

Supplementary material for the article:

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**Electronic Supplementary Information for RSC Advances**

**Cadmium specific proteomic responses of a highly resistant *Pseudomonas aeruginosa* san ai**

Table 1. Metalloproteins differentially expressed in the presence of 0.9 mM cadmium in *Pseudomonas aeruginosa*, classified according to COG<sup>a</sup> and identified on the basis of at least two matched peptides and FDR 1%.

Identified protein (strain, species)	Entry name	Easy Prot score	Number of matched peptides	Sequence coverage, %	Peptide sequence	Metal (according to Uniprot)	Molecular mass kDa
<b>C- Energy production and conversion</b>							
Azurin ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	AZUR_PSEAE	116	4	42	K DSVTFDVSK K LIGSGEKDSVTFDVSK K QFTVNLSHPGNLPK K LKEGEQYMFCTFPGHSALMK	Cu	13.9
Nitrous-oxide reductase, [CHAIN 0] ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	NOSZ_PSEAE	152	5	18	R AEKDGIDLMK R GNAYTTLFIDSQLVK R IPVFNVDSATGWGLTNESEK R LGDLFAGK K LSPTCTMIAIER R VLGVPSMR K WNLADAVR K YLFINDK	Ca, Cu	65.8
Nitrite reductase/ Cytochrome cd1 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	NIRS_PSEAE	58	4	9	R ALRFSAGSWR K ARLFDWLKR	Fe	62.6
Cytochrome c-551 ( <i>P. aeruginosa</i> ATCC	CY551_PSEAE	33	2	27	K FAGQAGAEELAQR K SKPCGACHSVQAK	Fe	10.9

15692/PAO1) Cytochrome c4 [CHAIN 0] ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	CYC4_PSEAE	23	2	7	M ALTVNTNIASLNTQR K EVAAQQAELTR	Fe	18.6
Phosphoenolpyruvate carboxylase (PEPCase) ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	CAPP_PSEAE	20	2	4	R AQEKLVEICR R EVLLLAR	Mg	97.8
Malate synthase G ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	MASZ_PSEAE	79	5	10	R AFLDEAAPLES GSHVDATSY SVK R TGDEIHTSMEAGAVVR R TGDEIHTSMEAGAVVR R VEDVLGLPR K VPDINDVGLMEDR R VVFINTGFLDR	Mg	78.5

**P- Inorganic ion transport and metabolism**

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Bacterioferritin ( <i>P. aeruginosa</i> ATCC15692/PAO1)	BFR_PSEAE	34	2	12	R ILLEGTPR R MGLENYLQSQIK	Fe	17.9
Fe(3+)-pyochelin receptor ( <i>P. aeruginosa</i> ATCC15692/PAO1)	FPTA_PSEAE	68	4	5	R AEVDVGGPLSASGNVR R EFAASTTLSAGR K LAEPLTLVVGGR R SLDANLNGPVR	Fe	76
Catalase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	CATA_PSEAE	73	4	8	R LTTAAGAPVVDNQNVQTAGPR R GVADALGLK K MYVQIMPEK R YNPFDLTK	Fe	55.5

