



Full wwPDB EM Validation Report ⓘ

Aug 6, 2026 – 04:57 AM JST

PDB ID : 8J9H / pdb_00008j9h
EMDB ID : EMD-36107
Title : Cryo-EM structure of Euglena gracilis respiratory complex I, deactive state
Authors : Wu, M.C.; He, Z.X.; Tian, H.T.; Hu, Y.Q.; Han, F.Z.; Zhou, L.
Deposited on : 2023-05-03
Resolution : 3.11 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

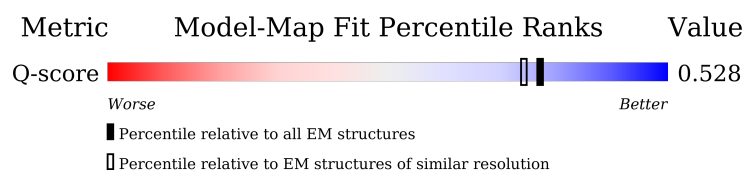
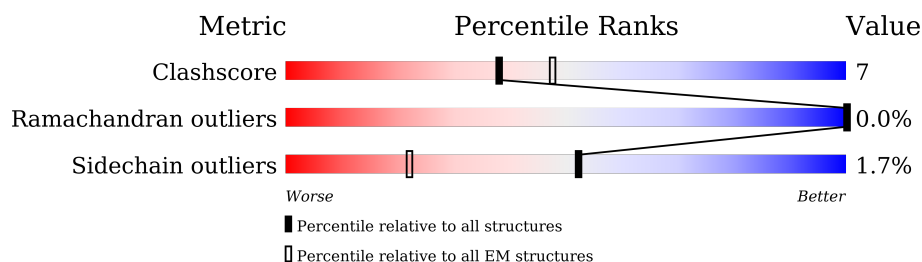
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14465 (2.61 - 3.61)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1A	385	
2	1B	527	
3	2B	142	
4	4L	171	

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Mol	Chain	Length	Quality of chain
5	A1	141	
6	A2	193	
7	A3	125	
8	A5	184	
9	A6	437	
10	A7	136	
11	A8	223	
12	A9	489	
13	AB	134	
14	AL	281	
15	AM	198	
16	AN	287	
17	B2	145	
18	B3	62	
19	B4	171	
20	B5	140	
21	B6	91	
22	B7	97	
23	B8	176	
24	B9	158	
25	BL	144	
26	BM	112	
27	C4	185	
28	E1	483	
29	E2	467	

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Mol	Chain	Length	Quality of chain
30	E3	434	
31	E4	368	
32	E5	290	
33	E6	371	
34	E8	205	
35	EA	126	
36	EB	101	
37	EC	101	
38	ED	151	
39	FX	325	
40	G1	436	
41	G2	267	
42	G3	261	
43	N1	670	
44	N2	300	
45	N3	293	
45	N6	293	
46	N4	478	
47	N5	584	
48	S2	395	
49	S3	277	
50	S4	208	
51	S5	122	
52	S6	147	
53	S7	207	

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Mol	Chain	Length	Quality of chain
54	S8	212	
55	U1	12	
55	U2	12	
56	V1	526	
57	V2	225	
58	E7	246	
59	AC	134	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
61	SF4	S8	297	-	-	X	-
61	SF4	S8	298	-	-	X	-

2 Entry composition [i](#)

There are 70 unique types of molecules in this entry. The entry contains 226135 atoms, of which 112544 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NDUS1A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1A	352	Total	C	H	N	O	S	0	0
			5501	1753	2700	488	537	23		

- Molecule 2 is a protein called NDUS1B.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1B	525	Total	C	H	N	O	S	1	0
			8357	2679	4159	743	765	11		

- Molecule 3 is a protein called NADH dehydrogenase subunit 5.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2B	140	Total	C	H	N	O	S	0	0
			2059	712	989	172	183	3		

- Molecule 4 is a protein called ND4L.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	4L	108	Total	C	H	N	O	S	0	0
			1768	606	878	133	145	6		

- Molecule 5 is a protein called NDUFA1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	A1	137	Total	C	H	N	O	S	0	0
			2097	684	1026	192	192	3		

- Molecule 6 is a protein called NDUFA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	A2	192	Total	C	H	N	O	S	0	0
			2967	942	1474	267	280	4		

- Molecule 7 is a protein called NDUFA3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	A3	124	Total	C	H	N	O	S	0	0
			2089	678	1039	191	175	6		

- Molecule 8 is a protein called NDUFA5.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	A5	154	Total	C	H	N	O	S	0	0
			2509	794	1248	221	244	2		

- Molecule 9 is a protein called NDUFA6.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	A6	423	Total	C	H	N	O	S	0	0
			6608	2091	3280	601	632	4		

- Molecule 10 is a protein called NDUFA7.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A7	136	Total	C	H	N	O	S	0	0
			2272	735	1118	219	194	6		

- Molecule 11 is a protein called NDUFA8.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	A8	223	Total	C	H	N	O	S	0	0
			3548	1160	1726	315	334	13		

- Molecule 12 is a protein called NDUFA9.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	A9	484	Total	C	H	N	O	S	0	0
			7679	2449	3850	662	700	18		

- Molecule 13 is a protein called NDUFAB1-alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AB	88	Total	C	H	N	O	S	0	0
			1367	437	673	114	139	4		

- Molecule 14 is a protein called NDUFA12.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AL	265	Total	C	H	N	O	S	0	0
			4409	1439	2172	414	379	5		

- Molecule 15 is a protein called NDUFA13.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AM	184	Total	C	H	N	O	S	0	0
			2935	953	1448	264	263	7		

- Molecule 16 is a protein called NDUFA11.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AN	287	Total	C	H	N	O	S	0	0
			4573	1501	2267	396	399	10		

- Molecule 17 is a protein called NDUFB2.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	B2	105	Total	C	H	N	O	S	0	0
			1770	604	857	142	166	1		

- Molecule 18 is a protein called NDUFB3.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	B3	61	Total	C	H	N	O	S	0	0
			758	292	309	88	68	1		

- Molecule 19 is a protein called NDUFB4.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	B4	171	Total	C	H	N	O	S	0	0
			2735	885	1358	250	236	6		

- Molecule 20 is a protein called NDUFB5.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	B5	140	Total	C	H	N	O	S	0	0
			2181	708	1069	207	195	2		

- Molecule 21 is a protein called NDUFB6.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	B6	91	Total	C	H	N	O	S	0	0
			1520	509	747	132	128	4		

- Molecule 22 is a protein called NDUFB7.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	B7	97	Total	C	H	N	O	S	0	0
			1692	536	835	165	149	7		

- Molecule 23 is a protein called NDUFB8.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	B8	147	Total	C	H	N	O	S	0	0
			2351	804	1127	199	213	8		

- Molecule 24 is a protein called NDUFB9.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	B9	151	Total	C	H	N	O	S	0	0
			2443	795	1207	216	222	3		

- Molecule 25 is a protein called NDUFB10.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	BL	144	Total	C	H	N	O	S	0	0
			2406	786	1179	215	216	10		

- Molecule 26 is a protein called NDUFB11.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	BM	112	Total	C	H	N	O	S	0	0
			1737	577	827	164	167	2		

- Molecule 27 is a protein called NDUFC2.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	C4	183	Total	C	H	N	O	S	0	0
			3062	1000	1517	268	271	6		

- Molecule 28 is a protein called NDUEG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	E1	450	Total	C	H	N	O	S	0	0
			7008	2244	3496	601	654	13		

- Molecule 29 is a protein called NDUEG2.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	E2	466	Total	C	H	N	O	S	0	0
			7103	2286	3540	618	655	4		

- Molecule 30 is a protein called NDUEG3.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	E3	432	Total	C	H	N	O	S	0	0
			6518	2071	3263	565	612	7		

- Molecule 31 is a protein called NDUEG4.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	E4	351	Total	C	H	N	O	S	0	0
			5502	1774	2732	477	504	15		

- Molecule 32 is a protein called NDUEG5.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	E5	276	Total	C	H	N	O	S	0	0
			4046	1265	2069	341	369	2		

- Molecule 33 is a protein called NDUEG6.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	E6	318	Total	C	H	N	O	S	0	0
			5228	1703	2554	477	482	12		

- Molecule 34 is a protein called NDUEG8.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	E8	205	Total	C	H	N	O	S	0	0
			3354	1100	1663	288	292	11		

- Molecule 35 is a protein called NDUEG10.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	EA	124	Total	C	H	N	O	S	0	0
			1793	630	832	172	156	3		

- Molecule 36 is a protein called NDUEG11.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	EB	101	Total	C	H	N	O	S	0	0
			1405	473	631	150	144	7		

- Molecule 37 is a protein called NDUEG12.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	EC	85	Total	C	H	N	O	S	0	0
			1323	424	663	116	118	2		

- Molecule 38 is a protein called NDUEG13.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	ED	138	Total	C	H	N	O	S	0	0
			2273	736	1131	205	196	5		

- Molecule 39 is a protein called NDUFEX.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	FX	237	Total	C	H	N	O	S	0	0
			3816	1263	1849	338	359	7		

- Molecule 40 is a protein called NDUCA1.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	G1	403	Total	C	H	N	O	S	0	0
			6146	1979	2999	558	594	16		

- Molecule 41 is a protein called NDUCA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	G2	236	Total	C	H	N	O	S	0	0
			3650	1138	1846	323	338	5		

- Molecule 42 is a protein called NDUCA3.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	G3	261	Total	C	H	N	O	S	0	0
			3905	1226	1944	356	373	6		

- Molecule 43 is a protein called ND1.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	N1	310	Total	C	H	N	O	S	0	0
			5331	1783	2726	380	435	7		

- Molecule 44 is a protein called ND2A.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	N2	296	Total	C	H	N	O	S	0	0
			5101	1725	2589	362	418	7		

- Molecule 45 is a protein called ND3.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	N3	121	Total	C	H	N	O	S	0	0
			2094	720	1057	143	172	2		
45	N6	154	Total	C	H	N	O	S	0	0
			2642	857	1385	187	210	3		

- Molecule 46 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	N4	478	Total	C	H	N	O	S	0	0
			8215	2743	4214	582	663	13		

- Molecule 47 is a protein called ND5.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	N5	584	Total	C	H	N	O	S	0	0
			9869	3293	5032	711	808	25		

- Molecule 48 is a protein called NDUFS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	S2	394	Total	C	H	N	O	S	0	0
			6274	2041	3101	541	569	22		

- Molecule 49 is a protein called NDUFS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	S3	248	Total	C	H	N	O	S	0	0
			3978	1307	1928	346	384	13		

- Molecule 50 is a protein called NDUFS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	S4	190	Total	C	H	N	O	S	0	0
			3038	956	1502	300	273	7		

- Molecule 51 is a protein called NDUFS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	S5	122	Total	C	H	N	O	S	0	0
			1886	625	895	173	188	5		

- Molecule 52 is a protein called NDUFS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	S6	147	Total	C	H	N	O	S	0	0
			2392	759	1192	225	208	8		

- Molecule 53 is a protein called NDUFS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	S7	201	Total	C	H	N	O	S	0	0
			3045	975	1500	272	284	14		

- Molecule 54 is a protein called NDUFS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	S8	182	Total	C	H	N	O	S	0	0
			2843	915	1392	245	275	16		

- Molecule 55 is a protein called UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	U1	12	Total	C	H	N	O	0	0
			76	36	16	12	12		
55	U2	12	Total	C	H	N	O	0	0
			76	36	16	12	12		

- Molecule 56 is a protein called NDUFV1.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	V1	504	Total	C	H	N	O	S	0	0
			7724	2463	3827	680	727	27		

- Molecule 57 is a protein called NDUFV2.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	V2	225	Total	C	H	N	O	S	0	0
			3460	1124	1701	299	319	17		

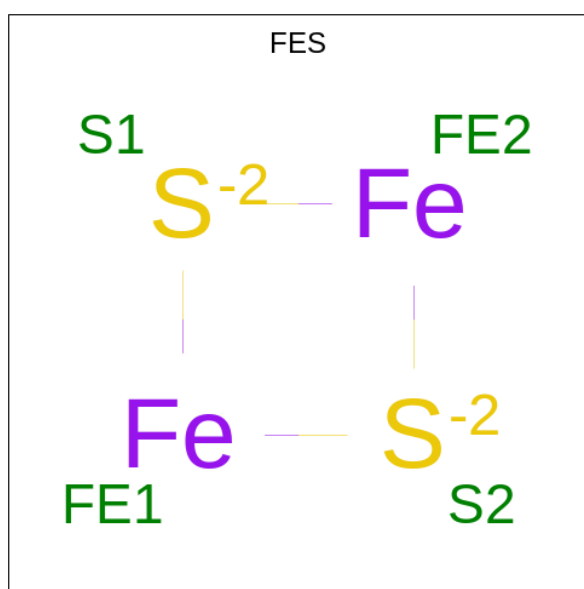
- Molecule 58 is a protein called NDUEG7.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	E7	246	Total	C	H	N	O	S	0	0
			3780	1205	1892	332	344	7		

- Molecule 59 is a protein called NDUFAB1-beta.

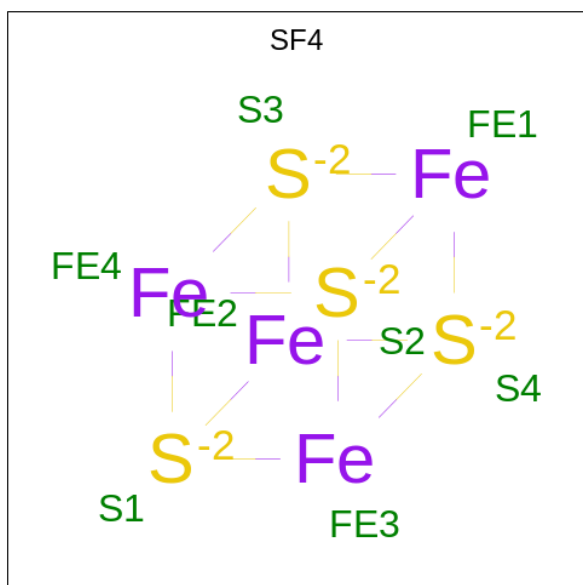
Mol	Chain	Residues	Atoms						AltConf	Trace
59	AC	92	Total	C	H	N	O	S	0	0
			1418	461	697	116	140	4		

- Molecule 60 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			AltConf
60	1A	1	Total	Fe	S	0
			4	2	2	
60	V2	1	Total	Fe	S	0
			4	2	2	

- Molecule 61 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).

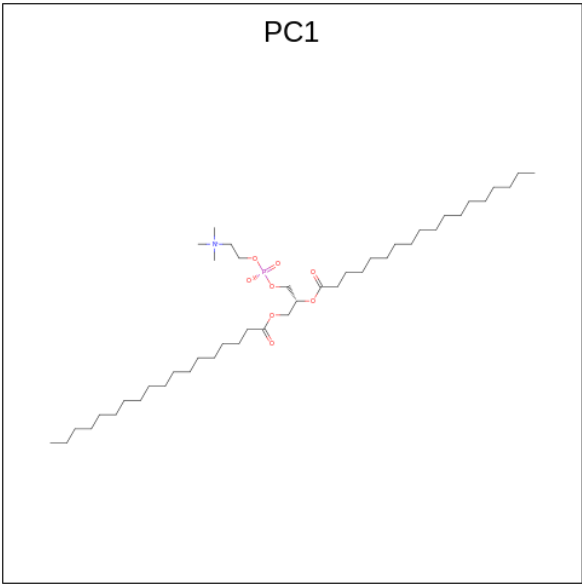


Mol	Chain	Residues	Atoms			AltConf
61	1A	1	Total	Fe	S	0
			8	4	4	
61	1A	1	Total	Fe	S	0
			8	4	4	
61	S7	1	Total	Fe	S	0
			8	4	4	
61	S8	1	Total	Fe	S	0
			8	4	4	
61	S8	1	Total	Fe	S	0
			8	4	4	
61	V1	1	Total	Fe	S	0
			8	4	4	

- Molecule 62 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
62	1A	1	Total	K	0
			1	1	

- Molecule 63 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



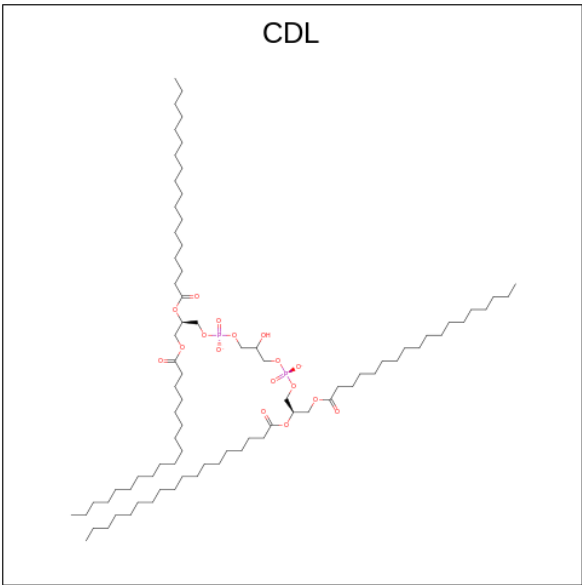
Mol	Chain	Residues	Atoms						AltConf
63	A1	1	Total	C	H	N	O	P	0
			124	39	75	1	8	1	
63	A1	1	Total	C	H	N	O	P	0
			67	21	36	1	8	1	
63	A9	1	Total	C	H	N	O	P	0
			73	23	40	1	8	1	
63	A9	1	Total	C	H	N	O	P	0
			73	23	40	1	8	1	
63	AL	1	Total	C	H	N	O	P	0
			127	40	77	1	8	1	
63	AM	1	Total	C	H	N	O	P	0
			124	39	75	1	8	1	
63	AM	1	Total	C	H	N	O	P	0
			121	38	73	1	8	1	
63	AN	1	Total	C	H	N	O	P	0
			121	38	73	1	8	1	
63	B5	1	Total	C	H	N	O	P	0
			142	44	88	1	8	1	
63	B5	1	Total	C	H	N	O	P	0
			142	44	88	1	8	1	
63	C4	1	Total	C	H	N	O	P	0
			88	28	50	1	8	1	
63	E4	1	Total	C	H	N	O	P	0
			130	41	79	1	8	1	

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Mol	Chain	Residues	Atoms						AltConf
63	E8	1	Total 142	C 44	H 88	N 1	O 8	P 1	0
63	E8	1	Total 142	C 44	H 88	N 1	O 8	P 1	0
63	E8	1	Total 73	C 23	H 40	N 1	O 8	P 1	0
63	E8	1	Total 64	C 20	H 34	N 1	O 8	P 1	0
63	ED	1	Total 142	C 44	H 88	N 1	O 8	P 1	0
63	N1	1	Total 124	C 39	H 75	N 1	O 8	P 1	0
63	N1	1	Total 94	C 30	H 54	N 1	O 8	P 1	0
63	N2	1	Total 85	C 27	H 48	N 1	O 8	P 1	0
63	N3	1	Total 103	C 32	H 61	N 1	O 8	P 1	0
63	N4	1	Total 91	C 29	H 52	N 1	O 8	P 1	0
63	N4	1	Total 73	C 23	H 40	N 1	O 8	P 1	0
63	N5	1	Total 142	C 44	H 88	N 1	O 8	P 1	0
63	N5	1	Total 97	C 31	H 56	N 1	O 8	P 1	0
63	N5	1	Total 82	C 26	H 46	N 1	O 8	P 1	0

- Molecule 64 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



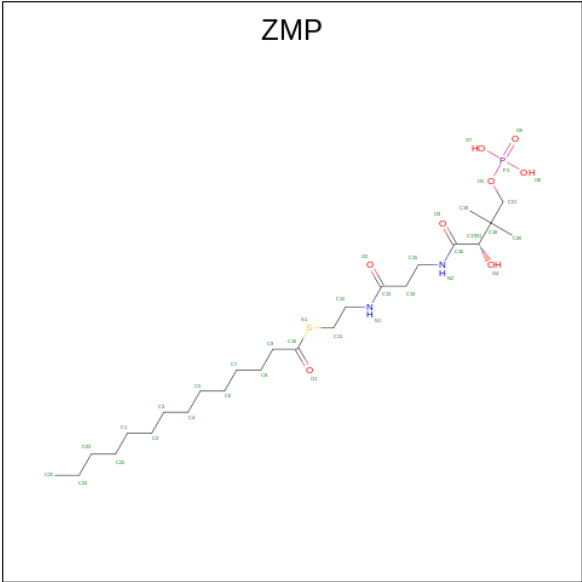
Mol	Chain	Residues	Atoms					AltConf
64	A3	1	Total	C	H	O	P	0
			118	39	60	17	2	
64	AL	1	Total	C	H	O	P	0
			148	49	80	17	2	
64	AL	1	Total	C	H	O	P	0
			136	45	72	17	2	
64	AL	1	Total	C	H	O	P	0
			154	51	84	17	2	
64	AM	1	Total	C	H	O	P	0
			163	53	91	17	2	
64	AM	1	Total	C	H	O	P	0
			163	53	91	17	2	
64	AM	1	Total	C	H	O	P	0
			163	53	91	17	2	
64	B3	1	Total	C	H	O	P	0
			139	46	74	17	2	
64	B5	1	Total	C	H	O	P	0
			118	39	60	17	2	
64	C4	1	Total	C	H	O	P	0
			235	75	141	17	2	
64	C4	1	Total	C	H	O	P	0
			151	50	82	17	2	
64	E6	1	Total	C	H	O	P	0
			136	45	72	17	2	
64	EA	1	Total	C	H	O	P	0
			121	40	62	17	2	
64	EA	1	Total	C	H	O	P	0
			109	36	54	17	2	

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Mol	Chain	Residues	Atoms					AltConf
64	N4	1	Total 247	C 79	H 149	O 17	P 2	0
64	N5	1	Total 157	C 51	H 87	O 17	P 2	0
64	N5	1	Total 229	C 74	H 136	O 17	P 2	0
64	E7	1	Total 148	C 49	H 80	O 17	P 2	0

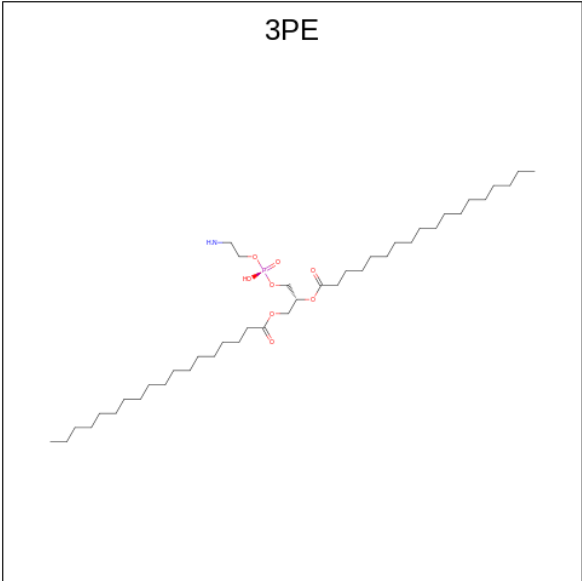
- # NDP

- Molecule 66 is S-[2-($\{N-[(2S)-2\text{-hydroxy-}3,3\text{-dimethyl-}4\text{-(phosphonooxy)butanoyl]-}\beta\text{-alanine}\}$)amino)ethyl] tetradecanethioate (CCD ID: ZMP) (formula: $C_{25}H_{49}N_2O_8PS$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
66	AB	1	Total	C	N	O	P	S	0
			36	25	2	7	1	1	
66	AC	1	Total	C	N	O	P	S	0
			36	25	2	7	1	1	

- Molecule 67 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



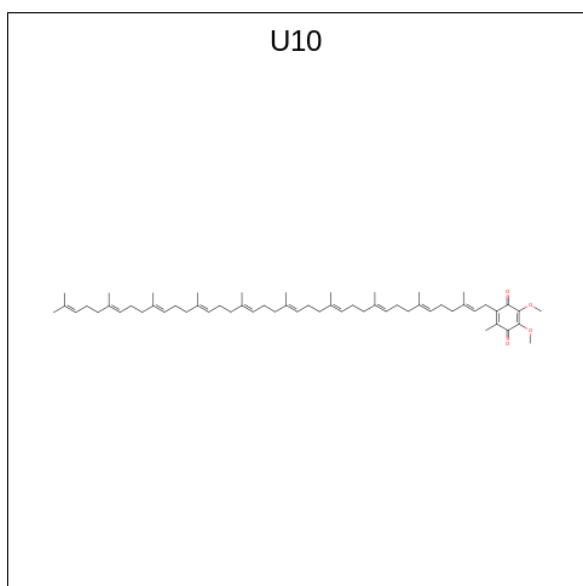
Mol	Chain	Residues	Atoms						AltConf
67	AN	1	Total	C	H	N	O	P	0
			132	41	81	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
67	G1	1	Total	C	H	N	O	P
			96	30	56	1	8	1
67	N4	1	Total	C	H	N	O	P
			96	31	55	1	8	1
67	N5	1	Total	C	H	N	O	P
			132	41	81	1	8	1

- Molecule 68 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).

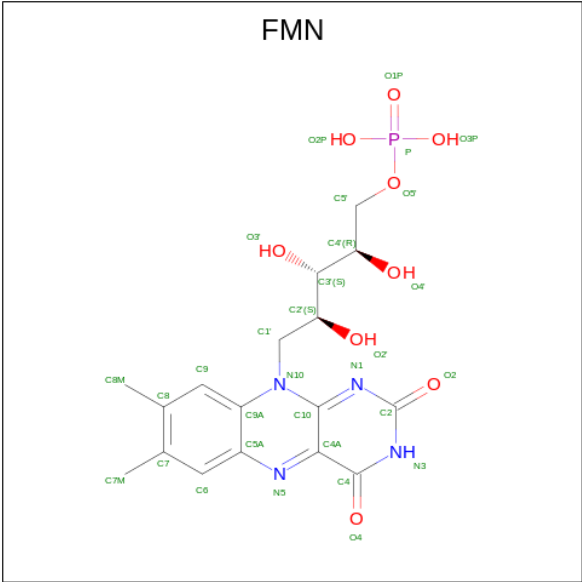


Mol	Chain	Residues	Atoms				AltConf
68	N4	1	Total	C	H	O	
			98	39	55	4	0

- Molecule 69 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
69	S6	1	Total	Zn	
			1	1	0
69	E7	1	Total	Zn	
			1	1	0

- Molecule 70 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).

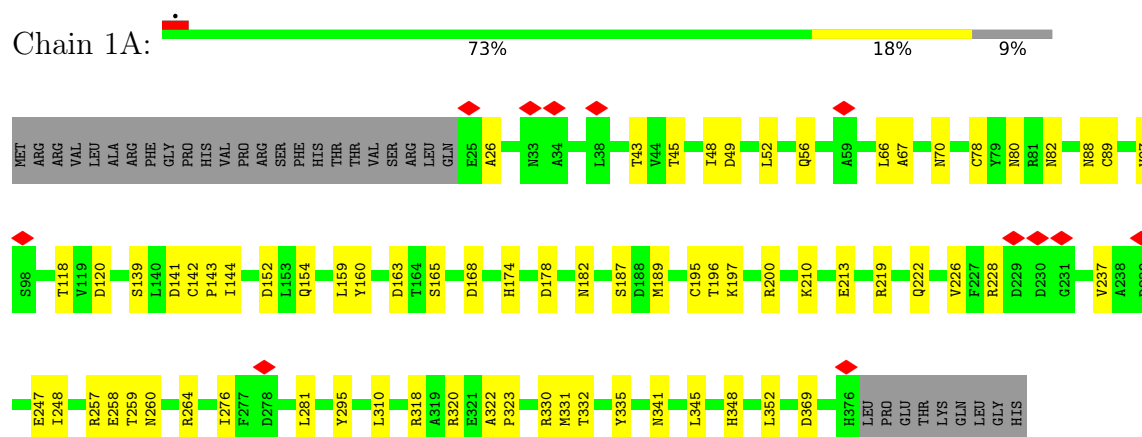


Mol	Chain	Residues	Atoms						AltConf
70	V1	1	Total	C	H	N	O	P	0
			50	17	19	4	9	1	

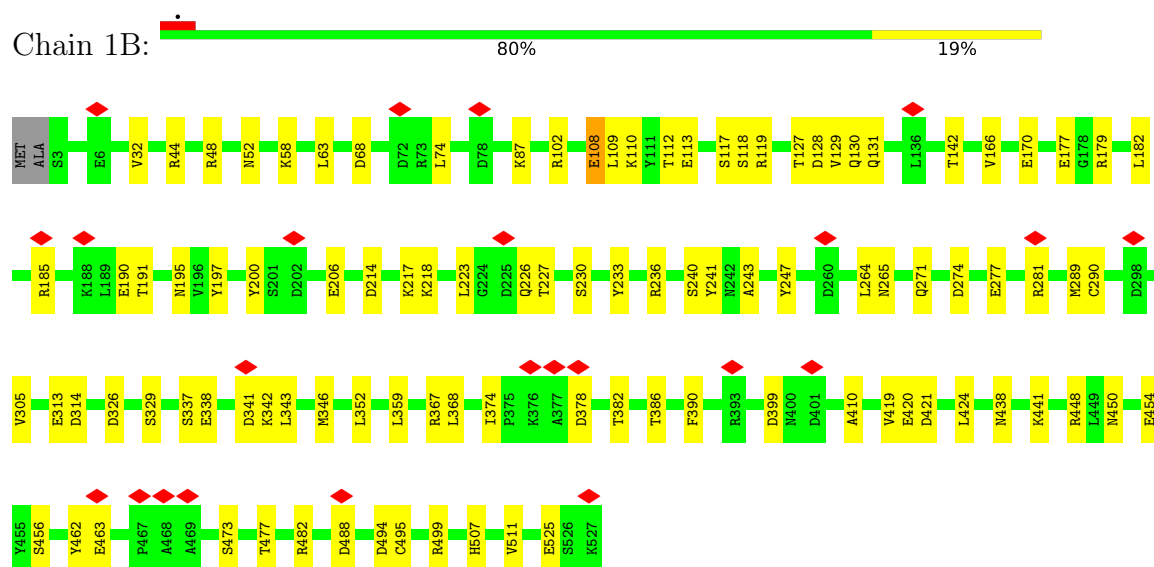
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

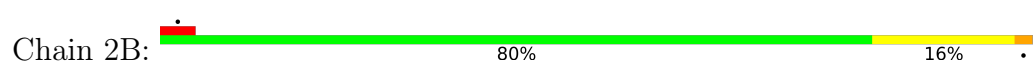
• Molecule 1: NDUS1A

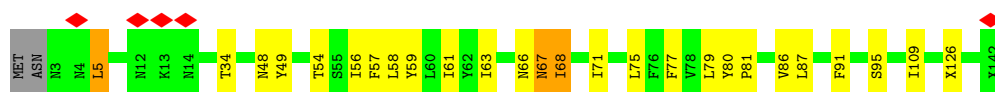


• Molecule 2: NDUS1B

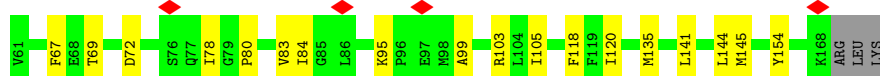
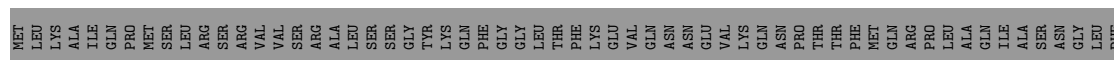


• Molecule 3: NADH dehydrogenase subunit 5

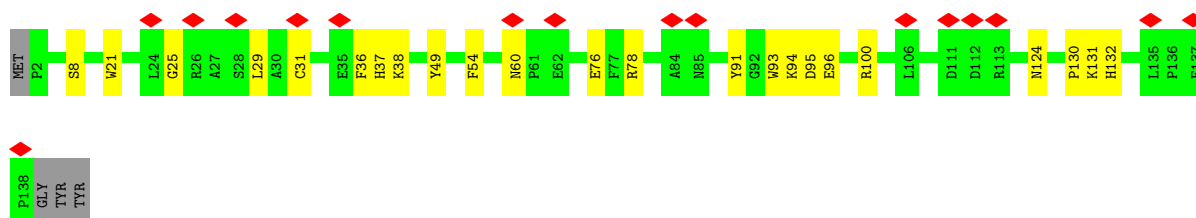
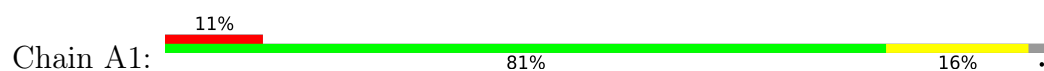




• Molecule 4: ND4L



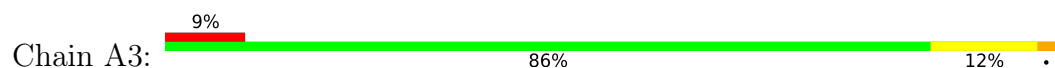
• Molecule 5: NDUFA1



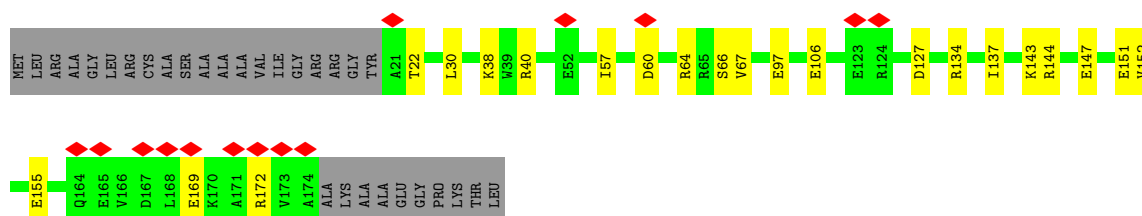
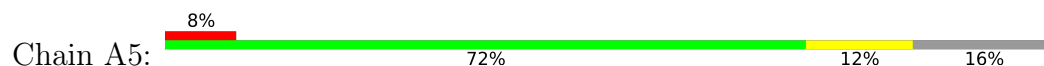
• Molecule 6: NDUFA2



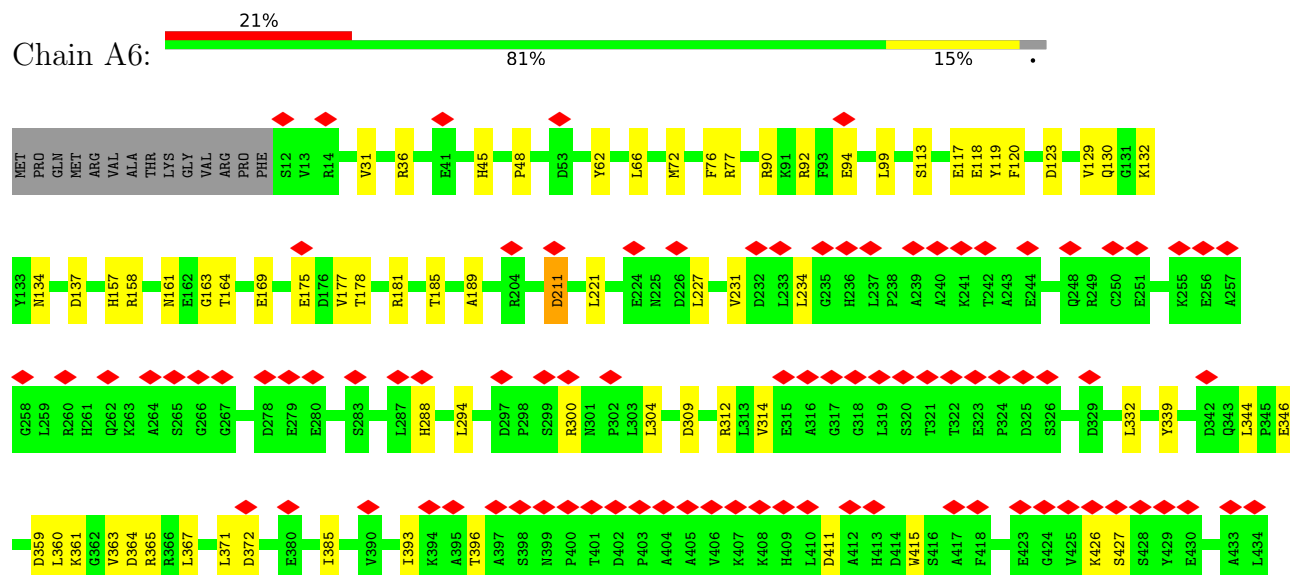
• Molecule 7: NDUFA3



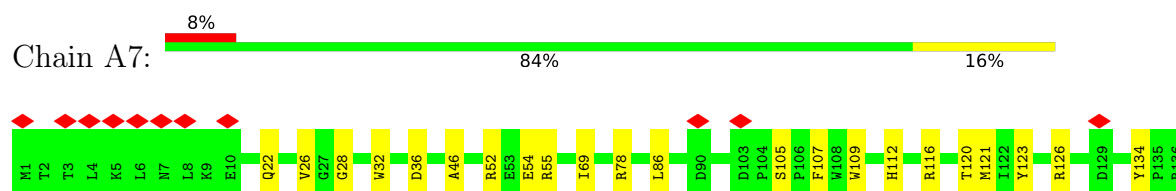
• Molecule 8: NDUFA5



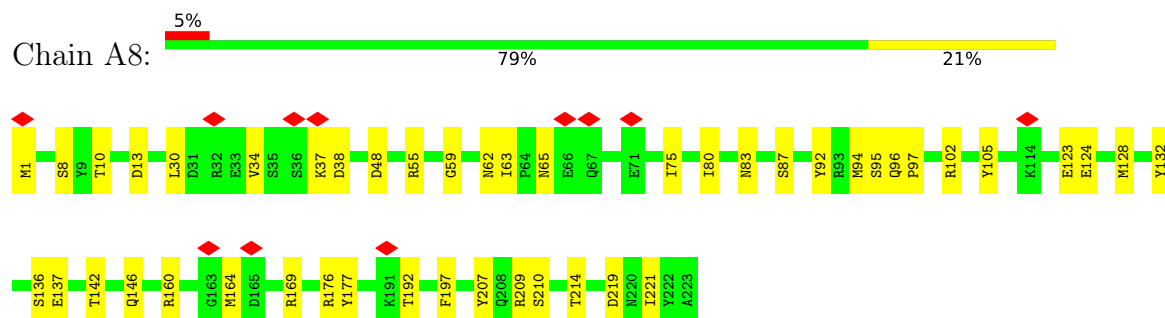
- Molecule 9: NDUFA6



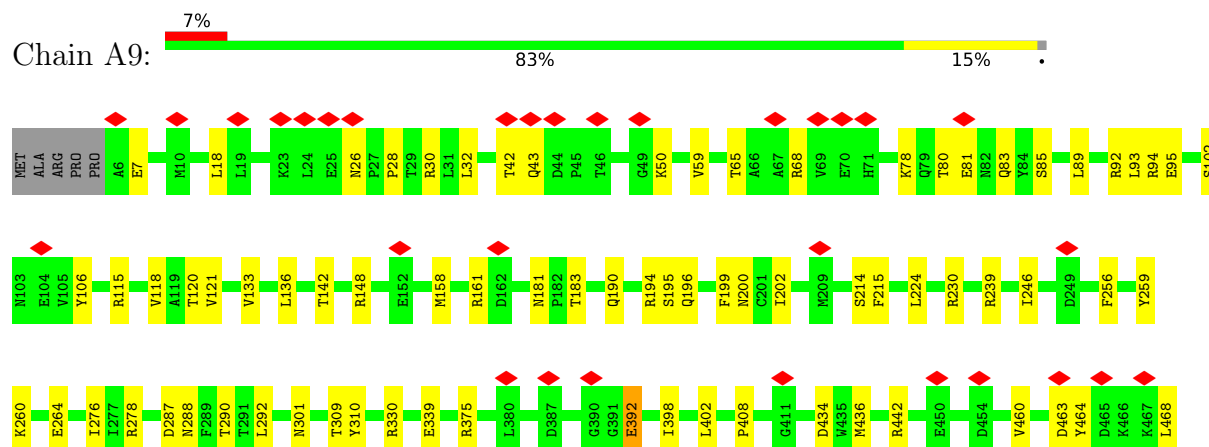
- Molecule 10: NDUFA7

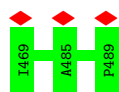


- Molecule 11: NDUFA8

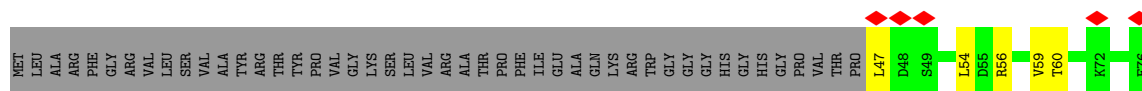


- Molecule 12: NDUFA9

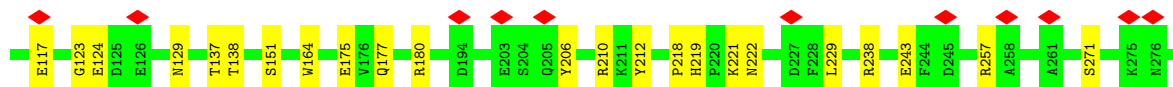
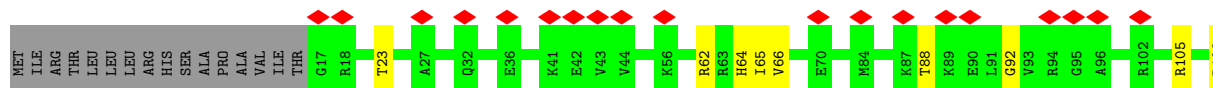
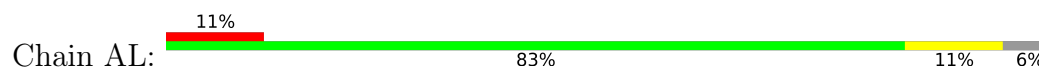




