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Supporting Information

Bioactive Pentacyclic Triterpene Ester Derivatives from *Alnus viridis* ssp. viridis *Bark*

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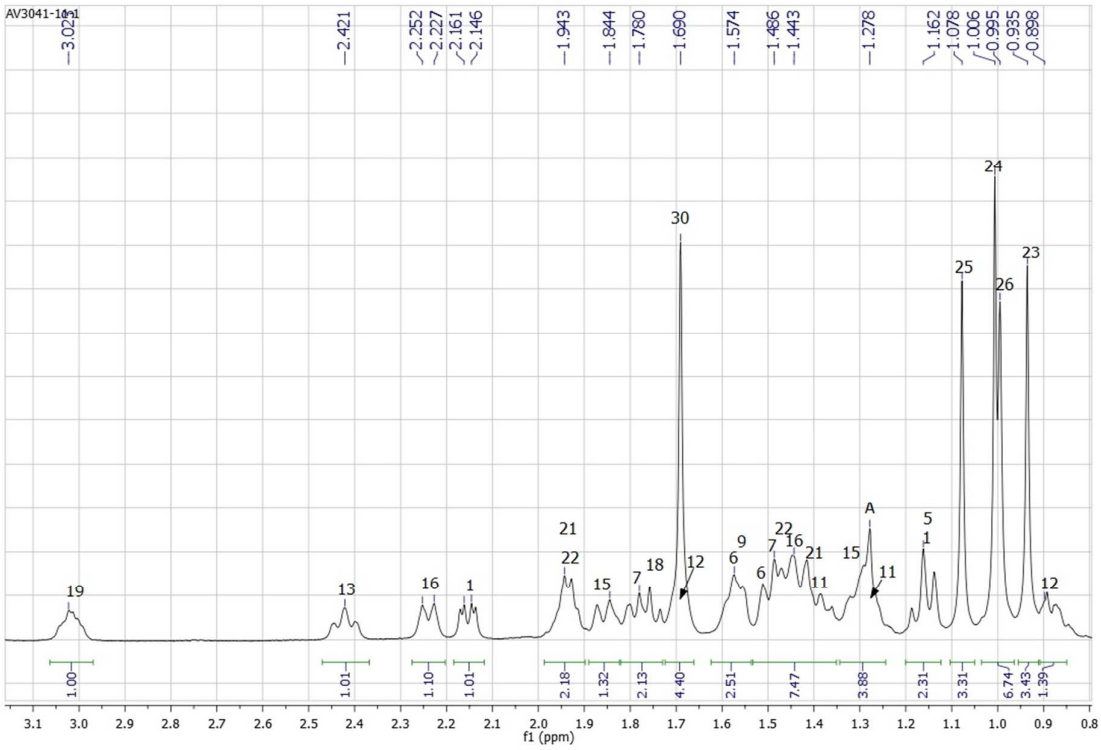

Figure S1. The 1st part of the ^{1}H NMR spectrum of **1** (CD_3OD, 500 MHz).

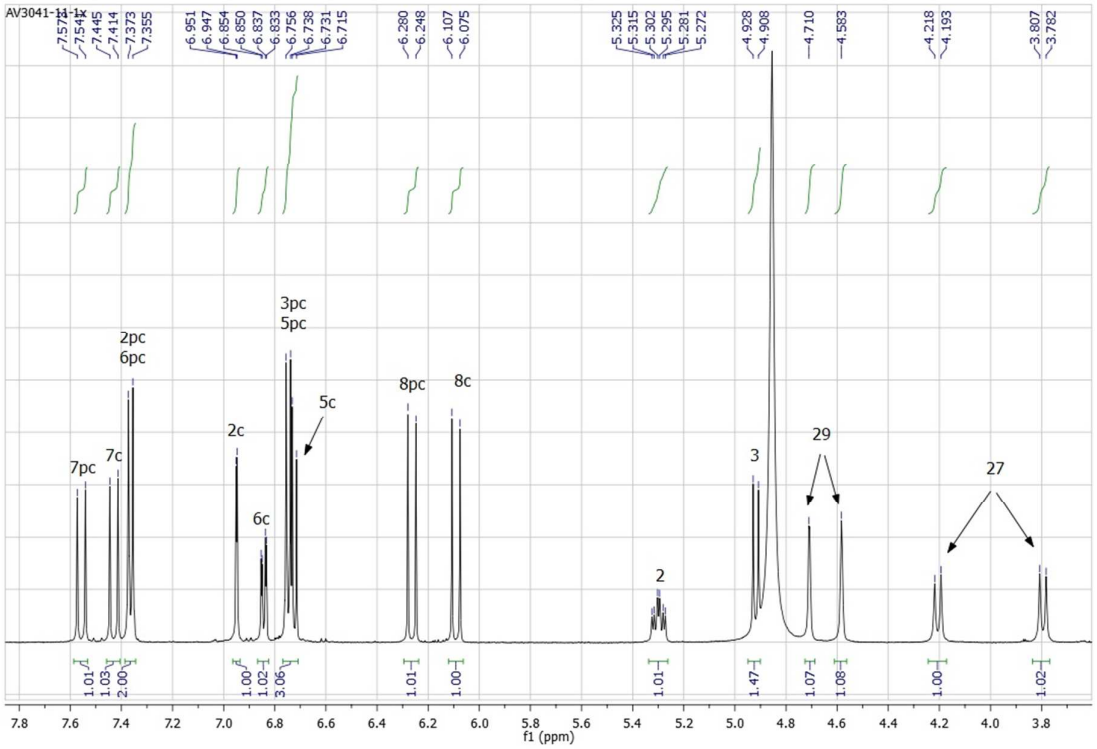

Figure S2. The 2nd part of the ^{1}H NMR spectrum of **1** (CD_3OD, 500 MHz).

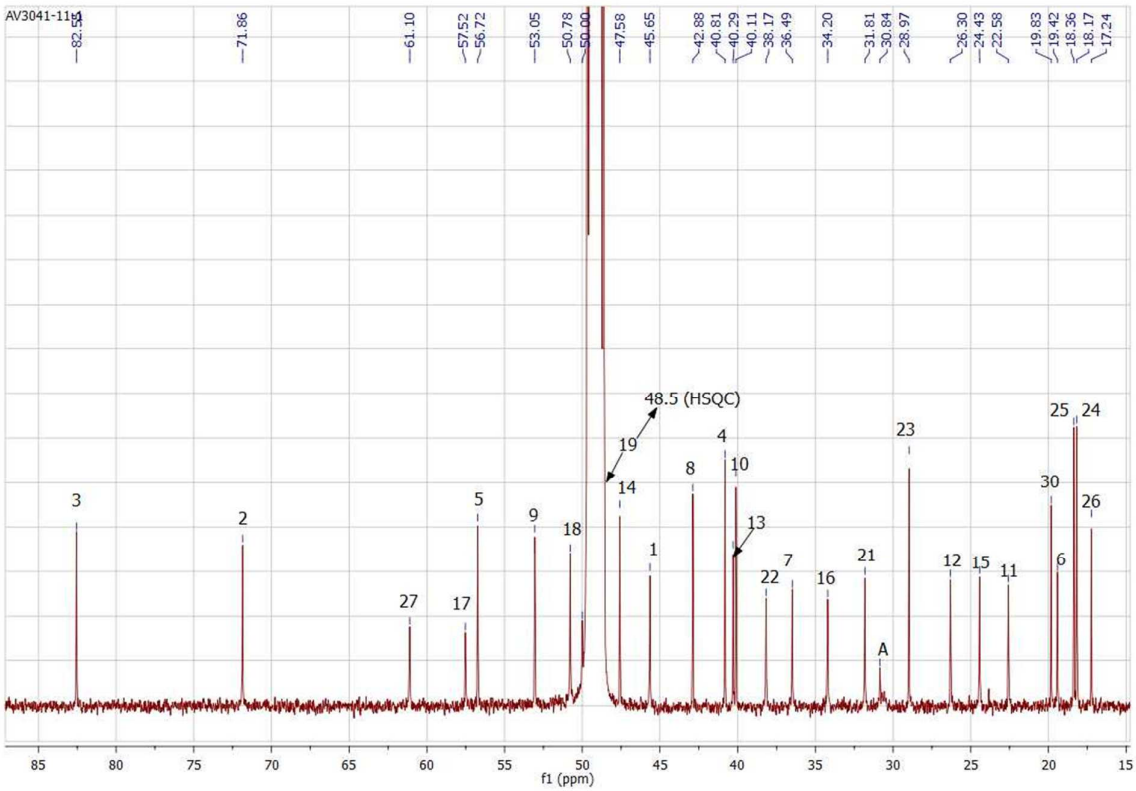

Figure S3. The 1st part of the ^{13}C NMR spectrum of **1** (CD_3OD, 125 MHz).

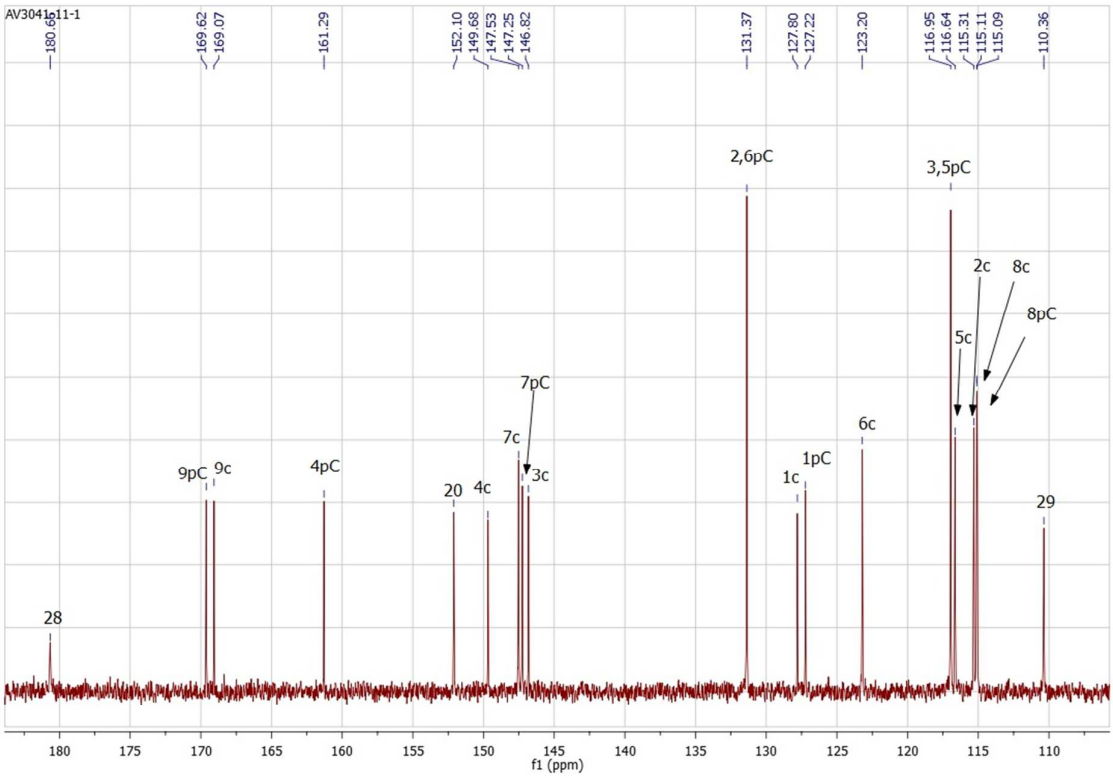

Figure S4. The 2nd part of the ^{13}C NMR spectrum of **1** (CD_3OD, 125 MHz).

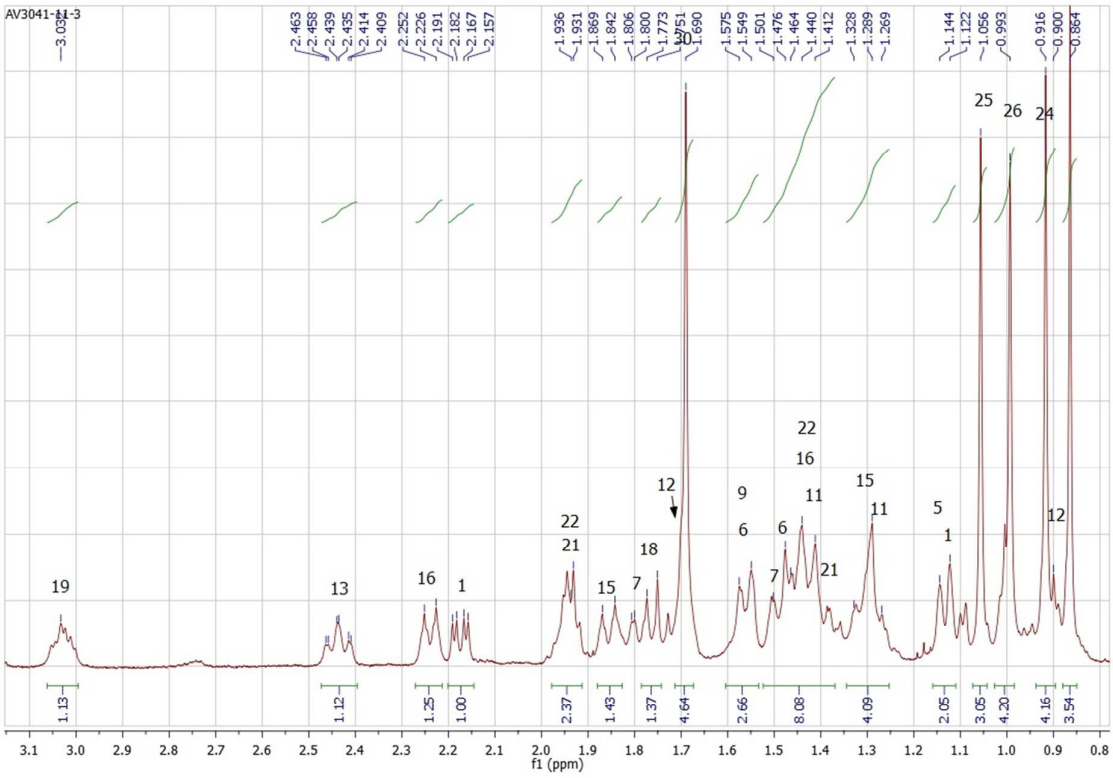

Figure S5. The 1st part of the ^{1}H NMR spectrum of **2** (CD_3OD, 500 MHz).

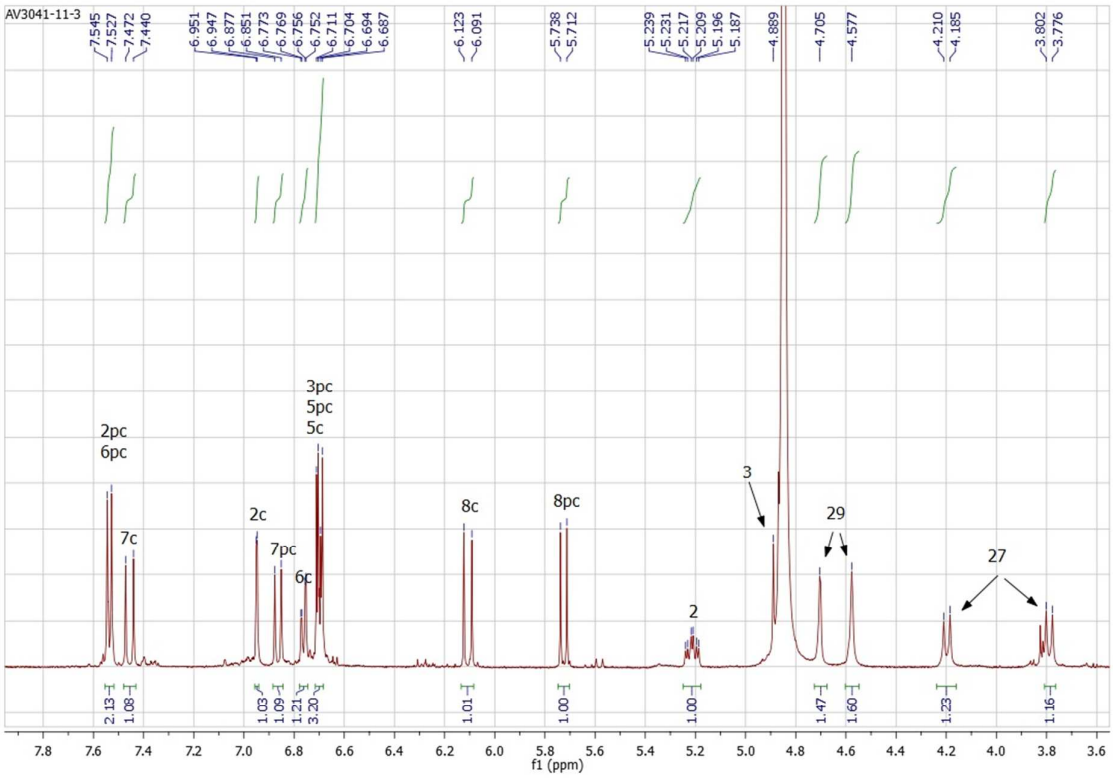

Figure S6. The 2nd part of the ^{1}H NMR spectrum of **2** (CD_3OD, 500 MHz).