Ferric uptake regulation protein	FUR_PSEAE	92	3	30	K ALMEAGEDVGTVYR R VLTQFEAAGLVVR K ILQMLDSAEQR	Fe, Zn	15.2
Superoxide dismutase [Fe] ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	SODF_PSEAE	14	1	6	M AFELPPLPYEK	Fe	21.3
Mercuric transport protein periplasmic component ( <i>P. aeruginosa</i> )	MERP_PSEAI	77	3	55	R ATQTVTLSPGMTCSACPITVKK R QAVVTFDDAK T K VDVTFETR Q	Hg	9.3
<b>G- Carbohydrate transport and metabolism</b>							
Phosphoheptose isomerase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GMHA_PSEAE	55	3	19	R DGGGMASLLLPEDVEIR R EMLVVALTGR R QLFQASIETK	Zn	21.4
<b>H- Coenzyme transport and metabolism</b>							
Molybdenum cofactor biosynthesis protein A 1 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	MOAA1_PSEAE	36	4	9	R CDFRCVYCMAEDMRFLPR R CVYCMAEDMR R CVYCMAEDMRFLPR	Fe, 4Fe-4S	36.6
Ketol-acid reductoisomerase (NADP(+)) ( <i>P. aeruginosa</i> , strain LESB58)	ILVC_PSEA8	101	4	15	R ADLDVIMIAPK K DSGVDVTVGLR R NNAAHPIEQIGEK K NVALSYACGVGGGR	Mg	36.4
<b>M- Cell wall/membrane biogenesis</b>							
Outer membrane porin F ( <i>P. aeruginosa</i> ATCC15692/PAO1)	PORF_PSEAE	111	6	28	R DVLVNEYGVEGGR R RVEAEVEAEAK R YFTDSVRNMK R VQLDVKFDKSK	Ca	37.6

R|VNAVGYGESRPVADNA  
TAEGR  
K|QYPSTSTTVEGHTDSVGTDA  
YNQK

<sup>a</sup>according to <https://www.ncbi.nlm.nih.gov/COG/>

Table 2. Proteins differentially expressed in the presence of 0.9 mM cadmium in *Pseudomonas aeruginosa*, classified according to COG<sup>a</sup> and identified on the basis of at least two matched peptides and FDR 1%.

COG category/ Identified protein (strain, species)	Entry name	Easy Prot score	Number of matched peptides	Peptide sequence	Coverage %	Fraction <sup>b</sup>	Molecular mass, kDa
<b>C- Energy production and conversion</b>							
Electron transfer flavoprotein subunit beta ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ETFB_PSEAE	101	4	K AVVDKEQPQLVILGK K GVATEIVAVSVGPTAAQREQ LR K MSMNPFCIEAVEEAVR K VEVAGDKVNVTR	23	I	26.3
Electron transfer flavoprotein subunit alpha ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ETFA_PSEAE	92	5	R AAVDAGFVPNDMQVGQTG K K NYSHVLAPATTNGK K RPIYAGNAIATVQSSAAVK K SAFVGEELAK K VLVADNAAYAHQLPENVA PLIAELGK	16	I	31.4
ATP synthase subunit alpha ( <i>P. aeruginosa</i> , strain LESB58)	ATPA_PSEA8	75	4	R GQRELIIGDR R ILEVPVGPPELLGR R NEGATIVSVSDGIVR	10	I	55.3

ATP synthase subunit beta ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ATPB_PSEAE	39	3	R VVDALGNPIDGK R NDSSLIAR R RLEAAGYR R YATNSETAGFFR	7	I	49.5
ATP synthase epsilon chain ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ATPE_PSEAE	35	2	R AGDLDEAAAQEALK K VLADTVVR	16	I	14.7
Dihydrolipoyl dehydrogenase1 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	DLDH1_PSEAE	160	7	R AMAQGEMVAELIAGK R AMTLEANEGFVR K VISSTEALAPGSLPK K AVSELSTAFASLEMGA R R EIAADQVLVAVGR R SALGIQVQAPSIDIAR K SVAVELAGGGSQR	25	I	48.6
Aldehyde dehydrogenase ( <i>Pseudomonas oleovorans</i> )	ALDH_PSEOL	34	4	K FNEILVKEIVR K GAKILQGGQVDATE R R RSADYCR K VKQLGITVK	9	I	52.8
Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ODO2_PSEAE	50	3	K APTFPESVADGTVATWHK K LAEEAGIDPNSIAGTGK K PIMDLR	10	I	42.9
Glycerol kinase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GLPK1_PSEAE	190	9	R DGLEDYIR R DVLDAMQR R ETTGLVTDYPYFSGTK R MLEVLDIPR R REKLYAGWKKAVERTR R SAAICAQLKR	22	I	55.9

