

Interactions between a heparin trisaccharide library and FGF-1 analyzed by NMR methods

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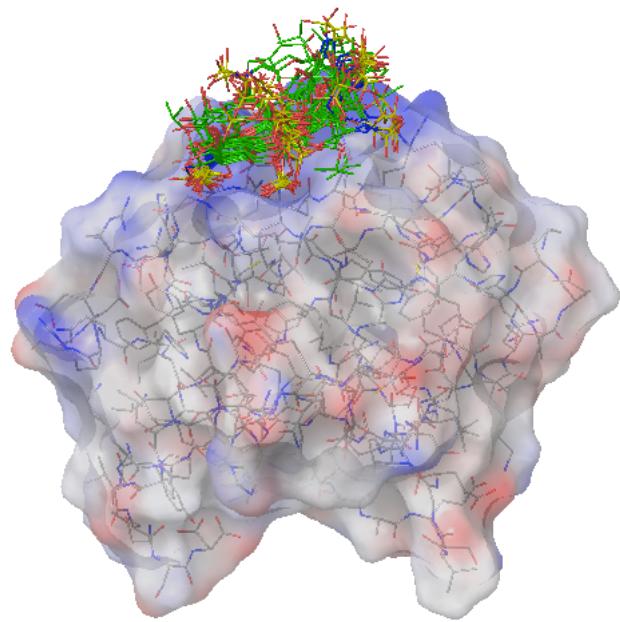


Figure S1. Docking results for **1**. Superimposition of the 10 structures with better docking score centered at the canonical binding site.

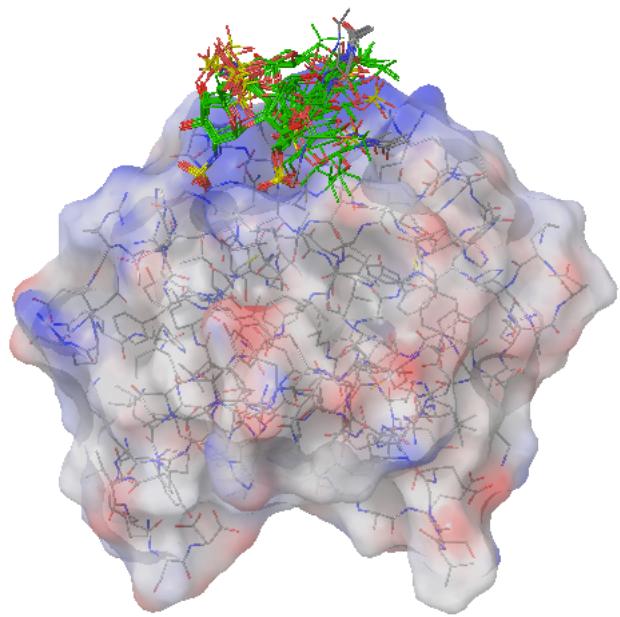


Figure S2. Docking results for **2**. Superimposition of the 10 structures with better docking score centered at the canonical binding site.

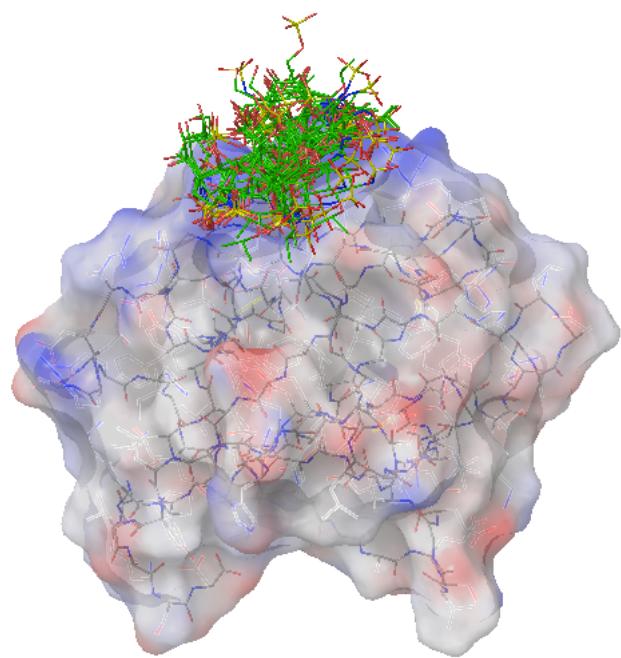


Figure S3. Docking results for **3**. Superimposition of the 10 structures with better docking score centered at the canonical binding site.

