

Supporting Information

Binding Free Energy Calculation Based on the Fragment Molecular Orbital Method and Its Application in Designing Novel SHP-2 Allosteric Inhibitors

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Table S1. Results for ranking with different affinity prediction methods in Schrödinger FEP+ benchmark set.

Protein	FMO					FMOScore					FEP+				
	N	R	ρ	τ	RMSE	N	R	ρ	τ	RMSE	N	R	ρ	τ	RMSE
CDK8	32	0.78 ^{0.71} _{0.85}	0.82 ^{0.73} _{0.89}	0.64 ^{0.52} _{0.73}	0.93 ^{0.64} _{1.26}	32	0.81 ^{0.72} _{0.88}	0.84 ^{0.75} _{0.92}	0.67 ^{0.56} _{0.78}	0.88 ^{0.63} _{1.15}	32	0.64 ^{0.44} _{0.81}	0.67 ^{0.46} _{0.84}	0.53 ^{0.36} _{0.69}	1.11 ^{0.66} _{1.55}
c-Met	24	0.83 ^{0.72} _{0.91}	0.79 ^{0.60} _{0.92}	0.65 ^{0.47} _{0.80}	1.04 ^{0.71} _{1.37}	24	0.90 ^{0.82} _{0.96}	0.90 ^{0.79} _{0.97}	0.77 ^{0.64} _{0.88}	0.78 ^{0.43} _{1.09}	24	0.91 ^{0.85} _{0.95}	0.88 ^{0.77} _{0.95}	0.75 ^{0.63} _{0.85}	0.76 ^{0.57} _{0.97}
Eg5	28	0.68 ^{0.48} _{0.83}	0.59 ^{0.31} _{0.81}	0.56 ^{0.22} _{0.65}	0.69 ^{0.47} _{0.91}	28	0.79 ^{0.66} _{0.88}	0.74 ^{0.54} _{0.89}	0.60 ^{0.41} _{0.76}	0.58 ^{0.41} _{0.76}	28	0.73 ^{0.57} _{0.86}	0.71 ^{0.52} _{0.86}	0.57 ^{0.40} _{0.73}	0.68 ^{0.47} _{0.92}
HIF-2 α	42	0.31 ^{0.05} _{0.54}	0.23 ^{-0.05} _{0.49}	0.16 ^{-0.03} _{0.36}	1.12 ^{0.78} _{1.46}	42	0.43 ^{0.13} _{0.67}	0.28 ^{0.01} _{0.53}	0.21 ^{0.01} _{0.40}	1.07 ^{0.77} _{1.38}	42	0.57 ^{0.23} _{0.80}	0.54 ^{0.29} _{0.74}	0.41 ^{0.22} _{0.58}	0.98 ^{0.62} _{1.34}
PFKFB3	40	0.86 ^{0.80} _{0.91}	0.84 ^{0.75} _{0.90}	0.77 ^{0.56} _{0.76}	0.56 ^{0.42} _{0.69}	40	0.90 ^{0.85} _{0.93}	0.89 ^{0.81} _{0.94}	0.73 ^{0.63} _{0.81}	0.49 ^{0.37} _{0.63}	40	0.81 ^{0.73} _{0.88}	0.81 ^{0.71} _{0.89}	0.64 ^{0.53} _{0.74}	0.64 ^{0.47} _{0.80}
SHP-2	26	0.57 ^{0.34} _{0.74}	0.59 ^{0.33} _{0.79}	0.45 ^{0.26} _{0.63}	1.05 ^{0.76} _{1.39}	26	0.80 ^{0.70} _{0.88}	0.75 ^{0.56} _{0.88}	0.56 ^{0.39} _{0.70}	0.76 ^{0.50} _{1.02}	26	0.73 ^{0.58} _{0.85}	0.71 ^{0.50} _{0.87}	0.57 ^{0.39} _{0.73}	0.88 ^{0.64} _{1.15}
SYK	39	0.43 ^{0.27} _{0.57}	0.43 ^{0.21} _{0.63}	0.31 ^{0.15} _{0.27}	0.77 ^{0.57} _{0.96}	39	0.76 ^{0.62} _{0.87}	0.76 ^{0.61} _{0.88}	0.61 ^{0.46} _{0.74}	0.54 ^{0.37} _{0.72}	39	0.47 ^{0.18} _{0.70}	0.40 ^{0.16} _{0.60}	0.28 ^{0.11} _{0.43}	0.75 ^{0.56} _{0.94}
TNKS2	27	0.36 ^{0.05} _{0.58}	0.21 ^{-0.19} _{0.54}	0.10 ^{-0.19} _{0.37}	1.02 ^{0.65} _{1.35}	27	0.62 ^{0.29} _{0.85}	0.50 ^{0.17} _{0.77}	0.39 ^{0.12} _{0.63}	0.86 ^{0.51} _{1.19}	27	0.46 ^{0.16} _{0.70}	0.43 ^{0.10} _{0.69}	0.32 ^{0.07} _{0.54}	0.98 ^{0.66} _{1.29}
Total	258	0.62 ^{0.55} _{0.68}	0.64 ^{0.57} _{0.70}	0.47 ^{0.41} _{0.52}	1.14 ^{1.02} _{1.26}	258	0.87 ^{0.84} _{0.89}	0.87 ^{0.84} _{0.89}	0.69 ^{0.65} _{0.72}	0.71 ^{0.62} _{0.80}	258	0.78 ^{0.74} _{0.83}	0.77 ^{0.71} _{0.81}	0.58 ^{0.53} _{0.63}	0.89 ^{0.77} _{1.00}
<hr/>															
Protein	MM/GBSA					MM/PBSA					Vina				
	N	R	ρ	τ	RMSE	N	R	ρ	τ	RMSE	N	R	ρ	τ	RMSE
CDK8	32	0.30 ^{0.03} _{0.68}	0.45 ^{0.16} _{0.71}	0.33 ^{0.11} _{0.53}	1.42 ^{0.93} _{2.09}	32	0.02 ^{-0.34} _{0.38}	-0.04 ^{-0.34} _{0.38}	-0.02 ^{-0.27} _{0.24}	1.50 ^{1.02} _{2.03}	32	0.58 ^{0.35} _{0.79}	0.61 ^{0.36} _{0.80}	0.48 ^{0.27} _{0.66}	1.17 ^{0.73} _{1.70}
c-Met	24	0.68 ^{0.48} _{0.83}	0.72 ^{0.47} _{0.89}	0.59 ^{0.39} _{0.77}	1.43 ^{0.89} _{2.02}	24	0.23 ^{-0.16} _{0.56}	0.15 ^{-0.25} _{0.51}	0.10 ^{-0.19} _{0.39}	1.83 ^{1.26} _{2.46}	24	-0.31 ^{-0.56} _{0.05}	-0.37 ^{-0.62} _{0.07}	-0.22 ^{-0.44} _{0.0}	1.80 ^{0.26} _{2.32}
Eg5	28	0.43 ^{0.11} _{0.69}	0.41 ^{0.08} _{0.70}	0.30 ^{0.04} _{0.53}	0.88 ^{0.61} _{1.17}	28	0.02 ^{-0.27} _{0.31}	0.10 ^{-0.25} _{0.43}	0.05 ^{-0.20} _{0.29}	0.96 ^{0.65} _{1.27}	28	-0.44 ^{-0.65} _{0.22}	-0.47 ^{-0.69} _{0.20}	-0.31 ^{-0.50} _{0.10}	0.84 ^{0.51} _{1.15}
HIF-2 α	42	0.19 ^{-0.03} _{0.43}	0.23 ^{0.0003} _{0.45}	0.15 ^{-0.005} _{0.30}	1.15 ^{0.82} _{1.52}	42	0.26 ^{0.001} _{0.51}	0.20 ^{0.06} _{0.45}	0.15 ^{0.04} _{0.33}	1.14 ^{0.80} _{1.49}	42	0.28 ^{0.0003} _{0.54}	0.50 ^{0.26} _{0.70}	0.39 ^{0.21} _{0.56}	1.13 ^{0.76} _{1.50}
PFKFB3	40	0.48 ^{0.23} _{0.70}	0.45 ^{0.19} _{0.69}	0.33 ^{0.14} _{0.51}	0.99 ^{0.73} _{1.28}	40	0.26 ^{0.01} _{0.49}	0.28 ^{0.005} _{0.54}	0.21 ^{0.01} _{0.41}	1.10 ^{0.87} _{1.34}	40	0.35 ^{0.13} _{0.54}	0.33 ^{0.10} _{0.54}	0.22 ^{0.05} _{0.38}	1.06 ^{0.84} _{1.28}
SHP-2	26	0.34 ^{0.08} _{0.64}	0.35 ^{0.02} _{0.67}	0.31 ^{0.08} _{0.55}	1.24 ^{0.82} _{1.75}	26	0.50 ^{0.19} _{0.77}	0.48 ^{0.18} _{0.74}	0.38 ^{0.15} _{0.59}	1.19 ^{0.70} _{1.73}	26	0.37 ^{0.04} _{0.67}	0.35 ^{0.04} _{0.64}	0.35 ^{0.01} _{0.48}	1.17 ^{0.72} _{1.61}
SYK	39	0.50 ^{0.29} _{0.69}	0.47 ^{0.24} _{0.68}	0.36 ^{0.19} _{0.52}	0.74 ^{0.55} _{0.93}	39	0.18 ^{-0.12} _{0.43}	0.06 ^{-0.23} _{0.34}	0.04 ^{-0.16} _{0.24}	0.84 ^{0.61} _{1.06}	39	0.39 ^{0.21} _{0.56}	0.35 ^{0.14} _{0.54}	0.34 ^{0.09} _{0.37}	0.77 ^{0.55} _{0.99}
TNKS2	27	0.47 ^{0.19} _{0.69}	0.41 ^{0.13} _{0.65}	0.28 ^{0.07} _{0.48}	0.96 ^{0.63} _{1.27}	27	-0.21 ^{-0.48} _{0.07}	-0.11 ^{-0.43} _{0.20}	-0.09 ^{-0.31} _{0.12}	1.06 ^{0.68} _{1.36}	27	-0.06 ^{-0.35} _{0.25}	0.11 ^{0.22} _{0.44}	0.09 ^{-0.14} _{0.33}	1.10 ^{0.70} _{1.44}
Total	258	0.27 ^{0.18} _{0.36}	0.27 ^{0.17} _{0.26}	0.18 ^{0.12} _{0.25}	1.39 ^{1.25} _{1.54}	258	0.13 ^{0.03} _{0.23}	0.09 ^{0.01} _{0.19}	0.06 ^{0.01} _{0.19}	1.44 ^{1.30} _{1.57}	258	0.09 ^{0.008} _{0.18}	0.09 ^{0.00} _{0.18}	0.06 ^{0.00} _{0.12}	1.44 ^{1.30} _{1.57}

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Table S2. Linear coefficients of FMOSScore of 8 targets in Schrödinger FEP+ benchmark.

