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Table S4. Identification of protein spots and bands of standard peanut extract (SPE), control peanut and digested peanut samples (CPS and DPS, respectively) from Figs. 1, 3 and 2S, including complete peptide coverage of DPS protein identification results by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 algorithms.

Standard peanut extract (SPE) spots identification - Figure 1.

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
1	1	34	Q6PSU3|Q6PS	Ara h 1	Conarachin (Fragment) OS	99	169.82	14	7.72E+05	6	6	10	66575
	1	30	sp|P43237|AL	Ara h 1	Allergen Ara h 1 clone P17	99	169.82	13	7.72E+05	6	6	10	70283
	1	31	B3IXL2|B3IXL	Ara h 1	Main allergen Ara h1 OS=A	99	169.82	13	7.72E+05	6	6	10	70283
2	1	31	B3IXL2|B3IXL	Ara h 1	Main allergen Ara h1 OS=A	99.1	171.66	14	8.16E+04	6	6	11	70283
	1	34	Q6PSU3|Q6PS	Ara h 1	Conarachin (Fragment) OS	99.1	171.66	15	8.16E+04	6	6	11	66575
	1	30	sp|P43237|AL	Ara h 1	Allergen Ara h 1 clone P17	99.1	171.66	14	8.16E+04	6	6	11	70283
3	1	29	sp|P43238|AL	Ara h 1	Allergen Ara h 1 clone P41	99.1	183.28	14	4.86E+05	7	7	14	71345
4	1	5	Q647H4|Q647	Ara h 3	Arachin Ahy-1 OS=Arachis	99.1	177.17	20	3.98E+05	6	2	17	61506
	1	9	Q8LKN1|Q8LK	Ara h 3	Allergen Arah3/Arah4 OS=	99.1	177.17	20	3.98E+05	6	2	17	61738
	2	13	Q9FZ11|Q9FZ	Ara h 3	Gly1 OS=Arachis hypogaea	99	157.43	17	8.59E+05	5	1	14	60449
	2	7	B5TYU1|B5TY	Ara h 3	Arachin Arah3 isoform OS=	99	157.43	17	8.59E+05	5	1	14	60624
5	1	13	Q9FZ11|Q9FZ	Ara h 3	Gly1 OS=Arachis hypogaea	99.2	207.35	31	7.04E+06	12	4	83	60449
	2	3	Q647H3|Q647	Ara h 3	Arachin Ahy-2 OS=Arachis	99.1	187.49	27	8.79E+05	10	2	74	61532
	4	1	A1DZF0|A1DZ	Ara h 3	Arachin 6 OS=Arachis hyp	99.1	185.76	24	1.52E+05	8	1	66	60375
	3	15	Q5I6T2|Q5I6T	Ara h 3	Arachin Ahy-4 OS=Arachis	99.1	182.47	27	4.73E+04	9	1	67	60736
6	1	24	Q6IWG5|Q6I	Ara h 3	Glycinin (Fragment) OS=Ar	98.5	112.5	15	2.44E+06	4	3	10	58061
	1	26	Q0GM57|Q0	Ara h 3	Iso-Ara h3 OS=Arachis hyp	98.5	112.5	15	2.44E+06	4	3	10	58263
	1	27	E5G077|E5G0	Ara h 3	Ara h 3 allergen OS=Arachi	98.5	112.5	15	2.44E+06	4	3	10	58305
7-9	spots were not processed												
10	1	24	Q6IWG5|Q6IW	Ara h 3	Glycinin (Fragment) OS=Ara	99.2	232.01	31	3.96E+06	12	3	60	58061
	1	26	Q0GM57|Q0G	Ara h 3	Iso-Ara h3 OS=Arachis hyp	99.2	232.01	31	3.96E+06	12	3	60	58263
	2	27	E5G077|E5G0	Ara h 3	Ara h 3 allergen OS=Arachi	99.2	202.54	31	1.87E+05	9	1	39	58305
	4	1	A1DZF0|A1DZ	Ara h 3	Arachin 6 OS=Arachis hyp	98.8	148	9	2.44E+05	3	2	4	60375
	3	3	Q647H3|Q647	Ara h 3	Arachin Ahy-2 OS=Arachis	98.7	113.06	9	6.89E+05	4	2	5	61532

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

11	the spot was not processed												
12	1	5	Q647H4|Q647	Ara h 3	Arachin Ahy-1 OS=Arachis	99.2	259.77	30	2.72E+06	12	5	133	61506
	1	11	Q6T2T4|Q6T2	Ara h 3	Storage protein OS=Arachi	99.2	259.77	30	2.72E+06	12	5	133	61499
	3	3	Q647H3|Q647	Ara h 3	Arachin Ahy-2 OS=Arachis	99.1	201.43	24	0.00E+00	7	1	58	61532
13	the spot was not processed												
14	1	15	Q647H3|Q647	Ara h 3	Arachin Ahy-2 OS=Arachis	99.2	330.17	32	71800000	44	5	899	61532
	6	7	Q647H4|Q647	Ara h 3	Arachin Ahy-1 OS=Arachis	99.2	316.97	30	8200000	40	5	755	61506
	6	12	Q6T2T4|Q6T2	Ara h 3	Storage protein OS=Arachi	99.2	316.97	30	8200000	40	5	755	61499
15	the spot was not present/identified on the gel												
16	8	17551	sp|Q6PSU2|C	Ara h 2	Conglutin-7 OS=Arachis hy	92.6	100.56	23	2.10E+06	3	2	3	20114
	3	315	A0A0A6ZDT3|	n/a	Serine hydroxymethyltrans	34.4	22.48	1	4.31E+05	1	1	1	51979
	3	323	A0A0A6ZDR9|	n/a	Serine hydroxymethyltrans	34.4	22.48	1	4.31E+05	1	1	1	52010
17	8	17550	sp|Q6PSU2-3|	Ara h 2	Isoform 3 of Conglutin-7 C	92.6	140.56	23	4.10E+06	3	3	4	19795
	8	17551	sp|Q6PSU2|C	Ara h 2	Conglutin-7 OS=Arachis hy	92.6	140.56	23	4.10E+06	3	3	4	20114
	20	9619	A0A0A1EUV7|	n/a	Actin (Fragment) OS=Arach	69.8	53.04	6	1.56E+06	1	1	1	35884
18	8	17548	sp|Q6PSU2-4|	Ara h 2	Isoform 4 of Conglutin-7 C	86	81.31	21	8.36E+05	2	2	4	18380
	8	17549	sp|Q6PSU2-2|	Ara h 2	Isoform 2 of Conglutin-7 C	86	81.31	21	8.36E+05	2	2	4	18700
	8	17550	sp|Q6PSU2-3|	Ara h 2	Isoform 3 of Conglutin-7 C	85.7	81.31	19	8.36E+05	2	2	4	19795
	8	17551	sp|Q6PSU2|C	Ara h 2	Conglutin-7 OS=Arachis hy	85.7	81.31	19	8.36E+05	2	2	4	20114
	15	1975	A0A0A6ZDP1|	n/a	Glyceraldehyde-3-phospha	55.3	33.8	8	3.59E+02	1	1	2	20101
	15	1267	A0A0A6ZDT0|	n/a	Glyceraldehyde-3-phospha	55.3	33.8	8	3.59E+02	1	1	2	20099
	8	17548	sp|Q6PSU2-4|	Ara h 2	Isoform 4 of Conglutin-7 C	86	81.31	21	8.36E+05	2	2	4	18380
	8	17549	sp|Q6PSU2-2|	Ara h 2	Isoform 2 of Conglutin-7 C	86	81.31	21	8.36E+05	2	2	4	18700
19	6	269	E6Y6S5|E6Y6S	n/a	Acetyl-CoA carboxylase 4	86.7	34.93	0	2.70E+06	1	1	1	252122
	6	276	E6Y6S3|E6Y6S	n/a	Acetyl-CoA carboxylase 2	85.1	34.93	0	2.70E+06	1	1	1	251791
	6	143	E6Y6S2|E6Y6S	n/a	Acetyl-CoA carboxylase 1	70.6	34.93	0	2.70E+06	1	1	1	252204
20	6	3728	A5Z1R0|A5Z1	Ara h 6	Ara h 6 OS=Arachis hypoga	98.4	133.08	27	1.00E+07	3	3	24	16920
	6	3727	sp|Q647G9|C	Ara h 6	Conglutin OS=Arachis hypo	98.4	133.08	27	1.00E+07	3	3	24	16920
	11	1	A1DZF0|A1DZ	Ara h 3	Arachin 6 OS=Arachis hypo	84.3	81.48	5	3.09E+04	2	2	2	60375
	11	17	Q9SQH7|Q9S	Ara h 3	Glycinin OS=Arachis hypog	84.3	81.48	5	3.09E+04	2	2	2	61011
	11	5	Q647H4|Q647	Ara h 3	Arachin Ahy-1 OS=Arachis	84.3	81.48	5	3.09E+04	2	2	2	61506
	11	11	Q6T2T4|Q6T2	Ara h 3	Storage protein OS=Arachi	84.3	81.48	5	3.09E+04	2	2	2	61499
	11	9	Q8LKN1|Q8LK	Ara h 3	Allergen Arah3/Arah4 OS=	84.3	81.48	5	3.09E+04	2	2	2	61738

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
21	1	3728	A5Z1R0|A5Z1I	Ara h 6	Ara h 6 OS=Arachis hypoga	96.4	123.08	26	1.00E+07	3	3	23	16920
	1	3727	sp|Q647G9|C	Ara h 6	Conglutin OS=Arachis hypo	96.4	123.08	26	1.00E+07	3	3	23	16920
	6	99	E6Y6R4|E6Y6I	n/a	Biotin carboxylase 1 OS=A	88.6	49.41	1	1.89E+06	1	1	4	58975
	6	101	E6Y6R6|E6Y6I	n/a	Biotin carboxylase 3 OS=A	88.6	49.41	1	1.89E+06	1	1	4	58933
	6	191	E6Y6R7|E6Y6I	n/a	Biotin carboxylase 4 OS=A	81.7	49.41	1	1.89E+06	1	1	4	58984
22	6	15	Q647H3|Q647	Ara h 3	Arachin Ahy-2 OS=Arachis	99.1	132.13	17	8.07E+03	5	1	11	61532
	7	2	A1DZF0|A1DZ	Ara h 3	Arachin 6 OS=Arachis hypo	99.1	127.52	18	1.83E+03	5	1	10	60375
23-25	spots were not processed												
A	8	3728	R0|A5Z1R0_AR	Ara h 6	Ara h 6 OS=Arachis hypoga	63.5	65.55	8	2.39E+06	1	1	10	16920
	8	3727	47G9|CONG_A	Ara h 6	Conglutin OS=Arachis hypo	63.5	65.55	8	2.39E+06	1	1	10	16920
	10	1975	DP1|A0A0A6ZDP	n/a	Glyceraldehyde-3-phospha	82.2	57.47	12	1.21E+05	2	2	2	20101
	10	1267	DT0|A0A0A6ZDT	n/a	Glyceraldehyde-3-phospha	82.2	57.47	12	1.21E+05	2	2	2	20099
	11	2989	T2B9M0|T2B9	n/a	Fructose-bisphosphate ald	61.3	44.07	4	9.23E+03	1	1	1	38383
	21	2163	Q5UIP7|Q5UI	n/a	Alcohol dehydrodenase (Fr	59.2	35.49	5	1.18E+04	1	1	1	19734

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

Control Peanut Sample (CPS) spots identification Figure - 1.

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
1 to 7	The spots were not processed												
8	1	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypogaea PE=2	99.1	231.37	29	3.84E+06	13	7	104	60375
	5	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea GN=Gly1 P	98.8	139.6	8	3.95E+04	5	1	35	60449
	10	41	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypog	84.2	54.9	3	1.74E+05	1	1	5	58061
	10	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	84.2	54.9	3	1.74E+05	1	1	5	58263
	10	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis hypogaea	84.2	54.9	3	1.74E+05	1	1	5	58305
9	The spot was not present/identified in the gel												
10	1	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypogaea PE=2	99.1	231.37	29	3.84E+06	13	7	104	60375
	5	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea GN=Gly1 P	98.8	139.6	8	3.95E+04	5	1	35	60449
	10	41	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypog	84.2	54.9	3	1.74E+05	1	1	5	58061
	10	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	84.2	54.9	3	1.74E+05	1	1	5	58263
	10	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis hypogaea	84.2	54.9	3	1.74E+05	1	1	5	58305
11	The spot was not processed												
12	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea GN=Gly1 P	99.2	216.57	36	4.26E+04	16	1	132	60449
	1	5	Q5I6T2|Q5I	Ara h 3	Arachin Ahy-4 OS=Arachis hypogaea P	99.2	216.57	35	4.26E+04	16	1	132	60736
	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea P	99.2	216.57	35	4.26E+04	16	1	132	61532
	3	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea P	99.2	215.35	46	3.91E+04	17	3	124	61506
	9	41	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypog	79.4	52.07	5	3.03E+04	1	1	1	58061
	9	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	79.4	52.07	5	3.03E+04	1	1	1	58263
	9	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis hypogaea	79.4	52.07	5	3.03E+04	1	1	1	58305
13	The spot was not processed												
14	1	41	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypog	99.2	297.31	34	3.77E+07	43	5	859	58061
	1	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	99.2	297.31	34	3.77E+07	43	5	859	58263
	2	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis hypogaea	99.2	276.42	34	7.85E+05	33	1	659	58305
	3	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea P	99.2	232.93	35	5.03E+05	22	5	120	61506
	3	12	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis hypogaea	99.2	232.93	35	5.03E+05	22	5	120	61499
	4	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypogaea PE=2	99.2	229.37	36	8.75E+04	21	3	116	60375
	5	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea P	99.1	215.69	23	1.51E+06	19	1	112	61532
	6	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea GN=Gly1 P	99.1	194.28	22	4.33E+04	13	1	86	60449

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

15	The spot was not processed

Control Peanut Sample (CPS) Ara h 2 & 6 spots identification picked from Figure - 3

16	4	216	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	99.1	170.72	42	4.81E+06	17	17	75	58061
	4	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	99.1	170.72	42	4.81E+06	17	17	75	58263
	6	215	sp|Q6PSU2|	Ara h 2	Conglutin-7 OS=Arachis hypogaea PE=	99.1	137.02	69	1.23E+06	11	11	54	20114
	7	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea P	99.1	167.25	44	1.77E+05	16	1	27	61532
	8	87	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea P	99.1	164.27	40	6.65E+03	15	1	24	61506
	8	88	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis hypogaea	99.1	164.27	40	6.65E+03	15	1	24	61499
	11	85	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=Arachis hyp	99.1	154.03	32	3.50E+04	13	1	20	60624
	12	219	sp|Q647H2|	Ara h 3	Arachin Ahy-3 OS=Arachis hypogaea P	99.1	137.07	24	7.36E+05	7	7	20	54569
17	1	216	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	99.2	248.23	37	8.32E+06	26	21	153	58061
	1	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	99.2	248.23	37	8.32E+06	26	21	153	58263
	2	215	sp|Q6PSU2|	Ara h 2	Conglutin-7 OS=Arachis hypogaea PE=	99.1	185.99	73	1.58E+06	15	15	59	20114
	4	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea P	99.1	212.25	34	1.75E+05	19	4	31	61532
	5	84	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypogaea PE=2	99.1	204.86	36	8.57E+04	15	1	30	60375
	6	85	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=Arachis hyp	99.1	194.34	35	1.42E+04	15	1	26	60624
	10	219	sp|Q647H2|	Ara h 3	Arachin Ahy-3 OS=Arachis hypogaea P	99.1	154.19	18	8.67E+04	6	4	11	54569
18	4	216	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	99.1	207.01	33	1.42E+06	14	13	57	58061
	4	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	99.1	207.01	33	1.42E+06	14	13	57	58263
	5	215	sp|Q6PSU2|	Ara h 2	Conglutin-7 OS=Arachis hypogaea PE=	99	145.32	41	1.17E+06	6	6	51	20114
	7	87	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea P	99.1	153.45	29	0.00E+00	9	1	20	61506
	7	88	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis hypogaea	99.1	153.45	29	0.00E+00	9	1	20	61499
	9	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea P	99.1	160.75	27	1.26E+04	9	1	17	61532
	13	1745	E9LFE8|E9L	n/a	11S arachin (Fragment) OS=Arachis hy	89.4	43.54	11	4.33E+03	2	2	2	28290
	14	1679	Q38711|Q3	n/a	Galactose-binding lectin (Fragment) O	83.5	54.26	17	2.84E+04	2	2	2	29134
	14	1680	sp|P02872|	n/a	Galactose-binding lectin OS=Arachis hy	83.5	54.26	16	2.84E+04	2	2	2	29325
	14	1681	A0A089ZXL7	n/a	Peanut agglutinin variant OS=Arachis h	83.5	54.26	16	2.84E+04	2	2	2	29407
	19	518	A1DZE9|A1	Ara h 6	Conglutin 8 OS=Arachis hypogaea PE=	61.7	72.02	10	9.54E+03	1	1	1	16833
	19	516	A5Z1R0|A5Z	Ara h 6	Ara h 6 OS=Arachis hypogaea GN=Ara	61.4	72.02	10	9.54E+03	1	1	1	16920
	19	517	sp|Q647G9|	Ara h 6.01	Conglutin OS=Arachis hypogaea PE=1	61.4	72.02	10	9.54E+03	1	1	1	16920
	21	2784	Q647G4|Q6	Ara h 10.0	Oleosin 2 (Fragment) OS=Arachis hypo	61.2	39.36	7	1.99E+03	1	1	1	15527
	21	2785	Q647G5|Q6	Ara h 10.0	Oleosin 1 OS=Arachis hypogaea PE=2	61.2	39.36	7	1.99E+03	1	1	1	17753
19	2	216	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	99.1	241.19	28	5.39E+06	18	16	127	58061
	2	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	99.1	241.19	28	5.39E+06	18	16	127	58263
	4	215	sp|Q6PSU2|	Ara h 2	Conglutin-7 OS=Arachis hypogaea PE=	99	164.72	41	3.49E+06	9	9	76	20114
	7	87	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea P	99.1	161.05	21	3.80E+03	6	1	19	61506
	7	88	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis hypogaea	99.1	161.05	21	3.80E+03	6	1	19	61499
	8	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea P	99	160.46	19	1.80E+05	8	2	20	61532
	16	516	A5Z1R0|A5Z	Ara h 6	Ara h 6 OS=Arachis hypogaea GN=Ara	58.6	27.33	7	3.24E+03	1	1	1	16920
	16	517	sp|Q647G9|	Ara h 6.01	Conglutin OS=Arachis hypogaea PE=1	58.6	27.33	7	3.24E+03	1	1	1	16920

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
20	4	517	sp|Q647G9|	Ara h 6.010	Conglutin OS=Arachis hypogaea PE=1 S	99.1	180.32	57	6.48E+05	8	8	55	16920
	4	516	A5Z1R0|A5Z	Ara h 6	Ara h 6 OS=Arachis hypogaea GN=Ara	99.1	180.32	57	6.48E+05	8	8	55	16920
	6	429	Q5XXQ4|Q5	Ara h 8	PR10 protein OS=Arachis hypogaea GN	98.1	67.76	43	5.74E+04	3	3	8	16218
	6	430	B0YIU5|B0Y	Ara h 8	Ara h 8 allergen isoform OS=Arachis hy	98.1	67.76	42	5.74E+04	3	3	8	16413
	8	216	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	84.2	70.73	8	3.37E+04	2	2	6	58061
	8	217	Q0GM57|Q0	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	84.2	70.73	8	3.37E+04	2	2	6	58263
	8	218	E5G077|E5G	Ara h 3	Ara h 3 allergen OS=Arachis hypogaea	84.2	70.73	8	3.37E+04	2	2	6	58305
	9	87	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea PE	79.3	41.36	2	1.04E+03	1	1	1	61506
	9	88	Q6T2T4|Q6T	Ara h 3	Storage protein OS=Arachis hypogaea	79.3	41.36	2	1.04E+03	1	1	1	61499
	9	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea PE	79.3	41.36	2	1.04E+03	1	1	1	61532
	9	90	Q8LKN1|Q8	Ara h 3	Allergen Arah3/Arah4 OS=Arachis hypo	79.3	41.36	2	1.04E+03	1	1	1	61738
	10	2788	Q2PXN9|Q2	n/a	Dessication protectant protein LEA 14	61.3	40.7	12	2.27E+03	1	1	2	16112
	10	3802	E5FHZ5|E5F	n/a	Late embryogenesis abundant protein	61.3	40.7	11	2.27E+03	1	1	2	17041
	16	204	E9LFE7|E9L	Ara h 1	7S conarachin (Fragment) OS=Arachis h	58.5	28.38	11	1.36E+03	1	1	1	15873
	16	205	Q6PSU5|Q6	Ara h 1	Conarachin (Fragment) OS=Arachis hyp	58.5	28.38	5	1.36E+03	1	1	1	33604
	16	206	Q6PSU6|Q6	Ara h 1	Conarachin (Fragment) OS=Arachis hyp	58.5	28.38	5	1.36E+03	1	1	1	34133
	16	3470	Q6PSU4|Q6	Ara h 1	Conarachin (Fragment) OS=Arachis hyp	58.5	28.38	4	1.36E+03	1	1	1	48095
21	4	516	A5Z1R0|A5Z	Ara h 6	Ara h 6 OS=Arachis hypogaea GN=Ara	98.8	152.88	39	2.24E+05	8	8	36	16920
	4	517	sp|Q647G9|	Ara h 6.010	Conglutin OS=Arachis hypogaea PE=1 S	98.8	152.88	39	2.24E+05	8	8	36	16920
	7	216	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	86.9	84.99	7	2.74E+04	3	3	6	58061
	7	218	E5G077|E5G	Ara h 3	Ara h 3 allergen OS=Arachis hypogaea	86.9	84.99	7	2.74E+04	3	3	6	58305
	7	217	Q0GM57|Q0	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	86.9	84.99	7	2.74E+04	3	3	6	58263

cond't Control Peanut Sample (CPS) spots identification Figure - 1.

22 to 24	Spots were not processed												
25	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hypogaea PE	99.1	326.12	32	8.10E+07	41	5	840	61532
	4	3	B5TYU1|B5T	Ara h 3	Arachin Arah3 isoform OS=Arachis hyp	99.1	322.8	32	8.50E+07	34	2	679	60624
	6	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hypogaea PE	99.1	317.45	32	5.49E+06	38	6	673	61506
	6	12	Q6T2T4|Q6T	Ara h 3	Storage protein OS=Arachis hypogaea	99.1	317.45	32	5.49E+06	38	6	673	61499
	5	13	Q9FZ11|Q9F	Ara h 3	Gly1 OS=Arachis hypogaea GN=Gly1 PE	99.1	308.92	32	5.86E+06	32	3	714	60449
	9	41	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arachis hypoga	99.1	188.56	18	2.57E+05	13	1	31	58061
	9	42	Q0GM57|Q0	Ara h 3	Iso-Ara h3 OS=Arachis hypogaea PE=2	99.1	188.56	18	2.57E+05	13	1	31	58263

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

Digested Peanut Sample (DPS) spots identification Figure - 1.

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
1	2	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	205.33	28	5.40E+04	10	2	84	61532
	3	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.1	204.18	28	6.14E+03	10	1	78	60624
	4	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	191.6	28	1.64E+04	10	3	74	61506
	4	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	99.1	191.6	28	1.64E+04	10	3	74	61499
	6	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	99.1	128.17	14	9.75E+04	5	5	27	71345
	6	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	99.1	128.17	14	9.75E+04	5	5	27	71345
	6	27	Q6PSU4|Q	Ara h 1	Conarachin (Fragment) OS=A	99.1	128.17	21	9.75E+04	5	5	27	48095
	7	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	98.7	100.37	17	5.36E+04	4	3	11	58061
	7	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	98.7	100.37	17	5.36E+04	4	3	11	58263
2	The spot was not processed												
3	1	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	99.2	286.27	44	1.88E+06	30	6	282	71345
	1	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	99.2	286.27	44	1.88E+06	30	6	282	71345
	2	26	Q6PSU3|Q	Ara h 1	Conarachin (Fragment) OS=A	99.2	280.01	44	1.15E+05	28	4	248	66575
	2	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17 O	99.2	280.01	42	1.15E+05	28	4	248	70283
	2	23	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	99.2	280.01	42	1.15E+05	28	4	248	70283
	3	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	204.93	28	4.07E+05	12	2	101	61532
	5	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.1	202.39	28	1.16E+05	12	1	86	60624
	6	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	185.1	22	9.42E+03	9	1	80	61506
	6	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	99.1	185.1	22	9.42E+03	9	1	80	61499
	14	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	83.6	61.56	7	1.77E+05	2	1	2	58061
	14	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	83.6	61.56	7	1.77E+05	2	1	2	58263
	14	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis	83.6	61.56	7	1.77E+05	2	1	2	58305
4	The spot was not processed												
5	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.2	229.99	41	1.18E+05	16	1	187	60449
	8	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	83.8	56.1	7	4.93E+04	2	1	3	58061
	8	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	83.8	56.1	7	4.93E+04	2	1	3	58263
	8	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis	83.8	56.1	7	4.93E+04	2	1	3	58305

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
6	The spot was not processed												
7	1	69	Q6PSU5|Q	Ara h 1	Conarachin (Fragment) OS=A	99.1	263.37	45	1.12E+06	20	7	217	33604
	1	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	99.1	263.37	21	1.12E+06	20	7	217	71345
	1	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	99.1	263.37	21	1.12E+06	20	7	217	71345
	2	26	Q6PSU3|Q	Ara h 1	Conarachin (Fragment) OS=A	99.1	230.39	17	1.30E+03	14	1	174	66575
	2	23	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	99.1	230.39	16	1.30E+03	14	1	174	70283
	2	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17 O	99.1	230.39	16	1.30E+03	14	1	174	70283
	2	57	Q6PSU6|Q	Ara h 1	Conarachin (Fragment) OS=A	99.1	230.39	33	1.30E+03	14	1	174	34133
	3	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.1	160.62	36	6.10E+04	13	2	56	60449
	7	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypoga	99.1	147.7	37	3.91E+03	12	1	48	60375
	5	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	146.57	37	6.76E+03	12	1	50	61532
	12	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	97.9	55.98	12	6.44E+04	3	2	7	58061
	12	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	97.9	55.98	12	6.44E+04	3	2	7	58263
8	The spot was not processed												
9	1	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	253.41	31	14300000	23	4	184	58061
	1	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	253.41	31	14300000	23	4	184	58263
	4	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	192.61	26	577000	13	2	48	61532
	6	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.2	188.29	31	63300	12	3	41	61506
	6	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	99.2	188.29	31	63300	12	3	41	61499
	13	59	Q647H1|Q647H1_ARAHY		Conarachin OS=Arachis hypo	99.1	139.13	14	241000	6	6	15	75933
	12	27	Q6PSU4|Q	Ara h 1	Conarachin (Fragment) OS=A	98.2	95.52	12	90800	3	3	12	48095
	12	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	98.2	95.52	8	90800	3	3	12	71345
	12	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	98.2	95.52	8	90800	3	3	12	71345
	16	92	sp|Q647H2	Ara h 3	Arachin Ahy-3 OS=Arachis hy	88.2	72.23	5	54500	2	2	3	54569
10	5	272	D8KXX2|D8	n/a	AO2 OS=Arachis hypogaea P	37.3	30.55	1	3.44E+03	1	1	1	148235
11	1	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	235.54	28	6350000	20	4	300	61506
	1	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	99.1	235.54	28	6350000	20	4	300	61499
	5	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.1	193.59	22	564000	13	1	119	60449
	7	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	179.89	29	708000	14	2	98	58061
	7	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	179.89	29	708000	14	2	98	58263
	8	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis	99.1	164.64	29	0	11	1	74	58305

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
12	1	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	162.19	25	85400	8	1	38	61506
	1	12	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis h	99.1	162.19	25	85400	8	1	38	61499
	6	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	82.8	54.94	10	16700	2	2	3	58061
	6	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	82.8	54.94	10	16700	2	2	3	58263
13	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	304.12	26	15800000	24	1	506	61532
	3	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.1	303.67	28	6880000	23	2	499	60624
	5	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.1	287.35	22	4320000	20	2	478	60449
	6	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	286.03	28	1970000	22	4	418	61506
	6	12	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis h	99.1	286.03	28	1970000	22	4	418	61499
	9	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	198.84	18	3130000	11	5	35	58061
	9	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	198.84	18	3130000	11	5	35	58263
14	3	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.2	339.69	33	42100000	42	2	832	60624
	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.2	338.17	32	78800000	44	5	899	61532
	6	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.2	326.97	30	8200000	40	6	755	61506
	6	12	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis h	99.2	326.97	30	8200000	40	6	755	61499
	5	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.2	324.5	33	6980000	35	3	788	60449
	9	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	194.92	16	1980000	14	2	80	58061
	9	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	194.92	16	1980000	14	2	80	58263
15	1	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	98.9	116.4	10	17300	4	3	10	58061
	1	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis h	98.9	116.4	10	17300	4	3	10	58305
	1	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	98.9	116.4	10	17300	4	3	10	58263
	2	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	98.8	106.02	12	1480	5	1	6	60449
	2	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	98.8	106.02	11	1480	5	1	6	60736
	2	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	98.8	106.02	11	1480	5	1	6	61532
Digested Peanut Sample (DPS) Ara h 2 & 6 spots identification picked from Figure - 3													
16	1	216	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	279.74	44	1.10E+07	24	19	176	58061
	1	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	279.74	44	1.10E+07	24	19	176	58263
	2	215	sp|Q6PSU2	Ara h 2	Conglutin-7 OS=Arachis hypc	99.1	216.68	70	3.87E+06	16	16	82	20114
	3	219	sp|Q647H2	Ara h 3	Arachin Ahy-3 OS=Arachis hy	99.1	239.93	35	2.26E+06	13	11	45	54569
	6	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	219.97	40	1.83E+05	16	2	23	61532
	9	85	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.1	199.25	34	1.42E+04	12	1	17	60624
	15	1679	Q38711|Q3	n/a	Galactose-binding lectin (Fra	83	43.8	17	1.19E+04	2	2	2	29134
	15	1680	sp|P02872|	n/a	Galactose-binding lectin OS=	83	43.8	16	1.19E+04	2	2	2	29325
	15	1681	A0A089ZXL	n/a	Peanut agglutinin variant OS	83	43.8	16	1.19E+04	2	2	2	29407

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
17	1	216	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	250	27	1.76E+06	19	19	100	58061
	1	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	250	27	1.76E+06	19	19	100	58263
	2	215	sp|Q6PSU2	Ara h 2	Conglutin-7 OS=Arachis hypo	99.1	193.67	50	3.02E+05	9	9	34	20114
	5	84	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypoga	98.9	83.58	20	1.75E+04	5	3	8	60375
	5	87	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hy	98.9	83.58	20	1.75E+04	5	3	8	61506
	6	219	sp|Q647H2	Ara h 3	Arachin Ahy-3 OS=Arachis hy	98.5	127.14	10	1.74E+04	3	3	7	54569
	8	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	97.6	79.08	12	5.83E+03	3	1	4	61532
	8	83	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	97.2	79.08	12	5.83E+03	3	1	4	60449
	8	86	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	97.2	79.08	12	5.83E+03	3	1	4	60736
18	5	216	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	168.44	23	1.55E+06	12	11	57	58061
	5	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	168.44	23	1.55E+06	12	11	57	58263
	6	215	sp|Q6PSU2	Ara h 2	Conglutin-7 OS=Arachis hypo	99	118.27	38	4.95E+05	5	5	27	20114
	8	88	Q6T2T4|Q6	Ara h 3	Storage protein OS=Arachis h	99.1	137.79	20	3.81E+04	7	2	11	61499
	8	87	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	137.79	20	3.81E+04	7	2	11	61506
	14	204	E9LFE7|E9L	Ara h 1	7S conarachin (Fragment) OS	80.6	38.61	21	1.74E+04	2	2	2	15873
	14	205	Q6PSU5|Q6	Ara h 1	Conarachin (Fragment) OS=A	80.6	38.61	10	1.74E+04	2	2	2	33604
	14	206	Q6PSU6|Q6	Ara h 1	Conarachin (Fragment) OS=A	80.6	38.61	10	1.74E+04	2	2	2	34133
	14	3470	Q6PSU4|Q6	Ara h 1	Conarachin (Fragment) OS=A	80.6	38.61	7	1.74E+04	2	2	2	48095
	14	207	Q6PSU3|Q6	Ara h 1	Conarachin (Fragment) OS=A	80.6	38.61	5	1.74E+04	2	2	2	66575
	14	208	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	80.6	38.61	5	1.74E+04	2	2	2	70283
	14	209	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17 O	80.6	38.61	5	1.74E+04	2	2	2	70283
	14	274	N1NG13|N	Ara h 1	Seed storage protein Ara h1	80.6	38.61	5	1.74E+04	2	2	2	71345
	14	275	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	80.6	38.61	5	1.74E+04	2	2	2	71345
19	1	216	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	244.88	30	4.48E+06	28	23	147	58061
	1	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	99.1	244.88	30	4.48E+06	28	23	147	58263
	4	215	sp|Q6PSU2	Ara h 2	Conglutin-7 OS=Arachis hypo	99	154.39	41	9.36E+05	6	6	53	20114
	7	84	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypoga	99.1	157.89	22	1.04E+05	8	3	16	60375
20	3	89	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99	135.1	17	4.30E+04	7	3	15	61532
	5	516	A5Z1R0|A5	Ara h 6	Ara h 6 OS=Arachis hypogaea	84	112.57	20	4.59E+04	3	3	12	16920
	5	517	sp|Q647G9	Ara h 6.0101	Conglutin OS=Arachis hypoga	84	112.57	20	4.59E+04	3	3	12	16920
	8	84	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypoga	98.3	91.67	11	0.00E+00	4	1	7	60375
	10	216	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	61.4	56.21	5	1.83E+04	1	1	4	58061
	10	218	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis h	61.4	56.21	5	1.83E+04	1	1	4	58305
	10	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	61.4	56.21	5	1.83E+04	1	1	4	58263

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
21	1	516	A5Z1R0|A5	Ara h 6	Ara h 6 OS=Arachis hypogaea	84.2	130.16	20	8.56E+04	4	4	16	16920
	1	517	sp|Q647G9	Ara h 6.0101	Conglutin OS=Arachis hypoga	84.2	130.16	20	8.56E+04	4	4	16	16920
	8	216	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	61.2	64.77	5	3.59E+04	1	1	5	58061
	8	218	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis h	61.2	64.77	5	3.59E+04	1	1	5	58305
	8	217	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	61.2	64.77	5	3.59E+04	1	1	5	58263

cond't Digested Peanut Sample (DPS) spots identification Figure - 1.

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
22	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	98.9	127.76	15	21100	4	2	13	61532
	2	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypoga	98.6	103.49	15	10600	4	2	9	60375
23	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	181.68	24	830	10	1	170	61532
	1	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	99.1	181.68	24	830	10	1	170	60736
	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.1	181.68	24	830	10	1	170	60449
	2	7	Q647H4|Q6	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	178.08	22	1930	9	1	168	61506
	2	10	Q8LKN1|Q8	Ara h 3	Allergen Arah3/Arah4 OS=Ara	99.1	178.08	22	1930	9	1	168	61738
	6	41	Q6IWG5|Q6	Ara h 3	Glycinin (Fragment) OS=Arac	84.1	64.34	7	18300	2	1	7	58061
	6	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	84.1	64.34	7	18300	2	1	7	58263
	6	45	E5G077|E5G	Ara h 3	Ara h 3 allergen OS=Arachis h	84.1	64.34	7	18300	2	1	7	58305
	19	122	E9LFE7|E9L	Ara h 1	7S conarachin (Fragment) OS	61	35.48	9	6930	1	1	1	15873
	19	69	Q6PSU5|Q6	Ara h 1	Conarachin (Fragment) OS=A	61	35.48	4	6930	1	1	1	33604
	19	57	Q6PSU6|Q6	Ara h 1	Conarachin (Fragment) OS=A	61	35.48	4	6930	1	1	1	34133
	19	27	Q6PSU4|Q6	Ara h 1	Conarachin (Fragment) OS=A	61	35.48	3	6930	1	1	1	48095
	19	26	Q6PSU3|Q6	Ara h 1	Conarachin (Fragment) OS=A	61	35.48	2	6930	1	1	1	66575
	19	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17 O	61	35.48	2	6930	1	1	1	70283
	19	23	B3IXL2|B3IX	Ara h 1	Main allergen Ara h1 OS=Ara	61	35.48	2	6930	1	1	1	70283
	19	55	E5G076|E5G	Ara h 1	Ara h 1 allergen OS=Arachis h	61	35.48	2	6930	1	1	1	70788
	19	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1 O	61	35.48	2	6930	1	1	1	71345
	19	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	61	35.48	2	6930	1	1	1	71345
24	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	91	70.3	6	6910	2	2	3	60449
	1	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	91	70.3	6	6910	2	2	3	60736
	1	15	Q647H3|Q6	Ara h 3	Arachin Ahy-2 OS=Arachis hy	91	70.3	6	6910	2	2	3	61532

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

25	1	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	99	165.65	17	1500000	9	4	235	60375
	1	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99	165.65	17	1500000	9	4	235	60624
	1	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99	165.65	17	1500000	9	4	235	61506
	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99	165.65	17	1500000	9	4	235	60449
	1	29	Q9SQH7|Q	Ara h 3.0201	Glycinin OS=Arachis hypogae	99	165.65	17	1500000	9	4	235	61011
	1	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	99	165.65	17	1500000	9	4	235	60736
	1	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99	165.65	17	1500000	9	4	235	61532
	1	10	Q8LKN1|Q	Ara h 3	Allergen Arah3/Arah4 OS=Ar	99	165.65	17	1500000	9	4	235	61738
	1	83	Q8LL03|Q8	Ara h 3	Trypsin inhibitor (Fragment)	99	165.65	42	1500000	9	4	235	25499
	2	34	O82580|O	Ara h 3	Glycinin (Fragment) OS=Arac	99	142.03	17	3.17	6	1	159	58350
	4	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	98.8	94.98	17	3350000	5	4	79	58061
	4	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis	98.8	94.98	17	3350000	5	4	79	58305
	4	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	98.8	94.98	17	3350000	5	4	79	58263
B	1	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	49.4	30.83	6	11200	1	1	1	58061
	1	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	49.4	30.83	6	11200	1	1	1	58263
C	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.1	124.75	17	3050	6	1	24	60449
	1	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	99.1	124.75	17	3050	6	1	24	60736
	1	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	124.75	17	3050	6	1	24	61532
	5	69	Q6PSU5|Q	Ara h 1	Conarachin (Fragment) OS=A	66.8	34.65	4	2480	1	1	1	33604
	5	57	Q6PSU6|Q	Ara h 1	Conarachin (Fragment) OS=A	66.8	34.65	4	2480	1	1	1	34133
	5	27	Q6PSU4|Q	Ara h 1	Conarachin (Fragment) OS=A	66.8	34.65	3	2480	1	1	1	48095
	5	26	Q6PSU3|Q	Ara h 1	Conarachin (Fragment) OS=A	66.8	34.65	2	2480	1	1	1	66575
	5	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17	66.8	34.65	2	2480	1	1	1	70283
	5	23	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	66.8	34.65	2	2480	1	1	1	70283
	5	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	66.8	34.65	2	2480	1	1	1	71345
	5	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	66.8	34.65	2	2480	1	1	1	71345
D	1	26	Q6PSU3|Q	Ara h 1	Conarachin (Fragment) OS=A	99.2	315.98	41	819000	25	7	183	66575
	1	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17	99.2	315.98	39	819000	25	7	183	70283
	1	23	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	99.2	315.98	39	819000	25	7	183	70283
	2	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	99.2	298.73	31	2930	19	1	139	71345
	2	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	99.2	298.73	31	2930	19	1	139	71345
	4	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	97.7	75.57	5	2730	2	2	2	61506
	4	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	97.7	75.57	5	2730	2	2	2	61499
	4	10	Q8LKN1|Q	Ara h 3	Allergen Arah3/Arah4 OS=Ar	97.7	75.57	5	2730	2	2	2	61738
	4	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	97.7	75.57	5	2730	2	2	2	60375
E	1	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.2	216.57	36	42600	16	1	132	60449
	1	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	99.2	216.57	35	42600	16	1	132	60736
	1	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.2	216.57	35	42600	16	1	132	61532
	3	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.2	215.35	46	39100	17	3	124	61506
	9	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	79.4	52.07	5	30300	1	1	1	58061
	9	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	79.4	52.07	5	30300	1	1	1	58263
	9	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis	79.4	52.07	5	30300	1	1	1	58305

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
F	1	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.2	334.82	45	54900000	57	4	627	61532
	3	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.2	333.82	45	28300000	57	2	567	60624
	5	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.2	319.71	45	2310000	48	3	538	60449
	6	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.2	316.31	40	2030000	47	4	491	61506
	6	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	99.2	316.31	40	2030000	47	4	491	61499
	9	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	99.1	212.57	21	845000	19	3	82	58061
	9	42	Q0GM57|	Ara h 3	Iso-Ara h3 OS=Arachis hypo	99.1	212.57	21	845000	19	3	82	58263
G	3	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	99.2	218.27	23	2990000	13	1	129	71345
	3	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	99.2	218.27	23	2990000	13	1	129	71345
	20	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	121.78	19	67700	5	2	9	61532
	21	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	99	114.8	17	83200	4	1	9	60375
H	1	59	Q647H1|Q	n/a	Conarachin OS=Arachis hypo	99.1	277.04	18	42800000	16	7	161	75933
	3	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	99.1	215.02	16	434000	10	1	42	71345
	3	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	99.1	215.02	16	434000	10	1	42	71345
	4	26	Q6PSU3|Q	Ara h 1	Conarachin (Fragment) OS=	99.1	214.23	17	196000	10	1	38	66575
	4	23	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	99.1	214.23	16	196000	10	1	38	70283
	4	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17	99.1	214.23	16	196000	10	1	38	70283
	2	87	E9LFF0|E9L	n/a	11S arachin (Fragment) OS=	99.1	204.15	43	18800	10	1	65	19081
	7	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	139.35	21	523000	6	3	25	61532
	9	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99	132.27	19	163000	5	1	20	60624
	8	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	99	129.77	19	295000	5	1	22	60375
I	1	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	129.86	17	4460	6	1	10	61532
J	23	59	Q647H1|Q	n/a	Conarachin OS=Arachis hypo	70.9	41.92	1	4360	1	1	1	75933
	11	34	O82580|O	Ara h 3.0101	Glycinin (Fragment) OS=Arac	62.8	39.85	3	2480	1	1	1	58350
	11	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	62.8	39.85	2	2480	1	1	1	60449
	11	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	62.8	39.85	2	2480	1	1	1	60375
	11	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	62.8	39.85	2	2480	1	1	1	60624
	11	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	62.8	39.85	2	2480	1	1	1	60736
	11	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	62.8	39.85	2	2480	1	1	1	61506
	11	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	62.8	39.85	2	2480	1	1	1	61499
	11	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	62.8	39.85	2	2480	1	1	1	61532
	11	10	Q8LKN1|Q	Ara h 3	Allergen Arah3/Arah4 OS=Ar	62.8	39.85	2	2480	1	1	1	61738

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

# SPOT	Protein Group	Protein ID	Accession	Allergome	Description	Score (%)	Score (-10lgP)	Coverage (%)	Area under XIC	# Peptides	# Unique	# PSM	Avg. Mass (Da)
L	2	2	A1DZF0|A1	Ara h 3	Arachis hypogaea PE=2 SV=1	99.1	122.66	17	27600	7	3	16	60375
M	6	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	132.13	17	8070	5	1	11	61532
	7	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	99.1	127.52	18	1830	5	1	10	60375
	5	122	E9LFE7|E9L	Ara h 1	7S conarachin (Fragment) O	84.1	89.31	21	575000	2	2	39	15873
	5	69	Q6PSU5|Q	Ara h 1	Conarachin (Fragment) OS=A	84.1	89.31	10	575000	2	2	39	33604
	5	57	Q6PSU6|Q	Ara h 1	Conarachin (Fragment) OS=A	84.1	89.31	10	575000	2	2	39	34133
	5	27	Q6PSU4|Q	Ara h 1	Conarachin (Fragment) OS=A	84.1	89.31	7	575000	2	2	39	48095
	5	26	Q6PSU3|Q	Ara h 1	Conarachin (Fragment) OS=A	84.1	89.31	5	575000	2	2	39	66575
	5	23	B3IXL2|B3I	Ara h 1	Main allergen Ara h1 OS=Ara	84.1	89.31	5	575000	2	2	39	70283
	5	21	sp|P43237|	Ara h 1	Allergen Ara h 1 clone P17 O	84.1	89.31	5	575000	2	2	39	70283
	5	18	N1NG13|N	Ara h 1	Seed storage protein Ara h1	84.1	89.31	5	575000	2	2	39	71345
	5	20	sp|P43238|	Ara h 1	Allergen Ara h 1 clone P41B	84.1	89.31	5	575000	2	2	39	71345
N	5	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	99.1	230.11	32	16300	18	1	195	60624
	1	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	99.1	228.54	32	130000	18	1	228	60375
	2	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	99.1	227.16	29	180000	17	1	212	61532
	3	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	99.1	226.44	26	100000	17	2	203	60449
	6	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	99.1	217.96	29	84900	17	4	173	61506
	6	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	99.1	217.96	29	84900	17	4	173	61499
	11	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	98.7	93.26	12	30900	5	1	10	58061
	11	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	98.7	93.26	12	30900	5	1	10	58263
	10	59	Q647H1|Q	n/a	Conarachin OS=Arachis hypo	98.5	62.78	7	70900	4	4	10	75933
O	6	83	Q8LL03|Q8	Ara h 3	Trypsin inhibitor (Fragment)	62.3	44.29	20	11400	2	2	2	25499
	6	34	O82580|O	Ara h 3	Glycinin (Fragment) OS=Arac	62.3	44.29	9	11400	2	2	2	58350
	6	13	Q9FZ11|Q9	Ara h 3	Gly1 OS=Arachis hypogaea G	62.3	44.29	8	11400	2	2	2	60449
	6	2	A1DZF0|A1	Ara h 3	Arachin 6 OS=Arachis hypog	62.3	44.29	8	11400	2	2	2	60375
	6	3	B5TYU1|B5	Ara h 3	Arachin Arah3 isoform OS=A	62.3	44.29	8	11400	2	2	2	60624
	6	29	Q9SQH7|Q	Ara h 3	Glycinin OS=Arachis hypogae	62.3	44.29	8	11400	2	2	2	61011
	6	5	Q5I6T2|Q5	Ara h 3	Arachin Ahy-4 OS=Arachis hy	62.3	44.29	8	11400	2	2	2	60736
	6	7	Q647H4|Q	Ara h 3	Arachin Ahy-1 OS=Arachis hy	62.3	44.29	8	11400	2	2	2	61506
	6	12	Q6T2T4|Q	Ara h 3	Storage protein OS=Arachis	62.3	44.29	8	11400	2	2	2	61499
	6	15	Q647H3|Q	Ara h 3	Arachin Ahy-2 OS=Arachis hy	62.3	44.29	8	11400	2	2	2	61532
	6	10	Q8LKN1|Q	Ara h 3	Allergen Arah3/Arah4 OS=Ar	62.3	44.29	8	11400	2	2	2	61738
	6	116	A1DZF1|A1	Ara h 3	Arachin 7 (Fragment) OS=Ara	61	44.29	8	9750	1	1	1	23857
	7	92	sp|Q647H2	Ara h 3	Arachin Ahy-3 OS=Arachis hy	60.1	33.58	6	6840	1	1	1	54569
	7	41	Q6IWG5|Q	Ara h 3	Glycinin (Fragment) OS=Arac	60.1	33.58	5	6840	1	1	1	58061
	7	45	E5G077|E5	Ara h 3	Ara h 3 allergen OS=Arachis	60.1	33.58	5	6840	1	1	1	58305
	7	42	Q0GM57|Q	Ara h 3	Iso-Ara h3 OS=Arachis hypog	60.1	33.58	5	6840	1	1	1	58263

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

CPS bands identification 1D - Figure S2A

#band	Protein Group	Protein ID	Accession	Description	Score (%)	-10lgP	Coverage (%)	Area	#Peptides	#Unique	#PSM	Avg. Mass
1	1	25	B5TYU1|B	Arachin Arah3 isoform OS=	91.1	157.83	8	349000	6	6	35	60624
	1	27	Q5I6T2|Q	Arachin Ahy-4 OS=Arachis h	91.1	157.83	8	349000	6	6	35	60736
	1	6	A1DZF0|A	Arachin 6 OS=Arachis hypog	90.4	157.83	8	349000	6	6	35	60375
	1	51	Q8LL03|Q	Trypsin inhibitor (Fragment)	84.3	157.83	18	349000	6	6	35	25499
	1	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea	84.3	157.83	8	349000	6	6	35	60449
	1	31	Q9SQH7|C	Glycinin OS=Arachis hypoga	84.3	157.83	8	349000	6	6	35	61011
	1	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	84.3	157.83	7	349000	6	6	35	61506
	1	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	84.3	157.83	7	349000	6	6	35	61532
	1	18	Q8LKN1|C	Allergen Arah3/Arah4 OS=A	84.3	157.83	7	349000	6	6	35	61738
2	**no sensible identification**											
3	**no sensible identification**											
4	9	64	Q9M5D3|	Lipoxygenase OS=Arachis h	83.7	90.24	4	6660	2	2	2	97616
	9	67	Q4JME7|C	Lipoxygenase OS=Arachis h	83.7	90.24	4	6660	2	2	2	97596
	9	66	Q4JME6|C	Lipoxygenase OS=Arachis h	83.7	90.24	4	6660	2	2	2	97476
	8	6	A1DZF0|A	Arachin 6 OS=Arachis hypog	62.1	89.28	2	7510	1	1	2	60375
	8	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea	61.4	89.28	2	7510	1	1	2	60449
	8	25	B5TYU1|B	Arachin Arah3 isoform OS=	61.4	89.28	2	7510	1	1	2	60624
	8	31	Q9SQH7|C	Glycinin OS=Arachis hypoga	61.4	89.28	2	7510	1	1	2	61011
	8	27	Q5I6T2|Q	Arachin Ahy-4 OS=Arachis h	61.4	89.28	2	7510	1	1	2	60736
	8	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	61.4	89.28	2	7510	1	1	2	61506
	8	10	Q6T2T4|Q	Storage protein OS=Arachis	61.4	89.28	2	7510	1	1	2	61499
	8	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	61.4	89.28	2	7510	1	1	2	61532
	8	18	Q8LKN1|C	Allergen Arah3/Arah4 OS=A	61.4	89.28	2	7510	1	1	2	61738
	10	96	E9LFE8|E	11S arachin (Fragment) OS=	61.4	87.57	6	5200	1	1	2	28290
	21	47	Q38711|Q	Galactose-binding lectin (Fr	61.4	64.45	5	2240	1	1	1	29134
	21	45	sp|P02872	Galactose-binding lectin OS	61.4	64.45	5	2240	1	1	1	29325
	21	49	A0A089ZX	Peanut agglutinin variant O	61.4	64.45	5	2240	1	1	1	29407
	11	38	Q6IWG5|	Glycinin (Fragment) OS=Ara	40.5	30.39	5	12400	1	1	2	58061
	11	43	E5G077|E	Ara h 3 allergen OS=Arachis	40.5	30.39	5	12400	1	1	2	58305
	11	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypo	40.5	30.39	5	12400	1	1	2	58263

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

5	**no sensible identification**											
6	4	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	99.1	300.44	29	5610000	30	3	333	61532
	2	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	99.1	295.41	29	802000	31	5	386	61506
	2	10	Q6T2T4|Q	Storage protein OS=Arachis	99.1	295.41	29	802000	31	5	386	61499
	3	25	B5TYU1|B	Arachin Arah3 isoform OS=	99.1	293.23	32	2470000	28	2	337	60624
	6	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea	99.1	285.72	26	286000	24	2	304	60449
	8	38	Q6IWG5|C	Glycinin (Fragment) OS=Ara	99.1	256.15	31	18400000	21	16	157	58061
	8	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypo	99.1	256.15	31	18400000	21	16	157	58263
	9	42	O82580|O	Glycinin (Fragment) OS=Ara	99.1	247.87	22	7770	18	1	127	58350
	10	58	sp|Q647H	Arachin Ahy-3 OS=Arachis h	98.4	126.39	7	268000	3	2	9	54569
7	1	6	A1DZF0|A	Arachin 6 OS=Arachis hypog	98.4	166.65	8	0	3	1	11	60375
	1	25	B5TYU1|B	Arachin Arah3 isoform OS=	98.4	166.65	8	0	3	1	11	60624
	1	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	98.4	166.65	8	0	3	1	11	61506
	1	10	Q6T2T4|Q	Storage protein OS=Arachis	98.4	166.65	8	0	3	1	11	61499
	2	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea	98.4	159.94	8	4100	3	1	9	60449
	2	27	Q5I6T2|Q	Arachin Ahy-4 OS=Arachis h	98.4	159.94	8	4100	3	1	9	60736
	2	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	98.4	159.94	8	4100	3	1	9	61532
8	1	6	A1DZF0|A	Arachin 6 OS=Arachis hypog	99.1	211.18	33	900000	10	7	61	60375
	3	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	98.8	192.17	18	2520	8	2	22	61532
	2	27	Q5I6T2|Q	Arachin Ahy-4 OS=Arachis h	99	189.65	27	85700	8	2	24	60736
	4	38	Q6IWG5|C	Glycinin (Fragment) OS=Ara	81.2	45.2	11	33800	2	2	5	58061
	4	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypo	81.2	45.2	11	33800	2	2	5	58263
	5	124	A1E2B0|A	11S seed storage globulin B	51.5	28.2	4	17900	1	1	2	33520
9	1	45	sp|P02872	Galactose-binding lectin OS	99.1	268.42	70	615000	19	18	61	29325
	2	89	Q43373|Q	Galactose-binding lectin OS	89.8	116.12	14	19700	3	2	13	29566
	11	6	A1DZF0|A	Arachin 6 OS=Arachis hypog	84.2	115.64	5	1310	2	1	2	60375
	11	25	B5TYU1|B	Arachin Arah3 isoform OS=	84.2	115.64	5	1310	2	1	2	60624
	11	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	84.2	115.64	4	1310	2	1	2	61506
	11	10	Q6T2T4|Q	Storage protein OS=Arachis	84.2	115.64	4	1310	2	1	2	61499
	12	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea	83.4	105.76	5	2200	2	1	2	60449
	12	27	Q5I6T2|Q	Arachin Ahy-4 OS=Arachis h	83.4	105.76	5	2200	2	1	2	60736
	12	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	83.4	105.76	4	2200	2	1	2	61532
	7	38	Q6IWG5|C	Glycinin (Fragment) OS=Ara	60.4	39.62	5	12900	1	1	2	58061
	7	43	E5G077|E	Ara h 3 allergen OS=Arachis	60.4	39.62	5	12900	1	1	2	58305
	7	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypo	60.4	39.62	5	12900	1	1	2	58263

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

10 to 12	**no sensible identification**										
13	1	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	99.2	258.54	46	55400	20	3	143	61506
	7	12	N1NG13|N	Seed storage protein Ara h1	98.9	147.28	7	49500	4	4	4	71345
	7	14	sp|P43238	Allergen Ara h 1 clone P41	98.9	147.28	7	49500	4	4	4	71345
	7	15	Q6PSU4|C	Conarachin (Fragment) OS=	98.9	147.28	11	49500	4	4	4	48095
	6	38	Q6IWG5|(	Glycinin (Fragment) OS=Ara	98.8	132.45	17	616000	4	4	19	58061
	6	40	Q0GM57|(	Iso-Ara h3 OS=Arachis hypo	98.8	132.45	17	616000	4	4	19	58263
	6	43	E5G077|E	Ara h 3 allergen OS=Arachis	98.8	132.45	17	616000	4	4	19	58305
	11	77	T2B9M0|T	Fructose-bisphosphate aldo	61.8	38.14	6	32600	1	1	2	38383
14	**no sensible identification**										
15	2	24	Q6PSU3|C	Conarachin (Fragment) OS=	99.1	192	18	101000	9	1	54	66575
	2	19	sp|P43237	Allergen Ara h 1 clone P17	99.1	192	17	101000	9	1	54	70283
	2	21	B3IXL2|B3	Main allergen Ara h1 OS=Ar	99.1	192	17	101000	9	1	54	70283
	1	12	N1NG13|N	Seed storage protein Ara h1	99.1	190.75	16	53100	9	1	54	71345
	1	14	sp|P43238	Allergen Ara h 1 clone P41	99.1	190.75	16	53100	9	1	54	71345
	3	64	Q9M5D3|(	Lipoxygenase OS=Arachis h	98.9	177.92	8	77500	5	5	18	97616
	3	67	Q4JME7|C	Lipoxygenase OS=Arachis h	98.9	177.92	8	77500	5	5	18	97596
	3	66	Q4JME6|C	Lipoxygenase OS=Arachis h	98.9	177.92	8	77500	5	5	18	97476
	7	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea	83.8	138.75	8	0	3	1	8	60449
	7	27	Q5I6T2|Q	Arachin Ahy-4 OS=Arachis h	83.8	138.75	8	0	3	1	8	60736
	7	1	Q647H3|C	Arachin Ahy-2 OS=Arachis h	83.8	138.75	8	0	3	1	8	61532
	5	6	A1DZF0|A	Arachin 6 OS=Arachis hypog	98.3	132.72	8	0	3	1	8	60375
	5	25	B5TYU1|B	Arachin Arah3 isoform OS=	98.2	132.72	8	0	3	1	8	60624
	5	3	Q647H4|C	Arachin Ahy-1 OS=Arachis h	98.2	132.72	8	0	3	1	8	61506
	5	10	Q6T2T4|Q	Storage protein OS=Arachis	98.2	132.72	8	0	3	1	8	61499
	4	38	Q6IWG5|(	Glycinin (Fragment) OS=Ara	61.5	53.76	5	123000	1	1	7	58061
	4	40	Q0GM57|(	Iso-Ara h3 OS=Arachis hypo	61.5	53.76	5	123000	1	1	7	58263
	4	43	E5G077|E	Ara h 3 allergen OS=Arachis	61.5	53.76	5	123000	1	1	7	58305

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

DPS bands identification 1D - Figure S2A

#band	Protein Group	Protein ID	Accession	Description	Score (%)	-10lgP	Coverage (%)	Area	#Peptides	#Unique	#PSM	Avg. Mass
1	3	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	98.8	137.05	19	13900000	11	9	85	58061
	3	40	Q0GM57|Q	Iso-Ara h3 OS=Arachis hypoga	98.8	137.05	19	13900000	11	9	85	58263
	3	43	E5G077|E5	Ara h 3 allergen OS=Arachis hy	98.8	137.05	19	13900000	11	9	85	58305
2	1	6	A1DZF0|A1	Arachin 6 OS=Arachis hypogae	98.9	112.7	21	185000	6	6	20	60375
	3	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	59.8	34.6	7	18600	1	1	3	58061
	3	40	Q0GM57|Q	Iso-Ara h3 OS=Arachis hypoga	59.8	34.6	7	18600	1	1	3	58263
	3	43	E5G077|E5	Ara h 3 allergen OS=Arachis hy	59.8	34.6	7	18600	1	1	3	58305
3	**no sensible identification**											
4	**no sensible identification**											
5	1	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	99.1	276.25	34	12800000	33	4	262	61532
	2	6	A1DZF0|A1	Arachin 6 OS=Arachis hypogae	99.1	276	34	1080000	35	2	252	60375
	5	25	B5TYU1|B5	Arachin Arah3 isoform OS=Ara	99.1	270.64	31	1250000	31	3	216	60624
	4	7	Q9FZ11|Q9	Gly1 OS=Arachis hypogaea GN	99.1	260.68	26	97200	25	1	223	60449
	7	18	Q8LKN1|Q	Allergen Arah3/Arah4 OS=Arac	99.1	255.73	28	1380000	33	2	149	61738
	6	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	99.2	249.22	36	40100000	32	28	205	58061
	6	40	Q0GM57|Q	Iso-Ara h3 OS=Arachis hypoga	99.2	249.22	36	40100000	32	28	205	58263
	8	42	O82580|O8	Glycinin (Fragment) OS=Arachi	99.1	204.15	21	1630	15	2	48	58350
	11	206	G0Y6U4|G	Retrotransposon gag protein (	57.4	21.2	2	44600	1	1	1	104156
6	3	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	99.1	267.52	38	377000	22	5	112	61532
	5	25	B5TYU1|B5	Arachin Arah3 isoform OS=Ara	99.1	266.85	36	8050	17	1	92	60624
	7	18	Q8LKN1|Q	Allergen Arah3/Arah4 OS=Arac	99.1	241.3	37	886	14	1	73	61738
	8	42	O82580|O8	Glycinin (Fragment) OS=Arachi	99.1	196.99	27	606000	11	1	28	58350
	6	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	99.1	193.34	32	2580000	11	10	87	58061
	6	40	Q0GM57|Q	Iso-Ara h3 OS=Arachis hypoga	99.1	193.34	32	2580000	11	10	87	58263
	9	15	Q6PSU4|Q	Conarachin (Fragment) OS=Ara	98.8	100.7	17	303000	5	5	10	48095
	9	12	N1NG13|N	Seed storage protein Ara h1 O	98.8	100.7	12	303000	5	5	10	71345
	9	14	sp|P43238	Allergen Ara h 1 clone P41B O	98.8	100.7	12	303000	5	5	10	71345

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

7	1	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	99.1	281.33	52	32200	31	2	222	61532
	2	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea GN	99.1	280.17	46	47300	30	1	221	60449
	3	27	Q5I6T2|Q5	Arachin Ahy-4 OS=Arachis hyp	99.1	278.74	43	0	29	1	214	60736
	5	3	Q647H4|Q	Arachin Ahy-1 OS=Arachis hyp	99.1	274.43	43	148000	28	2	201	61506
	6	6	A1DZF0|A1	Arachin 6 OS=Arachis hypogae	99.1	269.93	43	8880	28	2	193	60375
	7	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	98.3	99.38	18	651000	5	3	19	58061
	7	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypoga	98.3	99.38	18	651000	5	3	19	58263
	14	47	Q38711|Q	Galactose-binding lectin (Frag	65	59.8	5	5950	1	1	1	29134
	14	45	sp|P02872	Galactose-binding lectin OS=A	65	59.8	5	5950	1	1	1	29325
	14	49	A0A089ZXL	Peanut agglutinin variant OS=	65	59.8	5	5950	1	1	1	29407
	17	124	A1E2B0|A1	11S seed storage globulin B1	55.3	26.38	4	8170	1	1	1	33520
	15	143	A0A109QJ	Long chain acyl-CoA syntheta	58.2	25.9	2	0	1	1	1	74266
8	1	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea GN	78.4	102.15	5	89000	1	1	16	60449
	1	27	Q5I6T2|Q5	Arachin Ahy-4 OS=Arachis hyp	78.4	102.15	5	89000	1	1	16	60736
	1	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	78.4	102.15	4	89000	1	1	16	61532
	2	25	B5TYU1|B	Arachin Arah3 isoform OS=Ar	78.4	95.3	5	37100	1	1	12	60624
	2	6	A1DZF0|A1	Arachin 6 OS=Arachis hypogae	68	95.3	5	37100	1	1	12	60375
	2	3	Q647H4|Q	Arachin Ahy-1 OS=Arachis hyp	68	95.3	4	37100	1	1	12	61506
	2	10	Q6T2T4|Q	Storage protein OS=Arachis hy	68	95.3	4	37100	1	1	12	61499
	3	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	30.8	39.81	5	4210	1	1	2	58061
	3	43	E5G077|E5	Ara h 3 allergen OS=Arachis hy	30.8	39.81	5	4210	1	1	2	58305
	3	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypoga	30.8	39.81	5	4210	1	1	2	58263
9	1	15	Q6PSU4|Q	Conarachin (Fragment) OS=Ar	95.9	135.4	7	225000	3	3	20	48095
	1	12	N1NG13|N	Seed storage protein Ara h1 O	95.9	135.4	5	225000	3	3	20	71345
	1	14	sp|P43238	Allergen Ara h 1 clone P41B O	95.9	135.4	5	225000	3	3	20	71345
	3	10	Q6T2T4|Q	Storage protein OS=Arachis hy	92.6	131.39	4	37000	2	1	10	61499
	4	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	88.7	124.11	4	8580	2	1	8	61532
	4	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea GN	84.2	124.11	5	8580	2	1	8	60449
	4	27	Q5I6T2|Q5	Arachin Ahy-4 OS=Arachis hyp	84.2	124.11	5	8580	2	1	8	60736
	2	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	98.6	123.46	10	265000	3	3	8	58061
	2	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypoga	98.6	123.46	10	265000	3	3	8	58263
	18	47	Q38711|Q	Galactose-binding lectin (Frag	84.3	112.57	9	16800	2	2	2	29134
	18	45	sp|P02872	Galactose-binding lectin OS=A	84.3	112.57	9	16800	2	2	2	29325
	5	81	B4UWA1|	Lactoylglutathione lyase (Frag	98.3	101.94	24	45700	4	4	7	22284
10	**no sensible identification**											

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

11	2	3	Q647H4|Q	Arachin Ahy-1 OS=Arachis hyp	98.4	123.02	11	3.19E+04	3	3	6	61506
	2	10	Q6T2T4|Q	Storage protein OS=Arachis hy	98.4	123.02	11	3.19E+04	3	3	6	61499
	2	6	A1DZF0|A1	Arachin 6 OS=Arachis hypogae	98.3	123.02	11	3.19E+04	3	3	6	60375
	18	380	A0A0F6VX	Annexin OS=Arachis hypogaea	24	27.73	7	7.08E+03	1	1	1	36080
	3	24	Q6PSU3|Q	Conarachin (Fragment) OS=Ar	8.5	23.95	5	5.51E+04	1	1	3	66575
	3	19	sp|P43237	Allergen Ara h 1 clone P17 OS	8.5	23.95	5	5.51E+04	1	1	3	70283
	3	21	B3IXL2|B3	Main allergen Ara h1 OS=Arac	8.5	23.95	5	5.51E+04	1	1	3	70283
	3	12	N1NG13|N	Seed storage protein Ara h1 O	8.5	23.95	5	5.51E+04	1	1	3	71345
	3	14	sp|P43238	Allergen Ara h 1 clone P41B O	8.5	23.95	5	5.51E+04	1	1	3	71345
	3	15	Q6PSU4|Q	Conarachin (Fragment) OS=Ar	7.3	23.95	7	5.51E+04	1	1	3	48095
	25	1427	A0A0F7GF	Annexin OS=Arachis hypogaea	5.6	20.96	2	1.89E+04	1	1	1	36291
	1	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea GN	99.2	258.39	46	150000	20	3	186	60449
	2	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	99.2	255.4	45	191000	19	3	182	61532
	3	25	B5TYU1|B	Arachin Arah3 isoform OS=Ara	99.2	253.28	37	2860	18	1	181	60624
	6	24	Q6PSU3|Q	Conarachin (Fragment) OS=Ar	99.1	148.17	24	59800	9	1	15	66575
	6	19	sp|P43237	Allergen Ara h 1 clone P17 OS	99.1	148.17	23	59800	9	1	15	70283
	6	21	B3IXL2|B3	Main allergen Ara h1 OS=Arac	99.1	148.17	23	59800	9	1	15	70283
	8	77	T2B9M0|T	Fructose-bisphosphate aldola	98.9	134.75	22	667000	4	4	15	38383
	9	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	98.3	94.51	15	1270000	3	2	11	58061
	9	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypoga	98.3	94.51	15	1270000	3	2	11	58263
	9	43	E5G077|E5	Ara h 3 allergen OS=Arachis hy	98.3	94.51	15	1270000	3	2	11	58305
	20	101	A0A0A6ZD	Glyceraldehyde-3-phosphate	61.5	66.05	8	0	1	1	1	20101
	20	104	A0A0A6ZD	Glyceraldehyde-3-phosphate	61.5	66.05	8	0	1	1	1	20099
12	4	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea GN	80.5	118.17	2	14400	1	1	1	60449
	1	38	Q6IWG5|Q	Glycinin (Fragment) OS=Arachi	59.6	45.12	5	145000	1	1	7	58061
	1	40	Q0GM57|	Iso-Ara h3 OS=Arachis hypoga	59.6	45.12	5	145000	1	1	7	58263
	1	43	E5G077|E5	Ara h 3 allergen OS=Arachis hy	59.6	45.12	5	145000	1	1	7	58305
	1	25	B5TYU1|B	Arachin Arah3 isoform OS=Ara	79.8	51.79	4	8000	1	1	1	60624
	1	27	Q5I6T2|Q5	Arachin Ahy-4 OS=Arachis hyp	79.8	51.79	4	8000	1	1	1	60736
	1	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	79.8	51.79	4	8000	1	1	1	61532

Table S4. Identification of protein spots and bands from standard peanut extract, control peanut and digested peanut samples by tandem bottom up proteomics on Orbitrap LTQ hybrid and PEAKS Suite 8.5 softwares

13	1	12	N1NG13|N	Seed storage protein Ara h1 O	99.2	358.28	55	10100000	58	15	384	71345
	1	14	sp|P43238	Allergen Ara h 1 clone P41B O	99.2	358.28	55	10100000	58	15	384	71345
	2	24	Q6PSU3|Q	Conarachin (Fragment) OS=Ar	99.2	346.49	56	3610000	52	9	341	66575
	2	19	sp|P43237	Allergen Ara h 1 clone P17 OS	99.2	346.49	52	3610000	52	9	341	70283
	2	21	B3IXL2|B3I	Main allergen Ara h1 OS=Arac	99.2	346.49	52	3610000	52	9	341	70283
	10	7	Q9FZ11|Q	Gly1 OS=Arachis hypogaea GN	63.5	87.17	2	44400	1	1	1	60449
	10	25	B5TYU1|B	Arachin Arah3 isoform OS=Ar	63.5	87.17	2	44400	1	1	1	60624
	10	1	Q647H3|Q	Arachin Ahy-2 OS=Arachis hyp	63.5	87.17	2	44400	1	1	1	61532
	10	27	Q5I6T2|Q5	Arachin Ahy-4 OS=Arachis hyp	63.4	87.17	2	44400	1	1	1	60736
	10	31	Q9SQH7|Q	Glycinin OS=Arachis hypogaea	63.2	87.17	2	44400	1	1	1	61011
	10	6	A1DZF0|A1	Arachin 6 OS=Arachis hypogae	63.1	87.17	2	44400	1	1	1	60375
	10	3	Q647H4|Q	Arachin Ahy-1 OS=Arachis hyp	61.9	87.17	2	44400	1	1	1	61506
	10	10	Q6T2T4|Q	Storage protein OS=Arachis hy	61.9	87.17	2	44400	1	1	1	61499
	10	18	Q8LKN1|Q	Allergen Arah3/Arah4 OS=Ara	61.9	87.17	2	44400	1	1	1	61738
14	5	64	Q9M5D3|	Lipoxygenase OS=Arachis hyp	88.3	113.85	2	2210	1	1	1	97616
	4	24	Q6PSU3|Q	Conarachin (Fragment) OS=Ar	75.7	88.45	2	4440	1	1	3	66575
	4	21	B3IXL2|B3I	Main allergen Ara h1 OS=Arac	75.7	88.45	2	4440	1	1	3	70283
	4	19	sp|P43237	Allergen Ara h 1 clone P17 OS	75.7	88.45	2	4440	1	1	3	70283
	1	15	Q6PSU4|Q	Conarachin (Fragment) OS=Ar	97.8	85.86	24	291000	4	4	12	48095
	1	12	N1NG13|N	Seed storage protein Ara h1 O	97.8	85.86	16	291000	4	4	12	71345
	1	14	sp|P43238	Allergen Ara h 1 clone P41B O	97.8	85.86	16	291000	4	4	12	71345
	10	134	E5FHY1|E5	Late embryogenesis abundant	40	29.59	14	3610	1	1	1	10140
	5	1056	H9L6X4|H	UDP-sulfoquinovose synthase	28.2	24.24	2	3610	1	1	1	53229
15	**no sensible identification**											

END OF THE BASIC TABLE S4.

Summary

1. Notes

Spot 1 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

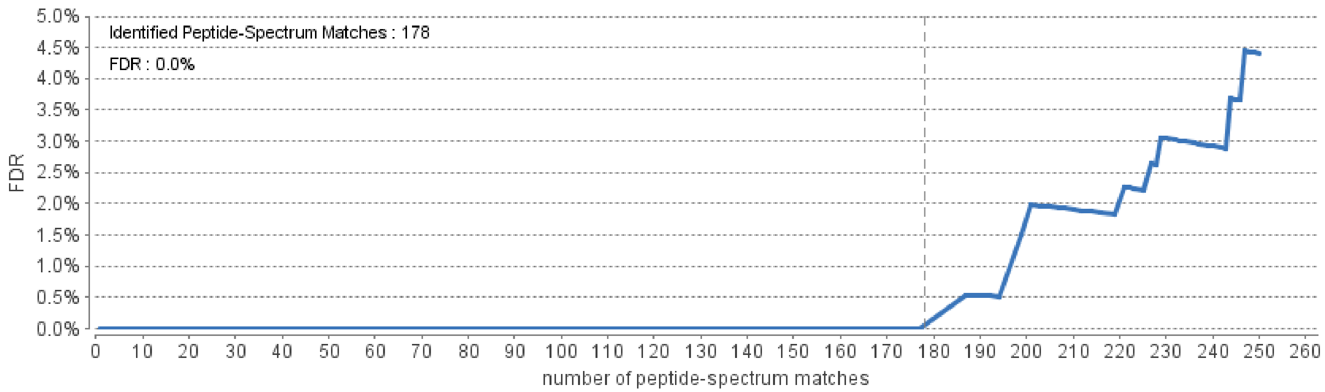
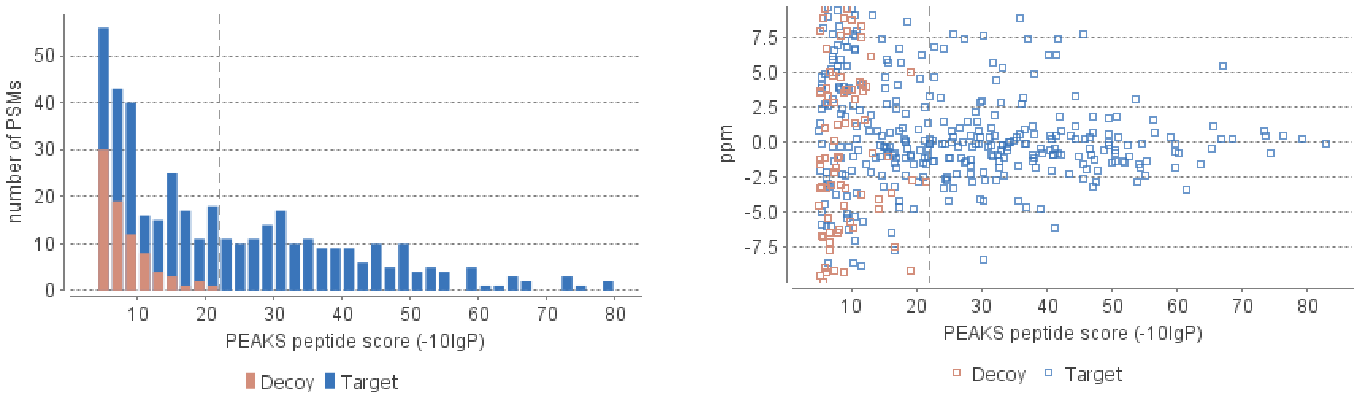


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.



(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

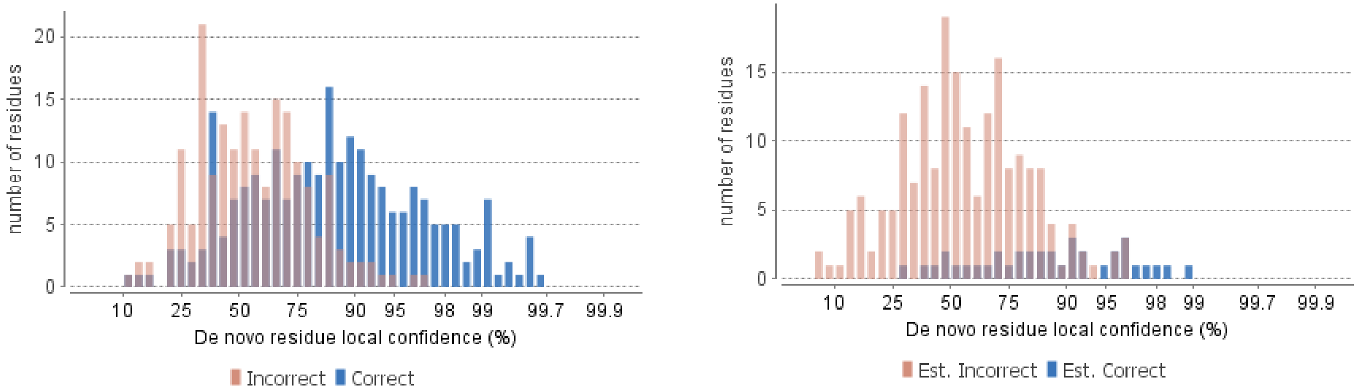


Table 1. Statistics of data.

# of MS scans	3073
# of MS/MS scans	2059

Table 2. Result filtration parameters.

Peptide -10lgP	≥22
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	129
Peptide sequences	40
Protein groups	4
Proteins	8
Proteins (#Unique Peptides)	7 (>2); 0 (=2); 1 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	25

Table 4. PTM profile.

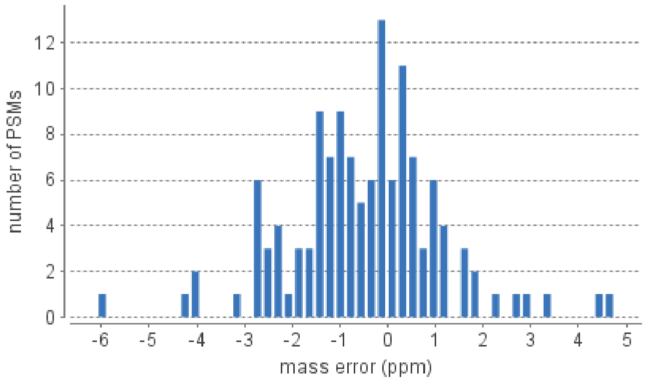
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Oxidation	15.99	M	12	55.11	6.39E3	1000.00
Deamidation	.98	NQ	11	53.76	4.3E3	49.37
Carbamidomethyl	57.02	C	7	68.35	2.03E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



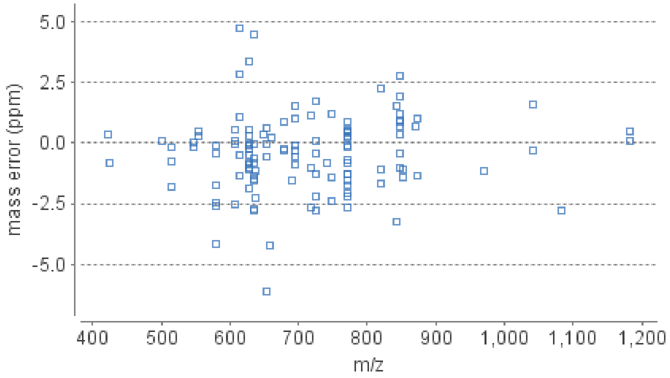


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 8	33	7	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3606.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 8	Area Sample 8	#Peptides	#Unique	#Spec Sample 8	PTM	Avg. Mass	Description
2	15	Q647H3|Q647H3_ARAHY	99.1	205.33	20	20	2.41E4	9	1	70	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
4	7	Q647H4|Q647H4_ARAHY	99.1	191.60	28	28	1.64E4	11	3	63	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
4	12	Q6T2T4|Q6T2T4_ARAHY	99.1	191.60	28	28	1.64E4	11	3	63	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
6	18	N1NG13|N1NG13_ARAHY	99.1	128.17	14	14	4.85E4	5	5	12	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
6	20	sp|P43238|ALL12_ARAHY	99.1	128.17	14	14	4.85E4	5	5	12	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
6	27	Q6PSU4|Q6PSU4_ARAHY	99.1	128.17	21	21	4.85E4	5	5	12	Y	48095	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
7	41	Q6IWG5|Q6IWG5_ARAHY	98.7	100.37	15	15	5.36E4	3	3	11	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
7	42	Q0GM57|Q0GM57_ARAHY	98.7	100.37	15	15	5.36E4	3	3	11	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 8 proteins													

Q647H3|Q647H3_ARAHY

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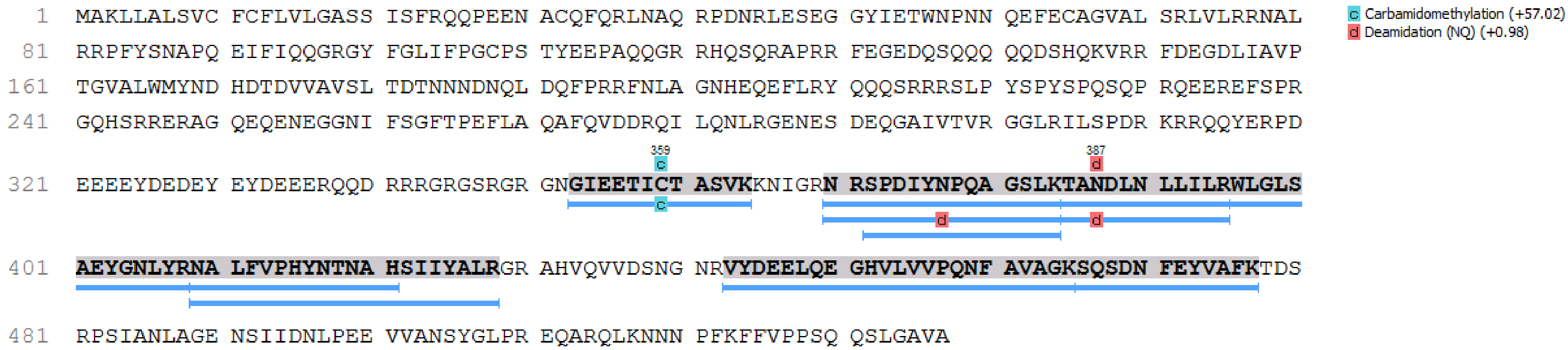
| Protein Coverage | Supporting Peptides |

Protein Coverage:



```
  1  MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
 81  RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161  TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241  GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321  EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS
401  AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS
481  RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA
```

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	82.94	1540.7673	13	-0.1	771.3909	2	32.61	8	1920	OB3606.raw	3.6E5	16	16	396	408	
K.SQSDNFEYVAFK.T	N	99.9	65.44	1433.6462	12	1.2	717.8312	2	30.04	8	1606	OB3606.raw	1.94E4	3	3	466	477	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	65.42	2540.2910	23	-0.4	847.7706	3	30.95	8	1712	OB3606.raw	6.48E5	11	11	443	465	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	60.27	2313.2019	20	-0.7	772.0740	3	30.42	8	1645	OB3606.raw	1.44E6	14	14	409	428	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	59.58	1306.6438	12	0.0	654.3292	2	27.53	8	1422	OB3606.raw	2.41E4	4	4	353	364	Carbamidomethylation
K.TANDLNLLILR.W	N	99.9	52.41	1254.7296	11	-0.2	628.3719	2	32.98	8	1963	OB3606.raw	4.8E5	12	12	385	395	
R.SPDIYNPQAGSLK.T	N	99.9	50.54	1388.6936	13	-0.5	695.3537	2	27.07	8	1391	OB3606.raw	4.12E4	6	6	372	384	
K.TAN(+.98)DLNLLILR.W	N	99.8	44.35	1255.7136	11	3.4	628.8662	2	33.08	8	1977	OB3606.raw	2.04E4	1	1	385	395	Deamidation (NQ)
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.8	40.74	1659.8217	15	0.3	554.2813	3	26.31	8	1348	OB3606.raw	5.99E3	1	1	370	384	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.7	40.53	1658.8376	15	0.5	553.9534	3	25.54	8	1301	OB3606.raw	3.5E3	1	1	370	384	
R.NALFVPHYNTNAH.S	N	87.5	22.52	1496.7161	13	0.1	499.9127	3	27.35	8	1408	OB3606.raw	2.22E3	1	1	409	421	

total 11 peptides

Q647H4|Q647H4_ARAHY

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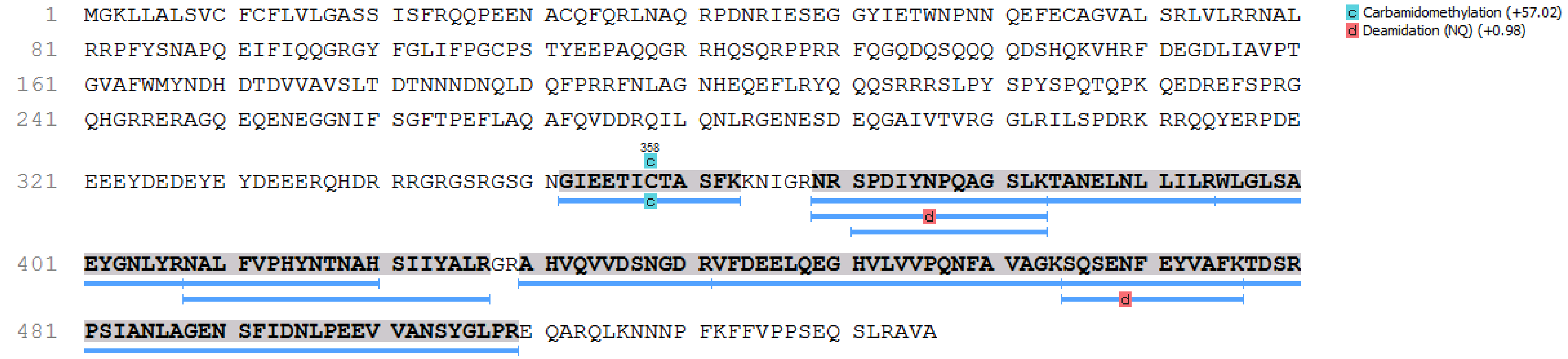
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG N**GIEETICTA SFK**KNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GR**A HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

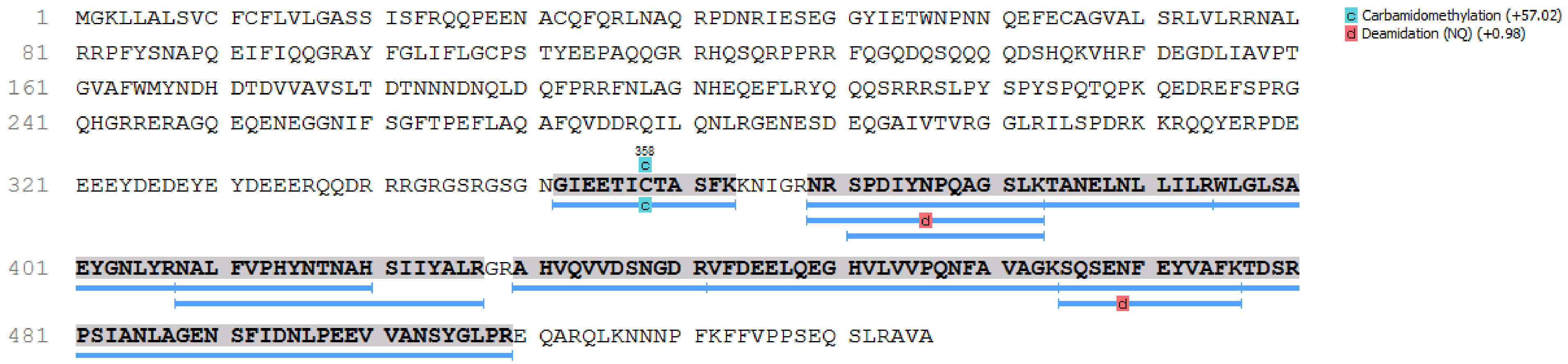
Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	82.94	1540.7673	13	-0.1	771.3909	2	32.61	8	1920	OB3606.raw	3.6E5	16	16	395	407	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	60.27	2313.2019	20	-0.7	772.0740	3	30.42	8	1645	OB3606.raw	1.44E6	14	14	408	427	
K.TANELNLLILR.W	N	99.9	59.78	1268.7452	11	-0.6	635.3795	2	33.08	8	1976	OB3606.raw	1.89E5	12	12	384	394	
R.AHVQVVDSNGDR.V	Y	99.9	59.04	1295.6218	12	0.4	648.8184	2	20.42	8	1043	OB3606.raw	6.33E3	1	1	430	441	
K.SQSENFEYVAFK.T	N	99.9	55.37	1447.6619	12	-1.3	724.8373	2	29.93	8	1597	OB3606.raw	2.09E4	4	4	465	476	
K.SQSEN(+.98)FEYVAFK.T	N	99.9	53.76	1448.6459	12	-2.8	725.3282	2	30.20	8	1620	OB3606.raw	4.3E3	1	1	465	476	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	50.54	1388.6936	13	-0.5	695.3537	2	27.07	8	1391	OB3606.raw	4.12E4	6	6	371	383	
N.GIEETIC(+57.02)TASFK.K	Y	99.8	42.10	1354.6438	12	0.9	678.3298	2	29.39	8	1554	OB3606.raw	2.19E3	2	2	352	363	Carbamidomethylation
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.8	40.74	1659.8217	15	0.3	554.2813	3	26.31	8	1348	OB3606.raw	5.99E3	1	1	369	383	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.7	40.53	1658.8376	15	0.5	553.9534	3	25.54	8	1301	OB3606.raw	3.5E3	1	1	369	383	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	97.3	28.36	3544.7434	33	0.5	1182.5890	3	35.63	8	2277	OB3606.raw	1.94E4	2	2	477	509	
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	94.4	27.74	2524.2961	23	1.5	842.4406	3	31.72	8	1809	OB3606.raw	7.83E3	2	2	442	464	
R.NALFVPHYNTNAH.S	N	87.5	22.52	1496.7161	13	0.1	499.9127	3	27.35	8	1408	OB3606.raw	2.22E3	1	1	408	420	
total 13 peptides																		

Q6T2T4|Q6T2T4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



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161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR
481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	82.94	1540.7673	13	-0.1	771.3909	2	32.61	8	1920	OB3606.raw	3.6E5	16	16	395	407	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	60.27	2313.2019	20	-0.7	772.0740	3	30.42	8	1645	OB3606.raw	1.44E6	14	14	408	427	
K.TANELNLLILR.W	N	99.9	59.78	1268.7452	11	-0.6	635.3795	2	33.08	8	1976	OB3606.raw	1.89E5	12	12	384	394	
R.AHVQVVDSNGDR.V	Y	99.9	59.04	1295.6218	12	0.4	648.8184	2	20.42	8	1043	OB3606.raw	6.33E3	1	1	430	441	
K.SQSENFEYVAFK.T	N	99.9	55.37	1447.6619	12	-1.3	724.8373	2	29.93	8	1597	OB3606.raw	2.09E4	4	4	465	476	
K.SQSEN(+.98)FEYVAFK.T	N	99.9	53.76	1448.6459	12	-2.8	725.3282	2	30.20	8	1620	OB3606.raw	4.3E3	1	1	465	476	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	50.54	1388.6936	13	-0.5	695.3537	2	27.07	8	1391	OB3606.raw	4.12E4	6	6	371	383	
N.GIEETIC(+57.02)TASFK.K	Y	99.8	42.10	1354.6438	12	0.9	678.3298	2	29.39	8	1554	OB3606.raw	2.19E3	2	2	352	363	Carbamidomethylation
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.8	40.74	1659.8217	15	0.3	554.2813	3	26.31	8	1348	OB3606.raw	5.99E3	1	1	369	383	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.7	40.53	1658.8376	15	0.5	553.9534	3	25.54	8	1301	OB3606.raw	3.5E3	1	1	369	383	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	97.3	28.36	3544.7434	33	0.5	1182.5890	3	35.63	8	2277	OB3606.raw	1.94E4	2	2	477	509	
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	94.4	27.74	2524.2961	23	1.5	842.4406	3	31.72	8	1809	OB3606.raw	7.83E3	2	2	442	464	
R.NALFVPHYNTNAH.S	N	87.5	22.52	1496.7161	13	0.1	499.9127	3	27.35	8	1408	OB3606.raw	2.22E3	1	1	408	420	
total 13 peptides																		

N1NG13|N1NG13_ARAHY

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| Protein Coverage | Supporting Peptides |

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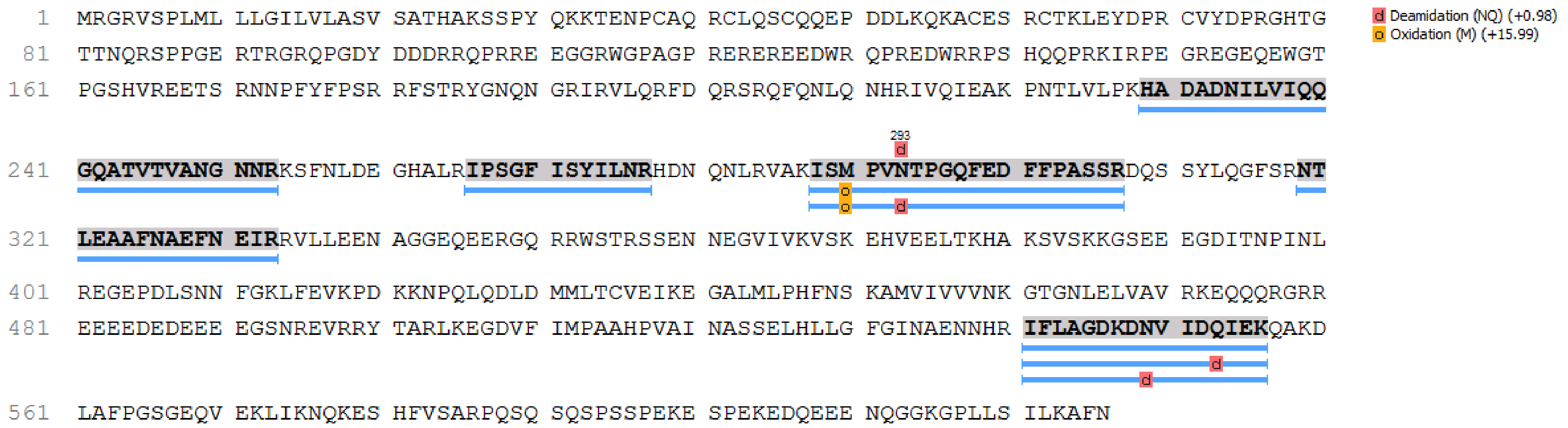

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81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPK**HA DADNILVIQQ**
241 **GQATVTVANG NNR**KSFNLDE GHALR**IPSGF ISYILNR**HDN QNLRVAK**ISM PVNTPGQFED FFPASSR**DQS SYLQGFSR**NT**
321 **LEAAFNAEFN EIR**RVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	Y	99.9	56.43	1737.8322	15	0.7	869.9240	2	33.47	8	2021	OB3606.raw	4.71E3	1	1	319	333	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	Y	99.9	55.11	2242.0364	20	-2.4	748.3510	3	32.22	8	1871	OB3606.raw	6.39E3	2	2	288	307	Oxidation (M)
R.IPSGFISYILNR.H	Y	99.9	54.18	1378.7609	12	-1.5	690.3867	2	34.14	8	2100	OB3606.raw	7.95E3	1	1	266	277	
R.IFLAGDKDNVIDQ(+.98)IEK.Q	Y	99.9	45.65	1817.9410	16	-2.5	606.9861	3	30.52	8	1658	OB3606.raw	1.83E1	1	1	541	556	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	Y	99.5	38.07	1816.9570	16	0.6	606.6600	3	30.44	8	1648	OB3606.raw	2.9E4	3	3	541	556	
K.HADADNILVIQQGQATVTVANGNNR.K	Y	98.8	31.59	2618.3162	25	1.0	873.7802	3	28.97	8	1524	OB3606.raw	4.51E2	2	2	229	253	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	Y	93.9	27.34	2243.0205	20	-1.4	748.6797	3	32.63	8	1923	OB3606.raw	0	1	1	288	307	Oxidation (M); Deamidation (NQ)
R.IFLAGDKDN(+.98)VIDQIEK.Q	Y	93.9	27.10	1817.9410	16	0.1	606.9877	3	30.71	8	1682	OB3606.raw	1.83E1	1	1	541	556	Deamidation (NQ)
total 8 peptides																		

sp|P43238|ALL12_ARAHY

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| Protein Coverage | Supporting Peptides |

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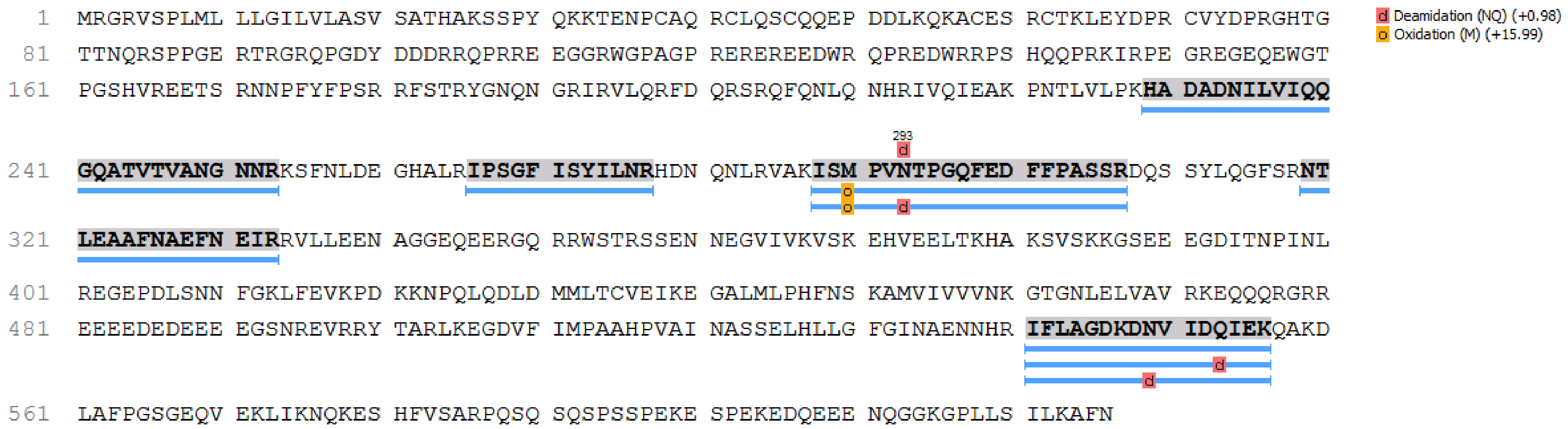

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81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPK**HA DADNILVIQQ**

241 **GQATVTVANG NNR**KSFNLDE GHALR**IPSGF ISYILNR**HDN QNLRVAK**ISM PVNTPGQFED FFPASSR**DQS SYLQGFSR**NT**

321 **LEAAFNAEFN EIR**RVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL

401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAKD

561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

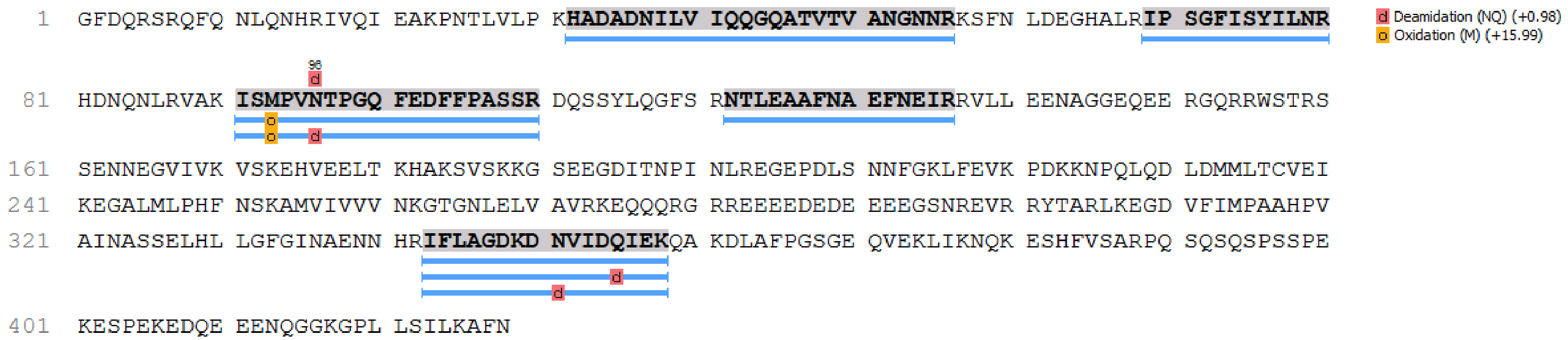
Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	Y	99.9	56.43	1737.8322	15	0.7	869.9240	2	33.47	8	2021	OB3606.raw	4.71E3	1	1	319	333	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	Y	99.9	55.11	2242.0364	20	-2.4	748.3510	3	32.22	8	1871	OB3606.raw	6.39E3	2	2	288	307	Oxidation (M)
R.IPSGFISYILNR.H	Y	99.9	54.18	1378.7609	12	-1.5	690.3867	2	34.14	8	2100	OB3606.raw	7.95E3	1	1	266	277	
R.IFLAGDKDNVIDQ(+.98)IEK.Q	Y	99.9	45.65	1817.9410	16	-2.5	606.9861	3	30.52	8	1658	OB3606.raw	1.83E1	1	1	541	556	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	Y	99.5	38.07	1816.9570	16	0.6	606.6600	3	30.44	8	1648	OB3606.raw	2.9E4	3	3	541	556	
K.HADADNILVIQQGQATVTVANGNNR.K	Y	98.8	31.59	2618.3162	25	1.0	873.7802	3	28.97	8	1524	OB3606.raw	4.51E2	2	2	229	253	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	Y	93.9	27.34	2243.0205	20	-1.4	748.6797	3	32.63	8	1923	OB3606.raw	0	1	1	288	307	Oxidation (M); Deamidation (NQ)
R.IFLAGDKDN(+.98)VIDQIEK.Q	Y	93.9	27.10	1817.9410	16	0.1	606.9877	3	30.71	8	1682	OB3606.raw	1.83E1	1	1	541	556	Deamidation (NQ)
total 8 peptides																		

Q6PSU4|Q6PSU4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 HDNQNLRVAK **ISMPVNTPGQ FEDFFPASSR** DQSSYLQGFS R**NTLEAAFNA EFNEIR**RVLL EENAGGEQEE RGQRRWSTRS

161 SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI

241 KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREEEEDEDE EEEGSNREVR RYTARLKEGD VFIMPAAHPV

321 AINASSELHL LGFGINAENN HR**IFLAGDKD NVIDQIEK**QA KDLAFPGSGE QVEKLIKNQK ESHFVSARPQ SQSQSPSSPE

401 KESPEKEDQE EENQGGKGPL LSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	Y	99.9	56.43	1737.8322	15	0.7	869.9240	2	33.47	8	2021	OB3606.raw	4.71E3	1	1	122	136	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	Y	99.9	55.11	2242.0364	20	-2.4	748.3510	3	32.22	8	1871	OB3606.raw	6.39E3	2	2	91	110	Oxidation (M)
R.IPSGFISYILNR.H	Y	99.9	54.18	1378.7609	12	-1.5	690.3867	2	34.14	8	2100	OB3606.raw	7.95E3	1	1	69	80	
R.IFLAGDKDNVIDQ(+.98)IEK.Q	Y	99.9	45.65	1817.9410	16	-2.5	606.9861	3	30.52	8	1658	OB3606.raw	1.83E1	1	1	343	358	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	Y	99.5	38.07	1816.9570	16	0.6	606.6600	3	30.44	8	1648	OB3606.raw	2.9E4	3	3	343	358	
K.HADADNILVIQQGQATVTVANGNNR.K	Y	98.8	31.59	2618.3162	25	1.0	873.7802	3	28.97	8	1524	OB3606.raw	4.51E2	2	2	32	56	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	Y	93.9	27.34	2243.0205	20	-1.4	748.6797	3	32.63	8	1923	OB3606.raw	0	1	1	91	110	Oxidation (M); Deamidation (NQ)
R.IFLAGDKDN(+.98)VIDQIEK.Q	Y	93.9	27.10	1817.9410	16	0.1	606.9877	3	30.71	8	1682	OB3606.raw	1.83E1	1	1	343	358	Deamidation (NQ)
total 8 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR **NAMFVPHYTL NAHTIVVALN**
401 **GR**AHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFK**T DSRPSIANLA GENSIIDNLP EEVVANSYR**L
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

d Deamidation (NQ) (+0.98)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.NAM(+15.99)FVPHYTLNAHTIVVALN(+.98)GR.A	Y	99.9	48.65	2454.2478	22	-0.5	614.5689	4	30.51	8	1656	OB3606.raw	3.29E4	5	5	381	402	Oxidation (M); Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.5	38.13	2453.2637	22	-1.1	818.7609	3	30.86	8	1701	OB3606.raw	1.85E4	3	3	381	402	Oxidation (M)
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	97.4	28.62	3243.6006	30	-2.8	1082.2045	3	33.97	8	2083	OB3606.raw	0	1	1	450	479	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	94.2	27.57	2554.3066	23	-1.4	852.4417	3	31.29	8	1756	OB3606.raw	2.17E3	2	2	415	437	
total 4 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

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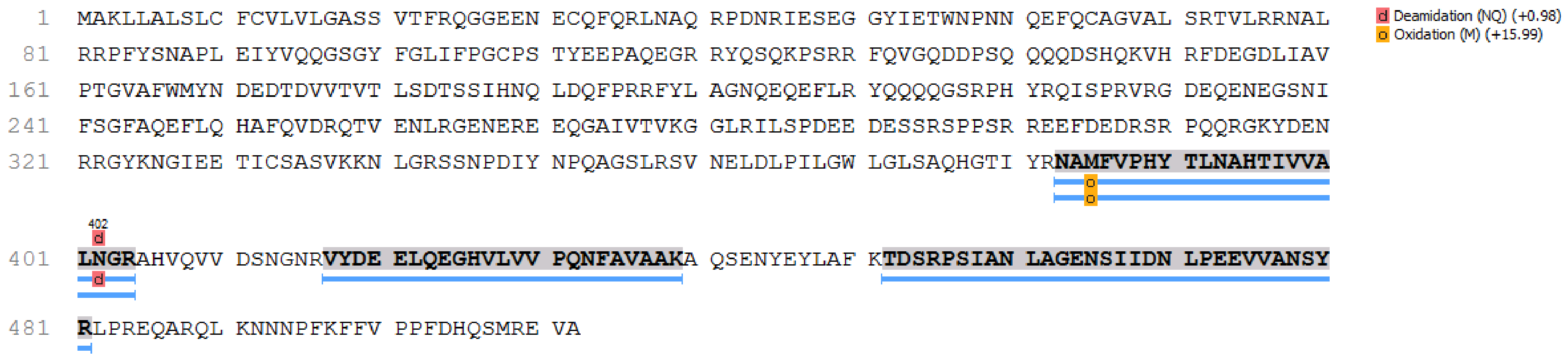


1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YR**NAMFVPHY TLNAHTIVVA**
401 **LNGR**AHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF K**TDSRPSIAN LAGENSIIDN LPEEVVANSY**
481 **R**LPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 8	#Spec	#Spec Sample 8	Start	End	PTM
R.NAM(+15.99)FVPHYTLNAHTIVVALN(+.98)GR.A	Y	99.9	48.65	2454.2478	22	-0.5	614.5689	4	30.51	8	1656	OB3606.raw	3.29E4	5	5	383	404	Oxidation (M); Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.5	38.13	2453.2637	22	-1.1	818.7609	3	30.86	8	1701	OB3606.raw	1.85E4	3	3	383	404	Oxidation (M)
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	97.4	28.62	3243.6006	30	-2.8	1082.2045	3	33.97	8	2083	OB3606.raw	0	1	1	452	481	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	94.2	27.57	2554.3066	23	-1.4	852.4417	3	31.29	8	1756	OB3606.raw	2.17E3	2	2	417	439	
total 4 peptides																		

Peptide List

Summary

1. Notes   Spot 3 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

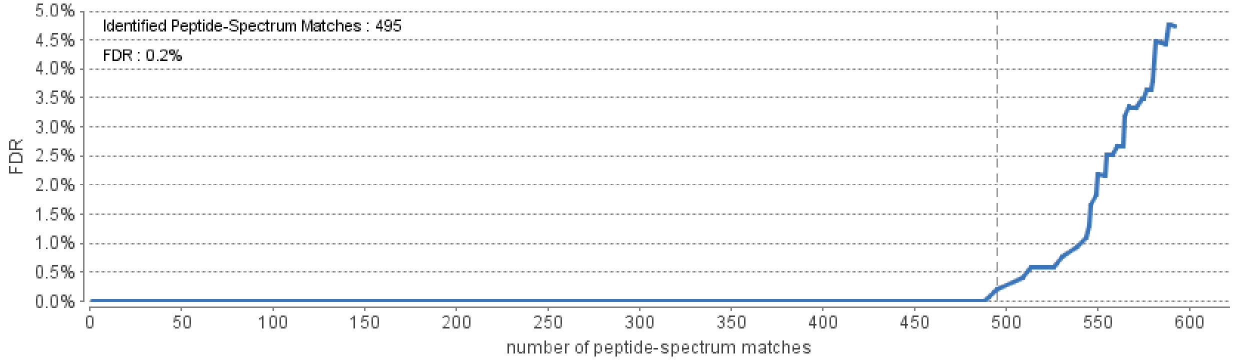
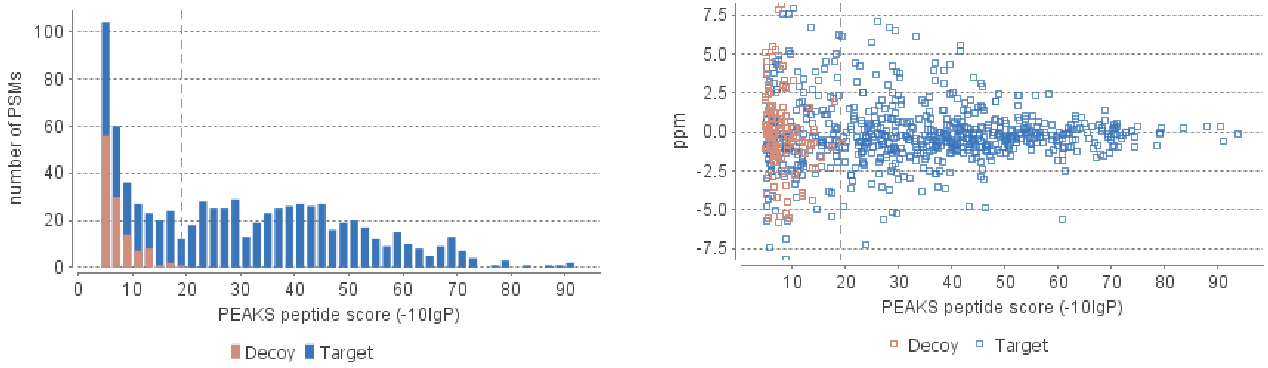


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

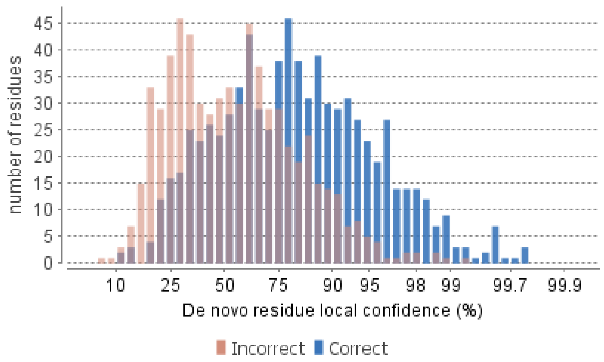

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



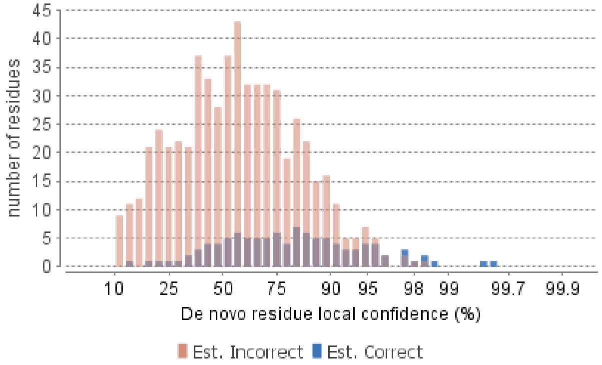


Table 1. Statistics of data.

# of MS scans	3006
# of MS/MS scans	2108

Table 2. Result filtration parameters.

Peptide -10lgP	≥19
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	405
Peptide sequences	121
Protein groups	6
Proteins	12
Proteins (#Unique Peptides)	5 (>2); 1 (=2); 6 (=1);
FDR (Peptide-Spectrum Matches)	0.2%
FDR (Peptide Sequences)	0.8%
FDR (Protein)	0.0%
De Novo Only Spectra	63

Table 4. PTM profile.

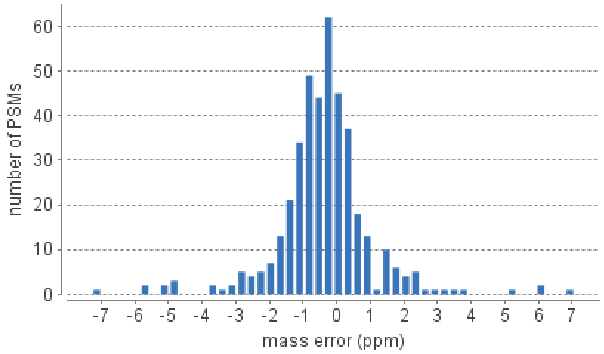
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Deamidation	.98	NQ	55	71.43	1.95E4	45.16
Oxidation	15.99	M	55	68.35	9.71E4	1000.00
Carbamidomethyl	57.02	C	20	68.26	3.95E4	1000.00
HydPro	15.99	P	2	67.63	6.97E4	38.03

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



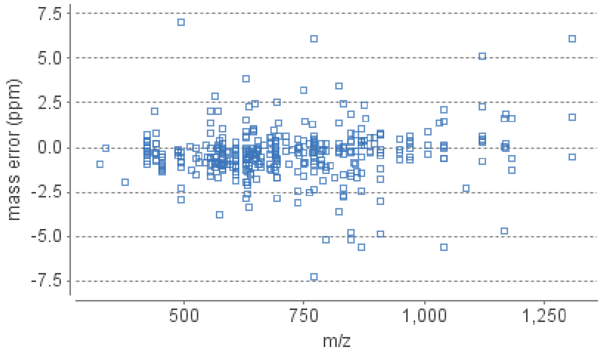


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 7	109	12	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3605.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 7	Area Sample 7	#Peptides	#Unique	#Spec Sample 7	PTM	Avg. Mass	Description
1	18	N1NG13|N1NG13_ARAHY	99.2	286.27	43	43	1.79E6	27	6	209	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
1	20	sp|P43238|ALL12_ARAHY	99.2	286.27	43	43	1.79E6	27	6	209	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
2	26	Q6PSU3|Q6PSU3_ARAHY	99.2	280.01	41	41	1.06E5	24	3	187	Y	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
2	21	sp|P43237|ALL11_ARAHY	99.2	280.01	39	39	1.06E5	24	3	187	Y	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
2	23	B3IXL2|B3IXL2_ARAHY	99.2	280.01	39	39	1.06E5	24	3	187	Y	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
3	15	Q647H3|Q647H3_ARAHY	99.1	204.93	26	26	1.72E5	9	2	69	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
5	3	B5TYU1|B5TYU1_ARAHY	99.1	202.39	26	26	4.88E4	9	1	63	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
6	7	Q647H4|Q647H4_ARAHY	99.1	185.10	22	22	9.42E3	8	1	54	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	99.1	185.10	22	22	9.42E3	8	1	54	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
14	41	Q6IWG5|Q6IWG5_ARAHY	83.6	61.56	5	5	1.77E5	1	1	1	N	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
14	42	Q0GM57|Q0GM57_ARAHY	83.6	61.56	4	4	1.77E5	1	1	1	N	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
14	45	E5G077|E5G077_ARAHY	83.6	61.56	4	4	1.77E5	1	1	1	N	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
total 12 proteins													

N1NG13|N1NG13_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG

81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS R**NNPFYFPSR** RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHR**IVQIEAK PNTLVLPKHA DADNILVIQQ**

241 **GQATVTVANG NNR**K**SFNLDE GHALRIPSGF ISYILNR**HDN QNLRVAK**ISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT**

321 **LEAAFNAEFN EIRRVLLEEN AGGEQEER**GQ RRWSTR**SSEN NEGVIVK**VSK **EHVEELTK**HA KSVSK**KGSEE EGDITNPINL**

401 **REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV R**KEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	91.13	1737.8322	15	-0.6	869.9229	2	33.43	7	2175	OB3605.raw	3.45E5	10	10	319	333	
R.VLLEENAGGEQEER.G	N	99.9	79.13	1571.7427	14	-0.2	786.8785	2	25.62	7	1220	OB3605.raw	8.24E4	4	4	335	348	
R.IPSGFISYILNR.H	N	99.9	74.81	1378.7609	12	0.3	690.3879	2	34.18	7	2277	OB3605.raw	6.36E5	10	10	266	277	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	73.94	2618.3162	25	0.1	873.7794	3	28.92	7	1572	OB3605.raw	4.19E5	5	5	229	253	
R.DQSSYLQGFSR.N	N	99.9	72.79	1286.5891	11	0.0	644.3018	2	29.22	7	1612	OB3605.raw	9.76E4	5	5	308	318	
K.GSEEEGDITNPINLR.E	Y	99.9	72.21	1642.7798	15	-0.2	822.3970	2	29.26	7	1619	OB3605.raw	1.71E5	7	7	387	401	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	71.43	1572.7267	14	-0.9	787.3699	2	26.05	7	1253	OB3605.raw	1.95E4	1	1	335	348	Deamidation (NQ)
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	71.16	2619.3000	25	0.4	874.1076	3	29.25	7	1617	OB3605.raw	8.83E5	1	1	229	253	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	N	99.9	70.69	1816.9570	16	-0.1	909.4857	2	30.45	7	1780	OB3605.raw	2.23E6	32	32	541	556	
K.GTGNLELVAVR.K	N	99.9	70.62	1127.6299	11	-0.9	564.8217	2	28.73	7	1545	OB3605.raw	8.29E5	6	6	461	471	
K.AMVIVVVNK.G	N	99.9	69.91	971.5837	9	-0.3	486.7990	2	28.00	7	1453	OB3605.raw	1.25E4	2	2	452	460	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.37	1287.5731	11	-0.3	644.7936	2	29.87	7	1701	OB3605.raw	5.71E4	1	1	308	318	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	68.35	2242.0364	20	0.3	1122.0258	2	32.26	7	2019	OB3605.raw	3.79E5	5	5	288	307	Oxidation (M)
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	68.26	2079.9526	17	0.0	1040.9836	2	32.26	7	2020	OB3605.raw	7.18E4	3	3	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation

R.NTLEAAFN(+.98)AEFNEIR.R	N	99.9	68.12	1738.8162	15	-1.5	870.4141	2	34.42	7	2309	OB3605.raw	2.98E4	1	1	319	333	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.63	2243.0205	20	0.5	1122.5181	2	32.93	7	2109	OB3605.raw	7.91E4	2	2	288	307	Hydroxylation Pro; Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.46	1257.6101	11	-0.9	629.8118	2	27.12	7	1353	OB3605.raw	6.15E4	6	6	255	265	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.20	2243.0205	20	-1.6	748.6796	3	32.98	7	2115	OB3605.raw	1.6E5	5	5	288	307	Oxidation (M); Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	66.89	1287.5731	11	-0.7	644.7934	2	29.70	7	1678	OB3605.raw	5.71E4	1	1	308	318	Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	64.35	1288.5571	11	0.9	645.2864	2	30.22	7	1749	OB3605.raw	1.25E4	1	1	308	318	Deamidation (NQ)
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	63.50	1817.9410	16	-1.2	909.9767	2	30.91	7	1841	OB3605.raw	3.83E4	4	4	541	556	Deamidation (NQ)
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	62.41	2078.9688	17	-1.0	693.9962	3	31.80	7	1959	OB3605.raw	1.8E5	4	4	423	439	Oxidation (M); Carbamidomethylation
R.EGEPDLSNNFGK.L	Y	99.9	61.81	1305.5836	12	0.0	653.7991	2	26.87	7	1329	OB3605.raw	6.85E4	4	4	402	413	
R.N(+.98)TLEAAFNAEFNEIR.R	N	99.9	61.43	1738.8162	15	-2.5	870.4132	2	34.60	7	2333	OB3605.raw	2.98E4	2	2	319	333	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVANGN(+.98)NR.K	N	99.9	58.34	2620.2842	25	2.4	874.4374	3	30.40	7	1774	OB3605.raw	0	1	1	229	253	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	56.11	987.5787	9	-0.3	494.7965	2	25.74	7	1233	OB3605.raw	9.29E4	5	5	452	460	Oxidation (M)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	54.76	1572.7267	14	-0.7	787.3701	2	26.23	7	1269	OB3605.raw	1.95E4	1	1	335	348	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	54.75	1140.5352	9	0.1	571.2749	2	30.09	7	1731	OB3605.raw	1.72E5	5	5	172	180	
K.KNPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.02	2207.0637	18	-0.1	736.6951	3	30.49	7	1786	OB3605.raw	5.62E4	1	1	422	439	Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	53.12	1358.6653	12	-0.1	680.3398	2	28.77	7	1551	OB3605.raw	5.19E5	13	13	440	451	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	52.48	1375.6619	13	1.0	688.8389	2	28.74	7	1547	OB3605.raw	1.12E5	2	2	560	572	
R.SSENNEGVIVK.V	Y	99.9	51.34	1174.5830	11	-0.2	588.2986	2	22.93	7	1069	OB3605.raw	3.52E4	3	3	357	367	
R.IVQ(+.98)IEAKPNTLVLPK.H	Y	99.9	51.13	1662.9919	15	-1.6	832.5020	2	29.09	7	1595	OB3605.raw	8.41E4	2	2	214	228	Deamidation (NQ)
K.KN(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	50.25	2208.0476	18	-1.3	737.0222	3	30.94	7	1845	OB3605.raw	5.34E4	3	3	422	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQIEAKPNTLVLPK.H	Y	99.9	50.12	1662.0079	15	-0.4	832.0109	2	28.31	7	1491	OB3605.raw	9.51E5	10	10	214	228	
K.KGSEEEGDITNPINLR.E	Y	99.9	47.82	1770.8748	16	-0.3	591.2987	3	27.56	7	1400	OB3605.raw	1.25E5	3	3	386	401	
R.IPSGFISYILN(+.98)R.H	N	99.9	47.63	1379.7449	12	-1.3	690.8788	2	34.51	7	2321	OB3605.raw	5.95E4	1	1	266	277	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQ(+.98)EER.G	N	99.9	47.46	1573.7107	14	-1.9	787.8611	2	26.59	7	1310	OB3605.raw	3.08E3	2	2	335	348	Deamidation (NQ)
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.9	46.35	1817.9410	16	-4.8	909.9734	2	31.00	7	1854	OB3605.raw	2.11E4	1	1	541	556	Deamidation (NQ)
R.IVQIEAKPN(+.98)TLVLPK.H	Y	99.9	46.16	1662.9919	15	1.4	555.3387	3	29.08	7	1593	OB3605.raw	2.52E5	2	2	214	228	Deamidation (NQ)
K.GTGN(+.98)LELVAVR.K	N	99.9	45.83	1128.6139	11	2.9	565.3159	2	29.30	7	1623	OB3605.raw	9.15E3	1	1	461	471	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.9	45.32	1893.9332	16	-0.1	947.9738	2	32.76	7	2086	OB3605.raw	1.67E5	6	6	319	334	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	44.71	2079.9526	17	-1.7	694.3237	3	32.31	7	2026	OB3605.raw	7.18E4	2	2	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.PNTLVLPK.H	N	99.9	43.52	880.5382	8	0.2	441.2765	2	27.12	7	1352	OB3605.raw	1.07E5	5	5	221	228	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	99.9	43.03	2062.9736	17	1.3	1032.4955	2	32.73	7	2083	OB3605.raw	1.44E4	1	1	423	439	Oxidation (M); Carbamidomethylation
K.DLAFPGSGEQ(+.98)VEK.L	N	99.8	41.70	1376.6459	13	0.3	689.3304	2	29.04	7	1588	OB3605.raw	1.96E4	1	1	560	572	Deamidation (NQ)
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.8	41.04	2062.9736	17	-1.1	688.6644	3	32.72	7	2082	OB3605.raw	1.29E4	1	1	423	439	Oxidation (M); Carbamidomethylation
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.8	40.46	2243.0205	20	0.6	1122.5182	2	33.17	7	2141	OB3605.raw	6.97E4	1	1	288	307	Oxidation (M); Deamidation (NQ)
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.8	40.17	2080.9368	17	2.5	694.6546	3	32.68	7	2076	OB3605.raw	8.05E3	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQ(+.98)IEAKPN(+.98)TLVLPK.H	Y	99.7	38.29	1663.9760	15	1.4	555.6667	3	29.39	7	1635	OB3605.raw	8.87E4	3	3	214	228	Deamidation (NQ)
K.GSEEEGDITN(+.98)PINLR.E	Y	99.6	37.39	1643.7638	15	-3.6	822.8862	2	29.47	7	1647	OB3605.raw	0	1	1	387	401	Deamidation (NQ)
N.TLVLPK.H	N	98.3	32.15	669.4425	6	0.0	335.7285	2	26.37	7	1284	OB3605.raw	1.78E4	1	1	223	228	
K.EHVEELTK.H	Y	98.1	28.95	983.4924	8	-2.3	492.7523	2	20.43	7	945	OB3605.raw	1.25E4	2	2	371	378	
R.IPSGFISY.I	N	96.8	26.65	882.4487	8	0.2	442.2317	2	32.31	7	2027	OB3605.raw	1.49E4	2	2	266	273	
K.LFEVKPDK.K	N	95.9	26.37	974.5436	8	-0.9	325.8549	3	24.46	7	1152	OB3605.raw	3.31E4	2	2	414	421	
K.AM(+15.99)VIVVVN(+.98)K.G	N	94.9	26.04	988.5627	9	7.1	495.2921	2	26.33	7	1279	OB3605.raw	0	1	1	452	460	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFN.S	N	93.1	24.89	1143.5382	10	-0.1	572.7763	2	31.12	7	1869	OB3605.raw	2.12E4	1	1	440	449	Oxidation (M)

total 57 peptides

sp|P43238|ALL12_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG

81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS R**NNPFYFPSR** RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHR**IVQIEAK PNTLVLPKHA DADNILVIQQ**

241 **GQATVTVANG NNR**K**SFNLDE GHALRIPSGF ISYILNR**HDN QNLRVAK**ISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT**

321 **LEAAFNAEFN EIRRVLLEEN AGGEQEER**GQ RRWSTR**SSEN NEGVIVK**VSK **EHVEELTK**HA KSVSK**KGSEE EGDITNPINL**

401 **REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV R**KEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	91.13	1737.8322	15	-0.6	869.9229	2	33.43	7	2175	OB3605.raw	3.45E5	10	10	319	333	
R.VLLEENAGGEQEER.G	N	99.9	79.13	1571.7427	14	-0.2	786.8785	2	25.62	7	1220	OB3605.raw	8.24E4	4	4	335	348	
R.IPSGFISYILNR.H	N	99.9	74.81	1378.7609	12	0.3	690.3879	2	34.18	7	2277	OB3605.raw	6.36E5	10	10	266	277	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	73.94	2618.3162	25	0.1	873.7794	3	28.92	7	1572	OB3605.raw	4.19E5	5	5	229	253	
R.DQSSYLQGFSR.N	N	99.9	72.79	1286.5891	11	0.0	644.3018	2	29.22	7	1612	OB3605.raw	9.76E4	5	5	308	318	
K.GSEEEGDITNPINLR.E	Y	99.9	72.21	1642.7798	15	-0.2	822.3970	2	29.26	7	1619	OB3605.raw	1.71E5	7	7	387	401	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	71.43	1572.7267	14	-0.9	787.3699	2	26.05	7	1253	OB3605.raw	1.95E4	1	1	335	348	Deamidation (NQ)
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	71.16	2619.3000	25	0.4	874.1076	3	29.25	7	1617	OB3605.raw	8.83E5	1	1	229	253	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	N	99.9	70.69	1816.9570	16	-0.1	909.4857	2	30.45	7	1780	OB3605.raw	2.23E6	32	32	541	556	

K.GTGNLELVAVR.K	N	99.9	70.62	1127.6299	11	-0.9	564.8217	2	28.73	7	1545	OB3605.raw	8.29E5	6	6	461	471	
K.AMVIVVVNK.G	N	99.9	69.91	971.5837	9	-0.3	486.7990	2	28.00	7	1453	OB3605.raw	1.25E4	2	2	452	460	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.37	1287.5731	11	-0.3	644.7936	2	29.87	7	1701	OB3605.raw	5.71E4	1	1	308	318	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	68.35	2242.0364	20	0.3	1122.0258	2	32.26	7	2019	OB3605.raw	3.79E5	5	5	288	307	Oxidation (M)
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	68.26	2079.9526	17	0.0	1040.9836	2	32.26	7	2020	OB3605.raw	7.18E4	3	3	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.9	68.12	1738.8162	15	-1.5	870.4141	2	34.42	7	2309	OB3605.raw	2.98E4	1	1	319	333	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.63	2243.0205	20	0.5	1122.5181	2	32.93	7	2109	OB3605.raw	7.91E4	2	2	288	307	Hydroxylation Pro; Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.46	1257.6101	11	-0.9	629.8118	2	27.12	7	1353	OB3605.raw	6.15E4	6	6	255	265	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.20	2243.0205	20	-1.6	748.6796	3	32.98	7	2115	OB3605.raw	1.6E5	5	5	288	307	Oxidation (M); Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	66.89	1287.5731	11	-0.7	644.7934	2	29.70	7	1678	OB3605.raw	5.71E4	1	1	308	318	Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	64.35	1288.5571	11	0.9	645.2864	2	30.22	7	1749	OB3605.raw	1.25E4	1	1	308	318	Deamidation (NQ)
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	63.50	1817.9410	16	-1.2	909.9767	2	30.91	7	1841	OB3605.raw	3.83E4	4	4	541	556	Deamidation (NQ)
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	62.41	2078.9688	17	-1.0	693.9962	3	31.80	7	1959	OB3605.raw	1.8E5	4	4	423	439	Oxidation (M); Carbamidomethylation
R.EGEPDLSNNFGK.L	Y	99.9	61.81	1305.5836	12	0.0	653.7991	2	26.87	7	1329	OB3605.raw	6.85E4	4	4	402	413	
R.N(+.98)TLEAAFNAEFNEIR.R	N	99.9	61.43	1738.8162	15	-2.5	870.4132	2	34.60	7	2333	OB3605.raw	2.98E4	2	2	319	333	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVANGN(+.98)NR.K	N	99.9	58.34	2620.2842	25	2.4	874.4374	3	30.40	7	1774	OB3605.raw	0	1	1	229	253	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	56.11	987.5787	9	-0.3	494.7965	2	25.74	7	1233	OB3605.raw	9.29E4	5	5	452	460	Oxidation (M)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	54.76	1572.7267	14	-0.7	787.3701	2	26.23	7	1269	OB3605.raw	1.95E4	1	1	335	348	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	54.75	1140.5352	9	0.1	571.2749	2	30.09	7	1731	OB3605.raw	1.72E5	5	5	172	180	
K.KNPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.02	2207.0637	18	-0.1	736.6951	3	30.49	7	1786	OB3605.raw	5.62E4	1	1	422	439	Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	53.12	1358.6653	12	-0.1	680.3398	2	28.77	7	1551	OB3605.raw	5.19E5	13	13	440	451	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	52.48	1375.6619	13	1.0	688.8389	2	28.74	7	1547	OB3605.raw	1.12E5	2	2	560	572	
R.SSENNEGVIVK.V	Y	99.9	51.34	1174.5830	11	-0.2	588.2986	2	22.93	7	1069	OB3605.raw	3.52E4	3	3	357	367	
R.IVQ(+.98)IEAKPNTLVLPK.H	Y	99.9	51.13	1662.9919	15	-1.6	832.5020	2	29.09	7	1595	OB3605.raw	8.41E4	2	2	214	228	Deamidation (NQ)
K.KN(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	50.25	2208.0476	18	-1.3	737.0222	3	30.94	7	1845	OB3605.raw	5.34E4	3	3	422	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQIEAKPNTLVLPK.H	Y	99.9	50.12	1662.0079	15	-0.4	832.0109	2	28.31	7	1491	OB3605.raw	9.51E5	10	10	214	228	
K.KGSEEEGDITNPINLR.E	Y	99.9	47.82	1770.8748	16	-0.3	591.2987	3	27.56	7	1400	OB3605.raw	1.25E5	3	3	386	401	
R.IPSGFISYILN(+.98)R.H	N	99.9	47.63	1379.7449	12	-1.3	690.8788	2	34.51	7	2321	OB3605.raw	5.95E4	1	1	266	277	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQ(+.98)EER.G	N	99.9	47.46	1573.7107	14	-1.9	787.8611	2	26.59	7	1310	OB3605.raw	3.08E3	2	2	335	348	Deamidation (NQ)
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.9	46.35	1817.9410	16	-4.8	909.9734	2	31.00	7	1854	OB3605.raw	2.11E4	1	1	541	556	Deamidation (NQ)
R.IVQIEAKPN(+.98)TLVLPK.H	Y	99.9	46.16	1662.9919	15	1.4	555.3387	3	29.08	7	1593	OB3605.raw	2.52E5	2	2	214	228	Deamidation (NQ)
K.GTGN(+.98)LELVAVR.K	N	99.9	45.83	1128.6139	11	2.9	565.3159	2	29.30	7	1623	OB3605.raw	9.15E3	1	1	461	471	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.9	45.32	1893.9332	16	-0.1	947.9738	2	32.76	7	2086	OB3605.raw	1.67E5	6	6	319	334	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	44.71	2079.9526	17	-1.7	694.3237	3	32.31	7	2026	OB3605.raw	7.18E4	2	2	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.PNTLVLPK.H	N	99.9	43.52	880.5382	8	0.2	441.2765	2	27.12	7	1352	OB3605.raw	1.07E5	5	5	221	228	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	99.9	43.03	2062.9736	17	1.3	1032.4955	2	32.73	7	2083	OB3605.raw	1.44E4	1	1	423	439	Oxidation (M); Carbamidomethylation
K.DLAFPGSGEQ(+.98)VEK.L	N	99.8	41.70	1376.6459	13	0.3	689.3304	2	29.04	7	1588	OB3605.raw	1.96E4	1	1	560	572	Deamidation (NQ)
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.8	41.04	2062.9736	17	-1.1	688.6644	3	32.72	7	2082	OB3605.raw	1.29E4	1	1	423	439	Oxidation (M); Carbamidomethylation
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.8	40.46	2243.0205	20	0.6	1122.5182	2	33.17	7	2141	OB3605.raw	6.97E4	1	1	288	307	Oxidation (M); Deamidation (NQ)
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.8	40.17	2080.9368	17	2.5	694.6546	3	32.68	7	2076	OB3605.raw	8.05E3	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQ(+.98)IEAKPN(+.98)TLVLPK.H	Y	99.7	38.29	1663.9760	15	1.4	555.6667	3	29.39	7	1635	OB3605.raw	8.87E4	3	3	214	228	Deamidation (NQ)
K.GSEEEGDITN(+.98)PINLR.E	Y	99.6	37.39	1643.7638	15	-3.6	822.8862	2	29.47	7	1647	OB3605.raw	0	1	1	387	401	Deamidation (NQ)

N.TLVLPK.H	N	98.3	32.15	669.4425	6	0.0	335.7285	2	26.37	7	1284	OB3605.raw	1.78E4	1	1	223	228	
K.EHVEELTK.H	Y	98.1	28.95	983.4924	8	-2.3	492.7523	2	20.43	7	945	OB3605.raw	1.25E4	2	2	371	378	
R.IPSGFISY.I	N	96.8	26.65	882.4487	8	0.2	442.2317	2	32.31	7	2027	OB3605.raw	1.49E4	2	2	266	273	
K.LFEVKPDK.K	N	95.9	26.37	974.5436	8	-0.9	325.8549	3	24.46	7	1152	OB3605.raw	3.31E4	2	2	414	421	
K.AM(+15.99)VIVVVN(+.98)K.G	N	94.9	26.04	988.5627	9	7.1	495.2921	2	26.33	7	1279	OB3605.raw	0	1	1	452	460	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFN.S	N	93.1	24.89	1143.5382	10	-0.1	572.7763	2	31.12	7	1869	OB3605.raw	2.12E4	1	1	440	449	Oxidation (M)
total 57 peptides																		

Q6PSU3|Q6PSU3_ARAHY

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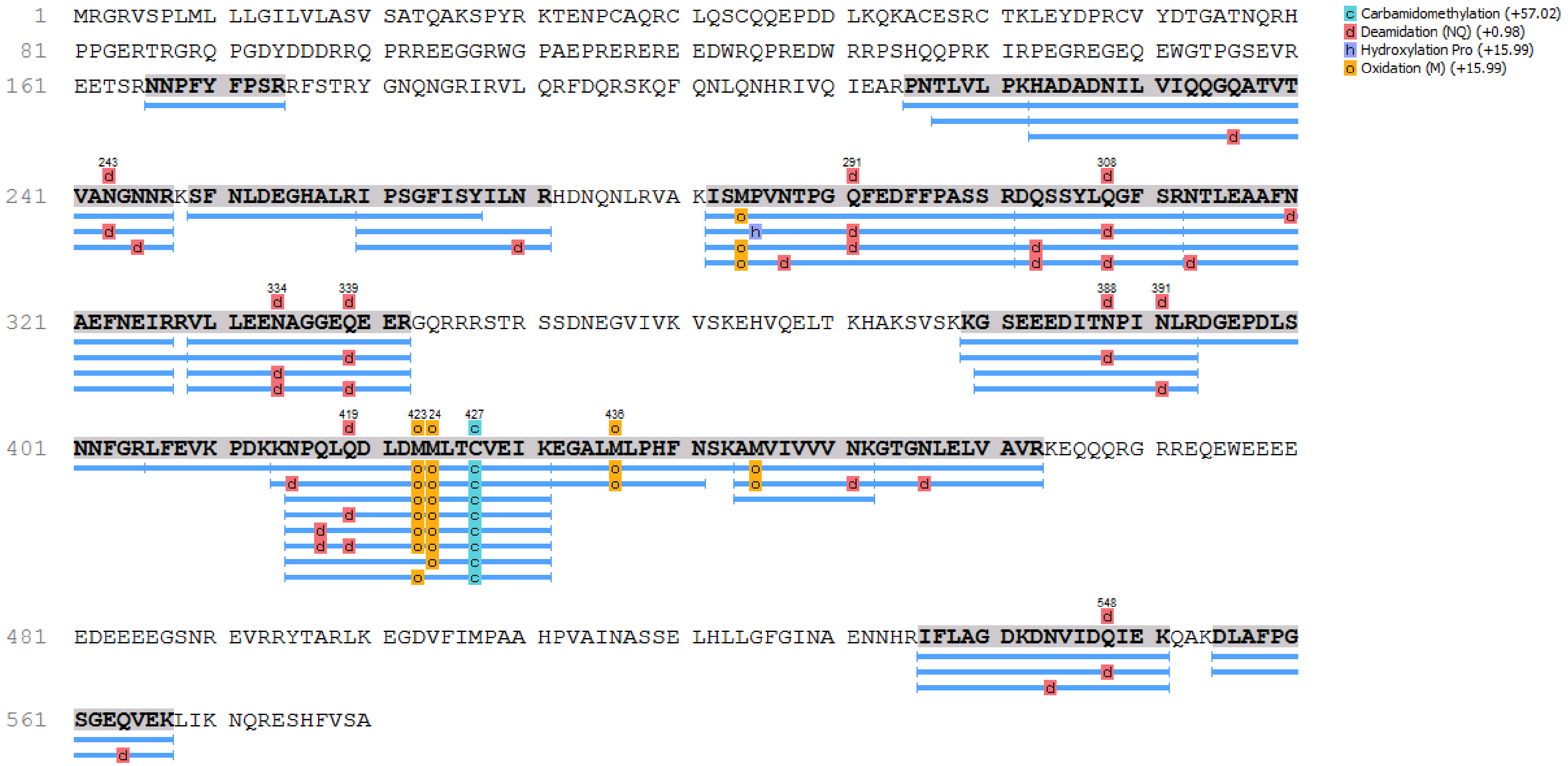
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	91.13	1737.8322	15	-0.6	869.9229	2	33.43	7	2175	OB3605.raw	3.45E5	10	10	313	327	
R.VLLEENAGGEQEER.G	N	99.9	79.13	1571.7427	14	-0.2	786.8785	2	25.62	7	1220	OB3605.raw	8.24E4	4	4	329	342	
R.IPSGFISYILNR.H	N	99.9	74.81	1378.7609	12	0.3	690.3879	2	34.18	7	2277	OB3605.raw	6.36E5	10	10	260	271	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	73.94	2618.3162	25	0.1	873.7794	3	28.92	7	1572	OB3605.raw	4.19E5	5	5	223	247	
R.DQSSYLQGFSR.N	N	99.9	72.79	1286.5891	11	0.0	644.3018	2	29.22	7	1612	OB3605.raw	9.76E4	5	5	302	312	

R.VLLEENAGGEQ(+.98)EER.G	N	99.9	71.43	1572.7267	14	-0.9	787.3699	2	26.05	7	1253	OB3605.raw	1.95E4	1	1	329	342	Deamidation (NQ)
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	71.16	2619.3000	25	0.4	874.1076	3	29.25	7	1617	OB3605.raw	8.83E5	1	1	223	247	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	N	99.9	70.69	1816.9570	16	-0.1	909.4857	2	30.45	7	1780	OB3605.raw	2.23E6	32	32	536	551	
K.GTGNLELVAVR.K	N	99.9	70.62	1127.6299	11	-0.9	564.8217	2	28.73	7	1545	OB3605.raw	8.29E5	6	6	453	463	
K.AMVIVVVNK.G	N	99.9	69.91	971.5837	9	-0.3	486.7990	2	28.00	7	1453	OB3605.raw	1.25E4	2	2	444	452	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.37	1287.5731	11	-0.3	644.7936	2	29.87	7	1701	OB3605.raw	5.71E4	1	1	302	312	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	68.35	2242.0364	20	0.3	1122.0258	2	32.26	7	2019	OB3605.raw	3.79E5	5	5	282	301	Oxidation (M)
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	68.26	2079.9526	17	0.0	1040.9836	2	32.26	7	2020	OB3605.raw	7.18E4	3	3	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.9	68.12	1738.8162	15	-1.5	870.4141	2	34.42	7	2309	OB3605.raw	2.98E4	1	1	313	327	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.63	2243.0205	20	0.5	1122.5181	2	32.93	7	2109	OB3605.raw	7.91E4	2	2	282	301	Hydroxylation Pro; Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.46	1257.6101	11	-0.9	629.8118	2	27.12	7	1353	OB3605.raw	6.15E4	6	6	249	259	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.20	2243.0205	20	-1.6	748.6796	3	32.98	7	2115	OB3605.raw	1.6E5	5	5	282	301	Oxidation (M); Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	66.89	1287.5731	11	-0.7	644.7934	2	29.70	7	1678	OB3605.raw	5.71E4	1	1	302	312	Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	64.35	1288.5571	11	0.9	645.2864	2	30.22	7	1749	OB3605.raw	1.25E4	1	1	302	312	Deamidation (NQ)
K.GSEEEDITNPINLR.D	Y	99.9	64.11	1585.7583	14	0.2	793.8866	2	29.44	7	1642	OB3605.raw	4.43E4	5	5	380	393	
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	63.50	1817.9410	16	-1.2	909.9767	2	30.91	7	1841	OB3605.raw	3.83E4	4	4	536	551	Deamidation (NQ)
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	62.41	2078.9688	17	-1.0	693.9962	3	31.80	7	1959	OB3605.raw	1.8E5	4	4	415	431	Oxidation (M); Carbamidomethylation
R.N(+.98)TLEAAFNAEFNEIR.R	N	99.9	61.43	1738.8162	15	-2.5	870.4132	2	34.60	7	2333	OB3605.raw	2.98E4	2	2	313	327	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVANGN(+.98)NR.K	N	99.9	58.34	2620.2842	25	2.4	874.4374	3	30.40	7	1774	OB3605.raw	0	1	1	223	247	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	56.11	987.5787	9	-0.3	494.7965	2	25.74	7	1233	OB3605.raw	9.29E4	5	5	444	452	Oxidation (M)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	54.76	1572.7267	14	-0.7	787.3701	2	26.23	7	1269	OB3605.raw	1.95E4	1	1	329	342	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	54.75	1140.5352	9	0.1	571.2749	2	30.09	7	1731	OB3605.raw	1.72E5	5	5	166	174	
K.KNPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.02	2207.0637	18	-0.1	736.6951	3	30.49	7	1786	OB3605.raw	5.62E4	1	1	414	431	Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	53.12	1358.6653	12	-0.1	680.3398	2	28.77	7	1551	OB3605.raw	5.19E5	13	13	432	443	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	52.48	1375.6619	13	1.0	688.8389	2	28.74	7	1547	OB3605.raw	1.12E5	2	2	555	567	
K.KN(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	50.25	2208.0476	18	-1.3	737.0222	3	30.94	7	1845	OB3605.raw	5.34E4	3	3	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.DGEPDLSNNFGR.L	Y	99.9	48.59	1319.5742	12	-1.1	660.7936	2	27.63	7	1410	OB3605.raw	1.99E4	2	2	394	405	
R.IPSGFISYILN(+.98)R.H	N	99.9	47.63	1379.7449	12	-1.3	690.8788	2	34.51	7	2321	OB3605.raw	5.95E4	1	1	260	271	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQ(+.98)EER.G	N	99.9	47.46	1573.7107	14	-1.9	787.8611	2	26.59	7	1310	OB3605.raw	3.08E3	2	2	329	342	Deamidation (NQ)
K.KGSEEEDITN(+.98)PINLR.D	Y	99.9	46.97	1714.8373	15	0.4	572.6199	3	28.27	7	1486	OB3605.raw	6.33E0	2	2	379	393	Deamidation (NQ)
K.KGSEEEDITNPINLR.D	Y	99.9	46.40	1713.8533	15	-0.9	572.2912	3	27.96	7	1448	OB3605.raw	4.14E4	5	5	379	393	
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.9	46.35	1817.9410	16	-4.8	909.9734	2	31.00	7	1854	OB3605.raw	2.11E4	1	1	536	551	Deamidation (NQ)
K.GTGN(+.98)LELVAVR.K	N	99.9	45.83	1128.6139	11	2.9	565.3159	2	29.30	7	1623	OB3605.raw	9.15E3	1	1	453	463	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.9	45.32	1893.9332	16	-0.1	947.9738	2	32.76	7	2086	OB3605.raw	1.67E5	6	6	313	328	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	44.71	2079.9526	17	-1.7	694.3237	3	32.31	7	2026	OB3605.raw	7.18E4	2	2	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.PNTLVLPK.H	N	99.9	43.52	880.5382	8	0.2	441.2765	2	27.12	7	1352	OB3605.raw	1.07E5	5	5	215	222	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	99.9	43.03	2062.9736	17	1.3	1032.4955	2	32.73	7	2083	OB3605.raw	1.44E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.DLAFPGSGEQ(+.98)VEK.L	N	99.8	41.70	1376.6459	13	0.3	689.3304	2	29.04	7	1588	OB3605.raw	1.96E4	1	1	555	567	Deamidation (NQ)
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.8	41.04	2062.9736	17	-1.1	688.6644	3	32.72	7	2082	OB3605.raw	1.29E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.8	40.46	2243.0205	20	0.6	1122.5182	2	33.17	7	2141	OB3605.raw	6.97E4	1	1	282	301	Oxidation (M); Deamidation (NQ)
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.8	40.17	2080.9368	17	2.5	694.6546	3	32.68	7	2076	OB3605.raw	8.05E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
N.TLVLPK.H	N	98.3	32.15	669.4425	6	0.0	335.7285	2	26.37	7	1284	OB3605.raw	1.78E4	1	1	217	222	

K.GSEEEDITNPIN(+.98)LR.D	Y	98.1	28.77	1586.7423	14	-5.2	794.3743	2	29.81	7	1693	OB3605.raw	0	1	1	380	393	Deamidation (NQ)
R.IPSGFISY.I	N	96.8	26.65	882.4487	8	0.2	442.2317	2	32.31	7	2027	OB3605.raw	1.49E4	2	2	260	267	
R.LFEVKPDK.K	N	95.9	26.37	974.5436	8	-0.9	325.8549	3	24.46	7	1152	OB3605.raw	3.31E4	2	2	406	413	
K.AM(+15.99)VIVVVN(+.98)K.G	N	94.9	26.04	988.5627	9	7.1	495.2921	2	26.33	7	1279	OB3605.raw	0	1	1	444	452	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFN.S	N	93.1	24.89	1143.5382	10	-0.1	572.7763	2	31.12	7	1869	OB3605.raw	2.12E4	1	1	432	441	Oxidation (M)
total 52 peptides																		

sp|P43237|ALL11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	91.13	1737.8322	15	-0.6	869.9229	2	33.43	7	2175	OB3605.raw	3.45E5	10	10	313	327	
R.VLLEENAGGEQEER.G	N	99.9	79.13	1571.7427	14	-0.2	786.8785	2	25.62	7	1220	OB3605.raw	8.24E4	4	4	329	342	
R.IPSGFISYILNR.H	N	99.9	74.81	1378.7609	12	0.3	690.3879	2	34.18	7	2277	OB3605.raw	6.36E5	10	10	260	271	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	73.94	2618.3162	25	0.1	873.7794	3	28.92	7	1572	OB3605.raw	4.19E5	5	5	223	247	
R.DQSSYLQGFSR.N	N	99.9	72.79	1286.5891	11	0.0	644.3018	2	29.22	7	1612	OB3605.raw	9.76E4	5	5	302	312	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	71.43	1572.7267	14	-0.9	787.3699	2	26.05	7	1253	OB3605.raw	1.95E4	1	1	329	342	Deamidation (NQ)

K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	71.16	2619.3000	25	0.4	874.1076	3	29.25	7	1617	OB3605.raw	8.83E5	1	1	223	247	Deamidation (NQ)
R.IFLAGDKDNVIDQIEK.Q	N	99.9	70.69	1816.9570	16	-0.1	909.4857	2	30.45	7	1780	OB3605.raw	2.23E6	32	32	536	551	
K.GTGNLELVAVR.K	N	99.9	70.62	1127.6299	11	-0.9	564.8217	2	28.73	7	1545	OB3605.raw	8.29E5	6	6	453	463	
K.AMVIVVVNK.G	N	99.9	69.91	971.5837	9	-0.3	486.7990	2	28.00	7	1453	OB3605.raw	1.25E4	2	2	444	452	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.37	1287.5731	11	-0.3	644.7936	2	29.87	7	1701	OB3605.raw	5.71E4	1	1	302	312	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	68.35	2242.0364	20	0.3	1122.0258	2	32.26	7	2019	OB3605.raw	3.79E5	5	5	282	301	Oxidation (M)
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	68.26	2079.9526	17	0.0	1040.9836	2	32.26	7	2020	OB3605.raw	7.18E4	3	3	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.9	68.12	1738.8162	15	-1.5	870.4141	2	34.42	7	2309	OB3605.raw	2.98E4	1	1	313	327	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.63	2243.0205	20	0.5	1122.5181	2	32.93	7	2109	OB3605.raw	7.91E4	2	2	282	301	Hydroxylation Pro; Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.46	1257.6101	11	-0.9	629.8118	2	27.12	7	1353	OB3605.raw	6.15E4	6	6	249	259	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.20	2243.0205	20	-1.6	748.6796	3	32.98	7	2115	OB3605.raw	1.6E5	5	5	282	301	Oxidation (M); Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	66.89	1287.5731	11	-0.7	644.7934	2	29.70	7	1678	OB3605.raw	5.71E4	1	1	302	312	Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	64.35	1288.5571	11	0.9	645.2864	2	30.22	7	1749	OB3605.raw	1.25E4	1	1	302	312	Deamidation (NQ)
K.GSEEEDITNPINLR.D	Y	99.9	64.11	1585.7583	14	0.2	793.8866	2	29.44	7	1642	OB3605.raw	4.43E4	5	5	380	393	
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	63.50	1817.9410	16	-1.2	909.9767	2	30.91	7	1841	OB3605.raw	3.83E4	4	4	536	551	Deamidation (NQ)
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	62.41	2078.9688	17	-1.0	693.9962	3	31.80	7	1959	OB3605.raw	1.8E5	4	4	415	431	Oxidation (M); Carbamidomethylation
R.N(+.98)TLEAAFNAEFNEIR.R	N	99.9	61.43	1738.8162	15	-2.5	870.4132	2	34.60	7	2333	OB3605.raw	2.98E4	2	2	313	327	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVANGN(+.98)NR.K	N	99.9	58.34	2620.2842	25	2.4	874.4374	3	30.40	7	1774	OB3605.raw	0	1	1	223	247	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	56.11	987.5787	9	-0.3	494.7965	2	25.74	7	1233	OB3605.raw	9.29E4	5	5	444	452	Oxidation (M)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	54.76	1572.7267	14	-0.7	787.3701	2	26.23	7	1269	OB3605.raw	1.95E4	1	1	329	342	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	54.75	1140.5352	9	0.1	571.2749	2	30.09	7	1731	OB3605.raw	1.72E5	5	5	166	174	
K.KNPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.02	2207.0637	18	-0.1	736.6951	3	30.49	7	1786	OB3605.raw	5.62E4	1	1	414	431	Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	53.12	1358.6653	12	-0.1	680.3398	2	28.77	7	1551	OB3605.raw	5.19E5	13	13	432	443	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	52.48	1375.6619	13	1.0	688.8389	2	28.74	7	1547	OB3605.raw	1.12E5	2	2	555	567	
K.KN(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	50.25	2208.0476	18	-1.3	737.0222	3	30.94	7	1845	OB3605.raw	5.34E4	3	3	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.DGEPDLSNNFGR.L	Y	99.9	48.59	1319.5742	12	-1.1	660.7936	2	27.63	7	1410	OB3605.raw	1.99E4	2	2	394	405	
R.IPSGFISYILN(+.98)R.H	N	99.9	47.63	1379.7449	12	-1.3	690.8788	2	34.51	7	2321	OB3605.raw	5.95E4	1	1	260	271	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQ(+.98)EER.G	N	99.9	47.46	1573.7107	14	-1.9	787.8611	2	26.59	7	1310	OB3605.raw	3.08E3	2	2	329	342	Deamidation (NQ)
K.KGSEEEDITN(+.98)PINLR.D	Y	99.9	46.97	1714.8373	15	0.4	572.6199	3	28.27	7	1486	OB3605.raw	6.33E0	2	2	379	393	Deamidation (NQ)
K.KGSEEEDITNPINLR.D	Y	99.9	46.40	1713.8533	15	-0.9	572.2912	3	27.96	7	1448	OB3605.raw	4.14E4	5	5	379	393	
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.9	46.35	1817.9410	16	-4.8	909.9734	2	31.00	7	1854	OB3605.raw	2.11E4	1	1	536	551	Deamidation (NQ)
K.GTGN(+.98)LELVAVR.K	N	99.9	45.83	1128.6139	11	2.9	565.3159	2	29.30	7	1623	OB3605.raw	9.15E3	1	1	453	463	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.9	45.32	1893.9332	16	-0.1	947.9738	2	32.76	7	2086	OB3605.raw	1.67E5	6	6	313	328	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	44.71	2079.9526	17	-1.7	694.3237	3	32.31	7	2026	OB3605.raw	7.18E4	2	2	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.PNTLVLPK.H	N	99.9	43.52	880.5382	8	0.2	441.2765	2	27.12	7	1352	OB3605.raw	1.07E5	5	5	215	222	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	99.9	43.03	2062.9736	17	1.3	1032.4955	2	32.73	7	2083	OB3605.raw	1.44E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.DLAFPGSGEQ(+.98)VEK.L	N	99.8	41.70	1376.6459	13	0.3	689.3304	2	29.04	7	1588	OB3605.raw	1.96E4	1	1	555	567	Deamidation (NQ)
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.8	41.04	2062.9736	17	-1.1	688.6644	3	32.72	7	2082	OB3605.raw	1.29E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.8	40.46	2243.0205	20	0.6	1122.5182	2	33.17	7	2141	OB3605.raw	6.97E4	1	1	282	301	Oxidation (M); Deamidation (NQ)
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.8	40.17	2080.9368	17	2.5	694.6546	3	32.68	7	2076	OB3605.raw	8.05E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
N.TLVLPK.H	N	98.3	32.15	669.4425	6	0.0	335.7285	2	26.37	7	1284	OB3605.raw	1.78E4	1	1	217	222	
K.GSEEEDITNPIN(+.98)LR.D	Y	98.1	28.77	1586.7423	14	-5.2	794.3743	2	29.81	7	1693	OB3605.raw	0	1	1	380	393	Deamidation (NQ)

R.IPSGFISY.I	N	96.8	26.65	882.4487	8	0.2	442.2317	2	32.31	7	2027	OB3605.raw	1.49E4	2	2	260	267	
R.LFEVKPDK.K	N	95.9	26.37	974.5436	8	-0.9	325.8549	3	24.46	7	1152	OB3605.raw	3.31E4	2	2	406	413	
K.AM(+15.99)VIVVVN(+.98)K.G	N	94.9	26.04	988.5627	9	7.1	495.2921	2	26.33	7	1279	OB3605.raw	0	1	1	444	452	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFN.S	N	93.1	24.89	1143.5382	10	-0.1	572.7763	2	31.12	7	1869	OB3605.raw	2.12E4	1	1	432	441	Oxidation (M)
total 52 peptides																		

B3IXL2|B3IXL2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	91.13	1737.8322	15	-0.6	869.9229	2	33.43	7	2175	OB3605.raw	3.45E5	10	10	313	327	
R.VLLEENAGGEQEER.G	N	99.9	79.13	1571.7427	14	-0.2	786.8785	2	25.62	7	1220	OB3605.raw	8.24E4	4	4	329	342	
R.IPSGFISYILNR.H	N	99.9	74.81	1378.7609	12	0.3	690.3879	2	34.18	7	2277	OB3605.raw	6.36E5	10	10	260	271	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	73.94	2618.3162	25	0.1	873.7794	3	28.92	7	1572	OB3605.raw	4.19E5	5	5	223	247	
R.DQSSYLQGFSR.N	N	99.9	72.79	1286.5891	11	0.0	644.3018	2	29.22	7	1612	OB3605.raw	9.76E4	5	5	302	312	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	71.43	1572.7267	14	-0.9	787.3699	2	26.05	7	1253	OB3605.raw	1.95E4	1	1	329	342	Deamidation (NQ)
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	71.16	2619.3000	25	0.4	874.1076	3	29.25	7	1617	OB3605.raw	8.83E5	1	1	223	247	Deamidation (NQ)

R.IFLAGDKDNVIDQIEK.Q	N	99.9	70.69	1816.9570	16	-0.1	909.4857	2	30.45	7	1780	OB3605.raw	2.23E6	32	32	536	551	
K.GTGNLELVAVR.K	N	99.9	70.62	1127.6299	11	-0.9	564.8217	2	28.73	7	1545	OB3605.raw	8.29E5	6	6	453	463	
K.AMVIVVVNK.G	N	99.9	69.91	971.5837	9	-0.3	486.7990	2	28.00	7	1453	OB3605.raw	1.25E4	2	2	444	452	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.37	1287.5731	11	-0.3	644.7936	2	29.87	7	1701	OB3605.raw	5.71E4	1	1	302	312	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	68.35	2242.0364	20	0.3	1122.0258	2	32.26	7	2019	OB3605.raw	3.79E5	5	5	282	301	Oxidation (M)
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	68.26	2079.9526	17	0.0	1040.9836	2	32.26	7	2020	OB3605.raw	7.18E4	3	3	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.9	68.12	1738.8162	15	-1.5	870.4141	2	34.42	7	2309	OB3605.raw	2.98E4	1	1	313	327	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.63	2243.0205	20	0.5	1122.5181	2	32.93	7	2109	OB3605.raw	7.91E4	2	2	282	301	Hydroxylation Pro; Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.46	1257.6101	11	-0.9	629.8118	2	27.12	7	1353	OB3605.raw	6.15E4	6	6	249	259	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	67.20	2243.0205	20	-1.6	748.6796	3	32.98	7	2115	OB3605.raw	1.6E5	5	5	282	301	Oxidation (M); Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	66.89	1287.5731	11	-0.7	644.7934	2	29.70	7	1678	OB3605.raw	5.71E4	1	1	302	312	Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	64.35	1288.5571	11	0.9	645.2864	2	30.22	7	1749	OB3605.raw	1.25E4	1	1	302	312	Deamidation (NQ)
K.GSEEEDITNPINLR.D	Y	99.9	64.11	1585.7583	14	0.2	793.8866	2	29.44	7	1642	OB3605.raw	4.43E4	5	5	380	393	
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	63.50	1817.9410	16	-1.2	909.9767	2	30.91	7	1841	OB3605.raw	3.83E4	4	4	536	551	Deamidation (NQ)
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	62.41	2078.9688	17	-1.0	693.9962	3	31.80	7	1959	OB3605.raw	1.8E5	4	4	415	431	Oxidation (M); Carbamidomethylation
R.N(+.98)TLEAAFNAEFNEIR.R	N	99.9	61.43	1738.8162	15	-2.5	870.4132	2	34.60	7	2333	OB3605.raw	2.98E4	2	2	313	327	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVANGN(+.98)NR.K	N	99.9	58.34	2620.2842	25	2.4	874.4374	3	30.40	7	1774	OB3605.raw	0	1	1	223	247	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	56.11	987.5787	9	-0.3	494.7965	2	25.74	7	1233	OB3605.raw	9.29E4	5	5	444	452	Oxidation (M)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	54.76	1572.7267	14	-0.7	787.3701	2	26.23	7	1269	OB3605.raw	1.95E4	1	1	329	342	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	54.75	1140.5352	9	0.1	571.2749	2	30.09	7	1731	OB3605.raw	1.72E5	5	5	166	174	
K.KNPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.02	2207.0637	18	-0.1	736.6951	3	30.49	7	1786	OB3605.raw	5.62E4	1	1	414	431	Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	53.12	1358.6653	12	-0.1	680.3398	2	28.77	7	1551	OB3605.raw	5.19E5	13	13	432	443	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	52.48	1375.6619	13	1.0	688.8389	2	28.74	7	1547	OB3605.raw	1.12E5	2	2	555	567	
K.KN(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	50.25	2208.0476	18	-1.3	737.0222	3	30.94	7	1845	OB3605.raw	5.34E4	3	3	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.DGEPDLSNNFGR.L	Y	99.9	48.59	1319.5742	12	-1.1	660.7936	2	27.63	7	1410	OB3605.raw	1.99E4	2	2	394	405	
R.IPSGFISYILN(+.98)R.H	N	99.9	47.63	1379.7449	12	-1.3	690.8788	2	34.51	7	2321	OB3605.raw	5.95E4	1	1	260	271	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQ(+.98)EER.G	N	99.9	47.46	1573.7107	14	-1.9	787.8611	2	26.59	7	1310	OB3605.raw	3.08E3	2	2	329	342	Deamidation (NQ)
K.KGSEEEDITN(+.98)PINLR.D	Y	99.9	46.97	1714.8373	15	0.4	572.6199	3	28.27	7	1486	OB3605.raw	6.33E0	2	2	379	393	Deamidation (NQ)
K.KGSEEEDITNPINLR.D	Y	99.9	46.40	1713.8533	15	-0.9	572.2912	3	27.96	7	1448	OB3605.raw	4.14E4	5	5	379	393	
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.9	46.35	1817.9410	16	-4.8	909.9734	2	31.00	7	1854	OB3605.raw	2.11E4	1	1	536	551	Deamidation (NQ)
K.GTGN(+.98)LELVAVR.K	N	99.9	45.83	1128.6139	11	2.9	565.3159	2	29.30	7	1623	OB3605.raw	9.15E3	1	1	453	463	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.9	45.32	1893.9332	16	-0.1	947.9738	2	32.76	7	2086	OB3605.raw	1.67E5	6	6	313	328	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	44.71	2079.9526	17	-1.7	694.3237	3	32.31	7	2026	OB3605.raw	7.18E4	2	2	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.PNTLVLPK.H	N	99.9	43.52	880.5382	8	0.2	441.2765	2	27.12	7	1352	OB3605.raw	1.07E5	5	5	215	222	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	99.9	43.03	2062.9736	17	1.3	1032.4955	2	32.73	7	2083	OB3605.raw	1.44E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.DLAFPGSGEQ(+.98)VEK.L	N	99.8	41.70	1376.6459	13	0.3	689.3304	2	29.04	7	1588	OB3605.raw	1.96E4	1	1	555	567	Deamidation (NQ)
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.8	41.04	2062.9736	17	-1.1	688.6644	3	32.72	7	2082	OB3605.raw	1.29E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.8	40.46	2243.0205	20	0.6	1122.5182	2	33.17	7	2141	OB3605.raw	6.97E4	1	1	282	301	Oxidation (M); Deamidation (NQ)
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.8	40.17	2080.9368	17	2.5	694.6546	3	32.68	7	2076	OB3605.raw	8.05E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
N.TLVLPK.H	N	98.3	32.15	669.4425	6	0.0	335.7285	2	26.37	7	1284	OB3605.raw	1.78E4	1	1	217	222	
K.GSEEEDITNPIN(+.98)LR.D	Y	98.1	28.77	1586.7423	14	-5.2	794.3743	2	29.81	7	1693	OB3605.raw	0	1	1	380	393	Deamidation (NQ)
R.IPSGFISY.I	N	96.8	26.65	882.4487	8	0.2	442.2317	2	32.31	7	2027	OB3605.raw	1.49E4	2	2	260	267	

R.LFEVKPDK.K	N	95.9	26.37	974.5436	8	-0.9	325.8549	3	24.46	7	1152	OB3605.raw	3.31E4	2	2	406	413	
K.AM(+15.99)VIVVVN(+.98)K.G	N	94.9	26.04	988.5627	9	7.1	495.2921	2	26.33	7	1279	OB3605.raw	0	1	1	444	452	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFN.S	N	93.1	24.89	1143.5382	10	-0.1	572.7763	2	31.12	7	1869	OB3605.raw	2.12E4	1	1	432	441	Oxidation (M)
total 52 peptides																		

Q647H3|Q647H3_ARAHY

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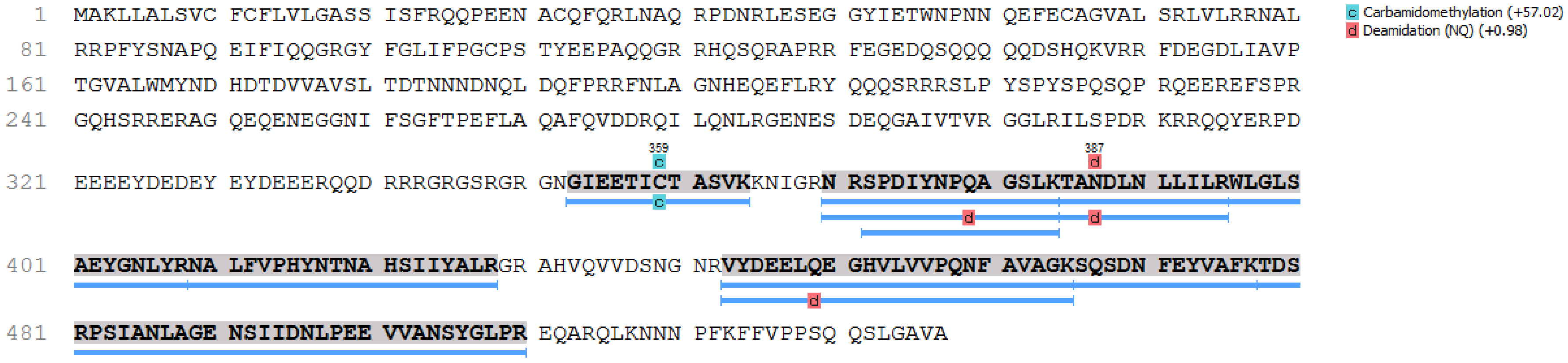
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP

161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR

241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD

321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GN**GIEETICT ASVK**KNIGR**N RSPDIYNPQA GSLKTANDLN LLILRWLGLS**

401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS**

481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	93.96	1540.7673	13	-0.1	771.3909	2	32.48	7	2049	OB3605.raw	5.16E5	13	13	396	408	
K.SQSDNFEYVAFK.T	N	99.9	70.25	1433.6462	12	-1.0	717.8297	2	30.14	7	1739	OB3605.raw	1.05E4	1	1	466	477	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	57.42	3510.7590	33	0.0	1171.2603	3	34.77	7	2356	OB3605.raw	1.56E5	4	4	478	510	
K.TANDLNLLILR.W	N	99.9	53.90	1254.7296	11	0.0	628.3721	2	32.30	7	2025	OB3605.raw	3.63E5	9	9	385	395	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	53.48	2540.2910	23	0.3	847.7712	3	31.16	7	1875	OB3605.raw	6.1E5	12	12	443	465	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	52.28	2313.2019	20	-0.5	579.3074	4	31.03	7	1857	OB3605.raw	1.62E6	19	19	409	428	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	45.43	1306.6438	12	0.4	654.3294	2	27.60	7	1406	OB3605.raw	1.54E4	1	1	353	364	Carbamidomethylation
K.TAN(+.98)DLNLLILR.W	N	99.9	44.81	1255.7136	11	1.5	628.8651	2	33.34	7	2163	OB3605.raw	1.37E4	2	2	385	395	Deamidation (NQ)
R.VYDEELQ(+.98)EGHVLVVPQNFAVAGK.S	N	99.8	42.41	2541.2751	23	1.9	848.1006	3	31.43	7	1911	OB3605.raw	5.52E5	1	1	443	465	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.8	42.01	1388.6936	13	0.6	695.3545	2	27.34	7	1373	OB3605.raw	2.22E4	4	4	372	384	
R.NRSPDIYNPQAGSLK.T	N	98.3	31.96	1658.8376	15	-0.5	553.9529	3	25.70	7	1229	OB3605.raw	3.95E3	1	1	370	384	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	98.1	28.66	1659.8217	15	0.8	554.2816	3	26.32	7	1278	OB3605.raw	6.42E3	2	2	370	384	Deamidation (NQ)
total 12 peptides																		

B5TYU1|B5TYU1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
352 c
321 EYDEDEYEYD EEDRRRGRGS RGSGN**GIEET ICTATVK**KNI GR**NRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY**
401 **RNALFVPHYN TNAHSIIYAL R**GRAHVQVVD SNGNR**VYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL**
481 **AGENSVIDNL PEEVVANSYG LPR**EQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	93.96	1540.7673	13	-0.1	771.3909	2	32.48	7	2049	OB3605.raw	5.16E5	13	13	389	401	
K.SQSDNFEYVAFK.T	N	99.9	70.25	1433.6462	12	-1.0	717.8297	2	30.14	7	1739	OB3605.raw	1.05E4	1	1	459	470	
K.TANELNLLILR.W	N	99.9	58.94	1268.7452	11	-0.2	635.3798	2	33.16	7	2139	OB3605.raw	1.68E5	6	6	378	388	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	53.48	2540.2910	23	0.3	847.7712	3	31.16	7	1875	OB3605.raw	6.1E5	12	12	436	458	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	52.28	2313.2019	20	-0.5	579.3074	4	31.03	7	1857	OB3605.raw	1.62E6	19	19	402	421	
N.GIEETIC(+57.02)TATVK.K	N	99.9	46.79	1320.6595	12	-0.8	661.3365	2	27.97	7	1449	OB3605.raw	1.26E4	1	1	346	357	Carbamidomethylation
R.VYDEELQ(+.98)EGHVLVVPQNFAVAGK.S	N	99.8	42.41	2541.2751	23	1.9	848.1006	3	31.43	7	1911	OB3605.raw	5.52E5	1	1	436	458	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.8	42.01	1388.6936	13	0.6	695.3545	2	27.34	7	1373	OB3605.raw	2.22E4	4	4	365	377	
R.NRSPDIYNPQAGSLK.T	N	98.3	31.96	1658.8376	15	-0.5	553.9529	3	25.70	7	1229	OB3605.raw	3.95E3	1	1	363	377	
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	98.1	28.70	3496.7434	33	1.6	1166.5903	3	34.38	7	2304	OB3605.raw	4.88E4	3	3	471	503	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	98.1	28.66	1659.8217	15	0.8	554.2816	3	26.32	7	1278	OB3605.raw	6.42E3	2	2	363	377	Deamidation (NQ)
total 11 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GR**A HVQVVDSNGD R**VFDEELQEG HVLVVPQNFA VAGK**SQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	93.96	1540.7673	13	-0.1	771.3909	2	32.48	7	2049	OB3605.raw	5.16E5	13	13	395	407	
R.AHVQVVDSNGDR.V	Y	99.9	59.08	1295.6218	12	-1.1	648.8174	2	20.49	7	950	OB3605.raw	9.42E3	2	2	430	441	

K.TANELNLLILR.W	N	99.9	58.94	1268.7452	11	-0.2	635.3798	2	33.16	7	2139	OB3605.raw	1.68E5	6	6	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	52.41	3544.7434	33	1.6	1182.5903	3	35.25	7	2421	OB3605.raw	1.26E5	6	6	477	509	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	52.28	2313.2019	20	-0.5	579.3074	4	31.03	7	1857	OB3605.raw	1.62E6	19	19	408	427	
R.SPDIYNPQAGSLK.T	N	99.8	42.01	1388.6936	13	0.6	695.3545	2	27.34	7	1373	OB3605.raw	2.22E4	4	4	371	383	
K.SQSENFEYVAFK.T	N	99.7	38.60	1447.6619	12	-0.1	724.8381	2	29.98	7	1716	OB3605.raw	2E4	1	1	465	476	
R.NRSPDIYNPQAGSLK.T	N	98.3	31.96	1658.8376	15	-0.5	553.9529	3	25.70	7	1229	OB3605.raw	3.95E3	1	1	369	383	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	98.1	28.66	1659.8217	15	0.8	554.2816	3	26.32	7	1278	OB3605.raw	6.42E3	2	2	369	383	Deamidation (NQ)
total 9 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GR**A HVQVVDSNGD R**VFDEELQEG HVLVVPQNFA VAGK**SQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	93.96	1540.7673	13	-0.1	771.3909	2	32.48	7	2049	OB3605.raw	5.16E5	13	13	395	407	
R.AHVQVVDSNGDR.V	Y	99.9	59.08	1295.6218	12	-1.1	648.8174	2	20.49	7	950	OB3605.raw	9.42E3	2	2	430	441	
K.TANELNLLILR.W	N	99.9	58.94	1268.7452	11	-0.2	635.3798	2	33.16	7	2139	OB3605.raw	1.68E5	6	6	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	52.41	3544.7434	33	1.6	1182.5903	3	35.25	7	2421	OB3605.raw	1.26E5	6	6	477	509	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	52.28	2313.2019	20	-0.5	579.3074	4	31.03	7	1857	OB3605.raw	1.62E6	19	19	408	427	
R.SPDIYNPQAGSLK.T	N	99.8	42.01	1388.6936	13	0.6	695.3545	2	27.34	7	1373	OB3605.raw	2.22E4	4	4	371	383	
K.SQSENFEYVAFK.T	N	99.7	38.60	1447.6619	12	-0.1	724.8381	2	29.98	7	1716	OB3605.raw	2E4	1	1	465	476	
R.NRSPDIYNPQAGSLK.T	N	98.3	31.96	1658.8376	15	-0.5	553.9529	3	25.70	7	1229	OB3605.raw	3.95E3	1	1	369	383	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	98.1	28.66	1659.8217	15	0.8	554.2816	3	26.32	7	1278	OB3605.raw	6.42E3	2	2	369	383	Deamidation (NQ)
total 9 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN

401 GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	86.1	22.38	2554.3066	23	-0.9	852.4421	3	31.22	7	1883	OB3605.raw	1.77E5	1	1	415	437	
total 1 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	86.1	22.38	2554.3066	23	-0.9	852.4421	3	31.22	7	1883	OB3605.raw	1.77E5	1	1	417	439	
total 1 peptides																		

E5G077|E5G077_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 7	#Spec	#Spec Sample 7	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	86.1	22.38	2554.3066	23	-0.9	852.4421	3	31.22	7	1883	OB3605.raw	1.77E5	1	1	417	439	
total 1 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

1. Notes

Spot 5 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

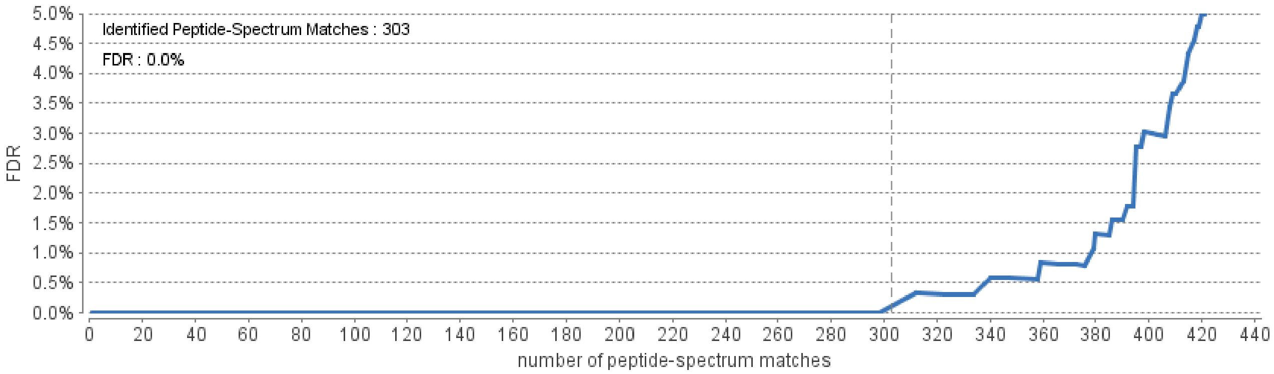
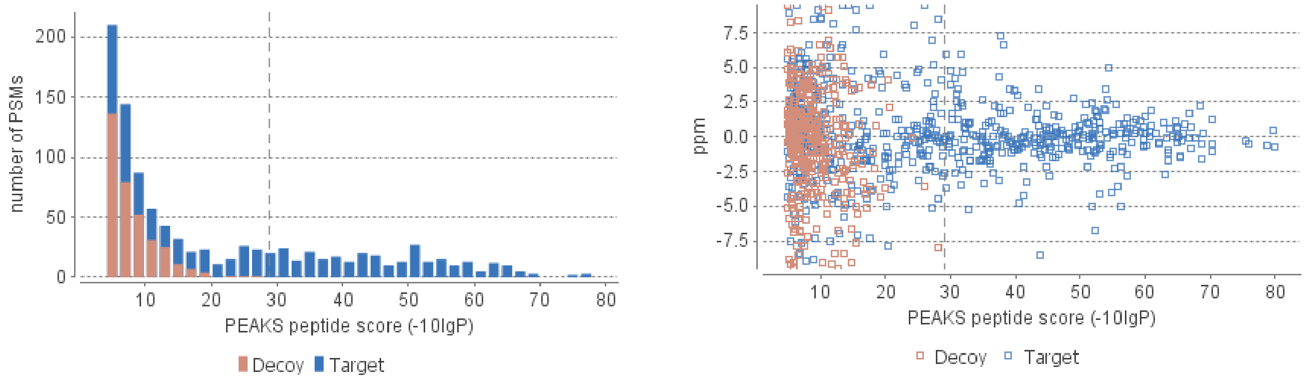


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

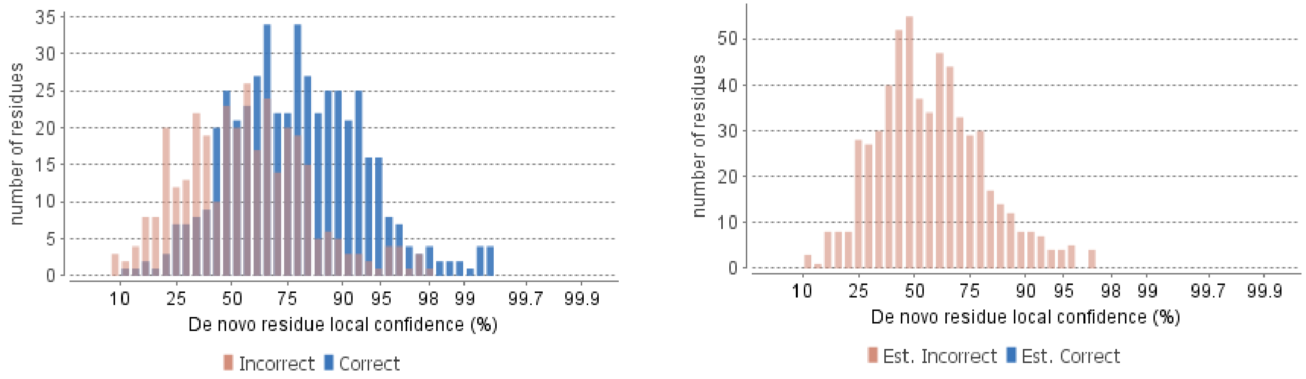


Table 1. Statistics of data.