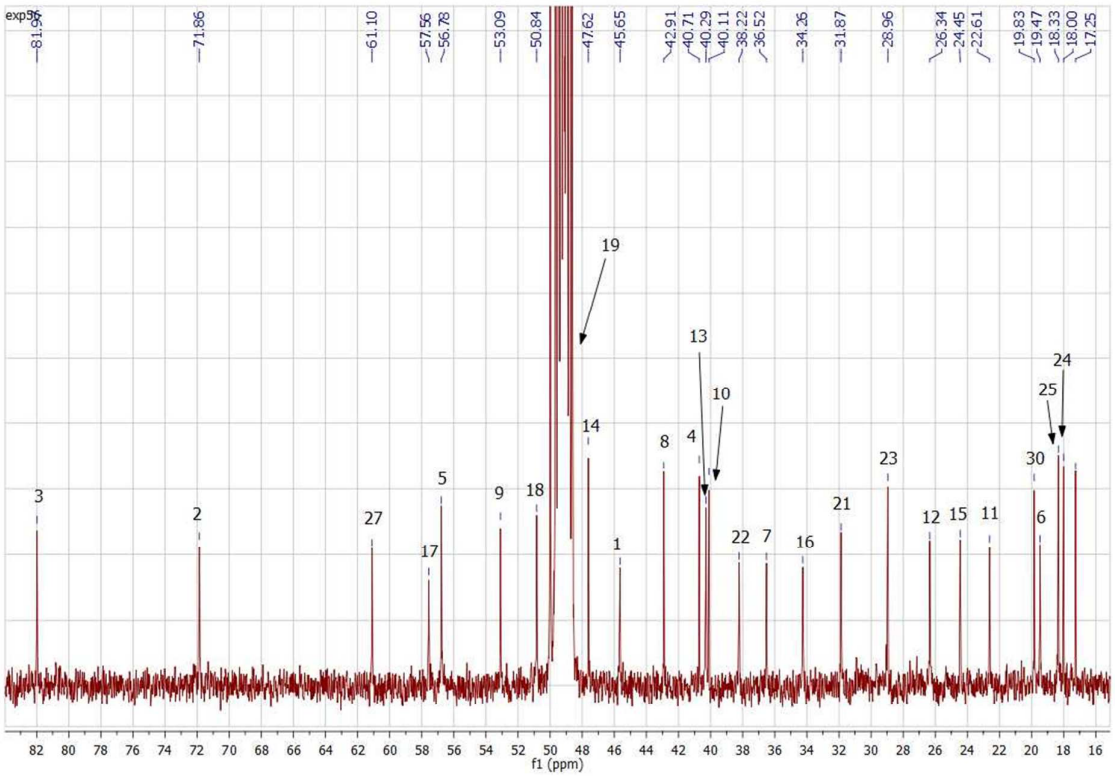

Figure S7. The 1st part of the ^{13}C NMR spectrum of **2** (CD_3OD, 125 MHz).

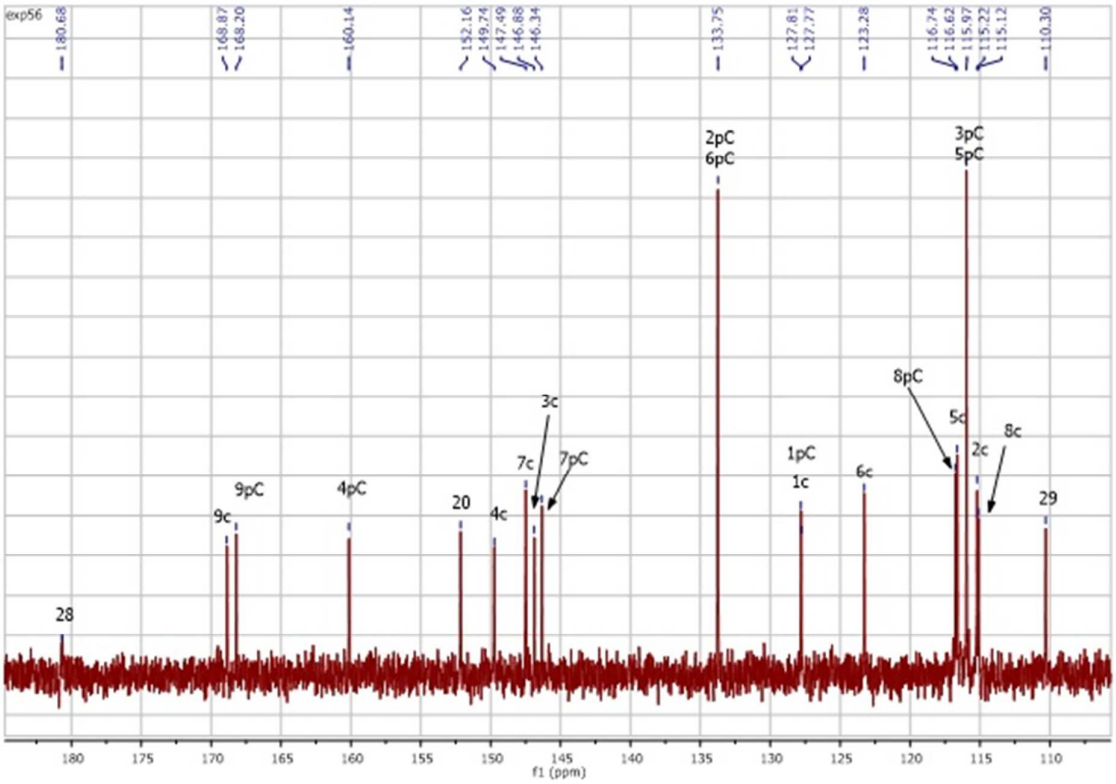

Figure S8. The 2nd part of the ^{13}C NMR spectrum of **2** (CD_3OD, 125 MHz).

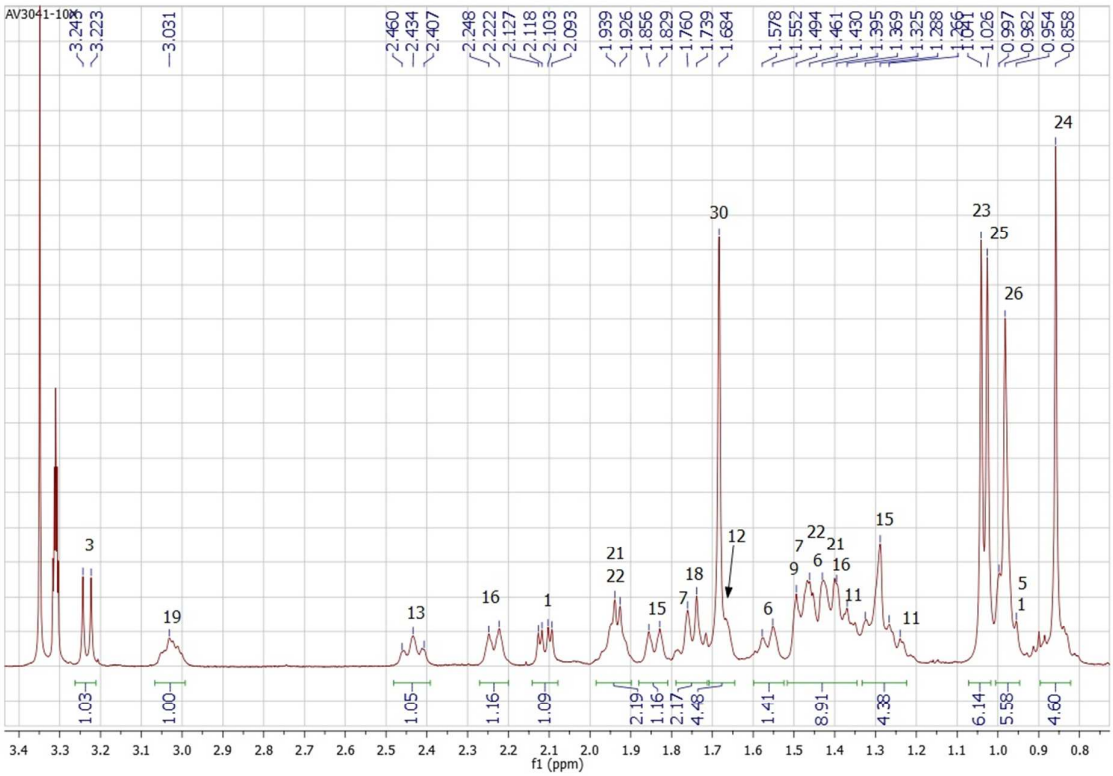

Figure S9. The 1st part of the ^{1}H NMR spectrum of **3** (CD_3OD, 500 MHz).

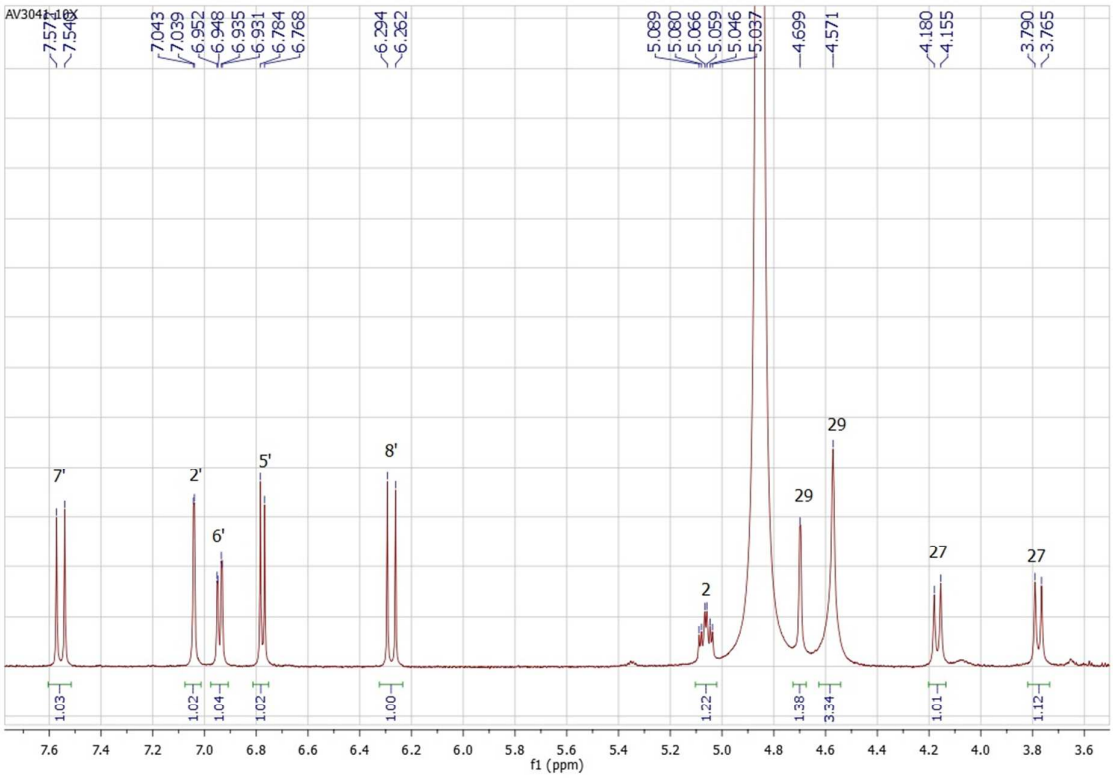

Figure S10. The 2nd part of the ^{1}H NMR spectrum of **3** (CD_3OD, 500 MHz).

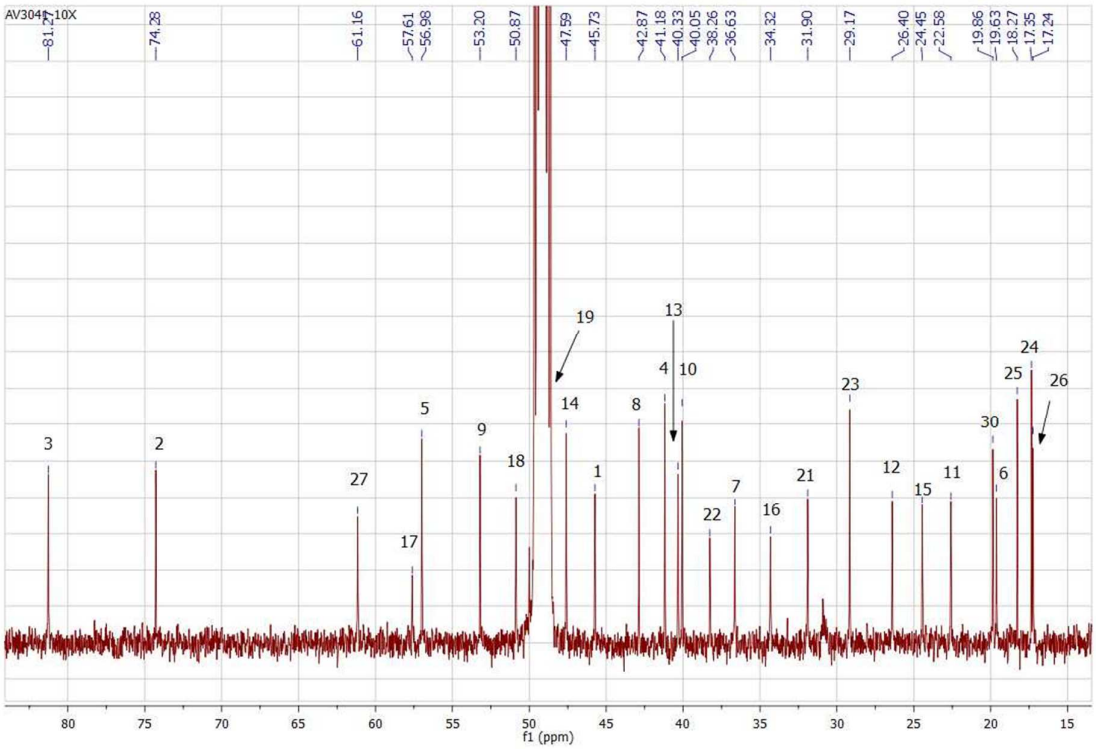

Figure S11. The 1st part of the ^{13}C NMR spectrum of **3** (CD_3OD, 125 MHz).

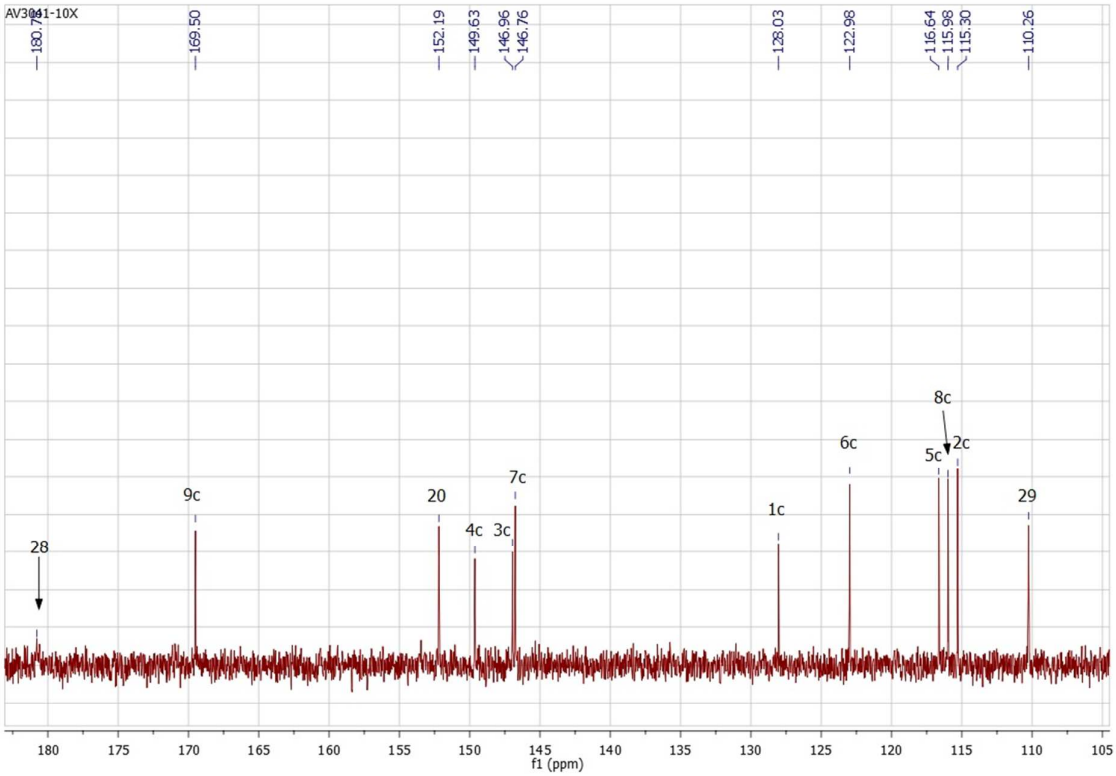

Figure S12. The 2nd part of the ^{13}C NMR spectrum of **3** (CD_3OD, 125 MHz).