Target	ΔE^{int}	ΔG^{sol}	$\Delta E_{\text{lig}}^{\text{def}}$	constant
CDK8	0.05066	-0.04087	0.02395	-3.05111
c-Met	0.04297	0.03001	0.04486	-3.85653
EG5	0.04591	-0.00677	0.01301	-6.73679
HIF-2 α	0.02229	0.01377	0.07526	-8.75932
PFKFB3	0.05389	-0.00547	0.03022	-3.05507
SHP2	0.02002	-0.02125	0.04421	-2.78159
SYK	0.01577	-0.0056	0.04735	-9.47309
TNKS2	0.08894	-0.03104	0.05194	-1.31775

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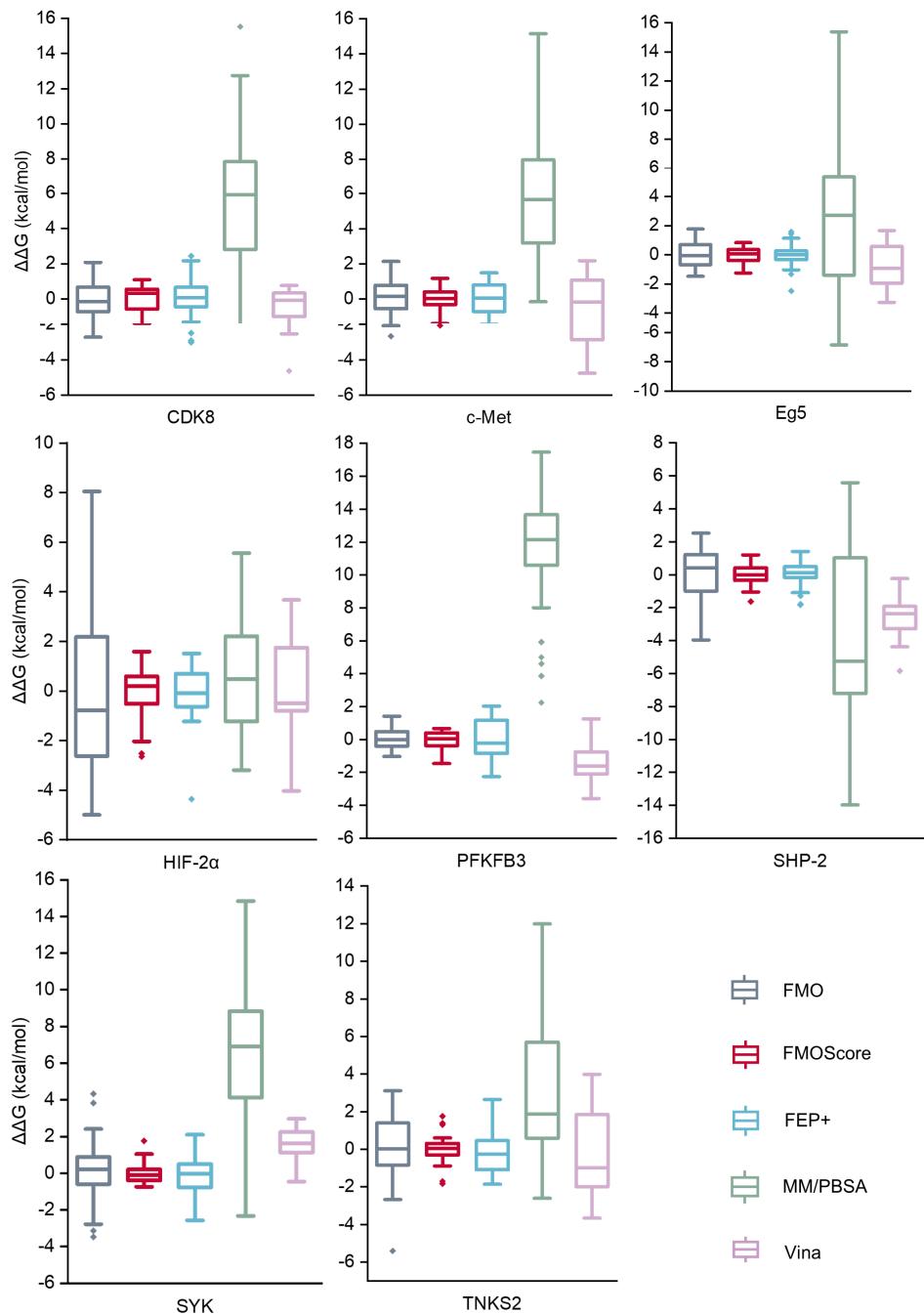


Figure S1. Box-plot diagrams of the error for pairwise relative affinities $|\Delta G_{\text{pred}} - \Delta G_{\text{exp}}|$.

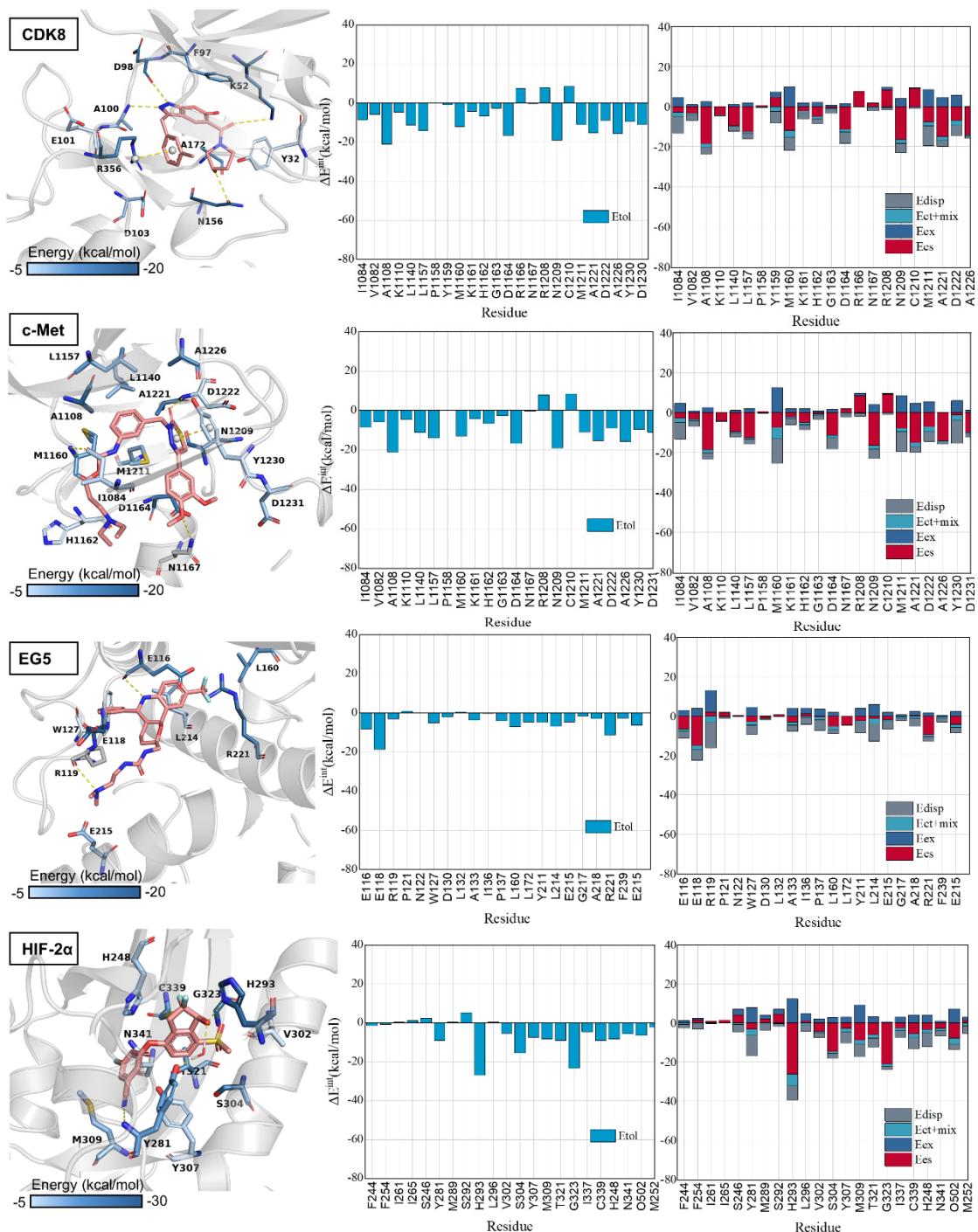
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Table S3. Results of different energy term contributions for eight targets with the FMOScore method on a literature curated benchmark set.