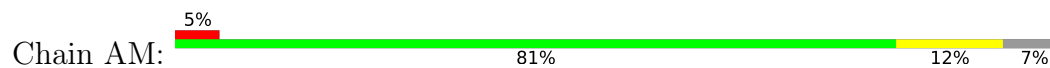
• Molecule 13: NDUFAB1-alpha



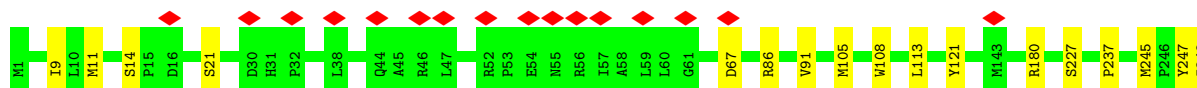
• Molecule 14: NDUFA12

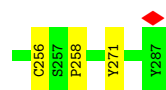


• Molecule 15: NDUFA13

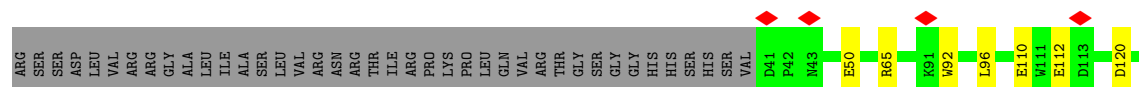


• Molecule 16: NDUFA11

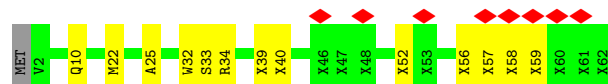
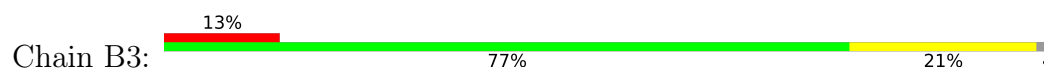




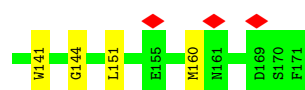
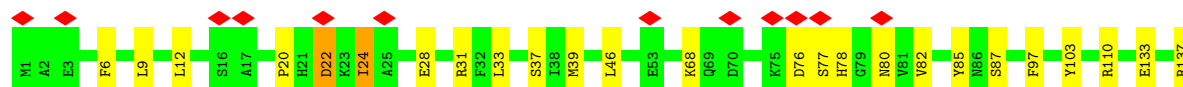
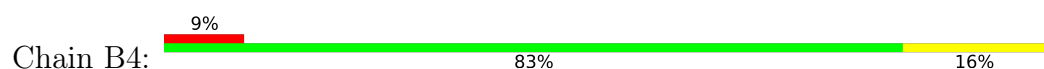
• Molecule 17: NDUFB2



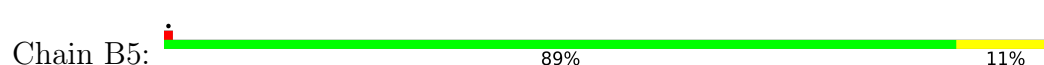
• Molecule 18: NDUFB3



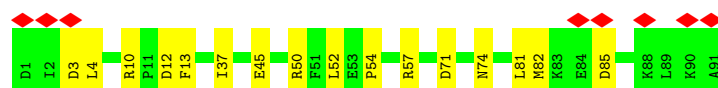
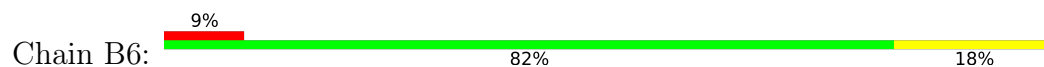
• Molecule 19: NDUFB4



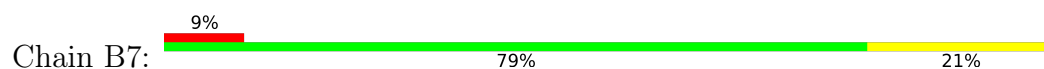
• Molecule 20: NDUFB5

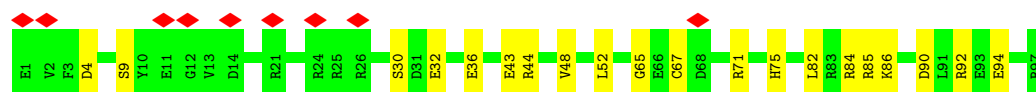


• Molecule 21: NDUFB6

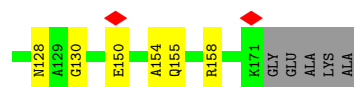
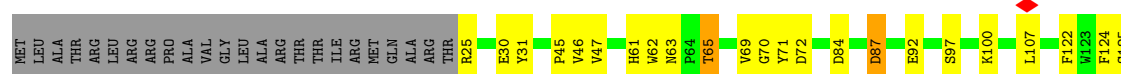


• Molecule 22: NDUFB7

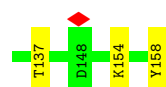
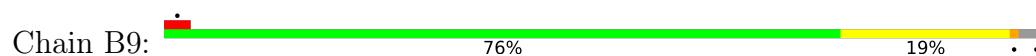




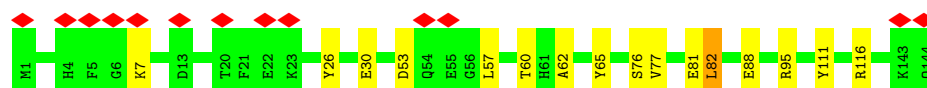
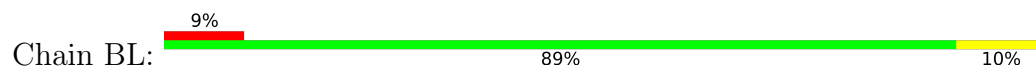
• Molecule 23: NDUFB8



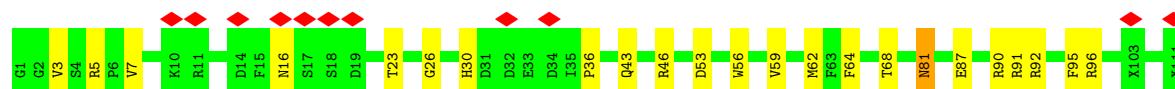
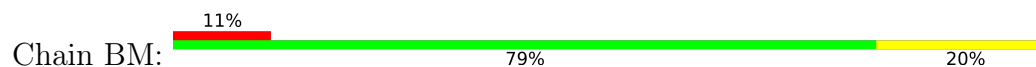
• Molecule 24: NDUFB9



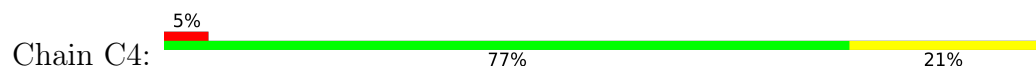
• Molecule 25: NDUFB10

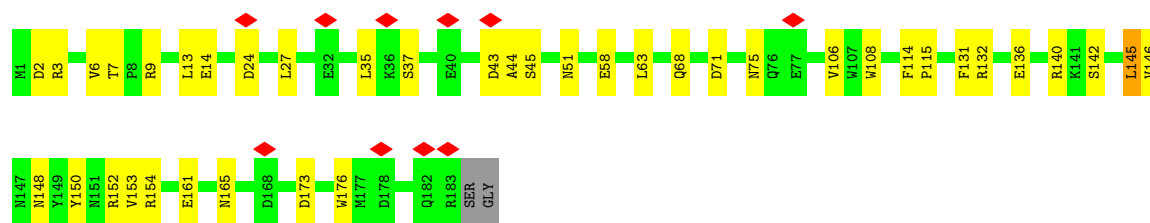


• Molecule 26: NDUFB11

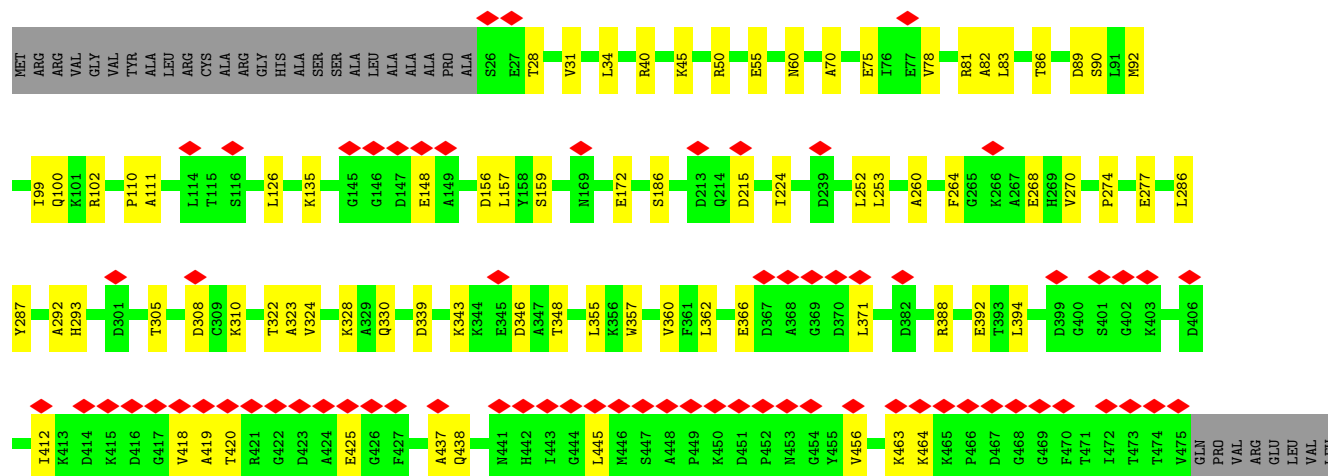
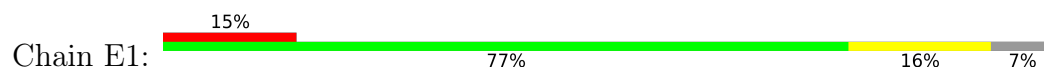


• Molecule 27: NDUFC2

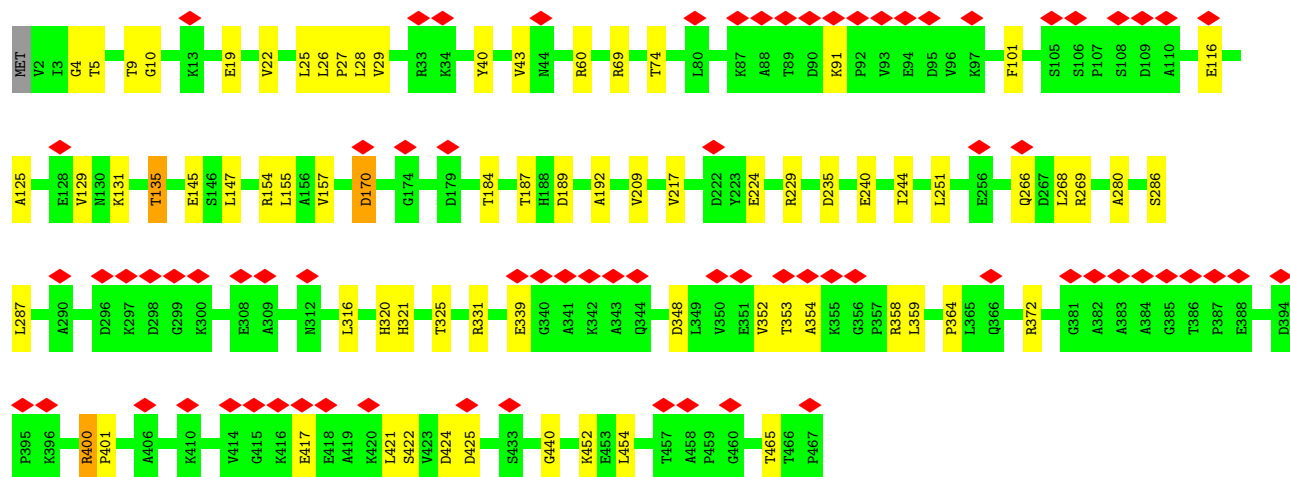
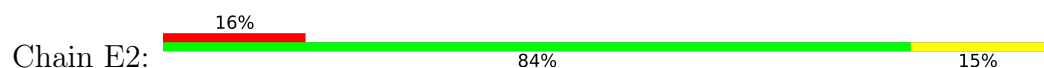




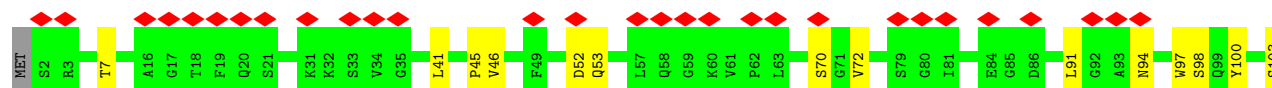
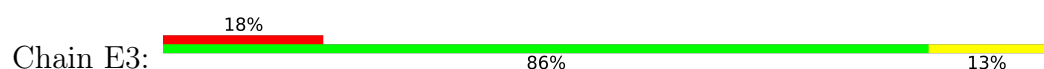
• Molecule 28: NDUEG1

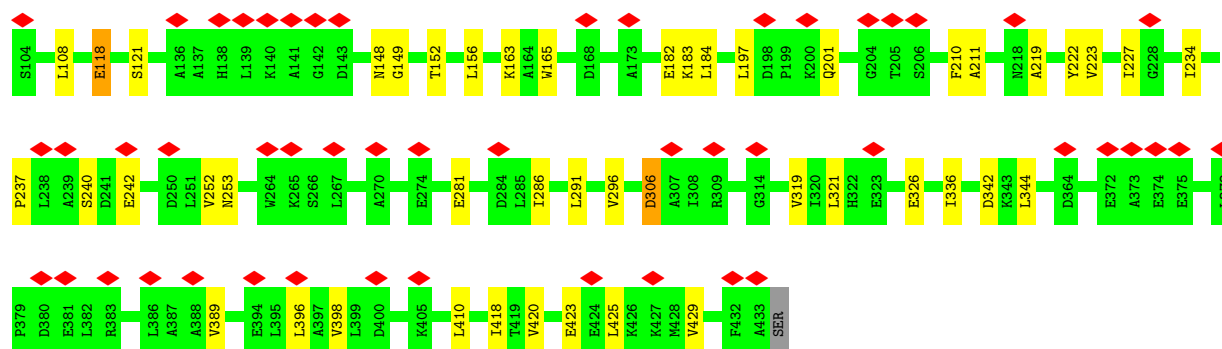


• Molecule 29: NDUEG2

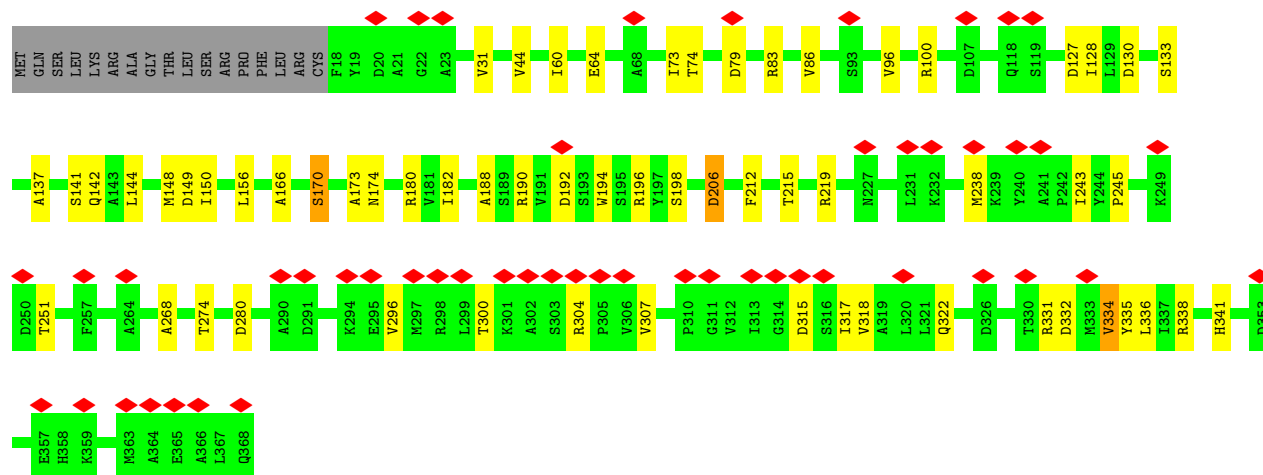
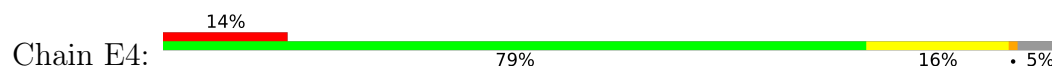


• Molecule 30: NDUEG3

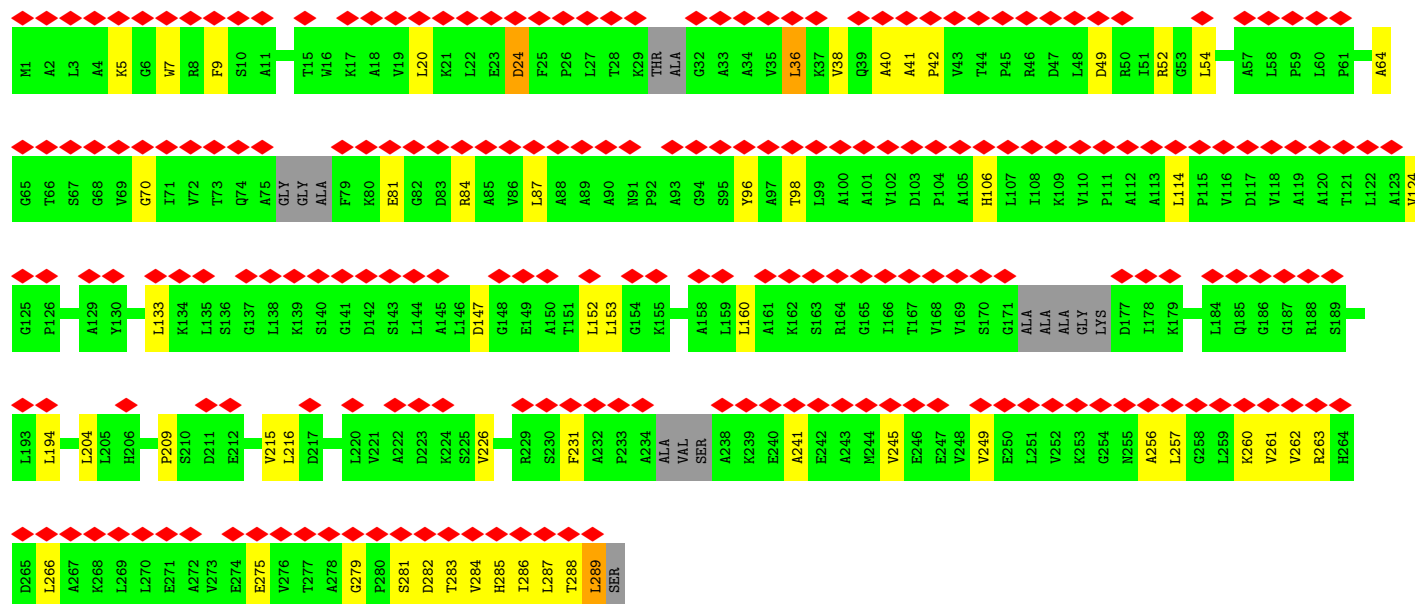
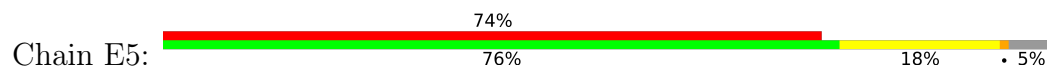




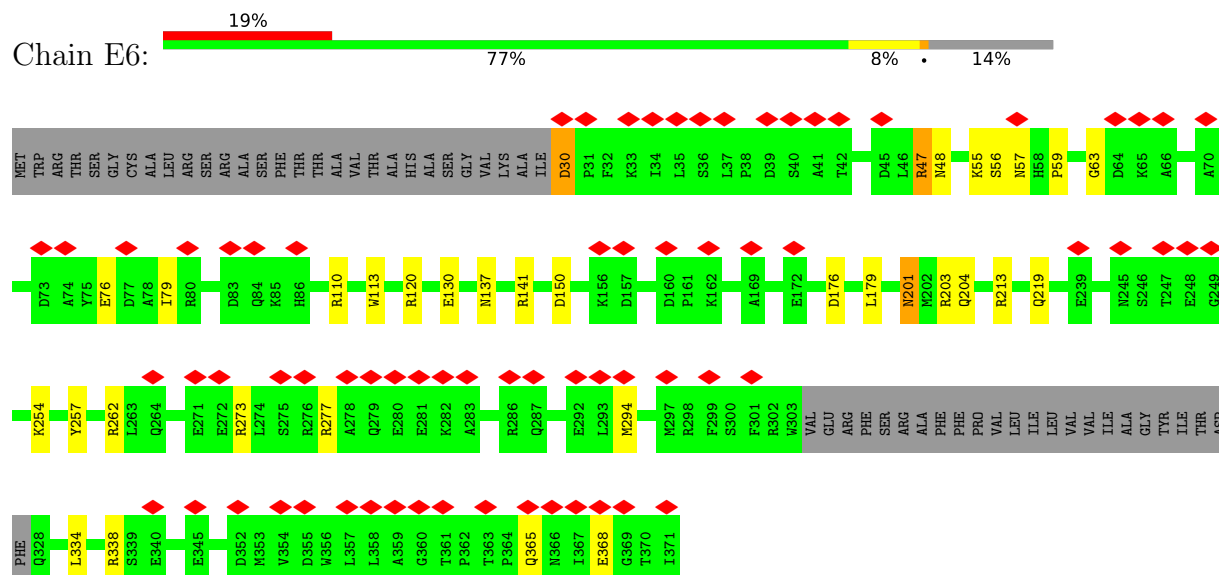
• Molecule 31: NDUEG4



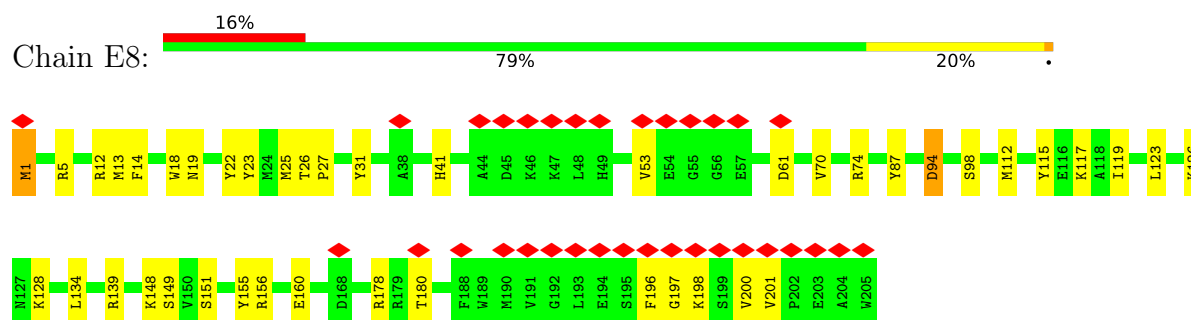
• Molecule 32: NDUEG5



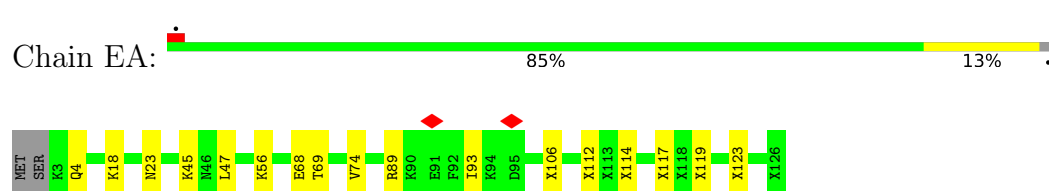
- Molecule 33: NDUEG6



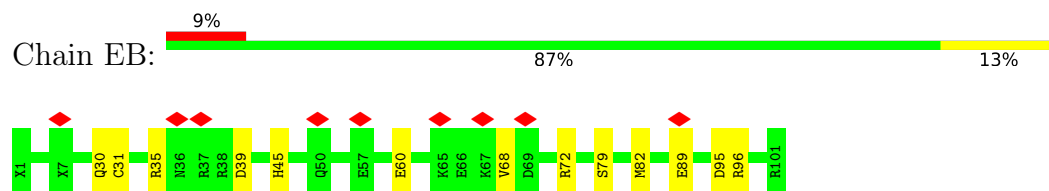
- Molecule 34: NDUEG8



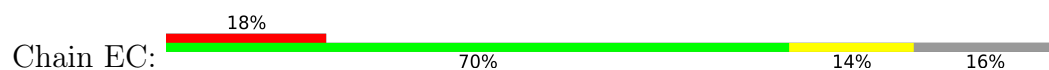
- Molecule 35: NDUEG10

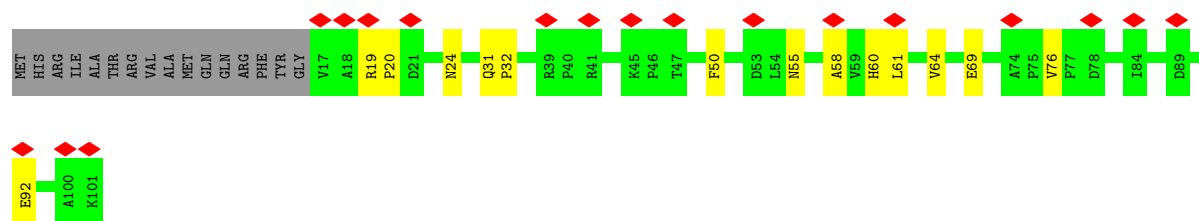


- Molecule 36: NDUEG11

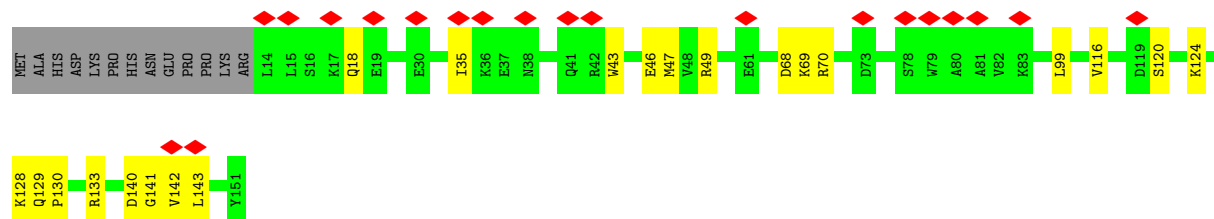
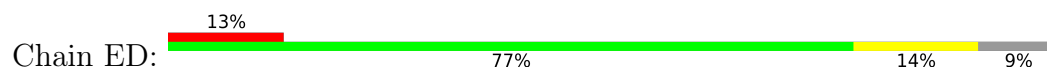


- Molecule 37: NDUEG12

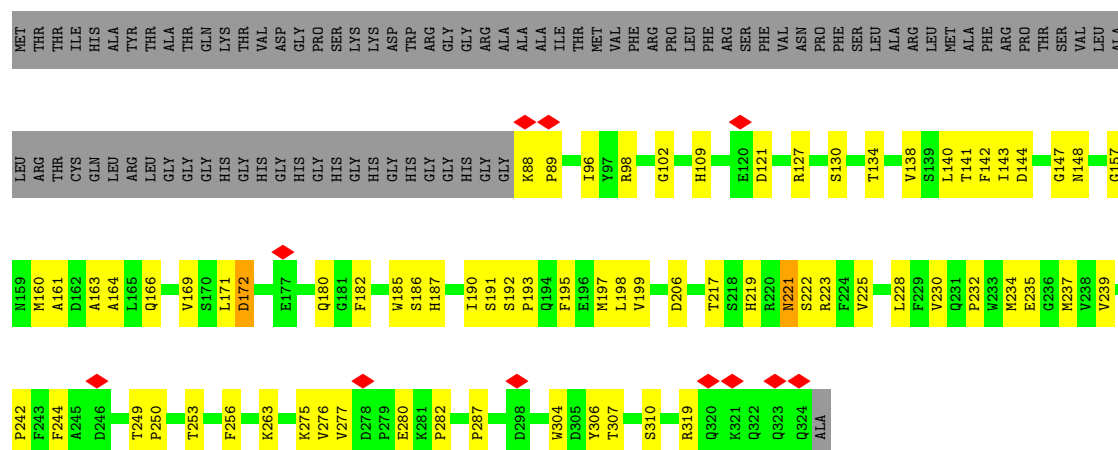




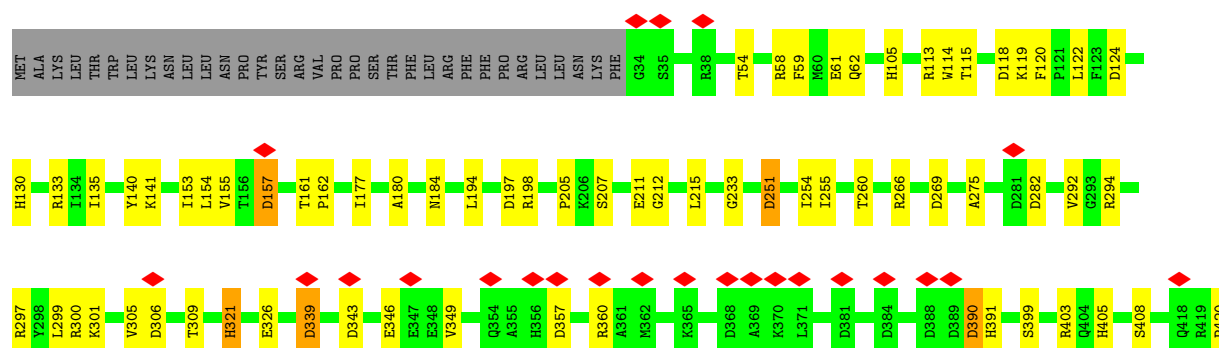
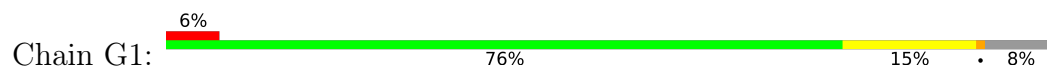
• Molecule 38: NDUEG13



• Molecule 39: NDUFX



• Molecule 40: NDUCA1



- Molecule 46: NADH-ubiquinone oxidoreductase chain 4

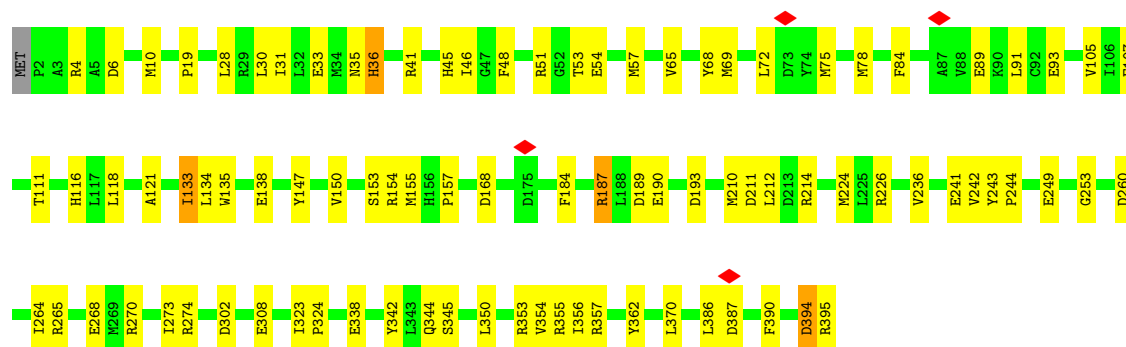
Frequency	Percentage
Often	70%
Sometimes	29%



Frequency	Percentage
Daily	69%
Weekly	29%
Monthly	2%

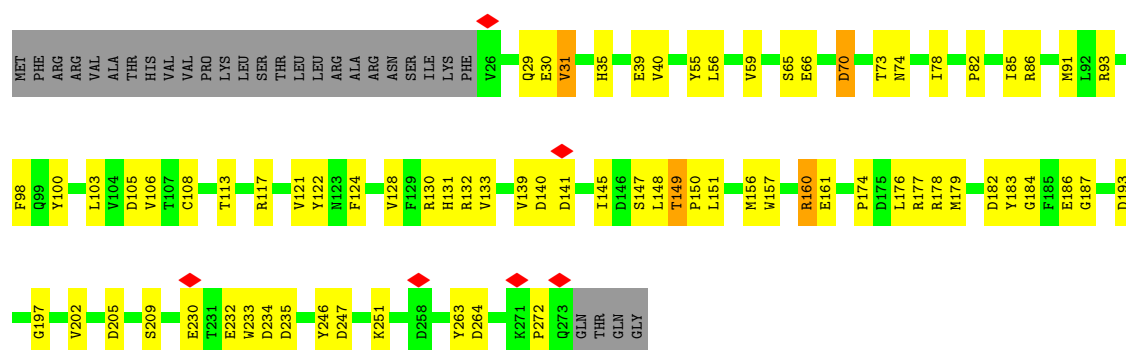


Opinion	Percentage
Doing a good job	77%
Doing a bad job	22%



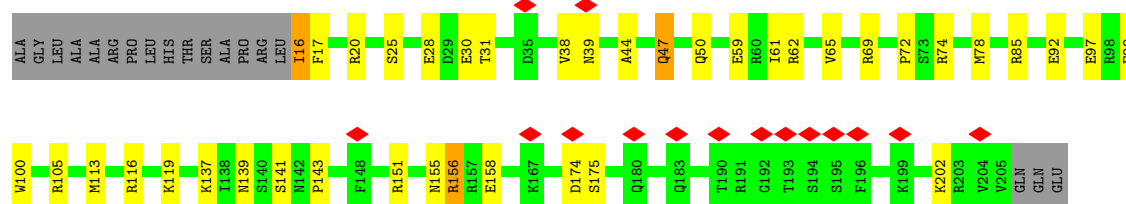
• Molecule 49: NDUFS3

Chain S3: 62% 26% 10%



• Molecule 50: NDUFS4

Chain S4: 72% 18% 9%



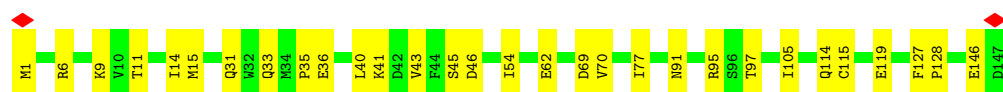
• Molecule 51: NDUFS5

Chain S5: 93% 7% 6%

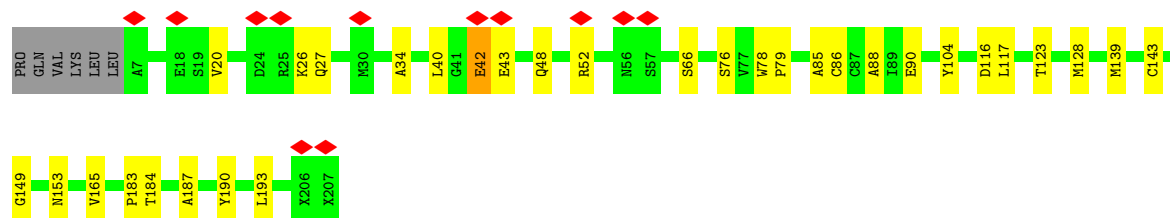
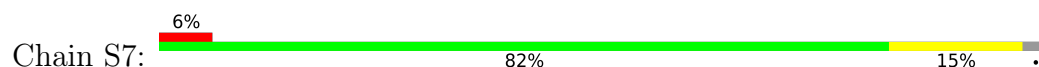


