

Table S3. Root mean square deviations, rotational and vibrational frequencies, and gradients of local minimum conformations obtained from NMODE-monitored energy minimization of protein-bound ligand conformations taken from the 100 crystal structures using the steepest descent minimization method with a gradient cutoff of 0.01 kcal/(mol•Å). All three translational frequencies were zero and are not listed.

PDB code	RSMD ^a (Å)	1 st rot. freq. ilevel = 0 ^b	2 nd rot. freq. ilevel = 0	3 rd rot. freq. ilevel = 0	1 st vib. freq. ilevel = 0 ^c	1 st vib. freq. ilevel = 1 ^d	Gradient ^e (kcal/mol•Å)
13GS	0.68	0.00	1.16	1.59	7.10	7.10	8.39E-03
1A42	0.91	0.00	0.19	1.44	12.76	12.76	9.43E-03
1A4K	0.41	0.00	1.29	1.77	13.88	13.88	9.46E-03
1A8T	1.06	0.00	0.05	1.46	6.27	6.27	9.30E-03
1AFQ	0.46	0.00	0.00	0.46	6.88	6.87	9.78E-03
1AOE	0.15	0.00	0.00	1.10	16.80	16.80	7.02E-03
1ATL	0.76	0.00	0.00	1.20	4.95	4.95	9.14E-03
1AZM	0.49	0.00	0.36	0.75	18.34	18.34	8.20E-03
1BNW	1.20	0.00	0.41	0.72	9.10	9.10	9.20E-03
1BQO	1.00	0.00	0.00	1.71	7.73	7.73	8.85E-03
1BR6	0.56	0.00	0.00	1.70	9.06	9.06	9.13E-03
1CET	0.38	0.00	0.00	1.16	6.85	6.82	9.22E-03
1CIM	0.54	0.00	0.50	1.22	21.52	21.52	9.31E-03
1D3P	0.94	0.00	0.81	1.56	7.81	7.80	9.09E-03
1D4P	1.21	0.00	0.00	2.20	16.86	16.86	9.06E-03
1D6V	0.81	0.00	0.00	0.36	13.41	13.41	9.92E-03
1DIB	0.43	0.00	0.00	0.65	11.65	11.65	9.28E-03
1DLR	0.41	0.00	0.68	1.84	8.91	8.89	8.76E-03
1EFY	0.41	0.00	0.18	0.50	34.30	34.30	9.35E-03
1ELA	1.08	0.00	0.36	0.87	9.27	9.27	9.44E-03
1ETR	0.40	0.00	0.57	1.69	9.62	9.62	9.14E-03
1ETT	0.68	0.00	0.20	1.79	7.71	7.71	8.33E-03
1EVE	0.44	0.00	0.44	1.01	10.42	10.41	9.75E-03
1EXA	0.16	0.00	1.07	1.35	4.60	4.60	9.60E-03
1EZQ	0.88	0.00	0.79	1.42	8.00	8.00	9.99E-03
1F0R	1.42	0.00	0.72	1.68	2.12	1.02	9.21E-03
1F0T	0.63	0.00	0.00	1.54	5.23	5.23	9.51E-03
1F4E	0.57	0.00	0.72	0.92	2.19	0.00	9.10E-03
1F4F	1.54	0.00	0.66	0.79	12.54	12.54	8.74E-03
1F4G	1.64	0.00	0.56	0.83	8.20	8.20	9.85E-03
1FCX	0.94	0.00	0.95	1.32	7.65	7.65	9.46E-03
1FCZ	0.34	0.00	0.00	0.00	24.82	24.82	9.96E-03
1FJS	0.77	0.00	0.00	0.70	4.74	4.74	9.64E-03
1FKG	1.12	0.00	0.00	1.56	6.52	6.51	9.89E-03
1FM6	0.30	0.00	0.00	1.29	7.96	7.96	9.70E-03
1FM9	0.42	0.00	0.00	0.53	1.30	0.00	8.40E-03
1FRB	1.03	0.00	1.27	1.42	4.21	4.21	9.89E-03
1G4O	0.86	0.00	0.24	1.13	11.97	11.97	8.84E-03
1GWX	1.63	0.00	0.53	1.76	5.34	5.34	9.44E-03
1H1P	0.68	0.00	0.00	0.22	17.29	17.29	7.67E-03
1H1S	0.74	0.00	0.00	1.27	12.98	12.98	9.63E-03
1H9U	0.26	0.00	0.00	1.42	21.95	21.95	6.86E-03
1HDQ	0.38	0.00	0.00	1.04	24.13	24.13	7.42E-03
1HFC	0.33	0.00	0.81	1.18	13.87	13.87	9.47E-03
1HPV	1.08	0.00	0.62	1.07	8.99	8.98	9.73E-03
1HTF	1.09	0.00	0.00	1.23	1.46	0.00	8.58E-03
1I7Z	0.38	0.00	0.00	1.48	18.01	18.01	8.14E-03
1I8Z	0.69	0.00	0.58	1.35	13.15	13.15	9.85E-03
1IF7	0.84	0.00	0.92	1.21	12.64	12.63	9.49E-03
1IY7	0.35	0.00	0.47	0.70	21.79	21.79	9.96E-03