Protein	PDB ID ^a	ΔG_{exp}^b	ΔG_{pred}^c	ΔE^{int}					ΔG^{sol}	$\Delta E_{\text{lig}}^{\text{def}}$
				Total ^d	ΔE_{es}	ΔE_{ex}	$\Delta E_{\text{ct+mix}}$	ΔE_{disp}		
CDK8	5HNB	-11.22	-11.86	-129.11	-93.83	61.14	-26.82	-69.60	61.73	12.63
c-Met	4R1Y	-8.73	-10.79	-174.79	-121.22	62.26	-28.53	-87.30	-30.36	32.47
Eg5	3L9H	-11.05	-11.04	-91.23	-43.25	58.82	-25.41	-81.39	119.70	44.91
HIF-2 α	5TBM	-11.01	-10.54	-135.58	-92.19	76.45	-32.98	-86.86	43.36	7.74
PFKFB3	6HV1	-10.3	-10.15	-134.46	-87.75	72.19	-28.62	-90.27	53.92	10.37
SHP-2	5EHR	-9.75	-9.76	-141.73	-131.02	98.16	-30.97	-77.90	196.22	7.55
SYK	4PV0	-11.42	-10.75	-132.67	-94.44	62.87	-24.57	-76.53	69.14	26.54
TNKS2	4UI5	-10.05	-10.93	-106.69	-68.45	69.01	-27.56	-79.69	46.88	14.78

^aThe structures of the lead compounds in each target in the FEP+ benchmark have been selected for presentation, which are usually the starting points for structural modifications. ^bExperimental affinities were converted to ΔG_{exp} values using the equation $\Delta G_{\text{exp}} \approx k_B T \log IC_{50}$. ^cPredicted binding free energy ΔG_{pred} was fitted to the three types of energies calculated by the FMOScore method, consisting of binding affinities in vacuo (ΔE^{int}), solvation free energy (ΔG^{sol}), and deformation energy into the isolated form ($\Delta E_{\text{lig}}^{\text{def}}$). ^dThe total fragment pair interaction energy (ΔE^{int}) was decomposed into the electrostatic term (ΔE_{es}), exchange-repulsion term (ΔE_{ex}), charge transfer terms ($\Delta E_{\text{ct+mix}}$), and dispersion term (ΔE_{disp}). All calculated values are in kcal/mol.

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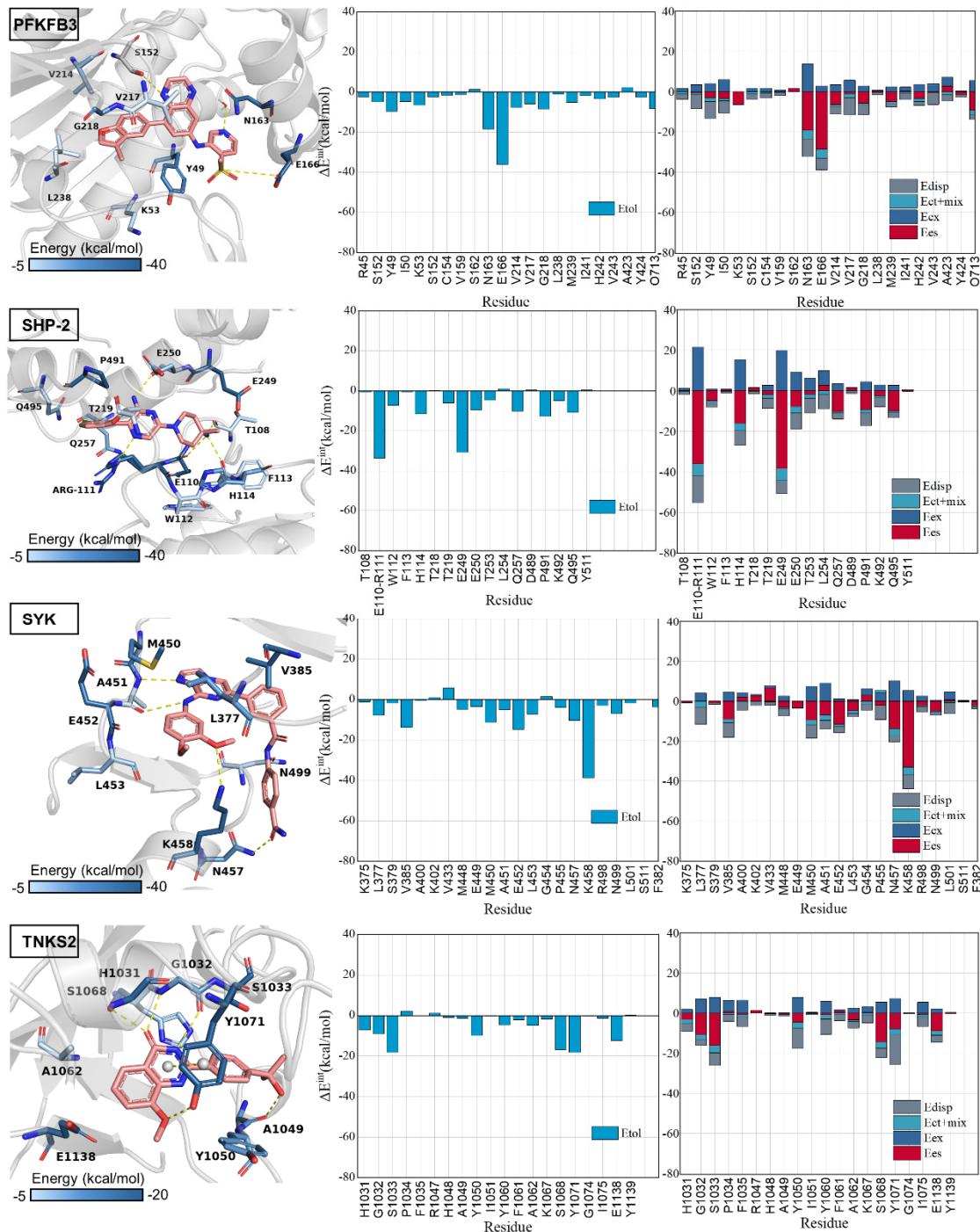


Figure S2. FMO results of eight targets: CDK8 (PDB: 5HNB), c-Met (PDB: 4R1Y), EG5 (PDB: 3I9H), HIF-2 α (PDB: 5TBM), PFKFB3 (PDB: 6HVJ), SHP-2 (PDB: SEHR), SYK (PDB: 4PV0), TNKS2 (PDB: 4UI5). The key interactions according to FMO calculations are marked as yellow dashed lines, and key residues are shown in dark blue sticks. The left-hand bar plots describe PIE between the residues at the active site and ligands, and the right-hand plots show the PIEDA of these key interactions.

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The electrostatics, charge-transfer, dispersion, and exchange-repulsion PIE terms are represented in red, blue, gray, and dark blue, respectively.

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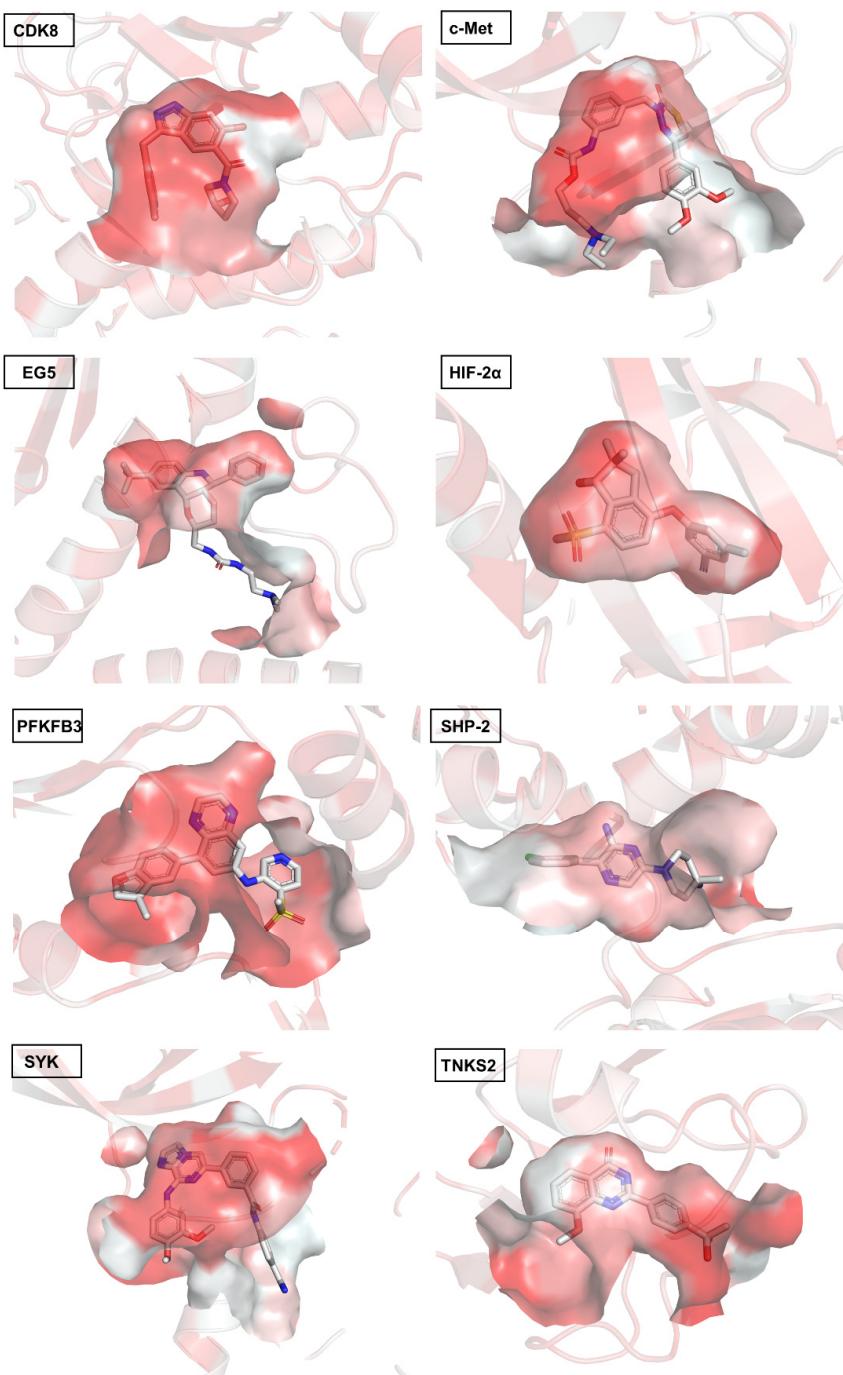


Figure S3. Pocket shapes and hydrophobic surfaces were rendered with PyMOL (version 2.3.0) for the eight targets: CDK8 (PDB: 5HNB), c-Met (PDB: 4R1Y), EG5 (PDB: 3I9H), HIF-2 α (PDB: 5TBM), PFKFB3 (PDB: 6HVJ), SHP-2 (PDB: 5EHR), SYK (PDB: 4PV0), TNKS2 (PDB: 4UI5). The redder color indicates a stronger hydrophobic surface.