• Molecule 52: NDUFS6

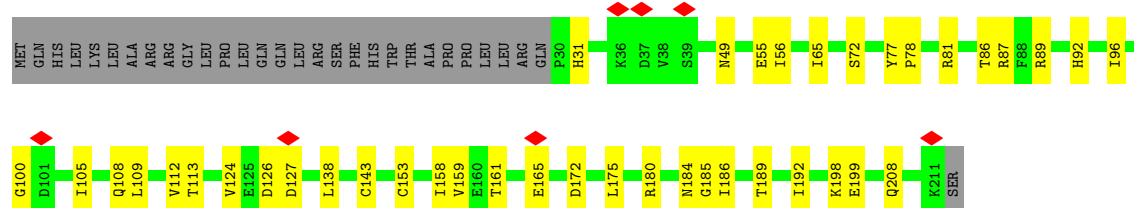
Chain S6: 80% 20%



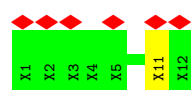
• Molecule 53: NDUF57



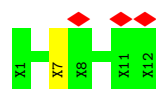
• Molecule 54: NDUF58



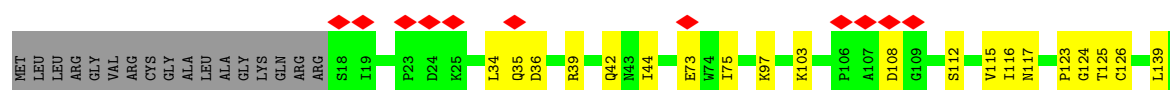
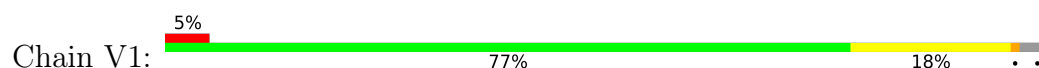
• Molecule 55: UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK

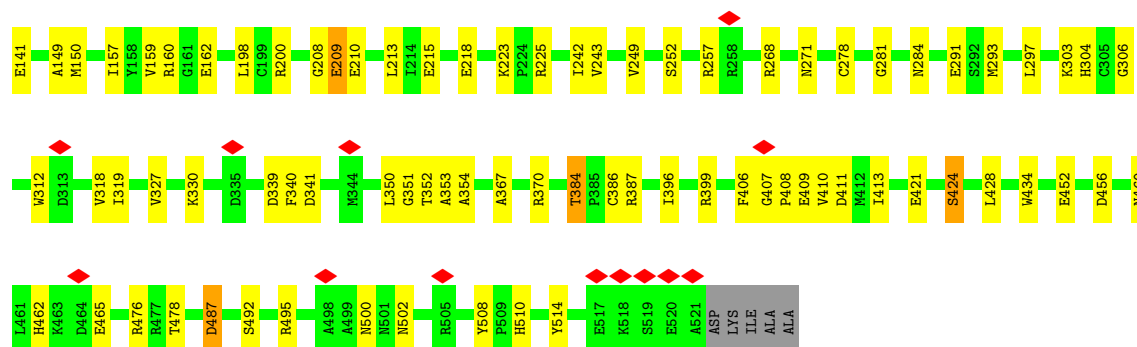


• Molecule 55: UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK

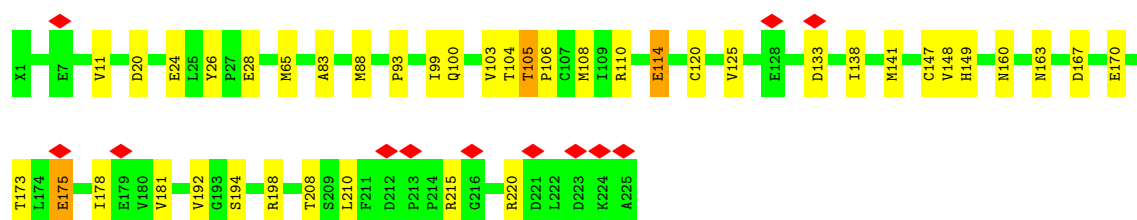
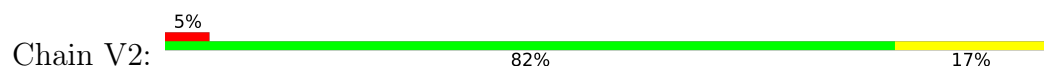


• Molecule 56: NDUFV1

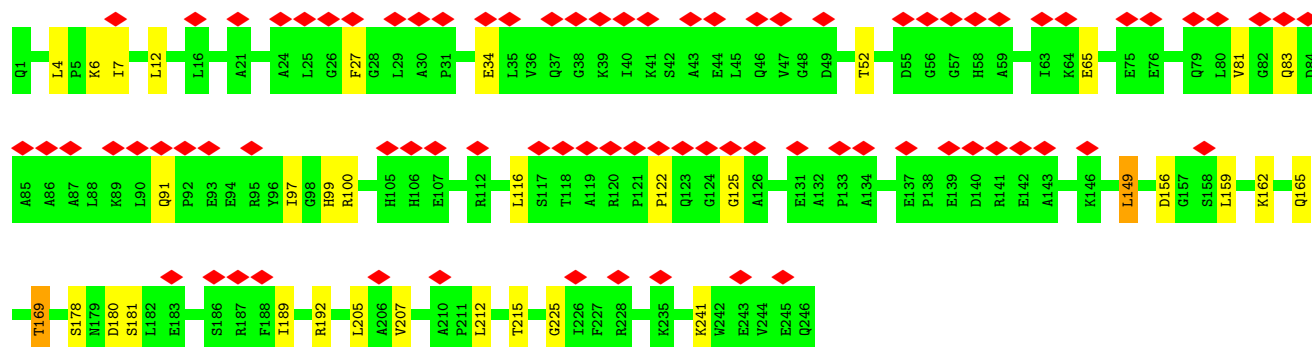
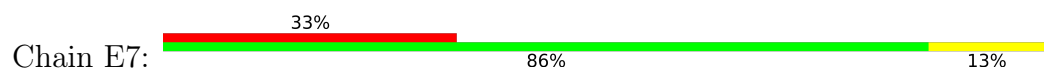




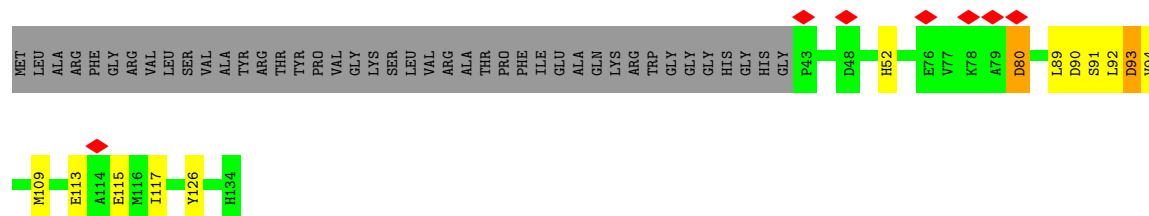
• Molecule 57: NDUFV2



• Molecule 58: NDUEG7



• Molecule 59: NDUFAB1-beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68660	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	41.957	Depositor
Minimum map value	-16.100	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.994	Depositor
Recommended contour level	5	Depositor
Map size (Å)	446.4, 446.4, 446.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MR, CDL, ZMP, K, NDP, ZN, 3PE, SF4, PC1, FMN, FES, U10

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1A	0.20	0/2858	0.33	0/3878
2	1B	0.17	0/4306	0.28	0/5854
3	2B	0.20	0/958	0.34	0/1306
4	4L	0.19	0/924	0.28	0/1261
5	A1	0.14	0/1108	0.27	0/1511
6	A2	0.15	0/1530	0.28	0/2089
7	A3	0.16	0/1079	0.29	0/1453
8	A5	0.16	0/1282	0.25	0/1737
9	A6	0.15	0/3395	0.27	0/4608
10	A7	0.17	0/1194	0.31	0/1619
11	A8	0.15	0/1879	0.26	0/2543
12	A9	0.17	0/3920	0.29	0/5335
13	AB	0.16	0/704	0.24	0/951
14	AL	0.15	0/2317	0.28	0/3136
15	AM	0.16	0/1533	0.24	0/2079
16	AN	0.15	0/2382	0.25	0/3249
17	B2	0.16	0/947	0.24	0/1291
18	B3	0.17	0/326	0.26	0/441
19	B4	0.18	0/1419	0.29	0/1922
20	B5	0.19	0/1111	0.29	0/1505
21	B6	0.17	0/803	0.27	0/1087
22	B7	0.15	0/877	0.25	0/1172
23	B8	0.19	0/1273	0.27	0/1733
24	B9	0.19	0/1274	0.32	0/1728
25	BL	0.19	0/1266	0.30	0/1710
26	BM	0.19	0/876	0.30	0/1192
27	C4	0.17	0/1592	0.28	0/2158
28	E1	0.14	0/3596	0.27	0/4879
29	E2	0.14	0/3658	0.26	0/4983
30	E3	0.14	0/3320	0.27	0/4520
31	E4	0.15	0/2850	0.26	0/3884
32	E5	0.13	0/2004	0.33	0/2721

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	E6	0.14	0/2750	0.25	0/3724
34	E8	0.16	0/1747	0.29	0/2367
35	EA	0.19	0/858	0.29	0/1163
36	EB	0.13	0/650	0.24	0/863
37	EC	0.15	0/676	0.27	0/925
38	ED	0.14	0/1176	0.27	0/1590
39	FX	0.20	0/2035	0.33	0/2763
40	G1	0.18	0/3234	0.31	0/4401
41	G2	0.17	0/1832	0.29	0/2476
42	G3	0.17	0/1957	0.30	0/2646
43	N1	0.17	0/2672	0.33	0/3639
44	N2	0.21	0/2582	0.32	0/3530
45	N3	0.19	0/1068	0.35	0/1456
45	N6	0.17	0/1275	0.32	0/1730
46	N4	0.21	0/4105	0.35	0/5594
47	N5	0.20	0/4963	0.35	0/6758
48	S2	0.21	0/3244	0.33	0/4403
49	S3	0.19	0/2112	0.32	0/2874
50	S4	0.17	0/1573	0.29	0/2107
51	S5	0.13	0/960	0.24	0/1291
52	S6	0.17	0/1232	0.29	0/1659
53	S7	0.18	0/1558	0.28	0/2120
54	S8	0.20	0/1485	0.30	0/2010
56	V1	0.16	0/3990	0.29	0/5394
57	V2	0.16	0/1787	0.29	0/2428
58	E7	0.15	0/1931	0.27	0/2618
59	AC	0.17	0/736	0.25	0/1000
All	All	0.17	0/112749	0.29	0/153064