1JSV	0.32	0.00	0.00	0.00	18.35	18.35	9.74E-03
1K1J	0.45	0.00	0.00	1.46	9.97	9.97	9.37E-03
1K22	1.09	0.00	1.33	1.58	8.40	8.39	9.94E-03
1K7E	0.53	0.00	0.00	0.70	5.75	5.74	8.79E-03
1K7F	0.53	0.00	1.31	1.40	12.35	12.35	9.98E-03
1KV1	0.31	0.00	0.53	1.79	10.76	10.76	9.60E-03
1KV2	0.73	0.00	0.00	0.88	5.34	5.34	9.08E-03
1L2S	0.62	0.00	0.99	1.24	5.31	5.30	8.09E-03
1L8G	0.50	0.00	0.00	0.48	9.58	9.58	6.20E-03
1LQD	1.10	0.00	0.00	1.99	6.35	6.35	9.69E-03
1M48	0.31	0.00	0.37	0.97	1.78	0.00	8.97E-03
1MMB	0.50	0.00	0.00	1.17	8.61	8.61	9.97E-03
1MNC	0.33	0.00	0.95	1.44	11.14	11.14	8.73E-03
1MQ5	0.54	0.00	0.33	0.88	8.64	8.64	9.72E-03
1MQ6	0.46	0.00	0.00	0.00	0.88	0.00	9.96E-03
1NHU	0.70	0.00	0.00	1.45	5.63	5.63	9.55E-03
1NHV	0.63	0.00	0.85	1.02	6.30	6.29	9.95E-03
1O86	0.74	0.00	0.00	0.91	12.74	12.74	7.98E-03
1OHR	0.93	0.00	0.85	1.37	8.22	8.22	9.39E-03
1PPC	1.00	0.00	0.00	1.80	6.38	6.37	9.60E-03
1PPH	0.45	0.00	0.00	1.76	8.60	8.60	9.14E-03
1QBU	1.11	0.00	0.89	1.02	4.76	4.66	9.39E-03
1QHI	0.29	0.00	0.00	0.86	16.13	16.13	9.43E-03
1QL9	0.64	0.00	0.00	1.45	2.03	0.00	9.96E-03
1QPE	0.30	0.00	0.00	0.59	28.78	28.78	6.95E-03
1R09	0.50	0.00	1.39	1.51	2.97	2.89	7.76E-03
1SYN	2.33	0.00	0.00	0.87	1.16	0.00	8.99E-03
1THL	0.53	0.00	0.00	1.31	8.00	8.00	9.75E-03
1UVS	0.94	0.00	0.55	1.26	6.16	6.16	9.24E-03
1UVT	0.79	0.00	0.00	0.00	1.41	0.00	9.88E-03
1YDR	0.31	0.00	0.00	1.43	13.37	13.37	8.73E-03
1YDS	0.41	0.00	1.15	1.30	25.03	25.03	8.12E-03
1YDT	0.75	0.00	0.00	0.99	1.32	0.00	9.53E-03
2CGR	1.12	0.00	0.98	1.58	7.23	7.23	9.42E-03
2CSN	0.96	0.00	1.32	1.63	37.68	37.68	7.64E-03
2PCP	0.24	0.00	0.00	1.43	33.14	33.14	8.50E-03
2QWI	0.49	0.00	0.92	1.18	25.45	25.45	1.00E-02
3CPA	0.43	0.00	0.40	0.83	11.60	11.59	7.43E-03
3ERK	0.42	0.00	0.00	1.20	21.72	21.72	9.67E-03
3ERT	0.39	0.00	0.77	0.99	17.96	17.96	8.88E-03
3STD ^f	0.72	0.69	1.11	1.28	13.34	13.34	3.81E-03
3TMN	0.24	0.00	1.12	1.45	14.37	14.37	9.90E-03
4DFR	1.22	0.00	1.39	1.63	6.60	6.60	9.89E-03
4STD	0.22	0.00	0.00	0.72	16.83	16.83	8.82E-03
5STD	0.60	0.00	1.10	1.33	14.60	14.60	9.54E-03
5TLN	1.06	0.00	0.58	0.69	7.06	7.05	9.21E-03
7DFR	1.14	0.00	0.14	0.78	6.23	6.20	7.90E-03
7EST	0.66	0.00	0.00	1.35	5.70	5.70	9.83E-03
830C	1.32	0.00	0.52	1.03	8.55	8.55	8.66E-03
966C	0.51	0.00	0.00	1.22	15.07	15.07	9.15E-03

- a: PDB: Protein Data Bank
b: RMSD of all ligand atoms between minimized and initial conformations.
c: First rotational frequency (cm^{-1}) computed with the second derivative matrix not adjusted to put rotation and translation vectors to a high frequency (ilevel = 0).
d: First vibrational frequency (cm^{-1}) computed with the second derivative matrix not adjusted to put rotation and translation vectors to a high frequency (ilevel = 0).
e: First vibrational frequency (cm^{-1}) computed with the second derivative matrix adjusted to put rotation and translation vectors to a high frequency (ilevel = 1).
f: Root mean square gradient.
g: Required cycles of 20 steps instead of 10 steps due to numeric truncations.