				R VFEPECDEPRR			
				K VINDSFDSEYFATK			
				K WILDNVEGAR E			
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ODP2_PSEAE	32	3	K ADTPAPVGAPSR	9	I	56.7
				K VGDEVGTGDLILK			
				K ANVIEVMVK			
<b>E- Amino acid transport metabolism</b>							
Arginine deiminase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ARCA_PSEAE	27	2	K GAAERVIVAGLPK	9	I	46.4
				R GGGHCMTCPIVR			
Ornithine carbamoyltransferase, catabolic ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	OTCC_PSEAE	68	4	R ITLTEDPKEAVK	13	I	38
				R MYDAIEYR			
				R NNMGNSLLLIGAK			
				K YTGTEQQHLKR			
N-acetyl-gamma-glutamyl-phosphate reductase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ARGC_PSEAE	30	2	R HLPEISQGLRR		I	36.7
				K VGIVGGTGYTGVELLR			
Glycine cleavage system H protein 1 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GCSH1_PSEAE	30	2	R FRPADAGAWEK	16	II	13.7
				K LLDQAAYDR			
Glycine cleavage system H protein 2 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GCSH2_PSEAE	28	2	K LKPSNPAELDK	15	II	13.6
				M SNIPAELR			
Glutaminase-asparaginase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ASPQ_PSEAE	32	2	K LSNVVILATGGTIAGAGASA	13	II	38.6
				ANSATYTAAK			
				K VPVDQLLASVPQLK			
Histidine ammonia-lyase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	HUTH_PSEAE	30	2	R DLLTASSEVAR	5	I	53.8
				R TAYGINTGFLLASTR			

Leucine-, isoleucine-, valine-, threonine- and alanine-binding protein ( <i>P. aeruginosa</i> ATCC15692/PAO1)	BRAC_PSEAE	58	3	K VAVFEGLNAGDKDFNALISK R TIGLDNMQGPVAGK K IALAGPVTGPVAQYGDMQR	23	I	39.7
Methylmalonate-semialdehyde dehydrogenase ( <i>P. aeruginosa</i> ATCC15692/PAO1)	MMSA_PSEAE	80	4	K AQVISNLVGASVGAAGQR K GVLQVVHGGK R LAELFLEAGAPK R LINESPYGNGTSIFTSSGAAAR	12	I	53.5
<b>G- Carbohydrate transport and metabolism</b>							
Phosphoglycerate kinase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	PGK_PSEAE	64	4	K EFAESAVATVK K SLYEADLVETAK K VAAAGPLLAELDALGK K VLPAVEILEQR	16	II	40.4
Glycosyltransferase alg8 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ALG8_PSEAE	19	2	R HINMCSMALSK R RLGWFTMLVLFDDQ R	5	I	56.5
Glucans biosynthesis glucosyltransferase H ( <i>P. aeruginosa</i> PA7)	OPGH_PSEA7	32	4	R ELRATDEYTYENR R MQQFATR R SNPPKPK K VIPEPWR	4	I	96
<b>I- Lipid transport and metabolism</b>							
Acetyl-CoA acetyltransferase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ATOB_PSEAE	20	2	- MQDVVIVAATR R TGLRMGHAK	3	II	40.3
Acyl carrier protein 1 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ACP1_PSEAE	50	2	K ITTVQEAIIDYIVAHQQ K IVAEQLGVK	19	III	8.7
<b>H- Coenzyme transport and metabolism</b>							