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	2801	2700	2710	53	0
2	1B	4198	4159	4175	76	0
3	2B	1070	989	1008	24	0
4	4L	890	878	880	19	0
5	A1	1071	1026	1030	15	0
6	A2	1493	1474	1478	15	0
7	A3	1050	1039	1041	15	0
8	A5	1261	1248	1251	15	0
9	A6	3328	3280	3293	57	0
10	A7	1154	1118	1123	23	0
11	A8	1822	1726	1736	40	0
12	A9	3829	3850	3857	57	0
13	AB	694	673	677	14	0
14	AL	2237	2172	2180	27	0
15	AM	1487	1448	1452	26	0
16	AN	2306	2267	2275	16	0
17	B2	913	857	858	13	0
18	B3	449	309	311	11	0
19	B4	1377	1358	1364	27	0
20	B5	1112	1069	1075	15	0
21	B6	773	747	751	19	0
22	B7	857	835	841	13	0
23	B8	1224	1127	1136	25	0
24	B9	1236	1207	1212	34	0
25	BL	1227	1179	1185	13	0
26	BM	910	827	830	25	0
27	C4	1545	1517	1519	30	0
28	E1	3512	3496	3510	48	0
29	E2	3563	3540	3554	44	0
30	E3	3255	3263	3279	45	0
31	E4	2770	2732	2742	51	0
32	E5	1977	2069	2075	45	0
33	E6	2674	2554	2562	25	0
34	E8	1691	1663	1668	37	0
35	EA	961	832	837	11	0
36	EB	774	631	636	11	0
37	EC	660	663	666	10	0
38	ED	1142	1131	1134	16	0
39	FX	1967	1849	1858	58	0
40	G1	3147	2999	3015	58	0
41	G2	1804	1846	1850	31	0
42	G3	1961	1944	1950	35	0
43	N1	2605	2726	2729	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	N2	2512	2589	2592	67	0
45	N3	1037	1057	1057	22	0
45	N6	1257	1385	1385	38	0
46	N4	4001	4214	4224	110	0
47	N5	4837	5032	5046	152	0
48	S2	3173	3101	3114	76	0
49	S3	2050	1928	1936	61	0
50	S4	1536	1502	1505	33	0
51	S5	991	895	898	7	0
52	S6	1200	1192	1198	23	0
53	S7	1545	1500	1503	27	0
54	S8	1451	1392	1397	38	0
55	U1	60	16	19	1	0
55	U2	60	16	17	1	0
56	V1	3897	3827	3837	76	0
57	V2	1759	1701	1711	28	0
58	E7	1888	1892	1903	24	0
59	AC	721	697	702	15	0
60	1A	4	0	0	0	0
60	V2	4	0	0	0	0
61	1A	16	0	0	0	0
61	S7	8	0	0	0	0
61	S8	16	0	0	5	0
61	V1	8	0	0	1	0
62	1A	1	0	0	0	0
63	A1	80	111	111	3	0
63	A9	66	80	80	1	0
63	AL	50	77	77	0	0
63	AM	97	148	148	1	0
63	AN	48	73	73	0	0
63	B5	108	176	176	2	0
63	C4	38	50	50	1	0
63	E4	51	79	79	0	0
63	E8	171	250	250	3	0
63	ED	54	88	88	1	0
63	N1	89	129	129	0	0
63	N2	37	48	48	1	0
63	N3	42	61	61	0	0
63	N4	72	92	92	2	0
63	N5	131	190	190	1	0
64	A3	58	60	60	1	0
64	AL	202	236	236	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	AM	216	273	273	10	0
64	B3	65	74	74	1	0
64	B5	58	60	60	1	0
64	C4	163	223	223	1	0
64	E6	64	72	72	0	0
64	E7	68	80	80	0	0
64	EA	114	116	116	1	0
64	N4	98	149	149	4	0
64	N5	163	223	223	4	0
65	A9	48	26	26	3	0
66	AB	36	0	47	6	0
66	AC	36	0	47	15	0
67	AN	51	81	82	0	0
67	G1	40	56	57	2	0
67	N4	41	55	56	0	0
67	N5	51	81	82	1	0
68	N4	43	55	55	5	0
69	E7	1	0	0	0	0
69	S6	1	0	0	0	0
70	V1	31	19	19	0	0
All	All	113591	112544	113046	1675	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (1675) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:E3:222:TYR:HH	37:EC:60:HIS:HE2	1.06	0.99
32:E5:287:LEU:O	32:E5:289:LEU:N	1.97	0.97
10:A7:105:SER:O	49:S3:130:ARG:NH1	2.02	0.93
46:N4:293:THR:HG21	46:N4:365:ILE:HD11	1.50	0.91
17:B2:120:ASP:OD2	17:B2:130:LYS:NZ	2.04	0.90
7:A3:17:HIS:ND1	31:E4:206:ASP:OD1	2.05	0.90
47:N5:255:LEU:O	47:N5:260:THR:OG1	1.90	0.90
9:A6:45:HIS:NE2	9:A6:117:GLU:OE1	2.05	0.89
6:A2:10:SER:OG	30:E3:182:GLU:OE2	1.92	0.88
46:N4:80:ILE:HD11	46:N4:337:ILE:HG23	1.55	0.88
11:A8:214:THR:OG1	11:A8:219:ASP:OD2	1.91	0.87
52:S6:91:ASN:ND2	52:S6:95:ARG:O	2.08	0.87
56:V1:424:SER:OG	61:V1:580:SF4:S2	2.31	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:S2:153:SER:OG	48:S2:155:MET:O	1.93	0.87
13:AB:92:LEU:HD13	66:AB:150:ZMP:H20A	1.58	0.86
46:N4:43:ILE:HD13	46:N4:472:LEU:HD21	1.57	0.86
56:V1:452:GLU:OE2	56:V1:508:TYR:OH	1.93	0.85
28:E1:86:THR:HG21	28:E1:92:MET:HE2	1.57	0.85
48:S2:116:HIS:NE2	48:S2:268:GLU:OE1	2.10	0.84
2:1B:421:ASP:OD2	2:1B:462:TYR:OH	1.96	0.84
17:B2:50:GLU:O	38:ED:70:ARG:NH2	2.11	0.84
7:A3:104:GLU:N	7:A3:104:GLU:OE1	2.11	0.84
14:AL:108:ARG:NH1	43:N1:403:GLY:O	2.10	0.83
34:E8:87:TYR:OH	64:N5:603:CDL:OA4	1.95	0.83
48:S2:111:THR:HG22	48:S2:147:TYR:OH	1.78	0.83
30:E3:53:GLN:NE2	30:E3:94:ASN:OD1	2.11	0.83
52:S6:41:LYS:O	52:S6:45:SER:OG	1.94	0.83
15:AM:74:ARG:NH2	43:N1:516:TYR:O	2.12	0.83
31:E4:238:MET:O	31:E4:304:ARG:NH1	2.11	0.83
49:S3:70:ASP:OD1	49:S3:73:THR:OG1	1.97	0.83
16:AN:248:ILE:O	27:C4:154:ARG:NH2	2.10	0.83
43:N1:514:LEU:O	43:N1:539:TYR:OH	1.96	0.83
41:G2:126:GLU:OE2	41:G2:141:TYR:OH	1.96	0.83
33:E6:254:LYS:NZ	53:S7:40:LEU:O	2.12	0.82
46:N4:67:ASN:N	46:N4:119:ASP:OD2	2.11	0.82
2:1B:399:ASP:OD2	12:A9:102:SER:OG	1.95	0.82
33:E6:120:ARG:NH1	52:S6:69:ASP:OD2	2.12	0.82
33:E6:76:GLU:OE1	33:E6:110:ARG:NH2	2.11	0.82
2:1B:214:ASP:OD2	2:1B:218:LYS:NZ	2.12	0.82
34:E8:123:LEU:O	34:E8:128:LYS:NZ	2.12	0.82
40:G1:133:ARG:NH1	42:G3:215:GLU:OE2	2.12	0.81
47:N5:355:LEU:HD11	47:N5:384:ILE:HG22	1.62	0.81
2:1B:217:LYS:NZ	2:1B:473:SER:OG	2.14	0.81
2:1B:110:LYS:NZ	2:1B:326:ASP:OD2	2.13	0.81
19:B4:85:TYR:OH	67:G1:516:3PE:O14	1.99	0.81
44:N2:32:GLU:N	44:N2:32:GLU:OE1	2.14	0.81
21:B6:57:ARG:NH1	21:B6:82:MET:SD	2.53	0.81
24:B9:66:ASP:OD2	34:E8:41:HIS:NE2	2.14	0.81
12:A9:95:GLU:OE1	50:S4:137:LYS:NZ	2.14	0.81
24:B9:63:GLU:OE1	34:E8:22:TYR:OH	1.98	0.81
11:A8:13:ASP:OD1	20:B5:115:ASN:ND2	2.13	0.81
1:1A:26:ALA:O	2:1B:448:ARG:NE	2.15	0.80
10:A7:46:ALA:O	15:AM:31:ARG:NH1	2.14	0.80
33:E6:137:ASN:OD1	33:E6:141:ARG:NH1	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C4:45:SER:O	27:C4:51:ASN:ND2	2.15	0.80
48:S2:107:PHE:O	48:S2:111:THR:HG23	1.80	0.80
11:A8:63:ILE:O	11:A8:95:SER:OG	1.99	0.80
50:S4:25:SER:OG	50:S4:30:GLU:OE2	1.99	0.80
25:BL:111:TYR:OH	47:N5:193:TYR:O	1.98	0.80
1:1A:165:SER:OG	1:1A:168:ASP:OD1	1.99	0.79
11:A8:102:ARG:NH1	11:A8:221:ILE:O	2.14	0.79
15:AM:46:ARG:NH2	31:E4:192:ASP:OD2	2.16	0.79
30:E3:118:GLU:OE1	30:E3:118:GLU:N	2.15	0.79
14:AL:212:TYR:OH	54:S8:175:LEU:O	1.99	0.79
34:E8:156:ARG:NH2	34:E8:180:THR:O	2.16	0.79
12:A9:230:ARG:NH1	33:E6:150:ASP:OD1	2.15	0.79
31:E4:128:ILE:HD11	31:E4:156:LEU:HD13	1.64	0.78
2:1B:113:GLU:OE2	50:S4:151:ARG:NH2	2.17	0.78
12:A9:161:ARG:NH1	65:A9:559:NDP:O1X	2.17	0.78
27:C4:132:ARG:NH1	27:C4:136:GLU:OE1	2.16	0.78
43:N1:386:GLU:OE2	43:N1:640:ARG:NH1	2.16	0.78
56:V1:411:ASP:OD2	56:V1:510:HIS:NE2	2.16	0.78
40:G1:133:ARG:NH2	40:G1:339:ASP:OD1	2.17	0.78
40:G1:294:ARG:HG2	41:G2:181:VAL:HG21	1.65	0.78
47:N5:97:SER:OG	47:N5:125:THR:HG21	1.84	0.78
40:G1:207:SER:OG	40:G1:233:GLY:O	2.01	0.77
28:E1:172:GLU:OE1	30:E3:183:LYS:NZ	2.17	0.77
46:N4:289:TYR:OH	47:N5:551:SER:OG	1.97	0.77
1:1A:222:GLN:OE1	56:V1:223:LYS:NZ	2.16	0.77
48:S2:226:ARG:NH2	48:S2:268:GLU:OE2	2.16	0.77
32:E5:41:ALA:O	32:E5:287:LEU:O	2.01	0.77
9:A6:132:LYS:NZ	49:S3:184:GLY:O	2.17	0.77
15:AM:47:TYR:OH	48:S2:193:ASP:OD1	2.02	0.77
35:EA:112:UNK:O	35:EA:114:UNK:N	2.18	0.77
29:E2:339:GLU:OE2	29:E2:358:ARG:NH1	2.18	0.76
1:1A:257:ARG:NH1	14:AL:271:SER:OG	2.18	0.76
25:BL:81:GLU:OE2	26:BM:92:ARG:NH1	2.18	0.76
30:E3:222:TYR:OH	37:EC:60:HIS:NE2	2.14	0.76
35:EA:18:LYS:O	35:EA:23:ASN:ND2	2.18	0.76
2:1B:58:LYS:NZ	2:1B:495:CYS:SG	2.56	0.76
29:E2:170:ASP:OD1	29:E2:170:ASP:N	2.18	0.76
38:ED:46:GLU:OE1	38:ED:49:ARG:NH1	2.19	0.76
58:E7:165:GLN:O	58:E7:169:THR:OG1	2.04	0.76
40:G1:133:ARG:NH2	41:G2:34:TYR:O	2.19	0.76
24:B9:137:THR:HG22	26:BM:23:THR:HG21	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:223:LEU:O	2:1B:227:THR:OG1	2.03	0.76
2:1B:118:SER:OG	2:1B:438:ASN:ND2	2.19	0.76
41:G2:150:GLU:OE1	41:G2:150:GLU:N	2.18	0.76
24:B9:70:SER:OG	34:E8:5:ARG:NH2	2.18	0.75
40:G1:211:GLU:OE1	40:G1:211:GLU:N	2.19	0.75
57:V2:160:ASN:OD1	57:V2:163:ASN:ND2	2.19	0.75
27:C4:2:ASP:OD1	27:C4:3:ARG:N	2.19	0.75
33:E6:150:ASP:OD2	33:E6:262:ARG:NH1	2.20	0.75
9:A6:31:VAL:HG11	39:FX:141:THR:HG21	1.67	0.75
12:A9:392:GLU:OE1	12:A9:392:GLU:N	2.18	0.75
22:B7:30:SER:OG	22:B7:32:GLU:OE1	2.04	0.75
26:BM:43:GLN:NE2	46:N4:449:ASP:OD1	2.20	0.75
39:FX:130:SER:OG	40:G1:297:ARG:NH2	2.19	0.75
54:S8:198:LYS:NZ	54:S8:199:GLU:OE2	2.19	0.75
2:1B:63:LEU:HD11	2:1B:352:LEU:HD12	1.69	0.74
28:E1:28:THR:O	29:E2:229:ARG:NH1	2.20	0.74
2:1B:102:ARG:O	2:1B:200:TYR:OH	2.04	0.74
14:AL:206:TYR:OH	53:S7:190:TYR:OH	2.03	0.74
56:V1:284:ASN:ND2	56:V1:306:GLY:O	2.20	0.74
46:N4:447:SER:OG	46:N4:449:ASP:OD2	2.05	0.74
33:E6:365:GLN:N	33:E6:365:GLN:OE1	2.20	0.74
12:A9:442:ARG:NH2	43:N1:484:ILE:O	2.20	0.74
18:B3:22:MET:SD	18:B3:34:ARG:NH1	2.60	0.74
46:N4:408:ASN:O	46:N4:412:SER:OG	2.06	0.74
49:S3:174:PRO:O	50:S4:20:ARG:NH1	2.21	0.74
12:A9:18:LEU:O	12:A9:50:LYS:NZ	2.17	0.74
27:C4:71:ASP:O	27:C4:75:ASN:ND2	2.21	0.74
29:E2:187:THR:HG22	29:E2:189:ASP:H	1.52	0.74
47:N5:358:TYR:OH	47:N5:464:ASN:OD1	2.05	0.74
56:V1:421:GLU:OE2	56:V1:434:TRP:NE1	2.20	0.74
24:B9:100:ARG:NH2	34:E8:31:TYR:O	2.21	0.73
39:FX:190:ILE:HG21	39:FX:198:LEU:HD11	1.70	0.73
43:N1:419:TYR:O	45:N3:199:ARG:NH2	2.20	0.73
31:E4:64:GLU:N	31:E4:64:GLU:OE1	2.21	0.73
4:4L:141:LEU:HB3	44:N2:116:VAL:HG11	1.70	0.73
10:A7:134:TYR:OH	31:E4:174:ASN:OD1	2.04	0.73
49:S3:93:ARG:NH1	49:S3:151:LEU:O	2.22	0.73
2:1B:48:ARG:NH1	6:A2:163:ASP:OD1	2.21	0.73
22:B7:67:CYS:SG	22:B7:71:ARG:NH1	2.61	0.73
47:N5:367:ASP:OD2	47:N5:369:ARG:NH1	2.22	0.73
34:E8:13:MET:O	34:E8:23:TYR:OH	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:E8:94:ASP:OD1	34:E8:117:LYS:NZ	2.17	0.73
11:A8:92:TYR:OH	11:A8:136:SER:OG	2.03	0.73
5:A1:49:TYR:OH	11:A8:83:ASN:ND2	2.20	0.73
9:A6:92:ARG:HB3	66:AB:150:ZMP:H7A	1.71	0.72
26:BM:87:GLU:OE2	26:BM:91:ARG:NE	2.19	0.72
48:S2:338:GLU:OE2	49:S3:132:ARG:NH2	2.22	0.72
64:A3:201:CDL:OA3	64:A3:201:CDL:O1	2.07	0.72
42:G3:235:GLY:O	45:N6:161:LYS:NZ	2.23	0.72
48:S2:308:GLU:N	48:S2:308:GLU:OE1	2.23	0.72
39:FX:219:HIS:N	39:FX:222:SER:OG	2.23	0.72
56:V1:35:GLN:N	56:V1:35:GLN:OE1	2.22	0.72
2:1B:68:ASP:OD1	6:A2:14:ARG:NH2	2.23	0.72
3:2B:95:SER:OG	23:B8:31:TYR:O	2.08	0.72
11:A8:209:ARG:NH1	15:AM:83:ASP:OD1	2.23	0.72
45:N3:251:ILE:CD1	45:N3:279:ILE:HD11	2.19	0.72
22:B7:84:ARG:NH1	55:U2:7:UNK:O	2.22	0.72
48:S2:105:VAL:HG21	48:S2:242:VAL:HG22	1.72	0.72
25:BL:30:GLU:OE1	25:BL:30:GLU:N	2.22	0.72
16:AN:180:ARG:NH1	39:FX:206:ASP:OD1	2.22	0.71
40:G1:357:ASP:OD2	40:G1:360:ARG:NE	2.23	0.71
53:S7:139:MET:HE3	53:S7:143:CYS:HB2	1.71	0.71
56:V1:462:HIS:ND1	56:V1:465:GLU:OE1	2.17	0.71
28:E1:392:GLU:N	28:E1:392:GLU:OE1	2.24	0.71
40:G1:118:ASP:O	40:G1:408:SER:OG	2.04	0.71
2:1B:374:ILE:HG21	2:1B:382:THR:HG21	1.72	0.71
2:1B:87:LYS:NZ	2:1B:240:SER:OG	2.23	0.71
46:N4:9:ARG:NH2	46:N4:70:TYR:OH	2.24	0.71
56:V1:36:ASP:O	57:V2:215:ARG:NH1	2.24	0.71
34:E8:115:TYR:CZ	34:E8:119:ILE:HD11	2.26	0.71
38:ED:18:GLN:N	38:ED:18:GLN:OE1	2.23	0.71
54:S8:165:GLU:N	54:S8:165:GLU:OE1	2.24	0.70
2:1B:277:GLU:O	2:1B:281:ARG:NH2	2.25	0.70
22:B7:94:GLU:OE2	58:E7:100:ARG:NH2	2.23	0.70
7:A3:5:GLU:OE1	10:A7:116:ARG:NH1	2.23	0.70
45:N3:245:PHE:HD2	45:N6:81:ILE:HD11	1.56	0.70
45:N6:163:SER:O	45:N6:165:ASN:ND2	2.25	0.70
5:A1:95:ASP:OD1	11:A8:160:ARG:NH2	2.25	0.70
9:A6:175:GLU:OE2	9:A6:178:THR:OG1	2.09	0.70
47:N5:272:ASN:O	47:N5:275:ILE:HG22	1.92	0.70
1:1A:152:ASP:OD1	49:S3:233:TRP:NE1	2.24	0.70
33:E6:47:ARG:NH1	33:E6:48:ASN:OD1	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:B9:21:SER:OG	24:B9:118:GLN:OE1	2.09	0.69
25:BL:88:GLU:OE1	36:EB:79:SER:OG	2.10	0.69
58:E7:34:GLU:OE1	58:E7:241:LYS:NZ	2.23	0.69
49:S3:182:ASP:OD1	49:S3:183:TYR:N	2.26	0.69
37:EC:20:PRO:O	37:EC:24:ASN:ND2	2.25	0.69
48:S2:249:GLU:OE1	48:S2:274:ARG:NH1	2.25	0.69
33:E6:55:LYS:NZ	52:S6:46:ASP:OD1	2.21	0.69
47:N5:337:ILE:HD11	47:N5:491:TYR:CG	2.27	0.69
56:V1:249:VAL:O	56:V1:252:SER:OG	2.10	0.69
29:E2:135:THR:OG1	29:E2:440:GLY:O	2.05	0.69
24:B9:18:GLN:NE2	24:B9:22:SER:O	2.26	0.69
48:S2:89:GLU:O	48:S2:93:GLU:N	2.25	0.69
9:A6:45:HIS:ND1	9:A6:113:SER:OG	2.25	0.69
17:B2:92:TRP:CH2	17:B2:96:LEU:HD11	2.28	0.69
21:B6:12:ASP:OD2	47:N5:116:ARG:NH2	2.26	0.69
23:B8:84:ASP:OD1	47:N5:166:LYS:NZ	2.26	0.69
31:E4:180:ARG:NH2	31:E4:274:THR:OG1	2.26	0.69
48:S2:19:PRO:HB3	53:S7:128:MET:HE1	1.73	0.69
10:A7:28:GLY:O	14:AL:64:HIS:NE2	2.26	0.69
27:C4:37:SER:OG	27:C4:58:GLU:OE2	2.03	0.69
11:A8:8:SER:OG	44:N2:95:ASN:O	2.11	0.69
43:N1:473:MET:HE3	43:N1:503:TYR:OH	1.93	0.69
56:V1:281:GLY:O	57:V2:110:ARG:NH1	2.26	0.68
1:1A:143:PRO:O	1:1A:264:ARG:NH2	2.27	0.68
48:S2:75:MET:SD	48:S2:118:LEU:HD22	2.33	0.68
47:N5:170:LYS:NZ	47:N5:244:ASP:OD2	2.20	0.68
47:N5:409:GLU:OE1	47:N5:495:SER:OG	2.12	0.68
48:S2:53:THR:HG21	48:S2:72:LEU:HD21	1.75	0.68
31:E4:31:VAL:HG21	48:S2:236:VAL:HG11	1.75	0.68
43:N1:395:ARG:NH2	48:S2:190:GLU:OE1	2.25	0.68
56:V1:351:GLY:O	56:V1:352:THR:OG1	2.11	0.68
8:A5:38:LYS:NZ	40:G1:391:HIS:O	2.25	0.68
32:E5:81:GLU:OE1	32:E5:81:GLU:N	2.26	0.68
44:N2:126:GLU:N	44:N2:126:GLU:OE1	2.27	0.68
47:N5:2:LEU:HD21	47:N5:133:ILE:HD12	1.74	0.68
64:AM:215:CDL:O1	31:E4:315:ASP:OD2	2.08	0.68
19:B4:24:ILE:O	19:B4:110:ARG:NH1	2.27	0.68
19:B4:133:GLU:OE1	46:N4:274:TYR:OH	2.09	0.68
24:B9:41:HIS:NE2	59:AC:115:GLU:OE2	2.27	0.68
2:1B:264:LEU:HD21	30:E3:344:LEU:HD13	1.76	0.67
48:S2:394:ASP:OD1	48:S2:394:ASP:N	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:V2:28:GLU:N	57:V2:28:GLU:OE1	2.27	0.67
8:A5:169:GLU:OE2	8:A5:172:ARG:NH2	2.27	0.67
44:N2:221:ILE:HD11	44:N2:252:ASN:CG	2.19	0.67
24:B9:59:SER:OG	34:E8:12:ARG:NH1	2.28	0.67
56:V1:97:LYS:NZ	56:V1:243:VAL:O	2.20	0.67
46:N4:284:ASN:O	46:N4:287:ILE:HG22	1.94	0.67
47:N5:111:ASP:OD1	47:N5:112:LYS:N	2.28	0.67
33:E6:59:PRO:O	33:E6:203:ARG:NH1	2.28	0.67
12:A9:26:ASN:O	12:A9:26:ASN:ND2	2.28	0.66
24:B9:158:TYR:O	46:N4:446:THR:HG22	1.95	0.66
46:N4:186:ASN:O	46:N4:190:ASN:ND2	2.26	0.66
59:AC:92:LEU:HD21	66:AC:201:ZMP:H19B	1.77	0.66
39:FX:263:LYS:NZ	40:G1:61:GLU:O	2.25	0.66
56:V1:291:GLU:OE2	56:V1:304:HIS:NE2	2.21	0.66
1:1A:88:ASN:OD1	1:1A:89:CYS:N	2.29	0.66
7:A3:53:ARG:NH2	44:N2:25:ILE:O	2.27	0.66
34:E8:156:ARG:NH1	34:E8:160:GLU:OE1	2.29	0.66
9:A6:118:GLU:OE2	49:S3:177:ARG:NE	2.26	0.66
18:B3:22:MET:HE1	18:B3:34:ARG:HD2	1.78	0.66
5:A1:78:ARG:NH2	63:A1:203:PC1:O12	2.28	0.66
39:FX:275:LYS:O	39:FX:277:VAL:N	2.27	0.66
41:G2:192:GLU:OE1	41:G2:192:GLU:N	2.29	0.66
7:A3:85:GLN:NE2	11:A8:207:TYR:O	2.29	0.66
56:V1:396:ILE:HB	56:V1:413:ILE:HD13	1.78	0.66
1:1A:318:ARG:NH2	2:1B:494:ASP:OD1	2.29	0.65
43:N1:379:SER:O	43:N1:383:THR:HG23	1.96	0.65
39:FX:185:TRP:O	39:FX:186:SER:OG	2.11	0.65
45:N3:275:LEU:HD23	45:N6:148:MET:SD	2.36	0.65
21:B6:50:ARG:NH2	36:EB:45:HIS:O	2.28	0.65
28:E1:75:GLU:OE2	28:E1:186:SER:OG	2.12	0.65
33:E6:368:GLU:OE1	33:E6:368:GLU:N	2.27	0.65
5:A1:132:HIS:O	15:AM:117:TYR:OH	2.08	0.65
11:A8:102:ARG:NH2	15:AM:93:CYS:O	2.30	0.65
47:N5:494:ILE:HD13	47:N5:499:HIS:HE1	1.60	0.65
12:A9:463:ASP:OD1	12:A9:464:TYR:N	2.28	0.65
59:AC:80:ASP:N	59:AC:80:ASP:OD1	2.29	0.65
47:N5:118:VAL:HG12	47:N5:122:MET:HE2	1.79	0.65
47:N5:393:LEU:HD11	47:N5:432:GLN:CG	2.27	0.65
56:V1:428:LEU:HD23	56:V1:428:LEU:O	1.96	0.65
11:A8:1:MET:HE2	44:N2:195:ILE:HG21	1.78	0.65
31:E4:31:VAL:HG21	48:S2:236:VAL:CG1	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:N5:246:MET:SD	47:N5:257:HIS:NE2	2.68	0.65
24:B9:50:ILE:HG13	66:AC:201:ZMP:H25A	1.79	0.65
47:N5:92:LEU:HD22	47:N5:343:PHE:HA	1.79	0.65
52:S6:62:GLU:N	52:S6:62:GLU:OE1	2.28	0.65
17:B2:112:GLU:O	17:B2:133:ARG:NH2	2.29	0.65
31:E4:180:ARG:NH2	31:E4:268:ALA:O	2.29	0.65
46:N4:295:ARG:NH1	47:N5:563:GLU:OE2	2.29	0.65
30:E3:149:GLY:O	30:E3:152:THR:OG1	2.13	0.64
9:A6:288:HIS:NE2	9:A6:411:ASP:OD1	2.29	0.64
26:BM:64:PHE:O	26:BM:68:THR:HG23	1.97	0.64
48:S2:241:GLU:O	56:V1:492:SER:OG	2.13	0.64
24:B9:154:LYS:N	26:BM:7:VAL:O	2.31	0.64
31:E4:318:VAL:HG21	31:E4:334:VAL:HG21	1.77	0.64
12:A9:214:SER:HA	53:S7:40:LEU:HD21	1.79	0.64
20:B5:116:LYS:N	27:C4:24:ASP:OD2	2.30	0.64
43:N1:402:ASN:OD1	43:N1:409:GLN:NE2	2.29	0.64
23:B8:150:GLU:N	23:B8:150:GLU:OE1	2.29	0.64
24:B9:99:ARG:NH2	47:N5:531:ASN:OD1	2.30	0.64
11:A8:75:ILE:N	11:A8:137:GLU:OE2	2.31	0.64
46:N4:90:LEU:HD23	46:N4:455:LEU:HD21	1.78	0.64
52:S6:54:ILE:HB	54:S8:186:ILE:HD11	1.80	0.64
24:B9:100:ARG:CD	66:AC:201:ZMP:H25B	2.28	0.64
29:E2:145:GLU:OE1	29:E2:147:LEU:N	2.31	0.64
31:E4:166:ALA:O	31:E4:170:SER:OG	2.15	0.64
47:N5:121:ILE:O	47:N5:125:THR:HG23	1.98	0.64
56:V1:125:THR:HG22	56:V1:354:ALA:HB2	1.80	0.64
13:AB:109:MET:HE1	13:AB:117:ILE:HD12	1.80	0.63
23:B8:25:ARG:NH2	39:FX:172:ASP:OD2	2.31	0.63
46:N4:354:TYR:O	46:N4:358:ASN:N	2.31	0.63
48:S2:189:ASP:OD1	48:S2:270:ARG:NH2	2.31	0.63
56:V1:36:ASP:OD2	57:V2:210:LEU:N	2.30	0.63
57:V2:114:GLU:OE1	57:V2:114:GLU:N	2.31	0.63
54:S8:92:HIS:CE1	61:S8:297:SF4:S4	2.91	0.63
9:A6:426:LYS:O	9:A6:427:SER:OG	2.13	0.63
31:E4:196:ARG:N	31:E4:332:ASP:OD1	2.30	0.63
35:EA:47:LEU:HD22	35:EA:56:LYS:HD3	1.80	0.63
44:N2:151:SER:O	44:N2:206:ASN:ND2	2.31	0.63
47:N5:533:HIS:N	64:N5:608:CDL:OB4	2.31	0.63
43:N1:367:GLN:OE1	45:N3:176:TYR:OH	2.15	0.63
47:N5:259:ALA:O	47:N5:260:THR:HG23	1.99	0.63
53:S7:42:GLU:N	53:S7:42:GLU:OE1	2.30	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:E5:152:LEU:HB2	32:E5:284:VAL:HG11	1.79	0.63
23:B8:25:ARG:NH1	23:B8:30:GLU:OE2	2.32	0.63
42:G3:87:LYS:NZ	42:G3:89:THR:OG1	2.20	0.63
58:E7:178:SER:OG	58:E7:180:ASP:OD1	2.16	0.63
31:E4:219:ARG:NH1	31:E4:280:ASP:OD2	2.32	0.63
44:N2:88:ILE:HG21	45:N6:143:LEU:HD21	1.80	0.63
46:N4:403:SER:O	46:N4:406:ILE:HG22	1.99	0.63
57:V2:173:THR:OG1	57:V2:175:GLU:OE1	2.09	0.63
25:BL:26:TYR:OH	26:BM:90:ARG:NH2	2.32	0.63
53:S7:85:ALA:O	53:S7:88:ALA:N	2.27	0.63
1:1A:259:THR:HG21	1:1A:295:TYR:O	1.98	0.63
24:B9:46:ALA:HB1	66:AC:201:ZMP:H24A	1.80	0.62
29:E2:4:GLY:O	29:E2:5:THR:OG1	2.17	0.62
46:N4:368:ASN:ND2	46:N4:444:THR:O	2.31	0.62
47:N5:389:LEU:HD21	47:N5:438:ILE:HD11	1.80	0.62
64:EA:202:CDL:OA3	64:EA:202:CDL:O1	2.17	0.62
36:EB:30:GLN:O	36:EB:35:ARG:NH2	2.32	0.62
8:A5:134:ARG:NH2	8:A5:147:GLU:OE2	2.32	0.62
9:A6:309:ASP:OD1	9:A6:312:ARG:NH2	2.32	0.62
20:B5:104:GLN:N	20:B5:104:GLN:OE1	2.32	0.62
47:N5:393:LEU:HD11	47:N5:432:GLN:HG2	1.81	0.62
45:N6:35:LEU:HD13	45:N6:46:ILE:HG22	1.80	0.62
58:E7:4:LEU:HD12	58:E7:4:LEU:O	2.00	0.62
26:BM:62:MET:HA	26:BM:62:MET:HE2	1.80	0.62
68:N4:505:U10:H18	68:N4:505:U10:H151	1.82	0.62
1:1A:213:GLU:N	1:1A:213:GLU:OE1	2.33	0.62
11:A8:164:MET:O	11:A8:169:ARG:NH2	2.32	0.62
31:E4:128:ILE:HD11	31:E4:156:LEU:CD1	2.29	0.62
40:G1:113:ARG:NH2	45:N6:166:TYR:OH	2.30	0.62
46:N4:43:ILE:HG12	46:N4:79:LEU:HD22	1.80	0.62
47:N5:494:ILE:HD13	47:N5:499:HIS:CE1	2.34	0.62
2:1B:206:GLU:OE1	2:1B:482:ARG:NH1	2.31	0.62
19:B4:28:GLU:OE1	19:B4:31:ARG:NH2	2.32	0.62
39:FX:172:ASP:OD1	39:FX:172:ASP:N	2.31	0.62
11:A8:94:MET:HE1	11:A8:197:PHE:CD1	2.35	0.62
48:S2:265:ARG:NE	48:S2:387:ASP:OD2	2.32	0.62
52:S6:115:CYS:O	52:S6:119:GLU:N	2.32	0.62
10:A7:32:TRP:O	48:S2:187:ARG:NH2	2.29	0.62
18:B3:52:UNK:O	18:B3:56:UNK:N	2.33	0.62
46:N4:43:ILE:HD12	46:N4:44:MET:N	2.14	0.62
48:S2:187:ARG:NH1	48:S2:190:GLU:OE2	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A6:181:ARG:O	9:A6:185:THR:OG1	2.17	0.62
12:A9:115:ARG:NH1	50:S4:97:GLU:OE2	2.33	0.61
17:B2:110:GLU:O	22:B7:92:ARG:NH1	2.33	0.61
32:E5:282:ASP:O	32:E5:284:VAL:HG13	1.98	0.61
39:FX:121:ASP:OD1	39:FX:127:ARG:NH2	2.33	0.61
48:S2:75:MET:HE1	48:S2:118:LEU:HD13	1.80	0.61
57:V2:20:ASP:OD1	57:V2:26:TYR:OH	2.17	0.61
57:V2:194:SER:OG	57:V2:198:ARG:O	2.17	0.61
6:A2:6:ARG:NH2	6:A2:135:GLU:OE1	2.32	0.61
11:A8:55:ARG:NH2	11:A8:210:SER:O	2.33	0.61
39:FX:161:ALA:N	39:FX:225:VAL:O	2.33	0.61
44:N2:272:TYR:CZ	44:N2:276:ILE:HD11	2.34	0.61
68:N4:505:U10:H151	68:N4:505:U10:C18	2.30	0.61
2:1B:236:ARG:NH2	2:1B:488:ASP:O	2.33	0.61
8:A5:144:ARG:NH1	49:S3:66:GLU:OE2	2.33	0.61
36:EB:89:GLU:N	36:EB:89:GLU:OE1	2.32	0.61
2:1B:441:LYS:HG2	29:E2:25:LEU:HD11	1.82	0.61
4:4L:84:ILE:HG23	45:N6:33:ILE:HD11	1.81	0.61
5:A1:54:PHE:O	33:E6:338:ARG:NH2	2.29	0.61
29:E2:187:THR:HG21	29:E2:192:ALA:HB3	1.82	0.61
56:V1:126:CYS:SG	57:V2:147:CYS:N	2.72	0.61
40:G1:141:LYS:NZ	42:G3:211:THR:HG21	2.16	0.61
56:V1:209:GLU:OE1	56:V1:210:GLU:N	2.34	0.61
28:E1:268:GLU:OE1	28:E1:322:THR:OG1	2.19	0.61
46:N4:293:THR:HG22	46:N4:362:LEU:HD23	1.83	0.61
47:N5:170:LYS:NZ	47:N5:540:ASP:OD2	2.34	0.61
48:S2:75:MET:HE2	48:S2:75:MET:HA	1.83	0.61
11:A8:102:ARG:HA	11:A8:128:MET:HE3	1.83	0.61
15:AM:52:LYS:NZ	64:AM:216:CDL:OB4	2.32	0.61
32:E5:114:LEU:HD11	32:E5:249:VAL:HG22	1.82	0.61
32:E5:241:ALA:O	32:E5:245:VAL:HG23	2.01	0.61
10:A7:36:ASP:OD1	14:AL:62:ARG:NH2	2.32	0.61
63:C4:203:PC1:O12	41:G2:11:ARG:NH1	2.34	0.61
4:4L:84:ILE:CG2	45:N6:33:ILE:HD11	2.31	0.60
9:A6:393:ILE:O	9:A6:396:THR:OG1	2.16	0.60
14:AL:221:LYS:NZ	53:S7:20:VAL:O	2.23	0.60
28:E1:50:ARG:NH1	28:E1:55:GLU:OE1	2.34	0.60
47:N5:311:VAL:O	47:N5:315:THR:HG23	2.01	0.60
10:A7:52:ARG:NH1	48:S2:302:ASP:OD2	2.34	0.60
17:B2:138:TRP:NE1	23:B8:155:GLN:OE1	2.33	0.60
29:E2:116:GLU:OE1	29:E2:116:GLU:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:FX:221:ASN:O	39:FX:223:ARG:N	2.34	0.60
2:1B:130:GLN:OE1	2:1B:131:GLN:NE2	2.34	0.60
11:A8:62:ASN:ND2	11:A8:62:ASN:O	2.34	0.60
28:E1:305:THR:N	28:E1:308:ASP:OD2	2.33	0.60
30:E3:253:ASN:ND2	32:E5:54:LEU:O	2.34	0.60
47:N5:161:ARG:NH1	47:N5:247:GLU:OE1	2.35	0.60
59:AC:92:LEU:CD2	66:AC:201:ZMP:H19B	2.31	0.60
1:1A:195:CYS:O	1:1A:196:THR:OG1	2.19	0.60
9:A6:304:LEU:HD21	9:A6:385:ILE:HG21	1.82	0.60
37:EC:60:HIS:O	37:EC:64:VAL:HG23	2.02	0.60
1:1A:331:MET:HE2	2:1B:305:VAL:CG1	2.32	0.60
12:A9:194:ARG:NH1	14:AL:219:HIS:O	2.34	0.60
31:E4:238:MET:HA	31:E4:238:MET:HE2	1.84	0.60
46:N4:173:ASN:ND2	46:N4:205:TYR:OH	2.30	0.60
46:N4:325:TYR:CE2	46:N4:329:ILE:HD11	2.37	0.60
58:E7:81:VAL:HG23	58:E7:83:GLN:H	1.67	0.60
1:1A:210:LYS:NZ	50:S4:174:ASP:OD2	2.34	0.60
7:A3:22:ASN:OD1	7:A3:23:ARG:NH1	2.33	0.60
28:E1:45:LYS:NZ	28:E1:293:HIS:O	2.32	0.60
46:N4:173:ASN:O	46:N4:177:ASN:ND2	2.33	0.60
56:V1:116:ILE:HG21	56:V1:139:LEU:HD11	1.84	0.60
19:B4:76:ASP:OD1	19:B4:77:SER:N	2.35	0.60
47:N5:260:THR:O	47:N5:263:THR:N	2.33	0.60
1:1A:160:TYR:OH	49:S3:235:ASP:OD1	2.19	0.59
15:AM:187:MET:O	51:S5:98:ARG:NH2	2.34	0.59
26:BM:81:ASN:ND2	47:N5:70:ASN:O	2.35	0.59
48:S2:51:ARG:HG2	53:S7:123:THR:HG21	1.83	0.59
49:S3:186:GLU:N	49:S3:186:GLU:OE1	2.36	0.59
9:A6:181:ARG:NH1	33:E6:176:ASP:OD1	2.35	0.59
28:E1:89:ASP:OD1	28:E1:90:SER:N	2.35	0.59
32:E5:42:PRO:HB3	32:E5:286:ILE:HG22	1.85	0.59
19:B4:20:PRO:O	19:B4:22:ASP:N	2.35	0.59
39:FX:164:ALA:CB	39:FX:171:LEU:HD21	2.32	0.59
48:S2:355:ARG:NH1	49:S3:105:ASP:OD1	2.35	0.59
2:1B:127:THR:O	2:1B:127:THR:HG23	2.01	0.59
14:AL:66:VAL:HG11	54:S8:65:ILE:HG22	1.85	0.59
16:AN:105:MET:SD	16:AN:113:LEU:HD12	2.43	0.59
17:B2:65:ARG:NH2	18:B3:39:UNK:O	2.30	0.59
32:E5:49:ASP:OD1	32:E5:52:ARG:NH1	2.34	0.59
37:EC:69:GLU:OE2	37:EC:76:VAL:N	2.34	0.59
44:N2:77:LYS:NZ	45:N3:281:TYR:OH	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:S2:31:ILE:HD12	48:S2:45:HIS:CE1	2.37	0.59
49:S3:263:TYR:OH	50:S4:85:ARG:NH1	2.35	0.59
66:AC:201:ZMP:H12A	66:AC:201:ZMP:HN2	1.66	0.59
30:E3:156:LEU:HD13	30:E3:184:LEU:HD22	1.84	0.59
43:N1:424:ARG:NH1	45:N3:202:SER:OG	2.36	0.59
46:N4:35:ILE:HG21	46:N4:108:TYR:OH	2.03	0.59
13:AB:56:ARG:O	13:AB:60:THR:HG23	2.03	0.59
14:AL:210:ARG:NH2	54:S8:172:ASP:OD1	2.31	0.59
8:A5:97:GLU:N	8:A5:97:GLU:OE1	2.36	0.59
19:B4:133:GLU:OE2	19:B4:137:ARG:NE	2.36	0.59
63:B5:203:PC1:O14	26:BM:46:ARG:NH2	2.35	0.59
48:S2:157:PRO:O	54:S8:89:ARG:NH2	2.33	0.59
27:C4:145:LEU:HD12	27:C4:145:LEU:O	2.02	0.58
39:FX:144:ASP:O	39:FX:147:GLY:N	2.34	0.58
46:N4:327:ILE:HG22	47:N5:72:TYR:CE2	2.38	0.58
58:E7:7:ILE:O	58:E7:212:LEU:HD12	2.02	0.58
23:B8:92:GLU:OE2	23:B8:97:SER:OG	2.14	0.58
28:E1:260:ALA:HB1	28:E1:292:ALA:HB2	1.85	0.58
52:S6:31:GLN:OE1	52:S6:31:GLN:N	2.36	0.58
1:1A:66:LEU:O	1:1A:70:ASN:ND2	2.36	0.58
1:1A:332:THR:OG1	14:AL:243:GLU:OE2	2.11	0.58
40:G1:141:LYS:HZ3	42:G3:211:THR:HG21	1.67	0.58
47:N5:102:ILE:HG23	47:N5:466:ILE:HD11	1.85	0.58
49:S3:117:ARG:NH2	49:S3:193:ASP:OD1	2.34	0.58
1:1A:43:THR:OG1	1:1A:56:GLN:NE2	2.36	0.58
2:1B:338:GLU:OE2	50:S4:105:ARG:NH1	2.37	0.58
32:E5:36:LEU:HD21	32:E5:70:GLY:HA3	1.83	0.58
28:E1:70:ALA:O	28:E1:102:ARG:NH1	2.36	0.58
32:E5:7:TRP:O	32:E5:96:TYR:HB2	2.02	0.58
40:G1:140:TYR:CE1	42:G3:211:THR:HG22	2.39	0.58
56:V1:73:GLU:OE2	56:V1:103:LYS:NZ	2.37	0.58
2:1B:177:GLU:OE1	2:1B:179:ARG:NH1	2.34	0.58
41:G2:47:ASN:OD1	41:G2:48:GLY:N	2.35	0.58
46:N4:273:ILE:HD12	46:N4:317:ILE:HD13	1.86	0.58
54:S8:161:THR:HG22	54:S8:192:ILE:HD11	1.86	0.58
44:N2:175:TYR:CG	44:N2:186:MET:HE1	2.38	0.58
56:V1:319:ILE:HG12	56:V1:327:VAL:HG12	1.85	0.58
1:1A:348:HIS:NE2	6:A2:176:ASN:O	2.30	0.58
9:A6:364:ASP:OD1	9:A6:365:ARG:N	2.36	0.58
19:B4:9:LEU:HD11	39:FX:253:THR:HG21	1.84	0.58
21:B6:45:GLU:OE2	47:N5:62:TYR:OH	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:B9:134:LYS:O	24:B9:137:THR:HG23	2.03	0.58
27:C4:6:VAL:HG22	44:N2:100:THR:OG1	2.04	0.58
40:G1:113:ARG:NH1	40:G1:115:THR:OG1	2.37	0.58
39:FX:164:ALA:HB1	39:FX:171:LEU:HD21	1.86	0.58
21:B6:45:GLU:CG	47:N5:64:LEU:HD11	2.34	0.57
3:2B:80:TYR:HB3	3:2B:81:PRO:HD3	1.85	0.57
4:4L:95:LYS:O	4:4L:103:ARG:NH2	2.38	0.57
8:A5:30:LEU:HD22	48:S2:212:LEU:HD22	1.85	0.57
31:E4:190:ARG:NH2	31:E4:341:HIS:O	2.35	0.57
47:N5:169:LEU:O	47:N5:173:VAL:HG23	2.04	0.57
56:V1:312:TRP:O	56:V1:330:LYS:NZ	2.37	0.57
57:V2:99:ILE:HB	57:V2:138:ILE:HD13	1.85	0.57
20:B5:55:TRP:O	20:B5:58:ARG:NH1	2.37	0.57
24:B9:54:PRO:HG3	34:E8:25:MET:HE3	1.86	0.57
56:V1:124:GLY:O	56:V1:354:ALA:HB1	2.04	0.57
21:B6:10:ARG:NH1	46:N4:368:ASN:O	2.36	0.57
42:G3:112:VAL:HG22	42:G3:128:PRO:HA	1.86	0.57
12:A9:120:THR:OG1	12:A9:195:SER:OG	2.11	0.57
47:N5:152:LEU:C	47:N5:152:LEU:HD23	2.30	0.57
3:2B:54:THR:HG21	64:N4:501:CDL:H792	1.85	0.57
28:E1:310:LYS:NZ	52:S6:146:GLU:OE1	2.37	0.57
34:E8:1:MET:HE3	34:E8:1:MET:HA	1.86	0.57
49:S3:82:PRO:HB3	49:S3:139:VAL:HG12	1.86	0.57
52:S6:105:ILE:HD11	52:S6:115:CYS:HB2	1.86	0.57
3:2B:56:ILE:HD12	44:N2:257:PHE:CZ	2.40	0.57
33:E6:334:LEU:O	55:U1:11:UNK:N	2.38	0.57
39:FX:160:MET:SD	39:FX:225:VAL:HG12	2.44	0.57
46:N4:130:GLN:OE1	46:N4:249:THR:HG21	2.04	0.57
47:N5:234:THR:HG21	47:N5:242:LEU:HB2	1.87	0.57
4:4L:69:THR:OG1	4:4L:72:ASP:OD1	2.23	0.57
33:E6:273:ARG:NH1	53:S7:26:LYS:O	2.37	0.57
48:S2:54:GLU:OE1	48:S2:353:ARG:NH2	2.34	0.57
52:S6:6:ARG:NH2	54:S8:208:GLN:O	2.38	0.57
53:S7:116:ASP:OD1	53:S7:116:ASP:N	2.38	0.57
56:V1:410:VAL:O	56:V1:413:ILE:HG22	2.04	0.57
3:2B:57:PHE:CE2	3:2B:61:ILE:HD11	2.40	0.57
9:A6:36:ARG:NH1	48:S2:6:ASP:OD2	2.37	0.57
17:B2:144:VAL:HG13	34:E8:139:ARG:NH2	2.19	0.57
22:B7:65:GLY:N	47:N5:487:ASP:OD2	2.35	0.57
32:E5:5:LYS:O	32:E5:98:THR:N	2.37	0.57
34:E8:70:VAL:HG22	58:E7:205:LEU:HD11	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A6:99:LEU:O	50:S4:47:GLN:NE2	2.35	0.56
12:A9:194:ARG:NH2	14:AL:222:ASN:O	2.38	0.56
34:E8:74:ARG:NH2	58:E7:207:VAL:O	2.37	0.56
48:S2:342:TYR:OH	48:S2:344:GLN:NE2	2.37	0.56
56:V1:218:GLU:OE2	56:V1:225:ARG:NH2	2.37	0.56
46:N4:189:HIS:CD2	46:N4:193:ILE:HD11	2.40	0.56
39:FX:287:PRO:CD	39:FX:307:THR:HG22	2.35	0.56
47:N5:132:ILE:O	47:N5:271:LYS:NZ	2.39	0.56
57:V2:104:THR:HG22	57:V2:105:THR:H	1.70	0.56
39:FX:182:PHE:O	39:FX:217:THR:OG1	2.22	0.56
47:N5:337:ILE:HD11	47:N5:491:TYR:CD1	2.41	0.56
56:V1:384:THR:OG1	56:V1:387:ARG:NH2	2.38	0.56
29:E2:101:PHE:CZ	29:E2:244:ILE:HG22	2.40	0.56
43:N1:481:ILE:O	43:N1:485:VAL:HG22	2.06	0.56
2:1B:233:TYR:O	2:1B:241:TYR:OH	2.13	0.56
29:E2:240:GLU:N	29:E2:240:GLU:OE1	2.38	0.56
43:N1:428:ILE:O	43:N1:431:LYS:NZ	2.35	0.56
46:N4:352:TYR:CG	46:N4:452:LEU:HD22	2.39	0.56
2:1B:112:THR:O	50:S4:155:ASN:ND2	2.35	0.56
56:V1:406:PHE:O	56:V1:409:GLU:N	2.30	0.56
11:A8:1:MET:HE1	44:N2:58:LEU:CD2	2.36	0.56
19:B4:151:LEU:HD22	47:N5:209:TYR:OH	2.06	0.56
35:EA:74:VAL:HG21	44:N2:15:SER:HA	1.88	0.56
38:ED:116:VAL:HG12	38:ED:116:VAL:O	2.05	0.56
9:A6:123:ASP:OD2	48:S2:45:HIS:NE2	2.39	0.56
15:AM:152:ARG:NH2	15:AM:185:GLU:OE2	2.39	0.56
39:FX:253:THR:HG23	39:FX:304:TRP:HE1	1.70	0.56
1:1A:247:GLU:OE2	1:1A:320:ARG:NH1	2.37	0.56
7:A3:102:GLU:OE2	35:EA:89:ARG:NH2	2.35	0.56
22:B7:44:ARG:HA	22:B7:48:VAL:CG1	2.35	0.56
32:E5:36:LEU:HD23	32:E5:36:LEU:O	2.05	0.56
45:N3:251:ILE:HD11	45:N3:279:ILE:HD11	1.88	0.56
48:S2:72:LEU:HD11	48:S2:356:ILE:HD13	1.87	0.56
10:A7:120:THR:OG1	10:A7:123:TYR:O	2.16	0.55
24:B9:38:ARG:NH2	24:B9:94:GLU:OE1	2.38	0.55
28:E1:425:GLU:OE1	28:E1:463:LYS:N	2.39	0.55
29:E2:147:LEU:HB2	29:E2:251:LEU:HD22	1.88	0.55
47:N5:54:ASN:OD1	47:N5:55:ILE:N	2.39	0.55
32:E5:275:GLU:O	32:E5:279:GLY:N	2.38	0.55
40:G1:113:ARG:NH2	40:G1:119:LYS:O	2.36	0.55
47:N5:315:THR:HG22	47:N5:349:LYS:HG2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:V1:117:ASN:ND2	56:V1:208:GLY:O	2.33	0.55
2:1B:32:VAL:HG21	2:1B:359:LEU:HD23	1.87	0.55
5:A1:124:ASN:N	15:AM:194:GLU:OE2	2.34	0.55
28:E1:34:LEU:HD22	28:E1:253:LEU:HD22	1.89	0.55
31:E4:100:ARG:NH2	31:E4:137:ALA:O	2.40	0.55
9:A6:137:ASP:OD2	12:A9:330:ARG:NH2	2.39	0.55
45:N3:261:ILE:HD13	45:N6:128:ILE:HB	1.88	0.55
9:A6:300:ARG:NH2	9:A6:415:TRP:O	2.38	0.55
28:E1:34:LEU:CD2	28:E1:253:LEU:HD22	2.37	0.55
30:E3:423:GLU:OE1	30:E3:423:GLU:N	2.36	0.55
32:E5:84:ARG:NH1	32:E5:114:LEU:O	2.39	0.55
48:S2:48:PHE:HB3	53:S7:128:MET:HE2	1.89	0.55
49:S3:264:ASP:OD1	50:S4:151:ARG:NH1	2.40	0.55
9:A6:72:MET:HE3	9:A6:120:PHE:HD1	1.71	0.55
12:A9:7:GLU:OE2	12:A9:30:ARG:NH2	2.39	0.55
12:A9:301:ASN:OD1	12:A9:375:ARG:NH2	2.39	0.55
31:E4:128:ILE:HD13	31:E4:148:MET:HE2	1.89	0.55
43:N1:447:LEU:HD11	43:N1:472:LEU:HD23	1.89	0.55
19:B4:80:ASN:O	19:B4:82:VAL:HG23	2.06	0.55
29:E2:364:PRO:O	29:E2:400:ARG:NH1	2.39	0.55
41:G2:207:LEU:HD21	42:G3:84:ASP:OD2	2.07	0.55
46:N4:427:LEU:HD11	47:N5:149:ILE:HD11	1.87	0.55
2:1B:329:SER:O	12:A9:94:ARG:NH2	2.39	0.55
24:B9:130:GLN:HG2	46:N4:444:THR:HG22	1.89	0.55
29:E2:266:GLN:OE1	29:E2:269:ARG:NH2	2.40	0.55
31:E4:318:VAL:HG21	31:E4:334:VAL:CG2	2.36	0.55
48:S2:324:PRO:O	48:S2:345:SER:OG	2.25	0.55
52:S6:40:LEU:HA	52:S6:43:VAL:HG22	1.89	0.55
6:A2:170:SER:OG	30:E3:326:GLU:OE2	2.11	0.54
17:B2:92:TRP:CZ2	17:B2:96:LEU:HD11	2.42	0.54
17:B2:125:PHE:CE2	47:N5:415:ILE:HG22	2.42	0.54
18:B3:10:GLN:OE1	24:B9:61:THR:HG21	2.07	0.54
24:B9:54:PRO:CG	34:E8:25:MET:HE3	2.37	0.54
47:N5:131:LEU:C	47:N5:131:LEU:HD23	2.31	0.54
49:S3:230:GLU:OE2	50:S4:119:LYS:NZ	2.33	0.54
50:S4:69:ARG:NH1	50:S4:143:PRO:O	2.38	0.54
12:A9:239:ARG:NH2	12:A9:339:GLU:OE2	2.41	0.54
39:FX:199:VAL:O	39:FX:223:ARG:NH2	2.40	0.54
41:G2:220:GLU:O	41:G2:223:THR:HG22	2.07	0.54
42:G3:74:SER:OG	42:G3:95:HIS:ND1	2.29	0.54
2:1B:117:SER:OG	2:1B:195:ASN:ND2	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BL:116:ARG:NH1	47:N5:214:TYR:OH	2.40	0.54
30:E3:41:LEU:HD12	30:E3:98:SER:O	2.07	0.54
44:N2:17:ILE:HD11	45:N6:146:LEU:HA	1.88	0.54
45:N6:45:ILE:HD11	45:N6:82:ILE:HG22	1.88	0.54
28:E1:366:GLU:O	28:E1:388:ARG:NH2	2.36	0.54
43:N1:543:GLN:OE1	43:N1:618:SER:N	2.41	0.54
2:1B:420:GLU:HG2	12:A9:89:LEU:HD13	1.89	0.54
46:N4:423:LEU:HD23	47:N5:176:ARG:CZ	2.38	0.54
21:B6:45:GLU:HG3	47:N5:64:LEU:HD11	1.90	0.54
2:1B:226:GLN:NE2	29:E2:29:VAL:O	2.38	0.54
9:A6:119:TYR:CE1	66:AB:150:ZMP:H24A	2.43	0.54
23:B8:87:ASP:OD2	47:N5:541:LYS:NZ	2.37	0.54
24:B9:100:ARG:HD3	66:AC:201:ZMP:H25B	1.90	0.54
31:E4:74:THR:HG1	31:E4:141:SER:HG	1.55	0.54
34:E8:126:LYS:O	34:E8:178:ARG:NH2	2.41	0.54
48:S2:355:ARG:NH1	49:S3:106:VAL:O	2.40	0.54
1:1A:345:LEU:HD23	9:A6:367:LEU:HD22	1.90	0.54
63:A1:202:PC1:C1	63:A1:202:PC1:H152	2.38	0.54
46:N4:286:ASN:ND2	47:N5:558:PHE:O	2.38	0.54
47:N5:336:GLU:HG2	47:N5:337:ILE:HD12	1.90	0.54
49:S3:29:GLN:OE1	49:S3:29:GLN:N	2.41	0.54
1:1A:330:ARG:NH2	2:1B:313:GLU:OE2	2.40	0.54
2:1B:454:GLU:OE2	6:A2:58:ARG:NH1	2.39	0.54
12:A9:460:VAL:CG1	40:G1:54:THR:HG23	2.38	0.54
21:B6:52:LEU:O	25:BL:95:ARG:NH1	2.36	0.54
53:S7:184:THR:O	53:S7:187:ALA:N	2.41	0.54
5:A1:76:GLU:OE1	5:A1:93:TRP:NE1	2.38	0.53
19:B4:68:LYS:NZ	24:B9:127:LEU:O	2.29	0.53
34:E8:22:TYR:O	34:E8:26:THR:OG1	2.26	0.53
46:N4:90:LEU:HD23	46:N4:455:LEU:CD2	2.38	0.53
4:4L:80:PRO:HD3	45:N6:112:ILE:HD11	1.89	0.53
9:A6:90:ARG:NE	9:A6:94:GLU:OE2	2.39	0.53
12:A9:148:ARG:NH2	65:A9:559:NDP:O3X	2.41	0.53
29:E2:316:LEU:O	29:E2:400:ARG:NH2	2.41	0.53
31:E4:212:PHE:O	31:E4:215:THR:HG23	2.07	0.53
43:N1:572:VAL:HG12	43:N1:572:VAL:O	2.06	0.53
56:V1:44:ILE:HG22	57:V2:210:LEU:HD11	1.91	0.53
1:1A:345:LEU:CD2	9:A6:367:LEU:HD22	2.39	0.53
31:E4:190:ARG:NE	40:G1:436:ALA:O	2.42	0.53
38:ED:43:TRP:CZ2	38:ED:47:MET:HE3	2.44	0.53
39:FX:134:THR:OG1	40:G1:282:ASP:OD1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S6:35:PRO:HD3	52:S6:77:ILE:HD11	1.90	0.53
56:V1:200:ARG:NH2	57:V2:88:MET:HE1	2.23	0.53
1:1A:352:LEU:HD11	9:A6:360:LEU:CD1	2.39	0.53
13:AB:92:LEU:HD22	66:AB:150:ZMP:H20	1.90	0.53
22:B7:4:ASP:OD2	22:B7:9:SER:OG	2.13	0.53
47:N5:310:ILE:HG21	47:N5:438:ILE:CG2	2.38	0.53
48:S2:210:MET:HE2	48:S2:370:LEU:HD21	1.90	0.53
49:S3:35:HIS:ND1	49:S3:39:GLU:OE1	2.37	0.53
1:1A:331:MET:HE2	2:1B:305:VAL:HG12	1.91	0.53
1:1A:331:MET:HE1	1:1A:335:TYR:CD2	2.43	0.53
16:AN:91:VAL:O	44:N2:169:TYR:OH	2.21	0.53
20:B5:101:GLN:NE2	64:N4:501:CDL:OA3	2.39	0.53
34:E8:14:PHE:O	34:E8:19:ASN:ND2	2.41	0.53
56:V1:456:ASP:OD1	56:V1:476:ARG:NH1	2.37	0.53
58:E7:91:GLN:OE1	58:E7:91:GLN:N	2.42	0.53
20:B5:11:PRO:O	68:N4:505:U10:H302	2.09	0.53
46:N4:269:LEU:HD22	46:N4:313:LEU:HD22	1.91	0.53
47:N5:156:ASN:OD1	47:N5:165:THR:HG22	2.09	0.53
59:AC:92:LEU:CG	66:AC:201:ZMP:H19B	2.39	0.53
12:A9:259:TYR:OH	53:S7:43:GLU:OE2	2.24	0.53
15:AM:54:VAL:HG13	64:AM:216:CDL:H532	1.89	0.53
40:G1:251:ASP:N	40:G1:251:ASP:OD1	2.41	0.53
47:N5:118:VAL:CG1	47:N5:122:MET:HE2	2.38	0.53
2:1B:119:ARG:NH1	29:E2:19:GLU:OE2	2.37	0.53
16:AN:108:TRP:HZ3	39:FX:307:THR:HG21	1.74	0.53
32:E5:41:ALA:HB3	32:E5:289:LEU:HB3	1.91	0.53
37:EC:50:PHE:O	37:EC:55:ASN:N	2.41	0.53
46:N4:99:ASN:ND2	68:N4:505:U10:O3	2.40	0.53
49:S3:148:LEU:HD22	49:S3:151:LEU:HD12	1.90	0.53
54:S8:78:PRO:O	54:S8:81:ARG:NE	2.36	0.53
58:E7:12:LEU:HD21	58:E7:212:LEU:HB3	1.90	0.53
39:FX:306:TYR:O	39:FX:310:SER:OG	2.06	0.53
48:S2:224:MET:SD	48:S2:386:LEU:HD23	2.48	0.53
51:S5:68:GLU:O	51:S5:72:GLY:N	2.42	0.53
46:N4:173:ASN:OD1	46:N4:177:ASN:ND2	2.42	0.52
53:S7:149:GLY:O	53:S7:153:ASN:ND2	2.42	0.52
1:1A:144:ILE:HG23	54:S8:105:ILE:HD12	1.90	0.52
1:1A:341:ASN:ND2	9:A6:363:VAL:O	2.43	0.52
5:A1:91:TYR:O	5:A1:94:LYS:NZ	2.34	0.52
39:FX:225:VAL:HG11	39:FX:239:VAL:HG11	1.90	0.52
42:G3:96:ILE:HG23	42:G3:100:VAL:HG11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A6:177:VAL:HG12	9:A6:177:VAL:O	2.10	0.52
14:AL:177:GLN:O	14:AL:180:ARG:NH1	2.35	0.52
15:AM:102:GLU:OE2	15:AM:106:LYS:NZ	2.36	0.52
20:B5:47:THR:HG22	63:B5:203:PC1:H2E1	1.92	0.52
32:E5:266:LEU:HG	32:E5:289:LEU:HD13	1.92	0.52
46:N4:316:LEU:HD21	46:N4:325:TYR:CZ	2.44	0.52
54:S8:92:HIS:CD2	54:S8:143:CYS:SG	3.02	0.52
15:AM:140:ALA:HA	51:S5:37:VAL:HG21	1.91	0.52
28:E1:277:GLU:OE1	28:E1:277:GLU:N	2.35	0.52
36:EB:60:GLU:HG3	36:EB:68:VAL:HG11	1.91	0.52
46:N4:293:THR:HG22	46:N4:362:LEU:CD2	2.40	0.52
50:S4:156:ARG:NH1	50:S4:158:GLU:OE2	2.41	0.52
16:AN:9:ILE:HA	44:N2:219:LEU:HD22	1.90	0.52
23:B8:100:LYS:NZ	47:N5:538:TYR:OH	2.40	0.52
40:G1:254:ILE:C	40:G1:255:ILE:HD12	2.35	0.52
58:E7:12:LEU:HD21	58:E7:212:LEU:CB	2.40	0.52
58:E7:27:PHE:HZ	58:E7:189:ILE:HG21	1.75	0.52
23:B8:70:GLY:HA2	47:N5:555:ILE:HG21	1.92	0.52
27:C4:148:ASN:OD1	27:C4:152:ARG:NH2	2.38	0.52
32:E5:245:VAL:O	32:E5:249:VAL:HG23	2.09	0.52
41:G2:101:ILE:HD13	41:G2:107:ILE:HD12	1.92	0.52
47:N5:567:ILE:HG22	47:N5:567:ILE:O	2.08	0.52
2:1B:314:ASP:OD2	2:1B:337:SER:OG	2.11	0.52
3:2B:34:THR:HG21	3:2B:91:PHE:CZ	2.45	0.52
18:B3:32:TRP:O	18:B3:33:SER:OG	2.20	0.52
19:B4:68:LYS:NZ	24:B9:129:GLN:O	2.41	0.52
29:E2:348:ASP:OD1	29:E2:372:ARG:NH2	2.41	0.52
47:N5:486:TYR:CZ	47:N5:490:ILE:HD12	2.44	0.52
51:S5:69:CYS:SG	51:S5:70:ARG:N	2.82	0.52
47:N5:336:GLU:OE1	47:N5:336:GLU:N	2.36	0.52
29:E2:91:LYS:HD3	29:E2:352:VAL:HG21	1.92	0.52
34:E8:197:GLY:O	34:E8:201:VAL:HG13	2.10	0.52
41:G2:135:GLN:OE1	41:G2:153:LYS:NZ	2.20	0.52
42:G3:98:GLU:OE1	42:G3:98:GLU:N	2.36	0.52
5:A1:100:ARG:NH1	15:AM:168:GLU:OE2	2.43	0.52
13:AB:47:LEU:HD21	39:FX:197:MET:SD	2.50	0.52
18:B3:57:UNK:O	18:B3:59:UNK:N	2.43	0.52
20:B5:126:GLU:OE1	20:B5:129:ARG:NH2	2.41	0.52
44:N2:98:ASN:O	51:S5:29:LYS:NZ	2.35	0.52
47:N5:144:TRP:NE1	47:N5:179:ASP:OD1	2.36	0.52
7:A3:28:GLN:O	54:S8:31:HIS:NE2	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E4:188:ALA:O	31:E4:198:SER:OG	2.23	0.51
33:E6:201:ASN:N	33:E6:201:ASN:OD1	2.41	0.51
42:G3:82:ARG:NH1	42:G3:84:ASP:OD2	2.43	0.51
52:S6:70:VAL:HG11	54:S8:100:GLY:O	2.10	0.51
2:1B:108:GLU:CG	2:1B:419:VAL:HG21	2.40	0.51
8:A5:127:ASP:OD1	10:A7:78:ARG:NH2	2.43	0.51
11:A8:146:GLN:OE1	11:A8:146:GLN:N	2.41	0.51
34:E8:53:VAL:HG12	34:E8:61:ASP:CG	2.35	0.51
47:N5:389:LEU:CD2	47:N5:438:ILE:HD11	2.40	0.51
48:S2:57:MET:SD	48:S2:354:VAL:HG11	2.50	0.51
21:B6:54:PRO:O	38:ED:128:LYS:NZ	2.33	0.51
40:G1:198:ARG:HH11	42:G3:202:LEU:HD21	1.75	0.51
40:G1:390:ASP:OD1	40:G1:390:ASP:N	2.42	0.51
41:G2:79:SER:OG	41:G2:100:HIS:ND1	2.28	0.51
2:1B:525:GLU:OE1	2:1B:525:GLU:N	2.39	0.51
18:B3:10:GLN:NE2	47:N5:447:SER:O	2.43	0.51
42:G3:54:VAL:HG21	42:G3:57:ILE:HG13	1.91	0.51
45:N3:249:ASP:O	45:N3:252:ILE:HG22	2.11	0.51
7:A3:53:ARG:NH2	44:N2:27:VAL:HG23	2.24	0.51
12:A9:118:VAL:N	12:A9:196:GLN:OE1	2.39	0.51
28:E1:156:ASP:OD2	28:E1:159:SER:OG	2.26	0.51
31:E4:149:ASP:OD1	31:E4:150:ILE:N	2.44	0.51
41:G2:174:GLN:N	41:G2:174:GLN:OE1	2.43	0.51
46:N4:9:ARG:NH1	46:N4:82:ASP:OD2	2.43	0.51
47:N5:52:ILE:HG22	47:N5:52:ILE:O	2.10	0.51
47:N5:285:LEU:HD12	47:N5:285:LEU:O	2.10	0.51
3:2B:86:VAL:HG12	44:N2:238:LEU:HD21	1.93	0.51
42:G3:148:LYS:C	42:G3:149:ILE:HD12	2.36	0.51
44:N2:68:SER:OG	44:N2:79:GLN:NE2	2.42	0.51
56:V1:500:ASN:O	56:V1:502:ASN:N	2.43	0.51
48:S2:241:GLU:N	56:V1:492:SER:OG	2.44	0.51
47:N5:34:LEU:O	47:N5:35:ILE:HD12	2.11	0.51
47:N5:285:LEU:HD13	64:N5:603:CDL:H721	1.92	0.51
54:S8:92:HIS:HE1	61:S8:297:SF4:S4	2.31	0.51
2:1B:271:GLN:O	2:1B:499:ARG:NH2	2.44	0.51
15:AM:57:ARG:NH2	64:AM:217:CDL:OA2	2.44	0.51
19:B4:103:TYR:HE2	23:B8:69:VAL:HG22	1.75	0.51
21:B6:71:ASP:OD1	25:BL:95:ARG:NH2	2.43	0.51
22:B7:85:ARG:NH2	23:B8:130:GLY:O	2.40	0.51
28:E1:31:VAL:HG12	28:E1:253:LEU:HD21	1.92	0.51
30:E3:46:VAL:HG22	30:E3:97:TRP:CZ2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:E6:257:TYR:HB2	53:S7:34:ALA:HB1	1.91	0.51
41:G2:114:VAL:HG22	41:G2:114:VAL:O	2.11	0.51
44:N2:146:LEU:C	44:N2:146:LEU:HD23	2.36	0.51
46:N4:89:ILE:HG22	46:N4:104:ILE:HG21	1.92	0.51
12:A9:264:GLU:OE1	12:A9:278:ARG:NH2	2.40	0.51
23:B8:122:PHE:O	23:B8:128:ASN:ND2	2.36	0.51
39:FX:223:ARG:NH2	39:FX:228:LEU:HD21	2.25	0.51
44:N2:81:ILE:CD1	45:N6:153:ILE:HD12	2.40	0.51
46:N4:11:ILE:O	46:N4:14:LEU:N	2.44	0.51
50:S4:174:ASP:OD1	50:S4:175:SER:N	2.44	0.51
56:V1:478:THR:O	56:V1:514:TYR:OH	2.29	0.51
6:A2:155:GLU:OE2	30:E3:163:LYS:NZ	2.31	0.50
28:E1:82:ALA:HB3	28:E1:99:ILE:HD13	1.94	0.50
47:N5:239:GLN:N	47:N5:240:PRO:CD	2.74	0.50
1:1A:142:CYS:SG	1:1A:154:GLN:NE2	2.78	0.50
31:E4:79:ASP:OD1	31:E4:79:ASP:N	2.44	0.50
35:EA:117:UNK:C	35:EA:119:UNK:H	2.23	0.50
40:G1:300:ARG:NH1	40:G1:301:LYS:O	2.45	0.50
2:1B:190:GLU:OE2	29:E2:22:VAL:HG11	2.11	0.50
3:2B:87:LEU:HD11	44:N2:242:SER:CB	2.41	0.50
29:E2:224:GLU:N	29:E2:224:GLU:OE1	2.44	0.50
48:S2:362:TYR:OH	49:S3:105:ASP:OD1	2.29	0.50
8:A5:137:ILE:N	49:S3:113:THR:O	2.40	0.50
11:A8:80:ILE:HD13	11:A8:136:SER:OG	2.12	0.50
49:S3:178:ARG:NH2	49:S3:187:GLY:O	2.41	0.50
52:S6:9:LYS:O	52:S6:33:GLN:NE2	2.44	0.50
56:V1:268:ARG:N	56:V1:271:ASN:O	2.44	0.50
58:E7:192:ARG:NH1	58:E7:225:GLY:O	2.43	0.50
59:AC:92:LEU:HG	66:AC:201:ZMP:H19B	1.94	0.50
9:A6:294:LEU:HD12	9:A6:393:ILE:HD11	1.92	0.50
12:A9:460:VAL:HG12	40:G1:54:THR:HG23	1.92	0.50
28:E1:274:PRO:O	28:E1:330:GLN:NE2	2.45	0.50
39:FX:221:ASN:OD1	39:FX:221:ASN:N	2.45	0.50
40:G1:62:GLN:OE1	48:S2:4:ARG:NE	2.44	0.50
44:N2:92:TYR:O	44:N2:96:ASN:ND2	2.45	0.50
47:N5:163:GLU:OE2	67:N5:607:3PE:N	2.28	0.50
48:S2:105:VAL:HG21	48:S2:242:VAL:CG2	2.41	0.50
48:S2:107:PHE:CZ	48:S2:150:VAL:HG21	2.46	0.50
17:B2:125:PHE:CZ	47:N5:415:ILE:HG22	2.47	0.50
46:N4:366:ASN:ND2	46:N4:369:ILE:HG23	2.27	0.50
47:N5:363:ILE:O	47:N5:363:ILE:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:V1:399:ARG:NH1	56:V1:409:GLU:OE1	2.39	0.50
9:A6:314:VAL:HG21	9:A6:332:LEU:HD21	1.93	0.50
19:B4:6:PHE:HD2	19:B4:12:LEU:HD11	1.77	0.50
21:B6:4:LEU:HD13	26:BM:36:PRO:CD	2.42	0.50
21:B6:4:LEU:HD13	26:BM:36:PRO:HD2	1.94	0.50
32:E5:260:LYS:C	32:E5:284:VAL:O	2.55	0.50
38:ED:140:ASP:OD1	38:ED:141:GLY:N	2.44	0.50
40:G1:260:THR:OG1	42:G3:140:ASN:ND2	2.42	0.50
41:G2:133:PRO:O	41:G2:151:GLY:N	2.38	0.50
49:S3:140:ASP:OD1	49:S3:141:ASP:N	2.36	0.50
56:V1:75:ILE:HG21	56:V1:149:ALA:HB2	1.94	0.50
56:V1:116:ILE:HD12	56:V1:249:VAL:HG11	1.93	0.50
56:V1:293:MET:HE1	56:V1:340:PHE:CD2	2.47	0.50
28:E1:360:VAL:HG11	28:E1:371:LEU:HD23	1.94	0.50
32:E5:124:VAL:O	32:E5:153:LEU:HD21	2.12	0.50
43:N1:582:ILE:HD11	45:N3:214:VAL:CG1	2.41	0.50
48:S2:33:GLU:OE1	48:S2:33:GLU:N	2.43	0.50
59:AC:90:ASP:O	59:AC:94:VAL:HG23	2.12	0.50
9:A6:48:PRO:HG2	49:S3:176:LEU:HD22	1.93	0.50
9:A6:361:LYS:NZ	9:A6:372:ASP:OD1	2.44	0.50
13:AB:92:LEU:CD1	66:AB:150:ZMP:H20A	2.36	0.50
64:AM:216:CDL:OA3	31:E4:322:GLN:NE2	2.44	0.50
20:B5:71:VAL:HG21	46:N4:50:ILE:HD11	1.94	0.50
25:BL:82:LEU:C	25:BL:82:LEU:HD23	2.37	0.50
30:E3:118:GLU:HB3	30:E3:296:VAL:HG11	1.92	0.50
30:E3:165:TRP:NE1	30:E3:281:GLU:OE2	2.34	0.50
6:A2:174:PHE:N	9:A6:359:ASP:OD2	2.39	0.49
11:A8:65:ASN:N	11:A8:65:ASN:OD1	2.45	0.49
14:AL:151:SER:OG	64:AL:303:CDL:OB3	2.14	0.49
28:E1:40:ARG:NH2	29:E2:235:ASP:OD2	2.45	0.49
3:2B:5:LEU:HD11	42:G3:224:LEU:HD11	1.94	0.49
11:A8:1:MET:HE2	44:N2:195:ILE:CG2	2.40	0.49
11:A8:59:GLY:O	35:EA:123:UNK:N	2.45	0.49
12:A9:468:LEU:HB3	63:A9:560:PC1:H142	1.92	0.49
50:S4:38:VAL:HG23	50:S4:39:ASN:N	2.26	0.49
33:E6:63:GLY:O	33:E6:203:ARG:NH2	2.46	0.49
36:EB:60:GLU:OE2	36:EB:72:ARG:NH1	2.45	0.49
37:EC:19:ARG:NH1	37:EC:92:GLU:OE1	2.39	0.49
52:S6:115:CYS:O	52:S6:119:GLU:CA	2.60	0.49
66:AC:201:ZMP:H21	66:AC:201:ZMP:O3	2.12	0.49
64:AM:215:CDL:OA4	31:E4:335:TYR:OH	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:FX:280:GLU:OE2	39:FX:319:ARG:NH2	2.46	0.49
46:N4:300:TYR:OH	46:N4:426:SER:N	2.46	0.49
47:N5:67:ASN:ND2	47:N5:75:ASN:OD1	2.37	0.49
45:N6:52:GLY:HA3	45:N6:75:ILE:HD13	1.93	0.49
45:N6:147:ILE:O	45:N6:150:MET:HG3	2.13	0.49
49:S3:105:ASP:OD1	49:S3:106:VAL:N	2.46	0.49
9:A6:129:VAL:HG12	9:A6:129:VAL:O	2.12	0.49
28:E1:418:VAL:HG22	28:E1:419:ALA:H	1.76	0.49
44:N2:131:TYR:CZ	44:N2:174:LEU:HD22	2.48	0.49
44:N2:221:ILE:HD11	44:N2:252:ASN:ND2	2.27	0.49
47:N5:360:ILE:HG23	47:N5:365:SER:O	2.13	0.49
56:V1:115:VAL:HG11	56:V1:213:LEU:HD22	1.94	0.49
9:A6:72:MET:HE3	9:A6:120:PHE:CD1	2.47	0.49
10:A7:86:LEU:HD23	49:S3:55:TYR:HB2	1.94	0.49
11:A8:30:LEU:O	11:A8:34:VAL:HG13	2.12	0.49
28:E1:148:GLU:OE1	28:E1:148:GLU:N	2.33	0.49
28:E1:339:ASP:OD2	28:E1:343:LYS:NZ	2.46	0.49
34:E8:18:TRP:CZ3	47:N5:436:LEU:HD12	2.46	0.49
43:N1:380:SER:O	43:N1:383:THR:OG1	2.19	0.49
44:N2:171:ILE:N	44:N2:172:PRO:CD	2.76	0.49
46:N4:37:ILE:O	46:N4:40:ILE:HG22	2.13	0.49
47:N5:34:LEU:C	47:N5:35:ILE:HD12	2.38	0.49
47:N5:242:LEU:HD11	47:N5:257:HIS:CE1	2.47	0.49
47:N5:393:LEU:HD11	47:N5:432:GLN:HG3	1.93	0.49
48:S2:184:PHE:CD2	48:S2:273:ILE:HG21	2.47	0.49
56:V1:487:ASP:O	56:V1:492:SER:HA	2.13	0.49
15:AM:54:VAL:HG13	64:AM:216:CDL:C53	2.43	0.49
19:B4:103:TYR:CE2	23:B8:69:VAL:HG22	2.47	0.49
26:BM:56:TRP:HA	26:BM:59:VAL:HG22	1.95	0.49
32:E5:283:THR:HG23	32:E5:283:THR:O	2.12	0.49
34:E8:18:TRP:CE3	47:N5:436:LEU:HD12	2.48	0.49
56:V1:157:ILE:HB	56:V1:198:LEU:HD12	1.93	0.49
5:A1:31:CYS:SG	43:N1:370:LEU:HD12	2.53	0.49
7:A3:37:LEU:O	7:A3:48:ARG:NH2	2.42	0.49
12:A9:287:ASP:OD2	12:A9:290:THR:OG1	2.31	0.49
30:E3:219:ALA:O	30:E3:223:VAL:HG23	2.13	0.49
31:E4:127:ASP:O	31:E4:130:ASP:N	2.43	0.49
63:N5:601:PC1:O13	63:N5:601:PC1:H143	2.12	0.49
49:S3:156:MET:HE2	50:S4:17:PHE:CE1	2.47	0.49
53:S7:139:MET:HE3	53:S7:143:CYS:CB	2.42	0.49
56:V1:160:ARG:NH2	56:V1:162:GLU:OE1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AL:105:ARG:NE	64:AL:303:CDL:OB3	2.46	0.49