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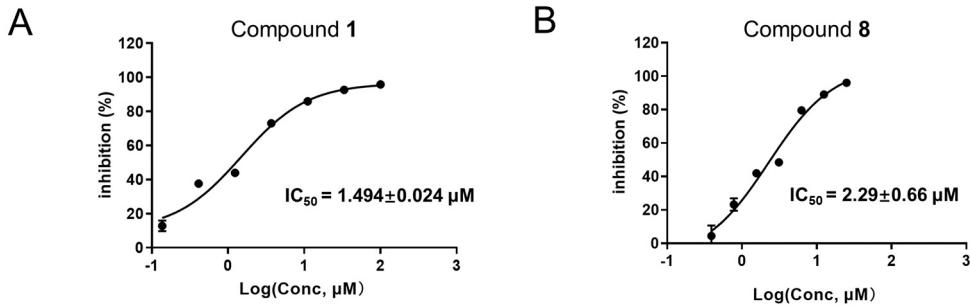
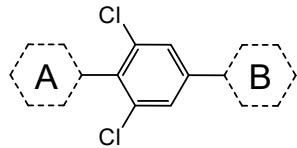


Figure S4. Identification of SHP-2 inhibitors through biochemical screening. (A-B) Compound **1** and **8** exhibited potent inhibitory activity against SHP-2. Phosphatase assays were conducted using the artificial substrate DIFMUP, and data represent mean \pm SD ($n = 3$).

Table S4. Structure activity relationship study of THR- β inhibition activities.



Ligand	Part A	Part B	THR- β $IC_{50} (\mu M)^a$	ΔG_{exp}^b	FMOSScore (kcal/mol)			
					ΔG_{pred}^c	ΔE^{int}	ΔE_{lig}^{def}	ΔG^{sol}
1			0.99 ± 0.08	-8.186	-9.629	-101.46	27.19	245.55
2			>33	-6.110	-6.318	-80.016	24.10	224.18
3			0.65 ± 0.07	-8.435	-8.475	-105.35	18.56	236.24
4			>100	-5.453	-5.925	-84.49	16.06	224.85

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5			>100	-5.453	-6.624	-78.58	19.95	236.48			
6			0.03±0.01	-10.257	-9.177	-112.88	22.27	232.94			
7			>3.7	-7.406	-7.832	-95.74	22.45	231.71			
8			>1.2	-8.072	-7.740	-91.58	20.76	237.49			
9			0.20±0.05	-9.133	-9.539	-107.01	21.70	245.91			
10			0.02±0.001	-10.497	-9.468	-101.48	25.28	245.88			
11			0.07±0.01	-9.755	-9.921	-106.95	26.54	244.73			
12			0.03±0.01	-10.257	-10.135	-107.75	27.03	246.33			
13			0.03±0.007	-10.257	-9.983	-110.78	27.52	239.90			
14			0.02±0.006	-10.497	-10.126	-100.10	32.65	246.69			
15			0.04±0.01	-10.086	-10.282	-106.87	35.74	236.90			

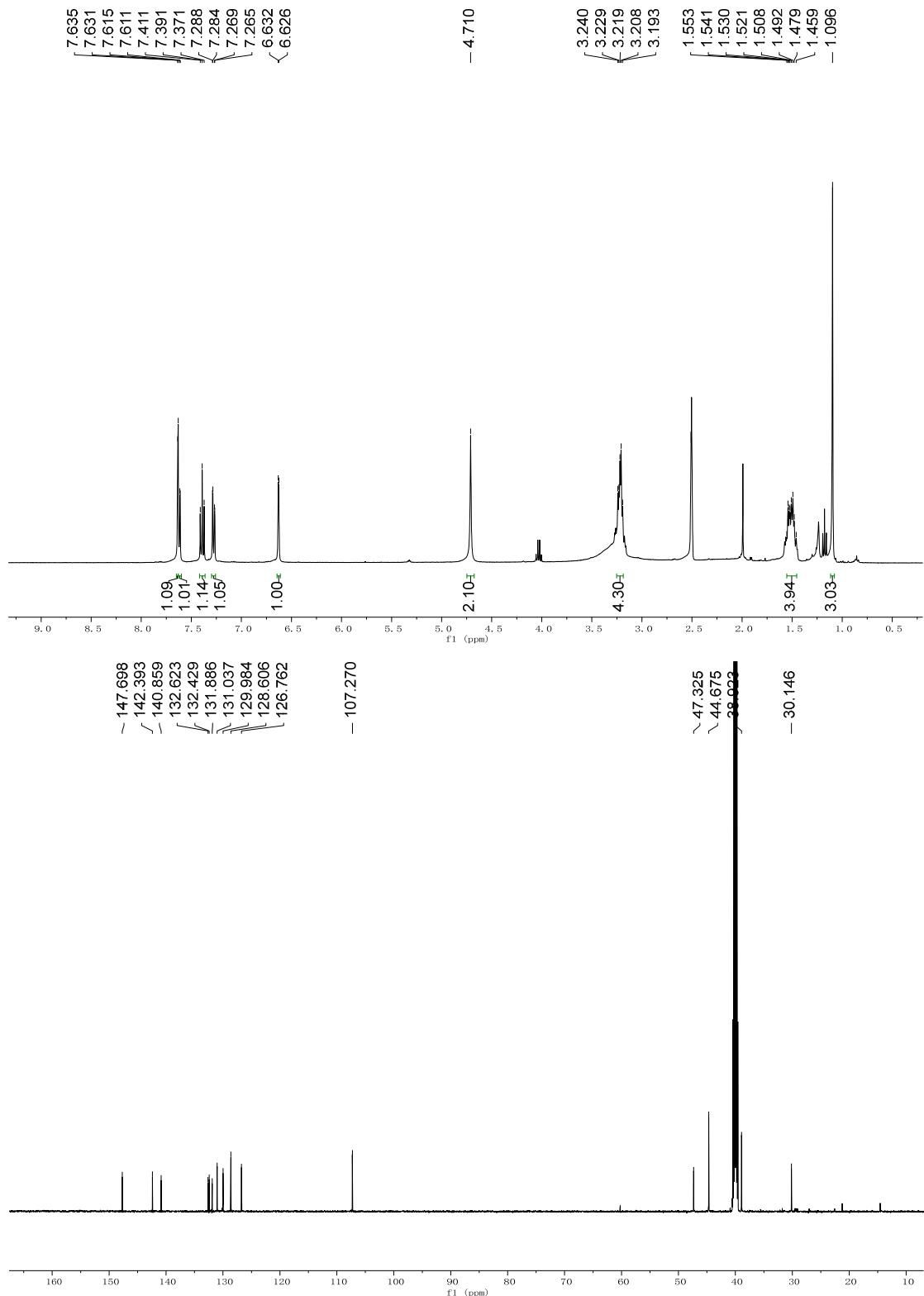
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16			0.21±0.06	-9.105	-10.820	-99.17	30.21	261.81
17			0.04±0.007	-10.086	-7.824	-75.72	24.64	251.07
18			0.009±0.003	-10.970	-10.192	-108.04	28.32	245.01
	<i>R</i> ²		-	-	0.71	0.46	0.40	0.37

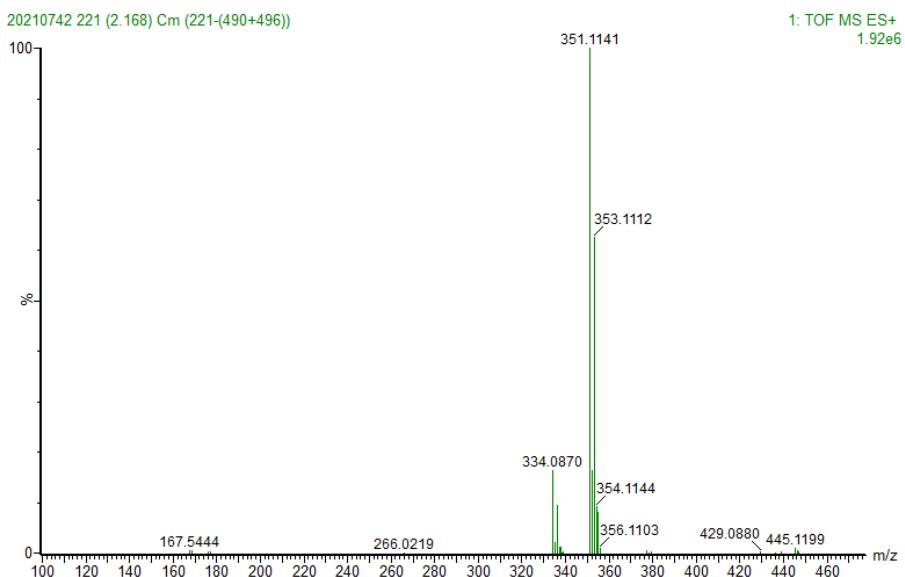
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The spectra of ^1H NMR, ^{13}C NMR and HRMS (ESI) of all final compounds