L-aspartate oxidase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	NADB_PSEAE	17	2	R LGIDCVYLDISHK K RCLGAYVLNR	4	I	60
Glutathione reductase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GSHR_PSEAE	22	3	K GLDLQFNSDIAR K IFESRFR K VKIFESR	5	I	49
<b>K- Transcription</b>							
Transcription elongation factor GreA ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GRE_A_PSEAE	77	3	K ISVNSPIAR K LSNAQVIDVTAIPHSKG R TPGGDVEYEIVEVR	25	I	17.1
DNA-binding protein HU-beta ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	DBHB_PSEAE	44	2	R ALDAVIESVTGALK K SELIDAI AASADIPK	32	III	9
<b>L- Replication and repair</b>							
DNA polymerase III subunit beta ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	DPO3B_PSEAE	51	3	R ATTGEFTFTSK R HQVIVPRK R TSFAMAQQDVR	8	I	40.6
<b>J- Translation, ribosomal structure and biogenesis</b>							
Elongation factor Tu ( <i>P. aeruginosa</i> UCBPP-PA14)	EFTU_PSEAB	38	2	R AGENVGILLR K FECEVYVLSK	5	III	43.3
50S ribosomal proteins L36 2 ( <i>P. aeruginosa</i> )	RL362_PSEAB	42	3	R FKCVQGR  R HRDCQVVKRRGRLYVICKSN PR - MKVLASLKQAKLR	86	III	5.9
50S ribosomal proteins L 20 ( <i>P. aeruginosa</i> ATCC15692/PAO1)	RL20_PSEAE	22	2	R DRRQRKRQFR K RQFRALWIAR	13	III	13.3

30S ribosomal proteins S14 ( <i>P. aeruginosa</i> ATCC15692/PAO1)	RS14_PSEAE	21	2	R CRLTGRPHGFYR R NKLREAAMR	21	III	11.5
50S ribosomal proteins L36 ( <i>P. aeruginosa</i> ATCC15692/PAO1)	RL36_PSEAE	24	2	K KLCRNCKIIRRDGIVR K VRASVKKLCRNCK	58	III	4.4
<b>M- Cell wall/membrane biogenesis</b>							
Peptidoglycan-associated lipoprotein ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	PAL_PSEAE	68	3	R EYNMALGER R VVLEGHTDER R YLVLQGVSPAQLELVSYGK	31	II	15.8
<b>N- Cell motility</b>							
Protein PilJ ( <i>P. aeruginosa</i> ATCC15692/PAO1)	PILJ_PSEAE	26	2	R LAQDAGVALEEIEK R SSAATKQIEALVK	4	I	72.5
Protein PilH ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	PILH_PSEAE	72	3	K DAETSAIPVIIVTTK D R ILIVDDSPTEMYK L R ILIVDDSPTEMYKLTAMLEK	23	II	13.2
A-type flagellin [CHAIN 0] ( <i>P. aeruginosa</i> )	FLICA_PSEAI	82	4	- ALTVENTNIASLNTQR R FDNTINNLK R NLNNSASLNTSLQR R LTSQVNGLNVATK	13	II	39.9
B-type flagellin ( <i>P. aeruginosa</i> ATCC15692/PAO1)	FLICB_PSEAE	30	2	M ALTVENTNIASLNTQR K EVAAQQAELTR	5	I	49
Flagellar motor switch protein FliG ( <i>P. aeruginosa</i> ATCC15692/PAO1)	FLIG_PSEAE	28	3	K EILTIARR R KMLTQALGEDK R EKVFKNMSKR A	9	II	37
<b>O- Posttranslational modification, protein turnover, chaperones</b>							
Thiol:disulfide interchange protein DsbA ( <i>P. aeruginosa</i> , UCBPP-PA14)	DSBA_PSEAB	35	2	R FDIGSAGGPEETLK K LADYLIEK	12	II	23.3
Thioredoxin	THIO_PSEAE	86	4	K LNIDENQDTPPK	43	II	11.8

( <i>P. aeruginosa</i> ATCC 15692/PAO1)					K MIAPVLDEVAR			
					K SQLAAFLDANI			
					M SEHIVNVTASFEQDVLK			
Chaperone protein DnaK ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	DNAK_PSEAB	123	6		K ALGELEAAVK	11	I	68.3
					K ASSGLSEDEIQQMVR			
					K FDLADIPPAPR			
					K MNALSQASTPLAQK			
					R NQG DALVHATR			
					R RFEENVVQK			
Alkyl hydroperoxide reductase subunit, Thioredoxin peroxidase ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	AHPF_PSEAE	22	3		K AKGVCFCPHCDGPLFK	12	II	20.5
					K GVCFCPHCDGPLFK			
					R HYEVDIMNLQR			

<sup>a</sup>According to <https://www.ncbi.nlm.nih.gov/COG/>

<sup>b</sup>Fraction in size exclusion chromatography

Table 3. Proteins differentially expressed in *Pseudomonas aeruginosa* grown in LB without addition of cadmium (control), classified according to COG<sup>a</sup> and identified on the basis of at least two matched peptides and FDR 1%.