50:S4:38:VAL:HG23	50:S4:39:ASN:H	1.77	0.49
54:S8:158:ILE:HG23	54:S8:158:ILE:O	2.12	0.49
56:V1:487:ASP:OD2	56:V1:495:ARG:NE	2.43	0.49
12:A9:93:LEU:HB3	50:S4:141:SER:HB3	1.95	0.49
12:A9:246:ILE:HD11	12:A9:408:PRO:HA	1.95	0.49
23:B8:63:ASN:ND2	23:B8:65:THR:OG1	2.41	0.49
30:E3:418:ILE:HG22	30:E3:420:VAL:HG13	1.95	0.49
39:FX:138:VAL:HG22	39:FX:232:PRO:HA	1.93	0.49
44:N2:108:ILE:HD12	44:N2:142:ILE:HG21	1.94	0.49
47:N5:209:TYR:O	47:N5:213:ASN:ND2	2.40	0.49
1:1A:331:MET:HE1	1:1A:335:TYR:HD2	1.76	0.48
2:1B:108:GLU:HG2	2:1B:419:VAL:HG21	1.95	0.48
9:A6:211:ASP:OD1	9:A6:211:ASP:N	2.43	0.48
11:A8:210:SER:N	15:AM:86:ASP:OD2	2.46	0.48
19:B4:97:PHE:HD2	46:N4:364:LEU:HD21	1.77	0.48
41:G2:149:MET:HE2	41:G2:168:GLU:HG3	1.94	0.48
9:A6:339:TYR:HB2	9:A6:344:LEU:HD12	1.96	0.48
18:B3:39:UNK:O	18:B3:40:UNK:CB	2.61	0.48
40:G1:59:PHE:O	42:G3:247:ARG:NH1	2.46	0.48
40:G1:212:GLY:O	42:G3:99:ARG:NE	2.46	0.48
52:S6:127:PHE:N	52:S6:128:PRO:CD	2.76	0.48
1:1A:174:HIS:O	1:1A:174:HIS:ND1	2.45	0.48
29:E2:125:ALA:O	29:E2:129:VAL:HG23	2.14	0.48
2:1B:166:VAL:HG21	2:1B:182:LEU:HD12	1.95	0.48
3:2B:63:ILE:HD13	44:N2:260:ILE:HD13	1.95	0.48
4:4L:99:ALA:HA	42:G3:256:ILE:HD11	1.95	0.48
45:N3:267:THR:HG21	45:N6:135:PHE:O	2.14	0.48
47:N5:102:ILE:CG2	47:N5:466:ILE:HD11	2.43	0.48
47:N5:328:ILE:HG22	47:N5:328:ILE:O	2.13	0.48
48:S2:210:MET:SD	48:S2:214:ARG:NH1	2.87	0.48
3:2B:79:LEU:HD11	63:N2:301:PC1:H2A1	1.94	0.48
10:A7:112:HIS:CD2	31:E4:31:VAL:HG13	2.48	0.48
25:BL:53:ASP:OD1	25:BL:57:LEU:N	2.45	0.48
31:E4:336:LEU:HD23	31:E4:336:LEU:C	2.38	0.48
32:E5:36:LEU:HD22	32:E5:87:LEU:HD11	1.96	0.48
41:G2:223:THR:HG23	41:G2:224:GLU:HG2	1.96	0.48
43:N1:442:ILE:HD11	45:N3:185:PHE:HA	1.96	0.48
44:N2:50:ILE:HD11	44:N2:87:ILE:HD11	1.95	0.48
47:N5:525:HIS:HB3	58:E7:4:LEU:HD23	1.96	0.48
11:A8:128:MET:HE2	11:A8:132:TYR:HE2	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:E3:197:LEU:C	30:E3:197:LEU:HD12	2.38	0.48
43:N1:446:LEU:HD12	45:N3:180:ASN:ND2	2.29	0.48
1:1A:276:ILE:HG22	1:1A:281:LEU:HD23	1.96	0.48
5:A1:38:LYS:NZ	5:A1:96:GLU:OE1	2.37	0.48
10:A7:69:ILE:O	10:A7:69:ILE:HG23	2.13	0.48
20:B5:129:ARG:NH1	51:S5:22:THR:OG1	2.39	0.48
30:E3:108:LEU:HD12	30:E3:108:LEU:N	2.28	0.48
33:E6:56:SER:OG	33:E6:57:ASN:ND2	2.47	0.48
43:N1:579:SER:OG	43:N1:645:ARG:NH1	2.47	0.48
49:S3:106:VAL:HG22	49:S3:122:TYR:CD1	2.48	0.48
2:1B:185:ARG:NH1	28:E1:215:ASP:OD2	2.43	0.48
46:N4:43:ILE:HG22	46:N4:75:ILE:HG23	1.96	0.48
48:S2:350:LEU:HD11	50:S4:116:ARG:NE	2.28	0.48
12:A9:136:LEU:HD11	12:A9:199:PHE:CE1	2.49	0.48
32:E5:64:ALA:O	32:E5:96:TYR:N	2.46	0.48
41:G2:95:ILE:HG23	41:G2:99:THR:HG21	1.95	0.48
47:N5:380:ILE:HG23	47:N5:381:LEU:N	2.29	0.48
52:S6:115:CYS:O	52:S6:119:GLU:HA	2.14	0.48
54:S8:108:GLN:N	61:S8:298:SF4:S1	2.78	0.48
54:S8:112:VAL:O	54:S8:112:VAL:HG22	2.14	0.48
2:1B:507:HIS:O	2:1B:511:VAL:HG23	2.13	0.48
4:4L:67:PHE:O	27:C4:13:LEU:N	2.40	0.48
5:A1:36:PHE:CG	43:N1:459:ILE:HD11	2.49	0.48
8:A5:57:ILE:O	8:A5:64:ARG:NH1	2.38	0.48
29:E2:154:ARG:O	29:E2:157:VAL:HG23	2.13	0.48
30:E3:286:ILE:HG13	30:E3:291:LEU:HD23	1.95	0.48
30:E3:389:VAL:CG2	30:E3:398:VAL:HG21	2.44	0.48
63:E8:301:PC1:H332	47:N5:223:MET:HE2	1.96	0.48
36:EB:95:ASP:OD1	36:EB:96:ARG:N	2.44	0.48
39:FX:192:SER:HB3	39:FX:193:PRO:HD3	1.96	0.48
40:G1:292:VAL:HG22	40:G1:299:LEU:HB2	1.96	0.48
49:S3:30:GLU:OE1	49:S3:246:TYR:OH	2.32	0.48
1:1A:331:MET:HE2	2:1B:305:VAL:HG11	1.95	0.47
13:AB:60:THR:HG22	13:AB:124:ILE:HG21	1.96	0.47
64:AM:215:CDL:O1	31:E4:338:ARG:NH2	2.39	0.47
16:AN:258:PRO:HG2	20:B5:91:ILE:HG21	1.95	0.47
33:E6:30:ASP:OD1	33:E6:30:ASP:N	2.47	0.47
40:G1:153:ILE:HG23	40:G1:162:PRO:HD2	1.96	0.47
43:N1:451:ILE:HD13	43:N1:536:LEU:HD11	1.96	0.47
47:N5:203:ILE:O	47:N5:206:SER:OG	2.31	0.47
2:1B:463:GLU:OE1	2:1B:463:GLU:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2B:59:TYR:CE1	44:N2:267:LEU:HD22	2.48	0.47
16:AN:108:TRP:CZ3	39:FX:307:THR:HG21	2.49	0.47
46:N4:264:ILE:HG22	46:N4:265:TYR:N	2.28	0.47
46:N4:377:ILE:HG23	46:N4:460:LEU:HD11	1.95	0.47
1:1A:120:ASP:N	1:1A:120:ASP:OD1	2.47	0.47
6:A2:2:ALA:N	30:E3:201:GLN:O	2.47	0.47
30:E3:425:LEU:O	30:E3:429:VAL:HG23	2.14	0.47
47:N5:270:TYR:CE2	47:N5:339:LEU:HD11	2.50	0.47
2:1B:341:ASP:OD1	2:1B:341:ASP:N	2.47	0.47
9:A6:31:VAL:CG1	39:FX:141:THR:HG21	2.42	0.47
63:AM:220:PC1:H143	31:E4:194:TRP:CZ3	2.48	0.47
27:C4:142:SER:O	27:C4:146:VAL:HG22	2.15	0.47
31:E4:296:VAL:O	31:E4:300:THR:HG22	2.14	0.47
49:S3:156:MET:HE1	49:S3:174:PRO:HG2	1.97	0.47
9:A6:90:ARG:NH2	13:AB:93:ASP:OD1	2.47	0.47
28:E1:264:PHE:CE2	28:E1:270:VAL:HG21	2.50	0.47
32:E5:281:SER:OG	32:E5:283:THR:HG22	2.13	0.47
47:N5:92:LEU:HD21	47:N5:259:ALA:HB2	1.95	0.47
47:N5:310:ILE:HG21	47:N5:438:ILE:HG21	1.97	0.47
54:S8:159:VAL:HG11	54:S8:192:ILE:HD12	1.96	0.47
2:1B:74:LEU:HD22	2:1B:390:PHE:HZ	1.80	0.47
7:A3:52:MET:HE1	40:G1:420:PRO:HG3	1.97	0.47
24:B9:30:ILE:HD13	24:B9:42:LEU:HD21	1.96	0.47
29:E2:60:ARG:NH1	29:E2:184:THR:OG1	2.46	0.47
31:E4:336:LEU:HD23	31:E4:336:LEU:O	2.15	0.47
38:ED:142:VAL:HG23	38:ED:143:LEU:N	2.28	0.47
40:G1:343:ASP:OD1	41:G2:33:ARG:NH2	2.43	0.47
48:S2:121:ALA:HB1	48:S2:133:ILE:HA	1.97	0.47
56:V1:159:VAL:CG2	56:V1:198:LEU:HD11	2.44	0.47
66:AC:201:ZMP:H12A	66:AC:201:ZMP:N2	2.30	0.47
1:1A:226:VAL:O	1:1A:228:ARG:N	2.47	0.47
2:1B:367:ARG:NE	30:E3:410:LEU:O	2.42	0.47
10:A7:126:ARG:NH2	15:AM:38:GLY:O	2.47	0.47
28:E1:81:ARG:NE	28:E1:126:LEU:O	2.46	0.47
29:E2:40:TYR:HA	29:E2:43:VAL:HG22	1.97	0.47
31:E4:130:ASP:OD2	31:E4:133:SER:OG	2.32	0.47
32:E5:38:VAL:HG11	32:E5:41:ALA:HB2	1.96	0.47
34:E8:148:LYS:O	34:E8:149:SER:OG	2.19	0.47
39:FX:143:ILE:HG21	39:FX:244:PHE:CD2	2.50	0.47
46:N4:258:ILE:HD11	46:N4:312:MET:SD	2.55	0.47
46:N4:398:LEU:HD11	47:N5:138:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:N5:131:LEU:HD23	47:N5:131:LEU:O	2.15	0.47
45:N6:45:ILE:HD11	45:N6:82:ILE:CG2	2.44	0.47
48:S2:33:GLU:HB2	48:S2:41:ARG:HB3	1.96	0.47
50:S4:65:VAL:O	50:S4:139:ASN:N	2.48	0.47
52:S6:97:THR:HG22	52:S6:97:THR:O	2.14	0.47
54:S8:159:VAL:HG11	54:S8:192:ILE:HG23	1.96	0.47
54:S8:159:VAL:CG1	54:S8:192:ILE:HD12	2.44	0.47
58:E7:159:LEU:HD23	58:E7:159:LEU:C	2.40	0.47
58:E7:212:LEU:O	58:E7:215:THR:OG1	2.26	0.47
1:1A:45:THR:HB	1:1A:52:LEU:HD11	1.96	0.47
6:A2:102:GLN:O	12:A9:78:LYS:NZ	2.36	0.47
7:A3:55:ALA:HB3	43:N1:658:TYR:HA	1.96	0.47
12:A9:42:THR:HG1	12:A9:43:GLN:CD	2.11	0.47
26:BM:96:ARG:NH2	36:EB:39:ASP:OD1	2.48	0.47
27:C4:13:LEU:HD23	27:C4:14:GLU:N	2.30	0.47
27:C4:43:ASP:O	27:C4:44:ALA:HB3	2.15	0.47
47:N5:60:LEU:HD22	47:N5:135:ASN:OD1	2.14	0.47
48:S2:253:GLY:H	48:S2:264:ILE:HD11	1.80	0.47
53:S7:76:SER:OG	53:S7:78:TRP:NE1	2.48	0.47
56:V1:319:ILE:CG1	56:V1:327:VAL:HG12	2.45	0.47
4:4L:141:LEU:HD21	45:N6:150:MET:HE1	1.97	0.47
11:A8:10:THR:HG22	20:B5:105:VAL:HG13	1.97	0.47
31:E4:188:ALA:HB1	31:E4:336:LEU:HD21	1.97	0.47
37:EC:69:GLU:HG2	37:EC:76:VAL:HG23	1.96	0.47
42:G3:68:THR:HB	42:G3:87:LYS:HZ3	1.80	0.47
46:N4:40:ILE:HD12	46:N4:43:ILE:HD11	1.97	0.47
46:N4:110:ILE:CG2	46:N4:126:ILE:HG23	2.45	0.47
2:1B:170:GLU:N	2:1B:170:GLU:OE1	2.48	0.47
14:AL:175:GLU:OE2	15:AM:31:ARG:NH2	2.47	0.47
40:G1:292:VAL:HG21	67:G1:516:3PE:H332	1.96	0.47
48:S2:211:ASP:OD1	48:S2:211:ASP:N	2.43	0.47
8:A5:152:VAL:HG21	12:A9:65:THR:HG22	1.97	0.46
27:C4:148:ASN:O	27:C4:152:ARG:NE	2.45	0.46
30:E3:52:ASP:OD1	30:E3:240:SER:OG	2.32	0.46
30:E3:306:ASP:OD1	30:E3:306:ASP:N	2.48	0.46
63:ED:201:PC1:H132	63:ED:201:PC1:O13	2.15	0.46
47:N5:126:TYR:CE2	47:N5:130:LEU:HD11	2.50	0.46
4:4L:141:LEU:HD11	45:N6:150:MET:HE1	1.96	0.46
11:A8:1:MET:HE1	44:N2:58:LEU:HD21	1.97	0.46
21:B6:37:ILE:HD12	47:N5:15:ILE:HD11	1.96	0.46
22:B7:36:GLU:OE1	38:ED:133:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:B9:66:ASP:CG	34:E8:41:HIS:HE2	2.18	0.46
29:E2:424:ASP:OD1	29:E2:425:ASP:N	2.48	0.46
43:N1:381:LEU:HA	43:N1:384:VAL:HG12	1.97	0.46
43:N1:605:ILE:HD11	43:N1:636:PHE:CE2	2.50	0.46
47:N5:117:PHE:CZ	47:N5:252:VAL:HG23	2.50	0.46
49:S3:202:VAL:CG2	53:S7:165:VAL:HG22	2.45	0.46
56:V1:487:ASP:OD1	56:V1:487:ASP:N	2.48	0.46
2:1B:109:LEU:HD21	2:1B:197:TYR:CZ	2.51	0.46
19:B4:33:LEU:HD21	19:B4:39:MET:HB2	1.97	0.46
19:B4:160:MET:HE1	23:B8:154:ALA:CB	2.45	0.46
64:B5:201:CDL:OA3	26:BM:46:ARG:NH1	2.44	0.46
56:V1:271:ASN:ND2	56:V1:341:ASP:OD2	2.45	0.46
29:E2:287:LEU:HD12	29:E2:454:LEU:HD12	1.97	0.46
35:EA:45:LYS:NZ	44:N2:29:ASP:OD2	2.46	0.46
39:FX:158:MET:HE2	39:FX:163:ALA:N	2.31	0.46
49:S3:85:ILE:HD11	49:S3:122:TYR:CD2	2.50	0.46
56:V1:213:LEU:O	56:V1:213:LEU:HD23	2.16	0.46
56:V1:407:GLY:O	56:V1:410:VAL:N	2.49	0.46
9:A6:163:GLY:N	9:A6:169:GLU:OE1	2.40	0.46
10:A7:109:TRP:CZ2	49:S3:128:VAL:HG22	2.50	0.46
44:N2:248:ILE:O	44:N2:252:ASN:ND2	2.46	0.46
12:A9:85:SER:HA	12:A9:92:ARG:O	2.15	0.46
12:A9:276:ILE:N	12:A9:276:ILE:HD12	2.30	0.46
21:B6:81:LEU:HD11	38:ED:124:LYS:HD3	1.98	0.46
46:N4:309:TYR:HE1	46:N4:336:MET:HE1	1.81	0.46
46:N4:374:ILE:HD11	46:N4:453:ILE:HG13	1.98	0.46
47:N5:16:MET:SD	47:N5:28:LEU:HD13	2.56	0.46
11:A8:83:ASN:O	11:A8:87:SER:OG	2.25	0.46
12:A9:288:ASN:O	12:A9:292:LEU:HD12	2.15	0.46
13:AB:60:THR:HG22	13:AB:124:ILE:HD13	1.97	0.46
16:AN:11:MET:HE1	47:N5:581:ILE:HG22	1.97	0.46
31:E4:182:ILE:HD12	31:E4:182:ILE:N	2.31	0.46
32:E5:7:TRP:HB2	32:E5:96:TYR:CB	2.46	0.46
46:N4:258:ILE:HD12	46:N4:261:TYR:CE2	2.51	0.46
45:N6:42:ILE:HD12	45:N6:43:ARG:N	2.30	0.46
52:S6:54:ILE:HG21	54:S8:96:ILE:HG12	1.98	0.46
59:AC:109:MET:HE1	59:AC:117:ILE:HD12	1.97	0.46
13:AB:54:LEU:HD23	13:AB:59:VAL:HG22	1.98	0.46
28:E1:50:ARG:NH2	28:E1:89:ASP:OD2	2.44	0.46
32:E5:204:LEU:HD21	32:E5:231:PHE:HB2	1.98	0.46
39:FX:142:PHE:HB3	39:FX:169:VAL:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:N1:602:TYR:HA	43:N1:605:ILE:HG22	1.98	0.46
1:1A:49:ASP:OD2	1:1A:118:THR:OG1	2.34	0.46
19:B4:6:PHE:CD2	19:B4:12:LEU:HD11	2.50	0.46
28:E1:83:LEU:HD13	28:E1:126:LEU:HD12	1.97	0.46
37:EC:58:ALA:HA	37:EC:61:LEU:HD12	1.97	0.46
41:G2:17:ARG:NH1	42:G3:30:GLY:O	2.47	0.46
43:N1:543:GLN:NE2	43:N1:615:LEU:O	2.49	0.46
1:1A:341:ASN:O	1:1A:345:LEU:HG	2.16	0.45
2:1B:52:ASN:ND2	2:1B:265:ASN:OD1	2.45	0.45
2:1B:368:LEU:HD21	30:E3:410:LEU:HD13	1.97	0.45
8:A5:155:GLU:OE1	12:A9:68:ARG:NH2	2.48	0.45
46:N4:121:ILE:HG23	64:N4:501:CDL:H801	1.98	0.45
46:N4:232:VAL:HG23	46:N4:233:GLU:HG2	1.97	0.45
47:N5:254:ALA:HB2	47:N5:353:PHE:HB3	1.98	0.45
53:S7:104:TYR:CD2	53:S7:193:LEU:HD21	2.50	0.45
6:A2:26:PRO:O	6:A2:27:GLU:HB3	2.16	0.45
19:B4:78:HIS:O	19:B4:80:ASN:ND2	2.48	0.45
23:B8:72:ASP:O	46:N4:432:LYS:NZ	2.49	0.45
34:E8:196:PHE:O	34:E8:200:VAL:HG22	2.17	0.45
40:G1:105:HIS:CE1	42:G3:241:ARG:HE	2.34	0.45
40:G1:194:LEU:HD22	40:G1:215:LEU:HD12	1.98	0.45
44:N2:215:ILE:O	44:N2:219:LEU:HG	2.16	0.45
3:2B:63:ILE:C	3:2B:63:ILE:HD12	2.41	0.45
9:A6:134:ASN:HD21	66:AB:150:ZMP:H24	1.81	0.45
21:B6:85:ASP:OD1	38:ED:120:SER:OG	2.25	0.45
27:C4:114:PHE:HB2	27:C4:115:PRO:HD3	1.97	0.45
28:E1:346:ASP:CG	28:E1:348:THR:HG1	2.24	0.45
29:E2:353:THR:HG22	29:E2:354:ALA:N	2.31	0.45
39:FX:144:ASP:OD1	39:FX:148:ASN:HB2	2.16	0.45
39:FX:158:MET:HE1	39:FX:166:GLN:NE2	2.32	0.45
46:N4:419:SER:O	46:N4:422:ASN:HB2	2.17	0.45
49:S3:139:VAL:HG11	49:S3:145:ILE:HB	1.97	0.45
3:2B:49:TYR:CG	44:N2:281:ILE:HG13	2.51	0.45
11:A8:124:GLU:OE1	11:A8:124:GLU:N	2.42	0.45
27:C4:161:GLU:OE1	27:C4:165:ASN:ND2	2.46	0.45
29:E2:280:ALA:HB1	29:E2:286:SER:HB3	1.98	0.45
30:E3:211:ALA:HB2	30:E3:227:ILE:HD13	1.98	0.45
36:EB:30:GLN:OE1	36:EB:31:CYS:N	2.41	0.45
38:ED:68:ASP:OD1	38:ED:69:LYS:N	2.49	0.45
47:N5:341:HIS:CE1	47:N5:400:LEU:HD11	2.52	0.45
47:N5:434:TYR:CD1	47:N5:435:SER:N	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:258:GLU:OE2	14:AL:238:ARG:NH2	2.36	0.45
11:A8:30:LEU:O	11:A8:34:VAL:HG22	2.17	0.45
45:N3:258:ILE:HD13	45:N3:271:THR:HG21	1.99	0.45
46:N4:211:LEU:HA	46:N4:254:HIS:CE1	2.52	0.45
46:N4:228:GLY:O	46:N4:232:VAL:HG13	2.16	0.45
47:N5:47:LEU:HB2	47:N5:91:ILE:HD11	1.98	0.45
14:AL:23:THR:O	14:AL:23:THR:HG22	2.16	0.45
16:AN:21:SER:OG	16:AN:67:ASP:OD1	2.19	0.45
40:G1:321:HIS:ND1	40:G1:321:HIS:C	2.75	0.45
44:N2:171:ILE:HD12	44:N2:247:THR:OG1	2.16	0.45
46:N4:191:ILE:HD11	46:N4:257:PHE:CE2	2.52	0.45
46:N4:302:ILE:O	46:N4:306:ASN:ND2	2.37	0.45
46:N4:308:TYR:HD2	46:N4:336:MET:HE2	1.81	0.45
47:N5:355:LEU:HD11	47:N5:384:ILE:CG2	2.39	0.45
56:V1:215:GLU:OE2	56:V1:225:ARG:NE	2.34	0.45
1:1A:78:CYS:O	1:1A:200:ARG:NH2	2.41	0.45
1:1A:139:SER:OG	1:1A:141:ASP:OD1	2.29	0.45
1:1A:163:ASP:OD1	10:A7:55:ARG:NH2	2.49	0.45
9:A6:99:LEU:HD21	50:S4:50:GLN:HG3	1.98	0.45
29:E2:421:LEU:HD11	29:E2:465:THR:OG1	2.17	0.45
31:E4:318:VAL:HG23	31:E4:331:ARG:HG2	1.99	0.45
33:E6:130:GLU:OE2	33:E6:213:ARG:NH2	2.49	0.45
43:N1:500:ILE:HG21	45:N6:84:LEU:HB2	1.97	0.45
43:N1:626:PHE:O	43:N1:629:ILE:HG13	2.16	0.45
45:N3:228:ILE:HD12	45:N3:228:ILE:N	2.32	0.45
47:N5:393:LEU:HD13	47:N5:393:LEU:O	2.15	0.45
48:S2:75:MET:CE	48:S2:118:LEU:HD13	2.47	0.45
48:S2:78:MET:HB2	48:S2:111:THR:HG21	1.98	0.45
49:S3:234:ASP:OD1	49:S3:235:ASP:N	2.49	0.45
56:V1:42:GLN:O	57:V2:210:LEU:HD13	2.17	0.45
59:AC:93:ASP:N	59:AC:93:ASP:OD1	2.50	0.45
12:A9:202:ILE:HD13	12:A9:224:LEU:HD21	1.99	0.45
17:B2:112:GLU:OE1	23:B8:158:ARG:NH1	2.50	0.45
19:B4:9:LEU:CD1	39:FX:253:THR:HG21	2.47	0.45
44:N2:58:LEU:HD22	44:N2:87:ILE:HG12	1.98	0.45
46:N4:357:THR:CG2	46:N4:369:ILE:HD13	2.47	0.45
47:N5:425:ILE:HG23	47:N5:509:ILE:HD13	1.98	0.45
12:A9:80:THR:HG22	12:A9:81:GLU:N	2.32	0.45
27:C4:27:LEU:HB3	27:C4:35:LEU:HD21	1.99	0.45
29:E2:217:VAL:HG11	29:E2:268:LEU:CD1	2.47	0.45
39:FX:140:LEU:HD22	39:FX:237:MET:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:N4:352:TYR:CD2	46:N4:452:LEU:HD22	2.51	0.45
59:AC:113:GLU:OE1	59:AC:126:TYR:OH	2.33	0.45
66:AC:201:ZMP:H4	66:AC:201:ZMP:H1	1.81	0.45
28:E1:324:VAL:HG23	28:E1:355:LEU:CD1	2.47	0.45
34:E8:1:MET:HE1	59:AC:89:LEU:CD2	2.46	0.45
40:G1:405:HIS:O	45:N6:169:ILE:HG22	2.17	0.45
56:V1:303:LYS:NZ	57:V2:208:THR:O	2.50	0.45
12:A9:106:TYR:OH	50:S4:92:GLU:OE1	2.29	0.44
15:AM:54:VAL:HG12	64:AM:215:CDL:HA31	1.98	0.44
27:C4:150:TYR:HA	27:C4:153:VAL:HG12	1.99	0.44
30:E3:98:SER:OG	30:E3:100:TYR:O	2.34	0.44
39:FX:249:THR:N	39:FX:250:PRO:HD2	2.32	0.44
43:N1:508:ILE:HG12	45:N3:248:LEU:HB3	1.98	0.44
44:N2:39:PHE:HA	44:N2:69:THR:HG21	1.98	0.44
57:V2:149:HIS:HB3	57:V2:170:GLU:HB3	1.98	0.44
11:A8:37:LYS:O	35:EA:106:UNK:N	2.51	0.44
12:A9:215:PHE:O	53:S7:48:GLN:NE2	2.48	0.44
14:AL:257:ARG:CD	54:S8:124:VAL:HG11	2.47	0.44
29:E2:348:ASP:HB3	29:E2:359:LEU:HD11	1.99	0.44
39:FX:157:GLY:N	39:FX:230:VAL:O	2.40	0.44
39:FX:234:MET:O	39:FX:235:GLU:C	2.60	0.44
46:N4:227:LEU:HD22	46:N4:231:HIS:CE1	2.52	0.44
46:N4:314:ILE:HG21	46:N4:404:LEU:CD1	2.47	0.44
45:N6:65:ILE:HG23	45:N6:66:LEU:N	2.33	0.44
49:S3:160:ARG:NH1	49:S3:177:ARG:O	2.50	0.44
57:V2:178:ILE:HA	57:V2:181:VAL:HG22	1.98	0.44
3:2B:59:TYR:CE1	3:2B:63:ILE:HG21	2.53	0.44
12:A9:202:ILE:HD13	12:A9:224:LEU:CD2	2.48	0.44
21:B6:3:ASP:OD2	59:AC:52:HIS:NE2	2.50	0.44
23:B8:46:VAL:HG23	23:B8:47:VAL:N	2.32	0.44
28:E1:324:VAL:HG23	28:E1:355:LEU:HD11	2.00	0.44
32:E5:24:ASP:OD1	32:E5:24:ASP:N	2.49	0.44
32:E5:87:LEU:N	32:E5:87:LEU:HD12	2.32	0.44
43:N1:502:LEU:HD21	43:N1:574:LEU:HD12	2.00	0.44
43:N1:506:TYR:C	43:N1:506:TYR:CD1	2.95	0.44
2:1B:129:VAL:O	2:1B:129:VAL:HG12	2.17	0.44
26:BM:3:VAL:O	41:G2:115:ARG:NH2	2.50	0.44
29:E2:9:THR:HG22	29:E2:10:GLY:N	2.32	0.44
32:E5:262:VAL:H	32:E5:285:HIS:HB2	1.82	0.44
40:G1:155:VAL:HG11	42:G3:221:ARG:NH2	2.32	0.44
41:G2:181:VAL:HG23	42:G3:176:VAL:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:N1:582:ILE:HD13	45:N3:212:TYR:HE2	1.83	0.44
46:N4:405:SER:OG	47:N5:187:ILE:HD12	2.17	0.44
56:V1:34:LEU:O	56:V1:39:ARG:NH1	2.45	0.44
56:V1:150:MET:CE	56:V1:242:ILE:HG21	2.48	0.44
56:V1:150:MET:SD	56:V1:242:ILE:HG21	2.58	0.44
24:B9:100:ARG:HD2	66:AC:201:ZMP:H25B	2.00	0.44
26:BM:16:ASN:N	26:BM:16:ASN:OD1	2.50	0.44
28:E1:323:ALA:HB2	28:E1:357:TRP:CE2	2.53	0.44
30:E3:252:VAL:HG11	32:E5:209:PRO:HG3	2.00	0.44
31:E4:251:THR:HG23	31:E4:251:THR:O	2.18	0.44
40:G1:275:ALA:HB1	41:G2:147:VAL:HG11	1.99	0.44
47:N5:466:ILE:HG23	47:N5:467:TYR:N	2.33	0.44
48:S2:118:LEU:HD23	48:S2:118:LEU:C	2.43	0.44
2:1B:177:GLU:HG3	2:1B:477:THR:HG21	1.99	0.44
11:A8:142:THR:HG21	11:A8:192:THR:HG21	1.99	0.44
12:A9:28:PRO:O	12:A9:59:VAL:HG22	2.17	0.44
16:AN:247:TYR:O	16:AN:271:TYR:OH	2.22	0.44
24:B9:39:VAL:HG21	66:AC:201:ZMP:H11	1.99	0.44
26:BM:62:MET:HE1	46:N4:457:ILE:CG2	2.48	0.44
30:E3:103:SER:HB3	30:E3:108:LEU:HD11	1.99	0.44
31:E4:170:SER:O	31:E4:173:ALA:HB3	2.17	0.44
32:E5:285:HIS:O	32:E5:286:ILE:HG23	2.18	0.44
33:E6:294:MET:SD	53:S7:52:ARG:NE	2.91	0.44
39:FX:88:LYS:N	39:FX:89:PRO:HD2	2.32	0.44
43:N1:511:LEU:O	43:N1:511:LEU:HD23	2.18	0.44
47:N5:310:ILE:HD13	47:N5:438:ILE:HG22	1.99	0.44
56:V1:123:PRO:O	57:V2:147:CYS:SG	2.75	0.44
3:2B:67:ASN:N	3:2B:67:ASN:OD1	2.51	0.44
3:2B:109:ILE:O	3:2B:109:ILE:HG23	2.18	0.44
8:A5:67:VAL:HG22	8:A5:106:GLU:OE2	2.18	0.44
8:A5:143:LYS:O	49:S3:251:LYS:NZ	2.29	0.44
9:A6:189:ALA:HB2	33:E6:219:GLN:HG3	1.98	0.44
14:AL:65:ILE:HG23	14:AL:66:VAL:HG13	2.00	0.44
24:B9:8:LEU:HD23	39:FX:96:ILE:HA	1.98	0.44
46:N4:62:ILE:HG23	46:N4:62:ILE:O	2.16	0.44
48:S2:395:ARG:NH2	49:S3:161:GLU:OE1	2.50	0.44
54:S8:180:ARG:NH1	54:S8:184:ASN:OD1	2.50	0.44
56:V1:456:ASP:O	56:V1:460:ASN:ND2	2.45	0.44
58:E7:122:PRO:O	58:E7:125:GLY:N	2.48	0.44
5:A1:21:TRP:CE3	43:N1:378:LEU:HD22	2.53	0.44
11:A8:105:TYR:OH	15:AM:104:GLN:NE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:B7:43:GLU:O	22:B7:48:VAL:HG12	2.18	0.44
40:G1:124:ASP:OD1	40:G1:403:ARG:NH2	2.37	0.44
40:G1:130:HIS:NE2	40:G1:346:GLU:OE1	2.51	0.44
40:G1:305:VAL:O	40:G1:309:THR:HG23	2.18	0.44
42:G3:149:ILE:HD12	42:G3:149:ILE:N	2.32	0.44
44:N2:214:ILE:HG23	44:N2:256:LEU:HD21	1.98	0.44
46:N4:131:THR:HG21	46:N4:164:SER:CB	2.48	0.44
47:N5:263:THR:HB	47:N5:342:LEU:HD11	2.00	0.44
56:V1:159:VAL:HG21	56:V1:198:LEU:HD11	2.00	0.44
3:2B:57:PHE:HB2	3:2B:77:PHE:CE1	2.53	0.44
4:4L:144:LEU:HD12	45:N6:154:ILE:HD11	2.00	0.44
11:A8:96:GLN:HB3	11:A8:97:PRO:HD3	1.99	0.44
41:G2:154:ILE:HD12	41:G2:154:ILE:N	2.33	0.44
47:N5:217:ILE:N	47:N5:217:ILE:HD12	2.32	0.44
56:V1:370:ARG:NH1	57:V2:103:VAL:O	2.41	0.44
2:1B:289:MET:SD	2:1B:305:VAL:HG13	2.58	0.43
2:1B:346:MET:HE2	9:A6:158:ARG:NE	2.33	0.43
4:4L:105:ILE:HG22	45:N6:36:ILE:HD11	2.00	0.43
7:A3:53:ARG:HH22	44:N2:27:VAL:HG23	1.83	0.43
11:A8:1:MET:N	44:N2:199:ASN:OD1	2.51	0.43
24:B9:30:ILE:HD13	24:B9:42:LEU:CD2	2.48	0.43
43:N1:582:ILE:HD11	45:N3:214:VAL:HG12	2.00	0.43
49:S3:157:TRP:HE1	50:S4:16:ILE:HG23	1.83	0.43
58:E7:52:THR:OG1	58:E7:65:GLU:OE2	2.33	0.43
2:1B:166:VAL:HG21	2:1B:182:LEU:CD1	2.48	0.43
9:A6:221:LEU:HD23	9:A6:221:LEU:C	2.43	0.43
10:A7:54:GLU:OE2	15:AM:28:ARG:NH2	2.48	0.43
20:B5:23:ILE:HG13	41:G2:114:VAL:HG21	1.99	0.43
25:BL:77:VAL:HG21	26:BM:87:GLU:HG2	2.01	0.43
32:E5:261:VAL:HA	32:E5:285:HIS:HA	1.99	0.43
39:FX:98:ARG:N	59:AC:113:GLU:OE2	2.44	0.43
40:G1:157:ASP:OD1	40:G1:157:ASP:N	2.50	0.43
42:G3:98:GLU:O	42:G3:122:PRO:HA	2.18	0.43
43:N1:654:LEU:O	43:N1:655:THR:C	2.61	0.43
44:N2:17:ILE:HD13	45:N6:145:ILE:HG22	2.00	0.43
46:N4:43:ILE:HD13	46:N4:472:LEU:CD2	2.39	0.43
46:N4:117:SER:OG	46:N4:123:ILE:HD12	2.18	0.43
46:N4:324:TYR:O	46:N4:327:ILE:HG12	2.19	0.43
47:N5:190:ILE:O	47:N5:194:ASN:HA	2.17	0.43
13:AB:86:ASP:OD1	13:AB:86:ASP:N	2.49	0.43
19:B4:160:MET:HE1	23:B8:154:ALA:HB1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:B7:75:HIS:HB3	47:N5:494:ILE:HD12	2.00	0.43
26:BM:5:ARG:HG3	40:G1:305:VAL:HG11	2.00	0.43
28:E1:135:LYS:O	28:E1:157:LEU:HD12	2.18	0.43
45:N3:255:ILE:HA	45:N3:258:ILE:HG22	2.00	0.43
46:N4:110:ILE:HG23	46:N4:126:ILE:HG23	2.01	0.43
47:N5:93:LEU:HD13	47:N5:259:ALA:O	2.18	0.43
49:S3:197:GLY:HA3	50:S4:113:MET:HE1	2.01	0.43
52:S6:11:THR:HA	52:S6:14:ILE:HD13	2.01	0.43
52:S6:114:GLN:N	52:S6:114:GLN:OE1	2.51	0.43
57:V2:175:GLU:O	57:V2:178:ILE:HG13	2.18	0.43
58:E7:4:LEU:HD13	58:E7:6:LYS:O	2.18	0.43
2:1B:128:ASP:OD1	2:1B:128:ASP:N	2.51	0.43
7:A3:16:LEU:O	10:A7:121:MET:HE3	2.18	0.43
9:A6:66:LEU:HB3	13:AB:99:MET:HE1	2.01	0.43
10:A7:26:VAL:HG12	15:AM:52:LYS:HD2	1.99	0.43
16:AN:237:PRO:HG2	27:C4:153:VAL:HG23	2.00	0.43
30:E3:242:GLU:OE1	30:E3:242:GLU:N	2.43	0.43
32:E5:7:TRP:HB2	32:E5:96:TYR:HB3	2.00	0.43
40:G1:58:ARG:NE	40:G1:61:GLU:OE1	2.37	0.43
46:N4:55:ILE:HG22	63:N4:502:PC1:H321	2.00	0.43
46:N4:73:ILE:N	46:N4:73:ILE:HD12	2.33	0.43
56:V1:350:LEU:HD11	56:V1:353:ALA:HB2	2.01	0.43
30:E3:45:PRO:HB2	30:E3:70:SER:HB2	2.00	0.43
31:E4:73:ILE:HD12	31:E4:96:VAL:HG13	2.01	0.43
40:G1:114:TRP:CE3	44:N2:30:ILE:HD13	2.53	0.43
46:N4:314:ILE:HG21	46:N4:404:LEU:HD11	2.00	0.43
47:N5:8:LYS:NZ	47:N5:38:LEU:HD12	2.34	0.43
53:S7:90:GLU:HG2	53:S7:183:PRO:O	2.19	0.43
1:1A:52:LEU:HD22	12:A9:32:LEU:HD12	1.99	0.43
9:A6:77:ARG:NH2	12:A9:434:ASP:O	2.46	0.43
16:AN:11:MET:HE1	47:N5:581:ILE:CG2	2.48	0.43
30:E3:321:LEU:HD12	30:E3:321:LEU:N	2.34	0.43
31:E4:144:LEU:HD12	31:E4:173:ALA:HB2	2.01	0.43
33:E6:277:ARG:NH1	53:S7:27:GLN:O	2.44	0.43
63:E8:301:PC1:H152	64:N5:603:CDL:OB4	2.19	0.43
46:N4:290:GLN:O	46:N4:362:LEU:HD12	2.18	0.43
46:N4:323:LEU:O	46:N4:327:ILE:HG23	2.19	0.43
45:N6:25:ASP:OD1	45:N6:25:ASP:N	2.51	0.43
51:S5:56:GLU:N	51:S5:56:GLU:OE1	2.51	0.43
2:1B:127:THR:O	2:1B:127:THR:CG2	2.66	0.43
2:1B:342:LYS:O	2:1B:343:LEU:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C4:176:TRP:HE3	46:N4:183:HIS:HE2	1.67	0.43
29:E2:101:PHE:CE1	29:E2:244:ILE:HG22	2.54	0.43
29:E2:422:SER:OG	29:E2:424:ASP:OD1	2.36	0.43
39:FX:144:ASP:HB3	39:FX:169:VAL:HG22	2.00	0.43
42:G3:55:ARG:N	42:G3:73:SER:O	2.52	0.43
46:N4:413:ILE:HG12	47:N5:184:LEU:HD22	1.99	0.43
48:S2:168:ASP:O	54:S8:87:ARG:NH2	2.47	0.43
49:S3:74:ASN:O	49:S3:131:HIS:NE2	2.52	0.43
1:1A:322:ALA:N	1:1A:323:PRO:HD2	2.33	0.43
2:1B:48:ARG:NE	30:E3:336:ILE:HD13	2.34	0.43
28:E1:328:LYS:HB2	28:E1:362:LEU:HD23	2.01	0.43
29:E2:320:HIS:O	29:E2:321:HIS:CG	2.72	0.43
36:EB:82:MET:HA	36:EB:82:MET:HE2	2.01	0.43
43:N1:643:LEU:HD21	54:S8:56:ILE:HG23	2.01	0.43
56:V1:396:ILE:HG21	56:V1:413:ILE:HB	2.01	0.43
26:BM:23:THR:OG1	26:BM:26:GLY:O	2.27	0.43
30:E3:91:LEU:HD12	30:E3:91:LEU:N	2.34	0.43
39:FX:98:ARG:HD2	39:FX:102:GLY:O	2.19	0.43
39:FX:190:ILE:HG12	39:FX:223:ARG:O	2.19	0.43
39:FX:219:HIS:H	39:FX:222:SER:HG	1.62	0.43
46:N4:305:MET:N	46:N4:305:MET:SD	2.92	0.43
47:N5:117:PHE:HZ	47:N5:252:VAL:HG23	1.83	0.43
48:S2:51:ARG:CD	53:S7:123:THR:HG21	2.49	0.43
54:S8:77:TYR:CG	54:S8:78:PRO:HA	2.54	0.43
56:V1:396:ILE:CB	56:V1:413:ILE:HD13	2.46	0.43
2:1B:386:THR:HA	30:E3:396:LEU:HD21	2.00	0.43
10:A7:54:GLU:OE2	15:AM:28:ARG:NH1	2.50	0.43
19:B4:37:SER:OG	19:B4:46:LEU:O	2.37	0.43
23:B8:124:PHE:CZ	47:N5:496:ILE:HB	2.52	0.43
24:B9:46:ALA:HB2	24:B9:97:ILE:HD11	2.01	0.43
39:FX:250:PRO:O	39:FX:253:THR:HG22	2.19	0.43
46:N4:420:CYS:SG	47:N5:180:VAL:HG22	2.59	0.43
56:V1:141:GLU:OE2	56:V1:257:ARG:NH1	2.48	0.43
58:E7:97:ILE:HG21	58:E7:116:LEU:HD13	2.01	0.43
2:1B:274:ASP:OD1	2:1B:274:ASP:N	2.51	0.42
4:4L:83:VAL:HG11	45:N6:104:PHE:HZ	1.84	0.42
9:A6:227:LEU:O	9:A6:231:VAL:HG23	2.18	0.42
11:A8:177:TYR:OH	43:N1:541:GLU:OE2	2.36	0.42
19:B4:24:ILE:HG22	19:B4:110:ARG:HH11	1.84	0.42
26:BM:95:PHE:CG	36:EB:82:MET:HE1	2.53	0.42
40:G1:135:ILE:HD13	40:G1:349:VAL:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:N2:175:TYR:CD1	44:N2:186:MET:HE1	2.54	0.42
46:N4:114:PHE:HB2	46:N4:126:ILE:HG21	2.00	0.42
46:N4:191:ILE:HD11	46:N4:257:PHE:CD2	2.54	0.42
46:N4:460:LEU:HD23	46:N4:463:ILE:HD11	2.01	0.42
47:N5:216:ASN:OD1	47:N5:216:ASN:N	2.48	0.42
47:N5:377:HIS:ND1	47:N5:455:ILE:HG21	2.34	0.42
50:S4:61:ILE:O	50:S4:61:ILE:HG23	2.19	0.42
50:S4:72:PRO:O	50:S4:74:ARG:NH1	2.52	0.42
1:1A:197:LYS:HB3	1:1A:248:ILE:CG2	2.49	0.42
12:A9:121:VAL:HG11	12:A9:133:VAL:HG23	2.00	0.42
32:E5:215:VAL:HG23	32:E5:215:VAL:O	2.19	0.42
42:G3:130:GLN:OE1	42:G3:148:LYS:NZ	2.52	0.42
68:N4:505:U10:H303	68:N4:505:U10:H261	2.02	0.42
47:N5:316:CYS:O	47:N5:320:SER:OG	2.34	0.42
3:2B:81:PRO:HB2	46:N4:165:ILE:HD11	2.01	0.42
16:AN:227:SER:OG	27:C4:173:ASP:OD2	2.30	0.42
24:B9:45:ARG:HG2	24:B9:97:ILE:HG21	2.02	0.42
28:E1:78:VAL:HG22	28:E1:224:ILE:HG23	2.00	0.42
28:E1:412:ILE:O	28:E1:420:THR:HG23	2.19	0.42
38:ED:43:TRP:CE2	38:ED:47:MET:HE3	2.54	0.42
43:N1:383:THR:HG22	43:N1:602:TYR:CG	2.54	0.42
43:N1:388:LYS:NZ	43:N1:397:ILE:O	2.45	0.42
46:N4:91:TYR:OH	46:N4:355:ASP:OD2	2.34	0.42
47:N5:28:LEU:HD11	47:N5:118:VAL:HG11	2.02	0.42
47:N5:352:ILE:HD12	47:N5:392:ILE:HG21	2.00	0.42
47:N5:377:HIS:O	47:N5:378:ILE:C	2.62	0.42
48:S2:46:ILE:HG12	49:S3:179:MET:HE2	2.02	0.42
48:S2:69:MET:HG3	48:S2:84:PHE:HB2	2.01	0.42
54:S8:92:HIS:CE1	61:S8:297:SF4:S2	3.11	0.42
54:S8:126:ASP:OD1	54:S8:127:ASP:N	2.44	0.42
54:S8:153:CYS:HB2	54:S8:158:ILE:HG22	2.01	0.42
54:S8:185:GLY:O	54:S8:189:THR:OG1	2.37	0.42
56:V1:200:ARG:HH21	57:V2:88:MET:HE1	1.84	0.42
56:V1:297:LEU:HD21	56:V1:318:VAL:HG11	2.01	0.42
29:E2:26:LEU:N	29:E2:27:PRO:CD	2.83	0.42
29:E2:69:ARG:NH2	29:E2:155:LEU:O	2.47	0.42
40:G1:154:LEU:HD12	40:G1:177:ILE:HG12	2.01	0.42
40:G1:306:ASP:O	40:G1:309:THR:OG1	2.30	0.42
47:N5:259:ALA:HA	47:N5:263:THR:HG21	2.01	0.42
45:N6:33:ILE:HA	45:N6:36:ILE:HG22	2.01	0.42
49:S3:31:VAL:HG21	49:S3:40:VAL:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:E7:81:VAL:HG11	58:E7:149:LEU:HD22	2.00	0.42
10:A7:109:TRP:HZ2	49:S3:128:VAL:HG22	1.85	0.42
26:BM:53:ASP:OD1	26:BM:53:ASP:N	2.44	0.42
34:E8:151:SER:O	34:E8:155:TYR:N	2.43	0.42
48:S2:28:LEU:HD22	48:S2:390:PHE:CZ	2.54	0.42
14:AL:117:GLU:OE1	14:AL:117:GLU:N	2.49	0.42
31:E4:128:ILE:HD13	31:E4:148:MET:CE	2.49	0.42
40:G1:197:ASP:OD1	40:G1:198:ARG:N	2.53	0.42
43:N1:510:PHE:CE2	43:N1:514:LEU:HD11	2.54	0.42
44:N2:10:ILE:HG22	44:N2:14:ILE:HD12	2.01	0.42
46:N4:14:LEU:HD11	63:N4:502:PC1:H362	2.01	0.42
49:S3:56:LEU:HD21	49:S3:78:ILE:HD11	2.02	0.42
66:AC:201:ZMP:H3A	66:AC:201:ZMP:H6	1.45	0.42
1:1A:178:ASP:OD1	1:1A:189:MET:N	2.47	0.42
4:4L:118:PHE:CD1	4:4L:135:MET:HE1	2.55	0.42
5:A1:25:GLY:O	5:A1:29:LEU:HG	2.20	0.42
63:A1:202:PC1:H152	63:A1:202:PC1:H11	2.01	0.42
14:AL:124:GLU:HA	14:AL:129:ASN:O	2.20	0.42
34:E8:1:MET:SD	59:AC:89:LEU:HD13	2.59	0.42
47:N5:57:ASN:HB3	47:N5:85:TYR:HD2	1.85	0.42
48:S2:35:ASN:O	48:S2:36:HIS:HB3	2.20	0.42
2:1B:410:ALA:HB1	6:A2:95:PHE:HB2	2.01	0.42
26:BM:53:ASP:OD2	46:N4:93:ARG:NE	2.52	0.42
27:C4:106:VAL:HG21	27:C4:108:TRP:CZ2	2.55	0.42
32:E5:262:VAL:O	32:E5:263:ARG:C	2.62	0.42
41:G2:126:GLU:HB3	41:G2:127:PRO:HD2	2.00	0.42
44:N2:254:TYR:OH	44:N2:275:THR:OG1	2.20	0.42
56:V1:407:GLY:N	56:V1:408:PRO:HD2	2.34	0.42
4:4L:72:ASP:OD1	4:4L:72:ASP:N	2.53	0.42
4:4L:154:TYR:OH	44:N2:129:TRP:NE1	2.52	0.42
9:A6:157:HIS:NE2	9:A6:161:ASN:OD1	2.53	0.42
15:AM:26:PHE:CD2	52:S6:15:MET:HE2	2.55	0.42
17:B2:144:VAL:HG22	34:E8:139:ARG:NH1	2.35	0.42
18:B3:25:ALA:O	38:ED:35:ILE:HG22	2.20	0.42
22:B7:86:LYS:NZ	22:B7:90:ASP:OD1	2.49	0.42
32:E5:256:ALA:C	32:E5:257:LEU:HD22	2.44	0.42
39:FX:253:THR:HG23	39:FX:304:TRP:NE1	2.35	0.42
40:G1:184:ASN:O	40:G1:205:PRO:HA	2.20	0.42
42:G3:169:GLN:OE1	42:G3:169:GLN:N	2.53	0.42
44:N2:150:LEU:HD13	44:N2:153:LEU:HD12	2.00	0.42
47:N5:328:ILE:O	47:N5:328:ILE:CG2	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:E7:156:ASP:OD2	58:E7:162:LYS:NZ	2.40	0.42
9:A6:90:ARG:NH1	13:AB:93:ASP:OD1	2.53	0.42
9:A6:164:THR:O	9:A6:164:THR:HG22	2.19	0.42
9:A6:294:LEU:CD1	9:A6:393:ILE:HD11	2.50	0.42
13:AB:90:ASP:OD1	13:AB:91:SER:N	2.49	0.42
23:B8:87:ASP:OD1	23:B8:87:ASP:N	2.52	0.42
28:E1:75:GLU:CD	28:E1:186:SER:HG	2.27	0.42
28:E1:438:GLN:HB3	28:E1:445:LEU:HD11	2.02	0.42
31:E4:74:THR:OG1	31:E4:141:SER:OG	2.33	0.42
32:E5:41:ALA:O	32:E5:287:LEU:C	2.63	0.42
34:E8:26:THR:N	34:E8:27:PRO:CD	2.83	0.42
47:N5:322:MET:O	47:N5:325:ILE:HG22	2.20	0.42
47:N5:334:ILE:O	47:N5:334:ILE:HG23	2.19	0.42
47:N5:393:LEU:HD21	47:N5:432:GLN:HA	2.01	0.42
48:S2:10:MET:HE2	48:S2:10:MET:HA	2.02	0.42
48:S2:357:ARG:O	48:S2:357:ARG:HG3	2.20	0.42
4:4L:78:ILE:HG21	4:4L:120:ILE:HG21	2.02	0.41
12:A9:78:LYS:NZ	12:A9:83:GLN:O	2.46	0.41
14:AL:137:THR:OG1	14:AL:138:THR:N	2.53	0.41
24:B9:103:MET:HE1	47:N5:305:LEU:HD11	2.02	0.41
28:E1:252:LEU:HD21	28:E1:287:TYR:CZ	2.55	0.41
40:G1:211:GLU:OE2	41:G2:87:ARG:NH1	2.53	0.41
40:G1:269:ASP:OD1	40:G1:269:ASP:N	2.53	0.41
41:G2:181:VAL:HG23	42:G3:176:VAL:CG2	2.50	0.41
42:G3:126:ILE:N	42:G3:126:ILE:HD12	2.35	0.41
46:N4:131:THR:HG21	46:N4:164:SER:HB2	2.01	0.41
49:S3:86:ARG:NE	49:S3:147:SER:O	2.42	0.41
53:S7:79:PRO:HA	53:S7:117:LEU:O	2.20	0.41
1:1A:276:ILE:HG22	1:1A:281:LEU:CD2	2.50	0.41
1:1A:369:ASP:HA	9:A6:234:LEU:HD13	2.02	0.41
2:1B:378:ASP:O	2:1B:382:THR:HG23	2.19	0.41
11:A8:142:THR:CG2	11:A8:192:THR:HG21	2.49	0.41
14:AL:88:THR:O	14:AL:92:GLY:N	2.50	0.41
16:AN:86:ARG:NH1	16:AN:121:TYR:OH	2.53	0.41
23:B8:45:PRO:HB3	23:B8:62:TRP:CE2	2.55	0.41
42:G3:136:TYR:CD2	42:G3:192:ILE:HG23	2.55	0.41
44:N2:81:ILE:HD11	45:N6:153:ILE:HD12	2.01	0.41
44:N2:131:TYR:CE2	44:N2:174:LEU:HD22	2.55	0.41
47:N5:491:TYR:OH	47:N5:493:ASN:ND2	2.52	0.41
48:S2:75:MET:SD	48:S2:118:LEU:HD13	2.59	0.41
56:V1:150:MET:HE1	56:V1:242:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:V2:105:THR:HB	57:V2:106:PRO:HD3	2.02	0.41
4:4L:144:LEU:HD11	45:N6:151:PHE:CZ	2.55	0.41
6:A2:27:GLU:HA	6:A2:30:ALA:HB3	2.02	0.41
8:A5:22:THR:O	8:A5:22:THR:HG23	2.20	0.41
9:A6:62:TYR:CZ	9:A6:66:LEU:HD11	2.56	0.41
9:A6:178:THR:HB	33:E6:179:LEU:HD13	2.02	0.41
23:B8:71:TYR:O	46:N4:363:TYR:OH	2.37	0.41
30:E3:286:ILE:CG1	30:E3:291:LEU:HD23	2.50	0.41
47:N5:260:THR:O	47:N5:261:LEU:C	2.64	0.41
48:S2:243:TYR:N	48:S2:244:PRO:HD2	2.36	0.41
1:1A:141:ASP:O	1:1A:142:CYS:C	2.64	0.41
1:1A:187:SER:HB2	1:1A:189:MET:HE2	2.03	0.41
3:2B:75:LEU:HD13	44:N2:221:ILE:HG21	2.02	0.41
19:B4:144:GLY:O	47:N5:216:ASN:ND2	2.53	0.41
24:B9:41:HIS:HE2	59:AC:115:GLU:CD	2.26	0.41
27:C4:63:LEU:HD11	27:C4:140:ARG:NH1	2.36	0.41
28:E1:437:ALA:HB2	28:E1:456:VAL:HG13	2.03	0.41
29:E2:417:GLU:OE1	29:E2:417:GLU:N	2.53	0.41
46:N4:299:LEU:HD23	46:N4:302:ILE:HD12	2.03	0.41
45:N6:46:ILE:HD12	45:N6:46:ILE:N	2.35	0.41
54:S8:86:THR:OG1	54:S8:199:GLU:OE2	2.38	0.41
54:S8:109:LEU:O	54:S8:113:THR:HG22	2.20	0.41
3:2B:48:ASN:ND2	3:2B:126:UNK:O	2.53	0.41
6:A2:45:LEU:HD22	49:S3:272:PRO:HD2	2.02	0.41
64:B3:102:CDL:OB3	38:ED:43:TRP:NE1	2.42	0.41
19:B4:141:TRP:CG	63:E8:302:PC1:H133	2.56	0.41
40:G1:120:PHE:O	40:G1:122:LEU:N	2.52	0.41
41:G2:132:SER:O	41:G2:133:PRO:C	2.61	0.41
46:N4:225:ILE:HG23	47:N5:568:MET:SD	2.60	0.41
46:N4:411:LEU:O	46:N4:415:LEU:HG	2.20	0.41
47:N5:250:THR:HG21	47:N5:357:GLY:HA2	2.02	0.41
47:N5:266:ILE:HD12	47:N5:266:ILE:N	2.36	0.41
47:N5:299:PHE:CE1	47:N5:430:LEU:HD11	2.55	0.41
48:S2:135:TRP:O	48:S2:138:GLU:HG3	2.20	0.41
49:S3:149:THR:N	49:S3:150:PRO:HD2	2.36	0.41
49:S3:205:ASP:O	49:S3:209:SER:N	2.52	0.41
50:S4:59:GLU:OE2	50:S4:62:ARG:NH2	2.45	0.41
56:V1:396:ILE:CG2	56:V1:413:ILE:HD13	2.50	0.41
12:A9:158:MET:N	53:S7:66:SER:OG	2.54	0.41
12:A9:200:ASN:ND2	12:A9:200:ASN:O	2.54	0.41
28:E1:100:GLN:NE2	28:E1:287:TYR:OH	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E4:243:ILE:HD12	31:E4:307:VAL:HG21	2.02	0.41
31:E4:245:PRO:HG2	31:E4:317:ILE:HD13	2.02	0.41
32:E5:260:LYS:HB2	32:E5:284:VAL:H	1.84	0.41
34:E8:112:MET:SD	34:E8:134:LEU:HD21	2.61	0.41
44:N2:81:ILE:HD12	45:N6:153:ILE:HD12	2.02	0.41
47:N5:63:LEU:HD11	47:N5:79:GLU:HB3	2.02	0.41
49:S3:59:VAL:CG1	49:S3:91:MET:HE1	2.49	0.41
49:S3:103:LEU:HD21	49:S3:106:VAL:CG2	2.51	0.41
50:S4:99:GLU:HG2	50:S4:100:TRP:N	2.35	0.41
56:V1:367:ALA:HA	57:V2:108:MET:HE2	2.02	0.41
56:V1:428:LEU:HD23	56:V1:428:LEU:C	2.46	0.41
57:V2:167:ASP:HB3	57:V2:192:VAL:HG13	2.01	0.41
2:1B:142:THR:HG21	50:S4:158:GLU:OE1	2.21	0.41
10:A7:107:PHE:CE2	10:A7:109:TRP:HA	2.55	0.41
12:A9:260:LYS:NZ	65:A9:559:NDP:O2D	2.42	0.41
26:BM:53:ASP:OD2	46:N4:93:ARG:NH2	2.53	0.41
30:E3:45:PRO:HD3	30:E3:121:SER:HB2	2.02	0.41
34:E8:115:TYR:CE2	34:E8:119:ILE:HD11	2.55	0.41
41:G2:117:VAL:HG22	41:G2:133:PRO:HA	2.03	0.41
44:N2:214:ILE:HG22	44:N2:218:PHE:CE2	2.56	0.41
14:AL:210:ARG:NH1	54:S8:172:ASP:OD1	2.54	0.41
16:AN:245:MET:O	27:C4:152:ARG:NH1	2.46	0.41
21:B6:12:ASP:OD1	21:B6:13:PHE:N	2.52	0.41
30:E3:156:LEU:CD1	30:E3:184:LEU:HD22	2.49	0.41
34:E8:25:MET:SD	47:N5:532:ILE:HG21	2.61	0.41
39:FX:171:LEU:HB3	39:FX:186:SER:HA	2.03	0.41
44:N2:122:ILE:N	44:N2:122:ILE:HD12	2.36	0.41
47:N5:241:TRP:HH2	47:N5:261:LEU:HD23	1.86	0.41
47:N5:329:ASP:HA	47:N5:334:ILE:HG22	2.03	0.41
49:S3:193:ASP:OD1	49:S3:193:ASP:N	2.51	0.41
54:S8:161:THR:HA	54:S8:192:ILE:HD11	2.02	0.41
57:V2:11:VAL:HG11	57:V2:93:PRO:HG3	2.02	0.41
1:1A:48:ILE:HD13	1:1A:67:ALA:HB2	2.03	0.41
2:1B:243:ALA:O	2:1B:247:TYR:N	2.53	0.41
10:A7:112:HIS:CD2	31:E4:31:VAL:HG22	2.56	0.41
11:A8:10:THR:HG22	20:B5:105:VAL:CG1	2.50	0.41
12:A9:181:ASN:OD1	12:A9:183:THR:OG1	2.34	0.41
64:AM:217:CDL:OB3	54:S8:49:ASN:ND2	2.53	0.41
21:B6:13:PHE:O	47:N5:21:ASN:ND2	2.54	0.41
25:BL:65:TYR:OH	46:N4:49:SER:O	2.38	0.41
27:C4:63:LEU:O	27:C4:68:GLN:NE2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:E5:9:PHE:HB3	32:E5:20:LEU:HD23	2.02	0.41
35:EA:4:GLN:OE1	44:N2:184:ASN:ND2	2.53	0.41
39:FX:191:SER:O	39:FX:195:PHE:HB2	2.21	0.41
42:G3:134:GLY:O	42:G3:196:ARG:NH2	2.51	0.41
43:N1:437:CYS:SG	43:N1:438:ILE:N	2.93	0.41
43:N1:527:LEU:C	43:N1:527:LEU:HD12	2.46	0.41
43:N1:660:LEU:HB3	43:N1:661:PRO:HD3	2.03	0.41
46:N4:89:ILE:CG2	46:N4:104:ILE:HG21	2.51	0.41
47:N5:431:SER:HA	47:N5:434:TYR:CE2	2.55	0.41
47:N5:481:LEU:N	47:N5:482:PRO:CD	2.84	0.41
48:S2:134:LEU:H	48:S2:134:LEU:HD12	1.86	0.41
49:S3:98:PHE:CD1	49:S3:98:PHE:N	2.87	0.41
49:S3:100:TYR:CE2	49:S3:133:VAL:HG13	2.56	0.41
54:S8:153:CYS:HA	61:S8:298:SF4:S3	2.61	0.41
57:V2:65:MET:HE2	57:V2:83:ALA:HB1	2.02	0.41
1:1A:97:VAL:HG12	1:1A:97:VAL:O	2.21	0.41
2:1B:44:ARG:O	2:1B:44:ARG:NH1	2.54	0.41
3:2B:57:PHE:CZ	3:2B:61:ILE:HD11	2.56	0.41
14:AL:123:GLY:HA3	14:AL:164:TRP:CZ2	2.56	0.41
27:C4:7:THR:HG23	27:C4:7:THR:O	2.21	0.41
28:E1:286:LEU:C	28:E1:286:LEU:HD23	2.46	0.41
32:E5:133:LEU:HD12	32:E5:160:LEU:HB3	2.03	0.41
32:E5:194:LEU:CD1	32:E5:226:VAL:HG11	2.51	0.41
39:FX:256:PHE:HB3	39:FX:282:PRO:HB3	2.02	0.41
44:N2:171:ILE:HD11	44:N2:248:ILE:HG13	2.01	0.41
45:N3:235:ASN:OD1	45:N3:235:ASN:N	2.53	0.41
46:N4:13:ILE:HG12	46:N4:35:ILE:HD13	2.02	0.41
47:N5:141:PHE:HB2	47:N5:186:ILE:HD11	2.03	0.41
47:N5:215:ILE:HG23	47:N5:216:ASN:N	2.35	0.41
47:N5:424:PHE:N	47:N5:424:PHE:CD1	2.89	0.41
50:S4:31:THR:O	50:S4:31:THR:HG22	2.20	0.41
56:V1:108:ASP:OD1	56:V1:108:ASP:N	2.53	0.41
4:4L:83:VAL:HG11	45:N6:104:PHE:CZ	2.56	0.40
9:A6:76:PHE:O	9:A6:130:GLN:NE2	2.54	0.40
12:A9:142:THR:HG21	14:AL:218:PRO:CG	2.51	0.40
19:B4:24:ILE:HG23	23:B8:61:HIS:O	2.22	0.40
20:B5:94:ARG:CZ	46:N4:179:TYR:OH	2.69	0.40
25:BL:60:THR:HG22	25:BL:62:ALA:H	1.86	0.40
29:E2:424:ASP:HA	29:E2:452:LYS:CE	2.51	0.40
30:E3:237:PRO:HG3	32:E5:216:LEU:HD22	2.03	0.40
31:E4:83:ARG:HA	31:E4:86:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:E8:98:SER:OG	34:E8:117:LYS:NZ	2.54	0.40
39:FX:187:HIS:O	39:FX:242:PRO:HD3	2.21	0.40
41:G2:222:GLN:HA	41:G2:228:ILE:HD12	2.03	0.40
43:N1:565:ILE:HG12	43:N1:572:VAL:HG11	2.03	0.40
44:N2:157:PHE:HA	44:N2:160:TYR:HB2	2.03	0.40
47:N5:503:ILE:HD12	47:N5:508:LEU:HD11	2.02	0.40
48:S2:270:ARG:O	48:S2:273:ILE:HG12	2.21	0.40
49:S3:232:GLU:HG3	50:S4:78:MET:HB3	2.03	0.40
1:1A:182:ASN:OD1	1:1A:237:VAL:HB	2.21	0.40
2:1B:191:THR:O	2:1B:227:THR:HG22	2.21	0.40
18:B3:58:UNK:O	18:B3:59:UNK:C	2.69	0.40
28:E1:110:PRO:O	28:E1:111:ALA:HB3	2.21	0.40
29:E2:331:ARG:NH1	29:E2:401:PRO:O	2.54	0.40
39:FX:287:PRO:HD3	39:FX:307:THR:HG22	2.02	0.40
48:S2:65:VAL:O	48:S2:68:TYR:HB2	2.22	0.40
48:S2:241:GLU:O	56:V1:492:SER:CB	2.69	0.40
49:S3:124:PHE:HB2	49:S3:133:VAL:HG23	2.03	0.40
57:V2:148:VAL:HG23	57:V2:149:HIS:CD2	2.57	0.40
58:E7:180:ASP:OD1	58:E7:181:SER:N	2.54	0.40
2:1B:63:LEU:CD1	2:1B:352:LEU:HD12	2.45	0.40
3:2B:58:LEU:HD12	64:N4:501:CDL:H831	2.04	0.40
5:A1:130:PRO:O	5:A1:131:LYS:HB3	2.20	0.40
8:A5:143:LYS:NZ	8:A5:151:GLU:OE2	2.29	0.40
12:A9:256:PHE:O	12:A9:260:LYS:HG3	2.22	0.40
12:A9:309:THR:OG1	12:A9:310:TYR:N	2.54	0.40
21:B6:74:ASN:ND2	38:ED:130:PRO:O	2.52	0.40
28:E1:252:LEU:HD12	28:E1:394:LEU:HD11	2.02	0.40
30:E3:72:VAL:HG12	30:E3:121:SER:HB3	2.04	0.40
30:E3:210:PHE:HZ	30:E3:234:ILE:HD12	1.87	0.40
32:E5:40:ALA:HA	32:E5:289:LEU:N	2.36	0.40
44:N2:50:ILE:HD12	44:N2:62:ILE:HG21	2.03	0.40
45:N6:118:ASN:OD1	45:N6:120:ASN:ND2	2.54	0.40
45:N6:151:PHE:O	45:N6:154:ILE:HG13	2.21	0.40
48:S2:72:LEU:CD1	48:S2:356:ILE:HD13	2.51	0.40
49:S3:73:THR:O	49:S3:74:ASN:HB2	2.21	0.40
49:S3:106:VAL:HG22	49:S3:122:TYR:HD1	1.86	0.40
2:1B:424:LEU:HB2	12:A9:89:LEU:HD11	2.03	0.40
27:C4:114:PHE:CZ	64:C4:202:CDL:OA7	2.74	0.40
27:C4:145:LEU:HD12	27:C4:145:LEU:C	2.47	0.40
29:E2:28:LEU:HD12	29:E2:29:VAL:HG23	2.03	0.40
35:EA:68:GLU:O	35:EA:69:THR:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:N2:174:LEU:HD23	44:N2:175:TYR:CE1	2.57	0.40
45:N3:239:TYR:OH	45:N6:88:ASN:ND2	2.43	0.40
46:N4:218:LEU:HD13	46:N4:309:TYR:CE1	2.55	0.40
48:S2:91:LEU:HD23	48:S2:323:ILE:CG2	2.52	0.40
1:1A:80:ASN:ND2	1:1A:82:ASN:OD1	2.53	0.40
2:1B:450:ASN:HA	2:1B:456:SER:OG	2.22	0.40
3:2B:68:ILE:O	3:2B:71:ILE:N	2.55	0.40
7:A3:70:TYR:N	7:A3:71:PRO:HD2	2.36	0.40
9:A6:367:LEU:O	9:A6:371:LEU:HG	2.22	0.40
12:A9:398:ILE:HG12	12:A9:402:LEU:HD12	2.03	0.40
27:C4:9:ARG:NH2	44:N2:147:ILE:O	2.49	0.40
31:E4:44:VAL:HG23	31:E4:60:ILE:HD11	2.03	0.40
37:EC:31:GLN:N	37:EC:32:PRO:HD2	2.37	0.40
40:G1:141:LYS:NZ	42:G3:207:GLU:OE2	2.49	0.40
40:G1:162:PRO:HA	40:G1:180:ALA:O	2.21	0.40
44:N2:186:MET:HE3	44:N2:282:TRP:CZ2	2.56	0.40
44:N2:293:ASN:OD1	44:N2:294:ASN:N	2.54	0.40
46:N4:2:ILE:HG23	46:N4:3:TYR:N	2.36	0.40
46:N4:376:PHE:CE2	46:N4:380:LEU:HD11	2.56	0.40
46:N4:376:PHE:CZ	46:N4:380:LEU:HD11	2.57	0.40
47:N5:393:LEU:CD2	47:N5:432:GLN:HA	2.52	0.40
50:S4:44:ALA:HB3	50:S4:47:GLN:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1A	350/385 (91%)	335 (96%)	15 (4%)	0	100	100
2	1B	523/527 (99%)	501 (96%)	22 (4%)	0	100	100
3	2B	112/142 (79%)	103 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4L	106/171 (62%)	104 (98%)	2 (2%)	0	100	100
5	A1	135/141 (96%)	124 (92%)	11 (8%)	0	100	100
6	A2	190/193 (98%)	186 (98%)	4 (2%)	0	100	100
7	A3	122/125 (98%)	117 (96%)	5 (4%)	0	100	100
8	A5	152/184 (83%)	149 (98%)	3 (2%)	0	100	100
9	A6	421/437 (96%)	405 (96%)	16 (4%)	0	100	100
10	A7	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
11	A8	221/223 (99%)	212 (96%)	9 (4%)	0	100	100
12	A9	482/489 (99%)	463 (96%)	19 (4%)	0	100	100
13	AB	86/134 (64%)	83 (96%)	3 (4%)	0	100	100
14	AL	263/281 (94%)	248 (94%)	15 (6%)	0	100	100
15	AM	182/198 (92%)	175 (96%)	7 (4%)	0	100	100
16	AN	285/287 (99%)	281 (99%)	4 (1%)	0	100	100
17	B2	103/145 (71%)	103 (100%)	0	0	100	100
18	B3	32/62 (52%)	31 (97%)	1 (3%)	0	100	100
19	B4	169/171 (99%)	154 (91%)	15 (9%)	0	100	100
20	B5	132/140 (94%)	130 (98%)	2 (2%)	0	100	100
21	B6	89/91 (98%)	89 (100%)	0	0	100	100
22	B7	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
23	B8	145/176 (82%)	133 (92%)	12 (8%)	0	100	100
24	B9	149/158 (94%)	140 (94%)	9 (6%)	0	100	100
25	BL	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
26	BM	99/112 (88%)	98 (99%)	1 (1%)	0	100	100
27	C4	181/185 (98%)	174 (96%)	7 (4%)	0	100	100
28	E1	448/483 (93%)	434 (97%)	14 (3%)	0	100	100
29	E2	464/467 (99%)	445 (96%)	19 (4%)	0	100	100
30	E3	430/434 (99%)	420 (98%)	10 (2%)	0	100	100
31	E4	349/368 (95%)	338 (97%)	11 (3%)	0	100	100
32	E5	266/290 (92%)	245 (92%)	20 (8%)	1 (0%)	30	60
33	E6	314/371 (85%)	310 (99%)	4 (1%)	0	100	100
34	E8	203/205 (99%)	191 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	EA	96/126 (76%)	92 (96%)	4 (4%)	0	100	100
36	EB	73/101 (72%)	72 (99%)	1 (1%)	0	100	100
37	EC	83/101 (82%)	77 (93%)	6 (7%)	0	100	100
38	ED	136/151 (90%)	130 (96%)	6 (4%)	0	100	100
39	FX	235/325 (72%)	224 (95%)	10 (4%)	1 (0%)	30	60
40	G1	401/436 (92%)	380 (95%)	21 (5%)	0	100	100
41	G2	234/267 (88%)	218 (93%)	16 (7%)	0	100	100
42	G3	253/261 (97%)	235 (93%)	18 (7%)	0	100	100
43	N1	308/670 (46%)	289 (94%)	19 (6%)	0	100	100
44	N2	294/300 (98%)	279 (95%)	15 (5%)	0	100	100
45	N3	119/293 (41%)	115 (97%)	4 (3%)	0	100	100
45	N6	152/293 (52%)	146 (96%)	6 (4%)	0	100	100
46	N4	476/478 (100%)	461 (97%)	15 (3%)	0	100	100
47	N5	582/584 (100%)	552 (95%)	30 (5%)	0	100	100
48	S2	391/395 (99%)	369 (94%)	21 (5%)	1 (0%)	36	65
49	S3	246/277 (89%)	235 (96%)	11 (4%)	0	100	100
50	S4	188/208 (90%)	174 (93%)	14 (7%)	0	100	100
51	S5	110/122 (90%)	108 (98%)	2 (2%)	0	100	100
52	S6	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
53	S7	195/207 (94%)	182 (93%)	13 (7%)	0	100	100
54	S8	180/212 (85%)	176 (98%)	4 (2%)	0	100	100
56	V1	502/526 (95%)	478 (95%)	24 (5%)	0	100	100
57	V2	220/225 (98%)	211 (96%)	9 (4%)	0	100	100
58	E7	244/246 (99%)	238 (98%)	6 (2%)	0	100	100
59	AC	90/134 (67%)	88 (98%)	2 (2%)	0	100	100
All	All	13527/15237 (89%)	12943 (96%)	581 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	E5	288	THR
48	S2	36	HIS
39	FX	276	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1A	310/340 (91%)	306 (99%)	4 (1%)	61	75
2	1B	453/454 (100%)	450 (99%)	3 (1%)	76	80
3	2B	109/111 (98%)	105 (96%)	4 (4%)	30	59
4	4L	96/151 (64%)	95 (99%)	1 (1%)	68	77
5	A1	115/118 (98%)	112 (97%)	3 (3%)	40	66
6	A2	159/160 (99%)	158 (99%)	1 (1%)	78	81
7	A3	104/104 (100%)	101 (97%)	3 (3%)	37	63
8	A5	134/152 (88%)	131 (98%)	3 (2%)	45	68
9	A6	346/358 (97%)	344 (99%)	2 (1%)	78	81
10	A7	119/119 (100%)	118 (99%)	1 (1%)	73	80
11	A8	196/196 (100%)	192 (98%)	4 (2%)	48	70
12	A9	420/424 (99%)	417 (99%)	3 (1%)	76	80
13	AB	79/114 (69%)	77 (98%)	2 (2%)	42	66
14	AL	228/242 (94%)	227 (100%)	1 (0%)	84	85
15	AM	156/168 (93%)	155 (99%)	1 (1%)	78	81
16	AN	241/241 (100%)	239 (99%)	2 (1%)	73	80
17	B2	97/131 (74%)	97 (100%)	0	100	100
18	B3	30/31 (97%)	30 (100%)	0	100	100
19	B4	144/144 (100%)	141 (98%)	3 (2%)	47	69
20	B5	108/108 (100%)	108 (100%)	0	100	100
21	B6	82/82 (100%)	82 (100%)	0	100	100
22	B7	93/93 (100%)	91 (98%)	2 (2%)	45	68
23	B8	127/148 (86%)	123 (97%)	4 (3%)	35	62
24	B9	132/139 (95%)	131 (99%)	1 (1%)	73	80
25	BL	132/132 (100%)	129 (98%)	3 (2%)	44	68
26	BM	93/93 (100%)	91 (98%)	2 (2%)	45	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	C4	166/167 (99%)	164 (99%)	2 (1%)	63	76
28	E1	381/404 (94%)	379 (100%)	2 (0%)	81	83
29	E2	379/380 (100%)	372 (98%)	7 (2%)	51	71
30	E3	339/341 (99%)	333 (98%)	6 (2%)	51	71
31	E4	302/317 (95%)	298 (99%)	4 (1%)	61	75
32	E5	200/205 (98%)	195 (98%)	5 (2%)	42	66
33	E6	272/314 (87%)	266 (98%)	6 (2%)	45	68
34	E8	179/179 (100%)	176 (98%)	3 (2%)	53	72
35	EA	84/86 (98%)	83 (99%)	1 (1%)	63	76
36	EB	70/70 (100%)	70 (100%)	0	100	100
37	EC	73/86 (85%)	73 (100%)	0	100	100
38	ED	121/133 (91%)	119 (98%)	2 (2%)	53	72
39	FX	212/276 (77%)	208 (98%)	4 (2%)	50	71
40	G1	333/365 (91%)	324 (97%)	9 (3%)	39	65
41	G2	192/214 (90%)	188 (98%)	4 (2%)	47	69
42	G3	202/202 (100%)	202 (100%)	0	100	100
43	N1	295/639 (46%)	291 (99%)	4 (1%)	59	74
44	N2	285/289 (99%)	278 (98%)	7 (2%)	42	66
45	N3	116/281 (41%)	111 (96%)	5 (4%)	26	55
45	N6	147/281 (52%)	143 (97%)	4 (3%)	39	65
46	N4	455/455 (100%)	447 (98%)	8 (2%)	51	71
47	N5	546/546 (100%)	533 (98%)	13 (2%)	43	67
48	S2	335/336 (100%)	330 (98%)	5 (2%)	57	73
49	S3	224/250 (90%)	216 (96%)	8 (4%)	31	59
50	S4	159/172 (92%)	154 (97%)	5 (3%)	35	62
51	S5	102/102 (100%)	102 (100%)	0	100	100
52	S6	130/130 (100%)	128 (98%)	2 (2%)	57	73
53	S7	165/171 (96%)	163 (99%)	2 (1%)	63	76
54	S8	160/187 (86%)	157 (98%)	3 (2%)	50	71
56	V1	412/427 (96%)	404 (98%)	8 (2%)	50	71
57	V2	190/190 (100%)	180 (95%)	10 (5%)	20	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	E7	192/192 (100%)	189 (98%)	3 (2%)	55	73
59	AC	80/111 (72%)	77 (96%)	3 (4%)	29	58
All	All	11801/13051 (90%)	11603 (98%)	198 (2%)	52	72