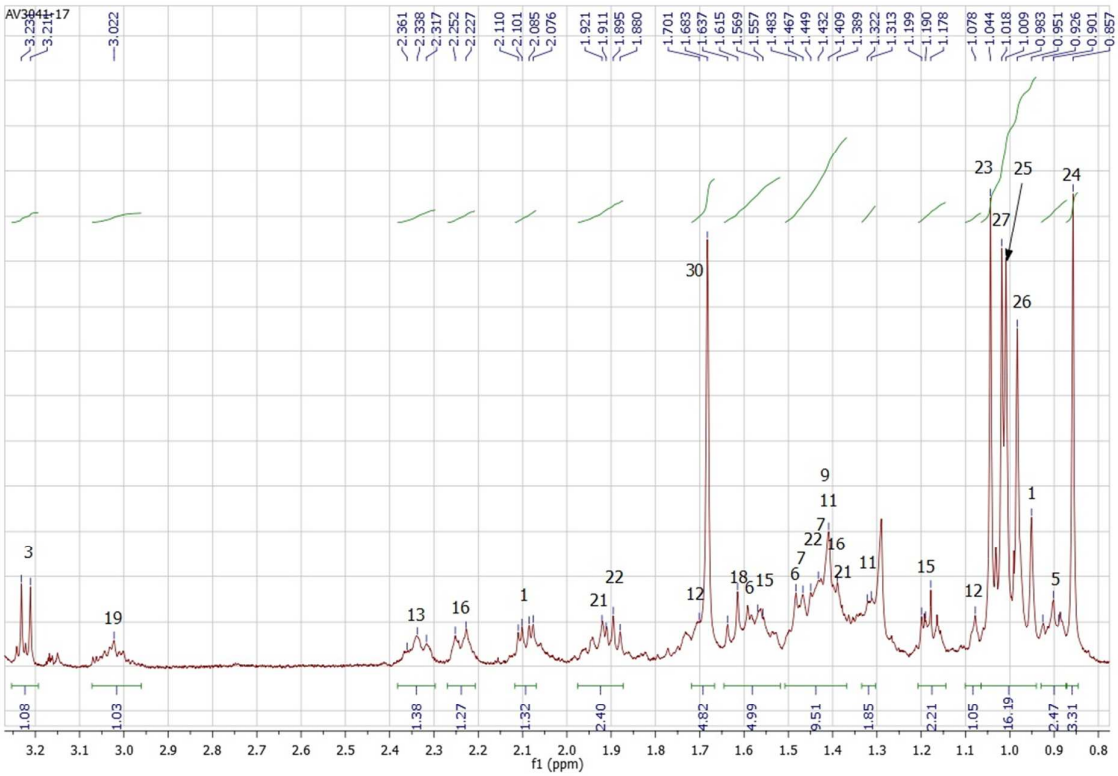

Figure S13. The 1st part of the ^{1}H NMR spectrum of **4** (CD_3OD, 500 MHz).

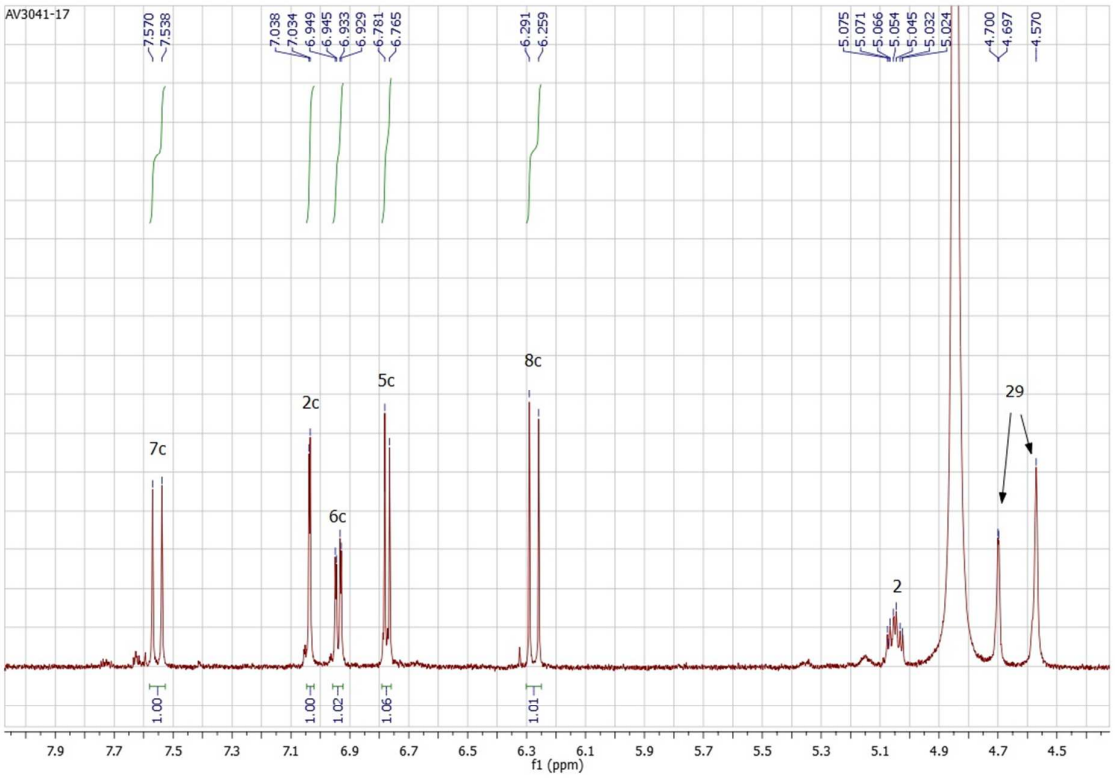

Figure S14. The 2nd part of the ^{1}H NMR spectrum of **4** (CD_3OD, 500 MHz).

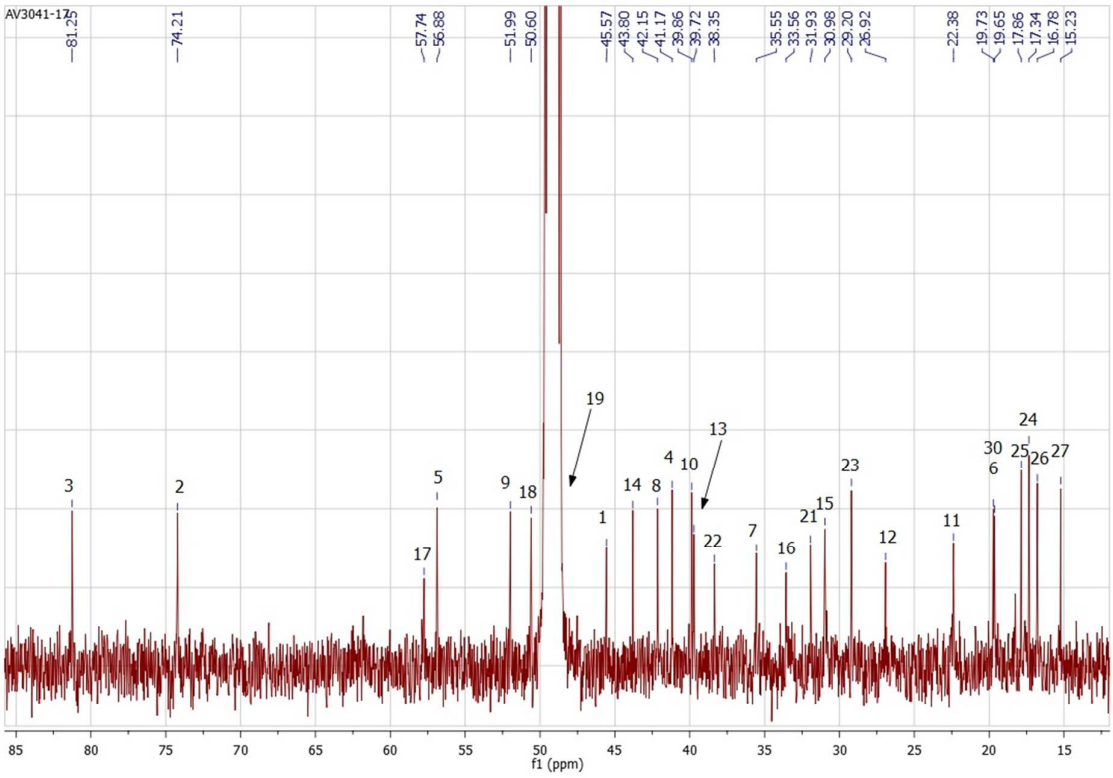

Figure S15. The 1st part of the ^{13}C NMR spectrum of **4** (CD_3OD, 125 MHz).

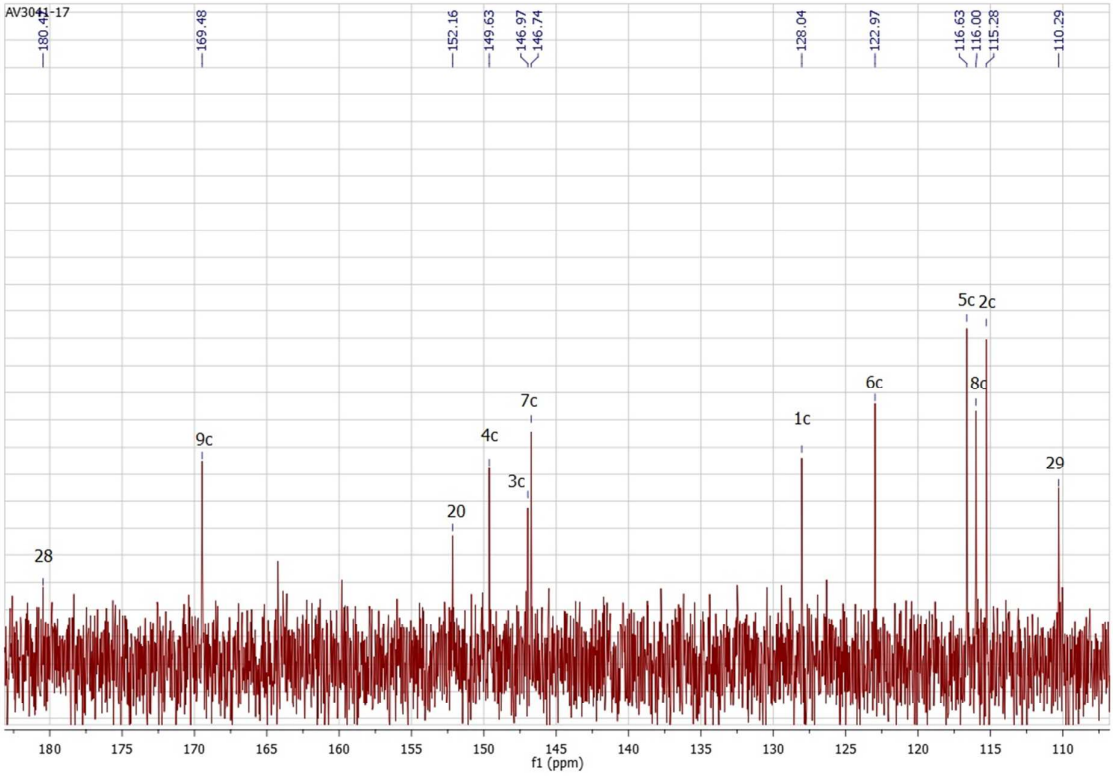

Figure S16. The 2nd part of the ^{13}C NMR spectrum of **4** (CD_3OD, 125 MHz).

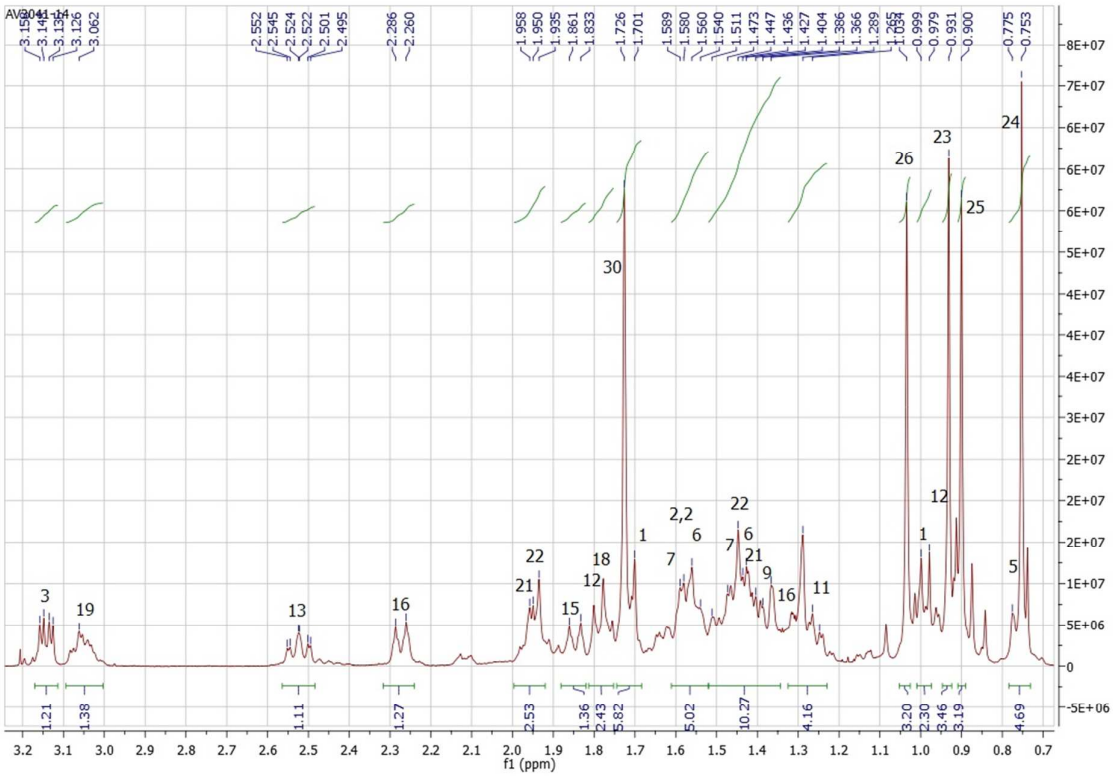

Figure S17. The 1st part of the ^{1}H NMR spectrum of **5** (CD_3OD, 500 MHz).

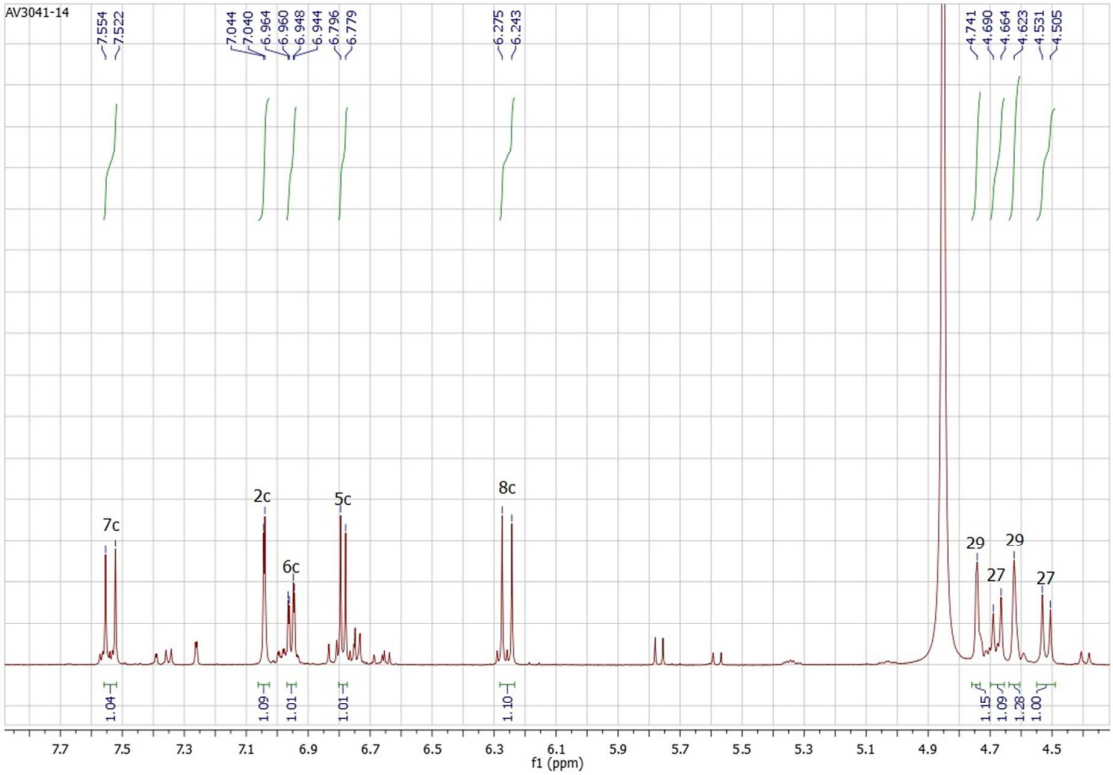

Figure S18. The 2nd part of the ^{1}H NMR spectrum of **5** (CD_3OD, 500 MHz).