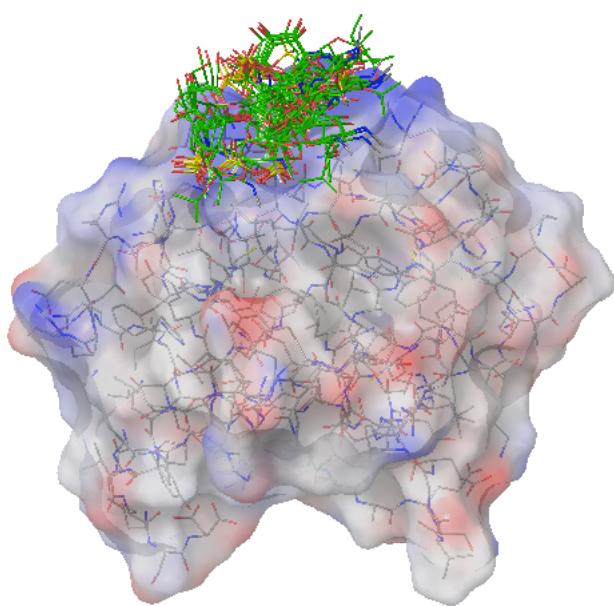


Figure S4. Docking results for **4**. Superimposition of the 10 structures with better docking score centered at the canonical binding site.

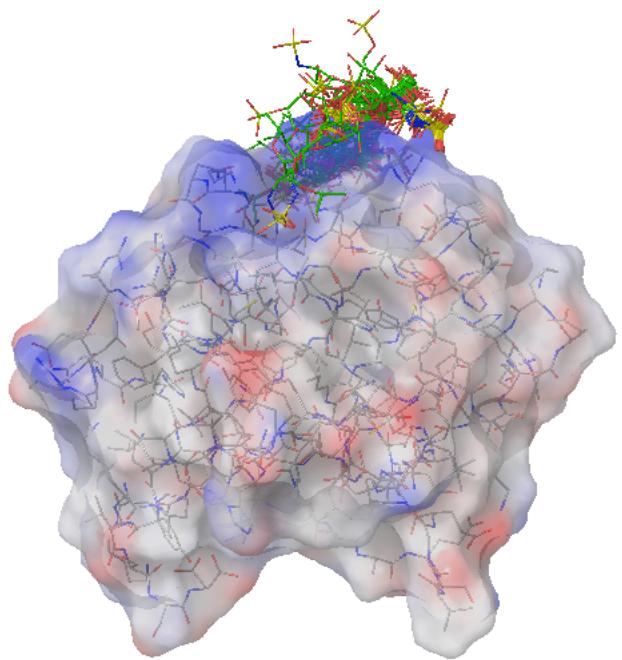


Figure S5. Docking results for **5**. Superimposition of the 10 structures with better docking score with the complete protein considered.

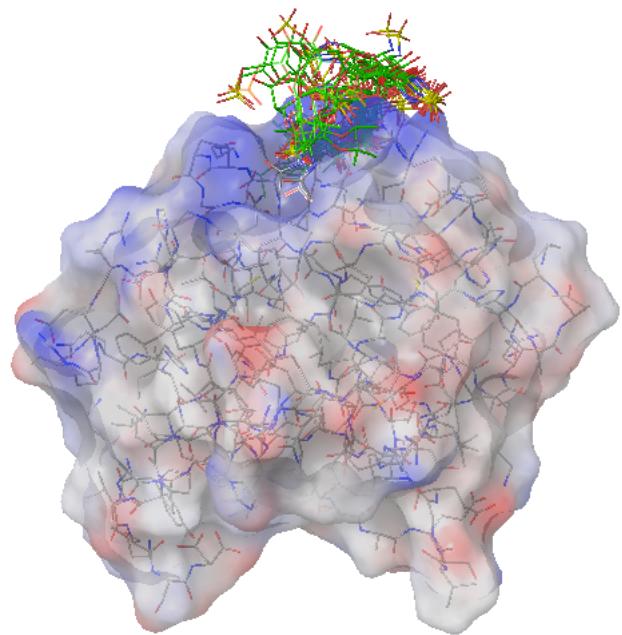


Figure S6. Docking results for **6**. Superimposition of the 10 structures with better docking score with the complete protein considered.