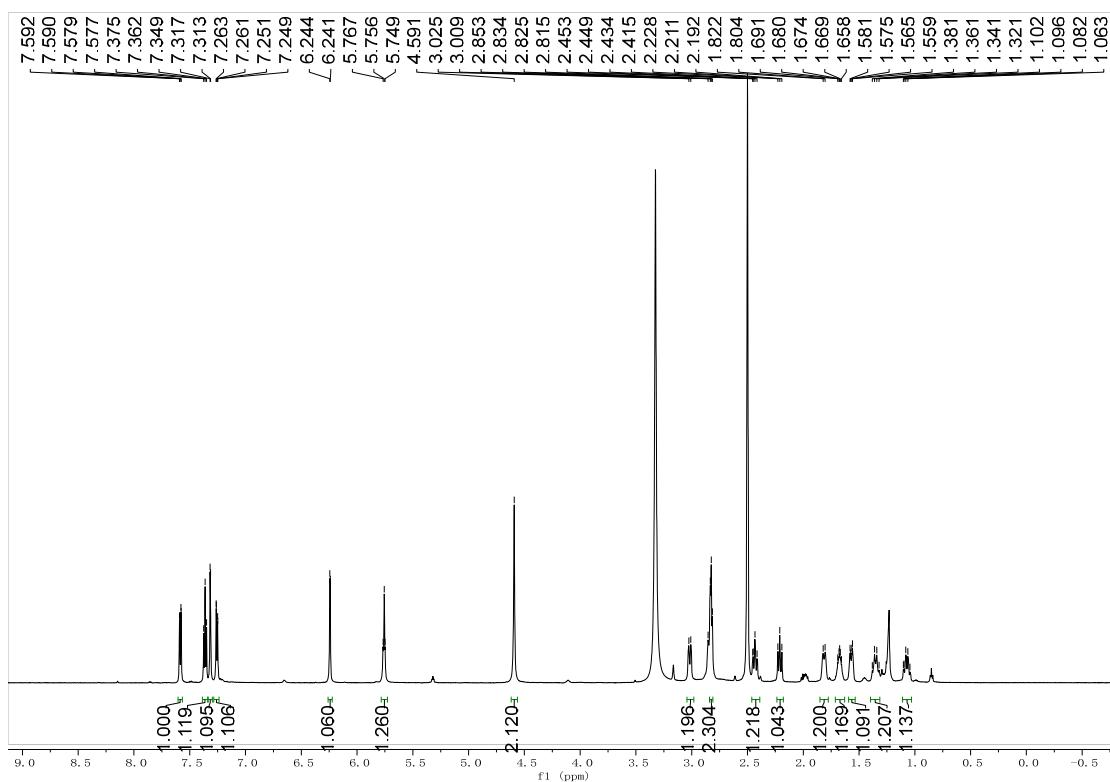
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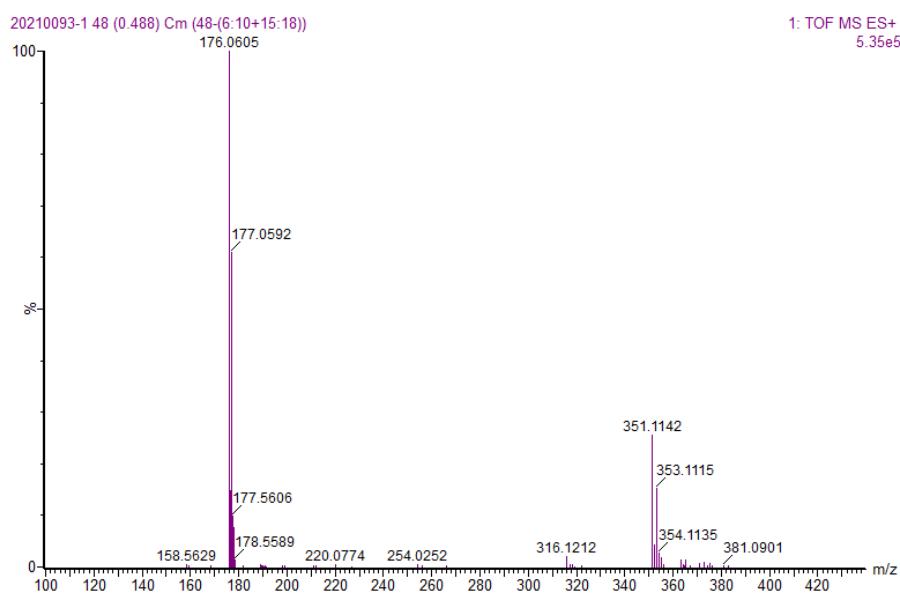
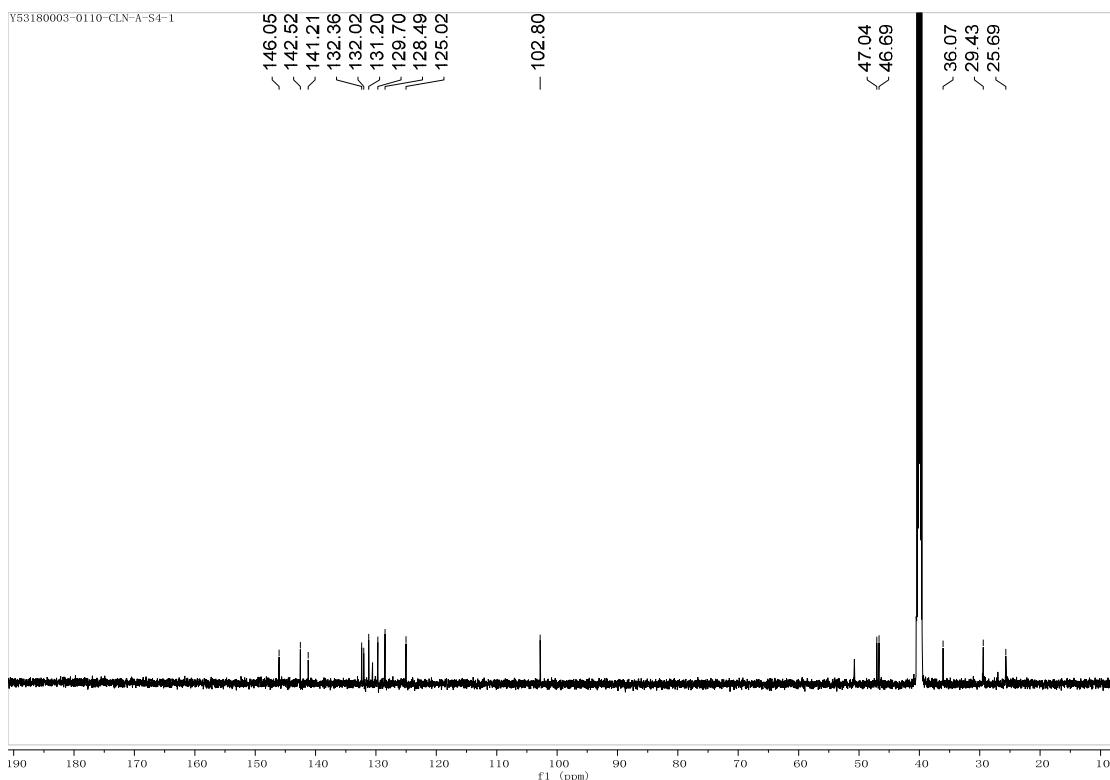
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Compound 2