# of MS scans	2921
# of MS/MS scans	3061

Table 2. Result filtration parameters.

Peptide -10lgP	≥29
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	285
Peptide sequences	62
Protein groups	2
Proteins	4
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 4 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	71

Table 4. PTM profile.

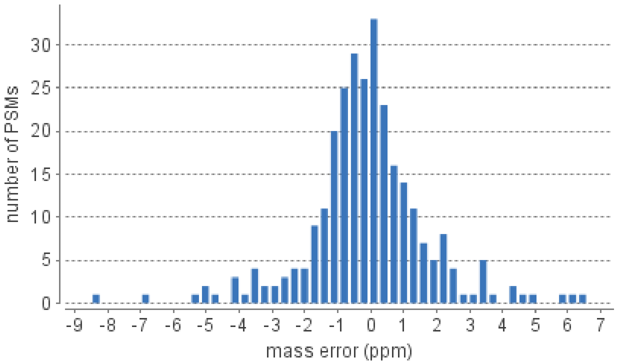
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	58	79.79	2E5	1000.00
Deamidation	.98	NQ	36	66.11		30.72
HydPro	15.99	P	25	66.99	3.83E5	83.88
Oxidation	15.99	M	7	52.90	2.43E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



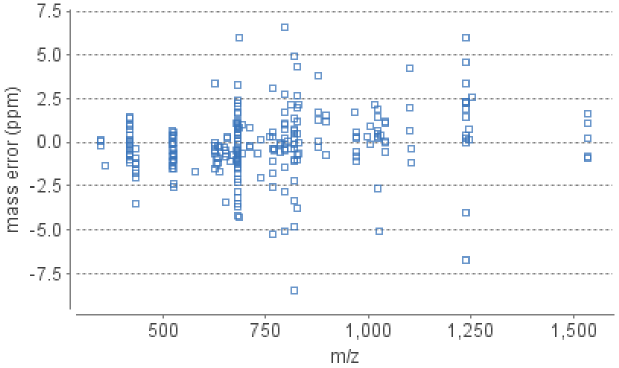


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 9	59	3	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3607.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:

Protein Sample Area >=
Protein Ptm Contains:

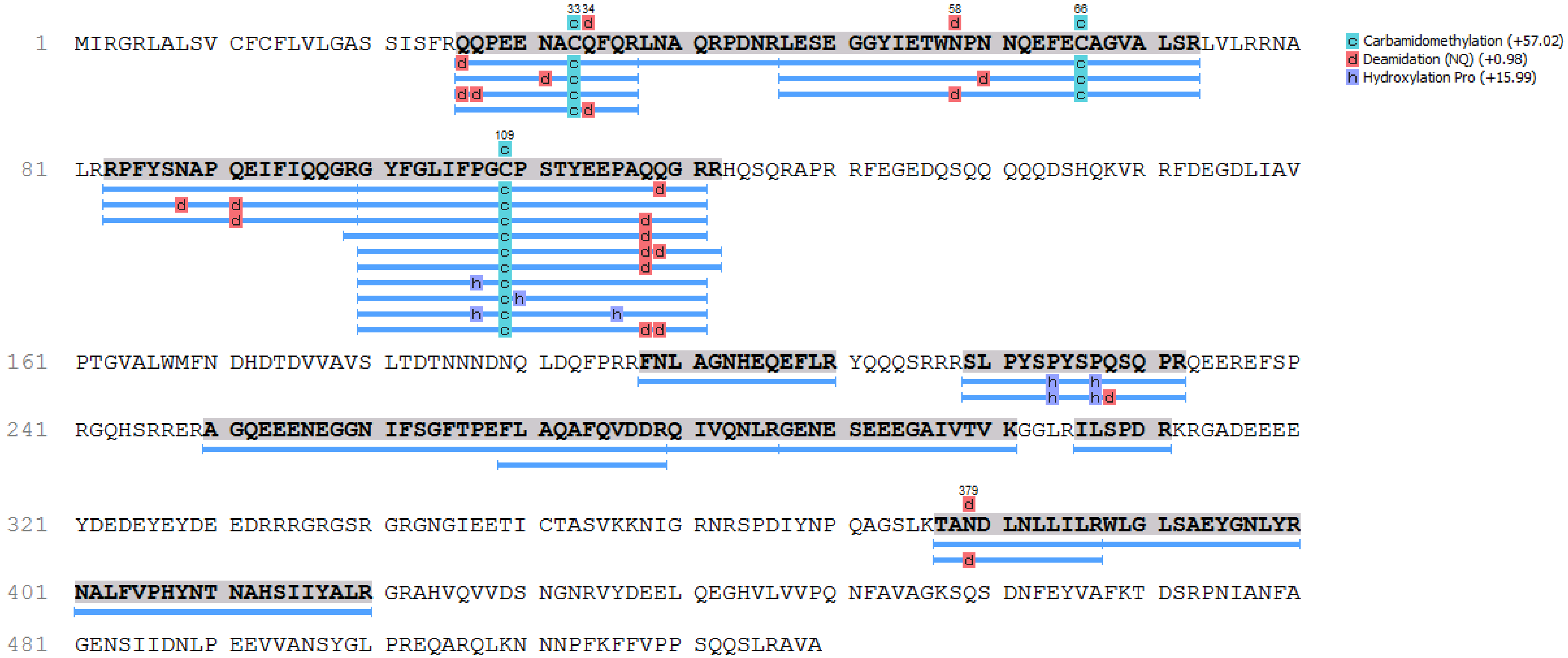
Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 9	Area Sample 9	#Peptides	#Unique	#Spec Sample 9	PTM	Avg. Mass	Description
1	13	Q9FZ11|Q9FZ11_ARAHY	99.2	229.99	41	41	1.18E5	17	1	182	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
8	41	Q6IWG5|Q6IWG5_ARAHY	83.8	56.10	7	7	4.93E4	2	1	3	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
8	42	Q0GM57|Q0GM57_ARAHY	83.8	56.10	7	7	4.93E4	2	1	3	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
8	45	E5G077|E5G077_ARAHY	83.8	56.10	7	7	4.93E4	2	1	3	Y	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
total 4 proteins													

Q9FZ11|Q9FZ11_ARAHY

back to list

| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



1 MIRGRLALSV CFCFLVLGAS SISFR**QQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSR**LVLRRNA

81 LR**RPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RR**HQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRR**FNL AGNHEQEFLR** YQQQSRRR**SL PYSPYSPQSQ PR**QEEREFSP

241 RGQHSRRER**A GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV K**GGLR**ILSPD R**KRGADEEEE

321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNRSPDIYNP QAGSLK**TAND LNLLILRWLG LSAEYGNLYR**

401 **NALFVPHYNT NAHSIIYALR** GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFKT DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 9	#Spec	#Spec Sample 9	Start	End	PTM
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	79.79	2473.1372	22	0.4	1237.5764	2	33.61	9	2192	OB3607.raw	9.53E5	15	15	100	121	Carbamidomethylation
R.WLGLSAEYGNLYR.N	N	99.9	75.99	1540.7673	13	-0.5	771.3906	2	32.18	9	2002	OB3607.raw	6.36E4	2	2	388	400	
R.GENESEEEGAIVTVK.G	Y	99.9	68.65	1589.7421	15	-0.5	795.8779	2	4.74	9	311	OB3607.raw	1.18E5	14	14	287	301	
R.SLPYSP(+15.99)YSP(+15.99)QSQPR.Q	N	99.9	66.99	1637.7684	14	0.7	819.8920	2	4.67	9	301	OB3607.raw	3.83E5	12	12	219	232	Hydroxylation Pro
R.RPFYSNAPQEIFIQQGR.G	N	99.9	66.94	2050.0383	17	-0.9	684.3528	3	3.87	9	185	OB3607.raw	1.02E6	49	49	83	99	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	66.11	2051.0225	17	0.8	684.6820	3	30.18	9	1752	OB3607.raw	0	1	1	83	99	Deamidation (NQ)

R.FNLAGNHEQEFLR.Y	N	99.9	65.12	1573.7637	13	0.0	787.8891	2	28.51	9	1585	OB3607.raw	3.06E5	17	17	198	210	
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	60.10	2474.1211	22	1.4	1238.0696	2	33.75	9	2210	OB3607.raw	3.65E5	5	5	100	121	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	57.15	3069.3774	27	0.3	1024.1334	3	32.40	9	2031	OB3607.raw	4.9E5	9	9	47	73	Carbamidomethylation
E.FLAQAFQVDDR.Q	N	99.9	56.24	1308.6462	11	0.3	655.3306	2	29.48	9	1672	OB3607.raw	7.99E3	2	2	269	279	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	54.98	2489.1321	22	0.1	1245.5735	2	33.34	9	2155	OB3607.raw	3.94E4	2	2	100	121	Hydroxylation Pro; Carbamidomethylation
K.TANDLNLLILR.W	N	99.9	54.54	1254.7296	11	-1.5	628.3712	2	32.45	9	2038	OB3607.raw	7.38E4	5	5	377	387	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPR.Q	N	99.9	54.33	1638.7524	14	5.0	820.3876	2	4.87	9	331	OB3607.raw	8.55E3	3	3	219	232	Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.9	54.24	2474.1211	22	2.6	825.7165	3	34.23	9	2275	OB3607.raw	2.7E5	3	3	100	121	Carbamidomethylation; Deamidation (NQ)
R.AGQEEENEGGNIFSGFTPEFLAQAFQVDDR.Q	N	99.9	53.68	3301.4800	30	2.0	1101.5028	3	36.90	9	2532	OB3607.raw	8.51E4	3	3	250	279	
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.9	51.28	2489.1321	22	0.0	830.7180	3	33.30	9	2151	OB3607.raw	3.21E4	3	3	100	121	Carbamidomethylation; Hydroxylation Pro
R.LESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	99.8	46.72	3070.3613	27	1.4	1024.4625	3	32.67	9	2067	OB3607.raw	1.78E5	2	2	47	73	Deamidation (NQ); Carbamidomethylation
K.TAN(+.98)DLNLLILR.W	N	99.8	45.03	1255.7136	11	0.0	628.8641	2	33.17	9	2133	OB3607.raw	4.4E3	2	2	377	387	Deamidation (NQ)
R.LESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	99.8	44.88	3070.3613	27	0.5	1024.4615	3	32.85	9	2091	OB3607.raw	1.63E5	1	1	47	73	Deamidation (NQ); Carbamidomethylation
R.QIVQNLR.G	N	99.8	43.79	869.5083	7	-0.4	435.7613	2	3.86	9	183	OB3607.raw	3.48E5	11	11	280	286	
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.5	41.28	2052.0063	17	-4.3	685.0065	3	30.70	9	1814	OB3607.raw	1.59E3	3	3	83	99	Deamidation (NQ)
R.ILSPDR.K	N	99.2	38.24	699.3915	6	0.1	350.7031	2	20.94	9	1230	OB3607.raw	1.01E5	3	3	306	311	
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.2	38.13	2631.2063	23	1.7	878.0775	3	32.27	9	2013	OB3607.raw	8.51E4	3	3	100	122	Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	98.9	36.49	1534.6470	12	-2.6	768.3288	2	5.17	9	376	OB3607.raw	3.53E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	98.9	36.18	1534.6470	12	-1.1	768.3300	2	5.49	9	424	OB3607.raw	9.79E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	98.9	36.05	1534.6470	12	-1.8	768.3294	2	5.80	9	466	OB3607.raw	9.79E3	1	1	26	37	Carbamidomethylation; Deamidation (NQ)
R.LNAQRPDNR.L	N	98.9	35.26	1082.5581	9	-1.3	361.8595	3	6.29	9	523	OB3607.raw	3.72E4	1	1	38	46	
R.NALFVPHYNTNAHSIIYALR.G	N	98.9	34.76	2313.2019	20	-1.7	579.3068	4	31.08	9	1858	OB3607.raw	5.88E4	1	1	401	420	
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	97.6	33.17	1535.6311	12	-1.8	768.8215	2	5.66	9	448	OB3607.raw	0	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	N	97.5	32.14	2630.2224	23	-0.2	877.7479	3	32.58	9	2055	OB3607.raw	1.64E5	1	1	100	122	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	97.5	31.29	2475.1052	22	3.4	1238.5641	2	34.76	9	2343	OB3607.raw	4.73E3	2	2	100	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEP(+15.99)AQQGR.R	N	96.5	30.95	2505.1270	22	2.6	1253.5740	2	34.12	9	2261	OB3607.raw	0	1	1	100	121	Hydroxylation Pro; Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	96.2	29.75	2630.2224	23	0.0	877.7481	3	31.96	9	1973	OB3607.raw	1.22E5	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
total 33 peptides																		

Q6IWG5|Q6IWG5_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQR**LNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR** TVLRRNALRR

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 9	#Spec	#Spec Sample 9	Start	End	PTM
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.3	38.47	3084.3882	27	0.4	1029.1371	3	33.48	9	2174	OB3607.raw	4.93E4	2	2	44	70	Hydroxylation Pro; Carbamidomethylation
R.LNAQRPDNR.I	N	98.9	35.26	1082.5581	9	-1.3	361.8595	3	6.29	9	523	OB3607.raw	3.72E4	1	1	35	43	
total 2 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 9	#Spec	#Spec Sample 9	Start	End	PTM
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.3	38.47	3084.3882	27	0.4	1029.1371	3	33.48	9	2174	OB3607.raw	4.93E4	2	2	46	72	Hydroxylation Pro; Carbamidomethylation
R.LNAQRPDNR.I	N	98.9	35.26	1082.5581	9	-1.3	361.8595	3	6.29	9	523	OB3607.raw	3.72E4	1	1	37	45	
total 2 peptides																		

E5G077|E5G077_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 9	#Spec	#Spec Sample 9	Start	End	PTM
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.3	38.47	3084.3882	27	0.4	1029.1371	3	33.48	9	2174	OB3607.raw	4.93E4	2	2	46	72	Hydroxylation Pro; Carbamidomethylation
R.LNAQRPDNR.I	N	98.9	35.26	1082.5581	9	-1.3	361.8595	3	6.29	9	523	OB3607.raw	3.72E4	1	1	37	45	
total 2 peptides																		

Peptide List

1. Notes

Spot 7 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

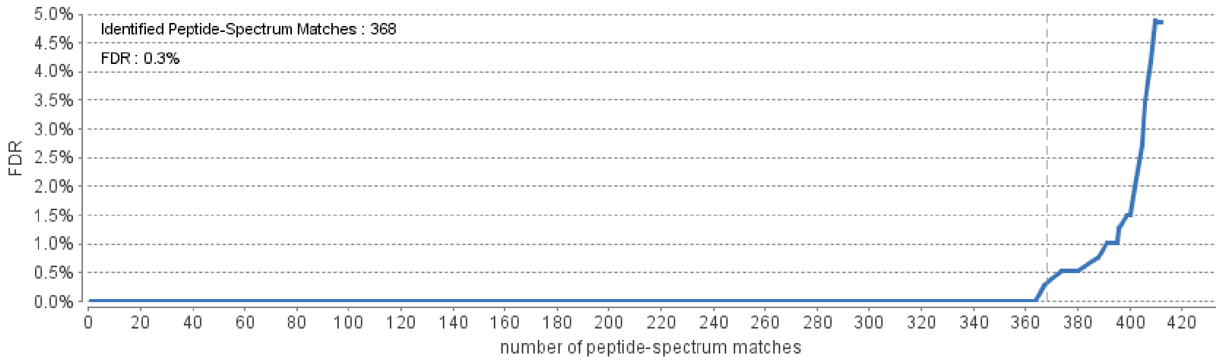
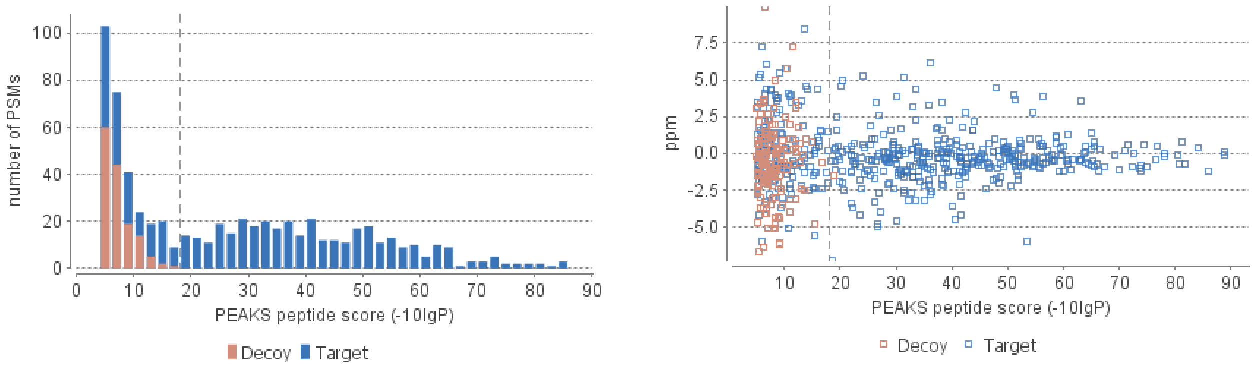


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

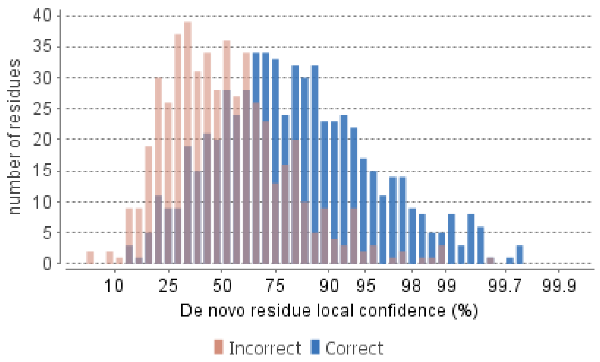

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



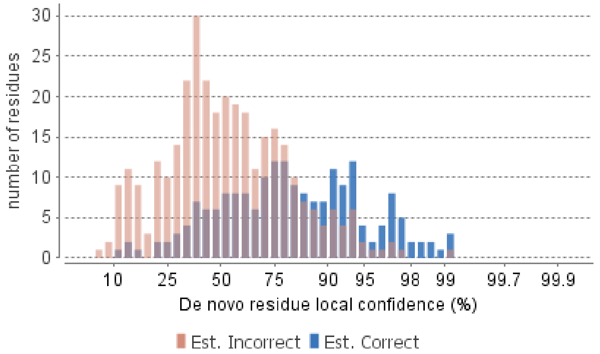


Table 1. Statistics of data.

# of MS scans	2768
# of MS/MS scans	3990

Table 2. Result filtration parameters.

Peptide -10lgP	≥18
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	345
Peptide sequences	128
Protein groups	6
Proteins	12
Proteins (#Unique Peptides)	3 (>2); 3 (=2); 6 (=1);
FDR (Peptide-Spectrum Matches)	0.3%
FDR (Peptide Sequences)	0.8%
FDR (Protein)	0.0%
De Novo Only Spectra	50

Table 4. PTM profile.

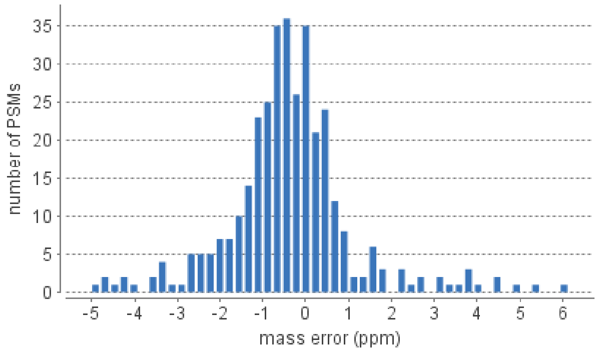
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Oxidation	15.99	M	91	88.73	1.68E4	1000.00
Deamidation	.98	NQ	59	88.73	1.68E4	0.00
Carbamidomethyl	57.02	C	59	88.73	1.68E4	1000.00
HydPro	15.99	P	12	35.76	5E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



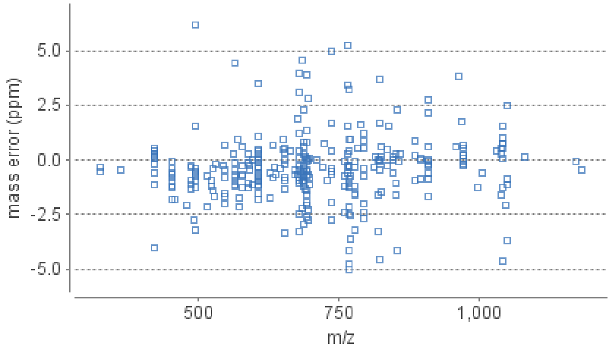


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 10	113	15	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3608.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 10	Area Sample 10	#Peptides	#Unique	#Spec Sample 10	PTM	Avg. Mass	Description
1	69	Q6PSU5|Q6PSU5_ARAHY	99.1	263.37	45	45	9.31E5	20	7	194	Y	33604	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
1	18	N1NG13|N1NG13_ARAHY	99.1	263.37	21	21	9.31E5	20	7	194	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
1	20	sp|P43238|ALL12_ARAHY	99.1	263.37	21	21	9.31E5	20	7	194	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
2	26	Q6PSU3|Q6PSU3_ARAHY	99.1	230.39	17	17	1.3E3	14	1	164	Y	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
2	23	B3IXL2|B3IXL2_ARAHY	99.1	230.39	16	16	1.3E3	14	1	164	Y	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
2	21	sp|P43237|ALL11_ARAHY	99.1	230.39	16	16	1.3E3	14	1	164	Y	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
2	57	Q6PSU6|Q6PSU6_ARAHY	99.1	230.39	33	33	1.3E3	14	1	164	Y	34133	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
3	13	Q9FZ11|Q9FZ11_ARAHY	99.1	160.62	36	36	3.27E4	13	2	46	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
7	2	A1DZF0|A1DZF0_ARAHY	99.1	147.70	37	37	3.91E3	12	1	40	Y	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
5	15	Q647H3|Q647H3_ARAHY	99.1	146.57	37	37	6.76E3	12	1	41	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
12	41	Q6IWG5|Q6IWG5_ARAHY	97.9	55.98	12	12	6.44E4	3	2	4	N	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
12	42	Q0GM57|Q0GM57_ARAHY	97.9	55.98	12	12	6.44E4	3	2	4	N	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 12 proteins													

Q6PSU5|Q6PSU5_ARAHY

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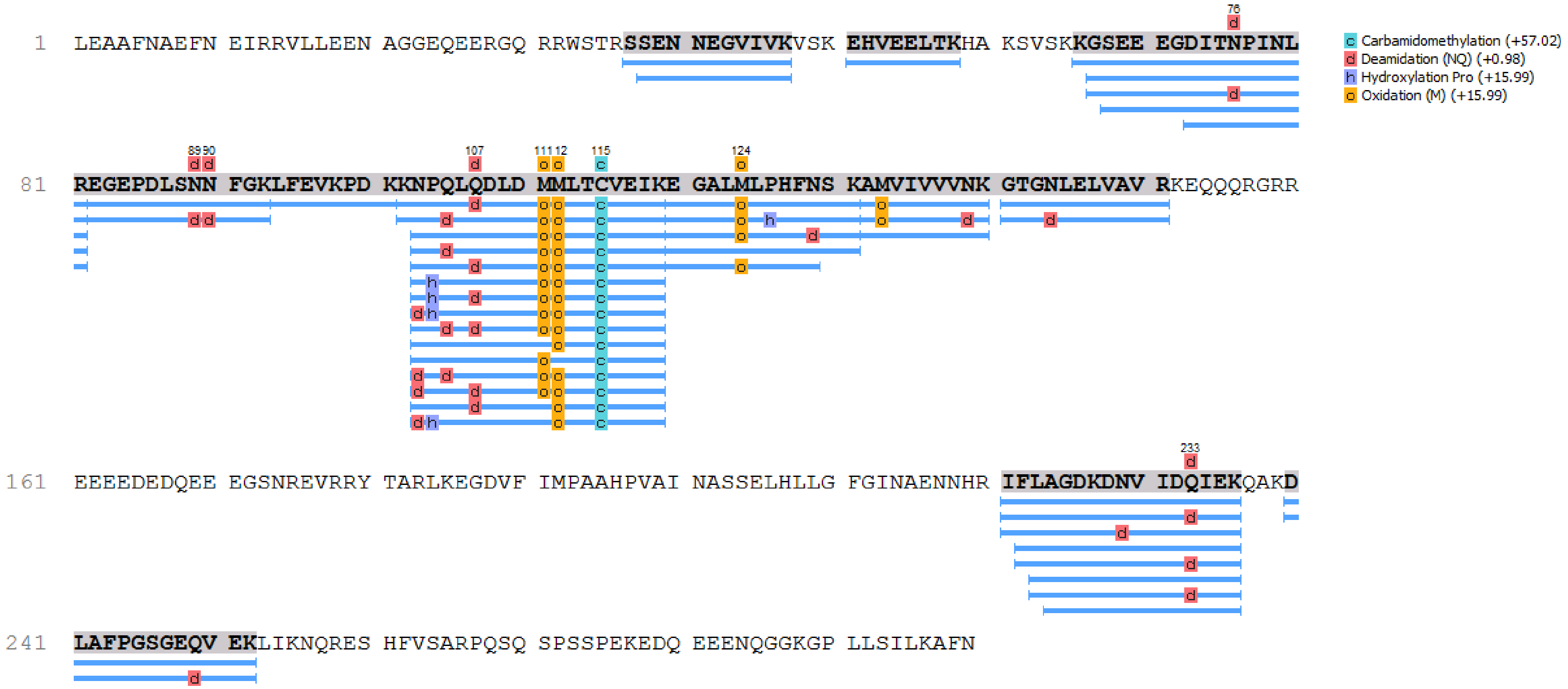
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
K.GSEEEGDITNPINLR.E	Y	99.9	88.96	1642.7798	15	-0.1	822.3971	2	29.01	10	1628	OB3608.raw	3.64E5	10	10	67	81	
																		Deamidation (NQ);

K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	103	119	Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	103	119	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	221	236	
R.EGEPDLSNNFGK.L	Y	99.9	78.16	1305.5836	12	0.0	653.7991	2	26.86	10	1384	OB3608.raw	3.66E5	6	6	82	93	
K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	141	151	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	103	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	132	140	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	103	119	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	103	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	120	131	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	240	252	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	132	140	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	224	236	
K.KGSEEEGDITNPINLR.E	Y	99.9	56.99	1770.8748	16	0.2	886.4448	2	27.48	10	1441	OB3608.raw	1.44E5	5	5	66	81	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	103	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	221	236	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	240	252	Deamidation (NQ)
K.GSEEEGDITN(+.98)PINLR.E	Y	99.9	51.34	1643.7638	15	3.7	822.8922	2	29.78	10	1729	OB3608.raw	0	2	2	67	81	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	120	131	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	102	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	223	236	
R.EGEPDLSN(+.98)N(+.98)FGK.L	Y	99.9	48.70	1307.5516	12	-0.8	654.7826	2	28.01	10	1494	OB3608.raw	0	1	1	82	93	Deamidation (NQ)
G.SEEEGDITNPINLR.E	Y	99.9	48.46	1585.7583	14	-2.0	793.8848	2	28.94	10	1619	OB3608.raw	1.1E4	1	1	68	81	
R.SSENNEGVIVK.V	Y	99.9	48.08	1174.5830	11	-1.1	588.2982	2	22.56	10	1086	OB3608.raw	2.81E4	4	4	37	47	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	141	151	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	120	131	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	222	236	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	222	236	Deamidation (NQ)
K.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	94	101	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	103	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	221	236	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	103	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	132	140	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	120	131	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	223	236	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	103	119	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
G.DITNPINLR.E	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	73	81	
K.EHVEELTK.H	Y	98.2	32.67	983.4924	8	-2.8	492.7521	2	20.40	10	984	OB3608.raw	1.33E4	1	1	51	58	
K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	103	119	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation

K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	120	129	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	103	119	Hydroxylation Pro; Deamidation (NQ); Oxidation (M); Carbamidomethylation
S.SENNEGVIVK.V	Y	79.9	22.47	1087.5509	10	-0.2	544.7826	2	22.67	10	1094	OB3608.raw	4.64E3	1	1	38	47	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	103	119	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	102	119	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	103	119	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
total 46 peptides																		

N1NG13|N1NG13_ARAHY

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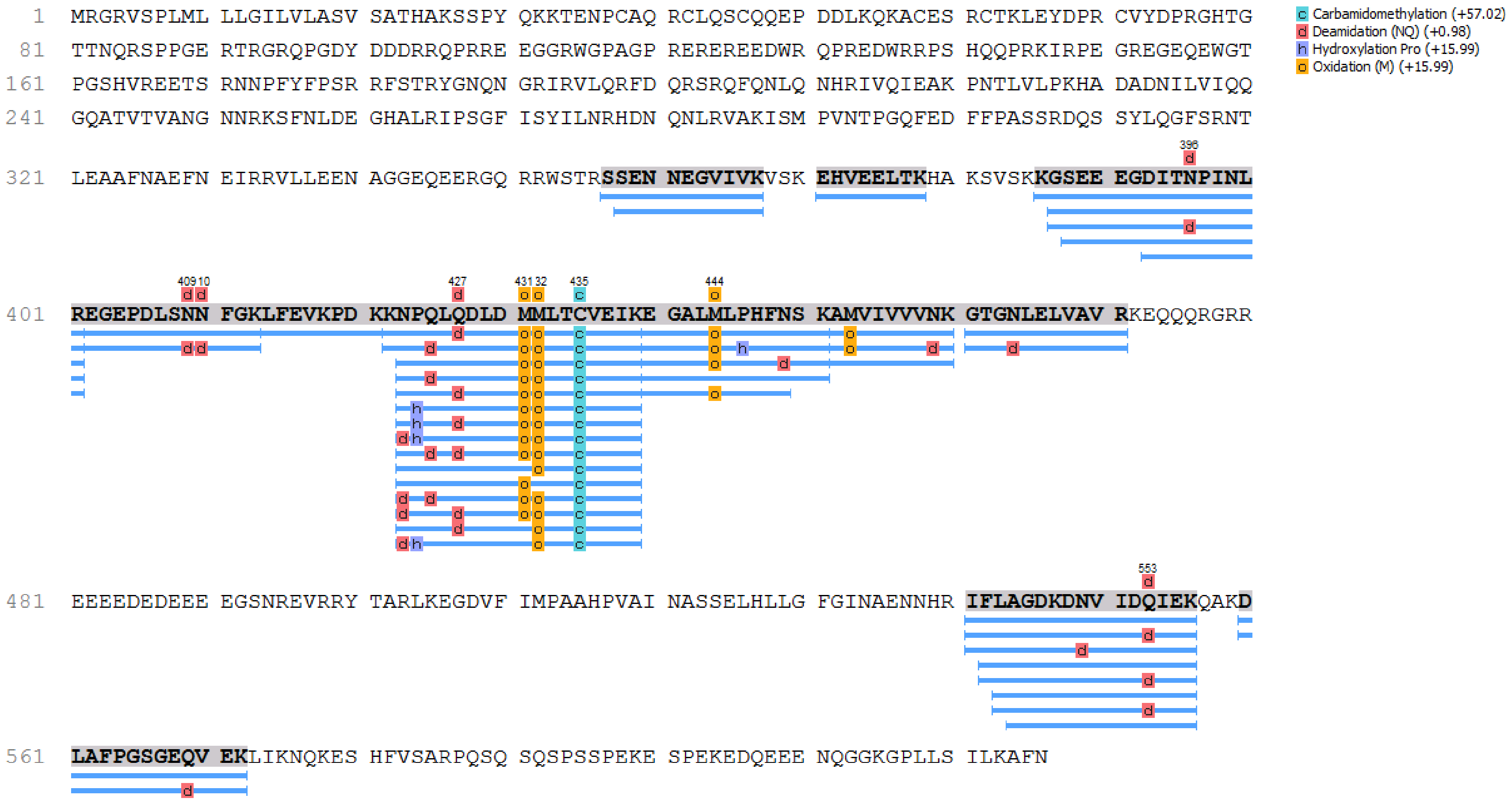
| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG

81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ

241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT

321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTR**SSEN NEGVIVK**VSK **EHVEELTK**HA KSVSK**KGSEE EGDITNPINL**

401 **REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV R**KEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM

K.GSEEEGDITNPINLR.E	Y	99.9	88.96	1642.7798	15	-0.1	822.3971	2	29.01	10	1628	OB3608.raw	3.64E5	10	10	387	401	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	423	439	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	541	556	
R.EGEPDLSNNFGK.L	Y	99.9	78.16	1305.5836	12	0.0	653.7991	2	26.86	10	1384	OB3608.raw	3.66E5	6	6	402	413	
K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	461	471	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	452	460	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	423	439	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	440	451	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	560	572	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	452	460	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	544	556	
K.KGSEEEGDITNPINLR.E	Y	99.9	56.99	1770.8748	16	0.2	886.4448	2	27.48	10	1441	OB3608.raw	1.44E5	5	5	386	401	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	541	556	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	560	572	Deamidation (NQ)
K.GSEEEGDITN(+.98)PINLR.E	Y	99.9	51.34	1643.7638	15	3.7	822.8922	2	29.78	10	1729	OB3608.raw	0	2	2	387	401	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	440	451	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	422	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	543	556	
R.EGEPDLSN(+.98)N(+.98)FGK.L	Y	99.9	48.70	1307.5516	12	-0.8	654.7826	2	28.01	10	1494	OB3608.raw	0	1	1	402	413	Deamidation (NQ)
G.SEEEGDITNPINLR.E	Y	99.9	48.46	1585.7583	14	-2.0	793.8848	2	28.94	10	1619	OB3608.raw	1.1E4	1	1	388	401	
R.SSENNEGVIVK.V	Y	99.9	48.08	1174.5830	11	-1.1	588.2982	2	22.56	10	1086	OB3608.raw	2.81E4	4	4	357	367	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	461	471	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	440	451	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	542	556	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	542	556	Deamidation (NQ)
K.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	414	421	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	541	556	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	452	460	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	440	451	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	543	556	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	423	439	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
G.DITNPINLR.E	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	393	401	
K.EHVEELTK.H	Y	98.2	32.67	983.4924	8	-2.8	492.7521	2	20.40	10	984	OB3608.raw	1.33E4	1	1	371	378	
																		Deamidation (NQ);

K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	423	439	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	440	449	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	423	439	Hydroxylation Pro; Deamidation (NQ); Oxidation (M); Carbamidomethylation
S.SENNEGVIVK.V	Y	79.9	22.47	1087.5509	10	-0.2	544.7826	2	22.67	10	1094	OB3608.raw	4.64E3	1	1	358	367	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	423	439	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	422	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	423	439	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
total 46 peptides																		

sp|P43238|ALL12_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTR**SSEN NEGVIVK**VSK **EHVEELTK**HA KSVSK**KGSEE EGDITNPINL**
401 **REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV R**KEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**
561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
K.GSEEEGDITNPINLR.E	Y	99.9	88.96	1642.7798	15	-0.1	822.3971	2	29.01	10	1628	OB3608.raw	3.64E5	10	10	387	401	
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	423	439	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	541	556	
R.EGEPDLSNNFGK.L	Y	99.9	78.16	1305.5836	12	0.0	653.7991	2	26.86	10	1384	OB3608.raw	3.66E5	6	6	402	413	
K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	461	471	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	452	460	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	423	439	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	440	451	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	560	572	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	452	460	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	544	556	
K.KGSEEEGDITNPINLR.E	Y	99.9	56.99	1770.8748	16	0.2	886.4448	2	27.48	10	1441	OB3608.raw	1.44E5	5	5	386	401	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	541	556	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	560	572	Deamidation (NQ)
K.GSEEEGDITN(+.98)PINLR.E	Y	99.9	51.34	1643.7638	15	3.7	822.8922	2	29.78	10	1729	OB3608.raw	0	2	2	387	401	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	440	451	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	422	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	543	556	
R.EGEPDLSN(+.98)N(+.98)FGK.L	Y	99.9	48.70	1307.5516	12	-0.8	654.7826	2	28.01	10	1494	OB3608.raw	0	1	1	402	413	Deamidation (NQ)
G.SEEEGDITNPINLR.E	Y	99.9	48.46	1585.7583	14	-2.0	793.8848	2	28.94	10	1619	OB3608.raw	1.1E4	1	1	388	401	
R.SSENNEGVIVK.V	Y	99.9	48.08	1174.5830	11	-1.1	588.2982	2	22.56	10	1086	OB3608.raw	2.81E4	4	4	357	367	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	461	471	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	440	451	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	542	556	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	542	556	Deamidation (NQ)
K.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	414	421	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	541	556	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	452	460	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	440	451	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	543	556	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	423	439	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
G.DITNPINLR.E	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	393	401	

K.EHVEELTK.H	Y	98.2	32.67	983.4924	8	-2.8	492.7521	2	20.40	10	984	OB3608.raw	1.33E4	1	1	371	378	
K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	423	439	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	440	449	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	423	439	Hydroxylation Pro; Deamidation (NQ); Oxidation (M); Carbamidomethylation
S.SENNEGVIVK.V	Y	79.9	22.47	1087.5509	10	-0.2	544.7826	2	22.67	10	1094	OB3608.raw	4.64E3	1	1	358	367	
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	423	439	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	422	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	423	439	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
total 46 peptides																		

Q6PSU3|Q6PSU3_ARAHY

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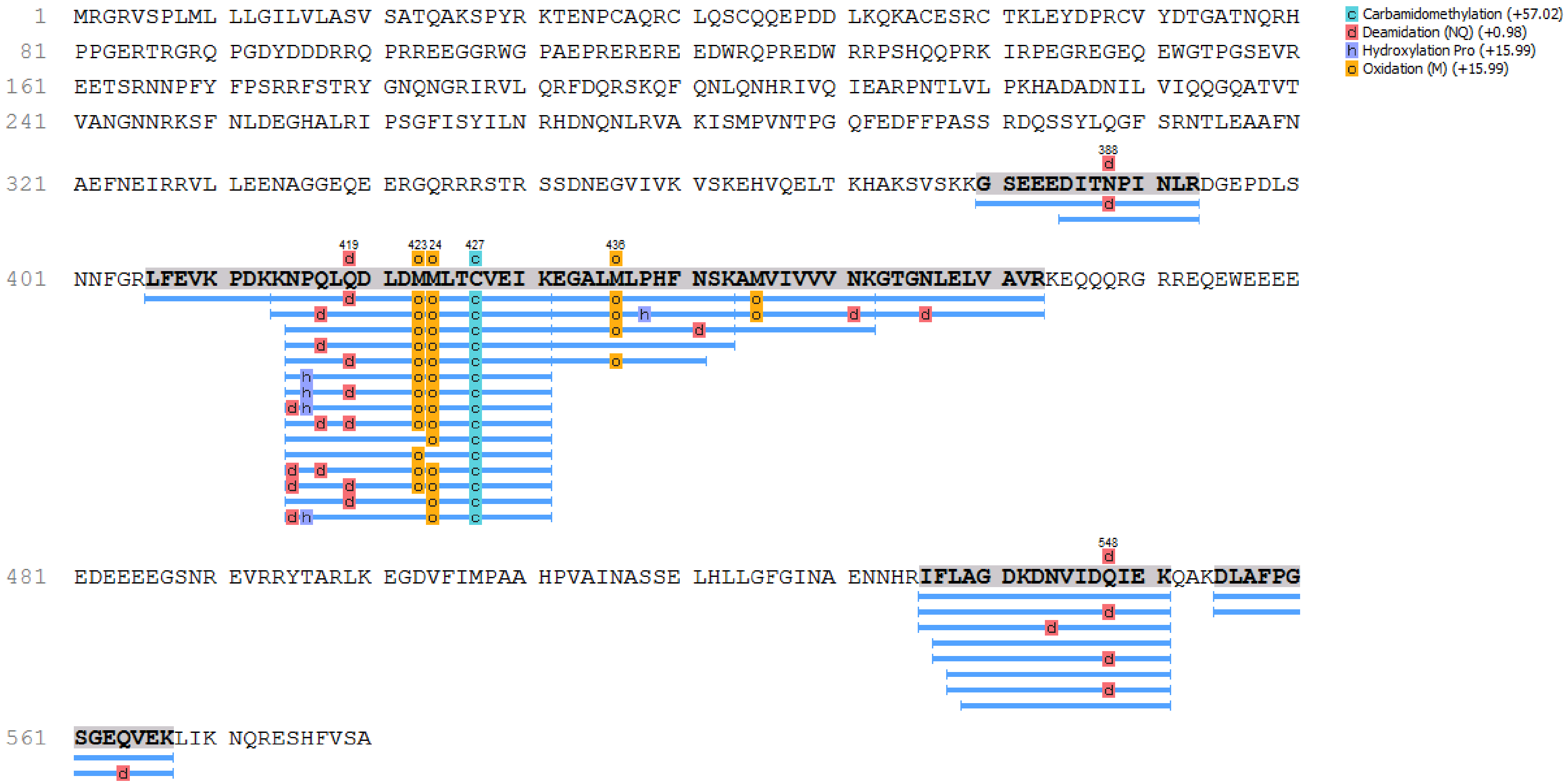
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKK**G SEEEDITNPI NLR**DGEPDLS
401 NNFGR**LFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVR**KEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**
561 **SGEQVEK**LIK NQRESHFVSA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	415	431	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	536	551	
K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	453	463	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	444	452	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	415	431	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	432	443	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	555	567	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	444	452	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	539	551	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	536	551	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	555	567	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	432	443	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	538	551	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	453	463	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	432	443	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	537	551	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	537	551	Deamidation (NQ)
R.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	406	413	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	536	551	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	444	452	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	432	443	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	538	551	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	415	431	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
E.DITNPINLR.D	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	385	393	
K.GSEEEDITN(+.98)PINLR.D	Y	97.9	31.32	1586.7423	14	-2.7	794.3763	2	29.40	10	1679	OB3608.raw	1.3E3	1	1	380	393	Deamidation (NQ)
K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	415	431	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	432	441	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	415	431	Hydroxylation Pro; Deamidation (NQ);

																		Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	415	431	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
total 38 peptides																		

B3IXL2|B3IXL2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKK**G SEEEDITNPI NLR**DGEPDLS
401 NNFGR**LFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVR**KEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**
561 **SGEQVEK**LIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	415	431	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	536	551	

K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	453	463	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	444	452	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	415	431	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	432	443	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	555	567	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	444	452	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	539	551	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	536	551	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	555	567	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	432	443	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	538	551	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	453	463	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	432	443	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	537	551	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	537	551	Deamidation (NQ)
R.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	406	413	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	536	551	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	444	452	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	432	443	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	538	551	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	415	431	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
E.DITNPINLR.D	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	385	393	
K.GSEEEDITN(+.98)PINLR.D	Y	97.9	31.32	1586.7423	14	-2.7	794.3763	2	29.40	10	1679	OB3608.raw	1.3E3	1	1	380	393	Deamidation (NQ)
K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	415	431	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	432	441	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	415	431	Hydroxylation Pro; Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	415	431	Deamidation (NQ); Hydroxylation Pro; Oxidation (M);

																	Carbamidomethylation

total 38 peptides

sp|P43237|ALL11_ARAHY

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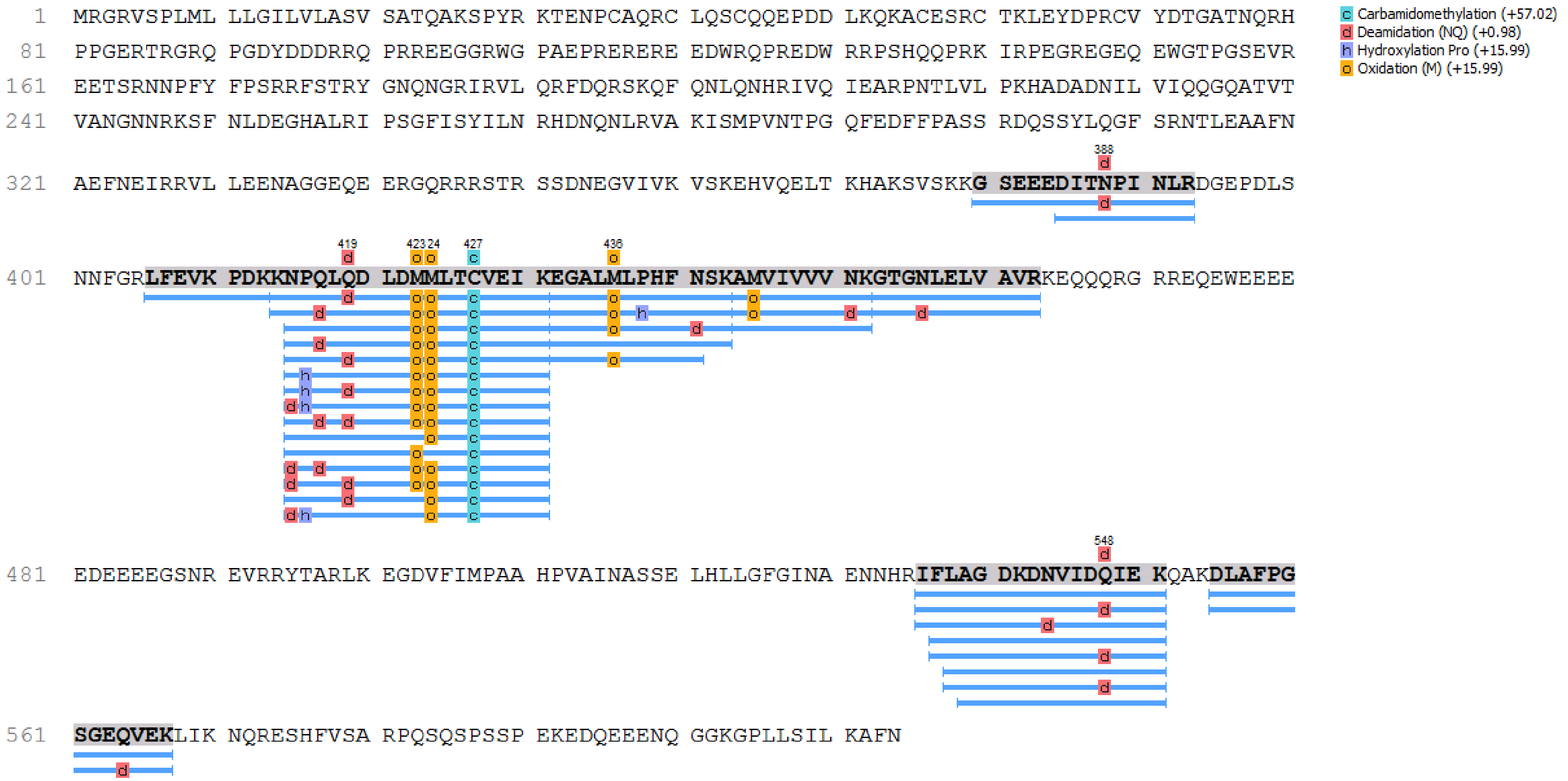
Protein Coverage:



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161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKK**G SEEEDITNPI NLR**DGEPDLS
401 NNFGR**LFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVR**KEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**
561 **SGEQVEK**LIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	415	431	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	536	551	
K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	453	463	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	444	452	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	415	431	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	415	431	Deamidation (NQ); Oxidation (M);

																		Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	432	443	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	555	567	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	444	452	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	539	551	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	536	551	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	555	567	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	432	443	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	538	551	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	453	463	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	432	443	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	537	551	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	537	551	Deamidation (NQ)
R.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	406	413	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	536	551	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	444	452	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	432	443	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	538	551	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	415	431	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
E.DITNPINLR.D	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	385	393	
K.GSEEEDITN(+.98)PINLR.D	Y	97.9	31.32	1586.7423	14	-2.7	794.3763	2	29.40	10	1679	OB3608.raw	1.3E3	1	1	380	393	Deamidation (NQ)
K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	415	431	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	432	441	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	415	431	Hydroxylation Pro; Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	415	431	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	414	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	415	431	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
total 38 peptides																		

Q6PSU6|Q6PSU6_ARAHY

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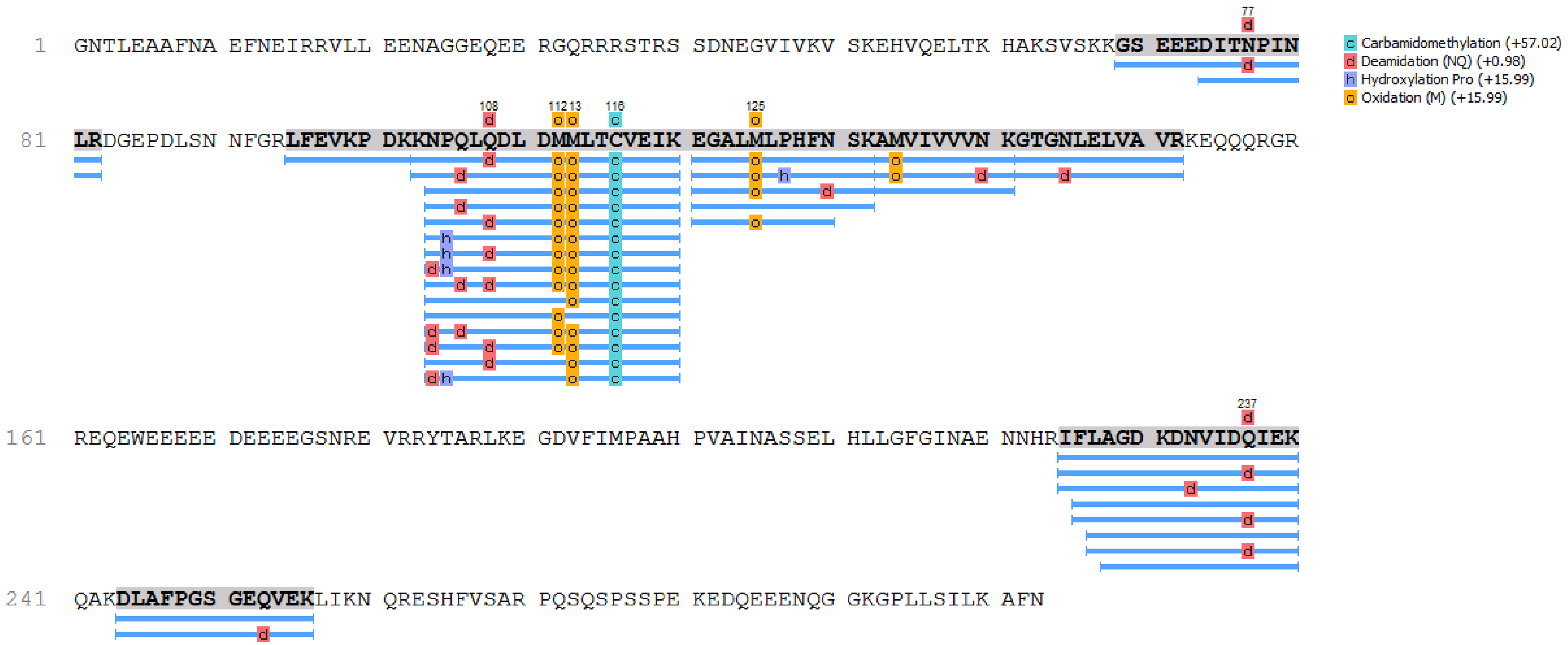
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
K.NPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	88.73	2079.9526	17	0.0	1040.9836	2	32.16	10	2046	OB3608.raw	6.76E4	6	6	104	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	84.04	2062.9736	17	0.4	1032.4945	2	32.52	10	2093	OB3608.raw	5.32E4	1	1	104	120	Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQIEK.Q	N	99.9	80.55	1816.9570	16	-0.1	909.4857	2	30.34	10	1805	OB3608.raw	8.34E6	39	39	225	240	
K.GTGNLELVAVR.K	N	99.9	76.60	1127.6299	11	-0.5	564.8220	2	28.48	10	1556	OB3608.raw	1.44E6	11	11	142	152	
K.N(+.98)PQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	73.89	2080.9368	17	-1.2	1041.4744	2	32.53	10	2095	OB3608.raw	1.35E4	1	1	104	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AMVIVVVNK.G	N	99.9	69.93	971.5837	9	-1.2	486.7986	2	28.00	10	1493	OB3608.raw	4.43E4	3	3	133	141	
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	66.57	2078.9688	17	0.3	1040.4919	2	31.89	10	2010	OB3608.raw	8.2E5	11	11	104	120	Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	65.55	2079.9526	17	0.8	694.3254	3	31.98	10	2021	OB3608.raw	5.26E4	4	4	104	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFNSK.A	N	99.9	65.39	1358.6653	12	-0.9	680.3393	2	28.70	10	1586	OB3608.raw	1.78E6	20	20	121	132	Oxidation (M)
K.DLAFPGSGEQVEK.L	N	99.9	62.87	1375.6619	13	-0.6	688.8378	2	28.62	10	1575	OB3608.raw	4.49E5	12	12	244	256	
K.AM(+15.99)VIVVVNK.G	N	99.9	62.72	987.5787	9	-0.6	494.7963	2	25.50	10	1264	OB3608.raw	1.72E5	10	10	133	141	Oxidation (M)
L.AGDKDNVIDQIEK.Q	N	99.9	57.45	1443.7205	13	-0.4	722.8672	2	30.22	10	1789	OB3608.raw	2.2E4	1	1	228	240	
K.NPQLQ(+.98)DLDMM(+15.99)LTC(+57.02)VEIK.E	N	99.9	54.38	2063.9578	17	-0.9	688.9926	3	32.91	10	2145	OB3608.raw	1.21E4	1	1	104	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDNVIDQ(+.98)IEK.Q	N	99.9	53.83	1817.9410	16	-0.6	606.9872	3	28.92	10	1616	OB3608.raw	1E5	3	3	225	240	Deamidation (NQ)
K.DLAFPGSGEQ(+.98)VEK.L	N	99.9	52.86	1376.6459	13	-0.8	689.3297	2	28.97	10	1623	OB3608.raw	7.97E4	1	1	244	256	Deamidation (NQ)
K.EGALM(+15.99)LPHFN(+.98)SK.A	N	99.9	51.20	1359.6493	12	3.9	680.8346	2	29.13	10	1642	OB3608.raw	2.16E5	3	3	121	132	Oxidation (M); Deamidation (NQ)
K.KNPQ(+.98)LQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.9	51.18	2208.0476	18	-0.5	737.0228	3	30.75	10	1859	OB3608.raw	4.9E4	1	1	103	120	Deamidation (NQ); Oxidation (M);

																		Carbamidomethylation
F.LAGDKDNVIDQIEK.Q	N	99.9	48.71	1556.8046	14	-1.6	779.4083	2	30.21	10	1787	OB3608.raw	5.76E4	4	4	227	240	
K.GTGN(+.98)LELVAVR.K	N	99.9	47.82	1128.6139	11	4.4	565.3167	2	29.11	10	1639	OB3608.raw	5.27E4	1	1	142	152	Deamidation (NQ)
K.EGALMLPHFNSK.A	N	99.8	44.12	1342.6703	12	-0.5	672.3421	2	29.07	10	1636	OB3608.raw	9.42E3	1	1	121	132	
I.FLAGDKDNVIDQIEK.Q	N	99.8	42.30	1703.8729	15	-1.6	852.9424	2	30.21	10	1788	OB3608.raw	2.73E4	1	1	226	240	
I.FLAGDKDNVIDQ(+.98)IEK.Q	N	99.8	41.58	1704.8569	15	-4.2	853.4322	2	30.73	10	1857	OB3608.raw	1.72E3	1	1	226	240	Deamidation (NQ)
R.LFEVKPDK.K	N	99.6	38.95	974.5436	8	-0.3	488.2790	2	24.37	10	1191	OB3608.raw	8.33E4	5	5	95	102	
K.NPQ(+.98)LQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.6	38.46	2080.9368	17	-2.2	694.6513	3	32.50	10	2091	OB3608.raw	2.49E4	1	1	104	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IFLAGDKDN(+.98)VIDQIEK.Q	N	99.6	38.30	1817.9410	16	3.5	606.9897	3	30.84	10	1871	OB3608.raw	3.88E5	1	1	225	240	Deamidation (NQ)
K.N(+.98)PQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.2	36.25	2080.9368	17	-2.8	694.6509	3	32.66	10	2112	OB3608.raw	3.83E4	2	2	104	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.AM(+15.99)VIVVVN(+.98)K.G	N	99.2	36.06	988.5627	9	6.1	495.2917	2	26.20	10	1323	OB3608.raw	6.95E3	2	2	133	141	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LP(+15.99)HFNSK.A	N	99.2	35.76	1374.6602	12	-1.8	459.2265	3	28.93	10	1617	OB3608.raw	5E4	1	1	121	132	Oxidation (M); Hydroxylation Pro
F.LAGDKDNVIDQ(+.98)IEK.Q	N	99.2	35.13	1557.7886	14	-3.2	779.8990	2	30.70	10	1853	OB3608.raw	7.34E3	2	2	227	240	Deamidation (NQ)
K.NP(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	99.1	34.51	2094.9636	17	-0.8	699.3279	3	32.03	10	2028	OB3608.raw	6.55E4	3	3	104	120	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
E.DITNPINLR.D	N	98.2	32.88	1054.5771	9	-1.6	528.2950	2	29.21	10	1653	OB3608.raw	4.27E3	1	1	74	82	
K.GSEEEDITN(+.98)PINLR.D	Y	97.9	31.32	1586.7423	14	-2.7	794.3763	2	29.40	10	1679	OB3608.raw	1.3E3	1	1	69	82	Deamidation (NQ)
K.N(+.98)P(+15.99)QLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	97.8	30.68	2095.9475	17	-1.2	699.6556	3	32.31	10	2065	OB3608.raw	3.53E4	2	2	104	120	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.EGALM(+15.99)LPHFN.S	N	92.8	26.19	1143.5382	10	-1.7	572.7754	2	30.95	10	1887	OB3608.raw	1.43E4	1	1	121	130	Oxidation (M)
K.NP(+15.99)QLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	85.0	23.56	2095.9475	17	-0.9	1048.9801	2	32.31	10	2066	OB3608.raw	4.25E4	3	3	104	120	Hydroxylation Pro; Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)MLTC(+57.02)VEIK.E	N	79.5	22.29	2062.9736	17	-0.5	688.6648	3	32.53	10	2094	OB3608.raw	4.06E4	1	1	104	120	Oxidation (M); Carbamidomethylation
K.KNPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	60.1	20.49	2208.0476	18	5.0	737.0268	3	30.58	10	1837	OB3608.raw	4.9E4	1	1	103	120	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.N(+.98)P(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	59.0	19.86	2079.9526	17	-1.9	694.3235	3	33.13	10	2174	OB3608.raw	3.47E4	1	1	104	120	Deamidation (NQ); Hydroxylation Pro; Oxidation (M); Carbamidomethylation
total 38 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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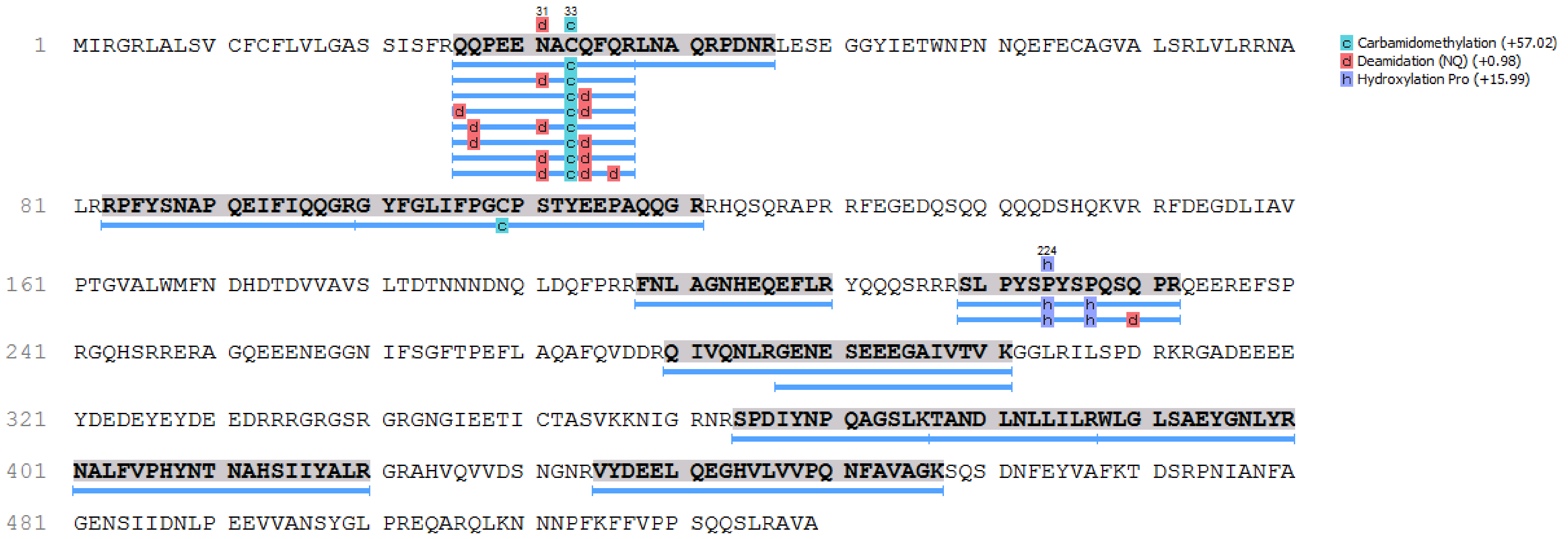
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MIRGRLALSV CFCFLVLGAS SISFR**QQPEE NACQFQRLNA QRPDNR**LESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA

81 LR**RPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG R**RHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRR**FNL AGNHEQEFLR** YQQQSRRR**SL PYSPYSPQSQ PR**QEEREFSP

241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDR**Q IVQNLRGENE SEEEGAIVTV K**GGLRILSPD RKRGADEEEE

321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNR**SPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR**

401 **NALFVPHYNT NAHSIIYALR** GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGK**SQS DNFEYVAFKT DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
R.GENESEEEGAIVTVK.G	Y	99.9	60.12	1589.7421	15	0.5	795.8787	2	26.28	10	1332	OB3608.raw	1.96E4	5	5	287	301	
R.WLGLSAEYGNLYR.N	N	99.9	55.63	1540.7673	13	0.9	771.3917	2	32.45	10	2084	OB3608.raw	4.44E4	2	2	388	400	
R.RPFYSNAPQEIFIQQGR.G	N	99.9	51.79	2050.0383	17	-0.6	684.3530	3	29.76	10	1727	OB3608.raw	3.25E4	3	3	83	99	
K.TANDLNLLILR.W	N	99.9	51.75	1254.7296	11	-1.8	628.3710	2	32.57	10	2100	OB3608.raw	3.1E4	2	2	377	387	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	48.55	2540.2910	23	0.1	847.7711	3	30.77	10	1863	OB3608.raw	1.07E5	3	3	435	457	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.8	41.38	1534.6470	12	-0.3	768.3306	2	24.65	10	1209	OB3608.raw	9.87E3	4	4	26	37	Deamidation (NQ); Carbamidomethylation
R.NALFVPHYNTNAHSIIYALR.G	N	99.6	40.03	2313.2019	20	-3.6	772.0718	3	30.41	10	1815	OB3608.raw	2.31E5	7	7	401	420	
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	39.26	1535.6311	12	-1.2	768.8219	2	25.38	10	1257	OB3608.raw	1.02E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.6	39.03	1388.6936	13	0.0	695.3541	2	27.03	10	1400	OB3608.raw	6.09E3	1	1	364	376	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.2	35.78	1535.6311	12	3.2	768.8253	2	24.62	10	1207	OB3608.raw	1.02E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.1	34.02	1534.6470	12	0.4	768.3311	2	24.25	10	1183	OB3608.raw	9.87E3	2	2	26	37	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QSQPR.Q	N	98.2	32.86	1637.7684	14	-1.6	819.8902	2	25.90	10	1291	OB3608.raw	3.02E3	1	1	219	232	Hydroxylation Pro
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	31.00	1535.6311	12	-1.2	768.8219	2	24.92	10	1227	OB3608.raw	1.02E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.QIVQNLRGENESEEEGAIVTVK.G	Y	97.8	30.65	2441.2397	22	0.1	814.7540	3	27.57	10	1450	OB3608.raw	1.31E4	1	1	280	301	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	97.8	30.41	2473.1372	22	-1.5	825.3851	3	34.06	10	2296	OB3608.raw	6.09E3	1	1	100	121	Carbamidomethylation
R.FNLAGNHEQEFLR.Y	N	95.8	28.25	1573.7637	13	-0.4	525.5950	3	28.90	10	1614	OB3608.raw	1.9E4	3	3	198	210	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	93.2	26.76	1535.6311	12	-5.0	768.8190	2	24.67	10	1211	OB3608.raw	0	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	93.1	26.59	1536.6151	12	-4.8	769.3112	2	25.72	10	1279	OB3608.raw	1.81E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	92.8	26.18	1533.6630	12	0.9	767.8395	2	23.84	10	1155	OB3608.raw	1.97E3	1	1	26	37	Carbamidomethylation
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	92.8	26.15	1638.7524	14	-3.3	820.3808	2	26.12	10	1315	OB3608.raw	3.73E3	1	1	219	232	Hydroxylation Pro; Deamidation (NQ)
R.LNAQRPDNR.L	N	91.0	25.71	1082.5581	9	-0.5	361.8598	3	18.07	10	832	OB3608.raw	5.89E3	1	1	38	46	
total 21 peptides																		

A1DZF0|A1DZF0_ARAHY

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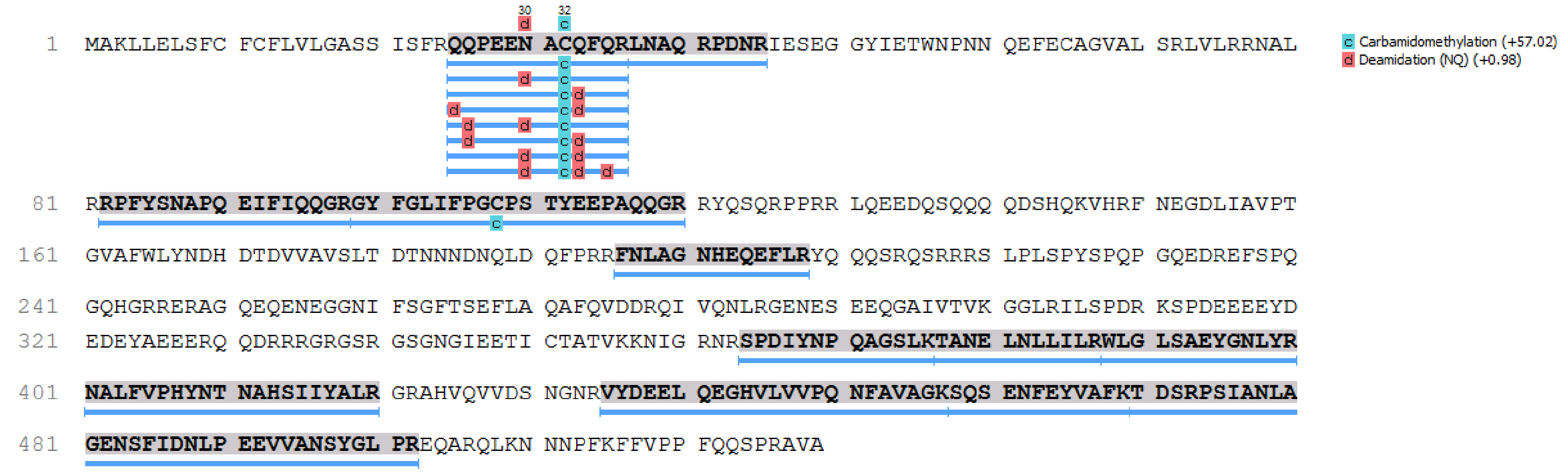
| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



1 MAKLLELSFC FCFLVLGASS ISFR**QQPEEN ACQFQRLNAQ RPDNR**IESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR** RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRR**FNLAG NHEQEFLR**YQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ

241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD

321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNR**SPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR**

401 **NALFVPHYNT NAHSIIYALR** GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA**

481 **GENSFIDNLP EEVVANSYGL PR**EQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	55.63	1540.7673	13	0.9	771.3917	2	32.45	10	2084	OB3608.raw	4.44E4	2	2	388	400	
K.TANELNLLILR.W	N	99.9	53.02	1268.7452	11	-0.3	635.3797	2	33.08	10	2167	OB3608.raw	2.74E4	2	2	377	387	
R.RPFYSNAPQEIFIQQGR.G	N	99.9	51.79	2050.0383	17	-0.6	684.3530	3	29.76	10	1727	OB3608.raw	3.25E4	3	3	82	98	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	48.55	2540.2910	23	0.1	847.7711	3	30.77	10	1863	OB3608.raw	1.07E5	3	3	435	457	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.8	41.38	1534.6470	12	-0.3	768.3306	2	24.65	10	1209	OB3608.raw	9.87E3	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.NALFVPHYNTNAHSIIYALR.G	N	99.6	40.03	2313.2019	20	-3.6	772.0718	3	30.41	10	1815	OB3608.raw	2.31E5	7	7	401	420	
K.SQSENFEYVAFK.T	N	99.6	39.51	1447.6619	12	0.7	724.8387	2	29.91	10	1748	OB3608.raw	3.23E3	1	1	458	469	
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	39.26	1535.6311	12	-1.2	768.8219	2	25.38	10	1257	OB3608.raw	1.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.6	39.03	1388.6936	13	0.0	695.3541	2	27.03	10	1400	OB3608.raw	6.09E3	1	1	364	376	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.2	35.78	1535.6311	12	3.2	768.8253	2	24.62	10	1207	OB3608.raw	1.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.1	34.02	1534.6470	12	0.4	768.3311	2	24.25	10	1183	OB3608.raw	9.87E3	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	31.00	1535.6311	12	-1.2	768.8219	2	24.92	10	1227	OB3608.raw	1.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	97.8	30.41	2473.1372	22	-1.5	825.3851	3	34.06	10	2296	OB3608.raw	6.09E3	1	1	99	120	Carbamidomethylation
R.FNLAGNHEQEFLR.Y	N	95.8	28.25	1573.7637	13	-0.4	525.5950	3	28.90	10	1614	OB3608.raw	1.9E4	3	3	196	208	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	93.2	26.76	1535.6311	12	-5.0	768.8190	2	24.67	10	1211	OB3608.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	93.1	26.59	1536.6151	12	-4.8	769.3112	2	25.72	10	1279	OB3608.raw	1.81E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	92.8	26.18	1533.6630	12	0.9	767.8395	2	23.84	10	1155	OB3608.raw	1.97E3	1	1	25	36	Carbamidomethylation
R.LNAQRPDNR.I	N	91.0	25.71	1082.5581	9	-0.5	361.8598	3	18.07	10	832	OB3608.raw	5.89E3	1	1	37	45	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	90.7	25.69	3544.7434	33	-0.4	1182.5879	3	35.00	10	2413	OB3608.raw	3.91E3	1	1	470	502	
total 19 peptides																		

Q647H3|Q647H3_ARAHY

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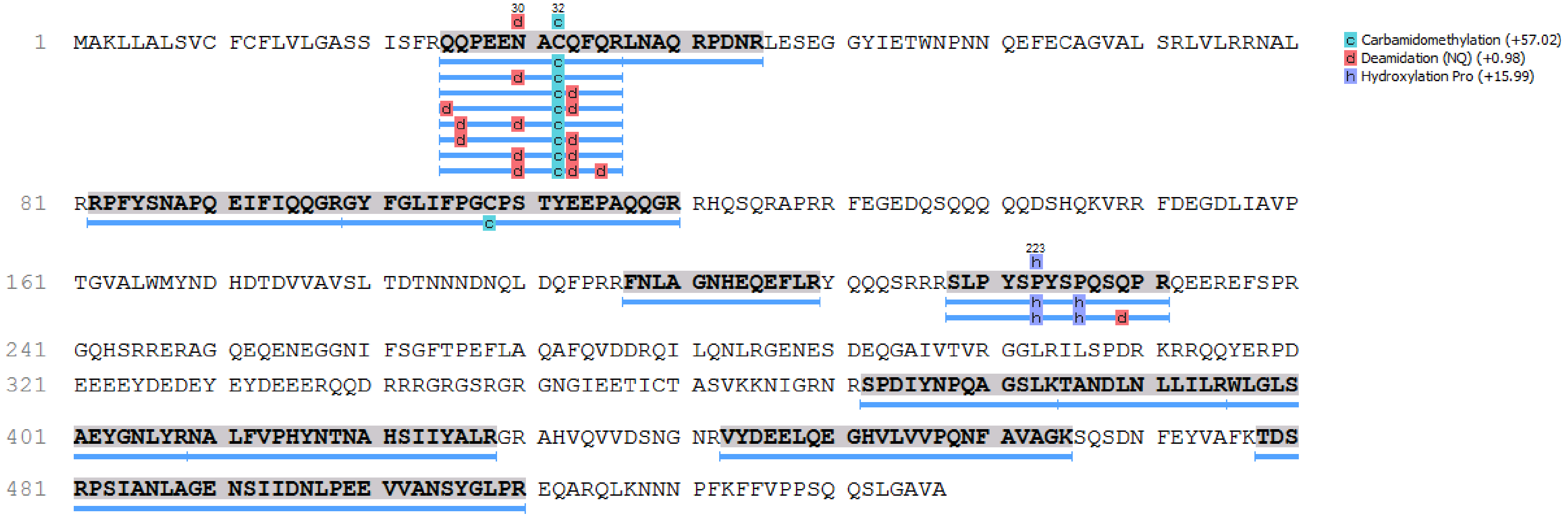
| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



1 MAKLLALSVC FCFLVLGASS ISFR**QQPEEN ACQFQRLNAQ RPDNR**LESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR** RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP

161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRR**FNLA GNHEQEFLR**Y QQQSRRR**SLP YSPYSPQSQP R**QEEREFSPR

241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD

321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN R**SPDIYNPQA GSLKTANDLN LLILRWLGLS**

401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS**

481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	55.63	1540.7673	13	0.9	771.3917	2	32.45	10	2084	OB3608.raw	4.44E4	2	2	396	408	
R.RPFYSNAPQEIFIQQGR.G	N	99.9	51.79	2050.0383	17	-0.6	684.3530	3	29.76	10	1727	OB3608.raw	3.25E4	3	3	82	98	
K.TANDLNLLILR.W	N	99.9	51.75	1254.7296	11	-1.8	628.3710	2	32.57	10	2100	OB3608.raw	3.1E4	2	2	385	395	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	48.55	2540.2910	23	0.1	847.7711	3	30.77	10	1863	OB3608.raw	1.07E5	3	3	443	465	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.8	41.38	1534.6470	12	-0.3	768.3306	2	24.65	10	1209	OB3608.raw	9.87E3	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.NALFVPHYNTNAHSIIYALR.G	N	99.6	40.03	2313.2019	20	-3.6	772.0718	3	30.41	10	1815	OB3608.raw	2.31E5	7	7	409	428	
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	39.26	1535.6311	12	-1.2	768.8219	2	25.38	10	1257	OB3608.raw	1.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.6	39.03	1388.6936	13	0.0	695.3541	2	27.03	10	1400	OB3608.raw	6.09E3	1	1	372	384	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.2	35.78	1535.6311	12	3.2	768.8253	2	24.62	10	1207	OB3608.raw	1.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.1	34.02	1534.6470	12	0.4	768.3311	2	24.25	10	1183	OB3608.raw	9.87E3	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QSQPR.Q	N	98.2	32.86	1637.7684	14	-1.6	819.8902	2	25.90	10	1291	OB3608.raw	3.02E3	1	1	218	231	Hydroxylation Pro
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	31.00	1535.6311	12	-1.2	768.8219	2	24.92	10	1227	OB3608.raw	1.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	97.8	30.41	2473.1372	22	-1.5	825.3851	3	34.06	10	2296	OB3608.raw	6.09E3	1	1	99	120	Carbamidomethylation
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	96.9	29.23	3510.7590	33	0.0	1171.2603	3	34.74	10	2384	OB3608.raw	6.76E3	1	1	478	510	
R.FNLAGNHEQEFLR.Y	N	95.8	28.25	1573.7637	13	-0.4	525.5950	3	28.90	10	1614	OB3608.raw	1.9E4	3	3	197	209	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	93.2	26.76	1535.6311	12	-5.0	768.8190	2	24.67	10	1211	OB3608.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	93.1	26.59	1536.6151	12	-4.8	769.3112	2	25.72	10	1279	OB3608.raw	1.81E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	92.8	26.18	1533.6630	12	0.9	767.8395	2	23.84	10	1155	OB3608.raw	1.97E3	1	1	25	36	Carbamidomethylation
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	92.8	26.15	1638.7524	14	-3.3	820.3808	2	26.12	10	1315	OB3608.raw	3.73E3	1	1	218	231	Hydroxylation Pro; Deamidation (NQ)
R.LNAQRPDNR.L	N	91.0	25.71	1082.5581	9	-0.5	361.8598	3	18.07	10	832	OB3608.raw	5.89E3	1	1	37	45	
total 20 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQR**LNAQRP DNR**IESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFK**T DSRPSIANLA GENSIIDNLP EEVVANSYR**L

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	97.9	31.83	2554.3066	23	-1.1	852.4419	3	31.08	10	1904	OB3608.raw	5.04E4	2	2	415	437	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	97.9	31.14	3243.6006	30	0.2	1082.2076	3	33.94	10	2282	OB3608.raw	1.4E4	1	1	450	479	
R.LNAQRPDNR.I	N	91.0	25.71	1082.5581	9	-0.5	361.8598	3	18.07	10	832	OB3608.raw	5.89E3	1	1	35	43	
total 3 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQR**LNAQ RPDNR**IESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF K**TDSRPSIAN LAGENSIIDN LPEEVVANSY**

481 **R**LPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 10	#Spec	#Spec Sample 10	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	97.9	31.83	2554.3066	23	-1.1	852.4419	3	31.08	10	1904	OB3608.raw	5.04E4	2	2	417	439	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	97.9	31.14	3243.6006	30	0.2	1082.2076	3	33.94	10	2282	OB3608.raw	1.4E4	1	1	452	481	
R.LNAQRPDNR.I	N	91.0	25.71	1082.5581	9	-0.5	361.8598	3	18.07	10	832	OB3608.raw	5.89E3	1	1	37	45	
total 3 peptides																		

Peptide List

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1. Notes

Spot 9 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

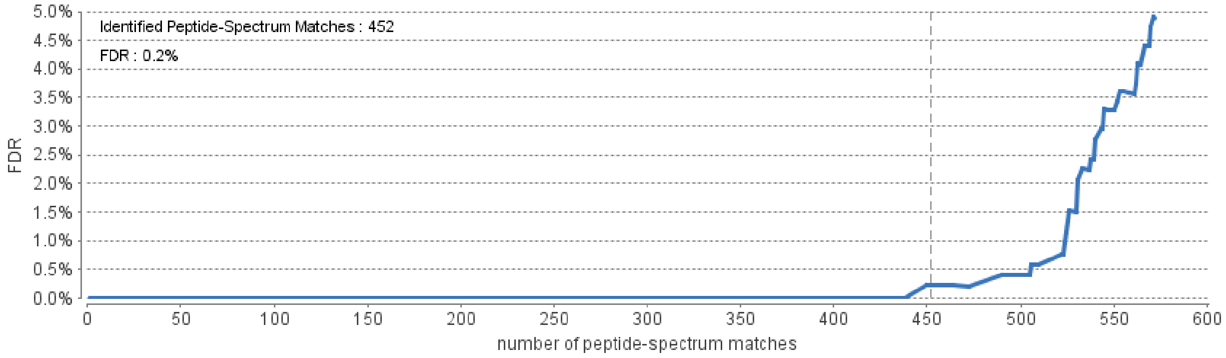
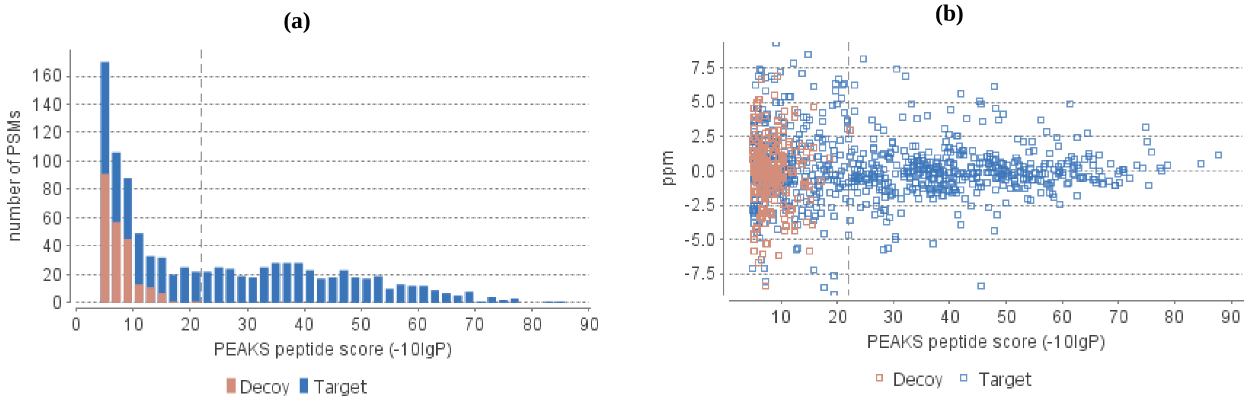


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

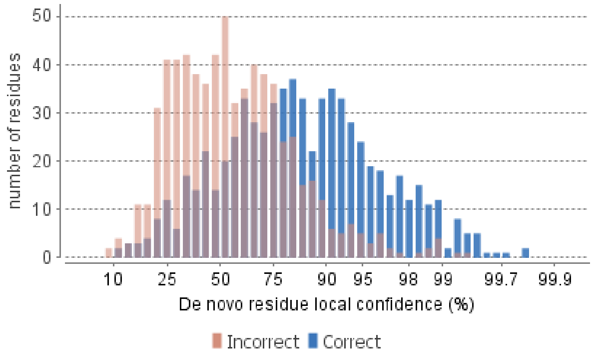

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



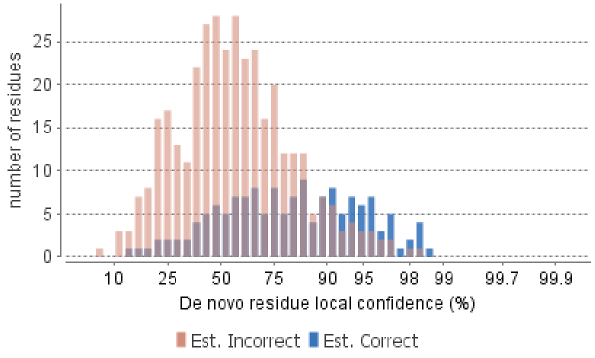


Table 1. Statistics of data.

# of MS scans	2760
# of MS/MS scans	4143

Table 2. Result filtration parameters.

Peptide -10lgP	≥22
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	402
Peptide sequences	143
Protein groups	6
Proteins	10
Proteins (#Unique Peptides)	8 (>2); 2 (=2); 0 (=1);
FDR (Peptide-Spectrum Matches)	0.2%
FDR (Peptide Sequences)	0.7%
FDR (Protein)	5.3%
De Novo Only Spectra	50

Table 4. PTM profile.

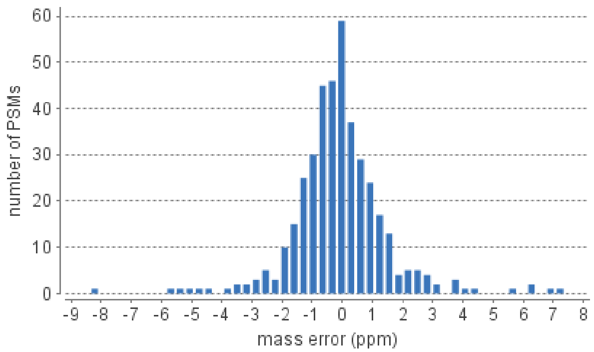
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Deamidation	.98	NQ	58	74.84	2.87E6	29.85
Oxidation	15.99	M	53	61.78	4.87E4	1000.00
Carbamidomethyl	57.02	C	30	66.60	2.66E5	1000.00
HydPro	15.99	P	3	38.38		1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



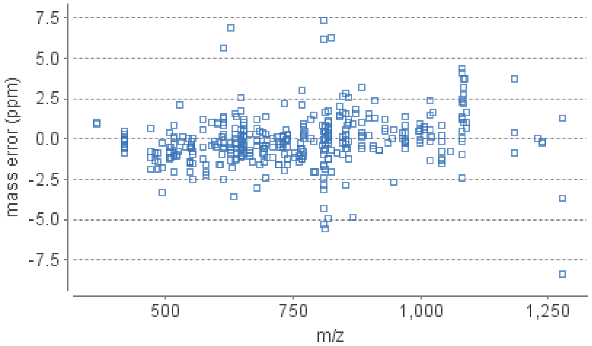


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 17	136	7	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3615.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein	Protein		Score		Coverage	Coverage (%)	Area			#Spec		Avg.	

Group	ID	Accession	(%)	-10lgP	(%)	Sample 17	Sample 17	#Peptides	#Unique	Sample 17	PTM	Mass	Description
1	41	Q6IWG5|Q6IWG5_ARAHY	99.1	253.41	31	31	1.09E7	24	4	155	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
1	42	Q0GM57|Q0GM57_ARAHY	99.1	253.41	31	31	1.09E7	24	4	155	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
4	15	Q647H3|Q647H3_ARAHY	99.1	192.61	26	26	5.77E5	14	2	48	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
6	7	Q647H4|Q647H4_ARAHY	99.2	188.29	31	31	6.33E4	12	3	39	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	99.2	188.29	31	31	6.33E4	12	3	39	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
13	59	Q647H1|Q647H1_ARAHY	99.1	139.13	11	11	1.76E5	5	5	11	Y	75933	Conarachin OS=Arachis hypogaea PE=2 SV=1
12	27	Q6PSU4|Q6PSU4_ARAHY	98.2	95.52	12	12	6.13E4	3	3	5	Y	48095	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
12	18	N1NG13|N1NG13_ARAHY	98.2	95.52	8	8	6.13E4	3	3	5	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
12	20	sp|P43238|ALL12_ARAHY	98.2	95.52	8	8	6.13E4	3	3	5	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
16	92	sp|Q647H2|AHY3_ARAHY	88.2	72.23	5	5	5.45E4	2	2	3	N	54569	Arachin Ahy-3 OS=Arachis hypogaea PE=1 SV=1
total 10 proteins													

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	87.90	3243.6006	30	1.2	1082.2087	3	34.06	17	2322	OB3615.raw	7.74E6	23	23	450	479	
R.SSNPDIYNPQAGSLR.S	N	99.9	78.83	1617.7747	15	0.4	809.8950	2	27.13	17	1408	OB3615.raw	4.75E5	5	5	342	356	
K.AQSENYEYLAFK.T	N	99.9	77.49	1461.6776	12	0.2	731.8463	2	29.95	17	1776	OB3615.raw	3.72E5	5	5	438	449	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVANSYR.L	Y	99.9	74.84	3244.5847	30	3.2	1082.5389	3	34.42	17	2370	OB3615.raw	2.87E6	2	2	450	479	Deamidation (NQ)

K.AQ(+.98)SENYEYLAFK.T	N	99.9	69.30	1462.6616	12	-1.0	732.3373	2	29.70	17	1741	OB3615.raw	5.92E4	3	3	438	449	Deamidation (NQ)
N.GIEETIC(+57.02)SASVK.K	N	99.9	66.60	1292.6282	12	0.0	647.3214	2	27.62	17	1466	OB3615.raw	3.35E5	12	12	325	336	Carbamidomethylation
R.SSNPDIYNPQ(+.98)AGSLR.S	N	99.9	65.41	1618.7587	15	-0.7	810.3860	2	27.57	17	1460	OB3615.raw	2.05E5	5	5	342	356	Deamidation (NQ)
R.PSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	65.40	2784.3928	26	0.4	929.1386	3	35.02	17	2452	OB3615.raw	1.04E5	3	3	454	479	
R.VYDEELQEGHVLVVPQNFAVAAK.A	N	99.9	64.68	2554.3066	23	1.3	1278.1622	2	31.09	17	1927	OB3615.raw	6.26E6	15	15	415	437	
K.TDSRPSIANLAGENSIIDNLPEEVVAN(+.98)SYR.L	Y	99.9	64.48	3244.5847	30	2.7	1082.5385	3	33.21	17	2208	OB3615.raw	4.15E4	2	2	450	479	Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALN(+.98)GR.A	N	99.9	59.41	2454.2478	22	1.8	819.0913	3	31.09	17	1928	OB3615.raw	4.42E5	8	8	381	402	Oxidation (M); Deamidation (NQ)
R.SSNPDIYN(+.98)PQ(+.98)AGSLR.S	N	99.9	57.86	1619.7427	15	-1.6	810.8773	2	28.09	17	1525	OB3615.raw	2.23E4	3	3	342	356	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGENSIIDN.L	N	99.9	57.03	1986.9493	19	0.5	994.4824	2	30.78	17	1887	OB3615.raw	2.84E4	1	1	450	468	Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	99.9	51.07	2453.2637	22	-0.3	818.7616	3	31.40	17	1968	OB3615.raw	7.94E5	4	4	381	402	Oxidation (M)
R.SSNPDIYN(+.98)PQAGSLR.S	N	99.9	48.35	1618.7587	15	-3.2	810.3840	2	28.37	17	1562	OB3615.raw	5.13E4	1	1	342	356	Deamidation (NQ)
R.SSN(+.98)PDIYNPQAGSLR.S	N	99.9	47.90	1618.7587	15	6.2	810.3916	2	27.38	17	1437	OB3615.raw	1.49E5	1	1	342	356	Deamidation (NQ)
K.NNNPFK.F	N	99.9	47.24	732.3555	6	0.9	367.1853	2	21.83	17	1083	OB3615.raw	1.74E4	2	2	490	495	
R.NAM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	99.9	47.02	2454.2478	22	1.1	819.0908	3	31.99	17	2046	OB3615.raw	1.27E5	6	6	381	402	Oxidation (M); Deamidation (NQ)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYR.L	Y	99.9	46.73	3244.5847	30	1.0	1082.5366	3	37.06	17	2720	OB3615.raw	5.59E4	1	1	450	479	Deamidation (NQ)
H.TIVVALN(+.98)GR.A	N	99.9	46.65	942.5498	9	-0.8	472.2818	2	27.63	17	1468	OB3615.raw	3.65E4	3	3	394	402	Deamidation (NQ)
R.VYDEELQEGHVLVVPQN(+.98)FAVAAK.A	N	99.8	45.68	2555.2908	23	-8.4	1278.6420	2	31.32	17	1957	OB3615.raw	0	1	1	415	437	Deamidation (NQ)
S.IANLAGENSIIDNLPEEVVANSYR.L	Y	99.8	45.52	2600.3081	24	0.9	867.7775	3	34.40	17	2368	OB3615.raw	2.52E4	2	2	456	479	
R.SVNELDLPILGWLGLSAQHGTIYR.N	N	99.8	44.71	2651.4070	24	-0.5	884.8092	3	37.31	17	2742	OB3615.raw	2.48E5	6	6	357	380	
K.TDSRPSIANLAGENSIID.N	N	99.8	44.39	1871.9225	18	-0.2	936.9683	2	30.74	17	1881	OB3615.raw	4.51E4	1	1	450	467	
H.VLVVPQNFAVAAK.A	N	99.7	42.38	1354.7972	13	1.2	678.4067	2	30.24	17	1815	OB3615.raw	9.6E3	1	1	425	437	
R.N(+.98)AM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	99.7	42.06	2455.2317	22	5.6	614.8187	4	32.32	17	2089	OB3615.raw	4.56E4	1	1	381	402	Deamidation (NQ); Oxidation (M)
H.YTLNAHTIVVALN(+.98)GR.A	N	99.7	40.46	1641.8838	15	-1.5	548.3010	3	30.14	17	1801	OB3615.raw	4.56E4	2	2	388	402	Deamidation (NQ)
H.YTLNAHTIVVALNGR.A	N	99.7	39.83	1640.8998	15	-1.4	547.9731	3	31.02	17	1918	OB3615.raw	3.38E4	2	2	388	402	
H.TIVVALNGR.A	N	99.6	38.78	941.5658	9	-1.8	471.7893	2	27.08	17	1402	OB3615.raw	1.27E4	1	1	394	402	
Y.TLNAHTIVVALNGR.A	N	99.6	38.64	1477.8365	14	-1.8	493.6186	3	29.63	17	1731	OB3615.raw	6.38E3	1	1	389	402	
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	99.6	38.54	2454.2478	22	-1.2	819.0889	3	32.18	17	2070	OB3615.raw	7.78E4	2	2	381	402	Deamidation (NQ); Oxidation (M)
K.FFVPPFDHQSM(+15.99)R.E	N	99.6	38.30	1522.7026	12	-1.1	508.5742	3	29.65	17	1734	OB3615.raw	1.72E5	5	5	496	507	Oxidation (M)
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.6	37.89	2837.4043	27	0.6	946.8093	3	33.97	17	2310	OB3615.raw	1.15E5	2	2	450	476	
K.TDSRPSIANLAGEN(+.98).S	N	99.5	36.81	1444.6793	14	-1.6	723.3458	2	27.99	17	1514	OB3615.raw	7.72E3	1	1	450	463	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.5	36.25	1443.6953	14	-0.2	722.8548	2	27.55	17	1458	OB3615.raw	1.26E4	3	3	450	463	
Y.TLNAHTIVVALN(+.98)GR.A	N	99.4	36.16	1478.8206	14	-0.2	493.9474	3	28.87	17	1629	OB3615.raw	3.51E3	2	2	389	402	Deamidation (NQ)
R.N(+.98)AM(+15.99)FVP(+15.99)HYTLN(+.98)AHTIVVALNGR.A	N	99.0	34.36	2471.2268	22	-2.0	824.7479	3	32.61	17	2128	OB3615.raw	4.13E4	1	1	381	402	Deamidation (NQ); Oxidation (M); Hydroxylation Pro
N.LAGENSIIDNLPEEVVANSYR.L	Y	98.7	33.44	2302.1440	21	-1.3	768.3876	3	33.62	17	2263	OB3615.raw	4.28E4	2	2	459	479	
R.NAM(+15.99)FVPHYTLNAH.T	N	98.2	32.98	1529.7085	13	-0.6	510.9098	3	27.45	17	1445	OB3615.raw	8.09E4	5	5	381	393	Oxidation (M)
N.SIIDNLPEEVVANSYR.L	N	96.1	30.36	1817.9159	16	-1.6	606.9783	3	32.91	17	2168	OB3615.raw	2.11E4	2	2	464	479	
R.SVNELDLPILGWLGLSAQ(+.98)HGTIYR.N	N	94.5	26.79	2652.3911	24	1.0	885.1385	3	36.88	17	2698	OB3615.raw	1.52E4	1	1	357	380	Deamidation (NQ)
K.FFVPPFDHQSM(+15.99)RE.V	N	88.6	25.62	1651.7452	13	-0.2	551.5889	3	29.52	17	1716	OB3615.raw	7.16E5	4	4	496	508	Oxidation (M)
R.N(+.98)AM(+15.99)FVP(+15.99)HYTLN(+.98)AHTIVVALN(+.98)GR.A	N	86.5	23.07	2472.2107	22	6.2	825.0826	3	31.97	17	2044	OB3615.raw	1.03E4	1	1	381	402	Deamidation (NQ); Oxidation (M); Hydroxylation Pro
R.VYDEELQEGHVLVVPQNF.A	N	83.6	22.54	2114.0320	18	-0.8	1058.0225	2	32.37	17	2097	OB3615.raw	1.59E4	1	1	415	432	
total 44 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	87.90	3243.6006	30	1.2	1082.2087	3	34.06	17	2322	OB3615.raw	7.74E6	23	23	452	481	
R.SSNPDIYNPQAGSLR.S	N	99.9	78.83	1617.7747	15	0.4	809.8950	2	27.13	17	1408	OB3615.raw	4.75E5	5	5	344	358	
K.AQSENYEYLAFK.T	N	99.9	77.49	1461.6776	12	0.2	731.8463	2	29.95	17	1776	OB3615.raw	3.72E5	5	5	440	451	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVANSYR.L	Y	99.9	74.84	3244.5847	30	3.2	1082.5389	3	34.42	17	2370	OB3615.raw	2.87E6	2	2	452	481	Deamidation (NQ)
K.AQ(+.98)SENYEYLAFK.T	N	99.9	69.30	1462.6616	12	-1.0	732.3373	2	29.70	17	1741	OB3615.raw	5.92E4	3	3	440	451	Deamidation (NQ)
N.GIEETIC(+57.02)SASVK.K	N	99.9	66.60	1292.6282	12	0.0	647.3214	2	27.62	17	1466	OB3615.raw	3.35E5	12	12	327	338	Carbamidomethylation
R.SSNPDIYNPQ(+.98)AGSLR.S	N	99.9	65.41	1618.7587	15	-0.7	810.3860	2	27.57	17	1460	OB3615.raw	2.05E5	5	5	344	358	Deamidation (NQ)
R.PSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	65.40	2784.3928	26	0.4	929.1386	3	35.02	17	2452	OB3615.raw	1.04E5	3	3	456	481	
R.VYDEELQEGHVLVVPQNFAVAAK.A	N	99.9	64.68	2554.3066	23	1.3	1278.1622	2	31.09	17	1927	OB3615.raw	6.26E6	15	15	417	439	
K.TDSRPSIANLAGENSIIDNLPEEVVAN(+.98)SYR.L	Y	99.9	64.48	3244.5847	30	2.7	1082.5385	3	33.21	17	2208	OB3615.raw	4.15E4	2	2	452	481	Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALN(+.98)GR.A	N	99.9	59.41	2454.2478	22	1.8	819.0913	3	31.09	17	1928	OB3615.raw	4.42E5	8	8	383	404	Oxidation (M); Deamidation (NQ)
R.SSNPDIYN(+.98)PQ(+.98)AGSLR.S	N	99.9	57.86	1619.7427	15	-1.6	810.8773	2	28.09	17	1525	OB3615.raw	2.23E4	3	3	344	358	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGENSIIDN.L	N	99.9	57.03	1986.9493	19	0.5	994.4824	2	30.78	17	1887	OB3615.raw	2.84E4	1	1	452	470	Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	99.9	51.07	2453.2637	22	-0.3	818.7616	3	31.40	17	1968	OB3615.raw	7.94E5	4	4	383	404	Oxidation (M)
R.SSNPDIYN(+.98)PQAGSLR.S	N	99.9	48.35	1618.7587	15	-3.2	810.3840	2	28.37	17	1562	OB3615.raw	5.13E4	1	1	344	358	Deamidation (NQ)

R.SSN(+.98)PDIYNPQAGSLR.S	N	99.9	47.90	1618.7587	15	6.2	810.3916	2	27.38	17	1437	OB3615.raw	1.49E5	1	1	344	358	Deamidation (NQ)
K.NNNPFK.F	N	99.9	47.24	732.3555	6	0.9	367.1853	2	21.83	17	1083	OB3615.raw	1.74E4	2	2	492	497	
R.NAM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	99.9	47.02	2454.2478	22	1.1	819.0908	3	31.99	17	2046	OB3615.raw	1.27E5	6	6	383	404	Oxidation (M); Deamidation (NQ)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYR.L	Y	99.9	46.73	3244.5847	30	1.0	1082.5366	3	37.06	17	2720	OB3615.raw	5.59E4	1	1	452	481	Deamidation (NQ)
H.TIVVALN(+.98)GR.A	N	99.9	46.65	942.5498	9	-0.8	472.2818	2	27.63	17	1468	OB3615.raw	3.65E4	3	3	396	404	Deamidation (NQ)
R.VYDEELQEGHVLVVPQN(+.98)FAVAAK.A	N	99.8	45.68	2555.2908	23	-8.4	1278.6420	2	31.32	17	1957	OB3615.raw	0	1	1	417	439	Deamidation (NQ)
S.IANLAGENSIIDNLPEEVVANSYR.L	Y	99.8	45.52	2600.3081	24	0.9	867.7775	3	34.40	17	2368	OB3615.raw	2.52E4	2	2	458	481	
R.SVNELDLPILGWLGLSAQHGTIYR.N	N	99.8	44.71	2651.4070	24	-0.5	884.8092	3	37.31	17	2742	OB3615.raw	2.48E5	6	6	359	382	
K.TDSRPSIANLAGENSIID.N	N	99.8	44.39	1871.9225	18	-0.2	936.9683	2	30.74	17	1881	OB3615.raw	4.51E4	1	1	452	469	
H.VLVVPQNFAVAAK.A	N	99.7	42.38	1354.7972	13	1.2	678.4067	2	30.24	17	1815	OB3615.raw	9.6E3	1	1	427	439	
R.N(+.98)AM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	99.7	42.06	2455.2317	22	5.6	614.8187	4	32.32	17	2089	OB3615.raw	4.56E4	1	1	383	404	Deamidation (NQ); Oxidation (M)
H.YTLNAHTIVVALN(+.98)GR.A	N	99.7	40.46	1641.8838	15	-1.5	548.3010	3	30.14	17	1801	OB3615.raw	4.56E4	2	2	390	404	Deamidation (NQ)
H.YTLNAHTIVVALNGR.A	N	99.7	39.83	1640.8998	15	-1.4	547.9731	3	31.02	17	1918	OB3615.raw	3.38E4	2	2	390	404	
H.TIVVALNGR.A	N	99.6	38.78	941.5658	9	-1.8	471.7893	2	27.08	17	1402	OB3615.raw	1.27E4	1	1	396	404	
Y.TLNAHTIVVALNGR.A	N	99.6	38.64	1477.8365	14	-1.8	493.6186	3	29.63	17	1731	OB3615.raw	6.38E3	1	1	391	404	
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	99.6	38.54	2454.2478	22	-1.2	819.0889	3	32.18	17	2070	OB3615.raw	7.78E4	2	2	383	404	Deamidation (NQ); Oxidation (M)
K.FFVPPFDHQSM(+15.99)R.E	N	99.6	38.30	1522.7026	12	-1.1	508.5742	3	29.65	17	1734	OB3615.raw	1.72E5	5	5	498	509	Oxidation (M)
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.6	37.89	2837.4043	27	0.6	946.8093	3	33.97	17	2310	OB3615.raw	1.15E5	2	2	452	478	
K.TDSRPSIANLAGEN(+.98).S	N	99.5	36.81	1444.6793	14	-1.6	723.3458	2	27.99	17	1514	OB3615.raw	7.72E3	1	1	452	465	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.5	36.25	1443.6953	14	-0.2	722.8548	2	27.55	17	1458	OB3615.raw	1.26E4	3	3	452	465	
Y.TLNAHTIVVALN(+.98)GR.A	N	99.4	36.16	1478.8206	14	-0.2	493.9474	3	28.87	17	1629	OB3615.raw	3.51E3	2	2	391	404	Deamidation (NQ)
R.N(+.98)AM(+15.99)FVP(+15.99)HYTLN(+.98)AHTIVVALNGR.A	N	99.0	34.36	2471.2268	22	-2.0	824.7479	3	32.61	17	2128	OB3615.raw	4.13E4	1	1	383	404	Deamidation (NQ); Oxidation (M); Hydroxylation Pro
N.LAGENSIIDNLPEEVVANSYR.L	Y	98.7	33.44	2302.1440	21	-1.3	768.3876	3	33.62	17	2263	OB3615.raw	4.28E4	2	2	461	481	
R.NAM(+15.99)FVPHYTLNAH.T	N	98.2	32.98	1529.7085	13	-0.6	510.9098	3	27.45	17	1445	OB3615.raw	8.09E4	5	5	383	395	Oxidation (M)
N.SIIDNLPEEVVANSYR.L	N	96.1	30.36	1817.9159	16	-1.6	606.9783	3	32.91	17	2168	OB3615.raw	2.11E4	2	2	466	481	
R.SVNELDLPILGWLGLSAQ(+.98)HGTIYR.N	N	94.5	26.79	2652.3911	24	1.0	885.1385	3	36.88	17	2698	OB3615.raw	1.52E4	1	1	359	382	Deamidation (NQ)
K.FFVPPFDHQSM(+15.99)RE.V	N	88.6	25.62	1651.7452	13	-0.2	551.5889	3	29.52	17	1716	OB3615.raw	7.16E5	4	4	498	510	Oxidation (M)
R.N(+.98)AM(+15.99)FVP(+15.99)HYTLN(+.98)AHTIVVALN(+.98)GR.A	N	86.5	23.07	2472.2107	22	6.2	825.0826	3	31.97	17	2044	OB3615.raw	1.03E4	1	1	383	404	Deamidation (NQ); Oxidation (M); Hydroxylation Pro
R.VYDEELQEGHVLVVPQNF.A	N	83.6	22.54	2114.0320	18	-0.8	1058.0225	2	32.37	17	2097	OB3615.raw	1.59E4	1	1	417	434	
total 44 peptides																		

Q647H3|Q647H3_ARAHY

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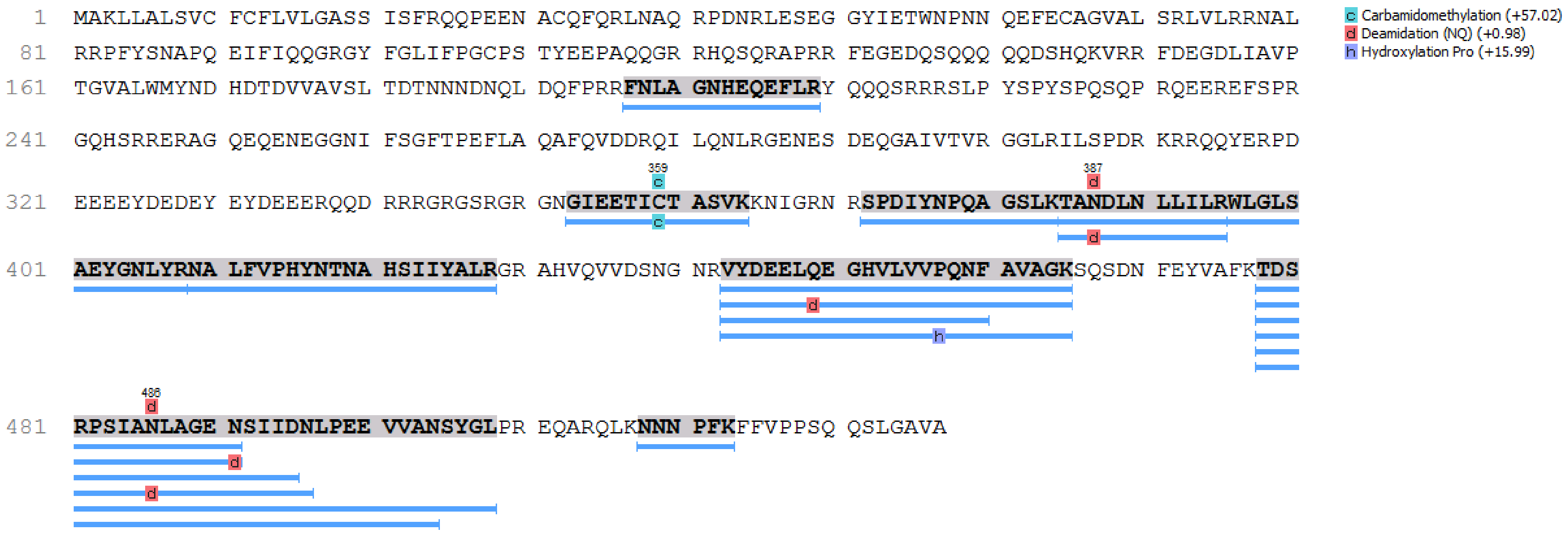
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRR**FNLA GNHEQEFLR**Y QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GN**GIEETICT ASVK**KNIGRN R**SPDIYNPQA GSLKTANDLN LLILRWLGLS**
401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS**
481 **RPSIANLAGE NSIIDNLPEE VVANSYGL**PR EQARQLK**NNN PFK**FFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	77.60	1540.7673	13	0.0	771.3909	2	32.81	17	2154	OB3615.raw	1.63E5	7	7	396	408	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	57.79	1306.6438	12	0.5	654.3295	2	27.39	17	1439	OB3615.raw	1.48E5	10	10	353	364	Carbamidomethylation
K.TDSRPSIAN(+.98)LAGENSIIDN.L	N	99.9	57.03	1986.9493	19	0.5	994.4824	2	30.78	17	1887	OB3615.raw	2.84E4	1	1	478	496	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	53.99	1388.6936	13	1.4	695.3550	2	27.10	17	1405	OB3615.raw	1.27E4	2	2	372	384	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	53.20	2540.2910	23	0.1	847.7711	3	30.93	17	1906	OB3615.raw	1.88E5	4	4	443	465	
K.TANDLNLLILR.W	N	99.9	51.48	1254.7296	11	-0.7	628.3716	2	32.63	17	2130	OB3615.raw	7.82E4	5	5	385	395	
K.NNNPFK.F	N	99.9	47.24	732.3555	6	0.9	367.1853	2	21.83	17	1083	OB3615.raw	1.74E4	2	2	518	523	
K.TDSRPSIANLAGENSIID.N	N	99.8	44.39	1871.9225	18	-0.2	936.9683	2	30.74	17	1881	OB3615.raw	4.51E4	1	1	478	495	
R.NALFVPHYNTNAHSIIYALR.G	N	99.7	42.78	2313.2019	20	-2.0	579.3066	4	30.28	17	1821	OB3615.raw	2.45E5	4	4	409	428	
R.VYDEELQ(+.98)EGHVLVVPQNFAVAGK.S	N	99.7	39.75	2541.2751	23	1.7	848.1004	3	31.37	17	1964	OB3615.raw	2.95E4	1	1	443	465	Deamidation (NQ)
R.VYDEELQEGHVLVVP(+15.99)QNFAVAGK.S	N	99.6	38.38	2556.2859	23	-0.6	853.1021	3	40.67	17	3038	OB3615.raw	0	1	1	443	465	Hydroxylation Pro
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.6	37.89	2837.4043	27	0.6	946.8093	3	33.97	17	2310	OB3615.raw	1.15E5	2	2	478	504	
K.TDSRPSIANLAGEN(+.98).S	N	99.5	36.81	1444.6793	14	-1.6	723.3458	2	27.99	17	1514	OB3615.raw	7.72E3	1	1	478	491	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.5	36.25	1443.6953	14	-0.2	722.8548	2	27.55	17	1458	OB3615.raw	1.26E4	3	3	478	491	
K.TAN(+.98)DLNLLILR.W	N	98.1	32.20	1255.7136	11	6.9	628.8684	2	33.23	17	2210	OB3615.raw	6.9E3	1	1	385	395	Deamidation (NQ)
R.FNLAGNHEQEFLR.Y	N	96.0	28.91	1573.7637	13	-0.8	525.5947	3	28.69	17	1606	OB3615.raw	2.33E3	1	1	197	209	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGL.P	Y	94.2	26.22	3257.6050	31	3.7	1086.8796	3	34.55	17	2388	OB3615.raw	4.29E5	1	1	478	508	
R.VYDEELQEGHVLVVPQNF.A	N	83.6	22.54	2114.0320	18	-0.8	1058.0225	2	32.37	17	2097	OB3615.raw	1.59E4	1	1	443	460	
total 18 peptides																		

Q647H4|Q647H4_ARAHY

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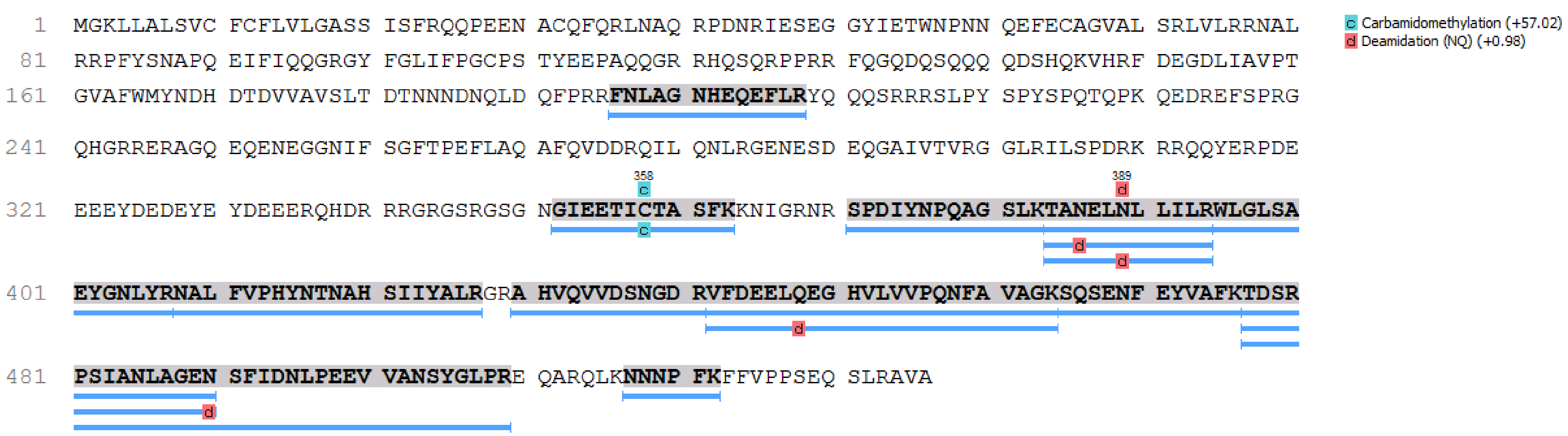
| Protein Coverage | Supporting Peptides |

Protein Coverage:



🟦c Carbamidomethylation (+57.02)
🟥d Deamidation (NQ) (+0.98)

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRR**FNLAG NHEQEFLR**YQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG N**GIEETICTA SFK**KNIGRNR **SPDIYNPQAG SLKTANELNL LILRWLGLSA**

401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GR**A HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**

481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLK**NNNP FK**FFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	77.60	1540.7673	13	0.0	771.3909	2	32.81	17	2154	OB3615.raw	1.63E5	7	7	395	407	
K.SQSENFEYVAFK.T	N	99.9	63.61	1447.6619	12	-0.5	724.8378	2	29.84	17	1761	OB3615.raw	1.11E4	2	2	465	476	
K.TANELNLLILR.W	N	99.9	54.14	1268.7452	11	-0.3	635.3797	2	32.50	17	2113	OB3615.raw	1.42E5	5	5	384	394	
R.SPDIYNPQAGSLK.T	N	99.9	53.99	1388.6936	13	1.4	695.3550	2	27.10	17	1405	OB3615.raw	1.27E4	2	2	371	383	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	48.76	3544.7434	33	3.7	1182.5928	3	35.31	17	2490	OB3615.raw	2.03E4	3	3	477	509	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	48.74	1354.6438	12	-0.5	678.3289	2	29.27	17	1682	OB3615.raw	5.67E3	1	1	352	363	Carbamidomethylation
K.NNNPFK.F	N	99.9	47.24	732.3555	6	0.9	367.1853	2	21.83	17	1083	OB3615.raw	1.74E4	2	2	517	522	
R.NALFVPHYNTNAHSIIYALR.G	N	99.7	42.78	2313.2019	20	-2.0	579.3066	4	30.28	17	1821	OB3615.raw	2.45E5	4	4	408	427	
K.TANELN(+.98)LLILR.W	N	99.7	42.53	1269.7292	11	1.5	635.8729	2	33.64	17	2265	OB3615.raw	0	1	1	384	394	Deamidation (NQ)
R.AHVQVVDSNGDR.V	Y	99.7	41.66	1295.6218	12	1.8	648.8193	2	20.26	17	1002	OB3615.raw	3.38E3	3	3	430	441	
K.TAN(+.98)ELNLLILR.W	N	99.7	40.19	1269.7292	11	0.7	635.8723	2	33.41	17	2234	OB3615.raw	0	1	1	384	394	Deamidation (NQ)
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.7	40.10	2524.2961	23	1.4	842.4405	3	31.64	17	2000	OB3615.raw	4.36E4	2	2	442	464	
K.TDSRPSIANLAGEN(+.98).S	N	99.5	36.81	1444.6793	14	-1.6	723.3458	2	27.99	17	1514	OB3615.raw	7.72E3	1	1	477	490	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.5	36.25	1443.6953	14	-0.2	722.8548	2	27.55	17	1458	OB3615.raw	1.26E4	3	3	477	490	
R.VFDEELQ(+.98)EGHVLVVPQNFAVAGK.S	Y	98.0	31.97	2525.2800	23	1.4	842.7685	3	32.01	17	2049	OB3615.raw	1.07E4	1	1	442	464	Deamidation (NQ)
R.FNLAGNHEQEFLR.Y	N	96.0	28.91	1573.7637	13	-0.8	525.5947	3	28.69	17	1606	OB3615.raw	2.33E3	1	1	196	208	
total 16 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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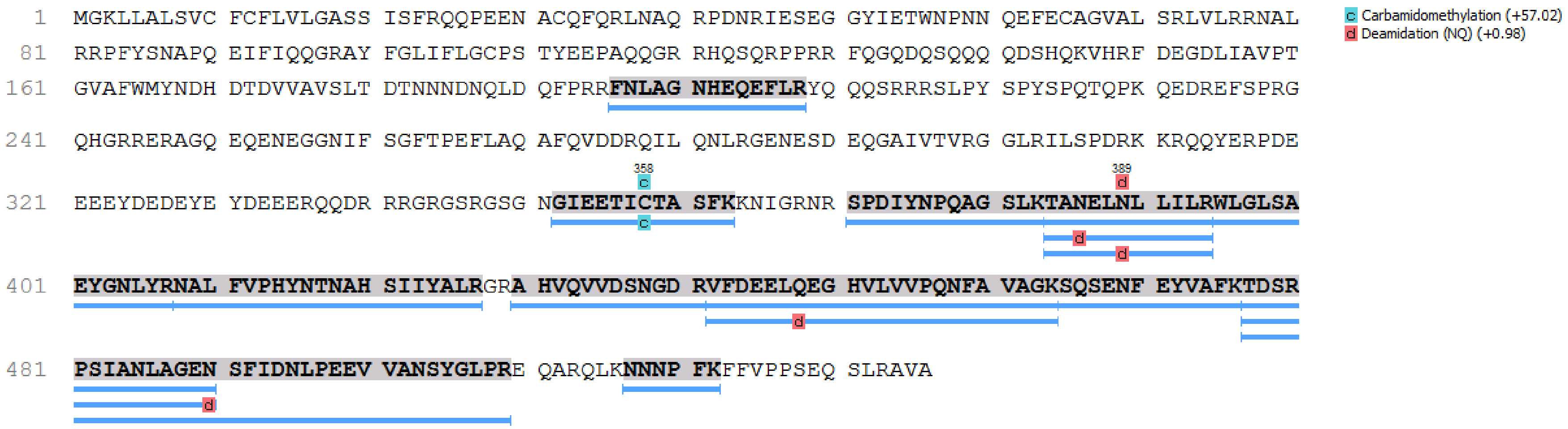
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRR**FNLAG NHEQEFLR**YQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE

321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG N**GIEETICTA SFK**KNIGRNR **SPDIYNPQAG SLKTANELNL LILRWLGLSA**

401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GR**A HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**

481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLK**NNNP FK**FFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	77.60	1540.7673	13	0.0	771.3909	2	32.81	17	2154	OB3615.raw	1.63E5	7	7	395	407	
K.SQSENFEYVAFK.T	N	99.9	63.61	1447.6619	12	-0.5	724.8378	2	29.84	17	1761	OB3615.raw	1.11E4	2	2	465	476	
K.TANELNLLILR.W	N	99.9	54.14	1268.7452	11	-0.3	635.3797	2	32.50	17	2113	OB3615.raw	1.42E5	5	5	384	394	
R.SPDIYNPQAGSLK.T	N	99.9	53.99	1388.6936	13	1.4	695.3550	2	27.10	17	1405	OB3615.raw	1.27E4	2	2	371	383	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	48.76	3544.7434	33	3.7	1182.5928	3	35.31	17	2490	OB3615.raw	2.03E4	3	3	477	509	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	48.74	1354.6438	12	-0.5	678.3289	2	29.27	17	1682	OB3615.raw	5.67E3	1	1	352	363	Carbamidomethylation
K.NNNPFK.F	N	99.9	47.24	732.3555	6	0.9	367.1853	2	21.83	17	1083	OB3615.raw	1.74E4	2	2	517	522	
R.NALFVPHYNTNAHSIIYALR.G	N	99.7	42.78	2313.2019	20	-2.0	579.3066	4	30.28	17	1821	OB3615.raw	2.45E5	4	4	408	427	
K.TANELN(+.98)LLILR.W	N	99.7	42.53	1269.7292	11	1.5	635.8729	2	33.64	17	2265	OB3615.raw	0	1	1	384	394	Deamidation (NQ)
R.AHVQVVDSNGDR.V	Y	99.7	41.66	1295.6218	12	1.8	648.8193	2	20.26	17	1002	OB3615.raw	3.38E3	3	3	430	441	
K.TAN(+.98)ELNLLILR.W	N	99.7	40.19	1269.7292	11	0.7	635.8723	2	33.41	17	2234	OB3615.raw	0	1	1	384	394	Deamidation (NQ)
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.7	40.10	2524.2961	23	1.4	842.4405	3	31.64	17	2000	OB3615.raw	4.36E4	2	2	442	464	
K.TDSRPSIANLAGEN(+.98).S	N	99.5	36.81	1444.6793	14	-1.6	723.3458	2	27.99	17	1514	OB3615.raw	7.72E3	1	1	477	490	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.5	36.25	1443.6953	14	-0.2	722.8548	2	27.55	17	1458	OB3615.raw	1.26E4	3	3	477	490	
R.VFDEELQ(+.98)EGHVLVVPQNFAVAGK.S	Y	98.0	31.97	2525.2800	23	1.4	842.7685	3	32.01	17	2049	OB3615.raw	1.07E4	1	1	442	464	Deamidation (NQ)
R.FNLAGNHEQEFLR.Y	N	96.0	28.91	1573.7637	13	-0.8	525.5947	3	28.69	17	1606	OB3615.raw	2.33E3	1	1	196	208	
total 16 peptides																		

Q647H1|Q647H1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVIGPFRLSL CVCLVFLTSA CFGTRLEESF NECQLDRLNA LTPDNRIESQ GGITETWNSN HPELRCAGVT LLKRTIFPNG

81 FHLPSYANYP QLIFIAQGNG VFGVSLPGCP VTYEEAESQS REDRRQRIVI KRESEQEQEQ QGDSHHKIYH FRQGHLLAIP

161 AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRRFYLA GNPEEEHPET QQQQPQTRRR HGQHQQDEYG SQGEEEGNNV

241 LSGFSTQLLA HAFGVDEEIA RILQNPPEQT KDQIVRVEGG FRDVISPRWG EGKQYEDELE ERQRQPPRRD EQGKGYDYDD

321 DRRPRHRQDP YREGDEDDRR PRGSRQGQGR GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY

456 c

401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRN**G VEETLCSPTL VEDIAR**PSRA DFYNPAAGR**I**

542 d

481 **SSANSLTFPI LRWFQLSAEH VLLYR**NGIYS PHWNNNANSI IYGLRGEGR**I QVVNSQGNAV FNGVLREGQI LLVPQNFAVG**

561 **K**QAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN

641 AQVDSKNNDG SRLWWPSSII IK

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.IQVVNSQGNAVFN(+.98)GVLR.E	Y	99.9	65.73	1814.9639	17	-0.6	908.4886	2	30.82	17	1892	OB3615.raw	1.94E4	2	2	530	546	Deamidation (NQ)
R.EGQILLVPQNFAVGK.Q	Y	99.9	62.21	1611.8984	15	0.8	806.9572	2	31.73	17	2011	OB3615.raw	5.64E4	2	2	547	561	
R.IQVVNSQ(+.98)GNAVFN(+.98)GVLR.E	Y	99.9	59.15	1815.9479	17	2.4	908.9834	2	30.74	17	1882	OB3615.raw	1.53E2	1	1	530	546	Deamidation (NQ)
R.ISSANSLTFPILR.W	Y	99.9	52.57	1417.7928	13	0.0	709.9037	2	31.83	17	2025	OB3615.raw	4.3E4	2	2	480	492	
R.IQVVNSQGNAVFNGVLR.E	Y	99.7	42.46	1813.9799	17	-0.2	605.6671	3	30.43	17	1840	OB3615.raw	2.13E3	1	1	530	546	
N.GVEETLC(+57.02)SPTLVEDIAR.P	Y	99.6	38.29	1887.9248	17	0.0	944.9697	2	31.87	17	2030	OB3615.raw	2.74E4	1	1	450	466	Carbamidomethylation
R.WFQLSAEHVLLYR.N	Y	99.0	34.83	1660.8726	13	-1.0	554.6309	3	32.54	17	2119	OB3615.raw	2.76E4	2	2	493	505	
total 7 peptides																		

Q6PSU4|Q6PSU4_ARAHY

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| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

52 d

1 GFDQRSRQFQ NLQNHR**IVQI EAKPNTLVLP KHADADNILV IQQGQATVTV ANGNNR**KSFN LDEGHALR**IP SGFISYILNR**

81 HDNQNLRVAK ISMPVNTPGQ FEDFFPASSR DQSSYLQGFS RNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRWSTRS

161 SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI

241 KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREEEEDEDE EEEGSNREVR RYTARLKEGD VFIMPAAHPV

321 AINASSELHL LGFGINAENN HRIFLAGDKD NVIDQIEKQA KDLAFPGSGE QVEKLIKNQK ESHFVSARPQ SQSQSPSSPE

401 KESPEKEDQE EENQGGKGPL LSILKAFN

d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.IPSGFISYILNR.H	Y	99.9	57.89	1378.7609	12	-0.9	690.3871	2	34.17	17	2337	OB3615.raw	5.31E3	1	1	69	80	
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	Y	99.7	40.70	2619.3000	25	1.5	874.1086	3	29.06	17	1654	OB3615.raw	2.76E4	1	1	32	56	Deamidation (NQ)
K.HADADNILVIQQGQATVTVANGNNR.K	Y	98.8	33.48	2618.3162	25	1.8	873.7809	3	28.80	17	1620	OB3615.raw	2.74E3	1	1	32	56	
R.IVQIEAKPNTLVLPK.H	Y	94.4	26.61	1662.0079	15	-0.8	555.0095	3	28.68	17	1603	OB3615.raw	2.57E4	2	2	17	31	
total 4 peptides																		

N1NG13|N1NG13_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHR**IVQIEAK PNTLVLPKHA DADNILVIQQ**

249
d
241 **GQATVTVANG NNR**KSFNLDE GHALR**IPSGF ISYILNR**HDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
d
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.IPSGFISYILNR.H	Y	99.9	57.89	1378.7609	12	-0.9	690.3871	2	34.17	17	2337	OB3615.raw	5.31E3	1	1	266	277	
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	Y	99.7	40.70	2619.3000	25	1.5	874.1086	3	29.06	17	1654	OB3615.raw	2.76E4	1	1	229	253	Deamidation (NQ)
K.HADADNILVIQQGQATVTVANGNNR.K	Y	98.8	33.48	2618.3162	25	1.8	873.7809	3	28.80	17	1620	OB3615.raw	2.74E3	1	1	229	253	
R.IVQIEAKPNTLVLPK.H	Y	94.4	26.61	1662.0079	15	-0.8	555.0095	3	28.68	17	1603	OB3615.raw	2.57E4	2	2	214	228	
total 4 peptides																		

sp|P43238|ALL12_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHR**IVQIEAK PNTLVLPKHA DADNILVIQQ**

249
d
241 **GQATVTVANG NNR**KSFNLDE GHALR**IPSGF ISYILNR**HDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
d
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.IPSGFISYILNR.H	Y	99.9	57.89	1378.7609	12	-0.9	690.3871	2	34.17	17	2337	OB3615.raw	5.31E3	1	1	266	277	
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	Y	99.7	40.70	2619.3000	25	1.5	874.1086	3	29.06	17	1654	OB3615.raw	2.76E4	1	1	229	253	Deamidation (NQ)
K.HADADNILVIQQGQATVTVANGNNR.K	Y	98.8	33.48	2618.3162	25	1.8	873.7809	3	28.80	17	1620	OB3615.raw	2.74E3	1	1	229	253	
R.IVQIEAKPNTLVLPK.H	Y	94.4	26.61	1662.0079	15	-0.8	555.0095	3	28.68	17	1603	OB3615.raw	2.57E4	2	2	214	228	
total 4 peptides																		

sp|Q647H2|AHY3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS VTFRQQGEEN ECQFQRLNAQ RPDNCIESEG GYIETWNPNN QEFQCAGVAL SRFVLRRNAL
81 RRPFYSNAPQ EIFIYQGSGY FGLIFPGCPG TFEEPIQGSE QFQRPSRHFQ GQDQSQRPLD THQKVHGFRE GDLIAVPHGV
161 AFWIYNDQDT DVVAISVLHT NSLHNQLDQF PRRFNLAGKQ EQEFLRYQQR SGRQSPKGEE QEQEQENEGG NVFSGFSTEF
241 LSHGFQVNED IVRNLRGENE REEQGAIVTV KGGLSILVPP EWRQSYQQPG RGDKDFNNGI EETICTATVK MNIGKSTSAD
321 IYNPQAGSVR **TVNELDLPIL NR**LGLSAEYG SIHRDAMFVP HYNMNANSMI YALHGGAHVQ VVDCNGNRVF DEELQEGQSL
401 VVPQNFAVAA K**SQSEHFLYV AFK**TNSRASI SNLAGKNSYM WNLPEDVVAN SYGLQYEQAR QLKNNNPFTF LVPPQDSQMI
481 RTVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 17	#Spec	#Spec Sample 17	Start	End	PTM
R.TVNELDLPILNR.L	Y	99.9	55.21	1395.7721	12	-0.1	698.8932	2	32.29	17	2086	OB3615.raw	3.26E4	2	2	331	342	
K.SQSEHFLYVAFK.T	Y	99.0	34.03	1454.7194	12	-0.9	485.9133	3	29.91	17	1770	OB3615.raw	2.19E4	1	1	412	423	
total 2 peptides																		

Peptide List

1. Notes Spot 11 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

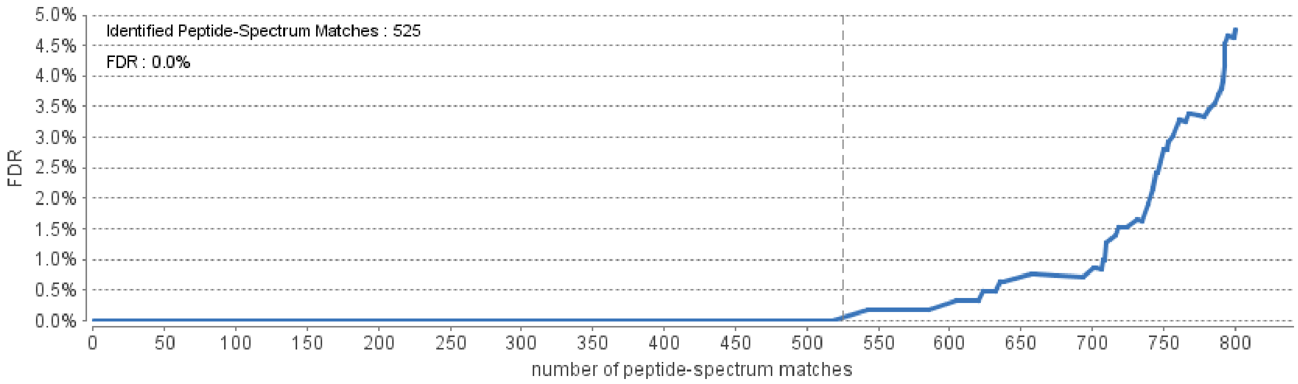
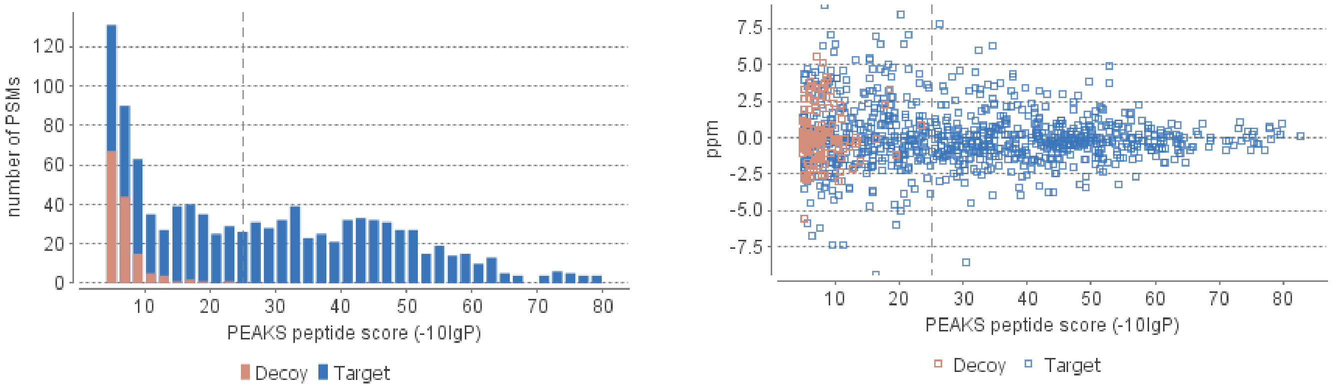


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.



(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

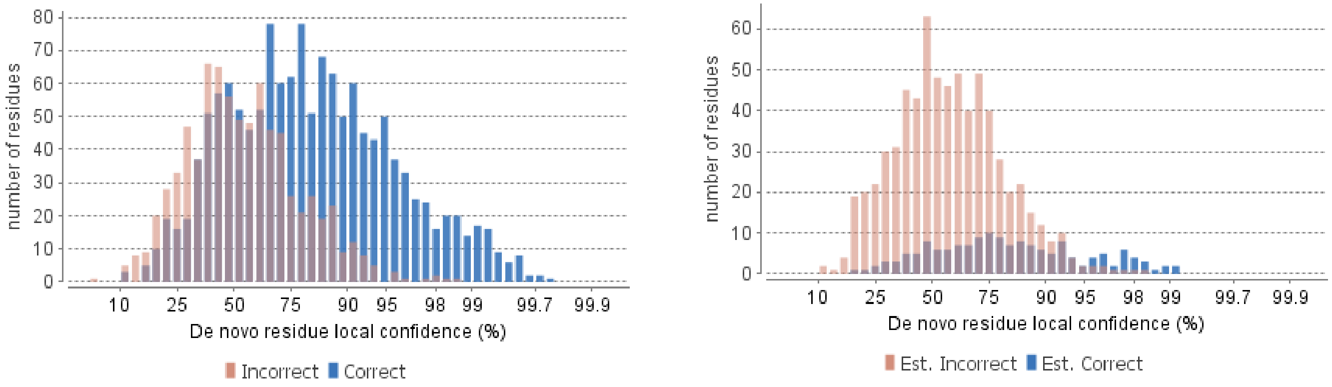


Table 1. Statistics of data.

# of MS scans	2960
# of MS/MS scans	2761

Table 2. Result filtration parameters.

Peptide -10lgP	≥25
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	462
Peptide sequences	82
Protein groups	2
Proteins	4
Proteins (#Unique Peptides)	2 (>2); 2 (=2); 0 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	83

Table 4. PTM profile.

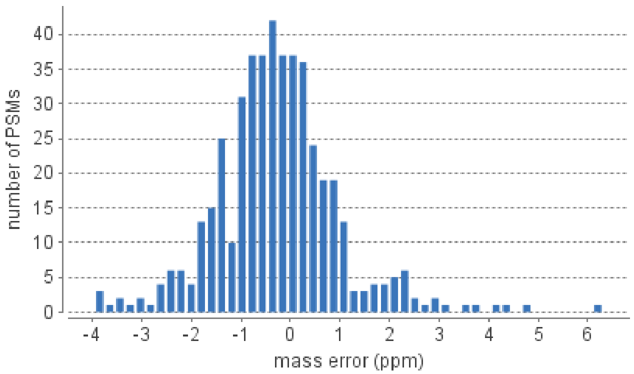
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	25	72.34	1.49E5	1000.00
Deamidation	.98	NQ	21	64.23	1.46E4	37.54
Oxidation	15.99	M	17	41.42	1.1E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



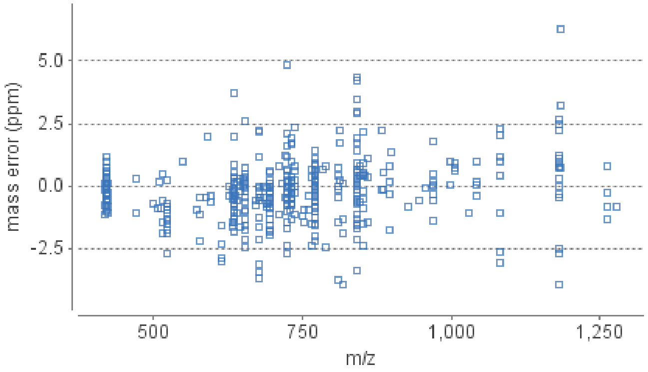


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 21	80	2	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3619.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 21	Area Sample 21	#Peptides	#Unique	#Spec Sample 21	PTM	Avg. Mass	Description
1	7	Q647H4|Q647H4_ARAHY	99.1	235.54	28	28	5.75E6	18	4	261	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
1	12	Q6T2T4|Q6T2T4_ARAHY	99.1	235.54	28	28	5.75E6	18	4	261	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
7	41	Q6IWG5|Q6IWG5_ARAHY	99.1	179.89	29	29	5.73E5	14	2	81	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
7	42	Q0GM57|Q0GM57_ARAHY	99.1	179.89	29	29	5.73E5	14	2	81	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 4 proteins													

Q647H4|Q647H4_ARAHY

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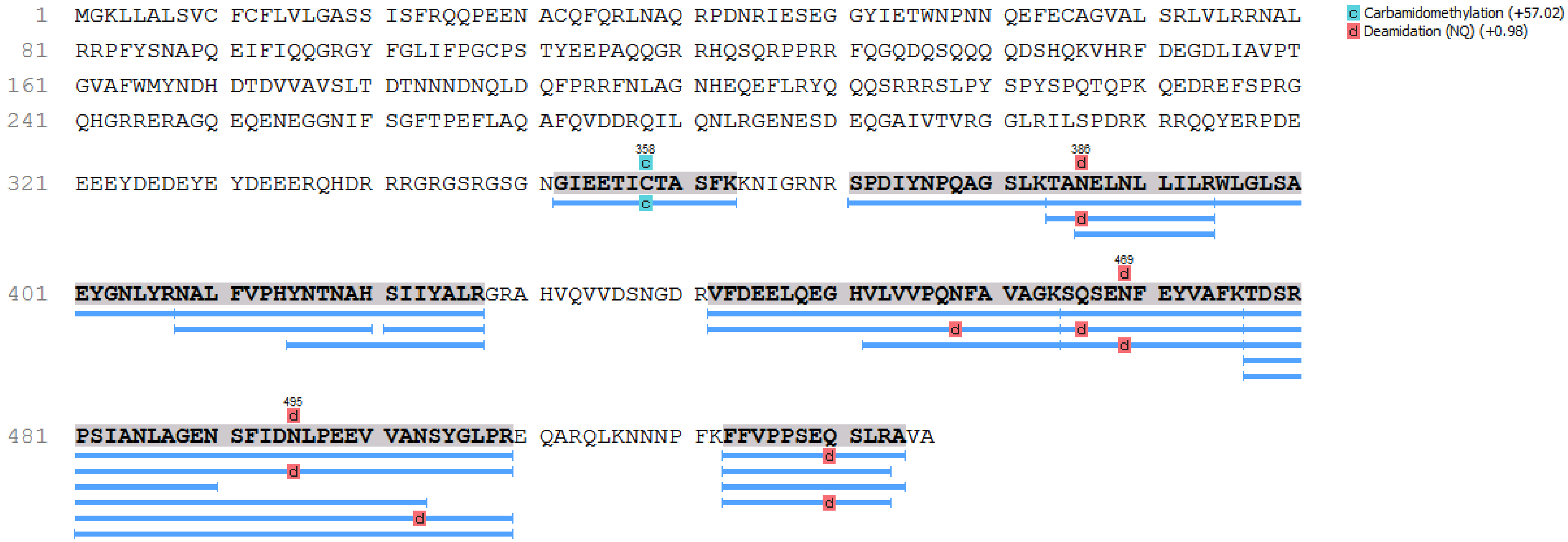
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG N**GIEETICTA SFK**KNIGRNR **SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GRA HVQVVDSNGD R**VFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FK**FFVPPSEQ SLRA**VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 21	#Spec	#Spec Sample 21	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	82.80	1540.7673	13	0.1	771.3911	2	32.29	21	2260	OB3619.raw	2.36E6	38	38	395	407	
K.SQSENFEYVAFK.T	N	99.9	75.49	1447.6619	12	-0.3	724.8380	2	29.81	21	1930	OB3619.raw	7.01E5	25	25	465	476	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	72.34	1354.6438	12	-0.6	678.3288	2	28.78	21	1800	OB3619.raw	4.29E5	16	16	352	363	Carbamidomethylation
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.9	68.52	2524.2961	23	-0.3	1263.1550	2	31.48	21	2154	OB3619.raw	3.76E6	37	37	442	464	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	63.72	2313.2019	20	-1.0	772.0738	3	30.21	21	1985	OB3619.raw	1.92E6	10	10	408	427	
K.TANELNLLILR.W	N	99.9	63.56	1268.7452	11	-0.4	635.3796	2	32.69	21	2314	OB3619.raw	3.79E6	37	37	384	394	
R.SPDIYNPQAGSLK.T	N	99.9	63.51	1388.6936	13	-0.8	695.3535	2	3.81	21	180	OB3619.raw	7.96E5	35	35	371	383	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	61.24	1448.6459	12	-1.7	725.3290	2	30.11	21	1972	OB3619.raw	4.29E4	1	1	465	476	Deamidation (NQ)

K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	55.00	3544.7434	33	0.8	1182.5894	3	34.85	21	2604	OB3619.raw	9.15E5	18	18	477	509	
K.SQSEN(+.98)FEYVAFK.T	N	99.9	52.75	1448.6459	12	4.9	725.3337	2	30.44	21	2016	OB3619.raw	0	1	1	465	476	Deamidation (NQ)
K.FFVPPSEQSLR.A	Y	99.9	51.13	1305.6716	11	-1.0	653.8424	2	6.18	21	529	OB3619.raw	8.32E5	20	20	523	533	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	44.43	3545.7273	33	0.7	1182.9172	3	34.22	21	2519	OB3619.raw	1.19E4	1	1	477	509	Deamidation (NQ)
K.TAN(+.98)ELNLLILR.W	N	99.8	41.10	1269.7292	11	2.0	635.8732	2	33.37	21	2404	OB3619.raw	0	2	2	384	394	Deamidation (NQ)
R.VFDEELQEGHVLVVPQN(+.98)FAVAGK.S	Y	99.6	37.64	2525.2800	23	4.3	842.7709	3	32.11	21	2236	OB3619.raw	5.9E5	1	1	442	464	Deamidation (NQ)
A.NELNLLILR.W	N	99.5	36.78	1096.6604	9	1.0	549.3380	2	32.31	21	2264	OB3619.raw	3.52E3	1	1	386	394	
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.3	34.53	3545.7273	33	6.3	1182.9238	3	4.94	21	349	OB3619.raw	1.51E5	2	2	477	509	Deamidation (NQ)
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.0	32.66	3085.5356	29	-1.1	1029.5181	3	35.69	21	2713	OB3619.raw	3.66E4	1	1	481	509	
H.SIIYALR.G	N	98.8	32.22	834.4963	7	0.1	418.2555	2	27.98	21	1705	OB3619.raw	1.67E5	4	4	421	427	
K.FFVPPSEQSLRA.V	Y	98.7	31.83	1376.7087	12	-0.8	689.3611	2	28.98	21	1825	OB3619.raw	2.34E4	1	1	523	534	
K.TDSRPSIANLAGEN.S	N	98.5	31.26	1443.6953	14	-0.4	722.8546	2	27.39	21	1647	OB3619.raw	2.24E3	2	2	477	490	
R.NALFVPHYNTNAH.S	N	97.9	30.35	1496.7161	13	-0.7	499.9123	3	27.12	21	1618	OB3619.raw	1.15E5	2	2	408	420	
K.FFVPPSEQ(+.98)SLRA.V	Y	97.8	29.32	1377.6927	12	-0.1	689.8536	2	29.50	21	1890	OB3619.raw	1.16E5	2	2	523	534	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	97.7	28.97	1534.7892	13	-0.9	512.6032	3	28.80	21	1803	OB3619.raw	2.32E4	1	1	415	427	
K.TDSRPSIANLAGENSFIDNLPEEVVAN.S	N	97.7	28.80	2871.3887	27	-0.1	958.1367	3	34.26	21	2525	OB3619.raw	1.53E4	1	1	477	503	
K.FFVPPSEQ(+.98)SLR.A	Y	97.2	28.72	1306.6556	11	2.6	654.3368	2	29.33	21	1867	OB3619.raw	0	1	1	523	533	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	96.4	28.37	1340.7816	13	-0.6	671.3977	2	29.54	21	1896	OB3619.raw	8.77E3	1	1	452	464	
total 26 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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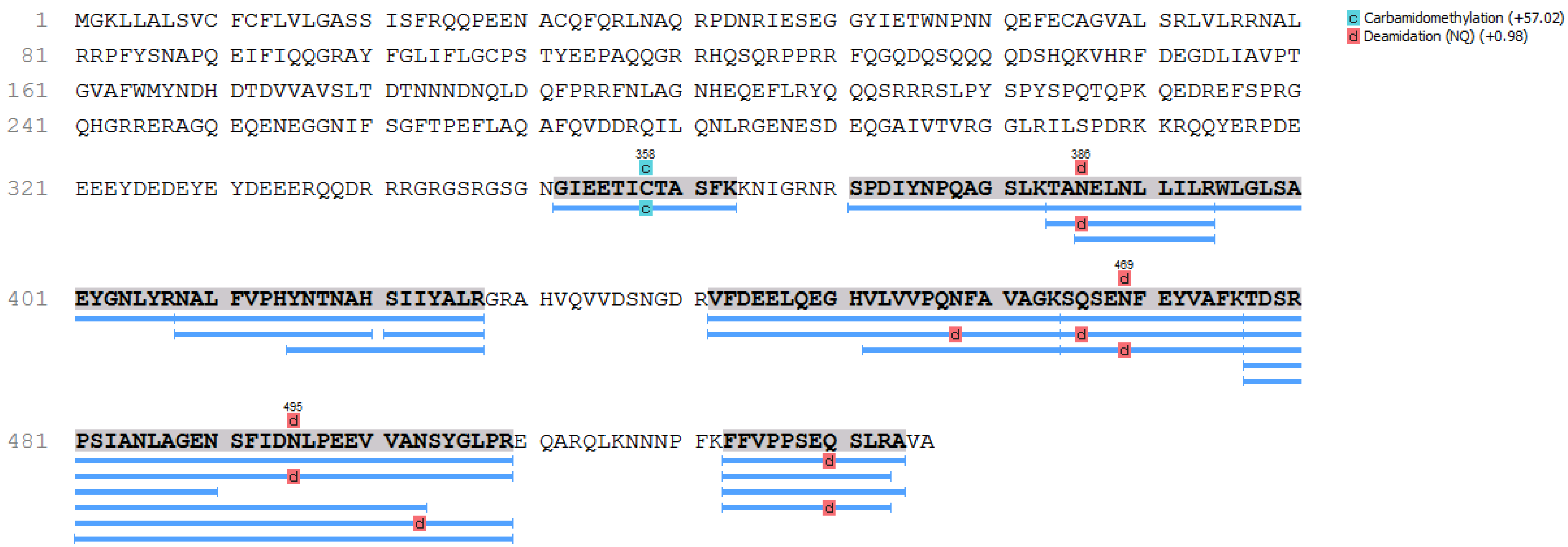
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE

321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA

401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 21	#Spec	#Spec Sample 21	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	82.80	1540.7673	13	0.1	771.3911	2	32.29	21	2260	OB3619.raw	2.36E6	38	38	395	407	

K.SQSENFEYVAFK.T	N	99.9	75.49	1447.6619	12	-0.3	724.8380	2	29.81	21	1930	OB3619.raw	7.01E5	25	25	465	476	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	72.34	1354.6438	12	-0.6	678.3288	2	28.78	21	1800	OB3619.raw	4.29E5	16	16	352	363	Carbamidomethylation
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.9	68.52	2524.2961	23	-0.3	1263.1550	2	31.48	21	2154	OB3619.raw	3.76E6	37	37	442	464	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	63.72	2313.2019	20	-1.0	772.0738	3	30.21	21	1985	OB3619.raw	1.92E6	10	10	408	427	
K.TANELNLLILR.W	N	99.9	63.56	1268.7452	11	-0.4	635.3796	2	32.69	21	2314	OB3619.raw	3.79E6	37	37	384	394	
R.SPDIYNPQAGSLK.T	N	99.9	63.51	1388.6936	13	-0.8	695.3535	2	3.81	21	180	OB3619.raw	7.96E5	35	35	371	383	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	61.24	1448.6459	12	-1.7	725.3290	2	30.11	21	1972	OB3619.raw	4.29E4	1	1	465	476	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	55.00	3544.7434	33	0.8	1182.5894	3	34.85	21	2604	OB3619.raw	9.15E5	18	18	477	509	
K.SQSEN(+.98)FEYVAFK.T	N	99.9	52.75	1448.6459	12	4.9	725.3337	2	30.44	21	2016	OB3619.raw	0	1	1	465	476	Deamidation (NQ)
K.FFVPPSEQSLR.A	Y	99.9	51.13	1305.6716	11	-1.0	653.8424	2	6.18	21	529	OB3619.raw	8.32E5	20	20	523	533	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	44.43	3545.7273	33	0.7	1182.9172	3	34.22	21	2519	OB3619.raw	1.19E4	1	1	477	509	Deamidation (NQ)
K.TAN(+.98)ELNLLILR.W	N	99.8	41.10	1269.7292	11	2.0	635.8732	2	33.37	21	2404	OB3619.raw	0	2	2	384	394	Deamidation (NQ)
R.VFDEELQEGHVLVVPQN(+.98)FAVAGK.S	Y	99.6	37.64	2525.2800	23	4.3	842.7709	3	32.11	21	2236	OB3619.raw	5.9E5	1	1	442	464	Deamidation (NQ)
A.NELNLLILR.W	N	99.5	36.78	1096.6604	9	1.0	549.3380	2	32.31	21	2264	OB3619.raw	3.52E3	1	1	386	394	
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.3	34.53	3545.7273	33	6.3	1182.9238	3	4.94	21	349	OB3619.raw	1.51E5	2	2	477	509	Deamidation (NQ)
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.0	32.66	3085.5356	29	-1.1	1029.5181	3	35.69	21	2713	OB3619.raw	3.66E4	1	1	481	509	
H.SIIYALR.G	N	98.8	32.22	834.4963	7	0.1	418.2555	2	27.98	21	1705	OB3619.raw	1.67E5	4	4	421	427	
K.FFVPPSEQSLRA.V	Y	98.7	31.83	1376.7087	12	-0.8	689.3611	2	28.98	21	1825	OB3619.raw	2.34E4	1	1	523	534	
K.TDSRPSIANLAGEN.S	N	98.5	31.26	1443.6953	14	-0.4	722.8546	2	27.39	21	1647	OB3619.raw	2.24E3	2	2	477	490	
R.NALFVPHYNTNAH.S	N	97.9	30.35	1496.7161	13	-0.7	499.9123	3	27.12	21	1618	OB3619.raw	1.15E5	2	2	408	420	
K.FFVPPSEQ(+.98)SLRA.V	Y	97.8	29.32	1377.6927	12	-0.1	689.8536	2	29.50	21	1890	OB3619.raw	1.16E5	2	2	523	534	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	97.7	28.97	1534.7892	13	-0.9	512.6032	3	28.80	21	1803	OB3619.raw	2.32E4	1	1	415	427	
K.TDSRPSIANLAGENSFIDNLPEEVVAN.S	N	97.7	28.80	2871.3887	27	-0.1	958.1367	3	34.26	21	2525	OB3619.raw	1.53E4	1	1	477	503	
K.FFVPPSEQ(+.98)SLR.A	Y	97.2	28.72	1306.6556	11	2.6	654.3368	2	29.33	21	1867	OB3619.raw	0	1	1	523	533	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	96.4	28.37	1340.7816	13	-0.6	671.3977	2	29.54	21	1896	OB3619.raw	8.77E3	1	1	452	464	
total 26 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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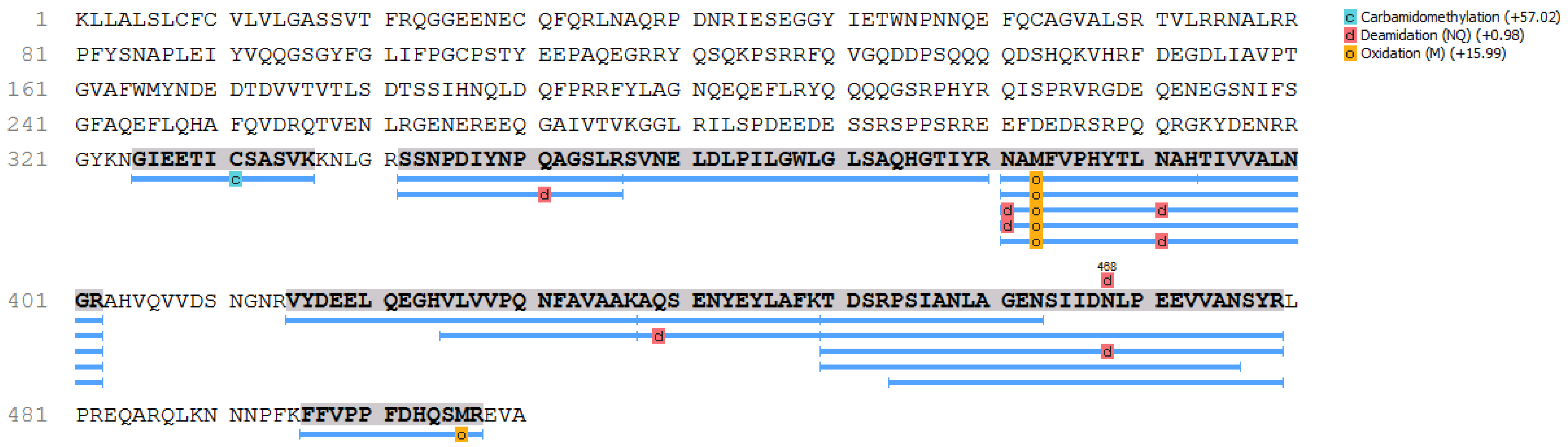
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKN**GIEETI CSASVK**KNLG R**SSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN**
401 **GR**AHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYR**L
481 PREQARQLKN NNPFK**FFVPP FDHQSMR**EVA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
o Oxidation (M) (+15.99)

Supporting Peptides:

													Area		**#Spec**			

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Sample 21	#Spec	Sample 21	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	N	99.9	68.48	1617.7747	15	0.0	809.8946	2	26.97	21	1603	OB3619.raw	2.33E5	6	6	342	356	
K.AQ(+.98)SENYEYLAFK.T	N	99.9	64.23	1462.6616	12	-0.5	732.3377	2	29.51	21	1892	OB3619.raw	1.46E4	2	2	438	449	Deamidation (NQ)
K.AQSENYEYLAFK.T	N	99.9	64.09	1461.6776	12	-0.4	731.8458	2	29.81	21	1931	OB3619.raw	4.18E5	19	19	438	449	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	61.97	3243.6006	30	0.4	1082.2079	3	33.77	21	2458	OB3619.raw	5.1E5	12	12	450	479	
R.VYDEELQEGHVLVVPQNFAVAAK.A	N	99.9	54.29	2554.3066	23	0.9	852.4436	3	30.88	21	2074	OB3619.raw	1.95E6	16	16	415	437	
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYR.L	Y	99.9	51.52	3244.5847	30	2.0	1082.5377	3	33.09	21	2368	OB3619.raw	4.8E4	1	1	450	479	Deamidation (NQ)
N.GIEETIC(+57.02)SASVK.K	N	99.9	50.67	1292.6282	12	-0.2	647.3212	2	27.28	21	1633	OB3619.raw	4.64E4	4	4	325	336	Carbamidomethylation
R.SSNPDIYNPQ(+.98)AGSLR.S	N	99.8	43.33	1618.7587	15	-3.8	810.3835	2	27.13	21	1619	OB3619.raw	4.57E4	1	1	342	356	Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	99.4	35.50	2453.2637	22	-1.9	818.7603	3	30.71	21	2052	OB3619.raw	5.33E4	5	5	381	402	Oxidation (M)
R.N(+.98)AM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	99.3	34.60	2455.2317	22	-3.9	819.4146	3	31.07	21	2100	OB3619.raw	1.6E3	1	1	381	402	Deamidation (NQ); Oxidation (M)
H.TIVVALNGR.A	N	99.3	34.40	941.5658	9	0.3	471.7903	2	26.39	21	1549	OB3619.raw	1.46E3	2	2	394	402	
R.PSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.3	34.38	2784.3928	26	-0.8	929.1375	3	34.81	21	2599	OB3619.raw	1.45E4	1	1	454	479	
R.SVNELDLPILGWLGLSAQHGTIYR.N	N	98.8	32.17	2651.4070	24	-0.2	884.8094	3	4.66	21	307	OB3619.raw	2.63E5	3	3	357	380	
R.NAM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	98.7	31.75	2454.2478	22	0.1	819.0900	3	31.62	21	2171	OB3619.raw	2.54E4	1	1	381	402	Oxidation (M); Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	98.5	31.26	1443.6953	14	-0.4	722.8546	2	27.39	21	1647	OB3619.raw	2.24E3	2	2	450	463	
H.VLVVPQNFAVAAK.A	N	97.8	29.58	1354.7972	13	-0.1	678.4058	2	29.73	21	1920	OB3619.raw	2.34E3	1	1	425	437	
K.FFVPPFDHQSM(+15.99)R.E	N	96.1	27.54	1522.7026	12	-0.9	508.5744	3	29.11	21	1838	OB3619.raw	4.29E4	1	1	496	507	Oxidation (M)
R.NAM(+15.99)FVPHYTLNAH.T	N	96.1	27.48	1529.7085	13	0.2	510.9102	3	27.25	21	1629	OB3619.raw	1.29E4	1	1	381	393	Oxidation (M)
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	95.6	26.53	2837.4043	27	-0.6	946.8082	3	33.69	21	2448	OB3619.raw	1.3E4	1	1	450	476	
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	95.3	26.28	2454.2478	22	-3.0	614.5674	4	31.58	21	2166	OB3619.raw	2.17E4	1	1	381	402	Deamidation (NQ); Oxidation (M)
total 20 peptides																		

Q0GM57|Q0GM57_ARAHY

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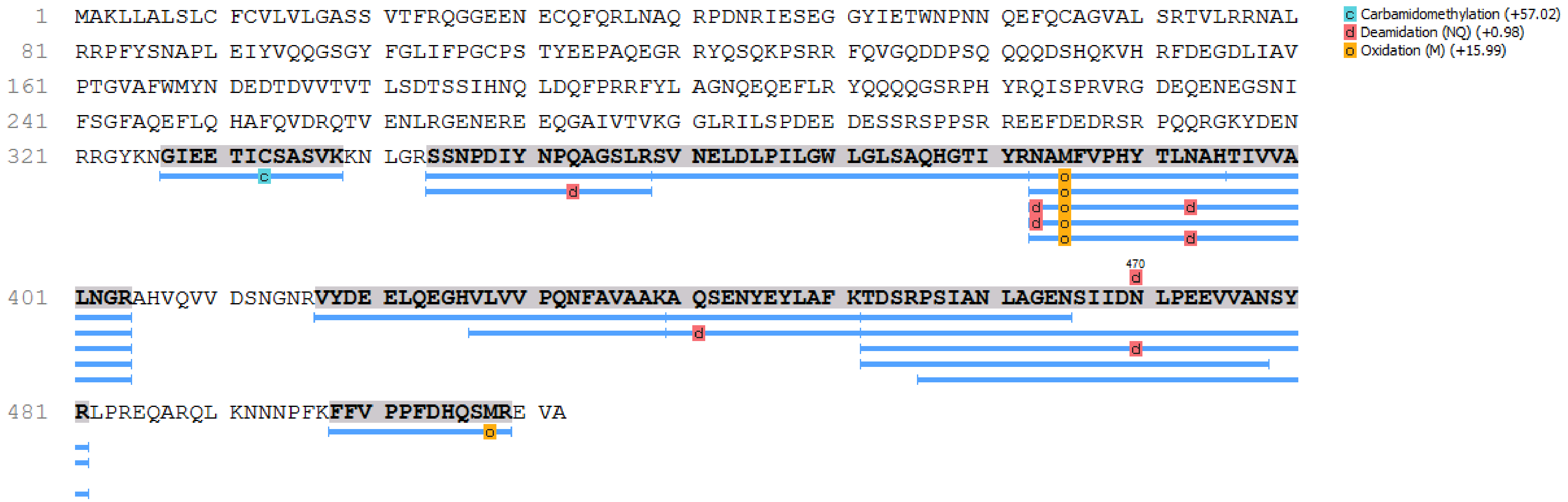
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKN**GIEE TICSASVK**KN LGR**SSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA**
401 **LNGR**AHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY**
481 **R**LPREQARQL KNNNPFK**FFV PPFDHQSMR**E VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 21	#Spec	#Spec Sample 21	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	N	99.9	68.48	1617.7747	15	0.0	809.8946	2	26.97	21	1603	OB3619.raw	2.33E5	6	6	344	358	
K.AQ(+.98)SENYEYLAFK.T	N	99.9	64.23	1462.6616	12	-0.5	732.3377	2	29.51	21	1892	OB3619.raw	1.46E4	2	2	440	451	Deamidation (NQ)
K.AQSENYEYLAFK.T	N	99.9	64.09	1461.6776	12	-0.4	731.8458	2	29.81	21	1931	OB3619.raw	4.18E5	19	19	440	451	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	61.97	3243.6006	30	0.4	1082.2079	3	33.77	21	2458	OB3619.raw	5.1E5	12	12	452	481	
R.VYDEELQEGHVLVVPQNFAVAAK.A	N	99.9	54.29	2554.3066	23	0.9	852.4436	3	30.88	21	2074	OB3619.raw	1.95E6	16	16	417	439	
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYR.L	Y	99.9	51.52	3244.5847	30	2.0	1082.5377	3	33.09	21	2368	OB3619.raw	4.8E4	1	1	452	481	Deamidation (NQ)
N.GIEETIC(+57.02)SASVK.K	N	99.9	50.67	1292.6282	12	-0.2	647.3212	2	27.28	21	1633	OB3619.raw	4.64E4	4	4	327	338	Carbamidomethylation
R.SSNPDIYNPQ(+.98)AGSLR.S	N	99.8	43.33	1618.7587	15	-3.8	810.3835	2	27.13	21	1619	OB3619.raw	4.57E4	1	1	344	358	Deamidation (NQ)
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	99.4	35.50	2453.2637	22	-1.9	818.7603	3	30.71	21	2052	OB3619.raw	5.33E4	5	5	383	404	Oxidation (M)
R.N(+.98)AM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	99.3	34.60	2455.2317	22	-3.9	819.4146	3	31.07	21	2100	OB3619.raw	1.6E3	1	1	383	404	Deamidation (NQ); Oxidation (M)
H.TIVVALNGR.A	N	99.3	34.40	941.5658	9	0.3	471.7903	2	26.39	21	1549	OB3619.raw	1.46E3	2	2	396	404	
R.PSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.3	34.38	2784.3928	26	-0.8	929.1375	3	34.81	21	2599	OB3619.raw	1.45E4	1	1	456	481	
R.SVNELDLPILGWLGLSAQHGTIYR.N	N	98.8	32.17	2651.4070	24	-0.2	884.8094	3	4.66	21	307	OB3619.raw	2.63E5	3	3	359	382	
R.NAM(+15.99)FVPHYTLN(+.98)AHTIVVALNGR.A	N	98.7	31.75	2454.2478	22	0.1	819.0900	3	31.62	21	2171	OB3619.raw	2.54E4	1	1	383	404	Oxidation (M); Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	98.5	31.26	1443.6953	14	-0.4	722.8546	2	27.39	21	1647	OB3619.raw	2.24E3	2	2	452	465	
H.VLVVPQNFAVAAK.A	N	97.8	29.58	1354.7972	13	-0.1	678.4058	2	29.73	21	1920	OB3619.raw	2.34E3	1	1	427	439	
K.FFVPPFDHQSM(+15.99)R.E	N	96.1	27.54	1522.7026	12	-0.9	508.5744	3	29.11	21	1838	OB3619.raw	4.29E4	1	1	498	509	Oxidation (M)
R.NAM(+15.99)FVPHYTLNAH.T	N	96.1	27.48	1529.7085	13	0.2	510.9102	3	27.25	21	1629	OB3619.raw	1.29E4	1	1	383	395	Oxidation (M)
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	95.6	26.53	2837.4043	27	-0.6	946.8082	3	33.69	21	2448	OB3619.raw	1.3E4	1	1	452	478	
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	N	95.3	26.28	2454.2478	22	-3.0	614.5674	4	31.58	21	2166	OB3619.raw	2.17E4	1	1	383	404	Deamidation (NQ); Oxidation (M)
total 20 peptides																		

Peptide List

Summary

1. Notes

Spot 12 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

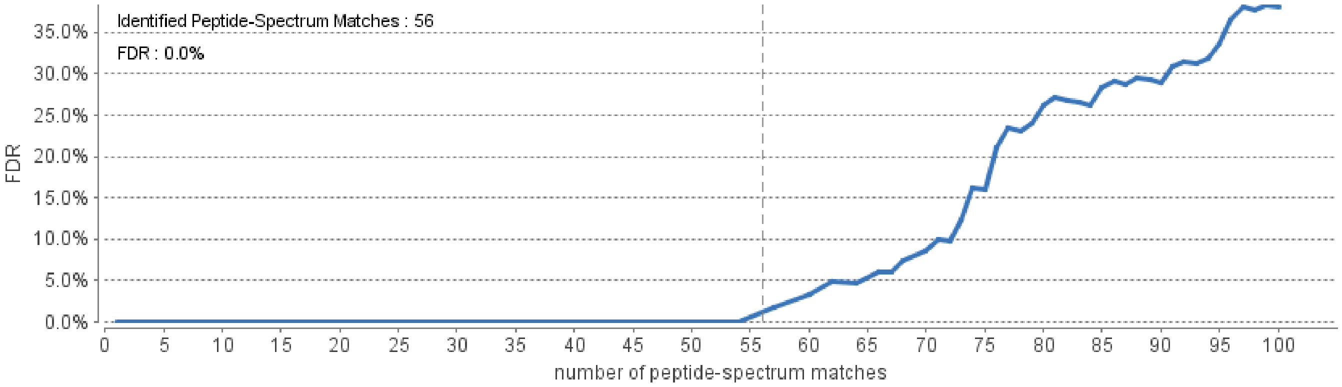


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

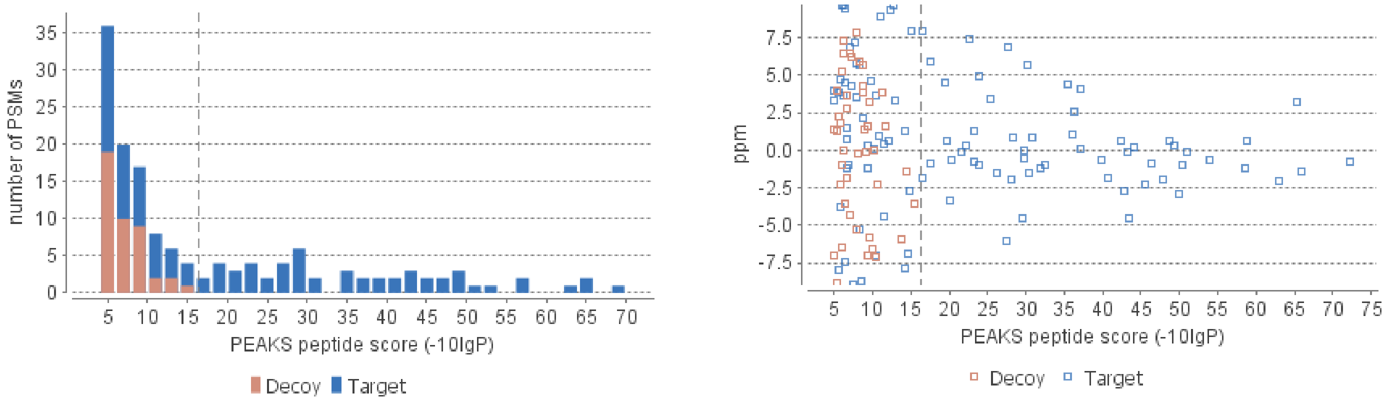

(a) **(b)**

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a) **(b)**

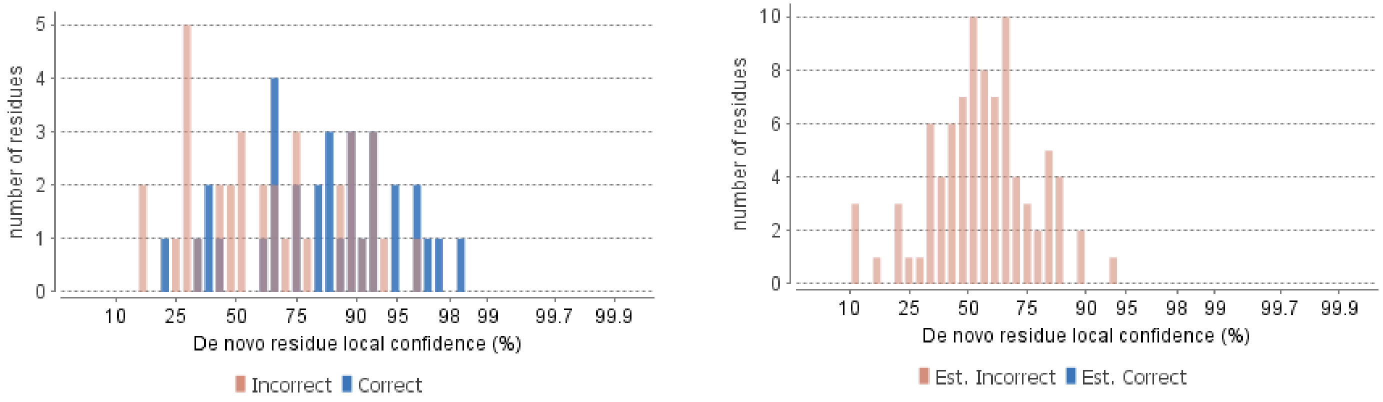


Table 1. Statistics of data.

# of MS scans	2943
# of MS/MS scans	2845

Table 2. Result filtration parameters.

Peptide -10lgP	≥16.4
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	44
Peptide sequences	20
Protein groups	3
Proteins	9
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 9 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	12

Table 4. PTM profile.

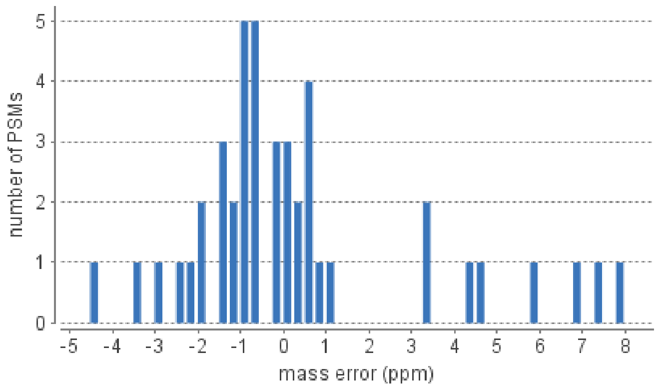
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Deamidation	.98	NQ	4	35.38		22.78
Carbamidomethyl	57.02	C	3	27.60	5.51E2	1000.00
HydPro	15.99	P	1	17.61		30.57
Oxidation	15.99	M	1	16.43	1.86E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm. ?