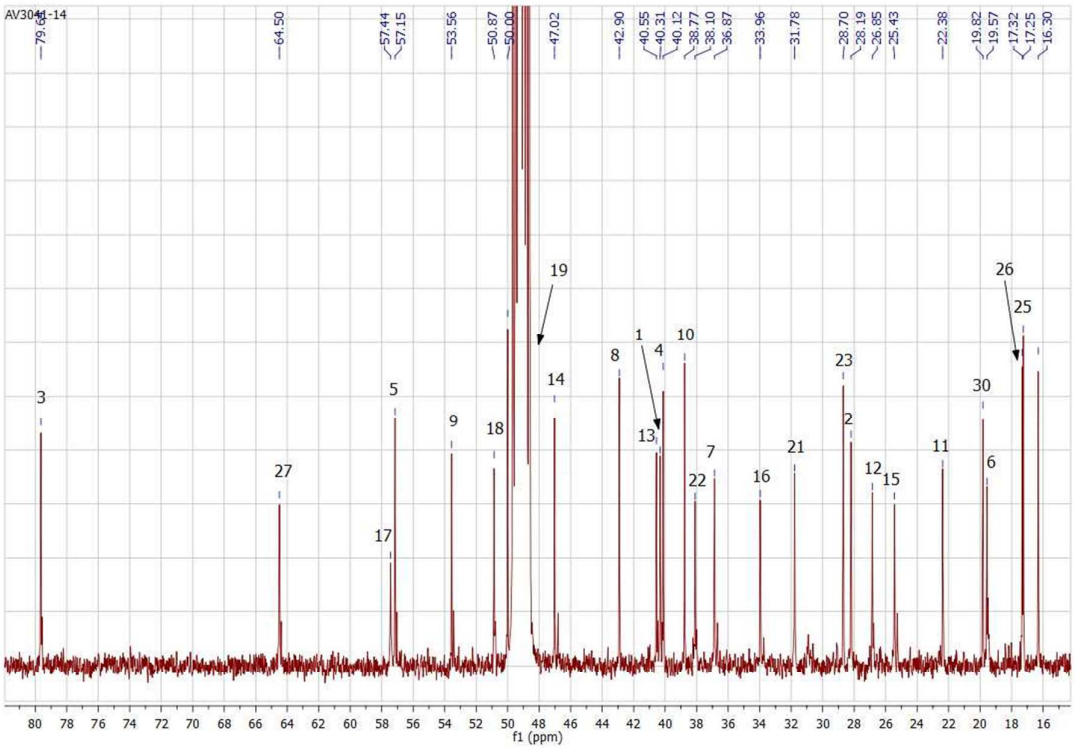

Figure S19. The 1st part of the ^{13}C NMR spectrum of **5** (CD_3OD, 125 MHz).

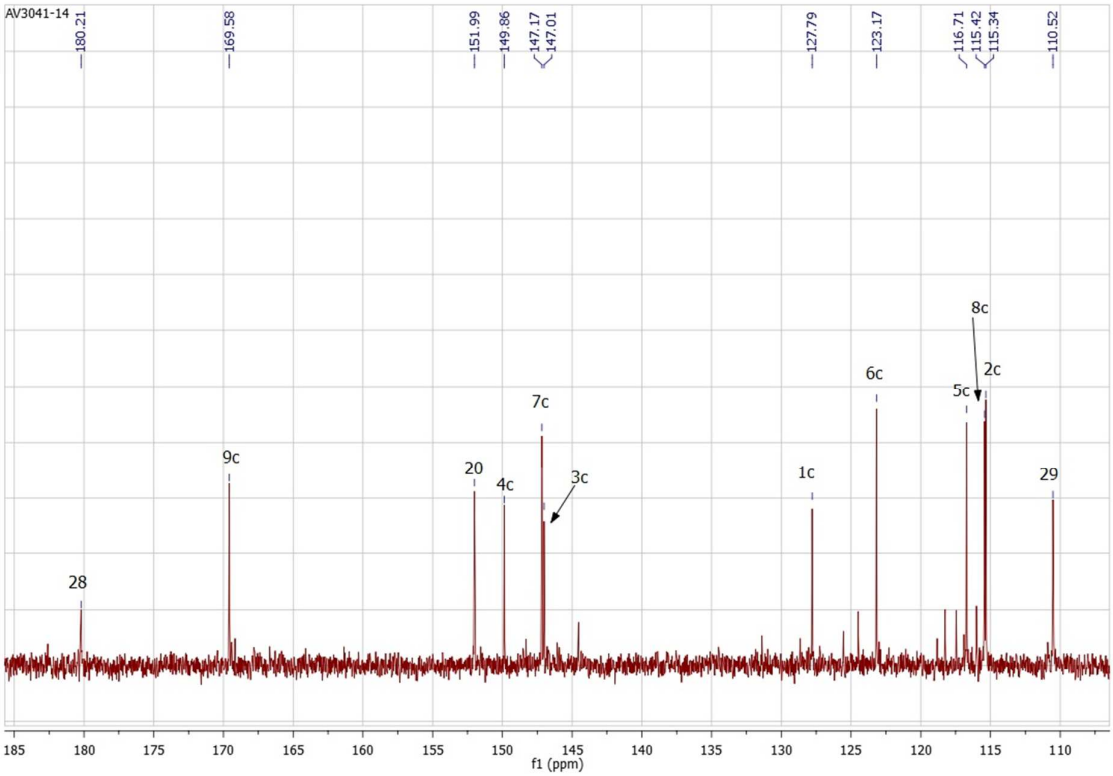

Figure S20. The 2nd part of the ^{13}C NMR spectrum of **5** (CD_3OD, 125 MHz).

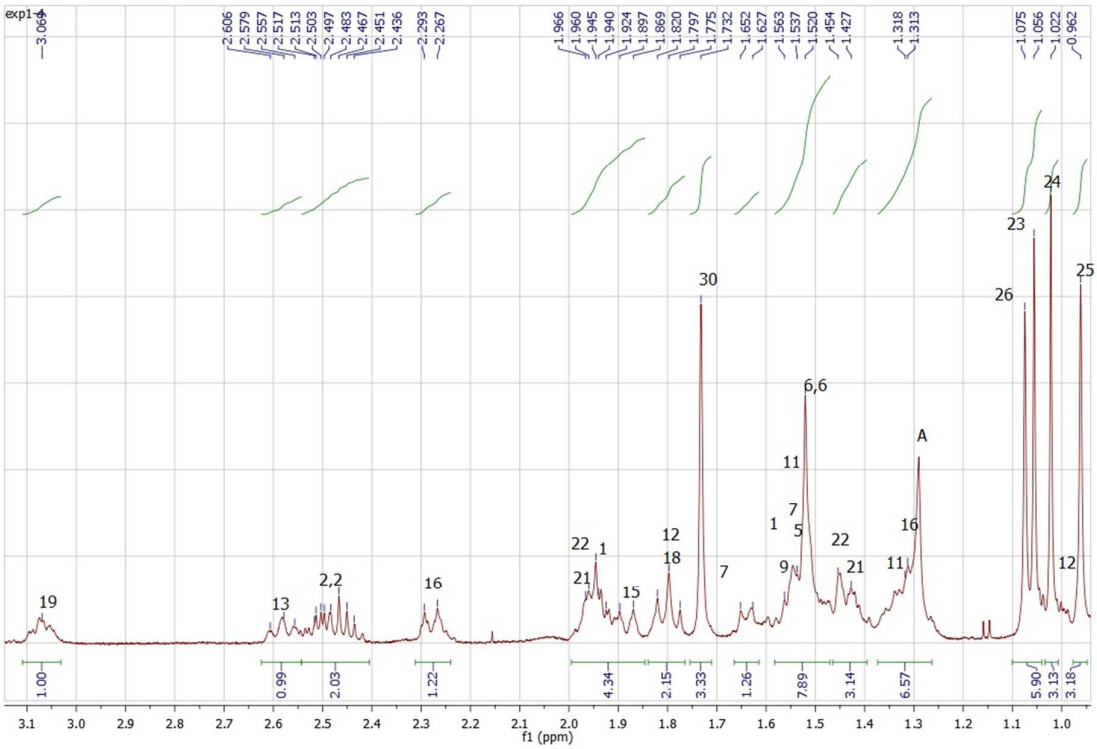

Figure S21. The 1st part of the ^{1}H NMR spectrum of **6** (CD_3OD, 500 MHz).

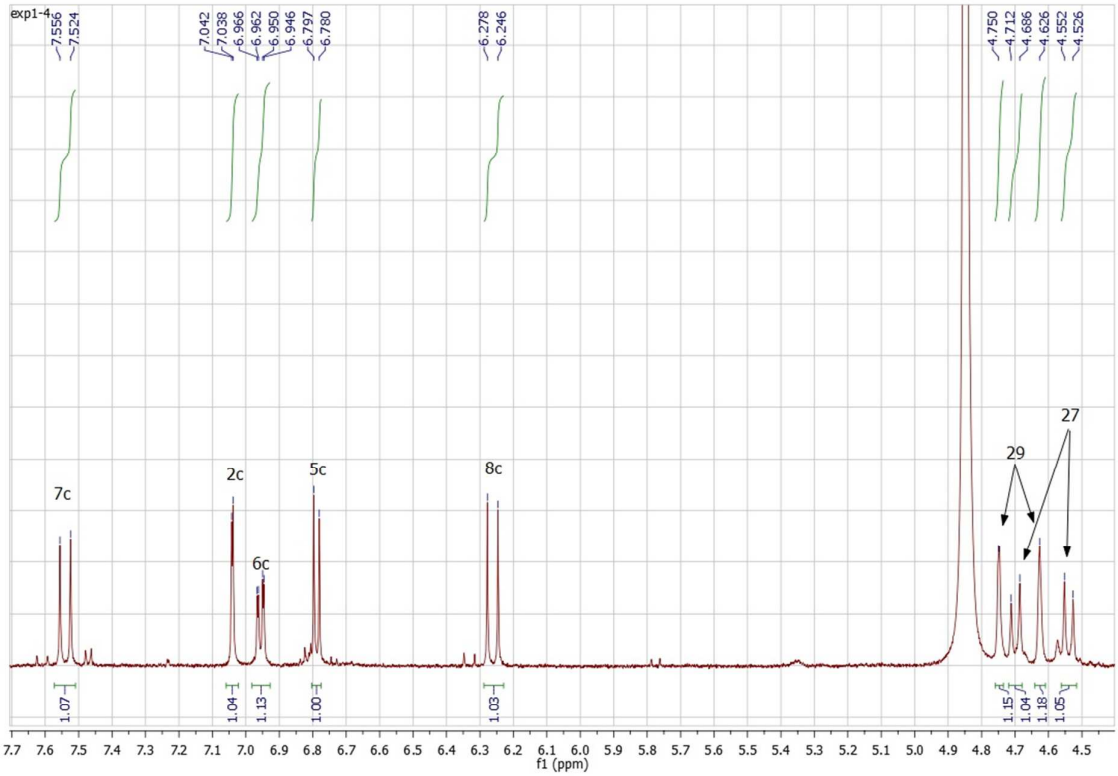

Figure S22. The 2nd part of the ^{1}H NMR spectrum of **6** (CD_3OD, 500 MHz).

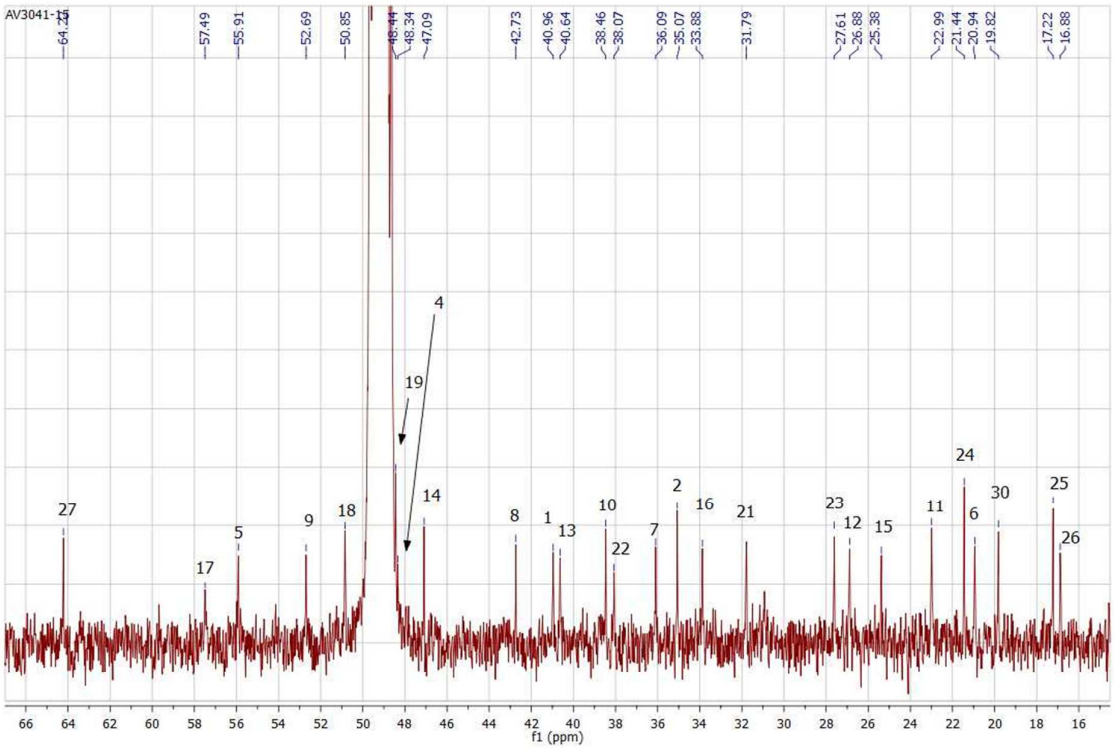

Figure S23. The 1st part of the ^{13}C NMR spectrum of **6** (CD_3OD, 125 MHz).

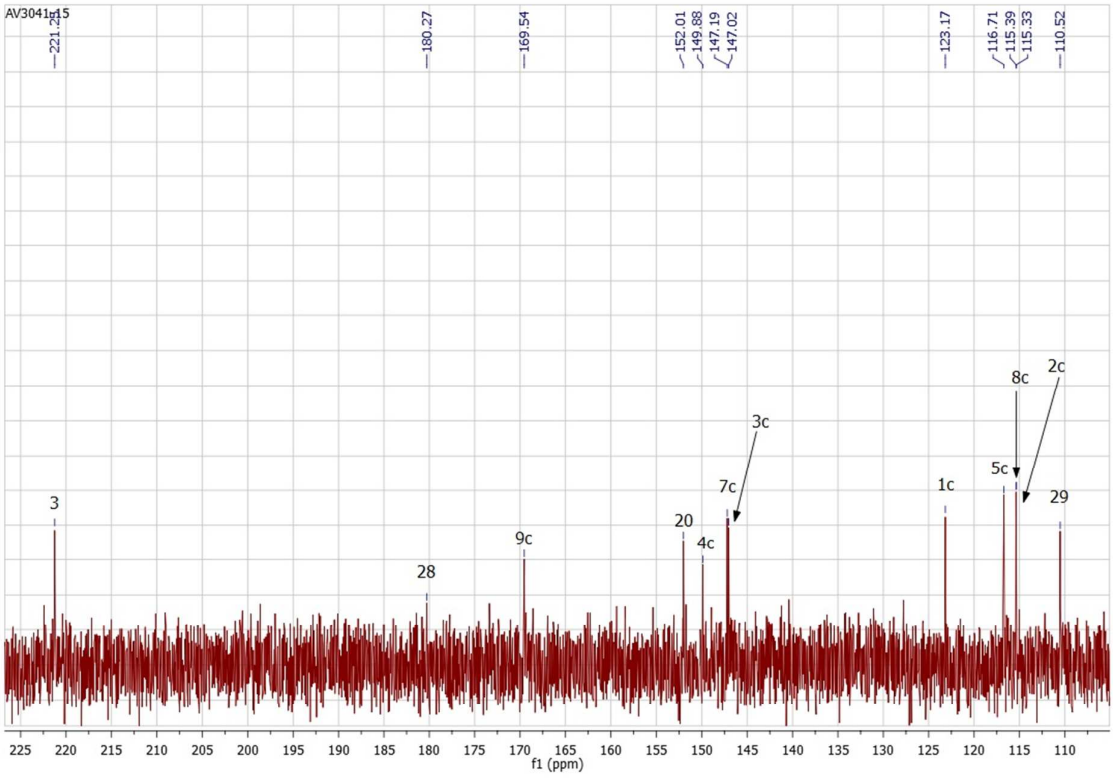

Figure S24. The 2nd part of the ^{13}C NMR spectrum of **6** (CD_3OD, 125 MHz).

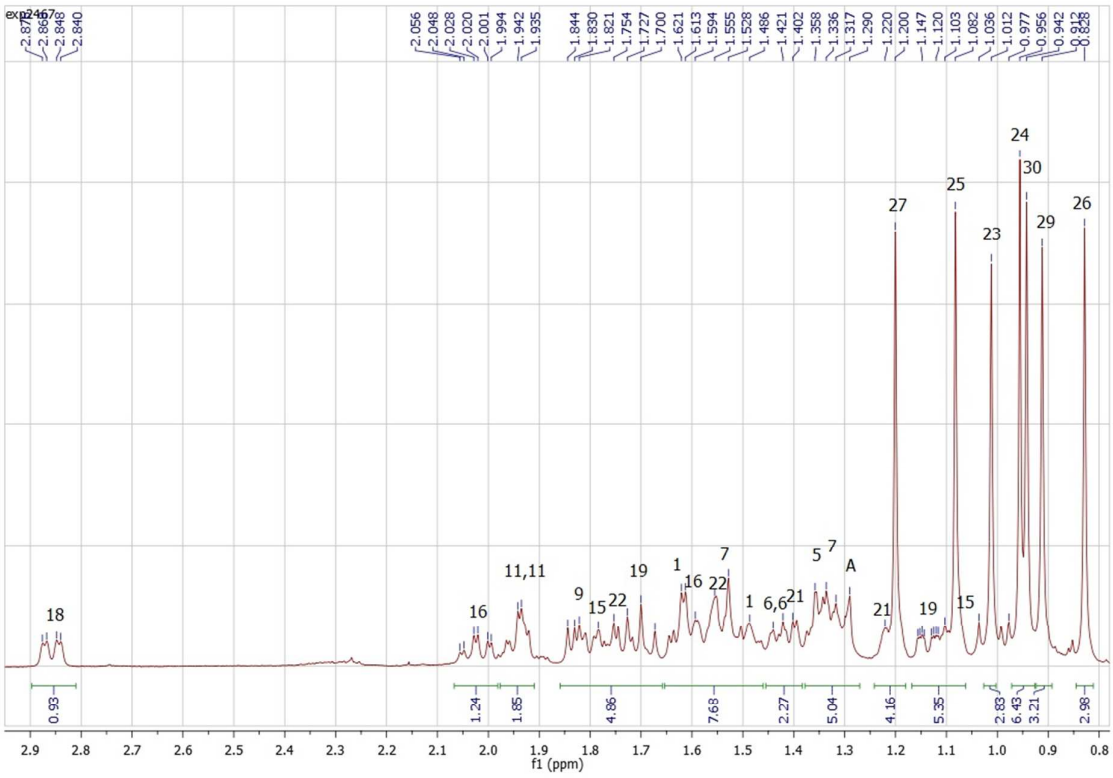

Figure S25. The 1st part of the ^{1}H NMR spectrum of **7** (CD_3OD, 500 MHz).