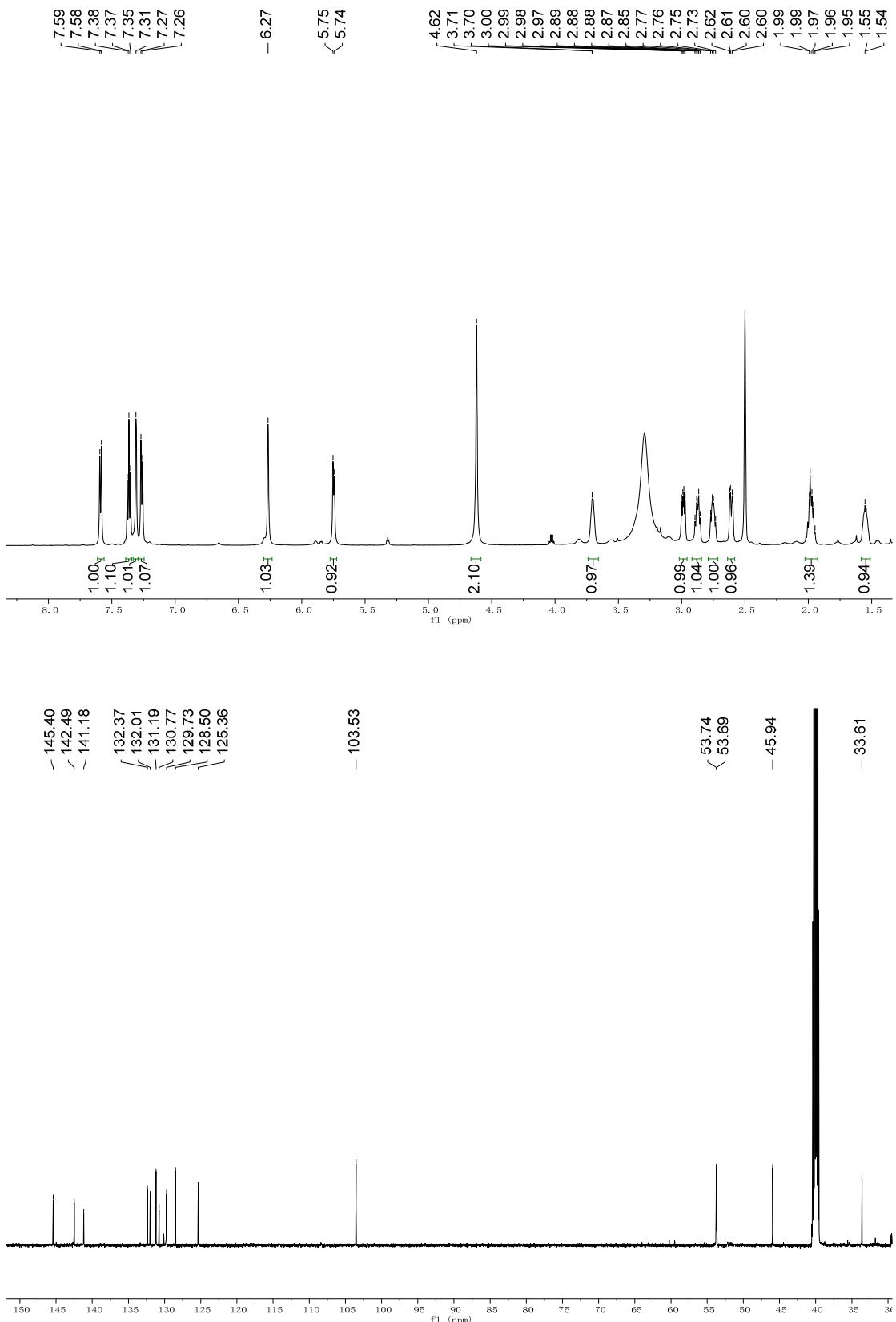


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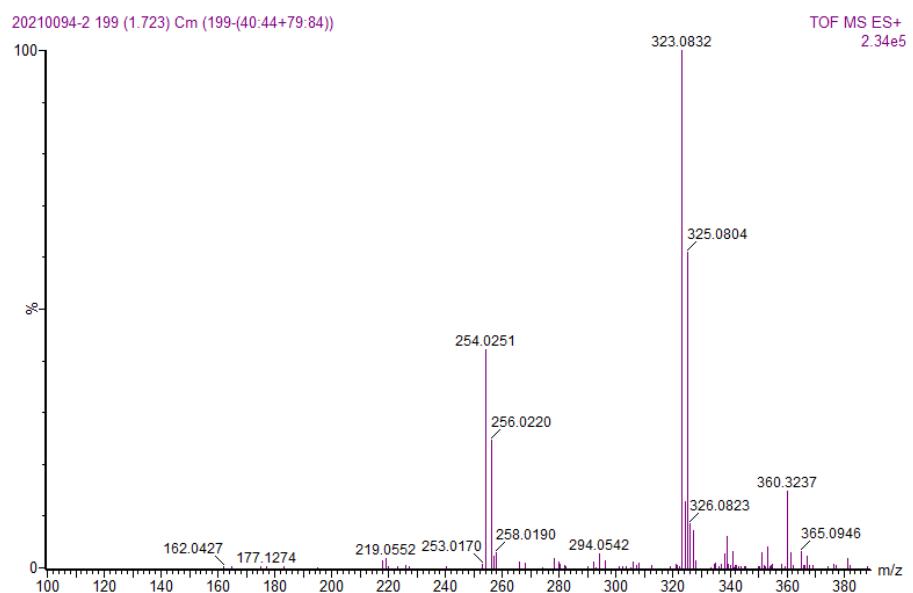


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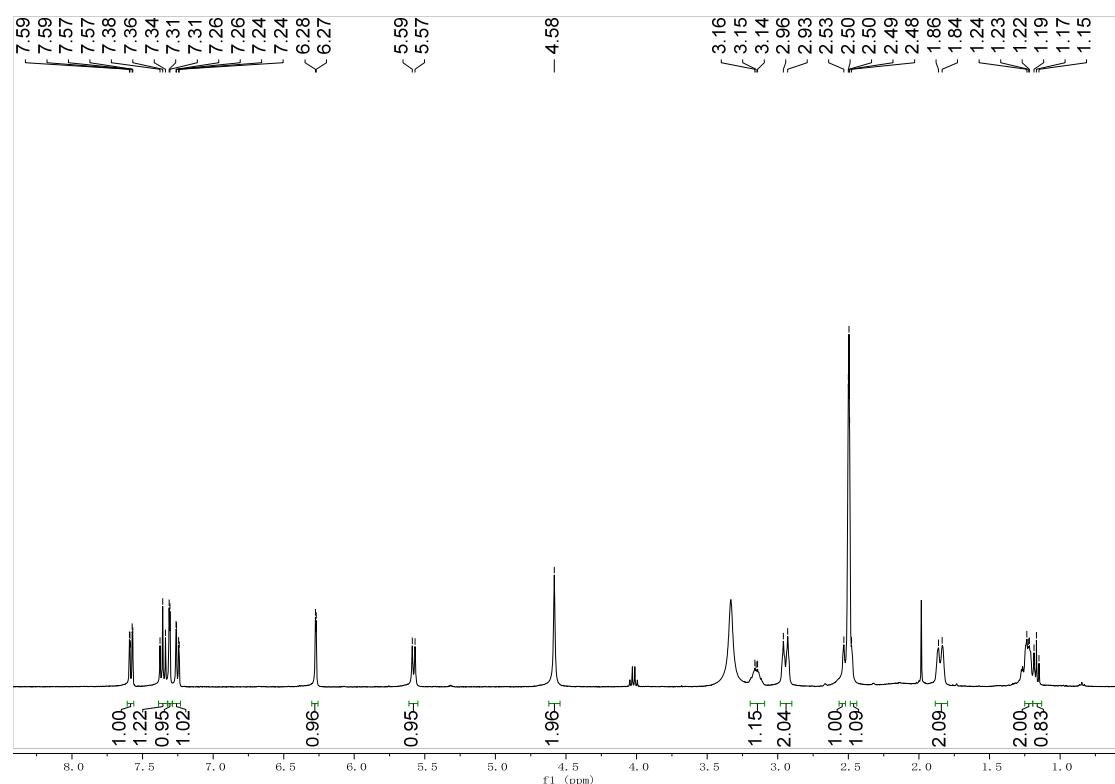
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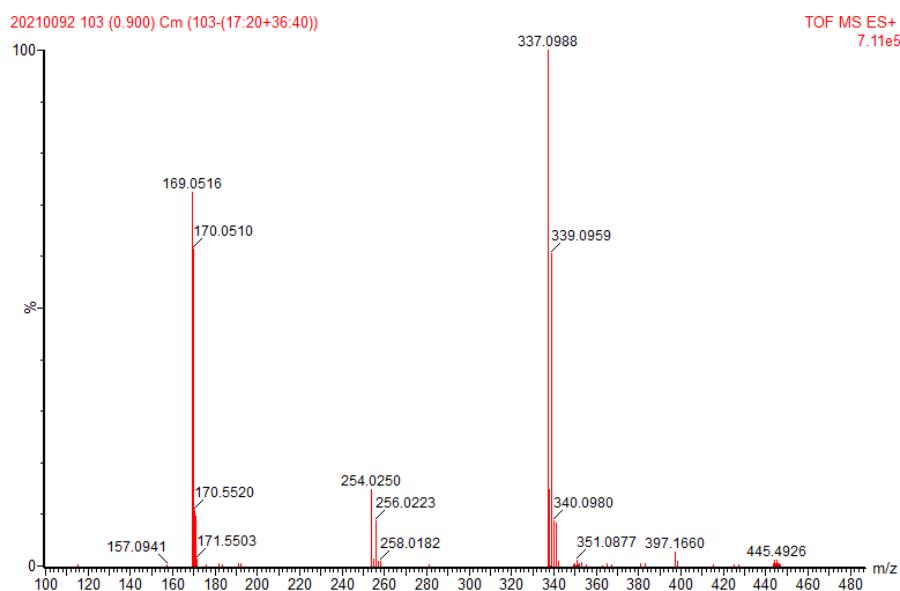
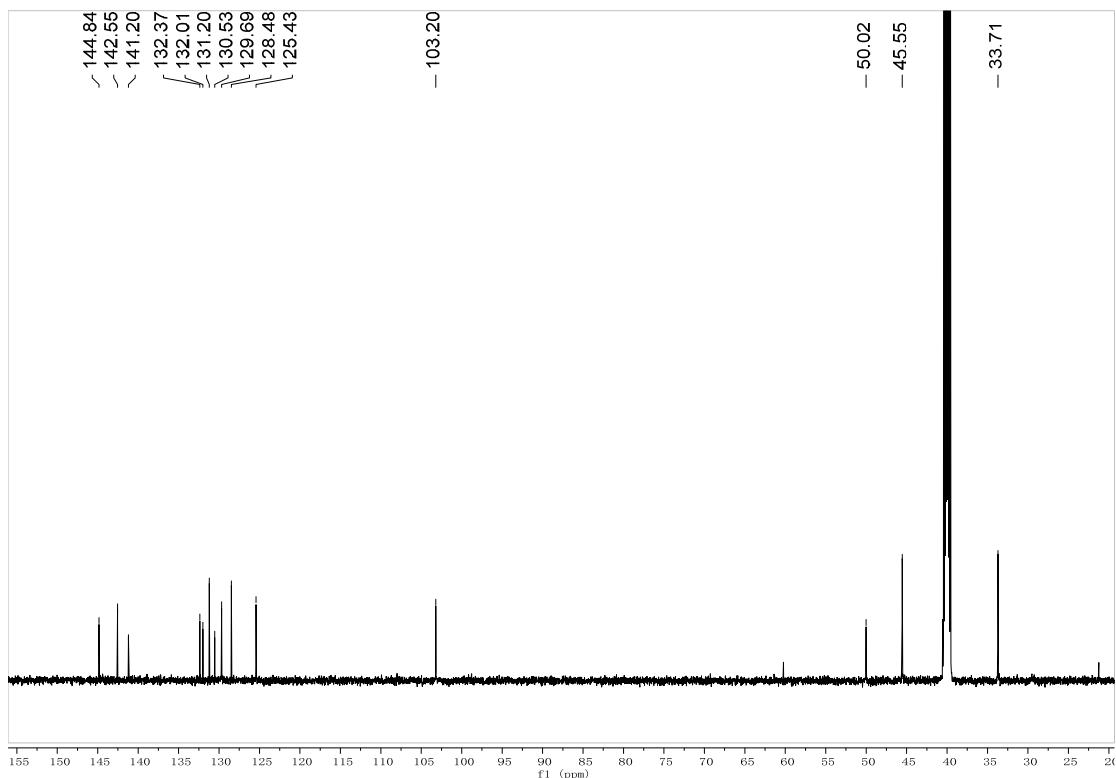
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Compound: 4