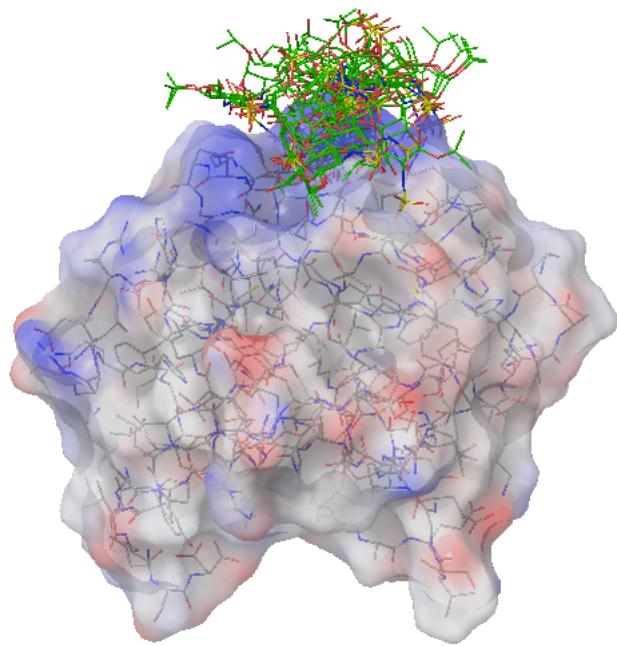


Figure S7. Docking results for **7**. Superimposition of the 10 structures with better docking score with the complete protein considered.

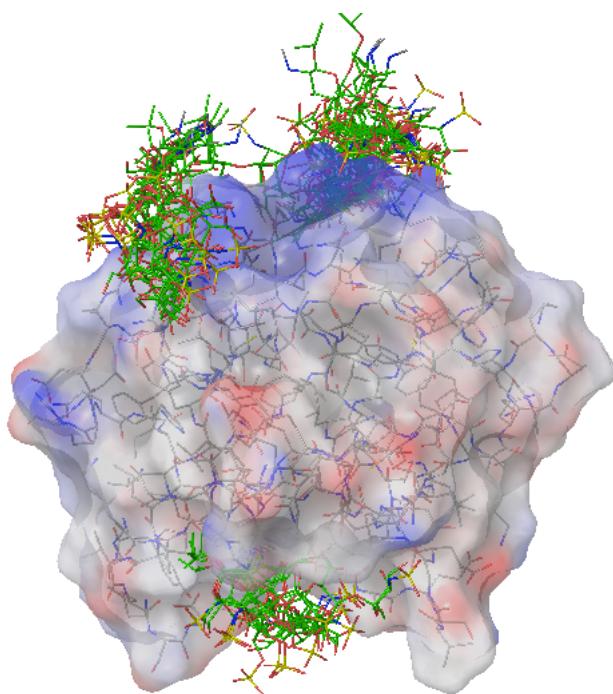


Figure S8. Docking results for **8**. Superimposition of the 20 structures with better docking score with the complete protein considered.

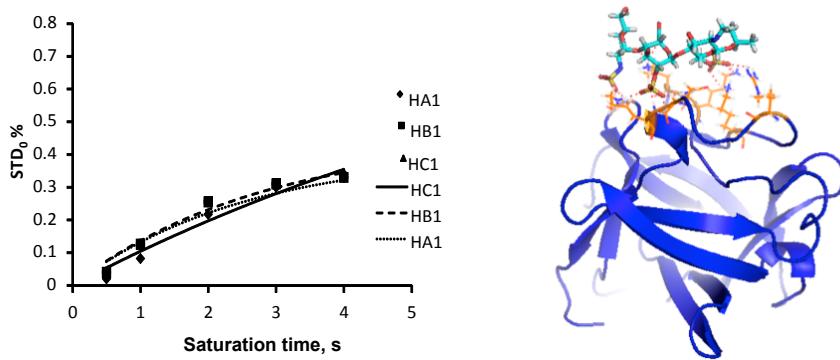


Figure S9. Docking results for compound 3. Absolute STD growth curve vs irradiation time (dots) and theoretical curves (lines). The structure (left) was obtained from the Docking calculations after energy minimization of the structure with the best docking coefficient.