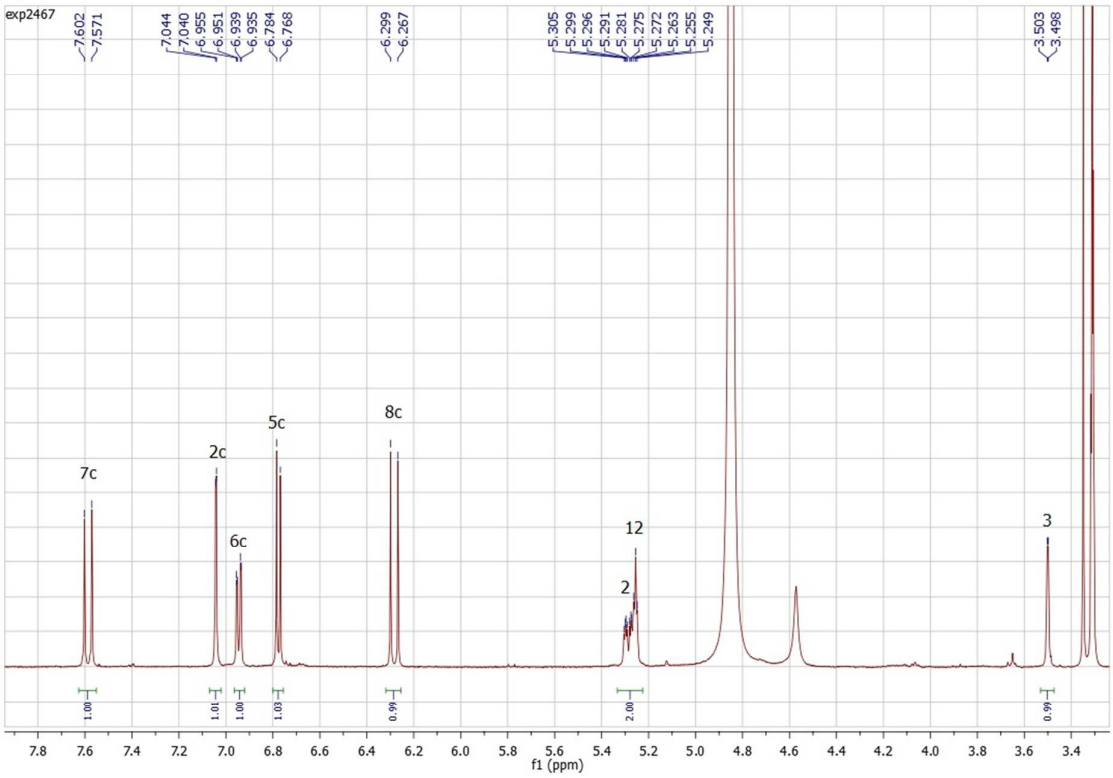

Figure S26. The 2nd part of the ^{1}H NMR spectrum of **7** (CD_3OD, 500 MHz).

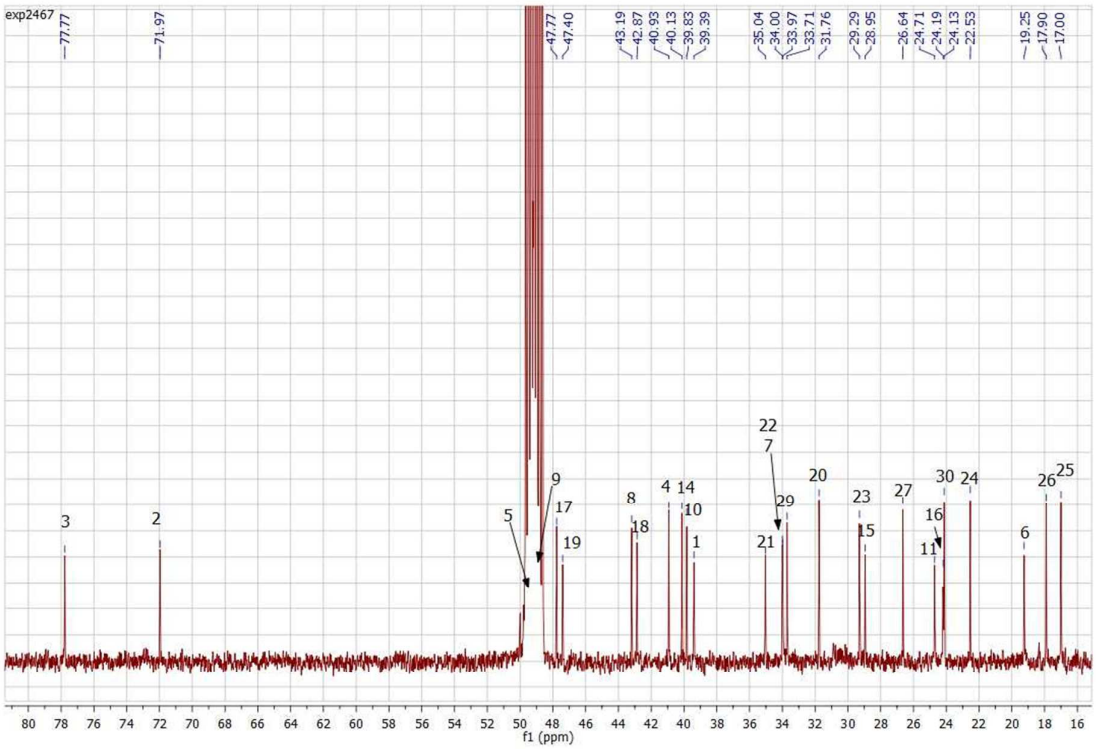

Figure S27. The 1st part of the ^{13}C NMR spectrum of **7** (CD_3OD, 125 MHz).

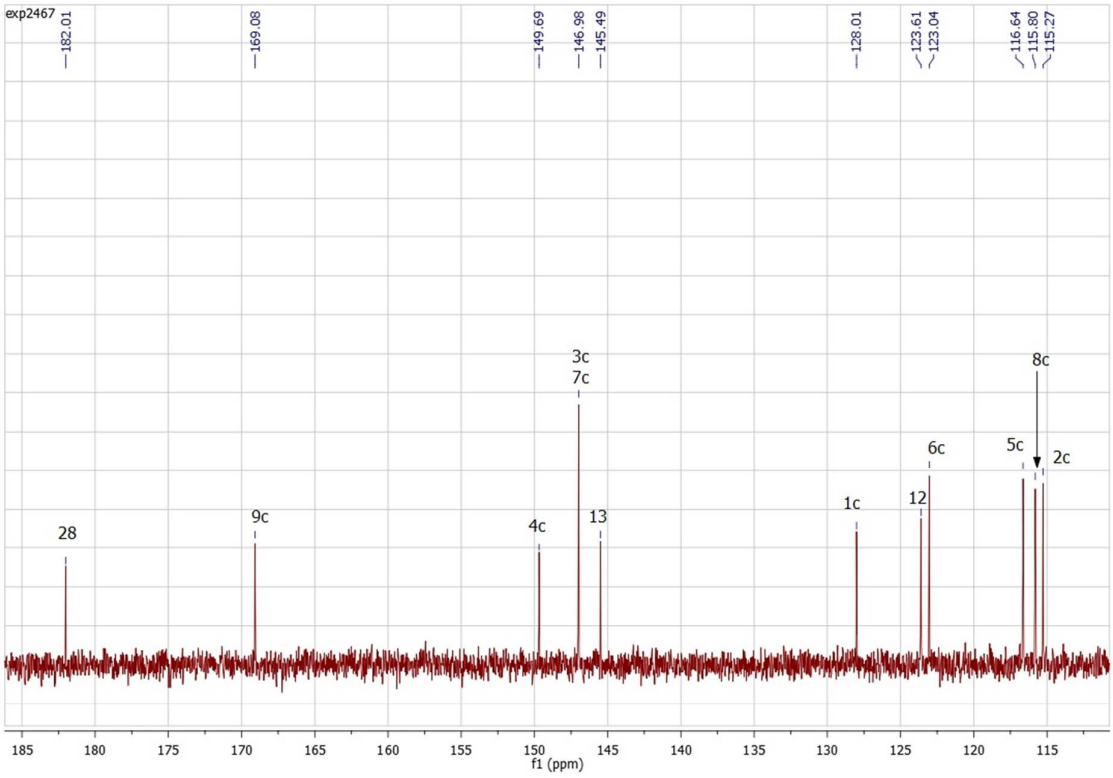

Figure S28. The 2nd part of the ^{13}C NMR spectrum of **7** (CD_3OD, 125 MHz).

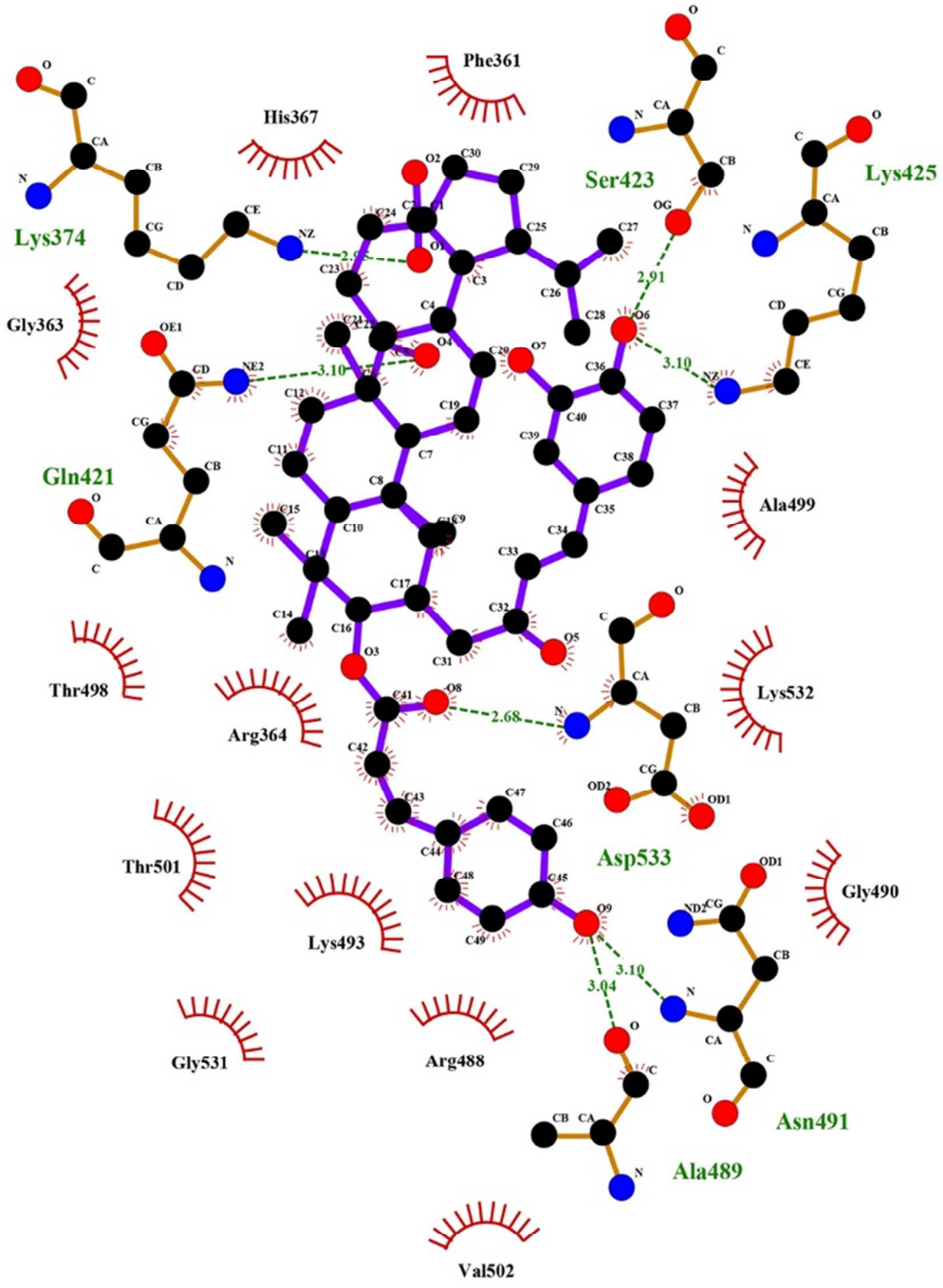

Figure S29. Two-dimensional representation of the best docking pose for compound **1** inside the topoisomerase I binding pocket.

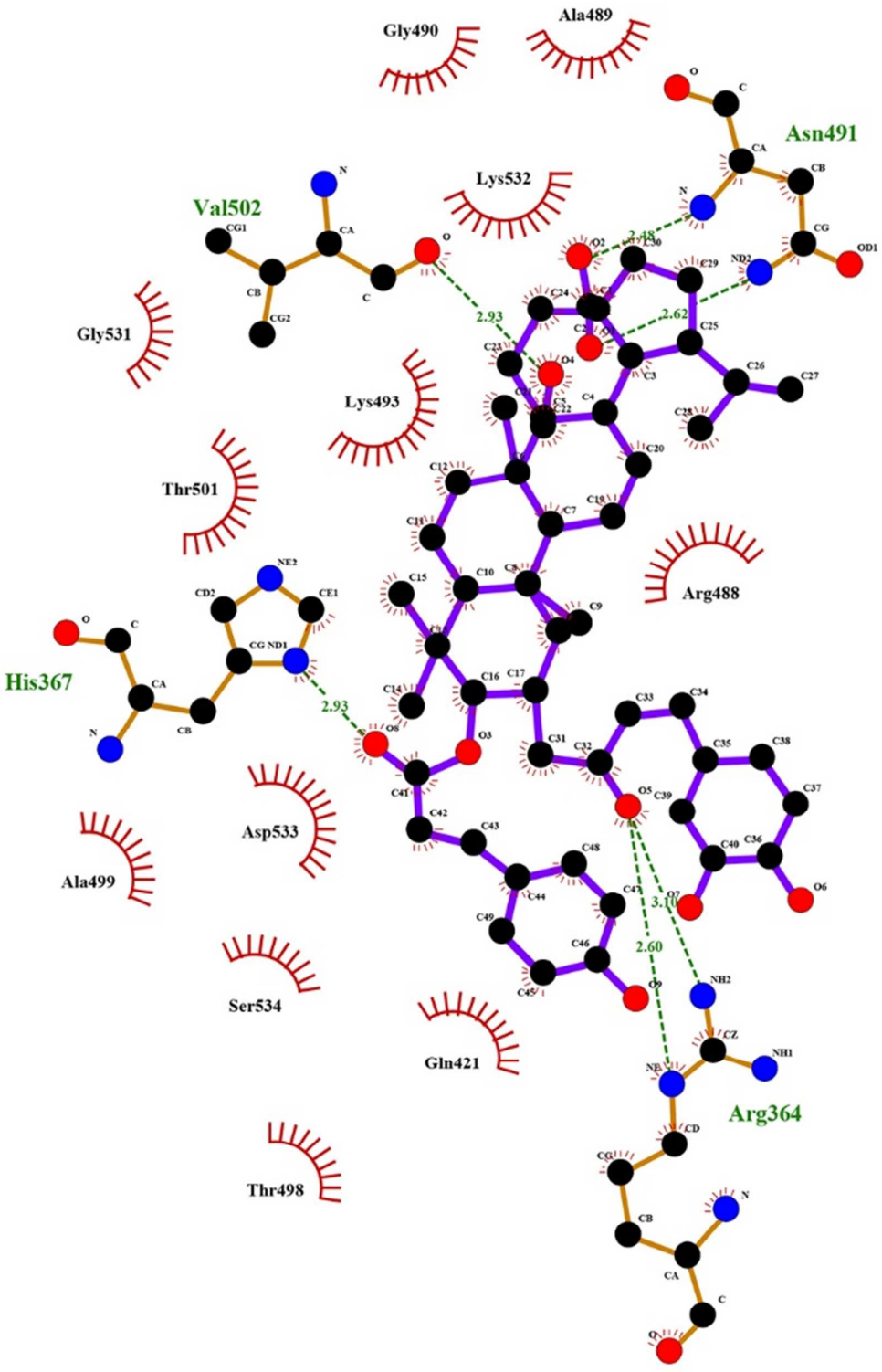

Figure S30. Two-dimensional representation of the best docking pose for compound **2** inside the topoisomerase I binding pocket.