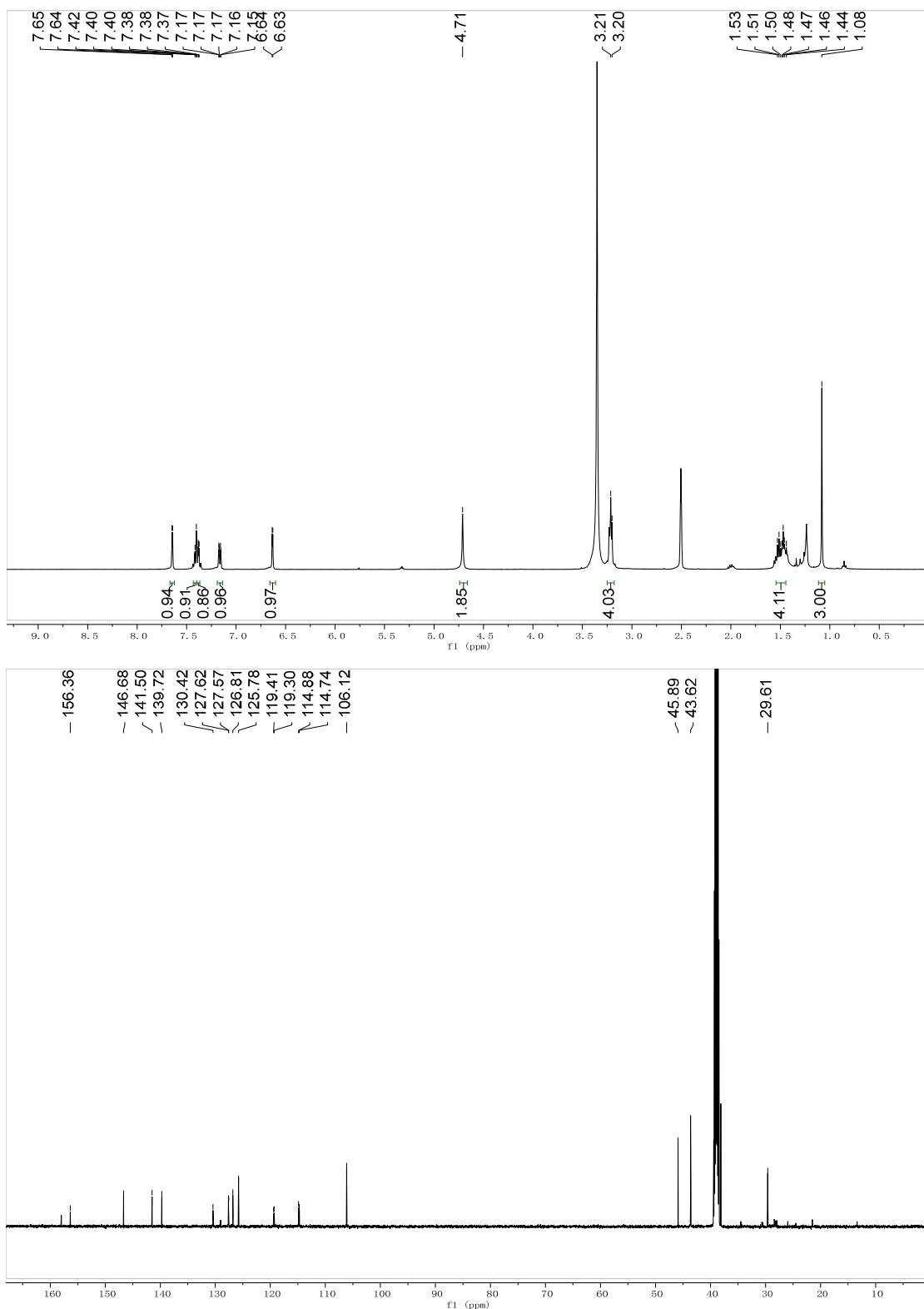


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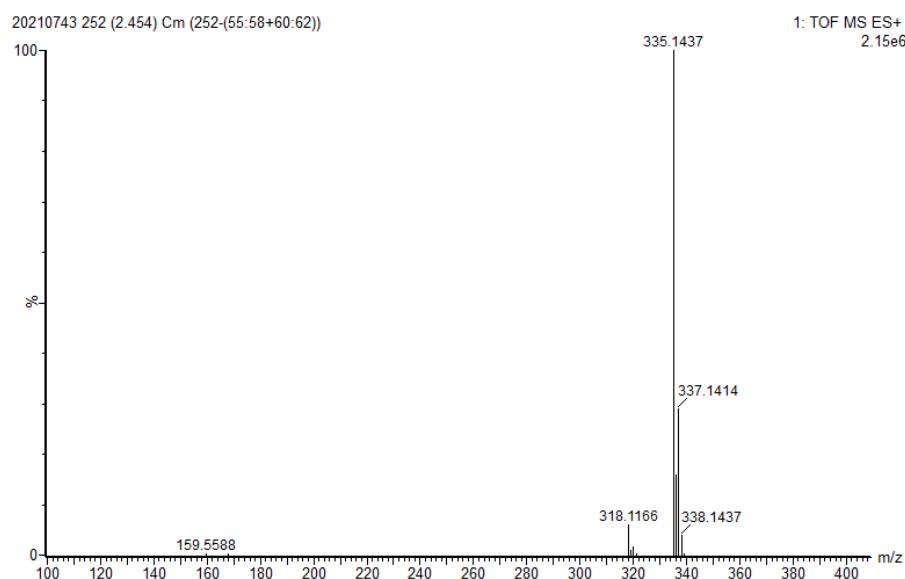


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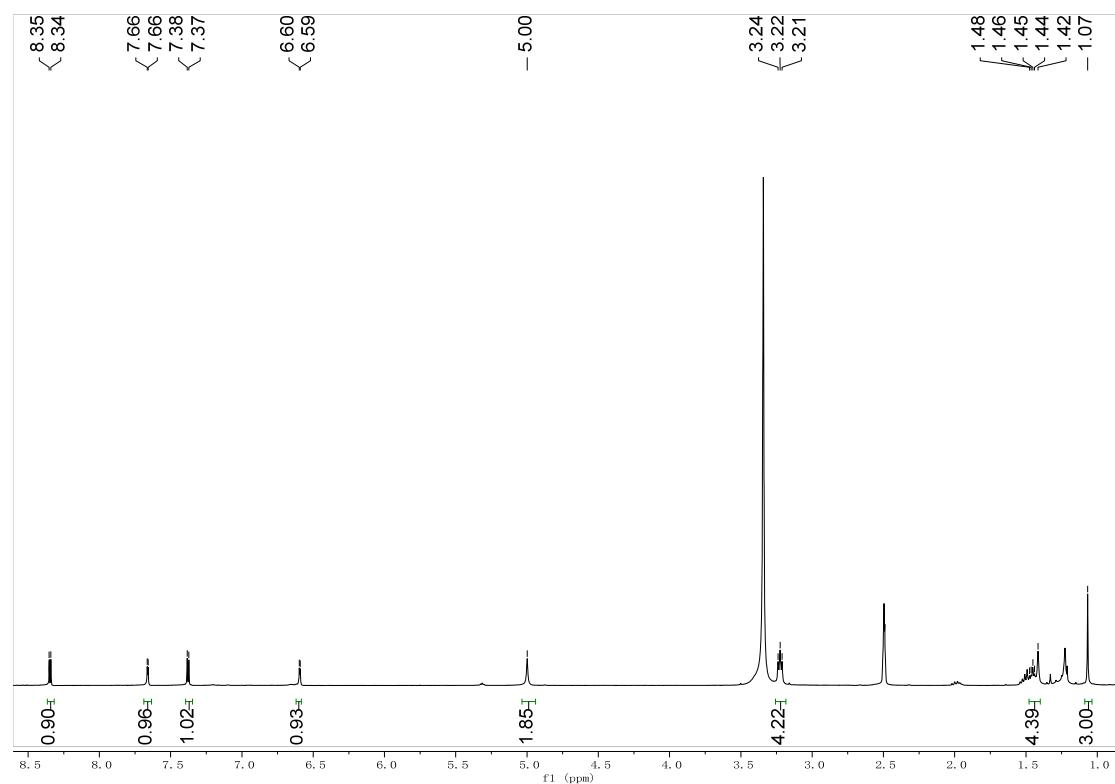
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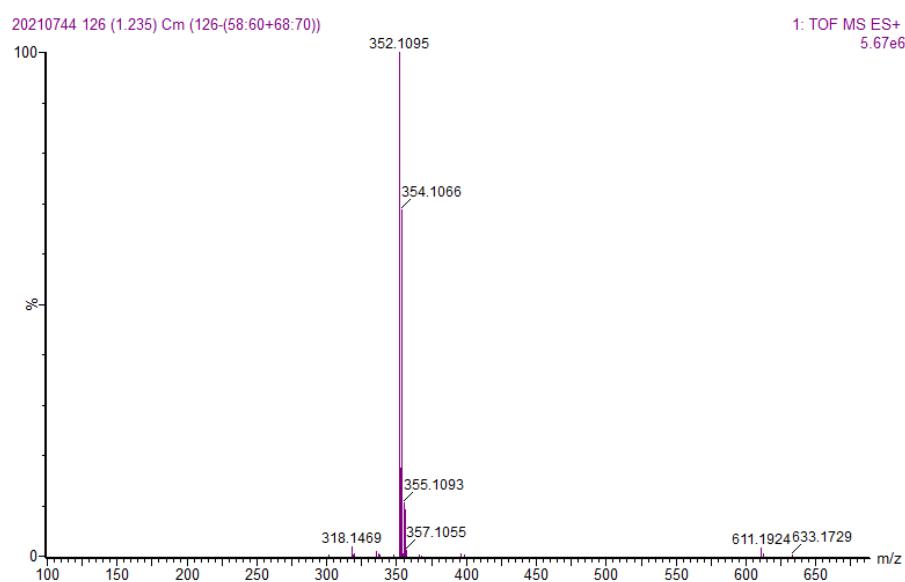
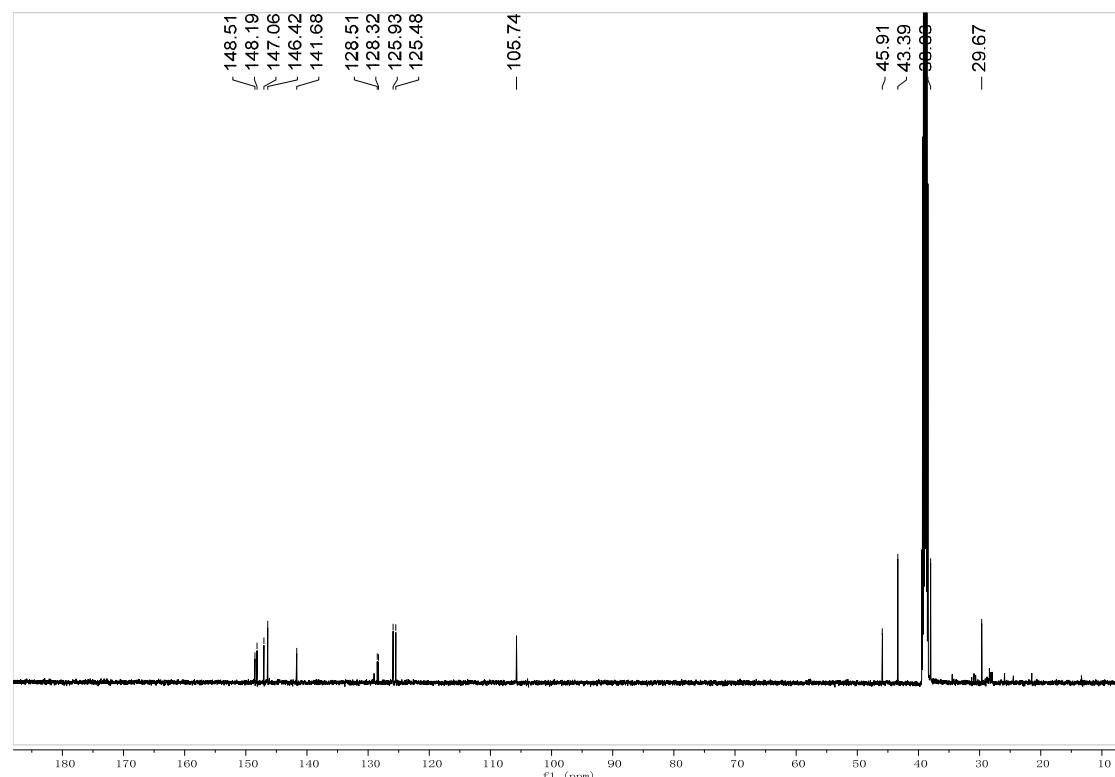
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Compound: 6