(a)

(b)



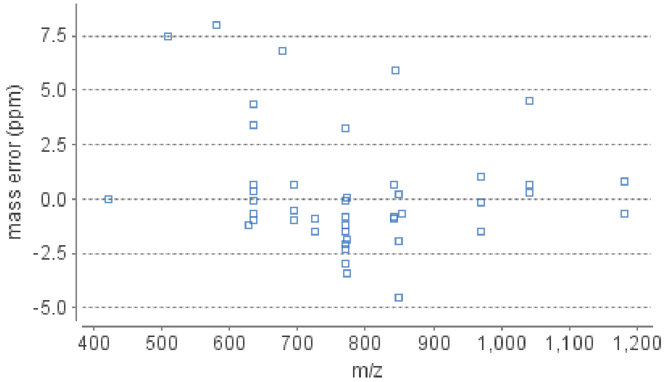


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 22	18	0	2	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3620.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 22	Area Sample 22	#Peptides	#Unique	#Spec Sample 22	PTM	Avg. Mass	Description
1	7	Q647H4|Q647H4_ARAHY	99.1	162.19	25	25	7.07E4	8	1	29	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
1	12	Q6T2T4|Q6T2T4_ARAHY	99.1	162.19	25	25	7.07E4	8	1	29	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
6	41	Q6IWG5|Q6IWG5_ARAHY	82.8	54.94	5	5	1.41E4	1	1	1	N	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
6	42	Q0GM57|Q0GM57_ARAHY	82.8	54.94	4	4	1.41E4	1	1	1	N	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
9	289	G0Y6V1|G0Y6V1_ARAHY	33.5	22.56	1	1	8.39E3	1	1	1	N	126434	NBS-LRR type disease resistance protein OS=Arachis hypogaea GN=205D04_1 PE=3 SV=1
9	1029	G0Y6V0|G0Y6V0_ARAHY	32.6	22.56	1	1	8.39E3	1	1	1	N	97063	TIR-NBS-LRR-TIR type disease resistance protein OS=Arachis hypogaea GN=303L13_20 PE=3 SV=1
9	713	G0Y6V4|G0Y6V4_ARAHY	32.6	22.56	1	1	8.39E3	1	1	1	N	98838	TIR-NBS-LRR type disease resistance protein OS=Arachis hypogaea GN=205D04_4 PE=3 SV=1
9	1033	G0Y6W5|G0Y6W5_ARAHY	32.6	22.56	1	1	8.39E3	1	1	1	N	105074	TIR-NBS-LRR type disease resistance protein OS=Arachis hypogaea GN=205D04_15 PE=4 SV=1
9	111	G0Y6W1|G0Y6W1_ARAHY	32.6	22.56	1	1	8.39E3	1	1	1	N	221451	TIR-NBS-LRR type disease resistance protein OS=Arachis hypogaea GN=205D04_11 PE=3 SV=1
total 9 proteins													

Q647H4|Q647H4_ARAHY

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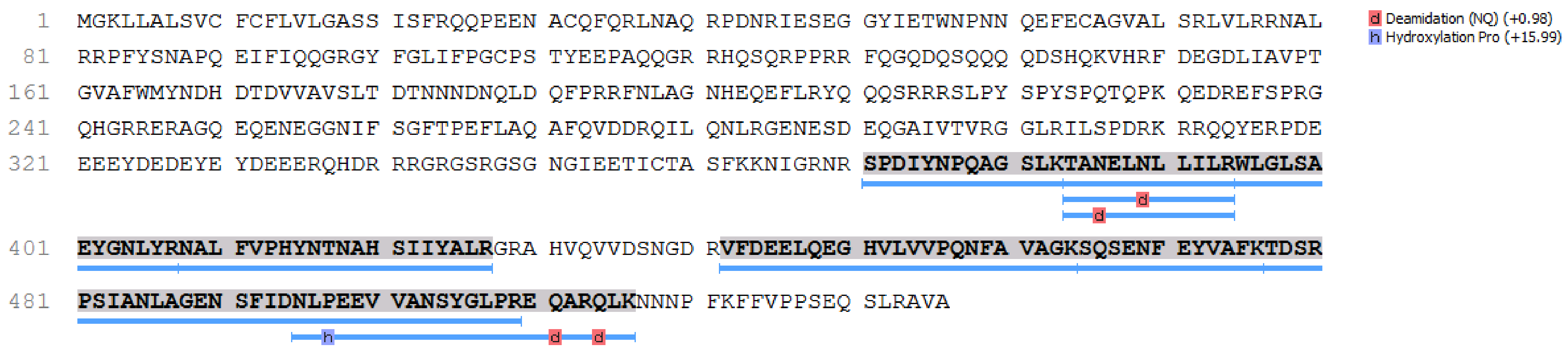
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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  1  MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
 81  RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161  GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241  QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321  EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
401  EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR
481  PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
```

🟥 d Deamidation (NQ) (+0.98)
🟦 h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	72.35	1540.7673	13	-0.8	771.3903	2	32.38	22	1650	OB3620.raw	4.16E4	8	8	395	407	
K.SQSENFEYVAFK.T	N	99.9	65.90	1447.6619	12	-1.5	724.8372	2	29.90	22	1436	OB3620.raw	3.23E3	2	2	465	476	
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.9	58.70	2524.2961	23	0.7	842.4399	3	31.40	22	1563	OB3620.raw	7.07E4	3	3	442	464	
K.TANELNLLILR.W	N	99.9	53.88	1268.7452	11	-0.7	635.3795	2	32.46	22	1658	OB3620.raw	2.17E4	5	5	384	394	
R.SPDIYNPQAGSLK.T	N	99.6	42.29	1388.6936	13	0.7	695.3546	2	27.03	22	1287	OB3620.raw	3.98E3	3	3	371	383	
R.NALFVPHYNTNAHSIIYALR.G	N	98.9	40.69	2313.2019	20	-1.9	772.0731	3	30.44	22	1477	OB3620.raw	6.84E3	3	3	408	427	

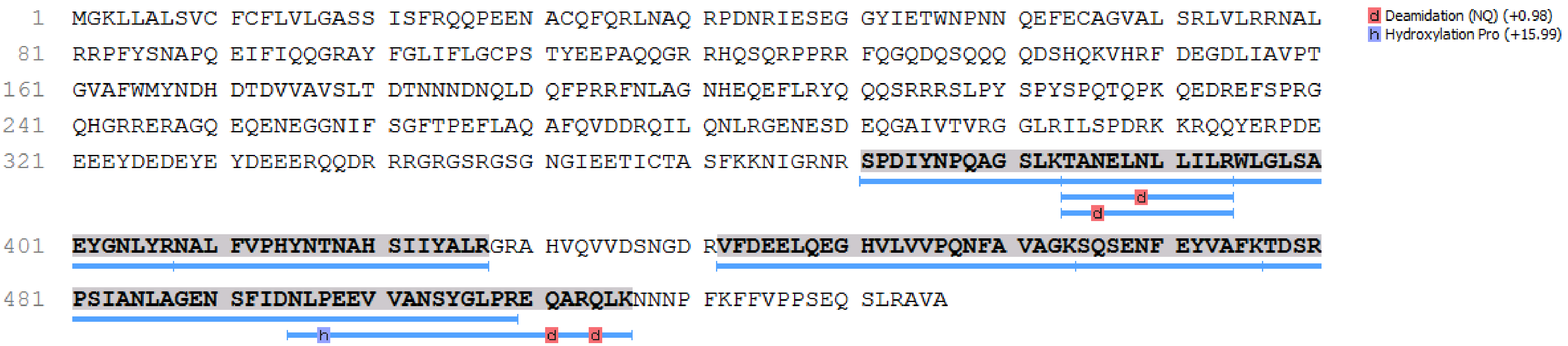
K.TANELN(+.98)LLILR.W	N	97.9	35.38	1269.7292	11	4.4	635.8747	2	33.14	22	1723	OB3620.raw	0	1	1	384	394	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	94.7	30.71	3544.7434	33	0.8	1182.5894	3	35.04	22	1896	OB3620.raw	1.61E4	2	2	477	509	
K.TAN(+.98)ELNLLILR.W	N	74.8	25.38	1269.7292	11	3.4	635.8741	2	33.17	22	1727	OB3620.raw	0	1	1	384	394	Deamidation (NQ)
D.NLP(+15.99)EEVVANSYGLPREQ(+.98)ARQ(+.98)LK.N	N	5.0	17.61	2528.2871	22	5.9	843.7747	3	32.25	22	1639	OB3620.raw	0	1	1	495	516	Hydroxylation Pro; Deamidation (NQ)
total 10 peptides																		

Q6T2T4|Q6T2T4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



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  1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
 81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR
481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	72.35	1540.7673	13	-0.8	771.3903	2	32.38	22	1650	OB3620.raw	4.16E4	8	8	395	407	
K.SQSENFEYVAFK.T	N	99.9	65.90	1447.6619	12	-1.5	724.8372	2	29.90	22	1436	OB3620.raw	3.23E3	2	2	465	476	
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.9	58.70	2524.2961	23	0.7	842.4399	3	31.40	22	1563	OB3620.raw	7.07E4	3	3	442	464	
K.TANELNLLILR.W	N	99.9	53.88	1268.7452	11	-0.7	635.3795	2	32.46	22	1658	OB3620.raw	2.17E4	5	5	384	394	
R.SPDIYNPQAGSLK.T	N	99.6	42.29	1388.6936	13	0.7	695.3546	2	27.03	22	1287	OB3620.raw	3.98E3	3	3	371	383	
R.NALFVPHYNTNAHSIIYALR.G	N	98.9	40.69	2313.2019	20	-1.9	772.0731	3	30.44	22	1477	OB3620.raw	6.84E3	3	3	408	427	
K.TANELN(+.98)LLILR.W	N	97.9	35.38	1269.7292	11	4.4	635.8747	2	33.14	22	1723	OB3620.raw	0	1	1	384	394	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	94.7	30.71	3544.7434	33	0.8	1182.5894	3	35.04	22	1896	OB3620.raw	1.61E4	2	2	477	509	
K.TAN(+.98)ELNLLILR.W	N	74.8	25.38	1269.7292	11	3.4	635.8741	2	33.17	22	1727	OB3620.raw	0	1	1	384	394	Deamidation (NQ)
D.NLP(+15.99)EEVVANSYGLPREQ(+.98)ARQ(+.98)LK.N	N	5.0	17.61	2528.2871	22	5.9	843.7747	3	32.25	22	1639	OB3620.raw	0	1	1	495	516	Hydroxylation Pro; Deamidation (NQ)
total 10 peptides																		

Q6IWG5|Q6IWG5_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN

401 GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	98.7	39.86	2554.3066	23	-0.7	852.4423	3	30.82	22	1504	OB3620.raw	1.41E4	1	1	415	437	
total 1 peptides																		

Q0GM57|Q0GM57_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	98.7	39.86	2554.3066	23	-0.7	852.4423	3	30.82	22	1504	OB3620.raw	1.41E4	1	1	417	439	
total 1 peptides																		

G0Y6V1|G0Y6V1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTVRRFKDGE MRYLKLLLIL VGAQKIKKTF CETNKNYHSL NRDEAVLVEN IAQHIHEILI PKLSSSMKNL VGIDSRVERV

81 ISQIGLGLND VRYIGLLGMG GIGKTTIARA VFETVRSRFE VTCFLADVRE QCEKKDIVRI QKQLLDQVNI NSNAVHNKYD

161 GRTIIQNSLR LKKVLLVLDD VNHEKQLENL AGEQDWFGPG SRIIITTRDV EVLKEQAVLE TYMVEGLVES EAFNLFCLKA

241 FKQAAEPTEG FLDLSEEVVK **YSGGLPLALK** VLGSYLNGRP IAVWHSAIEK IKKSSHSEII DVLKISYDGL DSMEKDIFLD

321 IACFFKGHPQ DYNLQMMLVS VADCGVTRML ILYLLKRRKL KQLIASFYMI CTVLHWTDCP METLPFRDHQ RYELVEIDLS

401 HSKIVQLWDG KKVLKKLVHL NLSYCKELKE MPDLSGAPNL KTLDLDGCEE LNYFHPSLAH HKSLVELNLR GCERLETLGD

481 KLEMSSLERL DLECCSSLRR LPEFGKCMKQ LSILILKRTG IEELPTTLGN LAGMSELDLT GCYKLTSLPF PLGCFVGLKK

561 LRLSRLVELS CVPYSTHGLE SLTVKDYSGS PNIVGLLCSL SHLTSLSSLK LQGCFSTSRE ESTDFGRLAS LTDLDLSENN

641 FLRVPISIHE LPRLTRLKLN NCRRLKVLPE LPLSLRELQA RDCDSLDASN ANDVILKACC GFAESASQDR EDLFQMWFSR

721 KKIPAWFEHH EEGNGVSVSF SHNCPSTETI ALALCFLLQG FLFSSEKPSV ICNGKEFINK SLLKASSGIS SENVYIVYVN

801 GYYLSKLLCQ HNCFQMLFPG TPSINIQVRR SSARWQQHKR FGKHDKTDSD SLQSEGENLH AIEAIKLIGI GLNDVCFVGI

881 WGMGGIGVLL VLDDVNEVNC LENLGENQDW FGPGSRIIIT ARDMHLLDMH GVHGTCGSAT HDESLYELAG GTGIVLKLIE

961 SALAEHVRFL LRSGREYDQT SSDSDKLSPR FLGCFLFRSS ERRQLLDKSY LMSGKELSKL VAFVKGTQFD LVLQMETLQS

1041 RLDADFLLAH MCSVKFKEWI VVLATLLRRS EVLFDLFPHD VRLWKAYSTT LQSHLKFVEY QDLLEDLEHK LSSISNKEE

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
K.YSGGLPLALK.V	Y	70.4	22.56	1017.5858	10	7.5	509.8040	2	32.70	22	1684	OB3620.raw	8.39E3	1	1	261	270	
total 1 peptides																		

G0Y6V0|G0Y6V0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKNLVGINSR VEQVITLIGL GLNDVRFIGI WGMGGIGKTT IARAVFETIR CSFEVTCFLA DVRENCEKKD ITHMQKQLLD

81 QMNISSNAVY NKYDGRTIIQ NSLRLKKVLL VLDDVNHEKQ LEDLAGEKAW FGPGSRIIIT TRDFHLLRKN KLHETYNVEG

161 LVENEALNLF SLEAFNLPKP SEEFLALSKE VVK**YSGGLPL ALK**VLGSYLN GRGIEVWHSA IEKIKHFSHS EIIDVLKISY

241 DGLDDMEKDI FLDIACFFKG WQKHHVTEIL KRCGHDAEIG IDILINRSLI TIDKYDYDYW LGMHDLLEEM GKRIVIQESQ

321 NVVCKRSRLW CLEDVEFVLT QKKKTKATHG IVLHEWYSET EVNQRDLSFS KLCQLKLLIL DGAKAPILCD IPCTLKVFCW

401 RRCPMKTLPL TDHQRYELVE INLSKSQIAE LWDGKKVLEN LEHLYLSWCK QLKQTPDLSG APNLKKLNLR GCEELDYIHP

481 SLAHHKRLVE LNLEDCKRLE TLGDKLEMSS LEKLDLDSCS SLRRLPEFGE CMKKLSILNL RNTGIEELPP TLGNLAGVSE

561 LNLSGCDKIT GLLLSLGCFV GLKKLVLRAL PQKTDGLESL TVRADYDDSD SSSREESTLS YDIAHLASLT YLDLSRNRFL

641 RVPISIHQLP RLTHLKLSFC DELEVLPELP SSLRELDAQG CYSLDKSYVD DVISKTCCGF AESASQDRED FLQMMITGEE

721 IPAWFEHQEE DEGVSVSFPL NCPSTEMVAL ALCFLFNGIE GLQPSVICNG KEFINASFYW WSSLYNLLFI VCVNGYYFSK

801 LLCHHNRFQM LFPYADHLGI RVQRCGARWV YKQDIQDFKK RKATLEDFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
K.YSGGLPLALK.V	Y	70.4	22.56	1017.5858	10	7.5	509.8040	2	32.70	22	1684	OB3620.raw	8.39E3	1	1	194	203	

total 1 peptides

G0Y6V4|G0Y6V4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKNLVGIDSR VEGVINLIGL GLNDVRYMVI WGMGGIGKTT IARAVFETIR SRFEVSCFLA DVREHCEKKD TVHIQKQLLD
81 QMNISSYAVY NKYDGRRIIQ NSLCLKKVLL VLDDVNHEKQ LEDLAGEKDW FGPGSRIIIT TRDVEVLKGP EVHEIYKVEG
161 LVESEALNLF CLKAFKQQEP TEGFLDLSKE VVK**YSGGLPL ALK**VLGSYLN GQKEKSSHED NYNIFMGVST LKISYEGLED
241 TEKDIFLDIA CFFKGRQKHH VTEMLKRCGY QAEIGLDILI NRSLVTLEEV KILGMVTLGM HDLLEEMGKQ IVIQESPNDA
321 SKRSRLWCYE DVDFVLTQKK ESEATHSIVS KVYYCETEEE WREYREIKEN WRDLSFSNIC QLKLLILDGV NAPILCDIPC
401 TLKVLHWEGC PMETLPFTDQ CYELVEIDLS HGKIVELWDG KKVLKKLEHL NLYFCEKLKQ TPDLSGAPNL KTLNLHGCKE
481 LNYINPSLAH HKRLVELNLG RCRSLETLGD KLEISSLEKL NLYECRSLRR LPEFGECMKQ LSILDLEKTG IEELPPTLGK
561 LAGVSELDLT GCHKLTSLPF PLGCFVGLKK LKLSRFVELS CVPYTTHGLE SLEAWDFSNS PIFVGLLCSL SRLTSLSSLK
641 LHGEYSRSRE VSTLYYDLGH LTSLTDLDLG YSDFLRVPIC IHALPRLTRL DLCYCYNLEV LPELPSSLRE LQVKGFEPLV
721 ASNVNAAISK ACCGFAESAS QDREDLLQMW ISGKEMPAWF KDQKKDNGIS VSFPHNCPST ETIALALCFL LQGVIMDLPE
801 QPSVICNVTC YAKTIASNCN FPVIIVESEY KDLEHVGCAS KTFNISSSLA SRRSSDPPEL LPFFPLHSHS TWFS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
K.YSGGLPLALK.V	Y	70.4	22.56	1017.5858	10	7.5	509.8040	2	32.70	22	1684	OB3620.raw	8.39E3	1	1	194	203	
total 1 peptides																		

G0Y6W5|G0Y6W5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALVVGEASS SLTPSPRSYT YHVFLSFRGE DTRTRFTSHL YAALNRNGIT TYIDDNNLRK GDVISDELLK AIEESMFAVI
81 VLSPNYASSS WCLDELCKIL DCSKKLGQHI VTVFYDVEPS DVRHQKGAFG EAFTKHEQRQ DGEKVKKWRD ALTQVAAYSG
161 WHSKNRNEAE LVESISKHIH EILIPKLPSS MKNLIGIDSR VEQVICQIGL GLNDVRYIGI WGMGGIVRER CEKKDIPDIQ
241 KQLLDQMGIS STALYSEYDG RAILQNSLRL KKVLLVLDDV NHEKQLENLA GEQDWFGSGS RIIITTRDQH LLQEQGVHET
321 YEVEGLVEIE AFNLFCSKAF KLPEPTEGFL DLTKEVVN**YS GGLPLALK**VL GSYLYCRSIE VWHSAIGKIK NSSHSDIIDV
401 LKISYDGLDS MEKNIFLDIS CFFKGRSRDY ATKILKLCGH HAEIGIDILI NRSLVTIEQD KYGEDTLKMH DLIEEMGKLI
481 VNQESPDDAS KRSRLWCEDD IDLVLRQNKE TKATRSIVLY DKRDELYWND LAFSNICQLK LLILDGVKSP ILCNIPCTLR
561 VLHWNGCPME TLPFTDEHYE LVEIDLYLSK IVHVWHGKKF LEKLKYLNLS NSHNLKQTPD LSGAPNLETL DLSCCSELND
641 IHQSLIHHKN LLELNLIKCG SLQTLGDKLE MSSLKELDLY ECNSLRKLPK FGECMKRLSI LTLSCTGITE LPTTVGNLVG
721 LSELDLQGCK RLTCLPDTIS GLKSLTALDV SDCPNLLLQS LDSLSTLTSL LLSWNKCVEA CCAFAASASQ DGDDVMQMLV
801 AGEEIPSWFV HREEGNGITA TFPHTETIAL AICFRLRSTS RRIRGEPSVI CNGEEFITET LLAMPLIGYS PHFFLLCLRS
881 DYFVDQSCQD YLFQMLFPND YYGDITVESS GARWVCTQDI QDLMKAGTET AT

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
N.YSGGLPLALK.V	Y	70.4	22.56	1017.5858	10	7.5	509.8040	2	32.70	22	1684	OB3620.raw	8.39E3	1	1	359	368	
total 1 peptides																		

G0Y6W1|G0Y6W1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSISDGAALH KLQKPGQTPF LLLRFFCRSS ILGLRPTSPF SGANVGNSSQ TYKEILFDLL NRDEAALVEN IAQHIFEILI
81 PKLPSSMKNL VGIESRVKQV ICRIGLGLND VRYINIWGMG GIGKTTIARV VFETIRSIFE VACFLADVRE QCEKKDIVHI
161 QRQLLDQTRI NSATVFSEYD GRTIIQNSLR LKKVLLVLDD VNQEKQLENL AGEQAWFGPG SRIIITTRDV EVLKELHETW
241 KVKGLVDSEA FNLFCLKAFK QPEPAEGFLD LFQEVIK**YSG GLPLALK**VLG SYLNGRPIAV WHSAIEKIKK SSHSDIIDVL
321 KISYDGLDSM ENDIFLDIAC FFKGRKKGYV TKILDGCGHH AVIGIDVLIN RALVTIDKYD ELGMHDLLEE MGKLIVIQES
401 PNDASKRSRL WWCEDVDSVL TQKKPNPHDM NQRHYCAKAR SLPGSNAPYG SSTVSKQEPL HRCPDVVLNE QGFSRFRERT
481 RVNKLVHKGK GKGRSDRRLR FGTWNIGTLT GKSMEVVDTM TRRKINIMCL QETKWVGAKA RELDTSGFKL WYTGKVKNRN
561 GVGIIVDKQW KKDVVDVKRV GDRIISIKLV VEGGAFHVIS AYAPQVGSDE QHKISFWEDL ESLVQGIPLG DKIFLGGDLN
641 GHVGREVTGY GSIHGGHGFG VINAEGKTIL DFSSTFDLLI ANTCFKKRDE HLITYKSGMT SSQIDFFLLR RVDRKFCINC
721 KIIPGESLTT QHRVLVLDFR VEQKLRKRHH TKNPRTRWWR MKGEEQRSFL RRVGEEAKWD GNGSAEEMWR EMAEVIRRTA
801 KESFGESKGI GPRDKESWWW NASIQEKIKI KRECFKEWSL CRNVDNWEKY KAAKKETKVA VSEARTRAYE GLYQSLDTKE
881 GEKGIYRIAK SRERRTRDLD QVKCIKDKDR EVLAQEEKIN ERWKSYFYEL FNEGQKTLPS LGRLCTREED QNFNYYRRIR
961 DFEVKEALKQ MKNGRAVGPD NIPIEVWKGL GGKGINWLTK LFYEILRSKK MPDEWRKSTL VPIYRIKGDI QSCGNYRGIK
1041 LMSHTMKLWG KGDRTEVEKR DTRYQGRFLW KVLEKRRVRI AYIRAIKDMY EGATTSVKTQ GGVTEEFPIG IGLHQGSSLS
1121 PYLFTLVLEV LTEHIQEPVP WCMLFADDIV LMGESREDLN KKLELWREAL EVYGLRISRS KTEYMECKFS LRRENSNIEV
1201 KIGENILRKV KSFKYLGCII QDNGEIEQDV NHRIQAGWSK WRSASGFICD KKVPLKLKGK FYRTAIRPAM LYGTECWAAK
1281 GEHEHKLSVA EMKMLRWMSG HTRLDKIRNE DIRERVGVAP IVEKMVESRL RWFGHVGRRP IEHLVRRVDE MEDGQKAKGR
1361 GRPKKTIHEV VKRDLHETEA IHSIVLHKVY RETEGKWRDL SFSNMCKLKL LVLDFVEAPI LCDIPSTLKV LHWKCCPMET
1441 LPFTDQHYEL VEIHLPDSKI VQLWDGKKVL KKLELLNLSC CYKLKETPDL SGAPVLKILN LEHCRELNYV HPSLALHKSL
1521 VELNLTGCYS IETLADKLEM CSLETLGLDC CTRLRRLPEF GECMKQLSIL ILTYTDIEEV PTTLGNLAGV SELDLTGCDK
1601 LTSLPLTGCF LKKLELHGFV ELSCLPHEAP SLKLEGCFST SKESTLYCDL GHLAQLTNLD LSDNCFIRVP ISIHQLPRLT
1681 CLKLSFCDEL EVLPELPSSL RELHAQGCDS LDASNVDDVI SKACCGFAES ASQDREDVLQ MLITGEEIPG WFEHQEEDEG
1761 VSVSFPLNCP STEMVALALC FLFERTKGYR TFTFYPSVIC NGKEFINASL YVVDSSDSLL IMITILISEY RDVEHVGCAS
1841 KTFKISGKQN PKQGKEKETL EWNMDMRSHS STSRNKMLVV GPPLCDEEEK HGATAEGAIG GLASRKSSDP PELLLLFPLH
1921 SPQHLVLILD KPLICCFFS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 22	#Spec	#Spec Sample 22	Start	End	PTM
K.YSGGLPLALK.V	Y	70.4	22.56	1017.5858	10	7.5	509.8040	2	32.70	22	1684	OB3620.raw	8.39E3	1	1	278	287	
total 1 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

Summary

1. Notes

Spot 13 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

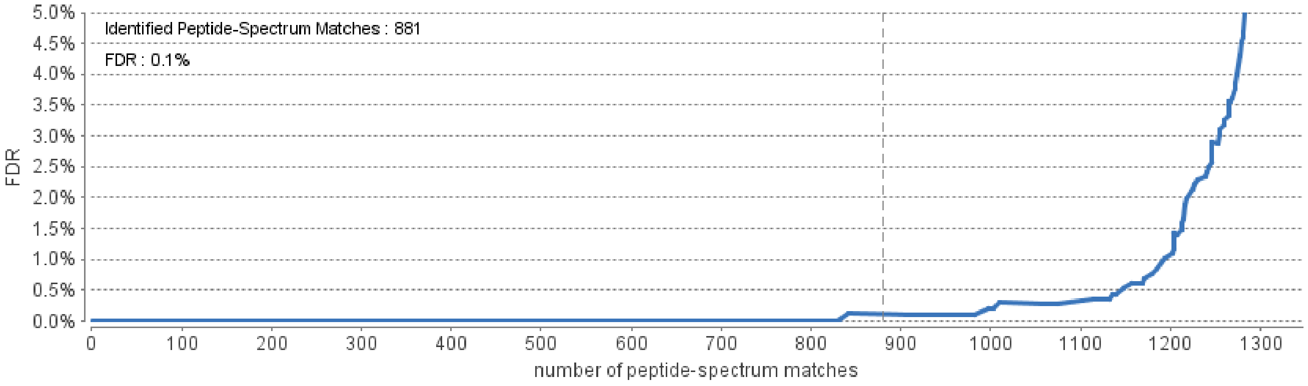
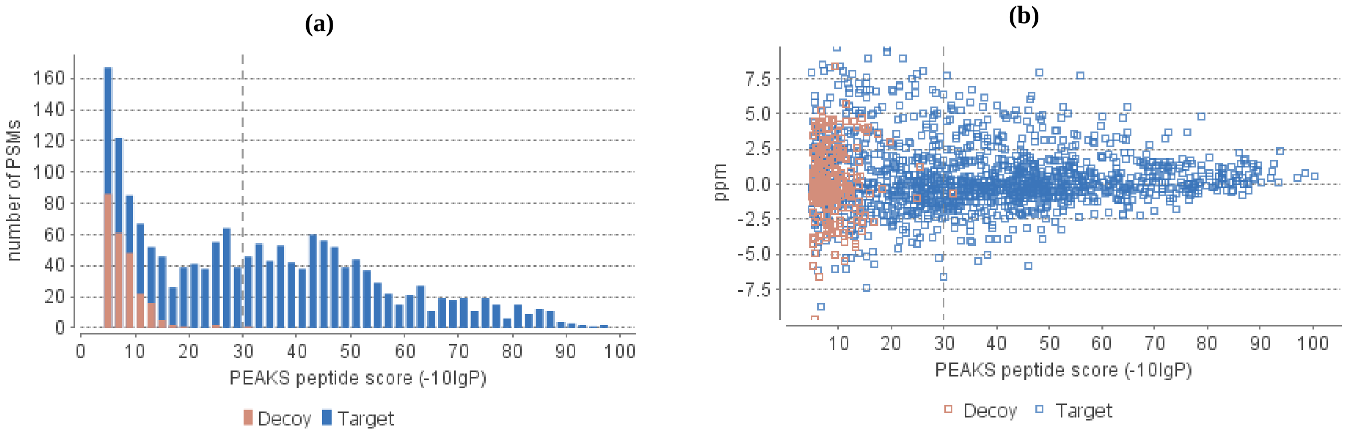


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

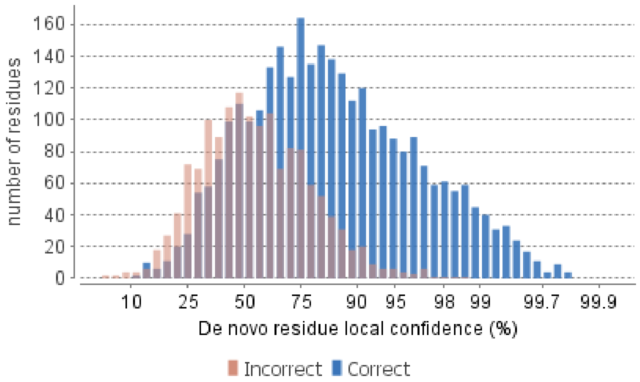

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



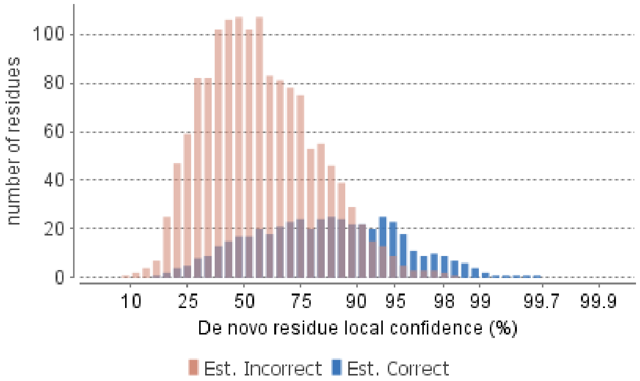


Table 1. Statistics of data.

# of MS scans	2892
# of MS/MS scans	3285

Table 2. Result filtration parameters.

Peptide -10lgP	≥30
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	753
Peptide sequences	93
Protein groups	5
Proteins	7
Proteins (#Unique Peptides)	4 (>2); 2 (=2); 1 (=1);
FDR (Peptide-Spectrum Matches)	0.1%
FDR (Peptide Sequences)	1.1%
FDR (Protein)	9.1%
De Novo Only Spectra	178

Table 4. PTM profile.

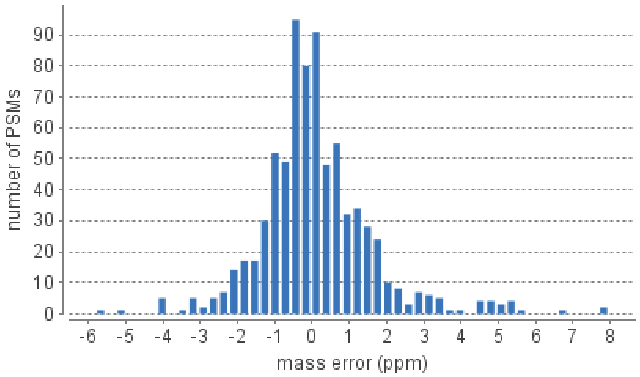
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Deamidation	.98	NQ	61	86.20	1.3E5	33.98
Carbamidomethyl	57.02	C	43	77.60	7.65E5	1000.00
HydPro	15.99	P	7	49.42	1.25E5	21.59
Oxidation	15.99	M	1	32.81	3.45E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



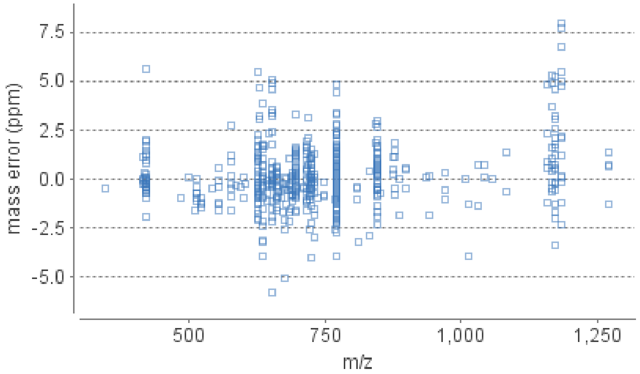


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 23	83	10	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3621.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 23	Area Sample 23	#Peptides	#Unique	#Spec Sample 23	PTM	Avg. Mass	Description
1	15	Q647H3|Q647H3_ARAHY	99.1	304.12	26	26	1.16E7	26	1	491	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
3	3	B5TYU1|B5TYU1_ARAHY	99.1	303.67	28	28	2.79E6	24	2	472	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
5	13	Q9FZ11|Q9FZ11_ARAHY	99.1	287.35	22	22	3.63E6	22	2	470	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
6	7	Q647H4|Q647H4_ARAHY	99.1	286.03	28	28	1.97E6	23	4	408	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	99.1	286.03	28	28	1.97E6	23	4	408	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
9	41	Q6IWG5|Q6IWG5_ARAHY	99.1	198.84	18	18	1.68E6	11	5	34	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
9	42	Q0GM57|Q0GM57_ARAHY	99.1	198.84	18	18	1.68E6	11	5	34	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 7 proteins													

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR G**NGIEETICT ASVK**KNIGR**N RSPDIYNPQA GSLKTANDLN LLILRWLGLS**
401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS**
481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	100.53	1540.7673	13	0.6	771.3914	2	33.21	23	2481	OB3621.raw	2.54E7	180	180	396	408	
K.SQSDNFEYVAFK.T	N	99.9	92.18	1433.6462	12	0.5	717.8307	2	30.27	23	2085	OB3621.raw	4.75E6	27	27	466	477	
R.VYDEELQEGHVLVVPQ(+.98)NFAVAGK.S	N	99.9	86.20	2541.2751	23	0.7	1271.6458	2	31.52	23	2254	OB3621.raw	1.3E5	1	1	443	465	Deamidation (NQ)
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	80.54	1434.6302	12	0.7	718.3229	2	30.67	23	2139	OB3621.raw	1.05E6	4	4	466	477	Deamidation (NQ)
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	77.63	2313.2019	20	0.6	1157.6089	2	30.63	23	2135	OB3621.raw	1.63E7	16	16	409	428	
N.GIEETIC(+57.02)TASVK.K	N	99.9	76.27	1306.6438	12	0.0	654.3292	2	27.74	23	1736	OB3621.raw	3.75E6	13	13	353	364	Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.9	76.05	1388.6936	13	-0.4	695.3538	2	26.97	23	1630	OB3621.raw	1.04E7	62	62	372	384	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	75.38	3510.7590	33	1.7	1171.2623	3	34.94	23	2715	OB3621.raw	7.09E6	20	20	478	510	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	74.80	2540.2910	23	1.4	1271.1545	2	30.94	23	2176	OB3621.raw	1.98E7	51	51	443	465	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	70.97	1389.6776	13	1.3	695.8470	2	28.06	23	1779	OB3621.raw	2.53E5	2	2	372	384	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.30	2314.1858	20	2.3	772.4043	3	31.60	23	2265	OB3621.raw	1.77E6	1	1	409	428	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYGLPR.E	Y	99.9	63.92	3511.7429	33	3.2	1171.5920	3	34.49	23	2655	OB3621.raw	1.79E6	1	1	478	510	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	58.27	3511.7429	33	3.0	1171.5918	3	34.32	23	2631	OB3621.raw	2.1E6	3	3	478	510	Deamidation (NQ)
N.TNAHSIIYALR.G	N	99.9	54.68	1257.6830	11	-0.8	629.8483	2	28.16	23	1794	OB3621.raw	1.37E4	1	1	418	428	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	53.61	2314.1858	20	-1.2	1158.0988	2	32.03	23	2323	OB3621.raw	9.47E4	2	2	409	428	Deamidation (NQ)
K.TANDLNLLILR.W	N	99.9	53.58	1254.7296	11	1.1	628.3727	2	32.68	23	2411	OB3621.raw	1.96E7	60	60	385	395	

K.TDSRPSIANLAGEN.S	N	99.9	53.46	1443.6953	14	-1.0	722.8542	2	27.80	23	1745	OB3621.raw	8.88E4	4	4	478	491	
K.TDSRPSIANLAGENSIID.N	N	99.9	53.05	1871.9225	18	0.1	936.9686	2	30.82	23	2161	OB3621.raw	4.21E4	1	1	478	495	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.16	1444.6793	14	-0.9	723.3463	2	28.32	23	1815	OB3621.raw	4.59E4	3	3	478	491	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	50.02	1329.6525	13	-0.8	665.8329	2	27.89	23	1757	OB3621.raw	3.59E4	2	2	478	490	
G.NGIEETIC(+57.02)TASVK.K	N	99.9	48.27	1420.6868	13	-0.4	711.3503	2	29.89	23	2034	OB3621.raw	1.32E4	1	1	352	364	Carbamidomethylation
A.NDLNLLILR.W	N	99.9	46.87	1082.6448	9	-0.5	542.3294	2	32.33	23	2362	OB3621.raw	3.22E4	1	1	387	395	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVANSYGLPR.E	Y	99.9	45.99	3511.7429	33	5.2	1171.5944	3	6.03	23	521	OB3621.raw	6.16E5	1	1	478	510	Deamidation (NQ)
P.DIYNPQAGSLK.T	N	99.9	44.14	1204.6088	11	-0.2	603.3115	2	27.11	23	1649	OB3621.raw	0	1	1	374	384	
R.NALFVPHYNTNAH.S	N	99.9	42.40	1496.7161	13	-0.8	749.3647	2	27.49	23	1703	OB3621.raw	4.55E5	4	4	409	421	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	42.01	1659.8217	15	-0.4	554.2809	3	26.52	23	1575	OB3621.raw	1.61E5	4	4	370	384	Deamidation (NQ)
N.AHSIIYALR.G	N	99.9	41.87	1042.5923	9	-0.5	348.5379	3	27.41	23	1691	OB3621.raw	3.52E3	1	1	420	428	
K.TAN(+.98)DLNLLILR.W	N	99.8	40.37	1255.7136	11	3.1	628.8660	2	33.43	23	2511	OB3621.raw	3.92E6	3	3	385	395	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.54	1200.6099	12	0.1	601.3123	2	27.76	23	1739	OB3621.raw	1.06E5	2	2	478	489	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.8	38.36	1660.8057	15	-1.3	554.6085	3	27.19	23	1660	OB3621.raw	3.8E4	1	1	370	384	Deamidation (NQ)
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.7	37.11	1659.8217	15	0.6	554.2815	3	26.87	23	1618	OB3621.raw	1.52E5	1	1	370	384	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGEN.S	N	99.6	36.49	1444.6793	14	0.1	723.3470	2	28.73	23	1873	OB3621.raw	3.98E4	1	1	478	491	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.5	35.61	2114.0320	18	0.0	1058.0233	2	32.34	23	2363	OB3621.raw	3.86E4	1	1	443	460	
H.SIIYALR.G	N	99.5	34.84	834.4963	7	-0.1	418.2554	2	28.45	23	1834	OB3621.raw	1.03E6	5	5	422	428	
H.VLVVPQNFAVAGK.S	N	99.5	34.67	1340.7816	13	-0.9	671.3975	2	30.01	23	2050	OB3621.raw	1.68E4	1	1	453	465	
R.N(+.98)RSPDIYN(+.98)PQAGSLK.T	N	99.4	33.31	1660.8057	15	-1.6	554.6083	3	27.01	23	1635	OB3621.raw	3.8E4	1	1	370	384	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	99.1	32.05	1534.7892	13	-2.6	768.3999	2	29.02	23	1913	OB3621.raw	3.67E4	3	3	416	428	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.1	31.72	1659.8217	15	-1.2	554.2805	3	26.35	23	1558	OB3621.raw	1.52E5	1	1	370	384	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	98.9	31.35	1658.8376	15	-0.1	553.9531	3	25.82	23	1519	OB3621.raw	4.1E3	1	1	370	384	
L.FVPHYNTNAHSIIYALR.G	N	98.8	31.24	2015.0377	17	-1.7	672.6854	3	30.59	23	2129	OB3621.raw	2.21E4	1	1	412	428	
N.DLNLLILR.W	N	98.7	31.14	968.6018	8	-1.0	485.3077	2	33.40	23	2507	OB3621.raw	7.09E3	1	1	388	395	
K.TDSRPSIANLAGENSIIDNLPEEVVANSY.G	N	98.7	30.52	3087.4995	29	-1.4	1030.1724	3	35.10	23	2737	OB3621.raw	2.8E4	1	1	478	506	
total 42 peptides																		

B5TYU1|B5TYU1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGN**GIEET ICTATVK**KNI GR**NRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY**
401 **RNALFVPHYN TNAHSIIYAL R**GRAHVQVVD SNGNR**VYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL**
481 **AGENSVIDNL PEEVVANSYG LPR**EQARQLK NNNPFK**FFVP PSQQSPR**AVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	100.53	1540.7673	13	0.6	771.3914	2	33.21	23	2481	OB3621.raw	2.54E7	180	180	389	401	
K.SQSDNFEYVAFK.T	N	99.9	92.18	1433.6462	12	0.5	717.8307	2	30.27	23	2085	OB3621.raw	4.75E6	27	27	459	470	
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	87.80	3496.7434	33	0.7	1166.5892	3	34.54	23	2661	OB3621.raw	2.19E6	12	12	471	503	
R.VYDEELQEGHVLVVPQ(+.98)NFAVAGK.S	N	99.9	86.20	2541.2751	23	0.7	1271.6458	2	31.52	23	2254	OB3621.raw	1.3E5	1	1	436	458	Deamidation (NQ)
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	80.54	1434.6302	12	0.7	718.3229	2	30.67	23	2139	OB3621.raw	1.05E6	4	4	459	470	Deamidation (NQ)
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	77.63	2313.2019	20	0.6	1157.6089	2	30.63	23	2135	OB3621.raw	1.63E7	16	16	402	421	
N.GIEETIC(+57.02)TATVK.K	N	99.9	77.60	1320.6595	12	-0.1	661.3370	2	28.10	23	1785	OB3621.raw	2.39E6	23	23	346	357	Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.9	76.05	1388.6936	13	-0.4	695.3538	2	26.97	23	1630	OB3621.raw	1.04E7	62	62	365	377	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	74.80	2540.2910	23	1.4	1271.1545	2	30.94	23	2176	OB3621.raw	1.98E7	51	51	436	458	
K.FFVPPSQQSPR.A	N	99.9	71.45	1288.6564	11	-0.3	645.3353	2	27.22	23	1664	OB3621.raw	1.24E5	4	4	517	527	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	70.97	1389.6776	13	1.3	695.8470	2	28.06	23	1779	OB3621.raw	2.53E5	2	2	365	377	Deamidation (NQ)
K.TDSRPSIANLAGENSVIDN(+.98)LPEEVVANSYGLPR.E	Y	99.9	64.90	3497.7273	33	3.7	1166.9207	3	4.05	23	210	OB3621.raw	2.01E5	1	1	471	503	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.30	2314.1858	20	2.3	772.4043	3	31.60	23	2265	OB3621.raw	1.77E6	1	1	402	421	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	62.88	1268.7452	11	0.7	635.3804	2	5.37	23	420	OB3621.raw	8.67E6	37	37	378	388	
K.TDSRPSIANLAGENSVIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	62.86	3497.7273	33	1.6	1166.9182	3	33.96	23	2583	OB3621.raw	3.67E5	2	2	471	503	Deamidation (NQ)
R.PSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	58.51	3037.5356	29	-1.3	1013.5179	3	35.28	23	2761	OB3621.raw	3.28E4	2	2	475	503	
N.TNAHSIIYALR.G	N	99.9	54.68	1257.6830	11	-0.8	629.8483	2	28.16	23	1794	OB3621.raw	1.37E4	1	1	411	421	

R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	53.61	2314.1858	20	-1.2	1158.0988	2	32.03	23	2323	OB3621.raw	9.47E4	2	2	402	421	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.9	53.46	1443.6953	14	-1.0	722.8542	2	27.80	23	1745	OB3621.raw	8.88E4	4	4	471	484	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.16	1444.6793	14	-0.9	723.3463	2	28.32	23	1815	OB3621.raw	4.59E4	3	3	471	484	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	50.02	1329.6525	13	-0.8	665.8329	2	27.89	23	1757	OB3621.raw	3.59E4	2	2	471	483	
K.FFVPPSQQSP(+15.99)R.A	N	99.9	47.46	1304.6512	11	-0.4	653.3326	2	26.83	23	1613	OB3621.raw	2.38E4	1	1	517	527	Hydroxylation Pro
P.DIYNPQAGSLK.T	N	99.9	44.14	1204.6088	11	-0.2	603.3115	2	27.11	23	1649	OB3621.raw	0	1	1	367	377	
R.NALFVPHYNTNAH.S	N	99.9	42.40	1496.7161	13	-0.8	749.3647	2	27.49	23	1703	OB3621.raw	4.55E5	4	4	402	414	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	42.01	1659.8217	15	-0.4	554.2809	3	26.52	23	1575	OB3621.raw	1.61E5	4	4	363	377	Deamidation (NQ)
N.AHSIIYALR.G	N	99.9	41.87	1042.5923	9	-0.5	348.5379	3	27.41	23	1691	OB3621.raw	3.52E3	1	1	413	421	
K.TAN(+.98)ELNLLILR.W	N	99.8	39.19	1269.7292	11	-3.1	635.8699	2	33.52	23	2523	OB3621.raw	9.38E5	1	1	378	388	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.54	1200.6099	12	0.1	601.3123	2	27.76	23	1739	OB3621.raw	1.06E5	2	2	471	482	
K.FFVPPSQ(+.98)QSP(+15.99)R.A	N	99.8	38.53	1305.6353	11	-0.4	653.8246	2	27.09	23	1646	OB3621.raw	8.48E3	1	1	517	527	Deamidation (NQ); Hydroxylation Pro
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.8	38.36	1660.8057	15	-1.3	554.6085	3	27.19	23	1660	OB3621.raw	3.8E4	1	1	363	377	Deamidation (NQ)
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.7	37.11	1659.8217	15	0.6	554.2815	3	26.87	23	1618	OB3621.raw	1.52E5	1	1	363	377	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGEN.S	N	99.6	36.49	1444.6793	14	0.1	723.3470	2	28.73	23	1873	OB3621.raw	3.98E4	1	1	471	484	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.5	35.61	2114.0320	18	0.0	1058.0233	2	32.34	23	2363	OB3621.raw	3.86E4	1	1	436	453	
H.SIIYALR.G	N	99.5	34.84	834.4963	7	-0.1	418.2554	2	28.45	23	1834	OB3621.raw	1.03E6	5	5	415	421	
H.VLVVPQNFAVAGK.S	N	99.5	34.67	1340.7816	13	-0.9	671.3975	2	30.01	23	2050	OB3621.raw	1.68E4	1	1	446	458	
R.N(+.98)RSPDIYN(+.98)PQAGSLK.T	N	99.4	33.31	1660.8057	15	-1.6	554.6083	3	27.01	23	1635	OB3621.raw	3.8E4	1	1	363	377	Deamidation (NQ)
K.TDSRPSIANLAGENSVIDNLPEEVVAN.S	N	99.1	32.79	2823.3887	27	-1.8	942.1351	3	33.62	23	2537	OB3621.raw	4.8E4	2	2	471	497	
K.FFVPPSQ(+.98)Q(+.98)SPR.A	N	99.1	32.57	1290.6244	11	2.3	646.3210	2	28.24	23	1804	OB3621.raw	5.1E4	1	1	517	527	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	99.1	32.05	1534.7892	13	-2.6	768.3999	2	29.02	23	1913	OB3621.raw	3.67E4	3	3	409	421	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.1	31.72	1659.8217	15	-1.2	554.2805	3	26.35	23	1558	OB3621.raw	1.52E5	1	1	363	377	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	98.9	31.35	1658.8376	15	-0.1	553.9531	3	25.82	23	1519	OB3621.raw	4.1E3	1	1	363	377	
L.FVPHYNTNAHSIIYALR.G	N	98.8	31.24	2015.0377	17	-1.7	672.6854	3	30.59	23	2129	OB3621.raw	2.21E4	1	1	405	421	
total 42 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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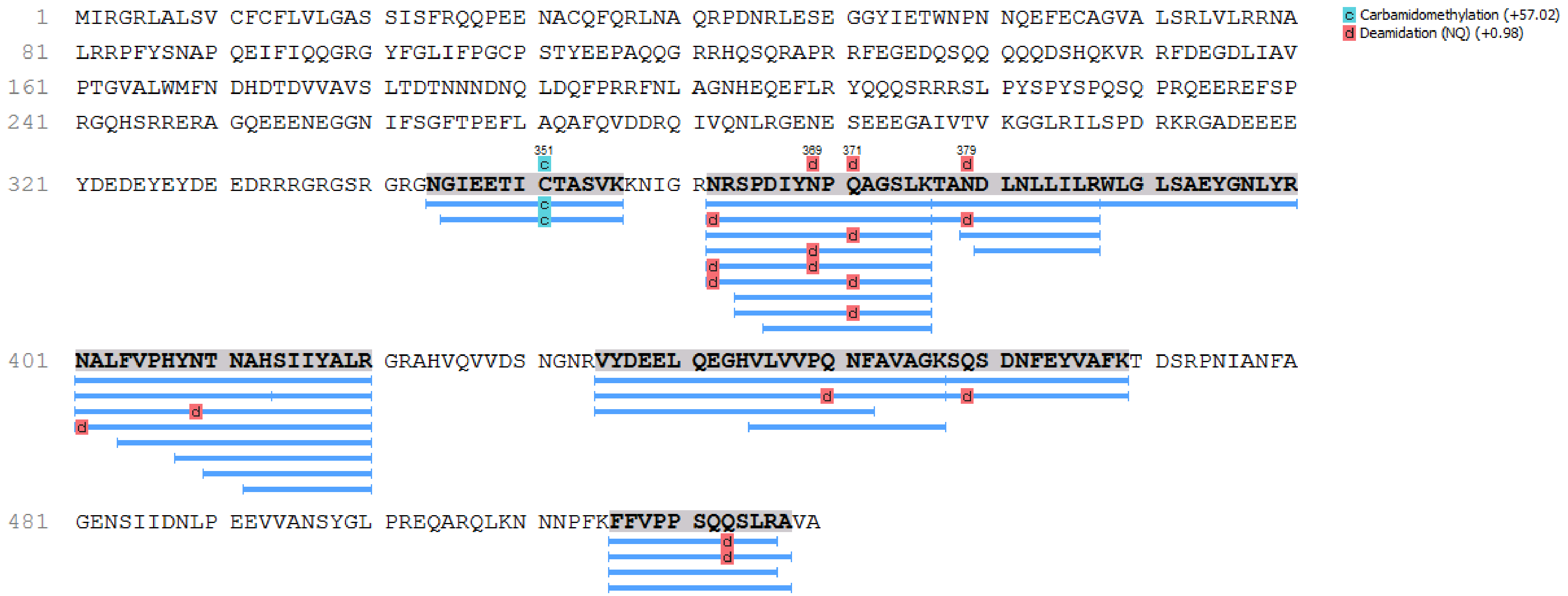
| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	100.53	1540.7673	13	0.6	771.3914	2	33.21	23	2481	OB3621.raw	2.54E7	180	180	388	400	
K.SQSDNFEYVAFK.T	N	99.9	92.18	1433.6462	12	0.5	717.8307	2	30.27	23	2085	OB3621.raw	4.75E6	27	27	458	469	
R.VYDEELQEGHVLVVPQ(+.98)NFAVAGK.S	N	99.9	86.20	2541.2751	23	0.7	1271.6458	2	31.52	23	2254	OB3621.raw	1.3E5	1	1	435	457	Deamidation (NQ)
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	80.54	1434.6302	12	0.7	718.3229	2	30.67	23	2139	OB3621.raw	1.05E6	4	4	458	469	Deamidation (NQ)
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	77.63	2313.2019	20	0.6	1157.6089	2	30.63	23	2135	OB3621.raw	1.63E7	16	16	401	420	
N.GIEETIC(+57.02)TASVK.K	N	99.9	76.27	1306.6438	12	0.0	654.3292	2	27.74	23	1736	OB3621.raw	3.75E6	13	13	345	356	Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.9	76.05	1388.6936	13	-0.4	695.3538	2	26.97	23	1630	OB3621.raw	1.04E7	62	62	364	376	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	74.80	2540.2910	23	1.4	1271.1545	2	30.94	23	2176	OB3621.raw	1.98E7	51	51	435	457	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	70.97	1389.6776	13	1.3	695.8470	2	28.06	23	1779	OB3621.raw	2.53E5	2	2	364	376	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.30	2314.1858	20	2.3	772.4043	3	31.60	23	2265	OB3621.raw	1.77E6	1	1	401	420	Deamidation (NQ)
K.FFVPPSQQSLR.A	Y	99.9	58.44	1304.6876	11	0.0	653.3511	2	28.76	23	1876	OB3621.raw	2.69E6	11	11	516	526	
N.TNAHSIIYALR.G	N	99.9	54.68	1257.6830	11	-0.8	629.8483	2	28.16	23	1794	OB3621.raw	1.37E4	1	1	410	420	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	53.61	2314.1858	20	-1.2	1158.0988	2	32.03	23	2323	OB3621.raw	9.47E4	2	2	401	420	Deamidation (NQ)
K.TANDLNLLILR.W	N	99.9	53.58	1254.7296	11	1.1	628.3727	2	32.68	23	2411	OB3621.raw	1.96E7	60	60	377	387	
G.NGIEETIC(+57.02)TASVK.K	N	99.9	48.27	1420.6868	13	-0.4	711.3503	2	29.89	23	2034	OB3621.raw	1.32E4	1	1	344	356	Carbamidomethylation
K.FFVPPSQQSLRA.V	Y	99.9	47.29	1375.7247	12	0.1	688.8697	2	29.10	23	1924	OB3621.raw	2.12E5	3	3	516	527	
A.NDLNLLILR.W	N	99.9	46.87	1082.6448	9	-0.5	542.3294	2	32.33	23	2362	OB3621.raw	3.22E4	1	1	379	387	
P.DIYNPQAGSLK.T	N	99.9	44.14	1204.6088	11	-0.2	603.3115	2	27.11	23	1649	OB3621.raw	0	1	1	366	376	
K.FFVPPSQQ(+.98)SLR.A	Y	99.9	43.94	1305.6716	11	0.3	653.8433	2	29.44	23	1971	OB3621.raw	3.76E5	3	3	516	526	Deamidation (NQ)
R.NALFVPHYNTNAH.S	N	99.9	42.40	1496.7161	13	-0.8	749.3647	2	27.49	23	1703	OB3621.raw	4.55E5	4	4	401	413	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	42.01	1659.8217	15	-0.4	554.2809	3	26.52	23	1575	OB3621.raw	1.61E5	4	4	362	376	Deamidation (NQ)
N.AHSIIYALR.G	N	99.9	41.87	1042.5923	9	-0.5	348.5379	3	27.41	23	1691	OB3621.raw	3.52E3	1	1	412	420	
K.TAN(+.98)DLNLLILR.W	N	99.8	40.37	1255.7136	11	3.1	628.8660	2	33.43	23	2511	OB3621.raw	3.92E6	3	3	377	387	Deamidation (NQ)

K.FFVPPSQQ(+.98)SLRA.V	Y	99.8	38.96	1376.7087	12	-0.1	689.3616	2	29.71	23	2008	OB3621.raw	3.58E5	1	1	516	527	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.8	38.36	1660.8057	15	-1.3	554.6085	3	27.19	23	1660	OB3621.raw	3.8E4	1	1	362	376	Deamidation (NQ)
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.7	37.11	1659.8217	15	0.6	554.2815	3	26.87	23	1618	OB3621.raw	1.52E5	1	1	362	376	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.5	35.61	2114.0320	18	0.0	1058.0233	2	32.34	23	2363	OB3621.raw	3.86E4	1	1	435	452	
H.SIIYALR.G	N	99.5	34.84	834.4963	7	-0.1	418.2554	2	28.45	23	1834	OB3621.raw	1.03E6	5	5	414	420	
H.VLVVPQNFAVAGK.S	N	99.5	34.67	1340.7816	13	-0.9	671.3975	2	30.01	23	2050	OB3621.raw	1.68E4	1	1	445	457	
R.N(+.98)RSPDIYN(+.98)PQAGSLK.T	N	99.4	33.31	1660.8057	15	-1.6	554.6083	3	27.01	23	1635	OB3621.raw	3.8E4	1	1	362	376	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	99.1	32.05	1534.7892	13	-2.6	768.3999	2	29.02	23	1913	OB3621.raw	3.67E4	3	3	408	420	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.1	31.72	1659.8217	15	-1.2	554.2805	3	26.35	23	1558	OB3621.raw	1.52E5	1	1	362	376	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	98.9	31.35	1658.8376	15	-0.1	553.9531	3	25.82	23	1519	OB3621.raw	4.1E3	1	1	362	376	
L.FVPHYNTNAHSIIYALR.G	N	98.8	31.24	2015.0377	17	-1.7	672.6854	3	30.59	23	2129	OB3621.raw	2.21E4	1	1	404	420	
N.DLNLLILR.W	N	98.7	31.14	968.6018	8	-1.0	485.3077	2	33.40	23	2507	OB3621.raw	7.09E3	1	1	380	387	
total 35 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG N**GIEETICTA SFK**KNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GRA HVQVVDSNGD R**VFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FK**FFVPPSEQ SLRA**VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM

R.WLGLSAEYGNLYR.N	N	99.9	100.53	1540.7673	13	0.6	771.3914	2	33.21	23	2481	OB3621.raw	2.54E7	180	180	395	407	
K.SQSENFEYVAFK.T	N	99.9	87.45	1447.6619	12	0.1	724.8383	2	30.14	23	2067	OB3621.raw	5.02E6	33	33	465	476	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	77.63	2313.2019	20	0.6	1157.6089	2	30.63	23	2135	OB3621.raw	1.63E7	16	16	408	427	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	77.36	1448.6459	12	-0.2	725.3301	2	30.53	23	2121	OB3621.raw	5.38E5	3	3	465	476	Deamidation (NQ)
N.GIEETIC(+57.02)TASFK.K	Y	99.9	76.78	1354.6438	12	-0.4	678.3289	2	29.29	23	1950	OB3621.raw	3.1E4	2	2	352	363	Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.9	76.05	1388.6936	13	-0.4	695.3538	2	26.97	23	1630	OB3621.raw	1.04E7	62	62	371	383	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	75.34	3544.7434	33	-0.1	1182.5883	3	34.90	23	2709	OB3621.raw	3.45E6	11	11	477	509	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	70.97	1389.6776	13	1.3	695.8470	2	28.06	23	1779	OB3621.raw	2.53E5	2	2	371	383	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.30	2314.1858	20	2.3	772.4043	3	31.60	23	2265	OB3621.raw	1.77E6	1	1	408	427	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	62.88	1268.7452	11	0.7	635.3804	2	5.37	23	420	OB3621.raw	8.67E6	37	37	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	61.36	3545.7273	33	2.2	1182.9189	3	34.55	23	2663	OB3621.raw	7.99E4	1	1	477	509	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	59.80	3545.7273	33	2.1	1182.9188	3	35.57	23	2799	OB3621.raw	1.12E6	4	4	477	509	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98)SFIDNLPEEVVANSYGLPR.E	N	99.9	55.87	3545.7273	33	7.8	1182.9255	3	4.46	23	276	OB3621.raw	2.82E5	1	1	477	509	Deamidation (NQ)
N.TNAHSIIYALR.G	N	99.9	54.68	1257.6830	11	-0.8	629.8483	2	28.16	23	1794	OB3621.raw	1.37E4	1	1	417	427	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	53.61	2314.1858	20	-1.2	1158.0988	2	32.03	23	2323	OB3621.raw	9.47E4	2	2	408	427	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.9	53.46	1443.6953	14	-1.0	722.8542	2	27.80	23	1745	OB3621.raw	8.88E4	4	4	477	490	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.16	1444.6793	14	-0.9	723.3463	2	28.32	23	1815	OB3621.raw	4.59E4	3	3	477	490	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	50.02	1329.6525	13	-0.8	665.8329	2	27.89	23	1757	OB3621.raw	3.59E4	2	2	477	489	
K.FFVPPSEQSLR.A	Y	99.9	46.62	1305.6716	11	-0.3	653.8429	2	29.27	23	1947	OB3621.raw	3.76E5	2	2	523	533	
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.9	44.56	2524.2961	23	2.8	842.4417	3	31.70	23	2278	OB3621.raw	5.89E4	2	2	442	464	
P.DIYNPQAGSLK.T	N	99.9	44.14	1204.6088	11	-0.2	603.3115	2	27.11	23	1649	OB3621.raw	0	1	1	373	383	
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	43.62	3085.5356	29	0.7	1029.5199	3	36.08	23	2869	OB3621.raw	1.09E4	1	1	481	509	
R.NALFVPHYNTNAH.S	N	99.9	42.40	1496.7161	13	-0.8	749.3647	2	27.49	23	1703	OB3621.raw	4.55E5	4	4	408	420	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	42.01	1659.8217	15	-0.4	554.2809	3	26.52	23	1575	OB3621.raw	1.61E5	4	4	369	383	Deamidation (NQ)
N.AHSIIYALR.G	N	99.9	41.87	1042.5923	9	-0.5	348.5379	3	27.41	23	1691	OB3621.raw	3.52E3	1	1	419	427	
K.TAN(+.98)ELNLLILR.W	N	99.8	39.19	1269.7292	11	-3.1	635.8699	2	33.52	23	2523	OB3621.raw	9.38E5	1	1	384	394	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.54	1200.6099	12	0.1	601.3123	2	27.76	23	1739	OB3621.raw	1.06E5	2	2	477	488	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.8	38.36	1660.8057	15	-1.3	554.6085	3	27.19	23	1660	OB3621.raw	3.8E4	1	1	369	383	Deamidation (NQ)
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.7	37.11	1659.8217	15	0.6	554.2815	3	26.87	23	1618	OB3621.raw	1.52E5	1	1	369	383	Deamidation (NQ)
K.FFVPPSEQSLRA.V	Y	99.7	37.02	1376.7087	12	-0.6	689.3613	2	30.10	23	2062	OB3621.raw	1.35E6	8	8	523	534	
K.TDSRPSIAN(+.98)LAGEN.S	N	99.6	36.49	1444.6793	14	0.1	723.3470	2	28.73	23	1873	OB3621.raw	3.98E4	1	1	477	490	Deamidation (NQ)
H.SIIYALR.G	N	99.5	34.84	834.4963	7	-0.1	418.2554	2	28.45	23	1834	OB3621.raw	1.03E6	5	5	421	427	
H.VLVVPQNFAVAGK.S	N	99.5	34.67	1340.7816	13	-0.9	671.3975	2	30.01	23	2050	OB3621.raw	1.68E4	1	1	452	464	
R.N(+.98)RSPDIYN(+.98)PQAGSLK.T	N	99.4	33.31	1660.8057	15	-1.6	554.6083	3	27.01	23	1635	OB3621.raw	3.8E4	1	1	369	383	Deamidation (NQ)
K.FFVPPSEQ(+.98)SLRA.V	Y	99.4	33.16	1377.6927	12	-0.8	689.8531	2	30.32	23	2093	OB3621.raw	1.57E5	1	1	523	534	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	99.1	32.05	1534.7892	13	-2.6	768.3999	2	29.02	23	1913	OB3621.raw	3.67E4	3	3	415	427	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.1	31.72	1659.8217	15	-1.2	554.2805	3	26.35	23	1558	OB3621.raw	1.52E5	1	1	369	383	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	98.9	31.35	1658.8376	15	-0.1	553.9531	3	25.82	23	1519	OB3621.raw	4.1E3	1	1	369	383	
L.FVPHYNTNAHSIIYALR.G	N	98.8	31.24	2015.0377	17	-1.7	672.6854	3	30.59	23	2129	OB3621.raw	2.21E4	1	1	411	427	
total 39 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG N**GIEETICTA SFK**KNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GRA HVQVVDSNGD R**VFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FK**FFVPPSEQ SLRA**VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	100.53	1540.7673	13	0.6	771.3914	2	33.21	23	2481	OB3621.raw	2.54E7	180	180	395	407	
K.SQSENFEYVAFK.T	N	99.9	87.45	1447.6619	12	0.1	724.8383	2	30.14	23	2067	OB3621.raw	5.02E6	33	33	465	476	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	77.63	2313.2019	20	0.6	1157.6089	2	30.63	23	2135	OB3621.raw	1.63E7	16	16	408	427	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	77.36	1448.6459	12	-0.2	725.3301	2	30.53	23	2121	OB3621.raw	5.38E5	3	3	465	476	Deamidation (NQ)
N.GIEETIC(+57.02)TASFK.K	Y	99.9	76.78	1354.6438	12	-0.4	678.3289	2	29.29	23	1950	OB3621.raw	3.1E4	2	2	352	363	Carbamidomethylation
R.SPDIYNPQAGSLK.T	N	99.9	76.05	1388.6936	13	-0.4	695.3538	2	26.97	23	1630	OB3621.raw	1.04E7	62	62	371	383	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	75.34	3544.7434	33	-0.1	1182.5883	3	34.90	23	2709	OB3621.raw	3.45E6	11	11	477	509	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	70.97	1389.6776	13	1.3	695.8470	2	28.06	23	1779	OB3621.raw	2.53E5	2	2	371	383	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.30	2314.1858	20	2.3	772.4043	3	31.60	23	2265	OB3621.raw	1.77E6	1	1	408	427	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	62.88	1268.7452	11	0.7	635.3804	2	5.37	23	420	OB3621.raw	8.67E6	37	37	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	61.36	3545.7273	33	2.2	1182.9189	3	34.55	23	2663	OB3621.raw	7.99E4	1	1	477	509	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	59.80	3545.7273	33	2.1	1182.9188	3	35.57	23	2799	OB3621.raw	1.12E6	4	4	477	509	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98)SFIDNLPEEVVANSYGLPR.E	N	99.9	55.87	3545.7273	33	7.8	1182.9255	3	4.46	23	276	OB3621.raw	2.82E5	1	1	477	509	Deamidation (NQ)
N.TNAHSIIYALR.G	N	99.9	54.68	1257.6830	11	-0.8	629.8483	2	28.16	23	1794	OB3621.raw	1.37E4	1	1	417	427	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	53.61	2314.1858	20	-1.2	1158.0988	2	32.03	23	2323	OB3621.raw	9.47E4	2	2	408	427	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	99.9	53.46	1443.6953	14	-1.0	722.8542	2	27.80	23	1745	OB3621.raw	8.88E4	4	4	477	490	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.16	1444.6793	14	-0.9	723.3463	2	28.32	23	1815	OB3621.raw	4.59E4	3	3	477	490	Deamidation (NQ)

K.TDSRPSIANLAGE.N	N	99.9	50.02	1329.6525	13	-0.8	665.8329	2	27.89	23	1757	OB3621.raw	3.59E4	2	2	477	489	
K.FFVPPSEQSLR.A	Y	99.9	46.62	1305.6716	11	-0.3	653.8429	2	29.27	23	1947	OB3621.raw	3.76E5	2	2	523	533	
R.VFDEELQEGHVLVVPQNFAVAGK.S	Y	99.9	44.56	2524.2961	23	2.8	842.4417	3	31.70	23	2278	OB3621.raw	5.89E4	2	2	442	464	
P.DIYNPQAGSLK.T	N	99.9	44.14	1204.6088	11	-0.2	603.3115	2	27.11	23	1649	OB3621.raw	0	1	1	373	383	
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	43.62	3085.5356	29	0.7	1029.5199	3	36.08	23	2869	OB3621.raw	1.09E4	1	1	481	509	
R.NALFVPHYNTNAH.S	N	99.9	42.40	1496.7161	13	-0.8	749.3647	2	27.49	23	1703	OB3621.raw	4.55E5	4	4	408	420	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	42.01	1659.8217	15	-0.4	554.2809	3	26.52	23	1575	OB3621.raw	1.61E5	4	4	369	383	Deamidation (NQ)
N.AHSIIYALR.G	N	99.9	41.87	1042.5923	9	-0.5	348.5379	3	27.41	23	1691	OB3621.raw	3.52E3	1	1	419	427	
K.TAN(+.98)ELNLLILR.W	N	99.8	39.19	1269.7292	11	-3.1	635.8699	2	33.52	23	2523	OB3621.raw	9.38E5	1	1	384	394	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.54	1200.6099	12	0.1	601.3123	2	27.76	23	1739	OB3621.raw	1.06E5	2	2	477	488	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.8	38.36	1660.8057	15	-1.3	554.6085	3	27.19	23	1660	OB3621.raw	3.8E4	1	1	369	383	Deamidation (NQ)
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.7	37.11	1659.8217	15	0.6	554.2815	3	26.87	23	1618	OB3621.raw	1.52E5	1	1	369	383	Deamidation (NQ)
K.FFVPPSEQSLRA.V	Y	99.7	37.02	1376.7087	12	-0.6	689.3613	2	30.10	23	2062	OB3621.raw	1.35E6	8	8	523	534	
K.TDSRPSIAN(+.98)LAGEN.S	N	99.6	36.49	1444.6793	14	0.1	723.3470	2	28.73	23	1873	OB3621.raw	3.98E4	1	1	477	490	Deamidation (NQ)
H.SIIYALR.G	N	99.5	34.84	834.4963	7	-0.1	418.2554	2	28.45	23	1834	OB3621.raw	1.03E6	5	5	421	427	
H.VLVVPQNFAVAGK.S	N	99.5	34.67	1340.7816	13	-0.9	671.3975	2	30.01	23	2050	OB3621.raw	1.68E4	1	1	452	464	
R.N(+.98)RSPDIYN(+.98)PQAGSLK.T	N	99.4	33.31	1660.8057	15	-1.6	554.6083	3	27.01	23	1635	OB3621.raw	3.8E4	1	1	369	383	Deamidation (NQ)
K.FFVPPSEQ(+.98)SLRA.V	Y	99.4	33.16	1377.6927	12	-0.8	689.8531	2	30.32	23	2093	OB3621.raw	1.57E5	1	1	523	534	Deamidation (NQ)
H.YNTNAHSIIYALR.G	N	99.1	32.05	1534.7892	13	-2.6	768.3999	2	29.02	23	1913	OB3621.raw	3.67E4	3	3	415	427	
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.1	31.72	1659.8217	15	-1.2	554.2805	3	26.35	23	1558	OB3621.raw	1.52E5	1	1	369	383	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	98.9	31.35	1658.8376	15	-0.1	553.9531	3	25.82	23	1519	OB3621.raw	4.1E3	1	1	369	383	
L.FVPHYNTNAHSIIYALR.G	N	98.8	31.24	2015.0377	17	-1.7	672.6854	3	30.59	23	2129	OB3621.raw	2.21E4	1	1	411	427	
total 39 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

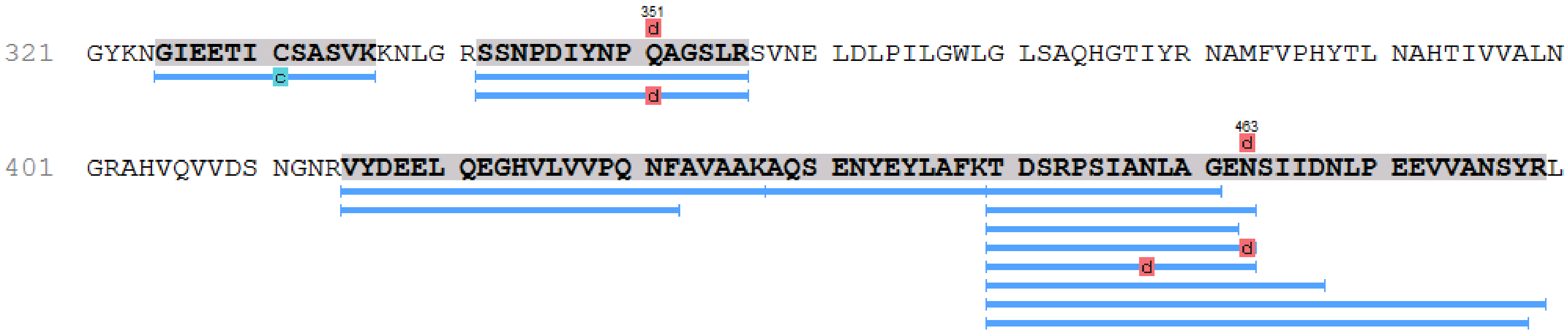
Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR



c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM

R.SSNPDIYNPQAGSLR.S	Y	99.9	68.82	1617.7747	15	-1.1	809.8937	2	27.36	23	1684	OB3621.raw	3.82E4	3	3	342	356	
K.AQSENYEYLAFK.T	Y	99.9	64.79	1461.6776	12	-1.5	731.8450	2	29.79	23	2019	OB3621.raw	1.43E6	10	10	438	449	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	63.25	3243.6006	30	-0.6	1082.2068	3	33.94	23	2581	OB3621.raw	1.41E5	3	3	450	479	
N.GIEETIC(+57.02)SASVK.K	Y	99.9	56.46	1292.6282	12	-0.2	647.3212	2	27.53	23	1707	OB3621.raw	1.17E4	1	1	325	336	Carbamidomethylation
K.TDSRPSIANLAGEN.S	N	99.9	53.46	1443.6953	14	-1.0	722.8542	2	27.80	23	1745	OB3621.raw	8.88E4	4	4	450	463	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.9	53.09	2554.3066	23	-0.7	852.4422	3	31.09	23	2196	OB3621.raw	4.65E4	1	1	415	437	
K.TDSRPSIANLAGENSIID.N	N	99.9	53.05	1871.9225	18	0.1	936.9686	2	30.82	23	2161	OB3621.raw	4.21E4	1	1	450	467	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.16	1444.6793	14	-0.9	723.3463	2	28.32	23	1815	OB3621.raw	4.59E4	3	3	450	463	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	50.02	1329.6525	13	-0.8	665.8329	2	27.89	23	1757	OB3621.raw	3.59E4	2	2	450	462	
R.SSNPDIYNPQ(+.98)AGSLR.S	Y	99.9	45.78	1618.7587	15	-3.2	810.3840	2	27.93	23	1764	OB3621.raw	1.3E4	1	1	342	356	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.54	1200.6099	12	0.1	601.3123	2	27.76	23	1739	OB3621.raw	1.06E5	2	2	450	461	
K.TDSRPSIAN(+.98)LAGEN.S	N	99.6	36.49	1444.6793	14	0.1	723.3470	2	28.73	23	1873	OB3621.raw	3.98E4	1	1	450	463	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.5	35.61	2114.0320	18	0.0	1058.0233	2	32.34	23	2363	OB3621.raw	3.86E4	1	1	415	432	
K.TDSRPSIANLAGENSIIDNLPEEVVANSY.R	N	98.7	30.52	3087.4995	29	-1.4	1030.1724	3	35.10	23	2737	OB3621.raw	2.8E4	1	1	450	478	
total 14 peptides																		

Q0GM57|Q0GM57_ARAHY

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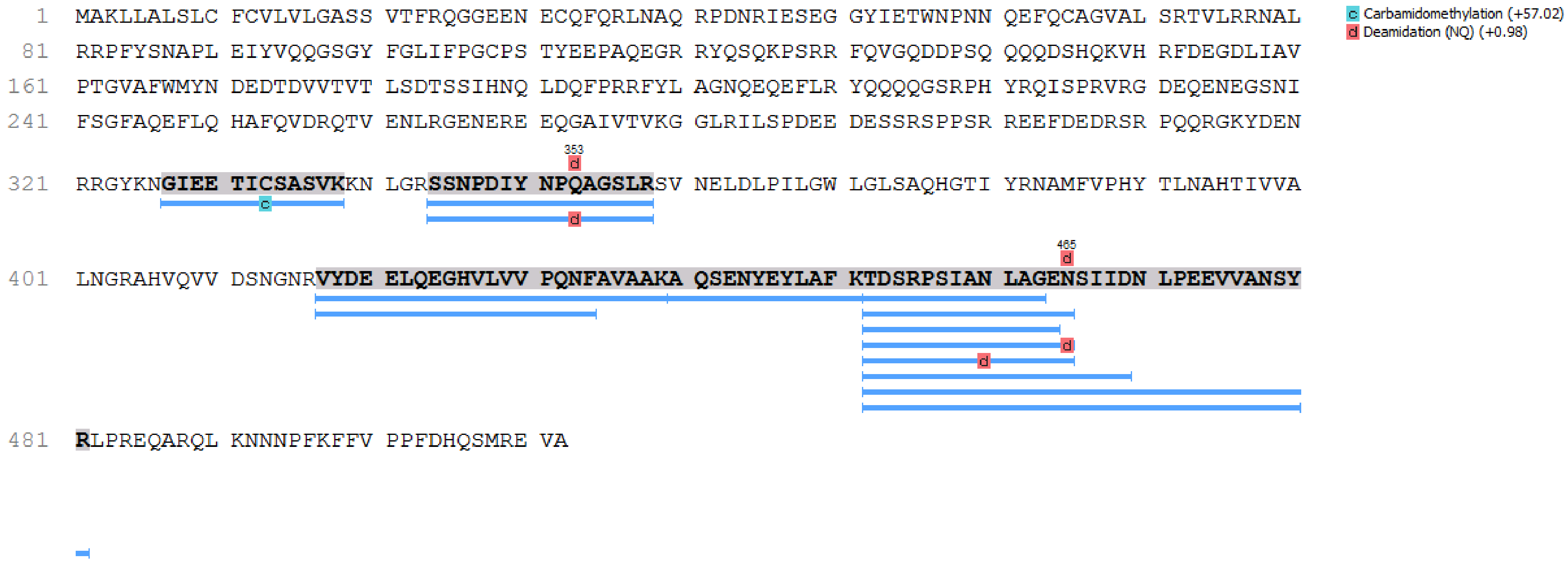
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKN**GIEE TICSASVK**KN LGR**SSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY**
481 **R**LPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 23	#Spec	#Spec Sample 23	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	Y	99.9	68.82	1617.7747	15	-1.1	809.8937	2	27.36	23	1684	OB3621.raw	3.82E4	3	3	344	358	
K.AQSENYEYLAFK.T	Y	99.9	64.79	1461.6776	12	-1.5	731.8450	2	29.79	23	2019	OB3621.raw	1.43E6	10	10	440	451	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	63.25	3243.6006	30	-0.6	1082.2068	3	33.94	23	2581	OB3621.raw	1.41E5	3	3	452	481	
N.GIEETIC(+57.02)SASVK.K	Y	99.9	56.46	1292.6282	12	-0.2	647.3212	2	27.53	23	1707	OB3621.raw	1.17E4	1	1	327	338	Carbamidomethylation

K.TDSRPSIANLAGEN.S	N	99.9	53.46	1443.6953	14	-1.0	722.8542	2	27.80	23	1745	OB3621.raw	8.88E4	4	4	452	465	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.9	53.09	2554.3066	23	-0.7	852.4422	3	31.09	23	2196	OB3621.raw	4.65E4	1	1	417	439	
K.TDSRPSIANLAGENSIID.N	N	99.9	53.05	1871.9225	18	0.1	936.9686	2	30.82	23	2161	OB3621.raw	4.21E4	1	1	452	469	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.16	1444.6793	14	-0.9	723.3463	2	28.32	23	1815	OB3621.raw	4.59E4	3	3	452	465	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	50.02	1329.6525	13	-0.8	665.8329	2	27.89	23	1757	OB3621.raw	3.59E4	2	2	452	464	
R.SSNPDIYNPQ(+.98)AGSLR.S	Y	99.9	45.78	1618.7587	15	-3.2	810.3840	2	27.93	23	1764	OB3621.raw	1.3E4	1	1	344	358	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.54	1200.6099	12	0.1	601.3123	2	27.76	23	1739	OB3621.raw	1.06E5	2	2	452	463	
K.TDSRPSIAN(+.98)LAGEN.S	N	99.6	36.49	1444.6793	14	0.1	723.3470	2	28.73	23	1873	OB3621.raw	3.98E4	1	1	452	465	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.5	35.61	2114.0320	18	0.0	1058.0233	2	32.34	23	2363	OB3621.raw	3.86E4	1	1	417	434	
K.TDSRPSIANLAGENSIIDNLPEEVVANSY.R	N	98.7	30.52	3087.4995	29	-1.4	1030.1724	3	35.10	23	2737	OB3621.raw	2.8E4	1	1	452	480	
total 14 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

1. Notes

Spot 14 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

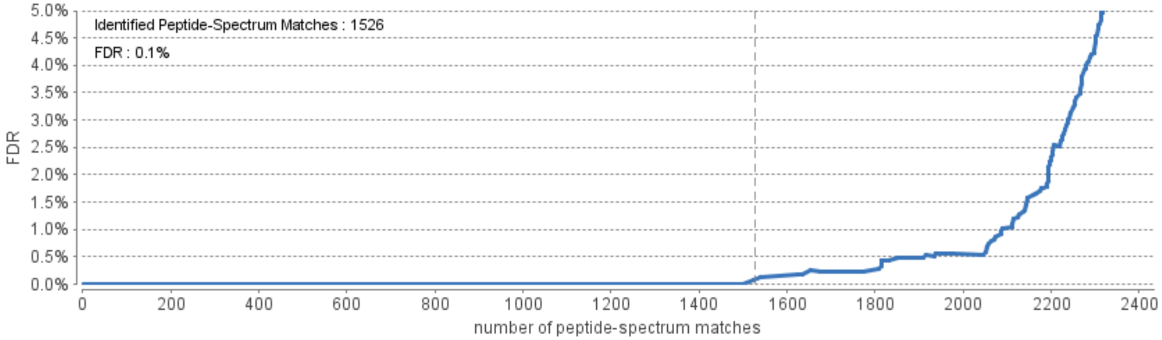


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

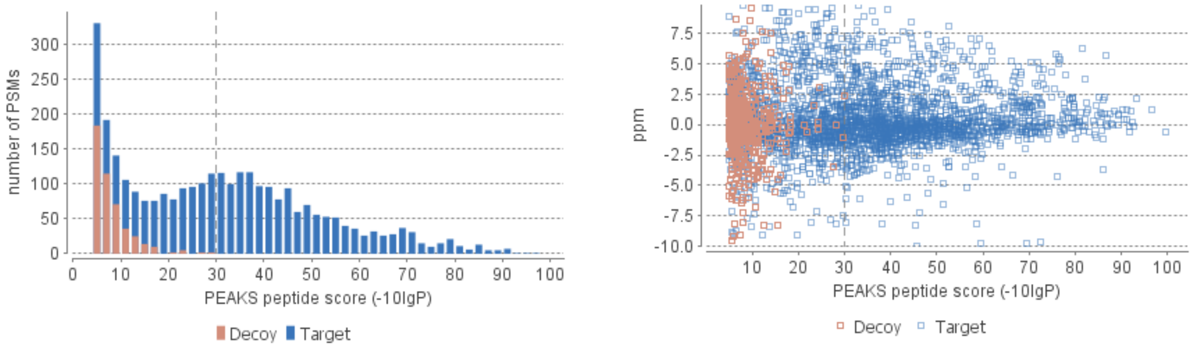


Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

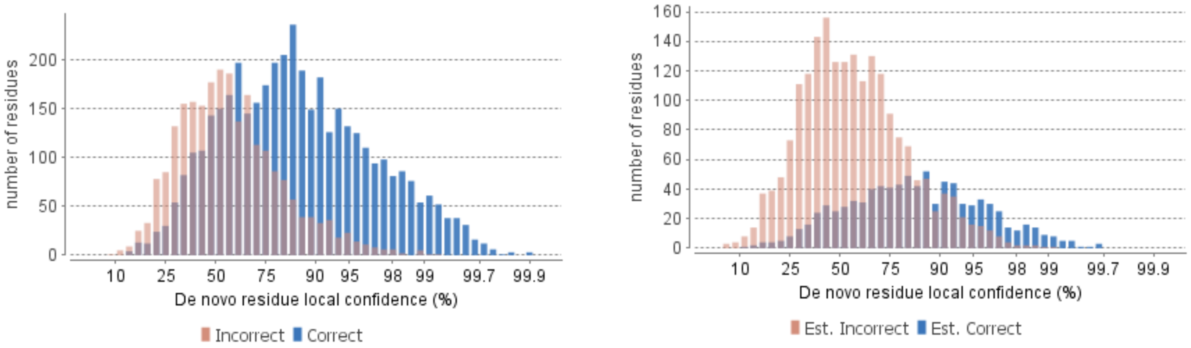


Table 1. Statistics of data.

# of MS scans	2422
# of MS/MS scans	6197

Table 2. Result filtration parameters.

Peptide -10lgP	≥30
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	1252
Peptide sequences	135
Protein groups	5
Proteins	7
Proteins (#Unique Peptides)	3 (>2); 4 (=2); 0 (=1);
FDR (Peptide-Spectrum Matches)	0.1%
FDR (Peptide Sequences)	0.7%
FDR (Protein)	9.1%
De Novo Only Spectra	264

Table 4. PTM profile.

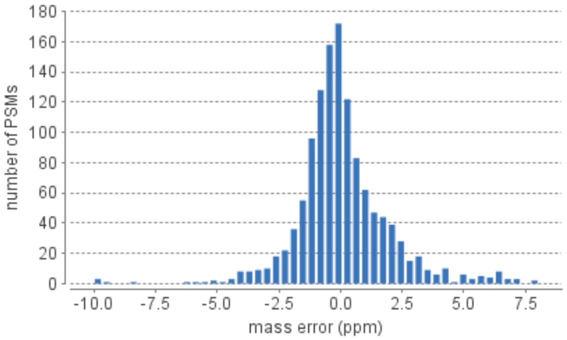
Name	∆Mass	Position	#PSM	-10lgP	Area	AScore
Deamidation	.98	NQ	121	86.17	8.16E2	32.52
Carbamidomethyl	57.02	C	69	71.61	3.83E6	1000.00
HydPro	15.99	P	23	69.12	3.63E5	103.33
Oxidation	15.99	M	1	32.10	2.62E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



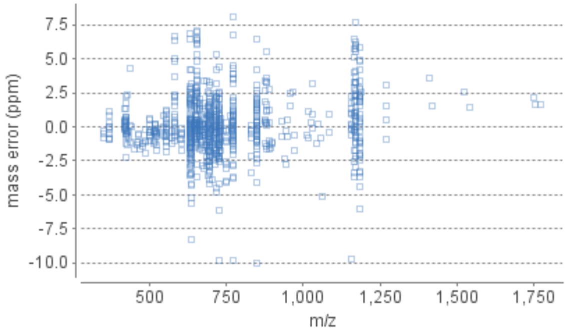


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 24	122	13	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3622.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 24	Area Sample 24	#Peptides	#Unique	#Spec Sample 24	PTM	Avg. Mass	Description
3	3	B5TYU1|B5TYU1_ARAHY	99.2	339.69	32	32	3.54E7	42	2	769	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1

1	15	Q647H3|Q647H3_ARAHY	99.2	338.17	32	32	5.51E7	44	5	842	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
6	7	Q647H4|Q647H4_ARAHY	99.2	326.97	30	30	8.2E6	39	6	690	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	99.2	326.97	30	30	8.2E6	39	6	690	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
5	13	Q9FZ11|Q9FZ11_ARAHY	99.2	324.50	26	26	6.43E6	34	2	773	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
9	41	Q6IWG5|Q6IWG5_ARAHY	99.1	194.92	15	15	1.98E6	13	2	60	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
9	42	Q0GM57|Q0GM57_ARAHY	99.1	194.92	15	15	1.98E6	13	2	60	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 7 proteins													

B5TYU1|B5TYU1_ARAHY

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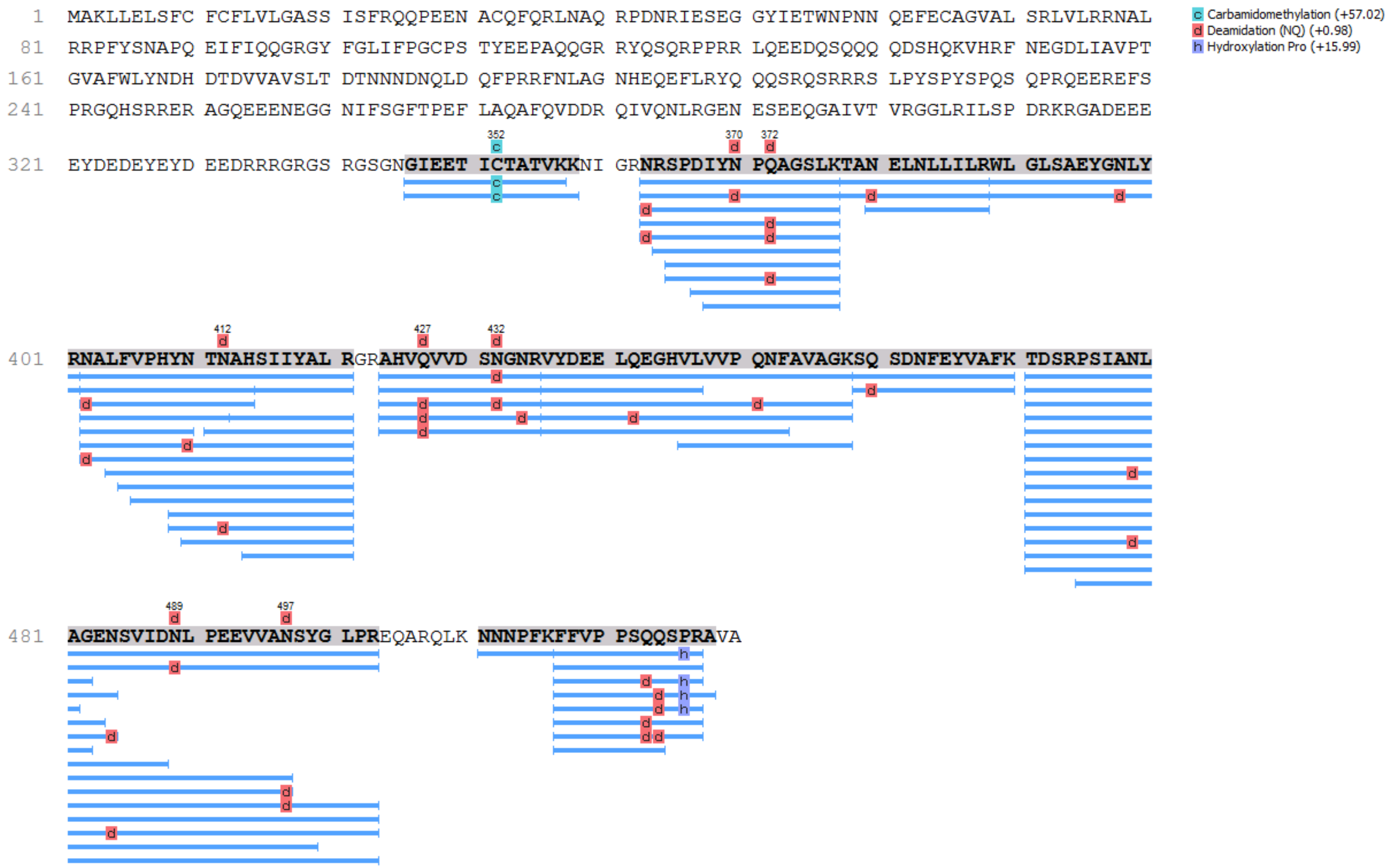
| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGNGIEET ICTATVKKNI GRNRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LPREQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	99.52	2313.2019	20	-0.6	1157.6075	2	31.20	24	2573	OB3622.raw	1.39E8	53	53	402	421	
R.WLGLSAEYGNLYR.N	N	99.9	96.69	1540.7673	13	1.3	771.3919	2	32.99	24	2817	OB3622.raw	4.78E7	114	114	389	401	

K.SQSDNFEYVAFK.T	N	99.9	89.30	1433.6462	12	0.8	717.8310	2	30.18	24	2433	OB3622.raw	1.37E7	52	52	459	470	
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	85.39	3496.7434	33	1.0	1166.5896	3	34.02	24	2955	OB3622.raw	1.7E7	26	26	471	503	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	82.52	2314.1858	20	1.0	1158.1013	2	32.05	24	2688	OB3622.raw	0	3	3	402	421	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	79.74	1388.6936	13	0.5	695.3544	2	27.06	24	2001	OB3622.raw	3.7E7	141	141	365	377	
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	77.76	1434.6302	12	4.2	718.3254	2	29.83	24	2385	OB3622.raw	2.73E6	3	3	459	470	Deamidation (NQ)
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	77.75	1389.6776	13	1.1	695.8469	2	27.79	24	2103	OB3622.raw	3.34E6	2	2	365	377	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98)SVIDNLPEEVVANSYGLPR.E	Y	99.9	75.81	3497.7273	33	5.8	1166.9231	3	35.07	24	3099	OB3622.raw	8.88E6	1	1	471	503	Deamidation (NQ)
K.TDSRPSIANLAGENSVIDN(+.98)LPEEVVANSYGLPR.E	Y	99.9	74.87	3497.7273	33	2.3	1166.9191	3	33.68	24	2909	OB3622.raw	9.25E6	3	3	471	503	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	74.54	2540.2910	23	0.5	1271.1534	2	30.64	24	2497	OB3622.raw	9.04E7	79	79	436	458	
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	72.62	2314.1858	20	3.9	772.4055	3	32.03	24	2685	OB3622.raw	6.33E6	4	4	402	421	Deamidation (NQ)
K.FFVPPSQQSPR.A	N	99.9	72.34	1288.6564	11	-0.2	645.3353	2	26.41	24	1911	OB3622.raw	9.6E5	8	8	517	527	
N.GIEETIC(+57.02)TATVK.K	N	99.9	71.61	1320.6595	12	-0.3	661.3369	2	28.01	24	2133	OB3622.raw	1.19E7	25	25	346	357	Carbamidomethylation
R.PSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	68.25	3037.5356	29	-0.6	1013.5186	3	35.13	24	3108	OB3622.raw	6.8E4	1	1	475	503	
R.VYDEELQEGHVLVVPQ(+.98)NFAVAGK.S	N	99.9	67.02	2541.2751	23	3.1	1271.6488	2	31.24	24	2579	OB3622.raw	1.57E6	1	1	436	458	Deamidation (NQ)
R.AHVQVVDSN(+.98)GNR.V	N	99.9	66.38	1295.6218	12	0.9	648.8188	2	4.85	24	333	OB3622.raw	2.26E6	6	6	424	435	Deamidation (NQ)
K.FFVPPSQQSP(+15.99)R.A	N	99.9	66.29	1304.6512	11	0.0	653.3329	2	26.06	24	1863	OB3622.raw	2.97E5	4	4	517	527	Hydroxylation Pro
K.FFVPPSQ(+.98)QSPR.A	N	99.9	66.27	1289.6404	11	2.0	645.8287	2	27.50	24	2063	OB3622.raw	3.68E5	1	1	517	527	Deamidation (NQ)
R.NALFVPHYNTNAH.S	N	99.9	65.14	1496.7161	13	-1.0	749.3646	2	27.67	24	2086	OB3622.raw	7.92E6	19	19	402	414	
R.VYDEELQEGHVL.V	N	99.9	64.92	1429.6725	12	0.0	715.8435	2	29.28	24	2311	OB3622.raw	1.14E5	2	2	436	447	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	64.27	1659.8217	15	-0.2	830.9180	2	26.24	24	1887	OB3622.raw	2.3E6	6	6	363	377	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	64.26	1268.7452	11	1.5	635.3809	2	32.55	24	2757	OB3622.raw	2.03E7	74	74	378	388	
R.NRSPDIYNPQAGSLK.T	N	99.9	62.82	1658.8376	15	-0.3	830.4258	2	25.58	24	1797	OB3622.raw	2.4E6	17	17	363	377	
K.TDSRPSIANLAGENSVIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	61.33	3497.7273	33	3.3	875.4420	4	33.76	24	2920	OB3622.raw	9.2E4	2	2	471	503	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.9	59.87	1294.6378	12	-0.1	648.3261	2	19.68	24	1394	OB3622.raw	3.06E5	7	7	424	435	
N.AHSIIYALR.G	N	99.9	57.60	1042.5923	9	-1.3	522.3027	2	27.33	24	2039	OB3622.raw	2.62E5	6	6	413	421	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.14	1660.8057	15	-0.8	831.4094	2	26.82	24	1968	OB3622.raw	7.69E5	3	3	363	377	Deamidation (NQ)
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.10	1659.8217	15	1.3	554.2819	3	26.02	24	1857	OB3622.raw	2.3E6	2	2	363	377	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	55.78	1340.7816	13	-0.4	671.3978	2	29.75	24	2375	OB3622.raw	5.67E4	1	1	446	458	
N.TNAHSIIYALR.G	N	99.9	55.69	1257.6830	11	-0.9	629.8482	2	27.43	24	2053	OB3622.raw	4.1E5	3	3	411	421	
K.TDSRPSIANLAGE.N	N	99.9	54.71	1329.6525	13	-1.0	665.8328	2	28.03	24	2137	OB3622.raw	9.7E4	2	2	471	483	
L.FVPHYNTNAHSIIYALR.G	N	99.9	53.28	2015.0377	17	-0.6	672.6861	3	30.41	24	2465	OB3622.raw	7.91E5	3	3	405	421	
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	52.66	1497.7001	13	-3.0	749.8550	2	28.25	24	2167	OB3622.raw	4.05E4	5	5	402	414	Deamidation (NQ)
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	52.64	1541.7513	13	8.1	771.8892	2	33.31	24	2859	OB3622.raw	1.05E7	2	2	389	401	Deamidation (NQ)
P.DIYNPQAGSLK.T	N	99.9	52.40	1204.6088	11	-0.4	603.3114	2	26.78	24	1963	OB3622.raw	4.79E4	3	3	367	377	
K.TDSRPSIANLAGENSVID.N	N	99.9	51.91	1857.9067	18	-0.7	929.9600	2	30.07	24	2419	OB3622.raw	5.72E4	2	2	471	488	
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.9	51.55	1659.8217	15	-0.2	554.2811	3	26.67	24	1947	OB3622.raw	2.15E6	1	1	363	377	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	50.96	1444.6793	14	-1.7	723.3457	2	28.05	24	2139	OB3622.raw	8.3E4	4	4	471	484	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	50.96	1296.6058	12	2.9	649.3121	2	20.84	24	1462	OB3622.raw	1.01E4	1	1	424	435	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	511	516	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	50.75	2128.1218	18	0.0	710.3812	3	30.41	24	2466	OB3622.raw	1.07E6	3	3	404	421	
K.FFVPPSQ(+.98)QSP(+15.99)R.A	N	99.9	49.86	1305.6353	11	1.9	653.8261	2	26.29	24	1895	OB3622.raw	2.59E5	1	1	517	527	Deamidation (NQ); Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	99.9	48.98	1534.7892	13	0.3	768.4021	2	28.37	24	2183	OB3622.raw	6.52E5	7	7	409	421	
K.TDSRPSIANLAGEN.S	N	99.9	48.50	1443.6953	14	-2.1	722.8534	2	27.55	24	2069	OB3622.raw	2.59E5	2	2	471	484	
R.NALFVPHYNTN.A	N	99.9	48.13	1288.6200	11	-0.7	645.3168	2	28.93	24	2262	OB3622.raw	7.75E4	5	5	402	412	
A.NELNLLILR.W	N	99.9	48.10	1096.6604	9	-0.7	549.3371	2	32.53	24	2755	OB3622.raw	1.95E4	1	1	380	388	
K.TDSRPSIANLAGENSVIDNLPEEVVANSY.G	N	99.9	47.77	3073.4839	29	0.3	1025.5022	3	34.74	24	3053	OB3622.raw	3.3E4	1	1	471	499	
Y.NTNAHSIIYALR.G	N	99.9	47.26	1371.7258	12	-1.3	458.2486	3	28.12	24	2149	OB3622.raw	5.29E4	1	1	410	421	
K.TDSRPSIANLA.G	N	99.9	46.27	1143.5884	11	-0.3	572.8013	2	27.32	24	2037	OB3622.raw	1.4E5	3	3	471	481	
A.HSIIYALR.G	N	99.9	45.89	971.5552	8	-1.0	486.7844	2	27.03	24	1998	OB3622.raw	3.35E4	2	2	414	421	
R.VYDEELQ(+.98)EGHVLVVPQNFAVAGK.S	N	99.9	45.69	2541.2751	23	0.6	636.3264	4	31.48	24	2610	OB3622.raw	6.72E5	1	1	436	458	Deamidation (NQ)
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	45.52	1295.6218	12	-1.0	648.8176	2	21.53	24	1504	OB3622.raw	1.85E4	1	1	424	435	Deamidation (NQ)
K.FFVPPSQ(+.98)Q(+.98)SPR.A	N	99.9	45.37	1290.6244	11	2.0	646.3207	2	28.02	24	2135	OB3622.raw	1.68E5	1	1	517	527	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.9	45.37	2114.0320	18	-0.8	1058.0225	2	32.13	24	2698	OB3622.raw	1.07E5	2	2	436	453	
K.FFVPPSQQ.S	N	99.9	45.30	948.4705	8	-1.2	475.2419	2	28.55	24	2209	OB3622.raw	9.93E3	1	1	517	524	
K.TAN(+.98)ELNLLILR.W	N	99.9	44.86	1269.7292	11	4.2	635.8746	2	33.44	24	2877	OB3622.raw	3.17E6	2	2	378	388	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	44.77	3497.7273	33	2.2	1749.8748	2	34.35	24	3001	OB3622.raw	8.25E4	1	1	471	503	Deamidation (NQ)

K.TDSRPSIANLAGENSVIDNLPEEVVAN.S	N	99.9	44.61	2823.3887	27	-0.3	942.1365	3	33.31	24	2860	OB3622.raw	1.98E5	2	2	471	497	
R.NALFVPHYN.T	N	99.8	40.12	1073.5294	9	-0.1	537.7719	2	28.67	24	2225	OB3622.raw	4.24E4	1	1	402	410	
K.FFVPPSQQ(+.98)SP(+15.99)RA.V	N	99.8	39.41	1376.6724	12	0.1	689.3435	2	27.11	24	2009	OB3622.raw	1.09E5	3	3	517	528	Deamidation (NQ); Hydroxylation Pro
K.TDSRPSIAN(+.98)LAG.E	N	99.8	38.95	1201.5939	12	-0.1	601.8041	2	28.38	24	2185	OB3622.raw	1.35E4	1	1	471	482	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.90	1200.6099	12	-0.5	601.3119	2	27.53	24	2067	OB3622.raw	3.15E5	4	4	471	482	
N.GIEETIC(+57.02)TATVKK.N	N	99.8	38.64	1448.7545	13	0.0	725.3845	2	26.33	24	1900	OB3622.raw	5.79E4	1	1	346	358	Carbamidomethylation
H.YNTN(+.98)AHSIIYALR.G	N	99.8	38.44	1535.7732	13	-1.3	512.9310	3	29.63	24	2359	OB3622.raw	3.41E4	1	1	409	421	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.60	834.4963	7	0.3	418.2556	2	28.19	24	2158	OB3622.raw	3.94E6	9	9	415	421	
N.RSPDIYNPQAGSLK.T	N	99.7	36.90	1544.7947	14	-0.5	515.9386	3	25.42	24	1775	OB3622.raw	5.99E4	3	3	364	377	
K.FFVPPSQQ(+.98)SP(+15.99)R.A	N	99.6	35.72	1305.6353	11	7.1	653.8295	2	26.73	24	1956	OB3622.raw	2.59E5	1	1	517	527	Deamidation (NQ); Hydroxylation Pro
K.TDSRPSIANLAGENSVIDNLPEEVVAN(+.98).S	N	99.5	35.40	2824.3726	27	3.6	1413.1986	2	33.63	24	2902	OB3622.raw	2.62E4	1	1	471	497	Deamidation (NQ)
R.AHVQ(+.98)VVDSNGN(+.98)R.V	N	99.4	33.69	1296.6058	12	4.3	433.2111	3	20.93	24	1468	OB3622.raw	1.25E5	1	1	424	435	Deamidation (NQ)
F.VPHYNTNAHSIIYALR.G	N	99.4	33.06	1867.9692	16	-1.6	467.9988	4	28.64	24	2221	OB3622.raw	3.03E4	1	1	406	421	
D.IYNPQAGSLK.T	N	98.8	30.17	1089.5818	10	0.9	545.7986	2	24.83	24	1726	OB3622.raw	1.67E3	1	1	368	377	
total 72 peptides																		

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS
401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	99.52	2313.2019	20	-0.6	1157.6075	2	31.20	24	2573	OB3622.raw	1.39E8	53	53	409	428	
R.WLGLSAEYGNLYR.N	N	99.9	96.69	1540.7673	13	1.3	771.3919	2	32.99	24	2817	OB3622.raw	4.78E7	114	114	396	408	
K.SQSDNFEYVAFK.T	N	99.9	89.30	1433.6462	12	0.8	717.8310	2	30.18	24	2433	OB3622.raw	1.37E7	52	52	466	477	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	86.72	3510.7590	33	5.7	1171.2670	3	34.86	24	3069	OB3622.raw	4.1E7	44	44	478	510	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	82.52	2314.1858	20	1.0	1158.1013	2	32.05	24	2688	OB3622.raw	0	3	3	409	428	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYGLPR.E	Y	99.9	81.57	3511.7429	33	6.3	1171.5956	3	35.16	24	3111	OB3622.raw	1.34E7	8	8	478	510	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	79.74	1388.6936	13	0.5	695.3544	2	27.06	24	2001	OB3622.raw	3.7E7	141	141	372	384	
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	77.76	1434.6302	12	4.2	718.3254	2	29.83	24	2385	OB3622.raw	2.73E6	3	3	466	477	Deamidation (NQ)
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	77.75	1389.6776	13	1.1	695.8469	2	27.79	24	2103	OB3622.raw	3.34E6	2	2	372	384	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	74.54	2540.2910	23	0.5	1271.1534	2	30.64	24	2497	OB3622.raw	9.04E7	79	79	443	465	
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	72.62	2314.1858	20	3.9	772.4055	3	32.03	24	2685	OB3622.raw	6.33E6	4	4	409	428	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	71.40	3511.7429	33	0.7	1171.5891	3	33.14	24	2838	OB3622.raw	5.3E4	3	3	478	510	Deamidation (NQ)
N.GIEETIC(+57.02)TASVK.K	N	99.9	71.40	1306.6438	12	0.2	654.3293	2	27.07	24	2002	OB3622.raw	1.63E7	37	37	353	364	Carbamidomethylation
R.VYDEELQEGHVLVVPQ(+.98)NFAVAGK.S	N	99.9	67.02	2541.2751	23	3.1	1271.6488	2	31.24	24	2579	OB3622.raw	1.57E6	1	1	443	465	Deamidation (NQ)
R.AHVQVVDSN(+.98)GNR.V	N	99.9	66.38	1295.6218	12	0.9	648.8188	2	4.85	24	333	OB3622.raw	2.26E6	6	6	431	442	Deamidation (NQ)
R.NALFVPHYNTNAH.S	N	99.9	65.14	1496.7161	13	-1.0	749.3646	2	27.67	24	2086	OB3622.raw	7.92E6	19	19	409	421	

R.VYDEELQEGHVL.V	N	99.9	64.92	1429.6725	12	0.0	715.8435	2	29.28	24	2311	OB3622.raw	1.14E5	2	2	443	454	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	64.27	1659.8217	15	-0.2	830.9180	2	26.24	24	1887	OB3622.raw	2.3E6	6	6	370	384	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.9	62.82	1658.8376	15	-0.3	830.4258	2	25.58	24	1797	OB3622.raw	2.4E6	17	17	370	384	
R.AHVQVVDSNGNR.V	N	99.9	59.87	1294.6378	12	-0.1	648.3261	2	19.68	24	1394	OB3622.raw	3.06E5	7	7	431	442	
R.PSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	57.72	3051.5513	29	1.1	1018.1922	3	35.92	24	3214	OB3622.raw	4.84E5	4	4	482	510	
N.AHSIIYALR.G	N	99.9	57.60	1042.5923	9	-1.3	522.3027	2	27.33	24	2039	OB3622.raw	2.62E5	6	6	420	428	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.14	1660.8057	15	-0.8	831.4094	2	26.82	24	1968	OB3622.raw	7.69E5	3	3	370	384	Deamidation (NQ)
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.10	1659.8217	15	1.3	554.2819	3	26.02	24	1857	OB3622.raw	2.3E6	2	2	370	384	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	55.78	1340.7816	13	-0.4	671.3978	2	29.75	24	2375	OB3622.raw	5.67E4	1	1	453	465	
N.TNAHSIIYALR.G	N	99.9	55.69	1257.6830	11	-0.9	629.8482	2	27.43	24	2053	OB3622.raw	4.1E5	3	3	418	428	
K.TDSRPSIANLAGE.N	N	99.9	54.71	1329.6525	13	-1.0	665.8328	2	28.03	24	2137	OB3622.raw	9.7E4	2	2	478	490	
K.TANDLNLLILR.W	N	99.9	53.64	1254.7296	11	-0.9	628.3715	2	6.34	24	555	OB3622.raw	5.11E7	121	121	385	395	
L.FVPHYNTNAHSIIYALR.G	N	99.9	53.28	2015.0377	17	-0.6	672.6861	3	30.41	24	2465	OB3622.raw	7.91E5	3	3	412	428	
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	52.66	1497.7001	13	-3.0	749.8550	2	28.25	24	2167	OB3622.raw	4.05E4	5	5	409	421	Deamidation (NQ)
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	52.64	1541.7513	13	8.1	771.8892	2	33.31	24	2859	OB3622.raw	1.05E7	2	2	396	408	Deamidation (NQ)
P.DIYNPQAGSLK.T	N	99.9	52.40	1204.6088	11	-0.4	603.3114	2	26.78	24	1963	OB3622.raw	4.79E4	3	3	374	384	
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.9	51.55	1659.8217	15	-0.2	554.2811	3	26.67	24	1947	OB3622.raw	2.15E6	1	1	370	384	Deamidation (NQ)
N.GIEETIC(+57.02)TASVKK.N	N	99.9	51.52	1434.7388	13	-0.1	718.3766	2	25.86	24	1835	OB3622.raw	1.07E5	3	3	353	365	Carbamidomethylation
K.TDSRPSIANLAGEN(+.98).S	N	99.9	50.96	1444.6793	14	-1.7	723.3457	2	28.05	24	2139	OB3622.raw	8.3E4	4	4	478	491	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	50.96	1296.6058	12	2.9	649.3121	2	20.84	24	1462	OB3622.raw	1.01E4	1	1	431	442	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	518	523	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	50.75	2128.1218	18	0.0	710.3812	3	30.41	24	2466	OB3622.raw	1.07E6	3	3	411	428	
A.NDLNLLILR.W	N	99.9	49.40	1082.6448	9	-0.6	542.3293	2	32.14	24	2700	OB3622.raw	1.13E5	2	2	387	395	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	49.01	2837.4043	27	1.5	1419.7115	2	33.95	24	2946	OB3622.raw	3.67E5	2	2	478	504	
H.YNTNAHSIIYALR.G	N	99.9	48.98	1534.7892	13	0.3	768.4021	2	28.37	24	2183	OB3622.raw	6.52E5	7	7	416	428	
K.TDSRPSIANLAGEN.S	N	99.9	48.50	1443.6953	14	-2.1	722.8534	2	27.55	24	2069	OB3622.raw	2.59E5	2	2	478	491	
R.NALFVPHYNTN.A	N	99.9	48.13	1288.6200	11	-0.7	645.3168	2	28.93	24	2262	OB3622.raw	7.75E4	5	5	409	419	
Y.NTNAHSIIYALR.G	N	99.9	47.26	1371.7258	12	-1.3	458.2486	3	28.12	24	2149	OB3622.raw	5.29E4	1	1	417	428	
K.TDSRPSIANLA.G	N	99.9	46.27	1143.5884	11	-0.3	572.8013	2	27.32	24	2037	OB3622.raw	1.4E5	3	3	478	488	
K.TAN(+.98)DLNLLILR.W	N	99.9	45.98	1255.7136	11	4.2	628.8667	2	32.64	24	2769	OB3622.raw	1.32E7	2	2	385	395	Deamidation (NQ)
A.HSIIYALR.G	N	99.9	45.89	971.5552	8	-1.0	486.7844	2	27.03	24	1998	OB3622.raw	3.35E4	2	2	421	428	
R.VYDEELQ(+.98)EGHVLVVPQNFAVAGK.S	N	99.9	45.69	2541.2751	23	0.6	636.3264	4	31.48	24	2610	OB3622.raw	6.72E5	1	1	443	465	Deamidation (NQ)
S.IANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	45.56	2867.4663	27	1.5	956.8308	3	35.05	24	3097	OB3622.raw	1.15E4	1	1	484	510	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	45.52	1295.6218	12	-1.0	648.8176	2	21.53	24	1504	OB3622.raw	1.85E4	1	1	431	442	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.9	45.37	2114.0320	18	-0.8	1058.0225	2	32.13	24	2698	OB3622.raw	1.07E5	2	2	443	460	
K.FFVPPSQQ.S	N	99.9	45.30	948.4705	8	-1.2	475.2419	2	28.55	24	2209	OB3622.raw	9.93E3	1	1	524	531	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVAN.S	N	99.9	43.75	2838.3882	27	0.6	947.1372	3	34.21	24	2983	OB3622.raw	1.82E5	1	1	478	504	Deamidation (NQ)
R.NALFVPHYN.T	N	99.8	40.12	1073.5294	9	-0.1	537.7719	2	28.67	24	2225	OB3622.raw	4.24E4	1	1	409	417	
K.TDSRPSIAN(+.98)LAG.E	N	99.8	38.95	1201.5939	12	-0.1	601.8041	2	28.38	24	2185	OB3622.raw	1.35E4	1	1	478	489	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.90	1200.6099	12	-0.5	601.3119	2	27.53	24	2067	OB3622.raw	3.15E5	4	4	478	489	
N.DLNLLILR.W	N	99.8	38.90	968.6018	8	-1.2	485.3076	2	33.23	24	2849	OB3622.raw	4.04E4	2	2	388	395	
K.TDSRPSIANLAGENSIID.N	N	99.8	38.66	1871.9225	18	-2.4	936.9663	2	30.90	24	2531	OB3622.raw	6.04E4	1	1	478	495	
H.YNTN(+.98)AHSIIYALR.G	N	99.8	38.44	1535.7732	13	-1.3	512.9310	3	29.63	24	2359	OB3622.raw	3.41E4	1	1	416	428	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.60	834.4963	7	0.3	418.2556	2	28.19	24	2158	OB3622.raw	3.94E6	9	9	422	428	
K.TDSRPSIANLAGENSIIDNLPEEVVANSY.G	N	99.8	37.59	3087.4995	29	-0.1	1030.1737	3	35.03	24	3094	OB3622.raw	8.25E3	1	1	478	506	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYG.L	Y	99.8	37.49	3144.5210	30	0.2	1049.1812	3	35.09	24	3102	OB3622.raw	9.89E4	1	1	478	507	
N.RSPDIYNPQAGSLK.T	N	99.7	36.90	1544.7947	14	-0.5	515.9386	3	25.42	24	1775	OB3622.raw	5.99E4	3	3	371	384	
K.FFVPPSQQSLGAV.A	Y	99.7	36.82	1375.7135	13	-1.8	688.8628	2	28.62	24	2219	OB3622.raw	5.21E4	1	1	524	536	
R.AHVQ(+.98)VVDSNGN(+.98)R.V	N	99.4	33.69	1296.6058	12	4.3	433.2111	3	20.93	24	1468	OB3622.raw	1.25E5	1	1	431	442	Deamidation (NQ)
F.VPHYNTNAHSIIYALR.G	N	99.4	33.06	1867.9692	16	-1.6	467.9988	4	28.64	24	2221	OB3622.raw	3.03E4	1	1	413	428	
K.TDSRPSIAN(+.98)LAGENSIIDNLPEEVVANSYGLPR.E	Y	98.8	30.29	3511.7429	33	3.3	878.9459	4	39.18	24	3655	OB3622.raw	7.51E0	1	1	478	510	Deamidation (NQ)
D.IYNPQAGSLK.T	N	98.8	30.17	1089.5818	10	0.9	545.7986	2	24.83	24	1726	OB3622.raw	1.67E3	1	1	375	384	
total 68 peptides																		

Q647H4|Q647H4_ARAHY

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Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	99.52	2313.2019	20	-0.6	1157.6075	2	31.20	24	2573	OB3622.raw	1.39E8	53	53	408	427	
R.WLGLSAEYGNLYR.N	N	99.9	96.69	1540.7673	13	1.3	771.3919	2	32.99	24	2817	OB3622.raw	4.78E7	114	114	395	407	
K.SQSENFEYVAFK.T	N	99.9	92.10	1447.6619	12	1.1	724.8390	2	29.52	24	2343	OB3622.raw	1.71E7	77	77	465	476	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	86.57	3544.7434	33	0.0	1182.5884	3	34.78	24	3058	OB3622.raw	1.22E7	34	34	477	509	
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	86.17	3545.7273	33	0.9	1182.9175	3	34.98	24	3087	OB3622.raw	1.1E7	6	6	477	509	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	82.52	2314.1858	20	1.0	1158.1013	2	32.05	24	2688	OB3622.raw	0	3	3	408	427	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	79.74	1388.6936	13	0.5	695.3544	2	27.06	24	2001	OB3622.raw	3.7E7	141	141	371	383	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	77.75	1389.6776	13	1.1	695.8469	2	27.79	24	2103	OB3622.raw	3.34E6	2	2	371	383	Deamidation (NQ)
K.SQ(+.98)SENFEYVAFK.T	N	99.9	74.98	1448.6459	12	4.4	725.3334	2	30.32	24	2453	OB3622.raw	1.64E6	4	4	465	476	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	72.62	2314.1858	20	3.9	772.4055	3	32.03	24	2685	OB3622.raw	6.33E6	4	4	408	427	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98)SFIDNLPEEVVANSYGLPR.E	N	99.9	71.13	3545.7273	33	3.4	1182.9204	3	34.24	24	2985	OB3622.raw	1.59E6	1	1	477	509	Deamidation (NQ)
R.AHVQVVDSNGDR.V	Y	99.9	68.28	1295.6218	12	2.0	648.8195	2	4.04	24	204	OB3622.raw	2.13E6	6	6	430	441	
R.NALFVPHYNTNAH.S	N	99.9	65.14	1496.7161	13	-1.0	749.3646	2	27.67	24	2086	OB3622.raw	7.92E6	19	19	408	420	

R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	64.27	1659.8217	15	-0.2	830.9180	2	26.24	24	1887	OB3622.raw	2.3E6	6	6	369	383	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	64.26	1268.7452	11	1.5	635.3809	2	32.55	24	2757	OB3622.raw	2.03E7	74	74	384	394	
R.NRSPDIYNPQAGSLK.T	N	99.9	62.82	1658.8376	15	-0.3	830.4258	2	25.58	24	1797	OB3622.raw	2.4E6	17	17	369	383	
N.AHSIIYALR.G	N	99.9	57.60	1042.5923	9	-1.3	522.3027	2	27.33	24	2039	OB3622.raw	2.62E5	6	6	419	427	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.14	1660.8057	15	-0.8	831.4094	2	26.82	24	1968	OB3622.raw	7.69E5	3	3	369	383	Deamidation (NQ)
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.10	1659.8217	15	1.3	554.2819	3	26.02	24	1857	OB3622.raw	2.3E6	2	2	369	383	Deamidation (NQ)
K.FFVPPSEQSLR.A	Y	99.9	55.97	1305.6716	11	2.7	653.8448	2	28.83	24	2247	OB3622.raw	1.61E6	7	7	523	533	
H.VLVVPQNFAVAGK.S	N	99.9	55.78	1340.7816	13	-0.4	671.3978	2	29.75	24	2375	OB3622.raw	5.67E4	1	1	452	464	
N.TNAHSIIYALR.G	N	99.9	55.69	1257.6830	11	-0.9	629.8482	2	27.43	24	2053	OB3622.raw	4.1E5	3	3	417	427	
K.TDSRPSIANLAGE.N	N	99.9	54.71	1329.6525	13	-1.0	665.8328	2	28.03	24	2137	OB3622.raw	9.7E4	2	2	477	489	
L.FVPHYNTNAHSIIYALR.G	N	99.9	53.28	2015.0377	17	-0.6	672.6861	3	30.41	24	2465	OB3622.raw	7.91E5	3	3	411	427	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	53.28	3545.7273	33	0.3	1182.9167	3	33.46	24	2880	OB3622.raw	1.44E5	3	3	477	509	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	52.66	1497.7001	13	-3.0	749.8550	2	28.25	24	2167	OB3622.raw	4.05E4	5	5	408	420	Deamidation (NQ)
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	52.64	1541.7513	13	8.1	771.8892	2	33.31	24	2859	OB3622.raw	1.05E7	2	2	395	407	Deamidation (NQ)
P.DIYNPQAGSLK.T	N	99.9	52.40	1204.6088	11	-0.4	603.3114	2	26.78	24	1963	OB3622.raw	4.79E4	3	3	373	383	
K.TDSRPSIANLAGENSFIDNLP(+15.99)EEVVANSYGLPR.E	N	99.9	52.06	3560.7383	33	2.6	1187.9231	3	36.69	24	3319	OB3622.raw	4.44E4	1	1	477	509	Hydroxylation Pro
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.9	51.55	1659.8217	15	-0.2	554.2811	3	26.67	24	1947	OB3622.raw	2.15E6	1	1	369	383	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	50.96	1444.6793	14	-1.7	723.3457	2	28.05	24	2139	OB3622.raw	8.3E4	4	4	477	490	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	517	522	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	50.75	2128.1218	18	0.0	710.3812	3	30.41	24	2466	OB3622.raw	1.07E6	3	3	410	427	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	50.48	1354.6438	12	-1.4	678.3282	2	29.06	24	2279	OB3622.raw	8.29E3	1	1	352	363	Carbamidomethylation
H.YNTNAHSIIYALR.G	N	99.9	48.98	1534.7892	13	0.3	768.4021	2	28.37	24	2183	OB3622.raw	6.52E5	7	7	415	427	
K.FFVPPSEQSLRA.V	Y	99.9	48.97	1376.7087	12	0.2	689.3618	2	29.78	24	2379	OB3622.raw	3.04E6	9	9	523	534	
K.TDSRPSIANLAGEN.S	N	99.9	48.50	1443.6953	14	-2.1	722.8534	2	27.55	24	2069	OB3622.raw	2.59E5	2	2	477	490	
R.NALFVPHYNTN.A	N	99.9	48.13	1288.6200	11	-0.7	645.3168	2	28.93	24	2262	OB3622.raw	7.75E4	5	5	408	418	
A.NELNLLILR.W	N	99.9	48.10	1096.6604	9	-0.7	549.3371	2	32.53	24	2755	OB3622.raw	1.95E4	1	1	386	394	
Y.NTNAHSIIYALR.G	N	99.9	47.26	1371.7258	12	-1.3	458.2486	3	28.12	24	2149	OB3622.raw	5.29E4	1	1	416	427	
K.TDSRPSIANLA.G	N	99.9	46.27	1143.5884	11	-0.3	572.8013	2	27.32	24	2037	OB3622.raw	1.4E5	3	3	477	487	
A.HSIIYALR.G	N	99.9	45.89	971.5552	8	-1.0	486.7844	2	27.03	24	1998	OB3622.raw	3.35E4	2	2	420	427	
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	45.35	3085.5356	29	1.0	1029.5201	3	35.84	24	3204	OB3622.raw	2.85E5	2	2	481	509	
K.TAN(+.98)ELNLLILR.W	N	99.9	44.86	1269.7292	11	4.2	635.8746	2	33.44	24	2877	OB3622.raw	3.17E6	2	2	384	394	Deamidation (NQ)
R.NALFVPHYN.T	N	99.8	40.12	1073.5294	9	-0.1	537.7719	2	28.67	24	2225	OB3622.raw	4.24E4	1	1	408	416	
K.TDSRPSIAN(+.98)LAG.E	N	99.8	38.95	1201.5939	12	-0.1	601.8041	2	28.38	24	2185	OB3622.raw	1.35E4	1	1	477	488	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.90	1200.6099	12	-0.5	601.3119	2	27.53	24	2067	OB3622.raw	3.15E5	4	4	477	488	
H.YNTN(+.98)AHSIIYALR.G	N	99.8	38.44	1535.7732	13	-1.3	512.9310	3	29.63	24	2359	OB3622.raw	3.41E4	1	1	415	427	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVAN.S	N	99.8	38.08	2872.3726	27	2.5	958.4672	3	34.53	24	3025	OB3622.raw	9.49E4	1	1	477	503	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGENSFIDNLPEEVVANSYGLPR.E	N	99.8	37.88	3545.7273	33	0.4	1182.9169	3	43.98	24	4301	OB3622.raw	1.23E5	1	1	477	509	Deamidation (NQ)
V.PPSEQSLR.A	Y	99.8	37.85	912.4664	8	-1.1	457.2400	2	28.81	24	2245	OB3622.raw	2.91E4	1	1	526	533	
H.SIIYALR.G	N	99.8	37.60	834.4963	7	0.3	418.2556	2	28.19	24	2158	OB3622.raw	3.94E6	9	9	421	427	
S.IANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.8	37.55	2901.4507	27	2.6	968.1600	3	35.43	24	3148	OB3622.raw	3.23E3	1	1	483	509	
K.FFVPPSEQ(+.98)SLR.A	Y	99.8	37.43	1306.6556	11	2.4	654.3367	2	29.58	24	2352	OB3622.raw	1.1E6	1	1	523	533	Deamidation (NQ)
N.RSPDIYNPQAGSLK.T	N	99.7	36.90	1544.7947	14	-0.5	515.9386	3	25.42	24	1775	OB3622.raw	5.99E4	3	3	370	383	
K.FFVPPSEQ(+.98)SLRA.V	Y	99.7	36.50	1377.6927	12	1.4	689.8546	2	29.95	24	2403	OB3622.raw	2.75E5	2	2	523	534	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGEN(+.98)SFIDN(+.98)LP(+15.99)EEVVAN(+.98)SYGLPR.E	N	99.5	34.77	3564.6743	33	-2.7	713.9402	5	35.18	24	3114	OB3622.raw	1.78E5	2	2	477	509	Deamidation (NQ); Hydroxylation Pro
R.PSIANLAGENSFIDN(+.98)LPEEVVAN(+.98)SYGLPR.E	N	99.4	34.48	3087.5037	29	3.2	1030.1785	3	36.82	24	3336	OB3622.raw	2.51E4	1	1	481	509	Deamidation (NQ)
F.VPHYNTNAHSIIYALR.G	N	99.4	33.06	1867.9692	16	-1.6	467.9988	4	28.64	24	2221	OB3622.raw	3.03E4	1	1	412	427	
K.FFVPPSEQ.S	Y	99.2	32.25	949.4545	8	-1.4	475.7339	2	29.24	24	2305	OB3622.raw	8.9E3	1	1	523	530	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYG.L	N	98.8	30.33	3178.5054	30	-5.1	1060.5037	3	35.44	24	3150	OB3622.raw	6.14E4	1	1	477	506	
D.IYNPQAGSLK.T	N	98.8	30.17	1089.5818	10	0.9	545.7986	2	24.83	24	1726	OB3622.raw	1.67E3	1	1	374	383	
total 62 peptides																		

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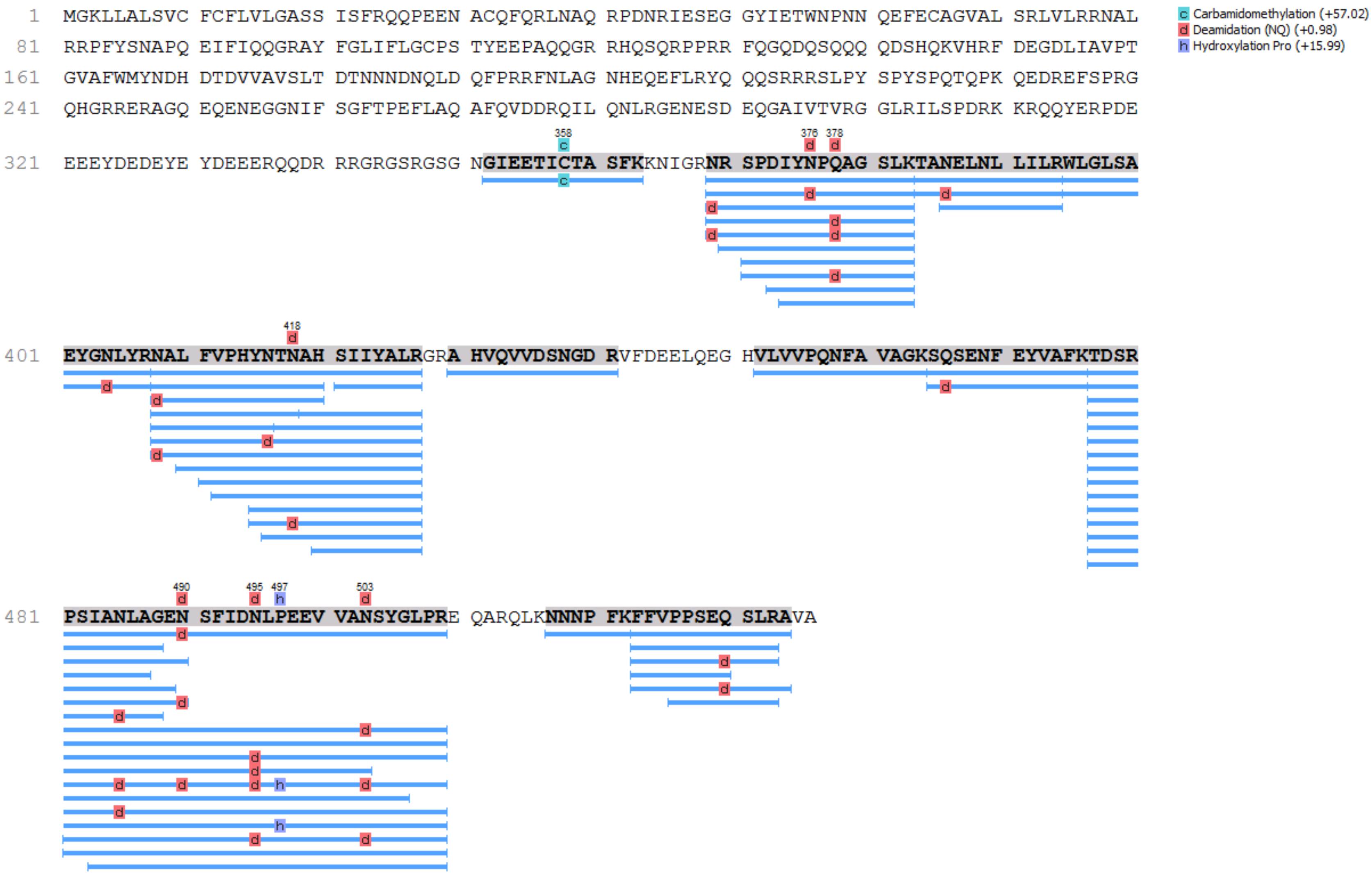
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	99.52	2313.2019	20	-0.6	1157.6075	2	31.20	24	2573	OB3622.raw	1.39E8	53	53	408	427	
R.WLGLSAEYGNLYR.N	N	99.9	96.69	1540.7673	13	1.3	771.3919	2	32.99	24	2817	OB3622.raw	4.78E7	114	114	395	407	
K.SQSENFEYVAFK.T	N	99.9	92.10	1447.6619	12	1.1	724.8390	2	29.52	24	2343	OB3622.raw	1.71E7	77	77	465	476	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	86.57	3544.7434	33	0.0	1182.5884	3	34.78	24	3058	OB3622.raw	1.22E7	34	34	477	509	
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	86.17	3545.7273	33	0.9	1182.9175	3	34.98	24	3087	OB3622.raw	1.1E7	6	6	477	509	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	82.52	2314.1858	20	1.0	1158.1013	2	32.05	24	2688	OB3622.raw	0	3	3	408	427	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	79.74	1388.6936	13	0.5	695.3544	2	27.06	24	2001	OB3622.raw	3.7E7	141	141	371	383	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	77.75	1389.6776	13	1.1	695.8469	2	27.79	24	2103	OB3622.raw	3.34E6	2	2	371	383	Deamidation (NQ)
K.SQ(+.98)SENFEYVAFK.T	N	99.9	74.98	1448.6459	12	4.4	725.3334	2	30.32	24	2453	OB3622.raw	1.64E6	4	4	465	476	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	72.62	2314.1858	20	3.9	772.4055	3	32.03	24	2685	OB3622.raw	6.33E6	4	4	408	427	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98)SFIDNLPEEVVANSYGLPR.E	N	99.9	71.13	3545.7273	33	3.4	1182.9204	3	34.24	24	2985	OB3622.raw	1.59E6	1	1	477	509	Deamidation (NQ)
R.AHVQVVDSNGDR.V	Y	99.9	68.28	1295.6218	12	2.0	648.8195	2	4.04	24	204	OB3622.raw	2.13E6	6	6	430	441	
R.NALFVPHYNTNAH.S	N	99.9	65.14	1496.7161	13	-1.0	749.3646	2	27.67	24	2086	OB3622.raw	7.92E6	19	19	408	420	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	64.27	1659.8217	15	-0.2	830.9180	2	26.24	24	1887	OB3622.raw	2.3E6	6	6	369	383	Deamidation (NQ)

K.TANELNLLILR.W	N	99.9	64.26	1268.7452	11	1.5	635.3809	2	32.55	24	2757	OB3622.raw	2.03E7	74	74	384	394	
R.NRSPDIYNPQAGSLK.T	N	99.9	62.82	1658.8376	15	-0.3	830.4258	2	25.58	24	1797	OB3622.raw	2.4E6	17	17	369	383	
N.AHSIIYALR.G	N	99.9	57.60	1042.5923	9	-1.3	522.3027	2	27.33	24	2039	OB3622.raw	2.62E5	6	6	419	427	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.14	1660.8057	15	-0.8	831.4094	2	26.82	24	1968	OB3622.raw	7.69E5	3	3	369	383	Deamidation (NQ)
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.10	1659.8217	15	1.3	554.2819	3	26.02	24	1857	OB3622.raw	2.3E6	2	2	369	383	Deamidation (NQ)
K.FFVPPSEQSLR.A	Y	99.9	55.97	1305.6716	11	2.7	653.8448	2	28.83	24	2247	OB3622.raw	1.61E6	7	7	523	533	
H.VLVVPQNFAVAGK.S	N	99.9	55.78	1340.7816	13	-0.4	671.3978	2	29.75	24	2375	OB3622.raw	5.67E4	1	1	452	464	
N.TNAHSIIYALR.G	N	99.9	55.69	1257.6830	11	-0.9	629.8482	2	27.43	24	2053	OB3622.raw	4.1E5	3	3	417	427	
K.TDSRPSIANLAGE.N	N	99.9	54.71	1329.6525	13	-1.0	665.8328	2	28.03	24	2137	OB3622.raw	9.7E4	2	2	477	489	
L.FVPHYNTNAHSIIYALR.G	N	99.9	53.28	2015.0377	17	-0.6	672.6861	3	30.41	24	2465	OB3622.raw	7.91E5	3	3	411	427	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	53.28	3545.7273	33	0.3	1182.9167	3	33.46	24	2880	OB3622.raw	1.44E5	3	3	477	509	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	52.66	1497.7001	13	-3.0	749.8550	2	28.25	24	2167	OB3622.raw	4.05E4	5	5	408	420	Deamidation (NQ)
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	52.64	1541.7513	13	8.1	771.8892	2	33.31	24	2859	OB3622.raw	1.05E7	2	2	395	407	Deamidation (NQ)
P.DIYNPQAGSLK.T	N	99.9	52.40	1204.6088	11	-0.4	603.3114	2	26.78	24	1963	OB3622.raw	4.79E4	3	3	373	383	
K.TDSRPSIANLAGENSFIDNLP(+15.99)EEVVANSYGLPR.E	N	99.9	52.06	3560.7383	33	2.6	1187.9231	3	36.69	24	3319	OB3622.raw	4.44E4	1	1	477	509	Hydroxylation Pro
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.9	51.55	1659.8217	15	-0.2	554.2811	3	26.67	24	1947	OB3622.raw	2.15E6	1	1	369	383	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	50.96	1444.6793	14	-1.7	723.3457	2	28.05	24	2139	OB3622.raw	8.3E4	4	4	477	490	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	517	522	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	50.75	2128.1218	18	0.0	710.3812	3	30.41	24	2466	OB3622.raw	1.07E6	3	3	410	427	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	50.48	1354.6438	12	-1.4	678.3282	2	29.06	24	2279	OB3622.raw	8.29E3	1	1	352	363	Carbamidomethylation
H.YNTNAHSIIYALR.G	N	99.9	48.98	1534.7892	13	0.3	768.4021	2	28.37	24	2183	OB3622.raw	6.52E5	7	7	415	427	
K.FFVPPSEQSLRA.V	Y	99.9	48.97	1376.7087	12	0.2	689.3618	2	29.78	24	2379	OB3622.raw	3.04E6	9	9	523	534	
K.TDSRPSIANLAGEN.S	N	99.9	48.50	1443.6953	14	-2.1	722.8534	2	27.55	24	2069	OB3622.raw	2.59E5	2	2	477	490	
R.NALFVPHYNTN.A	N	99.9	48.13	1288.6200	11	-0.7	645.3168	2	28.93	24	2262	OB3622.raw	7.75E4	5	5	408	418	
A.NELNLLILR.W	N	99.9	48.10	1096.6604	9	-0.7	549.3371	2	32.53	24	2755	OB3622.raw	1.95E4	1	1	386	394	
Y.NTNAHSIIYALR.G	N	99.9	47.26	1371.7258	12	-1.3	458.2486	3	28.12	24	2149	OB3622.raw	5.29E4	1	1	416	427	
K.TDSRPSIANLA.G	N	99.9	46.27	1143.5884	11	-0.3	572.8013	2	27.32	24	2037	OB3622.raw	1.4E5	3	3	477	487	
A.HSIIYALR.G	N	99.9	45.89	971.5552	8	-1.0	486.7844	2	27.03	24	1998	OB3622.raw	3.35E4	2	2	420	427	
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	45.35	3085.5356	29	1.0	1029.5201	3	35.84	24	3204	OB3622.raw	2.85E5	2	2	481	509	
K.TAN(+.98)ELNLLILR.W	N	99.9	44.86	1269.7292	11	4.2	635.8746	2	33.44	24	2877	OB3622.raw	3.17E6	2	2	384	394	Deamidation (NQ)
R.NALFVPHYN.T	N	99.8	40.12	1073.5294	9	-0.1	537.7719	2	28.67	24	2225	OB3622.raw	4.24E4	1	1	408	416	
K.TDSRPSIAN(+.98)LAG.E	N	99.8	38.95	1201.5939	12	-0.1	601.8041	2	28.38	24	2185	OB3622.raw	1.35E4	1	1	477	488	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.90	1200.6099	12	-0.5	601.3119	2	27.53	24	2067	OB3622.raw	3.15E5	4	4	477	488	
H.YNTN(+.98)AHSIIYALR.G	N	99.8	38.44	1535.7732	13	-1.3	512.9310	3	29.63	24	2359	OB3622.raw	3.41E4	1	1	415	427	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVAN.S	N	99.8	38.08	2872.3726	27	2.5	958.4672	3	34.53	24	3025	OB3622.raw	9.49E4	1	1	477	503	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGENSFIDNLPEEVVANSYGLPR.E	N	99.8	37.88	3545.7273	33	0.4	1182.9169	3	43.98	24	4301	OB3622.raw	1.23E5	1	1	477	509	Deamidation (NQ)
V.PPSEQSLR.A	Y	99.8	37.85	912.4664	8	-1.1	457.2400	2	28.81	24	2245	OB3622.raw	2.91E4	1	1	526	533	
H.SIIYALR.G	N	99.8	37.60	834.4963	7	0.3	418.2556	2	28.19	24	2158	OB3622.raw	3.94E6	9	9	421	427	
S.IANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.8	37.55	2901.4507	27	2.6	968.1600	3	35.43	24	3148	OB3622.raw	3.23E3	1	1	483	509	
K.FFVPPSEQ(+.98)SLR.A	Y	99.8	37.43	1306.6556	11	2.4	654.3367	2	29.58	24	2352	OB3622.raw	1.1E6	1	1	523	533	Deamidation (NQ)
N.RSPDIYNPQAGSLK.T	N	99.7	36.90	1544.7947	14	-0.5	515.9386	3	25.42	24	1775	OB3622.raw	5.99E4	3	3	370	383	
K.FFVPPSEQ(+.98)SLRA.V	Y	99.7	36.50	1377.6927	12	1.4	689.8546	2	29.95	24	2403	OB3622.raw	2.75E5	2	2	523	534	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAGEN(+.98)SFIDN(+.98)LP(+15.99)EEVVAN(+.98)SYGLPR.E	N	99.5	34.77	3564.6743	33	-2.7	713.9402	5	35.18	24	3114	OB3622.raw	1.78E5	2	2	477	509	Deamidation (NQ); Hydroxylation Pro
R.PSIANLAGENSFIDN(+.98)LPEEVVAN(+.98)SYGLPR.E	N	99.4	34.48	3087.5037	29	3.2	1030.1785	3	36.82	24	3336	OB3622.raw	2.51E4	1	1	481	509	Deamidation (NQ)
F.VPHYNTNAHSIIYALR.G	N	99.4	33.06	1867.9692	16	-1.6	467.9988	4	28.64	24	2221	OB3622.raw	3.03E4	1	1	412	427	
K.FFVPPSEQ.S	Y	99.2	32.25	949.4545	8	-1.4	475.7339	2	29.24	24	2305	OB3622.raw	8.9E3	1	1	523	530	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYG.L	N	98.8	30.33	3178.5054	30	-5.1	1060.5037	3	35.44	24	3150	OB3622.raw	6.14E4	1	1	477	506	
D.IYNPQAGSLK.T	N	98.8	30.17	1089.5818	10	0.9	545.7986	2	24.83	24	1726	OB3622.raw	1.67E3	1	1	374	383	
total 62 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA
81 LRRPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV
161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP
241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE
321 YDEDEYEYDE EDRRRGRGSR GRGN**GIEETI CTASVKK**NIG R**NRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR**
401 **NALFVPHYNT NAHSIIYALR** GR**AHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFK**T DSRPNIANFA
481 GENSIIDNLP EEVVANSYGL PREQARQLK**N NNPFKFFVPP SQQSLRA**VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	99.52	2313.2019	20	-0.6	1157.6075	2	31.20	24	2573	OB3622.raw	1.39E8	53	53	401	420	
R.WLGLSAEYGNLYR.N	N	99.9	96.69	1540.7673	13	1.3	771.3919	2	32.99	24	2817	OB3622.raw	4.78E7	114	114	388	400	
K.SQSDNFEYVAFK.T	N	99.9	89.30	1433.6462	12	0.8	717.8310	2	30.18	24	2433	OB3622.raw	1.37E7	52	52	458	469	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	82.52	2314.1858	20	1.0	1158.1013	2	32.05	24	2688	OB3622.raw	0	3	3	401	420	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	79.74	1388.6936	13	0.5	695.3544	2	27.06	24	2001	OB3622.raw	3.7E7	141	141	364	376	
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	77.76	1434.6302	12	4.2	718.3254	2	29.83	24	2385	OB3622.raw	2.73E6	3	3	458	469	Deamidation (NQ)
R.SPDIYNPQ(+.98)AGSLK.T	N	99.9	77.75	1389.6776	13	1.1	695.8469	2	27.79	24	2103	OB3622.raw	3.34E6	2	2	364	376	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	74.54	2540.2910	23	0.5	1271.1534	2	30.64	24	2497	OB3622.raw	9.04E7	79	79	435	457	
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	72.62	2314.1858	20	3.9	772.4055	3	32.03	24	2685	OB3622.raw	6.33E6	4	4	401	420	Deamidation (NQ)
N.GIEETIC(+57.02)TASVK.K	N	99.9	71.40	1306.6438	12	0.2	654.3293	2	27.07	24	2002	OB3622.raw	1.63E7	37	37	345	356	Carbamidomethylation
R.VYDEELQEGHVLVVPQ(+.98)NFAVAGK.S	N	99.9	67.02	2541.2751	23	3.1	1271.6488	2	31.24	24	2579	OB3622.raw	1.57E6	1	1	435	457	Deamidation (NQ)
R.AHVQVVDSN(+.98)GNR.V	N	99.9	66.38	1295.6218	12	0.9	648.8188	2	4.85	24	333	OB3622.raw	2.26E6	6	6	423	434	Deamidation (NQ)
R.NALFVPHYNTNAH.S	N	99.9	65.14	1496.7161	13	-1.0	749.3646	2	27.67	24	2086	OB3622.raw	7.92E6	19	19	401	413	
R.VYDEELQEGHVL.V	N	99.9	64.92	1429.6725	12	0.0	715.8435	2	29.28	24	2311	OB3622.raw	1.14E5	2	2	435	446	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	64.27	1659.8217	15	-0.2	830.9180	2	26.24	24	1887	OB3622.raw	2.3E6	6	6	362	376	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.9	62.82	1658.8376	15	-0.3	830.4258	2	25.58	24	1797	OB3622.raw	2.4E6	17	17	362	376	
K.FFVPPSQQSLR.A	Y	99.9	62.48	1304.6876	11	0.3	653.3513	2	28.61	24	2217	OB3622.raw	3.23E6	7	7	516	526	
R.AHVQVVDSNGNR.V	N	99.9	59.87	1294.6378	12	-0.1	648.3261	2	19.68	24	1394	OB3622.raw	3.06E5	7	7	423	434	
N.AHSIIYALR.G	N	99.9	57.60	1042.5923	9	-1.3	522.3027	2	27.33	24	2039	OB3622.raw	2.62E5	6	6	412	420	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.14	1660.8057	15	-0.8	831.4094	2	26.82	24	1968	OB3622.raw	7.69E5	3	3	362	376	Deamidation (NQ)
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	56.10	1659.8217	15	1.3	554.2819	3	26.02	24	1857	OB3622.raw	2.3E6	2	2	362	376	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	55.78	1340.7816	13	-0.4	671.3978	2	29.75	24	2375	OB3622.raw	5.67E4	1	1	445	457	
N.TNAHSIIYALR.G	N	99.9	55.69	1257.6830	11	-0.9	629.8482	2	27.43	24	2053	OB3622.raw	4.1E5	3	3	410	420	
K.TANDLNLLILR.W	N	99.9	53.64	1254.7296	11	-0.9	628.3715	2	6.34	24	555	OB3622.raw	5.11E7	121	121	377	387	
L.FVPHYNTNAHSIIYALR.G	N	99.9	53.28	2015.0377	17	-0.6	672.6861	3	30.41	24	2465	OB3622.raw	7.91E5	3	3	404	420	

R.N(+.98)ALFVPHYNTNAH.S	N	99.9	52.66	1497.7001	13	-3.0	749.8550	2	28.25	24	2167	OB3622.raw	4.05E4	5	5	401	413	Deamidation (NQ)
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	52.64	1541.7513	13	8.1	771.8892	2	33.31	24	2859	OB3622.raw	1.05E7	2	2	388	400	Deamidation (NQ)
P.DIYNPQAGSLK.T	N	99.9	52.40	1204.6088	11	-0.4	603.3114	2	26.78	24	1963	OB3622.raw	4.79E4	3	3	366	376	
R.NRSPDIYN(+.98)PQAGSLK.T	N	99.9	51.55	1659.8217	15	-0.2	554.2811	3	26.67	24	1947	OB3622.raw	2.15E6	1	1	362	376	Deamidation (NQ)
N.GIEETIC(+57.02)TASVKK.N	N	99.9	51.52	1434.7388	13	-0.1	718.3766	2	25.86	24	1835	OB3622.raw	1.07E5	3	3	345	357	Carbamidomethylation
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	50.96	1296.6058	12	2.9	649.3121	2	20.84	24	1462	OB3622.raw	1.01E4	1	1	423	434	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	510	515	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	50.75	2128.1218	18	0.0	710.3812	3	30.41	24	2466	OB3622.raw	1.07E6	3	3	403	420	
K.FFVPPSQQSLRA.V	Y	99.9	49.74	1375.7247	12	-0.9	688.8690	2	28.84	24	2249	OB3622.raw	2.02E5	2	2	516	527	
A.NDLNLLILR.W	N	99.9	49.40	1082.6448	9	-0.6	542.3293	2	32.14	24	2700	OB3622.raw	1.13E5	2	2	379	387	
H.YNTNAHSIIYALR.G	N	99.9	48.98	1534.7892	13	0.3	768.4021	2	28.37	24	2183	OB3622.raw	6.52E5	7	7	408	420	
R.NALFVPHYNTN.A	N	99.9	48.13	1288.6200	11	-0.7	645.3168	2	28.93	24	2262	OB3622.raw	7.75E4	5	5	401	411	
Y.NTNAHSIIYALR.G	N	99.9	47.26	1371.7258	12	-1.3	458.2486	3	28.12	24	2149	OB3622.raw	5.29E4	1	1	409	420	
K.TAN(+.98)DLNLLILR.W	N	99.9	45.98	1255.7136	11	4.2	628.8667	2	32.64	24	2769	OB3622.raw	1.32E7	2	2	377	387	Deamidation (NQ)
A.HSIIYALR.G	N	99.9	45.89	971.5552	8	-1.0	486.7844	2	27.03	24	1998	OB3622.raw	3.35E4	2	2	413	420	
R.VYDEELQ(+.98)EGHVLVVPQNFAVAGK.S	N	99.9	45.69	2541.2751	23	0.6	636.3264	4	31.48	24	2610	OB3622.raw	6.72E5	1	1	435	457	Deamidation (NQ)
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	45.52	1295.6218	12	-1.0	648.8176	2	21.53	24	1504	OB3622.raw	1.85E4	1	1	423	434	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.9	45.37	2114.0320	18	-0.8	1058.0225	2	32.13	24	2698	OB3622.raw	1.07E5	2	2	435	452	
K.FFVPPSQQ.S	N	99.9	45.30	948.4705	8	-1.2	475.2419	2	28.55	24	2209	OB3622.raw	9.93E3	1	1	516	523	
K.FFVPPSQQ(+.98)SLRA.V	Y	99.9	42.03	1376.7087	12	0.3	689.3619	2	29.39	24	2325	OB3622.raw	3E6	6	6	516	527	Deamidation (NQ)
R.NALFVPHYN.T	N	99.8	40.12	1073.5294	9	-0.1	537.7719	2	28.67	24	2225	OB3622.raw	4.24E4	1	1	401	409	
N.DLNLLILR.W	N	99.8	38.90	968.6018	8	-1.2	485.3076	2	33.23	24	2849	OB3622.raw	4.04E4	2	2	380	387	
H.YNTN(+.98)AHSIIYALR.G	N	99.8	38.44	1535.7732	13	-1.3	512.9310	3	29.63	24	2359	OB3622.raw	3.41E4	1	1	408	420	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.60	834.4963	7	0.3	418.2556	2	28.19	24	2158	OB3622.raw	3.94E6	9	9	414	420	
N.RSPDIYNPQAGSLK.T	N	99.7	36.90	1544.7947	14	-0.5	515.9386	3	25.42	24	1775	OB3622.raw	5.99E4	3	3	363	376	
R.AHVQ(+.98)VVDSNGN(+.98)R.V	N	99.4	33.69	1296.6058	12	4.3	433.2111	3	20.93	24	1468	OB3622.raw	1.25E5	1	1	423	434	Deamidation (NQ)
F.VPHYNTNAHSIIYALR.G	N	99.4	33.06	1867.9692	16	-1.6	467.9988	4	28.64	24	2221	OB3622.raw	3.03E4	1	1	405	420	
D.IYNPQAGSLK.T	N	98.8	30.17	1089.5818	10	0.9	545.7986	2	24.83	24	1726	OB3622.raw	1.67E3	1	1	367	376	
total 53 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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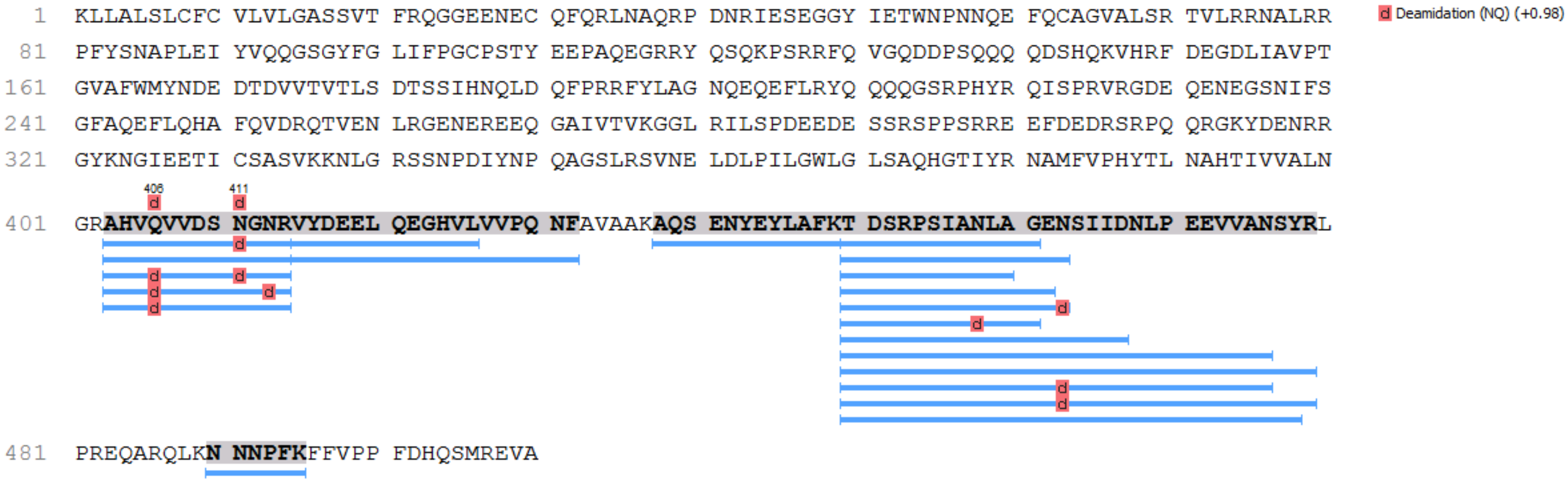
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GR**AHVQVVDS NGNRVYDEEL QEGHVLVVPQ NF**AVAAK**AQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYR**L
481 PREQARQLK**N NNPFK**FFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.AHVQVVDSN(+.98)GNR.V	N	99.9	66.38	1295.6218	12	0.9	648.8188	2	4.85	24	333	OB3622.raw	2.26E6	6	6	403	414	Deamidation (NQ)

R.VYDEELQEGHVL.V	N	99.9	64.92	1429.6725	12	0.0	715.8435	2	29.28	24	2311	OB3622.raw	1.14E5	2	2	415	426	
R.AHVQVVDSNGNR.V	N	99.9	59.87	1294.6378	12	-0.1	648.3261	2	19.68	24	1394	OB3622.raw	3.06E5	7	7	403	414	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVANSYR.L	Y	99.9	54.82	3244.5847	30	0.9	1082.5365	3	34.34	24	3000	OB3622.raw	3.76E4	1	1	450	479	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	54.71	1329.6525	13	-1.0	665.8328	2	28.03	24	2137	OB3622.raw	9.7E4	2	2	450	462	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	50.96	1444.6793	14	-1.7	723.3457	2	28.05	24	2139	OB3622.raw	8.3E4	4	4	450	463	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	50.96	1296.6058	12	2.9	649.3121	2	20.84	24	1462	OB3622.raw	1.01E4	1	1	403	414	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	490	495	
K.AQSENYEYLAFK.T	Y	99.9	50.05	1461.6776	12	-1.7	731.8448	2	29.97	24	2406	OB3622.raw	1.92E6	5	5	438	449	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	49.01	2837.4043	27	1.5	1419.7115	2	33.95	24	2946	OB3622.raw	3.67E5	2	2	450	476	
K.TDSRPSIANLAGEN.S	N	99.9	48.50	1443.6953	14	-2.1	722.8534	2	27.55	24	2069	OB3622.raw	2.59E5	2	2	450	463	
K.TDSRPSIANLA.G	N	99.9	46.27	1143.5884	11	-0.3	572.8013	2	27.32	24	2037	OB3622.raw	1.4E5	3	3	450	460	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	45.52	1295.6218	12	-1.0	648.8176	2	21.53	24	1504	OB3622.raw	1.85E4	1	1	403	414	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.9	45.37	2114.0320	18	-0.8	1058.0225	2	32.13	24	2698	OB3622.raw	1.07E5	2	2	415	432	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	45.12	3243.6006	30	-0.4	1082.2070	3	33.73	24	2916	OB3622.raw	1.64E4	1	1	450	479	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVAN.S	N	99.9	43.75	2838.3882	27	0.6	947.1372	3	34.21	24	2983	OB3622.raw	1.82E5	1	1	450	476	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAG.E	N	99.8	38.95	1201.5939	12	-0.1	601.8041	2	28.38	24	2185	OB3622.raw	1.35E4	1	1	450	461	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.90	1200.6099	12	-0.5	601.3119	2	27.53	24	2067	OB3622.raw	3.15E5	4	4	450	461	
K.TDSRPSIANLAGENSIID.N	N	99.8	38.66	1871.9225	18	-2.4	936.9663	2	30.90	24	2531	OB3622.raw	6.04E4	1	1	450	467	
K.TDSRPSIANLAGENSIIDNLPEEVVANSY.R	N	99.8	37.59	3087.4995	29	-0.1	1030.1737	3	35.03	24	3094	OB3622.raw	8.25E3	1	1	450	478	
R.AHVQ(+.98)VVDSNGN(+.98)R.V	N	99.4	33.69	1296.6058	12	4.3	433.2111	3	20.93	24	1468	OB3622.raw	1.25E5	1	1	403	414	Deamidation (NQ)
total 21 peptides																		

Q0GM57|Q0GM57_ARAHY

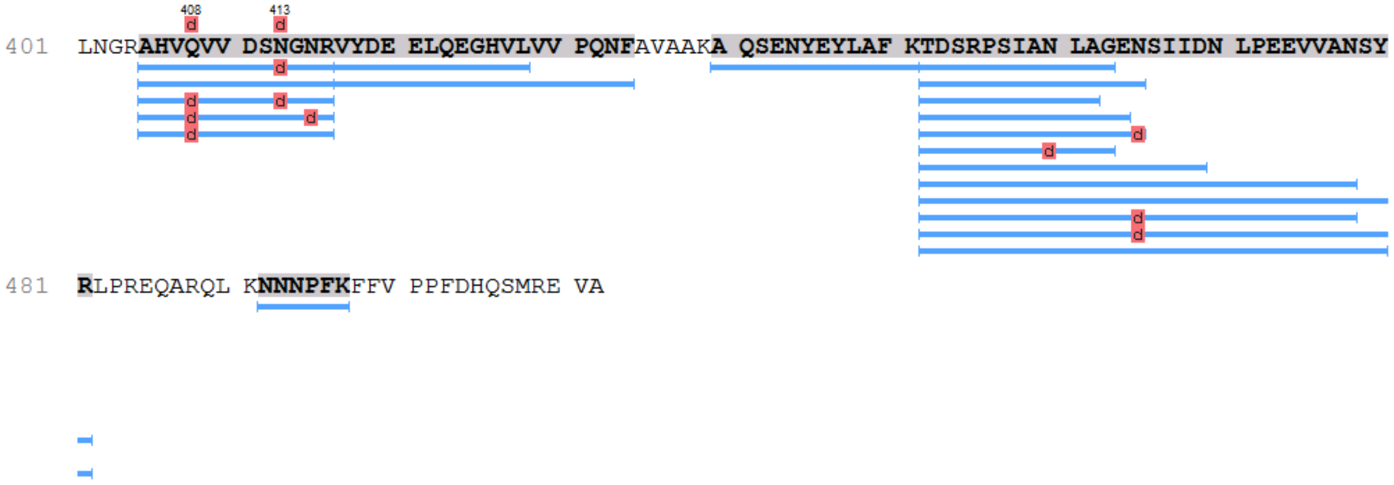
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

```
  1  MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
 81  RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161  PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241  FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321  RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
```



```
401  LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY
481  RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 24	#Spec	#Spec Sample 24	Start	End	PTM
R.AHVQVVDSN(+.98)GNR.V	N	99.9	66.38	1295.6218	12	0.9	648.8188	2	4.85	24	333	OB3622.raw	2.26E6	6	6	405	416	Deamidation (NQ)
R.VYDEELQEGHVL.V	N	99.9	64.92	1429.6725	12	0.0	715.8435	2	29.28	24	2311	OB3622.raw	1.14E5	2	2	417	428	
R.AHVQVVDSNGNR.V	N	99.9	59.87	1294.6378	12	-0.1	648.3261	2	19.68	24	1394	OB3622.raw	3.06E5	7	7	405	416	

K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVANSYR.L	Y	99.9	54.82	3244.5847	30	0.9	1082.5365	3	34.34	24	3000	OB3622.raw	3.76E4	1	1	452	481	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	54.71	1329.6525	13	-1.0	665.8328	2	28.03	24	2137	OB3622.raw	9.7E4	2	2	452	464	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	50.96	1444.6793	14	-1.7	723.3457	2	28.05	24	2139	OB3622.raw	8.3E4	4	4	452	465	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	50.96	1296.6058	12	2.9	649.3121	2	20.84	24	1462	OB3622.raw	1.01E4	1	1	405	416	Deamidation (NQ)
K.NNNPFK.F	N	99.9	50.79	732.3555	6	0.0	367.1850	2	21.88	24	1526	OB3622.raw	1.33E6	12	12	492	497	
K.AQSENYEYLAFK.T	Y	99.9	50.05	1461.6776	12	-1.7	731.8448	2	29.97	24	2406	OB3622.raw	1.92E6	5	5	440	451	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	49.01	2837.4043	27	1.5	1419.7115	2	33.95	24	2946	OB3622.raw	3.67E5	2	2	452	478	
K.TDSRPSIANLAGEN.S	N	99.9	48.50	1443.6953	14	-2.1	722.8534	2	27.55	24	2069	OB3622.raw	2.59E5	2	2	452	465	
K.TDSRPSIANLA.G	N	99.9	46.27	1143.5884	11	-0.3	572.8013	2	27.32	24	2037	OB3622.raw	1.4E5	3	3	452	462	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	45.52	1295.6218	12	-1.0	648.8176	2	21.53	24	1504	OB3622.raw	1.85E4	1	1	405	416	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.9	45.37	2114.0320	18	-0.8	1058.0225	2	32.13	24	2698	OB3622.raw	1.07E5	2	2	417	434	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	45.12	3243.6006	30	-0.4	1082.2070	3	33.73	24	2916	OB3622.raw	1.64E4	1	1	452	481	
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVAN.S	N	99.9	43.75	2838.3882	27	0.6	947.1372	3	34.21	24	2983	OB3622.raw	1.82E5	1	1	452	478	Deamidation (NQ)
K.TDSRPSIAN(+.98)LAG.E	N	99.8	38.95	1201.5939	12	-0.1	601.8041	2	28.38	24	2185	OB3622.raw	1.35E4	1	1	452	463	Deamidation (NQ)
K.TDSRPSIANLAG.E	N	99.8	38.90	1200.6099	12	-0.5	601.3119	2	27.53	24	2067	OB3622.raw	3.15E5	4	4	452	463	
K.TDSRPSIANLAGENSIID.N	N	99.8	38.66	1871.9225	18	-2.4	936.9663	2	30.90	24	2531	OB3622.raw	6.04E4	1	1	452	469	
K.TDSRPSIANLAGENSIIDNLPEEVVANSY.R	N	99.8	37.59	3087.4995	29	-0.1	1030.1737	3	35.03	24	3094	OB3622.raw	8.25E3	1	1	452	480	
R.AHVQ(+.98)VVDSNGN(+.98)R.V	N	99.4	33.69	1296.6058	12	4.3	433.2111	3	20.93	24	1468	OB3622.raw	1.25E5	1	1	405	416	Deamidation (NQ)
total 21 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

Summary

1. Notes Spot 15 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

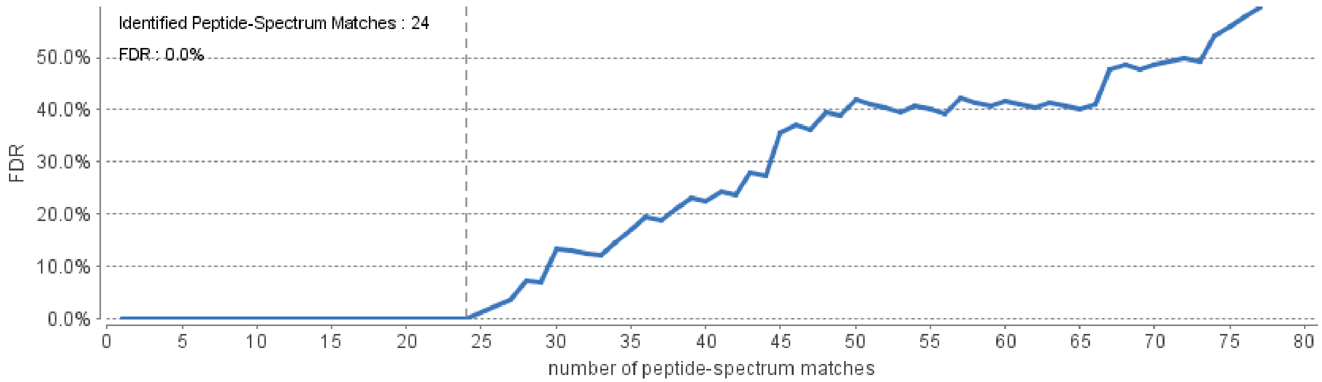
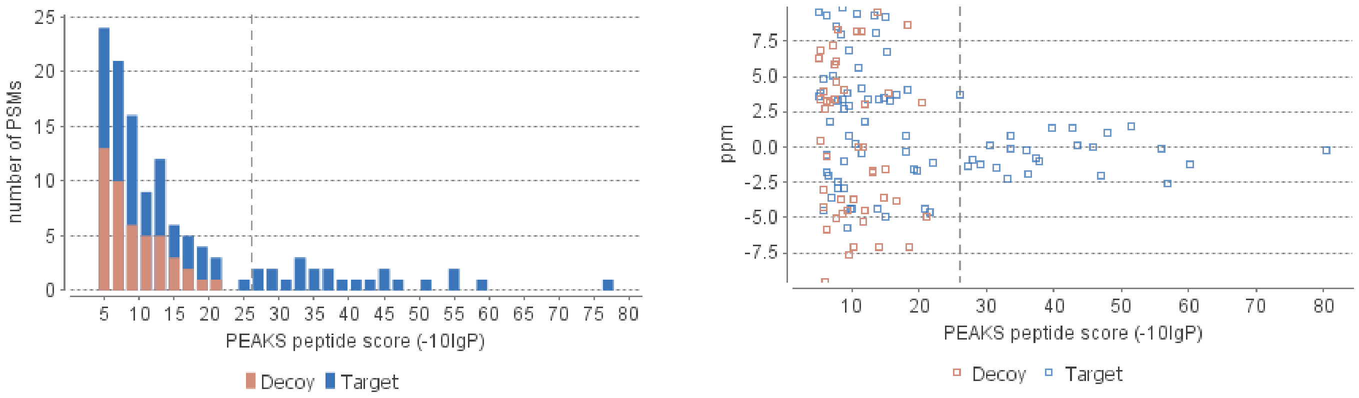


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

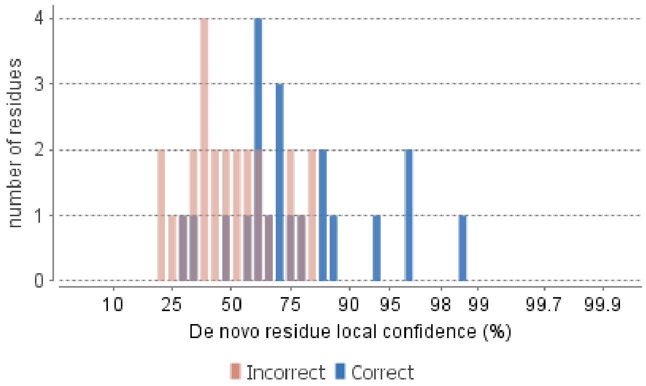

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



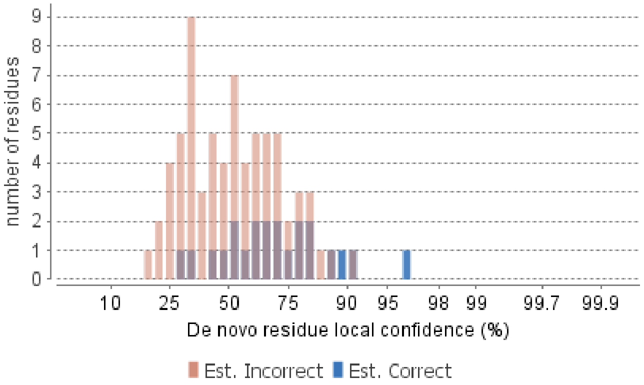


Table 1. Statistics of data.

# of MS scans	2872
# of MS/MS scans	3452

Table 2. Result filtration parameters.

Peptide -10lgP	≥26
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	19
Peptide sequences	12
Protein groups	3
Proteins	7
Proteins (#Unique Peptides)	3 (>2); 0 (=2); 4 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	7.7%
De Novo Only Spectra	13

Table 4. PTM profile.

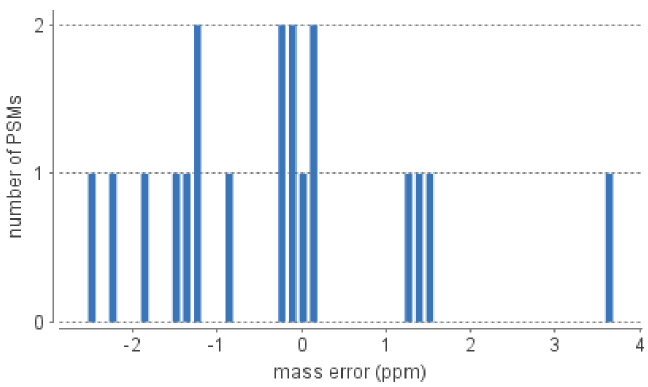
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	2	42.76	1.85E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



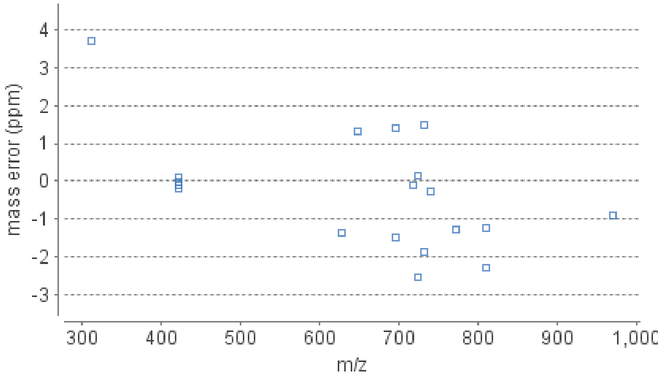


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 18	12	0	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3616.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 18	Area Sample 18	#Peptides	#Unique	#Spec Sample 18	PTM	Avg. Mass	Description
1	41	Q6IWG5|Q6IWG5_ARAHY	98.9	116.40	8	8	8.99E3	3	3	5	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
1	45	E5G077|E5G077_ARAHY	98.9	116.40	8	8	8.99E3	3	3	5	Y	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
1	42	Q0GM57|Q0GM57_ARAHY	98.9	116.40	8	8	8.99E3	3	3	5	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
2	13	Q9FZ11|Q9FZ11_ARAHY	98.8	106.02	9	9	1.48E3	4	1	5	N	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
2	5	Q5I6T2|Q5I6T2_ARAHY	98.8	106.02	9	9	1.48E3	4	1	5	N	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
2	15	Q647H3|Q647H3_ARAHY	98.8	106.02	9	9	1.48E3	4	1	5	N	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
9	181	H9L792|H9L792_ARAHY	20.9	26.11	2	2	7.87E3	1	1	1	Y	33305	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase OS=Arachis hypogaea GN=PGP1 PE=2 SV=1
total 7 proteins													

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

331
C
321 GYKN**GIEETI CSASVK**KNLG R**SSNPDIYNP QAGSLR**SVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
C

401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFK**T DSRPSIANLA GENSIIDNLP EEVVANSYRL

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	Y	99.9	60.27	1617.7747	15	-1.2	809.8936	2	27.86	18	1419	OB3616.raw	5.08E3	2	2	342	356	
K.AQSENYEYLAFK.T	Y	99.7	51.60	1461.6776	12	1.5	731.8472	2	30.58	18	1571	OB3616.raw	2.06E3	2	2	438	449	
N.GIEETIC(+57.02)SASVK.K	Y	99.1	42.76	1292.6282	12	1.3	647.3222	2	28.31	18	1442	OB3616.raw	1.85E3	1	1	325	336	Carbamidomethylation
total 3 peptides																		

E5G077|E5G077_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN

333
C
321 RRGYKN**GIEE TICSASVK**KN LGR**SSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
C

401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF K**TDSRPSIAN QAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	Y	99.9	60.27	1617.7747	15	-1.2	809.8936	2	27.86	18	1419	OB3616.raw	5.08E3	2	2	344	358	
K.AQSENYEYLAFK.T	Y	99.7	51.60	1461.6776	12	1.5	731.8472	2	30.58	18	1571	OB3616.raw	2.06E3	2	2	440	451	
N.GIEETIC(+57.02)SASVK.K	Y	99.1	42.76	1292.6282	12	1.3	647.3222	2	28.31	18	1442	OB3616.raw	1.85E3	1	1	327	338	Carbamidomethylation
total 3 peptides																		

Q0GM57|Q0GM57_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

333
C
321 RRGYKN**GIEE TICSASVK**KN LGR**SSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
C

401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF K**TDSRPSIAN LAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	Y	99.9	60.27	1617.7747	15	-1.2	809.8936	2	27.86	18	1419	OB3616.raw	5.08E3	2	2	344	358	
K.AQSENYEYLAFK.T	Y	99.7	51.60	1461.6776	12	1.5	731.8472	2	30.58	18	1571	OB3616.raw	2.06E3	2	2	440	451	
N.GIEETIC(+57.02)SASVK.K	Y	99.1	42.76	1292.6282	12	1.3	647.3222	2	28.31	18	1442	OB3616.raw	1.85E3	1	1	327	338	Carbamidomethylation
total 3 peptides																		

Q9FZ11|Q9FZ11_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA
81 LRRPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV
161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP
241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE
321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNR**SPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR**

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGK**SQS DNFEYVAFK**T DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
K.SQSDNFEYVAFK.T	Y	99.9	56.00	1433.6462	12	-0.1	717.8303	2	30.71	18	1583	OB3616.raw	1.48E3	1	1	458	469	
R.SPDIYNPQAGSLK.T	N	97.8	39.79	1388.6936	13	1.4	695.3550	2	27.72	18	1407	OB3616.raw	5.56E3	2	2	364	376	
R.WLGLSAEYGNLYR.N	N	80.5	29.21	1540.7673	13	-1.3	771.3900	2	33.50	18	1755	OB3616.raw	2.26E3	1	1	388	400	
K.TANDLNLLILR.W	N	78.7	27.20	1254.7296	11	-1.4	628.3712	2	33.41	18	1748	OB3616.raw	1.34E3	1	1	377	387	
total 4 peptides																		

Q5I6T2|Q5I6T2_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGRGNGIEET ICTASVKKNI GRNR**SPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY**

401 **R**NALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGK**SQ SDNFEYVAFK** TDSRPSIANL

481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
K.SQSDNFEYVAFK.T	Y	99.9	56.00	1433.6462	12	-0.1	717.8303	2	30.71	18	1583	OB3616.raw	1.48E3	1	1	459	470	
R.SPDIYNPQAGSLK.T	N	97.8	39.79	1388.6936	13	1.4	695.3550	2	27.72	18	1407	OB3616.raw	5.56E3	2	2	365	377	
R.WLGLSAEYGNLYR.N	N	80.5	29.21	1540.7673	13	-1.3	771.3900	2	33.50	18	1755	OB3616.raw	2.26E3	1	1	389	401	
K.TANDLNLLILR.W	N	78.7	27.20	1254.7296	11	-1.4	628.3712	2	33.41	18	1748	OB3616.raw	1.34E3	1	1	378	388	
total 4 peptides																		

Q647H3|Q647H3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN R**SPDIYNPQA GSLKTANDLN LLILRWLGLS**
401 **AEYGNLYR**NA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
K.SQSDNFEYVAFK.T	Y	99.9	56.00	1433.6462	12	-0.1	717.8303	2	30.71	18	1583	OB3616.raw	1.48E3	1	1	466	477	
R.SPDIYNPQAGSLK.T	N	97.8	39.79	1388.6936	13	1.4	695.3550	2	27.72	18	1407	OB3616.raw	5.56E3	2	2	372	384	
R.WLGLSAEYGNLYR.N	N	80.5	29.21	1540.7673	13	-1.3	771.3900	2	33.50	18	1755	OB3616.raw	2.26E3	1	1	396	408	
K.TANDLNLLILR.W	N	78.7	27.20	1254.7296	11	-1.4	628.3712	2	33.41	18	1748	OB3616.raw	1.34E3	1	1	385	395	
total 4 peptides																		

H9L792|H9L792_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

🟦C Carbamidomethylation (+57.02)

1 MTPLKLTATA SSFYVRTTAS APKPKPFFLR TWPSTTSTTK TTTVFYHQRT GRTITPCANI MLPPSQGSTR KSVTFAPHNN
81 NSFSRCISSD TAKDPDTRGP GPGPGPLPSH SEPSKLLTLP TMLTLGRVAS VPVLVATFYV DAPWGPAATT SIFIAAAVTD
161 WLDGYLARKM KLKSSFGAFL DPVADKLMVA ATLL**LLCSK**P LDVAAFSQAP WLLTVPSIAI IGREITMSAV REWAASQDTK
241 LLEAVAVNNL GKWKTATQMT ALTILLATRG WSDGGAALVV GSGVGLLYTS AGLAVWSLVV YMRKIWKVLM R

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 18	#Spec	#Spec Sample 18	Start	End	PTM
L.LLC(+57.02)SK.P	Y	67.2	26.11	619.3363	5	3.7	310.6766	2	33.30	18	1738	OB3616.raw	7.87E3	1	1	195	199	Carbamidomethylation
total 1 peptides																		

Peptide List

1. Notes

Spot 16 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

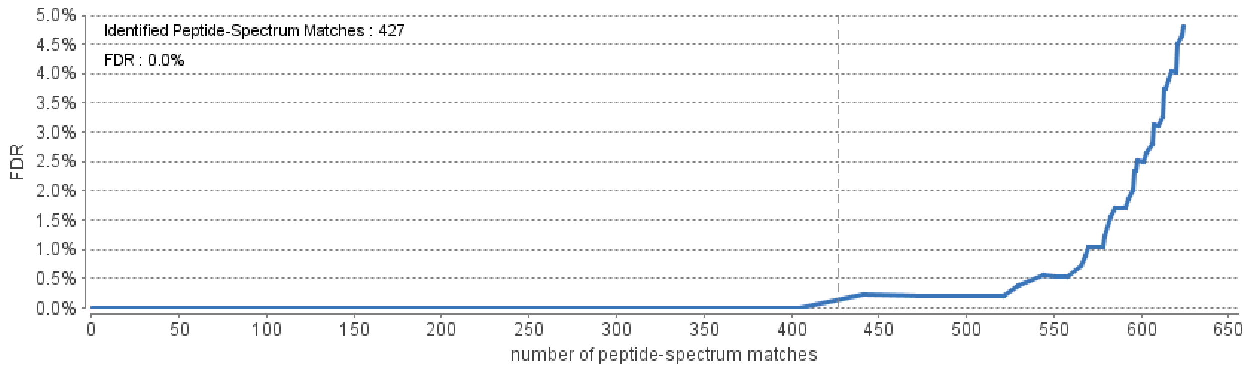
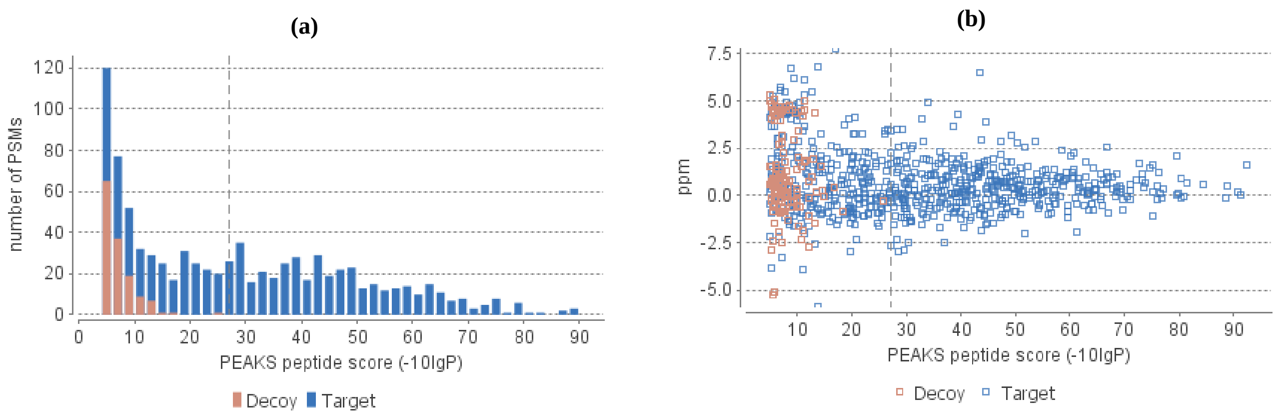


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

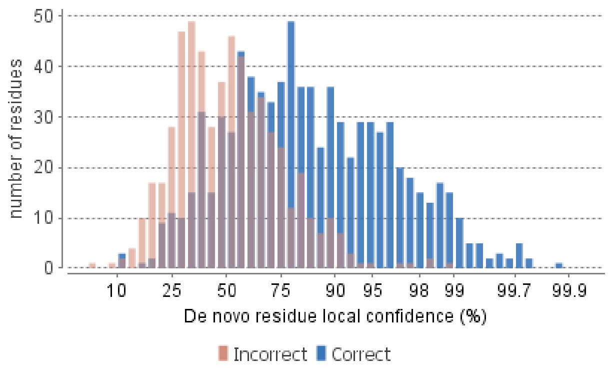

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



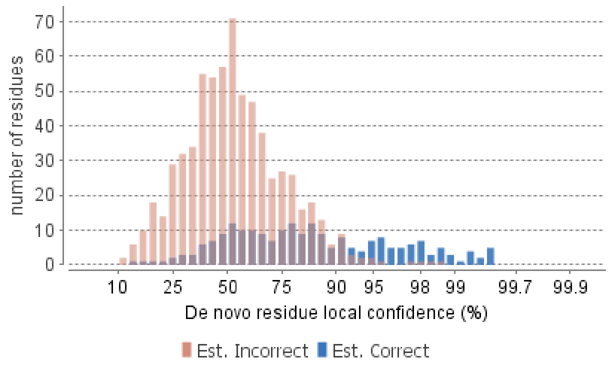


Table 1. Statistics of data.

# of MS scans	2225
# of MS/MS scans	1973

Table 2. Result filtration parameters.

Peptide -10lgP	≥27
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	417
Peptide sequences	127
Protein groups	11
Proteins	14
Proteins (#Unique Peptides)	8 (>2); 4 (=2); 2 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	102

Table 4. PTM profile.