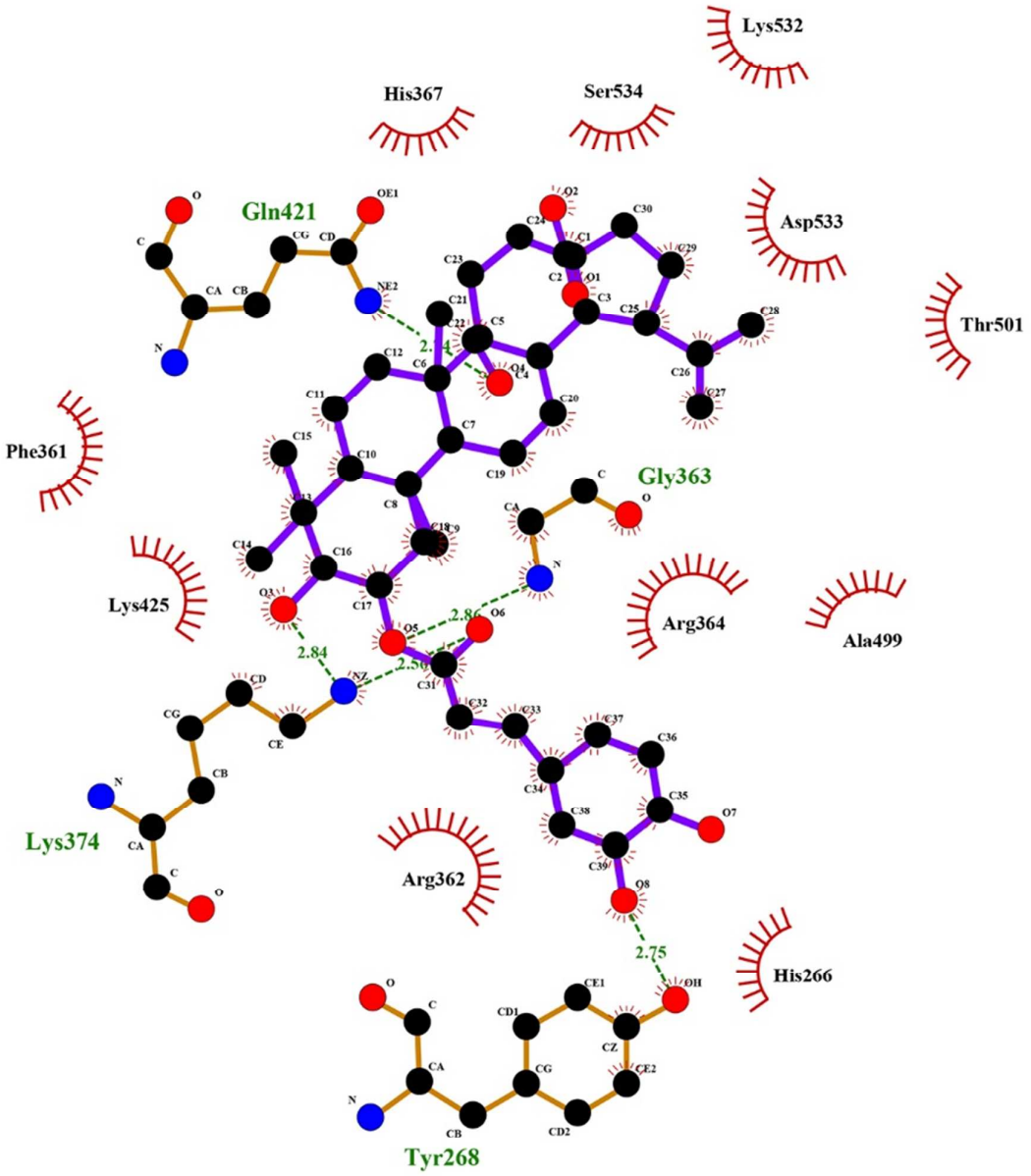

Figure S31. Two-dimensional representation of the best docking pose for compound **3** inside the topoisomerase I binding pocket.

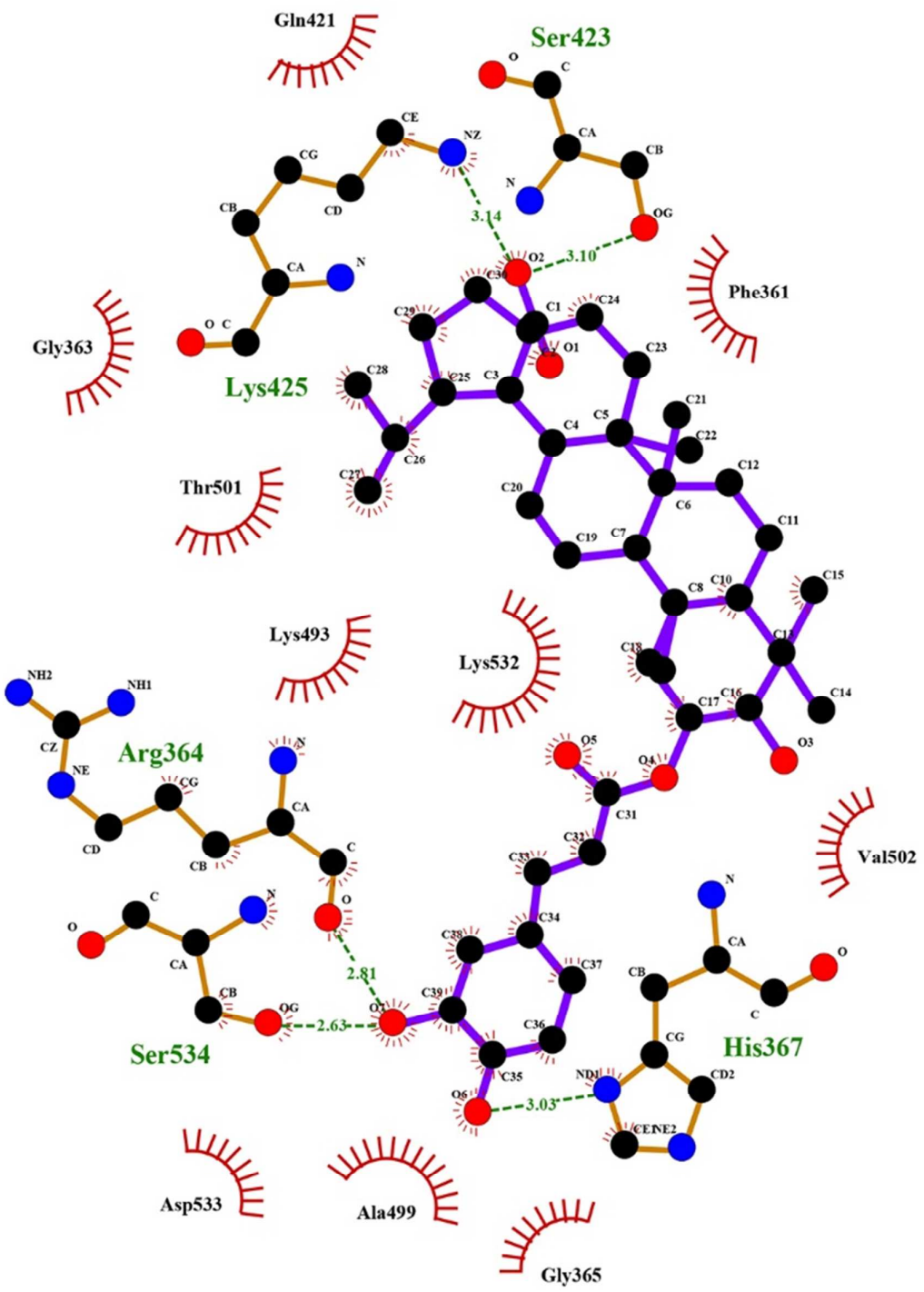

Figure S32. Two-dimensional representation of the best docking pose for compound **4** inside the topoisomerase I binding pocket.

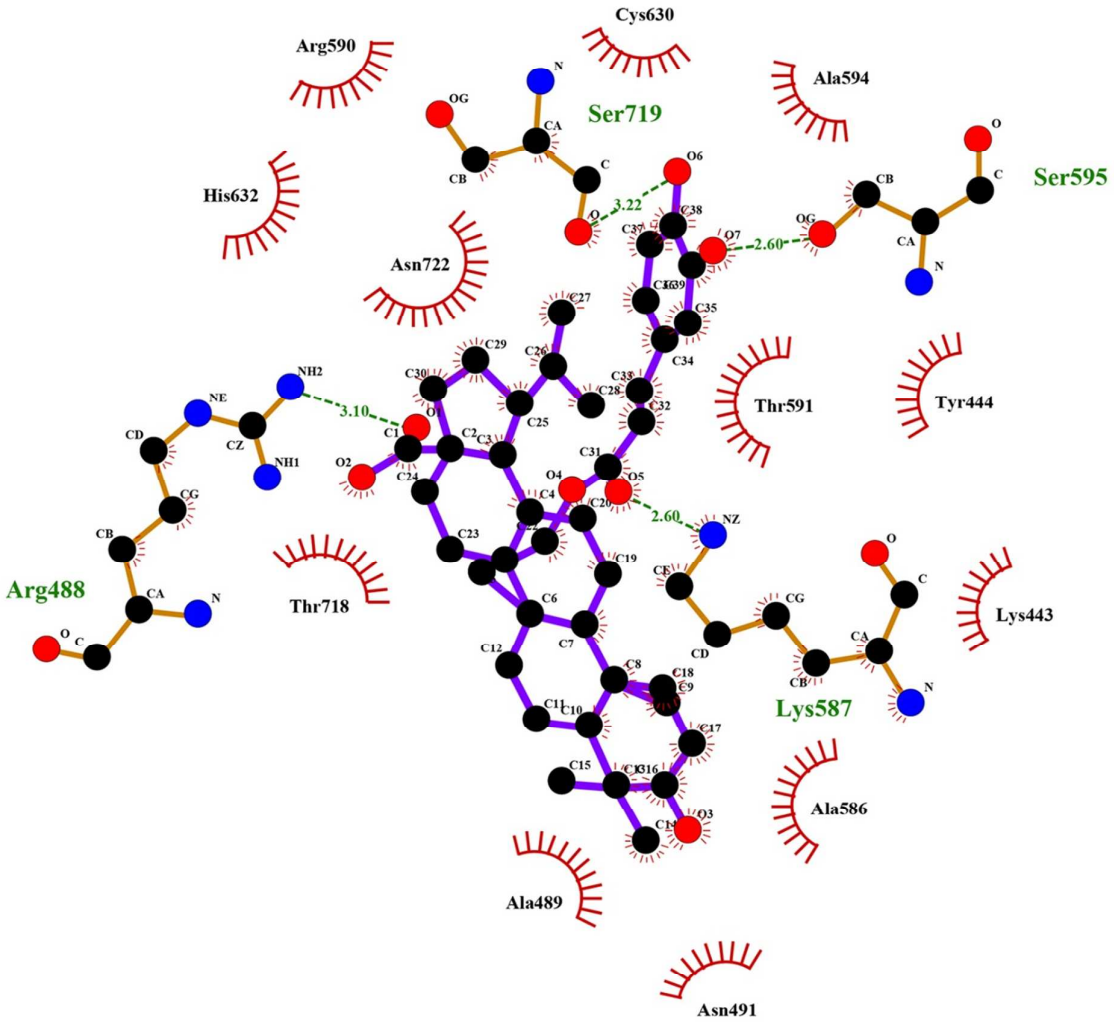

Figure S33. Two-dimensional representation of the best docking pose for compound **6** inside the topoisomerase I binding pocket.

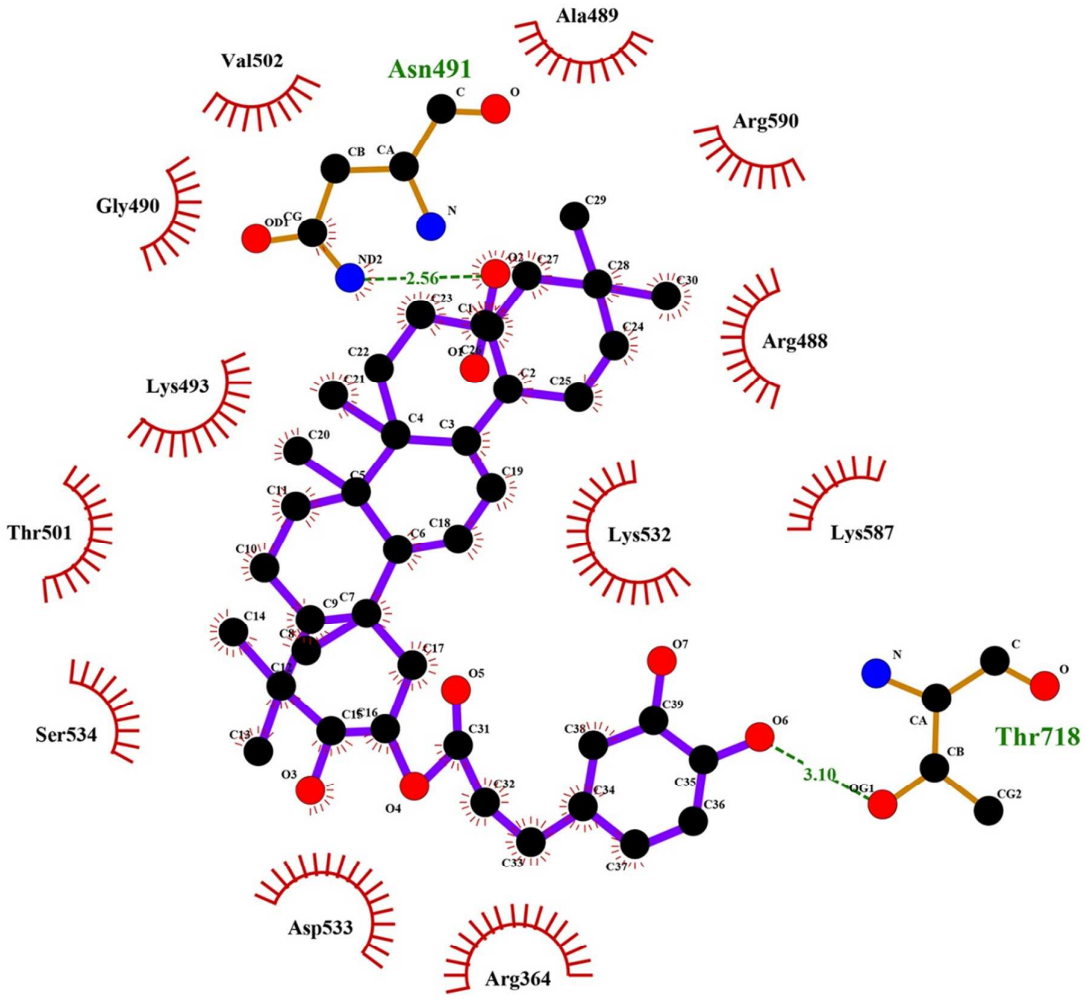

Figure S34. Two-dimensional representation of the best docking pose for compound **7** inside the topoisomerase I binding pocket.

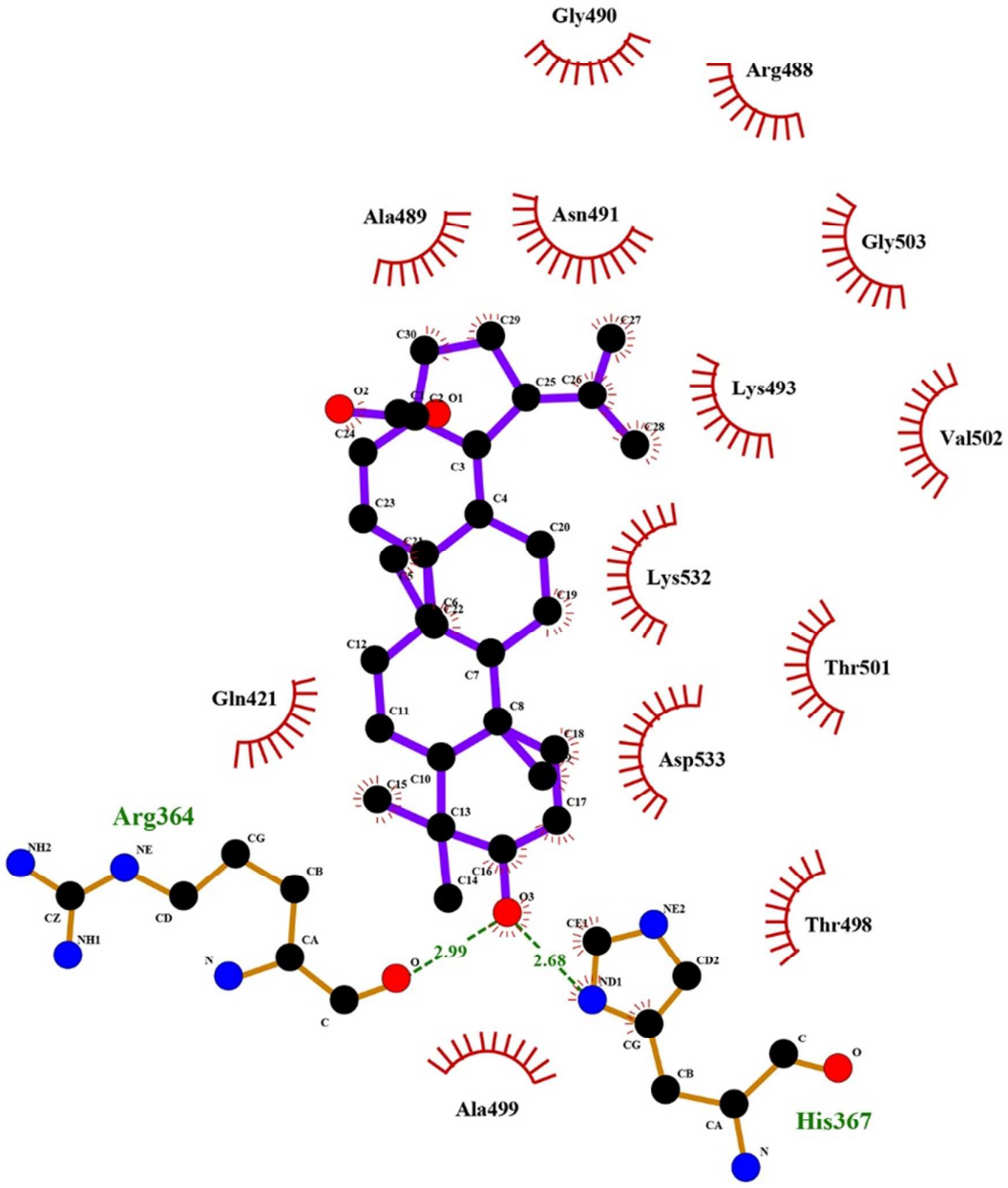

Figure S35. Two-dimensional representation of the best docking pose for betulinic acid inside the topoisomerase I binding pocket.