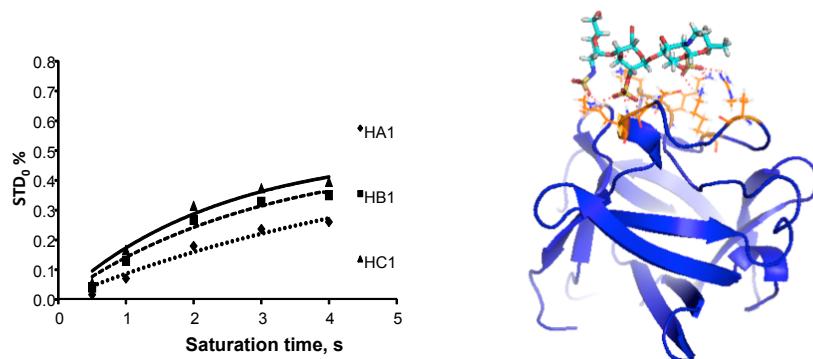
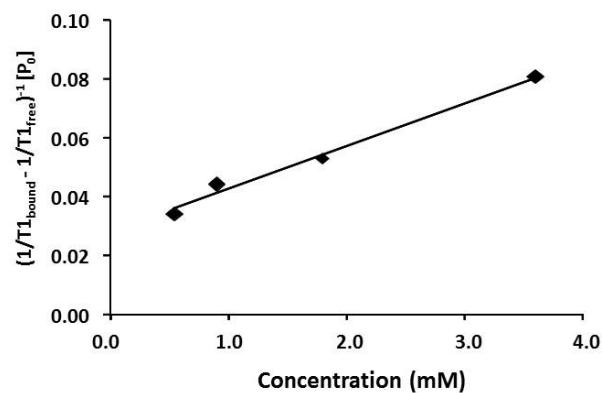
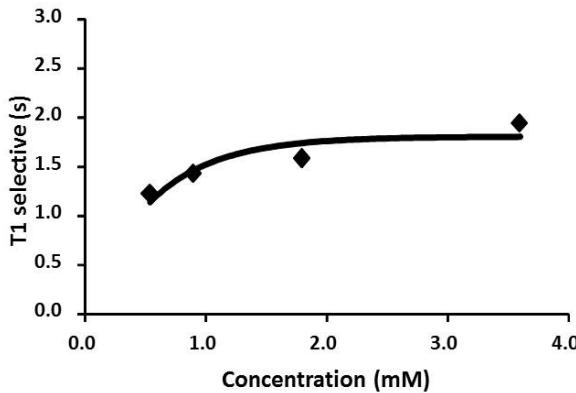


Figure S10. Docking results for compound 4. Absolute STD growth curve vs irradiation time (dots) and theoretical curves (lines). The structure (left) was obtained from the Docking calculations after energy minimization of the structure with the best docking coefficient.

Calculation of Binding Constants using $T_{1\text{sel}}$.

We have used the $T_{1\text{sel}}$ method for the evaluation of the K_D binding. In order to assess the validity of the method we performed a preliminary assay using the known system of the binding of GlcNAc to WGA (Wheat Germen Agglutinin) using a concentration of lectin of 20 uM. We obtained a K_D of 2.1 mM while the reported one is 2.5 mM.

$T_{1\text{sel}}$ method is described in the experimental section of the main paper.



Docking Results

We have performed a virtual screening by docking the ligands (8) using the tools provided by Schrodinger suite (Glide). Glide^{1,2} uses a series of hierarchical filters to search for possible locations of the ligand into the binding site. The shape and the properties of the receptor are represented on a grid by different set of fields that are progressively/sequentially applied. The exhaustive generation conformer by modification of the ligand torsions is done in order to generate a collection of possible structures. This are evaluated first into the torsional space and finally in the phase with a strong reduction on the number of hits. This are minimized and further processed.