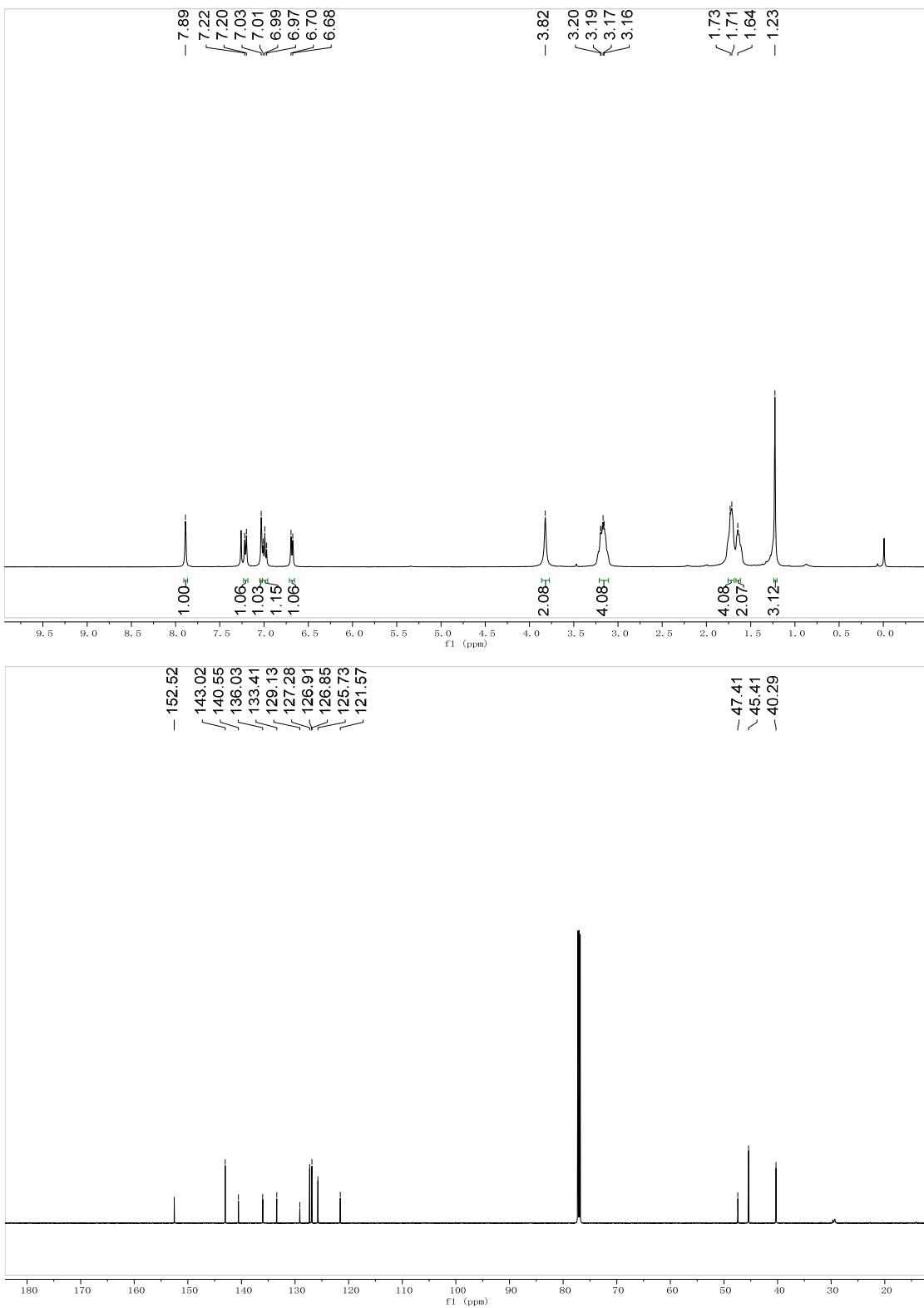


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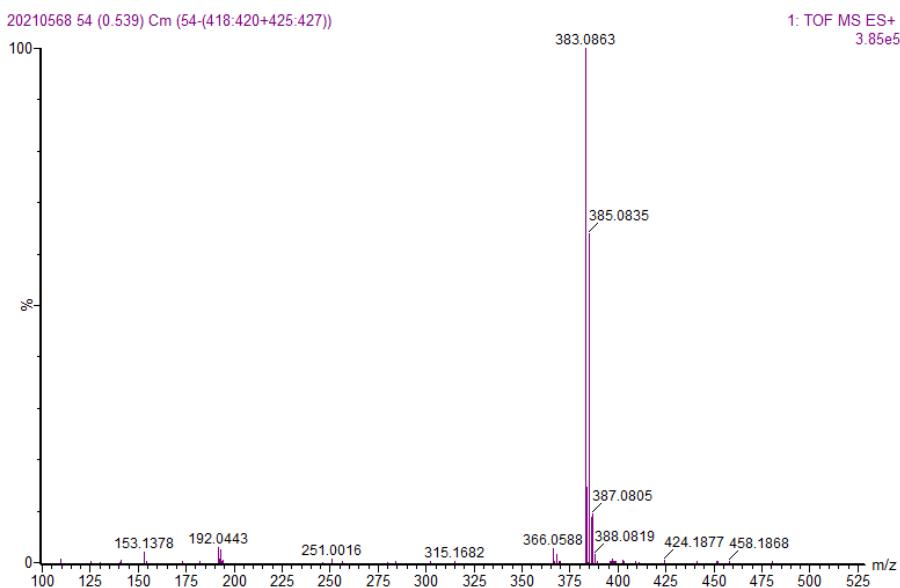


Compound: 7

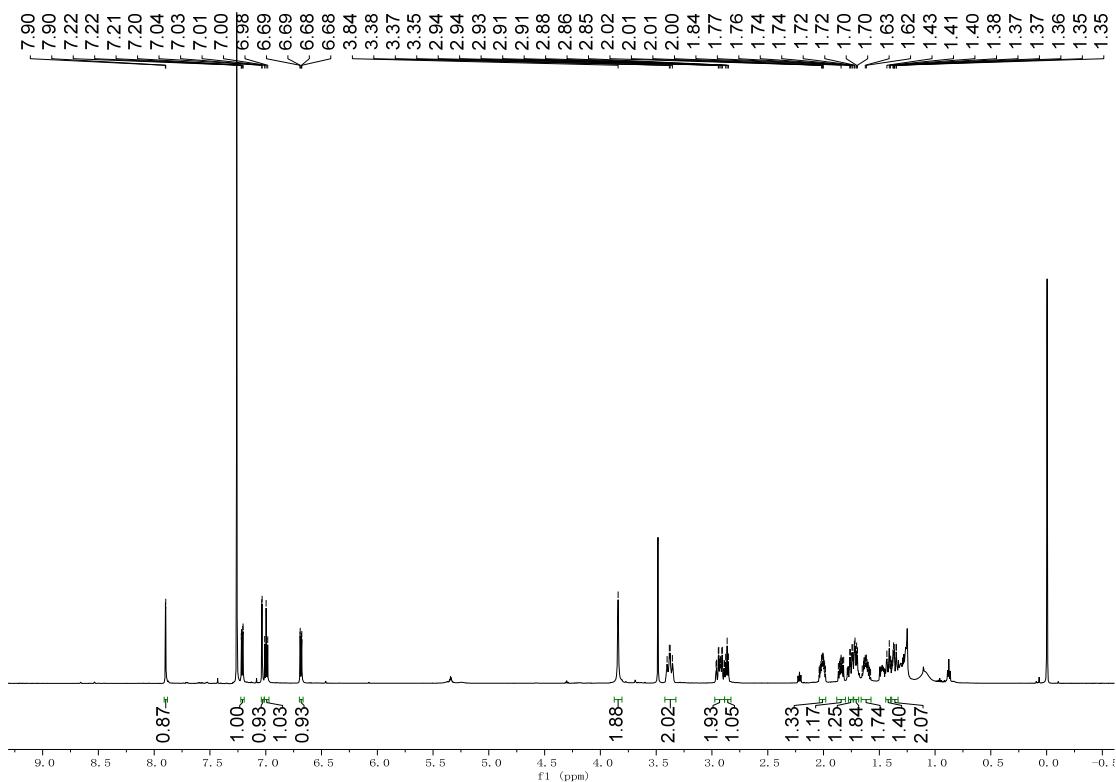
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Compound 8



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