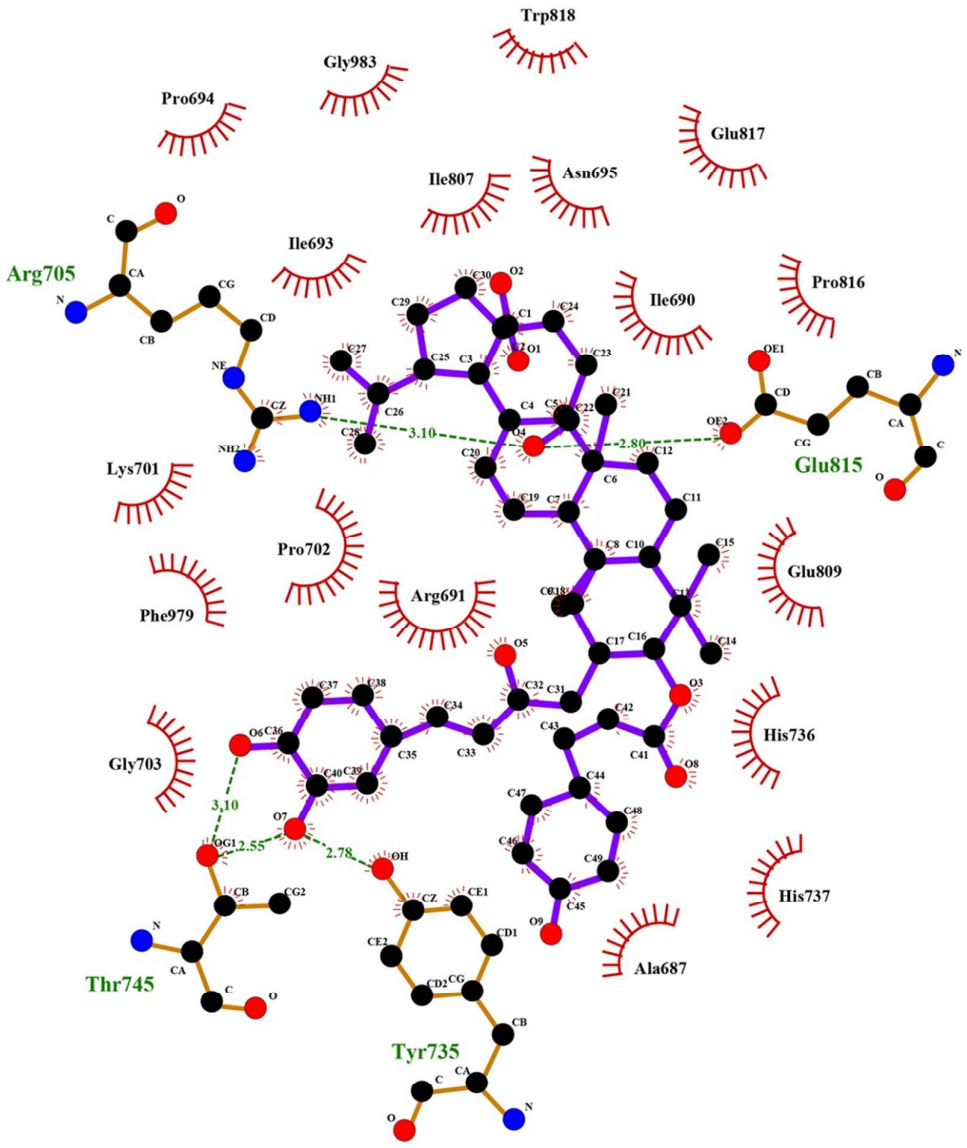

Figure S36. Two-dimensional representation of the best docking pose for compound **1** inside the topoisomerase IIα binding pocket.

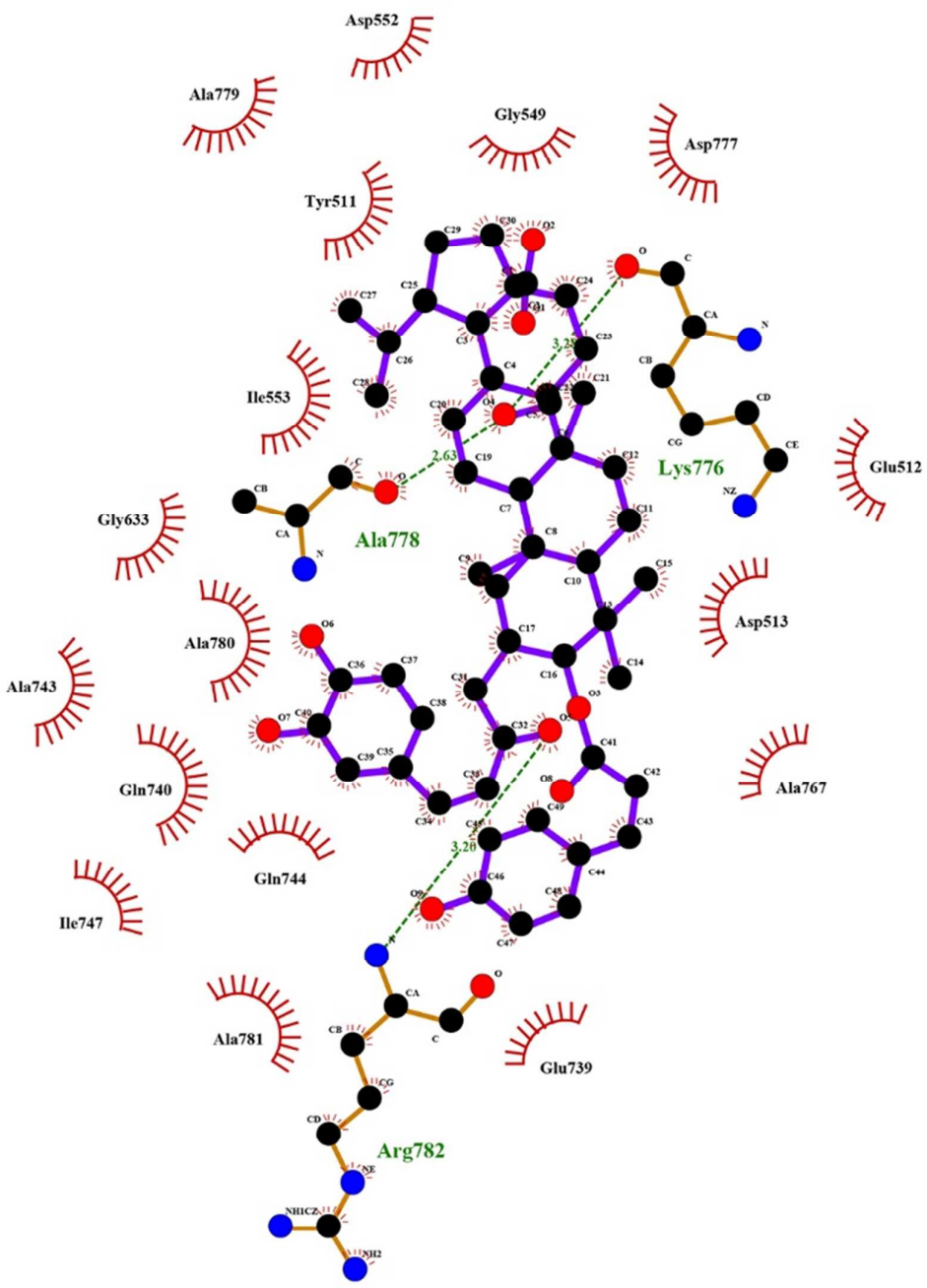

Figure S37. Two-dimensional representation of the best docking pose for compound **2** inside the topoisomerase IIα binding pocket.

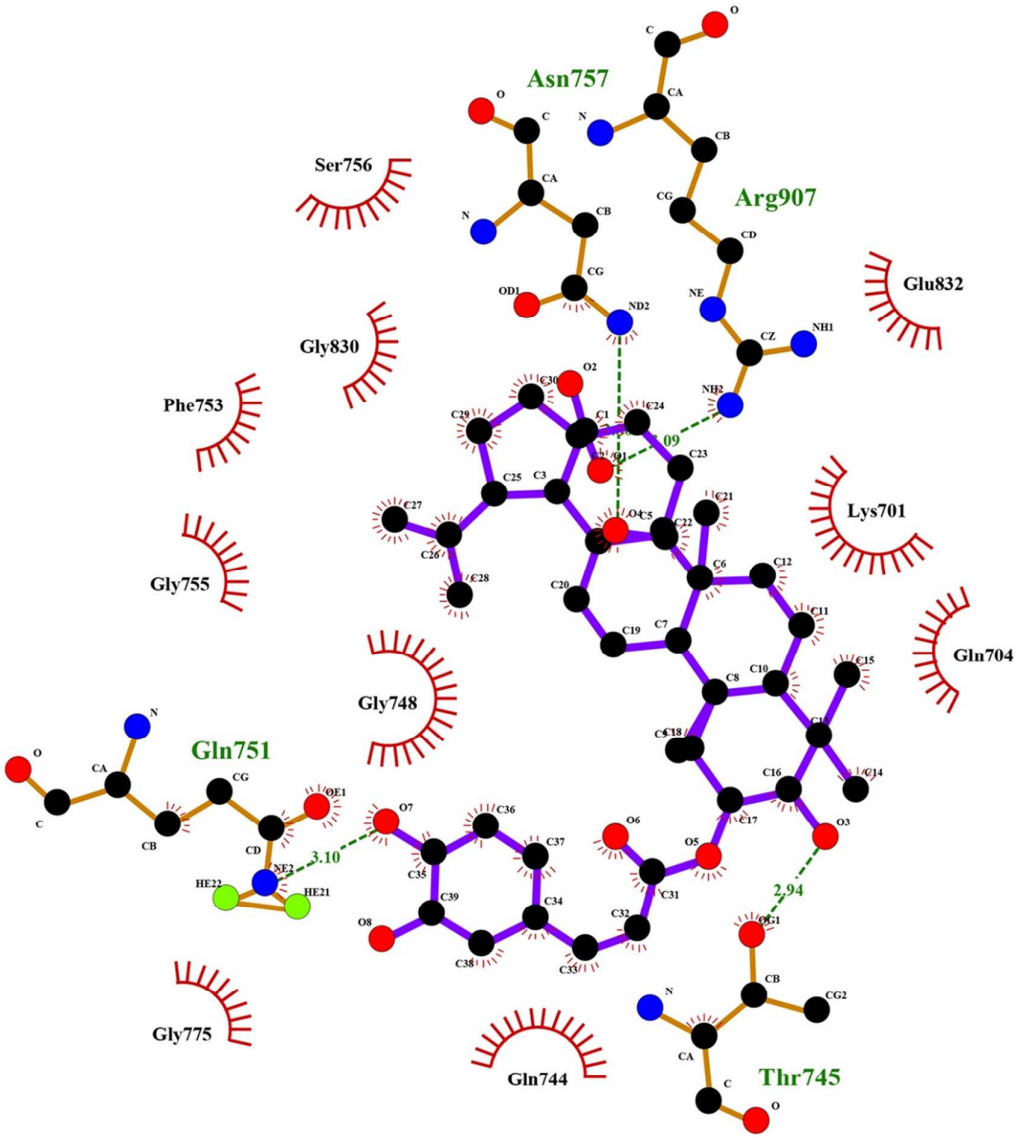

Figure S38. Two-dimensional representation of the best docking pose for compound **3** inside the topoisomerase IIα binding pocket.

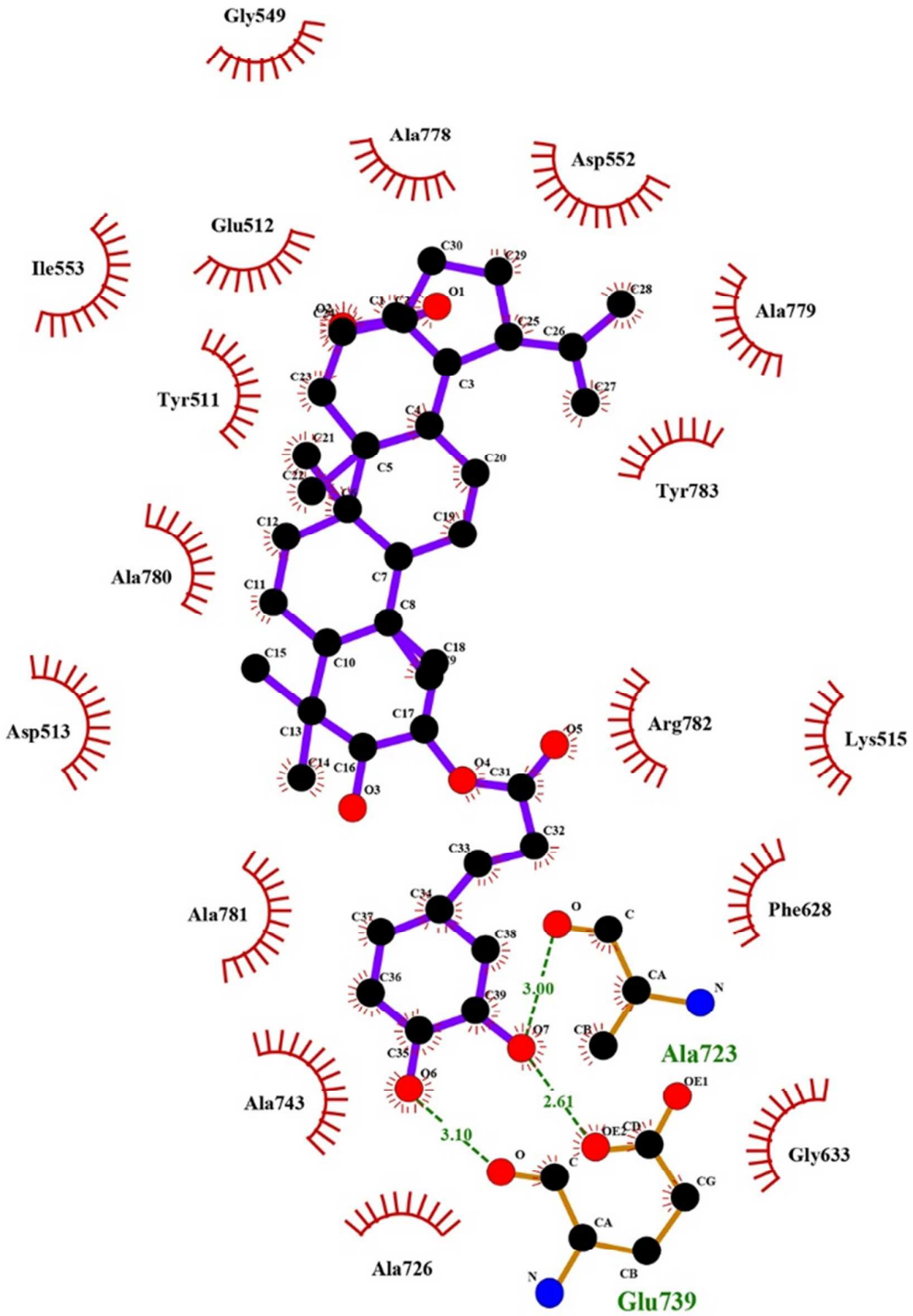

Figure S39. Two-dimensional representation of the best docking pose for compound **4** inside the topoisomerase IIα binding pocket.