Virtual screening stages:

- 1._Generation.- Conformational search of rotatable bonds,
- 2.- Site-point search. Exhaustive search of possible locations and orientations is performed using a grid of 2A spaced grid covering the active site. The pose is skipped if there is not a good enough mach.
- 3- Diameter test. If there is too many steric classes with the receptor the orientation is skipped.
- 4.- Subset test, small rotation about the ligand diameter. If this is good enough the interactions are scored.
- 5._ Scoring Software owned function of ChemScore.
- 6.- Energy minimization and annealing
- 7.- Poses were evaluated according to Schrodinger owned scoring function, including steric-class, buried polar terms, amide twist penalties, hydrophobic enclosure terms, and excluded volume penalties.

295	-6.041	-6.041	0	-0.984	-14.339	-54.566	0.072	-0.342	-129.611	-68.906	12.534
296	-6.035	-6.035	0	-0.835	-19.044	-43.358	0.072	-0.32	-123.07	-62.402	13.649
297	-6.033	-6.033	0	-0.954	-19.043	-40.349	0.072	-0.182	-110.138	-59.392	19.534
298	-5.995	-5.995	0	-0.913	-17.309	-43.858	0.072	-0.288	-116.303	-61.167	13.627
299	-5.977	-5.977	0	-0.913	-16.772	-44.852	0.072	-0.297	-116.855	-61.624	13.073
300	-5.969	-5.969	0	-0.903	-15.863	-46.933	0.072	-0.345	-123.286	-62.796	15.312
301	-5.963	-5.963	0	-1.043	-13.14	-51.116	0.072	-0.16	-120.325	-64.256	11.091
302	-5.958	-5.958	-0.032	-0.919	-17.672	-51.257	0.072	-0.157	-129.051	-68.928	12.493
303	-5.921	-5.921	0	-0.892	-15.515	-51.379	0.072	-0.325	-124.672	-66.894	12.913
304	-5.899	-5.899	0	-1.011	-15.285	-45.258	0.072	-0.171	-116.291	-60.542	9.329
305	-5.87	-5.87	0	-1.077	-11.918	-55.374	0.072	-0.269	-124.653	-67.292	12.638

Compound 2

	docking score	glide gscore	glide lipo	glide hbond	glide evdw	glide ecoul	glide erotb	glide esite	glide emodel	glide energy	glide einternal
1	-8.076	-8.076	-0.023	-1.518	-27.2	-64.047	0.095	-0.21	-233.573	-91.247	6.637
2	-7.379	-7.379	0	-1.635	-21.54	-69.86	0.095	-0.185	-217.627	-91.4	13.682
3	-7.372	-7.372	0	-1.679	-20.798	-69.435	0.095	-0.165	-215.512	-90.233	15.337
4	-7.369	-7.369	0	-1.693	-18.722	-76.895	0.095	-0.255	-221.296	-95.617	14.441
5	-7.228	-7.228	0	-1.699	-22.098	-61.565	0.095	-0.185	-204.4	-83.663	19.241
6	-7.214	-7.214	-0.038	-1.521	-23.537	-65.512	0.095	-0.193	-210.922	-89.049	16.465
7	-7.117	-7.117	-0.064	-1.248	-22.727	-64.818	0.095	-0.048	-186.263	-87.545	59.242
8	-7.077	-7.077	0	-1.555	-20.598	-67.576	0.095	-0.132	-207.941	-88.174	15.736
9	-7.033	-7.033	0	-1.26	-23.268	-58.644	0.095	-0.255	-200.507	-81.911	16.482
10	-6.976	-6.976	0	-1.181	-23.291	-63.167	0.095	-0.226	-207.2	-86.458	10.114
11	-6.933	-6.933	0	-1.649	-19.291	-65.669	0.095	-0.193	-201.265	-84.96	17.445
12	-6.92	-6.92	0	-1.378	-21.254	-62.306	0.095	-0.148	-201.627	-83.561	13.464
13	-6.855	-6.855	0	-1.452	-21.055	-67.179	0.095	-0.135	-202.47	-88.234	18.77
14	-6.315	-6.315	0	-0.977	-15.103	-57.727	0.095	-0.184	-177.886	-72.829	17.637
15	-6.173	-6.173	0	-0.761	-16.984	-50.317	0.095	-0.152	-174.38	-67.3	8.487
16	-6.145	-6.145	0	-1.044	-15.086	-54.677	0.095	-0.175	-174.34	-69.763	12.486
17	-6.035	-6.035	0	-1.138	-15.168	-53.674	0.095	-0.234	-170.918	-68.842	13.501
18	-5.966	-5.966	0	-1.098	-16.096	-55.775	0.095	-0.159	-171.351	-71.871	16.227