All (198) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1A	159	LEU
1	1A	219	ARG
1	1A	260	ASN
1	1A	310	LEU
2	1B	108	GLU
2	1B	230	SER
2	1B	290	CYS
3	2B	5	LEU
3	2B	66	ASN
3	2B	67	ASN
3	2B	68	ILE
4	4L	145	MET
5	A1	8	SER
5	A1	37	HIS
5	A1	60	ASN
6	A2	118	ASP
7	A3	15	THR
7	A3	53	ARG
7	A3	104	GLU
8	A5	40	ARG
8	A5	60	ASP
8	A5	66	SER
9	A6	211	ASP
9	A6	346	GLU
10	A7	22	GLN
11	A8	38	ASP
11	A8	48	ASP
11	A8	123	GLU
11	A8	176	ARG
12	A9	190	GLN
12	A9	392	GLU
12	A9	436	MET
13	AB	86	ASP
13	AB	92	LEU

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Mol	Chain	Res	Type
14	AL	229	LEU
15	AM	87	ASP
16	AN	14	SER
16	AN	256	CYS
19	B4	22	ASP
19	B4	24	ILE
19	B4	87	SER
22	B7	52	LEU
22	B7	82	LEU
23	B8	65	THR
23	B8	87	ASP
23	B8	107	LEU
23	B8	125	SER
24	B9	130	GLN
25	BL	7	LYS
25	BL	76	SER
25	BL	82	LEU
26	BM	30	HIS
26	BM	81	ASN
27	C4	131	PHE
27	C4	145	LEU
28	E1	60	ASN
28	E1	464	LYS
29	E2	74	THR
29	E2	131	LYS
29	E2	135	THR
29	E2	170	ASP
29	E2	209	VAL
29	E2	325	THR
29	E2	400	ARG
30	E3	7	THR
30	E3	118	GLU
30	E3	148	ASN
30	E3	306	ASP
30	E3	319	VAL
30	E3	342	ASP
31	E4	142	GLN
31	E4	170	SER
31	E4	206	ASP
31	E4	334	VAL
32	E5	24	ASP
32	E5	36	LEU