Identified protein (strain, species)	Entry name	EasyProt score	Number of matched peptides	Sequence coverage, %	Peptide sequence	Molecular mass, kDa	COG <sup>a</sup>	Fraction <sup>b</sup>
tRNA (guanine-N(1)- methyltransferase	TRMD_PSEAE	29	3	13	K RVPEVLLSGNHEHIRR R PEVYADKR	28.4	J	I



UPF0176 protein Pmen_1693 ( <i>P. mendoncina</i> )	Y1693_PSEMY	18	2	11	R CEKASSYMLGEGFEEV YHLKGGILK K SFREFPEYVK	35.5	/	I
UTP--glucose-1-phosphate uridylyltransferase (UDPGP) ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	GALU_PSEAE	18	2	12	R FLPATKAMPKEMPLV VNK K YGVIAGEMIRDDIFR	31.2	C	I
Type III pantothenate kinase ( <i>P. mendoncina</i> )	COAX_PSEMY	17	2	9	R CRLVSVR - MILELDCGNSFIKWR	26.7	H	I
Phenazine biosynthesis protein phzA 2 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	PHZA2_PSEAE	27	3	12	R EYQRLK - MREYQRLK R NREFMNPMPQKLR	19.3	Q	I
Nuclease sbcCD subunit C ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	SBCC_PSEAE	19	3	3	R ERQAQADNHLR R QQTLEAER R QRQQDEFQRLQADWQ AWR	139.0	L	I
Lipoprotein-releasing system ATP- binding protein LolD ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	LOLD_PSEAE	18	2	11	- MNDKSVLSCR R QRAAELLERVGLGHR	24.7	M	I
Putative quercetin 2,3-dioxygenase PA1205 (Putative quercetinase) ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	Y1205_PSEAE	18	2	10	R DCPERHEHLLQR R FGRLEDALEGPRLSAPPI PWK	24.4	R	I
tRNA sulfurtransferase ( <i>P. mendoncina</i> )	THII_PSEMY	17	2	5	K LIVKVFPEITIK R QECNAAGIDLKK	54.7	J	I
Peptide chain release factor 2 (RF-2) ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	RF2_PSEAE	36	4	11	R GRRRGRRRR R LRRHYHRAVRGR R PQRLEQPR R PQRLEQPRIRPEPRPRA	41.20	J	II

					R			
Protein sprT ( <i>P. aeruginosa</i> PA7)	SPRT_PSEA7	35	3	21	K GRRYYCR - MPEHLNARVEACYR R RCKATLVFSGEVTR	19.7	P	II
Outer membrane porin F [CHAIN 0] ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	PORF_PSEAE	28	2	7	R DVLVNEYGVVEGGR K SKVKENSYADIK	35.2	M	II
Translation initiation factor IF-2 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	IF2_PSEAE	23	3	5	K KTYVKRSPDEIEAERQ R K PAAVEERKKKEEPRRVP K K TVSVEVRKK	90.9	J	II
30S ribosomal protein S13 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	RS13_PSEAE	22	2	14	R HRRGLPVR K ITTEGDLR	13.2	J	II
Uncharacterized protein PA0525 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	Y525_PSEAE	22	3	4	R LLQLYR R RASQVLGGQPQKR R RQFACLR	69.47	/	II
SsrA-binding protein ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	SSRP_PSEAE	18	2	14	K GYACVALSMYWKK R HTEKERDSDR	18.0	J	II
30S ribosomal protein S3 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	RS3_PSEAE	18	2	15	- MGQKVHPNGIRLGIVK K PELDAMLVAQSVAQQ LER	25.8	J	II
Copper-binding periplasmic protein [CHAIN 0] ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	NOSD_PSEAE	17	2	6	R DSHPLMRMPAAEPRP - EPVDGLPLR	43.9	P	II
UPF0178 protein PLES_56411 ( <i>P. aeruginosa</i> , strain LESB58)	Y5641_PSEA8	20	2	14	R IWIDADACPKVAKELV CK	17.8	/	II