44	-6.085	-6.085	0	-1.457	-6.209	-83.528	0.106	-0.199	-208.463	-89.737	23.958
45	-6.072	-6.072	0	-1.174	-16.088	-67.358	0.106	-0.2	-173.615	-83.446	47.97
46	-6.065	-6.065	0	-1.087	-18.494	-75.374	0.106	-0.134	-199.58	-93.868	27.497
47	-6.039	-6.039	0	-1.041	-7.832	-86.597	0.106	-0.264	-217.038	-94.429	5.461
48	-6.034	-6.034	0	-1.341	-8.412	-102.018	0.106	-0.123	-218.718	-110.43	33.777
49	-5.974	-5.974	0	-1.013	-18.686	-78.006	0.106	-0.133	-207.915	-96.692	16.667
50	-5.928	-5.928	0	-0.933	-8.116	-77.274	0.106	-0.246	-197.194	-85.39	9.923
51	-5.926	-5.926	0	-1.065	-5.265	-73.252	0.106	-0.254	-190.513	-78.517	11.637
52	-5.906	-5.906	0	-1.073	-4.61	-78.992	0.106	-0.259	-185.516	-83.602	15.26
53	-5.861	-5.861	0	-1.082	-12.8	-65.599	0.106	-0.246	-193.137	-78.399	13.741
54	-5.696	-5.696	0	-1.042	-5.378	-84.158	0.106	-0.266	-186.725	-89.536	17.978
55	-5.58	-5.58	0	-0.989	-9.18	-84.887	0.106	-0.238	-194.678	-94.067	30.283
56	-5.537	-5.537	0	-0.98	-9.855	-72.74	0.106	-0.17	-169.674	-82.595	34.044
57	-5.534	-5.534	0	-1.045	-8.781	-83.684	0.106	-0.156	-187.928	-92.464	27.067
58	-5.49	-5.49	0	-1.196	-3.526	-79.862	0.106	-0.224	-188.763	-83.388	30.841
59	-5.488	-5.488	0	-0.892	-9.116	-81.883	0.106	-0.246	-188.56	-90.999	32.582
60	-5.427	-5.427	0	-0.808	-9.366	-70.165	0.106	-0.257	-173.847	-79.531	12.666
61	-5.381	-5.381	-0.002	-0.703	-11.052	-64.849	0.106	-0.229	-164.584	-75.902	24.959
62	-5.043	-5.043	0	-0.25	-13.587	-69.014	0.106	-0.219	-173.044	-82.601	17.758

Compound 4

	docking score	glide gscore	glide lipo	glide hbond	glide evdw	glide ecoul	glide erotb	glide esite	glide emodel	glide energy	glide einternal
1	-8.115	-8.115	0	-2.178	-19.239	-82.43	0.133	-0.285	-247.257	-101.669	17.165
2	-8.026	-8.026	0	-2.058	-20.152	-80.365	0.133	-0.248	-247.048	-100.516	11.901
3	-7.851	-7.851	0	-2.06	-15.174	-91.14	0.133	-0.204	-239.605	-106.314	31.727
4	-7.848	-7.848	0	-2.057	-15.398	-90.53	0.133	-0.203	-238.801	-105.928	32.452
5	-7.806	-7.806	-0.081	-1.576	-18.46	-81.913	0.133	-0.277	-234.974	-100.373	27.389
6	-7.501	-7.501	-0.051	-1.566	-18.011	-82.977	0.133	-0.249	-231.164	-100.988	24.631
7	-7.437	-7.437	0	-1.761	-15.224	-81.458	0.133	-0.268	-220.906	-96.681	34.101
8	-7.374	-7.374	0	-1.736	-14.715	-81.155	0.133	-0.262	-219.389	-95.87	33.154
9	-7.328	-7.328	0	-1.619	-21.492	-64.191	0.133	-0.141	-217.817	-85.683	14.162
10	-7.304	-7.304	0	-1.655	-16.444	-87.805	0.133	-0.228	-230.479	-104.249	25.066
11	-7.248	-7.248	0	-1.735	-16.598	-69.701	0.133	-0.286	-217.233	-86.299	13.532
12	-7.187	-7.187	0	-1.744	-13.149	-83.001	0.133	-0.237	-214.176	-96.151	37.005
13	-7.113	-7.113	0	-1.791	-12.867	-72.132	0.133	-0.296	-208.421	-84.998	23.423
14	-7.091	-7.091	0	-1.335	-22.646	-55.859	0.133	-0.215	-205.299	-78.504	15.833
15	-6.775	-6.775	0	-1.493	-20.762	-67.827	0.133	-0.143	-211.471	-88.589	11.638
16	-6.698	-6.698	-0.029	-1.068	-16.875	-57.262	0.133	-0.19	-192.557	-74.137	17.645
17	-6.677	-6.677	-0.035	-1.331	-18.749	-60.64	0.133	-0.149	-196.454	-79.389	19.574
18	-6.527	-6.527	0	-1.16	-21.302	-62.84	0.133	-0.21	-201.214	-84.142	13.835
19	-6.368	-6.368	0	-1.03	-20.465	-56.41	0.133	-0.223	-191.63	-76.874	12.441