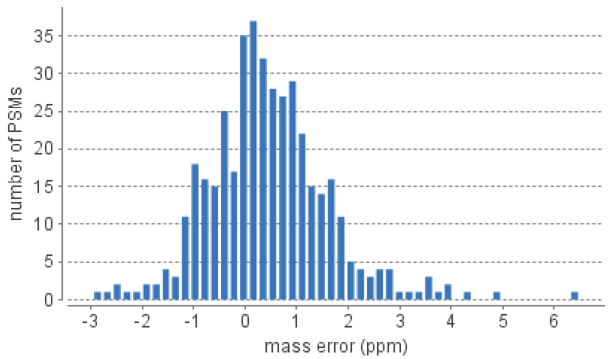
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	89	79.64	2.76E5	1000.00
Oxidation	15.99	M	69	80.92	1.87E5	1000.00
Deamidation	.98	N	9	66.08	7.4E4	100.79
HydPro	15.99	P	7	47.47	3.4E4	25.66

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



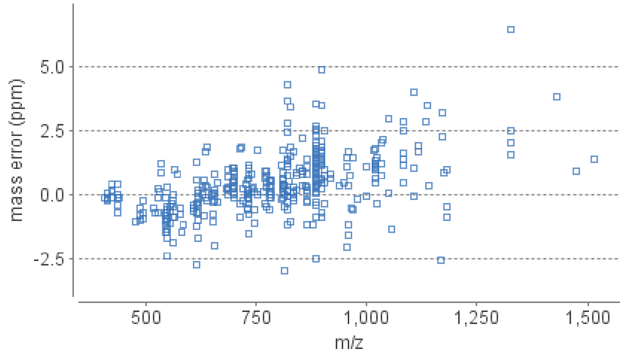


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
DS1 tacka 16 na Figuri 1	88	28	11	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: Uniprot_Peanut(3818)+cRAP_aug17
Taxon: All
Searched Entry: 1352
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB5184.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) DS1 tacka 16 na Figuri 1	Area DS1 tacka 16 na Figuri 1	#Peptides	#Unique	#Spec DS1 tacka 16 na Figuri 1	PTM	Avg. Mass	Description
1	216	Q6IWG5|Q6IWG5_ARAHY	99.1	279.74	44	44	1.1E7	24	19	176	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
1	217	Q0GM57|Q0GM57_ARAHY	99.1	279.74	44	44	1.1E7	24	19	176	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
3	219	sp|Q647H2|AHY3_ARAHY	99.1	239.93	35	35	2.26E6	13	11	45	Y	54569	Arachin Ahy-3 OS=Arachis hypogaea PE=1 SV=1
4	220	sp|K1C10_HUMAN|	99.1	226.69	37	37	1.68E6	19	19	40	Y	59519	sp|K1C10_HUMAN|
6	89	Q647H3|Q647H3_ARAHY	99.1	219.97	40	40	1.83E5	16	2	23	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
2	215	sp|Q6PSU2|CONG7_ARAHY	99.1	216.68	70	70	3.87E6	16	16	82	Y	20114	Conglutin-7 OS=Arachis hypogaea PE=1 SV=2
5	221	sp|K2C1_HUMAN|	99.1	212.55	22	22	6.78E5	11	10	22	Y	65886	sp|K2C1_HUMAN|
9	85	B5TYU1|B5TYU1_ARAHY	99.1	199.25	34	34	1.42E4	12	1	17	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
10	646	sp|K1C9_HUMAN|	99.1	161.27	14	14	1.64E5	6	6	10	N	62129	sp|K1C9_HUMAN|
12	964	sp|K22E_HUMAN|	99.1	144.53	22	22	2.21E5	7	6	9	N	65865	sp|K22E_HUMAN|
13	1193	sp|TRYP_PIG|	81.8	53.27	3	3	1.81E5	1	1	5	N	24409	sp|TRYP_PIG|
15	1679	Q38711|Q38711_ARAHY	83.0	43.80	17	17	1.19E4	2	2	2	N	29134	Galactose-binding lectin (Fragment) OS=Arachis hypogaea GN=lec PE=2 SV=1
15	1680	sp|P02872|LECG_ARAHY	83.0	43.80	16	16	1.19E4	2	2	2	N	29325	Galactose-binding lectin OS=Arachis hypogaea PE=1 SV=3
15	1681	A0A089ZXL7|A0A089ZXL7_ARAHY	83.0	43.80	16	16	1.19E4	2	2	2	N	29407	Peanut agglutinin variant OS=Arachis hypogaea PE=2 SV=1
total 14 proteins													

Q6IWG5|Q6IWG5_ARAHY

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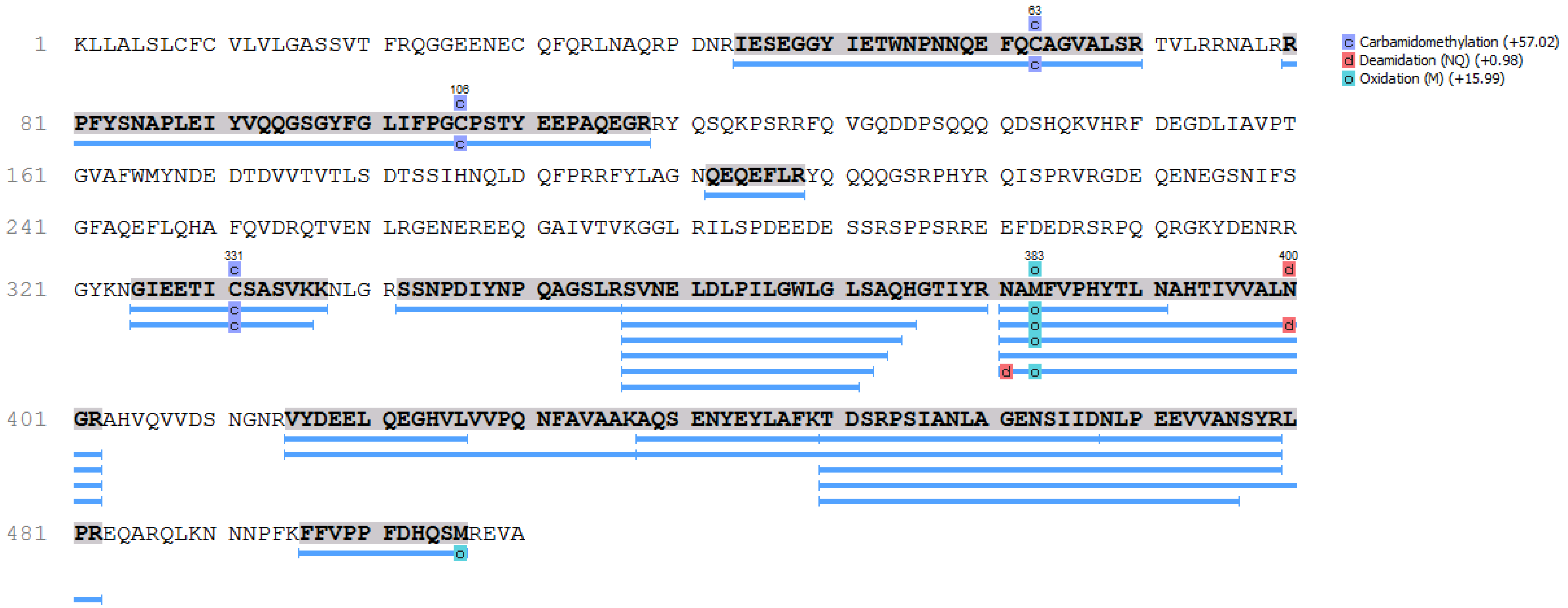
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	92.52	3243.6006	30	1.6	1082.2092	3	37.76	14	1902	OB5184.raw	8.24E5	10	10	450	479	
R.SSNPDIYNPQAGSLR.S	Y	99.9	81.54	1617.7747	15	0.7	809.8951	2	30.79	14	1495	OB5184.raw	7.23E5	12	12	342	356	
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.9	80.92	2453.2637	22	-0.1	818.7618	3	35.11	14	1749	OB5184.raw	3.75E5	5	5	381	402	Oxidation (M)
K.AQSENYEYLAFK.T	Y	99.9	80.31	1461.6776	12	-0.1	731.8460	2	33.59	14	1661	OB5184.raw	4.13E5	10	10	438	449	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	79.65	2651.4070	24	2.1	1326.7135	2	41.01	14	2092	OB5184.raw	5.33E6	70	70	357	380	
R.NAM(+15.99)FVPHYTLNAHTIVVALN(+.98)GR.A	Y	99.9	66.08	2454.2478	22	0.8	819.0905	3	34.67	14	1724	OB5184.raw	1.47E5	8	8	381	402	Oxidation (M); Deamidation (NQ)
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	N	99.9	64.14	3068.3933	27	1.4	1023.8065	3	36.26	14	1815	OB5184.raw	4.37E4	1	1	44	70	Carbamidomethylation
R.SVNELDLPILGWLGLSA.Q	Y	99.9	60.72	1795.9719	17	1.3	898.9944	2	46.20	14	2393	OB5184.raw	7.43E5	19	19	357	373	
R.SVNELDLPILGWLGLSAQH.G	Y	99.9	60.47	2061.0894	19	1.2	1031.5532	2	43.10	14	2212	OB5184.raw	6.24E4	3	3	357	375	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.9	60.37	2554.3066	23	0.9	852.4436	3	34.89	14	1737	OB5184.raw	2.07E5	4	4	415	437	
N.GIEETIC(+57.02)SASVK.K	Y	99.9	57.55	1292.6282	12	0.0	647.3214	2	31.19	14	1519	OB5184.raw	6.89E4	1	1	325	336	Carbamidomethylation
R.NAMFVPHYTLNAHTIVVALNGR.A	Y	99.9	57.40	2437.2688	22	-0.5	813.4298	3	35.81	14	1789	OB5184.raw	8.98E3	1	1	381	402	
D.NLPEEVVANSYR.L	Y	99.9	53.71	1389.6888	12	0.2	695.8519	2	32.53	14	1597	OB5184.raw	2.18E4	1	1	468	479	
N.GIEETIC(+57.02)SASVKK.N	Y	99.9	50.13	1420.7231	13	-0.9	711.3682	2	29.33	14	1411	OB5184.raw	2.84E4	2	2	325	337	Carbamidomethylation
K.TDSRPSIANLAGENSIID.N	N	99.9	49.58	1871.9225	18	0.4	936.9689	2	34.77	14	1730	OB5184.raw	3.29E4	1	1	450	467	
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.9	49.08	4424.0845	39	0.9	1475.7035	3	39.50	14	2004	OB5184.raw	9.55E4	4	4	80	118	Carbamidomethylation
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.9	49.03	3609.8386	33	0.7	903.4676	4	37.60	14	1893	OB5184.raw	9.85E5	6	6	450	482	
R.SVNELDLPILGWLGLSAQ.H	Y	99.9	47.74	1924.0305	18	0.7	963.0233	2	45.66	14	2361	OB5184.raw	1.3E4	1	1	357	374	
R.NAM(+15.99)FVPHYTLN.A	Y	99.9	47.56	1321.6125	11	-0.3	661.8134	2	32.71	14	1608	OB5184.raw	1.91E4	2	2	381	391	Oxidation (M)
R.SVNELDLPILGWLGL.S	Y	99.9	46.10	1637.9028	15	1.4	819.9598	2	47.49	14	2469	OB5184.raw	4.94E5	3	3	357	371	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	44.85	2837.4043	27	0.5	946.8091	3	37.97	14	1915	OB5184.raw	7.08E4	1	1	450	476	
K.FFVPPFDHQSM(+15.99).R	Y	99.8	41.97	1366.6016	11	0.2	684.3082	2	35.28	14	1759	OB5184.raw	1.23E5	5	5	496	506	Oxidation (M)
R.SVNELDLPILGWLGLS.A	Y	99.8	40.39	1724.9348	16	1.4	863.4759	2	46.52	14	2411	OB5184.raw	7.9E4	2	2	357	372	

R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.7	38.56	2454.2478	22	3.7	819.0929	3	35.91	14	1795	OB5184.raw	7.4E4	1	1	381	402	Deamidation (NQ); Oxidation (M)
R.VYDEELQEGHVL.V	N	99.0	34.29	1429.6725	12	1.9	715.8448	2	33.00	14	1625	OB5184.raw	3.92E3	1	1	415	426	
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	98.3	30.80	4687.2676	42	0.9	1172.8252	4	38.23	14	1930	OB5184.raw	1.59E5	1	1	438	479	
N.QEQEFLR.Y	N	96.6	27.86	948.4664	7	-1.1	475.2400	2	28.65	14	1370	OB5184.raw	0	1	1	202	208	
total 27 peptides																		

Q0GM57|Q0GM57_ARAHY

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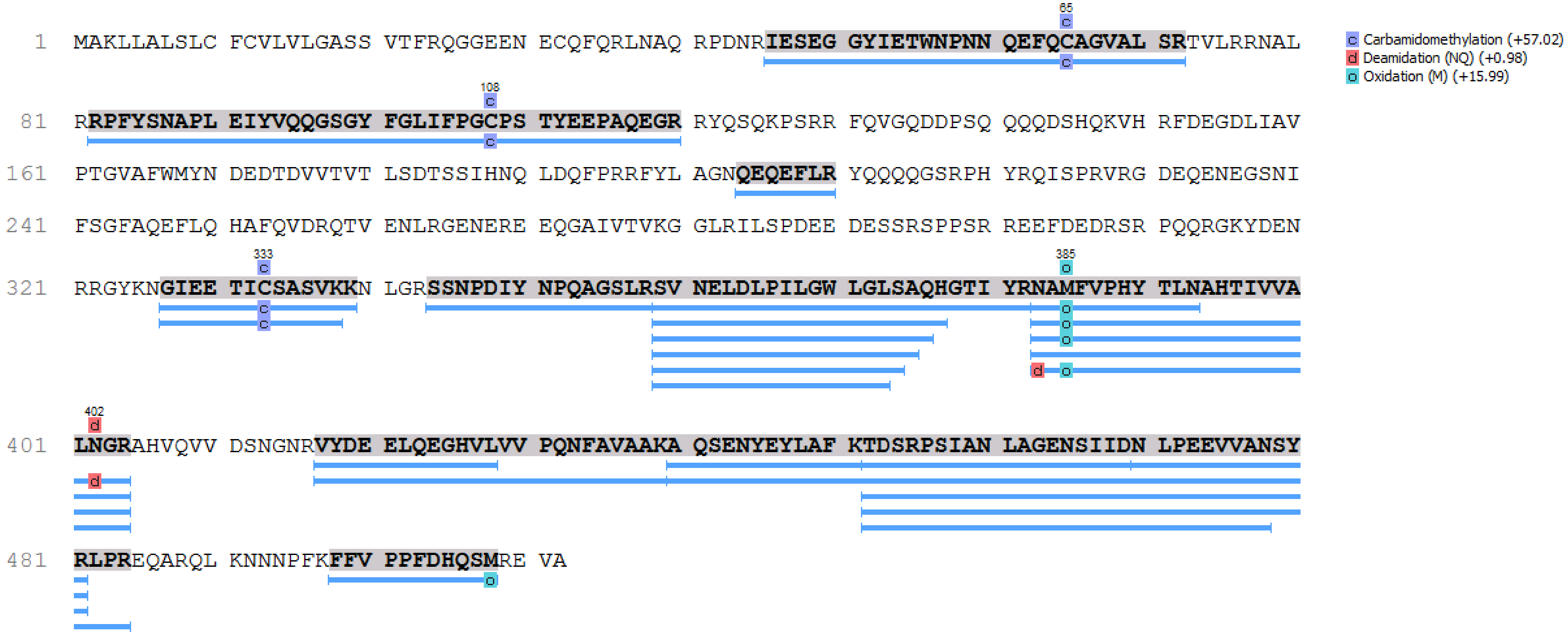
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNR**IESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

81 R**RPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR** RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGN**QEQEFLR** YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKN**GIEE TICSASVKK**N LGR**SSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA**

401 **LNGR**AHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY**

481 **RLPR**EQARQL KNNNPFK**FFV PPFDHQSM**RE VA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	92.52	3243.6006	30	1.6	1082.2092	3	37.76	14	1902	OB5184.raw	8.24E5	10	10	452	481	
R.SSNPDIYNPQAGSLR.S	Y	99.9	81.54	1617.7747	15	0.7	809.8951	2	30.79	14	1495	OB5184.raw	7.23E5	12	12	344	358	
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.9	80.92	2453.2637	22	-0.1	818.7618	3	35.11	14	1749	OB5184.raw	3.75E5	5	5	383	404	Oxidation (M)
K.AQSENYEYLAFK.T	Y	99.9	80.31	1461.6776	12	-0.1	731.8460	2	33.59	14	1661	OB5184.raw	4.13E5	10	10	440	451	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	79.65	2651.4070	24	2.1	1326.7135	2	41.01	14	2092	OB5184.raw	5.33E6	70	70	359	382	
R.NAM(+15.99)FVPHYTLNAHTIVVALN(+.98)GR.A	Y	99.9	66.08	2454.2478	22	0.8	819.0905	3	34.67	14	1724	OB5184.raw	1.47E5	8	8	383	404	Oxidation (M); Deamidation (NQ)
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	N	99.9	64.14	3068.3933	27	1.4	1023.8065	3	36.26	14	1815	OB5184.raw	4.37E4	1	1	46	72	Carbamidomethylation
R.SVNELDLPILGWLGLSA.Q	Y	99.9	60.72	1795.9719	17	1.3	898.9944	2	46.20	14	2393	OB5184.raw	7.43E5	19	19	359	375	
R.SVNELDLPILGWLGLSAQH.G	Y	99.9	60.47	2061.0894	19	1.2	1031.5532	2	43.10	14	2212	OB5184.raw	6.24E4	3	3	359	377	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.9	60.37	2554.3066	23	0.9	852.4436	3	34.89	14	1737	OB5184.raw	2.07E5	4	4	417	439	
N.GIEETIC(+57.02)SASVK.K	Y	99.9	57.55	1292.6282	12	0.0	647.3214	2	31.19	14	1519	OB5184.raw	6.89E4	1	1	327	338	Carbamidomethylation

R.NAMFVPHYTLNAHTIVVALNGR.A	Y	99.9	57.40	2437.2688	22	-0.5	813.4298	3	35.81	14	1789	OB5184.raw	8.98E3	1	1	383	404	
D.NLPEEVVANSYR.L	Y	99.9	53.71	1389.6888	12	0.2	695.8519	2	32.53	14	1597	OB5184.raw	2.18E4	1	1	470	481	
N.GIEETIC(+57.02)SASVKK.N	Y	99.9	50.13	1420.7231	13	-0.9	711.3682	2	29.33	14	1411	OB5184.raw	2.84E4	2	2	327	339	Carbamidomethylation
K.TDSRPSIANLAGENSIID.N	N	99.9	49.58	1871.9225	18	0.4	936.9689	2	34.77	14	1730	OB5184.raw	3.29E4	1	1	452	469	
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.9	49.08	4424.0845	39	0.9	1475.7035	3	39.50	14	2004	OB5184.raw	9.55E4	4	4	82	120	Carbamidomethylation
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.9	49.03	3609.8386	33	0.7	903.4676	4	37.60	14	1893	OB5184.raw	9.85E5	6	6	452	484	
R.SVNELDLPILGWLGLSAQ.H	Y	99.9	47.74	1924.0305	18	0.7	963.0233	2	45.66	14	2361	OB5184.raw	1.3E4	1	1	359	376	
R.NAM(+15.99)FVPHYTLN.A	Y	99.9	47.56	1321.6125	11	-0.3	661.8134	2	32.71	14	1608	OB5184.raw	1.91E4	2	2	383	393	Oxidation (M)
R.SVNELDLPILGWLGL.S	Y	99.9	46.10	1637.9028	15	1.4	819.9598	2	47.49	14	2469	OB5184.raw	4.94E5	3	3	359	373	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	44.85	2837.4043	27	0.5	946.8091	3	37.97	14	1915	OB5184.raw	7.08E4	1	1	452	478	
K.FFVPPFDHQSM(+15.99).R	Y	99.8	41.97	1366.6016	11	0.2	684.3082	2	35.28	14	1759	OB5184.raw	1.23E5	5	5	498	508	Oxidation (M)
R.SVNELDLPILGWLGLS.A	Y	99.8	40.39	1724.9348	16	1.4	863.4759	2	46.52	14	2411	OB5184.raw	7.9E4	2	2	359	374	
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.7	38.56	2454.2478	22	3.7	819.0929	3	35.91	14	1795	OB5184.raw	7.4E4	1	1	383	404	Deamidation (NQ); Oxidation (M)
R.VYDEELQEGHVL.V	N	99.0	34.29	1429.6725	12	1.9	715.8448	2	33.00	14	1625	OB5184.raw	3.92E3	1	1	417	428	
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	98.3	30.80	4687.2676	42	0.9	1172.8252	4	38.23	14	1930	OB5184.raw	1.59E5	1	1	440	481	
N.QEQEFLR.Y	N	96.6	27.86	948.4664	7	-1.1	475.2400	2	28.65	14	1370	OB5184.raw	0	1	1	204	210	
total 27 peptides																		

sp|Q647H2|AHY3_ARAHY

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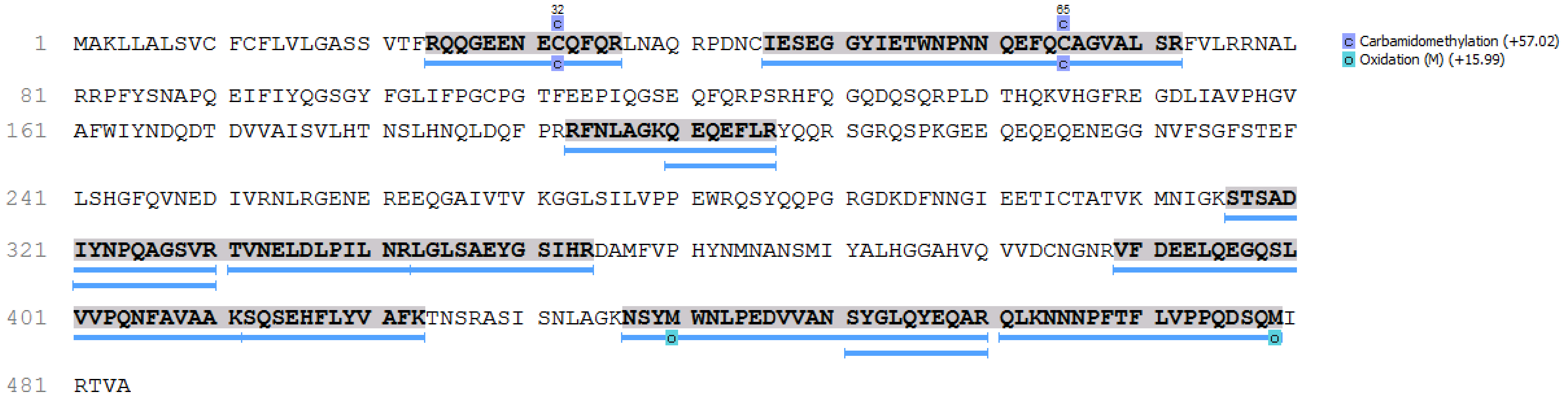
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 RRPFYSNAPQ EIFIYQGSGY FGLIFPGCPG TFEEPIQGSE QFQRPSRHFQ GQDQSQRPLD THQKVHGFRE GDLIAVPHGV
161 AFWIYNDQDT DVVAISVLHT NSLHNQLDQF PR**RFNLAGKQ EQEFLR**YQQR SGRQSPKGEE QEQEQENEGG NVFSGFSTEF
241 LSHGFQVNED IVRNLRGENE REEQGAIVTV KGGLSILVPP EWRQSYQQPG RGDKDFNNGI EETICTATVK MNIGK**STSAD**
321 **IYNPQAGSVR TVNELDLPIL NRLGLSAEYG SIHR**DAMFVP HYNMNANSMI YALHGGAHVQ VVDCNGNR**VF DEELQEGQSL**
401 **VVPQNFAVAA KSQSEHFLYV AFK**TNSRASI SNLAGK**NSYM WNLPEDVVAN SYGLQYEQAR QLKNNNPFTF LVPPQDSQM**I
481 RTVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
K.STSADIYNPQAGSVR.T	Y	99.9	91.27	1564.7482	15	0.0	783.3813	2	29.65	14	1430	OB5184.raw	2.92E5	6	6	316	330	
K.SQSEHFLYVAFK.T	Y	99.9	88.58	1454.7194	12	-0.1	728.3669	2	33.53	14	1657	OB5184.raw	2.12E5	6	6	412	423	
K.NSYM(+15.99)WNLPEDVVANSYGLQYEQAR.Q	Y	99.9	74.67	2862.2917	24	1.4	955.1059	3	37.56	14	1891	OB5184.raw	2.49E5	4	4	437	460	Oxidation (M)
R.LGLSAEYGSIHR.D	Y	99.9	69.76	1301.6727	12	-0.8	651.8431	2	30.44	14	1475	OB5184.raw	3.51E5	6	6	343	354	
R.TVNELDLPILNR.L	Y	99.9	69.26	1395.7721	12	0.5	698.8937	2	36.44	14	1826	OB5184.raw	9.27E5	11	11	331	342	
C.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.F	N	99.9	64.14	3068.3933	27	1.4	1023.8065	3	36.26	14	1815	OB5184.raw	4.37E4	1	1	46	72	Carbamidomethylation
R.VFDEELQEGQSLVVPQNFAVAAK.S	Y	99.9	62.38	2517.2751	23	0.2	840.0991	3	36.69	14	1841	OB5184.raw	7.62E4	3	3	389	411	
N.SYGLQYEQAR.Q	Y	99.9	59.55	1213.5728	10	-0.5	607.7933	2	29.74	14	1435	OB5184.raw	2.35E4	2	2	451	460	
F.RQQGEENEC(+57.02)QFQR.L	Y	99.5	36.76	1707.7383	13	0.8	570.2538	3	24.38	14	1122	OB5184.raw	6.22E3	1	1	24	36	Carbamidomethylation
R.QLKNNNPFTFLVPPQDSQM(+15.99).I	Y	99.5	36.49	2233.0837	19	1.9	1117.5513	2	37.46	14	1885	OB5184.raw	8.58E4	2	2	461	479	Oxidation (M)
R.RFNLAGKQEQEFLR.Y	Y	98.3	31.02	1734.9165	14	-1.4	579.3120	3	31.28	14	1524	OB5184.raw	3.2E4	1	1	193	206	

D.IYNPQAGSVR.T	Y	98.3	30.67	1103.5723	10	-1.1	552.7928	2	26.99	14	1274	OB5184.raw	4.06E3	1	1	321	330	
K.QEQEFLR.Y	N	96.6	27.86	948.4664	7	-1.1	475.2400	2	28.65	14	1370	OB5184.raw	0	1	1	200	206	
total 13 peptides																		

sp|K1C10_HUMAN|

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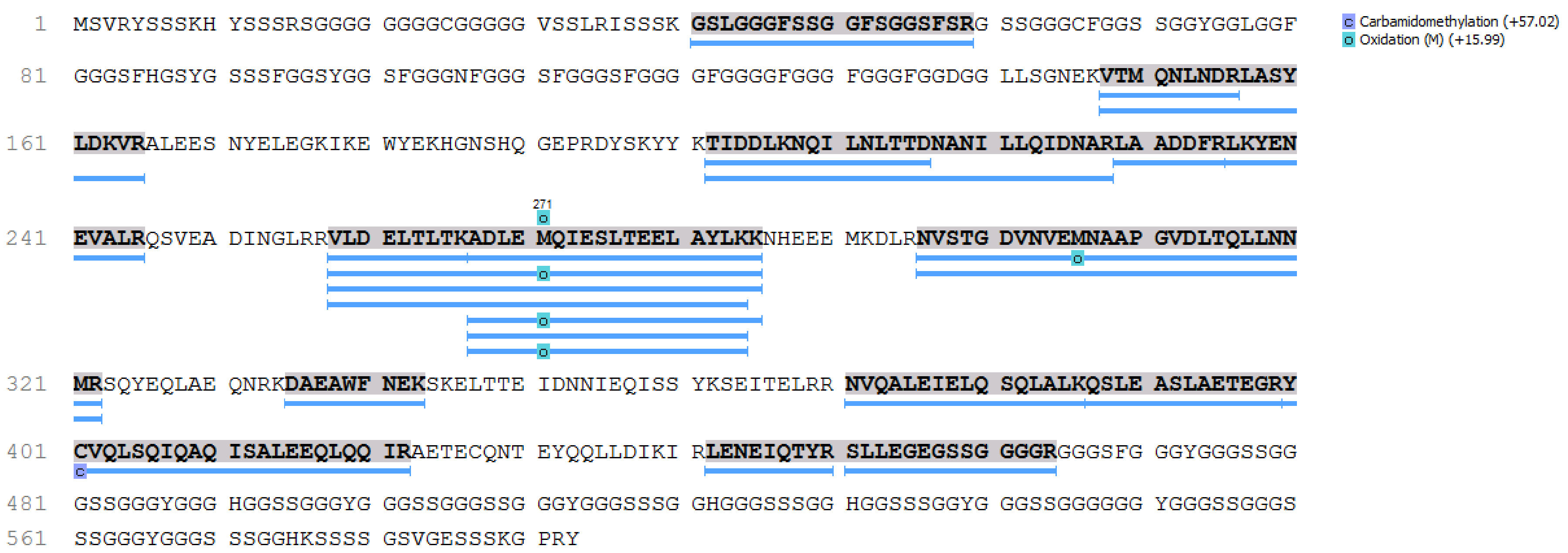
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MSVRYSSSKH YSSSRSGGGG GGGGCGGGGG VSSLRISSSK **GSLGGGFSSG GFSGGSFSR**G SSGGGCFGGS SGGYGGLGGF

81 GGGSFHGSYG SSSFGGSYGG SFGGGNFGGG SFGGGSFGGG GFGGGGFGGG FGGGFGGDGG LLSGNEK**VTM QNLNDRLASY**

161 **LDKVR**ALEES NYELEGKIKE WYEKHGNSHQ GEPRDYSKYY K**TIDDLKNQI LNLTTDNANI LLQIDNARLA ADDFRLKYEN**

241 **EVALR**QSVEA DINGLRR**VLD ELTLTKADLE MQIESLTEEL AYLKK**NHEEE MKDLR**NVSTG DVNVEMNAAP GVDLTQLLNN**

321 **MR**SQYEQLAE QNRK**DAEAWF NEK**SKELTTE IDNNIEQISS YKSEITELRR **NVQALEIELQ SQLALKQSLE ASLAETEGRY**

401 **CVQLSQIQAQ ISALEEQLQQ IR**AETECQNT EYQQLLDIKI R**LENEIQTYR SLLEGEGSSG GGR**GGGSFG GGYGGGSSGG

481 GSSGGGYGGG HGGSSGGGYG GGSSGGGSSG GGYGGGSSSG GHGGGSSSGG HGGSSSGGYG GGSSGGGGGG YGGGSSGGGS

561 SSGGGYGGGS SSGGHKSSSS GSVGESSSKG PRY

C Carbamidomethylation (+57.02)
O Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
K.GSLGGGFSSGGFSGGSFSR.G	Y	99.9	80.32	1706.7648	19	0.9	854.3904	2	33.67	14	1666	OB5184.raw	2.39E4	1	1	41	59	
R.YC(+57.02)VQLSQIQAQISALEEQLQQIR.A	Y	99.9	73.76	2745.4119	23	0.6	916.1451	3	41.56	14	2124	OB5184.raw	0	2	2	400	422	Carbamidomethylation
R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S	Y	99.9	72.69	2871.3855	27	1.7	958.1374	3	39.45	14	2001	OB5184.raw	1.5E5	4	4	296	322	
K.TIDDLKNQILNLTTDNANILLQIDNAR.L	Y	99.9	68.71	3051.6201	27	1.1	1018.2151	3	40.21	14	2045	OB5184.raw	7.83E5	9	9	202	228	
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNMR.S	Y	99.9	65.86	2887.3804	27	-0.5	963.4669	3	38.76	14	1961	OB5184.raw	3.42E4	1	1	296	322	Oxidation (M)
R.SLLEGEGSSGGGGR.G	Y	99.9	64.16	1261.5898	14	-0.8	631.8017	2	27.46	14	1301	OB5184.raw	8.24E3	2	2	451	464	
R.VLDELTLTKADLEMQIESLTEELAYLK.K	Y	99.9	47.24	3107.6199	27	2.2	1036.8828	3	42.71	14	2190	OB5184.raw	6.35E4	1	1	258	284	
R.LENEIQTYR.S	Y	99.9	47.20	1164.5775	9	-1.2	583.2953	2	29.02	14	1392	OB5184.raw	3.65E3	1	1	442	450	
R.LAADDFR.L	Y	99.9	46.23	806.3922	7	-0.1	404.2033	2	28.91	14	1386	OB5184.raw	2.05E4	1	1	229	235	
R.VLDELTLTKADLEM(+15.99)QIESLTEELAYLKK.N	Y	99.9	45.58	3251.7097	28	0.4	813.9350	4	40.81	14	2080	OB5184.raw	1.33E5	2	2	258	285	Oxidation (M)
K.ADLEMQIESLTEELAYLK.K	Y	99.9	43.74	2095.0396	18	3.0	1048.5302	2	42.04	14	2151	OB5184.raw	2.19E4	1	1	267	284	
K.ADLEM(+15.99)QIESLTEELAYLKK.N	Y	99.9	43.51	2239.1294	19	-0.6	747.3833	3	39.76	14	2019	OB5184.raw	7.19E4	2	2	267	285	Oxidation (M)
K.QSLEASLAETEGR.Y	Y	99.8	41.61	1389.6736	13	1.0	695.8448	2	32.02	14	1566	OB5184.raw	2.18E4	1	1	387	399	
K.ADLEM(+15.99)QIESLTEELAYLK.K	Y	99.8	41.61	2111.0344	18	-1.3	1056.5231	2	42.26	14	2164	OB5184.raw	0	1	1	267	284	Oxidation (M)
R.NVQALEIELQSQLALK.Q	Y	99.8	41.35	1796.0043	16	1.6	899.0109	2	37.91	14	1911	OB5184.raw	2.12E4	1	1	371	386	
K.TIDDLKNQILNLTTD.N	Y	99.7	39.19	1715.8942	15	0.3	858.9547	2	37.48	14	1886	OB5184.raw	8.3E3	1	1	202	216	
K.ADLEMQIESLTEELAYLKK.N	Y	99.3	35.79	2223.1343	19	0.3	742.0522	3	39.54	14	2006	OB5184.raw	7.68E4	1	1	267	285	
R.VLDELTLTK.A	Y	99.0	34.30	1030.5911	9	-0.5	516.3026	2	32.52	14	1596	OB5184.raw	2.17E4	1	1	258	266	
R.VLDELTLTKADLEMQIESLTEELAYLKK.N	Y	99.0	33.50	3235.7148	28	0.1	809.9361	4	40.90	14	2085	OB5184.raw	1.66E5	1	1	258	285	

K.VTMQNLNDR.L	Y	99.0	32.92	1089.5237	9	-0.9	545.7686	2	27.70	14	1315	OB5184.raw	6.75E3	1	1	148	156	
R.LKYENEVALR.Q	Y	98.4	31.95	1233.6716	10	0.0	412.2312	3	28.96	14	1389	OB5184.raw	2.47E4	3	3	236	245	
K.VTMQNLNDRLASYLDKVR.A	Y	97.4	28.23	2135.1157	18	1.8	712.7138	3	35.63	14	1779	OB5184.raw	8.68E3	1	1	148	165	
K.DAEAWFNEK.S	Y	96.4	27.06	1108.4825	9	-0.4	555.2484	2	33.51	14	1656	OB5184.raw	1.32E4	1	1	335	343	
total 23 peptides																		

Q647H3|Q647H3_ARAHY

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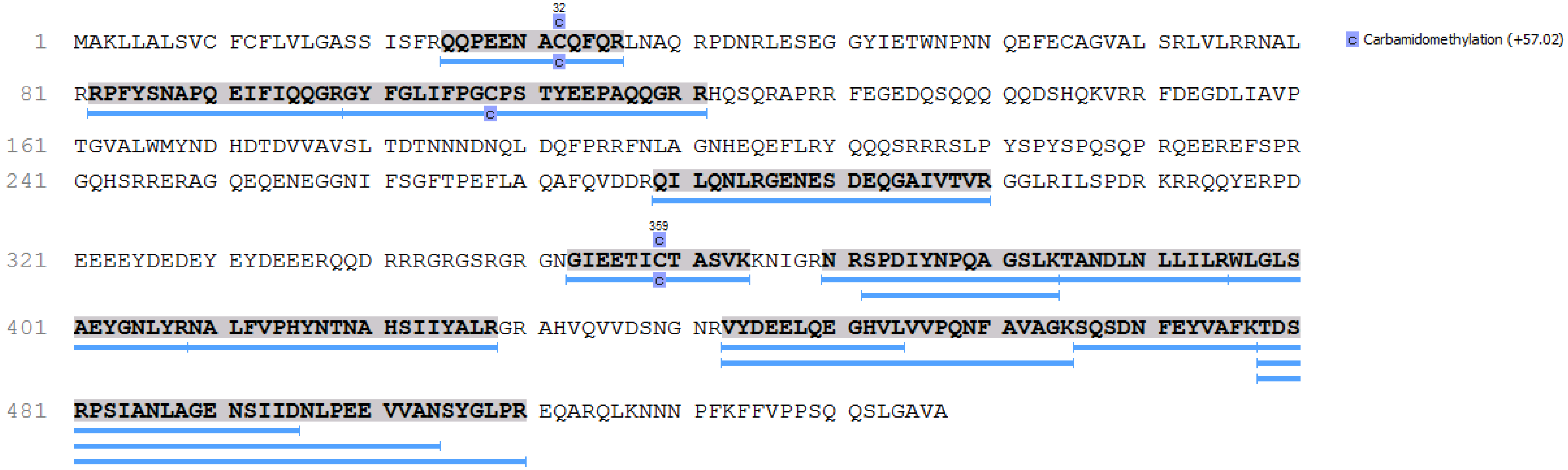
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**HQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP

161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR

241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDR**QI LQNLRGENES DEQGAIVTVR** GGLRILSPDR KRRQQYERPD

321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GN**GIEETICT ASVK**KNIGR**N RSPDIYNPQA GSLKTANDLN LLILRWLGLS**

401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS**

481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	88.82	1540.7673	13	0.5	771.3913	2	36.42	14	1825	OB5184.raw	2.01E5	4	4	396	408	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	63.56	1306.6438	12	0.1	654.3292	2	30.97	14	1506	OB5184.raw	1.38E5	3	3	353	364	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	62.89	1533.6630	12	0.9	767.8395	2	27.22	14	1287	OB5184.raw	2.25E3	1	1	25	36	Carbamidomethylation
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	61.19	2313.2019	20	-0.5	772.0742	3	34.63	14	1722	OB5184.raw	7.4E4	1	1	409	428	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	60.60	3510.7590	33	2.3	1171.2629	3	38.75	14	1960	OB5184.raw	4.55E4	2	2	478	510	
K.SQSDNFEYVAFK.T	N	99.9	57.07	1433.6462	12	0.2	717.8306	2	33.84	14	1676	OB5184.raw	4.53E3	1	1	466	477	
K.TDSRPSIANLAGENSIID.N	N	99.9	49.58	1871.9225	18	0.4	936.9689	2	34.77	14	1730	OB5184.raw	3.29E4	1	1	478	495	
R.SPDIYNPQAGSLK.T	N	99.9	46.87	1388.6936	13	0.5	695.3544	2	30.72	14	1491	OB5184.raw	1.39E4	1	1	372	384	
K.TANDLNLLILR.W	N	99.9	45.86	1254.7296	11	0.3	628.3723	2	36.45	14	1827	OB5184.raw	4.81E4	2	2	385	395	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	44.85	2837.4043	27	0.5	946.8091	3	37.97	14	1915	OB5184.raw	7.08E4	1	1	478	504	
R.QILQNLRGENESDEQGAIVTVR.G	N	99.5	37.18	2468.2620	22	0.6	823.7617	3	32.23	14	1578	OB5184.raw	0	1	1	279	300	
R.RPFYSNAPQEIFIQQGR.G	N	99.5	37.05	2050.0383	17	0.3	684.3536	3	33.50	14	1655	OB5184.raw	1.97E4	1	1	82	98	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.0	34.38	2540.2910	23	1.1	847.7719	3	35.04	14	1745	OB5184.raw	9.65E3	1	1	443	465	
R.VYDEELQEGHVL.V	N	99.0	34.29	1429.6725	12	1.9	715.8448	2	33.00	14	1625	OB5184.raw	3.92E3	1	1	443	454	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.H	N	99.0	33.73	2629.2383	23	-1.2	877.4190	3	36.51	14	1830	OB5184.raw	1.04E4	1	1	99	121	Carbamidomethylation
R.NRSPDIYNPQAGSLK.T	N	96.6	27.62	1658.8376	15	-0.6	553.9528	3	28.93	14	1387	OB5184.raw	1.58E4	1	1	370	384	
total 16 peptides																		

sp|Q6PSU2|CONG7_ARAHY

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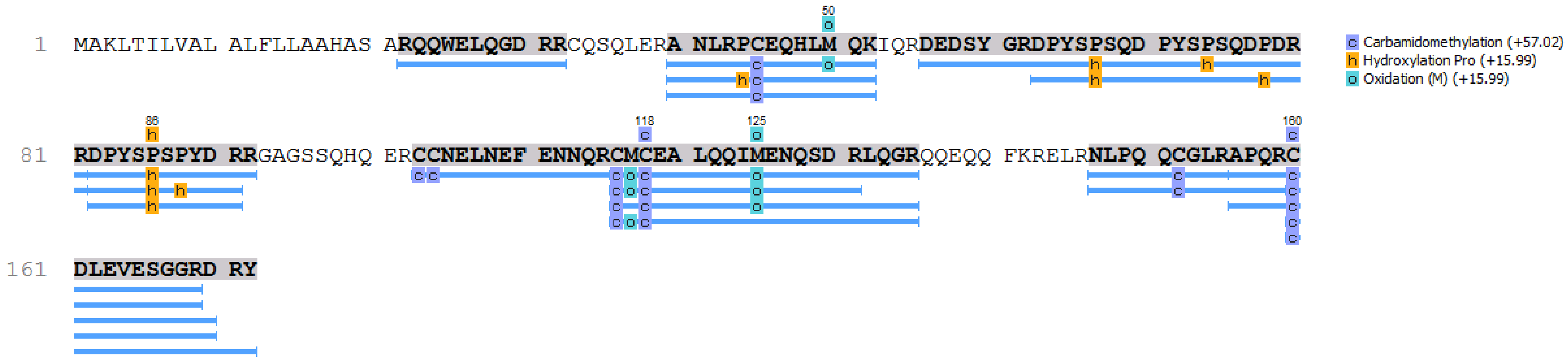
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.C(+57.02)C(+57.02)NELNEFENNQR.C	Y	99.9	79.64	1725.6835	13	0.1	863.8491	2	30.82	14	1497	OB5184.raw	3.73E5	9	9	103	115	Carbamidomethylation
R.ANLRPC(+57.02)EQHLM(+15.99)QK.I	Y	99.9	67.00	1639.7922	13	-0.9	547.6042	3	24.41	14	1124	OB5184.raw	9.73E5	21	21	40	52	Carbamidomethylation; Oxidation (M)
R.C(+57.02)M(+15.99)C(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.9	65.66	2498.0771	20	-0.1	833.6996	3	31.16	14	1517	OB5184.raw	5.09E5	7	7	116	135	Carbamidomethylation; Oxidation (M)
R.C(+57.02)DLEVESGGRDRY	Y	99.9	64.46	1554.6732	13	-0.1	778.3438	2	28.39	14	1355	OB5184.raw	4.45E5	6	6	160	172	Carbamidomethylation
R.C(+57.02)DLEVESGGR.D	Y	99.9	64.01	1120.4818	10	-0.5	561.2479	2	27.09	14	1280	OB5184.raw	5.76E4	5	5	160	169	Carbamidomethylation
R.APQRC(+57.02)DLEVESGGR.D	Y	99.9	52.41	1572.7314	14	-0.1	525.2510	3	26.20	14	1228	OB5184.raw	1.56E4	3	3	156	169	Carbamidomethylation
R.C(+57.02)MC(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.9	52.14	2482.0820	20	1.5	828.3692	3	32.87	14	1618	OB5184.raw	7.51E4	3	3	116	135	Carbamidomethylation; Oxidation (M)
R.NLPQQC(+57.02)GLR.A	Y	99.9	48.45	1084.5448	9	-0.7	543.2793	2	27.25	14	1289	OB5184.raw	4.66E5	5	5	147	155	Carbamidomethylation
R.ANLRPC(+57.02)EQHLMQK.I	Y	99.9	48.12	1623.7974	13	-1.0	542.2725	3	26.38	14	1238	OB5184.raw	3.75E4	2	2	40	52	Carbamidomethylation
R.C(+57.02)DLEVESGGRD.R	Y	99.9	48.10	1235.5088	11	-0.1	618.7616	2	27.63	14	1311	OB5184.raw	1.08E5	5	5	160	170	Carbamidomethylation
R.DPYSP(+15.99)SPYDR.R	Y	99.9	47.47	1211.5094	10	-0.4	606.7617	2	27.65	14	1312	OB5184.raw	3.4E4	2	2	82	91	Hydroxylation Pro
R.APQRC(+57.02)DLEVESGGRD.R	Y	99.9	43.03	1687.7583	15	1.0	563.5939	3	26.43	14	1241	OB5184.raw	4.6E4	2	2	156	170	Carbamidomethylation
R.NLPQQC(+57.02)GLRAPQR.C	Y	99.8	41.73	1536.7943	13	0.6	769.4049	2	27.36	14	1295	OB5184.raw	4.12E3	2	2	147	159	Carbamidomethylation
A.RQQWELQGDRR.C	Y	99.7	39.20	1470.7440	11	-0.7	491.2549	3	26.74	14	1259	OB5184.raw	1.84E5	3	3	22	32	
R.DPYSP(+15.99)SPYDRR.G	Y	99.7	38.98	1367.6105	11	0.7	684.8130	2	26.29	14	1233	OB5184.raw	5.84E4	1	1	82	92	Hydroxylation Pro
R.DEDSYGRDPYSP(+15.99)SQDPYSP(+15.99)SQDPDRR.D	Y	99.7	38.40	3060.2605	26	0.1	766.0725	4	28.73	14	1375	OB5184.raw	1.13E5	1	1	56	81	Hydroxylation Pro
R.DPYSP(+15.99)SQDPYSPSQDP(+15.99)DRR.D	Y	99.0	34.99	2237.9460	19	-1.1	746.9885	3	27.44	14	1300	OB5184.raw	1.08E4	1	1	63	81	Hydroxylation Pro
R.ANLRP(+15.99)C(+57.02)EQHLMQK.I	Y	99.0	33.58	1639.7922	13	-0.2	410.9553	4	25.82	14	1206	OB5184.raw	3.2E5	1	1	40	52	Hydroxylation Pro; Carbamidomethylation
R.DPYSP(+15.99)SP(+15.99)YDR.R	Y	98.3	29.96	1227.5043	10	0.6	614.7598	2	26.48	14	1244	OB5184.raw	1.55E4	1	1	82	91	Hydroxylation Pro
R.C(+57.02)M(+15.99)C(+57.02)EALQQIM(+15.99)ENQSDR.L	Y	96.7	27.93	2043.8119	16	0.3	682.2781	3	30.92	14	1503	OB5184.raw	1.41E4	1	1	116	131	Carbamidomethylation; Oxidation (M)
R.C(+57.02)M(+15.99)C(+57.02)EALQQIMENQSDRLQGR.Q	Y	96.5	27.12	2482.0820	20	3.4	828.3708	3	34.20	14	1697	OB5184.raw	1.03E4	1	1	116	135	Carbamidomethylation; Oxidation (M)
total 21 peptides																		

sp|K2C1_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

o Oxidation (M) (+15.99)

1 SRQFSSRSGY RSGGGFSSGS AGIINYQRRT TSSSTRRSGG GGGRFSSCGG GGGSFGAGGG FGSR**SLVNLG GSK**SISISVA

81 RGGGRGSGFG GGYGGGGFGG GGFGGGGFGG GGIGGGGFGG FGSGGGGFGG GGFGGGGYGG GYGPVCPPGG IQEVTINQSL

161 LQPLNVEIDP EIQKVKSRER EQIKSLNNQF ASFIDKVR**FL EQQNQVLQTK WELLQQVDTS TRTHNLEPYF ESFINNLRR**R

241 VDQLKSDQSR LDSELKNMQD MVEDYR**NKYE DEINKR**TNAE NEFVTIKKDV DGAYMTKVDL QAK**LDNLQQE IDFLTALYQA**

338

321 **ELSQMQTQIS ETNVILSMDN NRSLDLDSII AEVK**AQNEDI AQKSKAEAES LYQSKYEELQ ITAGRHGDSV RNSKIEISEL

401 NRVIQRLRSE IDNVKKQISN LQQSISDAEQ RGENALKDAK **NKLNDLEDAL QQAKEDLAR**L LRDYQELMNT K**LALDLEIAT**

481 **YR**TLLEGEES RMSGECAPNV SVSVSTSHTT ISGGGSRGGG GGGYGSGGSS YGSGGGSYGS GGGGGGGRGS YGSGGSSYGS

561 GGGSYGSGGG GGGHGSYGSG SSSGGYRGGS GGGGGGSSGG RGSGGGSSGG SIGGRGSSSG GVKSSGGSSS VRFVSTTYSG

641 VTR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.SLDLDSIIAEVK.A	Y	99.9	79.91	1301.7078	12	0.1	651.8612	2	38.14	14	1925	OB5184.raw	1.24E5	3	3	343	354	
R.FLEQQNQVLQTKWELLQQVDTSTR.T	Y	99.9	70.99	2931.5090	24	-0.2	978.1768	3	36.08	14	1805	OB5184.raw	7.52E4	1	1	199	222	
K.LALDLEIATYR.T	Y	99.9	69.76	1276.7026	11	-0.2	639.3585	2	36.10	14	1806	OB5184.raw	3.46E4	3	3	472	482	
K.NKLNDLEDALQQAKEDLAR.L	Y	99.9	63.24	2183.1182	19	0.0	728.7133	3	36.62	14	1837	OB5184.raw	1.39E5	4	4	441	459	
R.FLEQQNQVLQTK.W	N	99.9	61.41	1474.7780	12	0.2	738.3964	2	30.67	14	1488	OB5184.raw	1.85E4	1	1	199	210	
K.WELLQQVDTSTR.T	Y	99.9	59.03	1474.7416	12	0.8	738.3787	2	34.97	14	1741	OB5184.raw	1.62E4	1	1	211	222	
K.LDNLQQEIDFLTALYQA.E	Y	99.9	50.87	1993.9996	17	-0.1	998.0070	2	44.16	14	2273	OB5184.raw	1E4	2	2	304	320	
R.THNLEPYFESFINNLRR.R	Y	99.9	44.50	2149.0703	17	-0.2	717.3639	3	37.37	14	1880	OB5184.raw	1.04E5	1	1	223	239	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSM(+15.99)DNNR.S	Y	99.0	33.43	4558.1841	39	0.4	1140.5537	4	43.65	14	2244	OB5184.raw	3.09E4	1	1	304	342	Oxidation (M)
K.LDNLQQEIDFLTALYQAELSQMQTQISETNVILSMDNNR.S	Y	99.0	33.02	4526.1943	39	2.8	1132.5591	4	46.10	14	2387	OB5184.raw	6.45E4	1	1	304	342	
R.SLVNLGGSK.S	Y	98.4	32.32	873.4919	9	-0.1	437.7532	2	29.52	14	1422	OB5184.raw	1.42E4	1	1	65	73	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSMDNNR.S	Y	97.4	28.45	4542.1895	39	1.4	1515.0725	3	44.09	14	2269	OB5184.raw	6.19E4	2	2	304	342	Oxidation (M)
R.NKYEDEINKR.T	Y	96.8	27.99	1307.6470	10	0.4	436.8898	3	25.22	14	1171	OB5184.raw	3.77E3	1	1	267	276	
total 13 peptides																		

B5TYU1|B5TYU1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLELSFC FCFLVLGASS ISFR**QQPEEN ACQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**YQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGNGIEET ICTATVKKNI GR**NRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY**
401 **RNALFVPHYN TNAHSIIYAL R**GRAHVQVVD SNGNR**VYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL**
481 **AGENSVIDNL PEEVVANSYG LPR**EQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	88.82	1540.7673	13	0.5	771.3913	2	36.42	14	1825	OB5184.raw	2.01E5	4	4	389	401	
R.QQPEENAC(+57.02)QFQR.L	N	99.9	62.89	1533.6630	12	0.9	767.8395	2	27.22	14	1287	OB5184.raw	2.25E3	1	1	25	36	Carbamidomethylation
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	61.19	2313.2019	20	-0.5	772.0742	3	34.63	14	1722	OB5184.raw	7.4E4	1	1	402	421	
K.SQSDNFEYVAFK.T	N	99.9	57.07	1433.6462	12	0.2	717.8306	2	33.84	14	1676	OB5184.raw	4.53E3	1	1	459	470	
K.TANELNLLILR.W	N	99.9	51.37	1268.7452	11	-0.1	635.3798	2	36.61	14	1836	OB5184.raw	7.55E4	3	3	378	388	
R.SPDIYNPQAGSLK.T	N	99.9	46.87	1388.6936	13	0.5	695.3544	2	30.72	14	1491	OB5184.raw	1.39E4	1	1	365	377	
R.RPFYSNAPQEIFIQQGR.G	N	99.5	37.05	2050.0383	17	0.3	684.3536	3	33.50	14	1655	OB5184.raw	1.97E4	1	1	82	98	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.0	34.38	2540.2910	23	1.1	847.7719	3	35.04	14	1745	OB5184.raw	9.65E3	1	1	436	458	
R.VYDEELQEGHVL.V	N	99.0	34.29	1429.6725	12	1.9	715.8448	2	33.00	14	1625	OB5184.raw	3.92E3	1	1	436	447	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.Y	N	99.0	33.73	2629.2383	23	-1.2	877.4190	3	36.51	14	1830	OB5184.raw	1.04E4	1	1	99	121	Carbamidomethylation
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	98.3	30.32	3496.7434	33	-2.5	1166.5854	3	38.28	14	1933	OB5184.raw	1.42E4	1	1	471	503	
R.NRSPDIYNPQAGSLK.T	N	96.6	27.62	1658.8376	15	-0.6	553.9528	3	28.93	14	1387	OB5184.raw	1.58E4	1	1	363	377	
total 12 peptides																		

sp|K1C9_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCRQFSSSY LSR**SGGGGGG GLGSGGSIR**S SYSRFSSSGG RGGGGR**FSSS SGYGGGSSR**V CGRGGGGSFG YSYGGGSGGG
81 FSASSLGGGF GGGSRGFGGA SGGGYSSSGG FGGGFGGGSG GGFGGGYGSG FGGLGGFGGG AGGGDGGILT ANEK**STMQEL**
161 **NSR**LASYLDK VQALEEANND LENKIQDWYD KKGPAAIQK**N YSPYYNTIDD LKDQIVDLTV GNNKTLLDID NTR**MTLDDFR
241 IKFEMEQNLR QGVDADINGL RQVLDNLTME KSDLEMQYET LQEELMALKK NHKEEMSQLT GQNSGDVNVE INVAPGKDLT
321 KTLNDMRQEY EQLIAKNRKD IENQYETQIT QIEHEVSSSG QEVQSSAKEV TQLR**HGVQEL EIELQSQLSK K**AALEKSLED
401 TKNRYCGQLQ MIQEQISNLE AQITDVRQEI ECQNQEYSLL LSIKMRLEKE IETYHNLLEG GQEDFESSGA GKIGLGGRGG
481 SGGSYGRGSR GGSGGSYGGG GSGGGYGGGS GSRGGSGGSY GGGSGSGGGS GGGYGGGSGG GHSGGSGGGH SGGSGGNYGG
561 GSGSGGGSGG GYGGGSGSRG GSGGSHGGGS GFGGESGGSY GGGEEASGSG GGYGGGSGKS SHS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.SGGGGGGGLGSGGSIR.S	Y	99.9	76.68	1231.5905	16	0.1	616.8026	2	25.51	14	1188	OB5184.raw	4.75E3	2	2	14	29	
R.HGVQELEIELQSQLSKK.A	Y	99.9	61.21	1965.0531	17	-2.0	656.0237	3	34.27	14	1701	OB5184.raw	3.11E4	2	2	375	391	
K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	Y	99.9	56.47	2901.4031	25	-0.6	968.1411	3	38.93	14	1971	OB5184.raw	1.13E5	2	2	200	224	
K.STMQELNSR.L	Y	99.9	48.41	1064.4921	9	0.9	533.2538	2	26.24	14	1230	OB5184.raw	3.58E3	2	2	155	163	
K.TLLDIDNTR.M	Y	99.8	40.58	1059.5560	9	0.1	530.7853	2	32.19	14	1576	OB5184.raw	8.36E3	1	1	225	233	
R.FSSSSGYGGGSSR.V	Y	99.7	38.34	1234.5214	13	0.1	618.2680	2	24.84	14	1149	OB5184.raw	3.49E3	1	1	47	59	
total 6 peptides																		

sp|K22E_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCQISCKSR GRGGGGGGFR GFSSGSAVVS GGSRRSTSSF SCLSRHGGGG GGFGGGGFGS RSLVGLGGTK SISISVAGGG

81 GGFGAAGGFG GRGGGFGGGS GFGGGSGFGG GSGFSGGGFG GGGFGGGR**FG GFGGPGGVGG LGGPGGFGPG GYPGGIHEVS**

161 **VNQSLLQPLN VK**VDPEIQNV KAQEREQIKT LNNKFASFID KVR**FLEQQNQ VLQTK**WELLQ QMNVGTRPIN LEPIFQGYID

241 SLKRYLDGLT AER**TSQNSEL NNMQDLVEDY KK**KYEDEINK RTAAENDFVT LKKDVDNAYM IKVELQSKVD LLNQEIEFLK

321 **VLYDAEISQI HQSVTDTNVI LSMDNSRNLD LDSIIAEVKA QYEEIAQR**SK EEAEALYHSK YEELQVTVGR HGDSLKEIKI

401 EISELNRVIQ RLQGEIAHVK KQCKNVQDAI ADAEQRGEHA LKDAR**NKLND LEEALQQAKE DLAR**LLRDYQ ELMNVKLALD

481 VEIATYRKLL EGEECRMSGD LSSNVTVSVT SSTISSNVAS KAAFGGSGGR GSSSGGGYSS GSSSYGSGGR QSGSRGGSGG

561 GGSISGGGYG SGGGSGGRYG SGGGSKGGSI SGGGYGSGGG KHSSGGGSRG GSSSGGGYGS GGGGSSSVKG SSGEAFGSSV

641 TFSFR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.FLEQQNQVLQTK.W	N	99.9	61.41	1474.7780	12	0.2	738.3964	2	30.67	14	1488	OB5184.raw	1.85E4	1	1	204	215	
R.NLDLDSIIAEVKAQYEEIAQR.S	Y	99.9	59.41	2417.2437	21	1.2	806.7561	3	41.37	14	2113	OB5184.raw	1.49E5	2	2	348	368	
R.NKLNDLEEALQQAKEDLAR.L	Y	99.9	54.59	2197.1338	19	0.1	733.3853	3	36.89	14	1852	OB5184.raw	5.95E4	2	2	446	464	
K.VLYDAEISQIHQSVTDTNVILSMDNSR.N	Y	99.9	49.13	3047.4871	27	1.8	1016.8381	3	36.71	14	1842	OB5184.raw	7.25E3	1	1	321	347	
K.AQYEEIAQR.S	Y	99.9	43.05	1106.5356	9	-0.5	554.2748	2	27.49	14	1303	OB5184.raw	1.07E3	1	1	360	368	
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	Y	98.4	31.69	4091.0652	44	-0.4	1023.7732	4	38.08	14	1921	OB5184.raw	4.49E3	1	1	129	172	
R.TSQNSELNNMQDLVEDYKK.K	Y	97.3	28.18	2255.0376	19	1.8	752.6878	3	34.05	14	1688	OB5184.raw	0	1	1	254	272	
total 7 peptides																		

sp|TRYP_PIG|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FPTDDDDKIV GGYTCAANSI PYQVSLNSGS HFCGGSLINS QWVVSAAHCY KSRIQVRLGE HNIDVLEGNE QFINAAKIIT

81 HPNFNGNTLD NDIMLIKLSS PATLNSR**VAT VSLPR**SCAAA GTECLISGWG NTKSSGSSYP SLLQCLKAPV LSDSSCKSSY

161 PGQITGNMIC VGFLEGGKDS CQGDSGGPVV CNGQLQGIVS WGYGCAQKNK PGVYTKVCNY VNWIQQTIAA N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
R.VATVSLPR.S	Y	99.8	42.64	841.5021	8	-0.1	421.7583	2	29.46	14	1419	OB5184.raw	1.81E5	5	5	108	115	
total 1 peptides																		

Q38711|Q38711_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KPFCVFLTFF LLLAASKKVN SAETVSFNFN SFSEGNPAIN FQGDVTVLSN GNIQLTNLNK VNSVGRVLYA MPVRIWSSAT
81 GNVASFLTSF SFEMKDIKDY D**PADGIIFFI APEDTQIPAG SIGGGTLGVS DTK**GAGHFVG VEFDTYSNSE YNDPPTDHVG
161 IDVNSVDSVK TVPWNSVSGA VVQVTVIYDS STKTLSVAVT NENGDITTIA QVVDLKAKLP ERVKFGFSAS GSLGGRQIHL
241 IR**SWSFTSTL ITTTR**RSIDN NEKKIMNMAT A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
D.PADGIIFFIAPEDTQIPAGSIGGGTLGVSDTK.G	Y	98.3	29.68	3143.6025	32	0.1	1048.8749	3	39.69	14	2015	OB5184.raw	1.19E4	1	1	102	133	
R.SWSFTSTLITTTR.R	Y	97.4	28.24	1499.7620	13	0.0	750.8882	2	36.37	14	1822	OB5184.raw	0	1	1	243	255	
total 2 peptides																		

sp|P02872|LECG_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKPFCVFLTF FLLLAASSKK VDSAETVSFN FNSFSEGNPA INFQGDVTVL SNGNIQLTNL NKVNSVGRVL YAMPVRIWSS
81 ATGNVASFLT SFSFEMKDIK DYD**PADGIIF FIAPEDTQIP AGSIGGGTLG VSDTK**GAGHF VGVEFDTYSN SEYNDPPTDH
161 VGIDVNSVDS VKTVPWNSVS GAVVKVTVIY DSSTKTLSVA VTNDNGDITT IAQVVDLKAK LPERVKFGFS ASGSLGGRQI
241 HLIR**SWSFTS TLITTTR**RSI DNNEKKIMNM ASA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
D.PADGIIFFIAPEDTQIPAGSIGGGTLGVSDTK.G	Y	98.3	29.68	3143.6025	32	0.1	1048.8749	3	39.69	14	2015	OB5184.raw	1.19E4	1	1	104	135	
R.SWSFTSTLITTTR.R	Y	97.4	28.24	1499.7620	13	0.0	750.8882	2	36.37	14	1822	OB5184.raw	0	1	1	245	257	
total 2 peptides																		

A0A089ZXL7|A0A089ZXL7_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKPFCVFLTF FLLLAASSKK VNSAETVSFN FNSFSEGNPA INFQGDVTVL SNGNIQLTNL NKVNSVGRVL YAMPVRIWSS
81 ATGNVASFLT SFSFEMKDIK DYD**PADGIIF FIAPEDTQIP AGSIGGGTLG VSDTK**GAGYF VGVEFDTYSN SEYNDPPTDH
161 VGIDVNSVDS VKTVPWNSVS GAVVKVTVIY DSSTKTLSVA VTNDNGDITT IAQVVDLKAK LPERVKFGFS ASGSRAGRQI
241 HLIR**SWSFTS TLITTTR**RSI DNNEKKIMNM ASA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS1 tacka 16 na Figuri 1	#Spec	#Spec DS1 tacka 16 na Figuri 1	Start	End	PTM
D.PADGIIFFIAPEDTQIPAGSIGGGTLGVSDTK.G	Y	98.3	29.68	3143.6025	32	0.1	1048.8749	3	39.69	14	2015	OB5184.raw	1.19E4	1	1	104	135	
R.SWSFTSTLITTTR.R	Y	97.4	28.24	1499.7620	13	0.0	750.8882	2	36.37	14	1822	OB5184.raw	0	1	1	245	257	
total 2 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

1. Notes

Spot 17 from 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

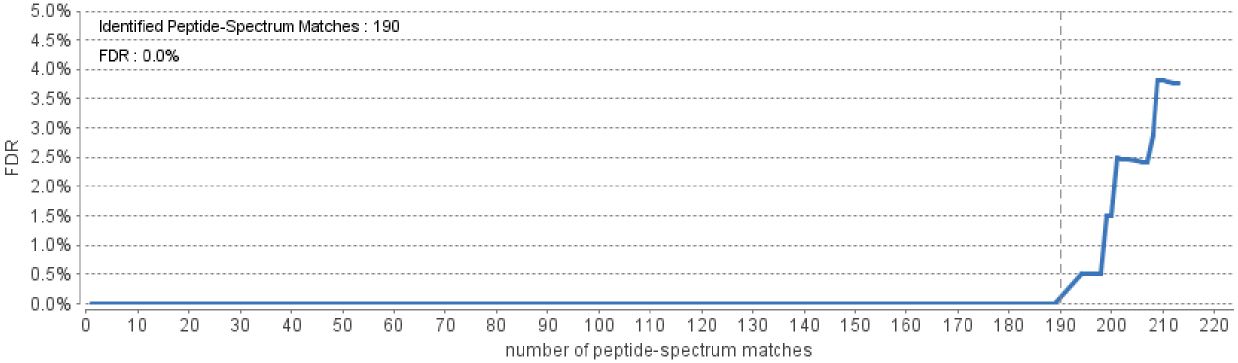


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

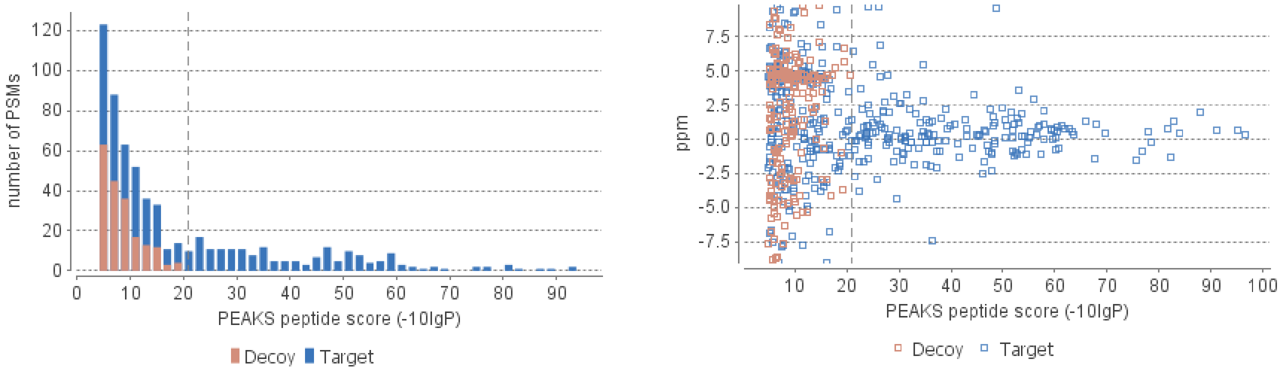


Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

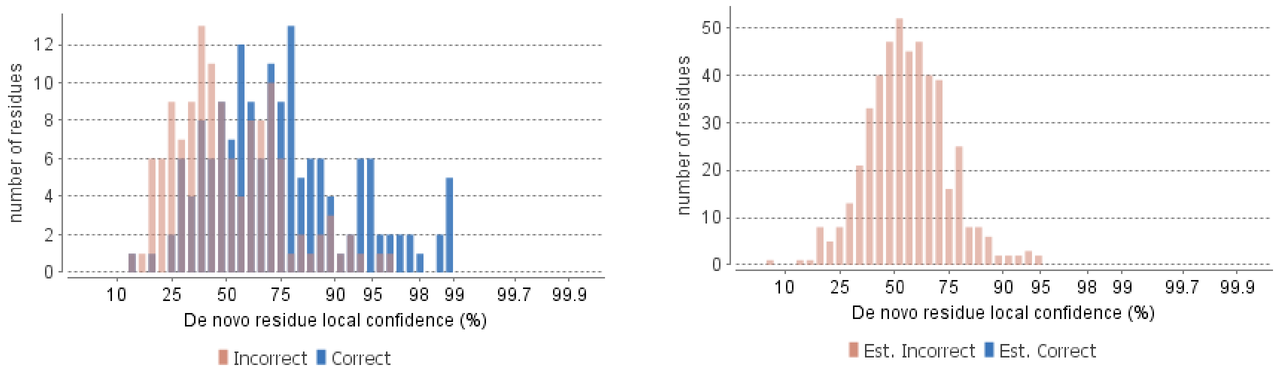


Table 1. Statistics of data.

# of MS scans	2513
# of MS/MS scans	1653

Table 2. Result filtration parameters.

Peptide -10lgP	≥21
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	183
Peptide sequences	63
Protein groups	10
Proteins	14
Proteins (#Unique Peptides)	9 (>2); 0 (=2); 5 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	77

Table 4. PTM profile.

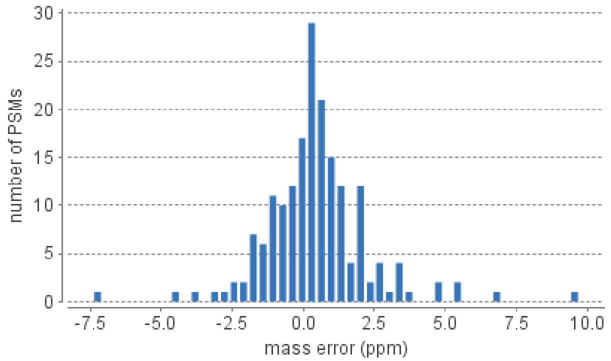
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	40	95.05	1.73E4	1000.00
Oxidation	15.99	M	22	67.58	3.44E3	54.40
Deamidation	.98	NQ	4	55.83		39.44
HydPro	15.99	P	3	67.58	3.44E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



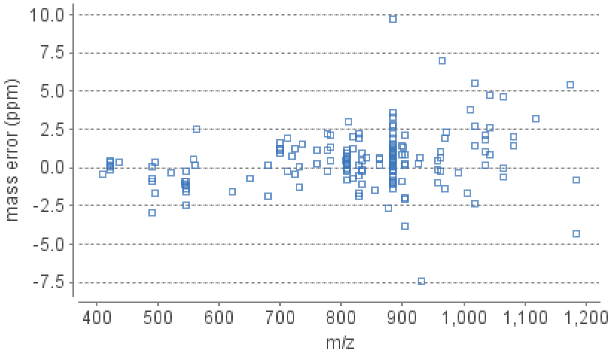


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
DS2 tacka 17 na Figuri 1	36	22	5	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: Uniprot_Peanut(3818)+cRAP_aug17
Taxon: All
Searched Entry: 1352
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB5186.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) DS2 tacka 17 na Figuri 1	Area DS2 tacka 17 na Figuri 1	#Peptides	#Unique	#Spec DS2 tacka 17 na Figuri 1	PTM	Avg. Mass	Description
1	216	Q6IWG5|Q6IWG5_ARAHY	99.1	250.00	27	27	1.76E6	19	19	100	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
1	217	Q0GM57|Q0GM57_ARAHY	99.1	250.00	27	27	1.76E6	19	19	100	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
2	215	sp|Q6PSU2|CONG7_ARAHY	99.1	193.67	50	50	3.02E5	9	9	34	Y	20114	Conglutin-7 OS=Arachis hypogaea PE=1 SV=2
3	220	sp|K1C10_HUMAN|	98.6	152.78	13	13	6.03E4	5	5	15	Y	59519	sp|K1C10_HUMAN|
4	1193	sp|TRYP_PIG|	98.5	130.24	16	16	1.84E5	6	6	13	N	24409	sp|TRYP_PIG|
6	219	sp|Q647H2|AHY3_ARAHY	98.5	127.14	10	10	1.74E4	3	3	7	Y	54569	Arachin Ahy-3 OS=Arachis hypogaea PE=1 SV=1
5	84	A1DZF0|A1DZF0_ARAHY	98.9	83.58	20	20	1.75E4	5	3	8	Y	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
5	87	Q647H4|Q647H4_ARAHY	98.9	83.58	20	20	1.75E4	5	3	8	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
9	221	sp|K2C1_HUMAN|	92.8	79.71	5	5	1.6E4	3	3	3	N	65886	sp|K2C1_HUMAN|
8	89	Q647H3|Q647H3_ARAHY	97.6	79.08	12	12	5.83E3	3	1	4	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
8	83	Q9FZ11|Q9FZ11_ARAHY	97.2	79.08	12	12	5.83E3	3	1	4	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
8	86	Q5I6T2|Q5I6T2_ARAHY	97.2	79.08	12	12	5.83E3	3	1	4	Y	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
13	646	sp|K1C9_HUMAN|	92.9	44.62	5	5	1.32E3	1	1	1	N	62129	sp|K1C9_HUMAN|
14	964	sp|K22E_HUMAN|	84.4	34.77	3	3	3.19E4	1	1	1	N	65865	sp|K22E_HUMAN|
total 14 proteins													

Q6IWG5|Q6IWG5_ARAHY

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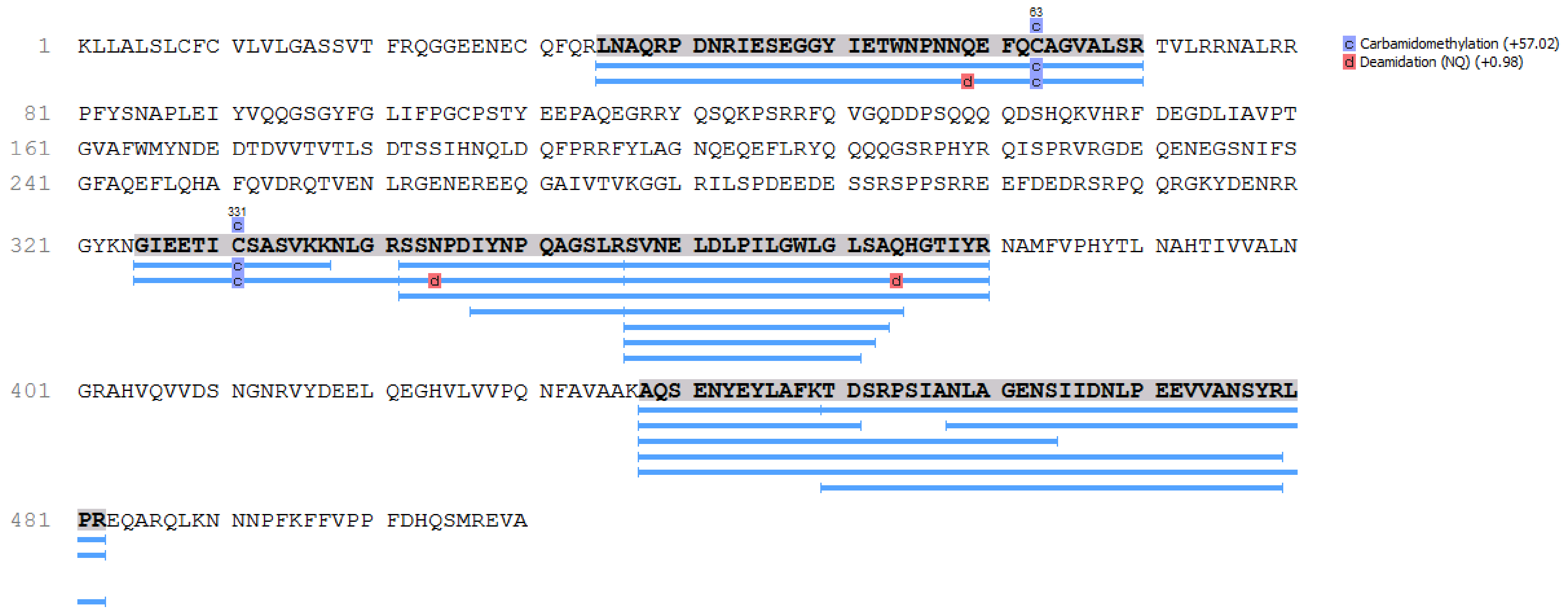
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQR**LNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR** TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKN**GIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR** NAMFVPHYTL NAHTIVVALN

401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL**

481 **PR**EQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	Y	99.9	96.69	1617.7747	15	0.3	809.8948	2	30.46	16	1425	OB5186.raw	2.64E5	16	16	342	356	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	87.87	3243.6006	30	2.0	1082.2096	3	37.53	16	1838	OB5186.raw	1.84E4	2	2	450	479	
K.AQSENYEYLAFK.T	Y	99.9	82.34	1461.6776	12	-1.3	731.8452	2	33.19	16	1587	OB5186.raw	2.08E4	2	2	438	449	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	65.84	2651.4070	24	1.3	884.8107	3	41.75	16	2084	OB5186.raw	8.88E5	46	46	357	380	
R.SVNELDLPILGWLGLSA.Q	Y	99.9	62.83	1795.9719	17	0.8	898.9940	2	45.88	16	2328	OB5186.raw	2E4	3	3	357	373	
K.AQSENYEYLAFKTD.S	Y	99.9	59.77	1677.7522	14	0.6	839.8839	2	33.74	16	1619	OB5186.raw	2.74E3	1	1	438	451	
R.SVNELDLPILGWLGLSAQ.H	Y	99.9	59.41	1924.0305	18	0.6	963.0231	2	45.44	16	2302	OB5186.raw	3.67E3	1	1	357	374	
R.SSN(+.98)PDIYNPQAGSLR.S	Y	99.9	55.83	1618.7587	15	3.0	810.3890	2	31.20	16	1467	OB5186.raw	0	1	1	342	356	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.5	42.95	3609.8386	33	0.2	903.4671	4	37.78	16	1852	OB5186.raw	1.38E5	7	7	450	482	
K.AQSENYEYLAFKTDSRPSIANLAGENS.I	Y	99.1	41.30	2974.3943	27	-0.4	992.4717	3	34.42	16	1658	OB5186.raw	0	1	1	438	464	
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.0	34.80	4687.2676	42	5.5	1172.8306	4	37.62	16	1843	OB5186.raw	2.14E4	1	1	438	479	
R.SVNELDLPILGWLGLS.A	Y	98.1	34.34	1724.9348	16	0.2	863.4749	2	46.04	16	2338	OB5186.raw	5.44E3	1	1	357	372	
N.GIEETIC(+57.02)SASVKK.N	Y	97.4	33.15	1420.7231	13	1.9	711.3702	2	29.31	16	1358	OB5186.raw	7.61E3	2	2	325	337	Carbamidomethylation
R.SSNPDIYNPQAGSLRSVNELDLPILGWLGLSAQHGTIYR.N	Y	97.3	31.86	4251.1714	39	-0.6	1063.7994	4	39.84	16	1973	OB5186.raw	7.91E4	4	4	342	380	
A.NLAGENSIIDNLPEEVVANSYRLPR.E	Y	94.4	29.49	2782.4248	25	0.6	928.4828	3	37.44	16	1833	OB5186.raw	2.64E4	1	1	458	482	
R.SVNELDLPILGWLGL.S	Y	94.0	28.22	1637.9028	15	2.0	819.9603	2	46.91	16	2392	OB5186.raw	2.87E4	3	3	357	371	
R.LNAQRPDNRIESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	93.3	26.97	4132.9409	36	2.1	1034.2446	4	34.31	16	1651	OB5186.raw	0	3	3	35	70	Carbamidomethylation
R.SVNELDLPILGWLGLSAQ(+.98)HGTIYR.N	Y	91.1	26.07	2652.3911	24	9.7	885.1462	3	44.67	16	2255	OB5186.raw	0	1	1	357	380	Deamidation (NQ)
D.IYNPQAGSLR.S	Y	90.9	25.58	1117.5880	10	0.5	559.8016	2	28.41	16	1307	OB5186.raw	1.21E3	1	1	347	356	
R.LNAQRPDNRIESEGGYIETWNPNNQ(+.98)EFQC(+57.02)AGVALSR.T	Y	90.2	23.87	4133.9248	36	1.0	1034.4895	4	34.65	16	1671	OB5186.raw	1.49E4	1	1	35	70	Deamidation (NQ); Carbamidomethylation
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	82.8	22.73	5053.5054	45	3.8	1011.7122	5	38.50	16	1894	OB5186.raw	1.98E5	1	1	438	482	
N.GIEETIC(+57.02)SASVKKNLGR.S	Y	82.3	22.41	1860.9727	17	-1.6	621.3305	3	30.25	16	1413	OB5186.raw	1.97E4	1	1	325	341	Carbamidomethylation
total 22 peptides																		

Q0GM57|Q0GM57_ARAHY

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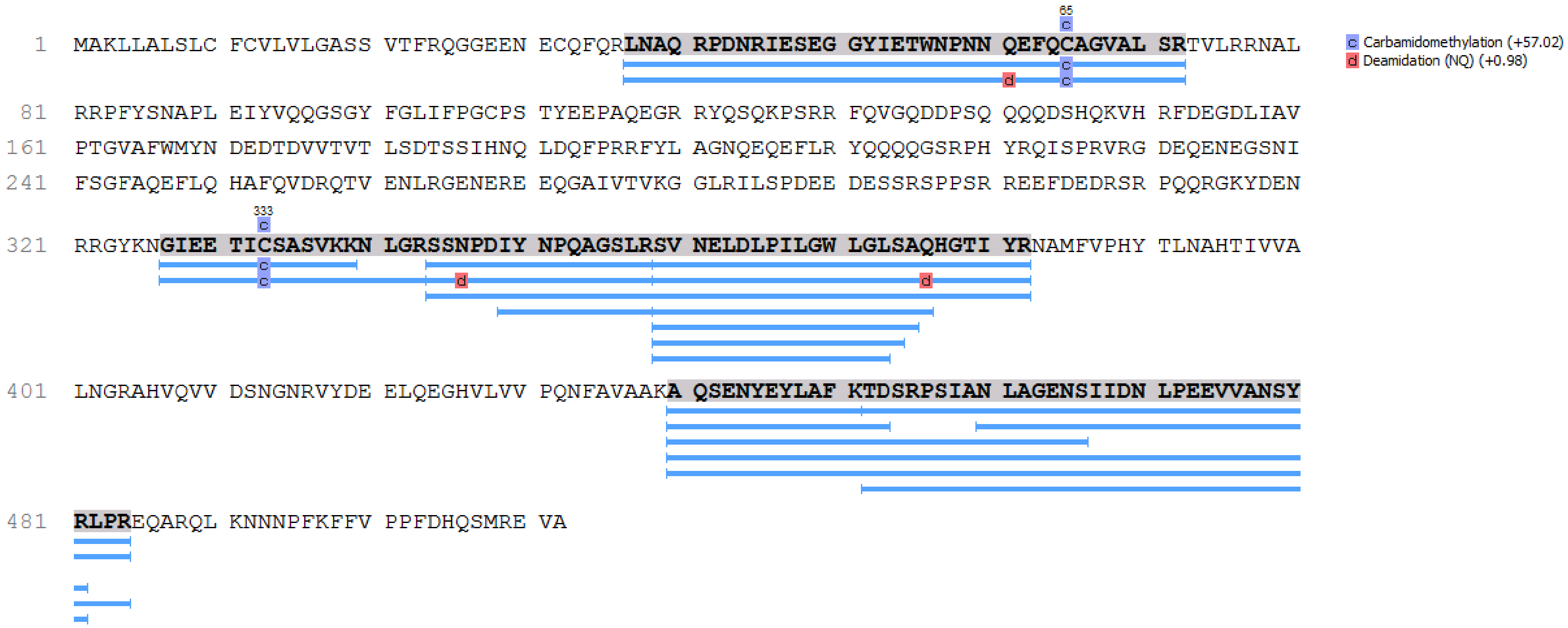
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.SSNPDIYNPQAGSLR.S	Y	99.9	96.69	1617.7747	15	0.3	809.8948	2	30.46	16	1425	OB5186.raw	2.64E5	16	16	344	358	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	87.87	3243.6006	30	2.0	1082.2096	3	37.53	16	1838	OB5186.raw	1.84E4	2	2	452	481	
K.AQSENYEYLAFK.T	Y	99.9	82.34	1461.6776	12	-1.3	731.8452	2	33.19	16	1587	OB5186.raw	2.08E4	2	2	440	451	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	65.84	2651.4070	24	1.3	884.8107	3	41.75	16	2084	OB5186.raw	8.88E5	46	46	359	382	
R.SVNELDLPILGWLGLSA.Q	Y	99.9	62.83	1795.9719	17	0.8	898.9940	2	45.88	16	2328	OB5186.raw	2E4	3	3	359	375	
K.AQSENYEYLAFKTD.S	Y	99.9	59.77	1677.7522	14	0.6	839.8839	2	33.74	16	1619	OB5186.raw	2.74E3	1	1	440	453	
R.SVNELDLPILGWLGLSAQ.H	Y	99.9	59.41	1924.0305	18	0.6	963.0231	2	45.44	16	2302	OB5186.raw	3.67E3	1	1	359	376	
R.SSN(+.98)PDIYNPQAGSLR.S	Y	99.9	55.83	1618.7587	15	3.0	810.3890	2	31.20	16	1467	OB5186.raw	0	1	1	344	358	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.5	42.95	3609.8386	33	0.2	903.4671	4	37.78	16	1852	OB5186.raw	1.38E5	7	7	452	484	
K.AQSENYEYLAFKTDSRPSIANLAGENS.I	Y	99.1	41.30	2974.3943	27	-0.4	992.4717	3	34.42	16	1658	OB5186.raw	0	1	1	440	466	
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.0	34.80	4687.2676	42	5.5	1172.8306	4	37.62	16	1843	OB5186.raw	2.14E4	1	1	440	481	
R.SVNELDLPILGWLGLS.A	Y	98.1	34.34	1724.9348	16	0.2	863.4749	2	46.04	16	2338	OB5186.raw	5.44E3	1	1	359	374	
N.GIEETIC(+57.02)SASVKK.N	Y	97.4	33.15	1420.7231	13	1.9	711.3702	2	29.31	16	1358	OB5186.raw	7.61E3	2	2	327	339	Carbamidomethylation
R.SSNPDIYNPQAGSLRSVNELDLPILGWLGLSAQHGTIYR.N	Y	97.3	31.86	4251.1714	39	-0.6	1063.7994	4	39.84	16	1973	OB5186.raw	7.91E4	4	4	344	382	
A.NLAGENSIIDNLPEEVVANSYRLPR.E	Y	94.4	29.49	2782.4248	25	0.6	928.4828	3	37.44	16	1833	OB5186.raw	2.64E4	1	1	460	484	
R.SVNELDLPILGWLGL.S	Y	94.0	28.22	1637.9028	15	2.0	819.9603	2	46.91	16	2392	OB5186.raw	2.87E4	3	3	359	373	
R.LNAQRPDNRIESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	93.3	26.97	4132.9409	36	2.1	1034.2446	4	34.31	16	1651	OB5186.raw	0	3	3	37	72	Carbamidomethylation
R.SVNELDLPILGWLGLSAQ(+.98)HGTIYR.N	Y	91.1	26.07	2652.3911	24	9.7	885.1462	3	44.67	16	2255	OB5186.raw	0	1	1	359	382	Deamidation (NQ)
D.IYNPQAGSLR.S	Y	90.9	25.58	1117.5880	10	0.5	559.8016	2	28.41	16	1307	OB5186.raw	1.21E3	1	1	349	358	
R.LNAQRPDNRIESEGGYIETWNPNNQ(+.98)EFQC(+57.02)AGVALSR.T	Y	90.2	23.87	4133.9248	36	1.0	1034.4895	4	34.65	16	1671	OB5186.raw	1.49E4	1	1	37	72	Deamidation (NQ); Carbamidomethylation
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	82.8	22.73	5053.5054	45	3.8	1011.7122	5	38.50	16	1894	OB5186.raw	1.98E5	1	1	440	484	
N.GIEETIC(+57.02)SASVKKNLGR.S	Y	82.3	22.41	1860.9727	17	-1.6	621.3305	3	30.25	16	1413	OB5186.raw	1.97E4	1	1	327	343	Carbamidomethylation

total 22 peptides

sp|Q6PSU2|CONG7_ARAHY

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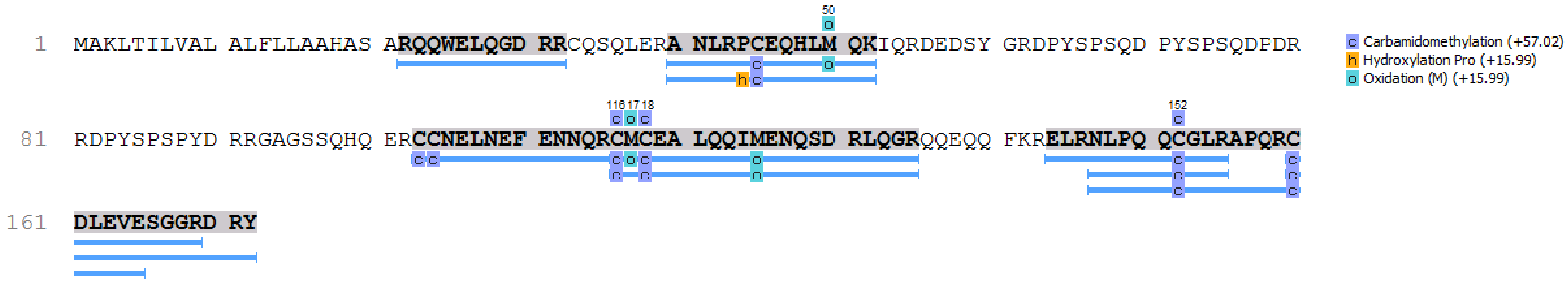
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.C(+57.02)C(+57.02)NELNEFENNQR.C	Y	99.9	95.05	1725.6835	13	0.6	863.8495	2	30.66	16	1436	OB5186.raw	1.73E4	2	2	103	115	Carbamidomethylation
R.NLPQQC(+57.02)GLR.A	Y	99.9	57.17	1084.5448	9	-1.1	543.2791	2	26.88	16	1222	OB5186.raw	1.73E4	2	2	147	155	Carbamidomethylation
R.ANLRPC(+57.02)EQHLM(+15.99)QK.I	Y	99.9	52.09	1639.7922	13	-1.3	547.6040	3	24.28	16	1093	OB5186.raw	3.32E4	6	6	40	52	Carbamidomethylation; Oxidation (M)
R.C(+57.02)MC(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.9	51.46	2482.0820	20	2.0	828.3696	3	32.71	16	1558	OB5186.raw	1.15E4	6	6	116	135	Carbamidomethylation; Oxidation (M)
R.C(+57.02)DLEVESGGRDRY	Y	99.9	48.29	1554.6732	13	1.2	778.3448	2	28.11	16	1290	OB5186.raw	1.1E4	3	3	160	172	Carbamidomethylation
R.C(+57.02)DLEVESGGR.D	Y	99.8	45.39	1120.4818	10	0.2	561.2483	2	26.80	16	1217	OB5186.raw	2.76E3	1	1	160	169	Carbamidomethylation
R.NLPQQC(+57.02)GLRAPQRC(+57.02)DLEVE.S	Y	99.1	40.70	2282.0896	19	1.1	761.7047	3	30.81	16	1445	OB5186.raw	6.49E4	2	2	147	165	Carbamidomethylation
R.C(+57.02)M(+15.99)C(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.0	39.80	2498.0771	20	0.9	833.7004	3	31.17	16	1465	OB5186.raw	6.59E4	5	5	116	135	Carbamidomethylation; Oxidation (M)
R.ELRNLPQQC(+57.02)GLR.A	Y	99.0	36.65	1482.7725	12	0.3	495.2649	3	28.34	16	1303	OB5186.raw	3.54E3	2	2	144	155	Carbamidomethylation
A.RQQWELQGDRR.C	Y	97.4	33.85	1470.7440	11	-0.7	491.2549	3	26.44	16	1200	OB5186.raw	4.5E4	4	4	22	32	
R.ANLRP(+15.99)C(+57.02)EQHLMQK.I	Y	90.3	24.02	1639.7922	13	-0.5	410.9551	4	24.74	16	1119	OB5186.raw	2.94E4	1	1	40	52	Hydroxylation Pro; Carbamidomethylation

total 11 peptides

sp|K1C10_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)
o Oxidation (M) (+15.99)

1 MSVRYSSSKH YSSSRSGGGG GGGGCGGGGG VSSLR**ISSSK GSLGGGFSSG GFSGGSFSR**G SSGGGCFGGS SGGYGGLGGF
81 GGGSFHGSYG SSSFGGSYGG SFGGGNFGGG SFGGGSFGGG GFGGGGFGGG FGGGFGGDGG LLSGNEKVTM QNLNDRLASY
161 LDKVRALEES NYELEGKIKE WYEKHGNSHQ GEPRDYSKYY K**TIDDLKNQI LNLTTDNANI LLQIDNAR**LA ADDFRLKYEN
241 EVALRQSVEA DINGLRRVLD ELTLTKADLE MQIESLTEEL AYLKKNHEEE MKDLR**NVSTG DVNVEMNAAP GVDLTQLLNN**
321 **MR**SQYEQLAE QNRKDAEAWF NEKSKELTTE IDNNIEQISS YKSEITELRR NVQALEIELQ SQLALKQSLE ASLAETEGRY
401 CVQLSQIQAQ ISALEEQLQQ IRAETECQNT EYQQLLDIKI RLENEIQTYR SLLEGEGSSG GGGRGGGSFG GGYGGGSSGG
481 GSSGGGYGGG HGGSSGGGYG GGSSGGGSSG GGYGGGSSSG GHGGGSSSGG HGGSSSGGYG GGSSGGGGGG YGGGSSGGGS
561 SSGGGYGGGS SSGGHKSSSS GSVGESSSKG PRY

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.GSLGGGFSSGGFSGGSFSR.G	Y	99.9	75.74	1706.7648	19	-1.5	854.3884	2	33.34	16	1596	OB5186.raw	1.61E3	1	1	41	59	
R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S	Y	99.9	69.59	2871.3855	27	0.4	958.1362	3	39.22	16	1936	OB5186.raw	1.73E4	3	3	296	322	
R.NVSTGDVNVEMNAAP(+15.99)GVDLTQLLNNM(+15.99)R.S	Y	99.9	67.58	2903.3752	27	-1.4	968.7977	3	36.46	16	1776	OB5186.raw	3.44E3	1	1	296	322	Hydroxylation Pro; Oxidation (M)
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNMR.S	Y	99.9	61.27	2887.3804	27	1.0	963.4684	3	38.43	16	1890	OB5186.raw	8.17E3	1	1	296	322	Oxidation (M)
R.ISSSKGSLGGGFSSGGFSGGSFSR.G	Y	99.9	52.82	2209.0398	24	1.5	737.3550	3	31.89	16	1506	OB5186.raw	2.09E3	1	1	36	59	
I.SSSKGSLGGGFSSGGFSGGSFSR.G	Y	99.9	48.01	2095.9558	23	1.6	699.6603	3	31.49	16	1483	OB5186.raw	3.5E3	1	1	37	59	
K.TIDDLKNQILNLTTDNANILLQIDNAR.L	Y	99.9	47.94	3051.6201	27	-2.3	1018.2116	3	40.15	16	1991	OB5186.raw	1.21E4	4	4	202	228	
R.NVSTGDVNVEMNAAP(+15.99)GVDLTQLLNNMR.S	Y	99.0	36.47	2887.3804	27	-0.2	963.4672	3	38.52	16	1895	OB5186.raw	8.17E3	1	1	296	322	Hydroxylation Pro
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNM(+15.99)R.S	Y	93.3	27.09	2903.3752	27	1.9	968.8009	3	36.61	16	1785	OB5186.raw	3.44E3	1	1	296	322	Oxidation (M)
R.NVSTGDVNVEM(+15.99)N(+.98)AAPGVDLTQLLNNMR.S	Y	92.9	26.39	2888.3645	27	6.9	963.8021	3	38.62	16	1901	OB5186.raw	4.31E2	1	1	296	322	Oxidation (M); Deamidation (NQ)
total 10 peptides																		

sp|TRYP_PIG|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FPTDDDDKIV GGYTCAANSI PYQVSLNSGS HFCGGSLINS QWVVSAAHCY KSRIQVR**LGE HNIDVLEGNE QFINAA**KIIT
81 HPNFNGNTLD NDIMLIK**LSS PATLNSRVAT VSLPR**SCAAA GTECLISGWG NTKSSGSSYP SLLQCLKAPV LSDSSCKSSY
161 PGQITGNMIC VGFLEGGKDS CQGDSGGPVV CNGQLQGIVS WGYGCAQKNK PGVYTKVCNY VNWIQQTIAA N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.LGEHNIDVLEGNEQFINAA.K	Y	99.9	60.36	2082.0017	19	0.9	1042.0090	2	35.35	16	1712	OB5186.raw	4.05E3	3	3	58	76	
R.VATVSLPR.S	Y	99.9	50.67	841.5021	8	0.1	421.7584	2	29.46	16	1367	OB5186.raw	1.43E5	6	6	108	115	
R.LGEHNIDVLEGNEQFIN.A	Y	99.9	49.86	1939.9275	17	2.3	970.9733	2	34.88	16	1685	OB5186.raw	1.21E4	1	1	58	74	
K.LSSPATLNSR.V	Y	99.9	48.35	1044.5564	10	-0.4	523.2853	2	27.08	16	1234	OB5186.raw	1.74E4	1	1	98	107	
R.LGEHNIDVLEGNEQFINA.A	Y	99.8	46.44	2010.9646	18	-1.7	1006.4879	2	35.32	16	1710	OB5186.raw	4.36E2	1	1	58	75	
R.LGEHNIDVLEGNE.Q	Y	99.0	39.24	1437.6736	13	0.7	719.8446	2	32.15	16	1522	OB5186.raw	7.67E3	1	1	58	70	
total 6 peptides																		

sp|Q647H2|AHY3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS VTFRQQGEEN ECQFQRLNAQ RPDNCIESEG GYIETWNPNN QEFQCAGVAL SRFVLRRNAL
81 RRPFYSNAPQ EIFIYQGSGY FGLIFPGCPG TFEEPIQGSE QFQRPSRHFQ GQDQSQRPLD THQKVHGFRE GDLIAVPHGV
161 AFWIYNDQDT DVVAISVLHT NSLHNQLDQF PRRFNLAGKQ EQEFLRYQQR SGRQSPKGEE QEQEQENEGG NVFSGFSTEF
241 LSHGFQVNED IVRNLRGENE REEQGAIVTV KGGLSILVPP EWRQSYQQPG RGDKDFNNGI EETICTATVK MNIGK**STSAD**
321 **IYNPQAGSVR TVNELDLPIL NR**LGLSAEYG SIHRDAMFVP HYNMNANSMI YALHGGAHVQ VVDCNGNRVF DEELQEGQSL
401 VVPQNFAVAA KSQSEHFLYV AFKTNSRASI SNLAGKNSYM WNLPEDVVAN SYGLQYEQAR **QLKNNNPFTF LVPPQDSQM**I
481 RTVA

o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.STSADIYNPQAGSVR.T	Y	99.9	84.04	1564.7482	15	0.5	783.3817	2	29.29	16	1357	OB5186.raw	4.93E3	3	3	316	330	
R.TVNELDLPILNR.L	Y	99.9	57.93	1395.7721	12	1.1	698.8941	2	35.87	16	1741	OB5186.raw	9.24E3	3	3	331	342	
R.QLKNNNPFTFLVPPQDSQM(+15.99).I	Y	94.2	28.82	2233.0837	19	3.2	1117.5527	2	37.01	16	1808	OB5186.raw	3.24E3	1	1	461	479	Oxidation (M)
total 3 peptides																		

A1DZF0|A1DZF0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

32
1 MAKLLELSFC FCFLVLGASS **ISFRQQPEEN ACQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR R**YQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLK**TANE LNLLILRWLG LSAEYGNLYR**
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGK**SQS ENFEYVAFKT DSRPSIANLA**
481 **GENSFIDNLP EEVVANSYGL PR**EQARQLKN NNPFKFFVPP FQQSPRAVA

C Carbamidomethylation (+57.02)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.0	37.75	3544.7434	33	-0.9	1182.5874	3	38.65	16	1903	OB5186.raw	1.25E4	2	2	470	502	
K.TANELNLLILRWLGLSAEYGNLYR.N	Y	99.0	36.51	2791.5020	24	-7.4	931.5010	3	42.62	16	2134	OB5186.raw	4.22E3	1	1	377	400	
K.SQSENFEYVAFK.T	Y	99.0	35.77	1447.6619	12	1.2	724.8391	2	33.29	16	1593	OB5186.raw	7.98E2	2	2	458	469	
S.ISFRQQPEENAC(+57.02)QFQR.L	N	99.0	35.27	2036.9486	16	-1.8	679.9889	3	29.81	16	1387	OB5186.raw	7.83E3	2	2	21	36	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.Y	N	75.0	21.56	2629.2383	23	-2.7	877.4177	3	36.21	16	1761	OB5186.raw	4.91E3	1	1	99	121	Carbamidomethylation
total 5 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

32
C

1 MGKLLALSVC FCFLVLGASS **ISFRQQPEEN ACQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

C Carbamidomethylation (+57.02)

81 RRPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR R**HQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLK**TANELNL LILRWLGLSA**

401 **EYGNLYR**NAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGK**SQSENF EYVAFKTDSR**

481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.0	37.75	3544.7434	33	-0.9	1182.5874	3	38.65	16	1903	OB5186.raw	1.25E4	2	2	477	509	
K.TANELNLLILRWLGLSAEYGNLYR.N	Y	99.0	36.51	2791.5020	24	-7.4	931.5010	3	42.62	16	2134	OB5186.raw	4.22E3	1	1	384	407	
K.SQSENFEYVAFK.T	Y	99.0	35.77	1447.6619	12	1.2	724.8391	2	33.29	16	1593	OB5186.raw	7.98E2	2	2	465	476	
S.ISFRQQPEENAC(+57.02)QFQR.L	N	99.0	35.27	2036.9486	16	-1.8	679.9889	3	29.81	16	1387	OB5186.raw	7.83E3	2	2	21	36	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.H	N	75.0	21.56	2629.2383	23	-2.7	877.4177	3	36.21	16	1761	OB5186.raw	4.91E3	1	1	99	121	Carbamidomethylation
total 5 peptides																		

sp|K2C1_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SRQFSSRSGY RSGGGFSSGS AGIINYQRRT TSSSTRRSGG GGGRFSSCGG GGGSFGAGGG FGSR**SLVNLG GSKSISISVA**

81 **R**GGGRGSGFG GGYGGGGFGG GGFGGGGFGG GGIGGGGFGG FGSGGGGFGG GGFGGGGYGG GYGPVCPPGG IQEVTINQSL

161 LQPLNVEIDP EIQKVKSRER EQIKSLNNQF ASFIDKVRFL EQQNQVLQTK WELLQQVDTS TRTHNLEPYF ESFINNLRRR
241 VDQLKSDQSR LDSELKNMQD MVEDYRNKYE DEINKRTNAE NEFVTIKKDV DGAYMTKVDL QAKLDNLQQE IDFLTALYQA
321 ELSQMQTQIS ETNVILSMDN NR**SLDLDSII AEVK**AQNEDI AQKSKAEAES LYQSKYEELQ ITAGRHGDSV RNSKIEISEL

401 NRVIQRLRSE IDNVKKQISN LQQSISDAEQ RGENALKDAK NKLNDLEDAL QQAKEDLARL LRDYQELMNT KLALDLEIAT
481 YRTLLEGEES RMSGECAPNV SVSVSTSHTT ISGGGSRGGG GGGYGSGGSS YGSGGGSYGS GGGGGGGRGS YGSGGSSYGS
561 GGGSYGSGGG GGGHGSYGSG SSSGGYRGGS GGGGGGSSGG RGSGGGSSGG SIGGRGSSSG GVKSSGGSSS VRFVSTTYSG
641 VTR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.SLDLDSIIAEVK.A	Y	99.9	60.08	1301.7078	12	-0.8	651.8607	2	37.90	16	1859	OB5186.raw	8.52E3	1	1	343	354	
R.SLVNLGGSKSISISVAR.G	Y	90.3	24.12	1686.9628	17	2.5	563.3296	3	32.60	16	1551	OB5186.raw	2.54E3	1	1	65	81	
R.SLVNLGGSK.S	Y	82.8	22.69	873.4919	9	0.3	437.7534	2	29.21	16	1352	OB5186.raw	4.94E3	1	1	65	73	
total 3 peptides																		

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS **ISFRQQPEEN ACQFQR**LNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

C Carbamidomethylation (+57.02)

81 RRPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR R**HQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP

161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLK**TANDLN LLILRWLGLS**

401 **AEYGNLYR**NA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS

481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.TANDLNLLILRWLGLSAEYGNLYR.N	Y	99.9	54.25	2777.4863	24	0.2	926.8362	3	42.60	16	2133	OB5186.raw	5.83E3	1	1	385	408	
S.ISFRQQPEENAC(+57.02)QFQR.L	N	99.0	35.27	2036.9486	16	-1.8	679.9889	3	29.81	16	1387	OB5186.raw	7.83E3	2	2	21	36	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.H	N	75.0	21.56	2629.2383	23	-2.7	877.4177	3	36.21	16	1761	OB5186.raw	4.91E3	1	1	99	121	Carbamidomethylation
total 3 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

33

1 MIRGRLALSV CFCFLVLGAS S**ISFRQQPEE NACQFQR**LNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA

81 LRRPFYSNAP QEIFIQQGR**G YFGLIFPGCP STYEEPAQQG RR**HQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP

241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE

321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNRSPDIYNP QAGSLK**TAND LNLLILRWLG LSAEYGNLYR**

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFKT DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

C Carbamidomethylation (+57.02)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.TANDLNLLILRWLGLSAEYGNLYR.N	Y	99.9	54.25	2777.4863	24	0.2	926.8362	3	42.60	16	2133	OB5186.raw	5.83E3	1	1	377	400	
S.ISFRQQPEENAC(+57.02)QFQR.L	N	99.0	35.27	2036.9486	16	-1.8	679.9889	3	29.81	16	1387	OB5186.raw	7.83E3	2	2	22	37	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.H	N	75.0	21.56	2629.2383	23	-2.7	877.4177	3	36.21	16	1761	OB5186.raw	4.91E3	1	1	100	122	Carbamidomethylation
total 3 peptides																		

Q5I6T2|Q5I6T2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

32

1 MAKLLELSFC FCFLVLGASS **ISFRQQPEEN ACQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR R**SQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS

241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE

321 EYDEDEYEYD EEDRRRGRGS RGRGNGIEET ICTASVKKNI GRNRSPDIYN PQAGSLK**TAN DLNLLILRWL GLSAEYGNLY**

401 **R**NALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL

481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

C Carbamidomethylation (+57.02)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
K.TANDLNLLILRWLGLSAEYGNLYR.N	Y	99.9	54.25	2777.4863	24	0.2	926.8362	3	42.60	16	2133	OB5186.raw	5.83E3	1	1	378	401	
S.ISFRQQPEENAC(+57.02)QFQR.L	N	99.0	35.27	2036.9486	16	-1.8	679.9889	3	29.81	16	1387	OB5186.raw	7.83E3	2	2	21	36	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGRR.S	N	75.0	21.56	2629.2383	23	-2.7	877.4177	3	36.21	16	1761	OB5186.raw	4.91E3	1	1	99	121	Carbamidomethylation
total 3 peptides																		

sp|K1C9_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCRQFSSSY LSRSGGGGGG GLGSGGSIRS SYSRFSSSGG RGGGGRFSSS SGYGGGSSRV CGR**GGGGSFG YSYGGGSGGG**

81 **FSASSLGGGF GGGSR**GFGGA SGGGYSSSGG FGGGFGGGSG GGFGGGYGSG FGGLGGFGGG AGGGDGGILT ANEKSTMQEL

161 NSRLASYLDK VQALEEANND LENKIQDWYD KKGPAAIQKN YSPYYNTIDD LKDQIVDLTV GNNKTLLDID NTRMTLDDFR
241 IKFEMEQNLR QGVDADINGL RQVLDNLTME KSDLEMQYET LQEELMALKK NHKEEMSQLT GQNSGDVNVE INVAPGKDLT
321 KTLNDMRQEY EQLIAKNRKD IENQYETQIT QIEHEVSSSG QEVQSSAKEV TQLRHGVQEL EIELQSQLSK KAALEKSLED
401 TKNRYCGQLQ MIQEQISNLE AQITDVRQEI ECQNQEYSLL LSIKMRLEKE IETYHNLLEG GQEDFESSGA GKIGLGGRGG
481 SGGSYGRGSR GGSGGSYGGG GSGGGYGGGS GSRGGSGGSY GGGSGSGGGS GGGYGGGSGG GHSGGSGGGH SGGSGGNYGG
561 GSGSGGGSGG GYGGGSGSRG GSGGSHGGGS GFGGESGGSY GGGEEASGSG GGYGGGSGKS SHS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	Y	99.0	36.30	2704.1538	32	1.3	902.3931	3	34.94	16	1688	OB5186.raw	1.32E3	1	1	64	95	
total 1 peptides																		

sp|K22E_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCQISCKSR GRGGGGGGFR GFSSGSAVVS GGSRRSTSSF SCLSRHGGGG GGFGGGGFGS RSLVGLGGTK SISISVAGGG
81 GGFGAAGGFG GRGGGFGGGS GFGGGSGFGG GSGFSGGGFG GGGFGGGRFG GFGGPGGVGG LGGPGGFGPG GYPGGIHEVS
161 VNQSLLQPLN VKVDPEIQNV KAQEREQIKT LNNKFASFID KVRFLEQQNQ VLQTKWELLQ QMNVGTRPIN LEPIFQGYID
241 SLKRYLDGLT AERTSQNSEL NNMQDLVEDY KKKYEDEINK RTAAENDFVT LKKDVDNAYM IKVELQSKVD LLNQEIEFLK
321 VLYDAEISQI HQSVTDTNVI LSMDNSR**NLD LDSIIAEVKA QYEEIAQR**SK EEAEALYHSK YEELQVTVGR HGDSLKEIKI

401 EISELNRVIQ RLQGEIAHVK KQCKNVQDAI ADAEQRGEHA LKDARNKLND LEEALQQAKE DLARLLRDYQ ELMNVKLALD
481 VEIATYRKLL EGEECRMSGD LSSNVTVSVT SSTISSNVAS KAAFGGSGGR GSSSGGGYSS GSSSYGSGGR QSGSRGGSGG
561 GGSISGGGYG SGGGSGGRYG SGGGSKGGSI SGGGYGSGGG KHSSGGGSRG GSSSGGGYGS GGGGSSSVKG SSGEAFGSSV
641 TFSFR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS2 tacka 17 na Figuri 1	#Spec	#Spec DS2 tacka 17 na Figuri 1	Start	End	PTM
R.NLDLDSIIAEVKAQYEEIAQR.S	Y	99.0	34.77	2417.2437	21	0.5	806.7556	3	41.21	16	2053	OB5186.raw	3.19E4	1	1	348	368	
total 1 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

1. Notes Spot 18 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

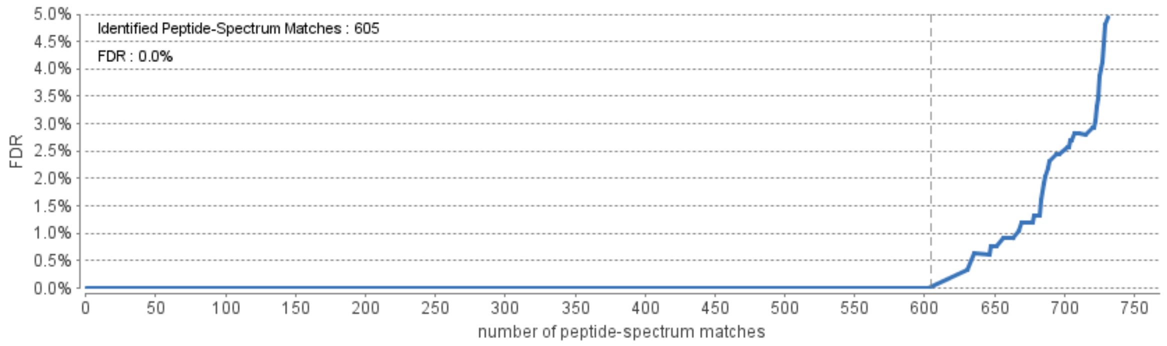
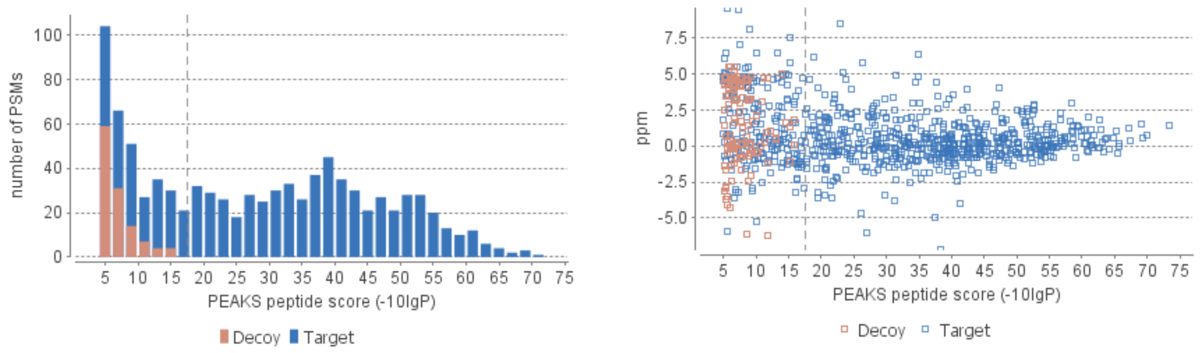


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

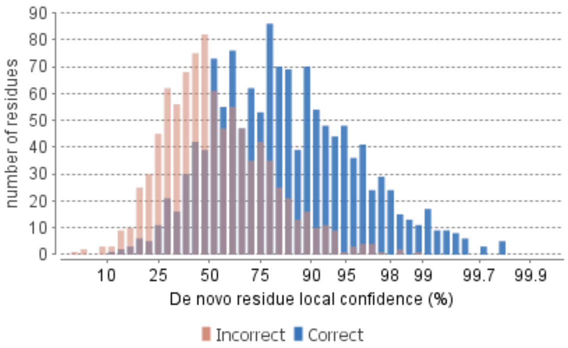

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



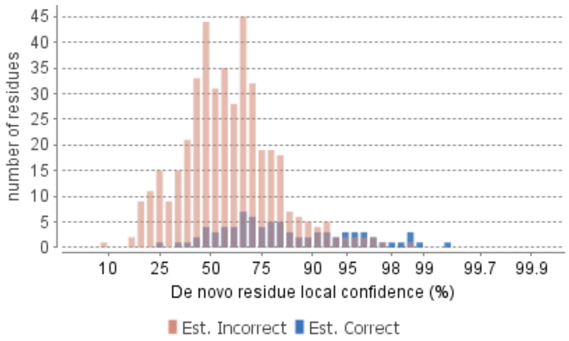


Table 1. Statistics of data.

# of MS scans	2223
# of MS/MS scans	1882

Table 2. Result filtration parameters.

Peptide -10lgP	≥17.5
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	599
Peptide sequences	210
Protein groups	12
Proteins	22
Proteins (#Unique Peptides)	8 (>2); 11 (=2); 3 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	69

Table 4. PTM profile.

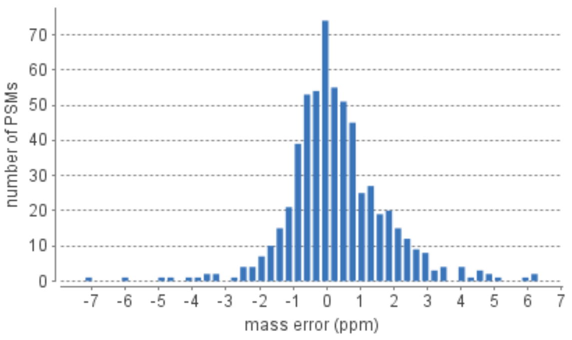
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Oxidation	15.99	M	66	61.02	2.73E4	1000.00
Carbamidomethyl	57.02	C	50	67.31	6.13E4	1000.00
Deamidation	.98	NQ	6	43.90	1.3E4	46.13
HydPro	15.99	P	2	37.36	9.83E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



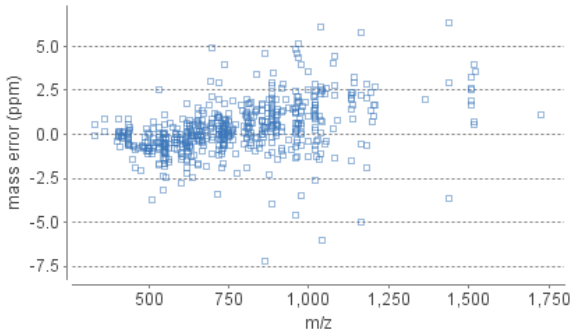


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
DS3 tacka 18 na Figuri 1	140	58	12	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: Uniprot_Peanut(3818)+cRAP_aug17
Taxon: All
Searched Entry: 1352
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB5188.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) DS3 tacka 18 na Figuri 1	Area DS3 tacka 18 na Figuri 1	#Peptides	#Unique	#Spec DS3 tacka 18 na Figuri 1	PTM	Avg. Mass	Description
1	221	sp|K2C1_HUMAN|	99.1	260.57	62	62	5.38E6	50	46	195	Y	65886	sp|K2C1_HUMAN|

2	220	sp|K1C10_HUMAN|	99.1	259.18	57	57	3.53E6	47	42	176	Y	59519	sp|K1C10_HUMAN|
4	964	sp|K22E_HUMAN|	99.1	239.38	63	63	6.56E5	32	28	66	Y	65865	sp|K22E_HUMAN|
3	646	sp|K1C9_HUMAN|	99.1	209.46	59	59	1.13E6	25	24	69	Y	62129	sp|K1C9_HUMAN|
5	216	Q6IWG5|Q6IWG5_ARAHY	99.1	168.44	23	23	1.55E6	12	11	57	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	217	Q0GM57|Q0GM57_ARAHY	99.1	168.44	23	23	1.55E6	12	11	57	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
8	88	Q6T2T4|Q6T2T4_ARAHY	99.1	137.79	20	20	3.81E4	7	2	11	N	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
8	87	Q647H4|Q647H4_ARAHY	99.1	137.79	20	20	3.81E4	7	2	11	N	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
7	1008	sp|K1C15_SHEEP|	98.8	119.68	9	9	1.48E4	5	1	16	Y	48770	sp|K1C15_SHEEP|
6	215	sp|Q6PSU2|CONG7_ARAHY	99.0	118.27	38	38	4.95E5	5	5	27	Y	20114	Conglutin-7 OS=Arachis hypogaea PE=1 SV=2
11	1193	sp|TRYP_PIG|	98.3	98.81	16	16	2.02E5	5	5	6	N	24409	sp|TRYP_PIG|
14	204	E9LFE7|E9LFE7_ARAHY	80.6	38.61	21	21	1.74E4	2	2	2	N	15873	7S conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
14	205	Q6PSU5|Q6PSU5_ARAHY	80.6	38.61	10	10	1.74E4	2	2	2	N	33604	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
14	206	Q6PSU6|Q6PSU6_ARAHY	80.6	38.61	10	10	1.74E4	2	2	2	N	34133	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
14	3470	Q6PSU4|Q6PSU4_ARAHY	80.6	38.61	7	7	1.74E4	2	2	2	N	48095	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
14	207	Q6PSU3|Q6PSU3_ARAHY	80.6	38.61	5	5	1.74E4	2	2	2	N	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
14	208	B3IXL2|B3IXL2_ARAHY	80.6	38.61	5	5	1.74E4	2	2	2	N	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
14	209	sp|P43237|ALL11_ARAHY	80.6	38.61	5	5	1.74E4	2	2	2	N	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
14	274	N1NG13|N1NG13_ARAHY	80.6	38.61	5	5	1.74E4	2	2	2	N	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
14	275	sp|P43238|ALL12_ARAHY	80.6	38.61	5	5	1.74E4	2	2	2	N	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
15	219	sp|Q647H2|AHY3_ARAHY	61.4	24.48	2	2	3.8E3	1	1	1	N	54569	Arachin Ahy-3 OS=Arachis hypogaea PE=1 SV=1
17	1758	sp|KRHB2_HUMAN|	52.6	21.05	2	2	5.32E3	1	1	1	Y	56683	sp|KRHB2_HUMAN|
total 22 proteins													

sp|K2C1_HUMAN|

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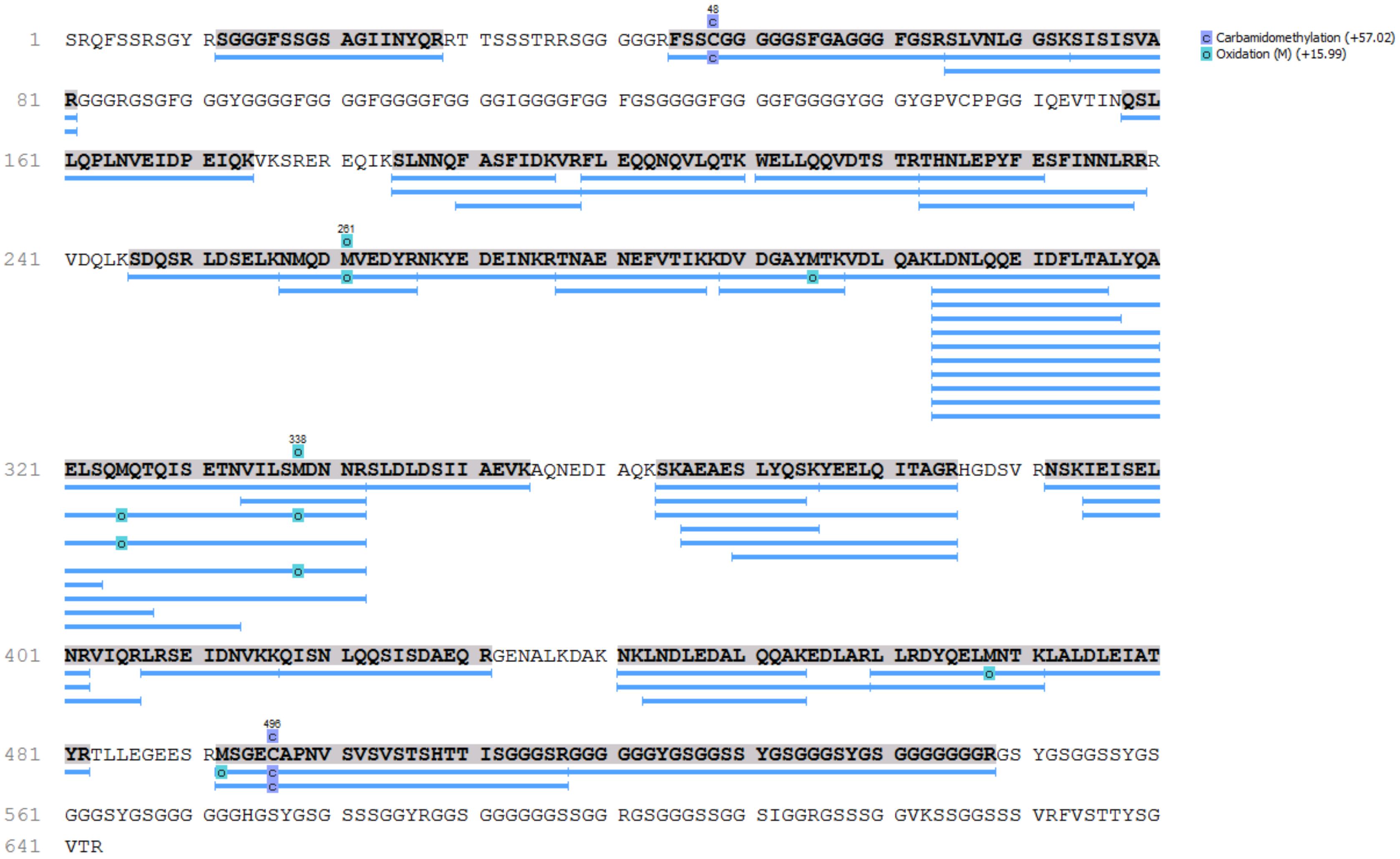
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 SRQFSSRSGY RSGGGFSSGS AGIINYQRRT TSSSTRRSGG GGGRFSSCGG GGGSFGAGGG FGSRSLVNLG GSKSISISVA
81 RGGGRGSGFG GGYGGGGFGG GGFGGGGFGG GGIGGGGFGG FGSGGGGFGG GGFGGGGYGG GYGPVCPPGG IQEVTINQSL
161 LQPLNVEIDP EIQKVKSRER EQIKSLNNQF ASFIDKVRFL EQQNQVLQTK WELLQQVDTS TRTHNLEPYF ESFINNLRRR
241 VDQLKSDQSR LDSELKNMQD MVEDYRNKYE DEINKRTNAE NEFVTIKKDV DGAYMTKVDL QAKLDNLQQE IDFLTALYQA
321 ELSQMQTQIS ETNVILSMDN NRSLDLDSII AEVKAQNEDI AQKSKAEAES LYQSKYEELQ ITAGRHGDSV RNSKIEISEL
401 NRVIQRLRSE IDNVKKQISN LQQSISDAEQ RGENALKDAK NKLNDLEDAL QQAKEDLARL LRDYQELMNT KLALDLEIAT
481 YRTLLEGEES RMSGECAPNV SVSVSTSHTT ISGGGSRGGG GGGYGSGGSS YGSGGGSYGS GGGGGGGRGS YGSGGSSYGS
561 GGGSYGSGGG GGGHGSYGSG SSSGGYRGGS GGGGGGSSGG RGSGGGSSGG SIGGRGSSSG GVKSSGGSSS VRFVSTTYSG
641 VTR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.FSSC(+57.02)GGGGGSFGAGGGFGSR.S	Y	99.9	67.31	1764.7274	20	0.4	883.3713	2	31.40	18	1510	OB5188.raw	6.13E4	2	2	45	64	Carbamidomethylation
R.FLEQQNQVLQTKWELLQQVDTSTR.T	Y	99.9	67.11	2931.5090	24	1.2	978.1782	3	36.42	18	1799	OB5188.raw	3.65E5	11	11	199	222	
R.SLDLDSIIAEVK.A	Y	99.9	64.78	1301.7078	12	0.5	651.8615	2	38.31	18	1905	OB5188.raw	4.17E5	15	15	343	354	
K.YEELQITAGR.H	Y	99.9	62.67	1178.5931	10	-0.1	590.3038	2	31.14	18	1495	OB5188.raw	1.08E5	5	5	376	385	
K.SKAEAESLYQSK.Y	Y	99.9	61.48	1339.6619	12	1.2	670.8390	2	25.44	18	1159	OB5188.raw	1.92E4	3	3	364	375	
R.FLEQQNQVLQTK.W	N	99.9	61.35	1474.7780	12	0.3	738.3965	2	30.79	18	1475	OB5188.raw	1.97E5	7	7	199	210	
K.WELLQQVDTSTR.T	Y	99.9	60.46	1474.7416	12	0.1	738.3782	2	35.09	18	1724	OB5188.raw	1.15E5	6	6	211	222	
K.QISNLQQSISDAEQR.G	Y	99.9	58.81	1715.8438	15	-0.2	858.9290	2	32.51	18	1574	OB5188.raw	0	1	1	417	431	
R.SGGGFSSGSAGIINYQR.R	Y	99.9	58.44	1656.7855	17	1.0	829.4009	2	32.16	18	1554	OB5188.raw	5.79E3	1	1	12	28	
K.LALDLEIATYR.T	Y	99.9	56.10	1276.7026	11	-0.1	639.3585	2	36.44	18	1800	OB5188.raw	9.77E4	4	4	472	482	
R.SLVNLGGSKSISISVAR.G	Y	99.9	55.54	1686.9628	17	-0.8	844.4880	2	33.02	18	1605	OB5188.raw	2.49E4	4	4	65	81	
R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	Y	99.9	55.53	2382.9446	31	1.4	1192.4812	2	27.13	18	1260	OB5188.raw	3.32E4	5	5	518	548	
K.NKLNDLEDALQQAKEDLAR.L	Y	99.9	55.30	2183.1182	19	-0.1	728.7133	3	36.81	18	1821	OB5188.raw	1.3E5	7	7	441	459	
R.MSGEC(+57.02)APNVSVSVSTSHTTISGGGSR.G	Y	99.9	54.82	2564.1594	26	0.0	855.7271	3	30.23	18	1442	OB5188.raw	4.28E4	2	2	492	517	Carbamidomethylation
K.SLNNQFASFIDK.V	Y	99.9	54.78	1382.6830	12	0.3	692.3490	2	35.28	18	1735	OB5188.raw	4.62E4	1	1	185	196	

K.AEAESLYQSK.Y	Y	99.9	54.37	1124.5349	10	-0.8	563.2743	2	27.15	18	1261	OB5188.raw	9.55E3	1	1	366	375	
R.TNAENEFVTIK.K	Y	99.9	54.23	1264.6299	11	0.0	633.3222	2	31.57	18	1520	OB5188.raw	5.81E4	2	2	277	287	
R.THNLEPYFESFINNLR.R	Y	99.9	54.16	1992.9694	16	-0.3	665.3302	3	38.51	18	1917	OB5188.raw	2.31E5	8	8	223	238	
K.SLNNQFASFIDKVR.F	Y	99.9	53.59	1637.8525	14	-0.6	819.9330	2	35.71	18	1759	OB5188.raw	4.28E5	8	8	185	198	
R.TNAENEFVTIKK.D	Y	99.9	53.22	1392.7249	12	0.6	697.3701	2	29.17	18	1379	OB5188.raw	1.58E5	4	4	277	288	
N.QSLLQPLNVEIDPEIQK.V	Y	99.9	51.20	1963.0625	17	1.6	982.5401	2	36.83	18	1822	OB5188.raw	3.07E4	1	1	158	174	
K.LDNLQQEIDFLTALYQAELSQMQTQISETNVILSMDNNR.S	Y	99.9	50.68	4526.1943	39	2.4	1132.5586	4	46.49	18	2371	OB5188.raw	1.58E6	16	16	304	342	
K.LDNLQQEIDFLTALYQA.E	Y	99.9	49.75	1993.9996	17	-0.4	998.0067	2	44.42	18	2252	OB5188.raw	2.29E4	2	2	304	320	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSMDNNR.S	Y	99.9	49.50	4542.1895	39	0.9	1136.5557	4	44.29	18	2245	OB5188.raw	2.67E5	4	4	304	342	Oxidation (M)
K.DVDGAYMTK.V	Y	99.9	48.40	998.4379	9	-0.8	500.2258	2	28.16	18	1320	OB5188.raw	4.61E4	4	4	289	297	
K.SKAEAESLYQSKYEELQITAGR.H	Y	99.9	48.01	2500.2444	22	0.5	626.0687	4	32.24	18	1559	OB5188.raw	9.08E4	4	4	364	385	
K.AEAESLYQSKYEELQITAGR.H	Y	99.9	47.78	2285.1174	20	1.9	762.7145	3	33.22	18	1617	OB5188.raw	1.77E4	1	1	366	385	
K.LDNLQQEIDFLTALYQAELSQMQTQISETNVILSM(+15.99)DNNR.S	Y	99.9	46.70	4542.1895	39	2.4	1136.5574	4	46.03	18	2345	OB5188.raw	1.68E5	2	2	304	342	Oxidation (M)
K.IEISELNR.V	N	99.9	46.44	972.5240	8	-0.5	487.2690	2	30.76	18	1473	OB5188.raw	3.26E4	3	3	395	402	
K.NMQDM(+15.99)VEDYR.N	Y	99.9	45.37	1315.5173	10	-0.4	658.7657	2	30.26	18	1444	OB5188.raw	2.79E3	2	2	257	266	Oxidation (M)
K.SISISVAR.G	Y	99.9	45.31	831.4814	8	0.1	416.7480	2	29.70	18	1411	OB5188.raw	6.84E4	1	1	74	81	
K.NMQDMVEDYR.N	Y	99.9	44.99	1299.5223	10	0.7	650.7689	2	32.71	18	1586	OB5188.raw	6.98E3	1	1	257	266	
K.LDNLQQEIDFLTALYQAELSQMQTQISETN.V	Y	99.9	44.37	3483.6714	30	-0.5	1162.2305	3	46.97	18	2398	OB5188.raw	3.17E4	3	3	304	333	
R.THNLEPYFESFINNLRR.R	Y	99.9	42.56	2149.0703	17	0.5	717.3644	3	37.40	18	1854	OB5188.raw	2.55E5	13	13	223	239	
R.SLVNLGGSK.S	Y	99.9	42.00	873.4919	9	0.2	437.7533	2	29.71	18	1412	OB5188.raw	9.31E4	5	5	65	73	
N.VILSMDNNR.S	Y	99.9	41.92	1060.5336	9	-0.8	531.2736	2	29.89	18	1422	OB5188.raw	9.02E3	1	1	334	342	
R.NKYEDEINKR.T	Y	99.8	38.82	1307.6470	10	-0.2	436.8895	3	25.66	18	1172	OB5188.raw	6.05E4	6	6	267	276	
K.SKAEAESLYQS.K	Y	99.8	38.63	1211.5669	11	0.9	606.7913	2	27.65	18	1290	OB5188.raw	4.09E3	1	1	364	374	
R.LLRDYQELMNTK.L	Y	99.8	38.09	1522.7814	12	-0.5	508.6008	3	32.55	18	1576	OB5188.raw	1.95E4	2	2	460	471	
K.LDNLQQEIDFLTALYQAELS.Q	Y	99.7	37.54	2323.1582	20	-5.0	1162.5806	2	45.91	18	2338	OB5188.raw	7.65E3	1	1	304	323	
K.LDNLQQEIDFLTAL.Y	Y	99.7	36.95	1631.8406	14	0.4	816.9279	2	44.01	18	2229	OB5188.raw	2.08E4	2	2	304	317	
R.M(+15.99)SGEC(+57.02)APNVSVSVSTSHTTISGGGSR.G	Y	99.7	36.52	2580.1545	26	0.2	861.0590	3	29.73	18	1413	OB5188.raw	1.35E4	2	2	492	517	Oxidation (M); Carbamidomethylation
R.NSKIEISELNR.V	Y	99.5	35.92	1301.6938	11	0.8	651.8547	2	29.29	18	1386	OB5188.raw	1.09E3	1	1	392	402	
K.SDQSRLDSELK.N	Y	99.2	32.70	1276.6259	11	0.6	639.3206	2	27.08	18	1257	OB5188.raw	4.63E3	1	1	246	256	
K.DVDGAYM(+15.99)TK.V	Y	99.1	31.16	1014.4328	9	-3.8	508.2218	2	24.36	18	1096	OB5188.raw	6.41E3	2	2	289	297	Oxidation (M)
K.LNDLEDALQQAK.E	Y	98.3	29.55	1356.6885	12	-0.2	679.3514	2	33.73	18	1647	OB5188.raw	0	1	1	443	454	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSM(+15.99)DNNR.S	Y	98.3	28.47	4558.1841	39	2.9	1140.5566	4	43.96	18	2226	OB5188.raw	9.54E4	3	3	304	342	Oxidation (M)
K.IEISELNRVIQR.L	N	95.7	27.60	1468.8362	12	0.3	735.4256	2	33.44	18	1630	OB5188.raw	0	1	1	395	406	
Q.FASFIDKVR.F	N	94.1	25.62	1081.5920	9	0.2	361.5380	3	31.62	18	1523	OB5188.raw	1.65E4	2	2	190	198	
K.VDLQAKLDNLQQEIDFLTALYQAELSQMQTQISETNVILSMDNNR.S	Y	92.9	22.97	5180.5645	45	2.7	1037.1229	5	45.42	18	2310	OB5188.raw	5.44E4	3	3	298	342	
R.LRSEIDNVKK.Q	Y	92.6	22.04	1200.6826	10	-0.4	401.2346	3	22.73	18	1011	OB5188.raw	1.25E4	1	1	407	416	
K.LDNLQQEIDFLTA.L	Y	92.5	21.92	1518.7566	13	0.1	760.3856	2	40.84	18	2049	OB5188.raw	1.22E4	1	1	304	316	
K.LDNLQQEIDFLTALYQAELSQMQT.Q	Y	92.5	21.65	2811.3635	24	-0.3	938.1282	3	46.39	18	2365	OB5188.raw	1.69E4	1	1	304	327	
R.THNLEPYFE.S	Y	92.4	21.63	1148.5138	9	0.4	575.2644	2	32.87	18	1596	OB5188.raw	0	1	1	223	231	
E.SLYQSKYEELQITAGR.H	Y	90.4	20.62	1884.9581	16	0.3	629.3268	3	32.37	18	1566	OB5188.raw	3.28E3	1	1	370	385	
K.NKLNDLEDALQQAK.E	Y	84.8	19.95	1598.8264	14	-0.4	533.9492	3	33.94	18	1659	OB5188.raw	3.41E3	1	1	441	454	
R.LLRDYQELM(+15.99)NTK.L	Y	84.0	19.38	1538.7762	12	0.7	513.9330	3	29.79	18	1416	OB5188.raw	4.25E3	1	1	460	471	Oxidation (M)
total 57 peptides																		

sp|K1C10_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVRYSSSKH YSSSR**SGGGG GGGGCGGGGG VSSLR**ISSSK **GSLGGGFSSG GFSGGSFSR**G SSGGGCFGGS SGGYGGLGGF

81 GGGSFHGSYG SSSFGGSYGG SFGGGNFGGG SFGGGSFGGG GFGGGGFGGG FGGGFGGDGG LLSGNEK**VTM QNLNDRLASY**

161 **LDKVRALEES NYELEGKIKE WYEK**HGNSHQ GEPR**DYSKYY KTIDDLKNQI LNLTTDNANI LLQIDNARLA ADDFRLKYEN**

241 **EVALRQSVEA DINGLRRVLD ELTLTKADLE MQIESLTEEL AYLKKNHEEE MKDLRNVSTG DVNVEMNAAP GVDLTQLLNN**

321 **MRSQYEQLAE QNRKDAEAWF NEKSKELTTE IDNNIEQISS YK**SEITELRR **NVQALEIELQ SQLALKQSLE ASLAETEGRY**

401 **CVQLSQIQAQ ISALEEQLQQ IRAETECQNT EYQQLLDIKI RLENEIQTYR SLLEGEGSSG GGGR**GGGSFG GGYGGGSSGG

481 GSSGGGYGGG HGGSSGGGYG GGSSGGGSSG GGYGGGSSSG GHGGGSSSGG HGGSSSGGYG GGSSGGGGGG YGGGSSGGGS

561 SSGGGYGGGS SSGGHKSSSS GSVGESSSKG PRY

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
K.GSLGGGFSSGGFSGGSFSR.G	Y	99.9	70.04	1706.7648	19	0.8	854.3903	2	33.80	18	1651	OB5188.raw	1.48E5	7	7	41	59	
R.SLLEGEGSSGGGGR.G	Y	99.9	65.62	1261.5898	14	0.2	631.8023	2	27.54	18	1284	OB5188.raw	4.95E4	3	3	451	464	
K.ADLEMQIESLTEELAYLK.K	Y	99.9	65.47	2095.0396	18	-0.5	1048.5265	2	42.18	18	2125	OB5188.raw	4.59E4	3	3	267	284	
R.ALEESNYELEGK.I	Y	99.9	63.69	1380.6409	12	0.5	691.3281	2	30.07	18	1433	OB5188.raw	1.12E5	1	1	166	177	
R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S	Y	99.9	62.89	2871.3855	27	1.2	958.1369	3	39.66	18	1982	OB5188.raw	3.87E5	17	17	296	322	
R.SQYEQLAEQNR.K	Y	99.9	62.49	1364.6321	11	-0.1	683.3232	2	28.35	18	1331	OB5188.raw	9.67E3	1	1	323	333	
R.NVQALEIELQSQLALK.Q	Y	99.9	61.03	1796.0043	16	2.0	899.0112	2	37.95	18	1885	OB5188.raw	6.57E4	4	4	371	386	
K.ADLEM(+15.99)QIESLTEELAYLK.K	Y	99.9	61.02	2111.0344	18	-0.4	1056.5240	2	42.41	18	2138	OB5188.raw	3.89E4	3	3	267	284	Oxidation (M)
K.ELTTEIDNNIEQISSYK.S	Y	99.9	59.91	1995.9636	17	1.0	998.9901	2	35.89	18	1769	OB5188.raw	1.67E4	2	2	346	362	
K.TIDDLKNQILNLTTDNANILLQIDNAR.L	Y	99.9	59.20	3051.6201	27	1.4	1018.2154	3	40.60	18	2035	OB5188.raw	9.16E5	22	22	202	228	
R.YC(+57.02)VQLSQIQAQISALEEQLQQIR.A	Y	99.9	58.43	2745.4119	23	0.2	916.1447	3	41.88	18	2108	OB5188.raw	1.06E5	7	7	400	422	Carbamidomethylation
K.IRLENEIQTYR.S	Y	99.9	55.33	1433.7627	11	0.9	717.8893	2	30.91	18	1482	OB5188.raw	5.23E4	4	4	440	450	
R.VLDELTLTK.A	N	99.9	55.26	1030.5911	9	-0.7	516.3024	2	32.64	18	1582	OB5188.raw	7.48E4	5	5	258	266	
K.QSLEASLAETEGR.Y	Y	99.9	54.69	1389.6736	13	-0.3	695.8439	2	32.04	18	1547	OB5188.raw	3.13E4	2	2	387	399	
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNMR.S	Y	99.9	54.43	2887.3804	27	-0.4	963.4670	3	38.89	18	1938	OB5188.raw	9.83E4	5	5	296	322	Oxidation (M)
R.SQYEQLAEQNRK.D	Y	99.9	53.09	1492.7269	12	-0.2	747.3706	2	26.54	18	1225	OB5188.raw	1.19E5	8	8	323	334	
K.VTMQNLNDR.L	Y	99.9	53.02	1089.5237	9	-0.6	545.7688	2	27.63	18	1289	OB5188.raw	5.13E4	3	3	148	156	
K.SKELTTEIDNNIEQISSYK.S	Y	99.9	52.91	2211.0906	19	-0.2	738.0374	3	34.66	18	1700	OB5188.raw	2.4E4	2	2	344	362	

R.LENEIQTYR.S	Y	99.9	51.50	1164.5775	9	0.1	583.2961	2	29.03	18	1371	OB5188.raw	3.72E4	2	2	442	450	
R.AETEC(+57.02)QNTEYQQLLDIK.I	Y	99.9	50.10	2081.9575	17	2.5	1041.9886	2	34.89	18	1713	OB5188.raw	1.31E4	2	2	423	439	Carbamidomethylation
K.YENEVALR.Q	Y	99.9	48.70	992.4927	8	-0.9	497.2531	2	28.37	18	1332	OB5188.raw	1.24E4	1	1	238	245	
K.NQILNLTTDNANILLQIDNAR.L	Y	99.9	47.83	2366.2554	21	1.7	789.7604	3	38.41	18	1911	OB5188.raw	9.71E3	1	1	208	228	
N.AAPGVDLTQLLNNMR.S	Y	99.9	47.37	1611.8402	15	-0.2	806.9272	2	38.53	18	1918	OB5188.raw	3.26E4	2	2	308	322	
D.NANILLQIDNAR.L	Y	99.9	47.01	1353.7365	12	0.3	677.8757	2	34.59	18	1696	OB5188.raw	2.02E4	2	2	217	228	
K.DAEAWFNEK.S	Y	99.9	45.37	1108.4825	9	-0.7	555.2482	2	33.49	18	1633	OB5188.raw	9.28E4	6	6	335	343	
R.LAADDFR.L	N	99.9	44.44	806.3922	7	0.1	404.2034	2	28.88	18	1362	OB5188.raw	9.82E4	6	6	229	235	
R.LASYLDKVR.A	Y	99.9	44.42	1063.6025	9	0.0	532.8085	2	29.22	18	1382	OB5188.raw	1.88E4	3	3	157	165	
K.ADLEM(+15.99)QIESLTEELAYLKK.N	Y	99.9	44.25	2239.1294	19	-0.2	747.3836	3	40.05	18	2004	OB5188.raw	1.05E5	6	6	267	285	Oxidation (M)
K.TIDDLKNQILNLTTD.N	Y	99.9	44.23	1715.8942	15	0.4	858.9547	2	37.62	18	1866	OB5188.raw	4.08E4	1	1	202	216	
R.LKYENEVALR.Q	Y	99.9	44.11	1233.6716	10	-1.9	617.8419	2	29.10	18	1375	OB5188.raw	1.02E5	4	4	236	245	
K.VTMQNLNDRLASYLDKVR.A	Y	99.9	44.00	2135.1157	18	1.0	712.7132	3	35.74	18	1761	OB5188.raw	1.53E4	2	2	148	165	
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNM(+15.99)R.S	Y	99.9	42.79	2903.3752	27	1.9	968.8008	3	37.03	18	1833	OB5188.raw	2.66E4	1	1	296	322	Oxidation (M)
R.QSVEADINGLR.R	N	99.9	42.79	1200.6099	11	-0.2	601.3121	2	31.82	18	1534	OB5188.raw	3.81E3	1	1	246	256	
K.NHEEEMKDLR.N	Y	99.9	42.47	1299.5878	10	0.0	434.2032	3	24.42	18	1099	OB5188.raw	4.43E4	3	3	286	295	
K.TIDDLKNQILNLTTDNA.N	Y	99.9	40.47	1900.9741	17	1.5	951.4957	2	37.74	18	1873	OB5188.raw	8.28E3	1	1	202	218	
K.ELTTEIDNN(+.98)IEQISSYK.S	Y	99.9	40.32	1996.9476	17	3.5	999.4846	2	36.35	18	1795	OB5188.raw	4.23E2	1	1	346	362	Deamidation (NQ)
A.NILLQIDNAR.L	Y	99.9	40.28	1168.6564	10	0.0	585.3354	2	34.04	18	1665	OB5188.raw	1.32E4	1	1	219	228	
K.ADLEMQIESLTEELAYLKK.N	Y	99.9	40.05	2223.1343	19	0.5	742.0524	3	39.72	18	1985	OB5188.raw	9.55E4	3	3	267	285	
R.SQYEQLAEQNRKDAEAWFNEK.S	Y	99.8	38.91	2583.1990	21	0.3	862.0739	3	34.08	18	1667	OB5188.raw	1.61E4	1	1	323	343	
R.VLDELTLTKADLEMQIESLTEELAYLK.K	Y	99.8	38.82	3107.6199	27	0.0	1036.8806	3	42.57	18	2147	OB5188.raw	4.36E4	3	3	258	284	
R.NVSTGDVNVEMNAAP(+15.99)GVDLTQLLNNMR.S	Y	99.7	37.36	2887.3804	27	1.7	963.4691	3	39.73	18	1986	OB5188.raw	9.83E4	1	1	296	322	Hydroxylation Pro
R.VLDELTLTKADLEM(+15.99)QIESLTEELAYLK.K	Y	99.6	36.13	3123.6147	27	2.4	1042.2147	3	42.89	18	2165	OB5188.raw	4.59E4	2	2	258	284	Oxidation (M)
R.SGGGGGGGGC(+57.02)GGGGGVSSLR.I	Y	99.5	35.32	1548.6699	20	-2.2	775.3405	2	25.73	18	1176	OB5188.raw	1.24E3	1	1	16	35	Carbamidomethylation
L.GGGFSSGGFSGGSFSR.G	Y	99.5	35.24	1449.6272	16	0.2	725.8210	2	32.35	18	1565	OB5188.raw	1.34E3	1	1	44	59	
R.LASYLDK.V	N	99.5	33.70	808.4330	7	0.0	405.2238	2	28.18	18	1321	OB5188.raw	1.48E4	1	1	157	163	
R.NVSTGDVNVEMNAAPGVDLTQLLNNM(+15.99)R.S	Y	99.2	33.17	2887.3804	27	0.3	963.4677	3	38.03	18	1889	OB5188.raw	9.83E4	2	2	296	322	Oxidation (M)
R.QSVEADINGLRR.V	N	99.1	31.52	1356.7109	12	-0.2	679.3626	2	30.33	18	1448	OB5188.raw	9.25E4	2	2	246	257	
R.DYSKYYK.T	Y	95.3	26.44	965.4494	7	-0.7	483.7316	2	27.34	18	1272	OB5188.raw	5.9E3	1	1	195	201	
K.IKEWYEK.H	Y	94.3	25.74	994.5123	7	-0.1	332.5114	3	28.28	18	1327	OB5188.raw	2.15E4	2	2	178	184	
S.ALEEQLQQIR.A	Y	93.7	24.82	1226.6619	10	-0.3	614.3380	2	31.90	18	1539	OB5188.raw	0	1	1	413	422	
R.NVSTGDVNVEMNAAPGVDLTQLLNN(+.98)M(+15.99)R.S	Y	93.4	23.81	2888.3645	27	4.6	963.7999	3	37.78	18	1875	OB5188.raw	2.79E4	1	1	296	322	Deamidation (NQ); Oxidation (M)
R.SQYEQLAEQN.R	Y	92.4	21.63	1208.5309	10	-0.7	605.2723	2	29.85	18	1420	OB5188.raw	0	1	1	323	332	
K.YYKTIDDLKNQILNLTTDNANILLQIDNAR.L	Y	90.3	20.50	3505.8416	30	2.0	877.4694	4	40.28	18	2017	OB5188.raw	8.99E3	2	2	199	228	
R.NVQALEIELQSQLALKQSLEASLAETEGRYC(+57.02)VQLSQIQAQISALEEQLQQIR.A	Y	90.3	20.49	5895.0688	52	-0.7	1180.0203	5	44.32	18	2247	OB5188.raw	1.79E5	2	2	371	422	Carbamidomethylation
R.QSVEADIN(+.98)GLRR.V	N	78.0	19.07	1357.6949	12	-0.7	453.5719	3	28.72	18	1353	OB5188.raw	9.85E3	1	1	246	257	Deamidation (NQ)
R.VLDELTLTKADLEMQIESLTEELAYLKK.N	Y	77.8	19.04	3235.7148	28	0.7	809.9366	4	41.74	18	2100	OB5188.raw	0	1	1	258	285	
R.VLDELTLTKADLEMQ(+.98)IESLTEELAYLK.K	Y	76.6	18.82	3108.6040	27	6.1	1037.2150	3	42.91	18	2166	OB5188.raw	1.29E4	1	1	258	284	Deamidation (NQ)
K.QSLEASLAETEGRYC(+57.02)VQLSQIQAQISALEEQLQQIR.A	Y	70.1	18.55	4117.0747	36	-0.3	1030.2756	4	42.56	18	2146	OB5188.raw	9.09E3	1	1	387	422	Carbamidomethylation
total 58 peptides																		

sp|K22E_HUMAN|

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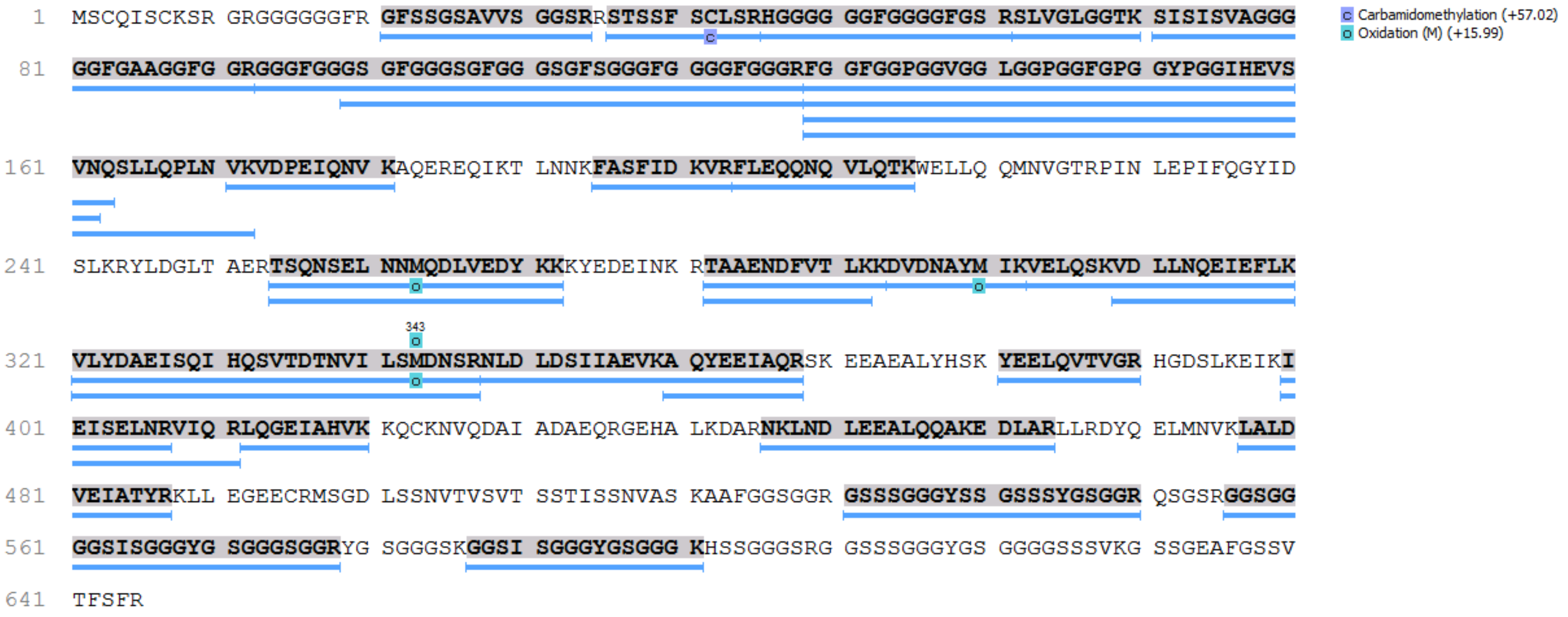
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MSCQISCKSR GRGGGGGGFR GFSSGSAVVS GGSRRSTSSF SCLSRHGGGG GGFGGGGFGS RSLVGLGGTK SISISVAGGG
81 GGFGAAGGFG GRGGGFGGGS GFGGGSGFGG GSGFSGGGFG GGGFGGGRFG GFGGPGGVGG LGGPGGFGPG GYPGGIHEVS
161 VNQSLLQPLN VKVDPEIQNV KAQEREQIKT LNNKFASFID KVRFLEQQNQ VLQTKWELLQ QMNVGTRPIN LEPIFQGYID
241 SLKRYLDGLT AERTSQNSEL NNMQDLVEDY KKKYEDEINK RTAAENDFVT LKKDVDNAYM IKVELQSKVD LLNQEIEFLK
321 VLYDAEISQI HQSVTDTNVI LSMDNSRNLD LDSIIAEVKA QYEEIAQRSK EEAEALYHSK YEELQVTVGR HGDSLKEIKI
401 EISELNRVIQ RLQGEIAHVK KQCKNVQDAI ADAEQRGEHA LKDARNKLND LEEALQQAKE DLARLLRDYQ ELMNVKLALD
481 VEIATYRKLL EGEECRMSGD LSSNVTVSVT SSTISSNVAS KAAFGGSGGR GSSSGGGYSS GSSSYGSGGR QSGSRGGSGG
561 GGSISGGGYG SGGGSGGRYG SGGGSKGGSI SGGGYGSGGG KHSSGGGSRG GSSSGGGYGS GGGGSSSVKG SSGEAFGSSV
641 TFSFR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
K.SISISVAGGGGGFGAAGGFGGR.G	Y	99.9	73.48	1837.9070	22	1.4	919.9620	2	35.14	18	1727	OB5188.raw	3.38E4	2	2	71	92	
R.GGSGGGGSISGGGYGSGGGSGGR.Y	Y	99.9	69.17	1740.7411	23	1.5	871.3792	2	25.12	18	1140	OB5188.raw	4.92E3	2	2	556	578	
R.NLDLDSIIAEVKAQYEEIAQR.S	Y	99.9	64.07	2417.2437	21	-0.3	806.7549	3	41.90	18	2109	OB5188.raw	1.02E5	7	7	348	368	
R.GFSSGSAVVSGGSR.R	Y	99.9	63.32	1253.6000	14	-0.4	627.8070	2	27.77	18	1297	OB5188.raw	2.54E4	2	2	21	34	
K.VDLLNQEIEFLK.V	Y	99.9	61.46	1459.7922	12	0.1	730.9034	2	37.92	18	1883	OB5188.raw	8.34E4	3	3	309	320	
R.FLEQQNQVLQTK.W	N	99.9	61.35	1474.7780	12	0.3	738.3965	2	30.79	18	1475	OB5188.raw	1.97E5	7	7	204	215	
R.HGGGGGGFGGGGFGSR.S	Y	99.9	55.59	1319.5754	16	0.0	660.7950	2	27.29	18	1269	OB5188.raw	2.82E4	3	3	46	61	
K.YEELQVTVGR.H	Y	99.9	53.69	1192.6088	10	0.0	597.3116	2	31.66	18	1525	OB5188.raw	1.18E4	1	1	381	390	
R.GSSSGGGYSSGSSSYGSGGR.Q	Y	99.9	53.30	1739.6982	20	0.7	870.8570	2	24.75	18	1118	OB5188.raw	4.33E3	2	2	531	550	
G.GSGFGGGSGFGGGSGFSGGGFGGGGFGGGR.F	Y	99.9	52.86	2398.0110	30	1.1	800.3452	3	35.48	18	1746	OB5188.raw	5.94E4	2	2	99	128	
K.LALDVEIATYR.K	Y	99.9	52.20	1262.6870	11	-0.8	632.3503	2	35.37	18	1740	OB5188.raw	1.39E4	2	2	477	487	
K.VLYDAEISQIHQSVTDTNVILSMDNSR.N	Y	99.9	50.92	3047.4871	27	2.2	1016.8385	3	36.85	18	1823	OB5188.raw	5.21E4	2	2	321	347	
K.AQYEEIAQR.S	Y	99.9	50.04	1106.5356	9	-0.6	554.2748	2	27.61	18	1288	OB5188.raw	3.32E4	2	2	360	368	
K.GGSISGGGYGSGGGK.H	Y	99.9	48.52	1196.5421	15	-1.1	599.2776	2	23.54	18	1054	OB5188.raw	3.06E3	3	3	587	601	
K.IEISELNR.V	N	99.9	46.44	972.5240	8	-0.5	487.2690	2	30.76	18	1473	OB5188.raw	3.26E4	3	3	400	407	
R.STSSFSC(+57.02)LSR.H	Y	99.9	43.13	1130.5026	10	0.6	566.2589	2	29.20	18	1381	OB5188.raw	2.99E3	1	1	36	45	Carbamidomethylation
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVS.V	Y	99.9	42.60	2757.2935	32	-1.2	920.1040	3	37.31	18	1849	OB5188.raw	0	1	1	129	160	
R.TSQNSELNNMQDLVEDYKK.K	Y	99.9	42.49	2255.0376	19	-0.1	752.6864	3	34.18	18	1673	OB5188.raw	6.48E4	2	2	254	272	
R.NKLNDLEEALQQAKEDLAR.L	Y	99.9	42.42	2197.1338	19	-0.6	733.3848	3	37.22	18	1844	OB5188.raw	3.83E4	2	2	446	464	
R.TAAENDFVTLK.K	Y	99.9	42.31	1207.6084	11	-0.3	604.8113	2	31.83	18	1535	OB5188.raw	1.37E4	1	1	282	292	
R.SLVGLGGTK.S	Y	99.9	41.20	830.4861	9	-0.3	416.2502	2	29.33	18	1389	OB5188.raw	3.08E4	1	1	62	70	
R.TAAENDFVTLKK.D	Y	99.9	41.01	1335.7034	12	1.4	668.8599	2	29.28	18	1385	OB5188.raw	3.76E3	1	1	282	293	
K.VLYDAEISQIHQSVTDTNVILSM(+15.99)DNSR.N	Y	99.8	39.11	3063.4819	27	-0.4	1022.1675	3	36.14	18	1783	OB5188.raw	1.18E4	2	2	321	347	Oxidation (M)
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVN.Q	Y	99.2	33.15	2970.4048	34	1.9	991.1440	3	37.42	18	1855	OB5188.raw	3.9E3	1	1	129	162	
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQ.S	Y	98.5	30.29	3098.4634	35	-1.5	1033.8269	3	37.33	18	1850	OB5188.raw	4.08E3	1	1	129	163	
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	Y	98.4	30.04	4091.0652	44	2.0	1364.6984	3	38.20	18	1899	OB5188.raw	1.47E4	1	1	129	172	
K.IEISELNRVIQR.L	N	95.7	27.60	1468.8362	12	0.3	735.4256	2	33.44	18	1630	OB5188.raw	0	1	1	400	411	
K.FASFIDKVR.F	N	94.1	25.62	1081.5920	9	0.2	361.5380	3	31.62	18	1523	OB5188.raw	1.65E4	2	2	195	203	

R.LQGEIAHVK.K	Y	93.8	25.25	993.5607	9	-1.1	497.7871	2	24.30	18	1093	OB5188.raw	2.88E3	1	1	412	420	
R.GGGFGGGSGFGGGSGFGGGSGFSGGGFGGGFGGGR.F	Y	93.5	24.32	2830.1868	36	-0.9	944.4020	3	36.53	18	1805	OB5188.raw	0	1	1	93	128	
R.TSQNSELNNM(+15.99)QDLVEDYKK.K	Y	93.5	24.12	2271.0325	19	0.2	758.0182	3	30.28	18	1445	OB5188.raw	5.1E3	1	1	254	272	Oxidation (M)
K.VELQSKVDLLNQEIEFLK.V	Y	90.4	20.64	2144.1729	18	-3.4	715.7291	3	37.12	18	1838	OB5188.raw	2.42E3	1	1	303	320	
N.VKVDPEIQNVK.A	Y	90.3	20.51	1267.7136	11	-1.6	634.8631	2	27.94	18	1307	OB5188.raw	8.05E2	1	1	171	181	
K.DVDNAYM(+15.99)IK.V	Y	84.1	19.50	1083.4906	9	-3.2	542.7509	2	29.66	18	1408	OB5188.raw	0	1	1	294	302	Oxidation (M)
total 34 peptides																		

sp|K1C9_HUMAN|

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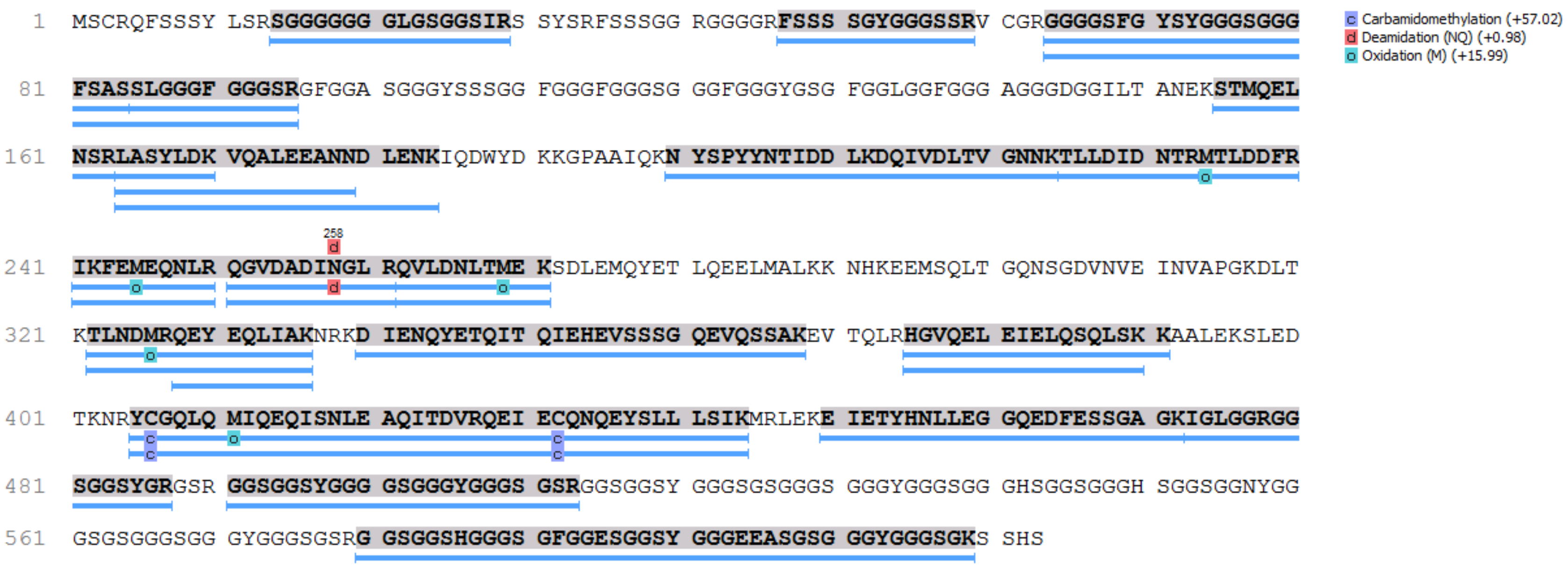
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.SGGGGGGGLGSGGSIR.S	Y	99.9	63.52	1231.5905	16	0.5	616.8028	2	25.76	18	1178	OB5188.raw	2.55E4	4	4	14	29	
R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	Y	99.9	60.32	2704.1538	32	1.1	902.3929	3	35.34	18	1738	OB5188.raw	3.49E4	2	2	64	95	
K.EIETYHNLLEGGQEDFESSGAGK.I	Y	99.9	59.50	2509.1245	23	1.3	837.3832	3	33.87	18	1655	OB5188.raw	5.49E4	4	4	450	472	
R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	Y	99.9	56.93	3222.2742	40	0.3	1075.0990	3	27.75	18	1296	OB5188.raw	1.41E4	2	2	580	619	
K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	Y	99.9	56.74	2901.4031	25	1.8	968.1434	3	39.08	18	1949	OB5188.raw	1.59E5	7	7	200	224	
R.FSSSSGYGGGSSR.V	Y	99.9	55.94	1234.5214	13	0.2	618.2681	2	24.67	18	1113	OB5188.raw	2.76E4	4	4	47	59	
R.QGVDADINGLR.Q	Y	99.9	55.23	1156.5836	11	-0.3	579.2989	2	30.88	18	1480	OB5188.raw	3.28E4	2	2	251	261	
R.GGSGGSYGGGGSGGGYGGGSGSR.G	Y	99.9	54.31	1790.7203	23	0.1	896.3675	2	24.52	18	1105	OB5188.raw	2.29E4	3	3	491	513	
K.STMQELNSR.L	Y	99.9	52.27	1064.4921	9	0.4	533.2535	2	26.23	18	1206	OB5188.raw	3.29E4	3	3	155	163	
K.TLNDMRQEYEQLIAK.N	Y	99.9	51.95	1850.9197	15	-0.4	617.9802	3	35.11	18	1725	OB5188.raw	1.06E5	6	6	322	336	
R.HGVQELEIELQSQLSK.K	Y	99.9	50.29	1836.9581	16	-0.5	613.3264	3	35.51	18	1748	OB5188.raw	9.35E4	2	2	375	390	
R.HGVQELEIELQSQLSKK.A	Y	99.9	48.71	1965.0531	17	0.2	656.0251	3	34.61	18	1697	OB5188.raw	4.4E4	2	2	375	391	
K.TLLDIDNTR.M	Y	99.9	46.75	1059.5560	9	-0.7	530.7849	2	32.17	18	1555	OB5188.raw	7.53E4	4	4	225	233	
R.QGVDADIN(+.98)GLR.Q	Y	99.9	43.90	1157.5676	11	-0.8	579.7906	2	30.38	18	1451	OB5188.raw	1.3E4	1	1	251	261	Deamidation (NQ)
R.QVLDNLTM(+15.99)EK.S	Y	99.9	43.43	1205.5962	10	-0.5	603.8051	2	30.36	18	1450	OB5188.raw	5.94E3	1	1	262	271	Oxidation (M)
R.IKFEMEQNLR.Q	Y	99.9	43.09	1306.6703	10	-1.7	654.3413	2	31.45	18	1513	OB5188.raw	5.08E4	3	3	241	250	
S.SLGGGFGGGSR.G	Y	99.9	40.72	950.4570	11	-2.1	476.2348	2	27.80	18	1299	OB5188.raw	9.67E3	1	1	85	95	

R.M(+15.99)TLDDFR.I	Y	99.9	39.69	912.4011	7	-0.8	457.2075	2	30.21	18	1441	OB5188.raw	1.37E4	2	2	234	240	Oxidation (M)
R.LASYLDKVQALEEANN.D	Y	99.8	39.17	1776.8894	16	0.5	889.4525	2	35.04	18	1721	OB5188.raw	2.18E3	1	1	164	179	
R.GGGGSFGYSYGGGSGGGFSAS.S	Y	99.8	37.80	1771.7074	21	3.5	886.8641	2	34.41	18	1686	OB5188.raw	0	1	1	64	84	
R.IKFEM(+15.99)EQNLR.Q	Y	99.5	35.54	1322.6653	10	-0.1	662.3398	2	28.62	18	1347	OB5188.raw	1.1E4	2	2	241	250	Oxidation (M)
R.LASYLDK.V	N	99.5	33.70	808.4330	7	0.0	405.2238	2	28.18	18	1321	OB5188.raw	1.48E4	1	1	164	170	
K.TLNDM(+15.99)RQEYEQLIAK.N	Y	99.5	33.66	1866.9146	15	0.1	623.3122	3	32.30	18	1562	OB5188.raw	1.57E4	2	2	322	336	Oxidation (M)
K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	Y	98.3	28.54	3263.5066	29	0.8	1088.8436	3	37.63	18	1867	OB5188.raw	7.51E4	1	1	340	368	
R.QVLDNLTMEK.S	Y	95.7	27.46	1189.6013	10	-0.3	595.8077	2	31.99	18	1544	OB5188.raw	2.1E3	1	1	262	271	
R.LASYLDKVQALEEANNDLENK.I	Y	94.2	25.67	2376.1809	21	1.4	793.0687	3	35.20	18	1730	OB5188.raw	0	1	1	164	184	
R.YC(+57.02)GQLQM(+15.99)IQEQISNLEAQITDVRQEIEC(+57.02)QNQEYSLLLSIK.M	Y	92.8	22.58	4828.3359	40	2.7	1208.0945	4	43.51	18	2200	OB5188.raw	8.3E4	2	2	405	444	Carbamidomethylation; Oxidation (M)
R.YC(+57.02)GQLQMIQEQISNLEAQITDVRQEIEC(+57.02)QNQEYSLLLSIK.M	Y	90.6	20.83	4812.3408	40	1.7	1204.0945	4	43.78	18	2216	OB5188.raw	1.15E5	2	2	405	444	Carbamidomethylation
K.IGLGGRGGSGGSYGR.G	Y	90.5	20.69	1349.6799	15	-1.5	450.8999	3	26.56	18	1226	OB5188.raw	6.98E3	1	1	473	487	
R.QEYEQLIAK.N	Y	84.0	19.36	1120.5764	9	-1.5	561.2946	2	30.67	18	1468	OB5188.raw	2.48E3	1	1	328	336	
total 30 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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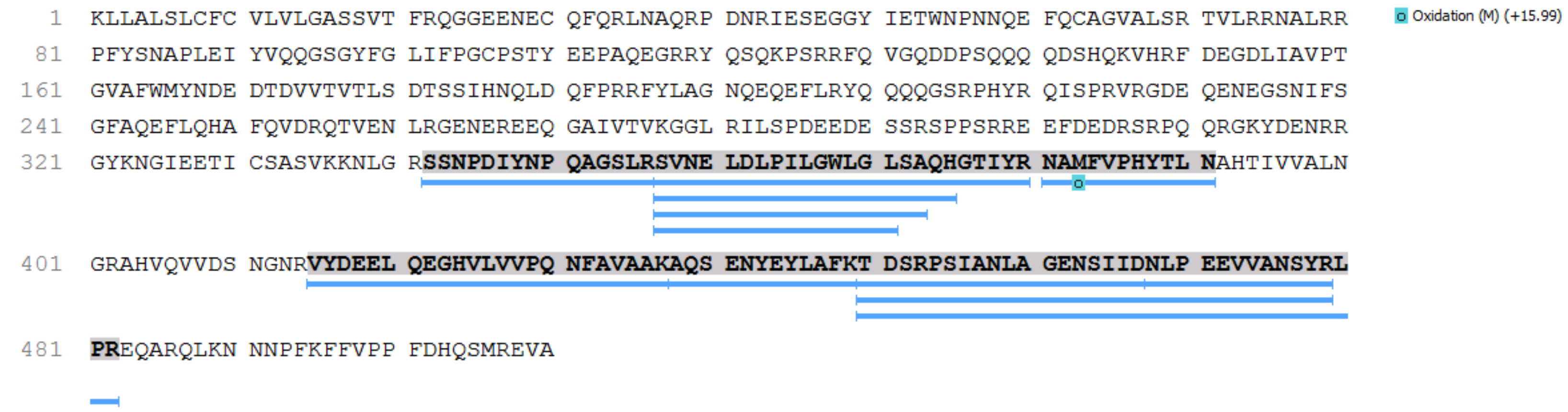
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG R**SSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL N**AHTIVVALN

401 GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL**

481 **PR**EQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
K.AQSENYEYLAFK.T	Y	99.9	65.65	1461.6776	12	0.0	731.8461	2	33.68	18	1644	OB5188.raw	6.47E4	6	6	438	449	
R.SSNPDIYNPQAGSLR.S	Y	99.9	63.18	1617.7747	15	0.3	809.8948	2	31.01	18	1488	OB5188.raw	1.46E5	7	7	342	356	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	52.72	3243.6006	30	2.8	1082.2104	3	38.36	18	1908	OB5188.raw	1.54E5	4	4	450	479	
R.SVNELDLPILGWLGLSA.Q	Y	99.9	52.10	1795.9719	17	1.3	898.9944	2	46.16	18	2352	OB5188.raw	7.97E4	4	4	357	373	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	51.28	2651.4070	24	1.4	884.8109	3	42.66	18	2152	OB5188.raw	9.26E5	22	22	357	380	
R.SVNELDLPILGWLGL.S	Y	99.9	40.51	1637.9028	15	0.1	819.9587	2	47.57	18	2433	OB5188.raw	1.04E5	5	5	357	371	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.8	38.76	2554.3066	23	1.3	852.4440	3	35.16	18	1728	OB5188.raw	1.58E4	2	2	415	437	
R.NAM(+15.99)FVPHYTLN.A	Y	99.8	37.90	1321.6125	11	0.4	661.8138	2	33.01	18	1604	OB5188.raw	3.17E3	1	1	381	391	Oxidation (M)
K.TDSRPSIANLAGENSIID.N	N	99.5	34.52	1871.9225	18	1.5	936.9699	2	34.95	18	1716	OB5188.raw	0	1	1	450	467	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.1	31.52	3609.8386	33	0.6	903.4675	4	38.22	18	1900	OB5188.raw	4.93E4	3	3	450	482	
D.NLPEEVVANSYR.L	Y	99.1	31.45	1389.6888	12	4.9	695.8551	2	32.76	18	1589	OB5188.raw	0	1	1	468	479	
R.SVNELDLPILGWLGLSAQH.G	Y	95.6	27.20	2061.0894	19	1.0	1031.5530	2	43.43	18	2195	OB5188.raw	4.05E3	1	1	357	375	
total 12 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

▣ Oxidation (M) (+15.99)

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGR**SSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLN**AHTIVVA

401 LNGRAHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY**

481 **RLPR**EQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
K.AQSENYEYLAFK.T	Y	99.9	65.65	1461.6776	12	0.0	731.8461	2	33.68	18	1644	OB5188.raw	6.47E4	6	6	440	451	
R.SSNPDIYNPQAGSLR.S	Y	99.9	63.18	1617.7747	15	0.3	809.8948	2	31.01	18	1488	OB5188.raw	1.46E5	7	7	344	358	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	52.72	3243.6006	30	2.8	1082.2104	3	38.36	18	1908	OB5188.raw	1.54E5	4	4	452	481	
R.SVNELDLPILGWLGLSA.Q	Y	99.9	52.10	1795.9719	17	1.3	898.9944	2	46.16	18	2352	OB5188.raw	7.97E4	4	4	359	375	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	51.28	2651.4070	24	1.4	884.8109	3	42.66	18	2152	OB5188.raw	9.26E5	22	22	359	382	
R.SVNELDLPILGWLGL.S	Y	99.9	40.51	1637.9028	15	0.1	819.9587	2	47.57	18	2433	OB5188.raw	1.04E5	5	5	359	373	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.8	38.76	2554.3066	23	1.3	852.4440	3	35.16	18	1728	OB5188.raw	1.58E4	2	2	417	439	
R.NAM(+15.99)FVPHYTLN.A	Y	99.8	37.90	1321.6125	11	0.4	661.8138	2	33.01	18	1604	OB5188.raw	3.17E3	1	1	383	393	Oxidation (M)
K.TDSRPSIANLAGENSIID.N	N	99.5	34.52	1871.9225	18	1.5	936.9699	2	34.95	18	1716	OB5188.raw	0	1	1	452	469	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.1	31.52	3609.8386	33	0.6	903.4675	4	38.22	18	1900	OB5188.raw	4.93E4	3	3	452	484	
D.NLPEEVVANSYR.L	Y	99.1	31.45	1389.6888	12	4.9	695.8551	2	32.76	18	1589	OB5188.raw	0	1	1	470	481	
R.SVNELDLPILGWLGLSAQH.G	Y	95.6	27.20	2061.0894	19	1.0	1031.5530	2	43.43	18	2195	OB5188.raw	4.05E3	1	1	359	377	
total 12 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDR**QIL QNLRGENESD EQGAIVTVR**G GLRILSPDRK KRQQYERPDE

321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**

401 **EYGNLYR**NAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGK**SQSENF EYVAFKTDSR**

481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	69.35	1540.7673	13	0.5	771.3914	2	36.63	18	1811	OB5188.raw	5.6E4	3	3	395	407	

K.TANELNLLILR.W	Y	99.9	47.41	1268.7452	11	-0.1	635.3798	2	36.87	18	1824	OB5188.raw	2.03E4	2	2	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.9	46.77	3544.7434	33	2.9	1182.5918	3	39.19	18	1955	OB5188.raw	1.78E4	2	2	477	509	
K.SQSENFEYVAFK.T	N	99.9	44.30	1447.6619	12	-0.4	724.8380	2	33.89	18	1656	OB5188.raw	5.21E3	1	1	465	476	
R.NRSPDIYNPQAGSLK.T	N	99.9	40.68	1658.8376	15	-1.4	553.9524	3	29.26	18	1384	OB5188.raw	5.71E3	1	1	369	383	
R.SPDIYNPQAGSLK.T	N	99.9	39.64	1388.6936	13	0.4	695.3544	2	30.93	18	1483	OB5188.raw	3.8E3	1	1	371	383	
R.QILQNLRGENESDEQGAIVTVR.G	N	93.0	23.25	2468.2620	22	0.6	823.7618	3	32.39	18	1567	OB5188.raw	1.24E3	1	1	278	299	
total 7 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDR**QIL QNLRGENESD EQGAIVTVR**G GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYR**NAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGK**SQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	69.35	1540.7673	13	0.5	771.3914	2	36.63	18	1811	OB5188.raw	5.6E4	3	3	395	407	
K.TANELNLLILR.W	Y	99.9	47.41	1268.7452	11	-0.1	635.3798	2	36.87	18	1824	OB5188.raw	2.03E4	2	2	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.9	46.77	3544.7434	33	2.9	1182.5918	3	39.19	18	1955	OB5188.raw	1.78E4	2	2	477	509	
K.SQSENFEYVAFK.T	N	99.9	44.30	1447.6619	12	-0.4	724.8380	2	33.89	18	1656	OB5188.raw	5.21E3	1	1	465	476	
R.NRSPDIYNPQAGSLK.T	N	99.9	40.68	1658.8376	15	-1.4	553.9524	3	29.26	18	1384	OB5188.raw	5.71E3	1	1	369	383	
R.SPDIYNPQAGSLK.T	N	99.9	39.64	1388.6936	13	0.4	695.3544	2	30.93	18	1483	OB5188.raw	3.8E3	1	1	371	383	
R.QILQNLRGENESDEQGAIVTVR.G	N	93.0	23.25	2468.2620	22	0.6	823.7618	3	32.39	18	1567	OB5188.raw	1.24E3	1	1	278	299	
total 7 peptides																		

sp|K1C15_SHEEP|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MATTLLQTSS STFGGSSTRG GSLLAGGGGF GGGSLYGGGG SRTISASSAR FVSSGSAGGY GGGFGGGAGS GYGGGFGGGF
81 GGGFGSGFGD FGGGDGGLLS GNEKITMQNL NDRLASYLEK VR**ALEEANAD LEVK**IRDWYQ RQSPTSPERD YSPYFKTTDE
161 LRDKILAAAI DNSRVILEID NAR**LAADDFR** LKYENEMALR **QSVEADINGL RRVLDELTLT K**TDLEMQIES LNEELAYLKK
241 NHEEEMKEFS NQLAGQVNVE MDAAPGVDLT RVLSEMREQY EAMAEKNRRD AEAWFFSKTE ELNKEVASNT EMIQTSKSEI
321 TDLRRTIQGL EIELQSQLSM KAGLESTLAE TDGRYAAQLQ QIQGLISSIE AQLSELRSEM EAQNQEYKML LDIKTRLEQE
401 IATYHSLLEG QDARMAGIGT GEASLGGGGG GKVRINVEES VDGKVVSSRK REI

d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.ALEEANADLEVK.I	Y	99.9	60.23	1300.6510	12	0.2	651.3329	2	30.35	18	1449	OB5188.raw	1.48E4	1	1	123	134	
R.VLDELTLTK.T	N	99.9	55.26	1030.5911	9	-0.7	516.3024	2	32.64	18	1582	OB5188.raw	7.48E4	5	5	213	221	

R.LAADDFR.L	N	99.9	44.44	806.3922	7	0.1	404.2034	2	28.88	18	1362	OB5188.raw	9.82E4	6	6	184	190	
R.QSVEADINGLR.R	N	99.9	42.79	1200.6099	11	-0.2	601.3121	2	31.82	18	1534	OB5188.raw	3.81E3	1	1	201	211	
R.QSVEADINGLRR.V	N	99.1	31.52	1356.7109	12	-0.2	679.3626	2	30.33	18	1448	OB5188.raw	9.25E4	2	2	201	212	
R.QSVEADIN(+.98)GLRR.V	N	78.0	19.07	1357.6949	12	-0.7	453.5719	3	28.72	18	1353	OB5188.raw	9.85E3	1	1	201	212	Deamidation (NQ)
total 6 peptides																		

sp|Q6PSU2|CONG7_ARAHY

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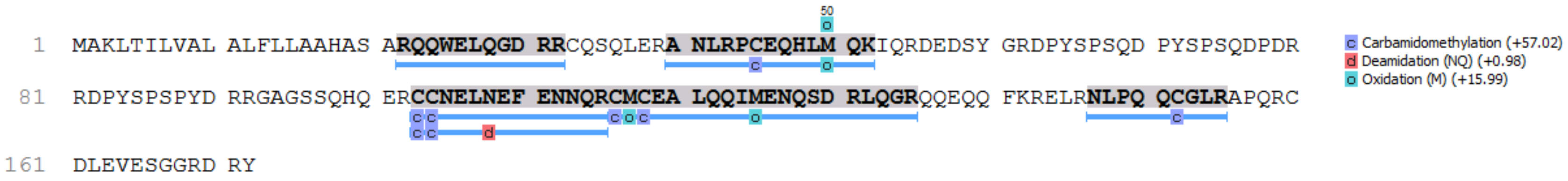
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM QKIQRDEDSY GRDPYSPSQD PYSPSQDPDR

81 RDPYSPSPYD RRGAGSSQHQ ERCCNELNEF ENNQRCMCEA LQQIMENQSD RLQGRQQEQQ FKRELRNLPQ QCGLRAPQRC

161 DLEVESGGRD RY

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.C(+57.02)C(+57.02)NELNEFENNQR.C	Y	99.9	60.86	1725.6835	13	0.7	863.8496	2	31.03	18	1489	OB5188.raw	4.47E4	2	2	103	115	Carbamidomethylation
R.ANLRPC(+57.02)EQHLM(+15.99)QK.I	Y	99.9	47.34	1639.7922	13	-1.0	547.6041	3	24.78	18	1120	OB5188.raw	1.77E5	14	14	40	52	Carbamidomethylation; Oxidation (M)
R.NLPQQC(+57.02)GLR.A	Y	99.9	47.22	1084.5448	9	-0.5	543.2794	2	27.32	18	1271	OB5188.raw	1.47E5	7	7	147	155	Carbamidomethylation
R.C(+57.02)M(+15.99)C(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.9	41.11	2498.0771	20	-0.2	833.6995	3	31.61	18	1522	OB5188.raw	8.48E4	2	2	116	135	Carbamidomethylation; Oxidation (M)
A.RQQWELQGDRR.C	Y	99.8	38.62	1470.7440	11	-0.9	491.2548	3	27.04	18	1255	OB5188.raw	4.19E4	1	1	22	32	
R.C(+57.02)C(+57.02)NELN(+.98)EFENNQR.C	Y	99.8	38.35	1726.6675	13	-7.2	864.3348	2	31.52	18	1517	OB5188.raw	0	1	1	103	115	Carbamidomethylation; Deamidation (NQ)
total 6 peptides																		

sp|TRYP_PIG|

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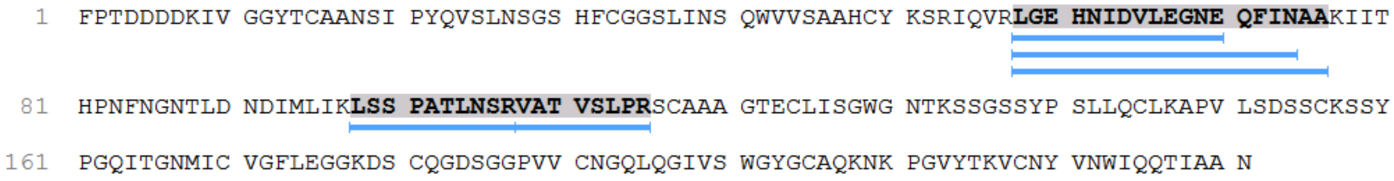
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 FPTDDDDKIV GGYTCAANSI PYQVSLNSGS HFCGGSLINS QWVVSAAHCY KSRIQVRLGE HNIDVLEGNE QFINAAKIIT

81 HPNFNGNTLD NDIMLIKLSS PATLNSRVAT VSLPRSCAAA GTECLISGWG NTKSSGSSYP SLLQCLKAPV LSDSSCKSSY

161 PGQITGNMIC VGFLEGGKDS CQGDSGGPVV CNGQLQGIVS WGYGCAQKNK PGVYTKVCNY VNWIQQTIAA N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.LGEHNIDVLEGNEQFINAA.K	Y	99.9	48.11	2082.0017	19	0.8	1042.0089	2	35.92	18	1771	OB5188.raw	0	1	1	58	76	
R.VATVSLPR.S	Y	99.9	41.09	841.5021	8	0.2	421.7584	2	29.52	18	1400	OB5188.raw	1.75E5	2	2	108	115	
K.LSSPATLNSR.V	Y	99.9	40.30	1044.5564	10	-0.5	523.2852	2	27.47	18	1280	OB5188.raw	1.63E4	1	1	98	107	
R.LGEHNIDVLEGNE.Q	Y	99.8	37.92	1437.6736	13	0.3	719.8443	2	32.67	18	1584	OB5188.raw	6.66E3	1	1	58	70	
R.LGEHNIDVLEGNEQFIN.A	Y	99.6	36.16	1939.9275	17	0.9	970.9719	2	35.44	18	1744	OB5188.raw	4.1E3	1	1	58	74	
total 5 peptides																		

E9LFE7|E9LFE7_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WEEEEEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

81 **LAFPGSGEQV EK**LIKNQRES HFVSARPQSQ SQFPSSPEKE DQEEENQGGK GPLLSILKAF N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	61	76	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	80	92	
total 2 peptides																		

Q6PSU5|Q6PSU5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
81 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
161 EEEEDEDQEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

241 **LAFPGSGEQV EK**LIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	221	236	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	240	252	
total 2 peptides																		

Q6PSU6|Q6PSU6_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRRSTRS SDNEGVIVKV SKEHVQELTK HAKSVSKKGS EEEDITNPIN
81 LRDGEPDLSN NFGRLFEVKP DKKNPQLQDL DMMLTCVEIK EGALMLPHFN SKAMVIVVVN KGTGNLELVA VRKEQQQRGR
161 REQEWEEEEE DEEEEGSNRE VRRYTARLKE GDVFIMPAAH PVAINASSEL HLLGFGINAE NNHR**IFLAGD KDNVIDQIEK**

241 QAK**DLAFPGS GEQVEK**LIKN QRESHFVSAR PQSQSPSSPE KEDQEEENQG GKGPLLSILK AFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	225	240	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	244	256	
total 2 peptides																		

Q6PSU4|Q6PSU4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GFDQRSRQFQ NLQNHRIVQI EAKPNTLVLP KHADADNILV IQQGQATVTV ANGNNRKSFN LDEGHALRIP SGFISYILNR

81 HDNQNLRVAK ISMPVNTPGQ FEDFFPASSR DQSSYLQGFS RNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRWSTRS

161 SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI

241 KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREEEEDEDE EEEGSNREVR RYTARLKEGD VFIMPAAHPV

321 AINASSELHL LGFGINAENN HR**IFLAGDKD NVIDQIEK**QA K**DLAFPGSGE QVEK**LIKNQK ESHFVSARPQ SQSQSPSSPE

401 KESPEKEDQE EENQGGKGPL LSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	343	358	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	362	374	
total 2 peptides																		

Q6PSU3|Q6PSU3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH

81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR

161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT

241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN

321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS

401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	536	551	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	555	567	
total 2 peptides																		

B3IXL2|B3IXL2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH

81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR

161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT

241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN

321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS

401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	536	551	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	555	567	
total 2 peptides																		

sp|P43237|ALL11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**
561 **SGEQVEK**LIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	536	551	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	555	567	
total 2 peptides																		

N1NG13|N1NG13_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**
561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	541	556	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	560	572	
total 2 peptides																		

sp|P43238|ALL12_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**
561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.IFLAGDKDNVIDQIEK.Q	Y	98.3	28.79	1816.9570	16	-1.2	606.6589	3	34.24	18	1676	OB5188.raw	9.97E3	1	1	541	556	
K.DLAFPGSGEQVEK.L	Y	84.3	19.64	1375.6619	13	1.7	688.8394	2	32.73	18	1587	OB5188.raw	7.46E3	1	1	560	572	
total 2 peptides																		

sp|Q647H2|AHY3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS VTFRQQGEEN ECQFQRLNAQ RPDNCIESEG GYIETWNPNN QEFQCAGVAL SRFVLRRNAL
81 RRPFYSNAPQ EIFIYQGSGY FGLIFPGCPG TFEEPIQGSE QFQRPSRHFQ GQDQSQRPLD THQKVHGFRE GDLIAVPHGV
161 AFWIYNDQDT DVVAISVLHT NSLHNQLDQF PRRFNLAGKQ EQEFLRYQQR SGRQSPKGEE QEQEQENEGG NVFSGFSTEF
241 LSHGFQVNED IVRNLRGENE REEQGAIVTV KGGLSILVPP EWRQSYQQPG RGDKDFNNGI EETICTATVK MNIGKSTSAD
321 IYNPQAGSVR **TVNELDLPIL NR**LGLSAEYG SIHRDAMFVP HYNMNANSMI YALHGGAHVQ VVDCNGNRVF DEELQEGQSL
401 VVPQNFAVAA KSQSEHFLYV AFKTNSRASI SNLAGKNSYM WNLPEDVVAN SYGLQYEQAR QLKNNNPFTF LVPPQDSQMI
481 RTVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM
R.TVNELDLPILNR.L	Y	93.6	24.48	1395.7721	12	2.2	698.8948	2	36.55	18	1806	OB5188.raw	3.8E3	1	1	331	342	
total 1 peptides																		

sp|KRHB2_HUMAN|

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSYHSFQPGS RCGSQSFSSY SAVMPRMVTH YAVSKGPCRP GGGRGLRALG CLGSRSLCNV GFGRPRVASR CGGTLPGFGY
81 RLGATCGPSA CITPVTINES LLVPLA**LEID PTVQRVKR**DE KEQIKCLNNR FASFINKVRF LEQKNKLLET KWNFMQQQRC
161 CQTNIEPIFE GYISALRRQL DCVSGDRVRL ESELCSLQAA LEGYKKKYEE ELSLRPCVEN EFVALKKDVD TAFLMKADLE
241 TNAEALVQEI DFLKSLYEEE ICLLQSQISE TSVIVKMDNS RELDVDGIIA EIKAQYDDIA SRSKAEAEAW YQCRYEELRV
321 TAGNHCDNLR NRKNEILEMN KLIQRLQQET ENVKAQRCKL EGAIAEAEQQ GEAALNDAKC KLAGLEEALQ KAKQDMACLL
401 KEYQEVMNSK LGLDIEIATY RRLLEGEEHR LCEGIGPVNI SVSSSKGAFL YEPCGVSMPV LSTGVLRSNG GCSIVGTGEL
481 YVPCEPQGLL SCGSGRKSSM TLGAGGSSPS HKH

h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS3 tacka 18 na Figuri 1	#Spec	#Spec DS3 tacka 18 na Figuri 1	Start	End	PTM

A.LEIDP(+15.99)TVQRVKR.D	Y	90.8	21.05	1468.8361	12	0.3	490.6194	3	33.42	18	1629	OB5188.raw	5.32E3	1	1	107	118	Hydroxylation Pro
total 1 peptides																		

Peptide List

1. Notes Spot 19 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

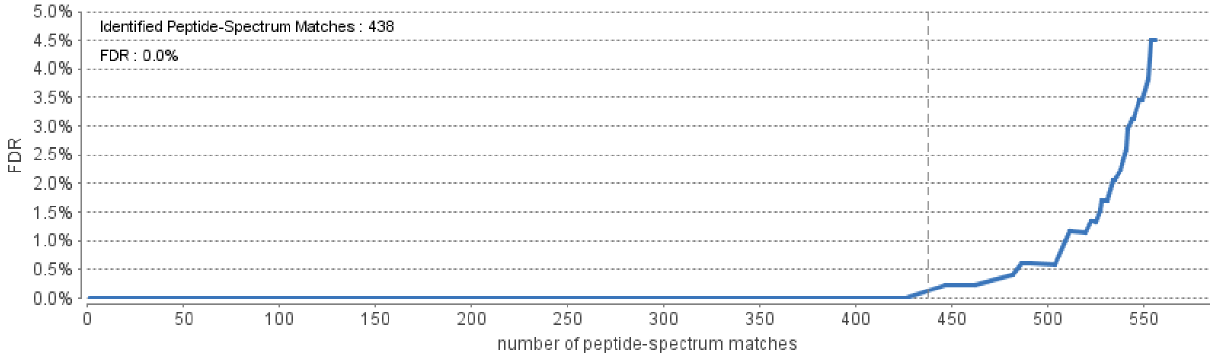


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

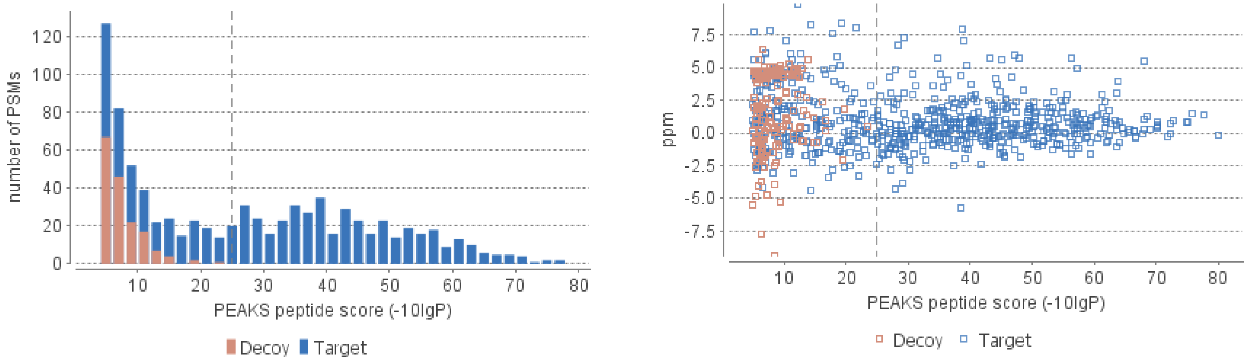
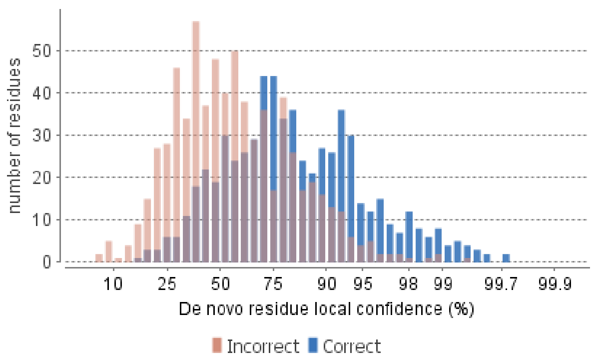


Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



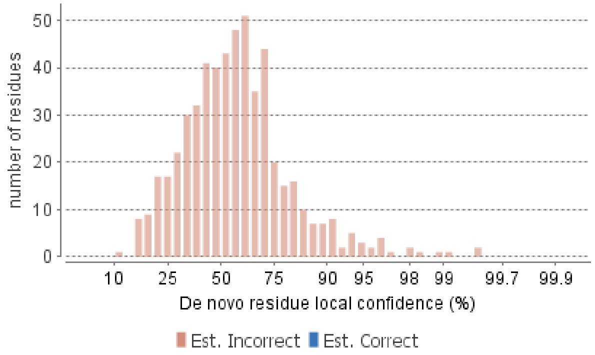


Table 1. Statistics of data.