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Mol	Chain	Res	Type
32	E5	106	HIS
32	E5	147	ASP
32	E5	289	LEU
33	E6	30	ASP
33	E6	47	ARG
33	E6	79	ILE
33	E6	113	TRP
33	E6	201	ASN
33	E6	204	GLN
34	E8	1	MET
34	E8	94	ASP
34	E8	198	LYS
35	EA	93	ILE
38	ED	99	LEU
38	ED	129	GLN
39	FX	109	HIS
39	FX	172	ASP
39	FX	180	GLN
39	FX	221	ASN
40	G1	157	ASP
40	G1	161	THR
40	G1	251	ASP
40	G1	266	ARG
40	G1	321	HIS
40	G1	326	GLU
40	G1	339	ASP
40	G1	390	ASP
40	G1	399	SER
41	G2	24	ASP
41	G2	108	ARG
41	G2	174	GLN
41	G2	228	ILE
43	N1	376	LEU
43	N1	452	TYR
43	N1	597	PHE
43	N1	652	PHE
44	N2	44	PHE
44	N2	84	ILE
44	N2	90	THR
44	N2	96	ASN
44	N2	128	ILE
44	N2	155	SER

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Mol	Chain	Res	Type
44	N2	230	PHE
45	N3	233	ILE
45	N3	235	ASN
45	N3	258	ILE
45	N3	264	ASN
45	N3	292	ASN
46	N4	28	GLU
46	N4	70	TYR
46	N4	76	TYR
46	N4	98	ASN
46	N4	156	SER
46	N4	191	ILE
46	N4	397	GLU
46	N4	412	SER
47	N5	72	TYR
47	N5	85	TYR
47	N5	92	LEU
47	N5	172	VAL
47	N5	285	LEU
47	N5	319	ILE
47	N5	320	SER
47	N5	350	SER
47	N5	369	ARG
47	N5	393	LEU
47	N5	503	ILE
47	N5	531	ASN
47	N5	533	HIS
45	N6	77	SER
45	N6	90	MET
45	N6	108	TYR
45	N6	150	MET
48	S2	30	LEU
48	S2	133	ILE
48	S2	187	ARG
48	S2	260	ASP
48	S2	394	ASP
49	S3	31	VAL
49	S3	65	SER
49	S3	70	ASP
49	S3	108	CYS
49	S3	121	VAL
49	S3	149	THR

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Mol	Chain	Res	Type
49	S3	160	ARG
49	S3	247	ASP
50	S4	16	ILE
50	S4	28	GLU
50	S4	47	GLN
50	S4	156	ARG
50	S4	202	LYS
52	S6	1	MET
52	S6	36	GLU
53	S7	42	GLU
53	S7	86	CYS
54	S8	55	GLU
54	S8	72	SER
54	S8	138	LEU
56	V1	112	SER
56	V1	209	GLU
56	V1	278	CYS
56	V1	339	ASP
56	V1	384	THR
56	V1	386	CYS
56	V1	424	SER
56	V1	487	ASP
57	V2	24	GLU
57	V2	100	GLN
57	V2	105	THR
57	V2	114	GLU
57	V2	120	CYS
57	V2	125	VAL
57	V2	133	ASP
57	V2	141	MET
57	V2	175	GLU
57	V2	220	ARG
58	E7	99	HIS
58	E7	149	LEU
58	E7	169	THR
59	AC	80	ASP
59	AC	91	SER
59	AC	93	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (217) such sidechains are listed below:

Mol	Chain	Res	Type
1	1A	56	GLN
1	1A	80	ASN
1	1A	82	ASN
1	1A	128	GLN
1	1A	260	ASN
1	1A	304	GLN
2	1B	33	ASN
2	1B	95	HIS
2	1B	155	HIS
2	1B	237	HIS
2	1B	315	ASN
2	1B	400	ASN
2	1B	465	GLN
2	1B	500	HIS
3	2B	3	ASN
3	2B	9	ASN
3	2B	26	ASN
3	2B	98	ASN
3	2B	99	HIS
3	2B	102	ASN
3	2B	113	ASN
4	4L	162	GLN
5	A1	55	ASN
5	A1	121	HIS
6	A2	12	HIS
6	A2	115	HIS
9	A6	74	GLN
9	A6	107	HIS
9	A6	130	GLN
9	A6	180	ASN
9	A6	350	GLN
10	A7	17	HIS
10	A7	22	GLN
10	A7	84	ASN
10	A7	124	GLN
11	A8	27	GLN
11	A8	52	HIS
11	A8	54	HIS
11	A8	83	ASN
11	A8	90	HIS
11	A8	110	HIS
11	A8	111	ASN
11	A8	134	HIS

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Mol	Chain	Res	Type
11	A8	182	GLN
12	A9	154	HIS
12	A9	159	ASN
12	A9	165	GLN
12	A9	174	GLN
12	A9	242	HIS
12	A9	288	ASN
12	A9	394	HIS
12	A9	401	HIS
13	AB	112	GLN
14	AL	20	GLN
14	AL	141	GLN
14	AL	201	HIS
14	AL	217	ASN
14	AL	219	HIS
14	AL	270	HIS
15	AM	25	GLN
15	AM	73	GLN
15	AM	104	GLN
16	AN	20	HIS
16	AN	114	HIS
16	AN	151	HIS
16	AN	152	ASN
16	AN	154	GLN
16	AN	221	HIS
17	B2	119	HIS
19	B4	50	GLN
19	B4	69	GLN
19	B4	92	HIS
20	B5	100	GLN
21	B6	22	HIS
23	B8	50	GLN
23	B8	156	GLN
24	B9	20	GLN
24	B9	48	HIS
24	B9	125	HIS
25	BL	24	HIS
25	BL	129	HIS
26	BM	30	HIS
26	BM	99	GLN
27	C4	10	GLN
27	C4	51	ASN

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Mol	Chain	Res	Type
27	C4	95	ASN
28	E1	61	GLN
28	E1	177	GLN
28	E1	204	ASN
28	E1	223	HIS
28	E1	395	ASN
28	E1	441	ASN
29	E2	20	GLN
29	E2	58	ASN
29	E2	99	GLN
29	E2	119	HIS
29	E2	153	HIS
29	E2	334	ASN
29	E2	344	GLN
30	E3	20	GLN
30	E3	53	GLN
30	E3	94	ASN
30	E3	99	GLN
30	E3	107	HIS
30	E3	232	HIS
30	E3	303	ASN
30	E3	313	HIS
30	E3	333	ASN
30	E3	355	GLN
31	E4	92	GLN
31	E4	160	GLN
31	E4	358	HIS
32	E5	255	ASN
32	E5	264	HIS
33	E6	49	GLN
33	E6	57	ASN
33	E6	72	GLN
33	E6	222	GLN
34	E8	19	ASN
34	E8	49	HIS
34	E8	146	ASN
35	EA	49	HIS
37	EC	97	HIS
38	ED	28	ASN
38	ED	139	HIS
39	FX	94	ASN
39	FX	124	HIS

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Mol	Chain	Res	Type
39	FX	133	GLN
40	G1	105	HIS
40	G1	148	ASN
40	G1	252	HIS
40	G1	314	ASN
40	G1	333	ASN
40	G1	413	ASN
42	G3	36	GLN
42	G3	140	ASN
43	N1	402	ASN
43	N1	409	GLN
43	N1	440	ASN
43	N1	476	HIS
43	N1	537	ASN
44	N2	6	ASN
44	N2	40	ASN
44	N2	55	ASN
44	N2	76	ASN
44	N2	79	GLN
44	N2	82	HIS
44	N2	89	ASN
44	N2	208	ASN
44	N2	209	HIS
44	N2	210	ASN
44	N2	237	ASN
45	N3	180	ASN
45	N3	219	ASN
45	N3	222	ASN
45	N3	264	ASN
45	N3	288	ASN
45	N3	292	ASN
46	N4	112	ASN
46	N4	157	ASN
46	N4	189	HIS
46	N4	204	ASN
46	N4	224	HIS
46	N4	231	HIS
46	N4	254	HIS
46	N4	304	HIS
46	N4	339	HIS
46	N4	366	ASN
47	N5	21	ASN

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Mol	Chain	Res	Type
47	N5	26	ASN
47	N5	49	ASN
47	N5	95	ASN
47	N5	235	GLN
47	N5	345	HIS
47	N5	366	GLN
47	N5	453	HIS
47	N5	463	ASN
47	N5	493	ASN
47	N5	499	HIS
47	N5	524	ASN
47	N5	525	HIS
47	N5	553	HIS
47	N5	572	HIS
45	N6	97	ASN
45	N6	115	ASN
45	N6	120	ASN
45	N6	124	ASN
45	N6	159	ASN
48	S2	36	HIS
48	S2	50	HIS
48	S2	158	ASN
48	S2	199	ASN
48	S2	278	GLN
48	S2	309	ASN
48	S2	344	GLN
48	S2	372	GLN
49	S3	153	HIS
49	S3	173	HIS
49	S3	238	HIS
50	S4	39	ASN
51	S5	75	GLN
51	S5	99	ASN
52	S6	85	HIS
53	S7	37	GLN
53	S7	159	HIS
54	S8	70	GLN
54	S8	76	HIS
56	V1	50	GLN
56	V1	282	HIS
56	V1	382	GLN
57	V2	42	GLN

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Mol	Chain	Res	Type
57	V2	149	HIS
57	V2	176	GLN
58	E7	1	GLN
58	E7	83	GLN
58	E7	166	HIS
59	AC	110	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
48	2MR	S2	154	48	10,12,13	2.43	2 (20%)	5,13,15	0.89	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	2MR	S2	154	48	-	2/10/13/15	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	S2	154	2MR	CZ-NH2	5.18	1.44	1.33
48	S2	154	2MR	CZ-NE	5.07	1.45	1.34

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	S2	154	2MR	CG-CD-NE-CZ
48	S2	154	2MR	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 3 are monoatomic - leaving 61 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
68	U10	N4	505	-	43,43,63	2.42	15 (34%)	52,55,79	1.65	15 (28%)
64	CDL	B5	201	-	57,57,99	0.39	0	63,69,111	0.34	0
64	CDL	C4	204	-	68,68,99	0.35	0	74,80,111	0.31	0
63	PC1	N5	601	-	53,53,53	0.30	0	59,61,61	0.30	0
61	SF4	S7	301	53	0,12,12	-	-	-		
64	CDL	AL	303	-	63,63,99	0.37	0	69,75,111	0.31	0
64	CDL	C4	202	-	93,93,99	0.32	0	99,105,111	0.30	0
64	CDL	EA	202	-	54,54,99	0.40	0	60,66,111	0.34	0
67	3PE	G1	516	-	39,39,50	0.34	0	42,44,55	0.30	0
66	ZMP	AB	150	13	29,35,36	0.69	1 (3%)	34,42,45	0.80	1 (2%)
63	PC1	B5	202	-	53,53,53	0.30	0	59,61,61	0.32	0
63	PC1	N1	701	-	48,48,53	0.30	0	54,56,61	0.28	0
64	CDL	N5	603	-	69,69,99	0.35	0	75,81,111	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	PC1	AM	220	-	47,47,53	0.31	0	53,55,61	0.26	0
63	PC1	N3	301	-	41,41,53	0.33	0	47,49,61	0.33	0
63	PC1	N1	702	-	39,39,53	0.34	0	45,47,61	0.29	0
64	CDL	N4	501	-	97,97,99	0.31	0	103,109,111	0.27	0
63	PC1	N4	503	-	32,32,53	0.36	0	38,40,61	0.33	0
64	CDL	AM	215	-	71,71,99	0.35	0	77,83,111	0.30	0
63	PC1	AL	301	-	49,49,53	0.31	0	55,57,61	0.29	0
64	CDL	B3	102	-	64,64,99	0.37	0	70,76,111	0.35	0
64	CDL	AL	302	-	67,67,99	0.36	0	73,79,111	0.31	0
65	NDP	A9	559	-	49,52,52	0.34	0	66,80,80	0.38	0
60	FES	V2	301	57	0,4,4	-	-	-		
63	PC1	A9	560	-	32,32,53	0.37	0	38,40,61	0.34	0
63	PC1	A1	203	-	30,30,53	0.37	0	36,38,61	0.33	0
63	PC1	E8	301	-	53,53,53	0.30	0	59,61,61	0.29	0
61	SF4	S8	298	54	0,12,12	-	-	-		
64	CDL	A3	201	-	57,57,99	0.39	0	63,69,111	0.35	0
63	PC1	A1	202	-	48,48,53	0.32	0	54,56,61	0.31	0
63	PC1	E8	303	-	32,32,53	0.36	0	38,40,61	0.35	0
63	PC1	E8	304	-	29,29,53	0.38	0	35,37,61	0.35	0
64	CDL	N5	608	-	92,92,99	0.31	0	98,104,111	0.29	0
64	CDL	E6	431	-	63,63,99	0.37	0	69,75,111	0.32	0
64	CDL	E7	301	-	67,67,99	0.36	0	73,79,111	0.30	0
61	SF4	V1	580	56	0,12,12	-	-	-		
66	ZMP	AC	201	59	29,35,36	0.68	1 (3%)	34,42,45	0.81	1 (2%)
60	FES	1A	401	1	0,4,4	-	-	-		
67	3PE	AN	302	-	50,50,50	0.30	0	53,55,55	0.29	0
67	3PE	N4	504	-	40,40,50	0.34	0	43,45,55	0.31	0
67	3PE	N5	607	-	50,50,50	0.31	0	53,55,55	0.30	0
70	FMN	V1	579	-	33,33,33	0.27	0	48,50,50	0.38	0
63	PC1	ED	201	-	53,53,53	0.30	0	59,61,61	0.29	0
61	SF4	1A	402	1	0,12,12	-	-	-		
63	PC1	B5	203	-	53,53,53	0.30	0	59,61,61	0.32	0
64	CDL	AM	217	-	71,71,99	0.36	0	77,83,111	0.33	0
63	PC1	N2	301	-	36,36,53	0.35	0	42,44,61	0.33	0
64	CDL	AM	216	-	71,71,99	0.35	0	77,83,111	0.33	0
61	SF4	S8	297	54	0,12,12	-	-	-		
63	PC1	A9	561	-	32,32,53	0.36	0	38,40,61	0.34	0
63	PC1	E8	302	-	53,53,53	0.30	0	59,61,61	0.29	0
63	PC1	AN	301	-	47,47,53	0.32	0	53,55,61	0.30	0
63	PC1	C4	203	-	37,37,53	0.34	0	43,45,61	0.30	0
64	CDL	AL	304	-	69,69,99	0.36	0	75,81,111	0.32	0
63	PC1	N5	605	-	40,40,53	0.33	0	46,48,61	0.29	0
61	SF4	1A	403	1	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	PC1	AM	218	-	48,48,53	0.31	0	54,56,61	0.28	0
63	PC1	E4	401	-	50,50,53	0.30	0	56,58,61	0.31	0
63	PC1	N5	606	-	35,35,53	0.35	0	41,43,61	0.30	0
63	PC1	N4	502	-	38,38,53	0.34	0	44,46,61	0.32	0
64	CDL	EA	201	-	58,58,99	0.39	0	64,70,111	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
68	U10	N4	505	-	-	8/39/63/87	0/1/1/1
64	CDL	B5	201	-	-	14/68/68/110	-
64	CDL	C4	204	-	-	12/79/79/110	-
63	PC1	N5	601	-	-	9/57/57/57	-
64	CDL	AL	303	-	-	11/74/74/110	-
64	CDL	C4	202	-	-	20/104/104/110	-
64	CDL	EA	202	-	-	16/65/65/110	-
61	SF4	S7	301	53	-	-	0/6/5/5
67	3PE	G1	516	-	-	8/43/43/54	-
66	ZMP	AB	150	13	-	14/40/42/43	-
63	PC1	B5	202	-	-	16/57/57/57	-
63	PC1	N1	701	-	-	15/52/52/57	-
64	CDL	N5	603	-	-	12/80/80/110	-
63	PC1	AM	220	-	-	9/51/51/57	-
63	PC1	N3	301	-	-	10/45/45/57	-
63	PC1	N1	702	-	-	11/43/43/57	-
64	CDL	N4	501	-	-	23/108/108/110	-
63	PC1	N4	503	-	-	6/36/36/57	-
64	CDL	AM	215	-	-	16/82/82/110	-
63	PC1	AL	301	-	-	9/53/53/57	-
64	CDL	B3	102	-	-	11/75/75/110	-
64	CDL	AL	302	-	-	9/78/78/110	-
65	NDP	A9	559	-	-	5/34/77/77	0/5/5/5
63	PC1	A9	560	-	-	12/36/36/57	-
63	PC1	E8	301	-	-	12/57/57/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	PC1	A1	203	-	-	6/34/34/57	-
64	CDL	A3	201	-	-	6/68/68/110	-
60	FES	V2	301	57	-	-	0/1/1/1
61	SF4	S8	298	54	-	-	0/6/5/5
63	PC1	A1	202	-	-	15/52/52/57	-
63	PC1	E8	303	-	-	8/36/36/57	-
63	PC1	E8	304	-	-	11/33/33/57	-
64	CDL	N5	608	-	-	17/103/103/110	-
64	CDL	E6	431	-	-	23/74/74/110	-
64	CDL	E7	301	-	-	19/78/78/110	-
66	ZMP	AC	201	59	-	23/40/42/43	-
67	3PE	AN	302	-	-	10/54/54/54	-
67	3PE	N4	504	-	-	10/44/44/54	-
67	3PE	N5	607	-	-	16/54/54/54	-
60	FES	1A	401	1	-	-	0/1/1/1
61	SF4	V1	580	56	-	-	0/6/5/5
70	FMN	V1	579	-	-	2/18/18/18	0/3/3/3
63	PC1	ED	201	-	-	8/57/57/57	-
61	SF4	1A	402	1	-	-	0/6/5/5
63	PC1	B5	203	-	-	16/57/57/57	-
64	CDL	AM	217	-	-	22/82/82/110	-
63	PC1	N2	301	-	-	9/40/40/57	-
64	CDL	AM	216	-	-	18/82/82/110	-
63	PC1	A9	561	-	-	9/36/36/57	-
63	PC1	E8	302	-	-	17/57/57/57	-
61	SF4	S8	297	54	-	-	0/6/5/5
63	PC1	AN	301	-	-	12/51/51/57	-
63	PC1	C4	203	-	-	11/41/41/57	-
64	CDL	AL	304	-	-	25/80/80/110	-
63	PC1	N5	605	-	-	13/44/44/57	-
63	PC1	AM	218	-	-	21/52/52/57	-
63	PC1	E4	401	-	-	13/54/54/57	-
61	SF4	1A	403	1	-	-	0/6/5/5
63	PC1	N5	606	-	-	10/39/39/57	-
63	PC1	N4	502	-	-	16/42/42/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
64	CDL	EA	201	-	-	13/69/69/110	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	N4	505	U10	C6-C1	10.33	1.54	1.35
68	N4	505	U10	C4-C3	4.21	1.53	1.36
68	N4	505	U10	C7-C8	3.11	1.55	1.50
68	N4	505	U10	C7-C6	2.89	1.56	1.51
68	N4	505	U10	C26-C24	2.66	1.56	1.51
68	N4	505	U10	C31-C29	2.59	1.56	1.51
68	N4	505	U10	C16-C14	2.54	1.56	1.51
66	AC	201	ZMP	C9-C10	-2.50	1.48	1.50
66	AB	150	ZMP	C9-C10	-2.50	1.48	1.50
68	N4	505	U10	C6-C5	2.46	1.53	1.46
68	N4	505	U10	O5-C5	-2.42	1.18	1.23
68	N4	505	U10	C21-C19	2.41	1.56	1.51
68	N4	505	U10	C11-C9	2.31	1.56	1.51
68	N4	505	U10	O2-C2	-2.27	1.18	1.23
68	N4	505	U10	O3-C3M	-2.16	1.40	1.45
68	N4	505	U10	C27-C28	2.09	1.57	1.50
68	N4	505	U10	C36-C34	2.07	1.55	1.50

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	N4	505	U10	C7-C8-C9	-3.67	120.69	126.79
68	N4	505	U10	C30-C29-C31	3.52	121.19	115.27
68	N4	505	U10	C22-C23-C24	-3.17	120.03	127.66
68	N4	505	U10	C15-C14-C16	3.03	120.37	115.27
68	N4	505	U10	C25-C24-C26	2.88	120.11	115.27
68	N4	505	U10	C20-C19-C21	2.78	119.95	115.27
68	N4	505	U10	C17-C18-C19	-2.62	121.35	127.66
68	N4	505	U10	C12-C13-C14	-2.56	121.49	127.66
68	N4	505	U10	C10-C9-C11	2.44	119.38	115.27
68	N4	505	U10	C1M-C1-C6	-2.39	120.50	124.40
66	AB	150	ZMP	C15-C14-C13	-2.36	108.42	112.36
68	N4	505	U10	C15-C14-C13	-2.26	117.87	123.68
68	N4	505	U10	C27-C28-C29	-2.25	122.24	127.66
68	N4	505	U10	C36-C34-C35	2.10	119.24	114.60
68	N4	505	U10	C7-C6-C5	2.09	120.99	118.48
66	AC	201	ZMP	C15-C14-C13	-2.07	108.91	112.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	N4	505	U10	C27-C26-C24	-2.02	106.34	112.98

There are no chirality outliers.