94	-6.063	-6.063	-0.004	-0.937	-20.049	-27.46	0.102	-0.207	-108.283	-47.509	9.877
95	-6.062	-6.062	-0.005	-0.931	-16.871	-33.456	0.102	-0.38	-110.437	-50.327	8.61
96	-6.04	-6.04	-0.002	-0.561	-17.143	-34.775	0.102	-0.261	-113.321	-51.918	8.105
97	-6.025	-6.025	0	-0.97	-13.916	-42.913	0.102	-0.461	-116.134	-56.828	9.438
98	-6.017	-6.017	-0.003	-0.61	-20.297	-43.153	0.102	-0.263	-123.937	-63.45	9.442
99	-6.011	-6.011	0	-0.611	-13.102	-40.012	0.071	-0.286	-113.736	-53.114	12.288
100	-5.998	-5.998	-0.07	-1.046	-13.653	-42.68	0.102	-0.302	-115.537	-56.333	9.059
101	-5.979	-5.979	-0.002	-0.885	-18.882	-40.095	0.102	-0.208	-114.691	-58.978	15.632
102	-5.867	-5.867	-0.018	-0.827	-17.597	-40.739	0.102	-0.204	-114.655	-58.336	12.036
103	-5.859	-5.859	0	-0.732	-20.574	-32.967	0.102	-0.2	-112.418	-53.541	6.76
104	-5.82	-5.82	-0.245	-0.883	-21.014	-23.772	0.102	-0.073	-104.29	-44.786	7.144
105	-5.807	-5.807	-0.242	-0.877	-20.661	-23.755	0.102	-0.076	-102.269	-44.416	10.172
106	-5.752	-5.752	-0.095	-0.781	-23.151	-24.267	0.102	-0.111	-103.685	-47.419	12.137
107	-5.689	-5.689	-0.051	-0.713	-25.627	-23.922	0.102	-0.102	-105.462	-49.55	11.499
108	-5.593	-5.593	-0.093	-0.829	-11.093	-28.939	0.102	-0.199	-92.517	-40.032	16.261
109	-5.575	-5.575	-0.094	-0.735	-22.693	-23.784	0.102	-0.106	-101.969	-46.477	9.859
110	-5.518	-5.518	-0.047	-0.908	-23.869	-22.198	0.102	-0.117	-102.593	-46.067	6.56
111	-5.516	-5.516	-0.032	-0.828	-21.383	-23.834	0.102	-0.113	-102.51	-45.217	4.97
112	-5.457	-5.457	-0.025	-0.985	-21.496	-22.393	0.102	-0.115	-100.471	-43.889	5.119
113	-5.448	-5.448	-0.022	-0.662	-13.1	-35.841	0.102	-0.211	-98.425	-48.94	19.125