# of MS scans	2377
# of MS/MS scans	1735

Table 2. Result filtration parameters.

Peptide -10lgP	≥25
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	433
Peptide sequences	153
Protein groups	8
Proteins	9
Proteins (#Unique Peptides)	9 (>2); 0 (=2); 0 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	69

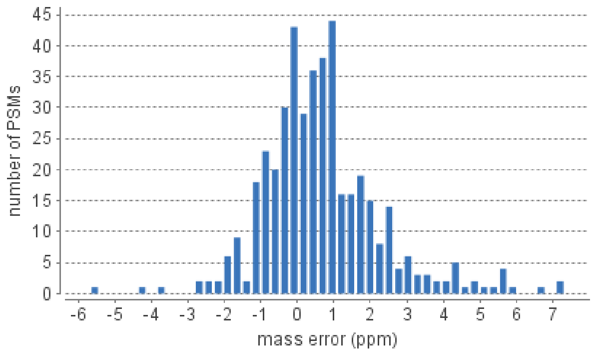
Table 4. PTM profile.

Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	56	75.15	8.15E4	1000.00
Oxidation	15.99	M	48	61.82	1.53E5	1000.00
Deamidation	.98	N	6	38.98	8E2	0.00
HydPro	15.99	P	5	43.28	3.52E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a) **(b)**



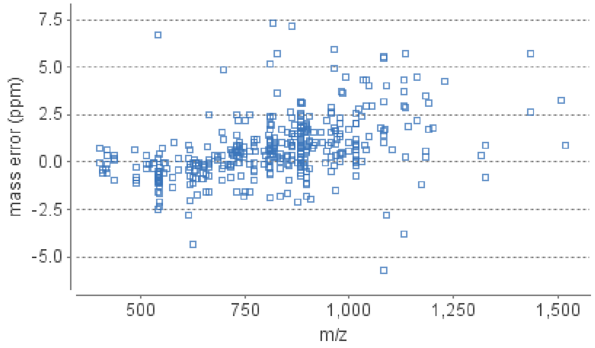


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
DS4 tacka 19 na Figuri 1	109	34	10	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: Uniprot_Peanut(3818)+cRAP_aug17
Taxon: All
Searched Entry: 1352
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB5190.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein	Protein		Score		Coverage	Coverage (%) DS4 tacka 19	Area DS4 tacka 19			#Spec DS4 tacka 19		Avg.	

Group	ID	Accession	(%)	-10lgP	(%)	na Figuri 1	na Figuri 1	#Peptides	#Unique	na Figuri 1	PTM	Mass	Description
2	221	sp|K2C1_HUMAN|	99.2	248.29	56	56	9.87E5	32	30	81	Y	65886	sp|K2C1_HUMAN|
3	220	sp|K1C10_HUMAN|	99.2	245.77	38	38	1.2E6	23	23	75	Y	59519	sp|K1C10_HUMAN|
1	216	Q6IWG5|Q6IWG5_ARAHY	99.1	244.88	30	30	4.48E6	28	23	147	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
1	217	Q0GM57|Q0GM57_ARAHY	99.1	244.88	30	30	4.48E6	28	23	147	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
6	964	sp|K22E_HUMAN|	99.2	195.89	43	43	1.09E5	16	14	23	N	65865	sp|K22E_HUMAN|
5	646	sp|K1C9_HUMAN|	99.2	186.80	46	46	3.69E5	15	15	30	N	62129	sp|K1C9_HUMAN|
7	84	A1DZF0|A1DZF0_ARAHY	99.1	157.89	22	22	1.04E5	8	3	16	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
4	215	sp|Q6PSU2|CONG7_ARAHY	99.0	154.39	41	41	9.36E5	6	6	53	Y	20114	Conglutin-7 OS=Arachis hypogaea PE=1 SV=2
9	1193	sp|TRYP_PIG|	98.4	117.26	16	16	3.25E5	5	5	11	N	24409	sp|TRYP_PIG|
total 9 proteins													

sp|K2C1_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SRQFSSRSGY R**SGGGFSSGS AGIINYQR**RT TSSSTRRSGG GGGR**FSSCGG GGGSFGAGGG FGSRSLVNLG GSKSISISVA**

81 **R**GGGRGSGFG GGYGGGGFGG GGFGGGGFGG GGIGGGGFGG FGSGGGGFGG GGFGGGGYGG GYGPVCPPGG IQEVTIN**QSL**

161 **LQPLNVEIDP EIQK**VKSRER EQIK**SLNNQF ASFIDKVRFL EQQNQVLQTK WELLQQVDTS TRTHNLEPYF ESFINNLRR**R

241 VDQLKSDQSR LDSELKNMQD MVEDYR**NKYE DEINKRTNAE NEFVTIKK**DV DGAYMTK**VDL QAKLDNLQQE IDFLTALYQA**

321 **ELSQMQTQIS ETNVILSMDN NRSLDLDSII AEVK**AQNEDI AQK**SKAEAES LYQSKYEELQ ITAGR**HGDSV RNSK**IEISEL**

401 **NR**VIQRLRSE IDNVKKQISN LQQSISDAEQ RGENALKDAK **NKLNDLEDAL QQAKEDLAR**L LRDYQELMNT K**LALDLEIAT**

481 **YR**TLLEGEES R**MSGECAPNV SVSVSTSHTT ISGGGSRGGG GGGYGSGGSS YGSGGGSYGS GGGGGGGRGS YGSGGSSYGS**

561 **GGGSYGSGGG GGGHGSYGSG SSSGGYR**GGS GGGGGGSSGG RGSGGGSSGG SIGGRGSSSG GVKSSGGSSS VRFVSTTYSG

641 VTR

Supporting Peptides:

													Area DS4		#Spec DS4			

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	tacka 19 na Figuri 1	#Spec	tacka 19 na Figuri 1	Start	End	PTM
R.SLDLDSIIAEVK.A	Y	99.9	71.81	1301.7078	12	-0.3	651.8610	2	38.47	20	1906	OB5190.raw	8.66E4	5	5	343	354	
K.YEELQITAGR.H	Y	99.9	66.29	1178.5931	10	0.2	590.3040	2	31.43	20	1501	OB5190.raw	1.37E4	2	2	376	385	
K.LALDLEIATYR.T	Y	99.9	64.75	1276.7026	11	0.0	639.3586	2	36.41	20	1788	OB5190.raw	1.29E4	2	2	472	482	
K.WELLQQVDTSTR.T	Y	99.9	63.70	1474.7416	12	0.2	738.3782	2	35.31	20	1726	OB5190.raw	1.83E4	2	2	211	222	
R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	Y	99.9	63.57	2382.9446	31	3.1	1192.4833	2	27.30	20	1262	OB5190.raw	9.14E3	4	4	518	548	
R.FLEQQNQVLQTKWELLQQVDTSTR.T	Y	99.9	62.02	2931.5090	24	1.3	978.1782	3	36.58	20	1798	OB5190.raw	5.02E4	8	8	199	222	
K.LDNLQQEIDFLTALYQA.E	Y	99.9	61.61	1993.9996	17	1.0	998.0081	2	44.61	20	2257	OB5190.raw	2.88E4	3	3	304	320	
R.FLEQQNQVLQTK.W	N	99.9	61.03	1474.7780	12	0.0	738.3962	2	30.91	20	1471	OB5190.raw	1.82E4	2	2	199	210	
R.THNLEPYFESFINNLR.R	Y	99.9	57.16	1992.9694	16	0.0	665.3304	3	38.51	20	1908	OB5190.raw	8.39E4	6	6	223	238	
R.TNAENEFVTIK.K	Y	99.9	56.86	1264.6299	11	0.0	633.3222	2	31.80	20	1522	OB5190.raw	6.43E3	1	1	277	287	
R.SGGGFSSGSAGIINYQR.R	Y	99.9	56.42	1656.7855	17	5.7	829.4048	2	32.32	20	1552	OB5190.raw	2.25E3	1	1	12	28	
K.SKAEAESLYQSKYEELQITAGR.H	Y	99.9	53.45	2500.2444	22	0.0	626.0684	4	32.62	20	1569	OB5190.raw	1.92E4	2	2	364	385	
R.FSSC(+57.02)GGGGGSFGAGGGFGSR.S	Y	99.9	53.12	1764.7274	20	1.6	883.3724	2	31.81	20	1523	OB5190.raw	6.57E3	1	1	45	64	Carbamidomethylation
R.TNAENEFVTIKK.D	Y	99.9	52.58	1392.7249	12	-0.4	697.3694	2	29.14	20	1369	OB5190.raw	1.01E4	2	2	277	288	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSM(+15.99)DNNR.S	Y	99.9	49.61	4558.1841	39	1.9	1140.5554	4	44.01	20	2221	OB5190.raw	4.88E4	2	2	304	342	Oxidation (M)
K.LDNLQQEIDFLTALYQAELSQMQTQISETNVILSMDNNR.S	Y	99.9	48.60	4526.1943	39	3.3	1509.7437	3	46.58	20	2375	OB5190.raw	2.49E5	5	5	304	342	
R.THNLEPYFESFINNLRR.R	Y	99.9	47.37	2149.0703	17	0.6	717.3645	3	37.53	20	1853	OB5190.raw	7.25E4	4	4	223	239	
K.AEAESLYQSKYEELQITAGR.H	Y	99.9	45.49	2285.1174	20	2.5	762.7150	3	33.48	20	1620	OB5190.raw	5.8E3	2	2	366	385	
N.QSLLQPLNVEIDPEIQK.V	Y	99.9	44.29	1963.0625	17	3.7	982.5422	2	36.96	20	1820	OB5190.raw	9.84E2	2	2	158	174	
R.MSGEC(+57.02)APNVSVSVSTSHTTISGGGSR.G	Y	99.9	43.80	2564.1594	26	-0.2	855.7269	3	30.42	20	1443	OB5190.raw	6.98E3	2	2	492	517	Carbamidomethylation
R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G	Y	99.9	43.64	3311.3008	39	0.6	1104.7749	3	28.16	20	1311	OB5190.raw	7.33E3	1	1	549	587	
R.SLVNLGGSKSISISVAR.G	Y	99.9	43.54	1686.9628	17	-0.3	563.3280	3	33.27	20	1608	OB5190.raw	2.24E3	1	1	65	81	
K.LDNLQQEIDFLTALYQAELS.Q	Y	99.9	43.41	2323.1582	20	2.1	1162.5889	2	46.08	20	2345	OB5190.raw	1.95E3	2	2	304	323	
R.SLVNLGGSK.S	Y	99.9	43.26	873.4919	9	0.2	437.7533	2	29.63	20	1398	OB5190.raw	2.41E4	2	2	65	73	
K.LDNLQQEIDFLTALYQAELSQMQTQISETNVILSM(+15.99)DNNR.S	Y	99.8	40.15	4542.1895	39	2.8	1136.5579	4	46.13	20	2348	OB5190.raw	2.83E4	1	1	304	342	Oxidation (M)
K.LDNLQQEIDFLTALY.Q	Y	99.8	39.54	1794.9039	15	1.3	898.4604	2	44.90	20	2274	OB5190.raw	9.73E3	3	3	304	318	
K.LDNLQQEIDFLTAL.Y	Y	99.8	39.14	1631.8406	14	0.3	816.9278	2	44.09	20	2226	OB5190.raw	2.78E4	2	2	304	317	
K.IEISELNR.V	N	99.8	38.28	972.5240	8	0.7	487.2696	2	31.10	20	1482	OB5190.raw	0	1	1	395	402	
E.SLYQSKYEELQITAGR.H	Y	99.7	37.37	1884.9581	16	-0.5	629.3264	3	32.48	20	1561	OB5190.raw	0	1	1	370	385	
K.NKLNDLEDALQQAKEDLAR.L	Y	99.6	36.92	2183.1182	19	0.6	728.7137	3	37.25	20	1837	OB5190.raw	6.88E3	1	1	441	459	
K.VDLQAKLDNLQQEIDFLTA.L	Y	99.6	35.75	2173.1267	19	1.7	1087.5725	2	40.82	20	2038	OB5190.raw	2.9E3	1	1	298	316	
K.SISISVAR.G	Y	99.6	35.30	831.4814	8	-0.3	416.7478	2	29.78	20	1407	OB5190.raw	2.04E4	1	1	74	81	
K.LDN(+.98)LQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSMDNNR.S	Y	99.4	34.81	4543.1733	39	5.7	1136.8071	4	44.44	20	2247	OB5190.raw	0	1	1	304	342	Deamidation (NQ); Oxidation (M)
R.NKYEDEINKR.T	Y	98.9	33.13	1307.6470	10	0.1	436.8896	3	25.52	20	1158	OB5190.raw	7.63E3	2	2	267	276	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSMDNNR.S	Y	98.4	31.72	4542.1895	39	0.3	1136.5549	4	44.64	20	2259	OB5190.raw	3.19E4	1	1	304	342	Oxidation (M)
K.SLNNQFASFIDKVR.F	Y	98.1	29.32	1637.8525	14	-1.0	546.9576	3	35.84	20	1756	OB5190.raw	8.37E4	2	2	185	198	
total 36 peptides																		

sp|K1C10_HUMAN|

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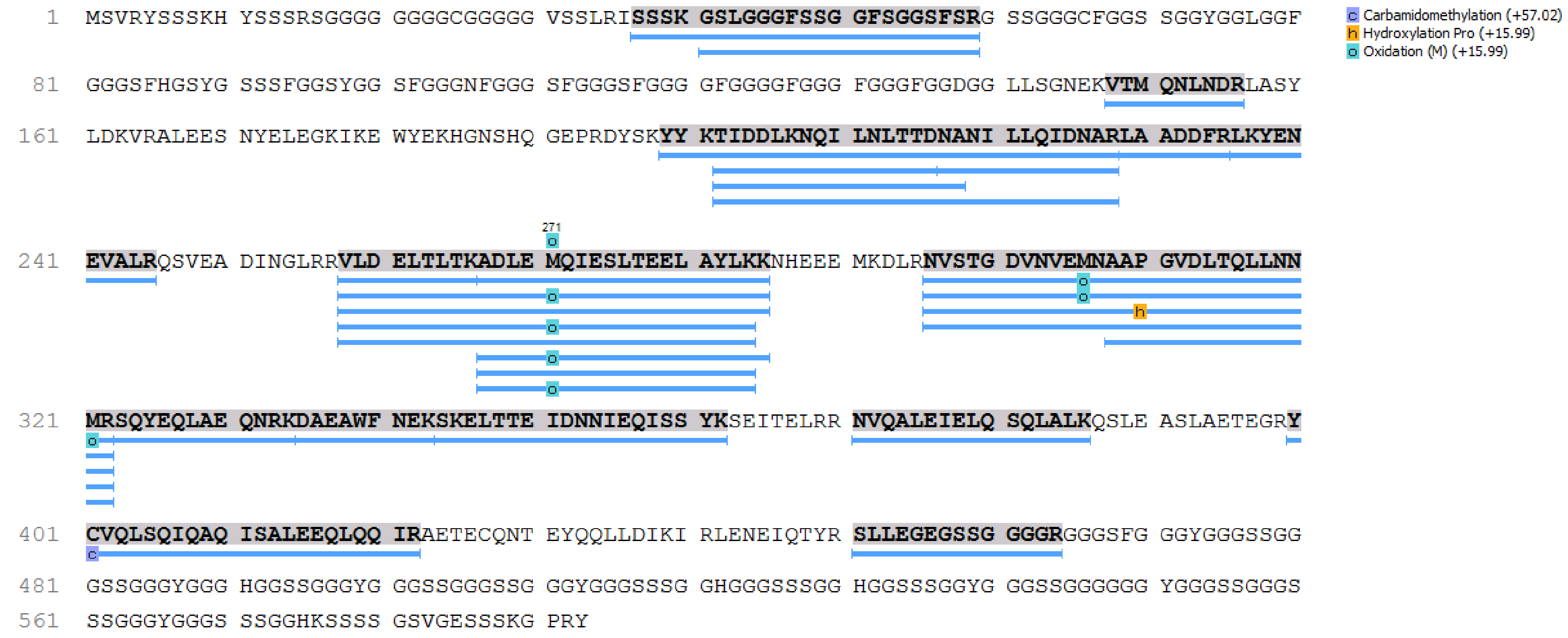
| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVRYSSSKH YSSSRSGGGG GGGGCGGGGG VSSLRI**SSSK GSLGGGFSSG GFSGGSFSR**G SSGGGCFGGS SGGYGGLGGF

81 GGGSFHGSYG SSSFGGSYGG SFGGGNFGGG SFGGGSFGGG GFGGGGFGGG FGGGFGGDGG LLSGNEK**VTM QNLNDR**LASY

161 LDKVRALEES NYELEGKIKE WYEKHGNSHQ GEPRDYSK**YY KTIDDLKNQI LNLTTDNANI LLQIDNARLA ADDFRLKYEN**

241 **EVALR**QSVEA DINGLRR**VLD ELTLTKADLE MQIESLTEEL AYLKK**NHEEE MKDLR**NVSTG DVNVEMNAAP GVDLTQLLNN**

321 **MRSQYEQLAE QNRKDAEAWF NEKSKELTTE IDNNIEQISS YK**SEITELRR **NVQALEIELQ SQLALK**QSLE ASLAETEGR**Y**

401 **CVQLSQIQAQ ISALEEQLQQ IR**AETECQNT EYQQLLDIKI RLENEIQTYR **SLLEGEGSSG GGGR**GGGSFG GGYGGGSSGG

481 GSSGGGYGGG HGGSSGGGYG GGSSGGGSSG GGYGGGSSSG GHGGGSSSGG HGGSSSGGYG GGSSGGGGGG YGGGSSGGGS

561 SSGGGYGGGS SSGGHKSSSS GSVGESSSKG PRY

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
K.GSLGGGFSSGGFSGGSFSR.G	Y	99.9	80.12	1706.7648	19	-0.2	854.3895	2	33.96	20	1649	OB5190.raw	4.54E4	3	3	41	59	
R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S	Y	99.9	75.78	2871.3855	27	1.6	958.1373	3	40.01	20	1992	OB5190.raw	1.51E5	9	9	296	322	
K.TIDDLKNQILNLTTDNANILLQIDNAR.L	Y	99.9	72.84	3051.6201	27	1.0	1018.2150	3	40.62	20	2027	OB5190.raw	4.34E5	18	18	202	228	
R.SLLEGEGSSGGGGR.G	Y	99.9	66.65	1261.5898	14	-0.4	631.8019	2	27.76	20	1288	OB5190.raw	1.38E4	3	3	451	464	
K.ADLEMQIESLTEELAYLK.K	Y	99.9	63.81	2095.0396	18	4.0	1048.5312	2	42.42	20	2129	OB5190.raw	7.78E3	2	2	267	284	
R.NVQALEIELQSQLALK.Q	Y	99.9	61.28	1796.0043	16	2.0	899.0112	2	38.10	20	1885	OB5190.raw	1.6E4	2	2	371	386	
R.YC(+57.02)VQLSQIQAQISALEEQLQQIR.A	Y	99.9	59.32	2745.4119	23	0.9	916.1454	3	42.10	20	2111	OB5190.raw	6.12E4	2	2	400	422	Carbamidomethylation
N.AAPGVDLTQLLNNMR.S	Y	99.9	58.91	1611.8402	15	-0.2	806.9272	2	38.74	20	1921	OB5190.raw	8.38E3	1	1	308	322	
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNMR.S	Y	99.9	57.28	2887.3804	27	5.0	963.4722	3	39.08	20	1940	OB5190.raw	3.52E4	1	1	296	322	Oxidation (M)
K.ADLEM(+15.99)QIESLTEELAYLK.K	Y	99.9	55.55	2111.0344	18	2.9	1056.5276	2	42.71	20	2146	OB5190.raw	1.03E4	1	1	267	284	Oxidation (M)
K.DAEAWFNEK.S	Y	99.9	51.91	1108.4825	9	-0.6	555.2482	2	33.78	20	1638	OB5190.raw	1.05E4	2	2	335	343	
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNM(+15.99)R.S	Y	99.9	51.73	2903.3752	27	1.6	968.8006	3	37.13	20	1830	OB5190.raw	3.48E3	1	1	296	322	Oxidation (M)
K.ADLEMQIESLTEELAYLKK.N	Y	99.9	51.59	2223.1343	19	0.4	742.0524	3	40.06	20	1995	OB5190.raw	5.57E4	2	2	267	285	
K.VTMQNLNDR.L	Y	99.9	50.88	1089.5237	9	-1.0	545.7686	2	27.92	20	1297	OB5190.raw	3.2E3	1	1	148	156	
K.ADLEM(+15.99)QIESLTEELAYLKK.N	Y	99.9	49.78	2239.1294	19	0.8	747.3843	3	40.22	20	2004	OB5190.raw	4.6E4	3	3	267	285	Oxidation (M)
D.NANILLQIDNAR.L	Y	99.9	49.44	1353.7365	12	0.3	677.8757	2	34.66	20	1689	OB5190.raw	2.77E3	1	1	217	228	
R.VLDELTLTK.A	Y	99.9	48.88	1030.5911	9	-0.1	516.3027	2	32.84	20	1582	OB5190.raw	7.32E3	2	2	258	266	
R.LAADDFR.L	Y	99.9	48.04	806.3922	7	0.7	404.2037	2	29.07	20	1365	OB5190.raw	1.67E4	2	2	229	235	
R.VLDELTLTKADLEM(+15.99)QIESLTEELAYLK.K	Y	99.9	46.76	3123.6147	27	4.3	1042.2167	3	42.98	20	2162	OB5190.raw	1.06E4	1	1	258	284	Oxidation (M)
R.LKYENEVALR.Q	Y	99.9	45.67	1233.6716	10	0.7	617.8435	2	29.43	20	1386	OB5190.raw	3.93E3	1	1	236	245	
R.SQYEQLAEQNRK.D	Y	99.9	45.54	1492.7269	12	-1.8	747.3694	2	26.70	20	1227	OB5190.raw	2.96E3	1	1	323	334	
R.NVSTGDVNVEMNAAP(+15.99)GVDLTQLLNNMR.S	Y	99.9	43.28	2887.3804	27	-0.2	963.4672	3	39.28	20	1951	OB5190.raw	3.52E4	1	1	296	322	Hydroxylation Pro
I.SSSKGSLGGGFSSGGFSGGSFSR.G	Y	99.8	40.79	2095.9558	23	-0.2	699.6591	3	32.04	20	1536	OB5190.raw	7.16E3	3	3	37	59	
K.TIDDLKNQILNLTTD.N	Y	99.8	40.59	1715.8942	15	1.1	858.9553	2	37.87	20	1872	OB5190.raw	6.3E3	2	2	202	216	
R.VLDELTLTKADLEMQIESLTEELAYLK.K	Y	99.7	37.68	3107.6199	27	0.9	1036.8815	3	43.21	20	2175	OB5190.raw	1.41E4	1	1	258	284	

K.TIDDLKNQILNLTTDNA.N	Y	99.7	37.21	1900.9741	17	0.9	951.4952	2	37.98	20	1878	OB5190.raw	1.05E3	1	1	202	218	
K.SKELTTEIDNNIEQISSYK.S	Y	99.6	36.40	2211.0906	19	0.8	738.0381	3	34.96	20	1706	OB5190.raw	1.55E3	1	1	344	362	
K.YYKTIDDLKNQILNLTTDNANILLQIDNAR.L	Y	98.8	32.81	3505.8416	30	-2.1	877.4658	4	40.40	20	2014	OB5190.raw	3.62E4	3	3	199	228	
R.VLDELTLTKADLEMQIESLTEELAYLKK.N	Y	98.1	29.21	3235.7148	28	-0.3	809.9357	4	41.53	20	2079	OB5190.raw	7.91E4	3	3	258	285	
R.VLDELTLTKADLEM(+15.99)QIESLTEELAYLKK.N	Y	98.1	28.89	3251.7097	28	0.6	813.9352	4	41.27	20	2064	OB5190.raw	7.14E4	1	1	258	285	Oxidation (M)
total 30 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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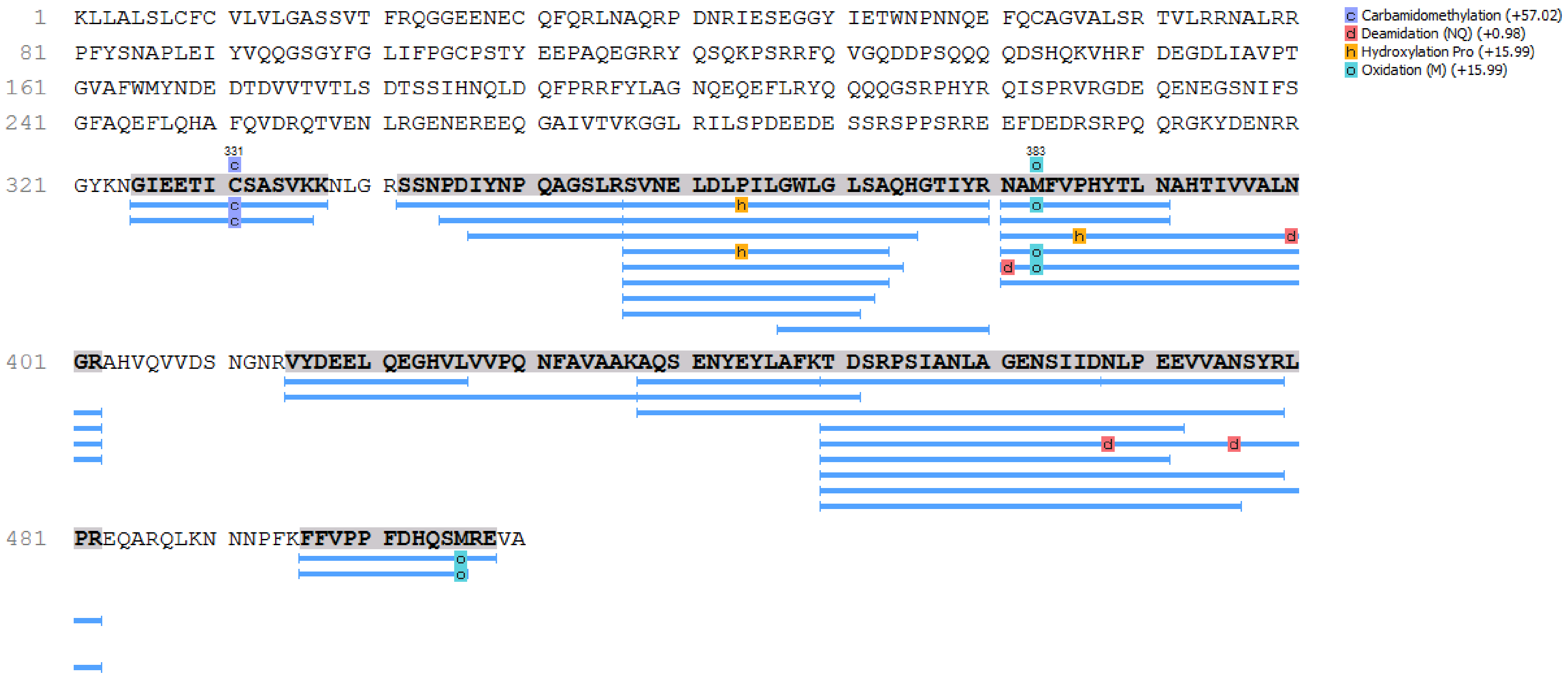
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKN**GIEETI CSASVKK**NLG R**SSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN**

401 **GR**AHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL**

481 **PR**EQARQLKN NNPFK**FFVPP FDHQSMRE**VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	77.55	3243.6006	30	1.4	1082.2090	3	38.26	20	1894	OB5190.raw	2.55E5	9	9	450	479	
R.SSNPDIYNPQAGSLR.S	Y	99.9	72.33	1617.7747	15	0.7	809.8952	2	31.15	20	1485	OB5190.raw	2.28E5	13	13	342	356	
K.AQSENYEYLAFK.T	Y	99.9	70.26	1461.6776	12	0.5	731.8464	2	33.93	20	1647	OB5190.raw	1.5E5	8	8	438	449	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.9	64.47	2554.3066	23	0.3	852.4431	3	35.30	20	1725	OB5190.raw	3.91E4	3	3	415	437	
R.SVNELDLPILGWLGLSA.Q	Y	99.9	61.91	1795.9719	17	0.9	898.9940	2	46.60	20	2376	OB5190.raw	3.93E5	16	16	357	373	
R.SVNELDLPILGWLGLSAQH.G	Y	99.9	61.74	2061.0894	19	2.4	1031.5544	2	43.39	20	2185	OB5190.raw	2.29E4	2	2	357	375	
R.SVNELDLPILGWLGLS.A	Y	99.9	58.27	1724.9348	16	1.5	863.4760	2	46.78	20	2386	OB5190.raw	5.25E4	4	4	357	372	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	57.16	2651.4070	24	0.4	884.8100	3	41.71	20	2089	OB5190.raw	2.31E6	49	49	357	380	
N.PDIYNPQAGSLR.S	Y	99.9	56.36	1329.6677	12	-0.8	665.8406	2	31.25	20	1491	OB5190.raw	9.45E3	2	2	345	356	
N.GIEETIC(+57.02)SASVK.K	Y	99.9	54.43	1292.6282	12	-0.9	647.3208	2	31.55	20	1508	OB5190.raw	2.34E4	1	1	325	336	Carbamidomethylation
K.TDSRPSIANLAGENSIID.N	N	99.9	50.36	1871.9225	18	1.0	936.9695	2	35.06	20	1712	OB5190.raw	1.6E4	1	1	450	467	
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.9	50.27	2453.2637	22	2.4	818.7638	3	35.51	20	1737	OB5190.raw	3.73E4	3	3	381	402	Oxidation (M)
R.SVNELDLPILGWLGLSAQ.H	Y	99.9	49.68	1924.0305	18	1.8	963.0243	2	46.17	20	2350	OB5190.raw	3.66E3	2	2	357	374	

K.TDSRPSIANLAGENSIIDNLPEE.V	N	99.9	44.10	2454.1873	23	4.2	1228.1061	2	37.15	20	1831	OB5190.raw	1.45E4	2	2	450	472	
R.SVNELDLPILGWLGL.S	Y	99.8	41.15	1637.9028	15	0.9	819.9594	2	48.09	20	2465	OB5190.raw	3.32E5	6	6	357	371	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.8	40.36	3609.8386	33	1.0	903.4678	4	38.45	20	1905	OB5190.raw	3.56E5	4	4	450	482	
R.SVNELDLP(+15.99)ILGWLGLSA.Q	Y	99.8	39.17	1811.9668	17	-2.0	906.9889	2	44.56	20	2254	OB5190.raw	1.21E4	1	1	357	373	Hydroxylation Pro
N.GIEETIC(+57.02)SASVKK.N	Y	99.8	38.81	1420.7231	13	-0.1	711.3688	2	29.65	20	1399	OB5190.raw	1.2E4	1	1	325	337	Carbamidomethylation
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.8	38.77	2837.4043	27	2.2	946.8108	3	38.29	20	1896	OB5190.raw	2.51E4	2	2	450	476	
L.GWLGLSAQHGTIYR.N	Y	99.6	36.29	1557.8052	14	1.2	779.9108	2	33.88	20	1644	OB5190.raw	2.09E3	1	1	367	380	
R.SVNELDLP(+15.99)ILGWLGLSAQHGTIYR.N	Y	99.6	36.03	2667.4021	24	0.0	890.1413	3	39.31	20	1953	OB5190.raw	2.83E4	2	2	357	380	Hydroxylation Pro
R.NAMFVPHYTLNAHTIVVALNGR.A	Y	99.6	35.48	2437.2688	22	1.9	813.4318	3	36.25	20	1779	OB5190.raw	0	1	1	381	402	
K.AQSENYEYLAFKTD.S	Y	99.5	34.96	1677.7522	14	1.7	839.8848	2	34.38	20	1673	OB5190.raw	4.07E3	1	1	438	451	
R.NAM(+15.99)FVPHYTLN.A	Y	99.4	34.35	1321.6125	11	0.8	661.8141	2	33.18	20	1603	OB5190.raw	8.05E3	1	1	381	391	Oxidation (M)
D.NLPEEVVANSYR.L	Y	99.3	34.07	1389.6888	12	-1.0	695.8510	2	33.04	20	1594	OB5190.raw	6.13E3	1	1	468	479	
D.IYNPQAGSLR.S	Y	98.9	33.16	1117.5880	10	0.0	559.8013	2	28.99	20	1360	OB5190.raw	4.12E3	1	1	347	356	
K.TDSRPSIANLAGENSIIDNLPE.E	N	98.5	31.96	2325.1448	22	0.6	776.0560	3	37.27	20	1838	OB5190.raw	0	1	1	450	471	
R.VYDEELQEGHVL.V	N	98.4	30.97	1429.6725	12	-0.3	715.8433	2	33.41	20	1616	OB5190.raw	0	1	1	415	426	
K.FFVPPFDHQSM(+15.99).R	Y	98.2	30.48	1366.6016	11	0.2	684.3082	2	35.70	20	1748	OB5190.raw	1.41E4	2	2	496	506	Oxidation (M)
R.NAMFVP(+15.99)HYTLNAHTIVVALN(+.98)GR.A	Y	98.2	30.29	2454.2478	22	-2.8	614.5675	4	35.19	20	1719	OB5190.raw	1.87E4	1	1	381	402	Hydroxylation Pro; Deamidation (NQ)
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	98.1	29.44	2454.2478	22	7.3	819.0959	3	35.88	20	1758	OB5190.raw	4.46E3	1	1	381	402	Deamidation (NQ); Oxidation (M)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVAN(+.98)SYRLPR.E	Y	97.6	27.61	3611.8066	33	2.4	903.9611	4	37.24	20	1836	OB5190.raw	5.35E2	1	1	450	482	Deamidation (NQ)
K.FFVPPFDHQSM(+15.99)RE.V	Y	97.4	27.06	1651.7452	13	0.7	551.5894	3	33.34	20	1612	OB5190.raw	1.57E5	1	1	496	508	Oxidation (M)
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	97.4	27.02	4687.2676	42	-1.2	1172.8228	4	38.38	20	1901	OB5190.raw	0	1	1	438	479	
R.NAMFVPHYTLN.A	Y	94.8	25.81	1305.6176	11	-0.2	653.8159	2	34.61	20	1686	OB5190.raw	0	1	1	381	391	
total 35 peptides																		

Q0GM57|Q0GM57_ARAHY

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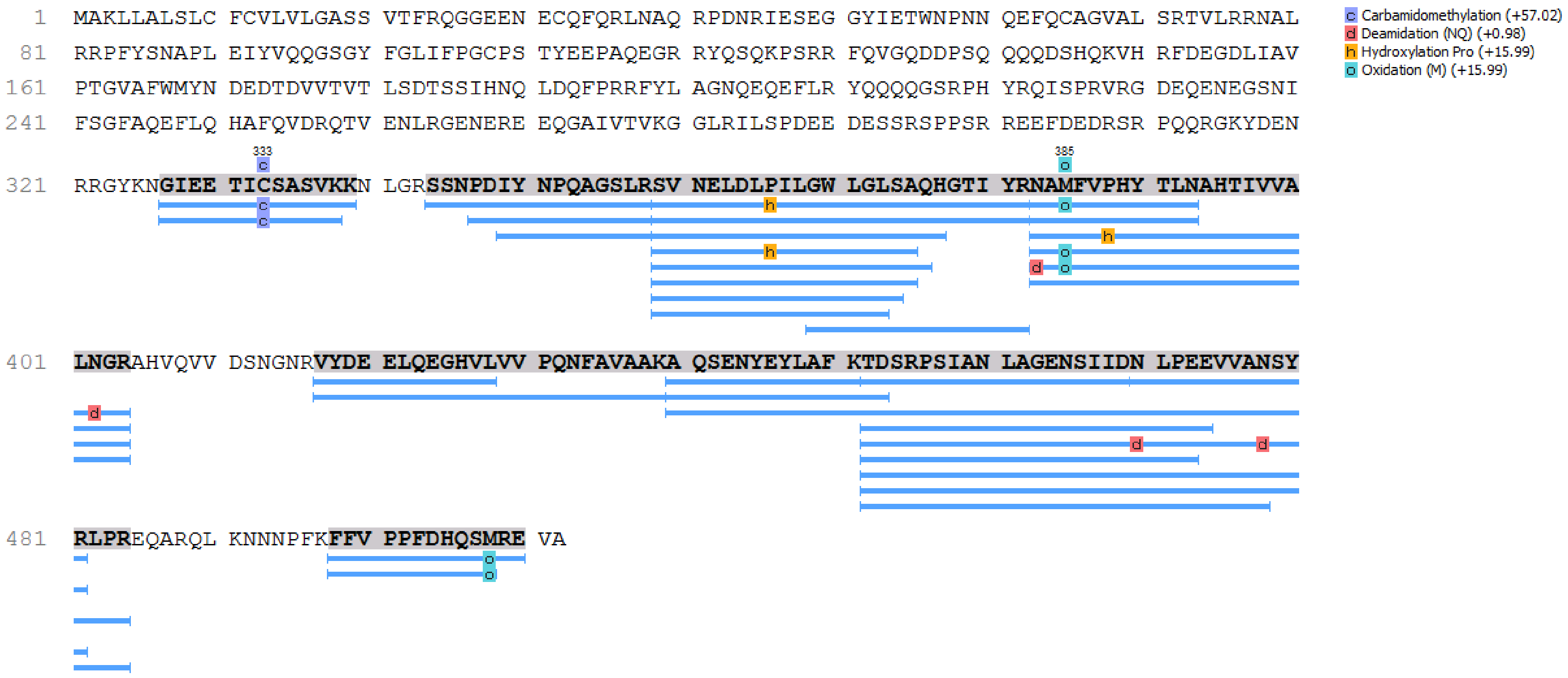
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	77.55	3243.6006	30	1.4	1082.2090	3	38.26	20	1894	OB5190.raw	2.55E5	9	9	452	481	
R.SSNPDIYNPQAGSLR.S	Y	99.9	72.33	1617.7747	15	0.7	809.8952	2	31.15	20	1485	OB5190.raw	2.28E5	13	13	344	358	
K.AQSENYEYLAFK.T	Y	99.9	70.26	1461.6776	12	0.5	731.8464	2	33.93	20	1647	OB5190.raw	1.5E5	8	8	440	451	
R.VYDEELQEGHVLVVPQNFAVAAK.A	Y	99.9	64.47	2554.3066	23	0.3	852.4431	3	35.30	20	1725	OB5190.raw	3.91E4	3	3	417	439	
R.SVNELDLPILGWLGLSA.Q	Y	99.9	61.91	1795.9719	17	0.9	898.9940	2	46.60	20	2376	OB5190.raw	3.93E5	16	16	359	375	
R.SVNELDLPILGWLGLSAQH.G	Y	99.9	61.74	2061.0894	19	2.4	1031.5544	2	43.39	20	2185	OB5190.raw	2.29E4	2	2	359	377	
R.SVNELDLPILGWLGLS.A	Y	99.9	58.27	1724.9348	16	1.5	863.4760	2	46.78	20	2386	OB5190.raw	5.25E4	4	4	359	374	
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	57.16	2651.4070	24	0.4	884.8100	3	41.71	20	2089	OB5190.raw	2.31E6	49	49	359	382	
N.PDIYNPQAGSLR.S	Y	99.9	56.36	1329.6677	12	-0.8	665.8406	2	31.25	20	1491	OB5190.raw	9.45E3	2	2	347	358	
N.GIEETIC(+57.02)SASVK.K	Y	99.9	54.43	1292.6282	12	-0.9	647.3208	2	31.55	20	1508	OB5190.raw	2.34E4	1	1	327	338	Carbamidomethylation
K.TDSRPSIANLAGENSIID.N	N	99.9	50.36	1871.9225	18	1.0	936.9695	2	35.06	20	1712	OB5190.raw	1.6E4	1	1	452	469	
R.NAM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	99.9	50.27	2453.2637	22	2.4	818.7638	3	35.51	20	1737	OB5190.raw	3.73E4	3	3	383	404	Oxidation (M)
R.SVNELDLPILGWLGLSAQ.H	Y	99.9	49.68	1924.0305	18	1.8	963.0243	2	46.17	20	2350	OB5190.raw	3.66E3	2	2	359	376	
K.TDSRPSIANLAGENSIIDNLPEE.V	N	99.9	44.10	2454.1873	23	4.2	1228.1061	2	37.15	20	1831	OB5190.raw	1.45E4	2	2	452	474	
R.SVNELDLPILGWLGL.S	Y	99.8	41.15	1637.9028	15	0.9	819.9594	2	48.09	20	2465	OB5190.raw	3.32E5	6	6	359	373	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR.E	Y	99.8	40.36	3609.8386	33	1.0	903.4678	4	38.45	20	1905	OB5190.raw	3.56E5	4	4	452	484	
R.SVNELDLP(+15.99)ILGWLGLSA.Q	Y	99.8	39.17	1811.9668	17	-2.0	906.9889	2	44.56	20	2254	OB5190.raw	1.21E4	1	1	359	375	Hydroxylation Pro
N.GIEETIC(+57.02)SASVKK.N	Y	99.8	38.81	1420.7231	13	-0.1	711.3688	2	29.65	20	1399	OB5190.raw	1.2E4	1	1	327	339	Carbamidomethylation
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.8	38.77	2837.4043	27	2.2	946.8108	3	38.29	20	1896	OB5190.raw	2.51E4	2	2	452	478	
L.GWLGLSAQHGTIYR.N	Y	99.6	36.29	1557.8052	14	1.2	779.9108	2	33.88	20	1644	OB5190.raw	2.09E3	1	1	369	382	
R.SVNELDLP(+15.99)ILGWLGLSAQHGTIYR.N	Y	99.6	36.03	2667.4021	24	0.0	890.1413	3	39.31	20	1953	OB5190.raw	2.83E4	2	2	359	382	Hydroxylation Pro
R.NAMFVPHYTLNAHTIVVALNGR.A	Y	99.6	35.48	2437.2688	22	1.9	813.4318	3	36.25	20	1779	OB5190.raw	0	1	1	383	404	
K.AQSENYEYLAFKTD.S	Y	99.5	34.96	1677.7522	14	1.7	839.8848	2	34.38	20	1673	OB5190.raw	4.07E3	1	1	440	453	
R.NAM(+15.99)FVPHYTLN.A	Y	99.4	34.35	1321.6125	11	0.8	661.8141	2	33.18	20	1603	OB5190.raw	8.05E3	1	1	383	393	Oxidation (M)

D.NLPEEVVANSYR.L	Y	99.3	34.07	1389.6888	12	-1.0	695.8510	2	33.04	20	1594	OB5190.raw	6.13E3	1	1	470	481	
D.IYNPQAGSLR.S	Y	98.9	33.16	1117.5880	10	0.0	559.8013	2	28.99	20	1360	OB5190.raw	4.12E3	1	1	349	358	
K.TDSRPSIANLAGENSIIDNLPE.E	N	98.5	31.96	2325.1448	22	0.6	776.0560	3	37.27	20	1838	OB5190.raw	0	1	1	452	473	
R.VYDEELQEGHVL.V	N	98.4	30.97	1429.6725	12	-0.3	715.8433	2	33.41	20	1616	OB5190.raw	0	1	1	417	428	
K.FFVPPFDHQSM(+15.99).R	Y	98.2	30.48	1366.6016	11	0.2	684.3082	2	35.70	20	1748	OB5190.raw	1.41E4	2	2	498	508	Oxidation (M)
R.NAMFVP(+15.99)HYTLNAHTIVVALN(+.98)GR.A	Y	98.2	30.29	2454.2478	22	-2.8	614.5675	4	35.19	20	1719	OB5190.raw	1.87E4	1	1	383	404	Hydroxylation Pro; Deamidation (NQ)
R.N(+.98)AM(+15.99)FVPHYTLNAHTIVVALNGR.A	Y	98.1	29.44	2454.2478	22	7.3	819.0959	3	35.88	20	1758	OB5190.raw	4.46E3	1	1	383	404	Deamidation (NQ); Oxidation (M)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVAN(+.98)SYRLPR.E	Y	97.6	27.61	3611.8066	33	2.4	903.9611	4	37.24	20	1836	OB5190.raw	5.35E2	1	1	452	484	Deamidation (NQ)
K.FFVPPFDHQSM(+15.99)RE.V	Y	97.4	27.06	1651.7452	13	0.7	551.5894	3	33.34	20	1612	OB5190.raw	1.57E5	1	1	498	510	Oxidation (M)
K.AQSENYEYLAFKTDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	97.4	27.02	4687.2676	42	-1.2	1172.8228	4	38.38	20	1901	OB5190.raw	0	1	1	440	481	
R.NAMFVPHYTLN.A	Y	94.8	25.81	1305.6176	11	-0.2	653.8159	2	34.61	20	1686	OB5190.raw	0	1	1	383	393	
total 35 peptides																		

sp|K22E_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCQISCKSR GRGGGGGGFR **GFSSGSAVVS GGSR**RSTSSF SCLSRHGGGG GGFGGGGFGS RSLVGLGGTK **SISISVAGGG**
81 **GGFGAAGGFG GRGGGFGGGS GFGGGSGFGG GSGFSGGGFG GGGFGGGRFG GFGGPGGVGG LGGPGGFGPG GYPGGIHEVS**
161 **VNQSLLQPLN VK**VDPEIQNV KAQEREQIKT LNNKFASFID KVR**FLEQQNQ VLQTK**WELLQ QMNVGTRPIN LEPIFQGYID
241 SLKRYLDGLT AER**TSQNSEL NNMQDLVEDY KK**KYEDEINK RTAAENDFVT LKKDVDNAYM IKVELQSK**VD LLNQEIEFLK**
321 **VLYDAEISQI HQSVTDTNVI LSMDNSRNLD LDSIIAEVKA QYEEIAQR**SK EEAEALYHSK YEELQVTVGR HGDSLKEIK**I**
401 **EISELNR**VIQ RLQGEIAHVK KQCKNVQDAI ADAEQRGEHA LKDAR**NKLND LEEALQQAKE DLAR**LLRDYQ ELMNVKLALD
481 VEIATYRKLL EGEECRMSGD LSSNVTVSVT SSTISSNVAS KAAFGGSGGR **GSSSGGGYSS GSSSYGSGGR** QSGSR**GGSGG**
561 **GGSISGGGYG SGGGSGGR**YG SGGGSKGGSI SGGGYGSGGG KHSSGGGSRG GSSSGGGYGS GGGGSSSVKG SSGEAFGSSV
641 TFSFR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
R.GGSGGGGSISGGGYGSGGGSGGR.Y	Y	99.9	68.53	1740.7411	23	1.3	871.3790	2	25.42	20	1152	OB5190.raw	4.16E3	1	1	556	578	
R.NLDLDSIIAEVKAQYEEIAQR.S	Y	99.9	65.46	2417.2437	21	0.1	806.7552	3	41.92	20	2101	OB5190.raw	5.44E4	3	3	348	368	
R.GFSSGSAVVSGGSR.R	Y	99.9	63.68	1253.6000	14	-1.1	627.8066	2	27.93	20	1298	OB5190.raw	5.42E3	2	2	21	34	
R.FLEQQNQVLQTK.W	N	99.9	61.03	1474.7780	12	0.0	738.3962	2	30.91	20	1471	OB5190.raw	1.82E4	2	2	204	215	
K.VDLLNQEIEFLK.V	Y	99.9	56.21	1459.7922	12	-1.6	730.9022	2	38.12	20	1886	OB5190.raw	5.08E3	1	1	309	320	
K.VLYDAEISQIHQSVTDTNVILSMDNSR.N	Y	99.9	55.45	3047.4871	27	2.5	1016.8389	3	37.04	20	1825	OB5190.raw	5.09E3	2	2	321	347	
K.SISISVAGGGGGFGAAGGFGGR.G	Y	99.9	54.26	1837.9070	22	1.0	919.9617	2	35.35	20	1728	OB5190.raw	6.34E3	1	1	71	92	
R.GSSSGGGYSSGSSSYGSGGR.Q	Y	99.9	45.94	1739.6982	20	2.0	870.8581	2	25.02	20	1130	OB5190.raw	3.07E3	1	1	531	550	
R.GGGFGGGSGFGGGSGFGGGSGFSGGGFGGGGFGGGR.F	Y	99.9	42.89	2830.1868	36	0.0	944.4028	3	36.62	20	1800	OB5190.raw	0	1	1	93	128	
G.GSGFGGGSGFGGGSGFSGGGFGGGGFGGGR.F	Y	99.8	39.88	2398.0110	30	0.3	800.3445	3	35.65	20	1745	OB5190.raw	9.07E3	2	2	99	128	
R.TSQNSELNNMQDLVEDYKK.K	Y	99.8	39.01	2255.0376	19	2.2	752.6881	3	34.35	20	1671	OB5190.raw	8.38E3	2	2	254	272	
K.IEISELNR.V	N	99.8	38.28	972.5240	8	0.7	487.2696	2	31.10	20	1482	OB5190.raw	0	1	1	400	407	

R.NKLNDLEEALQQAKEDLAR.L	Y	99.6	35.90	2197.1338	19	0.0	733.3852	3	37.41	20	1846	OB5190.raw	6.05E3	1	1	446	464	
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVN.Q	Y	99.6	35.24	2970.4048	34	4.5	991.1467	3	37.62	20	1858	OB5190.raw	2.26E3	1	1	129	162	
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQ.S	Y	96.9	26.90	3098.4634	35	4.3	1033.8329	3	37.59	20	1856	OB5190.raw	0	1	1	129	163	
R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	Y	94.7	25.51	4091.0652	44	2.8	1023.7764	4	38.37	20	1900	OB5190.raw	0	1	1	129	172	
total 16 peptides																		

sp|K1C9_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCRQFSSSY LSR**SGGGGGG GLGSGGSIR**S SYSRFSSSGG RGGGGR**FSSS SGYGGGSSR**V CGR**GGGGSFG YSYGGGSGGG**

81 **FSASSLGGGF GGGSR**GFGGA SGGGYSSSGG FGGGFGGGSG GGFGGGYGSG FGGLGGFGGG AGGGDGGILT ANEK**STMQEL**

161 **NSRLASYLDK VQALEEANND LENKIQD**WYD KKGPAAIQK**N YSPYYNTIDD LKDQIVDLTV GNNKTLLDID NTR**MTLDDFR

241 IKFEMEQNLR **QGVDADINGL R**QVLDNLTME KSDLEMQYET LQEELMALKK NHKEEMSQLT GQNSGDVNVE INVAPGKDLT

321 K**TLNDMRQEY EQLIAK**NRK**D IENQYETQIT QIEHEVSSSG QEVQSSAK**EV TQLR**HGVQEL EIELQSQLSK K**AALEKSLED

401 TKNRYCGQLQ MIQEQISNLE AQITDVRQEI ECQNQEYSLL LSIKMRLEK**E IETYHNLLEG GQEDFESSGA GK**IGLGGRGG

481 SGGSYGRGSR **GGSGGSYGGG GSGGGYGGGS GSR**GGSGGSY GGGSGSGGGS GGGYGGGSGG GHSGGSGGGH SGGSGGNYGG

561 GSGSGGGSGG GYGGGSGSR**G GSGGSHGGGS GFGGESGGSY GGGEEASGSG GGYGGGSGK**S SHS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
R.HGVQELEIELQSQLSKK.A	Y	99.9	64.09	1965.0531	17	-0.7	656.0245	3	34.64	20	1688	OB5190.raw	2.62E4	2	2	375	391	
R.SGGGGGGGLGSGGSIR.S	Y	99.9	63.95	1231.5905	16	0.9	616.8030	2	25.90	20	1180	OB5190.raw	7.04E3	2	2	14	29	
R.FSSSSGYGGGSSR.V	Y	99.9	59.43	1234.5214	13	-0.7	618.2675	2	25.14	20	1137	OB5190.raw	8.09E3	3	3	47	59	
R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	Y	99.9	57.16	2704.1538	32	0.8	902.3926	3	35.47	20	1735	OB5190.raw	9.11E3	2	2	64	95	
K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	Y	99.9	56.97	2901.4031	25	1.7	968.1432	3	39.24	20	1949	OB5190.raw	1.01E5	4	4	200	224	
R.GGSGGSYGGGGSGGGYGGGSGSR.G	Y	99.9	56.13	1790.7203	23	-0.3	896.3672	2	24.79	20	1117	OB5190.raw	5.79E3	3	3	491	513	
K.TLNDMRQEYEQLIAK.N	Y	99.9	47.36	1850.9197	15	-0.2	617.9804	3	35.26	20	1723	OB5190.raw	4.19E4	2	2	322	336	
K.STMQELNSR.L	Y	99.9	46.69	1064.4921	9	0.0	533.2533	2	26.37	20	1207	OB5190.raw	8.35E3	1	1	155	163	
R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	Y	99.9	43.83	3222.2742	40	1.8	1075.1006	3	27.81	20	1291	OB5190.raw	5.49E3	1	1	580	619	
K.TLLDIDNTR.M	Y	99.9	43.67	1059.5560	9	-0.4	530.7851	2	32.43	20	1558	OB5190.raw	8.5E3	2	2	225	233	
K.EIETYHNLLEGGQEDFESSGAGK.I	Y	99.8	39.79	2509.1245	23	1.1	837.3830	3	34.17	20	1661	OB5190.raw	5.66E3	1	1	450	472	
K.NYSPYYNTIDDLKDQIVDLTVGNNKTLLDIDNTR.M	Y	99.7	37.50	3942.9487	34	0.4	986.7449	4	40.03	20	1993	OB5190.raw	1.12E5	3	3	200	233	
R.QGVDADINGLR.Q	Y	99.7	37.44	1156.5836	11	1.0	579.2997	2	31.06	20	1480	OB5190.raw	3.88E3	1	1	251	261	
K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	Y	99.6	36.40	3263.5066	29	4.0	1088.8472	3	37.52	20	1852	OB5190.raw	2.26E4	2	2	340	368	
R.LASYLDKVQALEEANNDLENKIQD.W	Y	97.4	27.09	2732.3503	24	0.7	911.7914	3	36.16	20	1774	OB5190.raw	3.66E3	1	1	164	187	
total 15 peptides																		

A1DZF0|A1DZF0_ARAHY

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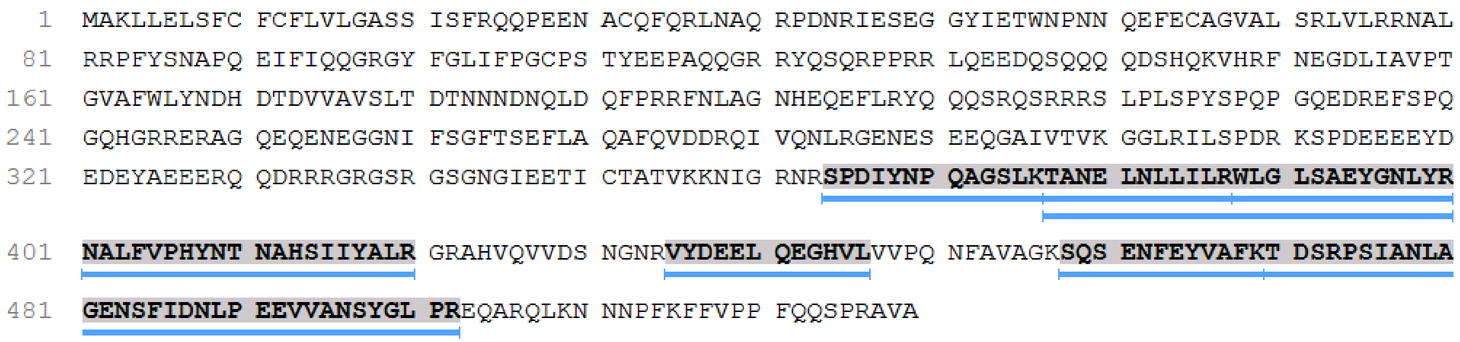
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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  1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
 81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA
481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	72.25	1540.7673	13	0.0	771.3909	2	36.87	20	1815	OB5190.raw	4.99E4	6	6	388	400	
K.SQSENFEYVAFK.T	N	99.9	56.79	1447.6619	12	0.3	724.8384	2	34.01	20	1652	OB5190.raw	1.13E4	1	1	458	469	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.9	56.55	3544.7434	33	0.6	1182.5891	3	39.26	20	1950	OB5190.raw	8E4	4	4	470	502	
K.TANELNLLILRWLGLSAEYGNLYR.N	Y	99.9	47.45	2791.5020	24	1.6	931.5094	3	43.42	20	2187	OB5190.raw	8.52E3	1	1	377	400	
K.TANELNLLILR.W	Y	99.9	45.56	1268.7452	11	-1.8	635.3788	2	36.92	20	1818	OB5190.raw	1.55E4	1	1	377	387	
R.SPDIYNPQAGSLK.T	N	99.8	41.39	1388.6936	13	1.6	695.3552	2	31.04	20	1479	OB5190.raw	2.95E3	1	1	364	376	
R.VYDEELQEGHVL.V	N	98.4	30.97	1429.6725	12	-0.3	715.8433	2	33.41	20	1616	OB5190.raw	0	1	1	435	446	
R.NALFVPHYNTNAHSIIYALR.G	N	98.0	28.71	2313.2019	20	-0.5	772.0742	3	35.21	20	1720	OB5190.raw	0	1	1	401	420	
total 8 peptides																		

sp|Q6PSU2|CONG7_ARAHY

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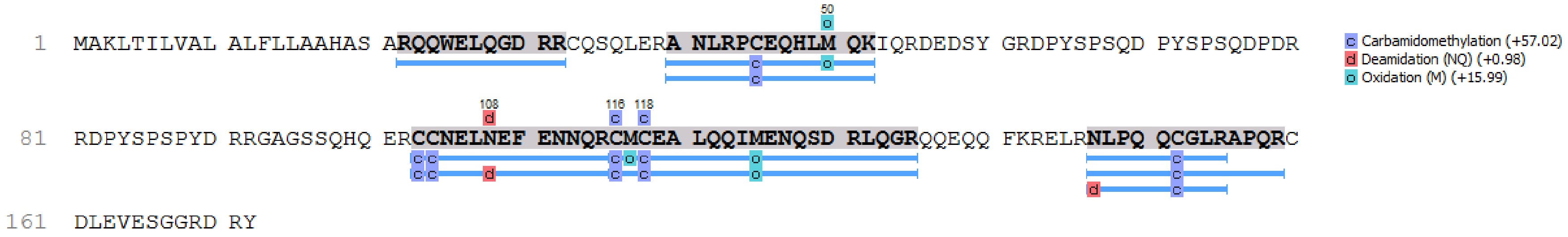
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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  1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM QKIQRDEDSY GRDPYSPSQD PYSPSQDPDR
 81 RDPYSPSPYD RRGAGSSQHQ ERCCNELNEF ENNQRCMCEA LQQIMENQSD RLQGRQQEQQ FKRELRNLPQ QCGLRAPQRC
161 DLEVESGGRD RY
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
R.C(+57.02)C(+57.02)NELNEFENNQR.C	Y	99.9	75.15	1725.6835	13	0.8	863.8497	2	31.18	20	1487	OB5190.raw	1.02E5	7	7	103	115	Carbamidomethylation
R.C(+57.02)M(+15.99)C(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.9	61.82	2498.0771	20	0.4	833.7000	3	31.74	20	1519	OB5190.raw	1.53E5	5	5	116	135	Carbamidomethylation; Oxidation (M)
R.NLPQQC(+57.02)GLR.A	Y	99.9	54.36	1084.5448	9	-0.9	543.2792	2	27.67	20	1283	OB5190.raw	1.95E5	10	10	147	155	Carbamidomethylation
R.ANLRPC(+57.02)EQHLM(+15.99)QK.I	Y	99.9	54.06	1639.7922	13	-0.8	547.6042	3	25.11	20	1135	OB5190.raw	3.2E5	20	20	40	52	Carbamidomethylation; Oxidation (M)
R.ANLRPC(+57.02)EQHLMQK.I	Y	99.9	44.73	1623.7974	13	-1.6	542.2722	3	26.95	20	1242	OB5190.raw	1.18E4	2	2	40	52	Carbamidomethylation
A.RQQWELQGDRR.C	Y	99.9	43.24	1470.7440	11	-0.8	491.2549	3	26.82	20	1234	OB5190.raw	1.35E5	4	4	22	32	
R.C(+57.02)MC(+57.02)EALQQIM(+15.99)ENQSDRLQGR.Q	Y	99.8	40.74	2482.0820	20	0.3	828.3682	3	33.20	20	1604	OB5190.raw	1.87E4	2	2	116	135	Carbamidomethylation; Oxidation (M)
R.C(+57.02)C(+57.02)NELN(+.98)EFENNQR.C	Y	99.8	38.98	1726.6675	13	7.1	864.3472	2	31.83	20	1524	OB5190.raw	8E2	1	1	103	115	Carbamidomethylation;

																		Deamidation (NQ)
R.NLPQQC(+57.02)GLRAPQR.C	Y	98.4	30.79	1536.7943	13	0.3	513.2722	3	28.37	20	1323	OB5190.raw	0	1	1	147	159	Carbamidomethylation
R.N(+.98)LPQQC(+57.02)GLR.A	Y	98.0	28.35	1085.5288	9	6.7	543.7753	2	28.82	20	1350	OB5190.raw	0	1	1	147	155	Deamidation (NQ); Carbamidomethylation
total 10 peptides																		

sp|TRYP_PIG|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FPTDDDDKIV GGYTCAANSI PYQVSLNSGS HFCGGSLINS QWVVSAAHCY KSRIQVR**LGE HNIDVLEGNE QFINAA**KIIT

81 HPNFNGNTLD NDIMLIK**LSS PATLNSRVAT VSLPR**SCAAA GTECLISGWG NTKSSGSSYP SLLQCLKAPV LSDSSCKSSY

161 PGQITGNMIC VGFLEGGKDS CQGDSGGPVV CNGQLQGIVS WGYGCAQKNK PGVYTKVCNY VNWIQQTIAA N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS4 tacka 19 na Figuri 1	#Spec	#Spec DS4 tacka 19 na Figuri 1	Start	End	PTM
R.LGEHNIDVLEGNEQFINAA.K	Y	99.9	61.26	2082.0017	19	3.0	1042.0112	2	35.97	20	1763	OB5190.raw	1.33E4	2	2	58	76	
R.VATVSLPR.S	Y	99.9	46.80	841.5021	8	0.3	421.7585	2	29.87	20	1412	OB5190.raw	2.36E5	5	5	108	115	
K.LSSPATLNSR.V	Y	99.9	45.11	1044.5564	10	-0.1	523.2854	2	27.53	20	1275	OB5190.raw	2.59E4	1	1	98	107	
R.LGEHNIDVLEGNE.Q	Y	99.8	41.56	1437.6736	13	0.5	719.8444	2	32.79	20	1579	OB5190.raw	2.86E4	2	2	58	70	
R.LGEHNIDVLEGNEQFIN.A	Y	99.6	35.80	1939.9275	17	1.2	970.9722	2	35.67	20	1746	OB5190.raw	2.07E4	1	1	58	74	
total 5 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

1. Notes

Spot 20 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

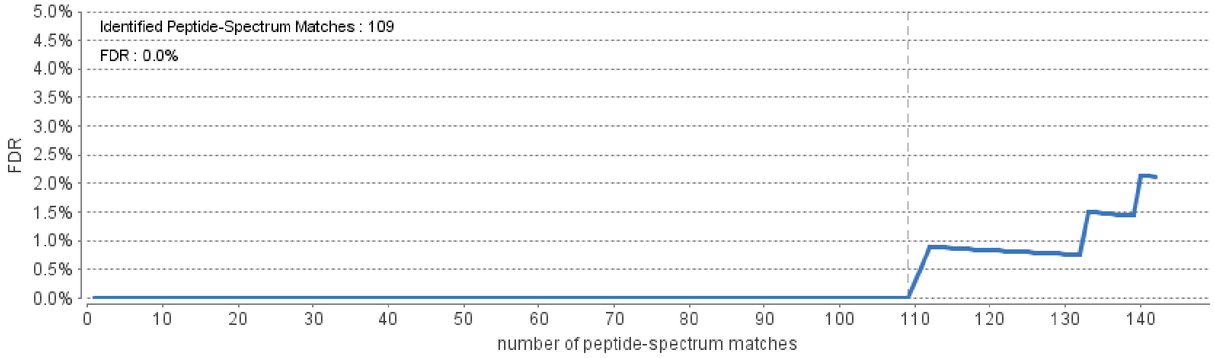


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a) **(b)**

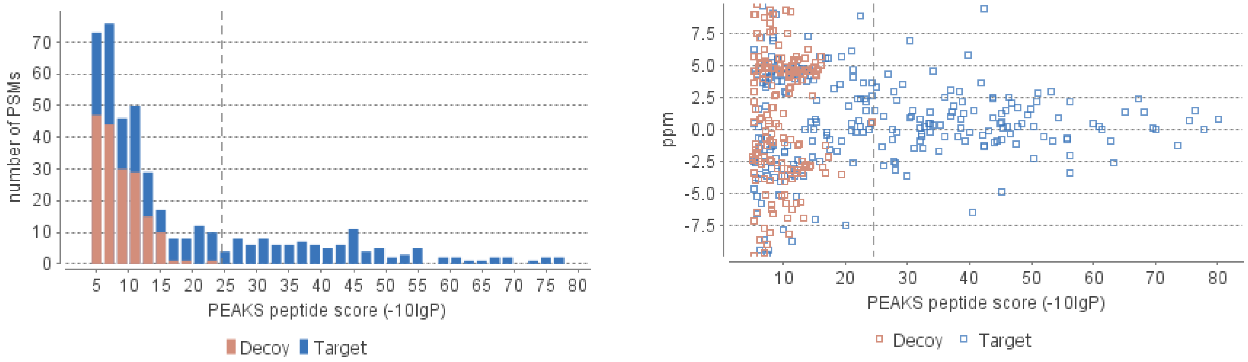
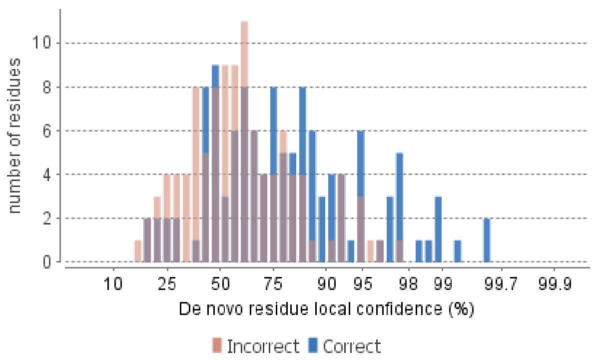


Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a) **(b)**



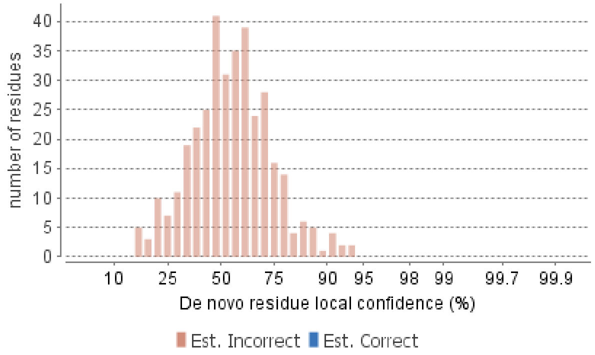


Table 1. Statistics of data.

# of MS scans	2714
# of MS/MS scans	1339

Table 2. Result filtration parameters.

Peptide -10lgP	≥24.5
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	107
Peptide sequences	53
Protein groups	9
Proteins	12
Proteins (#Unique Peptides)	7 (>2); 1 (=2); 4 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	57

Table 4. PTM profile.

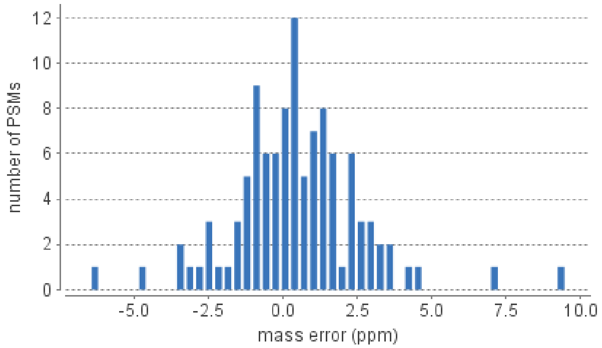
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Oxidation	15.99	M	15	77.71	1.95E4	1000.00
Carbamidomethyl	57.02	C	8	73.67	2.81E3	1000.00
HydPro	15.99	P	4	41.80	1.55E3	32.97

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



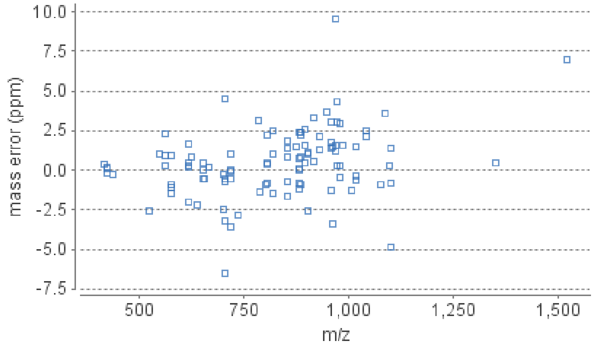


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
DS5 tacka 20 na Figuri 1	36	15	2	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: Uniprot_Peanut(3818)+cRAP_aug17
Taxon: All
Searched Entry: 1352
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB5192.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein	Protein		Score		Coverage	Coverage (%) DS5 tacka	Area DS5 tacka 20			#Spec DS5 tacka		Avg.	

Group	ID	Accession	(%)	-10lgP	(%)	20 na Figuri 1	na Figuri 1	#Peptides	#Unique	20 na Figuri 1	PTM	Mass	Description
1	221	sp|K2C1_HUMAN|	99.1	185.35	31	31	6.68E4	13	13	22	Y	65886	sp|K2C1_HUMAN|
2	646	sp|K1C9_HUMAN|	99.1	162.91	33	33	8.56E4	9	9	17	N	62129	sp|K1C9_HUMAN|
4	220	sp|K1C10_HUMAN|	98.9	158.89	17	17	5.73E4	7	7	18	Y	59519	sp|K1C10_HUMAN|
3	89	Q647H3|Q647H3_ARAHY	99.0	135.10	17	17	4.3E4	7	3	15	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
5	516	A5Z1R0|A5Z1R0_ARAHY	84.0	112.57	20	20	4.59E4	3	3	12	Y	16920	Ara h 6 OS=Arachis hypogaea GN=Ara h 6 PE=4 SV=1
5	517	sp|Q647G9|CONG_ARAHY	84.0	112.57	20	20	4.59E4	3	3	12	Y	16920	Conglutin OS=Arachis hypogaea PE=1 SV=1
7	1193	sp|TRYP_PIG|	98.3	110.49	18	18	1.54E5	6	6	14	Y	24409	sp|TRYP_PIG|
8	84	A1DZF0|A1DZF0_ARAHY	98.3	91.67	11	11	0E0	4	1	7	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
9	964	sp|K22E_HUMAN|	90.8	75.43	8	8	2.36E4	2	2	4	N	65865	sp|K22E_HUMAN|
10	216	Q6IWG5|Q6IWG5_ARAHY	61.4	56.21	5	5	1.83E4	1	1	4	N	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
10	218	E5G077|E5G077_ARAHY	61.4	56.21	5	5	1.83E4	1	1	4	N	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
10	217	Q0GM57|Q0GM57_ARAHY	61.4	56.21	5	5	1.83E4	1	1	4	N	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 12 proteins													

sp|K2C1_HUMAN|

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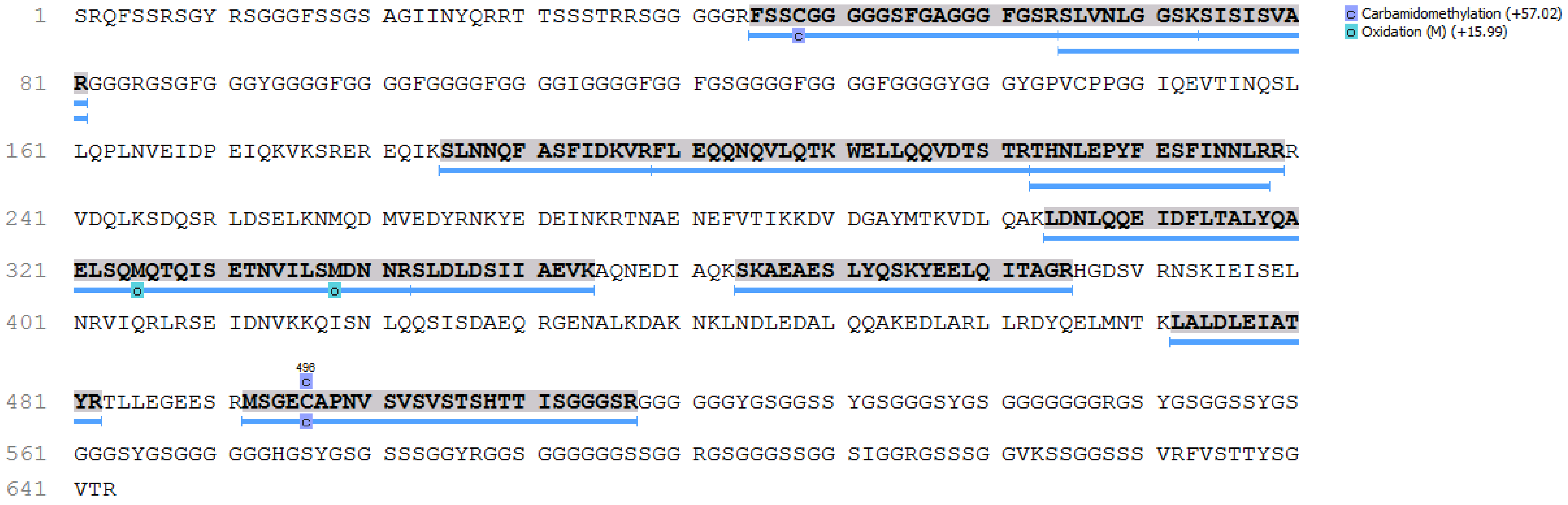
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 SRQFSSRSGY RSGGGFSSGS AGIINYQRRT TSSSTRRSGG GGGR**FSSCGG GGGSFGAGGG FGSRSLVNLG GSKSISISVA**

81 **R**GGGRGSGFG GGYGGGGFGG GGFGGGGFGG GGIGGGGFGG FGSGGGGFGG GGFGGGGYGG GYGPVCPPGG IQEVTINQSL

161 LQPLNVEIDP EIQKVKSRER EQIK**SLNNQF ASFIDKVRFL EQQNQVLQTK WELLQQVDTS TRTHNLEPYF ESFINNLRR**R

241 VDQLKSDQSR LDSELKNMQD MVEDYRNKYE DEINKRTNAE NEFVTIKKDV DGAYMTKVDL QAK**LDNLQQE IDFLTALYQA**

321 **ELSQMQTQIS ETNVILSMDN NRSLDLDSII AEVK**AQNEDI AQK**SKAEAES LYQSKYEELQ ITAGR**HGDSV RNSKIEISEL

401 NRVIQRLRSE IDNVKKQISN LQQSISDAEQ RGENALKDAK NKLNDLEDAL QQAKEDLARL LRDYQELMNT K**LALDLEIAT**

481 **YR**TLLEGEES R**MSGECAPNV SVSVSTSHTT ISGGGSR**GGG GGGYGSGGSS YGSGGGSYGS GGGGGGGRGS YGSGGSSYGS

561 GGGSYGSGGG GGGHGSYGSG SSSGGYRGGS GGGGGGSSGG RGSGGGSSGG SIGGRGSSSG GVKSSGGSSS VRFVSTTYSG

641 VTR

C Carbamidomethylation (+57.02)
O Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.FSSC(+57.02)GGGGGSFGAGGGFGSR.S	Y	99.9	73.67	1764.7274	20	-1.2	883.3699	2	32.01	22	1538	OB5192.raw	2.81E3	1	1	45	64	Carbamidomethylation
R.SLDLDSIIAEVK.A	Y	99.9	70.04	1301.7078	12	0.0	651.8611	2	39.05	22	1930	OB5192.raw	1.43E4	3	3	343	354	
R.SLVNLGGSKSISISVAR.G	Y	99.9	60.98	1686.9628	17	0.3	563.3284	3	33.70	22	1637	OB5192.raw	4.13E3	3	3	65	81	
R.FLEQQNQVLQTKWELLQQVDTSTR.T	Y	99.9	51.04	2931.5090	24	2.9	978.1798	3	37.03	22	1818	OB5192.raw	6.97E3	3	3	199	222	
K.LALDLEIATYR.T	Y	99.9	50.38	1276.7026	11	-2.2	639.3572	2	36.98	22	1815	OB5192.raw	1.97E3	1	1	472	482	

R.THNLEPYFESFINNLR.R	Y	99.8	45.35	1992.9694	16	0.2	665.3305	3	38.98	22	1926	OB5192.raw	7.81E3	1	1	223	238	
K.SKAEAESLYQSKYEELQITAGR.H	Y	99.4	38.58	2500.2444	22	0.9	626.0689	4	32.92	22	1590	OB5192.raw	3.11E3	1	1	364	385	
R.MSGEC(+57.02)APNVSVSVSTSHTTISGGGSR.G	Y	99.1	37.43	2564.1594	26	1.8	855.7286	3	30.94	22	1478	OB5192.raw	3.69E3	3	3	492	517	Carbamidomethylation
K.SISISVAR.G	Y	98.1	34.04	831.4814	8	0.3	416.7481	2	30.31	22	1443	OB5192.raw	4.56E3	1	1	74	81	
R.SLVNLGGSK.S	Y	98.0	33.55	873.4919	9	-0.2	437.7531	2	30.21	22	1437	OB5192.raw	5.3E3	1	1	65	73	
R.THNLEPYFESFINNLRR.R	Y	97.8	32.13	2149.0703	17	-0.6	717.3636	3	38.46	22	1895	OB5192.raw	4.84E3	2	2	223	239	
K.LDNLQQEIDFLTALYQAELSQM(+15.99)QTQISETNVILSM(+15.99)DNNR.S	Y	95.7	30.37	4558.1841	39	7.0	1520.4126	3	44.58	22	2230	OB5192.raw	0	1	1	304	342	Oxidation (M)
K.SLNNQFASFIDKVR.F	Y	84.6	26.17	1637.8525	14	1.0	546.9587	3	36.43	22	1788	OB5192.raw	7.35E3	1	1	185	198	
total 13 peptides																		

sp|K1C9_HUMAN| back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCRQFSSSY LSR**SGGGGGG GLGSGGSIR**S SYSRFSSSGG RGGGGRFSSS SGYGGGSSRV CGR**GGGGSFG YSYGGGSGGG**

81 **FSASSLGGGF GGGSR**GFGGA SGGGYSSSGG FGGGFGGGSG GGFGGGYGSG FGGLGGFGGG AGGGDGGILT ANEKSTMQEL

161 NSRLASYLDK VQALEEANND LENKIQDWYD KKGPAAIQK**N YSPYYNTIDD LKDQIVDLTV GNNKTLLDID NTR**MTLDDFR

241 IKFEMEQNLR QGVDADINGL RQVLDNLTME KSDLEMQYET LQEELMALKK NHKEEMSQLT GQNSGDVNVE INVAPGKDLT

321 K**TLNDMRQEY EQLIAK**NRK**D IENQYETQIT QIEHEVSSSG QEVQSSAK**EV TQLR**HGVQEL EIELQSQLSK K**AALEKSLED

401 TKNRYCGQLQ MIQEQISNLE AQITDVRQEI ECQNQEYSLL LSIKMRLEKE IETYHNLLEG GQEDFESSGA GKIGLGGRGG

481 SGGSYGRGSR **GGSGGSYGGG GSGGGYGGGS GSR**GGSGGSY GGGSGSGGGS GGGYGGGSGG GHSGGSGGGH SGGSGGNYGG

561 GSGSGGGSGG GYGGGSGSR**G GSGGSHGGGS GFGGESGGSY GGGEEASGSG GGYGGGSGK**S SHS

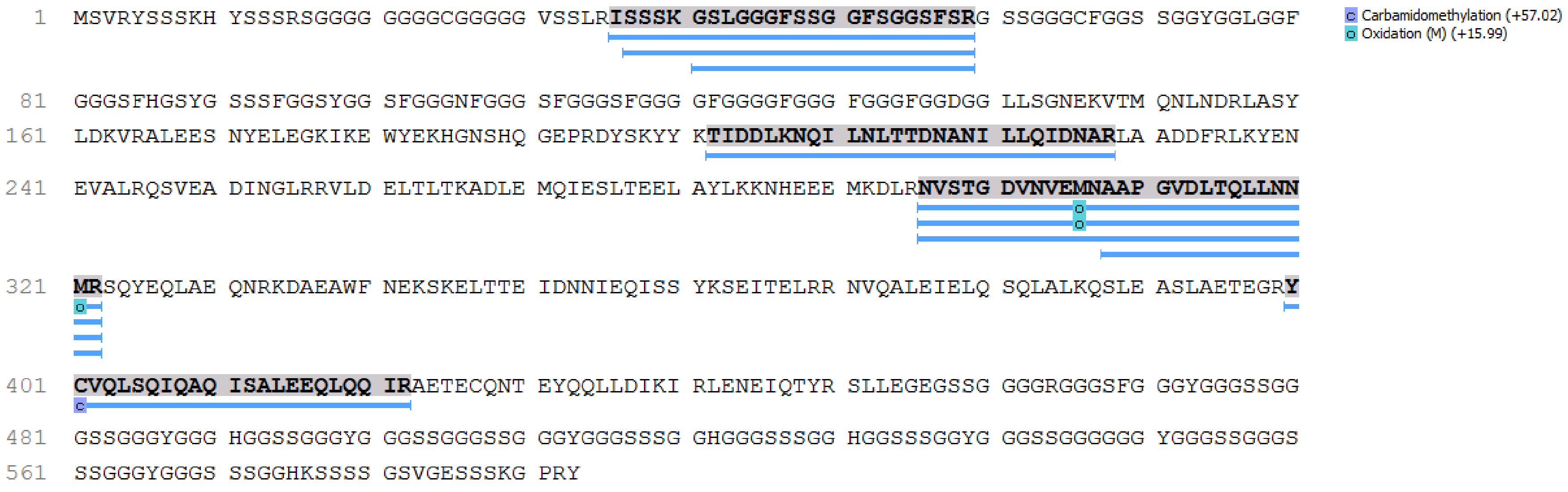
Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.SGGGGGGGLGSGGSIR.S	Y	99.9	69.53	1231.5905	16	0.2	616.8026	2	26.34	22	1243	OB5192.raw	7.28E3	3	3	14	29	
R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	Y	99.9	63.19	2704.1538	32	-2.5	902.3896	3	35.92	22	1759	OB5192.raw	1.39E4	4	4	64	95	
R.HGVQELEIELQSQLSKK.A	Y	99.9	51.98	1965.0531	17	-0.6	656.0246	3	35.26	22	1721	OB5192.raw	2.51E3	1	1	375	391	
R.GGSGGSYGGGGSGGGYGGGSGSR.G	Y	99.8	46.46	1790.7203	23	2.6	896.3698	2	25.14	22	1182	OB5192.raw	2.71E3	2	2	491	513	
K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	Y	99.8	45.20	2901.4031	25	1.2	968.1428	3	39.77	22	1970	OB5192.raw	1.2E4	2	2	200	224	
R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	Y	99.8	43.92	3222.2742	40	-0.9	1075.0977	3	28.46	22	1344	OB5192.raw	2.49E3	1	1	580	619	
K.TLNDMRQEYEQLIAK.N	Y	98.0	33.68	1850.9197	15	0.4	617.9808	3	35.62	22	1742	OB5192.raw	1.3E4	2	2	322	336	
K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	Y	93.6	29.09	3263.5066	29	3.6	1088.8467	3	37.92	22	1866	OB5192.raw	2.33E3	1	1	340	368	
K.NYSPYYNTIDDLKDQIVDLTVGNNKTLLDIDNTR.M	Y	84.1	24.63	3942.9487	34	1.5	986.7460	4	40.67	22	2022	OB5192.raw	2.94E4	1	1	200	233	
total 9 peptides																		

sp|K1C10_HUMAN| back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:


🟪 Carbamidomethylation (+57.02)
🟦 Oxidation (M) (+15.99)

1 MSVRYSSSKH YSSSRSGGGG GGGGCGGGGG VSSLR**ISSSK GSLGGGFSSG GFSGGSFSR**G SSGGGCFGGS SGGYGGLGGF
81 GGGSFHGSYG SSSFGGSYGG SFGGGNFGGG SFGGGSFGGG GFGGGGFGGG FGGGFGGDGG LLSGNEKVTM QNLNDRLASY
161 LDKVRALEES NYELEGKIKE WYEKHGNSHQ GEPRDYSKYY K**TIDDLKNQI LNLTTDNANI LLQIDNAR**LA ADDFRLKYEN
241 EVALRQSVEA DINGLRRVLD ELTLTKADLE MQIESLTEEL AYLKKNHEEE MKDLR**NVSTG DVNVEMNAAP GVDLTQLLNN**
321 **MR**SQYEQLAE QNRKDAEAWF NEKSKELTTE IDNNIEQISS YKSEITELRR NVQALEIELQ SQLALKQSLE ASLAETEGR**Y**
401 **CVQLSQIQAQ ISALEEQLQQ IR**AETECQNT EYQQLLDIKI RLENEIQTYR SLLEGEGSSG GGGRGGGSFG GGYGGGSSGG
481 GSSGGGYGGG HGGSSGGGYG GGSSGGGSSG GGYGGGSSSG GHGGGSSSGG HGGSSSGGYG GGSSGGGGGG YGGGSSGGGS
561 SSGGGYGGGS SSGGHKSSSS GSVGESSSKG PRY

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
K.GSLGGGFSSGGFSGGSFSR.G	Y	99.9	80.29	1706.7648	19	0.8	854.3904	2	34.39	22	1674	OB5192.raw	4.11E3	2	2	41	59	
R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S	Y	99.9	65.16	2871.3855	27	1.4	958.1371	3	40.37	22	2005	OB5192.raw	2.15E4	4	4	296	322	
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNMR.S	Y	99.9	56.23	2887.3804	27	-3.4	963.4642	3	39.63	22	1962	OB5192.raw	7.21E3	2	2	296	322	Oxidation (M)
K.TIDDLKNQILNLTTDNANILLQIDNAR.L	Y	99.9	55.72	3051.6201	27	-0.7	1018.2133	3	41.40	22	2063	OB5192.raw	1.18E4	3	3	202	228	
R.YC(+57.02)VQLSQIQAQISALEEQLQQIR.A	Y	99.8	45.16	2745.4119	23	0.6	916.1451	3	42.57	22	2129	OB5192.raw	4.7E3	2	2	400	422	Carbamidomethylation
R.NVSTGDVNVEM(+15.99)NAAPGVDLTQLLNNM(+15.99)R.S	Y	99.7	42.41	2903.3752	27	9.5	968.8082	3	37.68	22	1854	OB5192.raw	1.39E3	1	1	296	322	Oxidation (M)
N.AAPGVDLTQLLNNMR.S	Y	98.1	35.24	1611.8402	15	0.4	806.9277	2	39.15	22	1936	OB5192.raw	1.3E3	1	1	308	322	
I.SSSKGSLGGGFSSGGFSGGSFSR.G	Y	97.8	32.24	2095.9558	23	-0.3	699.6590	3	32.51	22	1568	OB5192.raw	3.41E3	2	2	37	59	
R.ISSSKGSLGGGFSSGGFSGGSFSR.G	Y	84.6	26.10	2209.0398	24	-2.8	737.3518	3	32.97	22	1593	OB5192.raw	1.92E3	1	1	36	59	
total 9 peptides																		

Q647H3|Q647H3_ARAHY

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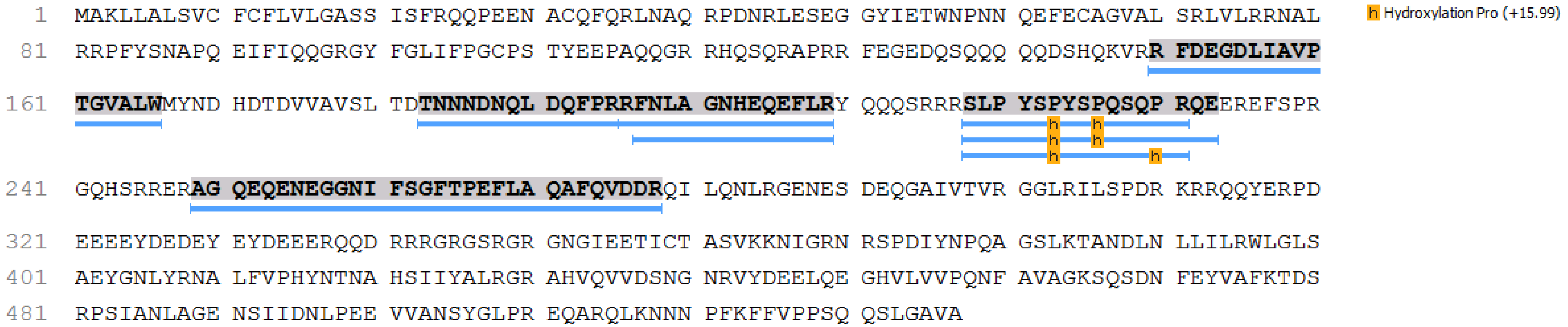
| Protein Coverage | Supporting Peptides |

Protein Coverage:


🟧 Hydroxylation Pro (+15.99)

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVR**R FDEGDLIAVP**
161 **TGVALW**MYND HDTDVVAVSL TD**TNNNDNQL DQFPRRFNLA GNHEQEFLR**Y QQQSRRR**SLP YSPYSPQSQP RQE**EREFSPR
241 GQHSRRER**AG QEQENEGGNI FSGFTPEFLA QAFQVDDR**QI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS
401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM

R.AGQEQENEGGNIFSGFTPEFLAQAFQVDDR.Q	N	99.9	62.87	3300.4958	30	-0.8	1101.1716	3	42.07	22	2101	OB5192.raw	8.64E3	3	3	249	278	
R.RFNLAGNHEQEFLR.Y	N	99.9	47.46	1729.8647	14	-1.1	577.6282	3	31.84	22	1528	OB5192.raw	2.69E4	4	4	196	209	
R.RFDEGDLIAVPTGVALW.M	Y	99.9	46.71	1857.9624	17	2.1	929.9904	2	40.64	22	2020	OB5192.raw	2.77E4	2	2	150	166	
D.TNNNDNQLDQFPR.R	N	99.7	42.28	1574.7073	13	-1.3	788.3599	2	31.49	22	1507	OB5192.raw	7.09E2	1	1	183	195	
R.SLPYSP(+15.99)YSP(+15.99)QSQPRQE.E	Y	99.5	41.80	1894.8696	16	3.7	948.4456	2	30.24	22	1439	OB5192.raw	1.55E3	1	1	218	233	Hydroxylation Pro
R.SLPYSP(+15.99)YSP(+15.99)QSQPR.Q	Y	99.0	36.97	1637.7684	14	1.0	819.8923	2	30.07	22	1429	OB5192.raw	6.89E3	2	2	218	231	Hydroxylation Pro
R.SLPYSP(+15.99)YSPQSQP(+15.99)R.Q	Y	96.1	31.00	1637.7684	14	-1.4	819.8903	2	30.33	22	1444	OB5192.raw	6.89E3	1	1	218	231	Hydroxylation Pro
R.FNLAGNHEQEFLR.Y	N	93.3	27.97	1573.7637	13	-2.6	525.5938	3	33.08	22	1600	OB5192.raw	4.26E3	1	1	197	209	
total 8 peptides																		

A5Z1R0|A5Z1R0_ARAHY

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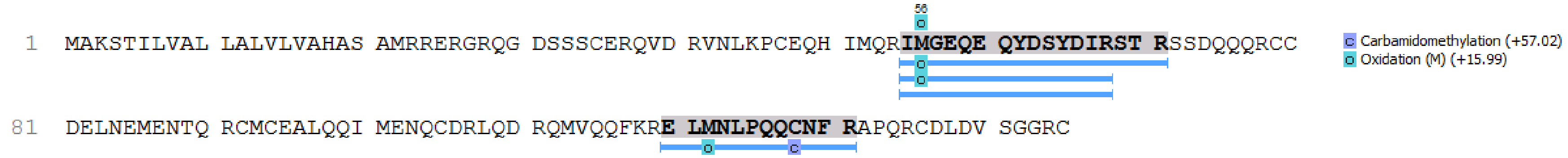
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

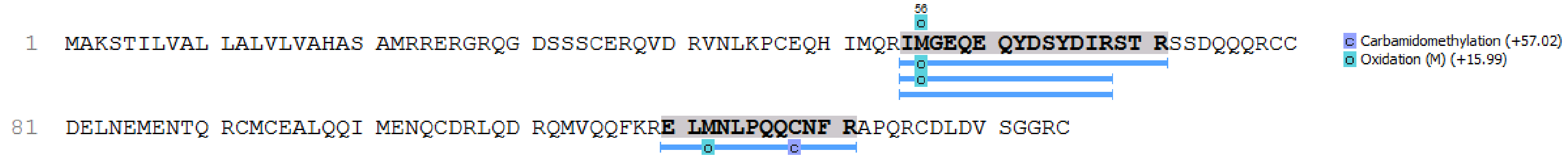
Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.IM(+15.99)GEQEQYDSYDIR.S	Y	99.9	77.71	1761.7516	14	0.0	881.8831	2	31.61	22	1514	OB5192.raw	1.95E4	5	5	55	68	Oxidation (M)
R.IMGEQEQYDSYDIR.S	Y	99.9	76.34	1745.7566	14	1.5	873.8868	2	32.94	22	1591	OB5192.raw	8.67E2	1	1	55	68	
R.IM(+15.99)GEQEQYDSYDIRSTR.S	Y	99.8	45.06	2105.9324	17	-0.8	702.9842	3	30.01	22	1425	OB5192.raw	2.33E4	5	5	55	71	Oxidation (M)
R.ELM(+15.99)NLPQQC(+57.02)NFR.A	Y	99.0	36.96	1564.7126	12	3.1	783.3660	2	31.81	22	1526	OB5192.raw	2.29E3	1	1	120	131	Oxidation (M); Carbamidomethylation
total 4 peptides																		

sp|Q647G9|CONG_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.IM(+15.99)GEQEQYDSYDIR.S	Y	99.9	77.71	1761.7516	14	0.0	881.8831	2	31.61	22	1514	OB5192.raw	1.95E4	5	5	55	68	Oxidation (M)
R.IMGEQEQYDSYDIR.S	Y	99.9	76.34	1745.7566	14	1.5	873.8868	2	32.94	22	1591	OB5192.raw	8.67E2	1	1	55	68	
R.IM(+15.99)GEQEQYDSYDIRSTR.S	Y	99.8	45.06	2105.9324	17	-0.8	702.9842	3	30.01	22	1425	OB5192.raw	2.33E4	5	5	55	71	Oxidation (M)
R.ELM(+15.99)NLPQQC(+57.02)NFR.A	Y	99.0	36.96	1564.7126	12	3.1	783.3660	2	31.81	22	1526	OB5192.raw	2.29E3	1	1	120	131	Oxidation (M); Carbamidomethylation
total 4 peptides																		

sp|TRYP_PIG|

back to list

| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 FPTDDDDKIV GGYTCAANSI PYQVSLNSGS HFCGGSLINS QWVVSAAHCY KSRIQVR**LGE HNIDVLEGNE QFINAA**KIIT

81 HPNFNGNTLD NDIMLIKLSS PATLNSR**VAT VSLPR**SCAAA GTECLISGWG NTKSSGSSYP SLLQCLKAPV LSDSSCKSSY

161 PGQITGNMIC VGFLEGGKDS CQGDSGGPVV CNGQLQGIVS WGYGCAQKNK PGVYTK**VCNY VNWIQQTIAA N**

C

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.LGEHNIDVLEGNEQFIN.A	Y	99.9	53.23	1939.9275	17	3.0	970.9739	2	35.94	22	1760	OB5192.raw	2.03E4	3	3	58	74	
R.LGEHNIDVLEGNEQFINAA.K	Y	99.8	43.81	2082.0017	19	2.5	1042.0107	2	36.47	22	1790	OB5192.raw	3.81E3	2	2	58	76	
R.LGEHNIDVLEGNE.Q	Y	99.7	43.09	1437.6736	13	-0.1	719.8440	2	33.18	22	1606	OB5192.raw	1.49E4	3	3	58	70	
R.VATVSLPR.S	Y	99.4	39.93	841.5021	8	-0.2	421.7583	2	30.36	22	1446	OB5192.raw	1.14E5	4	4	108	115	
K.VC(+57.02)NYVNWIQQTIAAN	Y	98.0	33.49	1792.8567	15	0.5	897.4360	2	40.69	22	2023	OB5192.raw	0	1	1	217	231	Carbamidomethylation
R.LGEHNIDVLEGNEQFINA.A	Y	84.3	25.81	2010.9646	18	-1.3	1006.4883	2	36.40	22	1786	OB5192.raw	4.38E2	1	1	58	75	
total 6 peptides																		

A1DZF0|A1DZF0_ARAHY

back to list

| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT D**TNNNDNQLD QFPRRFNLAG NHEQEFLR**YQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ

241 GQHGRRER**AG QEQENEGGNI FSGFTSEFLA QAFQVDDR**QI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD

321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA

481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.RFNLAGNHEQEFLR.Y	N	99.9	47.46	1729.8647	14	-1.1	577.6282	3	31.84	22	1528	OB5192.raw	2.69E4	4	4	195	208	
R.AGQEQENEGGNIFSGFTSEFLAQAFQVDDR.Q	Y	99.8	46.23	3290.4751	30	0.3	1097.8326	3	42.76	22	2140	OB5192.raw	0	1	1	249	278	
D.TNNNDNQLDQFPR.R	N	99.7	42.28	1574.7073	13	-1.3	788.3599	2	31.49	22	1507	OB5192.raw	7.09E2	1	1	182	194	
R.FNLAGNHEQEFLR.Y	N	93.3	27.97	1573.7637	13	-2.6	525.5938	3	33.08	22	1600	OB5192.raw	4.26E3	1	1	196	208	
total 4 peptides																		

sp|K22E_HUMAN|

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| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

1 MSCQISCKSR GRGGGGGGFR GFSSGSAVVS GGSRRSTSSF SCLSRHGGGG GGFGGGGFGS RSLVGLGGTK SISISVAGGG
81 GGFGAAGGFG GRGGGFGG**GS GFGGGSGFGG GSGFSGGGFG GGGFGGGR**FG GFGGPGGVGG LGGPGGFGPG GYPGGIHEVS
161 VNQSLLQPLN VKVDPEIQNV KAQEREQIKT LNNKFASFID KVRFLEQQNQ VLQTKWELLQ QMNVGTRPIN LEPIFQGYID
241 SLKRYLDGLT AERTSQNSEL NNMQDLVEDY KKKYEDEINK RTAAENDFVT LKKDVDNAYM IKVELQSKVD LLNQEIEFLK
321 VLYDAEISQI HQSVTDTNVI LSMDNSR**NLD LDSIIAEVKA QYEEIAQR**SK EEAEALYHSK YEELQVTVGR HGDSLKEIKI
401 EISELNRVIQ RLQGEIAHVK KQCKNVQDAI ADAEQRGEHA LKDARNKLND LEEALQQAKE DLARLLRDYQ ELMNVKLALD
481 VEIATYRKLL EGEECRMSGD LSSNVTVSVT SSTISSNVAS KAAFGGSGGR GSSSGGGYSS GSSSYGSGGR QSGSRGGSGG
561 GGSISGGGYG SGGGSGGRYG SGGGSKGGSI SGGGYGSGGG KHSSGGGSRG GSSSGGGYGS GGGGSSSVKG SSGEAFGSSV
641 TFSFR

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.NLDLDSIIAEVKAQYEEIAQR.S	Y	99.9	55.76	2417.2437	21	-0.8	806.7545	3	42.69	22	2136	OB5192.raw	2.16E4	3	3	348	368	
G.GSGFGGGSGFGGGSGFSGGGFGGGGFGGGR.F	Y	99.4	39.33	2398.0110	30	-0.9	800.3436	3	36.05	22	1767	OB5192.raw	2.02E3	1	1	99	128	
total 2 peptides																		

Q6IWG5|Q6IWG5_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLR**SVNE LDLPILGWLG LSAQHGTIYR** NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	56.21	2651.4070	24	2.2	884.8116	3	41.90	22	2091	OB5192.raw	1.83E4	4	4	357	380	
total 1 peptides																		

E5G077|E5G077_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YR**NAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	56.21	2651.4070	24	2.2	884.8116	3	41.90	22	2091	OB5192.raw	1.83E4	4	4	359	382	
total 1 peptides																		

Q0GM57|Q0GM57_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YR**NAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS5 tacka 20 na Figuri 1	#Spec	#Spec DS5 tacka 20 na Figuri 1	Start	End	PTM
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.9	56.21	2651.4070	24	2.2	884.8116	3	41.90	22	2091	OB5192.raw	1.83E4	4	4	359	382	
total 1 peptides																		

Peptide List

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1. Notes

Spot 21 2D gel DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

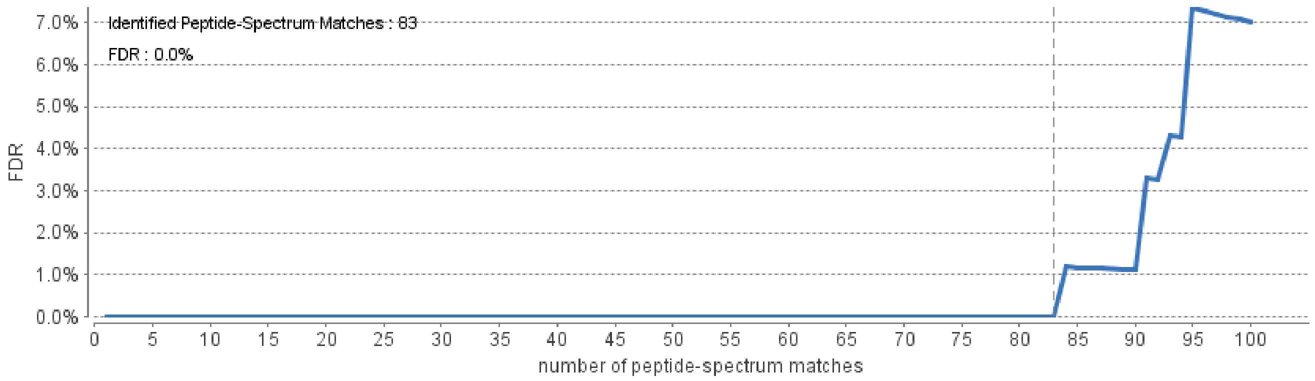
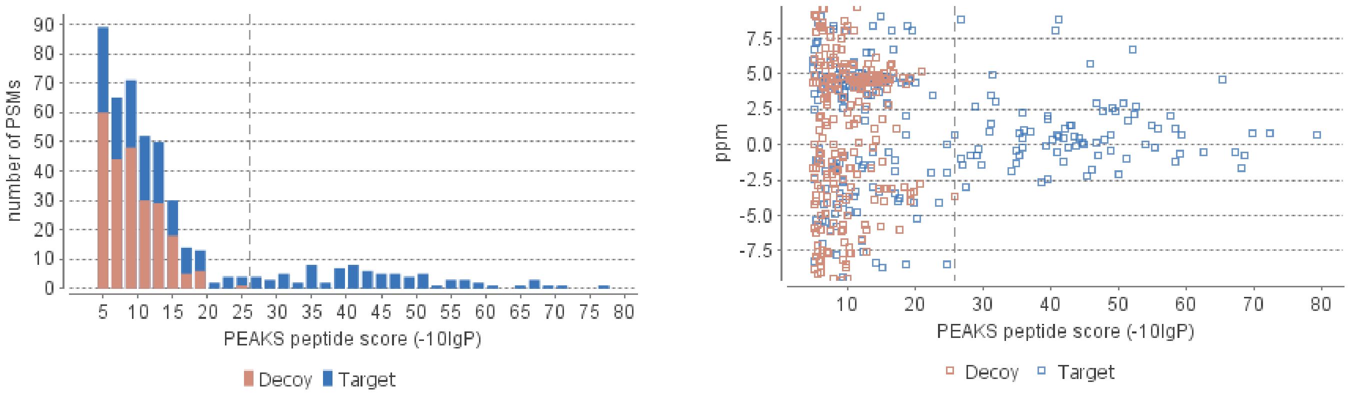


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

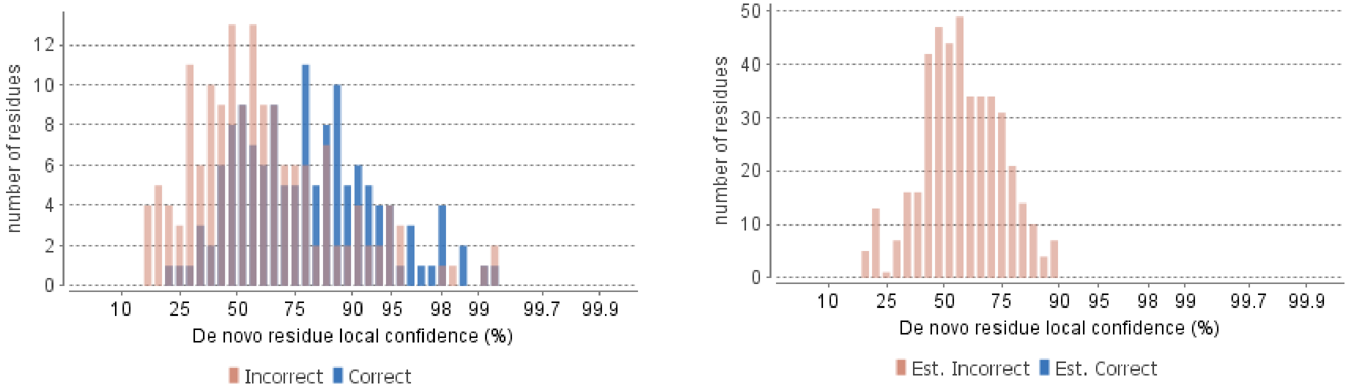


Table 1. Statistics of data.

# of MS scans	2636
# of MS/MS scans	1430

Table 2. Result filtration parameters.

Peptide -10lgP	≥26
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	79
Peptide sequences	29
Protein groups	7
Proteins	10
Proteins (#Unique Peptides)	5 (>2); 1 (=2); 4 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	68

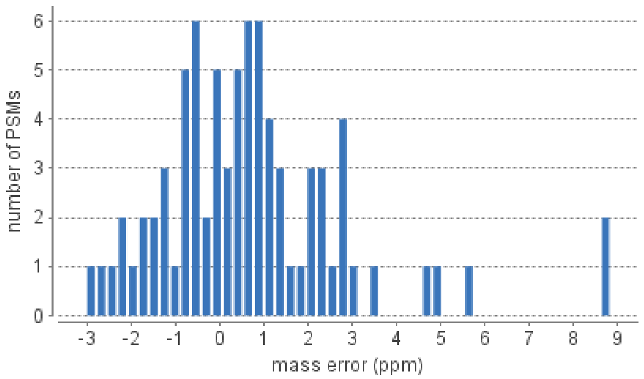
Table 4. PTM profile.

Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Oxidation	15.99	M	15	79.45	2.93E4	1000.00
HydPro	15.99	P	7	59.30	1.37E4	55.36
Carbamidomethyl	57.02	C	4	65.30	1.56E3	1000.00
Deamidation	.98	Q	3	50.83		0.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm. ?

(a) **(b)**



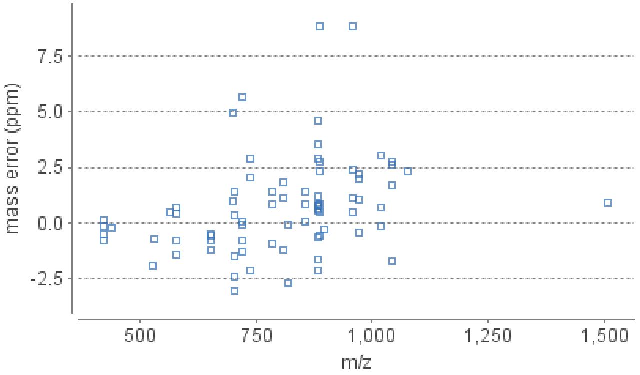


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
DS6 tacka 21 na Figuri 1	20	9	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: Uniprot_Peanut(3818)+cRAP_aug17
Taxon: All
Searched Entry: 1352
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB5194.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

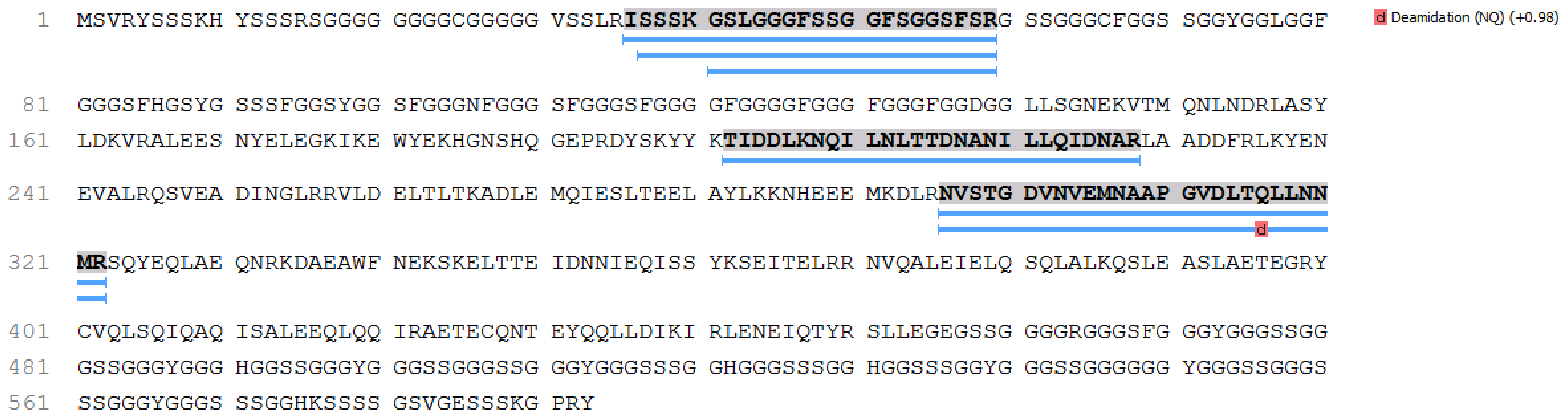
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) DS6 tacka 21 na Figuri 1	Area DS6 tacka 21 na Figuri 1	#Peptides	#Unique	#Spec DS6 tacka 21 na Figuri 1	PTM	Avg. Mass	Description
5	220	sp|K1C10_HUMAN|	98.4	138.79	13	13	3.1E4	5	5	15	Y	59519	sp|K1C10_HUMAN|
6	221	sp|K2C1_HUMAN|	98.8	138.01	14	14	1.82E4	5	5	8	Y	65886	sp|K2C1_HUMAN|
1	516	A5Z1R0|A5Z1R0_ARAHY	84.2	130.16	20	20	8.56E4	4	4	16	Y	16920	Ara h 6 OS=Arachis hypogaea GN=Ara h 6 PE=4 SV=1
1	517	sp|Q647G9|CONG_ARAHY	84.2	130.16	20	20	8.56E4	4	4	16	Y	16920	Conglutin OS=Arachis hypogaea PE=1 SV=1
2	1193	sp|TRYP_PIG|	84.1	105.75	12	12	1.66E5	4	4	18	N	24409	sp|TRYP_PIG|
8	216	Q6IWG5|Q6IWG5_ARAHY	61.2	64.77	5	5	3.59E4	1	1	5	N	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
8	218	E5G077|E5G077_ARAHY	61.2	64.77	5	5	3.59E4	1	1	5	N	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
8	217	Q0GM57|Q0GM57_ARAHY	61.2	64.77	5	5	3.59E4	1	1	5	N	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
15	646	sp|K1C9_HUMAN|	96.7	64.44	10	10	4.03E3	2	2	2	N	62129	sp|K1C9_HUMAN|
12	964	sp|K22E_HUMAN|	77.9	55.91	3	3	9.45E3	1	1	3	N	65865	sp|K22E_HUMAN|
total 10 proteins													

sp|K1C10_HUMAN| back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MSVRYSSSKH YSSSRSGGGG GGGGCGGGGG VSSLR**ISSSK GSLGGGFSSG GFSGGSFSR**G SSGGGCFGGS SGGYGGLGGF
81 GGGSFHGSYG SSSFGGSYGG SFGGGNFGGG SFGGGSFGGG GFGGGGFGGG FGGGFGGDGG LLSGNEKVTM QNLNDRLASY
161 LDKVRALEES NYELEGKIKE WYEKHGNSHQ GEPRDYSKYY K**TIDDLKNQI LNLTTDNANI LLQIDNAR**LA ADDFRLKYEN
241 EVALRQSVEA DINGLRRVLD ELTLTKADLE MQIESLTEEL AYLKKNHEEE MKDLR**NVSTG DVNVEMNAAP GVDLTQLLNN**
321 **MR**SQYEQLAE QNRKDAEAWF NEKSKELTTE IDNNIEQISS YKSEITELRR NVQALEIELQ SQLALKQSLE ASLAETEGRY
401 CVQLSQIQAQ ISALEEQLQQ IRAETECQNT EYQQLLDIKI RLENEIQTYR SLLEGEGSSG GGGRGGGSFG GGYGGGSSGG
481 GSSGGGYGGG HGGSSGGGYG GGSSGGGSSG GGYGGGSSSG GHGGGSSSGG HGGSSSGGYG GGSSGGGGGG YGGGSSGGGS
561 SSGGGYGGGS SSGGHKSSSS GSVGESSSKG PRY

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
K.GSLGGGFSSGGFSGGSFSR.G	Y	99.9	72.25	1706.7648	19	0.8	854.3904	2	35.43	24	1724	OB5194.raw	9.14E3	3	3	41	59	
R.ISSSKGSLGGGFSSGGFSGGSFSR.G	Y	99.9	57.78	2209.0398	24	2.1	737.3554	3	33.97	24	1642	OB5194.raw	4.08E3	3	3	36	59	
K.TIDDLKNQILNLTTDNANILLQIDNAR.L	Y	99.9	55.46	3051.6201	27	-0.2	1018.2138	3	42.45	24	2111	OB5194.raw	5.26E3	3	3	202	228	
R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S	Y	99.8	47.74	2871.3855	27	2.4	958.1381	3	41.45	24	2052	OB5194.raw	7.5E3	3	3	296	322	
R.NVSTGDVNVEMNAAPGVDLTQ(+.98)LLNNMR.S	Y	99.6	41.19	2872.3694	27	8.9	958.4722	3	41.35	24	2046	OB5194.raw	7.75E2	1	1	296	322	Deamidation (NQ)

I.SSSKGSLGGGFSSGGFSGGSFSR.G	Y	98.3	36.10	2095.9558	23	1.0	699.6599	3	33.56	24	1619	OB5194.raw	4.27E3	2	2	37	59	
total 6 peptides																		

sp|K2C1_HUMAN|

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SRQFSSRSGY RSGGGFSSGS AGIINYQRRT TSSSTRRSGG GGGR**FSSCGG GGGSFGAGGG FGSRSLVNLG GSKSISISVA**

81 **R**GGGRGSGFG GGYGGGGFGG GGFGGGGFGG GGIGGGGFGG FGSGGGGFGG GGFGGGGYGG GYGPVCPPGG IQEVTINQSL

161 LQPLNVEIDP EIQKVKSRER EQIKSLNNQF ASFIDKVRFL EQQNQVLQTK WELLQQVDTS TRTHNLEPYF ESFINNLRRR

241 VDQLKSDQSR LDSELKNMQD MVEDYRNKYE DEINKRTNAE NEFVTIKKDV DGAYMTKVDL QAK**LDNLQQE IDFLTALYQA**

321 **ELSQMQTQIS ETNVILSMDN NRSLDLDSII AEVK**AQNEDI AQKSKAEAES LYQSKYEELQ ITAGRHGDSV RNSKIEISEL

401 NRVIQRLRSE IDNVKKQISN LQQSISDAEQ RGENALKDAK NKLNDLEDAL QQAKEDLARL LRDYQELMNT KLALDLEIAT

481 YRTLLEGEES RMSGECAPNV SVSVSTSHTT ISGGGSRGGG GGGYGSGGSS YGSGGGSYGS GGGGGGGRGS YGSGGSSYGS

561 GGGSYGSGGG GGGHGSYGSG SSSGGYRGGS GGGGGGSSGG RGSGGGSSGG SIGGRGSSSG GVKSSGGSSS VRFVSTTYSG

641 VTR

C Carbamidomethylation (+57.02)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.SLDLDSIIAEVK.A	Y	99.9	68.74	1301.7078	12	-0.8	651.8607	2	40.03	24	1970	OB5194.raw	9.91E3	4	4	343	354	
R.FSSC(+57.02)GGGGGSFGAGGGFGSR.S	Y	99.9	65.30	1764.7274	20	4.6	883.3751	2	33.12	24	1594	OB5194.raw	1.56E3	1	1	45	64	Carbamidomethylation
R.SLVNLGGSK.S	Y	99.6	42.55	873.4919	9	-0.2	437.7531	2	31.31	24	1492	OB5194.raw	4.21E3	1	1	65	73	
R.SLVNLGGSKSISISVAR.G	Y	99.6	41.95	1686.9628	17	0.5	563.3285	3	34.87	24	1695	OB5194.raw	2.54E3	1	1	65	81	
K.LDNLQQEIDFLTALYQAELSQMQTQISETNVILSMDNNR.S	Y	92.2	31.08	4526.1943	39	0.9	1509.7401	3	48.08	24	2412	OB5194.raw	0	1	1	304	342	
total 5 peptides																		

A5Z1R0|A5Z1R0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

56 61

1 MAKSTILVAL LALVLVAHAS AMRRERGRQG DSSSCERQVD RVNLKPCEQH IMQR**IMGEQE QYDSYDIRST R**SSDQQQRCC

81 DELNEMENTQ RCMCEALQQI MENQCDRLQD RQMVQQFKR**E LMNLPQQCNF R**APQRCDLDV SGGRC

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na	#Spec	#Spec DS6 tacka 21 na	Start	End	PTM

		(%)											Figuri 1		Figuri 1			
R.IM(+15.99)GEQEQYDSYDIR.S	Y	99.9	79.45	1761.7516	14	0.7	881.8837	2	32.73	24	1571	OB5194.raw	2.93E4	6	6	55	68	Oxidation (M)
R.ELM(+15.99)NLPQQC(+57.02)NFR.A	Y	99.9	51.28	1564.7126	12	-1.0	783.3629	2	32.83	24	1577	OB5194.raw	5.59E3	3	3	120	131	Oxidation (M); Carbamidomethylation
R.IM(+15.99)GEQEQ(+.98)YDSYDIR.S	Y	99.9	50.83	1762.7356	14	2.9	882.3776	2	33.17	24	1597	OB5194.raw	0	1	1	55	68	Oxidation (M); Deamidation (NQ)
R.IM(+15.99)GEQEQYDSYDIRSTR.S	Y	99.6	43.07	2105.9324	17	1.4	702.9857	3	31.66	24	1512	OB5194.raw	4.91E4	5	5	55	71	Oxidation (M)
E.QYDSYDIR.S	Y	88.6	29.13	1058.4668	8	-0.7	530.2403	2	30.99	24	1473	OB5194.raw	1.65E3	1	1	61	68	
total 5 peptides																		

sp|Q647G9|CONG_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKSTILVAL LALVLVAHAS AMRRERGRQG DSSSCERQVD RVNLKPCEQH IMQR**IMGEQE QYDSYDIRST R**SSDQQQRCC

81 DELNEMENTQ RCMCEALQQI MENQCDRLQD RQMVQQFKR**E LMNLPQQCNF R**APQRCDLDV SGGRC

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.IM(+15.99)GEQEQYDSYDIR.S	Y	99.9	79.45	1761.7516	14	0.7	881.8837	2	32.73	24	1571	OB5194.raw	2.93E4	6	6	55	68	Oxidation (M)
R.ELM(+15.99)NLPQQC(+57.02)NFR.A	Y	99.9	51.28	1564.7126	12	-1.0	783.3629	2	32.83	24	1577	OB5194.raw	5.59E3	3	3	120	131	Oxidation (M); Carbamidomethylation
R.IM(+15.99)GEQEQ(+.98)YDSYDIR.S	Y	99.9	50.83	1762.7356	14	2.9	882.3776	2	33.17	24	1597	OB5194.raw	0	1	1	55	68	Oxidation (M); Deamidation (NQ)
R.IM(+15.99)GEQEQYDSYDIRSTR.S	Y	99.6	43.07	2105.9324	17	1.4	702.9857	3	31.66	24	1512	OB5194.raw	4.91E4	5	5	55	71	Oxidation (M)
E.QYDSYDIR.S	Y	88.6	29.13	1058.4668	8	-0.7	530.2403	2	30.99	24	1473	OB5194.raw	1.65E3	1	1	61	68	
total 5 peptides																		

sp|TRYP_PIG|

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FPTDDDDKIV GGYTCAANSI PYQVSLNSGS HFCGGSLINS QWVVSAAHCY KSRIQVR**LGE HNIDVLEGNE QFINAA**KIIT

81 HPNFNGNTLD NDIMLIKLSS PATLNSR**VAT VSLPR**SCAAA GTECLISGWG NTKSSGSSYP SLLQCLKAPV LSDSSCKSSY

161 PGQITGNMIC VGFLEGGKDS CQGDSGGPVV CNGQLQGIVS WGYGCAQKNK PGVYTKVCNY VNWIQQTIAA N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.LGEHNIDVLEGNEQFINAA.K	Y	99.9	52.57	2082.0017	19	2.7	1042.0110	2	37.51	24	1834	OB5194.raw	3.13E3	4	4	58	76	
R.LGEHNIDVLEGNEQFIN.A	Y	99.9	52.28	1939.9275	17	2.2	970.9731	2	37.11	24	1814	OB5194.raw	1.75E4	4	4	58	74	
R.VATVSLPR.S	Y	99.8	46.72	841.5021	8	0.1	421.7584	2	31.24	24	1488	OB5194.raw	1.26E5	5	5	108	115	

R.LGEHNIDVLEGNE.Q	Y	99.7	45.83	1437.6736	13	5.7	719.8481	2	34.22	24	1657	OB5194.raw	1.85E4	5	5	58	70	
total 4 peptides																		

Q6IWG5|Q6IWG5_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLR**SVNE LDLPILGWLG LSAQHGTIYR** NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.7	44.31	2651.4070	24	0.5	884.8101	3	43.07	24	2147	OB5194.raw	3.59E4	5	5	357	380	
total 1 peptides																		

E5G077|E5G077_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YR**NAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.7	44.31	2651.4070	24	0.5	884.8101	3	43.07	24	2147	OB5194.raw	3.59E4	5	5	359	382	
total 1 peptides																		

Q0GM57|Q0GM57_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YR**NAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.SVNELDLPILGWLGLSAQHGTIYR.N	Y	99.7	44.31	2651.4070	24	0.5	884.8101	3	43.07	24	2147	OB5194.raw	3.59E4	5	5	359	382	
total 1 peptides																		

sp|K1C9_HUMAN|

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSCRQFSSSY LSRSGGGGGG GLGSGGSIRS SYSRFSSSGG RGGGGRFSSS SGYGGGSSRV CGRGGGGSFG YSYGGGSGGG

81 FSASSLGGGF GGGSRGFGGA SGGGYSSSGG FGGGFGGGSG GGFGGGYGSG FGGLGGFGGG AGGGDGGILT ANEKSTMQEL

161 NSRLASYLDK VQALEEANND LENKIQDWYD KKGPAAIQKN YSPYYNTIDD LKDQIVDLTV GNNKTLLDID NTRMTLDDFR

241 IKFEMEQNLR QGVDADINGL RQVLDNLTME KSDLEMQYET LQEELMALKK NHKEEMSQLT GQNSGDVNVE INVAPGKDLT

321 KTLNDMRQEY EQLIAKNRKD IENQYETQIT QIEHEVSSSG QEVQSSAKEV TQLRHGVQEL EIELQSQLSK KAALEKSLED

401 TKNRYCGQLQ MIQEQISNLE AQITDVRQEI ECQNQEYSLL LSIKMRLEKE IETYHNLLEG GQEDFESSGA GKIGLGGRGG

481 SGGSYGRGSR **GGSGGSYGGG GSGGGYGGGS GSR**GGSGGSY GGGSGSGGGS GGGYGGGSGG GHSGGSGGGH SGGSGGNYGG

561 GSGSGGGSGG GYGGGSGSR**G GSGGSHGGGS GFGGESGGSY GGGEEASGSG GGYGGGSGK**S SHS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	Y	99.9	49.71	3222.2742	40	2.4	1075.1012	3	29.40	24	1394	OB5194.raw	1.97E3	1	1	580	619	
R.GGSGGSYGGGGSGGGYGGGSGSR.G	Y	89.0	29.45	1790.7203	23	-0.3	896.3672	2	26.30	24	1244	OB5194.raw	2.06E3	1	1	491	513	
total 2 peptides																		

sp|K22E_HUMAN|

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSCQISCKSR GRGGGGGGFR GFSSGSAVVS GGSRRSTSSF SCLSRHGGGG GGFGGGGFGS RSLVGLGGTK SISISVAGGG
 81  GGFGAAGGFG GRGGGFGGGS GFGGGSGFGG GSGFSGGGFG GGGFGGGRFG GFGGPGGVGG LGGPGGFGPG GYPGGIHEVS
161  VNQSLLQPLN VKVDPEIQNV KAQEREQIKT LNNKFASFID KVRFLEQQNQ VLQTKWELLQ QMNVGTRPIN LEPIFQGYID
241  SLKRYLDGLT AERTSQNSEL NNMQDLVEDY KKKYEDEINK RTAAENDFVT LKKDVDNAYM IKVELQSKVD LLNQEIEFLK
321  VLYDAEISQI HQSVTDTNVI LSMDNSRNLD LDSIIAEVKA QYEEIAQRSK EEAEALYHSK YEELQVTVGR HGDSLKEIKI

401  EISELNRVIQ RLQGEIAHVK KQCKNVQDAI ADAEQRGEHA LKDARNKLND LEEALQQAKE DLARLLRDYQ ELMNVKLALD
481  VEIATYRKLL EGEECRMSGD LSSNVTVSVT SSTISSNVAS KAAFGGSGGR GSSSGGGYSS GSSSYGSGGR QSGSRGGSGG
561  GGSISGGGYG SGGGSGGRYG SGGGSKGGSI SGGGYGSGGG KHSSGGGSRG GSSSGGGYGS GGGGSSSVKG SSGEAFGSSV
641  TFSFR
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area DS6 tacka 21 na Figuri 1	#Spec	#Spec DS6 tacka 21 na Figuri 1	Start	End	PTM
R.NLDLDSIIAEVKAQYEEIAQR.S	Y	99.9	55.91	2417.2437	21	1.1	806.7560	3	43.50	24	2172	OB5194.raw	9.45E3	3	3	348	368	
total 1 peptides																		

Peptide List

1. Notes

Spot 22 from DPS

2. Result Statistics

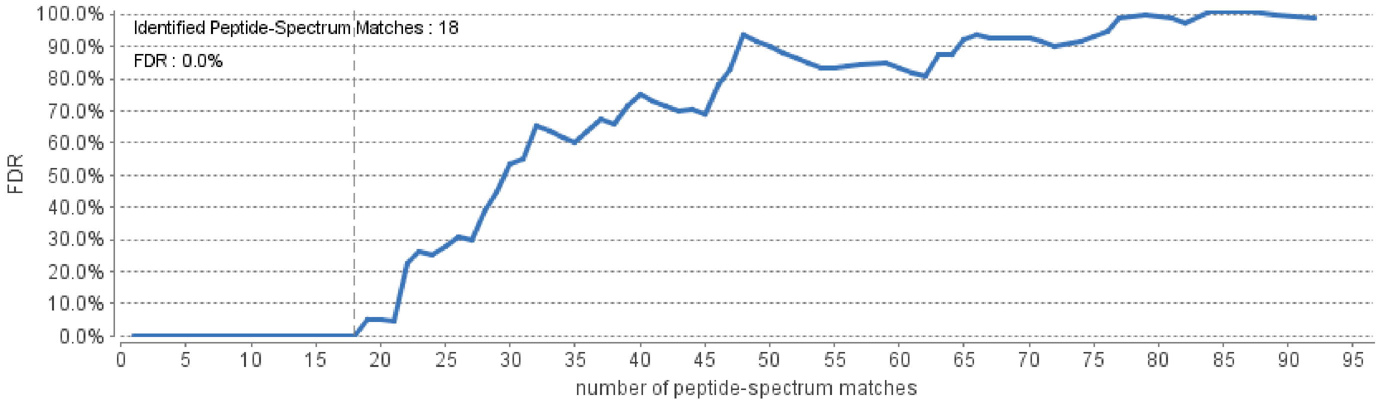
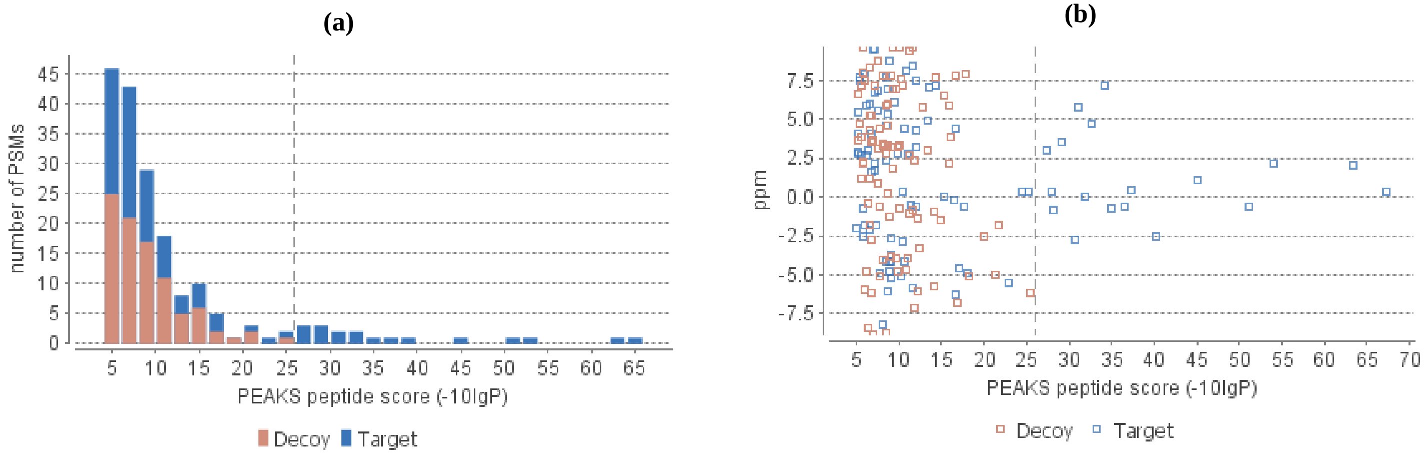


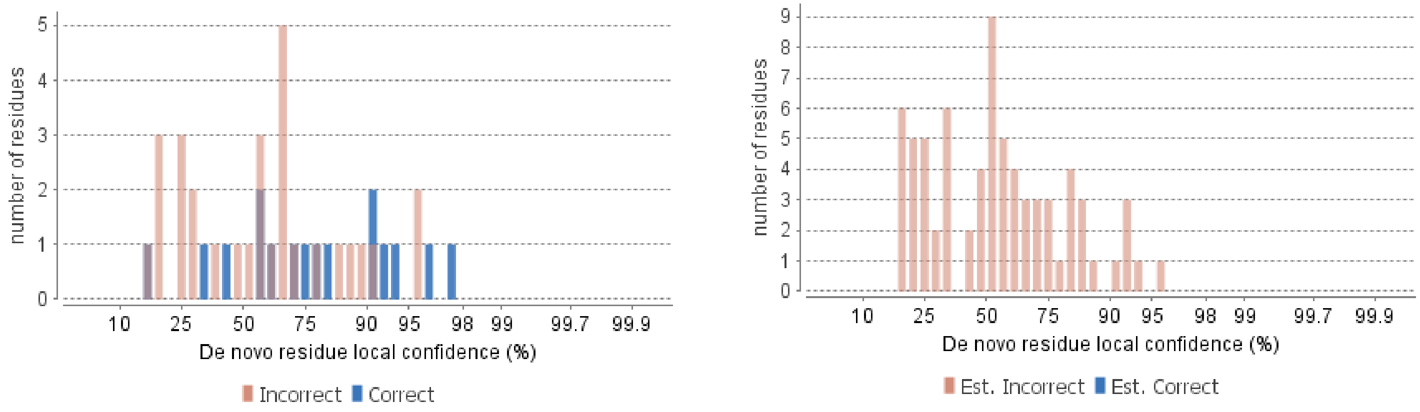
Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.


(a)

(b)

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.



(a)

(b)

Table 1. Statistics of data.

# of MS scans	3127
# of MS/MS scans	1942

Table 2. Result filtration parameters.

Peptide -10lgP	≥26
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	14
Peptide sequences	6
Protein groups	2
Proteins	2
Proteins (#Unique Peptides)	0 (>2); 1 (=2); 1 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	9

Table 4. PTM profile.

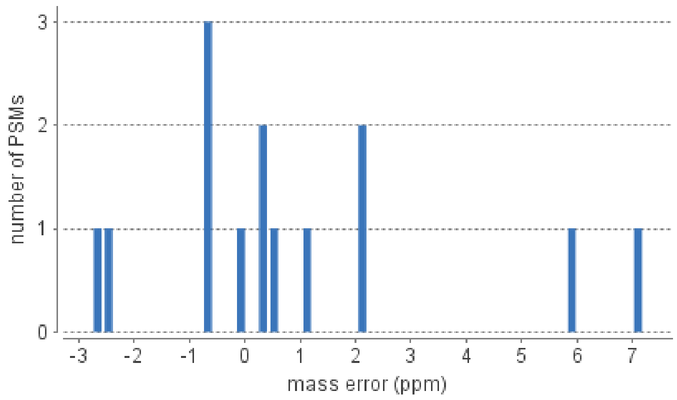
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm. ?

(a)

(b)



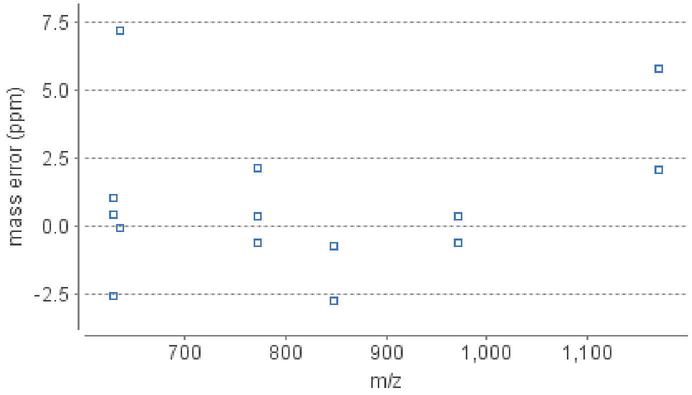


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 27	6	0	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3625.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 27	Area Sample 27	#Peptides	#Unique	#Spec Sample 27	PTM	Avg. Mass	Description
1	15	Q647H3|Q647H3_ARAHY	98.9	127.76	15	15	1.37E4	4	2	10	N	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
2	2	A1DZF0|A1DZF0_ARAHY	98.6	103.49	9	9	2.29E3	3	1	7	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
total 2 proteins													

Q647H3|Q647H3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLK**TANDLN LLILRWGLGS**
401 **AEYGNLYR**NA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS**
481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 27	#Spec	#Spec Sample 27	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	67.33	1540.7673	13	0.4	771.3912	2	32.74	27	1615	OB3625.raw	4.2E3	3	3	396	408	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	63.26	3510.7590	33	2.1	1171.2627	3	34.88	27	1873	OB3625.raw	0	2	2	478	510	
K.TANDLNLLILR.W	Y	98.5	45.08	1254.7296	11	1.1	628.3727	2	32.66	27	1605	OB3625.raw	1.37E4	3	3	385	395	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	95.5	34.94	2540.2910	23	-0.7	847.7703	3	30.84	27	1446	OB3625.raw	1.53E4	2	2	443	465	
total 4 peptides																		

A1DZF0|A1DZF0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ

241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD

321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLK**TANE LNLLILRWLG LSAEYGNLYR**

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGK**SQS ENFEYVAFKT DSRPSIANLA

481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 27	#Spec	#Spec Sample 27	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	67.33	1540.7673	13	0.4	771.3912	2	32.74	27	1615	OB3625.raw	4.2E3	3	3	388	400	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	95.5	34.94	2540.2910	23	-0.7	847.7703	3	30.84	27	1446	OB3625.raw	1.53E4	2	2	435	457	
K.TANELNLLILR.W	Y	95.0	34.16	1268.7452	11	7.2	635.3845	2	32.82	27	1622	OB3625.raw	2.29E3	2	2	377	387	
total 3 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

Summary

1. Notes Spot 23 DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

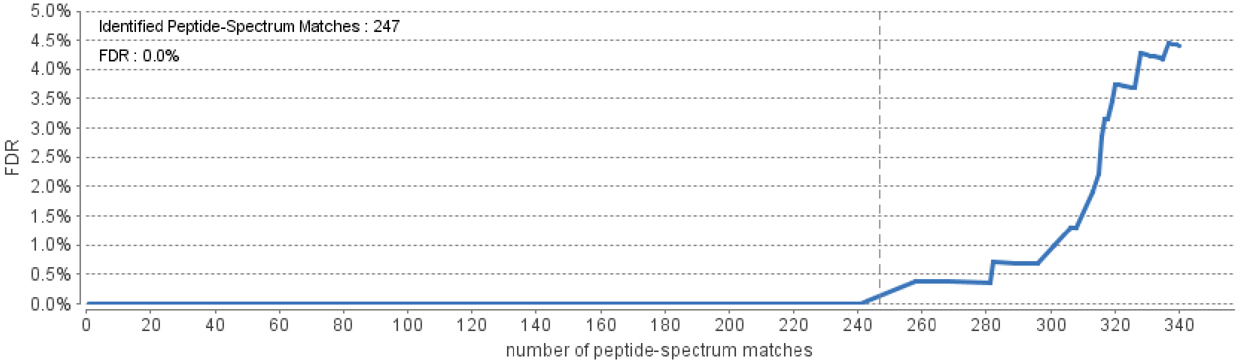
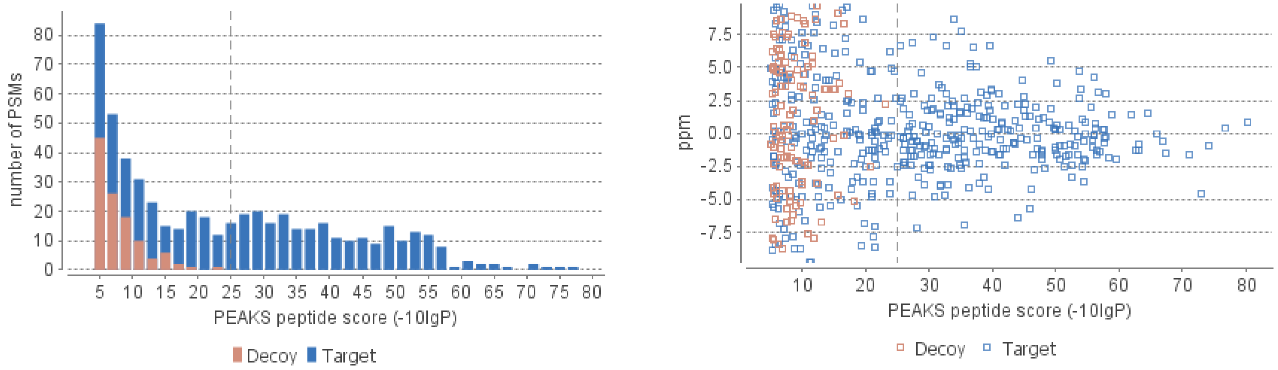


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.



(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

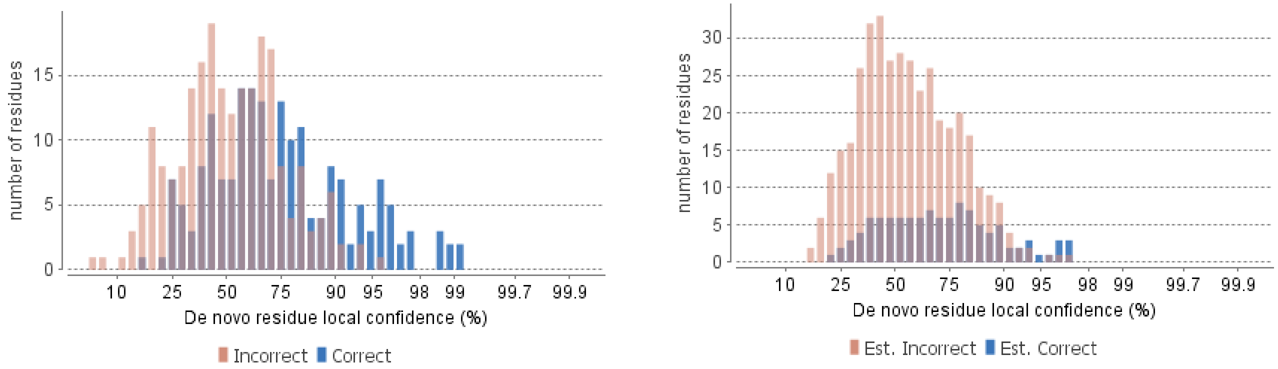


Table 1. Statistics of data.

# of MS scans	2925
# of MS/MS scans	3268

Table 2. Result filtration parameters.

Peptide -10lgP	≥25
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	234
Peptide sequences	86
Protein groups	4
Proteins	18
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 18 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	59

Table 4. PTM profile.