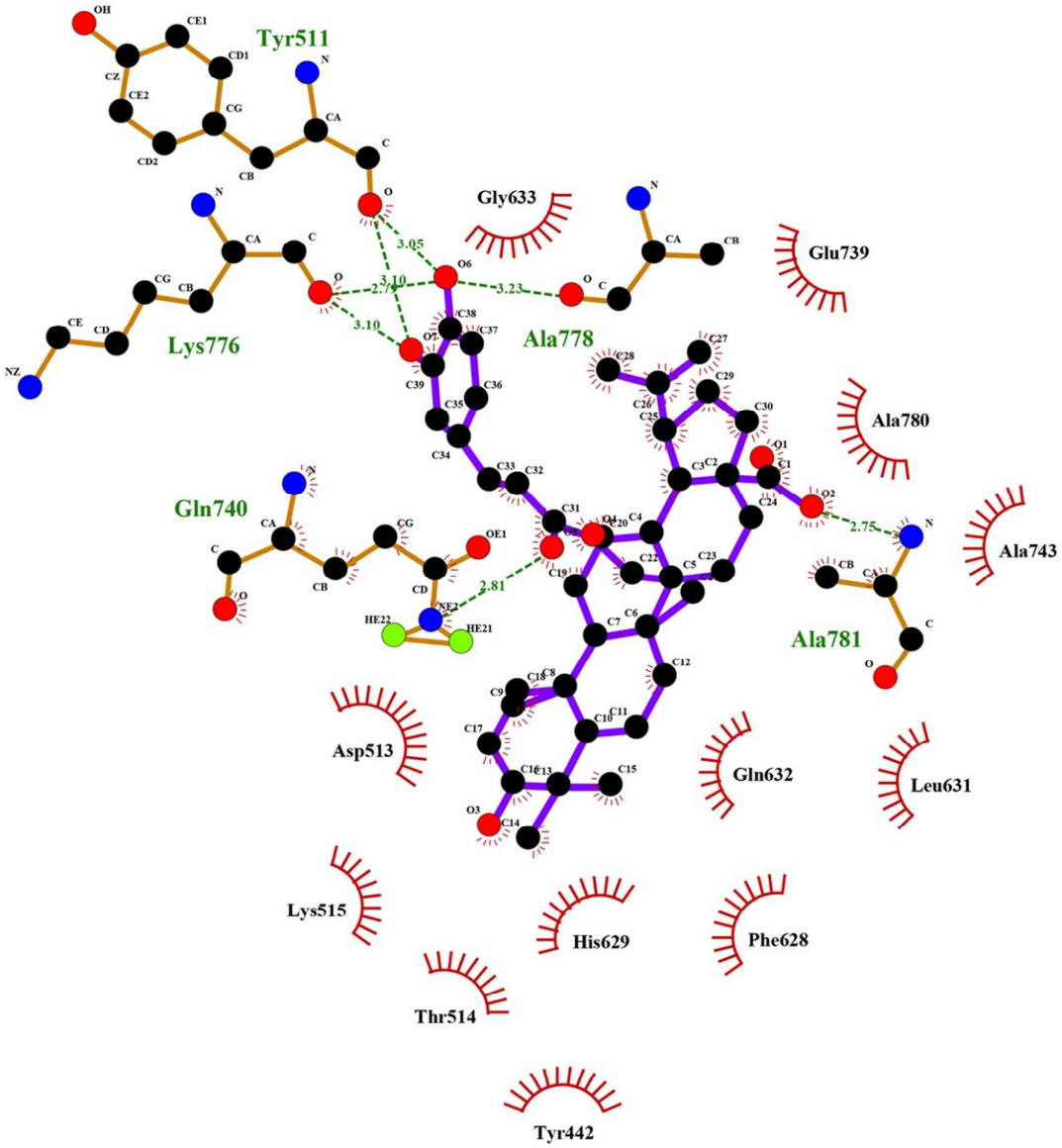

Figure S40. Two-dimensional representation of the best docking pose for compound **6** inside the topoisomerase IIα binding pocket.

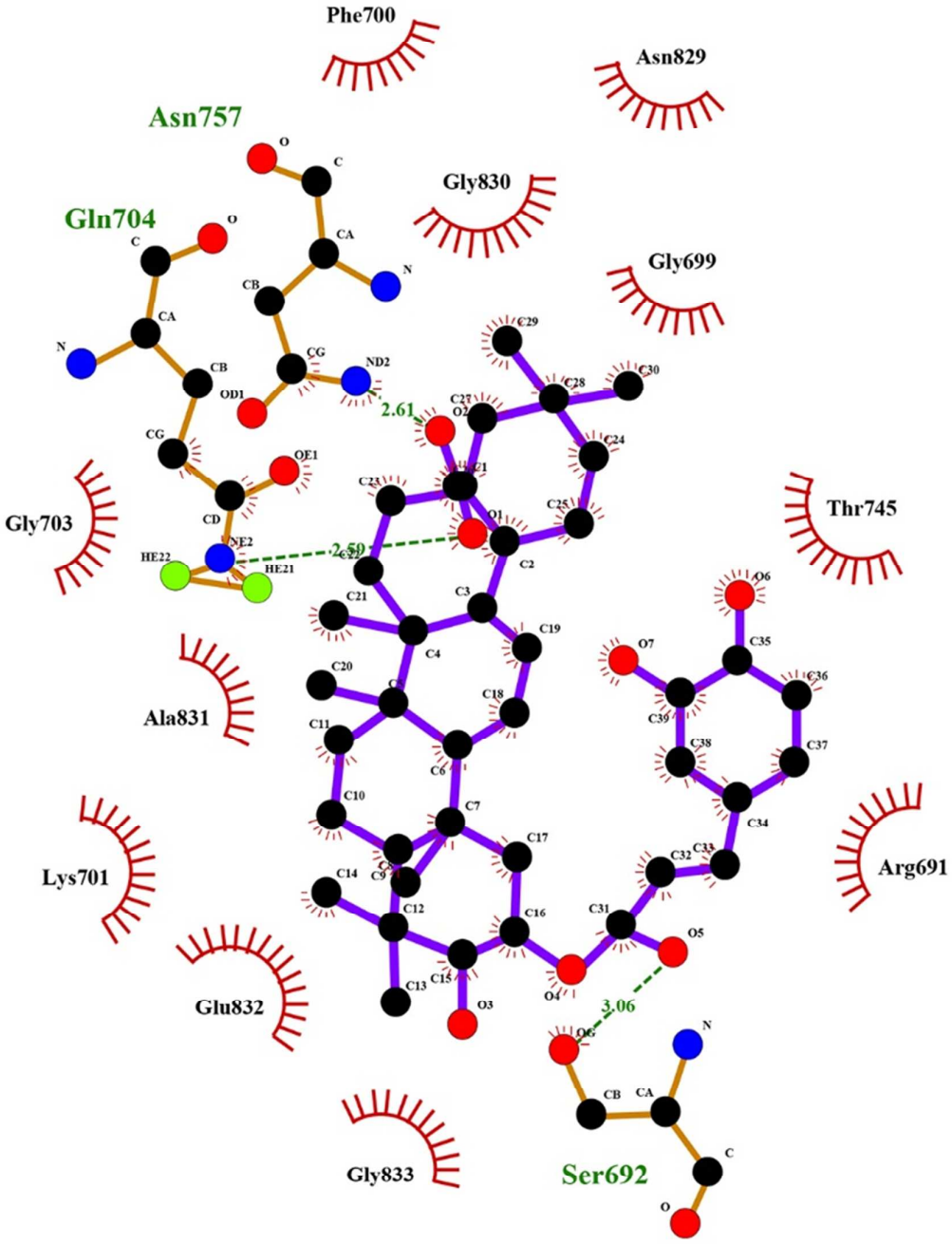

Figure S41. Two-dimensional representation of the best docking pose for compound **7** inside the topoisomerase IIα binding pocket.

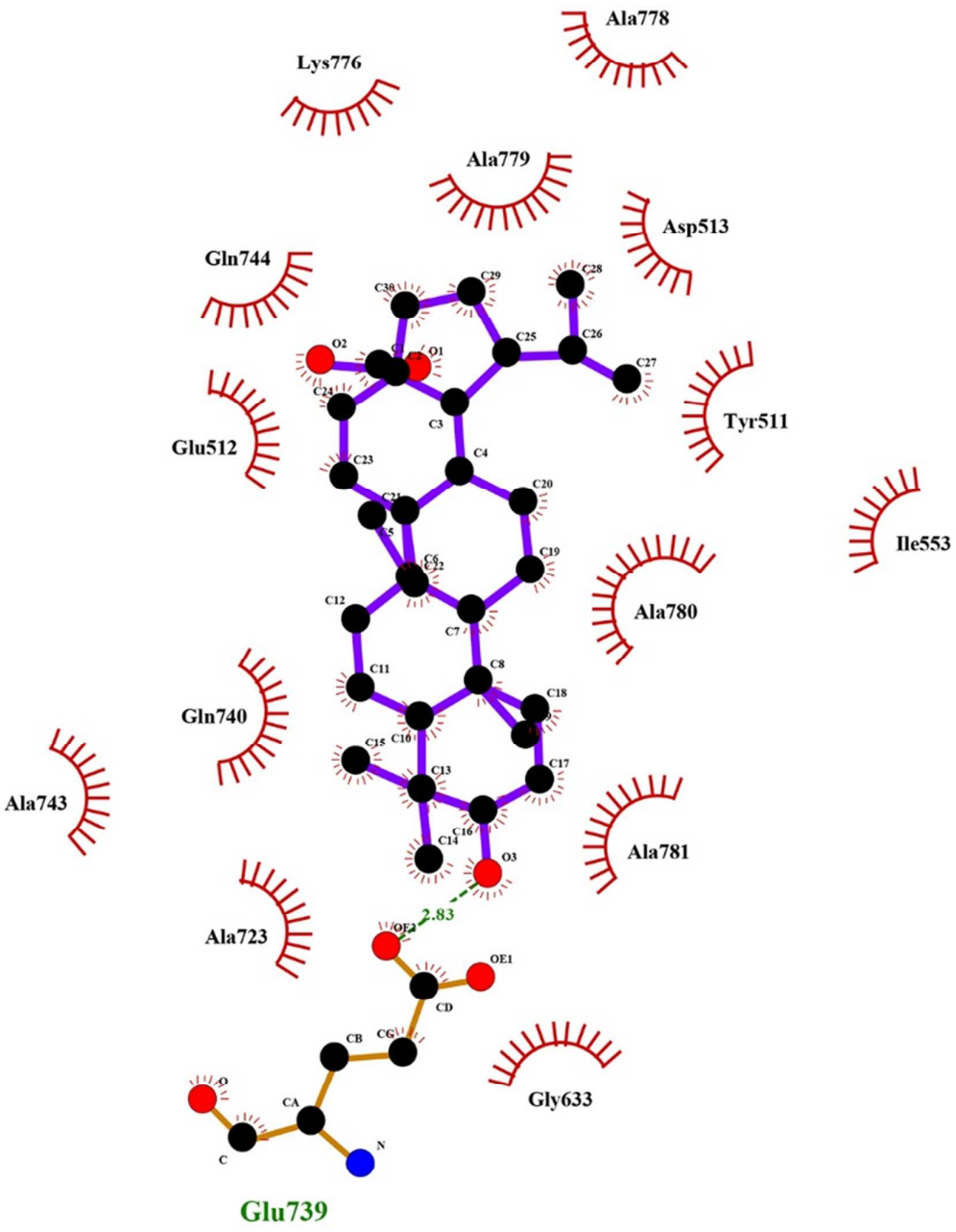

Figure S42. Two-dimensional representation of the best docking pose for betulinic acid inside the topoisomerase IIα binding pocket.

Table S1. ^{1}H and ^{13}C NMR Data of Compounds 4 and 5 Recorded in CD_3OD (500 MHz for ^{1}H and 125 MHz for ^{13}C)

position	4		5	
	δC	δH	δC	δH
1	45.6	0.95 m, 2.10 dd (12.5;4.5)[a]	40.3	0.98 m, 1.72 m
2	74.2	5.05 ddd (11.0;10.0;4.5)	28.2	1.58 m, 1.62 m
3	81.3	3.22 d (10.0)	79.6	3.14 dd (11.0;5.0)
4	41.2	-	40.1	-
5	56.9	0.89 m	57.2	0.76 m
6	19.7	1.48 m, 1.57 m	19.6	1.44 m, 1.55 m
7	35.6	1.42 m, 1.46 m	36.9	1.46 m, 1.56 m
8	42.2	-	42.9	-
9	52.0	1.42 m	53.6	1.37 m
10	39.9	-	38.8	-
11	22.4	1.30 m, 1.40 m	22.4	1.26 m, 1.51 m
12	26.9	1.07 m, 1.72 m	26.9	0.95 m, 1.77 m
13	39.7	2.34 bt (12.5)	40.6	2.52 td (12.5;2.5)
14	43.8	-	47.0	-
15	31.0	1.17 m, 1.55 m	25.4	1.45 m, 1.85 m
16	33.6	1.40 m, 2.24 d (12.5)	34.0	1.29 m, 2.27 bd (13.0)
17	57.7	-	57.4	-
18	50.6	1.62 m	50.9	1.78 m
19	48.6[b]	3.02 m	48.5[b]	3.06 m
20	152.2	-	152.0	-
21	31.9	1.36 m, 1.95 m	31.8	1.41 m, 1.96 m
22	38.4	1.45 m, 1.90 m	38.1	1.44 m, 1.94 m
23	29.2	1.04 s	28.7	0.93 s
24	17.3	0.86 s	16.3	0.75 s
25	17.9	1.01 s	17.3	0.90 s
26	16.8	0.98 s	17.3	1.03 s
27	15.2	1.02 s	64.5	4.52 d (13.0), 4.68 d (13.0)
28	180.5	-	180.2	-
29	110.3	4.57 bs, 4.70 bs	110.5	4.62 bs, 4.74 bs
30	19.7	1.70 s	19.8	1.73 s
1c[c]	128.0	-	127.8	-
2c	115.3	7.04 d (2.0)	115.3	7.04 d (2.0)
3c	147.0	-	147.0	-
4c	149.6	-	149.9	-
5c	116.6	6.78 d (8.0)	116.7	6.79 d (8.5)
6c	123.0	6.94 dd (8.0;2.0)	122.8	6.95 dd (8.5;2.0)
7c	146.7	7.55 d (16.0)	147.2	7.54 d (16.0)
8c	116.0	6.28 d (16.0)	115.4	6.26 d (16.0)
9c	169.5	-	169.6	-

[a] *J* values are given in parenthesis. [b] Signal overlapped with the signal of solvent; value obtained from the HSQC spectrum. [c] "c" – caffeoyl

Table S2. Score Values (kcal/mol) for All Studied Compounds 1–4, 6, 7 for Topoisomerase I Activity

compound	MolDock Score	RerankScore	PoseEnergy	LE1	LE3	HBond
1	-203.052	-101.365	-203,052	-350.009	-174.767	-166.501
2	-180.151	-426.024	-180,151	-310.606	-173.452	-117.429
3	-162.799	-125.187	-162,799	-346.382	-266.356	-142.554
4	-171.217	-123.581	-171,217	-372.212	-268.655	-166.678
6	-181.419	-976.498	-181,419	-394.389	-212.282	-99.534
7	-166.217	-121.19	-166,217	-361.342	-263.456	-71.593
BA[a]	-125.511	-901.372	-125,511	-380.336	-253.143	-53.574

[a] BA- betulinic acid

Table S3. Identified Hydrogen Bonds Between Studied Ligands and Amino Acids from Topoisomerase I Active Site

compound	identified hydrogen bonds between ligand and amino acids from the active site
1	Gly421(3.10 Å), Lys374(2.85 Å), Ser423(2.91 Å), Lys425(3.10 Å), Asp533(2.68 Å), Ala489(3.04 Å), Asn491(3.10 Å)
2	Asn491(2.48 Å and 2.62 Å), Val502(2.93 Å), His367(2.93 Å), Arg364(2.60 Å and 3.10 Å)
3	Gln421 (2.74 Å), Tyr268 (2.75 Å), Gly363(2.86 Å), Lys374(2.56 Å and 2.84 Å)
4	Ser423(3.10 Å and 3.14 Å), Ser535(2.63 Å and 2.81 Å), His367(3.03 Å)
6	Ser719(3.22 Å), Ser595(2.60 Å), Arg488(3.10 Å), Lys587(2.60 Å)
7	Asn491(2.56 Å), Thr781(3.10 Å)
BA[a]	Arg364(2.99 Å), His367(2.88 Å)

[a] BA- betulinic acid

Table S4. Score Values (kcal/mol) for All Studied Compounds 1–4, 6 and 7 for the Topoisomerase IIα Activity

compound	MolDock Score	RerankScore	PoseEnergy	LE1	LE3	HBond
1	-217.744	-384.338	-206.78	-375.421	-662.651	-145.673
2	-210.952	-592.479	-204.404	-363.714	-102.152	-156.712
3	-174.257	-118.666	-181.424	-370.759	-252.482	-180.17
4	-182.662	-137.408	-187.287	-397.091	-298.712	-114.963
6	-174.029	-664.934	-178.74	-378.324	-144.551	-168.656
7	-180.373	-139.764	-185.266	-392.115	-303.834	-126.776
BA[a]	-129.316	-608.735	-126.593	-391.868	-184.465	-5

[a] BA- betulinic acid

Table S5. Identified Hydrogen Bonds Between Studied Ligands and Amino Acids from the Topoisomerase IIα Active Site

compound	identified hydrogen bonds between ligand and amino acids from active site
1	Arg705(3.10 Å), Glu815(2.80 Å), Thr754(2.55 Å and 3.10 Å), Tyr735(2.78 Å)
2	Ala778(2.63 Å), Lys776(3.28 Å), Arg782(3.20 Å)
3	Asn757(2.86 Å), Arg907(3.09 Å), Gln751(3.10 Å), Thr(2.94 Å)
4	Ala723(3.00 Å), Glu739(2.61 Å and 3.10 Å)
6	Tyr511(3.05 Å and 3.10 Å), Lys776(2.79 Å and 3.10 Å), Ala778(3.23 Å), Gln740(2.81 Å), Ala781(2.75 Å)
7	Asn757(2.61 Å), Gln704(2.59 Å), Ser692(3.06 Å)
BA[a]	Glu739(2.83 Å)

[a] BA- betulinic acid

Table S6. Gradient Elution Program Used for the Silica Gel CC Separation of *A. viridis* ssp. *viridis* Extract

V (mL)	CH_2Cl_2	CH_3OH	fr. no.
200	100	0	-
800	90	10	-
400	85	15	0-13
400	80	20	14-34
600	75	25	35-63
700	70	30	64-100
600	65	35	101-132
400	60	40	133-155
600	50	50	156-189
400	40	60	190-211
800	0	100	212-240