94	-3.035	-3.035	-0.319	-0.16	-29.08	-5.164	0.141	-0.002	-58.197	-34.244	7.845
95	-3.028	-3.028	-0.125	-0.292	-22.485	-10.231	0.141	-0.083	-54.591	-32.716	11.872
96	-2.923	-2.923	-0.063	0	-18.467	-13.806	0.141	-0.006	-57.403	-32.273	7.327
97	-2.879	-2.879	-0.782	0	-32.202	-3.199	0.099	-0.001	-59.138	-35.401	5.425
98	-2.787	-2.787	-0.321	-0.344	-28.075	-3.764	0.141	-0.046	-52.929	-31.839	9.015
99	-2.686	-2.686	-0.579	0	-30.979	-3.635	0.099	-0.001	-55.238	-34.614	8.096
100	-2.685	-2.685	-0.573	-0.135	-27.598	-4.565	0.141	-0.002	-51.879	-32.163	9.899
101	-2.683	-2.683	-0.68	0	-30.974	-3.047	0.099	-0.001	-54.912	-34.02	7.51
102	-2.619	-2.619	-0.048	-0.048	-17.616	-11.607	0.141	-0.02	-48.662	-29.223	9.241
103	-2.564	-2.564	-0.444	-0.143	-28.513	-3.782	0.141	0	-51.41	-32.295	8.877
104	-2.546	-2.546	-0.562	0	-26.608	-4.523	0.099	-0.021	-50.686	-31.132	7.671
105	-2.453	-2.453	-0.644	-0.16	-24.023	-3.033	0.141	0	-41.962	-27.056	15.251
106	-2.446	-2.446	-0.477	-0.053	-28.223	-2.616	0.141	0	-48.007	-30.839	10.597
107	-2.437	-2.437	-0.538	-0.149	-25.338	-2.969	0.141	-0.061	-44.112	-28.307	13.17
108	-2.426	-2.426	-1.006	-0.117	-27.566	-0.329	0.141	-0.002	-44.039	-27.895	12.272
109	-2.363	-2.363	-0.584	0	-26.327	-3.275	0.099	-0.023	-47.236	-29.602	8.138
110	-2.362	-2.362	-0.213	0	-23.558	-6.488	0.141	0	-47.066	-30.046	9.346
111	-2.151	-2.151	-0.057	0	-14.949	-8.498	0.141	-0.062	-39.785	-23.447	6.834
112	-2.126	-2.126	-0.065	0	-15.732	-7.976	0.141	-0.069	-38.416	-23.709	9.635
113	-2.103	-2.103	-0.392	-0.16	-25.325	-1.272	0.141	-0.063	-42.735	-26.597	6.36
114	-1.984	-1.984	-0.201	-0.003	-23.514	-3.645	0.141	0	-39.254	-27.159	12.267
115	-1.981	-1.981	-0.203	-0.019	-24.94	-3.35	0.141	-0.001	-40.481	-28.29	12.015
116	-1.966	-1.966	-0.288	0	-25.321	-2.45	0.141	-0.002	-42.976	-27.771	5.714
117	-1.933	-1.933	-0.208	-0.059	-21.848	-3.775	0.141	0	-37.325	-25.623	12.112
118	-1.547	-1.547	-0.297	0	-21.322	-0.605	0.141	0	-31.039	-21.927	10.198

Glide emodel. Combines the energy of **glide score** (calculated from **glide energy**), which is the binding affinity predicted by glide score, and in the case of flexible docking also the internal strain energy (**glide internal**) that is used to model the potential used to direct the conformational-search algorithm.

Glide evdw: Van der Waals energy. This term is calculated with reduced net ionic charges on groups with formal charges, such as metals, carboxylates, and guanidiniums.

Glide ecoul: Coulomb energy. This term is calculated with reduced net ionic charges on groups with formal charges, such as metals, carboxylates, and guanidiniums.

Glide lipo: Lipophilic term, which is a pairwise term in SP but is derived from the hydrophobic grid potential for XP. Rewards favourable hydrophobic interactions.

Glide hbond: Hydrogen-bonding term. This term is separated into differently weighted components that depend on whether the donor and acceptor are neutral, one is neutral and the other is charged, or both are charged.

Glide erotb: Penalty for freezing rotatable bonds.

Glide esite: Site Polar interactions in the active site. Polar but non-hydrogen-bonding atoms in a hydrophobic region are rewarded.

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