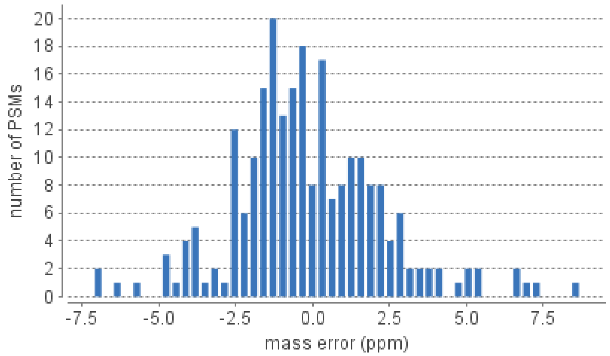
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	97	80.34	4.6E4	1000.00
Deamidation	.98	NQ	67	61.79		30.41
HydPro	15.99	P	14	56.67	6.81E3	0.00
Oxidation	15.99	M	1	27.27	1.33E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



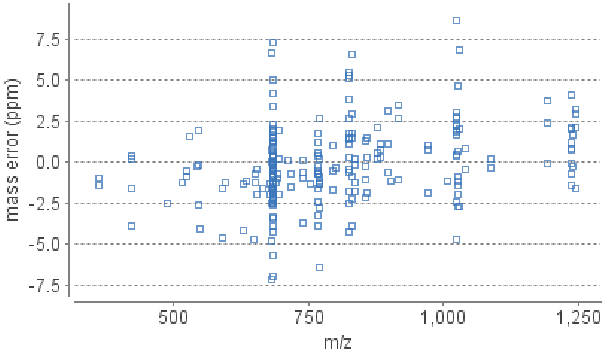


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 31	77	9	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3629.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 31	Area Sample 31	#Peptides	#Unique	#Spec Sample 31	PTM	Avg. Mass	Description
1	15	Q647H3|Q647H3_ARAHY	99.1	181.68	24	24	8.3E2	10	1	157	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
1	5	Q5I6T2|Q5I6T2_ARAHY	99.1	181.68	24	24	8.3E2	10	1	157	Y	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
1	13	Q9FZ11|Q9FZ11_ARAHY	99.1	181.68	24	24	8.3E2	10	1	157	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
2	7	Q647H4|Q647H4_ARAHY	99.1	178.08	22	22	1.93E3	9	1	155	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
2	10	Q8LKN1|Q8LKN1_ARAHY	99.1	178.08	22	22	1.93E3	9	1	155	Y	61738	Allergen Arah3/Arah4 OS=Arachis hypogaea PE=3 SV=1
6	41	Q6IWG5|Q6IWG5_ARAHY	84.1	64.34	7	7	1.83E4	2	1	6	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
6	42	Q0GM57|Q0GM57_ARAHY	84.1	64.34	7	7	1.83E4	2	1	6	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
6	45	E5G077|E5G077_ARAHY	84.1	64.34	7	7	1.83E4	2	1	6	Y	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
19	122	E9LFE7|E9LFE7_ARAHY	61.0	35.48	9	9	6.93E3	1	1	1	N	15873	7S conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
19	69	Q6PSU5|Q6PSU5_ARAHY	61.0	35.48	4	4	6.93E3	1	1	1	N	33604	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
19	57	Q6PSU6|Q6PSU6_ARAHY	61.0	35.48	4	4	6.93E3	1	1	1	N	34133	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
19	27	Q6PSU4|Q6PSU4_ARAHY	61.0	35.48	3	3	6.93E3	1	1	1	N	48095	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
19	26	Q6PSU3|Q6PSU3_ARAHY	61.0	35.48	2	2	6.93E3	1	1	1	N	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
19	21	sp|P43237|ALL11_ARAHY	61.0	35.48	2	2	6.93E3	1	1	1	N	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
19	23	B3IXL2|B3IXL2_ARAHY	61.0	35.48	2	2	6.93E3	1	1	1	N	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
19	55	E5G076|E5G076_ARAHY	61.0	35.48	2	2	6.93E3	1	1	1	N	70788	Ara h 1 allergen OS=Arachis hypogaea GN=ara h 1 PE=4 SV=1
19	18	N1NG13|N1NG13_ARAHY	61.0	35.48	2	2	6.93E3	1	1	1	N	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
19	20	sp|P43238|ALL12_ARAHY	61.0	35.48	2	2	6.93E3	1	1	1	N	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
total 18 proteins													

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	80.34	2473.1372	22	0.8	1237.5769	2	34.31	31	2107	OB3629.raw	1.05E5	10	10	99	120	Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	76.75	2050.0383	17	0.5	684.3537	3	30.01	31	1649	OB3629.raw	1.45E6	57	57	82	98	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	61.79	2051.0225	17	1.5	684.6824	3	30.67	31	1716	OB3629.raw	1.9E3	2	2	82	98	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.9	56.67	2489.1321	22	3.2	1245.5773	2	34.06	31	2074	OB3629.raw	3.37E4	3	3	99	120	Carbamidomethylation; Hydroxylation Pro
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	56.16	3069.3774	27	0.4	1024.1335	3	32.91	31	1932	OB3629.raw	1.62E5	5	5	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.9	55.50	2474.1211	22	2.0	1238.0703	2	34.44	31	2125	OB3629.raw	7.86E4	3	3	99	120	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	53.73	2474.1211	22	2.6	825.7165	3	34.52	31	2136	OB3629.raw	1.45E5	11	11	99	120	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQEIFIQQGR.G	N	99.9	53.56	2051.0225	17	4.7	1026.5233	2	30.56	31	1705	OB3629.raw	1.9E3	3	3	82	98	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	53.49	1534.6470	12	-0.3	768.3306	2	24.94	31	1228	OB3629.raw	3.89E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	53.36	2489.1321	22	-1.6	1245.5713	2	34.01	31	2067	OB3629.raw	6.81E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.9	52.53	1534.6470	12	-3.3	768.3282	2	24.42	31	1182	OB3629.raw	1.68E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	52.08	1533.6630	12	0.6	767.8392	2	24.20	31	1160	OB3629.raw	2.26E4	5	5	25	36	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.57	1535.6311	12	-2.8	768.8207	2	25.23	31	1252	OB3629.raw	5.14E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)

R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	45.81	2052.0063	17	-5.7	685.0055	3	31.03	31	1749	OB3629.raw	0	4	4	82	98	Deamidation (NQ)
R.LESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.9	44.91	3070.3613	27	2.8	1024.4639	3	33.22	31	1967	OB3629.raw	4.37E4	3	3	46	72	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.93	1535.6311	12	-6.4	768.8179	2	25.87	31	1300	OB3629.raw	5.14E4	3	3	25	36	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	99.8	41.99	3070.3613	27	-2.4	1024.4586	3	33.40	31	1989	OB3629.raw	4.37E4	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)Q(+.98)GR.R	N	99.7	41.84	2491.1001	22	2.1	1246.5599	2	35.61	31	2261	OB3629.raw	2.61E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	N	99.7	40.91	2490.1160	22	3.0	1246.0690	2	34.28	31	2104	OB3629.raw	1.68E4	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.7	40.78	1388.6936	13	0.2	695.3542	2	27.33	31	1423	OB3629.raw	4.69E3	2	2	372	384	
R.LNAQRPDNR.L	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	37	45	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.66	1535.6311	12	-1.4	768.8218	2	25.42	31	1265	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.7	39.43	2490.1160	22	6.6	831.0514	3	34.18	31	2090	OB3629.raw	1.38E3	2	2	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	38.37	1536.6151	12	0.2	769.3150	2	26.22	31	1327	OB3629.raw	6.79E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
K.TANDLNLLILR.W	N	99.4	36.36	1254.7296	11	-4.1	628.3695	2	32.87	31	1928	OB3629.raw	2.27E3	1	1	385	395	
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.4	35.60	1536.6151	12	2.7	769.3169	2	25.65	31	1281	OB3629.raw	8.11E1	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.3	34.68	1534.6470	12	-0.7	768.3302	2	25.04	31	1236	OB3629.raw	2.22E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.1	34.16	1535.6311	12	-0.9	768.8221	2	25.60	31	1278	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)P(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.1	33.50	3086.3562	27	-2.7	1029.7899	3	33.93	31	2057	OB3629.raw	0	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.1	33.04	2631.2063	23	2.1	878.0779	3	33.53	31	2004	OB3629.raw	1.74E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	99.1	32.96	2491.1001	22	-3.9	831.3707	3	35.65	31	2267	OB3629.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	99.1	32.60	2038.9166	16	6.7	680.6507	3	27.42	31	1434	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.1	30.88	2038.9166	16	-4.8	680.6429	3	27.56	31	1446	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
K.SQSDNFEYVAFK.T	Y	98.0	30.71	1433.6462	12	-1.6	717.8293	2	30.30	31	1679	OB3629.raw	8.3E2	2	2	466	477	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	98.0	30.33	2490.1160	22	1.7	831.0474	3	35.48	31	2246	OB3629.raw	7.21E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	97.9	29.73	2475.1052	22	1.7	1238.5620	2	35.35	31	2231	OB3629.raw	2.89E3	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	29.45	2039.9006	16	0.0	680.9742	3	27.87	31	1476	OB3629.raw	1.55E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.1	28.62	2039.9006	16	-1.6	680.9731	3	28.10	31	1505	OB3629.raw	1.55E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	97.0	28.13	2040.8846	16	-7.1	681.2973	3	28.24	31	1517	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.9	27.39	2040.8846	16	0.8	681.3027	3	28.36	31	1525	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	96.9	27.28	3085.3723	27	6.9	1029.4718	3	33.77	31	2035	OB3629.raw	6.29E1	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	95.1	26.50	2630.2224	23	0.2	877.7482	3	33.12	31	1954	OB3629.raw	3.19E4	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	94.7	25.99	1536.6151	12	-2.4	769.3130	2	26.32	31	1335	OB3629.raw	6.79E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
total 43 peptides																		

Q5I6T2|Q5I6T2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS

241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE

321 EYDEDEYEYD EEDRRRGRGS RGRGNGIEET ICTASVKKNI GRNRSPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY

401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL

481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	80.34	2473.1372	22	0.8	1237.5769	2	34.31	31	2107	OB3629.raw	1.05E5	10	10	99	120	Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	76.75	2050.0383	17	0.5	684.3537	3	30.01	31	1649	OB3629.raw	1.45E6	57	57	82	98	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	61.79	2051.0225	17	1.5	684.6824	3	30.67	31	1716	OB3629.raw	1.9E3	2	2	82	98	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.9	56.67	2489.1321	22	3.2	1245.5773	2	34.06	31	2074	OB3629.raw	3.37E4	3	3	99	120	Carbamidomethylation; Hydroxylation Pro
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	56.16	3069.3774	27	0.4	1024.1335	3	32.91	31	1932	OB3629.raw	1.62E5	5	5	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.9	55.50	2474.1211	22	2.0	1238.0703	2	34.44	31	2125	OB3629.raw	7.86E4	3	3	99	120	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	53.73	2474.1211	22	2.6	825.7165	3	34.52	31	2136	OB3629.raw	1.45E5	11	11	99	120	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQEIFIQQGR.G	N	99.9	53.56	2051.0225	17	4.7	1026.5233	2	30.56	31	1705	OB3629.raw	1.9E3	3	3	82	98	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	53.49	1534.6470	12	-0.3	768.3306	2	24.94	31	1228	OB3629.raw	3.89E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	53.36	2489.1321	22	-1.6	1245.5713	2	34.01	31	2067	OB3629.raw	6.81E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.9	52.53	1534.6470	12	-3.3	768.3282	2	24.42	31	1182	OB3629.raw	1.68E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation

R.QQPEENAC(+57.02)QFQR.L	N	99.9	52.08	1533.6630	12	0.6	767.8392	2	24.20	31	1160	OB3629.raw	2.26E4	5	5	25	36	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.57	1535.6311	12	-2.8	768.8207	2	25.23	31	1252	OB3629.raw	5.14E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	45.81	2052.0063	17	-5.7	685.0055	3	31.03	31	1749	OB3629.raw	0	4	4	82	98	Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.9	44.91	3070.3613	27	2.8	1024.4639	3	33.22	31	1967	OB3629.raw	4.37E4	3	3	46	72	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.93	1535.6311	12	-6.4	768.8179	2	25.87	31	1300	OB3629.raw	5.14E4	3	3	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	99.8	41.99	3070.3613	27	-2.4	1024.4586	3	33.40	31	1989	OB3629.raw	4.37E4	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)Q(+.98)GR.R	N	99.7	41.84	2491.1001	22	2.1	1246.5599	2	35.61	31	2261	OB3629.raw	2.61E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	N	99.7	40.91	2490.1160	22	3.0	1246.0690	2	34.28	31	2104	OB3629.raw	1.68E4	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.7	40.78	1388.6936	13	0.2	695.3542	2	27.33	31	1423	OB3629.raw	4.69E3	2	2	365	377	
R.LNAQRPDNR.I	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	37	45	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.66	1535.6311	12	-1.4	768.8218	2	25.42	31	1265	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.7	39.43	2490.1160	22	6.6	831.0514	3	34.18	31	2090	OB3629.raw	1.38E3	2	2	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	38.37	1536.6151	12	0.2	769.3150	2	26.22	31	1327	OB3629.raw	6.79E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
K.TANDLNLLILR.W	N	99.4	36.36	1254.7296	11	-4.1	628.3695	2	32.87	31	1928	OB3629.raw	2.27E3	1	1	378	388	
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.4	35.60	1536.6151	12	2.7	769.3169	2	25.65	31	1281	OB3629.raw	8.11E1	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.3	34.68	1534.6470	12	-0.7	768.3302	2	25.04	31	1236	OB3629.raw	2.22E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.1	34.16	1535.6311	12	-0.9	768.8221	2	25.60	31	1278	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)P(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.1	33.50	3086.3562	27	-2.7	1029.7899	3	33.93	31	2057	OB3629.raw	0	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.S	N	99.1	33.04	2631.2063	23	2.1	878.0779	3	33.53	31	2004	OB3629.raw	1.74E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	99.1	32.96	2491.1001	22	-3.9	831.3707	3	35.65	31	2267	OB3629.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	99.1	32.60	2038.9166	16	6.7	680.6507	3	27.42	31	1434	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.1	30.88	2038.9166	16	-4.8	680.6429	3	27.56	31	1446	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
K.SQSDNFEYVAFK.T	Y	98.0	30.71	1433.6462	12	-1.6	717.8293	2	30.30	31	1679	OB3629.raw	8.3E2	2	2	459	470	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	98.0	30.33	2490.1160	22	1.7	831.0474	3	35.48	31	2246	OB3629.raw	7.21E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	97.9	29.73	2475.1052	22	1.7	1238.5620	2	35.35	31	2231	OB3629.raw	2.89E3	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	29.45	2039.9006	16	0.0	680.9742	3	27.87	31	1476	OB3629.raw	1.55E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.1	28.62	2039.9006	16	-1.6	680.9731	3	28.10	31	1505	OB3629.raw	1.55E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	97.0	28.13	2040.8846	16	-7.1	681.2973	3	28.24	31	1517	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.9	27.39	2040.8846	16	0.8	681.3027	3	28.36	31	1525	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	96.9	27.28	3085.3723	27	6.9	1029.4718	3	33.77	31	2035	OB3629.raw	6.29E1	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.S	N	95.1	26.50	2630.2224	23	0.2	877.7482	3	33.12	31	1954	OB3629.raw	3.19E4	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	94.7	25.99	1536.6151	12	-2.4	769.3130	2	26.32	31	1335	OB3629.raw	6.79E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation

total 43 peptides

Q9FZ11|Q9FZ11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIRGRLALSV CFCFLVLGAS S**ISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSR**LVLRRNA

81 LR**RPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RR**HQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP

241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE

321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNR**SPDIYNP QAGSLKTAND LNLLILR**WLG LSAEYGNLYR

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGK**SQS DNFEYVAFK**T DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	80.34	2473.1372	22	0.8	1237.5769	2	34.31	31	2107	OB3629.raw	1.05E5	10	10	100	121	Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	76.75	2050.0383	17	0.5	684.3537	3	30.01	31	1649	OB3629.raw	1.45E6	57	57	83	99	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	61.79	2051.0225	17	1.5	684.6824	3	30.67	31	1716	OB3629.raw	1.9E3	2	2	83	99	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.9	56.67	2489.1321	22	3.2	1245.5773	2	34.06	31	2074	OB3629.raw	3.37E4	3	3	100	121	Carbamidomethylation; Hydroxylation Pro
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	56.16	3069.3774	27	0.4	1024.1335	3	32.91	31	1932	OB3629.raw	1.62E5	5	5	47	73	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.9	55.50	2474.1211	22	2.0	1238.0703	2	34.44	31	2125	OB3629.raw	7.86E4	3	3	100	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	53.73	2474.1211	22	2.6	825.7165	3	34.52	31	2136	OB3629.raw	1.45E5	11	11	100	121	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQEIFIQQGR.G	N	99.9	53.56	2051.0225	17	4.7	1026.5233	2	30.56	31	1705	OB3629.raw	1.9E3	3	3	83	99	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	53.49	1534.6470	12	-0.3	768.3306	2	24.94	31	1228	OB3629.raw	3.89E4	4	4	26	37	Deamidation (NQ); Carbamidomethylation

R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	53.36	2489.1321	22	-1.6	1245.5713	2	34.01	31	2067	OB3629.raw	6.81E3	1	1	100	121	Hydroxylation Pro; Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.9	52.53	1534.6470	12	-3.3	768.3282	2	24.42	31	1182	OB3629.raw	1.68E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	52.08	1533.6630	12	0.6	767.8392	2	24.20	31	1160	OB3629.raw	2.26E4	5	5	26	37	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.57	1535.6311	12	-2.8	768.8207	2	25.23	31	1252	OB3629.raw	5.14E4	1	1	26	37	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	45.81	2052.0063	17	-5.7	685.0055	3	31.03	31	1749	OB3629.raw	0	4	4	83	99	Deamidation (NQ)
R.LESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.9	44.91	3070.3613	27	2.8	1024.4639	3	33.22	31	1967	OB3629.raw	4.37E4	3	3	47	73	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.93	1535.6311	12	-6.4	768.8179	2	25.87	31	1300	OB3629.raw	5.14E4	3	3	26	37	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	99.8	41.99	3070.3613	27	-2.4	1024.4586	3	33.40	31	1989	OB3629.raw	4.37E4	4	4	47	73	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)Q(+.98)GR.R	N	99.7	41.84	2491.1001	22	2.1	1246.5599	2	35.61	31	2261	OB3629.raw	2.61E3	1	1	100	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	N	99.7	40.91	2490.1160	22	3.0	1246.0690	2	34.28	31	2104	OB3629.raw	1.68E4	2	2	100	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.7	40.78	1388.6936	13	0.2	695.3542	2	27.33	31	1423	OB3629.raw	4.69E3	2	2	364	376	
R.LNAQRPDNR.L	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	38	46	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.66	1535.6311	12	-1.4	768.8218	2	25.42	31	1265	OB3629.raw	5.14E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.7	39.43	2490.1160	22	6.6	831.0514	3	34.18	31	2090	OB3629.raw	1.38E3	2	2	100	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	38.37	1536.6151	12	0.2	769.3150	2	26.22	31	1327	OB3629.raw	6.79E3	2	2	26	37	Deamidation (NQ); Carbamidomethylation
K.TANDLNLLILR.W	N	99.4	36.36	1254.7296	11	-4.1	628.3695	2	32.87	31	1928	OB3629.raw	2.27E3	1	1	377	387	
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.4	35.60	1536.6151	12	2.7	769.3169	2	25.65	31	1281	OB3629.raw	8.11E1	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.3	34.68	1534.6470	12	-0.7	768.3302	2	25.04	31	1236	OB3629.raw	2.22E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.1	34.16	1535.6311	12	-0.9	768.8221	2	25.60	31	1278	OB3629.raw	5.14E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)P(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.1	33.50	3086.3562	27	-2.7	1029.7899	3	33.93	31	2057	OB3629.raw	0	1	1	47	73	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.1	33.04	2631.2063	23	2.1	878.0779	3	33.53	31	2004	OB3629.raw	1.74E4	2	2	100	122	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	99.1	32.96	2491.1001	22	-3.9	831.3707	3	35.65	31	2267	OB3629.raw	0	1	1	100	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	99.1	32.60	2038.9166	16	6.7	680.6507	3	27.42	31	1434	OB3629.raw	7.74E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.1	30.88	2038.9166	16	-4.8	680.6429	3	27.56	31	1446	OB3629.raw	7.74E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
K.SQSDNFEYVAFK.T	Y	98.0	30.71	1433.6462	12	-1.6	717.8293	2	30.30	31	1679	OB3629.raw	8.3E2	2	2	458	469	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	98.0	30.33	2490.1160	22	1.7	831.0474	3	35.48	31	2246	OB3629.raw	7.21E3	1	1	100	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	97.9	29.73	2475.1052	22	1.7	1238.5620	2	35.35	31	2231	OB3629.raw	2.89E3	2	2	100	121	Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	29.45	2039.9006	16	0.0	680.9742	3	27.87	31	1476	OB3629.raw	1.55E4	2	2	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.1	28.62	2039.9006	16	-1.6	680.9731	3	28.10	31	1505	OB3629.raw	1.55E4	1	1	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	97.0	28.13	2040.8846	16	-7.1	681.2973	3	28.24	31	1517	OB3629.raw	5.76E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.9	27.39	2040.8846	16	0.8	681.3027	3	28.36	31	1525	OB3629.raw	5.76E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	96.9	27.28	3085.3723	27	6.9	1029.4718	3	33.77	31	2035	OB3629.raw	6.29E1	1	1	47	73	Hydroxylation Pro; Carbamidomethylation

R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	95.1	26.50	2630.2224	23	0.2	877.7482	3	33.12	31	1954	OB3629.raw	3.19E4	1	1	100	122	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	94.7	25.99	1536.6151	12	-2.4	769.3130	2	26.32	31	1335	OB3629.raw	6.79E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
total 43 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**HQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELNL LILRWLGLSA

401 EYGNLYRNAL FVPHYNTNAH SIIYALRGR**A HVQVVDSNGD R**VFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	80.34	2473.1372	22	0.8	1237.5769	2	34.31	31	2107	OB3629.raw	1.05E5	10	10	99	120	Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	76.75	2050.0383	17	0.5	684.3537	3	30.01	31	1649	OB3629.raw	1.45E6	57	57	82	98	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	61.79	2051.0225	17	1.5	684.6824	3	30.67	31	1716	OB3629.raw	1.9E3	2	2	82	98	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.9	56.67	2489.1321	22	3.2	1245.5773	2	34.06	31	2074	OB3629.raw	3.37E4	3	3	99	120	Carbamidomethylation; Hydroxylation Pro
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	56.16	3069.3774	27	0.4	1024.1335	3	32.91	31	1932	OB3629.raw	1.62E5	5	5	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.9	55.50	2474.1211	22	2.0	1238.0703	2	34.44	31	2125	OB3629.raw	7.86E4	3	3	99	120	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	53.73	2474.1211	22	2.6	825.7165	3	34.52	31	2136	OB3629.raw	1.45E5	11	11	99	120	Carbamidomethylation; Deamidation (NQ)

R.RPFYSN(+.98)APQEIFIQQGR.G	N	99.9	53.56	2051.0225	17	4.7	1026.5233	2	30.56	31	1705	OB3629.raw	1.9E3	3	3	82	98	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	53.49	1534.6470	12	-0.3	768.3306	2	24.94	31	1228	OB3629.raw	3.89E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	53.36	2489.1321	22	-1.6	1245.5713	2	34.01	31	2067	OB3629.raw	6.81E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.9	52.53	1534.6470	12	-3.3	768.3282	2	24.42	31	1182	OB3629.raw	1.68E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	52.08	1533.6630	12	0.6	767.8392	2	24.20	31	1160	OB3629.raw	2.26E4	5	5	25	36	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.57	1535.6311	12	-2.8	768.8207	2	25.23	31	1252	OB3629.raw	5.14E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	45.81	2052.0063	17	-5.7	685.0055	3	31.03	31	1749	OB3629.raw	0	4	4	82	98	Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.9	44.91	3070.3613	27	2.8	1024.4639	3	33.22	31	1967	OB3629.raw	4.37E4	3	3	46	72	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.93	1535.6311	12	-6.4	768.8179	2	25.87	31	1300	OB3629.raw	5.14E4	3	3	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	99.8	41.99	3070.3613	27	-2.4	1024.4586	3	33.40	31	1989	OB3629.raw	4.37E4	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)Q(+.98)GR.R	N	99.7	41.84	2491.1001	22	2.1	1246.5599	2	35.61	31	2261	OB3629.raw	2.61E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	N	99.7	40.91	2490.1160	22	3.0	1246.0690	2	34.28	31	2104	OB3629.raw	1.68E4	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.7	40.78	1388.6936	13	0.2	695.3542	2	27.33	31	1423	OB3629.raw	4.69E3	2	2	371	383	
R.LNAQRPDNR.I	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	37	45	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.66	1535.6311	12	-1.4	768.8218	2	25.42	31	1265	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.7	39.43	2490.1160	22	6.6	831.0514	3	34.18	31	2090	OB3629.raw	1.38E3	2	2	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	38.37	1536.6151	12	0.2	769.3150	2	26.22	31	1327	OB3629.raw	6.79E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.4	35.60	1536.6151	12	2.7	769.3169	2	25.65	31	1281	OB3629.raw	8.11E1	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.3	34.68	1534.6470	12	-0.7	768.3302	2	25.04	31	1236	OB3629.raw	2.22E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.1	34.16	1535.6311	12	-0.9	768.8221	2	25.60	31	1278	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)P(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.1	33.50	3086.3562	27	-2.7	1029.7899	3	33.93	31	2057	OB3629.raw	0	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.1	33.04	2631.2063	23	2.1	878.0779	3	33.53	31	2004	OB3629.raw	1.74E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	99.1	32.96	2491.1001	22	-3.9	831.3707	3	35.65	31	2267	OB3629.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	99.1	32.60	2038.9166	16	6.7	680.6507	3	27.42	31	1434	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.AHVQVVDSNGDR.V	Y	99.1	32.58	1295.6218	12	-4.7	648.8151	2	20.59	31	947	OB3629.raw	1.93E3	1	1	430	441	
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.1	30.88	2038.9166	16	-4.8	680.6429	3	27.56	31	1446	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	98.0	30.33	2490.1160	22	1.7	831.0474	3	35.48	31	2246	OB3629.raw	7.21E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	97.9	29.73	2475.1052	22	1.7	1238.5620	2	35.35	31	2231	OB3629.raw	2.89E3	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	29.45	2039.9006	16	0.0	680.9742	3	27.87	31	1476	OB3629.raw	1.55E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.1	28.62	2039.9006	16	-1.6	680.9731	3	28.10	31	1505	OB3629.raw	1.55E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	97.0	28.13	2040.8846	16	-7.1	681.2973	3	28.24	31	1517	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.9	27.39	2040.8846	16	0.8	681.3027	3	28.36	31	1525	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation

R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	96.9	27.28	3085.3723	27	6.9	1029.4718	3	33.77	31	2035	OB3629.raw	6.29E1	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	95.1	26.50	2630.2224	23	0.2	877.7482	3	33.12	31	1954	OB3629.raw	3.19E4	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	94.7	25.99	1536.6151	12	-2.4	769.3130	2	26.32	31	1335	OB3629.raw	6.79E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
total 42 peptides																		

Q8LKN1|Q8LKN1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	80.34	2473.1372	22	0.8	1237.5769	2	34.31	31	2107	OB3629.raw	1.05E5	10	10	99	120	Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	76.75	2050.0383	17	0.5	684.3537	3	30.01	31	1649	OB3629.raw	1.45E6	57	57	82	98	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	61.79	2051.0225	17	1.5	684.6824	3	30.67	31	1716	OB3629.raw	1.9E3	2	2	82	98	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.9	56.67	2489.1321	22	3.2	1245.5773	2	34.06	31	2074	OB3629.raw	3.37E4	3	3	99	120	Carbamidomethylation; Hydroxylation Pro
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	56.16	3069.3774	27	0.4	1024.1335	3	32.91	31	1932	OB3629.raw	1.62E5	5	5	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.9	55.50	2474.1211	22	2.0	1238.0703	2	34.44	31	2125	OB3629.raw	7.86E4	3	3	99	120	Carbamidomethylation;

																		Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	53.73	2474.1211	22	2.6	825.7165	3	34.52	31	2136	OB3629.raw	1.45E5	11	11	99	120	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQEIFIQQGR.G	N	99.9	53.56	2051.0225	17	4.7	1026.5233	2	30.56	31	1705	OB3629.raw	1.9E3	3	3	82	98	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	53.49	1534.6470	12	-0.3	768.3306	2	24.94	31	1228	OB3629.raw	3.89E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	53.36	2489.1321	22	-1.6	1245.5713	2	34.01	31	2067	OB3629.raw	6.81E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.9	52.53	1534.6470	12	-3.3	768.3282	2	24.42	31	1182	OB3629.raw	1.68E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	52.08	1533.6630	12	0.6	767.8392	2	24.20	31	1160	OB3629.raw	2.26E4	5	5	25	36	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.57	1535.6311	12	-2.8	768.8207	2	25.23	31	1252	OB3629.raw	5.14E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	45.81	2052.0063	17	-5.7	685.0055	3	31.03	31	1749	OB3629.raw	0	4	4	82	98	Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.9	44.91	3070.3613	27	2.8	1024.4639	3	33.22	31	1967	OB3629.raw	4.37E4	3	3	46	72	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.93	1535.6311	12	-6.4	768.8179	2	25.87	31	1300	OB3629.raw	5.14E4	3	3	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	99.8	41.99	3070.3613	27	-2.4	1024.4586	3	33.40	31	1989	OB3629.raw	4.37E4	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)Q(+.98)GR.R	N	99.7	41.84	2491.1001	22	2.1	1246.5599	2	35.61	31	2261	OB3629.raw	2.61E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	N	99.7	40.91	2490.1160	22	3.0	1246.0690	2	34.28	31	2104	OB3629.raw	1.68E4	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.7	40.78	1388.6936	13	0.2	695.3542	2	27.33	31	1423	OB3629.raw	4.69E3	2	2	371	383	
R.LNAQRPDNR.I	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	37	45	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.66	1535.6311	12	-1.4	768.8218	2	25.42	31	1265	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	99.7	39.43	2490.1160	22	6.6	831.0514	3	34.18	31	2090	OB3629.raw	1.38E3	2	2	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.6	38.37	1536.6151	12	0.2	769.3150	2	26.22	31	1327	OB3629.raw	6.79E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.4	35.60	1536.6151	12	2.7	769.3169	2	25.65	31	1281	OB3629.raw	8.11E1	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.3	34.68	1534.6470	12	-0.7	768.3302	2	25.04	31	1236	OB3629.raw	2.22E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.1	34.16	1535.6311	12	-0.9	768.8221	2	25.60	31	1278	OB3629.raw	5.14E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)P(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.1	33.50	3086.3562	27	-2.7	1029.7899	3	33.93	31	2057	OB3629.raw	0	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.1	33.04	2631.2063	23	2.1	878.0779	3	33.53	31	2004	OB3629.raw	1.74E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	99.1	32.96	2491.1001	22	-3.9	831.3707	3	35.65	31	2267	OB3629.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	99.1	32.60	2038.9166	16	6.7	680.6507	3	27.42	31	1434	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.AHVQVVDSNGDR.V	Y	99.1	32.58	1295.6218	12	-4.7	648.8151	2	20.59	31	947	OB3629.raw	1.93E3	1	1	432	443	
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.1	30.88	2038.9166	16	-4.8	680.6429	3	27.56	31	1446	OB3629.raw	7.74E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	98.0	30.33	2490.1160	22	1.7	831.0474	3	35.48	31	2246	OB3629.raw	7.21E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	97.9	29.73	2475.1052	22	1.7	1238.5620	2	35.35	31	2231	OB3629.raw	2.89E3	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	97.9	29.45	2039.9006	16	0.0	680.9742	3	27.87	31	1476	OB3629.raw	1.55E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.1	28.62	2039.9006	16	-1.6	680.9731	3	28.10	31	1505	OB3629.raw	1.55E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
																		Deamidation (NQ);

S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	97.0	28.13	2040.8846	16	-7.1	681.2973	3	28.24	31	1517	OB3629.raw	5.76E3	1	1	21	36	Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.9	27.39	2040.8846	16	0.8	681.3027	3	28.36	31	1525	OB3629.raw	5.76E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	96.9	27.28	3085.3723	27	6.9	1029.4718	3	33.77	31	2035	OB3629.raw	6.29E1	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	95.1	26.50	2630.2224	23	0.2	877.7482	3	33.12	31	1954	OB3629.raw	3.19E4	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	94.7	25.99	1536.6151	12	-2.4	769.3130	2	26.32	31	1335	OB3629.raw	6.79E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
total 42 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQR**LNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR** TVLRRNALRR

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	99.8	44.27	3068.3933	27	0.4	1023.8054	3	32.53	31	1895	OB3629.raw	1.28E4	2	2	44	70	Carbamidomethylation
R.LNAQRPDNR.I	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	35	43	
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.1	33.94	3084.3882	27	2.1	1029.1388	3	33.60	31	2012	OB3629.raw	5.46E3	1	1	44	70	Hydroxylation Pro; Carbamidomethylation
total 3 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM

R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	99.8	44.27	3068.3933	27	0.4	1023.8054	3	32.53	31	1895	OB3629.raw	1.28E4	2	2	46	72	Carbamidomethylation
R.LNAQRPDNR.I	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	37	45	
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.1	33.94	3084.3882	27	2.1	1029.1388	3	33.60	31	2012	OB3629.raw	5.46E3	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
total 3 peptides																		

E5G077|E5G077_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQR**LNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	99.8	44.27	3068.3933	27	0.4	1023.8054	3	32.53	31	1895	OB3629.raw	1.28E4	2	2	46	72	Carbamidomethylation
R.LNAQRPDNR.I	N	99.7	40.13	1082.5581	9	-1.4	361.8595	3	18.39	31	832	OB3629.raw	2.83E4	3	3	37	45	
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.1	33.94	3084.3882	27	2.1	1029.1388	3	33.60	31	2012	OB3629.raw	5.46E3	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
total 3 peptides																		

E9LFE7|E9LFE7_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WEEEEEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAK**D**
81 **LAFPGSGEQV EK**LIKNQRES HFVSARPQSQ SQFPSSPEKE DQEEENQGGK GPLLSILKAF N

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	80	92	
total 1 peptides																		

Q6PSU5|Q6PSU5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL

81 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR

161 EEEEDEDQEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAK**D**

241 **LAFPGSGEQV EK**LIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	240	252	
total 1 peptides																		

Q6PSU6|Q6PSU6_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRRSTRS SDNEGVIVKV SKEHVQELTK HAKSVSKKGS EEEDITNPIN

81 LRDGEPDLSN NFGRLFEVKP DKKNPQLQDL DMMLTCVEIK EGALMLPHFN SKAMVIVVVN KGTGNLELVA VRKEQQQRGR

161 REQEWEEEEE DEEEEGSNRE VRRYTARLKE GDVFIMPAAH PVAINASSEL HLLGFGINAE NNHRIFLAGD KDNVIDQIEK

241 QAK**DLAFPGS GEQVEK**LIKN QRESHFVSAR PQSQSPSSPE KEDQEEENQG GKGPLLSILK AFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	244	256	
total 1 peptides																		

Q6PSU4|Q6PSU4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GFDQRSRQFQ NLQNHRIVQI EAKPNTLVLP KHADADNILV IQQGQATVTV ANGNNRKSFN LDEGHALRIP SGFISYILNR

81 HDNQNLRVAK ISMPVNTPGQ FEDFFPASSR DQSSYLQGFS RNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRWSTRS

161 SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI

241 KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREEEEDEDE EEEGSNREVR RYTARLKEGD VFIMPAAHPV

321 AINASSELHL LGFGINAENN HRIFLAGDKD NVIDQIEKQA K**DLAFPGSGE QVEK**LIKNQK ESHFVSARPQ SQSQSPSSPE

401 KESPEKEDQE EENQGGKGPL LSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	362	374	
total 1 peptides																		

Q6PSU3|Q6PSU3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	555	567	
total 1 peptides																		

sp|P43237|ALL11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	555	567	
total 1 peptides																		

B3IXL2|B3IXL2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH

81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR

161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT

241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN

321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS

401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	555	567	
total 1 peptides																		

E5G076|E5G076_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG

81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERERDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ

241 GQATVTVANG NNRRALILTR AMHSESHPFH FLHLDDMTPE LRVAKSHAVN TPGQFEDFFP ASSRDQSSYL QGFSRNTLEA

321 AFNAEFNEIR RVLLEENAGG EQEERGQRRW STRSSENNEG VIVEVSKEHV EELTKHAKSV SKKGSEEEGD ITNPINLREG

401 EPDLSDNFGR LFEVKPDKKN PQLQDLDMML TCVEIKEGAL MLPHFNSKAM VIVVINKGTG NLELVAVRKE QQQRGRREQE

481 WEEEEEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV VDQIEKQAK**D**

561 **LAFPGSGEQV EK**LIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	560	572	
total 1 peptides																		

N1NG13|N1NG13_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERΕEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	560	572	
total 1 peptides																		

sp|P43238|ALL12_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERΕEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 31	#Spec	#Spec Sample 31	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.4	35.48	1375.6619	13	-1.3	688.8373	2	28.82	31	1559	OB3629.raw	6.93E3	1	1	560	572	
total 1 peptides																		

Peptide List

Summary

1. Notes

Spot 25 DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

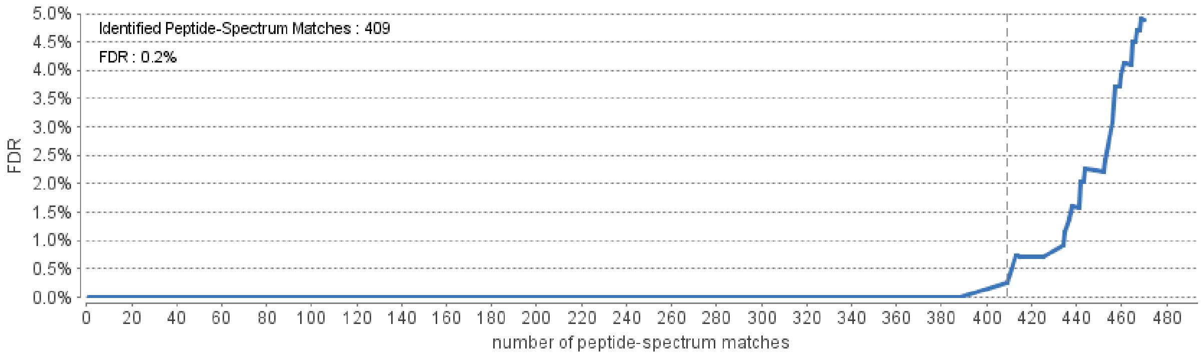
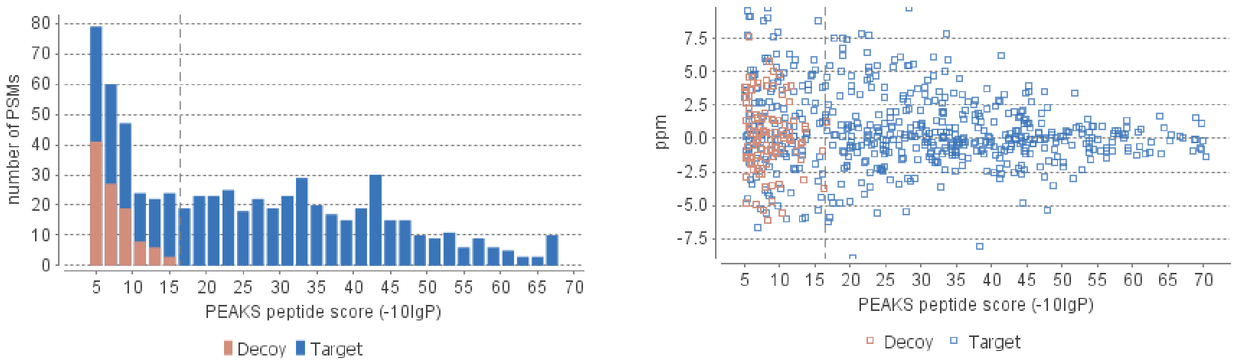


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

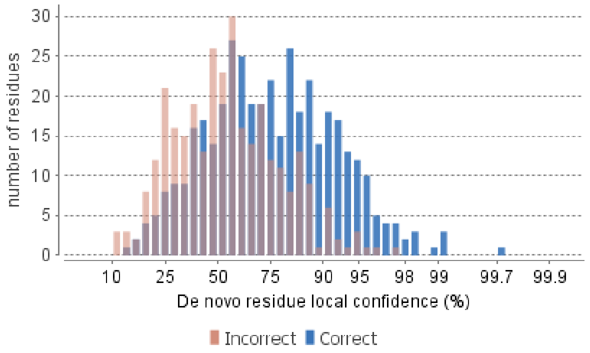

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



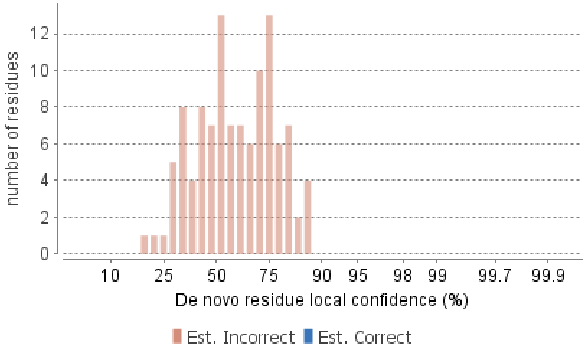


Table 1. Statistics of data.

# of MS scans	3090
# of MS/MS scans	1749

Table 2. Result filtration parameters.

Peptide -10lgP	≥16.5
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	397
Peptide sequences	95
Protein groups	3
Proteins	13
Proteins (#Unique Peptides)	12 (>2); 0 (=2); 1 (=1);
FDR (Peptide-Spectrum Matches)	0.3%
FDR (Peptide Sequences)	1.1%
FDR (Protein)	0.0%
De Novo Only Spectra	16

Table 4. PTM profile.

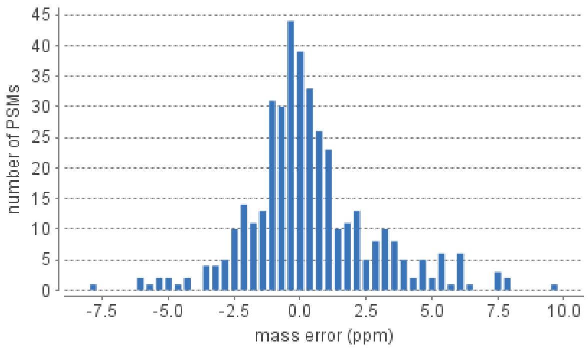
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	216	69.89	5.65E4	1000.00
Deamidation	.98	NQ	114	69.89	5.65E4	0.00
HydPro	15.99	P	39	51.62	2.85E4	7.77
Oxidation	15.99	M	3	40.29	2.75E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



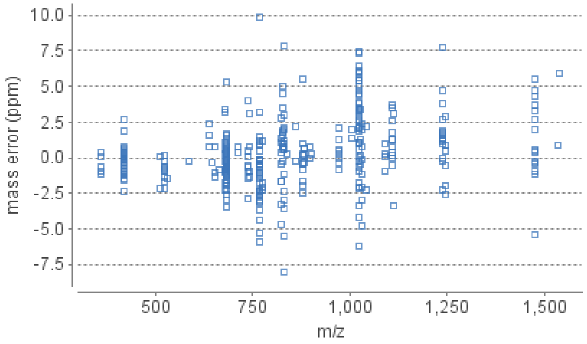


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 33	82	13	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3631.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein	Protein	Accession	Score	-10lgP	Coverage	Coverage (%)	Area Sample	#Peptides	#Unique	#Spec	PTM	Avg.	Description

Group	ID		(%)		(%)	Sample 33	33			Sample 33		Mass	
1	2	A1DZF0|A1DZF0_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
1	3	B5TYU1|B5TYU1_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
1	7	Q647H4|Q647H4_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
1	13	Q9FZ11|Q9FZ11_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
1	29	Q9SQH7|Q9SQH7_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	61011	Glycinin OS=Arachis hypogaea GN=Arah4 PE=2 SV=1
1	5	Q5I6T2|Q5I6T2_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
1	15	Q647H3|Q647H3_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
1	10	Q8LKN1|Q8LKN1_ARAHY	99.0	165.65	17	17	1.48E6	9	4	209	Y	61738	Allergen Arah3/Arah4 OS=Arachis hypogaea PE=3 SV=1
1	83	Q8LL03|Q8LL03_ARAHY	99.0	165.65	42	42	1.48E6	9	4	209	Y	25499	Trypsin inhibitor (Fragment) OS=Arachis hypogaea PE=2 SV=1
2	34	O82580|O82580_ARAHY	99.0	142.03	17	17	3.17E0	6	1	138	Y	58350	Glycinin (Fragment) OS=Arachis hypogaea GN=Arah3 PE=2 SV=1
4	41	Q6IWG5|Q6IWG5_ARAHY	98.8	94.98	17	17	3.1E6	4	3	72	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
4	45	E5G077|E5G077_ARAHY	98.8	94.98	17	17	3.1E6	4	3	72	Y	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
4	42	Q0GM57|Q0GM57_ARAHY	98.8	94.98	17	17	3.1E6	4	3	72	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 13 proteins													

A1DZF0|A1DZF0_ARAHY

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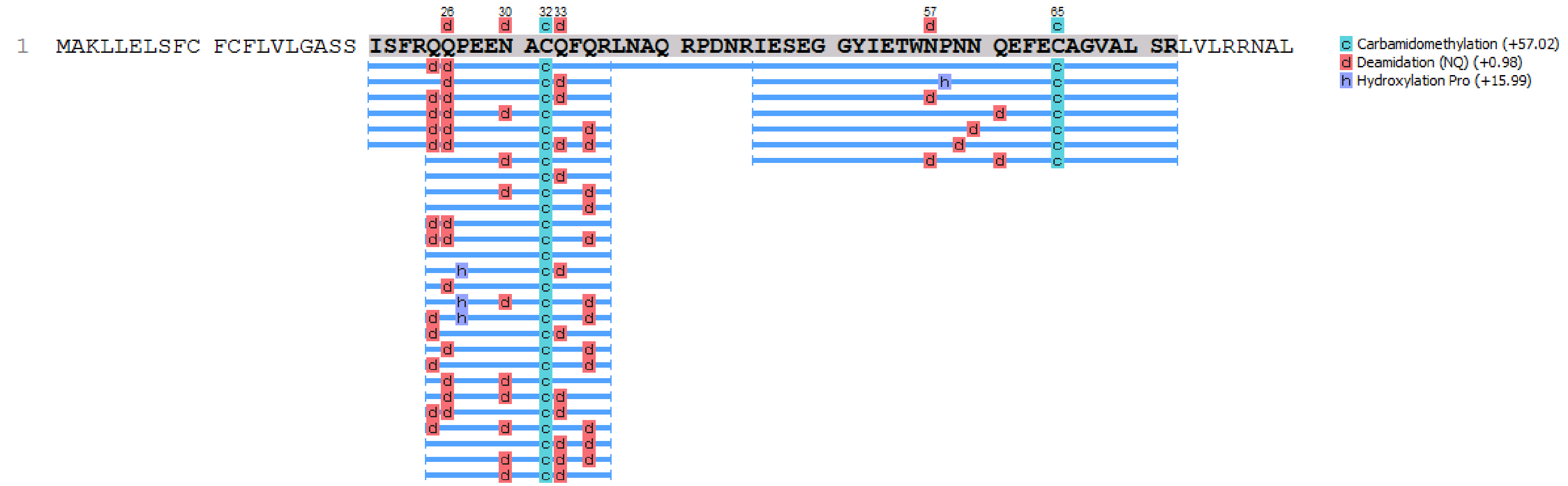
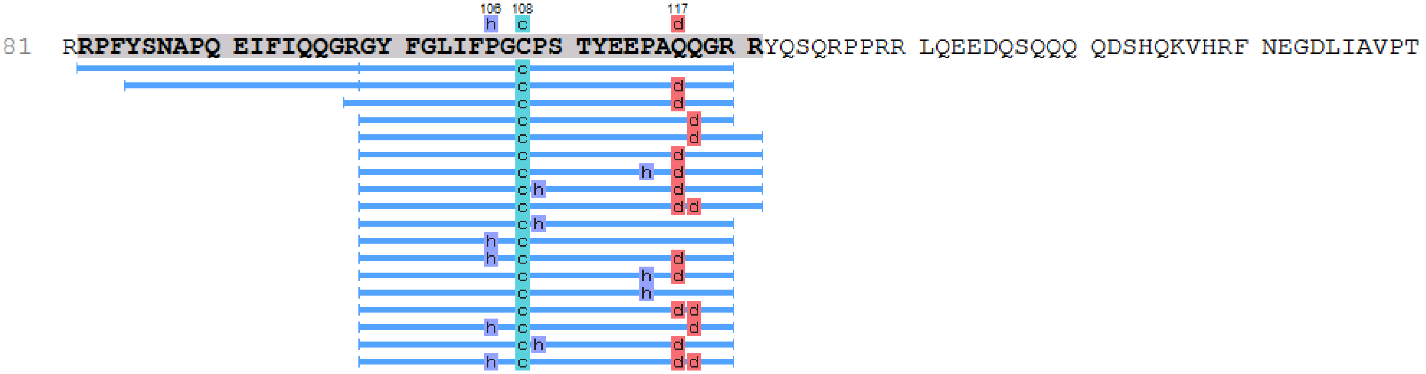
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL



81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA
481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.Y	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.Y	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.Y	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.Y	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.Y	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

B5TYU1|B5TYU1_ARAHY

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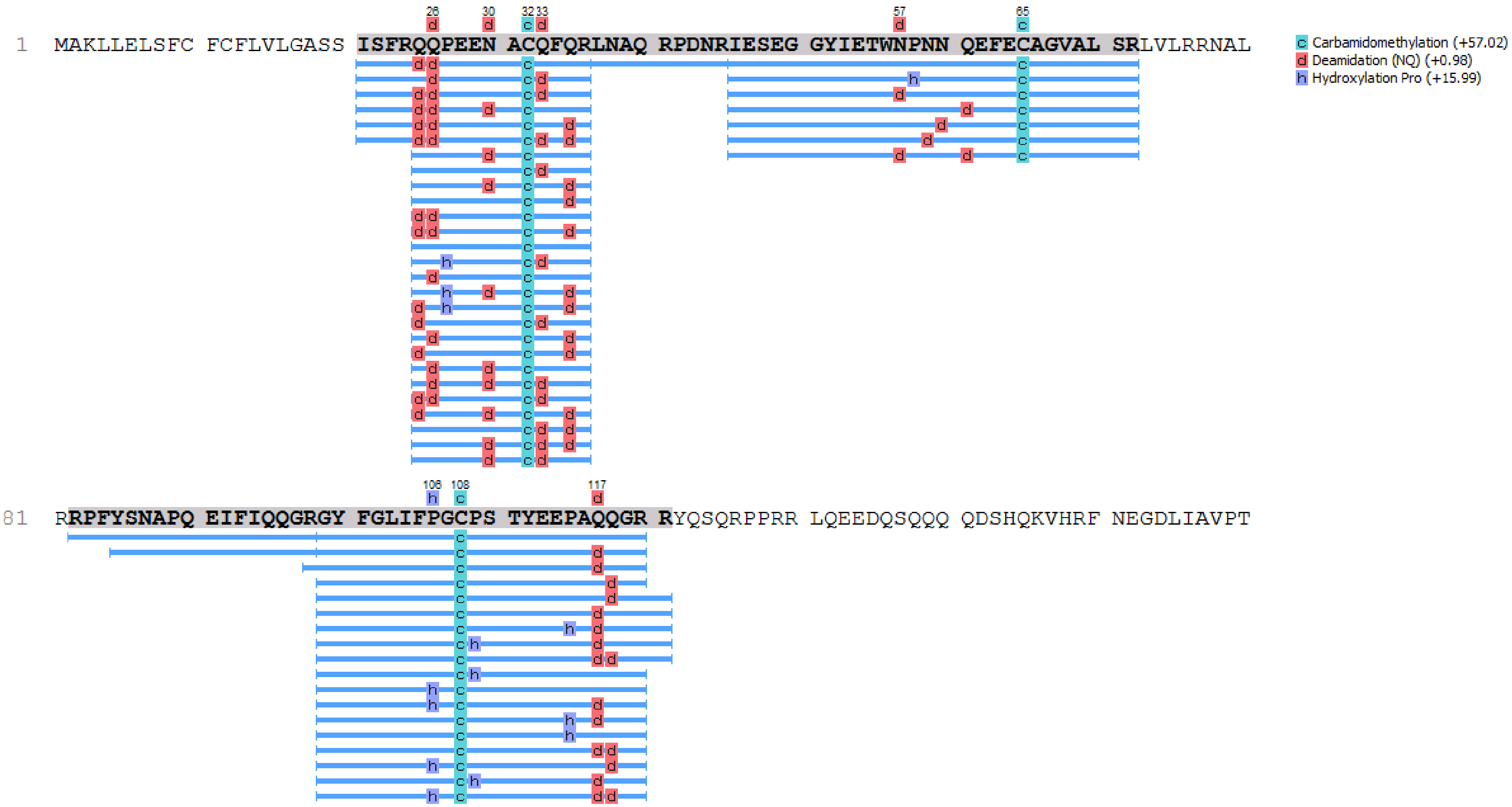
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLELSFC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**YQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGNGIEET ICTATVKKNI GRNRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LPREQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.Y	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.Y	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.Y	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.Y	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.Y	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q647H4|Q647H4_ARAHY

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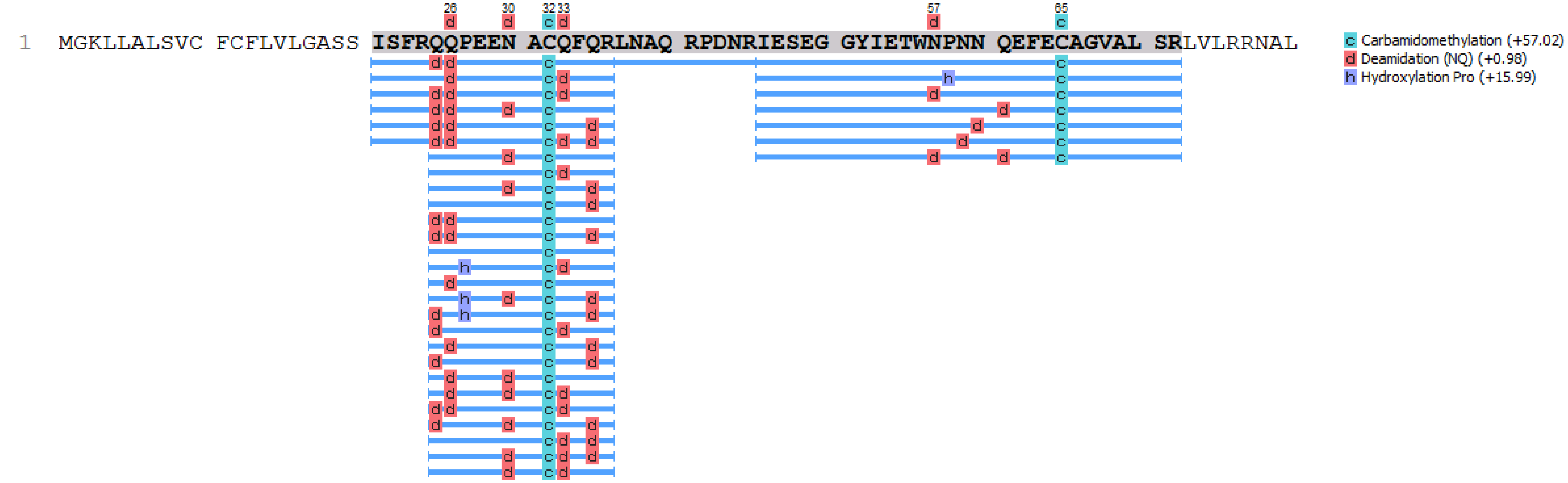
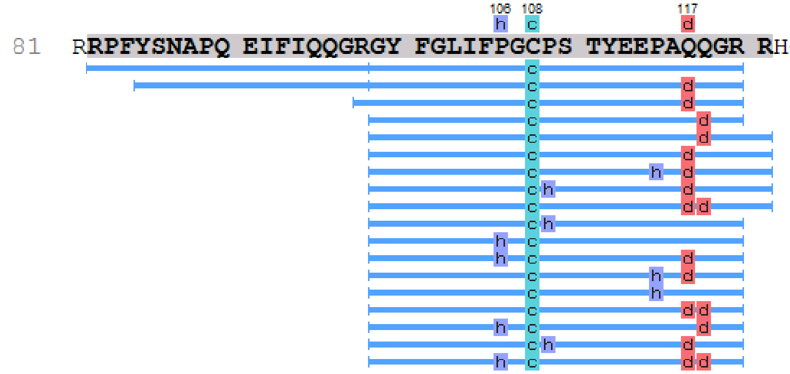
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MGKLLALSVC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL



81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**HQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA

401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.H	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA

81 LRRPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP

241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE

321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFKT DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	83	99	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	100	121	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	26	37	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	26	37	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	100	121	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	47	73	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	100	121	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	100	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	26	37	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	100	121	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	100	121	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	100	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	100	121	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	47	73	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	47	73	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	26	37	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	86	99	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	100	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	100	122	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.L	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	38	46	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	100	122	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	100	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	100	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	22	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	100	122	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	47	73	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	47	73	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	26	37	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	100	122	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.H	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	100	122	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	26	37	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	100	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	26	37	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	47	73	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	47	73	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q9SQH7|Q9SQH7_ARAHY

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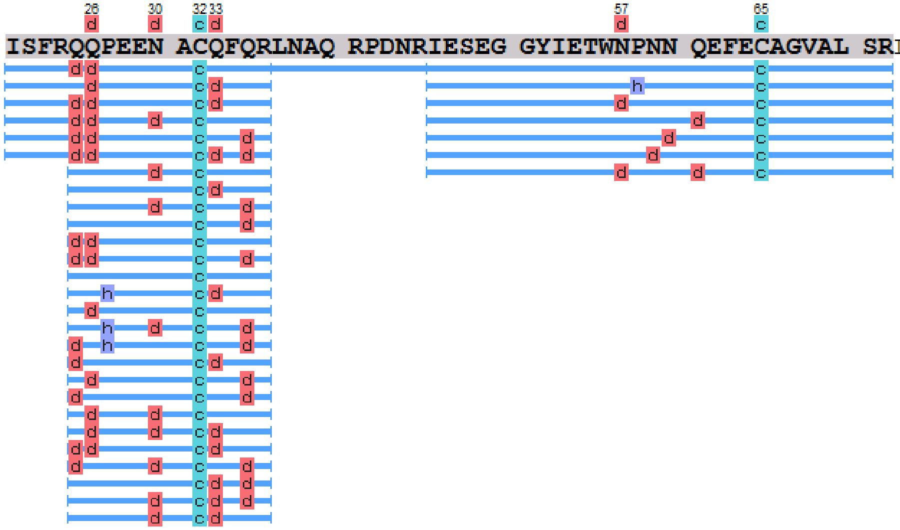
| Protein Coverage | Supporting Peptides |

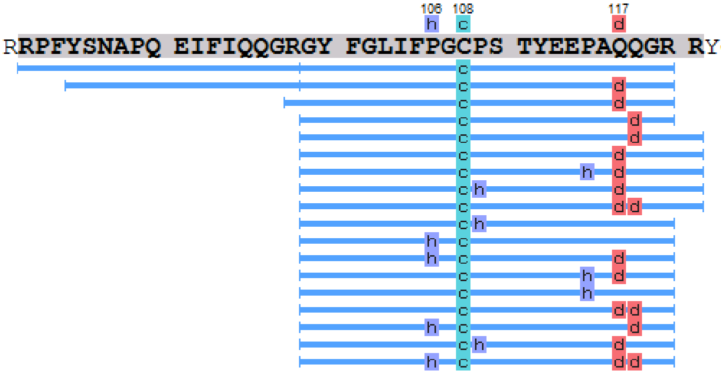
Protein Coverage:

1 MAKLLELSFC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL



c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**YQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT



161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPHS RPRREEREFR
241 PRGQHSRRER AGQEEEDEGG NIFSGFTPEF LEQAFQVDDR QIVQNLWGEN ESEEEGAIVT VRGGLRILSP DGTRGADEEE
321 EYDEDQYEYH EQDGRRGRGS RGGGNGIEET ICTACVKKNI GGNRSPHIYD PQRWFTQNCH DLNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SENFEYVAFK TDSRPSIANF
481 AGENSFIDNL PEEVVANSYG LPREQARQLK NNNPFKFFVP PFQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.Y	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.Y	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.Y	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.Y	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.Y	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q5I6T2|Q5I6T2_ARAHY

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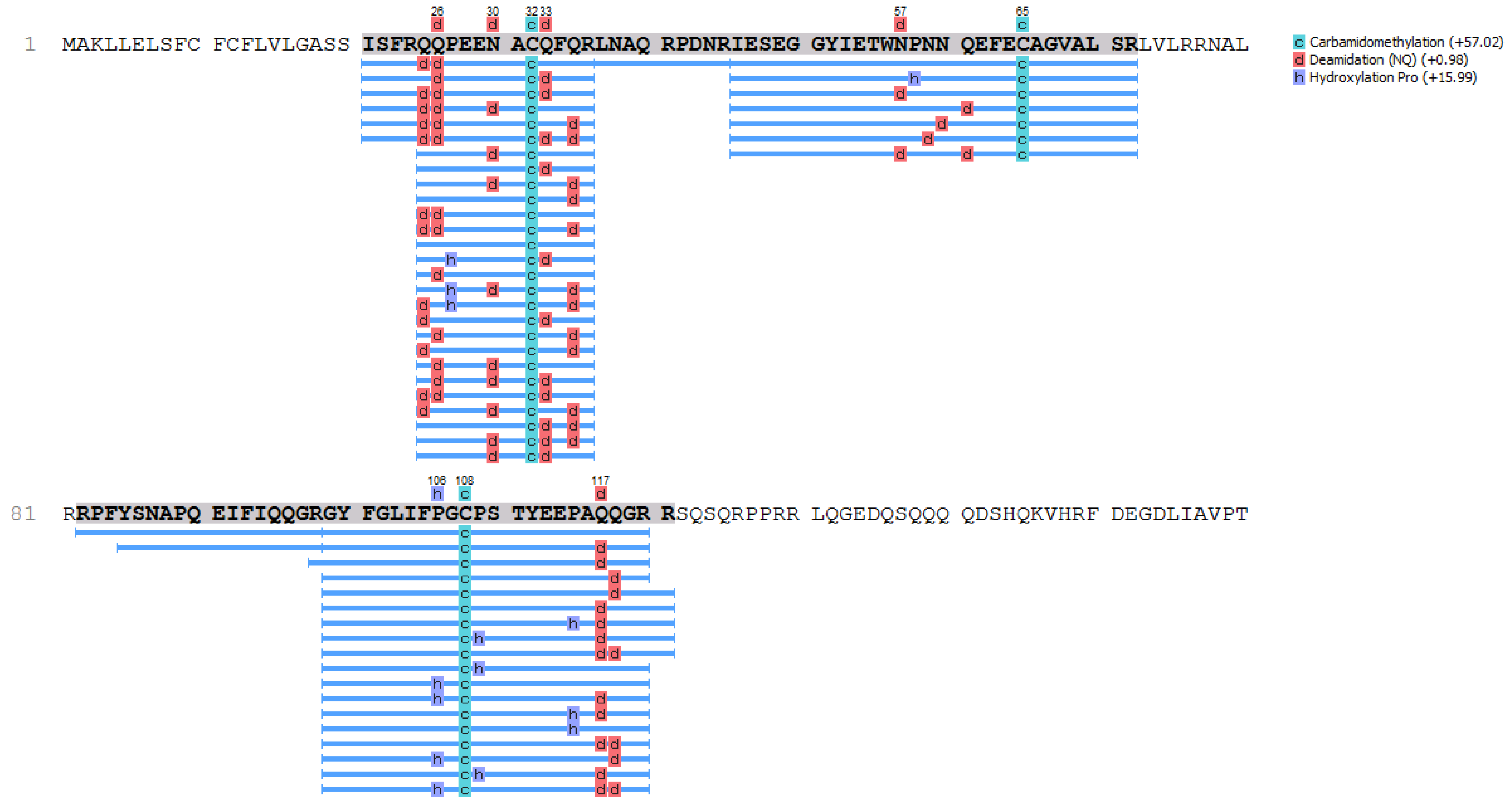
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLELSFC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**SQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS

241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE

321 EYDEDEYEYD EEDRRRGRGS RGRGNGIEET ICTASVKKNI GRNRSPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY

401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL

481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.S	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.S	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.S	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.S	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.S	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q647H3|Q647H3_ARAHY

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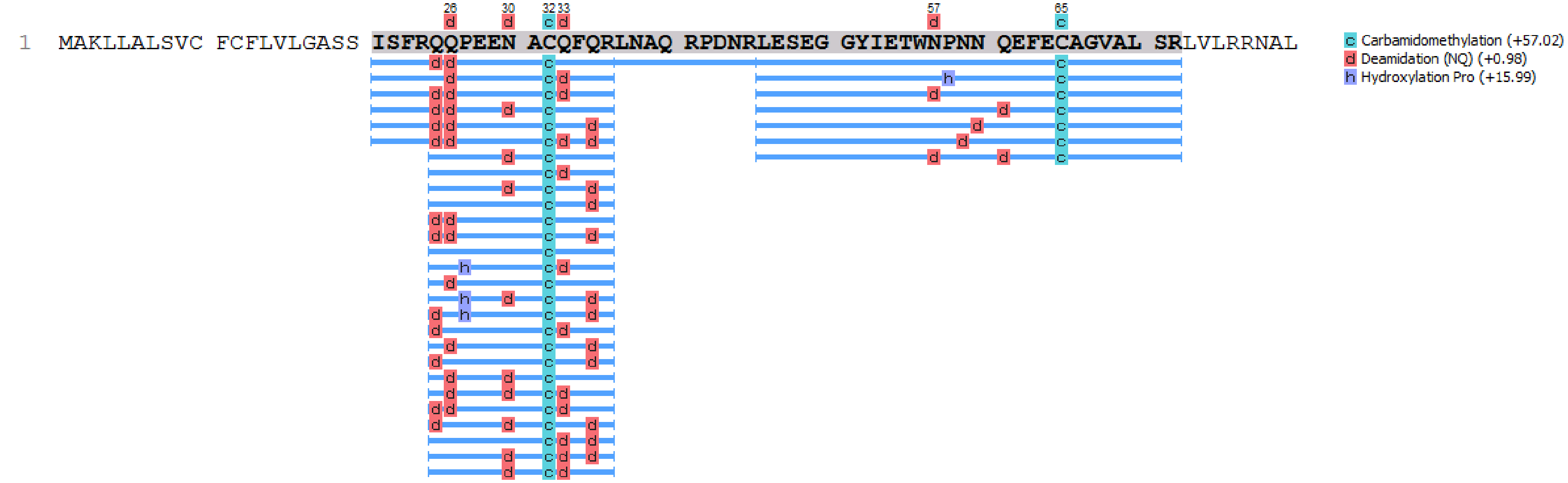
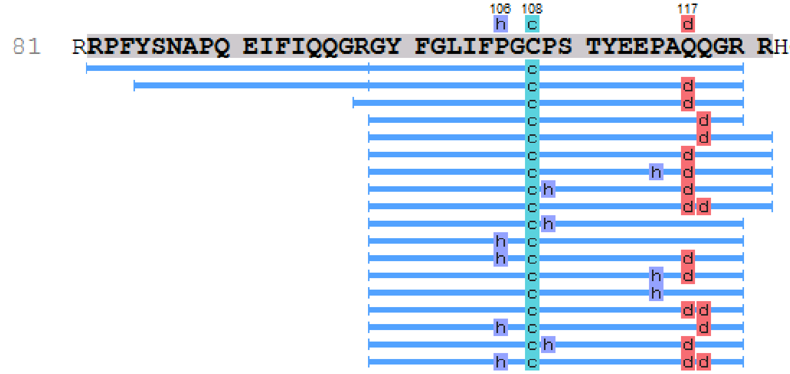
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSVC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL



81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**HQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP

161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR

241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD

321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS

401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS

481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.L	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.H	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q8LKN1|Q8LKN1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELQL NLLILRWLGL

401 SAEYGNLYRN ALFVPHYNTN AHSIIYALRG RAHVQVVDSN GDRVFDEELQ EGHVLVVPQN FAVAGKSQSE NFEYVAFKTD

481 SRPSIANLAG ENSFIDNLPE EVVANSYGLP REQARQLKNN NPFKFFVPPS EQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	82	98	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	25	36	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	46	72	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	99	120	Carbamidomethylation;

																		Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	46	72	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	85	98	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	46	72	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.H	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	25	36	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	99	120	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	25	36	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	46	72	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

Q8LL03|Q8LL03_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES EGGYIETWNP NNQEFECAGV ALSRLVLRRN

81 ALRRPFYSNA PQEIFIQQGR GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	27	38	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	84	100	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	Y	99.9	69.83	2473.1372	22	1.1	825.3873	3	34.09	33	2075	OB3631.raw	7.08E5	13	13	101	122	Carbamidomethylation
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	27	38	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	27	38	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.9	59.15	2474.1211	22	1.3	1238.0695	2	34.32	33	2106	OB3631.raw	1.74E5	10	10	101	122	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	48	74	Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	Y	99.9	51.62	2489.1321	22	-3.0	830.7155	3	34.18	33	2087	OB3631.raw	7.3E4	7	7	101	122	Carbamidomethylation; Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	27	38	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	99.9	45.52	2474.1211	22	0.8	825.7150	3	34.72	33	2159	OB3631.raw	1.65E5	7	7	101	122	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	27	38	Carbamidomethylation; Deamidation (NQ)

R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	Y	99.9	44.21	2489.1321	22	-2.6	1245.5701	2	34.49	33	2128	OB3631.raw	3.7E3	1	1	101	122	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	Y	99.9	43.45	2489.1321	22	0.6	830.7184	3	33.87	33	2047	OB3631.raw	3.46E4	2	2	101	122	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGR.R	Y	99.9	43.17	2490.1160	22	2.0	831.0476	3	35.62	33	2275	OB3631.raw	6.29E3	2	2	101	122	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	27	38	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	99.8	41.11	2475.1052	22	-2.2	1238.5571	2	34.90	33	2182	OB3631.raw	1.97E4	2	2	101	122	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	48	74	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	48	74	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	27	38	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	87	100	
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	99.7	37.63	2490.1160	22	2.9	1246.0688	2	34.01	33	2066	OB3631.raw	1.26E4	6	6	101	122	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	Y	99.5	35.79	2631.2063	23	-2.0	878.0743	3	33.70	33	2024	OB3631.raw	1.82E4	4	4	101	123	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	27	38	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	99.5	34.54	2039.9006	16	3.4	680.9764	3	28.00	33	1487	OB3631.raw	1.16E4	1	1	23	38	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	39	47	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	27	38	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEEN(+.98)AC(+57.02)QFQR.L	Y	99.0	32.29	2039.9006	16	-0.9	680.9735	3	27.90	33	1481	OB3631.raw	1.16E4	1	1	23	38	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	Y	99.0	31.94	2038.9166	16	-1.8	680.6450	3	27.60	33	1463	OB3631.raw	8.86E3	1	1	23	38	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	Y	98.9	31.65	2630.2224	23	-0.3	877.7478	3	32.78	33	1907	OB3631.raw	4.65E4	2	2	101	123	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGR.R	Y	97.8	30.11	2490.1160	22	1.1	831.0469	3	34.11	33	2078	OB3631.raw	1.02E4	1	1	101	122	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	Y	97.6	27.95	2491.1001	22	2.1	831.3757	3	35.57	33	2269	OB3631.raw	0	1	1	101	122	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
S.ISFRQQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	Y	97.6	27.74	2038.9166	16	0.3	680.6464	3	27.78	33	1472	OB3631.raw	8.86E3	1	1	23	38	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	Y	97.2	27.38	2039.9006	16	3.2	680.9763	3	28.10	33	1494	OB3631.raw	1.16E4	2	2	23	38	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	Y	97.0	26.85	2630.2224	23	-0.5	877.7477	3	33.10	33	1949	OB3631.raw	7.44E4	2	2	101	123	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	48	74	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	48	74	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	27	38	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	27	38	Deamidation (NQ); Carbamidomethylation
																		Deamidation (NQ);

R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	27	38	Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	Y	93.4	23.46	2646.2173	23	-0.3	883.0794	3	32.98	33	1934	OB3631.raw	1.08E4	1	1	101	123	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQ(+.98)QGRR.H	Y	92.8	22.39	2646.2173	23	0.6	883.0803	3	32.94	33	1928	OB3631.raw	1.08E4	2	2	101	123	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	27	38	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GR.R	Y	87.1	21.58	2490.1160	22	7.8	831.0524	3	35.37	33	2244	OB3631.raw	6.29E3	1	1	101	122	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	27	38	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	Y	85.8	19.62	2040.8846	16	-1.3	681.3013	3	28.22	33	1503	OB3631.raw	0	1	1	23	38	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	27	38	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	48	74	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	48	74	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	Y	64.8	17.69	2630.2224	23	0.3	877.7484	3	33.07	33	1945	OB3631.raw	5.71E4	1	1	100	122	Carbamidomethylation; Deamidation (NQ)
total 55 peptides																		

O82580|O82580_ARAHY

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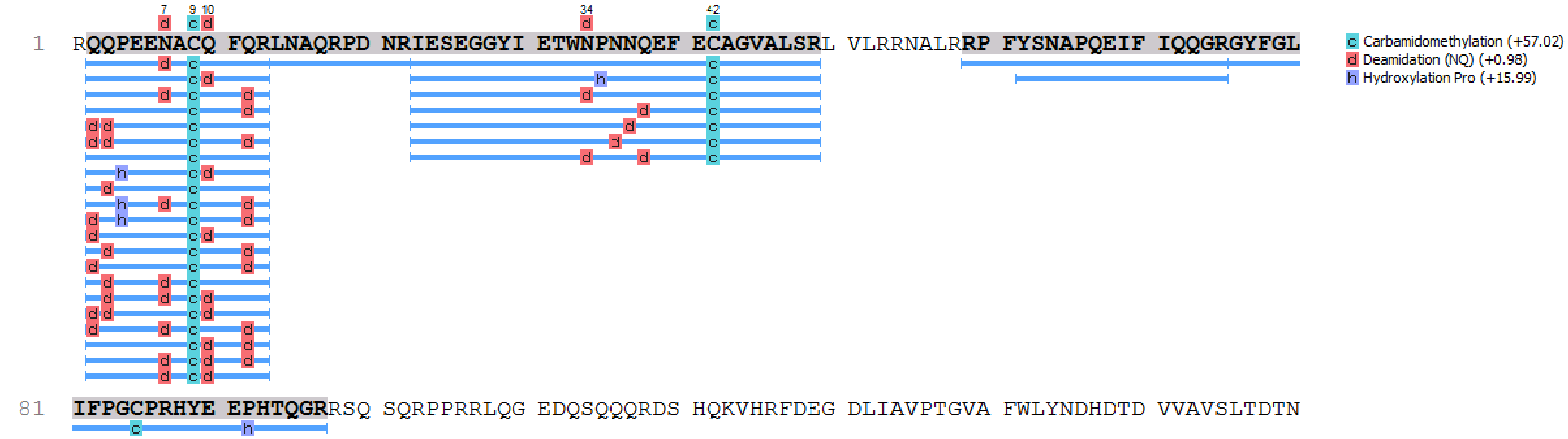
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 RQQPEENACQ FQRLNAQRPD NRIESEGGYI ETWNPNNQEF ECAGVALSRL VLRRNALRRP FYSNAPQEIF IQQGRGYFGL

81 IFPGCPRHYE EPHTQGRRSQ SQRPPRRLQG EDQSQQQRDS HQKVHRFDEG DLIAVPTGVA FWLYNDHDTD VVAVSLTDTN

161 NNDNQLDQFP RRFNLAGNTE QEFLRYQQQS RQSRRRSLPY SPYSPQSQPR QEEREFSPRG QHSRRERAGQ EEENEGGNIF

241 SGFTPEFLEQ AFQVDDRQIV QNLRGETESE EEGAIVTVRG GLRILSPDRK RRADEEEEYD EDEYEYDEED RRRGRGSRGR

321 GNGIEETICT ASAKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGPS AEYGNLYRNA LFVAHYNTNA HSIIYRLRGR

401 AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSEN FEYVAFKTDS RPSIANLAGE NSVIDNLPEE VVANSYGLQR

481 EQARQLKNNN PFKFFVPPSQ QSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample	#Spec	#Spec Sample	Start	End	PTM

													33		**33**			
R.QQ(+.98)PEENAC(+57.02)QFQR.L	N	99.9	69.89	1534.6470	12	-0.2	768.3306	2	24.84	33	1278	OB3631.raw	6.02E4	2	2	2	13	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.85	2050.0383	17	-0.8	684.3528	3	3.97	33	195	OB3631.raw	1.24E6	58	58	59	75	
R.QQPEENAC(+57.02)QFQR.L	N	99.9	65.24	1533.6630	12	-0.2	767.8386	2	24.63	33	1262	OB3631.raw	1.91E4	6	6	2	13	Carbamidomethylation
R.QQ(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	99.9	60.60	1535.6311	12	-1.2	768.8219	2	25.48	33	1325	OB3631.raw	3.99E4	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	59.23	1534.6470	12	-1.0	768.3300	2	25.19	33	1302	OB3631.raw	5.65E4	3	3	2	13	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.9	51.70	3069.3774	27	3.4	1024.1366	3	4.00	33	200	OB3631.raw	4.47E5	29	29	23	49	Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	47.81	1534.6470	12	-5.3	768.3267	2	4.18	33	226	OB3631.raw	2.15E4	4	4	2	13	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)QFQ(+.98)R.L	N	99.9	44.67	1534.6470	12	-2.3	768.3290	2	5.14	33	359	OB3631.raw	0	1	1	2	13	Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.8	41.70	1535.6311	12	3.2	768.8253	2	25.29	33	1309	OB3631.raw	2.64E0	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.8	41.41	1536.6151	12	-2.6	769.3128	2	26.29	33	1379	OB3631.raw	1.01E4	2	2	2	13	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.8	40.98	3070.3613	27	2.9	1024.4640	3	33.40	33	1987	OB3631.raw	3.56E5	1	1	23	49	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFEC(+57.02)AGVALSR.L	N	99.7	40.61	3085.3723	27	2.4	1029.4672	3	32.70	33	1897	OB3631.raw	1.25E4	3	3	23	49	Hydroxylation Pro; Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.7	40.25	1536.6151	12	-2.6	769.3129	2	25.84	33	1347	OB3631.raw	4.7E3	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	38.06	1535.6311	12	0.9	768.8235	2	26.32	33	1381	OB3631.raw	3.99E4	2	2	2	13	Carbamidomethylation; Deamidation (NQ)
F.YSNAPQEIFIQQGR.G	N	99.7	37.99	1649.8162	14	1.9	825.9169	2	29.58	33	1580	OB3631.raw	1.72E3	2	2	62	75	
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.5	34.80	1535.6311	12	-2.5	768.8209	2	26.40	33	1387	OB3631.raw	3.99E4	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	14	22	
R.Q(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.4	32.86	1536.6151	12	-3.7	769.3120	2	25.94	33	1354	OB3631.raw	4.7E3	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	97.6	28.39	1536.6151	12	-3.2	769.3124	2	26.40	33	1386	OB3631.raw	1.01E4	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	97.6	28.35	1536.6151	12	9.8	769.3224	2	5.33	33	384	OB3631.raw	0	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPN(+.98)NQEFEC(+57.02)AGVALSR.L	N	95.5	26.40	3070.3613	27	2.0	1024.4631	3	37.92	33	2566	OB3631.raw	1.87E3	1	1	23	49	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	95.5	26.18	3070.3613	27	5.9	1536.1970	2	32.84	33	1915	OB3631.raw	4.45E3	2	2	23	49	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	95.3	25.39	1535.6311	12	-1.0	768.8220	2	25.76	33	1342	OB3631.raw	3.99E4	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQ(+.98)R.L	N	95.2	24.82	1535.6311	12	-1.1	768.8220	2	25.66	33	1336	OB3631.raw	3.99E4	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	95.0	24.50	1535.6311	12	-2.2	768.8211	2	5.08	33	351	OB3631.raw	3.69E3	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QP(+15.99)EENAC(+57.02)QFQ(+.98)R.L	N	94.8	24.11	1551.6260	12	-2.3	776.8185	2	24.99	33	1290	OB3631.raw	5.38E3	1	1	2	13	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.GYFGLIFPGC(+57.02)PRHYEEP(+15.99)HTQGR.R	Y	93.0	22.83	2633.2234	22	-2.5	878.7462	3	4.83	33	318	OB3631.raw	3.17E0	1	1	76	97	Carbamidomethylation; Hydroxylation Pro
R.QQP(+15.99)EENAC(+57.02)Q(+.98)FQR.L	N	87.2	21.93	1550.6420	12	-1.7	776.3269	2	24.64	33	1263	OB3631.raw	1E4	1	1	2	13	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)Q(+.98)PEENAC(+57.02)QFQR.L	N	85.9	19.85	1535.6311	12	-0.5	768.8224	2	5.30	33	380	OB3631.raw	3.69E3	1	1	2	13	Deamidation (NQ); Carbamidomethylation
R.QQP(+15.99)EEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	82.8	19.46	1551.6260	12	-2.1	776.8187	2	25.30	33	1311	OB3631.raw	5.38E3	1	1	2	13	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	81.6	18.81	3071.3455	27	6.2	1024.7954	3	38.90	33	2653	OB3631.raw	0	1	1	23	49	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	81.3	18.66	3070.3613	27	5.0	1024.4662	3	37.48	33	2520	OB3631.raw	1.87E3	1	1	23	49	Deamidation (NQ); Carbamidomethylation
total 32 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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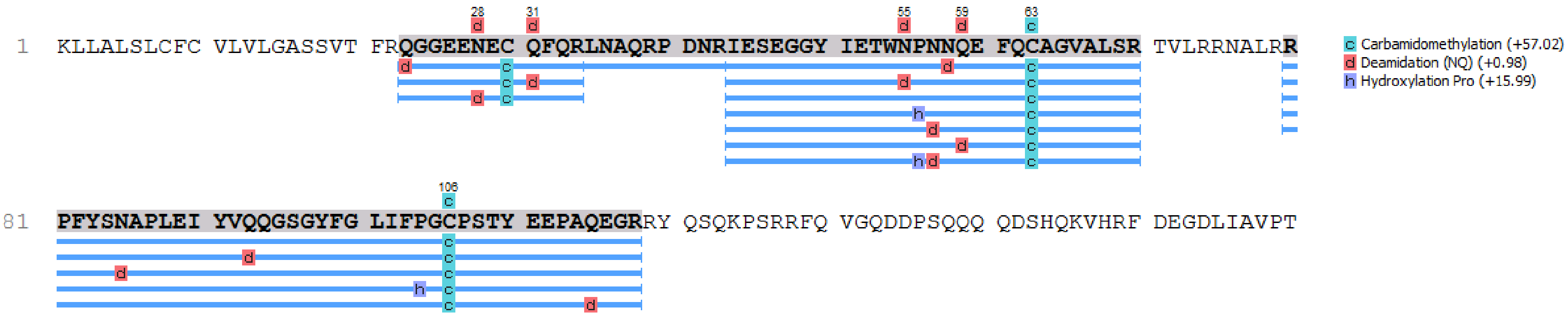
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR
81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS
241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR
321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL
481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	99.9	54.19	3068.3933	27	0.9	1023.8060	3	32.57	33	1880	OB3631.raw	1.16E6	13	13	44	70	Carbamidomethylation
R.IESEGGYIETWNPN(+.98)NQEFQC(+57.02)AGVALSR.T	Y	99.9	44.12	3069.3774	27	2.0	1024.1351	3	32.96	33	1931	OB3631.raw	3.05E5	4	4	44	70	Deamidation (NQ); Carbamidomethylation
R.RPFYSN(+.98)APLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.7	39.27	4425.0688	39	3.7	1476.0356	3	36.47	33	2391	OB3631.raw	2.06E5	6	6	80	118	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.7	38.90	4424.0845	39	-1.1	1475.7004	3	36.30	33	2368	OB3631.raw	3.39E5	19	19	80	118	Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.7	38.59	3084.3882	27	-0.2	1029.1365	3	33.78	33	2035	OB3631.raw	1.07E5	5	5	44	70	Hydroxylation Pro; Carbamidomethylation
R.QGGEENEC(+57.02)Q(+.98)FQR.L	Y	99.7	38.43	1481.5841	12	-0.9	741.7986	2	23.87	33	1212	OB3631.raw	3.24E4	3	3	23	34	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNN(+.98)QEFQC(+57.02)AGVALSR.T	Y	99.5	35.80	3069.3774	27	3.3	1024.1365	3	4.43	33	262	OB3631.raw	4.06E5	2	2	44	70	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQ(+.98)QGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.5	35.12	4425.0688	39	-0.5	1476.0295	3	36.68	33	2419	OB3631.raw	7.67E4	4	4	80	118	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFQC(+57.02)AGVALSR.T	Y	99.4	33.70	3069.3774	27	5.9	1024.1392	3	4.99	33	339	OB3631.raw	1E5	1	1	44	70	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	35	43	
R.Q(+.98)GGEENEC(+57.02)QFQR.L	Y	99.4	33.33	1481.5841	12	3.1	741.8016	2	23.57	33	1197	OB3631.raw	5.38E3	1	1	23	34	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQ(+.98)EFQC(+57.02)AGVALSR.T	Y	99.0	32.65	3069.3774	27	3.5	1024.1367	3	34.56	33	2137	OB3631.raw	3.05E5	4	4	44	70	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQEGR.R	Y	97.0	26.91	4440.0796	39	-3.4	1111.0234	4	35.63	33	2276	OB3631.raw	3.24E4	2	2	80	118	Hydroxylation Pro; Carbamidomethylation
R.QGGEEN(+.98)EC(+57.02)QFQR.L	Y	85.8	19.64	1481.5841	12	0.8	741.7999	2	24.37	33	1243	OB3631.raw	1.13E4	1	1	23	34	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)N(+.98)NQEFQC(+57.02)AGVALSR.T	Y	81.1	18.56	3085.3723	27	-4.9	1029.4597	3	34.67	33	2152	OB3631.raw	4.72E3	1	1	44	70	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)EGR.R	Y	63.4	16.80	4425.0688	39	2.6	1107.2773	4	37.17	33	2484	OB3631.raw	4.72E3	1	1	80	118	Carbamidomethylation; Deamidation (NQ)
total 16 peptides																		

E5G077|E5G077_ARAHY

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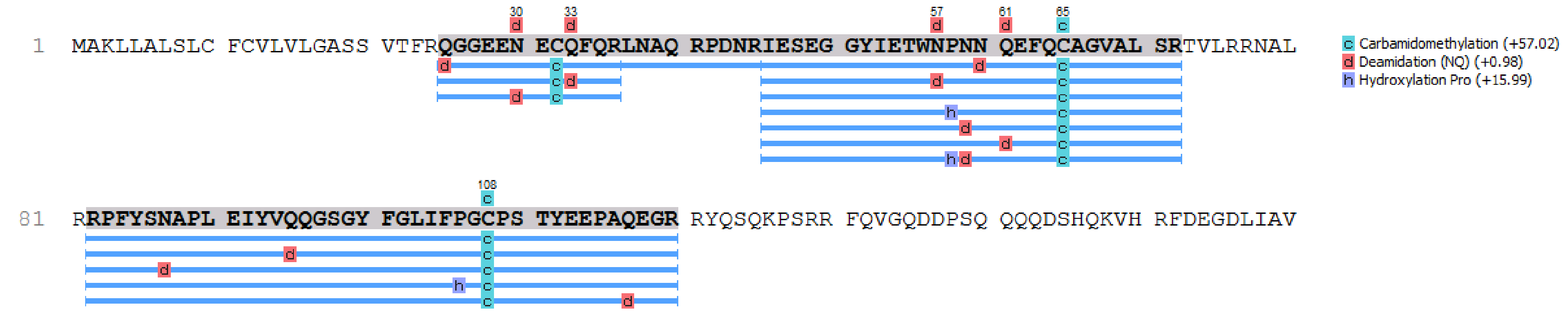
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSLC FCVLVLGASS VTFR**QGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

81 R**RPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR** RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

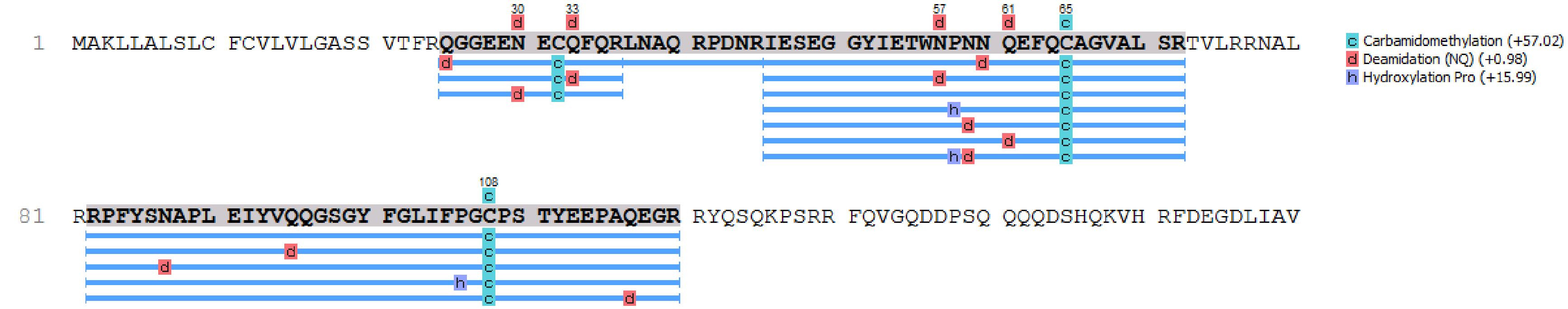
Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	99.9	54.19	3068.3933	27	0.9	1023.8060	3	32.57	33	1880	OB3631.raw	1.16E6	13	13	46	72	Carbamidomethylation
R.IESEGGYIETWNPN(+.98)NQEFQC(+57.02)AGVALSR.T	Y	99.9	44.12	3069.3774	27	2.0	1024.1351	3	32.96	33	1931	OB3631.raw	3.05E5	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.RPFYSN(+.98)APLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.7	39.27	4425.0688	39	3.7	1476.0356	3	36.47	33	2391	OB3631.raw	2.06E5	6	6	82	120	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.7	38.90	4424.0845	39	-1.1	1475.7004	3	36.30	33	2368	OB3631.raw	3.39E5	19	19	82	120	Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.7	38.59	3084.3882	27	-0.2	1029.1365	3	33.78	33	2035	OB3631.raw	1.07E5	5	5	46	72	Hydroxylation Pro; Carbamidomethylation
R.QGGEENEC(+57.02)Q(+.98)FQR.L	Y	99.7	38.43	1481.5841	12	-0.9	741.7986	2	23.87	33	1212	OB3631.raw	3.24E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNN(+.98)QEFQC(+57.02)AGVALSR.T	Y	99.5	35.80	3069.3774	27	3.3	1024.1365	3	4.43	33	262	OB3631.raw	4.06E5	2	2	46	72	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQ(+.98)QGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.5	35.12	4425.0688	39	-0.5	1476.0295	3	36.68	33	2419	OB3631.raw	7.67E4	4	4	82	120	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFQC(+57.02)AGVALSR.T	Y	99.4	33.70	3069.3774	27	5.9	1024.1392	3	4.99	33	339	OB3631.raw	1E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)GGEENEC(+57.02)QFQR.L	Y	99.4	33.33	1481.5841	12	3.1	741.8016	2	23.57	33	1197	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQ(+.98)EFQC(+57.02)AGVALSR.T	Y	99.0	32.65	3069.3774	27	3.5	1024.1367	3	34.56	33	2137	OB3631.raw	3.05E5	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQEGR.R	Y	97.0	26.91	4440.0796	39	-3.4	1111.0234	4	35.63	33	2276	OB3631.raw	3.24E4	2	2	82	120	Hydroxylation Pro; Carbamidomethylation
R.QGGEEN(+.98)EC(+57.02)QFQR.L	Y	85.8	19.64	1481.5841	12	0.8	741.7999	2	24.37	33	1243	OB3631.raw	1.13E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)N(+.98)NQEFQC(+57.02)AGVALSR.T	Y	81.1	18.56	3085.3723	27	-4.9	1029.4597	3	34.67	33	2152	OB3631.raw	4.72E3	1	1	46	72	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)EGR.R	Y	63.4	16.80	4425.0688	39	2.6	1107.2773	4	37.17	33	2484	OB3631.raw	4.72E3	1	1	82	120	Carbamidomethylation; Deamidation (NQ)
total 16 peptides																		

Q0GM57|Q0GM57_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 33	#Spec	#Spec Sample 33	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	99.9	54.19	3068.3933	27	0.9	1023.8060	3	32.57	33	1880	OB3631.raw	1.16E6	13	13	46	72	Carbamidomethylation
R.IESEGGYIETWNPN(+.98)NQEFQC(+57.02)AGVALSR.T	Y	99.9	44.12	3069.3774	27	2.0	1024.1351	3	32.96	33	1931	OB3631.raw	3.05E5	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.RPFYSN(+.98)APLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.7	39.27	4425.0688	39	3.7	1476.0356	3	36.47	33	2391	OB3631.raw	2.06E5	6	6	82	120	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.7	38.90	4424.0845	39	-1.1	1475.7004	3	36.30	33	2368	OB3631.raw	3.39E5	19	19	82	120	Carbamidomethylation
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	99.7	38.59	3084.3882	27	-0.2	1029.1365	3	33.78	33	2035	OB3631.raw	1.07E5	5	5	46	72	Hydroxylation Pro; Carbamidomethylation
R.QGGEENEC(+57.02)Q(+.98)FQR.L	Y	99.7	38.43	1481.5841	12	-0.9	741.7986	2	23.87	33	1212	OB3631.raw	3.24E4	3	3	25	36	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWNPNN(+.98)QEFQC(+57.02)AGVALSR.T	Y	99.5	35.80	3069.3774	27	3.3	1024.1365	3	4.43	33	262	OB3631.raw	4.06E5	2	2	46	72	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQ(+.98)QGSGYFGLIFPGC(+57.02)PSTYEEPAQEGR.R	Y	99.5	35.12	4425.0688	39	-0.5	1476.0295	3	36.68	33	2419	OB3631.raw	7.67E4	4	4	82	120	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)PNNQEFQC(+57.02)AGVALSR.T	Y	99.4	33.70	3069.3774	27	5.9	1024.1392	3	4.99	33	339	OB3631.raw	1E5	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNR.I	N	99.4	33.37	1082.5581	9	-0.7	361.8597	3	5.12	33	356	OB3631.raw	1.78E5	5	5	37	45	
R.Q(+.98)GGEENEC(+57.02)QFQR.L	Y	99.4	33.33	1481.5841	12	3.1	741.8016	2	23.57	33	1197	OB3631.raw	5.38E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQ(+.98)EFQC(+57.02)AGVALSR.T	Y	99.0	32.65	3069.3774	27	3.5	1024.1367	3	34.56	33	2137	OB3631.raw	3.05E5	4	4	46	72	Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQEGR.R	Y	97.0	26.91	4440.0796	39	-3.4	1111.0234	4	35.63	33	2276	OB3631.raw	3.24E4	2	2	82	120	Hydroxylation Pro; Carbamidomethylation
R.QGGEEN(+.98)EC(+57.02)QFQR.L	Y	85.8	19.64	1481.5841	12	0.8	741.7999	2	24.37	33	1243	OB3631.raw	1.13E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNP(+15.99)N(+.98)NQEFQC(+57.02)AGVALSR.T	Y	81.1	18.56	3085.3723	27	-4.9	1029.4597	3	34.67	33	2152	OB3631.raw	4.72E3	1	1	46	72	Hydroxylation Pro; Deamidation (NQ); Carbamidomethylation
R.RPFYSNAPLEIYVQQGSGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)EGR.R	Y	63.4	16.80	4425.0688	39	2.6	1107.2773	4	37.17	33	2484	OB3631.raw	4.72E3	1	1	82	120	Carbamidomethylation; Deamidation (NQ)
total 16 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

Summary

1. Notes

Spot C from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

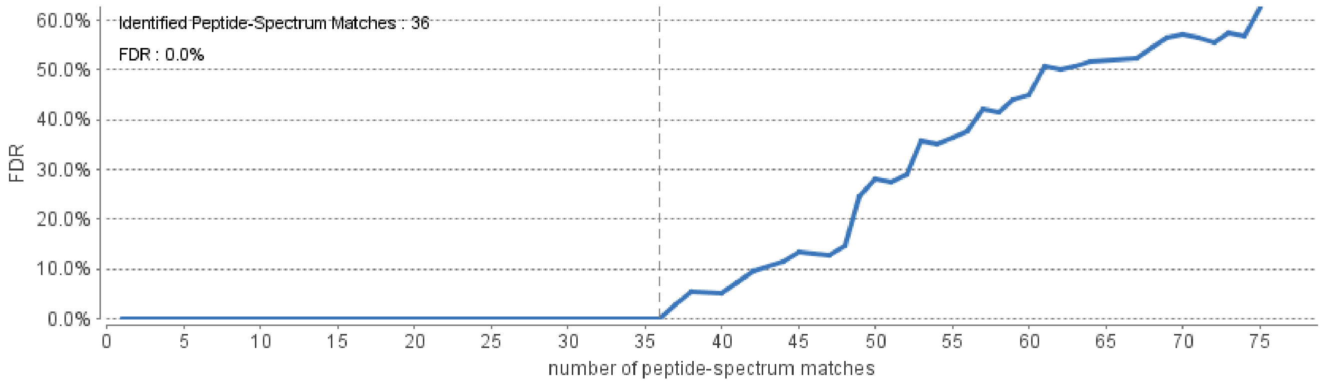
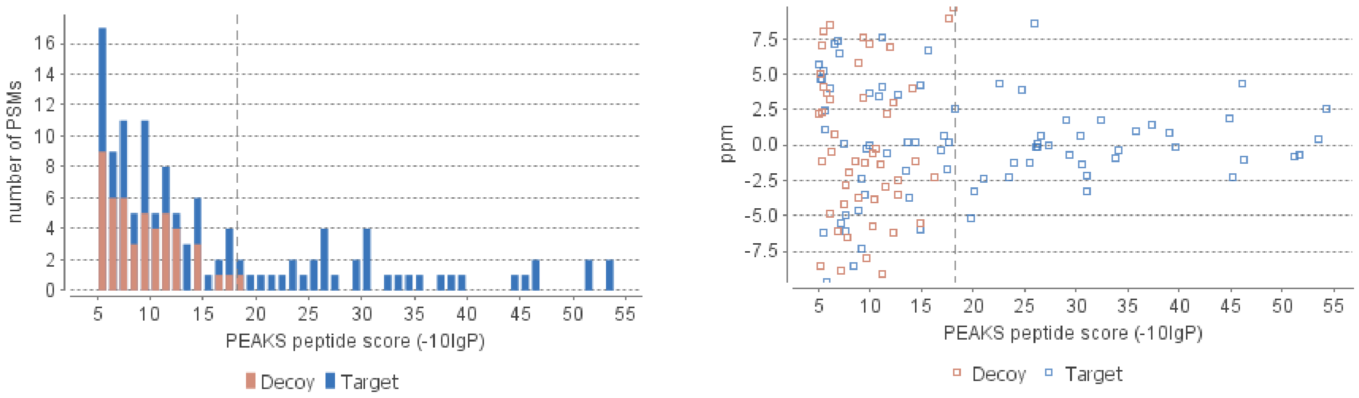


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.



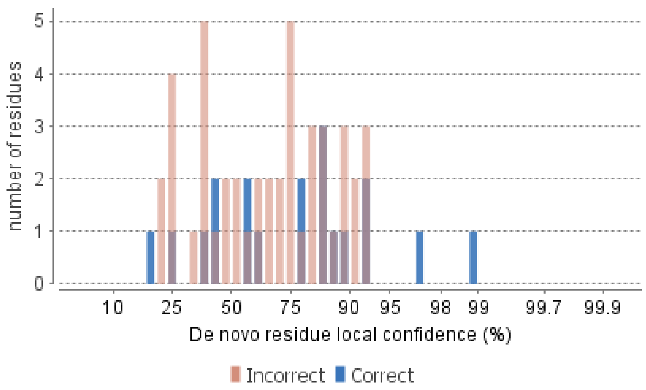
(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



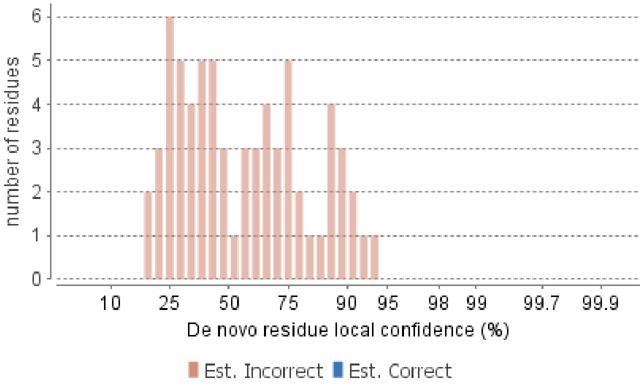


Table 1. Statistics of data.

# of MS scans	3184
# of MS/MS scans	1041

Table 2. Result filtration parameters.

Peptide -10lgP	≥18.2
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	32
Peptide sequences	15
Protein groups	4
Proteins	32
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 32 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	9

Table 4. PTM profile.

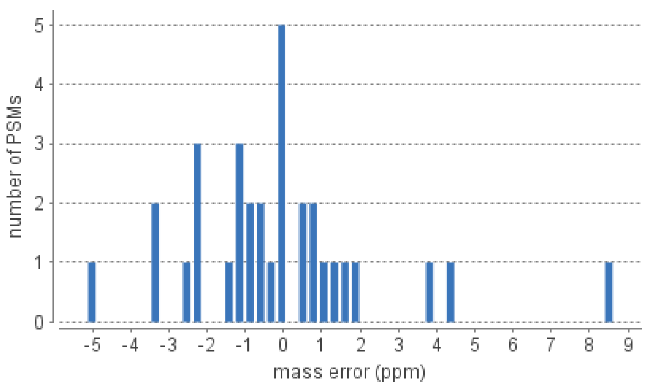
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Oxidation	15.99	M	2	26.29	9.84E3	1000.00
Carbamidomethyl	57.02	C	2	51.70	3.05E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



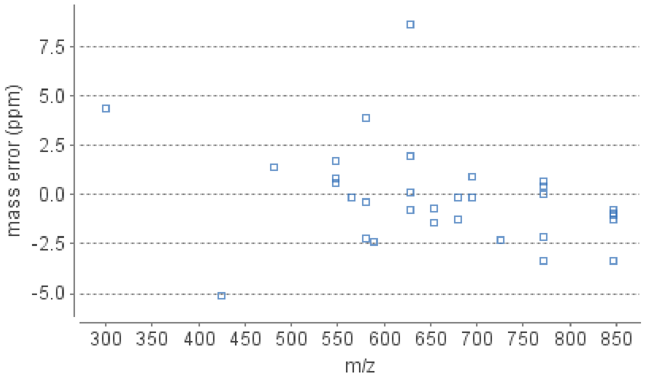


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 12	10	5	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3610.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 12	Area Sample 12	#Peptides	#Unique	#Spec Sample 12	PTM	Avg. Mass	Description
1	13	Q9FZ11|Q9FZ11_ARAHY	99.1	124.75	17	17	3.05E3	6	1	20	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
1	5	Q5I6T2|Q5I6T2_ARAHY	99.1	124.75	17	17	3.05E3	6	1	20	Y	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
1	15	Q647H3|Q647H3_ARAHY	99.1	124.75	17	17	3.05E3	6	1	20	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
5	69	Q6PSU5|Q6PSU5_ARAHY	66.8	34.65	4	4	2.48E3	1	1	1	N	33604	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	57	Q6PSU6|Q6PSU6_ARAHY	66.8	34.65	4	4	2.48E3	1	1	1	N	34133	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	27	Q6PSU4|Q6PSU4_ARAHY	66.8	34.65	3	3	2.48E3	1	1	1	N	48095	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	26	Q6PSU3|Q6PSU3_ARAHY	66.8	34.65	2	2	2.48E3	1	1	1	N	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
5	21	sp|P43237|ALL11_ARAHY	66.8	34.65	2	2	2.48E3	1	1	1	N	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
5	23	B3IXL2|B3IXL2_ARAHY	66.8	34.65	2	2	2.48E3	1	1	1	N	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
5	18	N1NG13|N1NG13_ARAHY	66.8	34.65	2	2	2.48E3	1	1	1	N	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
5	20	sp|P43238|ALL12_ARAHY	66.8	34.65	2	2	2.48E3	1	1	1	N	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
8	368	A0A0A6ZDX8|A0A0A6ZDX8_ARAHY	21.8	22.50	2	2	3.74E3	1	1	1	N	27063	40S ribosomal protein S3 OS=Arachis hypogaea PE=2 SV=1
9	790	Q2KPJ7|Q2KPJ7_ARAHY	14.9	21.06	11	11	5.57E3	1	1	1	N	9989	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	765	Q2KPK0|Q2KPK0_ARAHY	14.9	21.06	11	11	5.57E3	1	1	1	N	10062	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	766	Q2KPR1|Q2KPR1_ARAHY	14.9	21.06	8	8	5.57E3	1	1	1	N	13530	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	791	Q2KPR3|Q2KPR3_ARAHY	14.9	21.06	8	8	5.57E3	1	1	1	N	13837	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	769	Q2KPR2|Q2KPR2_ARAHY	14.9	21.06	8	8	5.57E3	1	1	1	N	14105	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	748	Q2KPY1|Q2KPY1_ARAHY	14.9	21.06	7	7	5.57E3	1	1	1	N	15692	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	770	Q2KPK3|Q2KPK3_ARAHY	14.9	21.06	7	7	5.57E3	1	1	1	N	16215	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	772	Q2KPL7|Q2KPL7_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	18731	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	777	Q2KPM5|Q2KPM5_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19261	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	780	Q2KPQ7|Q2KPQ7_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19262	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	793	Q2KPP3|Q2KPP3_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	18990	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	778	Q2KPL4|Q2KPL4_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19244	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	781	Q2KPL0|Q2KPL0_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19229	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	774	Q2KPP8|Q2KPP8_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19193	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	782	Q2KPM1|Q2KPM1_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19261	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1

9	787	Q2KPM0|Q2KPM0_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19462	Resistance protein PRG (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	750	Q2KPZ1|Q2KPZ1_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19524	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	364	Q2KQ67|Q2KQ67_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	20077	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	705	Q2KQ36|Q2KQ36_ARAHY	14.9	21.06	6	6	5.57E3	1	1	1	N	19688	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
9	713	G0Y6V4|G0Y6V4_ARAHY	14.9	21.06	1	1	5.57E3	1	1	1	N	98838	TIR-NBS-LRR type disease resistance protein OS=Arachis hypogaea GN=205D04_4 PE=3 SV=1
total 32 proteins													

Q9FZ11|Q9FZ11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA

81 LRRPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP

241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE

351 C

321 YDEDEYEYDE EDRRRGRGSR GRGN**GIEETI CTASVK**KNIG RNR**SPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR**

401 **NALFVPHYNT NAHSIIYALR** GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGK**SQS DNFEYVAFKT DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	53.54	1540.7673	13	0.5	771.3913	2	32.85	12	1824	OB3610.raw	3.46E3	1	1	388	400	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	51.70	1306.6438	12	-0.7	654.3287	2	27.59	12	1475	OB3610.raw	3.05E3	2	2	345	356	Carbamidomethylation
K.TANDLNLLILR.W	N	99.9	51.22	1254.7296	11	-0.8	628.3716	2	32.69	12	1810	OB3610.raw	8.88E3	3	3	377	387	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.7	46.33	2540.2910	23	-1.0	847.7701	3	31.01	12	1690	OB3610.raw	3.62E4	5	5	435	457	
R.SPDIYNPQAGSLK.T	N	98.2	39.64	1388.6936	13	-0.1	695.3540	2	27.22	12	1452	OB3610.raw	4.92E3	2	2	364	376	
R.NALFVPHYNTNAHSIIYALR.G	N	97.0	34.05	2313.2019	20	-0.3	579.3076	4	31.04	12	1693	OB3610.raw	1.11E5	7	7	401	420	
total 6 peptides																		

Q5I6T2|Q5I6T2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE

352
C
321 EYDEDEYEYD EEDRRRGRGS RGRGN**GIEET ICTASVK**KNI GRNR**SPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY**
C
401 **RNALFVPHYN TNAHSIIYAL R**GRAHVQVVD SNGNR**VYDEE LQEGHVLVVP QNFAVAGK**SQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	53.54	1540.7673	13	0.5	771.3913	2	32.85	12	1824	OB3610.raw	3.46E3	1	1	389	401	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	51.70	1306.6438	12	-0.7	654.3287	2	27.59	12	1475	OB3610.raw	3.05E3	2	2	346	357	Carbamidomethylation
K.TANDLNLLILR.W	N	99.9	51.22	1254.7296	11	-0.8	628.3716	2	32.69	12	1810	OB3610.raw	8.88E3	3	3	378	388	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.7	46.33	2540.2910	23	-1.0	847.7701	3	31.01	12	1690	OB3610.raw	3.62E4	5	5	436	458	
R.SPDIYNPQAGSLK.T	N	98.2	39.64	1388.6936	13	-0.1	695.3540	2	27.22	12	1452	OB3610.raw	4.92E3	2	2	365	377	
R.NALFVPHYNTNAHSIIYALR.G	N	97.0	34.05	2313.2019	20	-0.3	579.3076	4	31.04	12	1693	OB3610.raw	1.11E5	7	7	402	421	
total 6 peptides																		

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD

359
C
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GN**GIEETICT ASVK**KNIGRN R**SPDIYNPQA GSLKTANDLN LLILRWLGLS**
C
401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFKTDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	53.54	1540.7673	13	0.5	771.3913	2	32.85	12	1824	OB3610.raw	3.46E3	1	1	396	408	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	51.70	1306.6438	12	-0.7	654.3287	2	27.59	12	1475	OB3610.raw	3.05E3	2	2	353	364	Carbamidomethylation
K.TANDLNLLILR.W	N	99.9	51.22	1254.7296	11	-0.8	628.3716	2	32.69	12	1810	OB3610.raw	8.88E3	3	3	385	395	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.7	46.33	2540.2910	23	-1.0	847.7701	3	31.01	12	1690	OB3610.raw	3.62E4	5	5	443	465	
R.SPDIYNPQAGSLK.T	N	98.2	39.64	1388.6936	13	-0.1	695.3540	2	27.22	12	1452	OB3610.raw	4.92E3	2	2	372	384	
R.NALFVPHYNTNAHSIIYALR.G	N	97.0	34.05	2313.2019	20	-0.3	579.3076	4	31.04	12	1693	OB3610.raw	1.11E5	7	7	409	428	
total 6 peptides																		

Q6PSU5|Q6PSU5_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
81 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK **GTGNLELVAV R**KEQQQRGRR
161 EEEDEDQEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
241 LAFPGSGEQV EKLIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	141	151	
total 1 peptides																		

Q6PSU6|Q6PSU6_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRRSTRS SDNEGVIVKV SKEHVQELTK HAKSVSKKGS EEEDITNPIN
81 LRDGEPDLSN NFGRLFEVKP DKKNPQLQDL DMMLTCVEIK EGALMLPHFN SKAMVIVVVN K**GTGNLELVA VR**KEQQQRGR
161 REQEWEEEEE DEEEEGSNRE VRRYTARLKE GDVFIMPAAH PVAINASSEL HLLGFGINAE NNHRIFLAGD KDNVIDQIEK
241 QAKDLAFPGS GEQVEKLIKN QRESHFVSAR PQSQSPSSPE KEDQEEENQG GKGPLLSILK AFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	142	152	
total 1 peptides																		

Q6PSU4|Q6PSU4_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GFDQRSRQFQ NLQNHRIVQI EAKPNTLVLP KHADADNILV IQQGQATVTV ANGNNRKSFN LDEGHALRIP SGFISYILNR
81 HDNQNLRVAK ISMPVNTPGQ FEDFFPASSR DQSSYLQGFS RNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRWSTRS
161 SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI
241 KEGALMLPHF NSKAMVIVVV NK**GTGNLELV AVR**KEQQQRG RREEEEDEDE EEEGSNREVR RYTARLKEGD VFIMPAAHPV
321 AINASSELHL LGFGINAENN HRIFLAGDKD NVIDQIEKQA KDLAFPGSGE QVEKLIKNQK ESHFVSARPQ SQSQSPSSPE
401 KESPEKEDQE EENQGGKGPL LSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	263	273	
total 1 peptides																		

Q6PSU3|Q6PSU3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NK**GTGNLELV AVR**KEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG
561 SGEQVEKLIK NQRESHFVSA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	453	463	
total 1 peptides																		

sp|P43237|ALL11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NK**GTGNLELV AVR**KEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG
561 SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	453	463	
total 1 peptides																		

B3IXL2|B3IXL2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
 81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG
561 SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	453	463	
total 1 peptides																		

N1NG13|N1NG13_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
 81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERFEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	461	471	
total 1 peptides																		

sp|P43238|ALL12_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG

81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ

241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT

321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL

401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK **GTGNLELVAV R**KEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD

561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GTGNLELVAVR.K	Y	91.3	26.07	1127.6299	11	-0.1	564.8221	2	28.67	12	1537	OB3610.raw	2.48E3	1	1	461	471	
total 1 peptides																		

A0A0A6ZDX8|A0A0A6ZDX8_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAIQMSKKR KFVADGVFFA ELNEVLTREL AEDGYSGVEV RVTPMRTEII IRATRTQAVL GEKGRRIREL TSVVQKRFKF

81 PENSVELYAE RVNNRGLCAI AQAESLRYKL LGGLAVRRAC YGVLRFVMEN GAKGCEVIVS GKLRAQRAKS MKFKDGYMIS

161 SGQPVKDYID SAVRHVLLRQ GVLGIKVKIM LDWDPK**GKLG PK**TPLPDIVT IHPPKEEEEY NRIPVAAAVP ALANDIEAPA

241 VPVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
K.GKLGPK.T	Y	54.8	22.50	598.3802	6	4.3	300.1987	2	25.90	12	1382	OB3610.raw	3.74E3	1	1	197	202	
total 1 peptides																		

Q2KPJ7|Q2KPJ7_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NHGKRLEYLV GEQAWFGPGS RIIIATRDFH LVRKNKLHET YNVEGLVESE ALNLFSLEAF NLPKPSEE**FL DLSKEVVK**YS

81 GGLPFALN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	69	78	
total 1 peptides																		

Q2KPK0|Q2KPK0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DVNHGKQLEY LGGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVE SKALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

81 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	71	80	
total 1 peptides																		

Q2KPR1|Q2KPR1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ISSNSVHTKY HGRTIIQNSL RLKKVLLVLD HVNHGKQLEY LAGEQAWFGP ASRIIITTRD FHLLRKNKLH ETYNVEGLVE
81 SEALNLFSLE AFNLPKPSEE **FLDLSKEVVK** YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	101	110	
total 1 peptides																		

Q2KPR3|Q2KPR3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 IKISSNPVHN KYHGSTIIQN SSRLKKVLLV LHHVNHQNHL HSLAAEQHWF GPASRIMITT RDLEVLKEQE VHETYKVEGL
81 VESKSLNLFC LKAFKQQEPR EG**FLDLSKEV VK**YSGGLPFA L

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
G.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	103	112	
total 1 peptides																		

Q2KPR2|Q2KPR2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VDQMKISSNS VHNKYDGRTM IQNCLRLKKV LLVLDDVNHG KQLEYLAGEQ AWFGPGSRII ITTRDFHLVR KNKLHETYNV
81 EGLVESKALN LFSLEAFNLP KPSEE**FLDLS KEVVK**YSGGL PFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	106	115	
total 1 peptides																		

Q2KPY1|Q2KPY1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KKDITDMQKQ LLDQMNISSN AVYNQYDGRT IIQNSLRLKK VLLILDDVNQ ENQLENLTGE QAWFGPGSRI VITTRDVEAL

81 KGPEVHETYE VEGLVESEAL NLFCLKAFKQ QKPTEG**FLDL SKEVVK**YSGG LPFAFKVLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
G.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	117	126	
total 1 peptides																		

Q2KPK3|Q2KPK3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VRENCEKKDI SHMQKQLLDQ MKISSNSVHN KYDGRTMIQN SLRLKKVLLV LDDVNHGKRL EYLAGEQAWF GPGSRIIITT

81 RDFHLLRKNK LHETYNVEGL VESEALNLFS LEAFNLPKPS EE**FLDLSKEV VK**YSGGLPFA L

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	123	132	
total 1 peptides																		

Q2KPL7|Q2KPL7_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TIARAVFETI RCRFEVTCFL ADVRENCEKK DISHMQKQLL DQMKISSNSV HNKYDGRTMI QNSLRLKKVL LVLDDVNHGK

81 QLEYLAGEQA WFGPGSRIII TTRDFHLLRK NKLHETYNVE GLVESEALNL FSLEAFNLPK PSEE**FLDLSK EVVK**YSGGLP

161 FAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	145	154	
total 1 peptides																		

Q2KPM5|Q2KPM5_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGMGKTTIAR AVFETIRCRF EVTCFLADVR ENCEKKDISH MQKQLLDQMK ISSNSVHNKY DGRTMIQNSL RLKKVLLVLD

81 DVNHGKQLEY LAGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVK SEALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPQ7|Q2KPQ7_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGMGKTTIAR AVFETIRCRF EVTCFLADVR ENCEKKDISH MQKQLLDQMK ISSNSVHNKY DGRTMIQNSL RLKKVLLVLD

81 DVNHGKQLEY LAGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVE SEALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPP3|Q2KPP3_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGMGKTTIAR AVFETIRCRF EVTCFLADVR EQCEKKDITD IQKQLLDQMN ISSNAVHNKY DGGTIIQNSL RLKKVLLVLD

81 DVNHEKQLED LAGEQDWFGP GCRIIITTRD VEVLKGPEVH ETYKVEGLVE SEALNLFCLK AFKQQEPAEG **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
G.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPL4|Q2KPL4_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGVGKTTIAR AVFETIRCRF EVTCFLADVR ENCEKKDISH MQKQLVDQMK ISSNSVHNKY DGRTMIQNSL RLKKVLLVLD

81 DVNHGKRLEY LAGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVE SEALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPL0|Q2KPL0_ARAHY back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGVGKTTIAR AVFETIRCRF EVTCFLADVR ENCEKKDISH MQKQLLDQMK ISSNSVHNKY DGRTMIQNSL RLKKVLLVLD
81 DVNHGKQLEY LAGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVE SKALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPP8|Q2KPP8_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGMGKTTIAR AVFETIRCRF EVTCFLADVS ENCEKKDISH MQKQLLDQMK ISSNSVHNKY DGRTMIQNSL RLKKVLLVLD
81 DVNHGKQLEY LAGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVE SEALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPM1|Q2KPM1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGMGKTTIAR AVFETIRCRF EVTCFLADVR ENCEKKNISH MQKQLLDQMK ISSNSVHNKY DGRTMIQNSL RLKKVLLVLD
81 DVNHGKQLEY LAGEQAWFGP GSRIIITTRD FHLLRKNKLH ETYNVEGLVE SEALNLFSLE AFNLPKPSEE **FLDLSKEVVK**

161 YSGGLPFAL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	151	160	
total 1 peptides																		

Q2KPM0|Q2KPM0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SIGGMGKTTI ARAVFETIRC RFEVTCFLAD VRENCEKKDI SHMQKQLLDQ MKISSNSVHN KYDGRTMIQN SLRLKKVLLV
81 LDDVNHGKQL EYLAGEQAWF GPGSRIIITT RDFHLLRKNK LHETYNVEGL VESEALNLFS LEAFNLPKPS EE**FLDLSKEV**

161 **VK**YSGGLPFA L

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	153	162	
total 1 peptides																		

Q2KPZ1|Q2KPZ1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GMGGVGKTTI ARAVFETIRC GFEVTCFLAN VRENCEKKDI TDMQKQLLDQ MNISSNAVYN QYDGRTIIQN SLRLKKVLLI
81 LDDVNQENQL ENLAGEQAWF GPGSRIVITT RDVEALKGPE VHETYEVEGL VESEALNLFC LKAFKQQKPT EG**FLDLSKEV**

161 **VK**YSGGLPFA FKVLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
G.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	153	162	
total 1 peptides																		

Q2KQ67|Q2KQ67_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WMGGVGKTTL ARAVFETIRC RFEVTCFLAD VREHREKKDI TDIQKQLLKQ MNISSNAVHN KYDGRTIIQY SLRLKKVLLV
81 LDDVNHEKQL EDLAGEKDWF GPGSRIIITT RDFHLLRKNK LHETYNVEGL VESEALNLFS LEAFNLPKPS EE**FLDLSKEV**

161 **VK**YSGGFPLA LKVLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
E.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	153	162	
total 1 peptides																		

Q2KQ36|Q2KQ36_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GMGGVGKTTI ARAVFEIIRS RFEVTCFLAD VREHCEKKDI THIQKQLLDQ MKKSSNSVHN KYDGRTIIQN SLCLKKVLLV

81 LDDVNHEKQL EDLAGEKDWF GPGSRIIITT RDVEVLKGPE VHEIYKVEGL VESEALNLFC LKAFKQQEPT EG**FLDLSKEV**

161 **VK**YSGGLPLA FKVLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
G.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	153	162	
total 1 peptides																		

G0Y6V4|G0Y6V4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKNLVGIDSR VEGVINLIGL GLNDVRYMVI WGMGGIGKTT IARAVFETIR SRFEVSCFLA DVREHCEKKD TVHIQKQLLD

81 QMNISSYAVY NKYDGRRIIQ NSLCLKKVLL VLDDVNHEKQ LEDLAGEKDW FGPGSRIIIT TRDVEVLKGP EVHEIYKVEG

161 LVESEALNLF CLKAFKQQEP TEG**FLDLSKE VVK**YSGGLPL ALKVLGSYLN GQKEKSSHED NYNIFMGVST LKISYEGLED

241 TEKDIFLDIA CFFKGRQKHH VTEMLKRCGY QAEIGLDILI NRSLVTLEEV KILGMVTLGM HDLLEEMGKQ IVIQESPNDA

321 SKRSRLWCYE DVDFVLTQKK ESEATHSIVS KVYYCETEEE WREYREIKEN WRDLSFSNIC QLKLLILDGV NAPILCDIPC

401 TLKVLHWEGC PMETLPFTDQ CYELVEIDLS HGKIVELWDG KKVLKKLEHL NLYFCEKLKQ TPDLSGAPNL KTLNLHGCKE

481 LNYINPSLAH HKRLVELNLG RCRSLETLGD KLEISSLEKL NLYECRSLRR LPEFGECMKQ LSILDLEKTG IEELPPTLGK

561 LAGVSELDLT GCHKLTSLPF PLGCFVGLKK LKLSRFVELS CVPYTTHGLE SLEAWDFSNS PIFVGLLCSL SRLTSLSSLK

641 LHGEYSRSRE VSTLYYDLGH LTSLTDLDLG YSDFLRVPIC IHALPRLTRL DLCYCYNLEV LPELPSSLRE LQVKGFEPLV

721 ASNVNAAISK ACCGFAESAS QDREDLLQMW ISGKEMPAWF KDQKKDNGIS VSFPHNCPST ETIALALCFL LQGVIMDLPE

801 QPSVICNVTC YAKTIASNCN FPVIIVESEY KDLEHVGCAS KTFNISSSLA SRRSSDPPEL LPFFPLHSHS TWFS

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 12	#Spec	#Spec Sample 12	Start	End	PTM
G.FLDLSKEVVK.Y	Y	46.1	21.06	1176.6754	10	-2.4	589.3436	2	34.12	12	1930	OB3610.raw	5.57E3	1	1	184	193	
total 1 peptides																		

Peptide List

Summary

1. Notes

Spot D from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

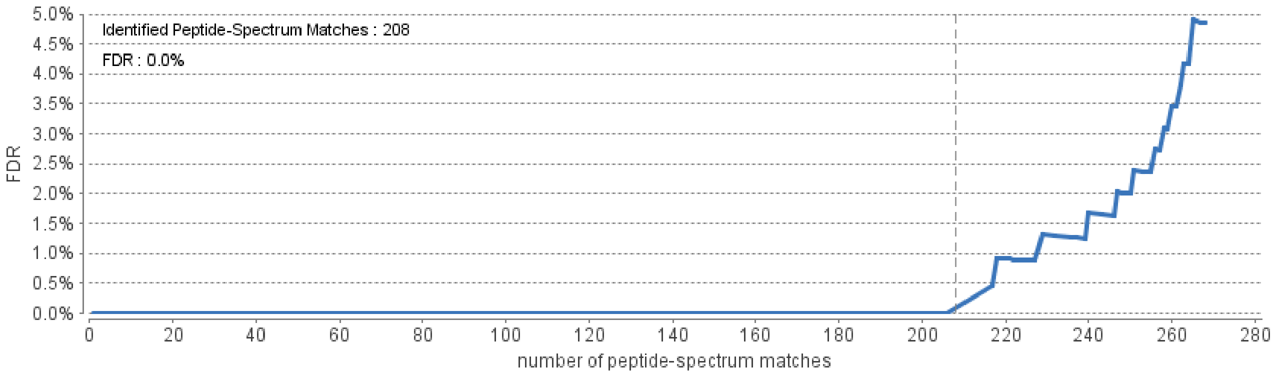
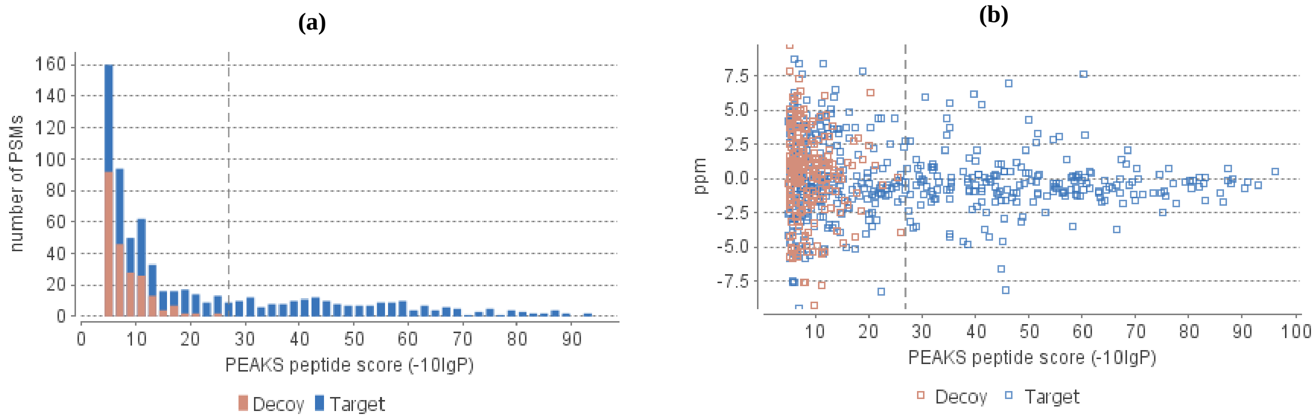


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

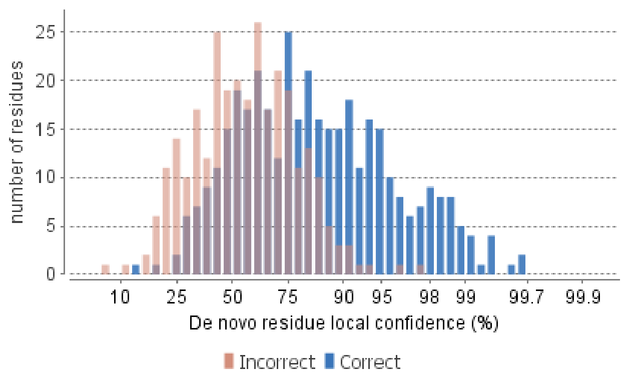

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



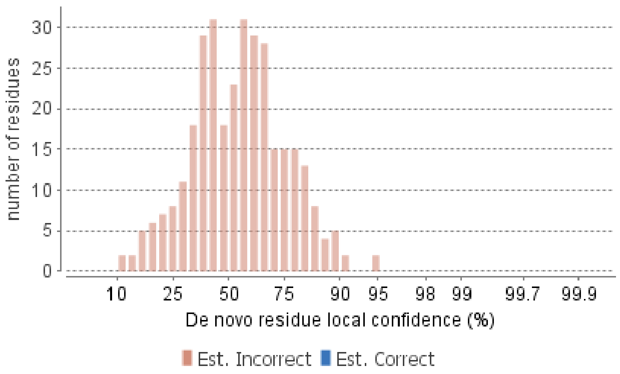


Table 1. Statistics of data.

# of MS scans	2957
# of MS/MS scans	3171

Table 2. Result filtration parameters.

Peptide -10lgP	≥27
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	181
Peptide sequences	53
Protein groups	4
Proteins	10
Proteins (#Unique Peptides)	3 (>2); 6 (=2); 1 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	39

Table 4. PTM profile.

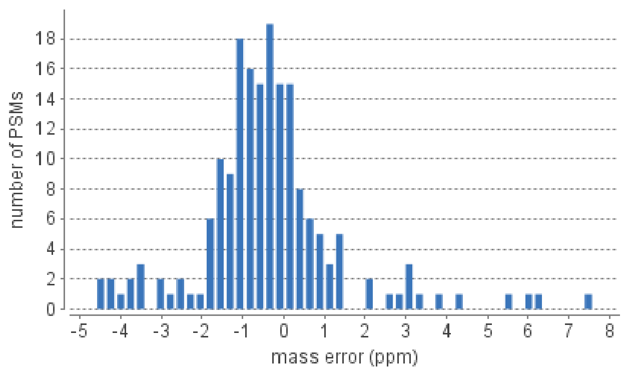
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Oxidation	15.99	M	36	93.00	3.74E4	1000.00
Deamidation	.98	NQ	30	90.33	4.8E4	90.87
Carbamidomethyl	57.02	C	6	44.37	2.92E3	1000.00
HydPro	15.99	P	1	37.69	8.18E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



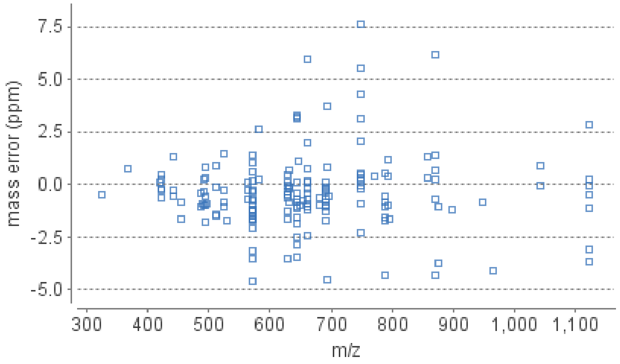


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 11	46	7	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3609.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:

Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 11	Area Sample 11	#Peptides	#Unique	#Spec Sample 11	PTM	Avg. Mass	Description
1	26	Q6PSU3|Q6PSU3_ARAHY	99.2	315.98	41	41	7.99E5	27	7	170	Y	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
1	21	sp|P43237|ALL11_ARAHY	99.2	315.98	39	39	7.99E5	27	7	170	Y	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
1	23	B3IXL2|B3IXL2_ARAHY	99.2	315.98	39	39	7.99E5	27	7	170	Y	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
2	18	N1NG13|N1NG13_ARAHY	99.2	298.73	33	33	1.01E4	22	2	131	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
2	20	sp|P43238|ALL12_ARAHY	99.2	298.73	33	33	1.01E4	22	2	131	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
4	7	Q647H4|Q647H4_ARAHY	97.7	75.57	5	5	2.73E3	2	2	2	N	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
4	12	Q6T2T4|Q6T2T4_ARAHY	97.7	75.57	5	5	2.73E3	2	2	2	N	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
4	10	Q8LKN1|Q8LKN1_ARAHY	97.7	75.57	5	5	2.73E3	2	2	2	N	61738	Allergen Arah3/Arah4 OS=Arachis hypogaea PE=3 SV=1
4	2	A1DZF0|A1DZF0_ARAHY	97.7	75.57	5	5	2.73E3	2	2	2	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
19	259	Q2KQ45|Q2KQ45_ARAHY	58.4	31.65	6	6	0E0	1	1	1	N	19632	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
total 10 proteins													

Q6PSU3|Q6PSU3_ARAHY

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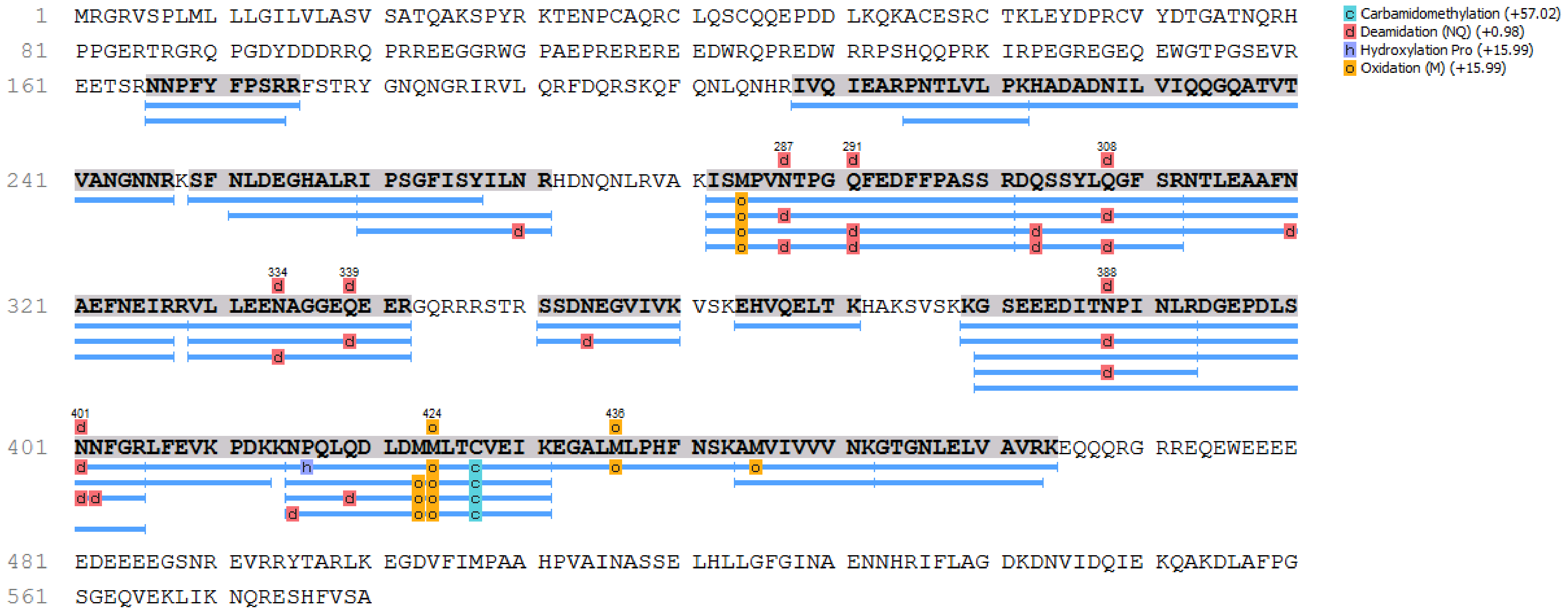
| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG
561 SGEQVEKLIK NQRESHFVSA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.VLLEENAGGEQEER.G	N	99.9	96.27	1571.7427	14	0.5	786.8790	2	25.36	11	1215	OB3609.raw	6.14E4	4	4	329	342	

K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	93.00	2242.0364	20	-0.5	1122.0249	2	32.20	11	1849	OB3609.raw	2E5	14	14	282	301	Oxidation (M)
K.SFNLDEGHALR.I	N	99.9	90.89	1257.6101	11	-0.3	629.8121	2	26.66	11	1317	OB3609.raw	6.94E5	9	9	249	259	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	90.33	1287.5731	11	-0.7	644.7934	2	29.47	11	1613	OB3609.raw	4.8E4	3	3	302	312	Deamidation (NQ)
R.IPSGFISYILNR.H	N	99.9	87.79	1378.7609	12	-0.4	690.3875	2	34.65	11	2127	OB3609.raw	8.13E5	18	18	260	271	
R.NTLEAAFNAEFNEIR.R	N	99.9	87.19	1737.8322	15	0.7	869.9240	2	33.41	11	1973	OB3609.raw	2.46E4	6	6	313	327	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	83.04	1572.7267	14	-1.6	787.3694	2	25.63	11	1236	OB3609.raw	1.65E4	2	2	329	342	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	83.01	1286.5891	11	0.1	644.3019	2	28.81	11	1540	OB3609.raw	9.08E4	9	9	302	312	
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	81.78	1572.7267	14	-0.6	787.3702	2	25.81	11	1250	OB3609.raw	1.65E4	1	1	329	342	Deamidation (NQ)
R.DGEPDLSNNFGR.L	Y	99.9	80.77	1319.5742	12	-0.2	660.7943	2	27.43	11	1388	OB3609.raw	1.39E5	9	9	394	405	
K.GTGNLELVAVR.K	N	99.9	80.54	1127.6299	11	-0.7	564.8218	2	28.24	11	1473	OB3609.raw	1.24E5	3	3	453	463	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	68.36	2243.0205	20	2.1	748.6823	3	32.77	11	1904	OB3609.raw	7.46E4	5	5	282	301	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	68.15	1288.5571	11	1.1	645.2866	2	29.84	11	1655	OB3609.raw	3.93E3	1	1	302	312	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	67.55	987.5787	9	-1.8	494.7957	2	25.17	11	1203	OB3609.raw	5.95E4	5	5	444	452	Oxidation (M)
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	66.46	2618.3162	25	-3.7	873.7761	3	28.53	11	1508	OB3609.raw	9.21E3	2	2	223	247	
K.KGSEEEDITNPINLR.D	Y	99.9	65.74	1713.8533	15	-0.7	572.2913	3	27.67	11	1412	OB3609.raw	2.41E5	14	14	379	393	
R.NNPFYFPSR.R	N	99.9	64.60	1140.5352	9	-0.8	571.2744	2	29.84	11	1654	OB3609.raw	9.43E4	9	9	166	174	
K.GSEEEDITN(+.98)PINLR.D	Y	99.9	64.27	1586.7423	14	-1.6	794.3771	2	29.37	11	1605	OB3609.raw	1.48E3	1	1	380	393	Deamidation (NQ)
R.SSDNEGVIVK.V	Y	99.9	62.96	1046.5244	10	-1.1	524.2689	2	22.41	11	1054	OB3609.raw	7.98E4	2	2	351	360	
K.GSEEEDITNPINLR.D	Y	99.9	61.70	1585.7583	14	0.4	793.8867	2	29.20	11	1584	OB3609.raw	3.3E4	4	4	380	393	
K.AMVIVVVNK.G	N	99.9	60.71	971.5837	9	-0.4	486.7990	2	27.64	11	1408	OB3609.raw	9.54E3	2	2	444	452	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	60.15	2243.0205	20	7.6	748.6865	3	32.42	11	1869	OB3609.raw	4.33E4	1	1	282	301	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFNSK.A	N	99.9	58.80	1358.6653	12	-0.6	680.3395	2	28.31	11	1481	OB3609.raw	3.54E5	4	4	432	443	Oxidation (M)
R.DGEPDLSN(+.98)NFGR.L	Y	99.9	58.17	1320.5582	12	0.2	661.2865	2	27.77	11	1423	OB3609.raw	2.76E4	2	2	394	405	Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	55.77	1287.5731	11	3.1	644.7958	2	29.27	11	1594	OB3609.raw	5.46E4	3	3	302	312	Deamidation (NQ)
K.EHVQELTK.H	Y	99.9	54.58	982.5084	8	-0.3	492.2613	2	19.06	11	872	OB3609.raw	4.1E4	3	3	364	371	
R.SSDN(+.98)EGVIVK.V	Y	99.9	51.35	1047.5084	10	-0.3	524.7614	2	23.26	11	1097	OB3609.raw	8.5E3	2	2	351	360	Deamidation (NQ)
K.ISM(+15.99)PVN(+.98)TPGQ(+.98)FEDFFPASSR.D	N	99.9	49.92	2244.0044	20	4.3	749.0120	3	32.84	11	1911	OB3609.raw	1.92E3	2	2	282	301	Oxidation (M); Deamidation (NQ)
F.NLDEGHALR.I	N	99.8	46.79	1023.5097	9	-1.4	512.7614	2	26.59	11	1311	OB3609.raw	6.96E3	4	4	251	259	
R.IPSGFISYILN(+.98)R.H	N	99.8	45.98	1379.7449	12	-0.8	690.8792	2	34.21	11	2071	OB3609.raw	3.14E5	1	1	260	271	Deamidation (NQ)
K.KGSEEEDITN(+.98)PINLR.D	Y	99.8	45.05	1714.8373	15	-4.6	572.6171	3	27.88	11	1430	OB3609.raw	0	1	1	379	393	Deamidation (NQ)
R.NNPFYFPSRR.F	N	99.8	44.49	1296.6364	10	-1.0	649.3248	2	27.78	11	1424	OB3609.raw	1.83E4	1	1	166	175	
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.6	42.58	1738.8162	15	-4.3	870.4116	2	34.02	11	2046	OB3609.raw	3.86E3	2	2	313	327	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.6	42.57	1893.9332	16	-0.1	632.3183	3	32.45	11	1873	OB3609.raw	2.57E5	5	5	313	328	
R.PNTLVLPK.H	N	99.6	41.97	880.5382	8	-0.2	441.2763	2	26.76	11	1324	OB3609.raw	4.14E4	2	2	215	222	
R.LFEVKPDK.K	N	99.5	39.98	974.5436	8	-0.4	325.8550	3	24.00	11	1139	OB3609.raw	4.68E4	2	2	406	413	
K.NP(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	98.0	37.69	2078.9688	17	-4.5	693.9937	3	31.42	11	1786	OB3609.raw	8.18E3	1	1	415	431	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.GSEEEDITNPINLRDGEPDLSNNFGR.L	Y	98.0	35.23	2887.3220	26	-4.1	963.4440	3	30.36	11	1708	OB3609.raw	4.74E3	1	1	380	405	
K.N(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	98.0	35.05	2079.9526	17	3.7	694.3274	3	31.91	11	1826	OB3609.raw	2.8E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQIEARPNTLVLPK.H	Y	96.9	33.11	1690.0140	15	-0.2	564.3452	3	28.58	11	1515	OB3609.raw	2.22E5	1	1	208	222	
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	32.04	2079.9526	17	0.8	694.3254	3	31.74	11	1811	OB3609.raw	2.53E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	31.68	2078.9688	17	0.9	1040.4926	2	31.49	11	1791	OB3609.raw	3.31E3	2	2	415	431	Oxidation (M); Carbamidomethylation
R.DGEPDLSN(+.98)N(+.98)FGR.L	Y	93.9	30.46	1321.5422	12	6.0	661.7823	2	28.51	11	1506	OB3609.raw	2.26E1	1	1	394	405	Deamidation (NQ)
R.LFEVKPDKK.N	N	93.5	29.20	1102.6385	9	0.8	368.5537	3	21.84	11	1024	OB3609.raw	9.66E3	1	1	406	414	
R.IPSGFISY.I	N	93.4	28.94	882.4487	8	1.4	442.2322	2	31.98	11	1832	OB3609.raw	1.5E3	1	1	260	267	
K.GTGNLELVAVRK.E	N	93.4	28.90	1255.7249	12	-3.5	628.8675	2	25.97	11	1261	OB3609.raw	6.28E3	2	2	453	464	

total 46 peptides

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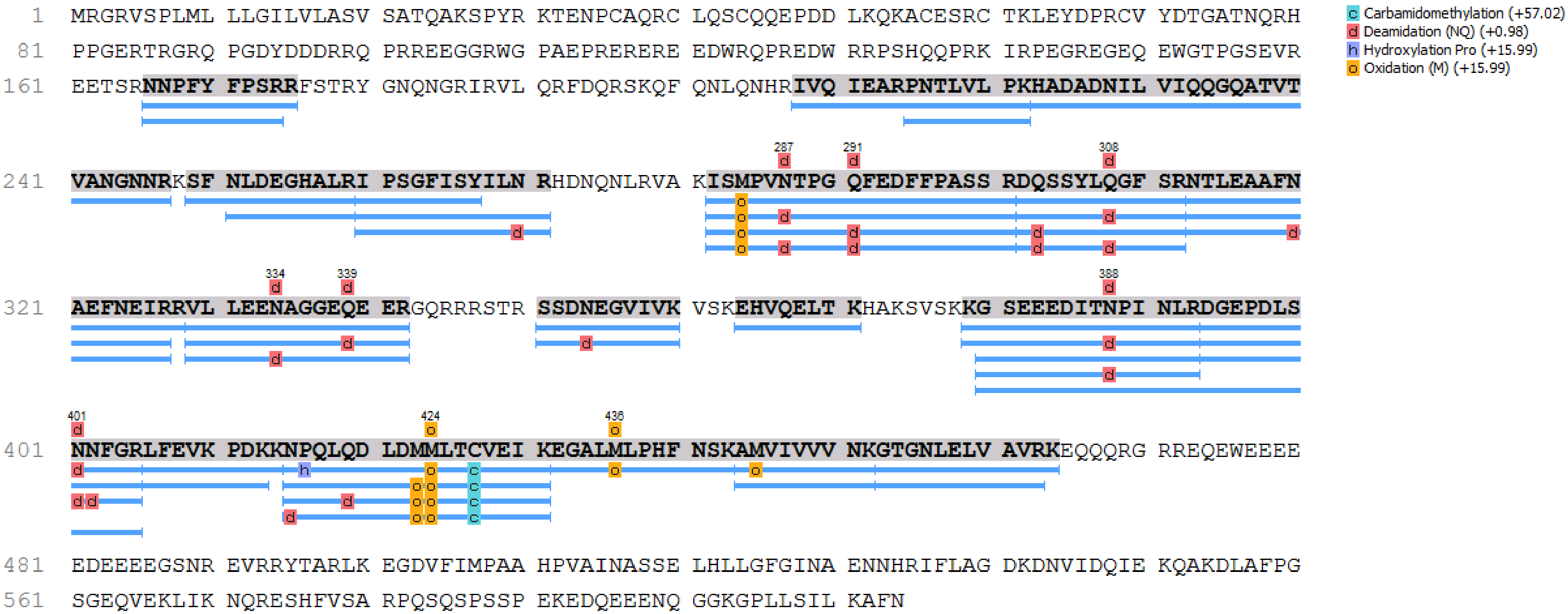
Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG
561 SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)
o Oxidation (M) (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.VLLEENAGGEQEER.G	N	99.9	96.27	1571.7427	14	0.5	786.8790	2	25.36	11	1215	OB3609.raw	6.14E4	4	4	329	342	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	93.00	2242.0364	20	-0.5	1122.0249	2	32.20	11	1849	OB3609.raw	2E5	14	14	282	301	Oxidation (M)
K.SFNLDEGHALR.I	N	99.9	90.89	1257.6101	11	-0.3	629.8121	2	26.66	11	1317	OB3609.raw	6.94E5	9	9	249	259	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	90.33	1287.5731	11	-0.7	644.7934	2	29.47	11	1613	OB3609.raw	4.8E4	3	3	302	312	Deamidation (NQ)
R.IPSGFISYILNR.H	N	99.9	87.79	1378.7609	12	-0.4	690.3875	2	34.65	11	2127	OB3609.raw	8.13E5	18	18	260	271	
R.NTLEAAFNAEFNEIR.R	N	99.9	87.19	1737.8322	15	0.7	869.9240	2	33.41	11	1973	OB3609.raw	2.46E4	6	6	313	327	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	83.04	1572.7267	14	-1.6	787.3694	2	25.63	11	1236	OB3609.raw	1.65E4	2	2	329	342	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	83.01	1286.5891	11	0.1	644.3019	2	28.81	11	1540	OB3609.raw	9.08E4	9	9	302	312	
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	81.78	1572.7267	14	-0.6	787.3702	2	25.81	11	1250	OB3609.raw	1.65E4	1	1	329	342	Deamidation (NQ)
R.DGEPDLSNNFGR.L	Y	99.9	80.77	1319.5742	12	-0.2	660.7943	2	27.43	11	1388	OB3609.raw	1.39E5	9	9	394	405	
K.GTGNLELVAVR.K	N	99.9	80.54	1127.6299	11	-0.7	564.8218	2	28.24	11	1473	OB3609.raw	1.24E5	3	3	453	463	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	68.36	2243.0205	20	2.1	748.6823	3	32.77	11	1904	OB3609.raw	7.46E4	5	5	282	301	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	68.15	1288.5571	11	1.1	645.2866	2	29.84	11	1655	OB3609.raw	3.93E3	1	1	302	312	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	67.55	987.5787	9	-1.8	494.7957	2	25.17	11	1203	OB3609.raw	5.95E4	5	5	444	452	Oxidation (M)
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	66.46	2618.3162	25	-3.7	873.7761	3	28.53	11	1508	OB3609.raw	9.21E3	2	2	223	247	
K.KGSEEEDITNPINLR.D	Y	99.9	65.74	1713.8533	15	-0.7	572.2913	3	27.67	11	1412	OB3609.raw	2.41E5	14	14	379	393	
R.NNPFYFPSR.R	N	99.9	64.60	1140.5352	9	-0.8	571.2744	2	29.84	11	1654	OB3609.raw	9.43E4	9	9	166	174	

K.GSEEEDITN(+.98)PINLR.D	Y	99.9	64.27	1586.7423	14	-1.6	794.3771	2	29.37	11	1605	OB3609.raw	1.48E3	1	1	380	393	Deamidation (NQ)
R.SSDNEGVIVK.V	Y	99.9	62.96	1046.5244	10	-1.1	524.2689	2	22.41	11	1054	OB3609.raw	7.98E4	2	2	351	360	
K.GSEEEDITNPINLR.D	Y	99.9	61.70	1585.7583	14	0.4	793.8867	2	29.20	11	1584	OB3609.raw	3.3E4	4	4	380	393	
K.AMVIVVVNK.G	N	99.9	60.71	971.5837	9	-0.4	486.7990	2	27.64	11	1408	OB3609.raw	9.54E3	2	2	444	452	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	60.15	2243.0205	20	7.6	748.6865	3	32.42	11	1869	OB3609.raw	4.33E4	1	1	282	301	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFNSK.A	N	99.9	58.80	1358.6653	12	-0.6	680.3395	2	28.31	11	1481	OB3609.raw	3.54E5	4	4	432	443	Oxidation (M)
R.DGEPDLSN(+.98)NFGR.L	Y	99.9	58.17	1320.5582	12	0.2	661.2865	2	27.77	11	1423	OB3609.raw	2.76E4	2	2	394	405	Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	55.77	1287.5731	11	3.1	644.7958	2	29.27	11	1594	OB3609.raw	5.46E4	3	3	302	312	Deamidation (NQ)
K.EHVQELTK.H	Y	99.9	54.58	982.5084	8	-0.3	492.2613	2	19.06	11	872	OB3609.raw	4.1E4	3	3	364	371	
R.SSDN(+.98)EGVIVK.V	Y	99.9	51.35	1047.5084	10	-0.3	524.7614	2	23.26	11	1097	OB3609.raw	8.5E3	2	2	351	360	Deamidation (NQ)
K.ISM(+15.99)PVN(+.98)TPGQ(+.98)FEDFFPASSR.D	N	99.9	49.92	2244.0044	20	4.3	749.0120	3	32.84	11	1911	OB3609.raw	1.92E3	2	2	282	301	Oxidation (M); Deamidation (NQ)
F.NLDEGHALR.I	N	99.8	46.79	1023.5097	9	-1.4	512.7614	2	26.59	11	1311	OB3609.raw	6.96E3	4	4	251	259	
R.IPSGFISYILN(+.98)R.H	N	99.8	45.98	1379.7449	12	-0.8	690.8792	2	34.21	11	2071	OB3609.raw	3.14E5	1	1	260	271	Deamidation (NQ)
K.KGSEEEDITN(+.98)PINLR.D	Y	99.8	45.05	1714.8373	15	-4.6	572.6171	3	27.88	11	1430	OB3609.raw	0	1	1	379	393	Deamidation (NQ)
R.NNPFYFPSRR.F	N	99.8	44.49	1296.6364	10	-1.0	649.3248	2	27.78	11	1424	OB3609.raw	1.83E4	1	1	166	175	
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.6	42.58	1738.8162	15	-4.3	870.4116	2	34.02	11	2046	OB3609.raw	3.86E3	2	2	313	327	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.6	42.57	1893.9332	16	-0.1	632.3183	3	32.45	11	1873	OB3609.raw	2.57E5	5	5	313	328	
R.PNTLVLPK.H	N	99.6	41.97	880.5382	8	-0.2	441.2763	2	26.76	11	1324	OB3609.raw	4.14E4	2	2	215	222	
R.LFEVKPDK.K	N	99.5	39.98	974.5436	8	-0.4	325.8550	3	24.00	11	1139	OB3609.raw	4.68E4	2	2	406	413	
K.NP(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	98.0	37.69	2078.9688	17	-4.5	693.9937	3	31.42	11	1786	OB3609.raw	8.18E3	1	1	415	431	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.GSEEEDITNPINLRDGEPDLSNNFGR.L	Y	98.0	35.23	2887.3220	26	-4.1	963.4440	3	30.36	11	1708	OB3609.raw	4.74E3	1	1	380	405	
K.N(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	98.0	35.05	2079.9526	17	3.7	694.3274	3	31.91	11	1826	OB3609.raw	2.8E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQIEARPNTLVLPK.H	Y	96.9	33.11	1690.0140	15	-0.2	564.3452	3	28.58	11	1515	OB3609.raw	2.22E5	1	1	208	222	
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	32.04	2079.9526	17	0.8	694.3254	3	31.74	11	1811	OB3609.raw	2.53E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	31.68	2078.9688	17	0.9	1040.4926	2	31.49	11	1791	OB3609.raw	3.31E3	2	2	415	431	Oxidation (M); Carbamidomethylation
R.DGEPDLSN(+.98)N(+.98)FGR.L	Y	93.9	30.46	1321.5422	12	6.0	661.7823	2	28.51	11	1506	OB3609.raw	2.26E1	1	1	394	405	Deamidation (NQ)
R.LFEVKPDKK.N	N	93.5	29.20	1102.6385	9	0.8	368.5537	3	21.84	11	1024	OB3609.raw	9.66E3	1	1	406	414	
R.IPSGFISY.I	N	93.4	28.94	882.4487	8	1.4	442.2322	2	31.98	11	1832	OB3609.raw	1.5E3	1	1	260	267	
K.GTGNLELVAVRK.E	N	93.4	28.90	1255.7249	12	-3.5	628.8675	2	25.97	11	1261	OB3609.raw	6.28E3	2	2	453	464	
total 46 peptides																		

B3IXL2|B3IXL2_ARAHY

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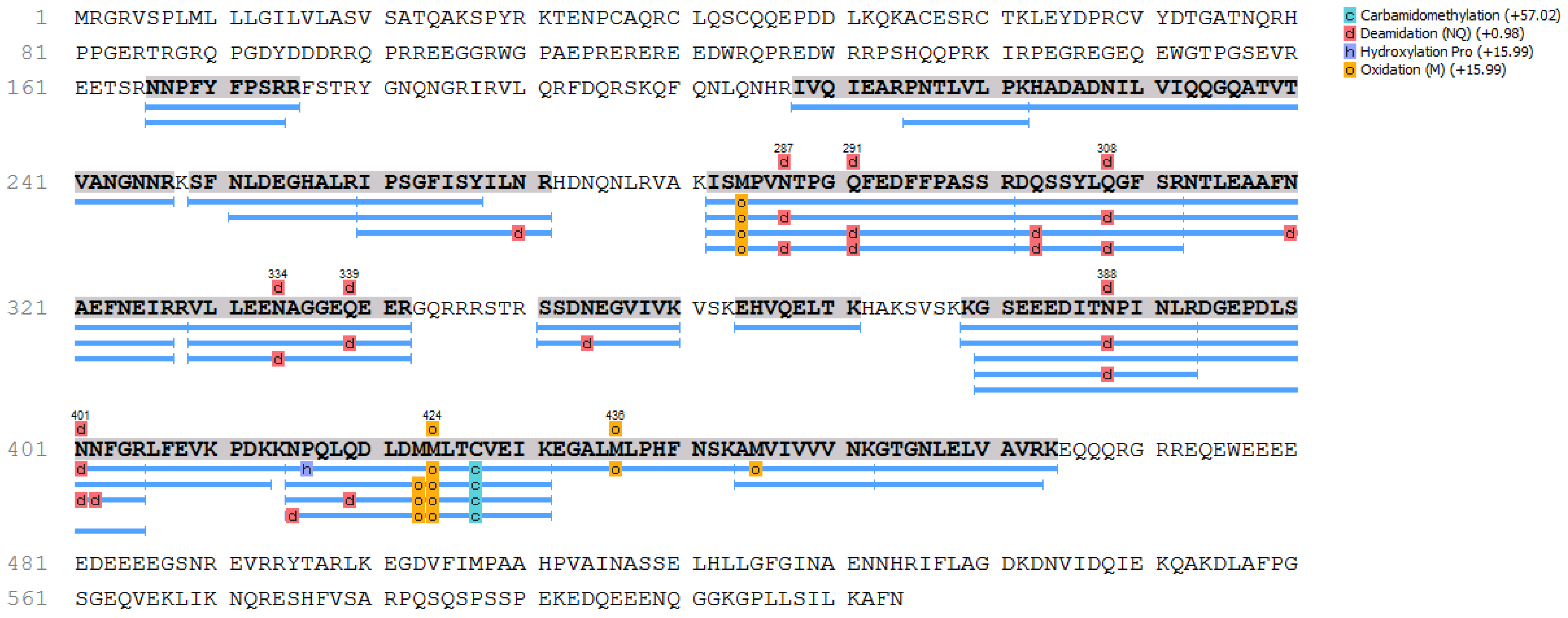
Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH

81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR

161 EETSR**NNPFY FPSRR**FSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHR**IVQ IEARPNTLVL PKHADADNIL VIQQGQATVT**

241 **VANGNNR**K**SF NLDEGHALRI PSGFISYILN R**HDNQNLRVA K**ISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN**

321 **AEFNEIRRVL LEENAGGEQE ER**GQRRRSTR **SSDNEGVIVK** VSK**EHVQELT K**HAKSVSK**KG SEEEDITNPI NLRDGEPDLS**

401 **NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRK**EQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG

561 SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.VLLEENAGGEQEER.G	N	99.9	96.27	1571.7427	14	0.5	786.8790	2	25.36	11	1215	OB3609.raw	6.14E4	4	4	329	342	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	93.00	2242.0364	20	-0.5	1122.0249	2	32.20	11	1849	OB3609.raw	2E5	14	14	282	301	Oxidation (M)
K.SFNLDEGHALR.I	N	99.9	90.89	1257.6101	11	-0.3	629.8121	2	26.66	11	1317	OB3609.raw	6.94E5	9	9	249	259	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	90.33	1287.5731	11	-0.7	644.7934	2	29.47	11	1613	OB3609.raw	4.8E4	3	3	302	312	Deamidation (NQ)
R.IPSGFISYILNR.H	N	99.9	87.79	1378.7609	12	-0.4	690.3875	2	34.65	11	2127	OB3609.raw	8.13E5	18	18	260	271	
R.NTLEAAFNAEFNEIR.R	N	99.9	87.19	1737.8322	15	0.7	869.9240	2	33.41	11	1973	OB3609.raw	2.46E4	6	6	313	327	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	83.04	1572.7267	14	-1.6	787.3694	2	25.63	11	1236	OB3609.raw	1.65E4	2	2	329	342	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	83.01	1286.5891	11	0.1	644.3019	2	28.81	11	1540	OB3609.raw	9.08E4	9	9	302	312	
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	81.78	1572.7267	14	-0.6	787.3702	2	25.81	11	1250	OB3609.raw	1.65E4	1	1	329	342	Deamidation (NQ)
R.DGEPDLSNNFGR.L	Y	99.9	80.77	1319.5742	12	-0.2	660.7943	2	27.43	11	1388	OB3609.raw	1.39E5	9	9	394	405	
K.GTGNLELVAVR.K	N	99.9	80.54	1127.6299	11	-0.7	564.8218	2	28.24	11	1473	OB3609.raw	1.24E5	3	3	453	463	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	68.36	2243.0205	20	2.1	748.6823	3	32.77	11	1904	OB3609.raw	7.46E4	5	5	282	301	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	68.15	1288.5571	11	1.1	645.2866	2	29.84	11	1655	OB3609.raw	3.93E3	1	1	302	312	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	67.55	987.5787	9	-1.8	494.7957	2	25.17	11	1203	OB3609.raw	5.95E4	5	5	444	452	Oxidation (M)
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	66.46	2618.3162	25	-3.7	873.7761	3	28.53	11	1508	OB3609.raw	9.21E3	2	2	223	247	
K.KGSEEEDITNPINLR.D	Y	99.9	65.74	1713.8533	15	-0.7	572.2913	3	27.67	11	1412	OB3609.raw	2.41E5	14	14	379	393	
R.NNPFYFPSR.R	N	99.9	64.60	1140.5352	9	-0.8	571.2744	2	29.84	11	1654	OB3609.raw	9.43E4	9	9	166	174	
K.GSEEEDITN(+.98)PINLR.D	Y	99.9	64.27	1586.7423	14	-1.6	794.3771	2	29.37	11	1605	OB3609.raw	1.48E3	1	1	380	393	Deamidation (NQ)
R.SSDNEGVIVK.V	Y	99.9	62.96	1046.5244	10	-1.1	524.2689	2	22.41	11	1054	OB3609.raw	7.98E4	2	2	351	360	
K.GSEEEDITNPINLR.D	Y	99.9	61.70	1585.7583	14	0.4	793.8867	2	29.20	11	1584	OB3609.raw	3.3E4	4	4	380	393	
K.AMVIVVVNK.G	N	99.9	60.71	971.5837	9	-0.4	486.7990	2	27.64	11	1408	OB3609.raw	9.54E3	2	2	444	452	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	60.15	2243.0205	20	7.6	748.6865	3	32.42	11	1869	OB3609.raw	4.33E4	1	1	282	301	Oxidation (M); Deamidation (NQ)

K.EGALM(+15.99)LPHFNSK.A	N	99.9	58.80	1358.6653	12	-0.6	680.3395	2	28.31	11	1481	OB3609.raw	3.54E5	4	4	432	443	Oxidation (M)
R.DGEPDLSN(+.98)NFGR.L	Y	99.9	58.17	1320.5582	12	0.2	661.2865	2	27.77	11	1423	OB3609.raw	2.76E4	2	2	394	405	Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	55.77	1287.5731	11	3.1	644.7958	2	29.27	11	1594	OB3609.raw	5.46E4	3	3	302	312	Deamidation (NQ)
K.EHVQELTK.H	Y	99.9	54.58	982.5084	8	-0.3	492.2613	2	19.06	11	872	OB3609.raw	4.1E4	3	3	364	371	
R.SSDN(+.98)EGVIVK.V	Y	99.9	51.35	1047.5084	10	-0.3	524.7614	2	23.26	11	1097	OB3609.raw	8.5E3	2	2	351	360	Deamidation (NQ)
K.ISM(+15.99)PVN(+.98)TPGQ(+.98)FEDFFPASSR.D	N	99.9	49.92	2244.0044	20	4.3	749.0120	3	32.84	11	1911	OB3609.raw	1.92E3	2	2	282	301	Oxidation (M); Deamidation (NQ)
F.NLDEGHALR.I	N	99.8	46.79	1023.5097	9	-1.4	512.7614	2	26.59	11	1311	OB3609.raw	6.96E3	4	4	251	259	
R.IPSGFISYILN(+.98)R.H	N	99.8	45.98	1379.7449	12	-0.8	690.8792	2	34.21	11	2071	OB3609.raw	3.14E5	1	1	260	271	Deamidation (NQ)
K.KGSEEEDITN(+.98)PINLR.D	Y	99.8	45.05	1714.8373	15	-4.6	572.6171	3	27.88	11	1430	OB3609.raw	0	1	1	379	393	Deamidation (NQ)
R.NNPFYFPSRR.F	N	99.8	44.49	1296.6364	10	-1.0	649.3248	2	27.78	11	1424	OB3609.raw	1.83E4	1	1	166	175	
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.6	42.58	1738.8162	15	-4.3	870.4116	2	34.02	11	2046	OB3609.raw	3.86E3	2	2	313	327	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.6	42.57	1893.9332	16	-0.1	632.3183	3	32.45	11	1873	OB3609.raw	2.57E5	5	5	313	328	
R.PNTLVLPK.H	N	99.6	41.97	880.5382	8	-0.2	441.2763	2	26.76	11	1324	OB3609.raw	4.14E4	2	2	215	222	
R.LFEVKPDK.K	N	99.5	39.98	974.5436	8	-0.4	325.8550	3	24.00	11	1139	OB3609.raw	4.68E4	2	2	406	413	
K.NP(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	98.0	37.69	2078.9688	17	-4.5	693.9937	3	31.42	11	1786	OB3609.raw	8.18E3	1	1	415	431	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.GSEEEDITNPINLRDGEPDLSNNFGR.L	Y	98.0	35.23	2887.3220	26	-4.1	963.4440	3	30.36	11	1708	OB3609.raw	4.74E3	1	1	380	405	
K.N(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	98.0	35.05	2079.9526	17	3.7	694.3274	3	31.91	11	1826	OB3609.raw	2.8E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
R.IVQIEARPNTLVLPK.H	Y	96.9	33.11	1690.0140	15	-0.2	564.3452	3	28.58	11	1515	OB3609.raw	2.22E5	1	1	208	222	
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	32.04	2079.9526	17	0.8	694.3254	3	31.74	11	1811	OB3609.raw	2.53E3	1	1	415	431	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	31.68	2078.9688	17	0.9	1040.4926	2	31.49	11	1791	OB3609.raw	3.31E3	2	2	415	431	Oxidation (M); Carbamidomethylation
R.DGEPDLSN(+.98)N(+.98)FGR.L	Y	93.9	30.46	1321.5422	12	6.0	661.7823	2	28.51	11	1506	OB3609.raw	2.26E1	1	1	394	405	Deamidation (NQ)
R.LFEVKPDKK.N	N	93.5	29.20	1102.6385	9	0.8	368.5537	3	21.84	11	1024	OB3609.raw	9.66E3	1	1	406	414	
R.IPSGFISY.I	N	93.4	28.94	882.4487	8	1.4	442.2322	2	31.98	11	1832	OB3609.raw	1.5E3	1	1	260	267	
K.GTGNLELVAVRK.E	N	93.4	28.90	1255.7249	12	-3.5	628.8675	2	25.97	11	1261	OB3609.raw	6.28E3	2	2	453	464	
total 46 peptides																		

N1NG13|N1NG13_ARAHY

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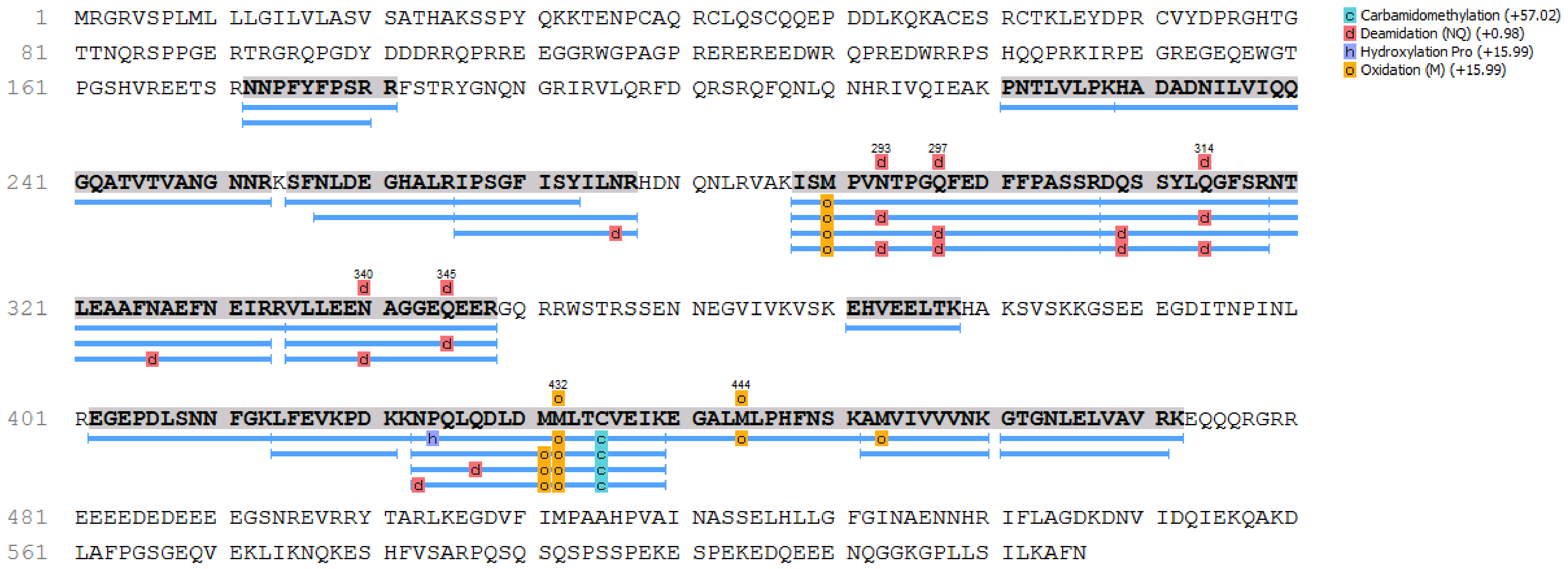
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.VLLEENAGGEQEER.G	N	99.9	96.27	1571.7427	14	0.5	786.8790	2	25.36	11	1215	OB3609.raw	6.14E4	4	4	335	348	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	93.00	2242.0364	20	-0.5	1122.0249	2	32.20	11	1849	OB3609.raw	2E5	14	14	288	307	Oxidation (M)
K.SFNLDEGHALR.I	N	99.9	90.89	1257.6101	11	-0.3	629.8121	2	26.66	11	1317	OB3609.raw	6.94E5	9	9	255	265	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	90.33	1287.5731	11	-0.7	644.7934	2	29.47	11	1613	OB3609.raw	4.8E4	3	3	308	318	Deamidation (NQ)
R.IPSGFISYILNR.H	N	99.9	87.79	1378.7609	12	-0.4	690.3875	2	34.65	11	2127	OB3609.raw	8.13E5	18	18	266	277	
R.NTLEAAFNAEFNEIR.R	N	99.9	87.19	1737.8322	15	0.7	869.9240	2	33.41	11	1973	OB3609.raw	2.46E4	6	6	319	333	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	83.04	1572.7267	14	-1.6	787.3694	2	25.63	11	1236	OB3609.raw	1.65E4	2	2	335	348	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	83.01	1286.5891	11	0.1	644.3019	2	28.81	11	1540	OB3609.raw	9.08E4	9	9	308	318	
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	81.78	1572.7267	14	-0.6	787.3702	2	25.81	11	1250	OB3609.raw	1.65E4	1	1	335	348	Deamidation (NQ)
K.GTGNLELVAVR.K	N	99.9	80.54	1127.6299	11	-0.7	564.8218	2	28.24	11	1473	OB3609.raw	1.24E5	3	3	461	471	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	68.36	2243.0205	20	2.1	748.6823	3	32.77	11	1904	OB3609.raw	7.46E4	5	5	288	307	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	68.15	1288.5571	11	1.1	645.2866	2	29.84	11	1655	OB3609.raw	3.93E3	1	1	308	318	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	67.55	987.5787	9	-1.8	494.7957	2	25.17	11	1203	OB3609.raw	5.95E4	5	5	452	460	Oxidation (M)
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	66.46	2618.3162	25	-3.7	873.7761	3	28.53	11	1508	OB3609.raw	9.21E3	2	2	229	253	
R.NNPFYFPSR.R	N	99.9	64.60	1140.5352	9	-0.8	571.2744	2	29.84	11	1654	OB3609.raw	9.43E4	9	9	172	180	
K.AMVIVVVNK.G	N	99.9	60.71	971.5837	9	-0.4	486.7990	2	27.64	11	1408	OB3609.raw	9.54E3	2	2	452	460	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	60.15	2243.0205	20	7.6	748.6865	3	32.42	11	1869	OB3609.raw	4.33E4	1	1	288	307	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFNSK.A	N	99.9	58.80	1358.6653	12	-0.6	680.3395	2	28.31	11	1481	OB3609.raw	3.54E5	4	4	440	451	Oxidation (M)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	55.77	1287.5731	11	3.1	644.7958	2	29.27	11	1594	OB3609.raw	5.46E4	3	3	308	318	Deamidation (NQ)
K.ISM(+15.99)PVN(+.98)TPGQ(+.98)FEDFFPASSR.D	N	99.9	49.92	2244.0044	20	4.3	749.0120	3	32.84	11	1911	OB3609.raw	1.92E3	2	2	288	307	Oxidation (M); Deamidation (NQ)
F.NLDEGHALR.I	N	99.8	46.79	1023.5097	9	-1.4	512.7614	2	26.59	11	1311	OB3609.raw	6.96E3	4	4	257	265	
R.IPSGFISYILN(+.98)R.H	N	99.8	45.98	1379.7449	12	-0.8	690.8792	2	34.21	11	2071	OB3609.raw	3.14E5	1	1	266	277	Deamidation (NQ)
R.NNPFYFPSRR.F	N	99.8	44.49	1296.6364	10	-1.0	649.3248	2	27.78	11	1424	OB3609.raw	1.83E4	1	1	172	181	
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.6	42.58	1738.8162	15	-4.3	870.4116	2	34.02	11	2046	OB3609.raw	3.86E3	2	2	319	333	Deamidation (NQ)

R.NTLEAAFNAEFNEIRR.V	N	99.6	42.57	1893.9332	16	-0.1	632.3183	3	32.45	11	1873	OB3609.raw	2.57E5	5	5	319	334	
K.PNTLVLPK.H	N	99.6	41.97	880.5382	8	-0.2	441.2763	2	26.76	11	1324	OB3609.raw	4.14E4	2	2	221	228	
K.LFEVKPDK.K	N	99.5	39.98	974.5436	8	-0.4	325.8550	3	24.00	11	1139	OB3609.raw	4.68E4	2	2	414	421	
R.EGEPDLSNNFGK.L	Y	99.4	38.94	1305.5836	12	-0.8	653.7986	2	26.40	11	1295	OB3609.raw	2.93E3	1	1	402	413	
K.NP(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	98.0	37.69	2078.9688	17	-4.5	693.9937	3	31.42	11	1786	OB3609.raw	8.18E3	1	1	423	439	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.N(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	98.0	35.05	2079.9526	17	3.7	694.3274	3	31.91	11	1826	OB3609.raw	2.8E3	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	32.04	2079.9526	17	0.8	694.3254	3	31.74	11	1811	OB3609.raw	2.53E3	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	31.68	2078.9688	17	0.9	1040.4926	2	31.49	11	1791	OB3609.raw	3.31E3	2	2	423	439	Oxidation (M); Carbamidomethylation
K.EHVEELTK.H	Y	93.5	29.32	983.4924	8	0.2	492.7536	2	19.95	11	924	OB3609.raw	7.17E3	1	1	371	378	
K.LFEVKPDKK.N	N	93.5	29.20	1102.6385	9	0.8	368.5537	3	21.84	11	1024	OB3609.raw	9.66E3	1	1	414	422	
R.IPSGFISY.I	N	93.4	28.94	882.4487	8	1.4	442.2322	2	31.98	11	1832	OB3609.raw	1.5E3	1	1	266	273	
K.GTGNLELVAVRK.E	N	93.4	28.90	1255.7249	12	-3.5	628.8675	2	25.97	11	1261	OB3609.raw	6.28E3	2	2	461	472	
total 36 peptides																		

sp|P43238|ALL12_ARAHY

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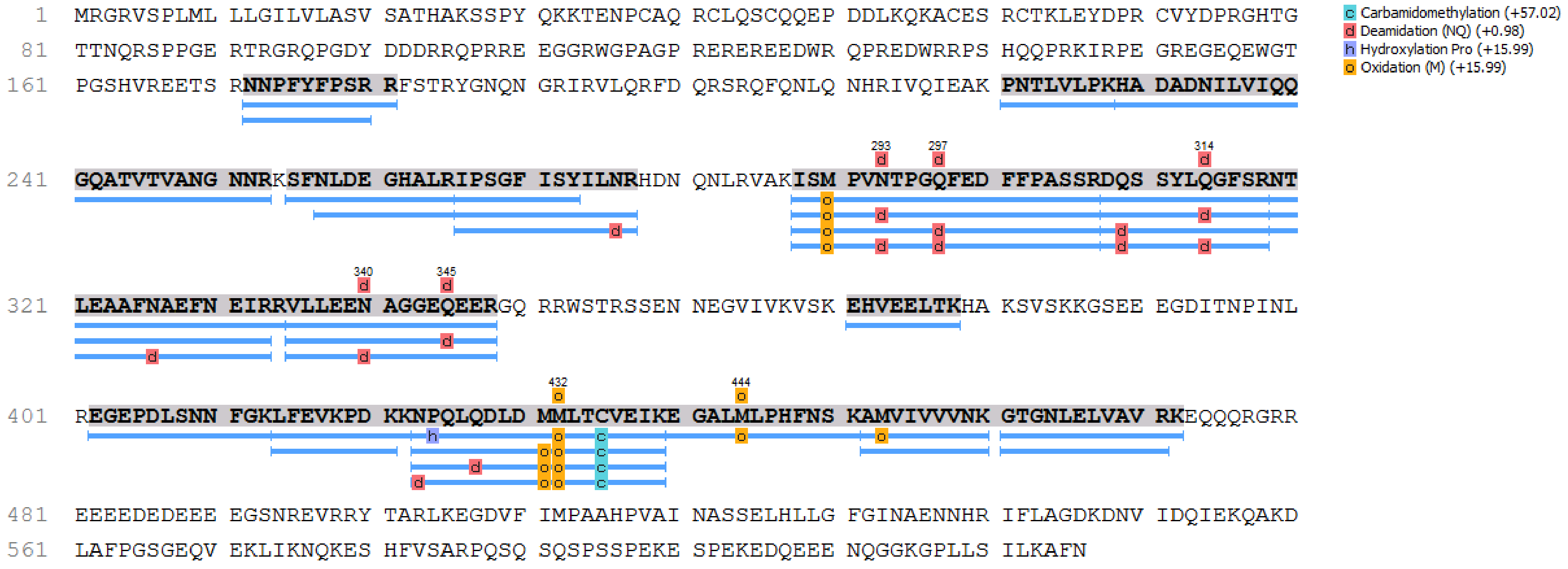
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS R**NNPFYFPSR R**FSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK **PNTLVLPKHA DADNILVIQQ**
241 **GQATVTVANG NNR**K**SFNLDE GHALRIPSGF ISYILNR**HDN QNLRVAK**ISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT**
321 **LEAAFNAEFN EIRRVLLEEN AGGEQEER**GQ RRWSTRSSEN NEGVIVKVSK **EHVEELTK**HA KSVSKKGSEE EGDITNPINL
401 R**EGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RK**EQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.VLLEENAGGEQEER.G	N	99.9	96.27	1571.7427	14	0.5	786.8790	2	25.36	11	1215	OB3609.raw	6.14E4	4	4	335	348	
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	93.00	2242.0364	20	-0.5	1122.0249	2	32.20	11	1849	OB3609.raw	2E5	14	14	288	307	Oxidation (M)
K.SFNLDEGHALR.I	N	99.9	90.89	1257.6101	11	-0.3	629.8121	2	26.66	11	1317	OB3609.raw	6.94E5	9	9	255	265	

R.DQ(+.98)SSYLQGFSR.N	N	99.9	90.33	1287.5731	11	-0.7	644.7934	2	29.47	11	1613	OB3609.raw	4.8E4	3	3	308	318	Deamidation (NQ)
R.IPSGFISYILNR.H	N	99.9	87.79	1378.7609	12	-0.4	690.3875	2	34.65	11	2127	OB3609.raw	8.13E5	18	18	266	277	
R.NTLEAAFNAEFNEIR.R	N	99.9	87.19	1737.8322	15	0.7	869.9240	2	33.41	11	1973	OB3609.raw	2.46E4	6	6	319	333	
R.VLLEENAGGEQ(+.98)EER.G	N	99.9	83.04	1572.7267	14	-1.6	787.3694	2	25.63	11	1236	OB3609.raw	1.65E4	2	2	335	348	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	83.01	1286.5891	11	0.1	644.3019	2	28.81	11	1540	OB3609.raw	9.08E4	9	9	308	318	
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	81.78	1572.7267	14	-0.6	787.3702	2	25.81	11	1250	OB3609.raw	1.65E4	1	1	335	348	Deamidation (NQ)
K.GTGNLELVAVR.K	N	99.9	80.54	1127.6299	11	-0.7	564.8218	2	28.24	11	1473	OB3609.raw	1.24E5	3	3	461	471	
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	68.36	2243.0205	20	2.1	748.6823	3	32.77	11	1904	OB3609.raw	7.46E4	5	5	288	307	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	68.15	1288.5571	11	1.1	645.2866	2	29.84	11	1655	OB3609.raw	3.93E3	1	1	308	318	Deamidation (NQ)
K.AM(+15.99)VIVVVNK.G	N	99.9	67.55	987.5787	9	-1.8	494.7957	2	25.17	11	1203	OB3609.raw	5.95E4	5	5	452	460	Oxidation (M)
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	66.46	2618.3162	25	-3.7	873.7761	3	28.53	11	1508	OB3609.raw	9.21E3	2	2	229	253	
R.NNPFYFPSR.R	N	99.9	64.60	1140.5352	9	-0.8	571.2744	2	29.84	11	1654	OB3609.raw	9.43E4	9	9	172	180	
K.AMVIVVVNK.G	N	99.9	60.71	971.5837	9	-0.4	486.7990	2	27.64	11	1408	OB3609.raw	9.54E3	2	2	452	460	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	60.15	2243.0205	20	7.6	748.6865	3	32.42	11	1869	OB3609.raw	4.33E4	1	1	288	307	Oxidation (M); Deamidation (NQ)
K.EGALM(+15.99)LPHFNSK.A	N	99.9	58.80	1358.6653	12	-0.6	680.3395	2	28.31	11	1481	OB3609.raw	3.54E5	4	4	440	451	Oxidation (M)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	55.77	1287.5731	11	3.1	644.7958	2	29.27	11	1594	OB3609.raw	5.46E4	3	3	308	318	Deamidation (NQ)
K.ISM(+15.99)PVN(+.98)TPGQ(+.98)FEDFFPASSR.D	N	99.9	49.92	2244.0044	20	4.3	749.0120	3	32.84	11	1911	OB3609.raw	1.92E3	2	2	288	307	Oxidation (M); Deamidation (NQ)
F.NLDEGHALR.I	N	99.8	46.79	1023.5097	9	-1.4	512.7614	2	26.59	11	1311	OB3609.raw	6.96E3	4	4	257	265	
R.IPSGFISYILN(+.98)R.H	N	99.8	45.98	1379.7449	12	-0.8	690.8792	2	34.21	11	2071	OB3609.raw	3.14E5	1	1	266	277	Deamidation (NQ)
R.NNPFYFPSRR.F	N	99.8	44.49	1296.6364	10	-1.0	649.3248	2	27.78	11	1424	OB3609.raw	1.83E4	1	1	172	181	
R.NTLEAAFN(+.98)AEFNEIR.R	N	99.6	42.58	1738.8162	15	-4.3	870.4116	2	34.02	11	2046	OB3609.raw	3.86E3	2	2	319	333	Deamidation (NQ)
R.NTLEAAFNAEFNEIRR.V	N	99.6	42.57	1893.9332	16	-0.1	632.3183	3	32.45	11	1873	OB3609.raw	2.57E5	5	5	319	334	
K.PNTLVLPK.H	N	99.6	41.97	880.5382	8	-0.2	441.2763	2	26.76	11	1324	OB3609.raw	4.14E4	2	2	221	228	
K.LFEVKPDK.K	N	99.5	39.98	974.5436	8	-0.4	325.8550	3	24.00	11	1139	OB3609.raw	4.68E4	2	2	414	421	
R.EGEPDLSNNFGK.L	Y	99.4	38.94	1305.5836	12	-0.8	653.7986	2	26.40	11	1295	OB3609.raw	2.93E3	1	1	402	413	
K.NP(+15.99)QLQDLDMM(+15.99)LTC(+57.02)VEIK.E	N	98.0	37.69	2078.9688	17	-4.5	693.9937	3	31.42	11	1786	OB3609.raw	8.18E3	1	1	423	439	Hydroxylation Pro; Oxidation (M); Carbamidomethylation
K.N(+.98)PQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	98.0	35.05	2079.9526	17	3.7	694.3274	3	31.91	11	1826	OB3609.raw	2.8E3	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQ(+.98)DLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	32.04	2079.9526	17	0.8	694.3254	3	31.74	11	1811	OB3609.raw	2.53E3	1	1	423	439	Deamidation (NQ); Oxidation (M); Carbamidomethylation
K.NPQLQDLDM(+15.99)M(+15.99)LTC(+57.02)VEIK.E	N	96.6	31.68	2078.9688	17	0.9	1040.4926	2	31.49	11	1791	OB3609.raw	3.31E3	2	2	423	439	Oxidation (M); Carbamidomethylation
K.EHVEELTK.H	Y	93.5	29.32	983.4924	8	0.2	492.7536	2	19.95	11	924	OB3609.raw	7.17E3	1	1	371	378	
K.LFEVKPDKK.N	N	93.5	29.20	1102.6385	9	0.8	368.5537	3	21.84	11	1024	OB3609.raw	9.66E3	1	1	414	422	
R.IPSGFISY.I	N	93.4	28.94	882.4487	8	1.4	442.2322	2	31.98	11	1832	OB3609.raw	1.5E3	1	1	266	273	
K.GTGNLELVAVRK.E	N	93.4	28.90	1255.7249	12	-3.5	628.8675	2	25.97	11	1261	OB3609.raw	6.28E3	2	2	461	472	
total 36 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELNL LILR**WLGLSA**

401 **EYGNLYR**NAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.WLGLSAEYGNLYR.N	Y	99.9	49.35	1540.7673	13	0.4	771.3912	2	32.49	11	1877	OB3609.raw	1.35E3	1	1	395	407	
R.SPDIYNPQAGSLK.T	Y	98.0	35.56	1388.6936	13	-0.5	695.3537	2	26.85	11	1335	OB3609.raw	1.38E3	1	1	371	383	
total 2 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE

321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELNL LILR**WLGLSA**

401 **EYGNLYR**NAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.WLGLSAEYGNLYR.N	Y	99.9	49.35	1540.7673	13	0.4	771.3912	2	32.49	11	1877	OB3609.raw	1.35E3	1	1	395	407	
R.SPDIYNPQAGSLK.T	Y	98.0	35.56	1388.6936	13	-0.5	695.3537	2	26.85	11	1335	OB3609.raw	1.38E3	1	1	371	383	
total 2 peptides																		

Q8LKN1|Q8LKN1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELQL NLLILR**WLGL**
401 **SAEYGNLYR**N ALFVPHYNTN AHSIIYALRG RAHVQVVDSN GDRVFDEELQ EGHVLVVPQN FAVAGKSQSE NFEYVAFKTD
481 SRPSIANLAG ENSFIDNLPE EVVANSYGLP REQARQLKNN NPFKFFVPPS EQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.WLGLSAEYGNLYR.N	Y	99.9	49.35	1540.7673	13	0.4	771.3912	2	32.49	11	1877	OB3609.raw	1.35E3	1	1	397	409	
R.SPDIYNPQAGSLK.T	Y	98.0	35.56	1388.6936	13	-0.5	695.3537	2	26.85	11	1335	OB3609.raw	1.38E3	1	1	371	383	
total 2 peptides																		

A1DZF0|A1DZF0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNR**SPDIYNP QAGSLK**TANE LNLLILR**WLG LSAEYGNLYR**
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA
481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
R.WLGLSAEYGNLYR.N	Y	99.9	49.35	1540.7673	13	0.4	771.3912	2	32.49	11	1877	OB3609.raw	1.35E3	1	1	388	400	
R.SPDIYNPQAGSLK.T	Y	98.0	35.56	1388.6936	13	-0.5	695.3537	2	26.85	11	1335	OB3609.raw	1.38E3	1	1	364	376	
total 2 peptides																		

Q2KQ45|Q2KQ45_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GMGGVGKTTI ARAVFETVRS RFEVTCFLAD VREQCEKKDI VRSQKQLLDQ VNINSNAVHN KYDGRTIIQN SLRLKKVLLV
81 LDDVNHEKLL ENLAGEQDWF GPGSRIIITT RDVEVLKEQA VLETYMVEGL VESEAFNLFC LKAFKQAAEP TEGFLDLSEE
161 VVK**HSGGLPL ALK**VLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 11	#Spec	#Spec Sample 11	Start	End	PTM
K.HSGGLPLALK.V	Y	96.6	31.65	991.5814	10	-0.9	496.7975	2	49.98	11	3105	OB3609.raw	0	1	1	164	173	
total 1 peptides																		

Peptide List

Summary

1. Notes

Spot E from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

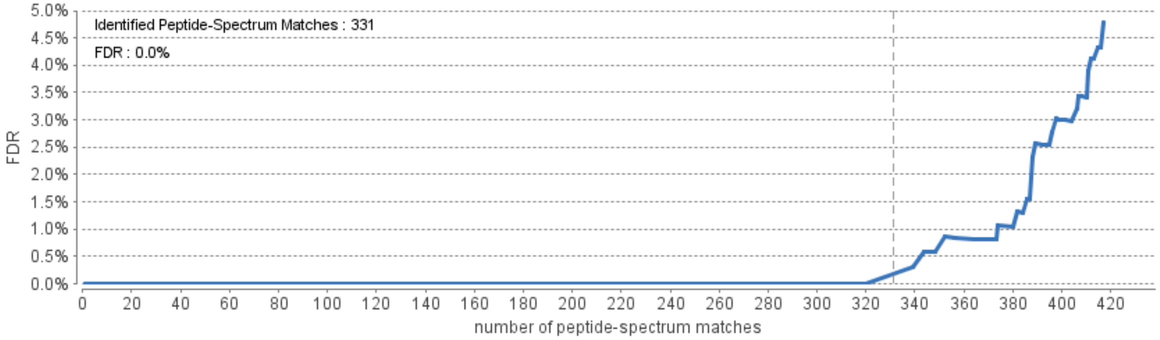
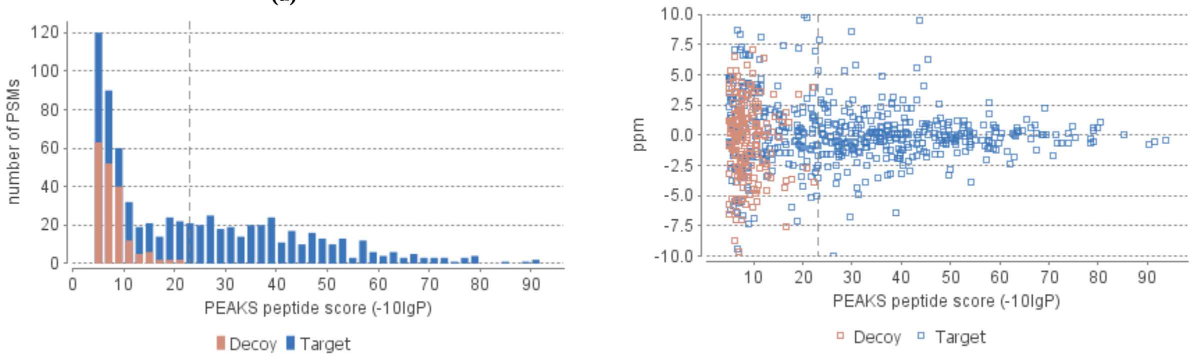


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

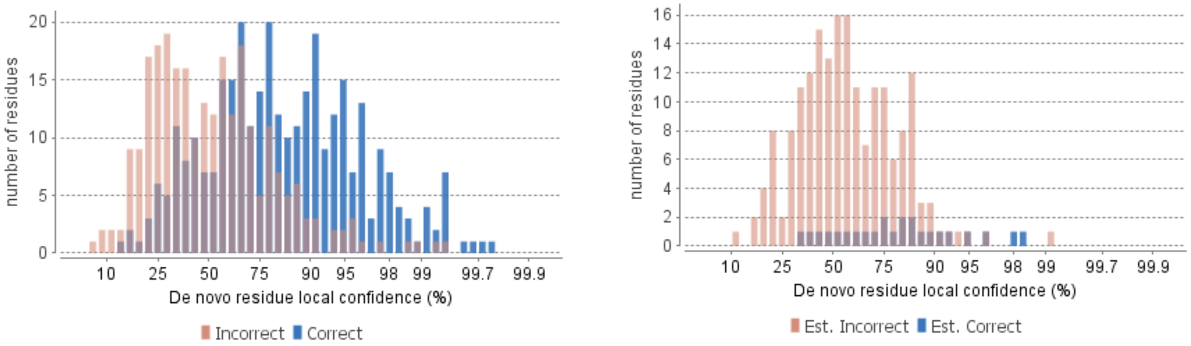


Table 1. Statistics of data.

# of MS scans	2995
# of MS/MS scans	2454

Table 2. Result filtration parameters.

Peptide -10lgP	≥23
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	309
Peptide sequences	129
Protein groups	3
Proteins	7
Proteins (#Unique Peptides)	1 (>2); 0 (=2); 6 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	24

Table 4. PTM profile.

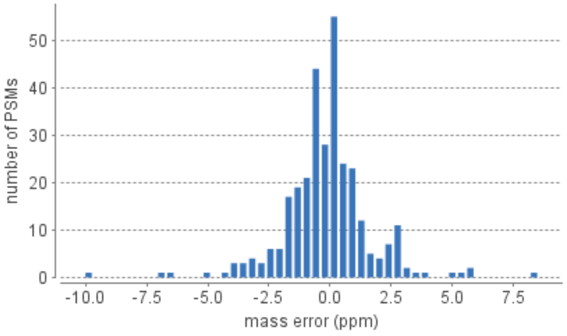
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	79	60.36	1.14E4	1000.00
Deamidation	.98	NQ	65	67.07	1.91E5	25.67
HydPro	15.99	P	19	52.70	2.19E4	12.33
Oxidation	15.99	M	8	49.72	3.28E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm. ?