					M RIWIDADACPKVAKE LVCKFALK			
Transcriptional regulatory protein AlgQ ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	ALGQ_PSEAE	18	2	8	R CDNGDCR - MLESCR	18.0	K	II
GTPase Der ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	DER_PSEAE	17	2	8	K STLFNRLTR K YTLIDTAGVRRRGKIF EAVEKFSVVK	55.0	R	II
50S ribosomal protein L31 ( <i>P. aeruginosa</i> ATCC 15692/PAO1)	RL31_PSEAE	20	2	23	K QKVLDTGGR K TRSTLCK	7.9	J	II
50S ribosomal protein L18 ( <i>P. mendoncina</i> )	RL18_PSEMY	20	2	22	R LKMHELEAVRLCVYR - MTDKKVTRLRR A	12.6	J	II
Beta-lactamase OXA-15 [CHAIN 0]	BLO15_PSEAI	19	2	12	R AMLVFDPVRSKRR K LYRNELPFRVEHQRLV K	29.3	V	II
Pyridoxine/pyridoxamine 5'-phosphate oxidase (PNPOx) ( <i>P. aeruginosa</i> )	PDXH_PSEAB	19	2	13	R AELERLLADTERR R LHDRLDYRRQDGGWS R	24.8	H	II

<sup>a</sup>According to <https://www.ncbi.nlm.nih.gov/COG/>

<sup>b</sup>Fraction in size exclusion chromatography

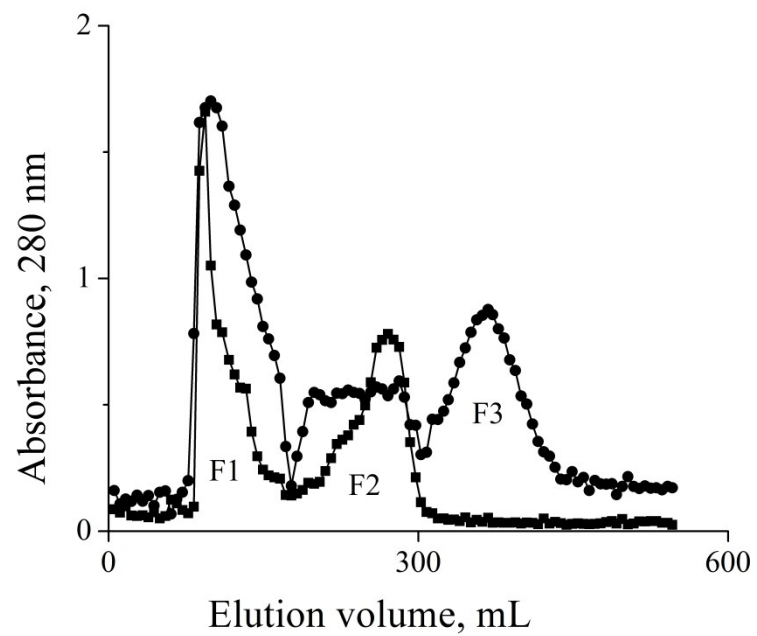


Figure 1. Size exclusion chromatography on Sephadex G-100 column (2.5 x 70 cm) equilibrated in buffer A (50 mM Tris buffer pH 7.5 supplemented with 0.1 mM PMSF and 0.5 mM DTT). Fractions (volumes of 5.5 mL) were collected and absorbance at 280 nm was recorded. Fractions were pooled according to absorbance. ■ - control, ● - cadmium amended biomass