

Computational Insights into the Binding of IN17

Inhibitors to MELK

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Supplementary Information

Table S1a:

Vdw-lambda/ele-lambda, and group restraints used for binding phase simulations

Vdw-lambda	Ele-lambda	Group restraint
1.0	1.0	0.0
1.0	0.95	1.0
1.0	0.9	2.0
1.0	0.8	4.0
1.0	0.7	6.0
1.0	0.6	8.0
1.0	0.5	10.0
1.0	0.4	12.0
1.0	0.3	14.0
1.0	0.2	15.0
1.0	0.1	15.0
1.0	0.0	15.0
0.95	0.0	15.0
0.9	0.0	15.0
0.85	0.0	15.0

0.8	0.0	15.0
0.75	0.0	15.0
0.70	0.0	15.0
0.65	0.0	15.0
0.63	0.0	15.0
0.61	0.0	15.0
0.59	0.0	15.0
0.57	0.0	15.0
0.55	0.0	15.0
0.5	0.0	15.0
0.4	0.0	15.0
0.0	0.0	15.0

Table S1b:

Vdw-lambda/ele-lambda, group restraint, and torsion restrains used for solvation phase simulations

Vdw-lambda	Ele-lambda	Torsion restraint
1.0	1.0	0.0
1.0	0.9	0.0
1.0	0.8	0.0
1.0	0.7	0.0
1.0	0.6	0.0
1.0	0.5	0.0
1.0	0.4	0.0
1.0	0.3	0.0
1.0	0.2	0.0
1.0	0.1	0.0
1.0	0.0	0.0
0.9	0.0	0.01
0.8	0.0	0.02
0.75	0.0	0.03
0.7	0.0	0.04
0.65	0.0	0.05
0.62	0.0	0.06
0.6	0.0	0.07
0.55	0.0	0.08
0.5	0.0	0.09
0.4	0.0	0.1
0.0	0.0	0.1

	binding enthalpy	binding enthalpy error	binding entropy (TΔS)	solvation enthalpy	solvation enthalpy error	solvation entropy TΔS	ΔH	TΔS
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16	-149.8	32.8	-76.4	-77.4	27.1	-22.8	-72.3	-53.6
22	-150.8	43.6	-73.7	-34.8	31.3	27.6	-116.0	-101.3
25	-127.7	37.1	-44.6	-100.5	28.8	-34.5	-27.2	-10.1
18a	-131.7	36.9	-61.3	-131.1	28.9	-78.2	-0.6	16.9
18b	-121.4	36.8	-41.3	-66.7	29.5	-4.9	-54.7	-36.3
18d	28.5	80.8	-110.3	-123.8	29.1	60.0	152.2	-170.4
18e	-120.8	80.6	-40.1	-172.2	29	-111.5	51.5	71.4
18g	-106.1	35.6	-24.7	-47.0	28.4	17.0	-59.1	-41.6
18i	-85.9	36.6	-8.3	-128.5	30.6	-69.6	42.6	61.3
18p	-273.6	36.4	-203.8	-84.1	28.5	-32.9	-189.6	-170.9
IN17	-94.9	32.9	-23.3	-115.1	15.1	-63.1	20.2	39.8

Table S2: Calculated binding and solvation entropy and enthalpy

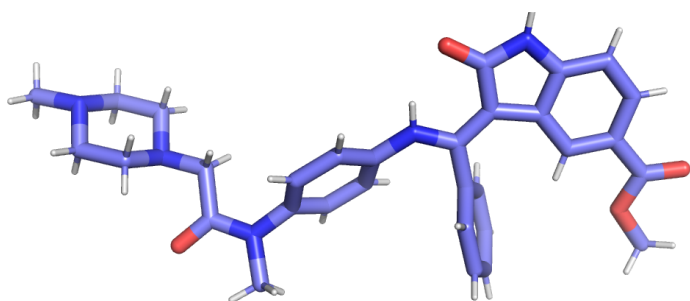


Figure S1: Solvent phase crystal structure of IN17