(a)

(b)



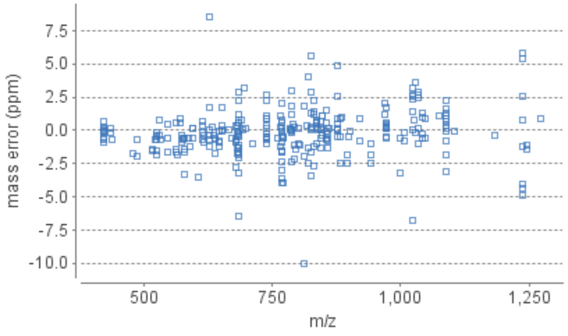


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 13	96	33	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3611.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 13	Area Sample 13	#Peptides	#Unique	#Spec Sample 13	PTM	Avg. Mass	Description
1	13	Q9FZ11|Q9FZ11_ARAHY	99.2	216.57	36	36	4.26E4	16	1	122	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1

1	5	Q5I6T2|Q5I6T2_ARAHY	99.2	216.57	35	35	4.26E4	16	1	122	Y	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
1	15	Q647H3|Q647H3_ARAHY	99.2	216.57	35	35	4.26E4	16	1	122	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
3	7	Q647H4|Q647H4_ARAHY	99.2	215.35	46	46	3.91E4	17	3	117	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
9	41	Q6IWG5|Q6IWG5_ARAHY	79.4	52.07	5	5	3.03E4	1	1	1	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
9	42	Q0GM57|Q0GM57_ARAHY	79.4	52.07	5	5	3.03E4	1	1	1	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
9	45	E5G077|E5G077_ARAHY	79.4	52.07	5	5	3.03E4	1	1	1	Y	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
total 7 proteins													

Q9FZ11|Q9FZ11_ARAHY

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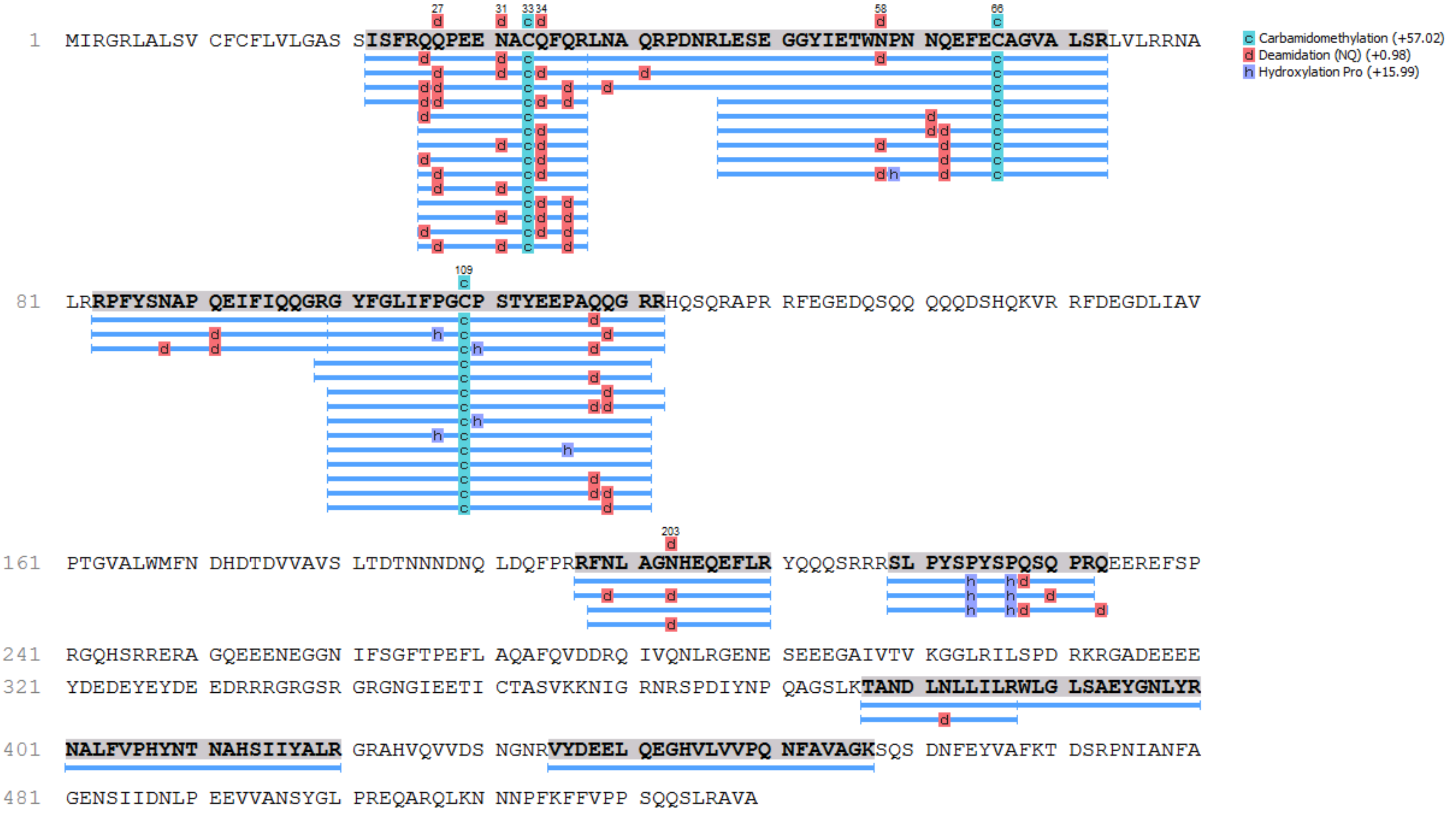
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA

81 LRRPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV

161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP

241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE

321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFKT DSRPNIANFA

481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	N	99.9	79.99	2050.0383	17	0.5	684.3538	3	29.81	13	1689	OB3611.raw	7.8E5	17	17	83	99	
R.WLGLSAEYGNLYR.N	N	99.9	79.06	1540.7673	13	-0.6	771.3905	2	32.83	13	2086	OB3611.raw	2.57E4	3	3	388	400	
R.FNLAGNHEQEFLR.Y	N	99.9	71.43	1573.7637	13	0.0	787.8891	2	28.61	13	1552	OB3611.raw	4.13E5	14	14	198	210	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	67.07	2051.0225	17	0.8	684.6820	3	30.37	13	1763	OB3611.raw	1.91E5	3	3	83	99	Deamidation (NQ)
R.FNLAGN(+.98)HEQEFLR.Y	N	99.9	62.08	1574.7477	13	-2.3	788.3793	2	28.98	13	1597	OB3611.raw	8.63E3	1	1	198	210	Deamidation (NQ)
K.TANDLNLLILR.W	Y	99.9	59.23	1254.7296	11	-1.2	628.3713	2	32.74	13	2074	OB3611.raw	3.9E4	5	5	377	387	

R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	56.66	2052.0063	17	0.8	685.0099	3	30.65	13	1799	OB3611.raw	0	2	2	83	99	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	54.71	2473.1372	22	0.2	825.3865	3	34.51	13	2306	OB3611.raw	1.45E5	6	6	100	121	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	53.34	1534.6470	12	0.1	768.3309	2	24.52	13	1218	OB3611.raw	1.07E4	2	2	26	37	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	52.70	2489.1321	22	1.2	830.7189	3	33.95	13	2234	OB3611.raw	3.14E4	2	2	100	121	Hydroxylation Pro; Carbamidomethylation
R.RFN(+.98)LAGN(+.98)HEQEFLR.Y	N	99.9	49.75	1731.8329	14	-3.3	578.2830	3	28.46	13	1533	OB3611.raw	2.86E4	1	1	197	210	Deamidation (NQ)
R.LESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	99.9	47.89	3070.3613	27	1.4	1024.4625	3	32.82	13	2085	OB3611.raw	4.73E4	2	2	47	73	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	47.61	2474.1211	22	2.6	1238.0710	2	34.27	13	2277	OB3611.raw	4.51E4	8	8	100	121	Carbamidomethylation; Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	47.14	2540.2910	23	1.1	847.7719	3	30.89	13	1831	OB3611.raw	6.43E4	3	3	435	457	
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.90	1535.6311	12	-1.6	768.8216	2	25.29	13	1271	OB3611.raw	1.07E4	1	1	26	37	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPR.Q	N	99.8	44.65	1638.7524	14	4.0	820.3868	2	26.38	13	1360	OB3611.raw	1.14E4	1	1	219	232	Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.8	43.73	2489.1321	22	-1.1	1245.5719	2	33.91	13	2230	OB3611.raw	3.14E4	4	4	100	121	Carbamidomethylation; Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.28	1535.6311	12	-1.7	768.8215	2	25.07	13	1256	OB3611.raw	1.07E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	41.71	1536.6151	12	-3.0	769.3126	2	25.56	13	1290	OB3611.raw	6.46E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.LNAQ(+.98)RPDNRLESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.7	40.31	4134.9087	36	2.9	1034.7374	4	31.25	13	1878	OB3611.raw	7.55E4	3	3	38	73	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	N	99.7	40.12	2630.2224	23	-0.5	877.7477	3	33.08	13	2118	OB3611.raw	2.09E5	3	3	100	122	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	99.7	40.11	1638.7524	14	-1.3	820.3824	2	26.29	13	1351	OB3611.raw	1.14E4	1	1	219	232	Hydroxylation Pro; Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.20	1535.6311	12	0.0	768.8228	2	25.12	13	1259	OB3611.raw	1.07E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNPNN(+.98)Q(+.98)EFEC(+57.02)AGVALSR.L	N	99.5	38.31	3071.3455	27	3.2	1024.7924	3	33.03	13	2112	OB3611.raw	2.63E4	1	1	47	73	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.5	38.03	3069.3774	27	2.7	1024.1359	3	32.49	13	2041	OB3611.raw	1.53E5	2	2	47	73	Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	99.5	37.22	2646.2173	23	0.8	883.0804	3	32.48	13	2040	OB3611.raw	4.26E4	1	1	100	122	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.5	37.03	1535.6311	12	-0.9	768.8221	2	24.87	13	1243	OB3611.raw	1.07E4	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	N	99.5	36.97	2489.1321	22	-1.2	830.7170	3	33.98	13	2238	OB3611.raw	2.19E4	1	1	100	121	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.4	36.50	2631.2063	23	0.1	878.0761	3	33.48	13	2172	OB3611.raw	2.18E4	2	2	100	122	Carbamidomethylation; Deamidation (NQ)
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.4	36.09	2630.2224	23	4.8	877.7523	3	32.47	13	2038	OB3611.raw	2.09E5	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.3	35.69	3071.3455	27	2.4	1024.7915	3	33.35	13	2154	OB3611.raw	2.63E4	1	1	47	73	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.0	35.12	1534.6470	12	-3.6	768.3280	2	24.18	13	1195	OB3611.raw	9.87E3	2	2	26	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	98.6	34.07	2630.2224	23	0.4	877.7485	3	32.73	13	2073	OB3611.raw	2.09E5	1	1	100	122	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	34.03	1536.6151	12	-0.9	769.3141	2	25.68	13	1298	OB3611.raw	6.46E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNRLESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	98.6	34.01	4134.9087	36	0.2	1034.7346	4	30.94	13	1838	OB3611.raw	7.55E4	1	1	38	73	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.6	33.55	2038.9166	16	-1.8	680.6450	3	27.18	13	1425	OB3611.raw	1.01E4	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	98.0	32.34	1536.6151	12	2.0	769.3164	2	25.81	13	1307	OB3611.raw	6.46E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	98.0	31.89	2629.2383	23	0.0	877.4200	3	32.42	13	2031	OB3611.raw	2.18E4	1	1	99	121	Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	98.0	31.32	2039.9006	16	-1.3	680.9733	3	27.50	13	1452	OB3611.raw	1.66E4	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	98.0	31.26	2475.1052	22	-4.9	1238.5538	2	34.92	13	2356	OB3611.raw	1.22E4	2	2	100	121	Carbamidomethylation; Deamidation (NQ)
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	98.0	31.07	1535.6311	12	-2.3	768.8210	2	25.25	13	1268	OB3611.raw	1.07E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
K.TANDLN(+.98)LLILR.W	Y	97.9	29.84	1255.7136	11	8.5	628.8694	2	33.27	13	2145	OB3611.raw	3.56E3	1	1	377	387	Deamidation (NQ)
R.LESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	96.6	29.48	3070.3613	27	-6.8	1024.4541	3	33.54	13	2180	OB3611.raw	0	1	1	47	73	Deamidation (NQ);

																		Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	96.5	29.28	2474.1211	22	2.6	1238.0710	2	35.21	13	2391	OB3611.raw	5.75E3	1	1	100	121	Carbamidomethylation; Deamidation (NQ)
R.RFNLAGNHEQEFLR.Y	N	96.4	28.36	1729.8647	14	-0.7	577.6285	3	27.43	13	1446	OB3611.raw	5.99E4	2	2	197	210	
R.NALFVPHYNTNAHSIIYALR.G	N	96.4	28.12	2313.2019	20	-1.4	579.3069	4	31.34	13	1890	OB3611.raw	7.24E4	2	2	401	420	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPRQ(+.98).E	N	96.3	27.88	1767.7950	15	1.0	884.9057	2	26.38	13	1359	OB3611.raw	2.62E3	1	1	219	233	Hydroxylation Pro; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.3	27.36	2040.8846	16	0.3	681.3024	3	27.95	13	1489	OB3611.raw	4.46E3	1	1	22	37	Deamidation (NQ); Carbamidomethylation
S.ISFRQQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	92.1	25.74	2039.9006	16	-0.1	680.9741	3	27.38	13	1442	OB3611.raw	1.66E4	1	1	22	37	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)P(+15.99)NNQ(+.98)EFEC(+57.02)AGVALSR.L	N	91.8	25.25	3087.3403	27	3.6	1030.1244	3	33.61	13	2189	OB3611.raw	1.5E3	1	1	47	73	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.LN(+.98)AQRPDNRLESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	90.0	23.76	4134.9087	36	2.6	1034.7372	4	31.12	13	1862	OB3611.raw	7.55E4	1	1	38	73	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	N	89.7	23.01	2646.2173	23	-2.5	883.0775	3	32.64	13	2061	OB3611.raw	4.26E4	1	1	100	122	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
total 52 peptides																		

Q5I6T2|Q5I6T2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	N	99.9	79.99	2050.0383	17	0.5	684.3538	3	29.81	13	1689	OB3611.raw	7.8E5	17	17	82	98	
R.WLGLSAEYGNLYR.N	N	99.9	79.06	1540.7673	13	-0.6	771.3905	2	32.83	13	2086	OB3611.raw	2.57E4	3	3	389	401	
R.FNLAGNHEQEFLR.Y	N	99.9	71.43	1573.7637	13	0.0	787.8891	2	28.61	13	1552	OB3611.raw	4.13E5	14	14	196	208	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	67.07	2051.0225	17	0.8	684.6820	3	30.37	13	1763	OB3611.raw	1.91E5	3	3	82	98	Deamidation (NQ)
R.FNLAGN(+.98)HEQEFLR.Y	N	99.9	62.08	1574.7477	13	-2.3	788.3793	2	28.98	13	1597	OB3611.raw	8.63E3	1	1	196	208	Deamidation (NQ)
K.TANDLNLLILR.W	Y	99.9	59.23	1254.7296	11	-1.2	628.3713	2	32.74	13	2074	OB3611.raw	3.9E4	5	5	378	388	
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	56.66	2052.0063	17	0.8	685.0099	3	30.65	13	1799	OB3611.raw	0	2	2	82	98	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	54.71	2473.1372	22	0.2	825.3865	3	34.51	13	2306	OB3611.raw	1.45E5	6	6	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	53.34	1534.6470	12	0.1	768.3309	2	24.52	13	1218	OB3611.raw	1.07E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	52.70	2489.1321	22	1.2	830.7189	3	33.95	13	2234	OB3611.raw	3.14E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.RFN(+.98)LAGN(+.98)HEQEFLR.Y	N	99.9	49.75	1731.8329	14	-3.3	578.2830	3	28.46	13	1533	OB3611.raw	2.86E4	1	1	195	208	Deamidation (NQ)
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	99.9	47.89	3070.3613	27	1.4	1024.4625	3	32.82	13	2085	OB3611.raw	4.73E4	2	2	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	47.61	2474.1211	22	2.6	1238.0710	2	34.27	13	2277	OB3611.raw	4.51E4	8	8	99	120	Carbamidomethylation; Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	47.14	2540.2910	23	1.1	847.7719	3	30.89	13	1831	OB3611.raw	6.43E4	3	3	436	458	
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.90	1535.6311	12	-1.6	768.8216	2	25.29	13	1271	OB3611.raw	1.07E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPR.Q	N	99.8	44.65	1638.7524	14	4.0	820.3868	2	26.38	13	1360	OB3611.raw	1.14E4	1	1	220	233	Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.8	43.73	2489.1321	22	-1.1	1245.5719	2	33.91	13	2230	OB3611.raw	3.14E4	4	4	99	120	Carbamidomethylation; Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.28	1535.6311	12	-1.7	768.8215	2	25.07	13	1256	OB3611.raw	1.07E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	41.71	1536.6151	12	-3.0	769.3126	2	25.56	13	1290	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LNAQ(+.98)RPDNRIESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.7	40.31	4134.9087	36	2.9	1034.7374	4	31.25	13	1878	OB3611.raw	7.55E4	3	3	37	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.S	N	99.7	40.12	2630.2224	23	-0.5	877.7477	3	33.08	13	2118	OB3611.raw	2.09E5	3	3	99	121	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	99.7	40.11	1638.7524	14	-1.3	820.3824	2	26.29	13	1351	OB3611.raw	1.14E4	1	1	220	233	Hydroxylation Pro; Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.20	1535.6311	12	0.0	768.8228	2	25.12	13	1259	OB3611.raw	1.07E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)Q(+.98)EFEC(+57.02)AGVALSR.L	N	99.5	38.31	3071.3455	27	3.2	1024.7924	3	33.03	13	2112	OB3611.raw	2.63E4	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.5	38.03	3069.3774	27	2.7	1024.1359	3	32.49	13	2041	OB3611.raw	1.53E5	2	2	46	72	Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GRR.S	N	99.5	37.22	2646.2173	23	0.8	883.0804	3	32.48	13	2040	OB3611.raw	4.26E4	1	1	99	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.5	37.03	1535.6311	12	-0.9	768.8221	2	24.87	13	1243	OB3611.raw	1.07E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	N	99.5	36.97	2489.1321	22	-1.2	830.7170	3	33.98	13	2238	OB3611.raw	2.19E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.S	N	99.4	36.50	2631.2063	23	0.1	878.0761	3	33.48	13	2172	OB3611.raw	2.18E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.4	36.09	2630.2224	23	4.8	877.7523	3	32.47	13	2038	OB3611.raw	2.09E5	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.3	35.69	3071.3455	27	2.4	1024.7915	3	33.35	13	2154	OB3611.raw	2.63E4	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.0	35.12	1534.6470	12	-3.6	768.3280	2	24.18	13	1195	OB3611.raw	9.87E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.S	N	98.6	34.07	2630.2224	23	0.4	877.7485	3	32.73	13	2073	OB3611.raw	2.09E5	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	34.03	1536.6151	12	-0.9	769.3141	2	25.68	13	1298	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNRIESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	98.6	34.01	4134.9087	36	0.2	1034.7346	4	30.94	13	1838	OB3611.raw	7.55E4	1	1	37	72	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.6	33.55	2038.9166	16	-1.8	680.6450	3	27.18	13	1425	OB3611.raw	1.01E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation

R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	98.0	32.34	1536.6151	12	2.0	769.3164	2	25.81	13	1307	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	98.0	31.89	2629.2383	23	0.0	877.4200	3	32.42	13	2031	OB3611.raw	2.18E4	1	1	98	120	Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	98.0	31.32	2039.9006	16	-1.3	680.9733	3	27.50	13	1452	OB3611.raw	1.66E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	98.0	31.26	2475.1052	22	-4.9	1238.5538	2	34.92	13	2356	OB3611.raw	1.22E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	98.0	31.07	1535.6311	12	-2.3	768.8210	2	25.25	13	1268	OB3611.raw	1.07E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TANDLN(+.98)LLILR.W	Y	97.9	29.84	1255.7136	11	8.5	628.8694	2	33.27	13	2145	OB3611.raw	3.56E3	1	1	378	388	Deamidation (NQ)
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	96.6	29.48	3070.3613	27	-6.8	1024.4541	3	33.54	13	2180	OB3611.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	96.5	29.28	2474.1211	22	2.6	1238.0710	2	35.21	13	2391	OB3611.raw	5.75E3	1	1	99	120	Carbamidomethylation; Deamidation (NQ)
R.RFNLAGNHEQEFLR.Y	N	96.4	28.36	1729.8647	14	-0.7	577.6285	3	27.43	13	1446	OB3611.raw	5.99E4	2	2	195	208	
R.NALFVPHYNTNAHSIIYALR.G	N	96.4	28.12	2313.2019	20	-1.4	579.3069	4	31.34	13	1890	OB3611.raw	7.24E4	2	2	402	421	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPRQ(+.98).E	N	96.3	27.88	1767.7950	15	1.0	884.9057	2	26.38	13	1359	OB3611.raw	2.62E3	1	1	220	234	Hydroxylation Pro; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.3	27.36	2040.8846	16	0.3	681.3024	3	27.95	13	1489	OB3611.raw	4.46E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	92.1	25.74	2039.9006	16	-0.1	680.9741	3	27.38	13	1442	OB3611.raw	1.66E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)P(+15.99)NNQ(+.98)EFEC(+57.02)AGVALSR.L	N	91.8	25.25	3087.3403	27	3.6	1030.1244	3	33.61	13	2189	OB3611.raw	1.5E3	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.LN(+.98)AQRPDNRIESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	90.0	23.76	4134.9087	36	2.6	1034.7372	4	31.12	13	1862	OB3611.raw	7.55E4	1	1	37	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.S	N	89.7	23.01	2646.2173	23	-2.5	883.0775	3	32.64	13	2061	OB3611.raw	4.26E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
total 52 peptides																		

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS **ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SR**LVLRRNAL

81 R**RPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR R**HQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP

161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPR**RFNLA GNHEQEFLR**Y QQQSRRR**SLP YSPYSPQSQP RQ**EEREFSPR

241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD

321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLK**TANDLN LLILRWLGLS**

401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFKTDS

481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	N	99.9	79.99	2050.0383	17	0.5	684.3538	3	29.81	13	1689	OB3611.raw	7.8E5	17	17	82	98	
R.WLGLSAEYGNLYR.N	N	99.9	79.06	1540.7673	13	-0.6	771.3905	2	32.83	13	2086	OB3611.raw	2.57E4	3	3	396	408	
R.FNLAGNHEQEFLR.Y	N	99.9	71.43	1573.7637	13	0.0	787.8891	2	28.61	13	1552	OB3611.raw	4.13E5	14	14	197	209	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	67.07	2051.0225	17	0.8	684.6820	3	30.37	13	1763	OB3611.raw	1.91E5	3	3	82	98	Deamidation (NQ)
R.FNLAGN(+.98)HEQEFLR.Y	N	99.9	62.08	1574.7477	13	-2.3	788.3793	2	28.98	13	1597	OB3611.raw	8.63E3	1	1	197	209	Deamidation (NQ)
K.TANDLNLLILR.W	Y	99.9	59.23	1254.7296	11	-1.2	628.3713	2	32.74	13	2074	OB3611.raw	3.9E4	5	5	385	395	
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	56.66	2052.0063	17	0.8	685.0099	3	30.65	13	1799	OB3611.raw	0	2	2	82	98	Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	54.71	2473.1372	22	0.2	825.3865	3	34.51	13	2306	OB3611.raw	1.45E5	6	6	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	53.34	1534.6470	12	0.1	768.3309	2	24.52	13	1218	OB3611.raw	1.07E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	52.70	2489.1321	22	1.2	830.7189	3	33.95	13	2234	OB3611.raw	3.14E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.RFN(+.98)LAGN(+.98)HEQEFLR.Y	N	99.9	49.75	1731.8329	14	-3.3	578.2830	3	28.46	13	1533	OB3611.raw	2.86E4	1	1	196	209	Deamidation (NQ)
R.LESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	99.9	47.89	3070.3613	27	1.4	1024.4625	3	32.82	13	2085	OB3611.raw	4.73E4	2	2	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	47.61	2474.1211	22	2.6	1238.0710	2	34.27	13	2277	OB3611.raw	4.51E4	8	8	99	120	Carbamidomethylation; Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	47.14	2540.2910	23	1.1	847.7719	3	30.89	13	1831	OB3611.raw	6.43E4	3	3	443	465	
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.90	1535.6311	12	-1.6	768.8216	2	25.29	13	1271	OB3611.raw	1.07E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)

R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPR.Q	N	99.8	44.65	1638.7524	14	4.0	820.3868	2	26.38	13	1360	OB3611.raw	1.14E4	1	1	218	231	Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.8	43.73	2489.1321	22	-1.1	1245.5719	2	33.91	13	2230	OB3611.raw	3.14E4	4	4	99	120	Carbamidomethylation; Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.28	1535.6311	12	-1.7	768.8215	2	25.07	13	1256	OB3611.raw	1.07E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	41.71	1536.6151	12	-3.0	769.3126	2	25.56	13	1290	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LNAQ(+.98)RPDNRLESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.7	40.31	4134.9087	36	2.9	1034.7374	4	31.25	13	1878	OB3611.raw	7.55E4	3	3	37	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	N	99.7	40.12	2630.2224	23	-0.5	877.7477	3	33.08	13	2118	OB3611.raw	2.09E5	3	3	99	121	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	99.7	40.11	1638.7524	14	-1.3	820.3824	2	26.29	13	1351	OB3611.raw	1.14E4	1	1	218	231	Hydroxylation Pro; Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.20	1535.6311	12	0.0	768.8228	2	25.12	13	1259	OB3611.raw	1.07E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNPNN(+.98)Q(+.98)EFEC(+57.02)AGVALSR.L	N	99.5	38.31	3071.3455	27	3.2	1024.7924	3	33.03	13	2112	OB3611.raw	2.63E4	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.5	38.03	3069.3774	27	2.7	1024.1359	3	32.49	13	2041	OB3611.raw	1.53E5	2	2	46	72	Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	99.5	37.22	2646.2173	23	0.8	883.0804	3	32.48	13	2040	OB3611.raw	4.26E4	1	1	99	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.5	37.03	1535.6311	12	-0.9	768.8221	2	24.87	13	1243	OB3611.raw	1.07E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	N	99.5	36.97	2489.1321	22	-1.2	830.7170	3	33.98	13	2238	OB3611.raw	2.19E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.4	36.50	2631.2063	23	0.1	878.0761	3	33.48	13	2172	OB3611.raw	2.18E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.4	36.09	2630.2224	23	4.8	877.7523	3	32.47	13	2038	OB3611.raw	2.09E5	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
R.LESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.3	35.69	3071.3455	27	2.4	1024.7915	3	33.35	13	2154	OB3611.raw	2.63E4	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.0	35.12	1534.6470	12	-3.6	768.3280	2	24.18	13	1195	OB3611.raw	9.87E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	98.6	34.07	2630.2224	23	0.4	877.7485	3	32.73	13	2073	OB3611.raw	2.09E5	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	34.03	1536.6151	12	-0.9	769.3141	2	25.68	13	1298	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNRLESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	98.6	34.01	4134.9087	36	0.2	1034.7346	4	30.94	13	1838	OB3611.raw	7.55E4	1	1	37	72	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.6	33.55	2038.9166	16	-1.8	680.6450	3	27.18	13	1425	OB3611.raw	1.01E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	98.0	32.34	1536.6151	12	2.0	769.3164	2	25.81	13	1307	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	98.0	31.89	2629.2383	23	0.0	877.4200	3	32.42	13	2031	OB3611.raw	2.18E4	1	1	98	120	Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	98.0	31.32	2039.9006	16	-1.3	680.9733	3	27.50	13	1452	OB3611.raw	1.66E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	98.0	31.26	2475.1052	22	-4.9	1238.5538	2	34.92	13	2356	OB3611.raw	1.22E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	98.0	31.07	1535.6311	12	-2.3	768.8210	2	25.25	13	1268	OB3611.raw	1.07E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TANDLN(+.98)LLILR.W	Y	97.9	29.84	1255.7136	11	8.5	628.8694	2	33.27	13	2145	OB3611.raw	3.56E3	1	1	385	395	Deamidation (NQ)
R.LESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	96.6	29.48	3070.3613	27	-6.8	1024.4541	3	33.54	13	2180	OB3611.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	96.5	29.28	2474.1211	22	2.6	1238.0710	2	35.21	13	2391	OB3611.raw	5.75E3	1	1	99	120	Carbamidomethylation; Deamidation (NQ)
R.RFNLAGNHEQEFLR.Y	N	96.4	28.36	1729.8647	14	-0.7	577.6285	3	27.43	13	1446	OB3611.raw	5.99E4	2	2	196	209	
R.NALFVPHYNTNAHSIIYALR.G	N	96.4	28.12	2313.2019	20	-1.4	579.3069	4	31.34	13	1890	OB3611.raw	7.24E4	2	2	409	428	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPRQ(+.98).E	N	96.3	27.88	1767.7950	15	1.0	884.9057	2	26.38	13	1359	OB3611.raw	2.62E3	1	1	218	232	Hydroxylation Pro; Deamidation (NQ)
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.3	27.36	2040.8846	16	0.3	681.3024	3	27.95	13	1489	OB3611.raw	4.46E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
S.ISFRQQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	92.1	25.74	2039.9006	16	-0.1	680.9741	3	27.38	13	1442	OB3611.raw	1.66E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.LESEGGYIETWN(+.98)P(+15.99)NNQ(+.98)EFEC(+57.02)AGVALSR.L	N	91.8	25.25	3087.3403	27	3.6	1030.1244	3	33.61	13	2189	OB3611.raw	1.5E3	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.LN(+.98)AQRPDNRLESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	90.0	23.76	4134.9087	36	2.6	1034.7372	4	31.12	13	1862	OB3611.raw	7.55E4	1	1	37	72	Deamidation (NQ);

																		Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	N	89.7	23.01	2646.2173	23	-2.5	883.0775	3	32.64	13	2061	OB3611.raw	4.26E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
total 52 peptides																		

Q647H4|Q647H4_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	N	99.9	79.99	2050.0383	17	0.5	684.3538	3	29.81	13	1689	OB3611.raw	7.8E5	17	17	82	98	
R.WLGLSAEYGNLYR.N	N	99.9	79.06	1540.7673	13	-0.6	771.3905	2	32.83	13	2086	OB3611.raw	2.57E4	3	3	395	407	
R.FNLAGNHEQEFLR.Y	N	99.9	71.43	1573.7637	13	0.0	787.8891	2	28.61	13	1552	OB3611.raw	4.13E5	14	14	196	208	
R.RPFYSNAPQ(+.98)EIFIQQGR.G	N	99.9	67.07	2051.0225	17	0.8	684.6820	3	30.37	13	1763	OB3611.raw	1.91E5	3	3	82	98	Deamidation (NQ)
R.FNLAGN(+.98)HEQEFLR.Y	N	99.9	62.08	1574.7477	13	-2.3	788.3793	2	28.98	13	1597	OB3611.raw	8.63E3	1	1	196	208	Deamidation (NQ)
R.RPFYSN(+.98)APQ(+.98)EIFIQQGR.G	N	99.9	56.66	2052.0063	17	0.8	685.0099	3	30.65	13	1799	OB3611.raw	0	2	2	82	98	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	54.88	1268.7452	11	-0.4	635.3796	2	32.91	13	2097	OB3611.raw	1.64E4	1	1	384	394	
R.GYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	99.9	54.71	2473.1372	22	0.2	825.3865	3	34.51	13	2306	OB3611.raw	1.45E5	6	6	99	120	Carbamidomethylation
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.9	53.34	1534.6470	12	0.1	768.3309	2	24.52	13	1218	OB3611.raw	1.07E4	2	2	25	36	Carbamidomethylation; Deamidation (NQ)

R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQGR.R	N	99.9	52.70	2489.1321	22	1.2	830.7189	3	33.95	13	2234	OB3611.raw	3.14E4	2	2	99	120	Hydroxylation Pro; Carbamidomethylation
R.RFN(+.98)LAGN(+.98)HEQEFLR.Y	N	99.9	49.75	1731.8329	14	-3.3	578.2830	3	28.46	13	1533	OB3611.raw	2.86E4	1	1	195	208	Deamidation (NQ)
R.IESEGGYIETWNPNN(+.98)QEFEC(+57.02)AGVALSR.L	N	99.9	47.89	3070.3613	27	1.4	1024.4625	3	32.82	13	2085	OB3611.raw	4.73E4	2	2	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.9	47.61	2474.1211	22	2.6	1238.0710	2	34.27	13	2277	OB3611.raw	4.51E4	8	8	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.9	46.90	1535.6311	12	-1.6	768.8216	2	25.29	13	1271	OB3611.raw	1.07E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQQGR.R	N	99.8	43.73	2489.1321	22	-1.1	1245.5719	2	33.91	13	2230	OB3611.raw	3.14E4	4	4	99	120	Carbamidomethylation; Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.8	43.28	1535.6311	12	-1.7	768.8215	2	25.07	13	1256	OB3611.raw	1.07E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.7	41.71	1536.6151	12	-3.0	769.3126	2	25.56	13	1290	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LNAQ(+.98)RPDNRIESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.7	40.31	4134.9087	36	2.9	1034.7374	4	31.25	13	1878	OB3611.raw	7.55E4	3	3	37	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGRR.H	N	99.7	40.12	2630.2224	23	-0.5	877.7477	3	33.08	13	2118	OB3611.raw	2.09E5	3	3	99	121	Carbamidomethylation; Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QTQPK.Q	Y	99.7	39.63	1623.7780	14	-2.0	812.8947	2	25.75	13	1303	OB3611.raw	5.91E3	1	1	217	230	Hydroxylation Pro
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.7	39.20	1535.6311	12	0.0	768.8228	2	25.12	13	1259	OB3611.raw	1.07E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNN(+.98)Q(+.98)EFEC(+57.02)AGVALSR.L	N	99.5	38.31	3071.3455	27	3.2	1024.7924	3	33.03	13	2112	OB3611.raw	2.63E4	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	99.5	38.03	3069.3774	27	2.7	1024.1359	3	32.49	13	2041	OB3611.raw	1.53E5	2	2	46	72	Carbamidomethylation
R.GYFGLIFP(+15.99)GC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	99.5	37.22	2646.2173	23	0.8	883.0804	3	32.48	13	2040	OB3611.raw	4.26E4	1	1	99	121	Hydroxylation Pro; Carbamidomethylation; Deamidation (NQ)
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	99.5	37.03	1535.6311	12	-0.9	768.8221	2	24.87	13	1243	OB3611.raw	1.07E4	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEP(+15.99)AQQGR.R	N	99.5	36.97	2489.1321	22	-1.2	830.7170	3	33.98	13	2238	OB3611.raw	2.19E4	1	1	99	120	Carbamidomethylation; Hydroxylation Pro
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GRR.H	N	99.4	36.50	2631.2063	23	0.1	878.0761	3	33.48	13	2172	OB3611.raw	2.18E4	2	2	99	121	Carbamidomethylation; Deamidation (NQ)
G.RGYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)QGR.R	N	99.4	36.09	2630.2224	23	4.8	877.7523	3	32.47	13	2038	OB3611.raw	2.09E5	1	1	98	120	Carbamidomethylation; Deamidation (NQ)
R.IESEGGYIETWN(+.98)PNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	99.3	35.69	3071.3455	27	2.4	1024.7915	3	33.35	13	2154	OB3611.raw	2.63E4	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.0	35.12	1534.6470	12	-3.6	768.3280	2	24.18	13	1195	OB3611.raw	9.87E3	2	2	25	36	Deamidation (NQ); Carbamidomethylation
R.SLPYSP(+15.99)YSP(+15.99)QTQ(+.98)PKQ(+.98)E.D	Y	98.9	34.81	1882.8472	16	-1.9	942.4291	2	26.55	13	1371	OB3611.raw	1.16E4	2	2	217	232	Hydroxylation Pro; Deamidation (NQ)
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GRR.H	N	98.6	34.07	2630.2224	23	0.4	877.7485	3	32.73	13	2073	OB3611.raw	2.09E5	1	1	99	121	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	34.03	1536.6151	12	-0.9	769.3141	2	25.68	13	1298	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.LNAQRPDNRIESEGGYIETWN(+.98)PNNQEFEC(+57.02)AGVALSR.L	N	98.6	34.01	4134.9087	36	0.2	1034.7346	4	30.94	13	1838	OB3611.raw	7.55E4	1	1	37	72	Deamidation (NQ); Carbamidomethylation
S.ISFRQ(+.98)QPEEN(+.98)AC(+57.02)QFQR.L	N	98.6	33.55	2038.9166	16	-1.8	680.6450	3	27.18	13	1425	OB3611.raw	1.01E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.SLPYSP(+15.99)YSP(+15.99)QTQ(+.98)PKQE.D	Y	98.5	33.01	1881.8632	16	-1.1	941.9379	2	26.11	13	1338	OB3611.raw	7.83E3	1	1	217	232	Hydroxylation Pro; Deamidation (NQ)
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	98.0	32.34	1536.6151	12	2.0	769.3164	2	25.81	13	1307	OB3611.raw	6.46E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
G.RGYFGLIFPGC(+57.02)PSTYEEPAQQGR.R	N	98.0	31.89	2629.2383	23	0.0	877.4200	3	32.42	13	2031	OB3611.raw	2.18E4	1	1	98	120	Carbamidomethylation
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)QFQ(+.98)R.L	N	98.0	31.32	2039.9006	16	-1.3	680.9733	3	27.50	13	1452	OB3611.raw	1.66E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQ(+.98)Q(+.98)GR.R	N	98.0	31.26	2475.1052	22	-4.9	1238.5538	2	34.92	13	2356	OB3611.raw	1.22E4	2	2	99	120	Carbamidomethylation; Deamidation (NQ)
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	98.0	31.07	1535.6311	12	-2.3	768.8210	2	25.25	13	1268	OB3611.raw	1.07E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWNPNNQ(+.98)EFEC(+57.02)AGVALSR.L	N	96.6	29.48	3070.3613	27	-6.8	1024.4541	3	33.54	13	2180	OB3611.raw	0	1	1	46	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)PSTYEEPAQQ(+.98)GR.R	N	96.5	29.28	2474.1211	22	2.6	1238.0710	2	35.21	13	2391	OB3611.raw	5.75E3	1	1	99	120	Carbamidomethylation; Deamidation (NQ)
R.RFNLAGNHEQEFLR.Y	N	96.4	28.36	1729.8647	14	-0.7	577.6285	3	27.43	13	1446	OB3611.raw	5.99E4	2	2	195	208	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	96.4	28.13	3544.7434	33	-0.3	1182.5880	3	35.18	13	2387	OB3611.raw	1.36E3	1	1	477	509	

R.NALFVPHYNTNAHSIIYALR.G	N	96.4	28.12	2313.2019	20	-1.4	579.3069	4	31.34	13	1890	OB3611.raw	7.24E4	2	2	408	427	
S.ISFRQ(+.98)Q(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	96.3	27.36	2040.8846	16	0.3	681.3024	3	27.95	13	1489	OB3611.raw	4.46E3	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.FDEGDLIAVP(+15.99)TGVAFWMYN(+.98)DHDTDVVAVSLTDTNNNDNQLDQFPR.R	Y	95.0	26.53	5085.2886	45	0.9	1272.3306	4	35.95	13	2462	OB3611.raw	1.38E4	1	1	150	194	Hydroxylation Pro; Deamidation (NQ)
S.ISFRQQ(+.98)PEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	92.1	25.74	2039.9006	16	-0.1	680.9741	3	27.38	13	1442	OB3611.raw	1.66E4	1	1	21	36	Deamidation (NQ); Carbamidomethylation
R.IESEGGYIETWN(+.98)P(+15.99)NNQ(+.98)EFEC(+57.02)AGVALSR.L	N	91.8	25.25	3087.3403	27	3.6	1030.1244	3	33.61	13	2189	OB3611.raw	1.5E3	1	1	46	72	Deamidation (NQ); Hydroxylation Pro; Carbamidomethylation
R.LN(+.98)AQRPDNRIESEGGYIETWNPNNQEFEC(+57.02)AGVALSR.L	N	90.0	23.76	4134.9087	36	2.6	1034.7372	4	31.12	13	1862	OB3611.raw	7.55E4	1	1	37	72	Deamidation (NQ); Carbamidomethylation
R.GYFGLIFPGC(+57.02)P(+15.99)STYEEPAQ(+.98)QGRR.H	N	89.7	23.01	2646.2173	23	-2.5	883.0775	3	32.64	13	2061	OB3611.raw	4.26E4	1	1	99	121	Carbamidomethylation; Hydroxylation Pro; Deamidation (NQ)
total 52 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNR**IESEGGY IETWNPNNQE FQCAGVALSR** TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN

401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	98.7	34.50	3084.3882	27	-0.2	1029.1365	3	33.21	13	2136	OB3611.raw	3.03E4	1	1	44	70	Hydroxylation Pro; Carbamidomethylation
total 1 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNR**IESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY

481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

c Carbamidomethylation (+57.02)
h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	98.7	34.50	3084.3882	27	-0.2	1029.1365	3	33.21	13	2136	OB3611.raw	3.03E4	1	1	46	72	Hydroxylation Pro; Carbamidomethylation

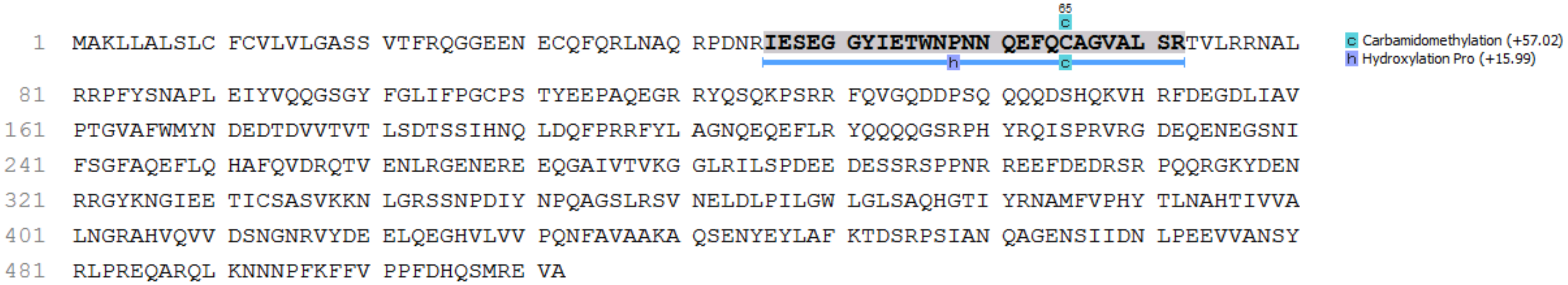
total 1 peptides

E5G077|E5G077_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



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  1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL
 81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 13	#Spec	#Spec Sample 13	Start	End	PTM
R.IESEGGYIETWNP(+15.99)NNQEFQC(+57.02)AGVALSR.T	Y	98.7	34.50	3084.3882	27	-0.2	1029.1365	3	33.21	13	2136	OB3611.raw	3.03E4	1	1	46	72	Hydroxylation Pro; Carbamidomethylation
total 1 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

Summary

1. Notes

Spot F from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

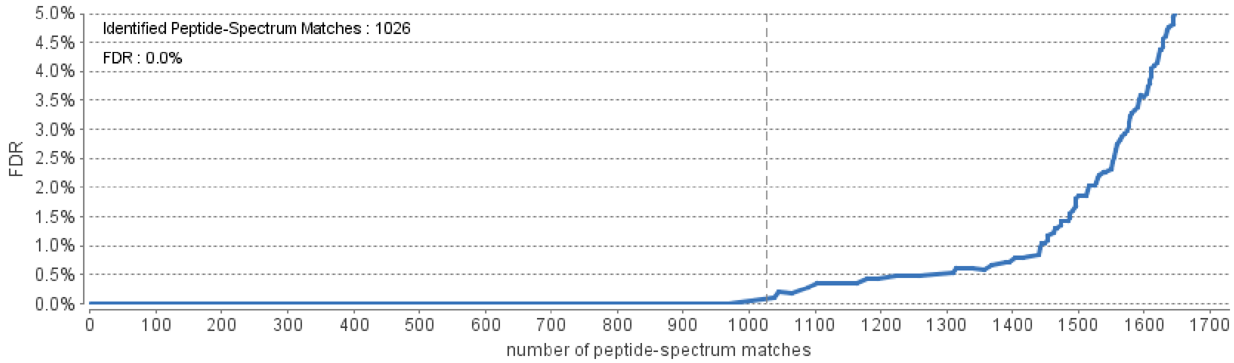
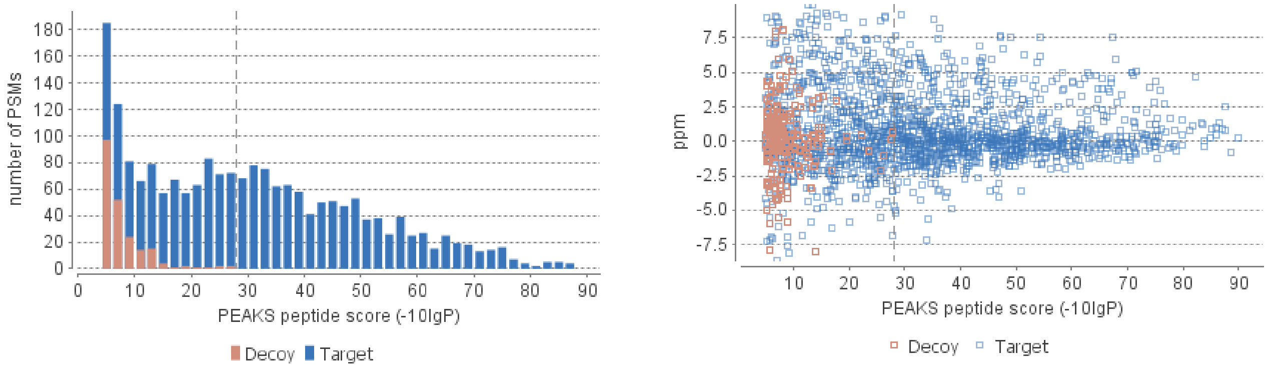


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

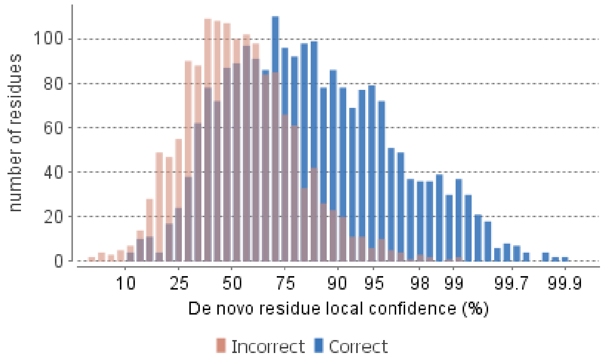

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



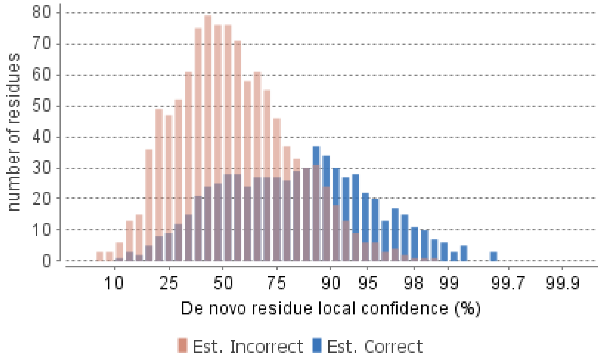


Table 1. Statistics of data.

# of MS scans	2643
# of MS/MS scans	5051

Table 2. Result filtration parameters.

Peptide -10lgP	≥28
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	808
Peptide sequences	173
Protein groups	5
Proteins	7
Proteins (#Unique Peptides)	5 (>2); 2 (=2); 0 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	151

Table 4. PTM profile.

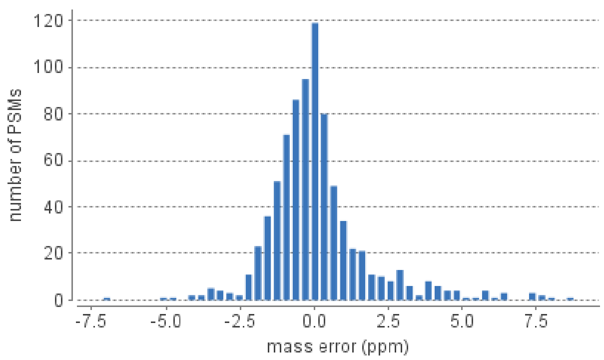
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Deamidation	.98	NQ	110	77.73	8.05E5	27.45
Carbamidomethyl	57.02	C	39	74.86	2.13E6	1000.00
HydPro	15.99	P	9	60.58	2.25E5	47.14
Oxidation	15.99	M	2	44.69	1.29E4	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



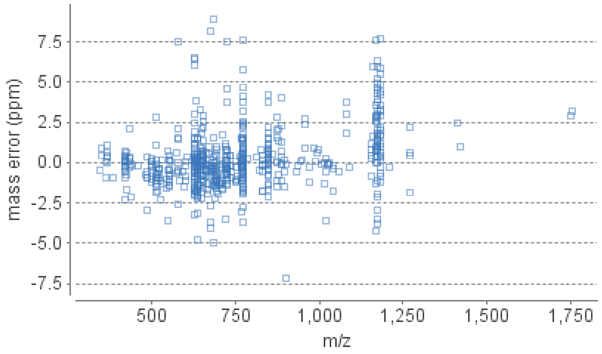


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 14	156	17	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3612.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 14	Area Sample 14	#Peptides	#Unique	#Spec Sample 14	PTM	Avg. Mass	Description
1	15	Q647H3|Q647H3_ARAHY	99.2	334.82	42	42	3.66E7	57	3	548	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
3	3	B5TYU1|B5TYU1_ARAHY	99.2	333.82	45	45	1.67E7	58	2	490	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
5	13	Q9FZ11|Q9FZ11_ARAHY	99.2	319.71	40	40	1.33E6	48	2	490	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
6	7	Q647H4|Q647H4_ARAHY	99.2	316.31	40	40	2.03E6	47	4	417	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	99.2	316.31	40	40	2.03E6	47	4	417	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
9	41	Q6IWG5|Q6IWG5_ARAHY	99.1	212.57	21	21	8.19E5	20	3	59	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
9	42	Q0GM57|Q0GM57_ARAHY	99.1	212.57	21	21	8.19E5	20	3	59	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
total 7 proteins													

Q647H3|Q647H3_ARAHY

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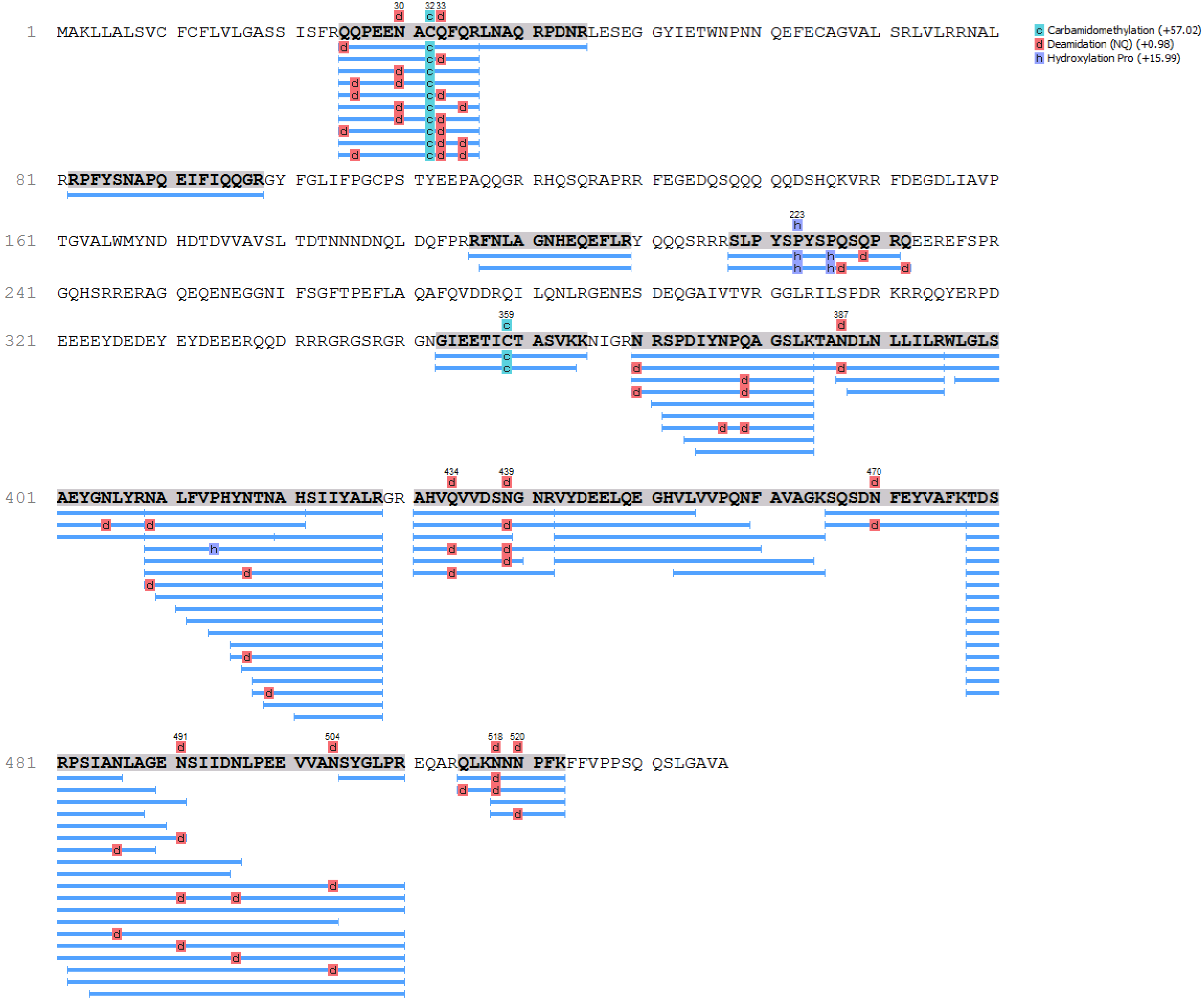
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

		Score											Area		#Spec			

Peptide	Uniq	(%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Sample 14	#Spec	Sample 14	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.00	1540.7673	13	0.2	771.3911	2	32.73	14	2386	OB3612.raw	1.51E7	127	127	396	408	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	88.61	2313.2019	20	-0.8	1157.6073	2	31.19	14	2179	OB3612.raw	1.07E8	18	18	409	428	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	86.94	3510.7590	33	0.9	1171.2614	3	34.94	14	2692	OB3612.raw	1.5E7	33	33	478	510	
K.SQSDNFEYVAFK.T	N	99.9	85.85	1433.6462	12	1.0	717.8311	2	30.10	14	2026	OB3612.raw	2.22E6	10	10	466	477	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	77.73	2314.1858	20	1.6	1158.1021	2	31.67	14	2243	OB3612.raw	8.07E5	2	2	409	428	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDN(+.98)LPEEVVANSYGLPR.E	Y	99.9	75.09	3511.7429	33	4.3	1171.5933	3	35.38	14	2752	OB3612.raw	9.85E6	3	3	478	510	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	75.03	1388.6936	13	0.1	695.3541	2	27.28	14	1636	OB3612.raw	4.8E6	21	21	372	384	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	73.38	2540.2910	23	0.4	1271.1533	2	31.14	14	2171	OB3612.raw	1.55E7	55	55	443	465	
N.GIEETIC(+57.02)TASVK.K	N	99.9	72.79	1306.6438	12	0.2	654.3293	2	27.58	14	1678	OB3612.raw	2.93E6	7	7	353	364	Carbamidomethylation
K.TDSRPSIANLAGEN(+.98)SIIDNLPEEVVANSYGLPR.E	Y	99.9	70.99	3511.7429	33	4.7	1171.5938	3	35.82	14	2813	OB3612.raw	9.84E6	3	3	478	510	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.9	70.64	1294.6378	12	0.2	648.3263	2	19.76	14	983	OB3612.raw	1.67E6	9	9	431	442	
R.AHVQVVDSN(+.98)GNR.V	N	99.9	69.99	1295.6218	12	-0.2	648.8181	2	20.35	14	1029	OB3612.raw	4.21E5	4	4	431	442	Deamidation (NQ)
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.65	2050.0383	17	-0.2	684.3533	3	29.88	14	1996	OB3612.raw	3.21E5	3	3	82	98	
V.PHYNTNAHSIIYALR.G	N	99.9	67.94	1768.9009	15	0.3	885.4580	2	30.91	14	2138	OB3612.raw	2.27E5	1	1	414	428	
K.SQSDN(+.98)FEYVAFK.T	N	99.9	67.76	1434.6302	12	-0.7	718.3219	2	30.86	14	2130	OB3612.raw	1.09E5	1	1	466	477	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	66.20	1296.6058	12	0.1	649.3102	2	20.90	14	1070	OB3612.raw	2.07E5	2	2	431	442	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.69	2314.1858	20	3.8	772.4055	3	31.92	14	2278	OB3612.raw	5.24E6	4	4	409	428	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	64.69	3511.7429	33	3.0	1171.5918	3	34.24	14	2596	OB3612.raw	1.43E6	5	5	478	510	Deamidation (NQ)
W.LGLSAEYGNLYR.N	N	99.9	61.15	1354.6881	12	-1.4	678.3504	2	30.16	14	2035	OB3612.raw	1.85E4	1	1	397	408	
N.TNAHSIIYALR.G	N	99.9	60.51	1257.6830	11	0.4	629.8490	2	27.94	14	1729	OB3612.raw	7.51E5	5	5	418	428	
R.NALFVPHYNTNAH.S	N	99.9	60.25	1496.7161	13	-0.3	749.3651	2	27.32	14	1642	OB3612.raw	1.33E6	11	11	409	421	
K.TDSRPSIANLAGENSIIDN.L	N	99.9	59.96	1985.9653	19	0.6	993.9905	2	30.56	14	2090	OB3612.raw	3.55E4	1	1	478	496	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	59.42	1295.6218	12	-1.1	648.8175	2	21.70	14	1122	OB3612.raw	4.28E5	2	2	431	442	Deamidation (NQ)
R.VYDEELQEGHVL.V	N	99.9	58.80	1429.6725	12	-0.8	715.8430	2	29.23	14	1908	OB3612.raw	4.23E4	2	2	443	454	
H.YNTNAHSIIYALR.G	N	99.9	58.66	1534.7892	13	0.1	768.4020	2	28.98	14	1872	OB3612.raw	8.43E5	10	10	416	428	
R.PSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	58.04	3051.5513	29	0.2	1018.1913	3	36.09	14	2849	OB3612.raw	3.38E5	3	3	482	510	
R.SPDIYN(+.98)PQ(+.98)AGSLK.T	N	99.9	57.39	1390.6616	13	-1.9	696.3367	2	28.27	14	1774	OB3612.raw	1.51E5	1	1	372	384	Deamidation (NQ)
K.TDSRPSIANLAGENSIID.N	N	99.9	57.32	1871.9225	18	-0.2	936.9683	2	30.89	14	2135	OB3612.raw	1.34E5	1	1	478	495	
R.NRSPDIYNPQAGSLK.T	N	99.9	57.29	1658.8376	15	-1.1	553.9526	3	25.54	14	1421	OB3612.raw	6.28E5	8	8	370	384	
K.TANDLNLLILR.W	N	99.9	57.11	1254.7296	11	-1.2	628.3713	2	32.42	14	2344	OB3612.raw	3.04E7	89	89	385	395	
K.TDSRPSIANLAGEN.S	N	99.9	55.66	1443.6953	14	-0.3	722.8547	2	27.71	14	1696	OB3612.raw	1.31E5	5	5	478	491	
N.AHSIIYALR.G	N	99.9	53.88	1042.5923	9	-0.4	522.3032	2	27.28	14	1637	OB3612.raw	1.92E5	3	3	420	428	
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	53.78	1541.7513	13	5.8	771.8874	2	33.15	14	2446	OB3612.raw	6.85E6	2	2	396	408	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	53.37	1340.7816	13	-0.2	671.3979	2	30.15	14	2034	OB3612.raw	5.71E4	1	1	453	465	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	53.09	2128.1218	18	-1.3	710.3803	3	31.20	14	2180	OB3612.raw	7.71E5	4	4	411	428	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	53.03	1659.8217	15	-0.5	830.9177	2	26.37	14	1516	OB3612.raw	8.5E5	3	3	370	384	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.71	1444.6793	14	-0.4	723.3467	2	28.24	14	1770	OB3612.raw	7.9E4	1	1	478	491	Deamidation (NQ)
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	518	523	
Y.NTNAHSIIYALR.G	N	99.9	51.22	1371.7258	12	-0.4	686.8699	2	28.06	14	1744	OB3612.raw	1.45E5	2	2	417	428	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	50.24	2837.4043	27	0.2	946.8089	3	33.91	14	2552	OB3612.raw	2.9E5	3	3	478	504	
L.FVPHYNTNAHSIIYALR.G	N	99.9	50.06	2015.0377	17	0.6	672.6869	3	31.15	14	2173	OB3612.raw	1.38E6	2	2	412	428	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	49.90	1534.6470	12	-1.1	768.3299	2	24.54	14	1327	OB3612.raw	3.85E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.81	1659.8217	15	0.2	554.2812	3	26.15	14	1488	OB3612.raw	8.5E5	2	2	370	384	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.77	1660.8057	15	-1.8	831.4086	2	26.98	14	1595	OB3612.raw	2.5E5	2	2	370	384	Deamidation (NQ)
A.NDLNLLILR.W	N	99.9	49.30	1082.6448	9	-1.0	542.3291	2	32.61	14	2370	OB3612.raw	9.72E4	2	2	387	395	
A.HSIIYALR.G	N	99.9	48.25	971.5552	8	-0.9	486.7845	2	27.02	14	1601	OB3612.raw	3.57E4	2	2	421	428	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	99.9	46.96	1535.6311	12	-3.0	768.8205	2	24.95	14	1364	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.PSIANLAGENSIIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	46.25	3052.5352	29	-3.6	1018.5154	3	35.14	14	2720	OB3612.raw	3.6E4	1	1	482	510	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	46.14	1497.7001	13	-1.2	749.8564	2	28.28	14	1776	OB3612.raw	1.39E5	3	3	409	421	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	45.80	1329.6525	13	-1.9	665.8322	2	28.04	14	1742	OB3612.raw	5.27E4	1	1	478	490	

R.NALFVPHYNTN.A	N	99.9	45.46	1288.6200	11	-0.2	645.3171	2	29.02	14	1878	OB3612.raw	3.47E4	2	2	409	419	
R.LNAQRPDNR.L	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	37	45	
P.DIYNPQAGSLK.T	N	99.9	42.96	1204.6088	11	0.4	603.3119	2	26.84	14	1578	OB3612.raw	8.34E3	2	2	374	384	
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.8	40.81	1534.6470	12	-0.3	768.3305	2	24.19	14	1295	OB3612.raw	7.29E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIANLAG.E	N	99.8	40.01	1200.6099	12	-0.2	601.3121	2	27.54	14	1673	OB3612.raw	1.58E5	2	2	478	489	
R.VYDEELQEGHVLVVPQNFAVAG.K	N	99.8	39.87	2412.1960	22	-0.3	1207.1050	2	32.70	14	2381	OB3612.raw	3.31E4	1	1	443	464	
N.ALFVPHYNTNAHSIIYALR.G	N	99.8	39.75	2199.1589	19	0.4	734.0605	3	30.90	14	2137	OB3612.raw	2.97E5	1	1	410	428	
R.AHVQVVDSN(+.98)G.N	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	431	440	Deamidation (NQ)
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	515	523	Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.8	38.20	1535.6311	12	-0.1	768.8228	2	25.05	14	1374	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	518	523	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.90	834.4963	7	0.0	418.2554	2	28.71	14	1835	OB3612.raw	1.05E6	4	4	422	428	
N.DLNLLILR.W	N	99.8	37.67	968.6018	8	-1.0	485.3077	2	33.63	14	2513	OB3612.raw	3.43E4	1	1	388	395	
K.TDSRPSIANLAGEN(+.98)SIIDN(+.98)LPEEVVANSYGLPR.E	Y	99.8	37.56	3512.7271	33	6.3	1171.9237	3	33.68	14	2521	OB3612.raw	8.63E4	1	1	478	510	Deamidation (NQ)
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.7	36.76	1534.6470	12	-0.7	768.3303	2	24.71	14	1341	OB3612.raw	1.11E4	4	4	25	36	Carbamidomethylation; Deamidation (NQ)
N.TN(+.98)AHSIIYALR.G	N	99.7	36.73	1258.6670	11	0.1	630.3408	2	29.11	14	1892	OB3612.raw	5.53E3	2	2	418	428	Deamidation (NQ)
T.NAHSIIYALR.G	N	99.7	36.68	1156.6353	10	-0.9	386.5520	3	27.65	14	1688	OB3612.raw	2.27E4	1	1	419	428	
R.VYDEELQEGHVLVVPQNF.A	N	99.7	36.57	2114.0320	18	-0.5	1058.0227	2	32.43	14	2346	OB3612.raw	1.29E5	1	1	443	460	
R.NALFVP(+15.99)HYNTNAHSIIYALR.G	N	99.6	35.76	2329.1968	20	-1.1	583.3058	4	30.64	14	2100	OB3612.raw	1.77E4	1	1	409	428	Hydroxylation Pro
N.GIEETIC(+57.02)TASVKK.N	N	99.6	35.24	1434.7388	13	-0.1	718.3766	2	25.88	14	1457	OB3612.raw	4.72E4	1	1	353	365	Carbamidomethylation
K.TDSRPSIANLA.G	N	99.6	35.20	1143.5884	11	-0.7	572.8011	2	27.78	14	1706	OB3612.raw	5.94E4	1	1	478	488	
R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	515	523	Deamidation (NQ)
H.YN(+.98)TNAHSIIYALR.G	N	99.6	34.60	1535.7732	13	-3.0	768.8915	2	29.68	14	1970	OB3612.raw	0	1	1	416	428	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.5	33.83	1535.6311	12	0.5	768.8232	2	25.16	14	1385	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.RFNLAGNHEQEFLR.Y	N	99.5	33.64	1729.8647	14	-2.6	577.6274	3	27.60	14	1681	OB3612.raw	2.7E4	1	1	196	209	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPRQ(+.98).E	N	99.5	33.49	1767.7950	15	0.7	884.9054	2	26.43	14	1524	OB3612.raw	3.53E3	1	1	218	232	Hydroxylation Pro; Deamidation (NQ)
K.TAN(+.98)DLNLLILR.W	N	99.5	32.90	1255.7136	11	6.0	628.8679	2	33.49	14	2494	OB3612.raw	6.09E6	3	3	385	395	Deamidation (NQ)
D.IYNPQAGSLK.T	N	99.5	32.86	1089.5818	10	0.8	545.7986	2	24.84	14	1351	OB3612.raw	9.56E3	1	1	375	384	
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.1	31.79	1535.6311	12	1.4	768.8239	2	25.38	14	1406	OB3612.raw	1.25E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.1	31.34	1535.6311	12	1.6	768.8240	2	25.31	14	1398	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
N.SYGLPR.E	N	99.1	31.30	691.3653	6	-0.5	346.6898	2	25.05	14	1373	OB3612.raw	1.53E4	1	1	505	510	
S.IANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.1	31.18	2867.4663	27	2.4	956.8317	3	35.43	14	2760	OB3612.raw	8.21E3	1	1	484	510	
K.TDSRPSIAN(+.98)LAGENSIIDNLPEEVVANSYGLPR.E	Y	99.1	31.03	3511.7429	33	-1.3	703.3549	5	34.03	14	2567	OB3612.raw	3.33E4	1	1	478	510	Deamidation (NQ)
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	99.1	30.73	1638.7524	14	-0.5	820.3831	2	26.35	14	1514	OB3612.raw	9.77E3	1	1	218	231	Hydroxylation Pro; Deamidation (NQ)
K.TDSRPSIAN.L	N	99.1	30.69	959.4672	9	-0.7	480.7405	2	20.71	14	1057	OB3612.raw	5.09E3	1	1	478	486	
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	431	439	
N.RSPDIYNPQAGSLK.T	N	98.7	30.18	1544.7947	14	-1.8	515.9379	3	25.49	14	1415	OB3612.raw	1.64E4	1	1	371	384	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	98.7	30.00	1535.6311	12	-1.1	768.8220	2	25.29	14	1396	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAG.E	N	98.6	29.68	1201.5939	12	0.1	601.8043	2	28.43	14	1796	OB3612.raw	1.36E4	1	1	478	489	Deamidation (NQ)
R.VYDEELQEGHVLVVPQN.F	N	98.6	29.18	1966.9636	17	0.9	984.4899	2	30.02	14	2016	OB3612.raw	3.6E4	1	1	443	459	
R.FNLAGNHEQEFLR.Y	N	98.6	29.05	1573.7637	13	-1.1	525.5946	3	28.84	14	1852	OB3612.raw	1.24E5	2	2	197	209	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	28.91	1536.6151	12	-0.7	769.3143	2	25.70	14	1437	OB3612.raw	4.4E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
total 92 peptides																		

B5TYU1|B5TYU1_ARAHY

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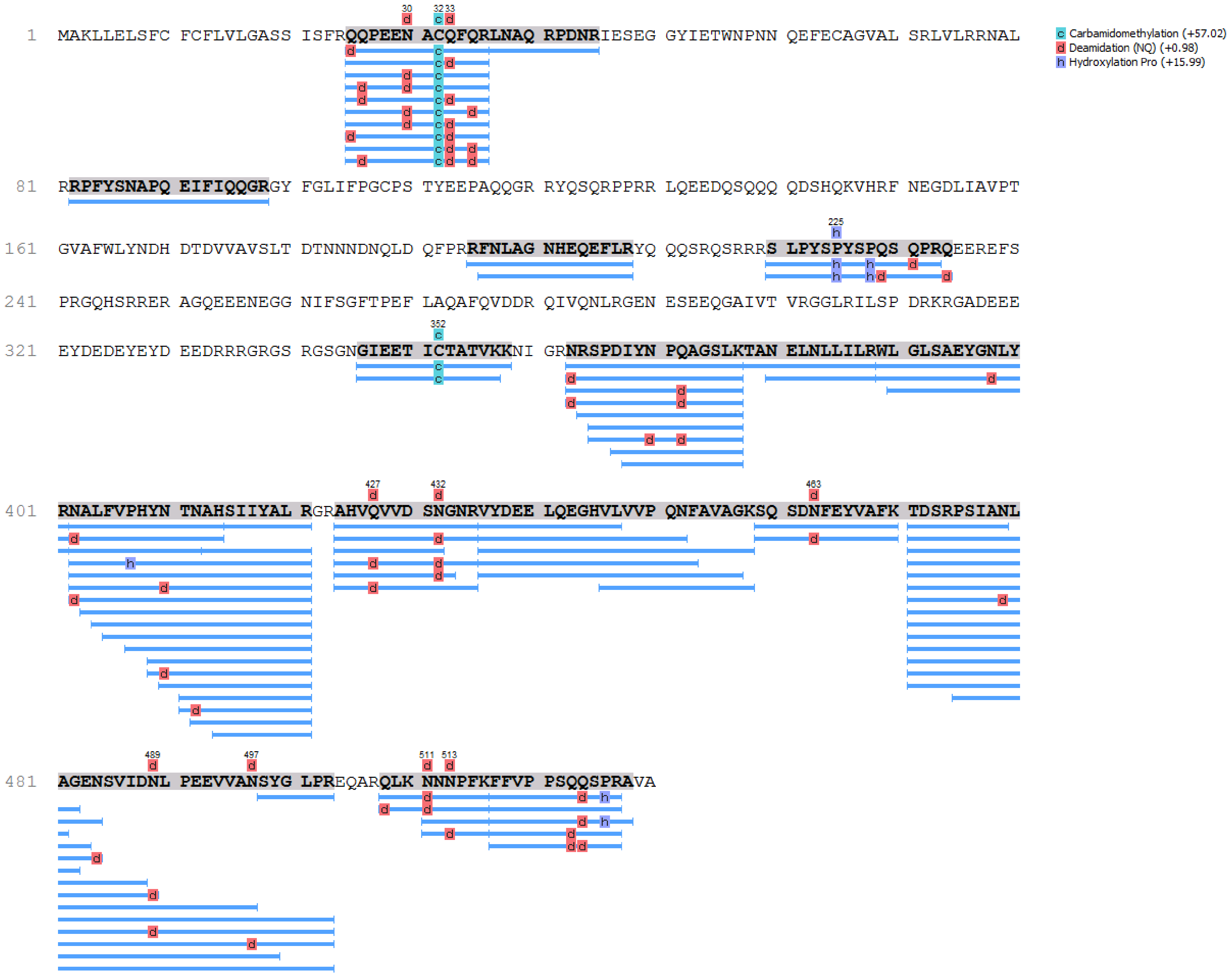
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 14	#Spec	#Spec Sample 14	Start	End	PTM

R.WLGLSAEYGNLYR.N	N	99.9	90.00	1540.7673	13	0.2	771.3911	2	32.73	14	2386	OB3612.raw	1.51E7	127	127	389	401	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	88.61	2313.2019	20	-0.8	1157.6073	2	31.19	14	2179	OB3612.raw	1.07E8	18	18	402	421	
K.SQSDNFEYVAFK.T	N	99.9	85.85	1433.6462	12	1.0	717.8311	2	30.10	14	2026	OB3612.raw	2.22E6	10	10	459	470	
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	78.41	3496.7434	33	0.8	1166.5894	3	34.38	14	2614	OB3612.raw	1.07E7	18	18	471	503	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	77.73	2314.1858	20	1.6	1158.1021	2	31.67	14	2243	OB3612.raw	8.07E5	2	2	402	421	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	75.03	1388.6936	13	0.1	695.3541	2	27.28	14	1636	OB3612.raw	4.8E6	21	21	365	377	
N.GIEETIC(+57.02)TATVK.K	N	99.9	74.86	1320.6595	12	-0.1	661.3370	2	28.01	14	1738	OB3612.raw	3.45E6	12	12	346	357	Carbamidomethylation
K.TDSRPSIANLAGENSVIDN(+.98)LPEEVVANSYGLPR.E	Y	99.9	74.69	3497.7273	33	2.8	1166.9197	3	34.95	14	2693	OB3612.raw	4.71E6	3	3	471	503	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	73.38	2540.2910	23	0.4	1271.1533	2	31.14	14	2171	OB3612.raw	1.55E7	55	55	436	458	
R.AHVQVVDSNGNR.V	N	99.9	70.64	1294.6378	12	0.2	648.3263	2	19.76	14	983	OB3612.raw	1.67E6	9	9	424	435	
R.AHVQVVDSN(+.98)GNR.V	N	99.9	69.99	1295.6218	12	-0.2	648.8181	2	20.35	14	1029	OB3612.raw	4.21E5	4	4	424	435	Deamidation (NQ)
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.65	2050.0383	17	-0.2	684.3533	3	29.88	14	1996	OB3612.raw	3.21E5	3	3	82	98	
V.PHYNTNAHSIIYALR.G	N	99.9	67.94	1768.9009	15	0.3	885.4580	2	30.91	14	2138	OB3612.raw	2.27E5	1	1	407	421	
K.SQSDN(+.98)FEYVAFK.T	N	99.9	67.76	1434.6302	12	-0.7	718.3219	2	30.86	14	2130	OB3612.raw	1.09E5	1	1	459	470	Deamidation (NQ)
K.TDSRPSIANLAGENSVIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.9	66.83	3497.7273	33	3.6	1166.9205	3	33.95	14	2556	OB3612.raw	1.24E6	2	2	471	503	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	66.20	1296.6058	12	0.1	649.3102	2	20.90	14	1070	OB3612.raw	2.07E5	2	2	424	435	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.69	2314.1858	20	3.8	772.4055	3	31.92	14	2278	OB3612.raw	5.24E6	4	4	402	421	Deamidation (NQ)
K.FFVPPSQQSPR.A	N	99.9	63.76	1288.6564	11	0.0	645.3354	2	27.06	14	1606	OB3612.raw	1.82E5	5	5	517	527	
K.TANELNLLILR.W	N	99.9	62.78	1268.7452	11	1.5	635.3809	2	33.07	14	2434	OB3612.raw	1.22E7	47	47	378	388	
W.LGLSAEYGNLYR.N	N	99.9	61.15	1354.6881	12	-1.4	678.3504	2	30.16	14	2035	OB3612.raw	1.85E4	1	1	390	401	
N.TNAHSIIYALR.G	N	99.9	60.51	1257.6830	11	0.4	629.8490	2	27.94	14	1729	OB3612.raw	7.51E5	5	5	411	421	
R.NALFVPHYNTNAH.S	N	99.9	60.25	1496.7161	13	-0.3	749.3651	2	27.32	14	1642	OB3612.raw	1.33E6	11	11	402	414	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	59.42	1295.6218	12	-1.1	648.8175	2	21.70	14	1122	OB3612.raw	4.28E5	2	2	424	435	Deamidation (NQ)
R.VYDEELQEGHVL.V	N	99.9	58.80	1429.6725	12	-0.8	715.8430	2	29.23	14	1908	OB3612.raw	4.23E4	2	2	436	447	
H.YNTNAHSIIYALR.G	N	99.9	58.66	1534.7892	13	0.1	768.4020	2	28.98	14	1872	OB3612.raw	8.43E5	10	10	409	421	
R.PSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	58.57	3037.5356	29	-0.1	1013.5191	3	35.66	14	2791	OB3612.raw	1.18E5	2	2	475	503	
R.SPDIYN(+.98)PQ(+.98)AGSLK.T	N	99.9	57.39	1390.6616	13	-1.9	696.3367	2	28.27	14	1774	OB3612.raw	1.51E5	1	1	365	377	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.9	57.29	1658.8376	15	-1.1	553.9526	3	25.54	14	1421	OB3612.raw	6.28E5	8	8	363	377	
K.TDSRPSIANLAGENSVID.N	N	99.9	55.75	1857.9067	18	-0.5	929.9601	2	30.11	14	2029	OB3612.raw	7.38E4	1	1	471	488	
K.TDSRPSIANLAGEN.S	N	99.9	55.66	1443.6953	14	-0.3	722.8547	2	27.71	14	1696	OB3612.raw	1.31E5	5	5	471	484	
K.TDSRPSIANLAGENSVIDNLPEEVVAN.S	N	99.9	54.57	2823.3887	27	0.1	942.1369	3	33.36	14	2476	OB3612.raw	1.21E5	2	2	471	497	
N.AHSIIYALR.G	N	99.9	53.88	1042.5923	9	-0.4	522.3032	2	27.28	14	1637	OB3612.raw	1.92E5	3	3	413	421	
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	53.78	1541.7513	13	5.8	771.8874	2	33.15	14	2446	OB3612.raw	6.85E6	2	2	389	401	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	53.37	1340.7816	13	-0.2	671.3979	2	30.15	14	2034	OB3612.raw	5.71E4	1	1	446	458	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	53.09	2128.1218	18	-1.3	710.3803	3	31.20	14	2180	OB3612.raw	7.71E5	4	4	404	421	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	53.03	1659.8217	15	-0.5	830.9177	2	26.37	14	1516	OB3612.raw	8.5E5	3	3	363	377	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.71	1444.6793	14	-0.4	723.3467	2	28.24	14	1770	OB3612.raw	7.9E4	1	1	471	484	Deamidation (NQ)
K.FFVPPSQQ(+.98)SP(+15.99)R.A	N	99.9	52.38	1305.6353	11	0.0	653.8249	2	27.06	14	1607	OB3612.raw	2.87E5	2	2	517	527	Deamidation (NQ); Hydroxylation Pro
K.TDSRPSIANLAGENSVIDN(+.98).L	N	99.9	52.00	1972.9337	19	0.0	987.4742	2	30.20	14	2041	OB3612.raw	2.36E4	1	1	471	489	Deamidation (NQ)
K.FFVPPSQ(+.98)QSPR.A	N	99.9	51.84	1289.6404	11	1.0	645.8281	2	28.59	14	1818	OB3612.raw	5.56E4	1	1	517	527	Deamidation (NQ)
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	511	516	
Y.NTNAHSIIYALR.G	N	99.9	51.22	1371.7258	12	-0.4	686.8699	2	28.06	14	1744	OB3612.raw	1.45E5	2	2	410	421	
L.FVPHYNTNAHSIIYALR.G	N	99.9	50.06	2015.0377	17	0.6	672.6869	3	31.15	14	2173	OB3612.raw	1.38E6	2	2	405	421	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	49.90	1534.6470	12	-1.1	768.3299	2	24.54	14	1327	OB3612.raw	3.85E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.81	1659.8217	15	0.2	554.2812	3	26.15	14	1488	OB3612.raw	8.5E5	2	2	363	377	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.77	1660.8057	15	-1.8	831.4086	2	26.98	14	1595	OB3612.raw	2.5E5	2	2	363	377	Deamidation (NQ)
A.HSIIYALR.G	N	99.9	48.25	971.5552	8	-0.9	486.7845	2	27.02	14	1601	OB3612.raw	3.57E4	2	2	414	421	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	99.9	46.96	1535.6311	12	-3.0	768.8205	2	24.95	14	1364	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
N.GIEETIC(+57.02)TATVKK.N	N	99.9	46.46	1448.7545	13	-0.8	725.3840	2	26.31	14	1509	OB3612.raw	4.52E4	1	1	346	358	Carbamidomethylation
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	46.14	1497.7001	13	-1.2	749.8564	2	28.28	14	1776	OB3612.raw	1.39E5	3	3	402	414	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	45.80	1329.6525	13	-1.9	665.8322	2	28.04	14	1742	OB3612.raw	5.27E4	1	1	471	483	

A.NELNLLILR.W	N	99.9	45.51	1096.6604	9	-0.5	549.3372	2	33.04	14	2430	OB3612.raw	2.23E4	1	1	380	388	
R.NALFVPHYNTN.A	N	99.9	45.46	1288.6200	11	-0.2	645.3171	2	29.02	14	1878	OB3612.raw	3.47E4	2	2	402	412	
R.LNAQRPDNR.I	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	37	45	
K.TDSRPSIANLAGENSVIDNLPEEVVANSY.G	N	99.9	43.12	3073.4839	29	-0.1	1025.5018	3	34.79	14	2672	OB3612.raw	4.4E4	1	1	471	499	
P.DIYNPQAGSLK.T	N	99.9	42.96	1204.6088	11	0.4	603.3119	2	26.84	14	1578	OB3612.raw	8.34E3	2	2	367	377	
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.8	40.81	1534.6470	12	-0.3	768.3305	2	24.19	14	1295	OB3612.raw	7.29E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIANLAG.E	N	99.8	40.01	1200.6099	12	-0.2	601.3121	2	27.54	14	1673	OB3612.raw	1.58E5	2	2	471	482	
R.VYDEELQEGHVLVVPQNFAVAG.K	N	99.8	39.87	2412.1960	22	-0.3	1207.1050	2	32.70	14	2381	OB3612.raw	3.31E4	1	1	436	457	
N.ALFVPHYNTNAHSIIYALR.G	N	99.8	39.75	2199.1589	19	0.4	734.0605	3	30.90	14	2137	OB3612.raw	2.97E5	1	1	403	421	
R.AHVQVVDSN(+.98)G.N	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	424	433	Deamidation (NQ)
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	508	516	Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.8	38.20	1535.6311	12	-0.1	768.8228	2	25.05	14	1374	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	511	516	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.90	834.4963	7	0.0	418.2554	2	28.71	14	1835	OB3612.raw	1.05E6	4	4	415	421	
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.7	36.76	1534.6470	12	-0.7	768.3303	2	24.71	14	1341	OB3612.raw	1.11E4	4	4	25	36	Carbamidomethylation; Deamidation (NQ)
N.TN(+.98)AHSIIYALR.G	N	99.7	36.73	1258.6670	11	0.1	630.3408	2	29.11	14	1892	OB3612.raw	5.53E3	2	2	411	421	Deamidation (NQ)
T.NAHSIIYALR.G	N	99.7	36.68	1156.6353	10	-0.9	386.5520	3	27.65	14	1688	OB3612.raw	2.27E4	1	1	412	421	
R.VYDEELQEGHVLVVPQNF.A	N	99.7	36.57	2114.0320	18	-0.5	1058.0227	2	32.43	14	2346	OB3612.raw	1.29E5	1	1	436	453	
R.NALFVP(+15.99)HYNTNAHSIIYALR.G	N	99.6	35.76	2329.1968	20	-1.1	583.3058	4	30.64	14	2100	OB3612.raw	1.77E4	1	1	402	421	Hydroxylation Pro
K.TDSRPSIANLA.G	N	99.6	35.20	1143.5884	11	-0.7	572.8011	2	27.78	14	1706	OB3612.raw	5.94E4	1	1	471	481	
R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	508	516	Deamidation (NQ)
H.YN(+.98)TNAHSIIYALR.G	N	99.6	34.60	1535.7732	13	-3.0	768.8915	2	29.68	14	1970	OB3612.raw	0	1	1	409	421	Deamidation (NQ)
K.FFVPPSQ(+.98)Q(+.98)SPR.A	N	99.5	34.36	1290.6244	11	3.3	646.3216	2	28.03	14	1741	OB3612.raw	4.91E4	1	1	517	527	Deamidation (NQ)
K.FFVPPSQQ(+.98)SP(+15.99)RA.V	N	99.5	34.32	1376.6724	12	0.5	689.3438	2	27.12	14	1615	OB3612.raw	2.78E4	1	1	517	528	Deamidation (NQ); Hydroxylation Pro
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.5	33.83	1535.6311	12	0.5	768.8232	2	25.16	14	1385	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.RFNLAGNHEQEFLR.Y	N	99.5	33.64	1729.8647	14	-2.6	577.6274	3	27.60	14	1681	OB3612.raw	2.7E4	1	1	195	208	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPRQ(+.98).E	N	99.5	33.49	1767.7950	15	0.7	884.9054	2	26.43	14	1524	OB3612.raw	3.53E3	1	1	220	234	Hydroxylation Pro; Deamidation (NQ)
D.IYNPQAGSLK.T	N	99.5	32.86	1089.5818	10	0.8	545.7986	2	24.84	14	1351	OB3612.raw	9.56E3	1	1	368	377	
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.1	31.79	1535.6311	12	1.4	768.8239	2	25.38	14	1406	OB3612.raw	1.25E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.1	31.34	1535.6311	12	1.6	768.8240	2	25.31	14	1398	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
N.SYGLPR.E	N	99.1	31.30	691.3653	6	-0.5	346.6898	2	25.05	14	1373	OB3612.raw	1.53E4	1	1	498	503	
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	99.1	30.73	1638.7524	14	-0.5	820.3831	2	26.35	14	1514	OB3612.raw	9.77E3	1	1	220	233	Hydroxylation Pro; Deamidation (NQ)
K.TDSRPSIAN.L	N	99.1	30.69	959.4672	9	-0.7	480.7405	2	20.71	14	1057	OB3612.raw	5.09E3	1	1	471	479	
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	424	432	
N.RSPDIYNPQAGSLK.T	N	98.7	30.18	1544.7947	14	-1.8	515.9379	3	25.49	14	1415	OB3612.raw	1.64E4	1	1	364	377	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	98.7	30.00	1535.6311	12	-1.1	768.8220	2	25.29	14	1396	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAG.E	N	98.6	29.68	1201.5939	12	0.1	601.8043	2	28.43	14	1796	OB3612.raw	1.36E4	1	1	471	482	Deamidation (NQ)
R.VYDEELQEGHVLVVPQN.F	N	98.6	29.18	1966.9636	17	0.9	984.4899	2	30.02	14	2016	OB3612.raw	3.6E4	1	1	436	452	
R.FNLAGNHEQEFLR.Y	N	98.6	29.05	1573.7637	13	-1.1	525.5946	3	28.84	14	1852	OB3612.raw	1.24E5	2	2	196	208	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	28.91	1536.6151	12	-0.7	769.3143	2	25.70	14	1437	OB3612.raw	4.4E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
total 91 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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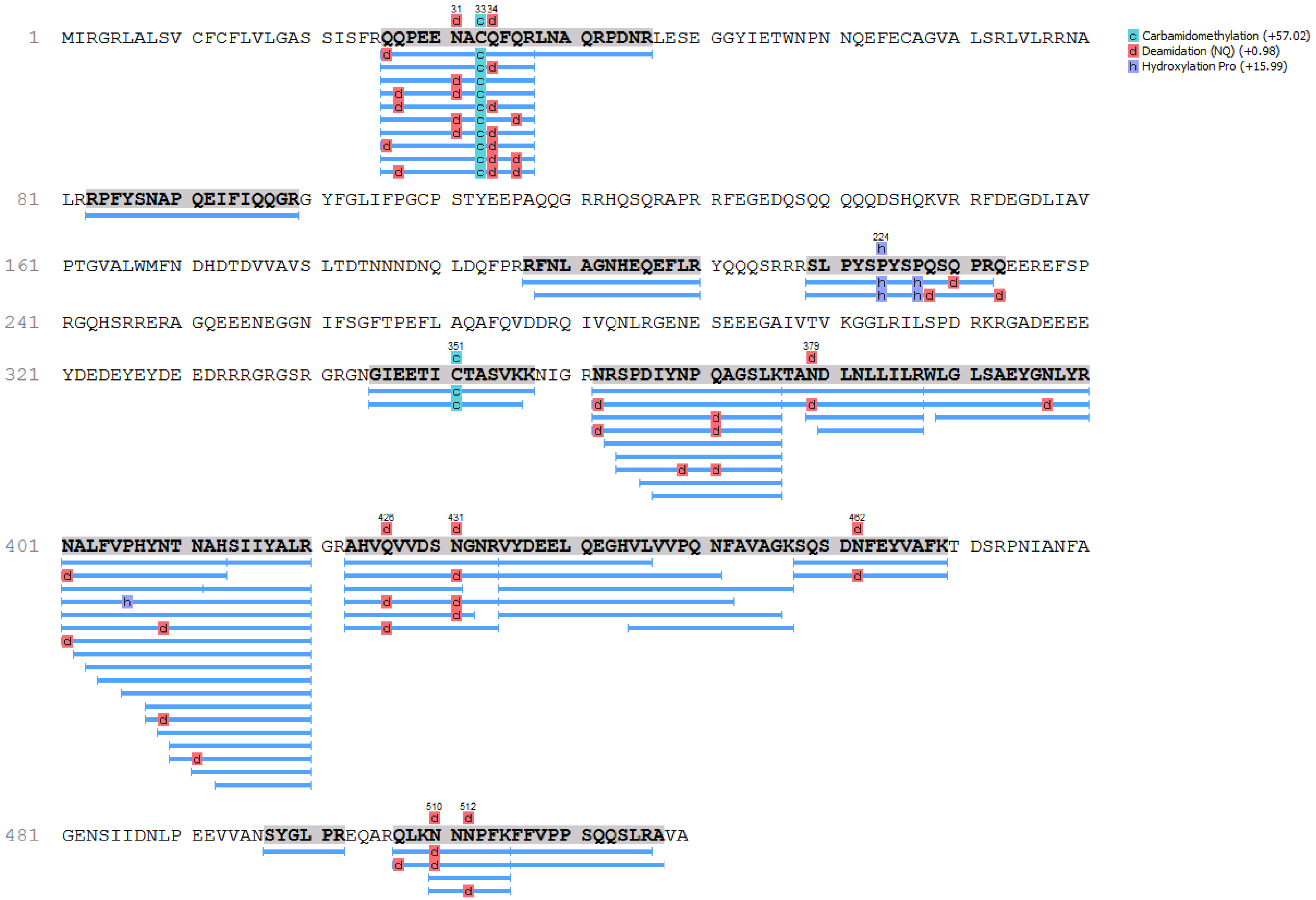
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 14	#Spec	#Spec Sample 14	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.00	1540.7673	13	0.2	771.3911	2	32.73	14	2386	OB3612.raw	1.51E7	127	127	388	400	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	88.61	2313.2019	20	-0.8	1157.6073	2	31.19	14	2179	OB3612.raw	1.07E8	18	18	401	420	
K.SQSDNFEYVAFK.T	N	99.9	85.85	1433.6462	12	1.0	717.8311	2	30.10	14	2026	OB3612.raw	2.22E6	10	10	458	469	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	77.73	2314.1858	20	1.6	1158.1021	2	31.67	14	2243	OB3612.raw	8.07E5	2	2	401	420	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	75.03	1388.6936	13	0.1	695.3541	2	27.28	14	1636	OB3612.raw	4.8E6	21	21	364	376	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	73.38	2540.2910	23	0.4	1271.1533	2	31.14	14	2171	OB3612.raw	1.55E7	55	55	435	457	
N.GIEETIC(+57.02)TASVK.K	N	99.9	72.79	1306.6438	12	0.2	654.3293	2	27.58	14	1678	OB3612.raw	2.93E6	7	7	345	356	Carbamidomethylation
R.AHVQVVDSNGNR.V	N	99.9	70.64	1294.6378	12	0.2	648.3263	2	19.76	14	983	OB3612.raw	1.67E6	9	9	423	434	

R.AHVQVVDSN(+.98)GNR.V	N	99.9	69.99	1295.6218	12	-0.2	648.8181	2	20.35	14	1029	OB3612.raw	4.21E5	4	4	423	434	Deamidation (NQ)
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.65	2050.0383	17	-0.2	684.3533	3	29.88	14	1996	OB3612.raw	3.21E5	3	3	83	99	
V.PHYNTNAHSIIYALR.G	N	99.9	67.94	1768.9009	15	0.3	885.4580	2	30.91	14	2138	OB3612.raw	2.27E5	1	1	406	420	
K.SQSDN(+.98)FEYVAFK.T	N	99.9	67.76	1434.6302	12	-0.7	718.3219	2	30.86	14	2130	OB3612.raw	1.09E5	1	1	458	469	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	66.20	1296.6058	12	0.1	649.3102	2	20.90	14	1070	OB3612.raw	2.07E5	2	2	423	434	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.69	2314.1858	20	3.8	772.4055	3	31.92	14	2278	OB3612.raw	5.24E6	4	4	401	420	Deamidation (NQ)
W.LGLSAEYGNLYR.N	N	99.9	61.15	1354.6881	12	-1.4	678.3504	2	30.16	14	2035	OB3612.raw	1.85E4	1	1	389	400	
N.TNAHSIIYALR.G	N	99.9	60.51	1257.6830	11	0.4	629.8490	2	27.94	14	1729	OB3612.raw	7.51E5	5	5	410	420	
R.NALFVPHYNTNAH.S	N	99.9	60.25	1496.7161	13	-0.3	749.3651	2	27.32	14	1642	OB3612.raw	1.33E6	11	11	401	413	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	59.42	1295.6218	12	-1.1	648.8175	2	21.70	14	1122	OB3612.raw	4.28E5	2	2	423	434	Deamidation (NQ)
R.VYDEELQEGHVL.V	N	99.9	58.80	1429.6725	12	-0.8	715.8430	2	29.23	14	1908	OB3612.raw	4.23E4	2	2	435	446	
H.YNTNAHSIIYALR.G	N	99.9	58.66	1534.7892	13	0.1	768.4020	2	28.98	14	1872	OB3612.raw	8.43E5	10	10	408	420	
K.FFVPPSQQSLR.A	Y	99.9	58.04	1304.6876	11	0.1	653.3511	2	28.58	14	1816	OB3612.raw	9.81E5	6	6	516	526	
R.SPDIYN(+.98)PQ(+.98)AGSLK.T	N	99.9	57.39	1390.6616	13	-1.9	696.3367	2	28.27	14	1774	OB3612.raw	1.51E5	1	1	364	376	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.9	57.29	1658.8376	15	-1.1	553.9526	3	25.54	14	1421	OB3612.raw	6.28E5	8	8	362	376	
K.TANDLNLLILR.W	N	99.9	57.11	1254.7296	11	-1.2	628.3713	2	32.42	14	2344	OB3612.raw	3.04E7	89	89	377	387	
N.AHSIIYALR.G	N	99.9	53.88	1042.5923	9	-0.4	522.3032	2	27.28	14	1637	OB3612.raw	1.92E5	3	3	412	420	
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	53.78	1541.7513	13	5.8	771.8874	2	33.15	14	2446	OB3612.raw	6.85E6	2	2	388	400	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	53.37	1340.7816	13	-0.2	671.3979	2	30.15	14	2034	OB3612.raw	5.71E4	1	1	445	457	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	53.09	2128.1218	18	-1.3	710.3803	3	31.20	14	2180	OB3612.raw	7.71E5	4	4	403	420	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	53.03	1659.8217	15	-0.5	830.9177	2	26.37	14	1516	OB3612.raw	8.5E5	3	3	362	376	Deamidation (NQ)
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	510	515	
Y.NTNAHSIIYALR.G	N	99.9	51.22	1371.7258	12	-0.4	686.8699	2	28.06	14	1744	OB3612.raw	1.45E5	2	2	409	420	
L.FVPHYNTNAHSIIYALR.G	N	99.9	50.06	2015.0377	17	0.6	672.6869	3	31.15	14	2173	OB3612.raw	1.38E6	2	2	404	420	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	49.90	1534.6470	12	-1.1	768.3299	2	24.54	14	1327	OB3612.raw	3.85E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.81	1659.8217	15	0.2	554.2812	3	26.15	14	1488	OB3612.raw	8.5E5	2	2	362	376	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.77	1660.8057	15	-1.8	831.4086	2	26.98	14	1595	OB3612.raw	2.5E5	2	2	362	376	Deamidation (NQ)
A.NDLNLLILR.W	N	99.9	49.30	1082.6448	9	-1.0	542.3291	2	32.61	14	2370	OB3612.raw	9.72E4	2	2	379	387	
A.HSIIYALR.G	N	99.9	48.25	971.5552	8	-0.9	486.7845	2	27.02	14	1601	OB3612.raw	3.57E4	2	2	413	420	
K.FFVPPSQQSLRA.V	Y	99.9	47.27	1375.7247	12	-1.5	688.8686	2	29.22	14	1906	OB3612.raw	3.53E5	4	4	516	527	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	99.9	46.96	1535.6311	12	-3.0	768.8205	2	24.95	14	1364	OB3612.raw	1.25E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	46.14	1497.7001	13	-1.2	749.8564	2	28.28	14	1776	OB3612.raw	1.39E5	3	3	401	413	Deamidation (NQ)
R.NALFVPHYNTN.A	N	99.9	45.46	1288.6200	11	-0.2	645.3171	2	29.02	14	1878	OB3612.raw	3.47E4	2	2	401	411	
R.LNAQRPDNR.L	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	38	46	
P.DIYNPQAGSLK.T	N	99.9	42.96	1204.6088	11	0.4	603.3119	2	26.84	14	1578	OB3612.raw	8.34E3	2	2	366	376	
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.8	40.81	1534.6470	12	-0.3	768.3305	2	24.19	14	1295	OB3612.raw	7.29E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.VYDEELQEGHVLVVPQNFAVAG.K	N	99.8	39.87	2412.1960	22	-0.3	1207.1050	2	32.70	14	2381	OB3612.raw	3.31E4	1	1	435	456	
N.ALFVPHYNTNAHSIIYALR.G	N	99.8	39.75	2199.1589	19	0.4	734.0605	3	30.90	14	2137	OB3612.raw	2.97E5	1	1	402	420	
R.AHVQVVDSN(+.98)G.N	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	423	432	Deamidation (NQ)
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	507	515	Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.8	38.20	1535.6311	12	-0.1	768.8228	2	25.05	14	1374	OB3612.raw	1.25E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	510	515	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.90	834.4963	7	0.0	418.2554	2	28.71	14	1835	OB3612.raw	1.05E6	4	4	414	420	
N.DLNLLILR.W	N	99.8	37.67	968.6018	8	-1.0	485.3077	2	33.63	14	2513	OB3612.raw	3.43E4	1	1	380	387	
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.7	36.76	1534.6470	12	-0.7	768.3303	2	24.71	14	1341	OB3612.raw	1.11E4	4	4	26	37	Carbamidomethylation; Deamidation (NQ)
N.TN(+.98)AHSIIYALR.G	N	99.7	36.73	1258.6670	11	0.1	630.3408	2	29.11	14	1892	OB3612.raw	5.53E3	2	2	410	420	Deamidation (NQ)
T.NAHSIIYALR.G	N	99.7	36.68	1156.6353	10	-0.9	386.5520	3	27.65	14	1688	OB3612.raw	2.27E4	1	1	411	420	
R.VYDEELQEGHVLVVPQNF.A	N	99.7	36.57	2114.0320	18	-0.5	1058.0227	2	32.43	14	2346	OB3612.raw	1.29E5	1	1	435	452	
R.NALFVP(+15.99)HYNTNAHSIIYALR.G	N	99.6	35.76	2329.1968	20	-1.1	583.3058	4	30.64	14	2100	OB3612.raw	1.77E4	1	1	401	420	Hydroxylation Pro
N.GIEETIC(+57.02)TASVKK.N	N	99.6	35.24	1434.7388	13	-0.1	718.3766	2	25.88	14	1457	OB3612.raw	4.72E4	1	1	345	357	Carbamidomethylation

R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	507	515	Deamidation (NQ)
H.YN(+.98)TNAHSIIYALR.G	N	99.6	34.60	1535.7732	13	-3.0	768.8915	2	29.68	14	1970	OB3612.raw	0	1	1	408	420	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.5	33.83	1535.6311	12	0.5	768.8232	2	25.16	14	1385	OB3612.raw	1.25E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.RFNLAGNHEQEFLR.Y	N	99.5	33.64	1729.8647	14	-2.6	577.6274	3	27.60	14	1681	OB3612.raw	2.7E4	1	1	197	210	
R.SLPYSP(+15.99)YSP(+15.99)Q(+.98)SQPRQ(+.98).E	N	99.5	33.49	1767.7950	15	0.7	884.9054	2	26.43	14	1524	OB3612.raw	3.53E3	1	1	219	233	Hydroxylation Pro; Deamidation (NQ)
K.TAN(+.98)DLNLLILR.W	N	99.5	32.90	1255.7136	11	6.0	628.8679	2	33.49	14	2494	OB3612.raw	6.09E6	3	3	377	387	Deamidation (NQ)
D.IYNPQAGSLK.T	N	99.5	32.86	1089.5818	10	0.8	545.7986	2	24.84	14	1351	OB3612.raw	9.56E3	1	1	367	376	
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.1	31.79	1535.6311	12	1.4	768.8239	2	25.38	14	1406	OB3612.raw	1.25E4	1	1	26	37	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.1	31.34	1535.6311	12	1.6	768.8240	2	25.31	14	1398	OB3612.raw	1.25E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
N.SYGLPR.E	N	99.1	31.30	691.3653	6	-0.5	346.6898	2	25.05	14	1373	OB3612.raw	1.53E4	1	1	497	502	
R.SLPYSP(+15.99)YSP(+15.99)QSQ(+.98)PR.Q	N	99.1	30.73	1638.7524	14	-0.5	820.3831	2	26.35	14	1514	OB3612.raw	9.77E3	1	1	219	232	Hydroxylation Pro; Deamidation (NQ)
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	423	431	
N.RSPDIYNPQAGSLK.T	N	98.7	30.18	1544.7947	14	-1.8	515.9379	3	25.49	14	1415	OB3612.raw	1.64E4	1	1	363	376	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	98.7	30.00	1535.6311	12	-1.1	768.8220	2	25.29	14	1396	OB3612.raw	1.25E4	1	1	26	37	Deamidation (NQ); Carbamidomethylation
R.VYDEELQEGHVLVVPQN.F	N	98.6	29.18	1966.9636	17	0.9	984.4899	2	30.02	14	2016	OB3612.raw	3.6E4	1	1	435	451	
R.FNLAGNHEQEFLR.Y	N	98.6	29.05	1573.7637	13	-1.1	525.5946	3	28.84	14	1852	OB3612.raw	1.24E5	2	2	198	210	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	28.91	1536.6151	12	-0.7	769.3143	2	25.70	14	1437	OB3612.raw	4.4E3	1	1	26	37	Deamidation (NQ); Carbamidomethylation
total 75 peptides																		

Q647H4|Q647H4_ARAHY

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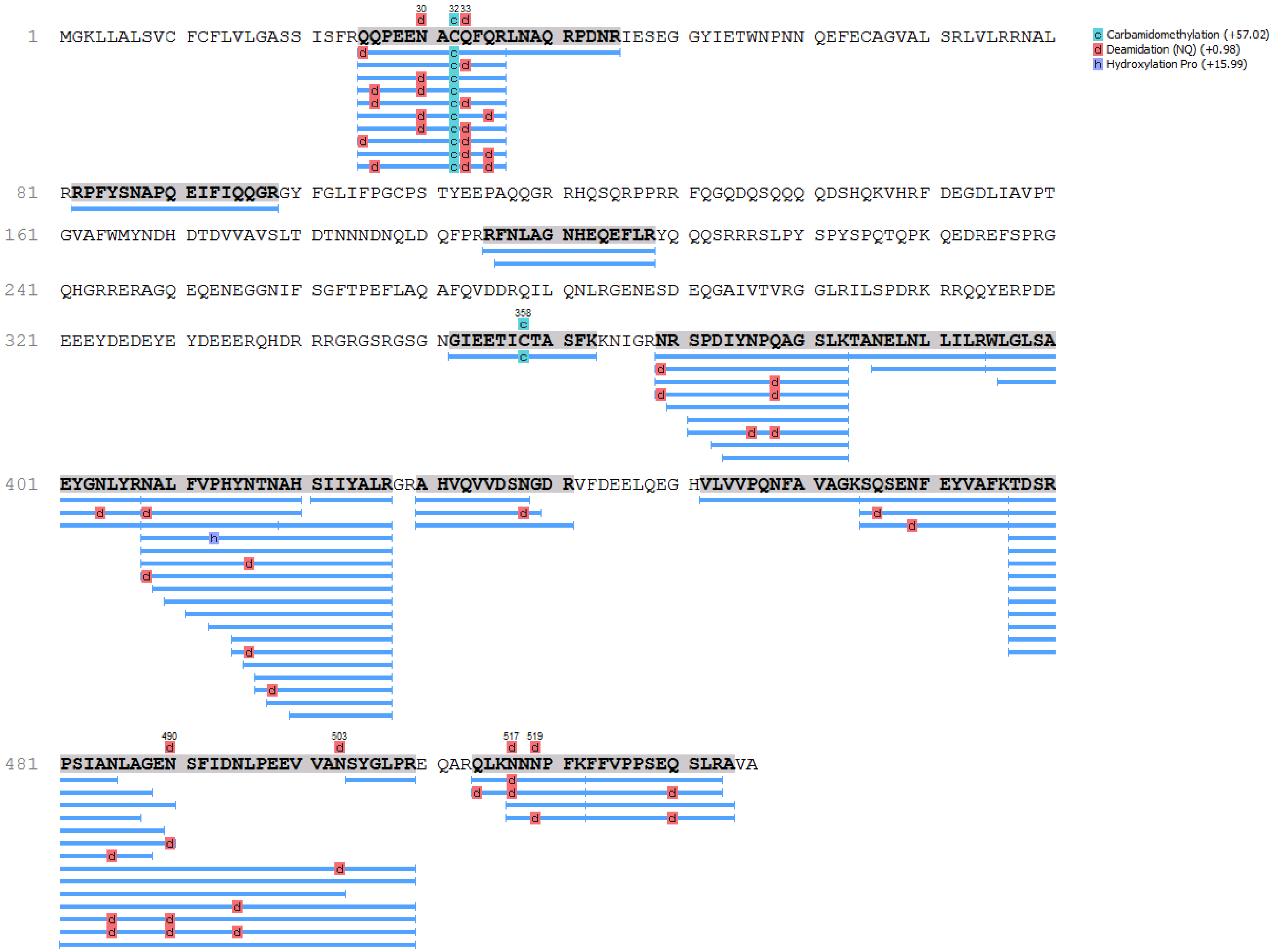
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 14	#Spec	#Spec Sample 14	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.00	1540.7673	13	0.2	771.3911	2	32.73	14	2386	OB3612.raw	1.51E7	127	127	395	407	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	88.61	2313.2019	20	-0.8	1157.6073	2	31.19	14	2179	OB3612.raw	1.07E8	18	18	408	427	
K.SQSENFEYVAFK.T	N	99.9	87.38	1447.6619	12	0.7	724.8387	2	29.96	14	2008	OB3612.raw	3.29E6	13	13	465	476	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	77.73	2314.1858	20	1.6	1158.1021	2	31.67	14	2243	OB3612.raw	8.07E5	2	2	408	427	Deamidation (NQ)

K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	75.32	3544.7434	33	1.6	1182.5903	3	35.34	14	2746	OB3612.raw	1.06E7	23	23	477	509	
R.SPDIYNPQAGSLK.T	N	99.9	75.03	1388.6936	13	0.1	695.3541	2	27.28	14	1636	OB3612.raw	4.8E6	21	21	371	383	
R.RPFYSNAPQEIFIQQGR.G	N	99.9	69.65	2050.0383	17	-0.2	684.3533	3	29.88	14	1996	OB3612.raw	3.21E5	3	3	82	98	
V.PHYNTNAHSIIYALR.G	N	99.9	67.94	1768.9009	15	0.3	885.4580	2	30.91	14	2138	OB3612.raw	2.27E5	1	1	413	427	
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	67.34	3545.7273	33	2.2	1182.9189	3	34.83	14	2677	OB3612.raw	2.02E6	7	7	477	509	Deamidation (NQ)
K.SQSEN(+.98)FEYVAFK.T	N	99.9	66.60	1448.6459	12	3.8	725.3329	2	30.36	14	2062	OB3612.raw	2.42E5	1	1	465	476	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.69	2314.1858	20	3.8	772.4055	3	31.92	14	2278	OB3612.raw	5.24E6	4	4	408	427	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	62.78	1268.7452	11	1.5	635.3809	2	33.07	14	2434	OB3612.raw	1.22E7	47	47	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	62.40	3545.7273	33	0.6	1182.9171	3	34.64	14	2650	OB3612.raw	1.04E6	5	5	477	509	Deamidation (NQ)
W.LGLSAEYGNLYR.N	N	99.9	61.15	1354.6881	12	-1.4	678.3504	2	30.16	14	2035	OB3612.raw	1.85E4	1	1	396	407	
N.TNAHSIIYALR.G	N	99.9	60.51	1257.6830	11	0.4	629.8490	2	27.94	14	1729	OB3612.raw	7.51E5	5	5	417	427	
R.NALFVPHYNTNAH.S	N	99.9	60.25	1496.7161	13	-0.3	749.3651	2	27.32	14	1642	OB3612.raw	1.33E6	11	11	408	420	
H.YNTNAHSIIYALR.G	N	99.9	58.66	1534.7892	13	0.1	768.4020	2	28.98	14	1872	OB3612.raw	8.43E5	10	10	415	427	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	57.99	1354.6438	12	-0.4	678.3289	2	29.40	14	1931	OB3612.raw	6.41E3	1	1	352	363	Carbamidomethylation
R.SPDIYN(+.98)PQ(+.98)AGSLK.T	N	99.9	57.39	1390.6616	13	-1.9	696.3367	2	28.27	14	1774	OB3612.raw	1.51E5	1	1	371	383	Deamidation (NQ)
K.SQ(+.98)SENFEYVAFK.T	N	99.9	57.35	1448.6459	12	4.5	725.3335	2	30.18	14	2038	OB3612.raw	3.37E5	2	2	465	476	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.9	57.29	1658.8376	15	-1.1	553.9526	3	25.54	14	1421	OB3612.raw	6.28E5	8	8	369	383	
K.TDSRPSIANLAGEN.S	N	99.9	55.66	1443.6953	14	-0.3	722.8547	2	27.71	14	1696	OB3612.raw	1.31E5	5	5	477	490	
N.AHSIIYALR.G	N	99.9	53.88	1042.5923	9	-0.4	522.3032	2	27.28	14	1637	OB3612.raw	1.92E5	3	3	419	427	
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	53.78	1541.7513	13	5.8	771.8874	2	33.15	14	2446	OB3612.raw	6.85E6	2	2	395	407	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	53.37	1340.7816	13	-0.2	671.3979	2	30.15	14	2034	OB3612.raw	5.71E4	1	1	452	464	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	53.09	2128.1218	18	-1.3	710.3803	3	31.20	14	2180	OB3612.raw	7.71E5	4	4	410	427	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	53.03	1659.8217	15	-0.5	830.9177	2	26.37	14	1516	OB3612.raw	8.5E5	3	3	369	383	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.71	1444.6793	14	-0.4	723.3467	2	28.24	14	1770	OB3612.raw	7.9E4	1	1	477	490	Deamidation (NQ)
R.AHVQVVDSNGDR.V	Y	99.9	52.04	1295.6218	12	0.7	648.8187	2	22.07	14	1150	OB3612.raw	4.21E5	4	4	430	441	
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	517	522	
Y.NTNAHSIIYALR.G	N	99.9	51.22	1371.7258	12	-0.4	686.8699	2	28.06	14	1744	OB3612.raw	1.45E5	2	2	416	427	
K.TDSRPSIANLAGENSFIDNLPEEVVAN.S	N	99.9	51.16	2871.3887	27	0.9	958.1377	3	34.34	14	2609	OB3612.raw	1.62E5	2	2	477	503	
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	50.74	3085.5356	29	-0.1	1029.5190	3	36.50	14	2905	OB3612.raw	1.73E5	2	2	481	509	
L.FVPHYNTNAHSIIYALR.G	N	99.9	50.06	2015.0377	17	0.6	672.6869	3	31.15	14	2173	OB3612.raw	1.38E6	2	2	411	427	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	49.90	1534.6470	12	-1.1	768.3299	2	24.54	14	1327	OB3612.raw	3.85E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.81	1659.8217	15	0.2	554.2812	3	26.15	14	1488	OB3612.raw	8.5E5	2	2	369	383	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.77	1660.8057	15	-1.8	831.4086	2	26.98	14	1595	OB3612.raw	2.5E5	2	2	369	383	Deamidation (NQ)
K.FFVPPSEQSLR.A	Y	99.9	49.41	1305.6716	11	0.5	653.8434	2	29.27	14	1912	OB3612.raw	6E5	4	4	523	533	
A.HSIIYALR.G	N	99.9	48.25	971.5552	8	-0.9	486.7845	2	27.02	14	1601	OB3612.raw	3.57E4	2	2	420	427	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	99.9	46.96	1535.6311	12	-3.0	768.8205	2	24.95	14	1364	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAGEN(+.98)SFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	46.17	3547.6953	33	3.3	1183.5763	3	40.41	14	3425	OB3612.raw	1.9E3	1	1	477	509	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	46.14	1497.7001	13	-1.2	749.8564	2	28.28	14	1776	OB3612.raw	1.39E5	3	3	408	420	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	45.80	1329.6525	13	-1.9	665.8322	2	28.04	14	1742	OB3612.raw	5.27E4	1	1	477	489	
A.NELNLLILR.W	N	99.9	45.51	1096.6604	9	-0.5	549.3372	2	33.04	14	2430	OB3612.raw	2.23E4	1	1	386	394	
R.NALFVPHYNTN.A	N	99.9	45.46	1288.6200	11	-0.2	645.3171	2	29.02	14	1878	OB3612.raw	3.47E4	2	2	408	418	
R.LNAQRPDNR.I	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	37	45	
P.DIYNPQAGSLK.T	N	99.9	42.96	1204.6088	11	0.4	603.3119	2	26.84	14	1578	OB3612.raw	8.34E3	2	2	373	383	
K.FFVPPSEQSLRA.V	Y	99.8	41.22	1376.7087	12	-0.8	689.3611	2	29.61	14	1960	OB3612.raw	5.14E5	2	2	523	534	
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.8	40.81	1534.6470	12	-0.3	768.3305	2	24.19	14	1295	OB3612.raw	7.29E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIANLAG.E	N	99.8	40.01	1200.6099	12	-0.2	601.3121	2	27.54	14	1673	OB3612.raw	1.58E5	2	2	477	488	
N.ALFVPHYNTNAHSIIYALR.G	N	99.8	39.75	2199.1589	19	0.4	734.0605	3	30.90	14	2137	OB3612.raw	2.97E5	1	1	409	427	
R.AHVQVVDSN(+.98)G.D	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	430	439	Deamidation (NQ)
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	514	522	Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.8	38.20	1535.6311	12	-0.1	768.8228	2	25.05	14	1374	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation

K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	517	522	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.90	834.4963	7	0.0	418.2554	2	28.71	14	1835	OB3612.raw	1.05E6	4	4	421	427	
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.7	36.76	1534.6470	12	-0.7	768.3303	2	24.71	14	1341	OB3612.raw	1.11E4	4	4	25	36	Carbamidomethylation; Deamidation (NQ)
N.TN(+.98)AHSIIYALR.G	N	99.7	36.73	1258.6670	11	0.1	630.3408	2	29.11	14	1892	OB3612.raw	5.53E3	2	2	417	427	Deamidation (NQ)
T.NAHSIIYALR.G	N	99.7	36.68	1156.6353	10	-0.9	386.5520	3	27.65	14	1688	OB3612.raw	2.27E4	1	1	418	427	
K.FFVPPSEQ(+.98)SLRA.V	Y	99.7	36.27	1377.6927	12	0.0	689.8536	2	30.01	14	2014	OB3612.raw	2.55E5	1	1	523	534	Deamidation (NQ)
R.NALFVP(+15.99)HYNTNAHSIIYALR.G	N	99.6	35.76	2329.1968	20	-1.1	583.3058	4	30.64	14	2100	OB3612.raw	1.77E4	1	1	408	427	Hydroxylation Pro
K.TDSRPSIANLA.G	N	99.6	35.20	1143.5884	11	-0.7	572.8011	2	27.78	14	1706	OB3612.raw	5.94E4	1	1	477	487	
R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	514	522	Deamidation (NQ)
H.YN(+.98)TNAHSIIYALR.G	N	99.6	34.60	1535.7732	13	-3.0	768.8915	2	29.68	14	1970	OB3612.raw	0	1	1	415	427	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.5	33.83	1535.6311	12	0.5	768.8232	2	25.16	14	1385	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.RFNLAGNHEQEFLR.Y	N	99.5	33.64	1729.8647	14	-2.6	577.6274	3	27.60	14	1681	OB3612.raw	2.7E4	1	1	195	208	
D.IYNPQAGSLK.T	N	99.5	32.86	1089.5818	10	0.8	545.7986	2	24.84	14	1351	OB3612.raw	9.56E3	1	1	374	383	
K.FFVPPSEQ(+.98)SLR.A	Y	99.5	32.64	1306.6556	11	2.9	654.3370	2	29.57	14	1954	OB3612.raw	2.32E5	1	1	523	533	Deamidation (NQ)
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.1	31.79	1535.6311	12	1.4	768.8239	2	25.38	14	1406	OB3612.raw	1.25E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.1	31.34	1535.6311	12	1.6	768.8240	2	25.31	14	1398	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
N.SYGLPR.E	N	99.1	31.30	691.3653	6	-0.5	346.6898	2	25.05	14	1373	OB3612.raw	1.53E4	1	1	504	509	
K.TDSRPSIAN.L	N	99.1	30.69	959.4672	9	-0.7	480.7405	2	20.71	14	1057	OB3612.raw	5.09E3	1	1	477	485	
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	430	438	
N.RSPDIYNPQAGSLK.T	N	98.7	30.18	1544.7947	14	-1.8	515.9379	3	25.49	14	1415	OB3612.raw	1.64E4	1	1	370	383	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	98.7	30.00	1535.6311	12	-1.1	768.8220	2	25.29	14	1396	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAG.E	N	98.6	29.68	1201.5939	12	0.1	601.8043	2	28.43	14	1796	OB3612.raw	1.36E4	1	1	477	488	Deamidation (NQ)
R.FNLAGNHEQEFLR.Y	N	98.6	29.05	1573.7637	13	-1.1	525.5946	3	28.84	14	1852	OB3612.raw	1.24E5	2	2	196	208	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	28.91	1536.6151	12	-0.7	769.3143	2	25.70	14	1437	OB3612.raw	4.4E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAGEN(+.98)SFIDNLPEEVVANSYGLPR.E	N	98.6	28.82	3546.7114	33	5.9	1183.2513	3	41.26	14	3535	OB3612.raw	0	1	1	477	509	Deamidation (NQ)
total 79 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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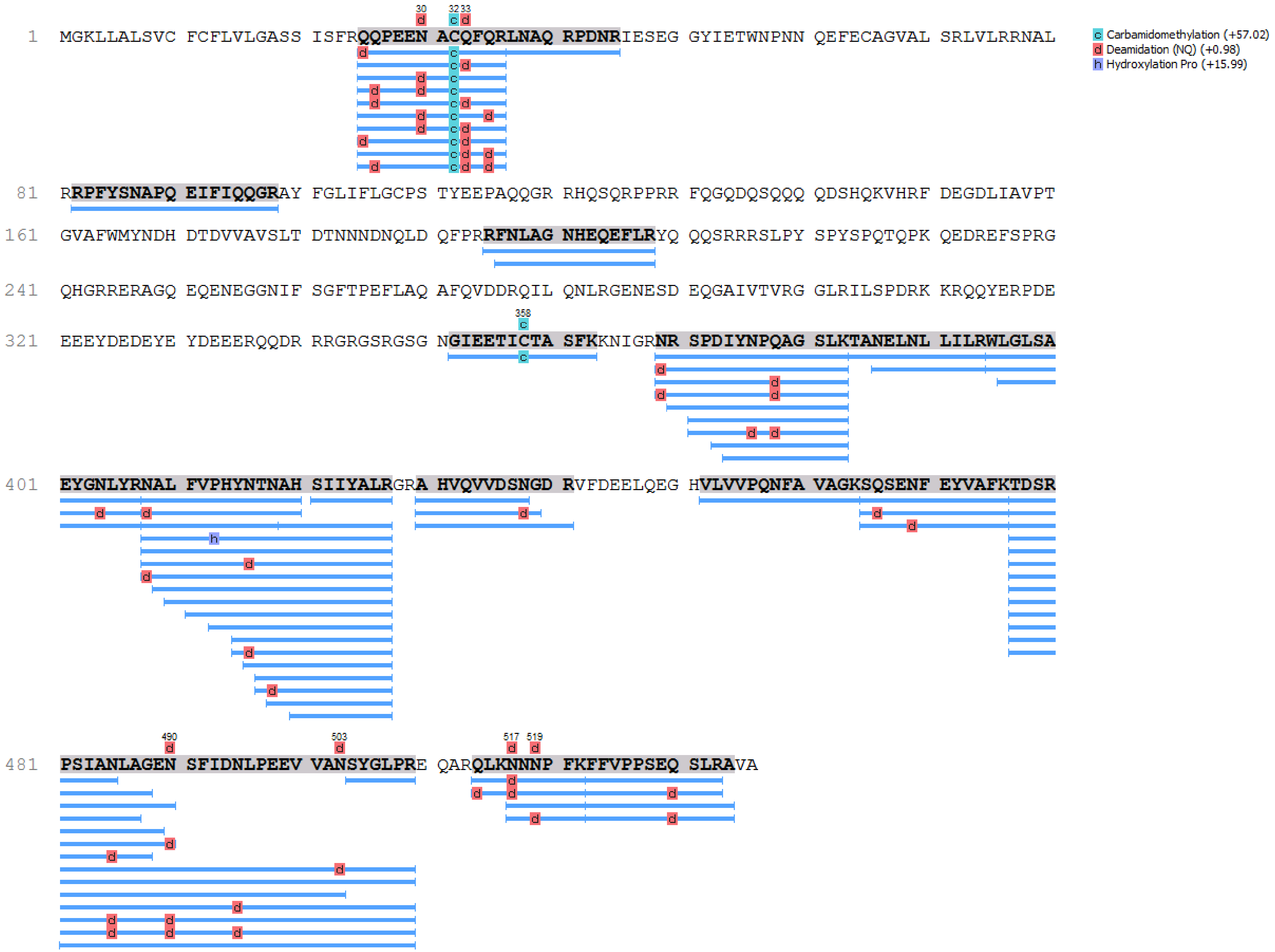
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 14	#Spec	#Spec Sample 14	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.00	1540.7673	13	0.2	771.3911	2	32.73	14	2386	OB3612.raw	1.51E7	127	127	395	407	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	88.61	2313.2019	20	-0.8	1157.6073	2	31.19	14	2179	OB3612.raw	1.07E8	18	18	408	427	
K.SQSENFEYVAFK.T	N	99.9	87.38	1447.6619	12	0.7	724.8387	2	29.96	14	2008	OB3612.raw	3.29E6	13	13	465	476	
R.N(+.98)ALFVPHYNTNAHSIIYALR.G	N	99.9	77.73	2314.1858	20	1.6	1158.1021	2	31.67	14	2243	OB3612.raw	8.07E5	2	2	408	427	Deamidation (NQ)

K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	75.32	3544.7434	33	1.6	1182.5903	3	35.34	14	2746	OB3612.raw	1.06E7	23	23	477	509	
R.SPDIYNPQAGSLK.T	N	99.9	75.03	1388.6936	13	0.1	695.3541	2	27.28	14	1636	OB3612.raw	4.8E6	21	21	371	383	
R.RPFYSNAPQEIFIQQGR.A	N	99.9	69.65	2050.0383	17	-0.2	684.3533	3	29.88	14	1996	OB3612.raw	3.21E5	3	3	82	98	
V.PHYNTNAHSIIYALR.G	N	99.9	67.94	1768.9009	15	0.3	885.4580	2	30.91	14	2138	OB3612.raw	2.27E5	1	1	413	427	
K.TDSRPSIANLAGENSFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	67.34	3545.7273	33	2.2	1182.9189	3	34.83	14	2677	OB3612.raw	2.02E6	7	7	477	509	Deamidation (NQ)
K.SQSEN(+.98)FEYVAFK.T	N	99.9	66.60	1448.6459	12	3.8	725.3329	2	30.36	14	2062	OB3612.raw	2.42E5	1	1	465	476	Deamidation (NQ)
R.NALFVPHYN(+.98)TNAHSIIYALR.G	N	99.9	64.69	2314.1858	20	3.8	772.4055	3	31.92	14	2278	OB3612.raw	5.24E6	4	4	408	427	Deamidation (NQ)
K.TANELNLLILR.W	N	99.9	62.78	1268.7452	11	1.5	635.3809	2	33.07	14	2434	OB3612.raw	1.22E7	47	47	384	394	
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	99.9	62.40	3545.7273	33	0.6	1182.9171	3	34.64	14	2650	OB3612.raw	1.04E6	5	5	477	509	Deamidation (NQ)
W.LGLSAEYGNLYR.N	N	99.9	61.15	1354.6881	12	-1.4	678.3504	2	30.16	14	2035	OB3612.raw	1.85E4	1	1	396	407	
N.TNAHSIIYALR.G	N	99.9	60.51	1257.6830	11	0.4	629.8490	2	27.94	14	1729	OB3612.raw	7.51E5	5	5	417	427	
R.NALFVPHYNTNAH.S	N	99.9	60.25	1496.7161	13	-0.3	749.3651	2	27.32	14	1642	OB3612.raw	1.33E6	11	11	408	420	
H.YNTNAHSIIYALR.G	N	99.9	58.66	1534.7892	13	0.1	768.4020	2	28.98	14	1872	OB3612.raw	8.43E5	10	10	415	427	
N.GIEETIC(+57.02)TASFK.K	Y	99.9	57.99	1354.6438	12	-0.4	678.3289	2	29.40	14	1931	OB3612.raw	6.41E3	1	1	352	363	Carbamidomethylation
R.SPDIYN(+.98)PQ(+.98)AGSLK.T	N	99.9	57.39	1390.6616	13	-1.9	696.3367	2	28.27	14	1774	OB3612.raw	1.51E5	1	1	371	383	Deamidation (NQ)
K.SQ(+.98)SENFEYVAFK.T	N	99.9	57.35	1448.6459	12	4.5	725.3335	2	30.18	14	2038	OB3612.raw	3.37E5	2	2	465	476	Deamidation (NQ)
R.NRSPDIYNPQAGSLK.T	N	99.9	57.29	1658.8376	15	-1.1	553.9526	3	25.54	14	1421	OB3612.raw	6.28E5	8	8	369	383	
K.TDSRPSIANLAGEN.S	N	99.9	55.66	1443.6953	14	-0.3	722.8547	2	27.71	14	1696	OB3612.raw	1.31E5	5	5	477	490	
N.AHSIIYALR.G	N	99.9	53.88	1042.5923	9	-0.4	522.3032	2	27.28	14	1637	OB3612.raw	1.92E5	3	3	419	427	
R.WLGLSAEYGN(+.98)LYR.N	N	99.9	53.78	1541.7513	13	5.8	771.8874	2	33.15	14	2446	OB3612.raw	6.85E6	2	2	395	407	Deamidation (NQ)
H.VLVVPQNFAVAGK.S	N	99.9	53.37	1340.7816	13	-0.2	671.3979	2	30.15	14	2034	OB3612.raw	5.71E4	1	1	452	464	
A.LFVPHYNTNAHSIIYALR.G	N	99.9	53.09	2128.1218	18	-1.3	710.3803	3	31.20	14	2180	OB3612.raw	7.71E5	4	4	410	427	
R.N(+.98)RSPDIYNPQAGSLK.T	N	99.9	53.03	1659.8217	15	-0.5	830.9177	2	26.37	14	1516	OB3612.raw	8.5E5	3	3	369	383	Deamidation (NQ)
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.71	1444.6793	14	-0.4	723.3467	2	28.24	14	1770	OB3612.raw	7.9E4	1	1	477	490	Deamidation (NQ)
R.AHVQVVDSNGDR.V	Y	99.9	52.04	1295.6218	12	0.7	648.8187	2	22.07	14	1150	OB3612.raw	4.21E5	4	4	430	441	
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	517	522	
Y.NTNAHSIIYALR.G	N	99.9	51.22	1371.7258	12	-0.4	686.8699	2	28.06	14	1744	OB3612.raw	1.45E5	2	2	416	427	
K.TDSRPSIANLAGENSFIDNLPEEVVAN.S	N	99.9	51.16	2871.3887	27	0.9	958.1377	3	34.34	14	2609	OB3612.raw	1.62E5	2	2	477	503	
R.PSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	50.74	3085.5356	29	-0.1	1029.5190	3	36.50	14	2905	OB3612.raw	1.73E5	2	2	481	509	
L.FVPHYNTNAHSIIYALR.G	N	99.9	50.06	2015.0377	17	0.6	672.6869	3	31.15	14	2173	OB3612.raw	1.38E6	2	2	411	427	
R.QQPEEN(+.98)AC(+57.02)QFQR.L	N	99.9	49.90	1534.6470	12	-1.1	768.3299	2	24.54	14	1327	OB3612.raw	3.85E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.NRSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.81	1659.8217	15	0.2	554.2812	3	26.15	14	1488	OB3612.raw	8.5E5	2	2	369	383	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	99.9	49.77	1660.8057	15	-1.8	831.4086	2	26.98	14	1595	OB3612.raw	2.5E5	2	2	369	383	Deamidation (NQ)
K.FFVPPSEQSLR.A	Y	99.9	49.41	1305.6716	11	0.5	653.8434	2	29.27	14	1912	OB3612.raw	6E5	4	4	523	533	
A.HSIIYALR.G	N	99.9	48.25	971.5552	8	-0.9	486.7845	2	27.02	14	1601	OB3612.raw	3.57E4	2	2	420	427	
R.QQ(+.98)PEEN(+.98)AC(+57.02)QFQR.L	N	99.9	46.96	1535.6311	12	-3.0	768.8205	2	24.95	14	1364	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAGEN(+.98)SFIDN(+.98)LPEEVVANSYGLPR.E	N	99.9	46.17	3547.6953	33	3.3	1183.5763	3	40.41	14	3425	OB3612.raw	1.9E3	1	1	477	509	Deamidation (NQ)
R.N(+.98)ALFVPHYNTNAH.S	N	99.9	46.14	1497.7001	13	-1.2	749.8564	2	28.28	14	1776	OB3612.raw	1.39E5	3	3	408	420	Deamidation (NQ)
K.TDSRPSIANLAGE.N	N	99.9	45.80	1329.6525	13	-1.9	665.8322	2	28.04	14	1742	OB3612.raw	5.27E4	1	1	477	489	
A.NELNLLILR.W	N	99.9	45.51	1096.6604	9	-0.5	549.3372	2	33.04	14	2430	OB3612.raw	2.23E4	1	1	386	394	
R.NALFVPHYNTN.A	N	99.9	45.46	1288.6200	11	-0.2	645.3171	2	29.02	14	1878	OB3612.raw	3.47E4	2	2	408	418	
R.LNAQRPDNR.I	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	37	45	
P.DIYNPQAGSLK.T	N	99.9	42.96	1204.6088	11	0.4	603.3119	2	26.84	14	1578	OB3612.raw	8.34E3	2	2	373	383	
K.FFVPPSEQSLRA.V	Y	99.8	41.22	1376.7087	12	-0.8	689.3611	2	29.61	14	1960	OB3612.raw	5.14E5	2	2	523	534	
R.Q(+.98)QPEENAC(+57.02)QFQR.L	N	99.8	40.81	1534.6470	12	-0.3	768.3305	2	24.19	14	1295	OB3612.raw	7.29E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIANLAG.E	N	99.8	40.01	1200.6099	12	-0.2	601.3121	2	27.54	14	1673	OB3612.raw	1.58E5	2	2	477	488	
N.ALFVPHYNTNAHSIIYALR.G	N	99.8	39.75	2199.1589	19	0.4	734.0605	3	30.90	14	2137	OB3612.raw	2.97E5	1	1	409	427	
R.AHVQVVDSN(+.98)G.D	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	430	439	Deamidation (NQ)
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	514	522	Deamidation (NQ)
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQR.L	N	99.8	38.20	1535.6311	12	-0.1	768.8228	2	25.05	14	1374	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation

K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	517	522	Deamidation (NQ)
H.SIIYALR.G	N	99.8	37.90	834.4963	7	0.0	418.2554	2	28.71	14	1835	OB3612.raw	1.05E6	4	4	421	427	
R.QQPEENAC(+57.02)Q(+.98)FQR.L	N	99.7	36.76	1534.6470	12	-0.7	768.3303	2	24.71	14	1341	OB3612.raw	1.11E4	4	4	25	36	Carbamidomethylation; Deamidation (NQ)
N.TN(+.98)AHSIIYALR.G	N	99.7	36.73	1258.6670	11	0.1	630.3408	2	29.11	14	1892	OB3612.raw	5.53E3	2	2	417	427	Deamidation (NQ)
T.NAHSIIYALR.G	N	99.7	36.68	1156.6353	10	-0.9	386.5520	3	27.65	14	1688	OB3612.raw	2.27E4	1	1	418	427	
K.FFVPPSEQ(+.98)SLRA.V	Y	99.7	36.27	1377.6927	12	0.0	689.8536	2	30.01	14	2014	OB3612.raw	2.55E5	1	1	523	534	Deamidation (NQ)
R.NALFVP(+15.99)HYNTNAHSIIYALR.G	N	99.6	35.76	2329.1968	20	-1.1	583.3058	4	30.64	14	2100	OB3612.raw	1.77E4	1	1	408	427	Hydroxylation Pro
K.TDSRPSIANLA.G	N	99.6	35.20	1143.5884	11	-0.7	572.8011	2	27.78	14	1706	OB3612.raw	5.94E4	1	1	477	487	
R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	514	522	Deamidation (NQ)
H.YN(+.98)TNAHSIIYALR.G	N	99.6	34.60	1535.7732	13	-3.0	768.8915	2	29.68	14	1970	OB3612.raw	0	1	1	415	427	Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)QFQ(+.98)R.L	N	99.5	33.83	1535.6311	12	0.5	768.8232	2	25.16	14	1385	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
R.RFNLAGNHEQEFLR.Y	N	99.5	33.64	1729.8647	14	-2.6	577.6274	3	27.60	14	1681	OB3612.raw	2.7E4	1	1	195	208	
D.IYNPQAGSLK.T	N	99.5	32.86	1089.5818	10	0.8	545.7986	2	24.84	14	1351	OB3612.raw	9.56E3	1	1	374	383	
K.FFVPPSEQ(+.98)SLR.A	Y	99.5	32.64	1306.6556	11	2.9	654.3370	2	29.57	14	1954	OB3612.raw	2.32E5	1	1	523	533	Deamidation (NQ)
R.QQPEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	99.1	31.79	1535.6311	12	1.4	768.8239	2	25.38	14	1406	OB3612.raw	1.25E4	1	1	25	36	Carbamidomethylation; Deamidation (NQ)
R.QQPEEN(+.98)AC(+57.02)Q(+.98)FQR.L	N	99.1	31.34	1535.6311	12	1.6	768.8240	2	25.31	14	1398	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
N.SYGLPR.E	N	99.1	31.30	691.3653	6	-0.5	346.6898	2	25.05	14	1373	OB3612.raw	1.53E4	1	1	504	509	
K.TDSRPSIAN.L	N	99.1	30.69	959.4672	9	-0.7	480.7405	2	20.71	14	1057	OB3612.raw	5.09E3	1	1	477	485	
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	430	438	
N.RSPDIYNPQAGSLK.T	N	98.7	30.18	1544.7947	14	-1.8	515.9379	3	25.49	14	1415	OB3612.raw	1.64E4	1	1	370	383	
R.Q(+.98)QPEENAC(+57.02)Q(+.98)FQR.L	N	98.7	30.00	1535.6311	12	-1.1	768.8220	2	25.29	14	1396	OB3612.raw	1.25E4	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAG.E	N	98.6	29.68	1201.5939	12	0.1	601.8043	2	28.43	14	1796	OB3612.raw	1.36E4	1	1	477	488	Deamidation (NQ)
R.FNLAGNHEQEFLR.Y	N	98.6	29.05	1573.7637	13	-1.1	525.5946	3	28.84	14	1852	OB3612.raw	1.24E5	2	2	196	208	
R.QQ(+.98)PEENAC(+57.02)Q(+.98)FQ(+.98)R.L	N	98.6	28.91	1536.6151	12	-0.7	769.3143	2	25.70	14	1437	OB3612.raw	4.4E3	1	1	25	36	Deamidation (NQ); Carbamidomethylation
K.TDSRPSIAN(+.98)LAGEN(+.98)SFIDNLPEEVVANSYGLPR.E	N	98.6	28.82	3546.7114	33	5.9	1183.2513	3	41.26	14	3535	OB3612.raw	0	1	1	477	509	Deamidation (NQ)
total 79 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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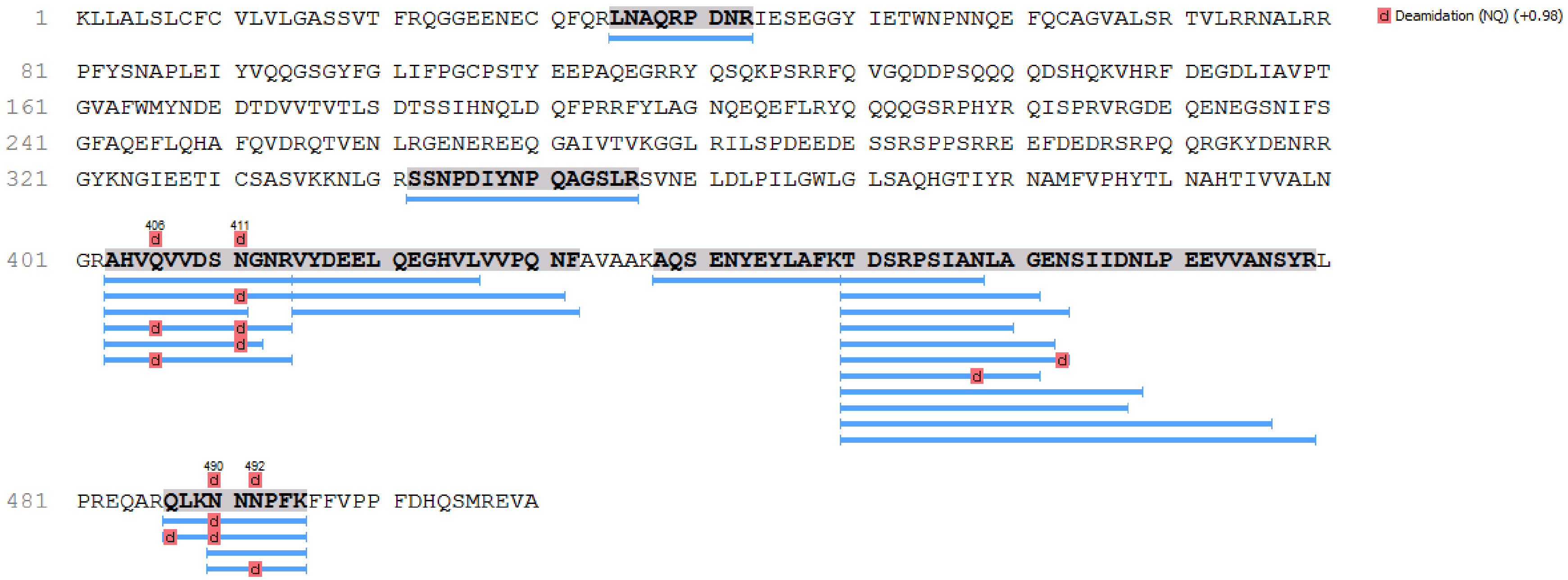
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQR**LNAQRP DNR**IESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG R**SSNPDIYNP QAGSLR**SVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN

401 GR**AHVQVVDS NGNRVYDEEL QEGHVLVVPQ NF**AVAAK**AQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYR**L

481 PREQAR**QLKN NNPFK**FFVPP FDHQSMREVA

d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 14	#Spec	#Spec Sample 14	Start	End	PTM
R.AHVQVVDSNGNR.V	N	99.9	70.64	1294.6378	12	0.2	648.3263	2	19.76	14	983	OB3612.raw	1.67E6	9	9	403	414	
R.AHVQVVDSN(+.98)GNR.V	N	99.9	69.99	1295.6218	12	-0.2	648.8181	2	20.35	14	1029	OB3612.raw	4.21E5	4	4	403	414	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	66.20	1296.6058	12	0.1	649.3102	2	20.90	14	1070	OB3612.raw	2.07E5	2	2	403	414	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	65.75	3243.6006	30	1.9	1082.2095	3	34.08	14	2575	OB3612.raw	1.13E5	3	3	450	479	
K.TDSRPSIANLAGENSIIDN.L	N	99.9	59.96	1985.9653	19	0.6	993.9905	2	30.56	14	2090	OB3612.raw	3.55E4	1	1	450	468	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	59.42	1295.6218	12	-1.1	648.8175	2	21.70	14	1122	OB3612.raw	4.28E5	2	2	403	414	Deamidation (NQ)
R.VYDEELQEGHVL.V	N	99.9	58.80	1429.6725	12	-0.8	715.8430	2	29.23	14	1908	OB3612.raw	4.23E4	2	2	415	426	
K.TDSRPSIANLAGENSIID.N	N	99.9	57.32	1871.9225	18	-0.2	936.9683	2	30.89	14	2135	OB3612.raw	1.34E5	1	1	450	467	
K.TDSRPSIANLAGEN.S	N	99.9	55.66	1443.6953	14	-0.3	722.8547	2	27.71	14	1696	OB3612.raw	1.31E5	5	5	450	463	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.71	1444.6793	14	-0.4	723.3467	2	28.24	14	1770	OB3612.raw	7.9E4	1	1	450	463	Deamidation (NQ)
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	490	495	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	50.24	2837.4043	27	0.2	946.8089	3	33.91	14	2552	OB3612.raw	2.9E5	3	3	450	476	
R.SSNPDIYNPQAGSLR.S	Y	99.9	48.74	1617.7747	15	0.4	809.8949	2	27.20	14	1626	OB3612.raw	6.64E3	1	1	342	356	
K.TDSRPSIANLAGE.N	N	99.9	45.80	1329.6525	13	-1.9	665.8322	2	28.04	14	1742	OB3612.raw	5.27E4	1	1	450	462	
R.LNAQRPDNR.I	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	35	43	
K.TDSRPSIANLAG.E	N	99.8	40.01	1200.6099	12	-0.2	601.3121	2	27.54	14	1673	OB3612.raw	1.58E5	2	2	450	461	
R.AHVQVVDSN(+.98)G.N	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	403	412	Deamidation (NQ)
K.AQSENYEYLAFK.T	Y	99.8	39.21	1461.6776	12	-0.2	731.8459	2	30.93	14	2141	OB3612.raw	6.99E5	1	1	438	449	
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	487	495	Deamidation (NQ)
K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	490	495	Deamidation (NQ)
R.VYDEELQEGHVLVVPQNF.A	N	99.7	36.57	2114.0320	18	-0.5	1058.0227	2	32.43	14	2346	OB3612.raw	1.29E5	1	1	415	432	
K.TDSRPSIANLA.G	N	99.6	35.20	1143.5884	11	-0.7	572.8011	2	27.78	14	1706	OB3612.raw	5.94E4	1	1	450	460	
R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	487	495	Deamidation (NQ)
K.TDSRPSIAN.L	N	99.1	30.69	959.4672	9	-0.7	480.7405	2	20.71	14	1057	OB3612.raw	5.09E3	1	1	450	458	
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	403	411	
K.TDSRPSIAN(+.98)LAG.E	N	98.6	29.68	1201.5939	12	0.1	601.8043	2	28.43	14	1796	OB3612.raw	1.36E4	1	1	450	461	Deamidation (NQ)
R.VYDEELQEGHVLVVPQN.F	N	98.6	29.18	1966.9636	17	0.9	984.4899	2	30.02	14	2016	OB3612.raw	3.6E4	1	1	415	431	
total 27 peptides																		

Q0GM57|Q0GM57_ARAHY

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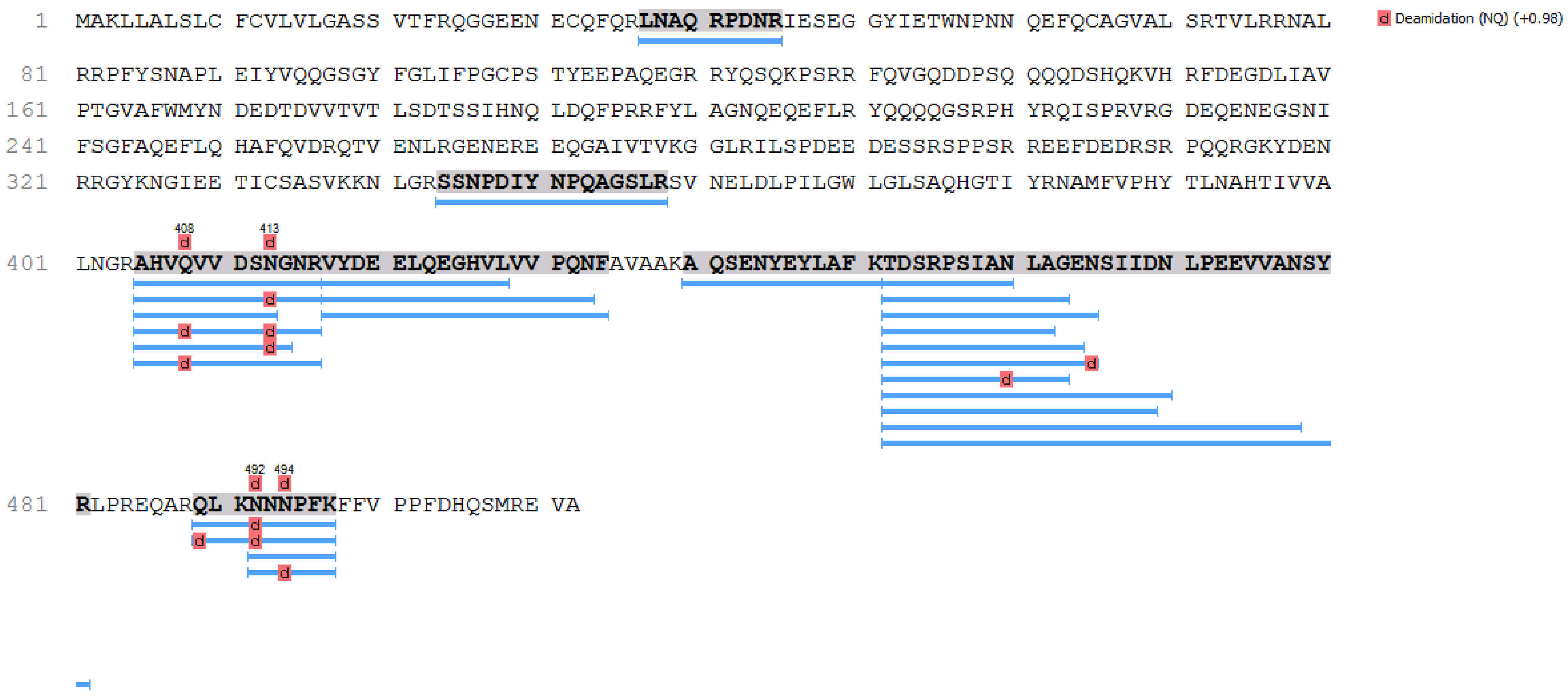
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQR**LNAQ RPDNR**IESEG GYIETWNPNN QEFQCAGVAL SRTVLRRNAL

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV

161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI

241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN

321 RRGYKNGIEE TICSASVKKN LGR**SSNPDIY NPQAGSLR**SV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA

401 LNGR**AHVQVV DSNGNRVYDE ELQEGHVLVV PQNF**AVAAK**A QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY**

481 **R**LPREQAR**QL KNNNPFK**FFV PPFDHQSMRE VA

d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 14	#Spec	#Spec Sample 14	Start	End	PTM
R.AHVQVVDSNGNR.V	N	99.9	70.64	1294.6378	12	0.2	648.3263	2	19.76	14	983	OB3612.raw	1.67E6	9	9	405	416	
R.AHVQVVDSN(+.98)GNR.V	N	99.9	69.99	1295.6218	12	-0.2	648.8181	2	20.35	14	1029	OB3612.raw	4.21E5	4	4	405	416	Deamidation (NQ)
R.AHVQ(+.98)VVDSN(+.98)GNR.V	N	99.9	66.20	1296.6058	12	0.1	649.3102	2	20.90	14	1070	OB3612.raw	2.07E5	2	2	405	416	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVANSYR.L	Y	99.9	65.75	3243.6006	30	1.9	1082.2095	3	34.08	14	2575	OB3612.raw	1.13E5	3	3	452	481	
K.TDSRPSIANLAGENSIIDN.L	N	99.9	59.96	1985.9653	19	0.6	993.9905	2	30.56	14	2090	OB3612.raw	3.55E4	1	1	452	470	
R.AHVQ(+.98)VVDSNGNR.V	N	99.9	59.42	1295.6218	12	-1.1	648.8175	2	21.70	14	1122	OB3612.raw	4.28E5	2	2	405	416	Deamidation (NQ)
R.VYDEELQEGHVL.V	N	99.9	58.80	1429.6725	12	-0.8	715.8430	2	29.23	14	1908	OB3612.raw	4.23E4	2	2	417	428	
K.TDSRPSIANLAGENSIID.N	N	99.9	57.32	1871.9225	18	-0.2	936.9683	2	30.89	14	2135	OB3612.raw	1.34E5	1	1	452	469	
K.TDSRPSIANLAGEN.S	N	99.9	55.66	1443.6953	14	-0.3	722.8547	2	27.71	14	1696	OB3612.raw	1.31E5	5	5	452	465	
K.TDSRPSIANLAGEN(+.98).S	N	99.9	52.71	1444.6793	14	-0.4	723.3467	2	28.24	14	1770	OB3612.raw	7.9E4	1	1	452	465	Deamidation (NQ)
K.NNNPFK.F	N	99.9	51.80	732.3555	6	0.5	367.1852	2	21.94	14	1141	OB3612.raw	3.57E5	5	5	492	497	
K.TDSRPSIANLAGENSIIDNLPEEVVAN.S	N	99.9	50.24	2837.4043	27	0.2	946.8089	3	33.91	14	2552	OB3612.raw	2.9E5	3	3	452	478	
R.SSNPDIYNPQAGSLR.S	Y	99.9	48.74	1617.7747	15	0.4	809.8949	2	27.20	14	1626	OB3612.raw	6.64E3	1	1	344	358	
K.TDSRPSIANLAGE.N	N	99.9	45.80	1329.6525	13	-1.9	665.8322	2	28.04	14	1742	OB3612.raw	5.27E4	1	1	452	464	
R.LNAQRPDNR.I	N	99.9	45.20	1082.5581	9	0.1	361.8600	3	18.13	14	862	OB3612.raw	1.91E4	2	2	37	45	
K.TDSRPSIANLAG.E	N	99.8	40.01	1200.6099	12	-0.2	601.3121	2	27.54	14	1673	OB3612.raw	1.58E5	2	2	452	463	
R.AHVQVVDSN(+.98)G.N	N	99.8	39.26	1025.4778	10	2.8	513.7476	2	21.66	14	1117	OB3612.raw	9.6E3	3	3	405	414	Deamidation (NQ)
K.AQSENYEYLAFK.T	Y	99.8	39.21	1461.6776	12	-0.2	731.8459	2	30.93	14	2141	OB3612.raw	6.99E5	1	1	440	451	
R.Q(+.98)LKN(+.98)NNPFK.F	N	99.8	38.25	1103.5610	9	0.2	552.7879	2	24.52	14	1325	OB3612.raw	9.82E4	3	3	489	497	Deamidation (NQ)
K.NNN(+.98)PFK.F	N	99.8	37.92	733.3395	6	0.4	367.6772	2	22.62	14	1185	OB3612.raw	2.91E4	1	1	492	497	Deamidation (NQ)

R.VYDEELQEGHVLVVPQNF.A	N	99.7	36.57	2114.0320	18	-0.5	1058.0227	2	32.43	14	2346	OB3612.raw	1.29E5	1	1	417	434	
K.TDSRPSIANLA.G	N	99.6	35.20	1143.5884	11	-0.7	572.8011	2	27.78	14	1706	OB3612.raw	5.94E4	1	1	452	462	
R.QLKN(+.98)NNPFK.F	N	99.6	34.70	1102.5770	9	-1.4	552.2950	2	24.06	14	1283	OB3612.raw	4.06E4	1	1	489	497	Deamidation (NQ)
K.TDSRPSIAN.L	N	99.1	30.69	959.4672	9	-0.7	480.7405	2	20.71	14	1057	OB3612.raw	5.09E3	1	1	452	460	
R.AHVQVVDSN.G	N	98.8	30.39	967.4723	9	-3.0	484.7420	2	20.75	14	1061	OB3612.raw	2E3	1	1	405	413	
K.TDSRPSIAN(+.98)LAG.E	N	98.6	29.68	1201.5939	12	0.1	601.8043	2	28.43	14	1796	OB3612.raw	1.36E4	1	1	452	463	Deamidation (NQ)
R.VYDEELQEGHVLVVPQN.F	N	98.6	29.18	1966.9636	17	0.9	984.4899	2	30.02	14	2016	OB3612.raw	3.6E4	1	1	417	433	
total 27 peptides																		

Peptide List

Summary

1. Notes

Spot G from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

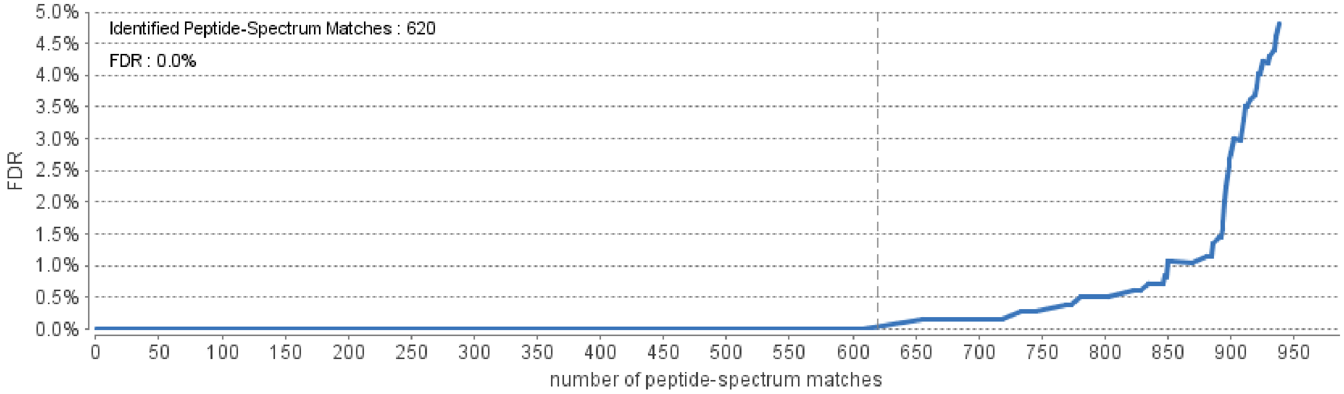
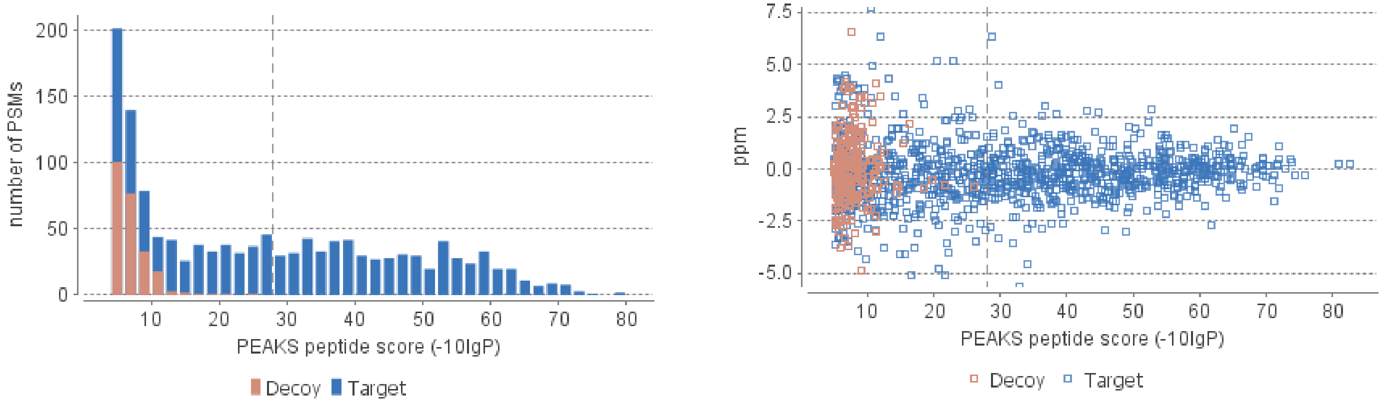


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

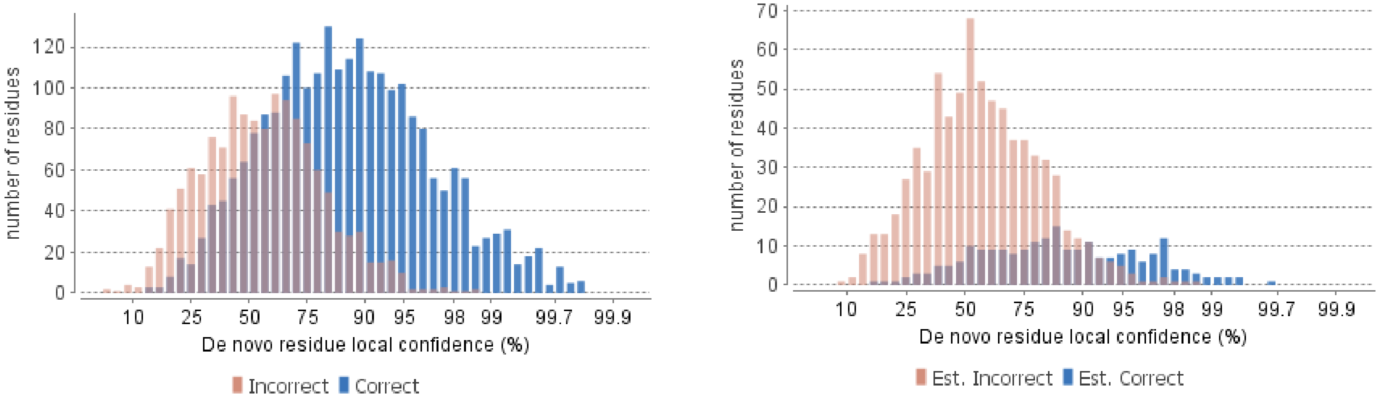


Table 1. Statistics of data.

# of MS scans	2637
# of MS/MS scans	5060

Table 2. Result filtration parameters.

Peptide -10lgP	≥28
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	597
Peptide sequences	145
Protein groups	3
Proteins	4
Proteins (#Unique Peptides)	0 (>2); 1 (=2); 3 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	96

Table 4. PTM profile.

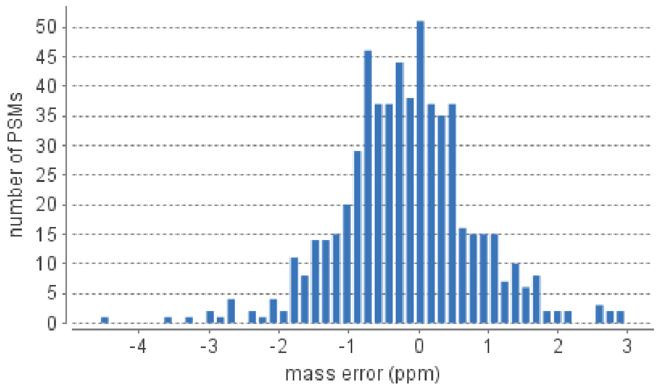
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	125	82.73	1.03E5	1000.00
Deamidation	.98	NQ	22	69.47	7.61E4	110.71
Oxidation	15.99	M	7	67.41	1.15E5	1000.00
HydPro	15.99	P	4	60.35	7.96E4	58.99

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm. ?

(a)

(b)



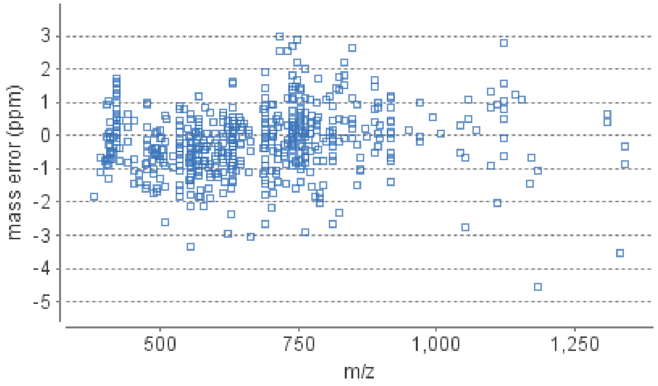


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 15	111	31	3	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3613.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 15	Area Sample 15	#Peptides	#Unique	#Spec Sample 15	PTM	Avg. Mass	Description
3	18	N1NG13|N1NG13_ARAHY	99.2	218.27	21	21	2.98E6	11	1	110	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
3	20	sp|P43238|ALL12_ARAHY	99.2	218.27	21	21	2.98E6	11	1	110	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
20	15	Q647H3|Q647H3_ARAHY	99.1	121.78	19	19	6.77E4	5	2	7	N	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
21	2	A1DZF0|A1DZF0_ARAHY	99.0	114.80	17	17	8.32E4	4	1	7	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
total 4 proteins													

N1NG13|N1NG13_ARAHY

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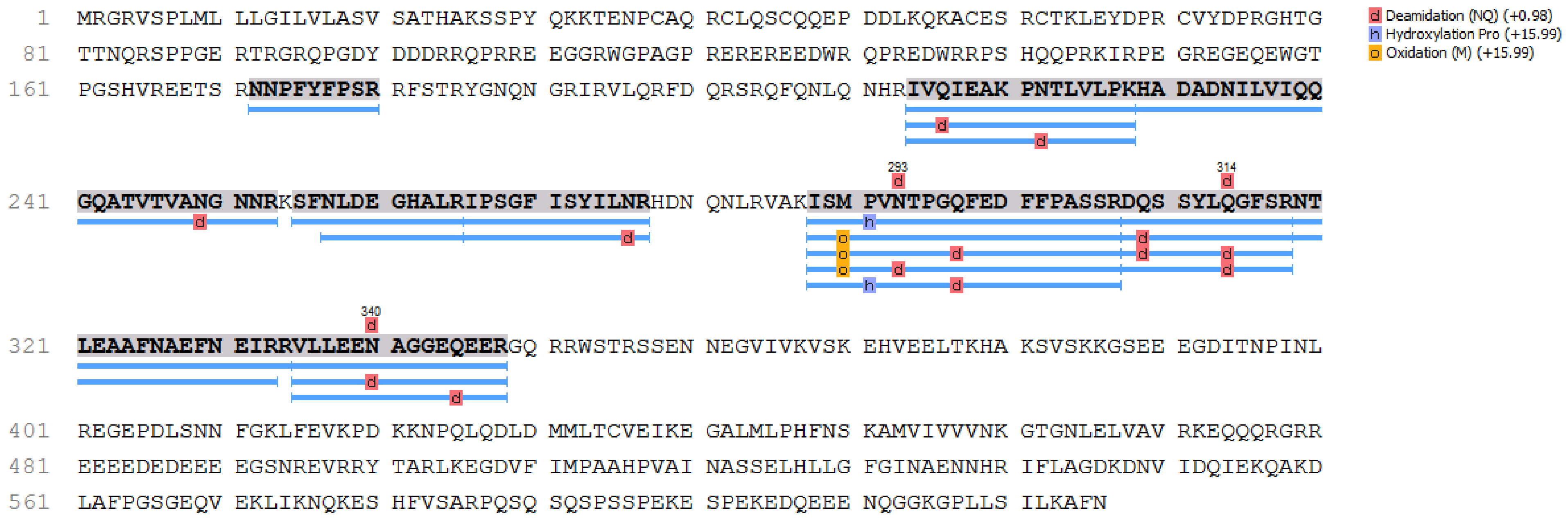
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERЕEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS R**NNPFYFPSR** RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHR**IVQIEAK PNTLVLPKHA DADNILVIQQ**
241 **GQATVTVANG NNR**K**SFNLDE GHALRIPSGF ISYILNR**HDN QNLRVAK**ISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT**
321 **LEAAFNAEFN EIRRVLLEEN AGGEQEER**GQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 15	#Spec	#Spec Sample 15	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	80.97	1737.8322	15	0.2	869.9235	2	33.25	15	2874	OB3613.raw	4.2E4	2	2	319	333	
K.SFNLDEGHALR.I	N	99.9	71.22	1257.6101	11	-0.3	629.8121	2	26.57	15	1982	OB3613.raw	1.45E6	15	15	255	265	
R.IPSGFISYILNR.H	N	99.9	70.33	1378.7609	12	0.2	690.3878	2	34.64	15	3062	OB3613.raw	5.13E6	26	26	266	277	
R.VLLEENAGGEQEER.G	N	99.9	69.90	1571.7427	14	-0.4	786.8783	2	24.91	15	1760	OB3613.raw	4.21E4	3	3	335	348	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.47	1287.5731	11	-0.3	644.7936	2	29.27	15	2346	OB3613.raw	9.89E4	3	3	308	318	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	68.54	1286.5891	11	-0.2	644.3017	2	28.73	15	2274	OB3613.raw	2.63E5	4	4	308	318	

K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	67.41	2243.0205	20	1.6	1122.5193	2	32.40	15	2761	OB3613.raw	1.15E5	1	1	288	307	Oxidation (M); Deamidation (NQ)
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	63.03	2243.0205	20	0.8	1122.5184	2	32.67	15	2797	OB3613.raw	2.61E5	4	4	288	307	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	60.72	1288.5571	11	0.5	645.2861	2	29.68	15	2401	OB3613.raw	2.47E4	2	2	308	318	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQFEDFFPASSR.D	N	99.9	60.35	2242.0364	20	0.5	1122.0260	2	32.00	15	2709	OB3613.raw	7.96E4	2	2	288	307	Hydroxylation Pro
R.IPSGFISYILN(+.98)R.H	N	99.9	58.66	1379.7449	12	-0.4	690.8795	2	34.94	15	3102	OB3613.raw	0	2	2	266	277	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	54.99	2243.0205	20	1.6	748.6820	3	32.76	15	2808	OB3613.raw	1.46E5	2	2	288	307	Hydroxylation Pro; Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	53.43	1287.5731	11	0.4	644.7941	2	29.96	15	2439	OB3613.raw	0	1	1	308	318	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	52.15	1572.7267	14	-2.0	787.3690	2	25.53	15	1841	OB3613.raw	1.74E4	2	2	335	348	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	50.49	2242.0364	20	0.0	748.3527	3	31.90	15	2695	OB3613.raw	2.71E5	2	2	288	307	Oxidation (M)
R.NNPFYFPSR.R	N	99.9	49.42	1140.5352	9	-0.8	571.2744	2	29.99	15	2442	OB3613.raw	1.07E6	15	15	172	180	
K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	49.06	2619.3000	25	-0.1	874.1072	3	28.55	15	2250	OB3613.raw	7.03E4	1	1	229	253	Deamidation (NQ)
R.IVQIEAKPNTLVLPK.H	Y	99.9	47.28	1662.0079	15	0.4	832.0116	2	27.93	15	2166	OB3613.raw	2.54E6	14	14	214	228	
R.VLLEENAGGEQ(+.98)EER.G	N	99.8	44.17	1572.7267	14	-1.7	787.3693	2	25.71	15	1865	OB3613.raw	1.74E4	1	1	335	348	Deamidation (NQ)
F.NLDEGHALR.I	N	99.7	40.38	1023.5097	9	0.5	512.7624	2	26.21	15	1933	OB3613.raw	2.74E3	1	1	257	265	
R.NTLEAAFNAEFNEIRR.V	N	99.6	38.29	1893.9332	16	0.2	947.9741	2	32.57	15	2784	OB3613.raw	5.78E5	4	4	319	334	
R.IVQ(+.98)IEAKPNTLVLPK.H	Y	98.9	34.90	1662.9919	15	-0.1	832.5032	2	28.24	15	2208	OB3613.raw	2.21E5	2	2	214	228	Deamidation (NQ)
R.IVQIEAKPN(+.98)TLVLPK.H	Y	96.9	29.70	1662.9919	15	-3.4	555.3361	3	28.91	15	2298	OB3613.raw	2.19E5	1	1	214	228	Deamidation (NQ)
total 23 peptides																		

sp|P43238|ALL12_ARAHY

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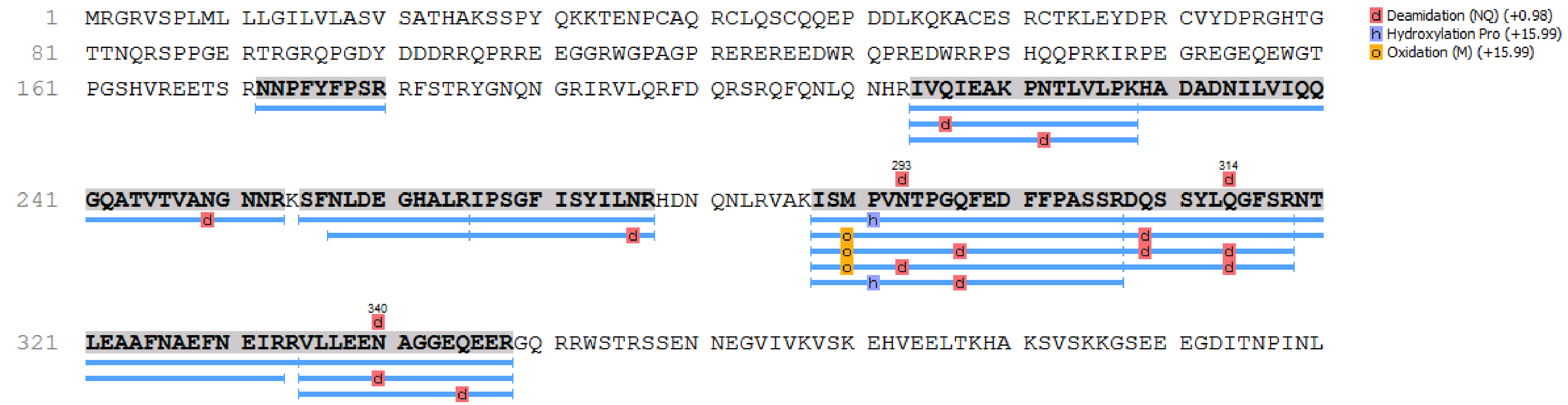
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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  1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
 81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 15	#Spec	#Spec Sample 15	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	80.97	1737.8322	15	0.2	869.9235	2	33.25	15	2874	OB3613.raw	4.2E4	2	2	319	333	
K.SFNLDEGHALR.I	N	99.9	71.22	1257.6101	11	-0.3	629.8121	2	26.57	15	1982	OB3613.raw	1.45E6	15	15	255	265	
R.IPSGFISYILNR.H	N	99.9	70.33	1378.7609	12	0.2	690.3878	2	34.64	15	3062	OB3613.raw	5.13E6	26	26	266	277	
R.VLLEENAGGEQEER.G	N	99.9	69.90	1571.7427	14	-0.4	786.8783	2	24.91	15	1760	OB3613.raw	4.21E4	3	3	335	348	
R.DQ(+.98)SSYLQGFSR.N	N	99.9	69.47	1287.5731	11	-0.3	644.7936	2	29.27	15	2346	OB3613.raw	9.89E4	3	3	308	318	Deamidation (NQ)
R.DQSSYLQGFSR.N	N	99.9	68.54	1286.5891	11	-0.2	644.3017	2	28.73	15	2274	OB3613.raw	2.63E5	4	4	308	318	
K.ISM(+15.99)PVN(+.98)TPGQFEDFFPASSR.D	N	99.9	67.41	2243.0205	20	1.6	1122.5193	2	32.40	15	2761	OB3613.raw	1.15E5	1	1	288	307	Oxidation (M); Deamidation (NQ)
K.ISM(+15.99)PVNTPGQ(+.98)FEDFFPASSR.D	N	99.9	63.03	2243.0205	20	0.8	1122.5184	2	32.67	15	2797	OB3613.raw	2.61E5	4	4	288	307	Oxidation (M); Deamidation (NQ)
R.DQ(+.98)SSYLQ(+.98)GFSR.N	N	99.9	60.72	1288.5571	11	0.5	645.2861	2	29.68	15	2401	OB3613.raw	2.47E4	2	2	308	318	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQFEDFFPASSR.D	N	99.9	60.35	2242.0364	20	0.5	1122.0260	2	32.00	15	2709	OB3613.raw	7.96E4	2	2	288	307	Hydroxylation Pro
R.IPSGFISYILN(+.98)R.H	N	99.9	58.66	1379.7449	12	-0.4	690.8795	2	34.94	15	3102	OB3613.raw	0	2	2	266	277	Deamidation (NQ)
K.ISMP(+15.99)VNTPGQ(+.98)FEDFFPASSR.D	N	99.9	54.99	2243.0205	20	1.6	748.6820	3	32.76	15	2808	OB3613.raw	1.46E5	2	2	288	307	Hydroxylation Pro; Deamidation (NQ)
R.DQSSYLQ(+.98)GFSR.N	N	99.9	53.43	1287.5731	11	0.4	644.7941	2	29.96	15	2439	OB3613.raw	0	1	1	308	318	Deamidation (NQ)
R.VLLEEN(+.98)AGGEQEER.G	N	99.9	52.15	1572.7267	14	-2.0	787.3690	2	25.53	15	1841	OB3613.raw	1.74E4	2	2	335	348	Deamidation (NQ)
K.ISM(+15.99)PVNTPGQFEDFFPASSR.D	N	99.9	50.49	2242.0364	20	0.0	748.3527	3	31.90	15	2695	OB3613.raw	2.71E5	2	2	288	307	Oxidation (M)
R.NNPFYFPSR.R	N	99.9	49.42	1140.5352	9	-0.8	571.2744	2	29.99	15	2442	OB3613.raw	1.07E6	15	15	172	180	

K.HADADNILVIQQGQATVTVAN(+.98)GNNR.K	N	99.9	49.06	2619.3000	25	-0.1	874.1072	3	28.55	15	2250	OB3613.raw	7.03E4	1	1	229	253	Deamidation (NQ)
R.IVQIEAKPNTLVLPK.H	Y	99.9	47.28	1662.0079	15	0.4	832.0116	2	27.93	15	2166	OB3613.raw	2.54E6	14	14	214	228	
R.VLLEENAGGEQ(+.98)EER.G	N	99.8	44.17	1572.7267	14	-1.7	787.3693	2	25.71	15	1865	OB3613.raw	1.74E4	1	1	335	348	Deamidation (NQ)
F.NLDEGHALR.I	N	99.7	40.38	1023.5097	9	0.5	512.7624	2	26.21	15	1933	OB3613.raw	2.74E3	1	1	257	265	
R.NTLEAAFNAEFNEIRR.V	N	99.6	38.29	1893.9332	16	0.2	947.9741	2	32.57	15	2784	OB3613.raw	5.78E5	4	4	319	334	
R.IVQ(+.98)IEAKPNTLVLPK.H	Y	98.9	34.90	1662.9919	15	-0.1	832.5032	2	28.24	15	2208	OB3613.raw	2.21E5	2	2	214	228	Deamidation (NQ)
R.IVQIEAKPN(+.98)TLVLPK.H	Y	96.9	29.70	1662.9919	15	-3.4	555.3361	3	28.91	15	2298	OB3613.raw	2.19E5	1	1	214	228	Deamidation (NQ)
total 23 peptides																		

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLK**TANDLN LLILRWLGLS**
401 **AEYGNLYRNA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS**
481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 15	#Spec	#Spec Sample 15	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	64.90	1540.7673	13	-0.5	771.3906	2	32.31	15	2749	OB3613.raw	4.25E4	2	2	396	408	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.8	45.32	2540.2910	23	0.3	847.7712	3	30.58	15	2521	OB3613.raw	7.42E4	2	2	443	465	
K.TANDLNLLILR.W	Y	99.7	40.51	1254.7296	11	-0.9	628.3715	2	32.13	15	2726	OB3613.raw	8.41E3	1	1	385	395	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.6	38.50	3510.7590	33	-0.7	1171.2595	3	34.69	15	3069	OB3613.raw	5.93E4	1	1	478	510	
R.NALFVPHYNTNAHSIIYALR.G	N	99.5	37.53	2313.2019	20	-0.8	579.3073	4	30.80	15	2550	OB3613.raw	1.31E5	1	1	409	428	
total 5 peptides																		

A1DZF0|A1DZF0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ

241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD

321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILR**WLG LSAEYGNLYR**

401 **NALFVPHYNT NAHSIIYALR** GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGK**SQS ENFEYVAFK**T DSRPSIANLA**

481 **GENSFIDNLP EEVVANSYGL PR**EQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 15	#Spec	#Spec Sample 15	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	64.90	1540.7673	13	-0.5	771.3906	2	32.31	15	2749	OB3613.raw	4.25E4	2	2	388	400	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.8	45.32	2540.2910	23	0.3	847.7712	3	30.58	15	2521	OB3613.raw	7.42E4	2	2	435	457	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.7	40.67	3544.7434	33	-1.1	1182.5872	3	35.09	15	3121	OB3613.raw	8.32E4	2	2	470	502	
R.NALFVPHYNTNAHSIIYALR.G	N	99.5	37.53	2313.2019	20	-0.8	579.3073	4	30.80	15	2550	OB3613.raw	1.31E5	1	1	401	420	
total 4 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

1. Notes

Spot H from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

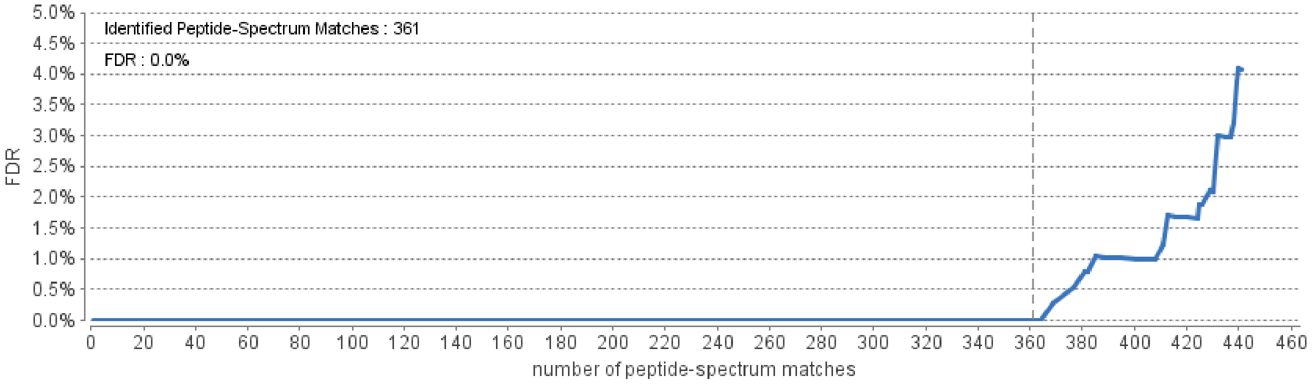
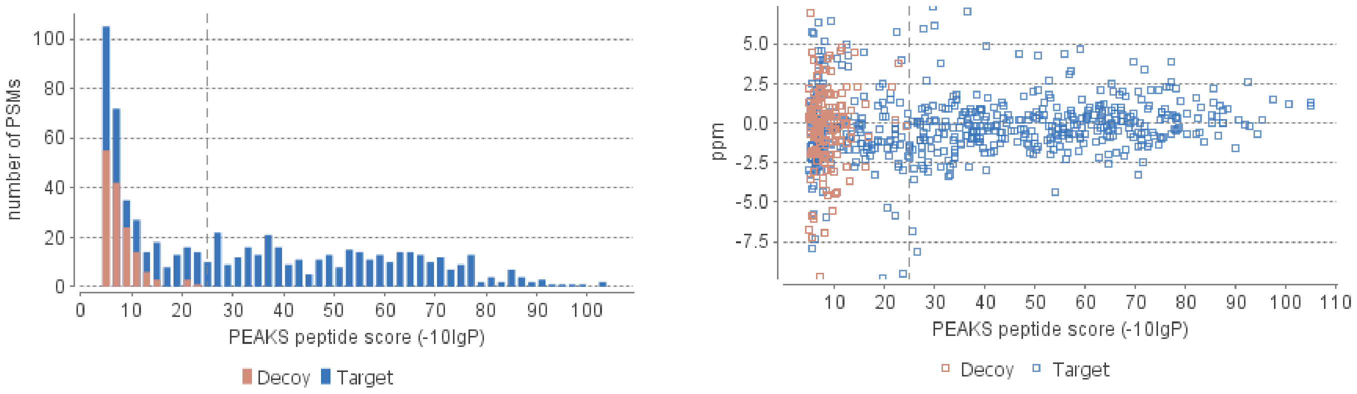


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

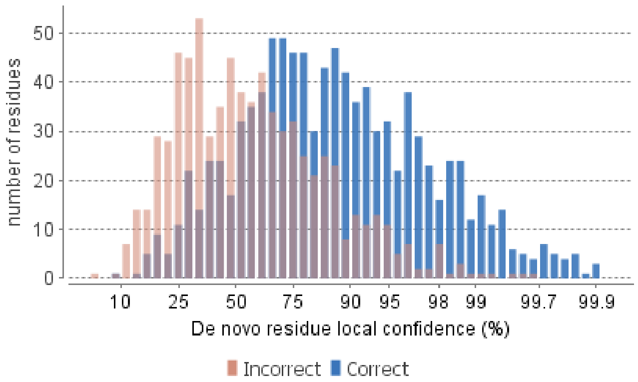

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



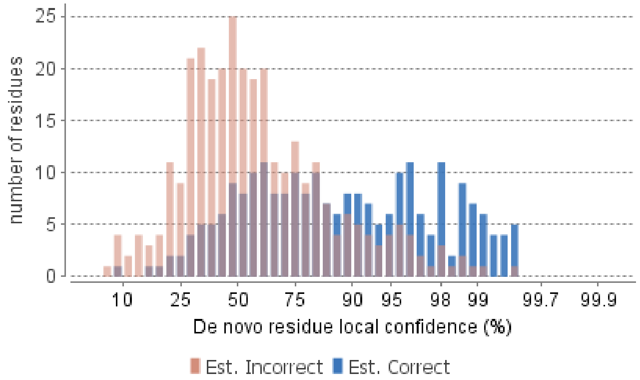


Table 1. Statistics of data.

# of MS scans	2737
# of MS/MS scans	4013

Table 2. Result filtration parameters.

Peptide -10lgP	≥25
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	313
Peptide sequences	120
Protein groups	8
Proteins	14
Proteins (#Unique Peptides)	2 (>2); 0 (=2); 12 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	45

Table 4. PTM profile.

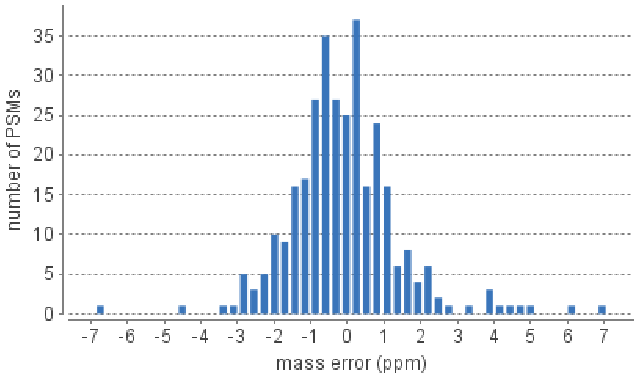
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Deamidation	.98	NQ	48	105.11	4.12E6	30.36
Carbamidomethyl	57.02	C	36	82.69	1.03E4	1000.00
HydPro	15.99	P	7	53.43	2.43E4	1000.00
Oxidation	15.99	M	4	54.15	2.6E5	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



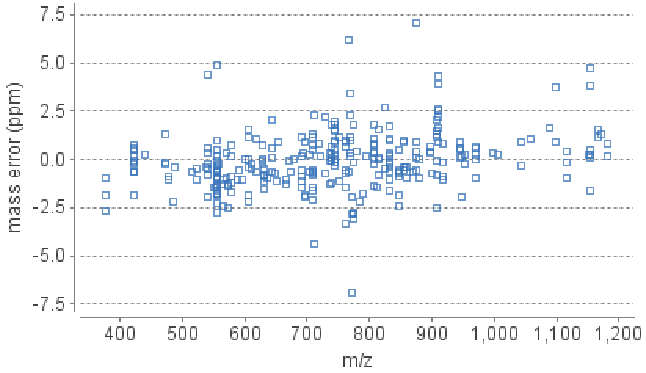


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 16	112	8	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3614.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 16	Area Sample 16	#Peptides	#Unique	#Spec Sample 16	PTM	Avg. Mass	Description
1	59	Q647H1|Q647H1_ARAHY	99.1	277.04	18	18	3.97E7	16	7	138	Y	75933	Conarachin OS=Arachis hypogaea PE=2 SV=1
3	18	N1NG13|N1NG13_ARAHY	99.1	215.02	16	16	3.88E5	9	1	32	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
3	20	sp|P43238|ALL12_ARAHY	99.1	215.02	16	16	3.88E5	9	1	32	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
4	26	Q6PSU3|Q6PSU3_ARAHY	99.1	214.23	17	17	1.96E5	9	1	30	Y	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
4	23	B3IXL2|B3IXL2_ARAHY	99.1	214.23	16	16	1.96E5	9	1	30	Y	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
4	21	sp|P43237|ALL11_ARAHY	99.1	214.23	16	16	1.96E5	9	1	30	Y	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
2	87	E9LFF0|E9LFF0_ARAHY	99.1	204.15	43	43	1.88E4	10	1	48	Y	19081	11S arachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
7	15	Q647H3|Q647H3_ARAHY	99.1	139.35	21	21	3.64E5	6	3	17	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
9	3	B5TYU1|B5TYU1_ARAHY	99.0	132.27	19	19	1.36E5	5	1	15	N	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
8	2	A1DZF0|A1DZF0_ARAHY	99.0	129.77	19	19	2.07E5	5	1	15	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
19	212	Q2KPX7|Q2KPX7_ARAHY	51.7	25.07	7	7	1.08E4	1	1	1	N	19768	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
19	217	Q2KQ57|Q2KQ57_ARAHY	51.7	25.07	7	7	1.08E4	1	1	1	N	19784	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
19	206	Q2KQ05|Q2KQ05_ARAHY	51.7	25.07	7	7	1.08E4	1	1	1	N	19965	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
19	209	Q2KPY0|Q2KPY0_ARAHY	51.7	25.07	7	7	1.08E4	1	1	1	N	20173	Resistance protein PLTR (Fragment) OS=Arachis hypogaea PE=4 SV=1
total 14 proteins													

Q647H1|Q647H1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MVIGPFRLSL CVCLVFLTSA CFGTRLEESF NECQLDRLNA LTPDNRIESQ GGITETWNSN HPELRCAGVT LLKRTIFPNG
 81 FHLPSYANYP QLIFIAQGNG VFGVSLPGCP VTYEEAESQS REDRRQRIVI KRESEQEQEQ QGDSHHKIYH FRQGHLLAIP
161 AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRRFYLA GNPEEEHPET QQQQPQTRRR HGQHQQDEYG SQGEEEGNNV
241 LSGFSTQLLA HAFGVDEEIA RILQNPPEQT KDQIVRVEGG FRDVISPRWG EGKQYEDELE ERQRQPPRRD EQGKGYDYDD
321 DRRPRHRQDP YREGDEDDRR PRGSRQGQGR GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY
401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRNG VEETLCSPTL VEDIARPSRA DFYNPAAGRI
481 SSANSLTFPI LRWFQLSAEH VLLYRNGIYS PHWNNNANSI IYGLRGEGRI QVVNSQGNAV FNGVLREGQI LLVPQNFAVG
561 KQAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN
641 AQVDSKNNDG SRLWWPSSII IK
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.IQVVNSQ(+.98)GNAVFNGVLR.E	Y	100.0	105.11	1814.9639	17	1.3	908.4904	2	32.10	16	1827	OB3614.raw	4.12E6	1	1	530	546	Deamidation (NQ)
R.IQVVNSQGNAVFN(+.98)GVLR.E	Y	100.0	104.83	1814.9639	17	1.1	908.4902	2	31.48	16	1744	OB3614.raw	5.04E6	6	6	530	546	Deamidation (NQ)
R.IQVVN(+.98)SQGNAVFNGVLR.E	Y	99.9	97.60	1814.9639	17	1.5	908.4905	2	32.32	16	1857	OB3614.raw	4.12E6	1	1	530	546	Deamidation (NQ)
R.WFQLSAEHVLLYR.N	Y	99.9	95.25	1660.8726	13	0.2	831.4437	2	33.50	16	2019	OB3614.raw	6.61E6	34	34	493	505	
R.IQVVNSQ(+.98)GN(+.98)AVFNGVLR.E	Y	99.9	92.35	1815.9479	17	2.6	908.9836	2	32.50	16	1881	OB3614.raw	7.66E5	1	1	530	546	Deamidation (NQ)
R.ISSANSLTFPILR.W	Y	99.9	87.40	1417.7928	13	0.8	709.9042	2	33.42	16	2008	OB3614.raw	3.27E6	13	13	480	492	
R.N(+.98)GIYSPHWNNNANSIIYGLR.G	N	99.9	87.35	2303.1084	20	0.0	1152.5615	2	33.00	16	1949	OB3614.raw	3.35E6	4	4	506	525	Deamidation (NQ)
R.IQVVNSQGN(+.98)AVFNGVLR.E	Y	99.9	86.38	1814.9639	17	-0.8	908.4885	2	33.27	16	1987	OB3614.raw	4.12E6	1	1	530	546	Deamidation (NQ)
R.IQ(+.98)VVNSQGN(+.98)AVFNGVLR.E	Y	99.9	85.47	1815.9479	17	2.2	908.9832	2	33.08	16	1960	OB3614.raw	7.66E5	2	2	530	546	Deamidation (NQ)
R.IQVVNSQGNAVFNGVLR.E	Y	99.9	85.33	1813.9799	17	0.0	605.6672	3	31.71	16	1774	OB3614.raw	5.69E5	2	2	530	546	
R.N(+.98)GIYSPHWN(+.98)NNANSIIYGLR.G	N	99.9	85.18	2304.0923	20	0.5	1153.0540	2	33.78	16	2057	OB3614.raw	8.07E4	3	3	506	525	Deamidation (NQ)
R.IQVVN(+.98)SQGNAVFN(+.98)GVLR.E	Y	99.9	82.14	1815.9479	17	1.6	908.9827	2	32.68	16	1905	OB3614.raw	8.09E5	2	2	530	546	Deamidation (NQ)
R.ADFYNPAAGR.I	N	99.9	78.55	1080.4988	10	-0.2	541.2565	2	28.13	16	1365	OB3614.raw	2.72E5	9	9	470	479	
K.QAGNEGFEYVAFK.T	N	99.9	78.02	1458.6779	13	2.2	730.3478	2	31.34	16	1725	OB3614.raw	2.51E5	2	2	562	574	
R.IQVVNSQGN(+.98)AVFN(+.98)GVLR.E	Y	99.9	77.12	1815.9479	17	2.5	908.9835	2	31.79	16	1785	OB3614.raw	7.66E5	1	1	530	546	Deamidation (NQ)
R.IQ(+.98)VVNSQ(+.98)GNAVFN(+.98)GVLR.E	Y	99.9	77.06	1816.9319	17	3.9	909.4767	2	33.04	16	1955	OB3614.raw	8.02E4	1	1	530	546	Deamidation (NQ)
R.ISSAN(+.98)SLTFPILR.W	Y	99.9	76.96	1418.7769	13	2.3	710.3973	2	33.77	16	2055	OB3614.raw	2.81E5	2	2	480	492	Deamidation (NQ)
R.N(+.98)GIYSPHWNNN(+.98)ANSIIYGLR.G	N	99.9	76.35	2304.0923	20	2.3	769.0398	3	33.86	16	2067	OB3614.raw	1.51E6	1	1	506	525	Deamidation (NQ)

R.EGQILLVPQNFAVGK.Q	N	99.9	75.27	1611.8984	15	0.7	806.9571	2	33.16	16	1971	OB3614.raw	2.98E6	8	8	547	561	
R.N(+.98)GIYSPHWNN(+.98)NANSIIYGLR.G	N	99.9	71.76	2304.0923	20	3.4	769.0406	3	34.43	16	2145	OB3614.raw	1.51E6	1	1	506	525	Deamidation (NQ)
R.EGQILLVPQN(+.98)FAVGK.Q	N	99.9	66.75	1612.8824	15	1.8	807.4500	2	33.59	16	2031	OB3614.raw	7.07E5	1	1	547	561	Deamidation (NQ)
R.IQ(+.98)VVNSQGNAVFN(+.98)GVLR.E	Y	99.9	66.12	1815.9479	17	-1.9	606.3221	3	32.74	16	1914	OB3614.raw	4.29E4	1	1	530	546	Deamidation (NQ)
R.NGIYSPHWNNNANSIIYGLR.G	N	99.9	63.64	2302.1243	20	1.2	768.3829	3	32.41	16	1869	OB3614.raw	7.95E5	3	3	506	525	
N.GVEETLC(+57.02)SPTLVEDIAR.P	Y	99.9	63.42	1887.9248	17	0.6	944.9702	2	33.04	16	1954	OB3614.raw	1.44E6	5	5	450	466	Carbamidomethylation
R.N(+.98)GIYSPHWNN(+.98)N(+.98)ANSIIYGLR.G	N	99.9	59.14	2305.0764	20	4.7	1153.5509	2	34.23	16	2118	OB3614.raw	0	1	1	506	525	Deamidation (NQ)
R.NGIYSP(+15.99)HWN(+.98)N(+.98)NANSIIYGLR.G	N	99.9	53.43	2320.0872	20	-0.2	774.3695	3	33.12	16	1967	OB3614.raw	2.43E4	1	1	506	525	Hydroxylation Pro; Deamidation (NQ)
R.IQ(+.98)VVN(+.98)SQGNAVFNGVLR.E	Y	99.9	50.50	1815.9479	17	4.3	908.9851	2	31.70	16	1773	OB3614.raw	7.66E5	1	1	530	546	Deamidation (NQ)
N.GVEETLC(+57.02)SPTLVEDIARPSR.A	Y	99.9	49.77	2228.1106	20	2.0	743.7123	3	31.65	16	1767	OB3614.raw	4.79E6	14	14	450	469	Carbamidomethylation
R.EGQILLVPQ(+.98)N(+.98)FAVGK.Q	N	99.9	48.64	1613.8665	15	-1.4	807.9394	2	33.95	16	2080	OB3614.raw	5.92E4	1	1	547	561	Deamidation (NQ)
W.NNNANSIIYGLR.G	N	99.9	48.02	1347.6895	12	-0.7	674.8516	2	30.39	16	1599	OB3614.raw	5.03E3	1	1	514	525	
N.GVEETLC(+57.02)SP(+15.99)TLVEDIAR.P	Y	99.8	47.17	1903.9197	17	0.2	952.9673	2	32.51	16	1882	OB3614.raw	2.32E5	2	2	450	466	Carbamidomethylation; Hydroxylation Pro
R.ADFYN(+.98)PAAGR.I	N	99.8	46.71	1081.4828	10	4.4	541.7510	2	28.43	16	1394	OB3614.raw	1.31E3	1	1	470	479	Deamidation (NQ)
R.WFQ(+.98)LSAEHVLLYR.N	Y	99.6	40.36	1661.8566	13	4.9	554.9622	3	33.72	16	2049	OB3614.raw	1.1E6	1	1	493	505	Deamidation (NQ)
N.SLTFPILR.W	N	99.6	38.49	945.5647	8	-0.2	473.7895	2	32.94	16	1941	OB3614.raw	2.01E5	1	1	485	492	
R.NGIYSP(+15.99)HWNNNANSIIYGLR.G	N	99.6	38.47	2318.1191	20	1.8	773.7150	3	30.99	16	1679	OB3614.raw	4.98E4	2	2	506	525	Hydroxylation Pro
N.NNANSIIYGLR.G	N	99.5	37.32	1233.6466	11	-0.6	617.8302	2	30.41	16	1602	OB3614.raw	2.71E3	1	1	515	525	
R.NGIYSP(+15.99)HWNN(+.98)NANSIIYGLR.G	N	98.1	33.03	2319.1033	20	-2.8	774.0396	3	32.20	16	1841	OB3614.raw	7.21E4	1	1	506	525	Hydroxylation Pro; Deamidation (NQ)
R.N(+.98)GIYSPHWNNNAN.S	N	96.0	29.62	1500.6382	13	1.1	751.3272	2	30.11	16	1562	OB3614.raw	5.15E3	1	1	506	518	Deamidation (NQ)
Y.SPHWNNNANSIIYGLR.G	N	95.8	27.91	1854.9125	16	1.0	619.3121	3	30.94	16	1673	OB3614.raw	9.26E3	1	1	510	525	
R.N(+.98)GIYSP(+15.99)HWNNNANSIIYGLR.G	N	95.7	27.70	2319.1033	20	-2.9	774.0395	3	32.52	16	1884	OB3614.raw	7.21E4	1	1	506	525	Deamidation (NQ); Hydroxylation Pro
C.SPTLVEDIARPSR.A	Y	90.0	25.49	1439.7732	13	0.2	720.8940	2	28.66	16	1418	OB3614.raw	5.34E3	1	1	457	469	
C.SPTLVEDIAR.P	Y	89.8	25.02	1099.5873	10	-1.5	550.8001	2	29.88	16	1533	OB3614.raw	4.69E3	1	1	457	466	
total 42 peptides																		

N1NG13|N1NG13_ARAHY

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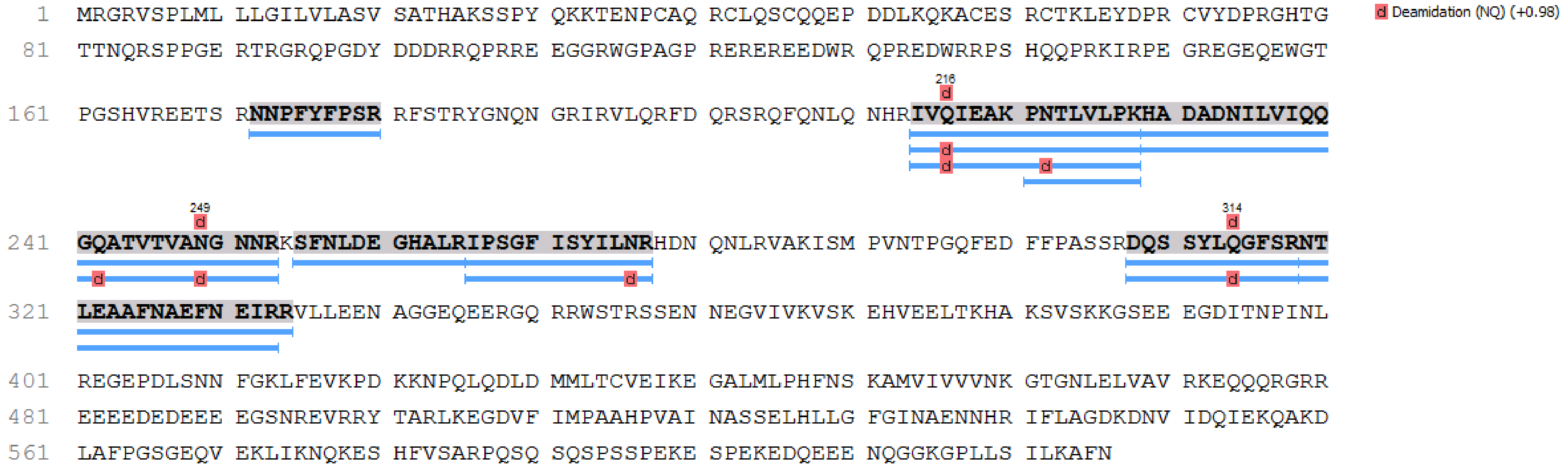
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG

81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT

161 PGSHVREETS R**NNPFYFPSR** RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHR**IVQIEAK PNTLVLPKHA DADNILVIQQ**

241 **GQATVTVANG NNR**K**SFNLDE GHALRIPSGF ISYILNR**HDN QNLRVAKISM PVNTPGQFED FFPASSR**DQS SYLQGFSRNT**

321 **LEAAFNAEFN EIRR**VLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL

401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR

481 EEEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD

561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	94.45	1737.8322	15	-0.6	869.9228	2	34.61	16	2170	OB3614.raw	3.74E4	1	1	319	333	
R.DQSSYLQGFSR.N	N	99.9	76.61	1286.5891	11	0.5	644.3022	2	30.21	16	1575	OB3614.raw	1.87E4	3	3	308	318	
R.IPSGFISYILNR.H	N	99.9	74.90	1378.7609	12	-0.9	690.3871	2	35.46	16	2286	OB3614.raw	3.13E5	3	3	266	277	
R.DQSSYLQ(+.98)GFSR.N	N	99.9	68.92	1287.5731	11	-0.7	644.7934	2	30.62	16	1629	OB3614.raw	1.42E4	1	1	308	318	Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.08	1257.6101	11	0.8	629.8128	2	28.06	16	1360	OB3614.raw	3.33E4	3	3	255	265	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	63.30	2618.3162	25	0.1	873.7794	3	29.99	16	1546	OB3614.raw	2.33E4	4	4	229	253	
R.IPSGFISYILN(+.98)R.H	N	99.9	61.99	1379.7449	12	-1.2	690.8789	2	35.80	16	2333	OB3614.raw	3.83E4	2	2	266	277	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	53.18	1140.5352	9	-1.0	571.2743	2	31.04	16	1685	OB3614.raw	1.46E4	2	2	172	180	
R.NTLEAAFNAEFNEIRR.V	N	99.9	51.54	1893.9332	16	0.2	947.9741	2	33.60	16	2033	OB3614.raw	3.49E5	4	4	319	334	
R.IVQIEAKPNTLVLPK.H	Y	99.7	43.39	1662.0079	15	-0.6	555.0096	3	29.60	16	1498	OB3614.raw	3.46E5	5	5	214	228	
R.IVQ(+.98)IEAKPNTLVLPK.H	Y	99.6	38.31	1662.9919	15	-0.5	555.3376	3	29.87	16	1530	OB3614.raw	2.97E4	1	1	214	228	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVAN(+.98)GNNR.K	N	99.4	36.54	2620.2842	25	7.1	874.4415	3	30.40	16	1600	OB3614.raw	5.44E3	1	1	229	253	Deamidation (NQ)
R.IVQ(+.98)IEAKPN(+.98)TLVLPK.H	Y	97.3	31.78	1663.9760	15	-1.8	555.6649	3	30.26	16	1581	OB3614.raw	1.3E4	1	1	214	228	Deamidation (NQ)
K.PNTLVLPK.H	N	96.0	29.96	880.5382	8	0.2	441.2765	2	28.01	16	1355	OB3614.raw	5.66E3	1	1	221	228	
total 14 peptides																		

sp|P43238|ALL12_ARAHY

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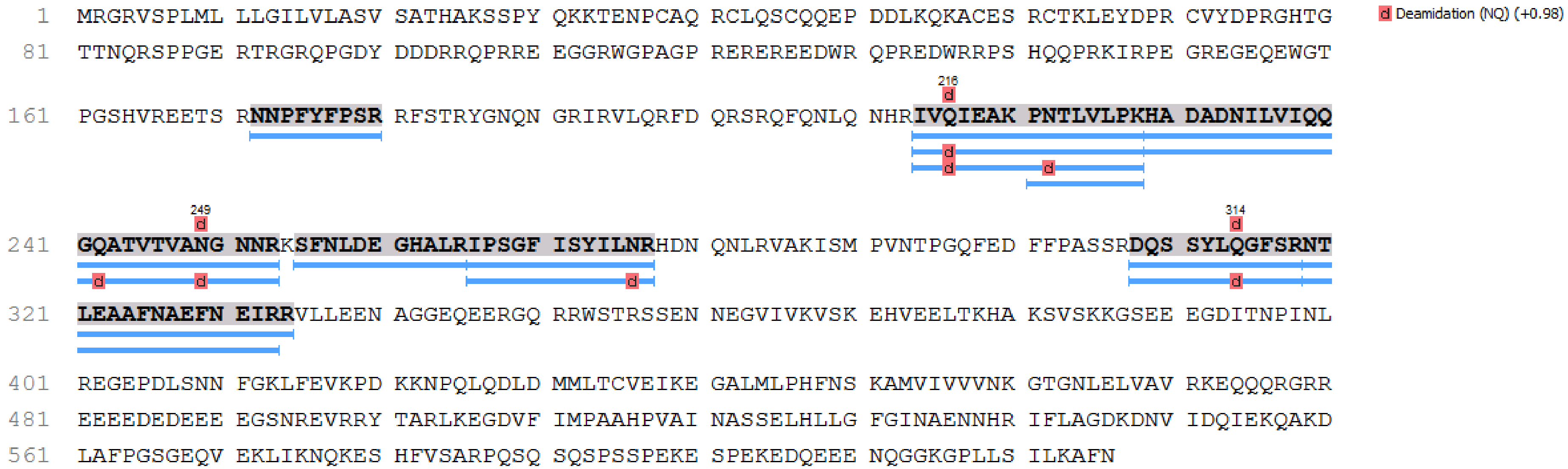
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
561 LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN
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Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	94.45	1737.8322	15	-0.6	869.9228	2	34.61	16	2170	OB3614.raw	3.74E4	1	1	319	333	
R.DQSSYLQGFSR.N	N	99.9	76.61	1286.5891	11	0.5	644.3022	2	30.21	16	1575	OB3614.raw	1.87E4	3	3	308	318	

R.IPSGFISYILNR.H	N	99.9	74.90	1378.7609	12	-0.9	690.3871	2	35.46	16	2286	OB3614.raw	3.13E5	3	3	266	277	
R.DQSSYLQ(+.98)GFSR.N	N	99.9	68.92	1287.5731	11	-0.7	644.7934	2	30.62	16	1629	OB3614.raw	1.42E4	1	1	308	318	Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.08	1257.6101	11	0.8	629.8128	2	28.06	16	1360	OB3614.raw	3.33E4	3	3	255	265	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	63.30	2618.3162	25	0.1	873.7794	3	29.99	16	1546	OB3614.raw	2.33E4	4	4	229	253	
R.IPSGFISYILN(+.98)R.H	N	99.9	61.99	1379.7449	12	-1.2	690.8789	2	35.80	16	2333	OB3614.raw	3.83E4	2	2	266	277	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	53.18	1140.5352	9	-1.0	571.2743	2	31.04	16	1685	OB3614.raw	1.46E4	2	2	172	180	
R.NTLEAAFNAEFNEIRR.V	N	99.9	51.54	1893.9332	16	0.2	947.9741	2	33.60	16	2033	OB3614.raw	3.49E5	4	4	319	334	
R.IVQIEAKPNTLVLPK.H	Y	99.7	43.39	1662.0079	15	-0.6	555.0096	3	29.60	16	1498	OB3614.raw	3.46E5	5	5	214	228	
R.IVQ(+.98)IEAKPNTLVLPK.H	Y	99.6	38.31	1662.9919	15	-0.5	555.3376	3	29.87	16	1530	OB3614.raw	2.97E4	1	1	214	228	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVAN(+.98)GNNR.K	N	99.4	36.54	2620.2842	25	7.1	874.4415	3	30.40	16	1600	OB3614.raw	5.44E3	1	1	229	253	Deamidation (NQ)
R.IVQ(+.98)IEAKPN(+.98)TLVLPK.H	Y	97.3	31.78	1663.9760	15	-1.8	555.6649	3	30.26	16	1581	OB3614.raw	1.3E4	1	1	214	228	Deamidation (NQ)
K.PNTLVLPK.H	N	96.0	29.96	880.5382	8	0.2	441.2765	2	28.01	16	1355	OB3614.raw	5.66E3	1	1	221	228	
total 14 peptides																		

Q6PSU3|Q6PSU3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH

81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR

161 EETSR**NNPFY FPSR**RFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHR**IVQ IEARPNTLVL PKHADADNIL VIQQGQATVT**

243 d   308 d

241 **VANGNNR**K**SF NLDEGHALRI PSGFISYILN R**HDNQNLRVA KISMPVNTPG QFEDFFPASS R**DQSSYLQGF SRNTLEAAFN**

321 **AEFNEIRR**VL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS

401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG

561 SGEQVEKLIK NQRESHFVSA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	94.45	1737.8322	15	-0.6	869.9228	2	34.61	16	2170	OB3614.raw	3.74E4	1	1	313	327	
R.DQSSYLQGFSR.N	N	99.9	76.61	1286.5891	11	0.5	644.3022	2	30.21	16	1575	OB3614.raw	1.87E4	3	3	302	312	
R.IPSGFISYILNR.H	N	99.9	74.90	1378.7609	12	-0.9	690.3871	2	35.46	16	2286	OB3614.raw	3.13E5	3	3	260	271	
R.DQSSYLQ(+.98)GFSR.N	N	99.9	68.92	1287.5731	11	-0.7	644.7934	2	30.62	16	1629	OB3614.raw	1.42E4	1	1	302	312	Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.08	1257.6101	11	0.8	629.8128	2	28.06	16	1360	OB3614.raw	3.33E4	3	3	249	259	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	63.30	2618.3162	25	0.1	873.7794	3	29.99	16	1546	OB3614.raw	2.33E4	4	4	223	247	
R.IPSGFISYILN(+.98)R.H	N	99.9	61.99	1379.7449	12	-1.2	690.8789	2	35.80	16	2333	OB3614.raw	3.83E4	2	2	260	271	Deamidation (NQ)

R.NNPFYFPSR.R	N	99.9	53.18	1140.5352	9	-1.0	571.2743	2	31.04	16	1685	OB3614.raw	1.46E4	2	2	166	174	
R.NTLEAAFNAEFNEIRR.V	N	99.9	51.54	1893.9332	16	0.2	947.9741	2	33.60	16	2033	OB3614.raw	3.49E5	4	4	313	328	
R.IVQIEARPN(+.98)TLVLPK.H	Y	99.4	37.01	1690.9980	15	-1.3	564.6725	3	30.26	16	1582	OB3614.raw	6.49E4	1	1	208	222	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVAN(+.98)GNNR.K	N	99.4	36.54	2620.2842	25	7.1	874.4415	3	30.40	16	1600	OB3614.raw	5.44E3	1	1	223	247	Deamidation (NQ)
R.IVQIEARPNTLVLPK.H	Y	98.8	35.23	1690.0140	15	-1.3	564.3445	3	29.91	16	1536	OB3614.raw	6.24E4	2	2	208	222	
R.IVQ(+.98)IEARPNTLVLPK.H	Y	97.9	32.63	1690.9980	15	-2.4	564.6719	3	30.06	16	1556	OB3614.raw	6.85E4	2	2	208	222	Deamidation (NQ)
R.PNTLVLPK.H	N	96.0	29.96	880.5382	8	0.2	441.2765	2	28.01	16	1355	OB3614.raw	5.66E3	1	1	215	222	
total 14 peptides																		

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| Protein Coverage | Supporting Peptides |

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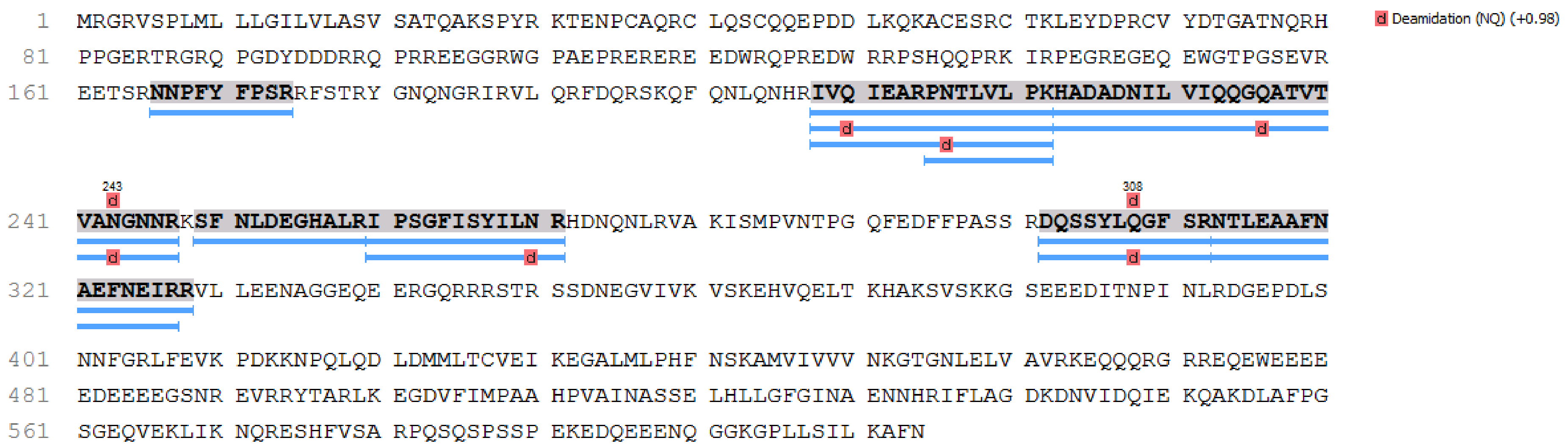

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81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR

161 EETSR**NNPFY FPSR**RFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHR**IVQ IEARPNTLVL PKHADADNIL VIQQGQATVT**

241 **VANGNNR**K**SF NLDEGHALRI PSGFISYILN R**HDNQNLRVA KISMPVNTPG QFEDFFPASS R**DQSSYLQGF SRNTLEAAFN**

321 **AEFNEIRR**VL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS

401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE

481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG

561 SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	94.45	1737.8322	15	-0.6	869.9228	2	34.61	16	2170	OB3614.raw	3.74E4	1	1	313	327	
R.DQSSYLQGFSR.N	N	99.9	76.61	1286.5891	11	0.5	644.3022	2	30.21	16	1575	OB3614.raw	1.87E4	3	3	302	312	
R.IPSGFISYILNR.H	N	99.9	74.90	1378.7609	12	-0.9	690.3871	2	35.46	16	2286	OB3614.raw	3.13E5	3	3	260	271	
R.DQSSYLQ(+.98)GFSR.N	N	99.9	68.92	1287.5731	11	-0.7	644.7934	2	30.62	16	1629	OB3614.raw	1.42E4	1	1	302	312	Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.08	1257.6101	11	0.8	629.8128	2	28.06	16	1360	OB3614.raw	3.33E4	3	3	249	259	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	63.30	2618.3162	25	0.1	873.7794	3	29.99	16	1546	OB3614.raw	2.33E4	4	4	223	247	
R.IPSGFISYILN(+.98)R.H	N	99.9	61.99	1379.7449	12	-1.2	690.8789	2	35.80	16	2333	OB3614.raw	3.83E4	2	2	260	271	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	53.18	1140.5352	9	-1.0	571.2743	2	31.04	16	1685	OB3614.raw	1.46E4	2	2	166	174	
R.NTLEAAFNAEFNEIRR.V	N	99.9	51.54	1893.9332	16	0.2	947.9741	2	33.60	16	2033	OB3614.raw	3.49E5	4	4	313	328	
R.IVQIEARPN(+.98)TLVLPK.H	Y	99.4	37.01	1690.9980	15	-1.3	564.6725	3	30.26	16	1582	OB3614.raw	6.49E4	1	1	208	222	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVAN(+.98)GNNR.K	N	99.4	36.54	2620.2842	25	7.1	874.4415	3	30.40	16	1600	OB3614.raw	5.44E3	1	1	223	247	Deamidation (NQ)
R.IVQIEARPNTLVLPK.H	Y	98.8	35.23	1690.0140	15	-1.3	564.3445	3	29.91	16	1536	OB3614.raw	6.24E4	2	2	208	222	

R.IVQ(+.98)IEARPNTLVLPK.H	Y	97.9	32.63	1690.9980	15	-2.4	564.6719	3	30.06	16	1556	OB3614.raw	6.85E4	2	2	208	222	Deamidation (NQ)
R.PNTLVLPK.H	N	96.0	29.96	880.5382	8	0.2	441.2765	2	28.01	16	1355	OB3614.raw	5.66E3	1	1	215	222	
total 14 peptides																		

sp|P43237|ALL11_ARAHY

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| Protein Coverage | Supporting Peptides |

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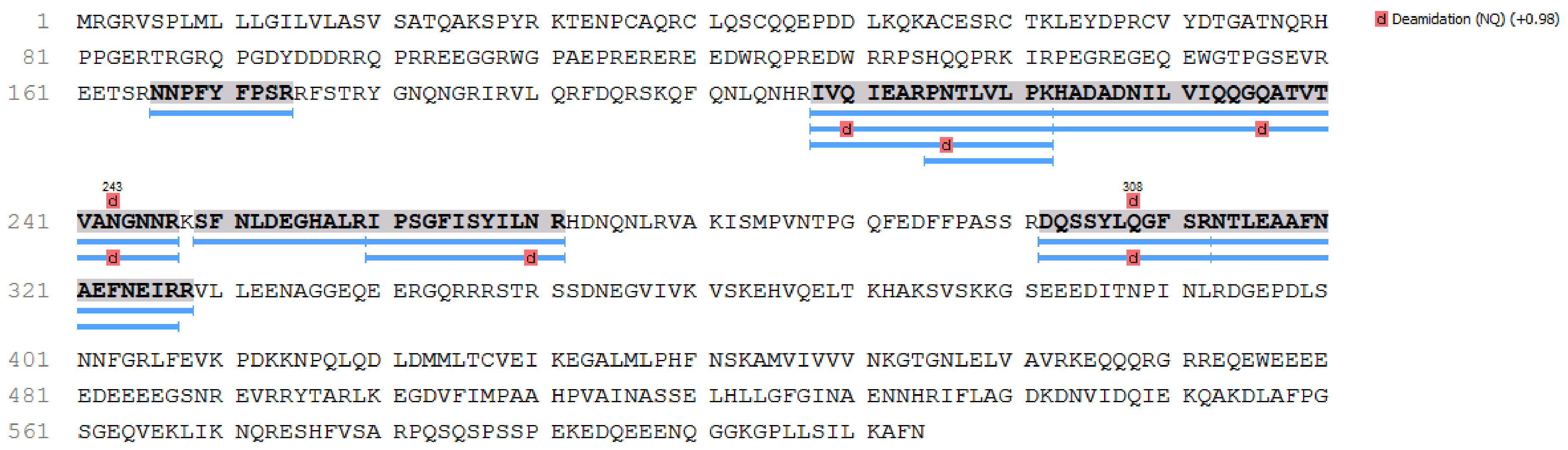

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81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSR**NNPFY FPSR**RFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHR**IVQ IEARPNTLVL PKHADADNIL VIQQGQATVT**
241 **VANGNNR**K**SF NLDEGHALRI PSGFISYILN R**HDNQNLRVA KISMPVNTPG QFEDFFPASS R**DQSSYLQGF SRNTLEAAFN**
321 **AEFNEIRR**VL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE KQAKDLAFPG
561 SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ GGKGPLLSIL KAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.NTLEAAFNAEFNEIR.R	N	99.9	94.45	1737.8322	15	-0.6	869.9228	2	34.61	16	2170	OB3614.raw	3.74E4	1	1	313	327	
R.DQSSYLQGFSR.N	N	99.9	76.61	1286.5891	11	0.5	644.3022	2	30.21	16	1575	OB3614.raw	1.87E4	3	3	302	312	
R.IPSGFISYILNR.H	N	99.9	74.90	1378.7609	12	-0.9	690.3871	2	35.46	16	2286	OB3614.raw	3.13E5	3	3	260	271	
R.DQSSYLQ(+.98)GFSR.N	N	99.9	68.92	1287.5731	11	-0.7	644.7934	2	30.62	16	1629	OB3614.raw	1.42E4	1	1	302	312	Deamidation (NQ)
K.SFNLDEGHALR.I	N	99.9	67.08	1257.6101	11	0.8	629.8128	2	28.06	16	1360	OB3614.raw	3.33E4	3	3	249	259	
K.HADADNILVIQQGQATVTVANGNNR.K	N	99.9	63.30	2618.3162	25	0.1	873.7794	3	29.99	16	1546	OB3614.raw	2.33E4	4	4	223	247	
R.IPSGFISYILN(+.98)R.H	N	99.9	61.99	1379.7449	12	-1.2	690.8789	2	35.80	16	2333	OB3614.raw	3.83E4	2	2	260	271	Deamidation (NQ)
R.NNPFYFPSR.R	N	99.9	53.18	1140.5352	9	-1.0	571.2743	2	31.04	16	1685	OB3614.raw	1.46E4	2	2	166	174	
R.NTLEAAFNAEFNEIRR.V	N	99.9	51.54	1893.9332	16	0.2	947.9741	2	33.60	16	2033	OB3614.raw	3.49E5	4	4	313	328	
R.IVQIEARPN(+.98)TLVLPK.H	Y	99.4	37.01	1690.9980	15	-1.3	564.6725	3	30.26	16	1582	OB3614.raw	6.49E4	1	1	208	222	Deamidation (NQ)
K.HADADNILVIQQGQ(+.98)ATVTVAN(+.98)GNNR.K	N	99.4	36.54	2620.2842	25	7.1	874.4415	3	30.40	16	1600	OB3614.raw	5.44E3	1	1	223	247	Deamidation (NQ)
R.IVQIEARPNTLVLPK.H	Y	98.8	35.23	1690.0140	15	-1.3	564.3445	3	29.91	16	1536	OB3614.raw	6.24E4	2	2	208	222	
R.IVQ(+.98)IEARPNTLVLPK.H	Y	97.9	32.63	1690.9980	15	-2.4	564.6719	3	30.06	16	1556	OB3614.raw	6.85E4	2	2	208	222	Deamidation (NQ)
R.PNTLVLPK.H	N	96.0	29.96	880.5382	8	0.2	441.2765	2	28.01	16	1355	OB3614.raw	5.66E3	1	1	215	222	
total 14 peptides																		

E9LFF0|E9LFF0_ARAHY

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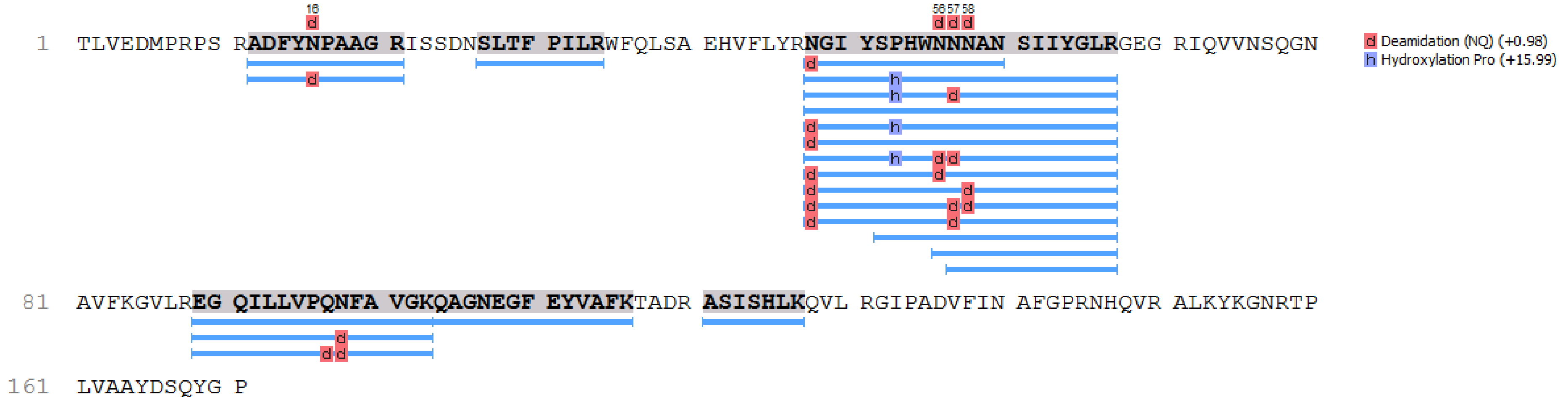
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.N(+.98)GIYSPHWNNNANSIIYGLR.G	N	99.9	87.35	2303.1084	20	0.0	1152.5615	2	33.00	16	1949	OB3614.raw	3.35E6	4	4	48	67	Deamidation (NQ)
R.N(+.98)GIYSPHWN(+.98)NNANSIIYGLR.G	N	99.9	85.18	2304.0923	20	0.5	1153.0540	2	33.78	16	2057	OB3614.raw	8.07E4	3	3	48	67	Deamidation (NQ)
R.ADFYNPAAGR.I	N	99.9	78.55	1080.4988	10	-0.2	541.2565	2	28.13	16	1365	OB3614.raw	2.72E5	9	9	12	21	
K.QAGNEGFEYVAFK.T	N	99.9	78.02	1458.6779	13	2.2	730.3478	2	31.34	16	1725	OB3614.raw	2.51E5	2	2	104	116	
R.N(+.98)GIYSPHWNNN(+.98)ANSIIYGLR.G	N	99.9	76.35	2304.0923	20	2.3	769.0398	3	33.86	16	2067	OB3614.raw	1.51E6	1	1	48	67	Deamidation (NQ)
R.EGQILLVPQNFAVGK.Q	N	99.9	75.27	1611.8984	15	0.7	806.9571	2	33.16	16	1971	OB3614.raw	2.98E6	8	8	89	103	
R.N(+.98)GIYSPHWNN(+.98)NANSIIYGLR.G	N	99.9	71.76	2304.0923	20	3.4	769.0406	3	34.43	16	2145	OB3614.raw	1.51E6	1	1	48	67	Deamidation (NQ)
R.EGQILLVPQN(+.98)FAVGK.Q	N	99.9	66.75	1612.8824	15	1.8	807.4500	2	33.59	16	2031	OB3614.raw	7.07E5	1	1	89	103	Deamidation (NQ)
R.NGIYSPHWNNNANSIIYGLR.G	N	99.9	63.64	2302.1243	20	1.2	768.3829	3	32.41	16	1869	OB3614.raw	7.95E5	3	3	48	67	
R.N(+.98)GIYSPHWNN(+.98)N(+.98)ANSIIYGLR.G	N	99.9	59.14	2305.0764	20	4.7	1153.5509	2	34.23	16	2118	OB3614.raw	0	1	1	48	67	Deamidation (NQ)
R.NGIYSP(+15.99)HWN(+.98)N(+.98)NANSIIYGLR.G	N	99.9	53.43	2320.0872	20	-0.2	774.3695	3	33.12	16	1967	OB3614.raw	2.43E4	1	1	48	67	Hydroxylation Pro; Deamidation (NQ)
R.EGQILLVPQ(+.98)N(+.98)FAVGK.Q	N	99.9	48.64	1613.8665	15	-1.4	807.9394	2	33.95	16	2080	OB3614.raw	5.92E4	1	1	89	103	Deamidation (NQ)
W.NNNANSIIYGLR.G	N	99.9	48.02	1347.6895	12	-0.7	674.8516	2	30.39	16	1599	OB3614.raw	5.03E3	1	1	56	67	
R.ADFYN(+.98)PAAGR.I	N	99.8	46.71	1081.4828	10	4.4	541.7510	2	28.43	16	1394	OB3614.raw	1.31E3	1	1	12	21	Deamidation (NQ)
R.ASISHLK.Q	Y	99.7	41.04	754.4337	7	-1.9	378.2234	2	18.42	16	851	OB3614.raw	1.88E4	3	3	121	127	
N.SLTFPILR.W	N	99.6	38.49	945.5647	8	-0.2	473.7895	2	32.94	16	1941	OB3614.raw	2.01E5	1	1	27	34	
R.NGIYSP(+15.99)HWNNNANSIIYGLR.G	N	99.6	38.47	2318.1191	20	1.8	773.7150	3	30.99	16	1679	OB3614.raw	4.98E4	2	2	48	67	Hydroxylation Pro
N.NNANSIIYGLR.G	N	99.5	37.32	1233.6466	11	-0.6	617.8302	2	30.41	16	1602	OB3614.raw	2.71E3	1	1	57	67	
R.NGIYSP(+15.99)HWNN(+.98)NANSIIYGLR.G	N	98.1	33.03	2319.1033	20	-2.8	774.0396	3	32.20	16	1841	OB3614.raw	7.21E4	1	1	48	67	Hydroxylation Pro; Deamidation (NQ)

R.N(+.98)GIYSPHWNNNAN.S	N	96.0	29.62	1500.6382	13	1.1	751.3272	2	30.11	16	1562	OB3614.raw	5.15E3	1	1	48	60	Deamidation (NQ)
Y.SPHWNNNANSIIYGLR.G	N	95.8	27.91	1854.9125	16	1.0	619.3121	3	30.94	16	1673	OB3614.raw	9.26E3	1	1	52	67	
R.N(+.98)GIYSP(+15.99)HWNNNANSIIYGLR.G	N	95.7	27.70	2319.1033	20	-2.9	774.0395	3	32.52	16	1884	OB3614.raw	7.21E4	1	1	48	67	Deamidation (NQ); Hydroxylation Pro
total 22 peptides																		

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
359 C
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GN**GIEETICT ASVK**KNIGRN R**SPDIYNPQA GSLKTANDLN LLILR**WLGLS
C
401 AEYGNLYR**NA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS**
481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	58.89	2540.2910	23	-0.7	847.7704	3	31.89	16	1800	OB3614.raw	2.14E5	2	2	443	465	
K.TANDLNLLILR.W	Y	99.9	52.76	1254.7296	11	-0.2	628.3719	2	33.60	16	2034	OB3614.raw	2.87E4	1	1	385	395	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	51.78	3510.7590	33	1.3	1171.2618	3	35.55	16	2298	OB3614.raw	3.33E5	3	3	478	510	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	49.74	2313.2019	20	-2.0	772.0731	3	31.44	16	1739	OB3614.raw	1E6	8	8	409	428	
R.SPDIYNPQAGSLK.T	N	99.6	39.85	1388.6936	13	-1.9	695.3528	2	28.20	16	1373	OB3614.raw	4.6E3	2	2	372	384	
N.GIEETIC(+57.02)TASVK.K	Y	99.6	38.91	1306.6438	12	0.9	654.3298	2	28.57	16	1408	OB3614.raw	2.15E3	1	1	353	364	Carbamidomethylation
total 6 peptides																		

B5TYU1|B5TYU1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS

241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE

321 EYDEDEYEYD EEDRRRGRGS RGSGNGIEET ICTATVKKNI GRNR**SPDIYN PQAGSLKTAN ELNLLILR**WL GLSAEYGNLY

401 R**NALFVPHYN TNAHSIIYAL R**GRAHVQVVD SNGNR**VYDEE LQEGHVLVVP QNFAVAGK**SQ SDNFEYVAFK **TDSRPSIANL**

481 **AGENSVIDNL PEEVVANSYG LPR**EQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	62.78	3496.7434	33	1.1	1166.5897	3	35.20	16	2249	OB3614.raw	1.36E5	2	2	471	503	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	58.89	2540.2910	23	-0.7	847.7704	3	31.89	16	1800	OB3614.raw	2.14E5	2	2	436	458	
K.TANELNLLILR.W	N	99.9	58.89	1268.7452	11	-1.0	635.3793	2	33.92	16	2076	OB3614.raw	1.08E4	1	1	378	388	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	49.74	2313.2019	20	-2.0	772.0731	3	31.44	16	1739	OB3614.raw	1E6	8	8	402	421	
R.SPDIYNPQAGSLK.T	N	99.6	39.85	1388.6936	13	-1.9	695.3528	2	28.20	16	1373	OB3614.raw	4.6E3	2	2	365	377	
total 5 peptides																		

A1DZF0|A1DZF0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ

241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD

321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNR**SPDIYNP QAGSLKTANE LNLLILR**WLG LSAEYGNLYR

401 **NALFVPHYNT NAHSIIYALR** GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGK**SQS ENFEYVAFK**T DSRPSIANLA**

481 **GENSFIDNLP EEVVANSYGL PR**EQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	99.9	60.28	3544.7434	33	0.2	1182.5886	3	35.89	16	2345	OB3614.raw	2.07E5	2	2	470	502	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	58.89	2540.2910	23	-0.7	847.7704	3	31.89	16	1800	OB3614.raw	2.14E5	2	2	435	457	
K.TANELNLLILR.W	N	99.9	58.89	1268.7452	11	-1.0	635.3793	2	33.92	16	2076	OB3614.raw	1.08E4	1	1	377	387	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	49.74	2313.2019	20	-2.0	772.0731	3	31.44	16	1739	OB3614.raw	1E6	8	8	401	420	
R.SPDIYNPQAGSLK.T	N	99.6	39.85	1388.6936	13	-1.9	695.3528	2	28.20	16	1373	OB3614.raw	4.6E3	2	2	364	376	
total 5 peptides																		

Q2KPX7|Q2KPX7_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GMGGVGKTTL ASVLYDKISY MFDAHCFIEN ASKSYR**EGSA ISVQRQILR**R TLEEQDLDKY SPSEIAGIIR NRLSSRKLLI

81 VLDNVDEREQ LDQLAINTKL LGRGSRMIIT SRDKHILESY GIDAIHNVSL LNSQDASELF FRKAFKSDHP SSSTCMELTP
161 IILEYAQGLP FALKVL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.EGSAISVQRQILR.R	Y	89.8	25.07	1455.8157	13	-2.2	486.2781	3	36.93	16	2486	OB3614.raw	1.08E4	1	1	37	49	
total 1 peptides																		

Q2KQ57|Q2KQ57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GMGGVGKTTL ASVLYDKISY MFDAHCFIEN VSKSYR**EGSA ISVQRQILR**R TLEEQGLDKY SPSEIAGIIR NRLSSRKLLI

81 VLDNVDEREQ LDQLAINTKL LGRGTRIIIT TRDKHILESY GIDAIHNVSL MNSQDAPELL FRKAFKSDRP SSSTCMELTP
161 IILEYAQGLP LALKVLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.EGSAISVQRQILR.R	Y	89.8	25.07	1455.8157	13	-2.2	486.2781	3	36.93	16	2486	OB3614.raw	1.08E4	1	1	37	49	
total 1 peptides																		

Q2KQ05|Q2KQ05_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 IGMGGVGKTT LASVLYDKIS YMFDAHCFIE NVSKSYR**EGS AISVQRQILR** RTLEEQDLDK YSPSEIAGII RNRLSSRKLL

81 IVLDNVDERE QLDQLAINTK LLGRGSRIII TTRDKHILES YGIDAIHNVS LMNSQDASEL LFRKAFKSDR PSSSTCMELT
161 PIILEYAQGL PLAFKVLG

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.EGSAISVQRQILR.R	Y	89.8	25.07	1455.8157	13	-2.2	486.2781	3	36.93	16	2486	OB3614.raw	1.08E4	1	1	38	50	
total 1 peptides																		

Q2KPY0|Q2KPY0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WGWGGVGKTT LASVLYDKIS YMFDAHCFIE NVSKSYR**EGS AISVQRQILR** RTLEEQDLDK YSPSEIAGII RNRLSSRKLL

81 IVLDNVDERE QLDQLAINTK LLGRGSRIII TTRDKHILES YGIDAIHNVS LMNSQDASEL LFRKAFKSDR PSSSTCMELT
161 PIILEYAQGL PLALKVLGN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 16	#Spec	#Spec Sample 16	Start	End	PTM
R.EGSAISVQRQILR.R	Y	89.8	25.07	1455.8157	13	-2.2	486.2781	3	36.93	16	2486	OB3614.raw	1.08E4	1	1	38	50	
total 1 peptides																		

Peptide List

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1. Notes

Spot I from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

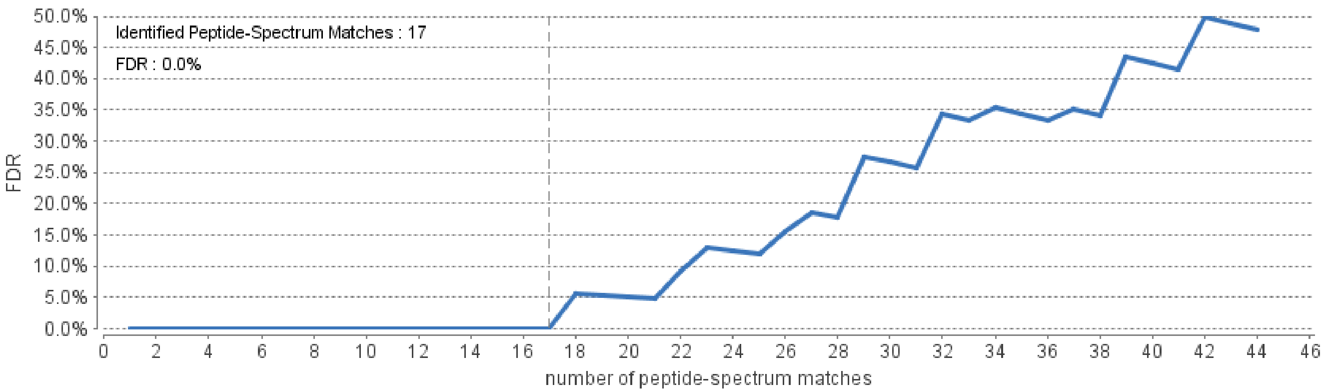
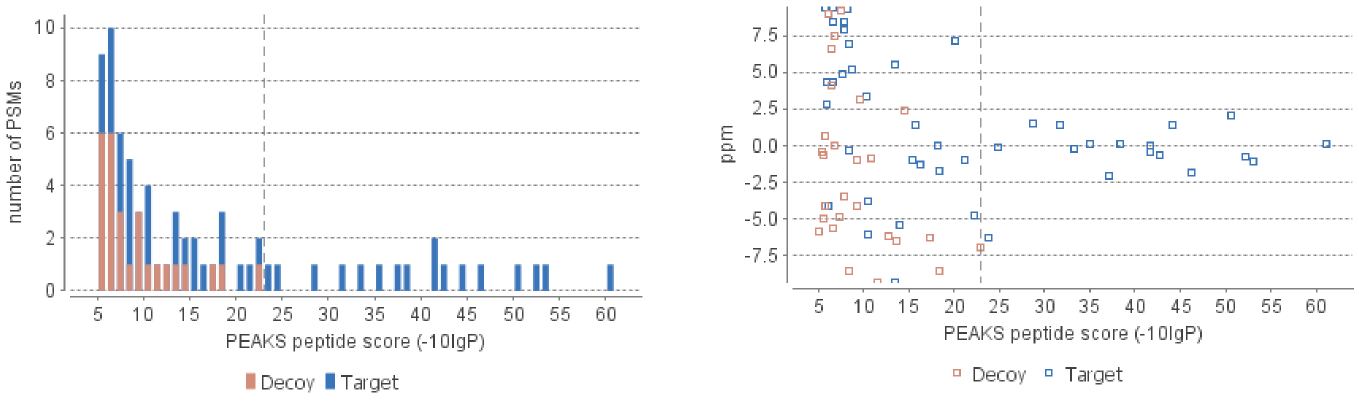


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.



(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

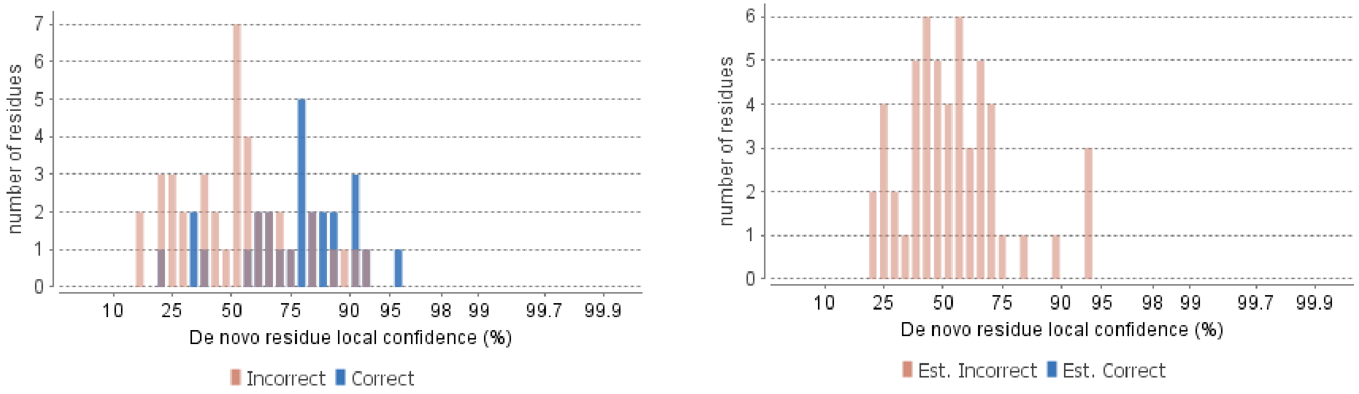


Table 1. Statistics of data.

# of MS scans	3039
# of MS/MS scans	2326

Table 2. Result filtration parameters.

Peptide -10lgP	≥23
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	15
Peptide sequences	10
Protein groups	2
Proteins	5
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 5 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	7

Table 4. PTM profile.

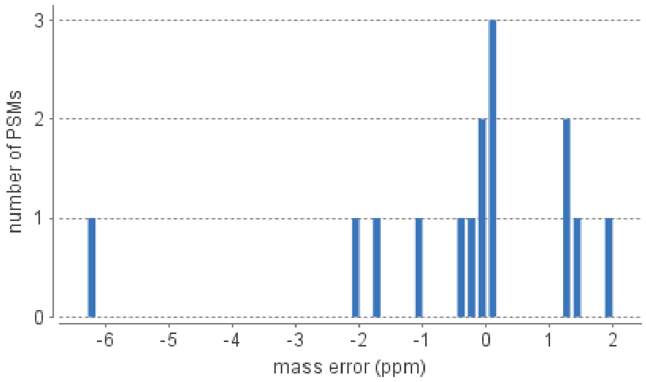
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	3	53.00	4.46E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



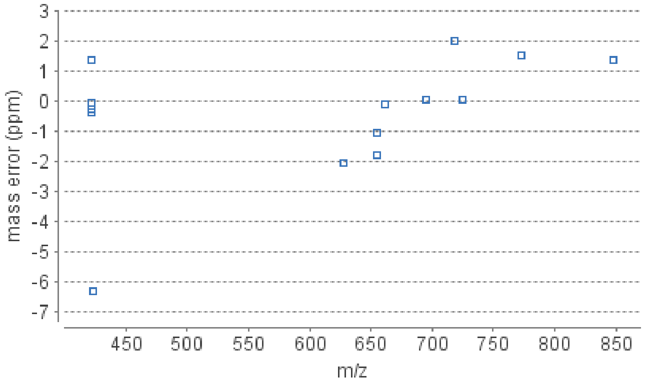


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 29	10	0	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3627.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 29	Area Sample 29	#Peptides	#Unique	#Spec Sample 29	PTM	Avg. Mass	Description
1	15	Q647H3|Q647H3_ARAHY	99.1	129.86	17	17	4.46E3	6	1	8	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
8	418	G3GD57|G3GD57_ARAHY	21.5	23.73	2	2	1.39E4	1	1	1	N	37502	Diacylglycerol acyltransferase type 2 OS=Arachis hypogaea GN=DGAT2a PE=2 SV=1
8	422	G3GD58|G3GD58_ARAHY	21.5	23.73	2	2	1.39E4	1	1	1	N	37540	Diacylglycerol acyltransferase type 2 OS=Arachis hypogaea GN=DGAT2b PE=2 SV=1
8	417	G3GD60|G3GD60_ARAHY	21.5	23.73	2	2	1.39E4	1	1	1	N	37528	Diacylglycerol acyltransferase type 2 OS=Arachis hypogaea GN=DGAT2d PE=2 SV=1
8	416	G3GD59|G3GD59_ARAHY	21.5	23.73	2	2	1.39E4	1	1	1	N	37556	Diacylglycerol acyltransferase type 2 OS=Arachis hypogaea GN=DGAT2c PE=2 SV=1
total 5 proteins													

Q647H3|Q647H3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carbamidomethylation (+57.02)

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GN**GIEETICT ASVK**KNIGRN R**SPDIYNPQA GSLKTANDLN LLILR**WLGLS
401 AEYGNLYR**NA LFVPHYNTNA HSIIYALR**GR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFK**TDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 29	#Spec	#Spec Sample 29	Start	End	PTM
R.SPDIYNPQAGSLK.T	N	99.9	61.20	1388.6936	13	0.1	695.3541	2	27.34	29	1404	OB3627.raw	5.49E3	2	2	372	384	
N.GIEETIC(+57.02)TASVK.K	Y	99.9	53.00	1306.6438	12	-1.0	654.3285	2	27.79	29	1427	OB3627.raw	4.46E3	2	2	353	364	Carbamidomethylation
K.SQSDNFEYVAFK.T	N	99.8	50.52	1433.6462	12	2.0	717.8318	2	30.38	29	1576	OB3627.raw	2.65E3	1	1	466	477	
K.TANDLNLLILR.W	N	97.6	37.18	1254.7296	11	-2.1	628.3708	2	32.93	29	1737	OB3627.raw	2.58E3	1	1	385	395	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	92.0	31.70	2540.2910	23	1.4	847.7721	3	31.26	29	1631	OB3627.raw	3.66E3	1	1	443	465	
R.NALFVPHYNTNAHSIIYALR.G	N	73.8	28.70	2313.2019	20	1.5	772.0757	3	30.75	29	1601	OB3627.raw	5.97E3	1	1	409	428	
total 6 peptides																		

G3GD57|G3GD57_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEDRGNVTAA PPAEEKVFRS TEVFAAESSS KSKGFKTTLA LALWLGAIHF NGALMLFALL FLPLSKALLV FALLFVFMVI

81 PIDEKSKFGR KLSRYICKNA CSYFPITLHV EDIKAFNSNR AYVFGFEPHS VLPIGVVALA DNTGFMPLPK IKVLASSAVF

161 YTPFLRHIWT WLGLTPATKK NFLSLLDNGY SCILIPGGVQ ETFLMEHGTE TAYLKARKGF IRIAMQKGQP LVPVFCFGQS

241 DIYKWWKPGG K**LILNFAR**AI KFTPIYFWGI FGSPIPFKHP MYVVVGRPIE LDKNPEPTTE EVATVHSQFV ASLQDLFERY

321 KARAGYPNLE LRIV

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 29	#Spec	#Spec Sample 29	Start	End	PTM
K.LILNFAR.A	Y	57.4	23.73	845.5123	7	-6.3	423.7607	2	34.81	29	1878	OB3627.raw	1.39E4	1	1	252	258	
total 1 peptides																		

G3GD58|G3GD58_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEVRGNVTVA PPAEEKVFRS TEVFAPESSS KSKGFKTTLA LALWLGAIHF NGALMLFALL FLPLSKALLV FALLFVFMVI

81 PIDEKSKFGR KLSRYICKNA CSYFPITLHV EDIKAFNSNR AYVFGFEPHS VLPIGVVALA DNTGFMPLPK IKVLASSAVF

161 YTPFLRHIWT WLGLTPATKK NFLSLLDNGY SCILIPGGVQ ETFLMEHGTE TAYLKARKGF IRIAMQKGQP LVPVFCFGQS

241 DIYKWWKPGG K**LILNFAR**AI KFTPIYFWGI FGSPIPFKHP MYVVVGRPIE LDKNPEPTTE EVATVHSQFV ASLQDLFERY

321 KARAGYPNLE LRIV

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 29	#Spec	#Spec Sample 29	Start	End	PTM
K.LILNFAR.A	Y	57.4	23.73	845.5123	7	-6.3	423.7607	2	34.81	29	1878	OB3627.raw	1.39E4	1	1	252	258	
total 1 peptides																		

G3GD60|G3GD60_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEDRGNVTAA PPAEEKVFRS TEVFAPESSS KSKGFKTTLA LALWLGAIHF NGALMLFALL FLPLSKALLV FALLFVFMVI

81 PIDEKSKFGR KLSRYICKNA CSYFPITLHV EDIKAFNSNR AYVFGFEPHS VLPIGVVALA DNTGFMPLPK IKVLASSAVF

161 YTPFLRHIWT WLGLTPATKK NFLSLLDNGY SCILIPGGVQ ETFLMEHGTE TAYLKARKGF IRIAMQKGQP LVPVFCFGQS

241 DIYKWWKPGG K**LILNFAR**AI KFTPIYFWGI FGSPIPFKHP MYVVVGRPIE LDKNPEPTTE EVATVHSQFV ASLQDLFERY

321 KARAGYPNLE LRIV

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 29	#Spec	#Spec Sample 29	Start	End	PTM
K.LILNFAR.A	Y	57.4	23.73	845.5123	7	-6.3	423.7607	2	34.81	29	1878	OB3627.raw	1.39E4	1	1	252	258	
total 1 peptides																		

G3GD59|G3GD59_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEDRGNVTVA PPAEEKVFRS TEVFAPESSS KSKGFKTTLA LALWLGAIHF NGALMLFALL FLPLSKALLV FALLFVFMVI
81 PIDEKSKFGR KLSRYICKNA CSYFPITLHV EDIKAFNSNR AYVFGFEPHS VLPIGVVALA DNTGFMPLPK IKVLASSAVF
161 YTPFLRHIWT WLGLTPATKK NFLSLLDNGY SCILIPGGVQ ETFLMEHGTE TAYLKARKGF IRIAMQKGQP LVPVFCFGQS
241 DIYKWWKPGG K**LILNFAR**AI KFTPIYFWGI FGSPIPFKHP MYVVVGRPIE LDKNPEPTTE EVATVHSQFV ASLQDLFERY
321 KARAGYPNLE LRIV

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 29	#Spec	#Spec Sample 29	Start	End	PTM
K.LILNFAR.A	Y	57.4	23.73	845.5123	7	-6.3	423.7607	2	34.81	29	1878	OB3627.raw	1.39E4	1	1	252	258	
total 1 peptides																		

Peptide List

1. Notes

Spot J from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

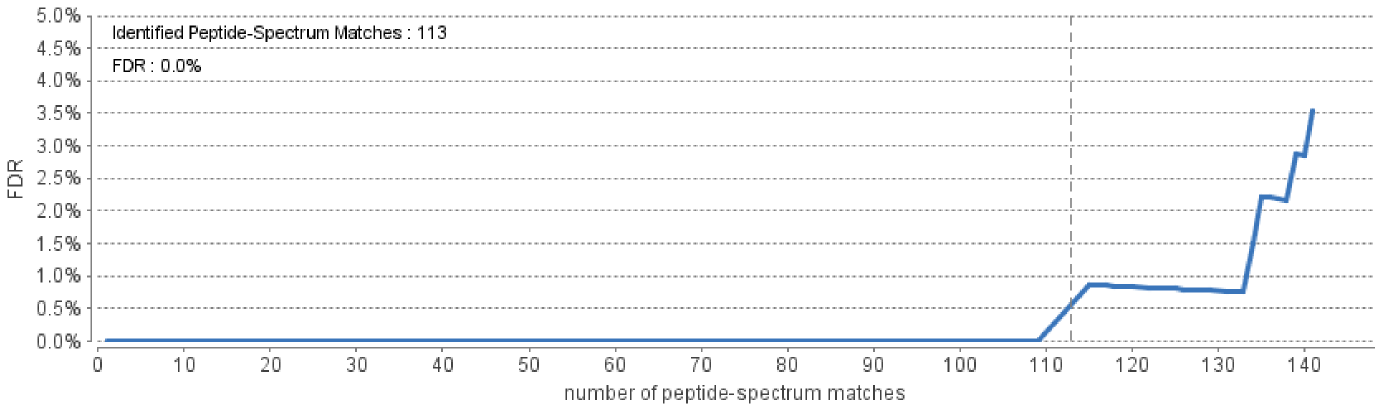
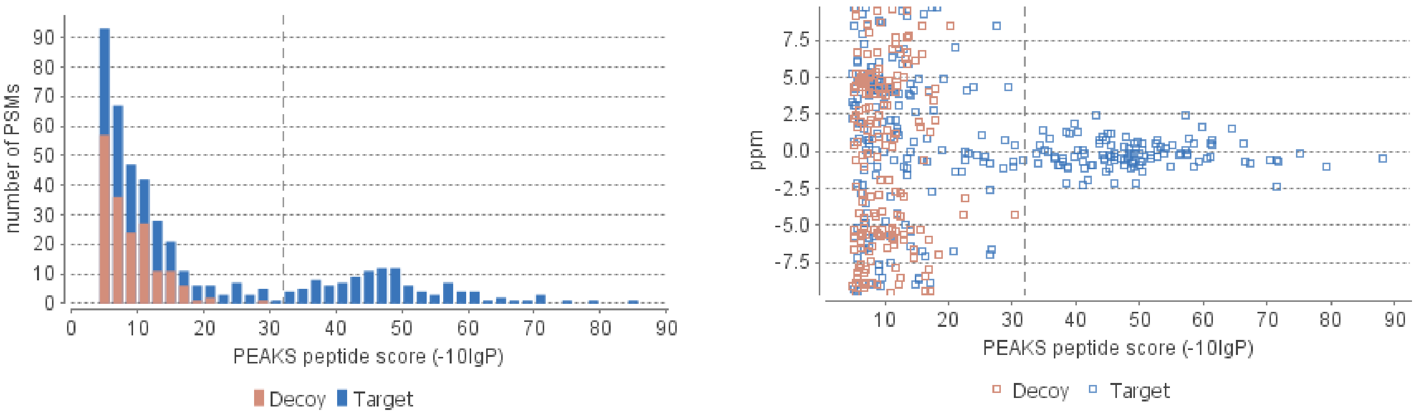


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

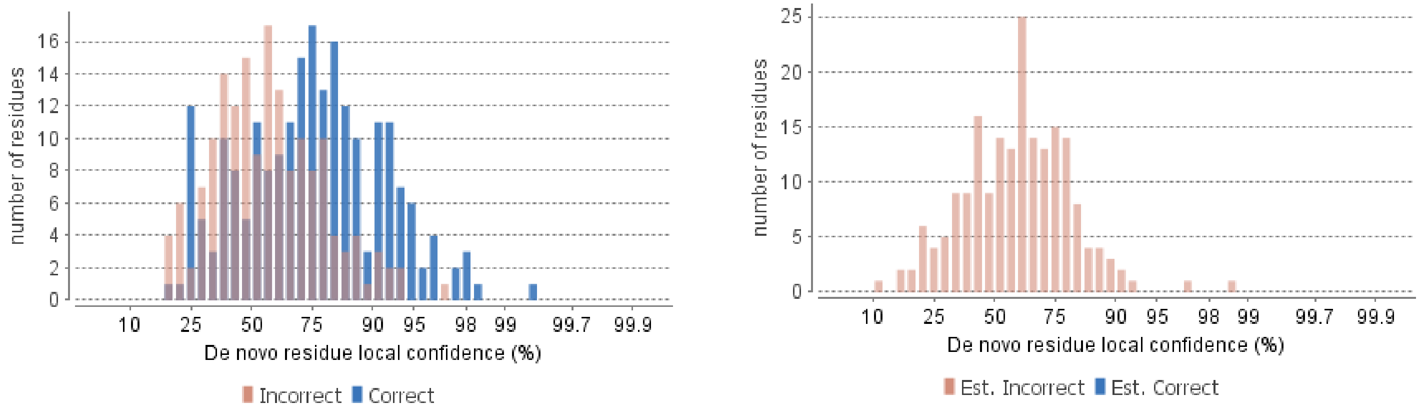


Table 1. Statistics of data.

# of MS scans	3063
# of MS/MS scans	1961

Table 2. Result filtration parameters.

Peptide -10lgP	≥32
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	113
Peptide sequences	33
Protein groups	2
Proteins	10
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 10 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	26

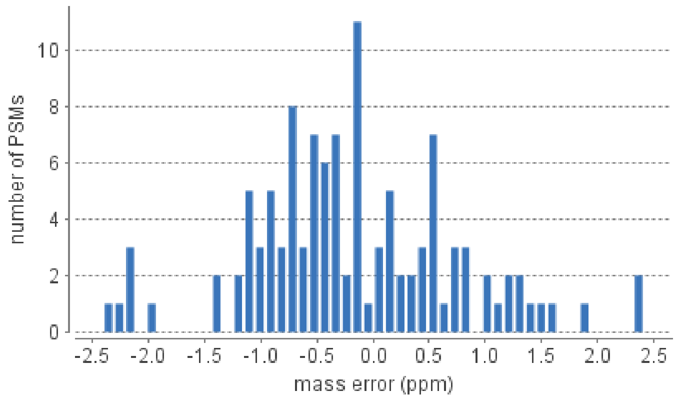
Table 4. PTM profile.

Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	7	60.50	6.36E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a) **(b)**



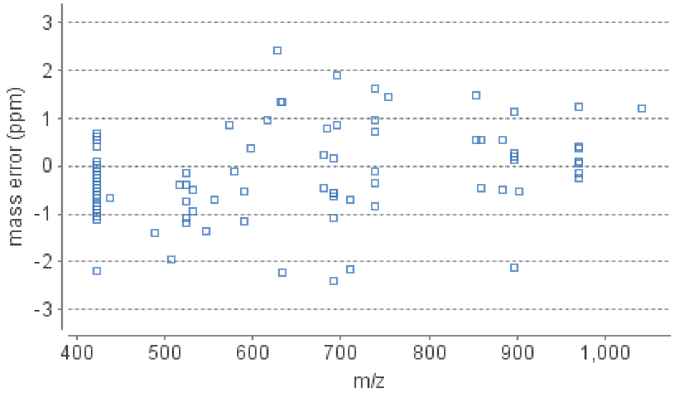


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 30	33	0	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3628.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 30	Area Sample 30	#Peptides	#Unique	#Spec Sample 30	PTM	Avg. Mass	Description
23	59	Q647H1|Q647H1_ARAHY	70.9	41.92	1	1	4.36E3	1	1	1	N	75933	Conarachin OS=Arachis hypogaea PE=2 SV=1
11	34	O82580|O82580_ARAHY	62.8	39.85	3	3	2.48E3	1	1	1	N	58350	Glycinin (Fragment) OS=Arachis hypogaea GN=Arah3 PE=2 SV=1
11	13	Q9FZ11|Q9FZ11_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
11	2	A1DZF0|A1DZF0_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
11	3	B5TYU1|B5TYU1_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
11	5	Q5I6T2|Q5I6T2_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
11	7	Q647H4|Q647H4_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
11	12	Q6T2T4|Q6T2T4_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
11	15	Q647H3|Q647H3_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
11	10	Q8LKN1|Q8LKN1_ARAHY	62.8	39.85	2	2	2.48E3	1	1	1	N	61738	Allergen Arah3/Arah4 OS=Arachis hypogaea PE=3 SV=1
total 10 proteins													

Q647H1|Q647H1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVIGPFRLSL CVCLVFLTSA CFGTRLEESF NECQLDR**LNA LTPDNR**IESQ GGITETWNSN HPELRCAGVT LLKRTIFPNG

81 FHLPSYANYP QLIFIAQGNG VFGVSLPGCP VTYEEAESQS REDRRQRIVI KRESEQEQEQ QGDSHHKIYH FRQGHLLAIP

161 AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRRFYLA GNPEEEHPET QQQQPQTRRR HGQHQQDEYG SQGEEEGNNV

241 LSGFSTQLLA HAFGVDEEIA RILQNPPEQT KDQIVRVEGG FRDVISPRWG EGKQYEDELE ERQRQPPRRD EQGKGYDYDD

321 DRRPRHRQDP YREGDEDDRR PRGSRQGQGR GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY

401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRNG VEETLCSPTL VEDIARPSRA DFYNPAAGRI

481 SSANSLTFPI LRWFQLSAEH VLLYRNGIYS PHWNNNANSI IYGLRGEGRI QVVNSQGNAV FNGVLREGQI LLVPQNFAVG

561 KQAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN

641 AQVDSKNNDG SRLWWPSSII IK

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.LNALTPDNR.I	Y	99.6	41.92	1012.5302	9	-2.0	507.2714	2	24.72	30	1139	OB3628.raw	4.36E3	1	1	38	46	
total 1 peptides																		

O82580|O82580_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RQQPEENACQ FQRLNAQRPD NRIESEGGYI ETWNPNNQEF ECAGVALSRL VLRRNALRRP FYSNAPQEIF IQQGRGYFGL
81 IFPGCPRHYE EPHTQGRRSQ SQRPPRRLQG EDQSQQQRDS HQKVHRFDEG DLIAVPTGVA FWLYNDHDTD VVAVSLTDTN
161 NNDNQLDQFP RRFNLAGNTE QEFLRYQQQS RQSRRRSLPY SPYSPQSQPR QEEREFSPRG QHSRRERAGQ EEENEGGNIF
241 SGFTPEFLEQ AFQVDDRQIV QNLRGETESE EEGAIVTVRG GLRILSPDRK RRADEEEEYD EDEYEYDEED RRRGRGSRGR
321 GNGIEETICT ASAKKNIGRN R**SPDIYNPQA GSLK**TANDLN LLILRWLGPS AEYGNLYRNA LFVAHYNTNA HSIIYRLRGR
401 AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSEN FEYVAFKTDS RPSIANLAGE NSVIDNLPEE VVANSYGLQR
481 EQARQLKNNN PFKFFVPPSQ QSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	342	354	
total 1 peptides																		

Q9FZ11|Q9FZ11_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA
81 LRRPFYSNAP QEIFIQQGRG YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV
161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP
241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE
321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNR**SPDIYNP QAGSLK**TAND LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFKT DSRPNIANFA
481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	364	376	
total 1 peptides																		

A1DZF0|A1DZF0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNR**SPDIYNP QAGSLK**TANE LNLLILRWLG LSAEYGNLYR

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA
481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	364	376	
total 1 peptides																		

B5TYU1|B5TYU1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGNGIEET ICTATVKKNI GRNR**SPDIYN PQAGSLK**TAN ELNLLILRWL GLSAEYGNLY

401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LPREQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	365	377	
total 1 peptides																		

Q5I6T2|Q5I6T2_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGRGNGIEET ICTASVKKNI GRNR**SPDIYN PQAGSLK**TAN DLNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	365	377	
total 1 peptides																		

Q647H4|Q647H4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELNL LILRWLGLSA
401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR
481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	371	383	
total 1 peptides																		

Q6T2T4|Q6T2T4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELNL LILRWLGLSA

401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR
481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	371	383	
total 1 peptides																		

Q647H3|Q647H3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN R**SPDIYNPQA GSLK**TANDLN LLILRWLGLS

401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	372	384	
total 1 peptides																		

Q8LKN1|Q8LKN1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR **SPDIYNPQAG SLK**TANELQL NLLILRWLGL
401 SAEYGNLYRN ALFVPHYNTN AHSIIYALRG RAHVQVVDSN GDRVFDEELQ EGHVLVVPQN FAVAGKSQSE NFEYVAFKTD
481 SRPSIANLAG ENSFIDNLPE EVVANSYGLP REQARQLKNN NPFKFFVPPS EQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 30	#Spec	#Spec Sample 30	Start	End	PTM
R.SPDIYNPQAGSLK.T	Y	99.3	39.85	1388.6936	13	1.9	695.3554	2	27.67	30	1309	OB3628.raw	2.48E3	1	1	371	383	
total 1 peptides																		

Peptide List

Prepared with PEAKS ™ (bioinfor.com)

Summary

1. Notes

Spot L from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

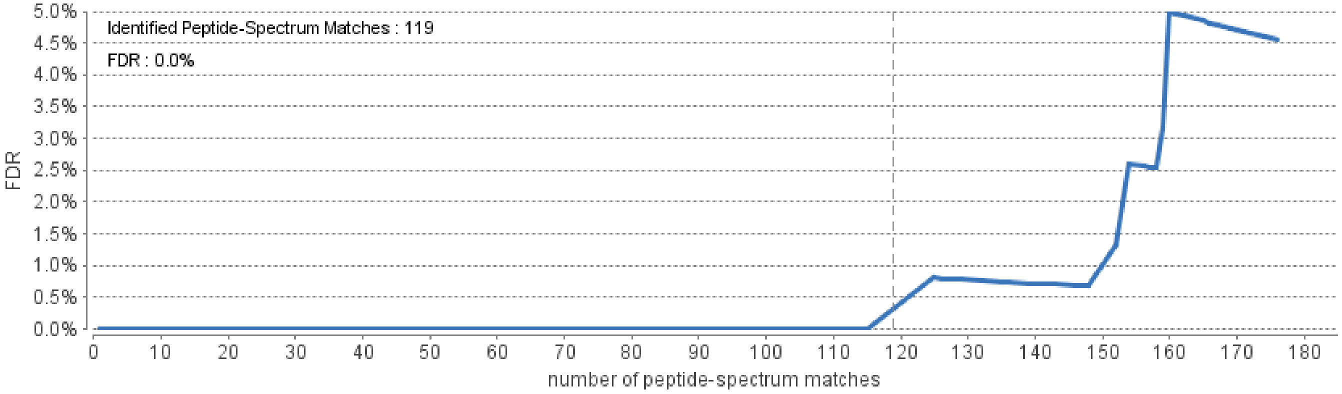
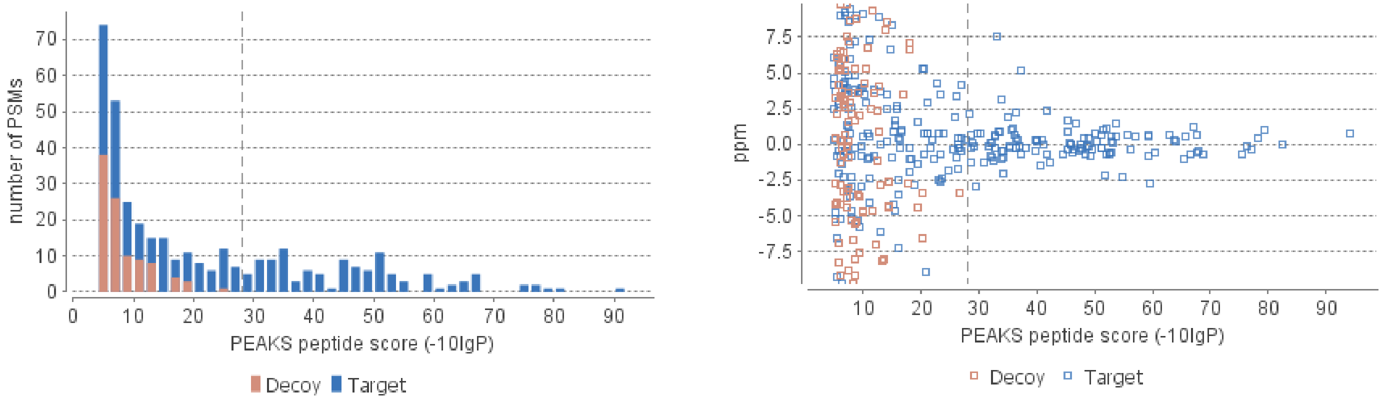


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

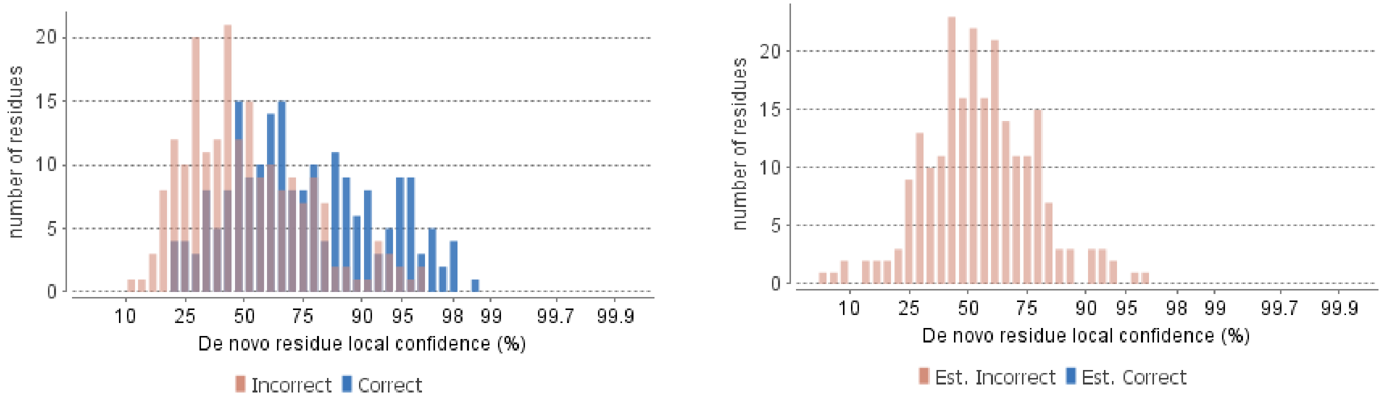


Table 1. Statistics of data.

# of MS scans	3101
# of MS/MS scans	1701

Table 2. Result filtration parameters.

Peptide -10lgP	≥28
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	116
Peptide sequences	53
Protein groups	1
Proteins	1
Proteins (#Unique Peptides)	1 (>2); 0 (=2); 0 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	28

Table 4. PTM profile.

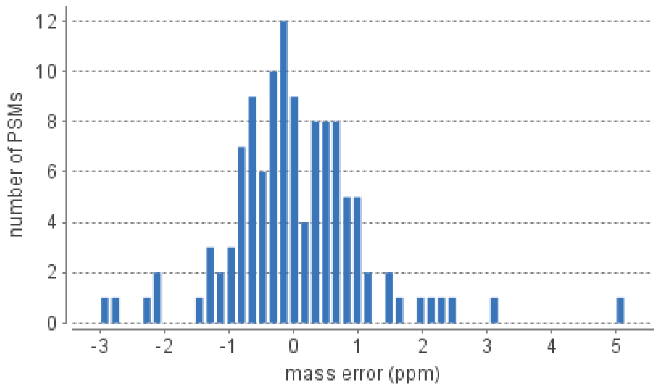
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Oxidation	15.99	M	6	50.01	1.2E3	1000.00
HydPro	15.99	P	5	46.85	9.01E3	45.01
Carbamidomethyl	57.02	C	4	63.76	2.09E4	1000.00
Deamidation	.98	Q	3	34.33	1.4E4	0.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



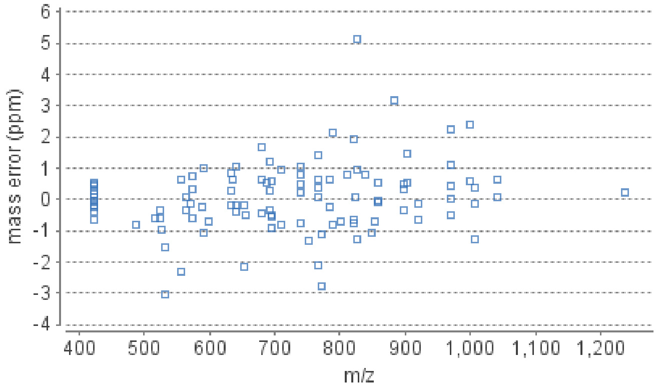


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 28	52	1	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3626.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 28	Area Sample 28	#Peptides	#Unique	#Spec Sample 28	PTM	Avg. Mass	Description
2	2	A1DZF0|A1DZF0_ARAHY	99.1	122.66	17	17	2.76E4	7	3	13	Y	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
total 1 proteins													

A1DZF0|A1DZF0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT

225 h 228 h

161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRR**FNLAG NHEQEFLR**YQ QQSRQSRRR**S LPLSPYSPQP GQED**REFSPQ

h h
h h d
h h d

241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD

321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNR**SPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR**

401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGK**SQS ENFEYVAFKT DSRPSIANLA

481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 28	#Spec	#Spec Sample 28	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	59.56	1540.7673	13	-2.8	771.3888	2	32.63	28	1887	OB3626.raw	2.51E3	2	2	388	400	
R.SLPLSP(+15.99)YSP(+15.99)QPGQE.D	Y	99.9	46.85	1530.7201	14	1.4	766.3684	2	28.68	28	1477	OB3626.raw	9.01E3	2	2	220	233	Hydroxylation Pro
R.SLPLSP(+15.99)YSP(+15.99)Q(+.98)PGQE.D	Y	98.8	34.33	1531.7041	14	-2.1	766.8577	2	28.88	28	1498	OB3626.raw	1.4E4	2	2	220	233	Hydroxylation Pro; Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	98.8	34.28	1388.6936	13	-0.9	695.3535	2	27.00	28	1360	OB3626.raw	2.78E3	1	1	364	376	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	98.7	34.04	2540.2910	23	-1.1	847.7700	3	30.93	28	1706	OB3626.raw	3.95E4	1	1	435	457	
R.FNLAGNHEQEFLR.Y	N	98.1	32.19	1573.7637	13	-1.0	525.5947	3	28.48	28	1457	OB3626.raw	1.02E5	3	3	196	208	
R.SLPLSP(+15.99)YSP(+15.99)Q(+.98)PGQED.R	Y	97.8	31.88	1646.7311	15	0.1	824.3729	2	29.03	28	1512	OB3626.raw	4.63E3	1	1	220	234	Hydroxylation Pro; Deamidation (NQ)
K.TANELNLLILR.W	Y	94.5	28.62	1268.7452	11	0.7	635.3803	2	32.90	28	1905	OB3626.raw	0	1	1	377	387	
total 8 peptides																		

Peptide List

Summary

1. Notes

Spot M from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR. ?

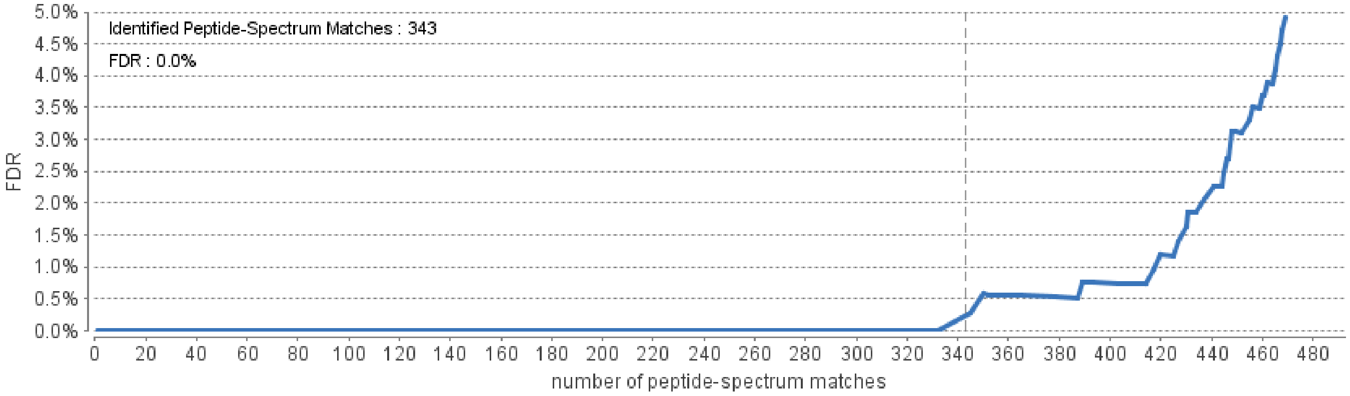


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error. ?

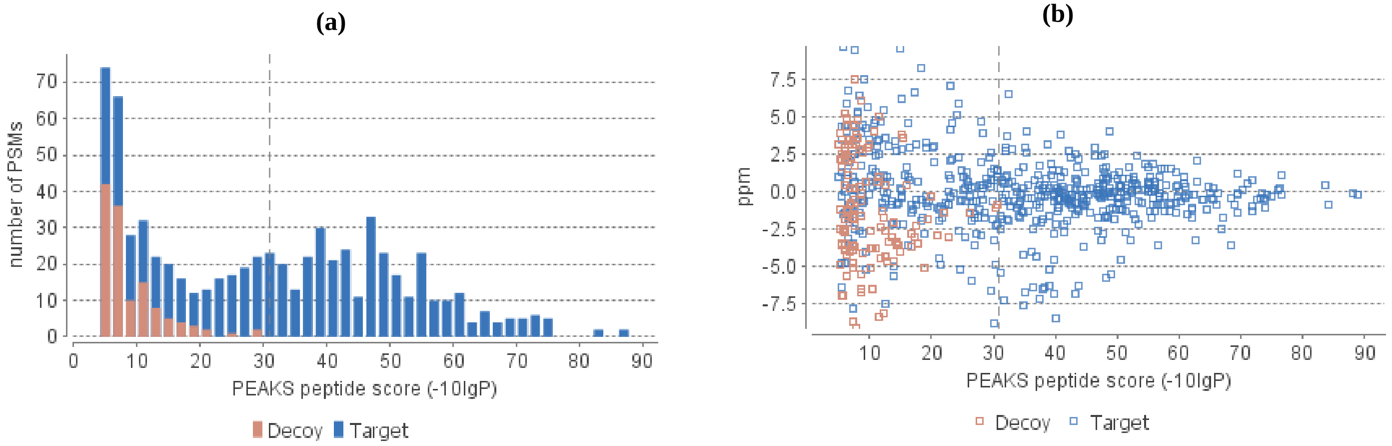


Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences. ?

(a)

(b)

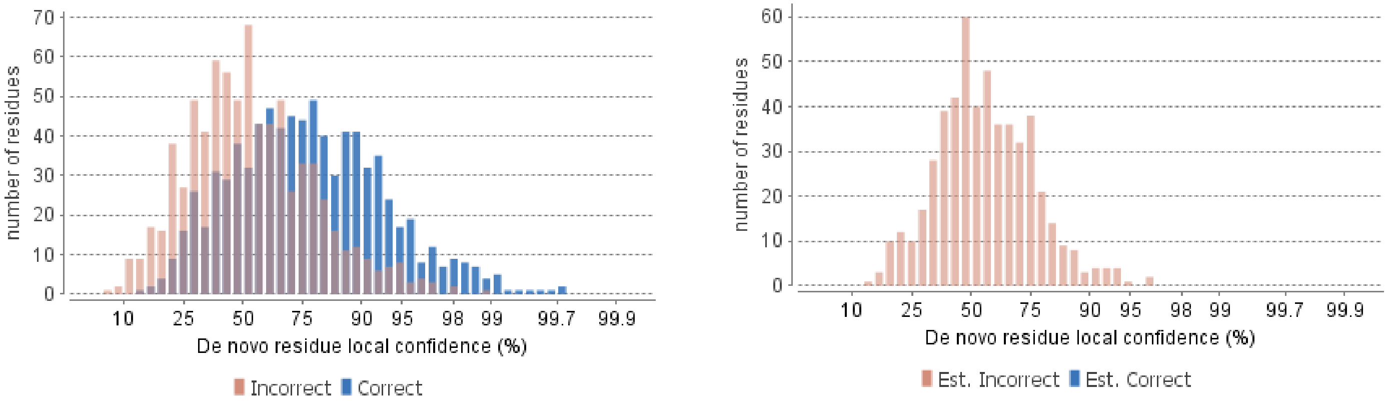


Table 1. Statistics of data.

# of MS scans	3083
# of MS/MS scans	2455

Table 2. Result filtration parameters.

Peptide -10lgP	≥31
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	341
Peptide sequences	62
Protein groups	3
Proteins	11
Proteins (#Unique Peptides)	0 (>2); 9 (=2); 2 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	63

Table 4. PTM profile.

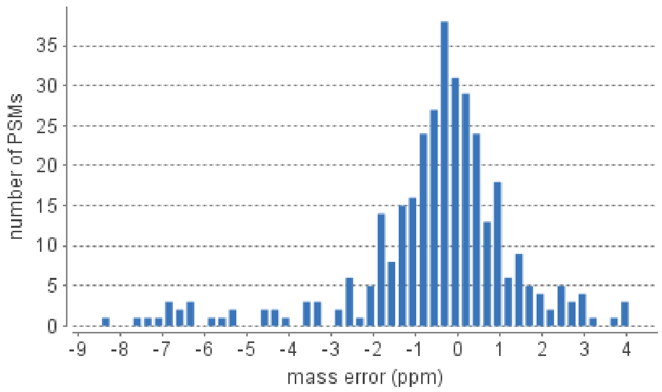
Name	ΔMass	Position	#PSM	-10lgP	Area	AScore
Carbamidomethyl	57.02	C	8	59.40	3.12E4	1000.00
Deamidation	.98	Q	2	42.14	4.24E4	1000.00
Oxidation	15.99	M	2	48.04	4.42E3	36.33

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



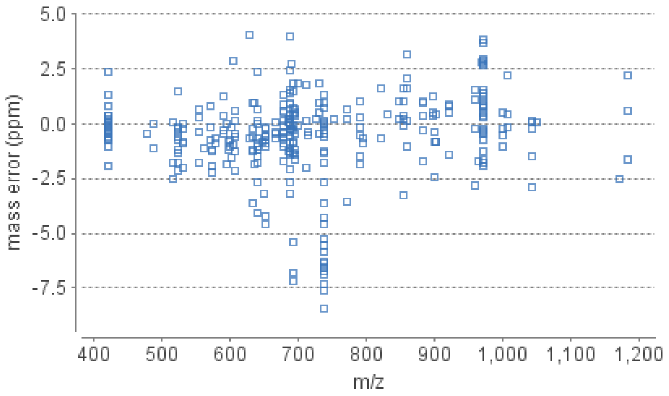


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 26	60	2	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3624.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 26	Area Sample 26	#Peptides	#Unique	#Spec Sample 26	PTM	Avg. Mass	Description
6	15	Q647H3|Q647H3_ARAHY	99.1	132.13	17	17	8.07E3	5	1	10	N	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
7	2	A1DZF0|A1DZF0_ARAHY	99.1	127.52	20	20	1.83E3	6	1	11	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
5	122	E9LFE7|E9LFE7_ARAHY	84.1	89.31	21	21	5.75E5	2	2	39	Y	15873	7S conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	69	Q6PSU5|Q6PSU5_ARAHY	84.1	89.31	10	10	5.75E5	2	2	39	Y	33604	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	57	Q6PSU6|Q6PSU6_ARAHY	84.1	89.31	10	10	5.75E5	2	2	39	Y	34133	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	27	Q6PSU4|Q6PSU4_ARAHY	84.1	89.31	7	7	5.75E5	2	2	39	Y	48095	Conarachin (Fragment) OS=Arachis hypogaea PE=2 SV=1
5	26	Q6PSU3|Q6PSU3_ARAHY	84.1	89.31	5	5	5.75E5	2	2	39	Y	66575	Conarachin (Fragment) OS=Arachis hypogaea PE=4 SV=1
5	23	B3IXL2|B3IXL2_ARAHY	84.1	89.31	5	5	5.75E5	2	2	39	Y	70283	Main allergen Ara h1 OS=Arachis hypogaea PE=2 SV=1
5	21	sp|P43237|ALL11_ARAHY	84.1	89.31	5	5	5.75E5	2	2	39	Y	70283	Allergen Ara h 1, clone P17 OS=Arachis hypogaea PE=1 SV=1
5	18	N1NG13|N1NG13_ARAHY	84.1	89.31	5	5	5.75E5	2	2	39	Y	71345	Seed storage protein Ara h1 OS=Arachis hypogaea GN=ARAX_AHF417E07-017 PE=4 SV=1
5	20	sp|P43238|ALL12_ARAHY	84.1	89.31	5	5	5.75E5	2	2	39	Y	71345	Allergen Ara h 1, clone P41B OS=Arachis hypogaea PE=1 SV=1
total 11 proteins													

Q647H3|Q647H3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN R**SPDIYNPQA GSLKTANDLN LLILRWLGLS**
401 **AEYGNLYR**NA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NR**VYDEELQE GHVLVVPQNF AVAGK**SQSDN FEYVAFK**TDS**
481 **RPSIANLAGE NSIIDNLPEE VVANSYGLPR** EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	68.43	1540.7673	13	-3.6	771.3882	2	32.58	26	2055	OB3624.raw	2.33E4	3	3	396	408	
K.TANDLNLLILR.W	N	99.9	53.61	1254.7296	11	-0.7	628.3716	2	32.08	26	1993	OB3624.raw	1.25E4	2	2	385	395	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.4	36.34	3510.7590	33	-2.5	1171.2573	3	34.72	26	2295	OB3624.raw	8.07E3	1	1	478	510	
R.SPDIYNPQAGSLK.T	N	99.3	34.97	1388.6936	13	-1.4	695.3531	2	27.03	26	1450	OB3624.raw	5.19E3	2	2	372	384	

R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.3	34.93	2540.2910	23	0.2	847.7711	3	31.25	26	1889	OB3624.raw	4.44E4	2	2	443	465	
total 5 peptides																		

A1DZF0|A1DZF0_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNR**SPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR**
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA**
481 **GENSFIDNLP EEVVANSYGL PR**EQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	68.43	1540.7673	13	-3.6	771.3882	2	32.58	26	2055	OB3624.raw	2.33E4	3	3	388	400	
K.TANELNLLILR.W	N	99.9	49.58	1268.7452	11	-1.8	635.3787	2	32.40	26	2032	OB3624.raw	2.54E3	2	2	377	387	
R.SPDIYNPQAGSLK.T	N	99.3	34.97	1388.6936	13	-1.4	695.3531	2	27.03	26	1450	OB3624.raw	5.19E3	2	2	364	376	
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.3	34.93	2540.2910	23	0.2	847.7711	3	31.25	26	1889	OB3624.raw	4.44E4	2	2	435	457	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	Y	98.9	32.60	3544.7434	33	0.6	1182.5891	3	35.11	26	2340	OB3624.raw	1.83E3	1	1	470	502	
K.SQSENFEYVAFK.T	N	98.8	31.23	1447.6619	12	0.2	724.8384	2	29.83	26	1716	OB3624.raw	2.54E3	1	1	458	469	
total 6 peptides																		

E9LFE7|E9LFE7_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WEEEEEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**
81 **LAFPGSGEQV EK**LIKNQRES HFVSARPQSQ SQFPSSPEKE DQEEENQGGK GPLLSILKAF N

d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	80	92	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	61	76	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	80	92	Deamidation (NQ)
total 3 peptides																		

Q6PSU5|Q6PSU5_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

```
  1 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
 81 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
161 EEEEDEDQEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD
241 LAFPGSGEQV EKLIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	240	252	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	221	236	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	240	252	Deamidation (NQ)
total 3 peptides																		

Q6PSU6|Q6PSU6_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

```
  1 GNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRRSTRS SDNEGVIVKV SKEHVQELTK HAKSVSKKGS EEEDITNPIN
 81 LRDGEPDLSN NFGRLFEVKP DKKNPQLQDL DMMLTCVEIK EGALMLPHFN SKAMVIVVVN KGTGNLELVA VRKEQQQRGR
161 REQEWEEEEE DEEEEGSNRE VRRYTARLKE GDVFIMPAAH PVAINASSEL HLLGFGINAE NNHRIFLAGD KDNVIDQIEK
241 QAKDLAFPGS GEQVEKLIKN QRESHFVSAR PQSQSPSSPE KEDQEEENQG GKGPLLSILK AFN
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	244	256	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	225	240	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	244	256	Deamidation (NQ)
total 3 peptides																		

Q6PSU4|Q6PSU4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 GFDQRSRQFQ NLQNHRIVQI EAKPNTLVLP KHADADNILV IQQGQATVTV ANGNNRKSFN LDEGHALRIP SGFISYILNR
81 HDNQNLRVAK ISMPVNTPGQ FEDFFPASSR DQSSYLQGFS RNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRWSTRS
161 SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI
241 KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREEEDEDE EEEGSNREVR RYTARLKEGD VFIMPAAHPV
321 AINASSELHL LGFGINAENN HR**IFLAGDKD NVIDQIEK**QA K**DLAFPGSGE QVEK**LIKNQK ESHFVSARPQ SQSQSPSSPE

401 KESPEKEDQE EENQGGKGPL LSILKAFN

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	362	374	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	343	358	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	362	374	Deamidation (NQ)
total 3 peptides																		

Q6PSU3|Q6PSU3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	555	567	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	536	551	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	555	567	Deamidation (NQ)
total 3 peptides																		

B3IXL2|B3IXL2_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA RPQSQPSSSP EKEDQEEENQ GGKGPLLSIL KAFN

d

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	555	567	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	536	551	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	555	567	Deamidation (NQ)
total 3 peptides																		

sp|P43237|ALL11_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD LKQKACESRC TKLEYDPRCV YDTGATNQRH
81 PPGERTRGRQ PGDYDDDRRQ PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ EWGTPGSEVR
161 EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT
241 VANGNNRKSF NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS RDQSSYLQGF SRNTLEAAFN
321 AEFNEIRRVL LEENAGGEQE ERGQRRRSTR SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREQEWEEEE
481 EDEEEEGSNR EVRRYTARLK EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHR**IFLAG DKDNVIDQIE K**QAK**DLAFPG**

561 **SGEQVEK**LIK NQRESHFVSA RPQSQPSSSP EKEDQEEENQ GGKGPLLSIL KAFN

d

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	555	567	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	536	551	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	555	567	Deamidation (NQ)
total 3 peptides																		

N1NG13|N1NG13_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

🟥d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

d

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	560	572	
R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	541	556	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	560	572	Deamidation (NQ)
total 3 peptides																		

sp|P43238|ALL12_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

🟥d Deamidation (NQ) (+0.98)

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP DDLKQKACES RCTKLEYDPR CVYDPRGHTG
81 TTNQRSPPGE RTRGRQPGDY DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE GREGEQEWGT
161 PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ
241 GQATVTVANG NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED FFPASSRDQS SYLQGFSRNT
321 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV RKEQQQRGRR
481 EEEDEDEEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR **IFLAGDKDNV IDQIEK**QAK**D**

561 **LAFPGSGEQV EK**LIKNQKES HFVSARPQSQ SQSPSSPEKE SPEKEDQEEE NQGGKGPLLS ILKAFN

d

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 26	#Spec	#Spec Sample 26	Start	End	PTM
K.DLAFPGSGEQVEK.L	Y	99.9	63.87	1375.6619	13	-0.6	688.8378	2	28.18	26	1547	OB3624.raw	4.02E5	31	31	560	572	

R.IFLAGDKDNVIDQIEK.Q	Y	99.9	50.88	1816.9570	16	-1.2	606.6589	3	30.55	26	1798	OB3624.raw	1.29E5	6	6	541	556	
K.DLAFPGSGEQ(+.98)VEK.L	Y	99.8	42.14	1376.6459	13	2.7	689.3321	2	28.92	26	1625	OB3624.raw	4.43E4	2	2	560	572	Deamidation (NQ)
total 3 peptides																		

Peptide List

1. Notes

Spot N from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

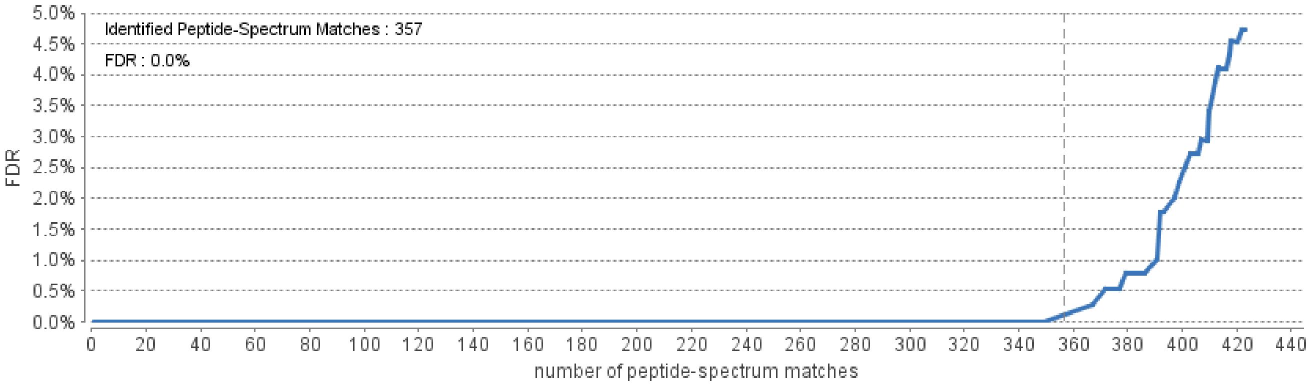


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)

(b)

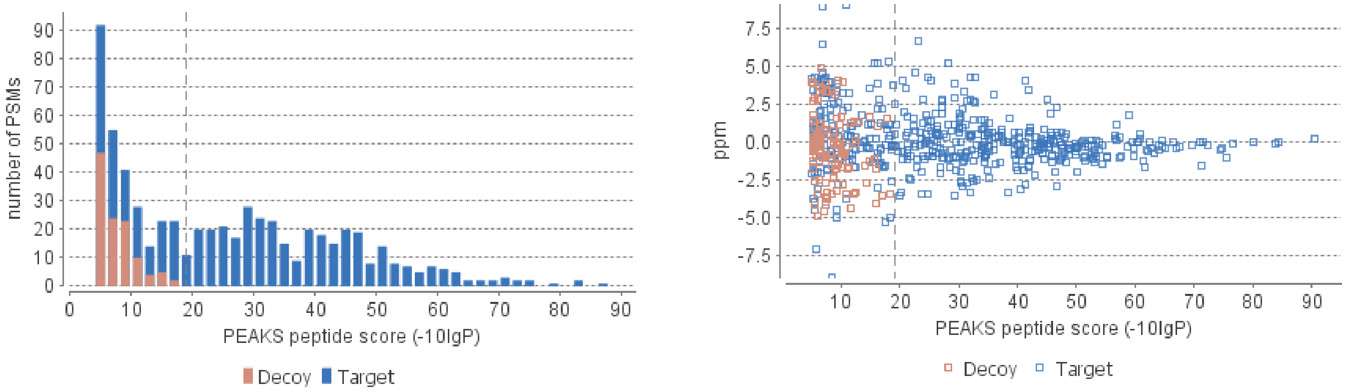


Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)

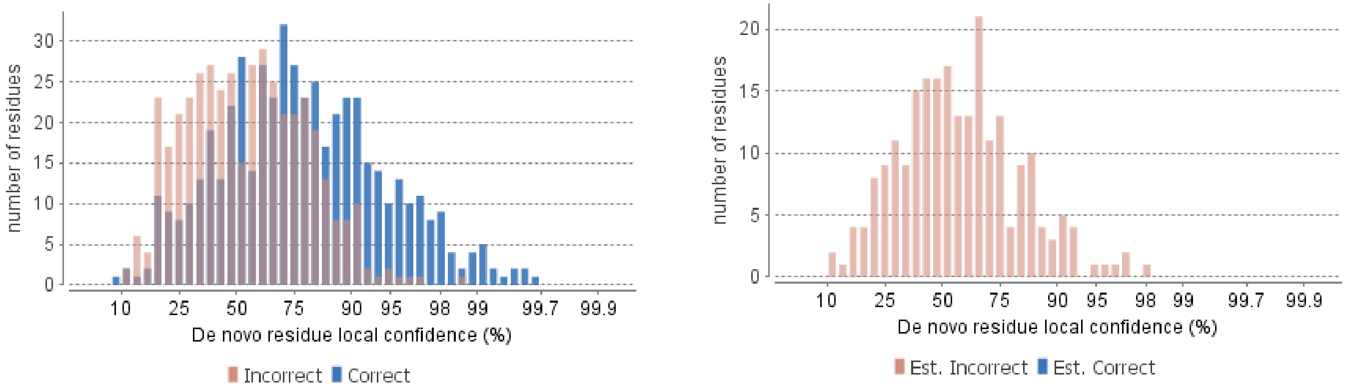


Table 1. Statistics of data.

# of MS scans	3030
# of MS/MS scans	2075

Table 2. Result filtration parameters.

Peptide -10lgP	≥19
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	299
Peptide sequences	64
Protein groups	7
Proteins	9
Proteins (#Unique Peptides)	3 (>2); 1 (=2); 5 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	0.0%
De Novo Only Spectra	29

Table 4. PTM profile.

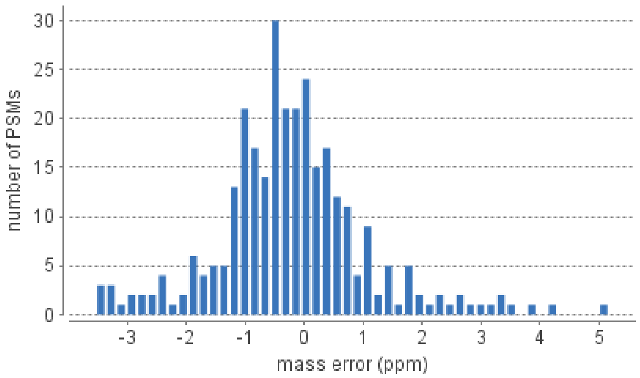
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	21	63.92	7.44E4	1000.00
Deamidation	.98	NQ	13	71.20	2.46E4	54.70
HydPro	15.99	P	2	22.67	1.42E4	1000.00
Oxidation	15.99	M	1	34.41	3.37E3	1000.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



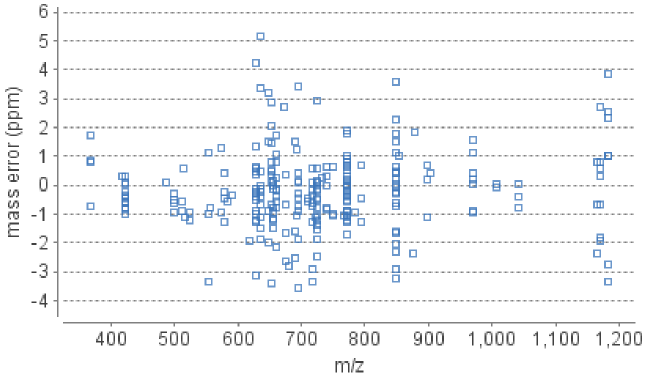


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 25	61	3	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3623.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:

Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 25	Area Sample 25	#Peptides	#Unique	#Spec Sample 25	PTM	Avg. Mass	Description
5	3	B5TYU1|B5TYU1_ARAHY	99.1	230.11	30	30	1.63E4	16	1	152	Y	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
1	2	A1DZF0|A1DZF0_ARAHY	99.1	228.54	32	32	3.04E4	17	1	166	Y	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
2	15	Q647H3|Q647H3_ARAHY	99.1	227.16	29	29	9.39E4	16	1	164	Y	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
3	13	Q9FZ11|Q9FZ11_ARAHY	99.1	226.44	26	26	5.57E4	16	2	161	Y	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
6	7	Q647H4|Q647H4_ARAHY	99.1	217.96	29	29	8.49E4	17	4	137	Y	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	99.1	217.96	29	29	8.49E4	17	4	137	Y	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
11	41	Q6IWG5|Q6IWG5_ARAHY	98.7	93.26	9	9	3.09E4	4	1	7	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
11	42	Q0GM57|Q0GM57_ARAHY	98.7	93.26	9	9	3.09E4	4	1	7	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
10	59	Q647H1|Q647H1_ARAHY	98.5	62.78	7	7	1.49E4	4	4	4	N	75933	Conarachin OS=Arachis hypogaea PE=2 SV=1
total 9 proteins													

B5TYU1|B5TYU1_ARAHY

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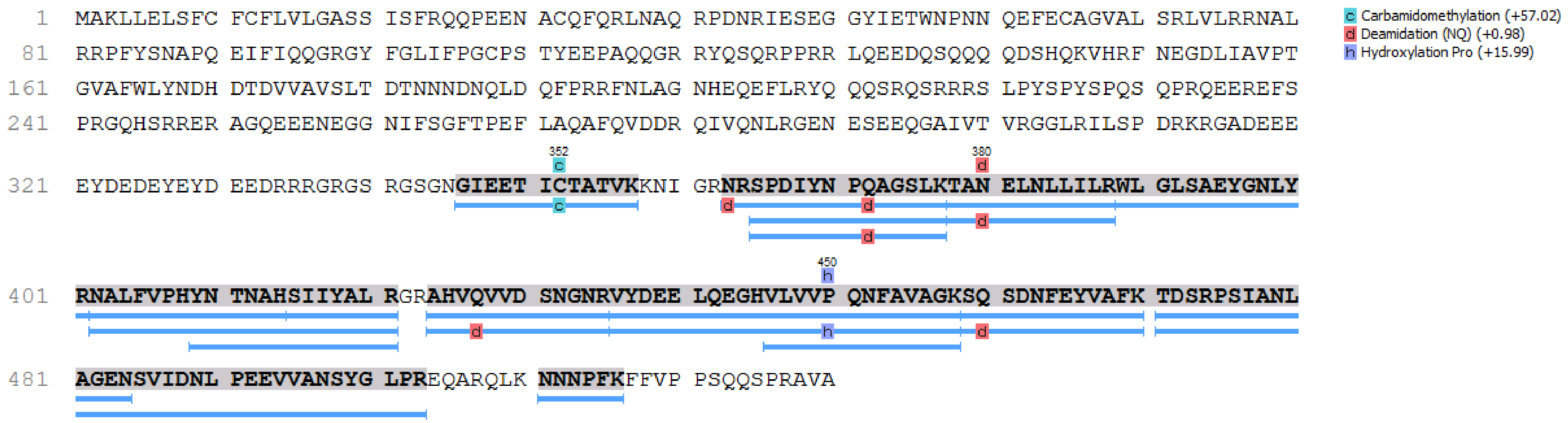
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGN**GIEET ICTATVK**KNI GR**NRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY**
401 **RNALFVPHYN TNAHSIIYAL R**GR**AHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL**
481 **AGENSVIDNL PEEVVANSYG LPR**EQARQLK **NNNPFK**FFVP PSQQSPRAVA

c Carbamidomethylation (+57.02)
d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.65	1540.7673	13	0.2	771.3911	2	32.75	25	1974	OB3623.raw	6.72E5	48	48	389	401	
K.SQSDNFEYVAFK.T	N	99.9	80.09	1433.6462	12	0.1	717.8304	2	30.04	25	1660	OB3623.raw	1.7E5	13	13	459	470	
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	70.93	1434.6302	12	0.1	718.3224	2	30.29	25	1680	OB3623.raw	5.52E4	1	1	459	470	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	64.66	1388.6936	13	-0.3	695.3539	2	27.09	25	1353	OB3623.raw	4.07E5	14	14	365	377	

N.GIEETIC(+57.02)TATVK.K	N	99.9	63.92	1320.6595	12	-0.2	661.3369	2	27.90	25	1437	OB3623.raw	1.08E5	10	10	346	357	Carbamidomethylation
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	56.54	2540.2910	23	0.2	847.7711	3	31.02	25	1762	OB3623.raw	4.24E5	24	24	436	458	
K.TANELNLLILR.W	N	99.9	54.46	1268.7452	11	-0.2	635.3798	2	32.92	25	1992	OB3623.raw	1.32E5	10	10	378	388	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	51.43	2313.2019	20	-0.9	772.0739	3	31.03	25	1763	OB3623.raw	5.99E5	6	6	402	421	
K.TDSRPSIANLAGENSVIDNLPEEVVANSYGLPR.E	Y	99.9	44.54	3496.7434	33	0.8	1166.5894	3	34.31	25	2160	OB3623.raw	1.63E4	3	3	471	503	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.8	41.84	1389.6776	13	3.4	695.8484	2	28.06	25	1452	OB3623.raw	8.41E4	1	1	365	377	Deamidation (NQ)
H.SIIYALR.G	N	99.4	36.28	834.4963	7	0.3	418.2556	2	28.66	25	1516	OB3623.raw	7.48E4	1	1	415	421	
R.AHVQ(+.98)VVDSNGNR.V	N	99.4	35.89	1295.6218	12	3.2	648.8203	2	20.50	25	991	OB3623.raw	1.36E4	1	1	424	435	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.4	34.34	1294.6378	12	1.5	648.3271	2	19.56	25	938	OB3623.raw	2.55E3	1	1	424	435	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	511	516	
R.NALFVPHYNTNAH.S	N	98.9	32.31	1496.7161	13	-0.5	499.9124	3	27.31	25	1374	OB3623.raw	2.23E5	7	7	402	414	
H.VLVVPQNFAVAGK.S	N	98.8	31.36	1340.7816	13	2.7	671.3999	2	30.07	25	1664	OB3623.raw	1.04E3	1	1	446	458	
K.TAN(+.98)ELNLLILR.W	N	98.8	30.93	1269.7292	11	3.3	635.8740	2	33.49	25	2057	OB3623.raw	0	2	2	378	388	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	96.5	28.09	1660.8057	15	1.2	554.6098	3	26.85	25	1330	OB3623.raw	2.81E3	2	2	363	377	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	471	484	
R.VYDEELQEGHVLVVP(+15.99)QNFAVAGK.S	N	86.4	22.26	2556.2859	23	1.0	853.1035	3	32.12	25	1901	OB3623.raw	4.76E3	1	1	436	458	Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	86.0	21.82	1534.7892	13	-0.9	512.6032	3	28.92	25	1548	OB3623.raw	1.82E4	2	2	409	421	
total 21 peptides																		

A1DZF0|A1DZF0_ARAHY

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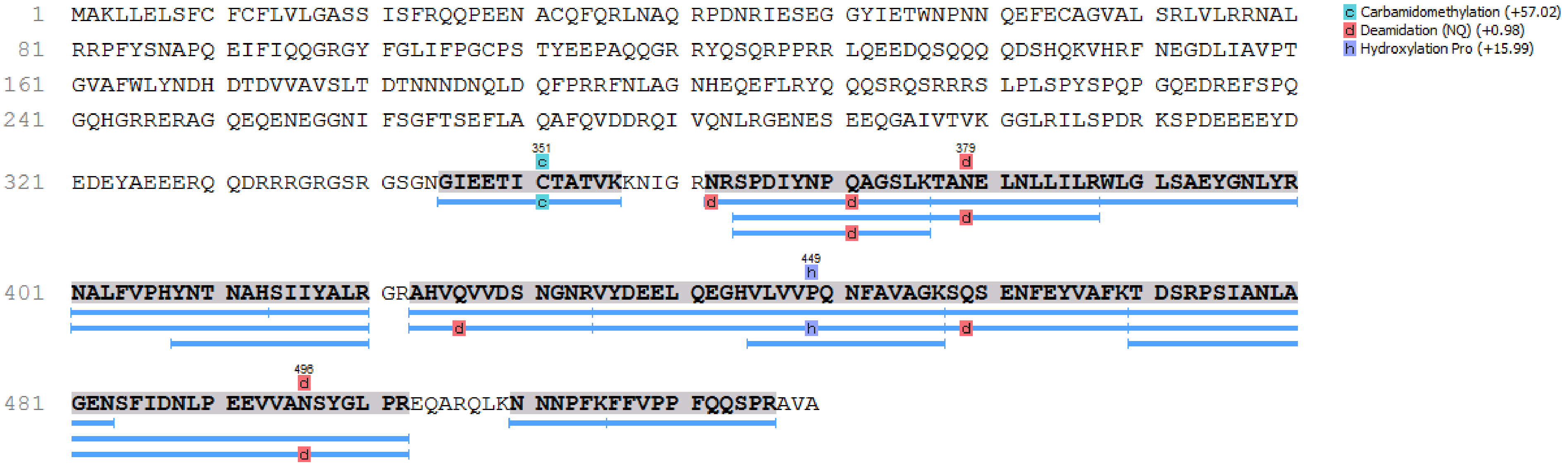
| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.65	1540.7673	13	0.2	771.3911	2	32.75	25	1974	OB3623.raw	6.72E5	48	48	388	400	
K.SQSENFEYVAFK.T	N	99.9	74.74	1447.6619	12	-0.4	724.8379	2	29.94	25	1649	OB3623.raw	1.92E5	19	19	458	469	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	71.20	1448.6459	12	-1.5	725.3291	2	30.12	25	1669	OB3623.raw	2.46E4	1	1	458	469	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	64.66	1388.6936	13	-0.3	695.3539	2	27.09	25	1353	OB3623.raw	4.07E5	14	14	364	376	
N.GIEETIC(+57.02)TATVK.K	N	99.9	63.92	1320.6595	12	-0.2	661.3369	2	27.90	25	1437	OB3623.raw	1.08E5	10	10	345	356	Carbamidomethylation

R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	56.54	2540.2910	23	0.2	847.7711	3	31.02	25	1762	OB3623.raw	4.24E5	24	24	435	457	
K.TANELNLLILR.W	N	99.9	54.46	1268.7452	11	-0.2	635.3798	2	32.92	25	1992	OB3623.raw	1.32E5	10	10	377	387	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	51.43	2313.2019	20	-0.9	772.0739	3	31.03	25	1763	OB3623.raw	5.99E5	6	6	401	420	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	46.53	3544.7434	33	2.3	1182.5912	3	35.04	25	2251	OB3623.raw	4.39E4	5	5	470	502	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.8	41.84	1389.6776	13	3.4	695.8484	2	28.06	25	1452	OB3623.raw	8.41E4	1	1	364	376	Deamidation (NQ)
K.FFVPPFQQSPR.A	Y	99.8	40.16	1348.6927	11	-0.7	675.3532	2	31.22	25	1786	OB3623.raw	3.04E4	4	4	516	526	
H.SIIYALR.G	N	99.4	36.28	834.4963	7	0.3	418.2556	2	28.66	25	1516	OB3623.raw	7.48E4	1	1	414	420	
R.AHVQ(+.98)VVDSNGNR.V	N	99.4	35.89	1295.6218	12	3.2	648.8203	2	20.50	25	991	OB3623.raw	1.36E4	1	1	423	434	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.4	34.34	1294.6378	12	1.5	648.3271	2	19.56	25	938	OB3623.raw	2.55E3	1	1	423	434	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	510	515	
R.NALFVPHYNTNAH.S	N	98.9	32.31	1496.7161	13	-0.5	499.9124	3	27.31	25	1374	OB3623.raw	2.23E5	7	7	401	413	
H.VLVVPQNFAVAGK.S	N	98.8	31.36	1340.7816	13	2.7	671.3999	2	30.07	25	1664	OB3623.raw	1.04E3	1	1	445	457	
K.TAN(+.98)ELNLLILR.W	N	98.8	30.93	1269.7292	11	3.3	635.8740	2	33.49	25	2057	OB3623.raw	0	2	2	377	387	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	97.8	29.32	3545.7273	33	3.8	1182.9209	3	35.63	25	2324	OB3623.raw	3.21E3	2	2	470	502	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	96.5	28.09	1660.8057	15	1.2	554.6098	3	26.85	25	1330	OB3623.raw	2.81E3	2	2	362	376	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	470	483	
R.VYDEELQEGHVLVVP(+15.99)QNFAVAGK.S	N	86.4	22.26	2556.2859	23	1.0	853.1035	3	32.12	25	1901	OB3623.raw	4.76E3	1	1	435	457	Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	86.0	21.82	1534.7892	13	-0.9	512.6032	3	28.92	25	1548	OB3623.raw	1.82E4	2	2	408	420	
total 23 peptides																		

Q647H3|Q647H3_ARAHY

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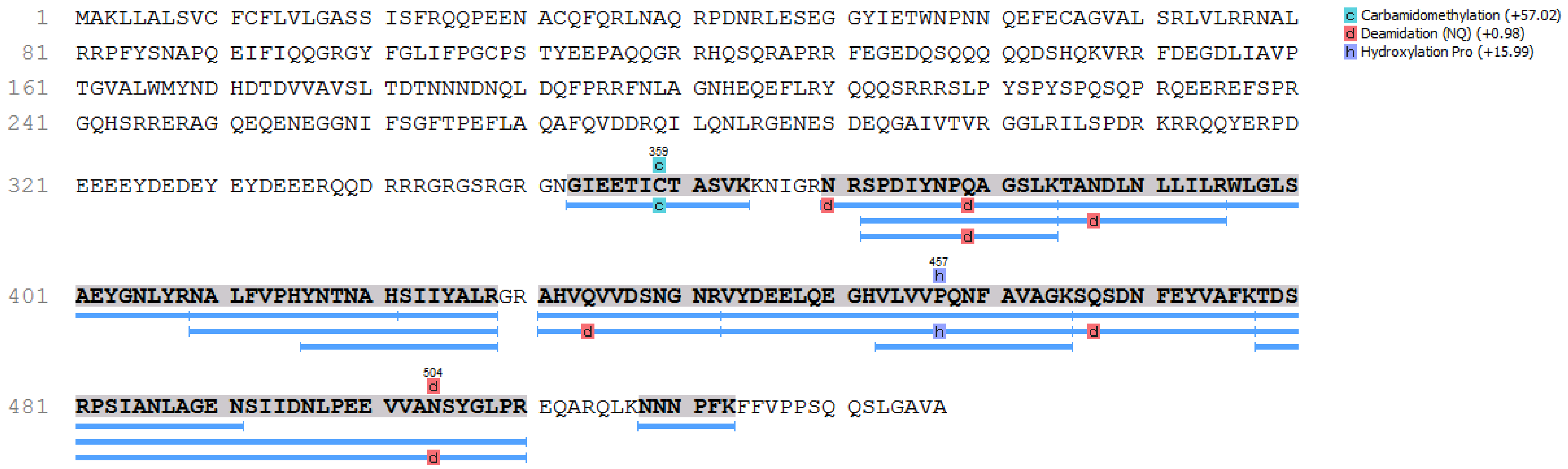
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS
401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA
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Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.65	1540.7673	13	0.2	771.3911	2	32.75	25	1974	OB3623.raw	6.72E5	48	48	396	408	
K.SQSDNFEYVAFK.T	N	99.9	80.09	1433.6462	12	0.1	717.8304	2	30.04	25	1660	OB3623.raw	1.7E5	13	13	466	477	
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	70.93	1434.6302	12	0.1	718.3224	2	30.29	25	1680	OB3623.raw	5.52E4	1	1	466	477	Deamidation (NQ)

R.SPDIYNPQAGSLK.T	N	99.9	64.66	1388.6936	13	-0.3	695.3539	2	27.09	25	1353	OB3623.raw	4.07E5	14	14	372	384	
N.GIEETIC(+57.02)TASVK.K	N	99.9	60.31	1306.6438	12	0.0	654.3292	2	27.50	25	1397	OB3623.raw	1.43E5	8	8	353	364	Carbamidomethylation
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	56.54	2540.2910	23	0.2	847.7711	3	31.02	25	1762	OB3623.raw	4.24E5	24	24	443	465	
K.TANDLNLLILR.W	N	99.9	52.03	1254.7296	11	-0.3	628.3719	2	32.79	25	1979	OB3623.raw	3.02E5	20	20	385	395	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	51.43	2313.2019	20	-0.9	772.0739	3	31.03	25	1763	OB3623.raw	5.99E5	6	6	409	428	
K.TDSRPSIANLAGENSIIDNLPEEVVANSYGLPR.E	Y	99.9	48.06	3510.7590	33	-0.7	1171.2595	3	34.73	25	2211	OB3623.raw	8.13E4	7	7	478	510	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.8	41.84	1389.6776	13	3.4	695.8484	2	28.06	25	1452	OB3623.raw	8.41E4	1	1	372	384	Deamidation (NQ)
K.TDSRPSIANLAGENSIIDNLPEEVVAN(+.98)SYGLPR.E	Y	99.4	36.64	3511.7429	33	0.3	1171.5886	3	35.56	25	2315	OB3623.raw	1.26E4	1	1	478	510	Deamidation (NQ)
H.SIIYALR.G	N	99.4	36.28	834.4963	7	0.3	418.2556	2	28.66	25	1516	OB3623.raw	7.48E4	1	1	422	428	
R.AHVQ(+.98)VVDSNGNR.V	N	99.4	35.89	1295.6218	12	3.2	648.8203	2	20.50	25	991	OB3623.raw	1.36E4	1	1	431	442	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.4	34.34	1294.6378	12	1.5	648.3271	2	19.56	25	938	OB3623.raw	2.55E3	1	1	431	442	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	518	523	
K.TAN(+.98)DLNLLILR.W	N	99.0	32.74	1255.7136	11	4.3	628.8668	2	33.00	25	2002	OB3623.raw	6.07E2	1	1	385	395	Deamidation (NQ)
R.NALFVPHYNTNAH.S	N	98.9	32.31	1496.7161	13	-0.5	499.9124	3	27.31	25	1374	OB3623.raw	2.23E5	7	7	409	421	
H.VLVVPQNFAVAGK.S	N	98.8	31.36	1340.7816	13	2.7	671.3999	2	30.07	25	1664	OB3623.raw	1.04E3	1	1	453	465	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	96.5	28.09	1660.8057	15	1.2	554.6098	3	26.85	25	1330	OB3623.raw	2.81E3	2	2	370	384	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	478	491	
R.VYDEELQEGHVLVVP(+15.99)QNFAVAGK.S	N	86.4	22.26	2556.2859	23	1.0	853.1035	3	32.12	25	1901	OB3623.raw	4.76E3	1	1	443	465	Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	86.0	21.82	1534.7892	13	-0.9	512.6032	3	28.92	25	1548	OB3623.raw	1.82E4	2	2	416	428	
total 22 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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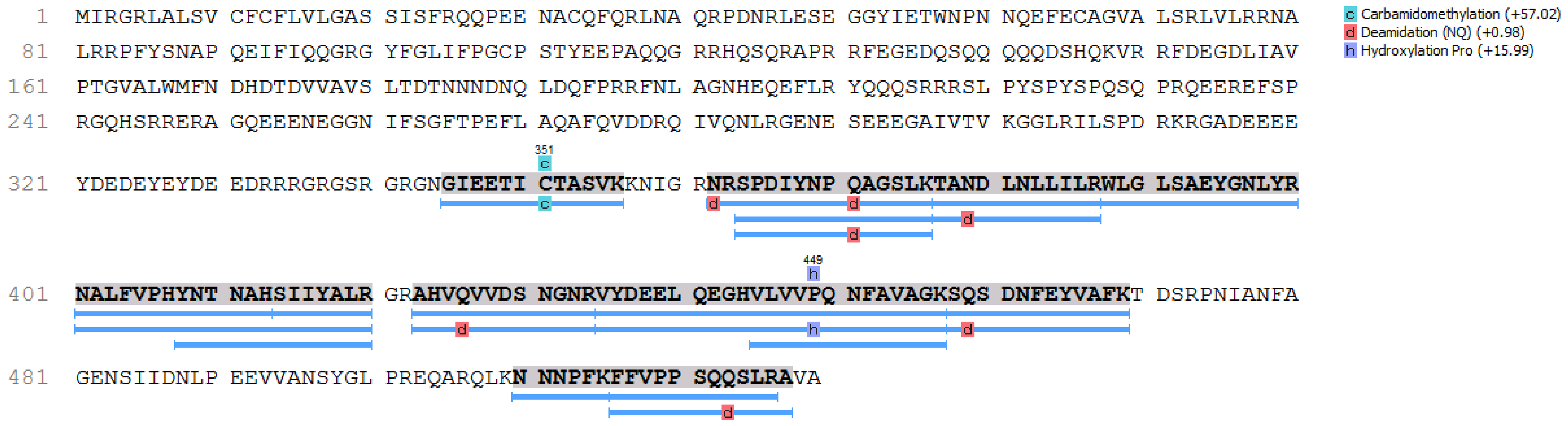
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP
241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE
321 YDEDEYEYDE EDRRRGRGSR GRGN**GIEETI CTASVK**KNIG R**NRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR**
401 **NALFVPHYNT NAHSIIYALR** GR**AHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFK**T DSRPNIANFA
481 GENSIIDNLP EEVVANSYGL PREQARQLK**N NNPFKFFVPP SQQSLRA**VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.65	1540.7673	13	0.2	771.3911	2	32.75	25	1974	OB3623.raw	6.72E5	48	48	388	400	
K.SQSDNFEYVAFK.T	N	99.9	80.09	1433.6462	12	0.1	717.8304	2	30.04	25	1660	OB3623.raw	1.7E5	13	13	458	469	
K.SQ(+.98)SDNFEYVAFK.T	N	99.9	70.93	1434.6302	12	0.1	718.3224	2	30.29	25	1680	OB3623.raw	5.52E4	1	1	458	469	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	64.66	1388.6936	13	-0.3	695.3539	2	27.09	25	1353	OB3623.raw	4.07E5	14	14	364	376	

N.GIEETIC(+57.02)TASVK.K	N	99.9	60.31	1306.6438	12	0.0	654.3292	2	27.50	25	1397	OB3623.raw	1.43E5	8	8	345	356	Carbamidomethylation
R.VYDEELQEGHVLVVPQNFAVAGK.S	N	99.9	56.54	2540.2910	23	0.2	847.7711	3	31.02	25	1762	OB3623.raw	4.24E5	24	24	435	457	
K.TANDLNLLILR.W	N	99.9	52.03	1254.7296	11	-0.3	628.3719	2	32.79	25	1979	OB3623.raw	3.02E5	20	20	377	387	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	51.43	2313.2019	20	-0.9	772.0739	3	31.03	25	1763	OB3623.raw	5.99E5	6	6	401	420	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.8	41.84	1389.6776	13	3.4	695.8484	2	28.06	25	1452	OB3623.raw	8.41E4	1	1	364	376	Deamidation (NQ)
K.FFVPPSQQSLR.A	Y	99.8	41.39	1304.6876	11	0.1	653.3511	2	28.67	25	1517	OB3623.raw	4.34E4	5	5	516	526	
H.SIIYALR.G	N	99.4	36.28	834.4963	7	0.3	418.2556	2	28.66	25	1516	OB3623.raw	7.48E4	1	1	414	420	
R.AHVQ(+.98)VVDSNGNR.V	N	99.4	35.89	1295.6218	12	3.2	648.8203	2	20.50	25	991	OB3623.raw	1.36E4	1	1	423	434	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.4	34.34	1294.6378	12	1.5	648.3271	2	19.56	25	938	OB3623.raw	2.55E3	1	1	423	434	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	510	515	
K.TAN(+.98)DLNLLILR.W	N	99.0	32.74	1255.7136	11	4.3	628.8668	2	33.00	25	2002	OB3623.raw	6.07E2	1	1	377	387	Deamidation (NQ)
R.NALFVPHYNTNAH.S	N	98.9	32.31	1496.7161	13	-0.5	499.9124	3	27.31	25	1374	OB3623.raw	2.23E5	7	7	401	413	
H.VLVVPQNFAVAGK.S	N	98.8	31.36	1340.7816	13	2.7	671.3999	2	30.07	25	1664	OB3623.raw	1.04E3	1	1	445	457	
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	96.5	28.09	1660.8057	15	1.2	554.6098	3	26.85	25	1330	OB3623.raw	2.81E3	2	2	362	376	Deamidation (NQ)
K.FFVPPSQQ(+.98)SLRA.V	Y	94.7	24.66	1376.7087	12	1.5	689.3627	2	29.36	25	1590	OB3623.raw	1.23E4	1	1	516	527	Deamidation (NQ)
R.VYDEELQEGHVLVVP(+15.99)QNFAVAGK.S	N	86.4	22.26	2556.2859	23	1.0	853.1035	3	32.12	25	1901	OB3623.raw	4.76E3	1	1	435	457	Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	86.0	21.82	1534.7892	13	-0.9	512.6032	3	28.92	25	1548	OB3623.raw	1.82E4	2	2	408	420	
total 21 peptides																		

Q647H4|Q647H4_ARAHY

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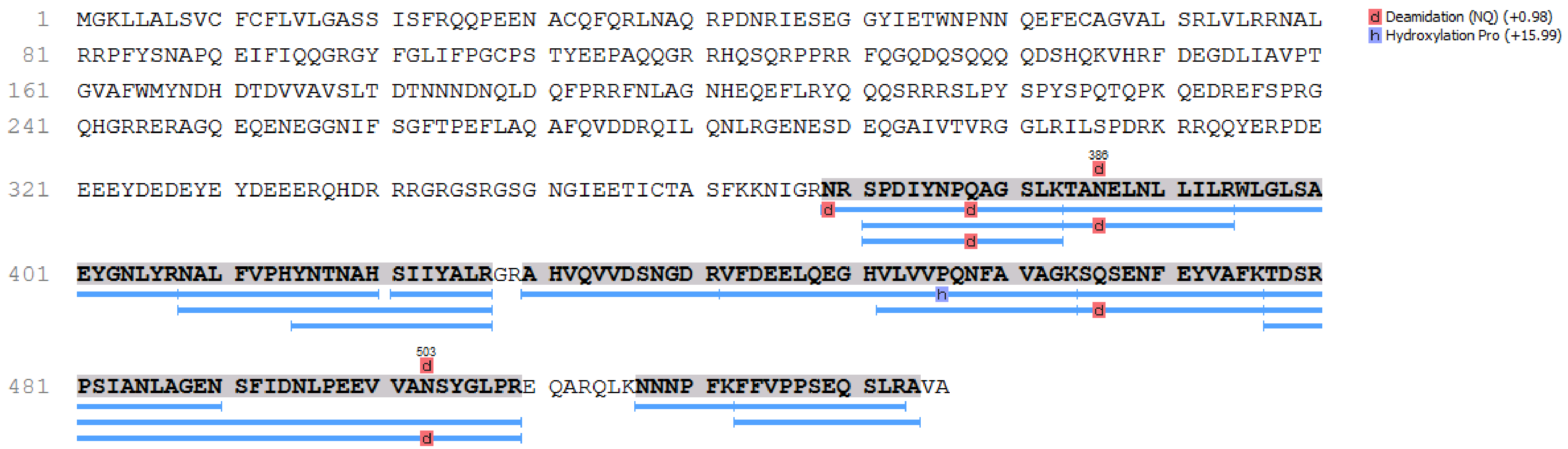
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 RRPFYSNAPQ EIFIQQGRGY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGR**NR SPDIYNPQAG SLKTANELNL LILRWLGLSA**
401 **EYGNLYRNAL FVPHYNTNAH SIIYALR**GR**A HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR**
481 **PSIANLAGEN SFIDNLPEEV VANSYGLPR**E QARQLK**NNNP FKFFVPPSEQ SLRA**VA

d Deamidation (NQ) (+0.98)
h Hydroxylation Pro (+15.99)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.65	1540.7673	13	0.2	771.3911	2	32.75	25	1974	OB3623.raw	6.72E5	48	48	395	407	
K.SQSENFEYVAFK.T	N	99.9	74.74	1447.6619	12	-0.4	724.8379	2	29.94	25	1649	OB3623.raw	1.92E5	19	19	465	476	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	71.20	1448.6459	12	-1.5	725.3291	2	30.12	25	1669	OB3623.raw	2.46E4	1	1	465	476	Deamidation (NQ)
R.SPDIYNPQAGSLK.T	N	99.9	64.66	1388.6936	13	-0.3	695.3539	2	27.09	25	1353	OB3623.raw	4.07E5	14	14	371	383	
R.AHVQVVDSNGDR.V	Y	99.9	55.17	1295.6218	12	-0.9	648.8176	2	20.33	25	980	OB3623.raw	1.36E4	2	2	430	441	

K.TANELNLLILR.W	N	99.9	54.46	1268.7452	11	-0.2	635.3798	2	32.92	25	1992	OB3623.raw	1.32E5	10	10	384	394	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	51.43	2313.2019	20	-0.9	772.0739	3	31.03	25	1763	OB3623.raw	5.99E5	6	6	408	427	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	46.53	3544.7434	33	2.3	1182.5912	3	35.04	25	2251	OB3623.raw	4.39E4	5	5	477	509	
K.FFVPPSEQSLR.A	Y	99.8	43.13	1305.6716	11	0.4	653.8433	2	29.08	25	1567	OB3623.raw	4.48E4	7	7	523	533	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.8	41.84	1389.6776	13	3.4	695.8484	2	28.06	25	1452	OB3623.raw	8.41E4	1	1	371	383	Deamidation (NQ)
H.SIIYALR.G	N	99.4	36.28	834.4963	7	0.3	418.2556	2	28.66	25	1516	OB3623.raw	7.48E4	1	1	421	427	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	517	522	
R.NALFVPHYNTNAH.S	N	98.9	32.31	1496.7161	13	-0.5	499.9124	3	27.31	25	1374	OB3623.raw	2.23E5	7	7	408	420	
H.VLVVPQNFAVAGK.S	N	98.8	31.36	1340.7816	13	2.7	671.3999	2	30.07	25	1664	OB3623.raw	1.04E3	1	1	452	464	
K.TAN(+.98)ELNLLILR.W	N	98.8	30.93	1269.7292	11	3.3	635.8740	2	33.49	25	2057	OB3623.raw	0	2	2	384	394	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	97.8	29.32	3545.7273	33	3.8	1182.9209	3	35.63	25	2324	OB3623.raw	3.21E3	2	2	477	509	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	96.5	28.09	1660.8057	15	1.2	554.6098	3	26.85	25	1330	OB3623.raw	2.81E3	2	2	369	383	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	477	490	
K.FFVPPSEQSLRA.V	Y	88.5	22.92	1376.7087	12	-1.6	689.3605	2	29.55	25	1609	OB3623.raw	1.23E4	2	2	523	534	
R.VFDEELQEGHVLVVP(+15.99)QNFAVAGK.S	Y	88.1	22.67	2540.2910	23	-0.1	636.0800	4	30.89	25	1745	OB3623.raw	1.42E4	1	1	442	464	Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	86.0	21.82	1534.7892	13	-0.9	512.6032	3	28.92	25	1548	OB3623.raw	1.82E4	2	2	415	427	
total 21 peptides																		

Q6T2T4|Q6T2T4_ARAHY

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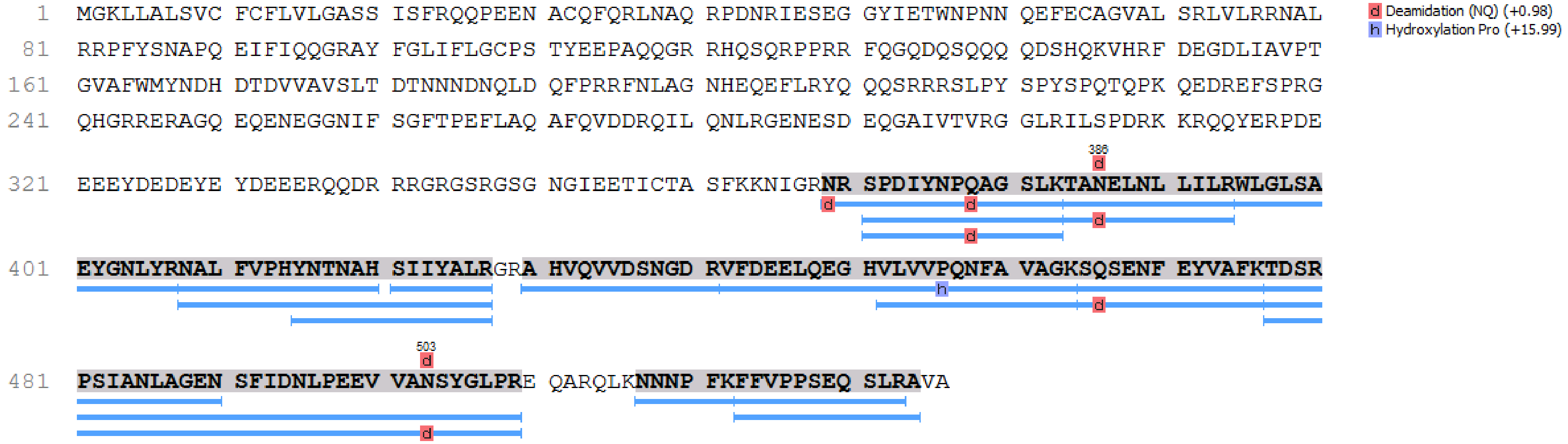
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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 81 RRPFYSNAPQ EIFIQQGRAY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR
481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
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Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.WLGLSAEYGNLYR.N	N	99.9	90.65	1540.7673	13	0.2	771.3911	2	32.75	25	1974	OB3623.raw	6.72E5	48	48	395	407	
K.SQSENFEYVAFK.T	N	99.9	74.74	1447.6619	12	-0.4	724.8379	2	29.94	25	1649	OB3623.raw	1.92E5	19	19	465	476	
K.SQ(+.98)SENFEYVAFK.T	N	99.9	71.20	1448.6459	12	-1.5	725.3291	2	30.12	25	1669	OB3623.raw	2.46E4	1	1	465	476	Deamidation (NQ)

R.SPDIYNPQAGSLK.T	N	99.9	64.66	1388.6936	13	-0.3	695.3539	2	27.09	25	1353	OB3623.raw	4.07E5	14	14	371	383	
R.AHVQVVDSNGDR.V	Y	99.9	55.17	1295.6218	12	-0.9	648.8176	2	20.33	25	980	OB3623.raw	1.36E4	2	2	430	441	
K.TANELNLLILR.W	N	99.9	54.46	1268.7452	11	-0.2	635.3798	2	32.92	25	1992	OB3623.raw	1.32E5	10	10	384	394	
R.NALFVPHYNTNAHSIIYALR.G	N	99.9	51.43	2313.2019	20	-0.9	772.0739	3	31.03	25	1763	OB3623.raw	5.99E5	6	6	408	427	
K.TDSRPSIANLAGENSFIDNLPEEVVANSYGLPR.E	N	99.9	46.53	3544.7434	33	2.3	1182.5912	3	35.04	25	2251	OB3623.raw	4.39E4	5	5	477	509	
K.FFVPPSEQSLR.A	Y	99.8	43.13	1305.6716	11	0.4	653.8433	2	29.08	25	1567	OB3623.raw	4.48E4	7	7	523	533	
R.SPDIYNPQ(+.98)AGSLK.T	N	99.8	41.84	1389.6776	13	3.4	695.8484	2	28.06	25	1452	OB3623.raw	8.41E4	1	1	371	383	Deamidation (NQ)
H.SIIYALR.G	N	99.4	36.28	834.4963	7	0.3	418.2556	2	28.66	25	1516	OB3623.raw	7.48E4	1	1	421	427	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	517	522	
R.NALFVPHYNTNAH.S	N	98.9	32.31	1496.7161	13	-0.5	499.9124	3	27.31	25	1374	OB3623.raw	2.23E5	7	7	408	420	
H.VLVVPQNFAVAGK.S	N	98.8	31.36	1340.7816	13	2.7	671.3999	2	30.07	25	1664	OB3623.raw	1.04E3	1	1	452	464	
K.TAN(+.98)ELNLLILR.W	N	98.8	30.93	1269.7292	11	3.3	635.8740	2	33.49	25	2057	OB3623.raw	0	2	2	384	394	Deamidation (NQ)
K.TDSRPSIANLAGENSFIDNLPEEVVAN(+.98)SYGLPR.E	N	97.8	29.32	3545.7273	33	3.8	1182.9209	3	35.63	25	2324	OB3623.raw	3.21E3	2	2	477	509	Deamidation (NQ)
R.N(+.98)RSPDIYNPQ(+.98)AGSLK.T	N	96.5	28.09	1660.8057	15	1.2	554.6098	3	26.85	25	1330	OB3623.raw	2.81E3	2	2	369	383	Deamidation (NQ)
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	477	490	
K.FFVPPSEQSLRA.V	Y	88.5	22.92	1376.7087	12	-1.6	689.3605	2	29.55	25	1609	OB3623.raw	1.23E4	2	2	523	534	
R.VFDEELQEGHVLVVP(+15.99)QNFAVAGK.S	Y	88.1	22.67	2540.2910	23	-0.1	636.0800	4	30.89	25	1745	OB3623.raw	1.42E4	1	1	442	464	Hydroxylation Pro
H.YNTNAHSIIYALR.G	N	86.0	21.82	1534.7892	13	-0.9	512.6032	3	28.92	25	1548	OB3623.raw	1.82E4	2	2	415	427	
total 21 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY IETWNPNNQE FQCAGVALSR TVLRRNALRR

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN

401 GR**AHVQVVDS NGNR**VYDEEL QEGHVLVVPQ NFAVAAK**AQS ENYEYLAFKT DSRPSIANLA GEN**SIIDNLP EEVVANSYRL

d

481 PREQARQLK**N NNPFK**FFVPP FDHQSMREVA

d Deamidation (NQ) (+0.98)

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.AHVQ(+.98)VVDSNGNR.V	N	99.4	35.89	1295.6218	12	3.2	648.8203	2	20.50	25	991	OB3623.raw	1.36E4	1	1	403	414	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.4	34.34	1294.6378	12	1.5	648.3271	2	19.56	25	938	OB3623.raw	2.55E3	1	1	403	414	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	490	495	
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	450	463	
K.AQSENYEYLAFK.T	Y	91.3	23.75	1461.6776	12	0.2	731.8463	2	30.59	25	1710	OB3623.raw	3.09E4	1	1	438	449	
total 5 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deamidation (NQ) (+0.98)

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81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGR**AHVQVV DSNGNR**VYDE ELQEGHVLVV PQNFAVAAK**A QSENYEYLAF KTDSRPSIAN LAGEN**SIIDN LPEEVVANSY
481 RLPREQARQL K**NNNPFK**FFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
R.AHVQ(+.98)VVDSNGNR.V	N	99.4	35.89	1295.6218	12	3.2	648.8203	2	20.50	25	991	OB3623.raw	1.36E4	1	1	405	416	Deamidation (NQ)
R.AHVQVVDSNGNR.V	N	99.4	34.34	1294.6378	12	1.5	648.3271	2	19.56	25	938	OB3623.raw	2.55E3	1	1	405	416	
K.NNNPFK.F	N	99.4	33.76	732.3555	6	0.9	367.1853	2	21.87	25	1061	OB3623.raw	1.9E4	3	3	492	497	
K.TDSRPSIANLAGEN.S	N	94.5	24.25	1443.6953	14	-1.1	722.8541	2	27.54	25	1404	OB3623.raw	3.64E3	1	1	452	465	
K.AQSENYEYLAFK.T	Y	91.3	23.75	1461.6776	12	0.2	731.8463	2	30.59	25	1710	OB3623.raw	3.09E4	1	1	440	451	
total 5 peptides																		

Q647H1|Q647H1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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161 AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRR**FYLA GNPEEEHPET QQQQPQTR**RR HGQHQQDEYG SQGEEEGNNV
241 LSGFSTQLLA H**AFGVDEEIA RILQNPPEQT K**DQIVRVEGG FRDVISPRWG EGKQYEDELE ERQRQPPRRD EQGKGYDYDD
321 DRRPRHRQDP YREGDEDDRR PRGSRQGQGR GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY
401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRNG VEETLCSPTL VEDIARPSRA DFYNPAAGRI
481 SSANSLTFPI LRWFQLSAEH VLLYRNGIYS PHWNNNANSI IYGLRGEGRI QVVNSQGNAV FNGVLREGQI LLVPQNFAVG
561 KQAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN
641 AQVDSKNNDG SRLWWPSSII IK

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 25	#Spec	#Spec Sample 25	Start	End	PTM
K.IYHFR.Q	Y	98.8	30.27	734.3864	5	1.7	368.2011	2	23.39	25	1136	OB3623.raw	2.92E3	1	1	148	152	
R.ILQNPPEQTK.D	Y	96.4	27.47	1166.6295	10	-0.5	584.3217	2	22.05	25	1070	OB3623.raw	4.57E3	1	1	262	271	
H.AFGVDEEIAR.I	Y	96.4	27.45	1105.5403	10	-1.0	553.7769	2	27.96	25	1442	OB3623.raw	4.34E3	1	1	252	261	
R.FYLAGNPEEEHPETQQQQPQTR.R	Y	85.7	21.44	2626.2048	22	-2.4	876.4068	3	26.62	25	1310	OB3623.raw	3.04E3	1	1	197	218	
total 4 peptides																		

Peptide List

Summary

1. Notes

Spot O from DPS

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

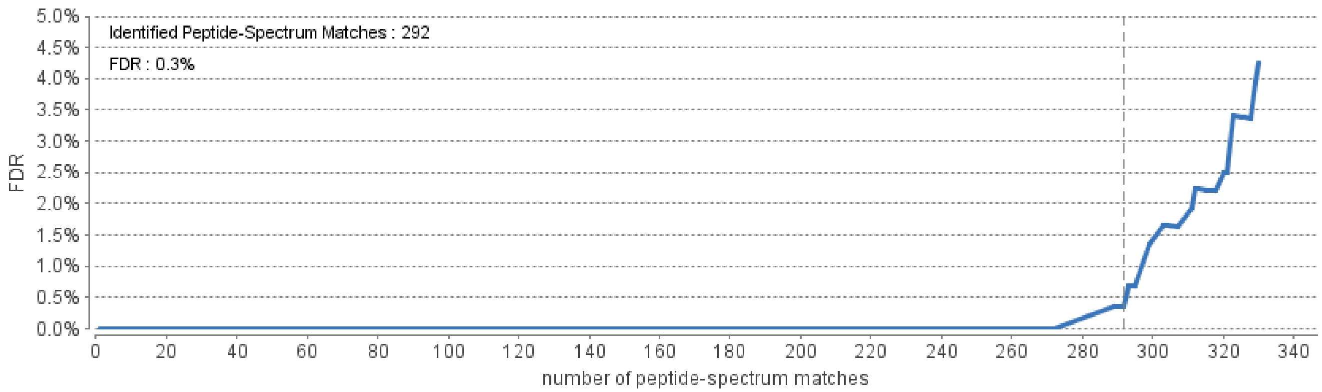
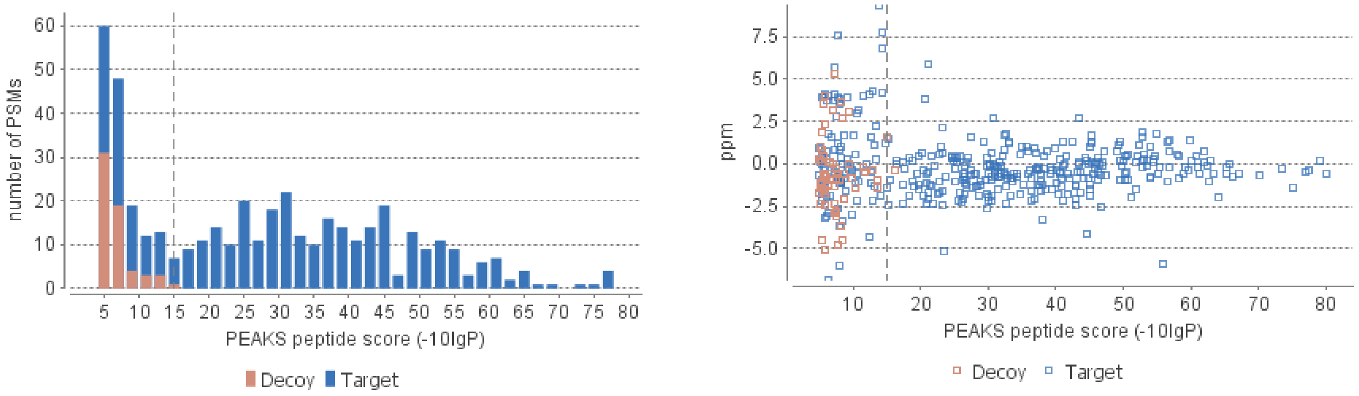


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

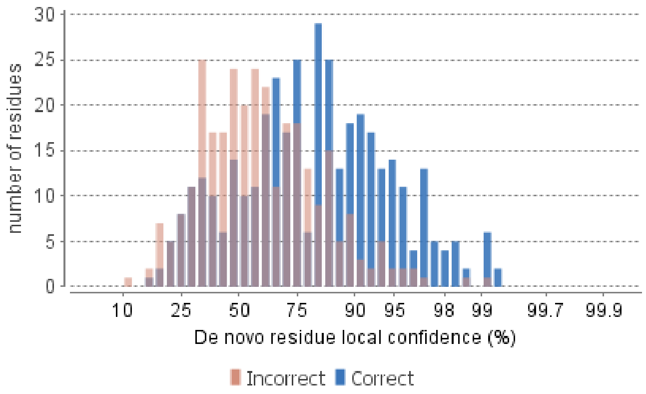

(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

(a)

(b)



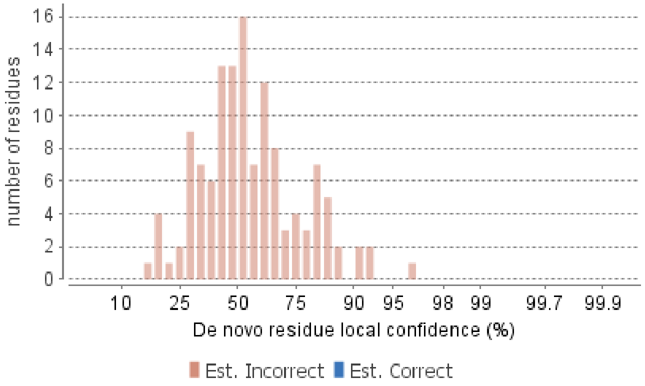


Table 1. Statistics of data.

# of MS scans	3115
# of MS/MS scans	2206

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Peptide Ascore	≥20
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	290
Peptide sequences	62
Protein groups	3
Proteins	18
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 18 (=1);
FDR (Peptide-Spectrum Matches)	0.3%
FDR (Peptide Sequences)	1.6%
FDR (Protein)	0.0%
De Novo Only Spectra	17

Table 4. PTM profile.

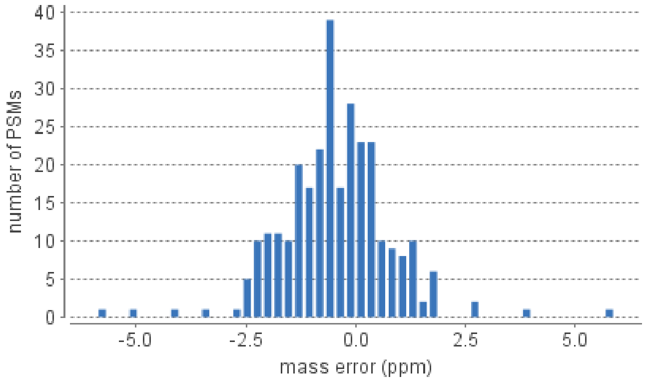
Name	**ΔMass**	**Position**	**#PSM**	**-10lgP**	**Area**	**AScore**
Carbamidomethyl	57.02	C	17	62.34	1.74E4	1000.00
Oxidation	15.99	M	4	36.17	6.12E3	1000.00
Deamidation	.98	N	2	36.17	6.12E3	0.00

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

(a)

(b)



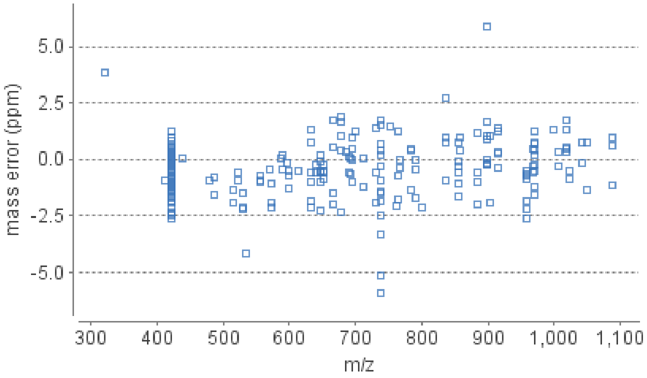


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 34	55	7	0	0	0

4. Other Information

Table 6. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.5 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 2
Non-specific Cleavage: both
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Deamidation (NQ): 0.98
  Oxidation (M): 15.99
  Hydroxylation Pro: 15.99
Max Variable PTM Per Peptide: 5
Database: UniProt_Peanut[3818]_Sep16
Taxon: All
Contaminant Database: cRAP_Oct16
Searched Entry: 1242
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: OB3632.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Accession Contains:
Protein Description Contains:
Protein Sample Area >=
Protein Ptm Contains:

Protein Group	Protein ID	Accession	Score (%)	-10lgP	Coverage (%)	Coverage (%) Sample 34	Area Sample 34	#Peptides	#Unique	#Spec Sample 34	PTM	Avg. Mass	Description
6	83	Q8LL03|Q8LL03_ARAHY	62.3	44.29	8	8	9.75E3	1	1	1	N	25499	Trypsin inhibitor (Fragment) OS=Arachis hypogaea PE=2 SV=1
6	34	O82580|O82580_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	58350	Glycinin (Fragment) OS=Arachis hypogaea GN=Arah3 PE=2 SV=1
6	13	Q9FZ11|Q9FZ11_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	60449	Gly1 OS=Arachis hypogaea GN=Gly1 PE=2 SV=1
6	2	A1DZF0|A1DZF0_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	60375	Arachin 6 OS=Arachis hypogaea PE=2 SV=1
6	3	B5TYU1|B5TYU1_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	60624	Arachin Arah3 isoform OS=Arachis hypogaea PE=1 SV=1
6	29	Q9SQH7|Q9SQH7_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	61011	Glycinin OS=Arachis hypogaea GN=Arah4 PE=2 SV=1
6	5	Q5I6T2|Q5I6T2_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	60736	Arachin Ahy-4 OS=Arachis hypogaea PE=2 SV=1
6	7	Q647H4|Q647H4_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	61506	Arachin Ahy-1 OS=Arachis hypogaea PE=2 SV=1
6	12	Q6T2T4|Q6T2T4_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	61499	Storage protein OS=Arachis hypogaea PE=2 SV=1
6	15	Q647H3|Q647H3_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	61532	Arachin Ahy-2 OS=Arachis hypogaea PE=2 SV=1
6	10	Q8LKN1|Q8LKN1_ARAHY	62.3	44.29	3	3	9.75E3	1	1	1	N	61738	Allergen Arah3/Arah4 OS=Arachis hypogaea PE=3 SV=1
6	116	A1DZF1|A1DZF1_ARAHY	61.0	44.29	8	8	9.75E3	1	1	1	N	23857	Arachin 7 (Fragment) OS=Arachis hypogaea PE=2 SV=1
7	92	sp|Q647H2|AHY3_ARAHY	60.1	33.58	6	6	6.84E3	1	1	1	Y	54569	Arachin Ahy-3 OS=Arachis hypogaea PE=1 SV=1
7	41	Q6IWG5|Q6IWG5_ARAHY	60.1	33.58	5	5	6.84E3	1	1	1	Y	58061	Glycinin (Fragment) OS=Arachis hypogaea PE=2 SV=1
7	45	E5G077|E5G077_ARAHY	60.1	33.58	5	5	6.84E3	1	1	1	Y	58305	Ara h 3 allergen OS=Arachis hypogaea GN=ara h 3 PE=3 SV=1
7	42	Q0GM57|Q0GM57_ARAHY	60.1	33.58	5	5	6.84E3	1	1	1	Y	58263	Iso-Ara h3 OS=Arachis hypogaea PE=2 SV=1
11	819	I1E3D2|I1E3D2_ARAHY	32.7	20.63	1	1	7.53E3	1	1	1	N	56020	3-ketoacyl-CoA synthase OS=Arachis hypogaea GN=kcs PE=2 SV=1
11	817	A0A0N7CRG1|A0A0N7CRG1_ARAHY	32.7	20.63	1	1	7.53E3	1	1	1	N	55974	3-ketoacyl-CoA synthase OS=Arachis hypogaea GN=kcs PE=2 SV=1
total 18 proteins													

Q8LL03|Q8LL03_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES EGGYIETWNP NNQEFECAGV ALSRLVLRRN
 81  ALRRPFYSNA PQEIFIQQGR GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH RFDEGDLIAV
161  PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRS
```

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM

R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	84	100	
total 1 peptides																		

O82580|O82580_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RQQPEENACQ FQRLNAQRPD NRIESEGGYI ETWNPNNQEF ECAGVALSRL VLRRNALR**RP FYSNAPQEIF IQQGR**GYFGL
81 IFPGCPRHYE EPHTQGRRSQ SQRPPRRLQG EDQSQQQRDS HQKVHRFDEG DLIAVPTGVA FWLYNDHDTD VVAVSLTDTN
161 NNDNQLDQFP RRFNLAGNTE QEFLRYQQQS RQSRRRSLPY SPYSPQSQPR QEEREFSPRG QHSRRERAGQ EEENEGGNIF
241 SGFTPEFLEQ AFQVDDRQIV QNLRGETESE EEGAIVTVRG GLRILSPDRK RRADEEEEYD EDEYEYDEED RRRGRGSRGR
321 GNGIEETICT ASAKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGPS AEYGNLYRNA LFVAHYNTNA HSIIYRLRGR
401 AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSEN FEYVAFKTDS RPSIANLAGE NSVIDNLPEE VVANSYGLQR
481 EQARQLKNNN PFKFFVPPSQ QSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	59	75	
total 1 peptides																		

Q9FZ11|Q9FZ11_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE GGYIETWNPN NQEFECAGVA LSRLVLRRNA
81 LR**RPFYSNAP QEIFIQQGR**G YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR RFDEGDLIAV
161 PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP
241 RGQHSRRERA GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV KGGLRILSPD RKRGADEEEE
321 YDEDEYEYDE EDRRRGRGSR GRGNGIEETI CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS DNFEYVAFKT DSRPNIANFA
481 GENSIIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP SQQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	83	99	
total 1 peptides																		

A1DZF0|A1DZF0_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ
241 GQHGRRERAG QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK GGLRILSPDR KSPDEEEEYD
321 EDEYAEEERQ QDRRRGRGSR GSGNGIEETI CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAGKSQS ENFEYVAFKT DSRPSIANLA
481 GENSFIDNLP EEVVANSYGL PREQARQLKN NNPFKFFVPP FQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

B5TYU1|B5TYU1_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LAQAFQVDDR QIVQNLRGEN ESEEQGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGSGNGIEET ICTATVKKNI GRNRSPDIYN PQAGSLKTAN ELNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LPREQARQLK NNNPFKFFVP PSQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

Q9SQH7|Q9SQH7_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF NEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPHS RPRREEREFR
241 PRGQHSRRER AGQEEEDEGG NIFSGFTPEF LEQAFQVDDR QIVQNLWGEN ESEEEGAIVT VRGGLRILSP DGTRGADEEE
321 EYDEDQYEYH EQDGRRGRGS RGGGNGIEET ICTACVKKNI GGNRSPHIYD PQRWFTQNCH DLNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SENFEYVAFK TDSRPSIANF
481 AGENSFIDNL PEEVVANSYG LPREQARQLK NNNPFKFFVP PFQQSPRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

Q5I6T2|Q5I6T2_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS
241 PRGQHSRRER AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT VRGGLRILSP DRKRGADEEE
321 EYDEDEYEYD EEDRRRGRGS RGRGNGIEET ICTASVKKNI GRNRSPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL
481 AGENSVIDNL PEEVVANSYG LQREQARQQL KNNNPFKFFV PPSQQSPRAV A

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

Q647H4|Q647H4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE

321 EEEYDEDEYE YDEEERQHDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA

401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

Q6T2T4|Q6T2T4_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL

81 R**RPFYSNAPQ EIFIQQGR**AY FGLIFLGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG

241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK KRQQYERPDE

321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA

401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG HVLVVPQNFA VAGKSQSENF EYVAFKTDSR

481 PSIANLAGEN SFIDNLPEEV VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.A	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

Q647H3|Q647H3_ARAHY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR FDEGDLIAVP
161 TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR
241 GQHSRRERAG QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR GGLRILSPDR KRRQQYERPD
321 EEEEYDEDEY EYDEEERQQD RRRGRGSRGR GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS
401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS
481 RPSIANLAGE NSIIDNLPEE VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

Q8LKN1|Q8LKN1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG GYIETWNPNN QEFECAGVAL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF DEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG
241 QHGRRERAGQ EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG GLRILSPDRK RRQQYERPDE
321 EEEYDEDEYE YDEEERQQDR RRGRGSRGSG NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELQL NLLILRWLGL
401 SAEYGNLYRN ALFVPHYNTN AHSIIYALRG RAHVQVVDSN GDRVFDEELQ EGHVLVVPQN FAVAGKSQSE NFEYVAFKTD
481 SRPSIANLAG ENSFIDNLPE EVVANSYGLP REQARQLKNN NPFKFFVPPS EQSLRAVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

A1DZF1|A1DZF1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNLIESEG GYIETWNPNN QEFECAGVTL SRLVLRRNAL
81 R**RPFYSNAPQ EIFIQQGR**GY FGLIFPGCPI TYEEPAQRGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF YEGDLIAVPT
161 GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPIRFNLAG NHEQEFL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.RPFYSNAPQEIFIQQGR.G	Y	99.9	44.29	2050.0383	17	0.4	684.3536	3	29.66	34	1484	OB3632.raw	9.75E3	1	1	82	98	
total 1 peptides																		

sp|Q647H2|AHY3_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

65 C

1 MAKLLALSVC FCFLVLGASS VTFRQQGEEN ECQFQRLNAQ RPDNC**IESEG GYIETWNPNN QEFQCAGVAL SR**FVLRRNAL

C Carbamidomethylation (+57.02)

81 RRPFYSNAPQ EIFIYQGSGY FGLIFPGCPG TFEEPIQGSE QFQRPSRHFQ GQDQSQRPLD THQKVHGFRE GDLIAVPHGV

161 AFWIYNDQDT DVVAISVLHT NSLHNQLDQF PRRFNLAGKQ EQEFLRYQQR SGRQSPKGEE QEQEQENEGG NVFSGFSTEF

241 LSHGFQVNED IVRNLRGENE REEQGAIVTV KGGLSILVPP EWRQSYQQPG RGDKDFNNGI EETICTATVK MNIGKSTSAD

321 IYNPQAGSVR TVNELDLPIL NRLGLSAEYG SIHRDAMFVP HYNMNANSMI YALHGGAHVQ VVDCNGNRVF DEELQEGQSL

401 VVPQNFAVAA KSQSEHFLYV AFKTNSRASI SNLAGKNSYM WNLPEDVVAN SYGLQYEQAR QLKNNNPFTF LVPPQDSQMI

481 RTVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
C.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.F	Y	98.9	33.58	3068.3933	27	-0.9	1023.8041	3	32.30	34	1784	OB3632.raw	6.84E3	1	1	46	72	Carbamidomethylation
total 1 peptides																		

Q6IWG5|Q6IWG5_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

63 C

1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNR**IESEGGY IETWNPNNQE FQCAGVALSR** TVLRRNALRR

C Carbamidomethylation (+57.02)

81 PFYSNAPLEI YVQQGSGYFG LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF DEGDLIAVPT

161 GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS

241 GFAQEFLQHA FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE EFDEDRSRPQ QRGKYDENRR

321 GYKNGIEETI CSASVKKNLG RSSNPDIYNP QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN

401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT DSRPSIANLA GENSIIDNLP EEVVANSYRL

481 PREQARQLKN NNPFKFFVPP FDHQSMREVA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	98.9	33.58	3068.3933	27	-0.9	1023.8041	3	32.30	34	1784	OB3632.raw	6.84E3	1	1	44	70	Carbamidomethylation
total 1 peptides																		

E5G077|E5G077_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

65
C

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNR**IESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

C Carbamidomethylation (+57.02)

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPNR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN QAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	98.9	33.58	3068.3933	27	-0.9	1023.8041	3	32.30	34	1784	OB3632.raw	6.84E3	1	1	46	72	Carbamidomethylation
total 1 peptides																		

Q0GM57|Q0GM57_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

65
C

1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNR**IESEG GYIETWNPNN QEFQCAGVAL SR**TVLRRNAL

C Carbamidomethylation (+57.02)

81 RRPFYSNAPL EIYVQQGSGY FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH RFDEGDLIAV
161 PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI
241 FSGFAQEFLQ HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR REEFDEDRSR PQQRGKYDEN
321 RRGYKNGIEE TICSASVKKN LGRSSNPDIY NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF KTDSRPSIAN LAGENSIIDN LPEEVVANSY
481 RLPREQARQL KNNNPFKFFV PPFDHQSMRE VA

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
R.IESEGGYIETWNPNNQEFQC(+57.02)AGVALSR.T	Y	98.9	33.58	3068.3933	27	-0.9	1023.8041	3	32.30	34	1784	OB3632.raw	6.84E3	1	1	46	72	Carbamidomethylation
total 1 peptides																		

I1E3D2|I1E3D2_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPPMLPDFSN SVKLKYVKLG YQYLVNHIIT LTLVPIMLGV SIEILRLGPQ EILNLWNSLH FNLVQILCSA FLIIFVATVY
81 FMSKPRTIYL VDYACFKPPV TCRVPFATFM EHSRLILKNN PKSVEFQMRI LERSGLGEET CLPPAIHYIP PKPTMEAARG
161 EAELVIFSAM DSLFKK**TGLK PK**DIDILIVN CSLFSPTPSL SAMVINKYKL RSNIKSFNLS GMGCSAGLIS IDLARDLLQV

241 HPNSNAVVVS TEIITPNYYQ GNERAMLLPN CLFRMGGAAI LLSNRRSERR RAKYRLVHVV RTHKGADDKA YRCVFEEEDK
321 EGKVGISLSK DLMAIAGEAL KSNITTMGPL VLPASEQLLF LLTLIGRKIF NPKWKPYIPD FKQAFEHFCI HAGGRAVIDE
401 LQKNLQLSTE HVEASRMTLH RFGNTSSSSL WYELNYIESK GRMKKGDRVW QIAFGSGFKC NSAVWKCNKT IKTPIDGPWT
481 DCIDRYPVHI PEIVKL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
K.TGLKPK.D	Y	75.0	20.63	642.4064	6	3.9	322.2117	2	25.80	34	1213	OB3632.raw	7.53E3	1	1	177	182	
total 1 peptides																		

A0A0N7CRG1|A0A0N7CRG1_ARAHY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPPMLPDFSN SVKLKYVKLG YQYLVNHIIT LTLVPIMLGV SIEILRLGPQ EILNLWNSLH FNLVQILCSA FLIIFVATVY
81 FMSKPRTIYL VDYACFKPPV TCRVPFATFM GHSRLILKNN PKSVEFQMRI LERSGLGEET CLPPAIHYIP PKPTMEAARG
161 EAELVIFSAM DSLFKK**TGLK PK**DIDILIVN CSLFSPTPSL SAMVINKYKL RSNIKSFNLS GMGCSAGLIS IDLARDLLQV

241 HPNSNAVVVS TEIITPNYYQ GNERAMLLPN CLFRMGGAAI LLSNRRSERR RAKYRLVHVV RTHKGADDKA YRCVFEEEDK
321 EGKVGISLSK DLMAIAGEAL KLNITTMGPL VLPASEQLLF LLTLIGRKIF NPKWKPYIPD FKQAFEHFCI HAGGRAVIDE
401 LQKNLQLSTE HVEASRMTLH RFGNTSSSSL WYELNYIESK GRMKKGDRVW QIAFGSGFKC NSAVWKCNKT IKTPIDGPWT
481 DCIDRYPVHI PEIVKL

Supporting Peptides:

Peptide	Uniq	Score (%)	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 34	#Spec	#Spec Sample 34	Start	End	PTM
K.TGLKPK.D	Y	75.0	20.63	642.4064	6	3.9	322.2117	2	25.80	34	1213	OB3632.raw	7.53E3	1	1	177	182	
total 1 peptides																		

Peptide List