All (687) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
63	A1	203	PC1	C11-O13-P-O12
63	A1	203	PC1	C11-O13-P-O14
63	A1	203	PC1	C1-O11-P-O12
63	A9	560	PC1	C1-O11-P-O12
63	A9	560	PC1	C1-O11-P-O14
63	A9	560	PC1	C1-O11-P-O13
63	A9	561	PC1	C11-O13-P-O14
63	A9	561	PC1	C1-O11-P-O12
63	A9	561	PC1	C1-O11-P-O14
63	AM	218	PC1	C1-O11-P-O14
63	AM	220	PC1	C1-O11-P-O14
63	AN	301	PC1	C11-O13-P-O11
63	AN	301	PC1	C1-O11-P-O14
63	B5	202	PC1	C11-O13-P-O11
63	B5	202	PC1	C1-O11-P-O13
63	B5	202	PC1	O13-C11-C12-N
63	B5	203	PC1	C1-O11-P-O12
63	B5	203	PC1	C1-O11-P-O14
63	C4	203	PC1	C11-O13-P-O11
63	E4	401	PC1	C11-O13-P-O12
63	E8	302	PC1	C1-O11-P-O12
63	E8	304	PC1	C1-O11-P-O14
63	E8	304	PC1	C1-O11-P-O13
63	ED	201	PC1	C11-O13-P-O11
63	N1	701	PC1	C1-O11-P-O13
63	N1	702	PC1	C1-O11-P-O12
63	N2	301	PC1	C1-O11-P-O12
63	N2	301	PC1	O13-C11-C12-N
63	N3	301	PC1	C1-O11-P-O13
63	N4	502	PC1	C11-O13-P-O14
63	N4	502	PC1	C1-O11-P-O12
63	N5	601	PC1	C11-O13-P-O14
63	N5	605	PC1	C11-O13-P-O12
63	N5	606	PC1	C1-O11-P-O14
64	AL	303	CDL	OB6-CB4-CB6-OB8
64	AL	304	CDL	CA2-OA2-PA1-OA4

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Mol	Chain	Res	Type	Atoms
64	AL	304	CDL	CB3-OB5-PB2-OB2
64	AM	215	CDL	CA3-OA5-PA1-OA3
64	AM	215	CDL	CB3-OB5-PB2-OB2
64	AM	215	CDL	OB5-CB3-CB4-OB6
64	AM	216	CDL	CA2-OA2-PA1-OA4
64	AM	217	CDL	CA3-OA5-PA1-OA4
64	AM	217	CDL	CB2-OB2-PB2-OB3
64	AM	217	CDL	CB2-OB2-PB2-OB4
64	AM	217	CDL	CB2-OB2-PB2-OB5
64	AM	217	CDL	CB3-OB5-PB2-OB3
64	B3	102	CDL	CA2-OA2-PA1-OA3
64	B3	102	CDL	CA3-OA5-PA1-OA3
64	B3	102	CDL	CA3-OA5-PA1-OA4
64	B3	102	CDL	CB3-OB5-PB2-OB4
64	B5	201	CDL	CB3-OB5-PB2-OB3
64	B5	201	CDL	CB3-OB5-PB2-OB4
64	C4	202	CDL	CA2-OA2-PA1-OA3
64	C4	202	CDL	CA2-OA2-PA1-OA4
64	C4	202	CDL	CA2-OA2-PA1-OA5
64	C4	202	CDL	CA3-OA5-PA1-OA2
64	C4	204	CDL	CA2-OA2-PA1-OA3
64	C4	204	CDL	CA3-OA5-PA1-OA2
64	C4	204	CDL	CA3-OA5-PA1-OA3
64	C4	204	CDL	CA3-OA5-PA1-OA4
64	E6	431	CDL	CA2-OA2-PA1-OA3
64	E6	431	CDL	CA3-OA5-PA1-OA3
64	E6	431	CDL	CA3-OA5-PA1-OA4
64	EA	201	CDL	CA2-OA2-PA1-OA3
64	EA	201	CDL	C1-CB2-OB2-PB2
64	EA	201	CDL	CB3-OB5-PB2-OB3
64	EA	201	CDL	CB3-OB5-PB2-OB4
64	EA	202	CDL	CB3-OB5-PB2-OB4
64	N4	501	CDL	CA2-OA2-PA1-OA3
64	N4	501	CDL	CA2-OA2-PA1-OA4
64	N5	603	CDL	CB2-OB2-PB2-OB3
64	N5	603	CDL	CB2-OB2-PB2-OB4
64	N5	608	CDL	O1-C1-CB2-OB2
64	E7	301	CDL	C1-CA2-OA2-PA1
64	E7	301	CDL	CA3-OA5-PA1-OA2
64	E7	301	CDL	OB5-CB3-CB4-OB6
65	A9	559	NDP	C2N-C3N-C7N-N7N
66	AB	150	ZMP	S1-C11-C12-N1

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Mol	Chain	Res	Type	Atoms
66	AB	150	ZMP	C7-C8-C9-C10
66	AC	201	ZMP	C19-C18-C21-O5
66	AC	201	ZMP	C17-C18-C21-O5
66	AC	201	ZMP	O4-C17-C18-C21
66	AC	201	ZMP	C16-C17-C18-C21
66	AC	201	ZMP	O4-C17-C18-C19
66	AC	201	ZMP	C16-C17-C18-C19
66	AC	201	ZMP	O4-C17-C18-C20
66	AC	201	ZMP	C16-C17-C18-C20
67	AN	302	3PE	C11-O13-P-O11
67	AN	302	3PE	C11-O13-P-O14
67	AN	302	3PE	O13-C11-C12-N
67	N4	504	3PE	C11-O13-P-O14
67	N5	607	3PE	C11-O13-P-O14
67	N5	607	3PE	O13-C11-C12-N
68	N4	505	U10	C1-C6-C7-C8
68	N4	505	U10	C5-C6-C7-C8
68	N4	505	U10	C28-C29-C31-C32
68	N4	505	U10	C30-C29-C31-C32
70	V1	579	FMN	N10-C1'-C2'-O2'
70	V1	579	FMN	N10-C1'-C2'-C3'
66	AB	150	ZMP	C14-C13-N1-C12
66	AC	201	ZMP	C14-C13-N1-C12
66	AC	201	ZMP	C3-C4-C5-C6
64	E6	431	CDL	O1-C1-CA2-OA2
66	AC	201	ZMP	C5-C6-C7-C8
64	A3	201	CDL	C1-CA2-OA2-PA1
64	AL	302	CDL	CB4-CB3-OB5-PB2
66	AB	150	ZMP	O2-C13-N1-C12
66	AC	201	ZMP	O2-C13-N1-C12
64	B3	102	CDL	CA7-C31-C32-C33
64	AL	304	CDL	CB2-C1-CA2-OA2
64	E6	431	CDL	CB2-C1-CA2-OA2
63	N3	301	PC1	C11-C12-N-C15
65	A9	559	NDP	O4D-C1D-N1N-C6N
64	N5	608	CDL	CB5-C51-C52-C53
64	AL	304	CDL	O1-C1-CA2-OA2
63	N1	702	PC1	O21-C2-C3-O31
63	B5	202	PC1	C21-C22-C23-C24
63	B5	202	PC1	C31-C32-C33-C34
63	N5	605	PC1	C21-C22-C23-C24
64	A3	201	CDL	CA5-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
63	B5	202	PC1	C24-C25-C26-C27
63	A1	202	PC1	C11-C12-N-C13
63	N1	701	PC1	C11-C12-N-C15
63	N3	301	PC1	C11-C12-N-C13
64	AL	302	CDL	CB5-C51-C52-C53
64	AM	217	CDL	CB5-C51-C52-C53
64	N4	501	CDL	CA5-C11-C12-C13
67	G1	516	3PE	C21-C22-C23-C24
63	A1	202	PC1	C11-O13-P-O11
63	A1	202	PC1	C1-O11-P-O13
63	A1	203	PC1	C11-O13-P-O11
63	A1	203	PC1	C1-O11-P-O13
63	A9	561	PC1	C1-O11-P-O13
63	AM	220	PC1	C1-O11-P-O13
63	AN	301	PC1	C1-O11-P-O13
63	B5	203	PC1	C1-O11-P-O13
63	E4	401	PC1	C11-O13-P-O11
63	E8	301	PC1	C11-O13-P-O11
63	E8	301	PC1	C1-O11-P-O13
63	E8	302	PC1	C1-O11-P-O13
63	E8	303	PC1	C1-O11-P-O13
63	N1	702	PC1	C1-O11-P-O13
63	N2	301	PC1	C1-O11-P-O13
63	N4	502	PC1	C11-O13-P-O11
63	N4	502	PC1	C1-O11-P-O13
63	N5	601	PC1	C11-O13-P-O11
63	N5	605	PC1	C1-O11-P-O13
63	N5	606	PC1	C1-O11-P-O13
64	AL	303	CDL	CA2-OA2-PA1-OA5
64	AL	304	CDL	CA2-OA2-PA1-OA5
64	AM	215	CDL	CB2-OB2-PB2-OB5
64	AM	217	CDL	CA3-OA5-PA1-OA2
64	AM	217	CDL	CB3-OB5-PB2-OB2
64	B3	102	CDL	CA3-OA5-PA1-OA2
64	B3	102	CDL	CB3-OB5-PB2-OB2
64	B5	201	CDL	CA3-OA5-PA1-OA2
64	B5	201	CDL	CB3-OB5-PB2-OB2
64	C4	204	CDL	CA2-OA2-PA1-OA5
64	E6	431	CDL	CA2-OA2-PA1-OA5
64	E6	431	CDL	CA3-OA5-PA1-OA2
64	EA	201	CDL	CB3-OB5-PB2-OB2
64	EA	202	CDL	CB3-OB5-PB2-OB2

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Mol	Chain	Res	Type	Atoms
64	N4	501	CDL	CA2-OA2-PA1-OA5
64	N4	501	CDL	CB3-OB5-PB2-OB2
64	N5	603	CDL	CA3-OA5-PA1-OA2
64	N5	603	CDL	CB2-OB2-PB2-OB5
64	E7	301	CDL	CA2-OA2-PA1-OA5
67	N4	504	3PE	C11-O13-P-O11
67	N5	607	3PE	C1-O11-P-O13
67	N5	607	3PE	C11-O13-P-O11
64	C4	202	CDL	CB7-C71-C72-C73
64	N5	608	CDL	CA2-C1-CB2-OB2
63	N3	301	PC1	C26-C27-C28-C29
63	B5	202	PC1	C26-C27-C28-C29
64	AL	304	CDL	C11-C12-C13-C14
66	AC	201	ZMP	C20-C18-C21-O5
63	C4	203	PC1	C21-C22-C23-C24
66	AB	150	ZMP	C6-C7-C8-C9
63	E8	304	PC1	C2-C1-O11-P
63	AM	218	PC1	C24-C25-C26-C27
64	B3	102	CDL	C51-C52-C53-C54
64	N4	501	CDL	C53-C54-C55-C56
66	AB	150	ZMP	C2-C3-C4-C5
64	AL	302	CDL	C32-C33-C34-C35
63	ED	201	PC1	C21-C22-C23-C24
63	AM	218	PC1	C25-C26-C27-C28
63	A9	561	PC1	C32-C33-C34-C35
66	AC	201	ZMP	C2-C3-C4-C5
63	B5	203	PC1	C2E-C2F-C2G-C2H
67	G1	516	3PE	C29-C2A-C2B-C2C
63	ED	201	PC1	C24-C25-C26-C27
64	AM	216	CDL	C37-C38-C39-C40
66	AB	150	ZMP	C3-C4-C5-C6
63	A1	202	PC1	C11-C12-N-C15
63	E8	304	PC1	C11-C12-N-C15
64	AL	303	CDL	C51-C52-C53-C54
64	C4	202	CDL	C51-C52-C53-C54
64	N4	501	CDL	C19-C20-C21-C22
64	N4	501	CDL	C38-C39-C40-C41
63	N1	701	PC1	C37-C38-C39-C3A
63	N5	601	PC1	C31-C32-C33-C34
63	AM	220	PC1	C23-C24-C25-C26
63	N5	601	PC1	C32-C33-C34-C35
64	EA	202	CDL	CA3-CA4-CA6-OA8

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Mol	Chain	Res	Type	Atoms
64	AL	302	CDL	C35-C36-C37-C38
64	C4	202	CDL	C61-C62-C63-C64
66	AB	150	ZMP	C1-C2-C3-C4
63	AN	301	PC1	C35-C36-C37-C38
64	AM	217	CDL	C33-C34-C35-C36
63	E4	401	PC1	C33-C34-C35-C36
63	A1	202	PC1	C11-C12-N-C14
63	N3	301	PC1	C11-C12-N-C14
64	C4	204	CDL	CA5-C11-C12-C13
64	N5	608	CDL	CA7-C31-C32-C33
63	AM	220	PC1	C2C-C2D-C2E-C2F
64	AL	304	CDL	C13-C14-C15-C16
63	N1	701	PC1	C2B-C2C-C2D-C2E
64	AL	303	CDL	CB7-C71-C72-C73
64	EA	202	CDL	C53-C54-C55-C56
67	G1	516	3PE	C25-C26-C27-C28
64	B5	201	CDL	C55-C56-C57-C58
63	N1	702	PC1	C27-C28-C29-C2A
63	B5	203	PC1	C2C-C2D-C2E-C2F
63	A9	560	PC1	C2-C3-O31-C31
63	AM	218	PC1	C11-C12-N-C13
63	N1	701	PC1	C11-C12-N-C14
63	AM	218	PC1	C37-C38-C39-C3A
63	ED	201	PC1	C3B-C3C-C3D-C3E
63	AM	220	PC1	C27-C28-C29-C2A
63	E8	302	PC1	C22-C23-C24-C25
64	A3	201	CDL	C71-C72-C73-C74
63	A9	561	PC1	C11-O13-P-O11
63	N5	605	PC1	C11-O13-P-O11
64	N5	608	CDL	CA2-OA2-PA1-OA5
63	C4	203	PC1	C2-C1-O11-P
64	N4	501	CDL	C78-C79-C80-C81
66	AC	201	ZMP	C1-C22-C23-C24
64	EA	202	CDL	OB5-CB3-CB4-CB6
64	E7	301	CDL	OA5-CA3-CA4-CA6
64	AM	216	CDL	CB7-C71-C72-C73
63	N4	502	PC1	C34-C35-C36-C37
63	A1	202	PC1	C22-C23-C24-C25
63	AM	218	PC1	C35-C36-C37-C38
67	AN	302	3PE	C27-C28-C29-C2A
64	C4	204	CDL	C11-C12-C13-C14
64	N5	608	CDL	C42-C43-C44-C45

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Mol	Chain	Res	Type	Atoms
63	E8	304	PC1	C11-C12-N-C13
63	N1	701	PC1	C11-C12-N-C13
63	B5	203	PC1	C1-C2-C3-O31
63	N4	502	PC1	C1-C2-C3-O31
64	AL	302	CDL	CA3-CA4-CA6-OA8
64	AL	303	CDL	CB3-CB4-CB6-OB8
64	AL	304	CDL	CB3-CB4-CB6-OB8
64	AM	216	CDL	CA3-CA4-CA6-OA8
63	AM	218	PC1	C39-C3A-C3B-C3C
67	N5	607	3PE	C35-C36-C37-C38
63	B5	202	PC1	C3B-C3C-C3D-C3E
64	A3	201	CDL	C52-C53-C54-C55
67	N5	607	3PE	C22-C23-C24-C25
66	AC	201	ZMP	O3-C16-C17-O4
64	N4	501	CDL	CA7-C31-C32-C33
63	N2	301	PC1	C24-C25-C26-C27
64	E6	431	CDL	C15-C16-C17-C18
64	AL	304	CDL	C14-C15-C16-C17
63	N5	605	PC1	C11-C12-N-C13
63	AM	220	PC1	C31-C32-C33-C34
63	E8	301	PC1	C31-C32-C33-C34
63	N4	502	PC1	C31-C32-C33-C34
64	N5	608	CDL	C17-C18-C19-C20
63	N2	301	PC1	C25-C26-C27-C28
63	E8	304	PC1	C11-C12-N-C14
63	B5	202	PC1	O11-C1-C2-C3
63	E4	401	PC1	O11-C1-C2-C3
64	AM	215	CDL	OB5-CB3-CB4-CB6
64	AM	216	CDL	OB5-CB3-CB4-CB6
64	AM	217	CDL	OA5-CA3-CA4-CA6
64	C4	202	CDL	OB5-CB3-CB4-CB6
64	E6	431	CDL	OB5-CB3-CB4-CB6
64	E7	301	CDL	OB5-CB3-CB4-CB6
63	AL	301	PC1	C2A-C2B-C2C-C2D
63	N2	301	PC1	C27-C28-C29-C2A
64	EA	202	CDL	CB7-C71-C72-C73
63	A1	203	PC1	C21-C22-C23-C24
63	ED	201	PC1	C28-C29-C2A-C2B
64	B5	201	CDL	C71-C72-C73-C74
63	A9	560	PC1	C2-C1-O11-P
63	B5	202	PC1	C2-C1-O11-P
63	N1	702	PC1	C2-C1-O11-P

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Mol	Chain	Res	Type	Atoms
63	N3	301	PC1	C2-C1-O11-P
64	EA	202	CDL	C1-CA2-OA2-PA1
66	AC	201	ZMP	S1-C11-C12-N1
64	C4	202	CDL	C59-C60-C61-C62
63	A1	202	PC1	C25-C26-C27-C28
63	A9	560	PC1	C1-C2-C3-O31
63	N1	702	PC1	C1-C2-C3-O31
64	EA	201	CDL	CB3-CB4-CB6-OB8
64	E7	301	CDL	CB3-CB4-CB6-OB8
63	N1	701	PC1	C2C-C2D-C2E-C2F
64	AM	217	CDL	C31-C32-C33-C34
66	AB	150	ZMP	N2-C16-C17-C18
63	AM	218	PC1	C11-C12-N-C14
63	AM	218	PC1	C11-O13-P-O11
64	E6	431	CDL	CB2-OB2-PB2-OB5
67	G1	516	3PE	C1-O11-P-O13
63	E4	401	PC1	C28-C29-C2A-C2B
63	E4	401	PC1	O11-C1-C2-O21
64	AM	217	CDL	OA5-CA3-CA4-OA6
64	C4	202	CDL	OB5-CB3-CB4-OB6
64	EA	202	CDL	OB5-CB3-CB4-OB6
64	N4	501	CDL	C83-C84-C85-C86
63	B5	203	PC1	O21-C2-C3-O31
64	AM	216	CDL	OA6-CA4-CA6-OA8
67	N4	504	3PE	O31-C31-C32-C33
63	AL	301	PC1	C2-C1-O11-P
63	N4	503	PC1	C2-C1-O11-P
64	AL	303	CDL	C1-CA2-OA2-PA1
64	AL	303	CDL	CA4-CA3-OA5-PA1
63	AN	301	PC1	C3A-C3B-C3C-C3D
64	AL	304	CDL	OB5-CB3-CB4-CB6
66	AC	201	ZMP	C6-C7-C8-C9
63	N5	601	PC1	C22-C23-C24-C25
64	N5	603	CDL	C58-C59-C60-C61
66	AC	201	ZMP	C22-C23-C24-C25
63	E4	401	PC1	C1-C2-C3-O31
64	AL	304	CDL	C1-CA2-OA2-PA1
64	E6	431	CDL	CA4-CA3-OA5-PA1
64	E6	431	CDL	CA3-CA4-CA6-OA8
64	N4	501	CDL	CA4-CA3-OA5-PA1
64	AM	216	CDL	OB5-CB3-CB4-OB6
64	E6	431	CDL	OB5-CB3-CB4-OB6

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Mol	Chain	Res	Type	Atoms
63	A9	560	PC1	O21-C2-C3-O31
63	AL	301	PC1	O21-C2-C3-O31
63	AM	218	PC1	O21-C2-C3-O31
63	E4	401	PC1	O21-C2-C3-O31
64	AL	302	CDL	OA6-CA4-CA6-OA8
64	E6	431	CDL	OA6-CA4-CA6-OA8
64	E6	431	CDL	OB6-CB4-CB6-OB8
63	E4	401	PC1	C21-C22-C23-C24
63	C4	203	PC1	C11-C12-N-C15
63	N5	605	PC1	C11-C12-N-C15
65	A9	559	NDP	C2B-O2B-P2B-O3X
63	N1	702	PC1	C33-C34-C35-C36
64	E7	301	CDL	C72-C73-C74-C75
64	AL	304	CDL	C31-C32-C33-C34
63	B5	203	PC1	C34-C35-C36-C37
63	C4	203	PC1	C24-C25-C26-C27
64	E7	301	CDL	C32-C33-C34-C35
64	AL	304	CDL	CB5-C51-C52-C53
64	AM	215	CDL	C56-C57-C58-C59
64	EA	201	CDL	CA2-OA2-PA1-OA5
64	EA	202	CDL	CA2-OA2-PA1-OA5
64	N5	603	CDL	CA2-OA2-PA1-OA5
63	AM	218	PC1	C2-C1-O11-P
64	AM	217	CDL	CA4-CA3-OA5-PA1
64	E6	431	CDL	C1-CB2-OB2-PB2
63	A1	202	PC1	C11-O13-P-O14
63	A1	202	PC1	C1-O11-P-O12
63	A1	202	PC1	C1-O11-P-O14
63	A9	561	PC1	C11-O13-P-O12
63	AM	218	PC1	C11-O13-P-O12
63	AM	220	PC1	C1-O11-P-O12
63	AN	301	PC1	C11-O13-P-O12
63	AN	301	PC1	C1-O11-P-O12
63	B5	202	PC1	C11-O13-P-O12
63	B5	202	PC1	C1-O11-P-O12
63	C4	203	PC1	C11-O13-P-O12
63	C4	203	PC1	C11-O13-P-O14
63	C4	203	PC1	C11-C12-N-C13
63	E4	401	PC1	C11-O13-P-O14
63	E8	301	PC1	C11-O13-P-O14
63	E8	303	PC1	C1-O11-P-O14
63	ED	201	PC1	C11-O13-P-O12

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Mol	Chain	Res	Type	Atoms
63	N1	701	PC1	C1-O11-P-O12
63	N3	301	PC1	C1-O11-P-O12
63	N4	502	PC1	C11-O13-P-O12
63	N5	601	PC1	C11-O13-P-O12
63	N5	605	PC1	C11-O13-P-O14
63	N5	605	PC1	C1-O11-P-O14
63	N5	606	PC1	C1-O11-P-O12
64	AL	303	CDL	CA2-OA2-PA1-OA3
64	AL	304	CDL	CB3-OB5-PB2-OB4
64	AM	215	CDL	CB2-OB2-PB2-OB3
64	AM	215	CDL	CB2-OB2-PB2-OB4
64	AM	215	CDL	CB3-OB5-PB2-OB4
64	AM	217	CDL	CB3-OB5-PB2-OB4
64	B5	201	CDL	CA3-OA5-PA1-OA3
64	C4	202	CDL	CA3-OA5-PA1-OA3
64	C4	202	CDL	CA3-OA5-PA1-OA4
64	C4	204	CDL	CA2-OA2-PA1-OA4
64	N4	501	CDL	CB3-OB5-PB2-OB3
64	N4	501	CDL	CB3-OB5-PB2-OB4
64	N5	603	CDL	CA3-OA5-PA1-OA3
64	N5	603	CDL	CA3-OA5-PA1-OA4
64	E7	301	CDL	CA2-OA2-PA1-OA3
64	E7	301	CDL	CA3-OA5-PA1-OA4
67	N4	504	3PE	C11-O13-P-O12
67	N5	607	3PE	C1-O11-P-O12
67	N5	607	3PE	C1-O11-P-O14
67	N5	607	3PE	C11-O13-P-O12
63	ED	201	PC1	O11-C1-C2-C3
63	N1	701	PC1	O11-C1-C2-C3
64	C4	204	CDL	OB5-CB3-CB4-CB6
63	B5	203	PC1	C3B-C3C-C3D-C3E
63	A1	202	PC1	C31-C32-C33-C34
67	N4	504	3PE	C22-C23-C24-C25
64	N4	501	CDL	C76-C77-C78-C79
63	B5	202	PC1	C12-C11-O13-P
63	E8	304	PC1	C12-C11-O13-P
64	B5	201	CDL	CA5-C11-C12-C13
63	E8	302	PC1	C39-C3A-C3B-C3C
63	B5	203	PC1	C24-C25-C26-C27
64	C4	202	CDL	C17-C18-C19-C20
63	B5	202	PC1	O11-C1-C2-O21
63	E8	302	PC1	O11-C1-C2-O21

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Mol	Chain	Res	Type	Atoms
63	ED	201	PC1	O11-C1-C2-O21
64	AL	304	CDL	OB5-CB3-CB4-OB6
64	C4	204	CDL	OB5-CB3-CB4-OB6
63	AN	301	PC1	O31-C31-C32-C33
64	AL	304	CDL	CB7-C71-C72-C73
63	E8	302	PC1	C11-C12-N-C14
63	N5	606	PC1	C11-C12-N-C15
63	A9	560	PC1	O13-C11-C12-N
63	A9	561	PC1	O13-C11-C12-N
63	AL	301	PC1	C1-C2-C3-O31
63	AM	218	PC1	C1-C2-C3-O31
63	AN	301	PC1	O13-C11-C12-N
63	E8	301	PC1	O13-C11-C12-N
63	E8	303	PC1	O13-C11-C12-N
63	E8	304	PC1	O13-C11-C12-N
63	N1	702	PC1	O13-C11-C12-N
63	N4	502	PC1	O13-C11-C12-N
63	N4	503	PC1	O13-C11-C12-N
63	N5	606	PC1	O13-C11-C12-N
64	E6	431	CDL	CB3-CB4-CB6-OB8
63	N4	502	PC1	O21-C2-C3-O31
64	AL	304	CDL	OB6-CB4-CB6-OB8
64	EA	201	CDL	OB6-CB4-CB6-OB8
64	EA	202	CDL	OA6-CA4-CA6-OA8
64	E7	301	CDL	OB6-CB4-CB6-OB8
63	A9	560	PC1	C32-C33-C34-C35
63	AM	218	PC1	C22-C23-C24-C25
66	AB	150	ZMP	O3-C16-C17-O4
63	E8	301	PC1	C27-C28-C29-C2A
67	N4	504	3PE	C36-C37-C38-C39
63	AM	218	PC1	C11-C12-N-C15
63	N5	605	PC1	C11-C12-N-C14
67	AN	302	3PE	C32-C33-C34-C35
63	AL	301	PC1	C31-C32-C33-C34
64	E7	301	CDL	CA7-C31-C32-C33
63	A1	202	PC1	C24-C25-C26-C27
64	C4	202	CDL	C38-C39-C40-C41
63	N1	701	PC1	O31-C31-C32-C33
63	AL	301	PC1	C3-C2-O21-C21
63	B5	202	PC1	C1-C2-O21-C21
63	N2	301	PC1	C1-C2-O21-C21
64	E6	431	CDL	CA6-CA4-OA6-CA5

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Mol	Chain	Res	Type	Atoms
64	E6	431	CDL	CB6-CB4-OB6-CB5
64	AL	304	CDL	CA7-C31-C32-C33
63	E8	301	PC1	C35-C36-C37-C38
64	AM	216	CDL	CB4-CB3-OB5-PB2
63	N1	701	PC1	O11-C1-C2-O21
64	E7	301	CDL	OA5-CA3-CA4-OA6
63	E8	302	PC1	C2C-C2D-C2E-C2F
63	B5	203	PC1	C3C-C3D-C3E-C3F
68	N4	505	U10	C24-C26-C27-C28
63	N2	301	PC1	C11-O13-P-O11
63	N4	503	PC1	C1-O11-P-O13
64	AL	304	CDL	CA3-OA5-PA1-OA2
64	AM	216	CDL	CB3-OB5-PB2-OB2
64	AM	217	CDL	CA2-OA2-PA1-OA5
64	C4	204	CDL	CB2-OB2-PB2-OB5
64	EA	202	CDL	CB2-OB2-PB2-OB5
64	N5	603	CDL	CB3-OB5-PB2-OB2
64	N5	608	CDL	CA3-OA5-PA1-OA2
63	E8	303	PC1	C1-C2-C3-O31
64	C4	202	CDL	C39-C40-C41-C42
64	EA	201	CDL	CB4-CB3-OB5-PB2
63	N5	606	PC1	C24-C25-C26-C27
64	N4	501	CDL	C73-C74-C75-C76
67	AN	302	3PE	C2C-C2D-C2E-C2F
63	B5	203	PC1	C21-C22-C23-C24
63	B5	203	PC1	C2A-C2B-C2C-C2D
66	AB	150	ZMP	C22-C23-C24-C25
63	B5	203	PC1	C25-C26-C27-C28
64	N4	501	CDL	C16-C17-C18-C19
63	E4	401	PC1	C11-C12-N-C13
63	E8	302	PC1	C11-C12-N-C13
63	N5	606	PC1	C11-C12-N-C14
68	N4	505	U10	C26-C27-C28-C29
64	AM	216	CDL	C31-C32-C33-C34
64	C4	202	CDL	C77-C78-C79-C80
66	AC	201	ZMP	O3-C16-C17-C18
63	N5	605	PC1	C23-C24-C25-C26
67	N5	607	3PE	C2-C1-O11-P
63	C4	203	PC1	C11-C12-N-C14
63	AM	220	PC1	C25-C26-C27-C28
63	AM	218	PC1	C3C-C3D-C3E-C3F
63	B5	203	PC1	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
63	E8	302	PC1	C3A-C3B-C3C-C3D
63	N3	301	PC1	C1-C2-C3-O31
64	N5	608	CDL	CA3-CA4-CA6-OA8
66	AC	201	ZMP	N2-C16-C17-C18
64	AM	217	CDL	C15-C16-C17-C18
63	A9	560	PC1	C1-C2-O21-C21
63	AN	301	PC1	C1-C2-O21-C21
63	N4	502	PC1	C3-C2-O21-C21
64	AL	304	CDL	CB3-CB4-OB6-CB5
64	AL	304	CDL	CB6-CB4-OB6-CB5
64	AM	216	CDL	CA6-CA4-OA6-CA5
64	AM	217	CDL	CA3-CA4-OA6-CA5
64	AM	215	CDL	C15-C16-C17-C18
63	N5	606	PC1	C11-C12-N-C13
63	N1	701	PC1	C2A-C2B-C2C-C2D
63	E8	301	PC1	C29-C2A-C2B-C2C
66	AC	201	ZMP	C4-C5-C6-C7
64	E6	431	CDL	C1-CA2-OA2-PA1
63	E8	301	PC1	C24-C25-C26-C27
64	N4	501	CDL	C22-C23-C24-C25
64	B5	201	CDL	OB5-CB3-CB4-OB6
67	N4	504	3PE	O11-C1-C2-O21
64	C4	202	CDL	C72-C71-CB7-OB8
66	AB	150	ZMP	C1-C22-C23-C24
63	N1	702	PC1	C32-C33-C34-C35
67	AN	302	3PE	C38-C39-C3A-C3B
63	E8	302	PC1	C11-C12-N-C15
66	AC	201	ZMP	C12-C11-S1-C10
63	E8	303	PC1	O21-C2-C3-O31
64	N5	608	CDL	OA6-CA4-CA6-OA8
63	AL	301	PC1	C2D-C2E-C2F-C2G
66	AB	150	ZMP	C5-C6-C7-C8
64	AL	302	CDL	C32-C31-CA7-OA8
64	AM	216	CDL	C42-C43-C44-C45
64	B3	102	CDL	C35-C36-C37-C38
63	E8	304	PC1	O11-C1-C2-O21
63	E8	302	PC1	C3D-C3E-C3F-C3G
67	AN	302	3PE	C34-C35-C36-C37
63	E8	304	PC1	O11-C1-C2-C3
67	N4	504	3PE	O11-C1-C2-C3
63	N2	301	PC1	O21-C21-C22-C23
68	N4	505	U10	C29-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
63	E8	303	PC1	O31-C31-C32-C33
63	N4	502	PC1	O21-C21-C22-C23
63	N5	605	PC1	O21-C21-C22-C23
64	N5	608	CDL	C12-C11-CA5-OA6
64	N5	608	CDL	C1-CB2-OB2-PB2
63	N5	606	PC1	C35-C36-C37-C38
63	B5	203	PC1	C38-C39-C3A-C3B
63	N4	503	PC1	C36-C37-C38-C39
63	N3	301	PC1	C11-O13-P-O11
64	B3	102	CDL	CA2-OA2-PA1-OA5
64	B5	201	CDL	CB2-OB2-PB2-OB5
64	E7	301	CDL	CB3-OB5-PB2-OB2
63	AN	301	PC1	C32-C33-C34-C35
64	N4	501	CDL	C54-C55-C56-C57
63	N4	502	PC1	C11-C12-N-C13
64	AL	303	CDL	C12-C11-CA5-OA6
64	AL	304	CDL	C12-C11-CA5-OA6
67	AN	302	3PE	C29-C2A-C2B-C2C
64	A3	201	CDL	C11-C12-C13-C14
63	N1	701	PC1	O21-C21-C22-C23
63	A1	202	PC1	C1-C2-O21-C21
63	B5	202	PC1	C3-C2-O21-C21
64	AM	216	CDL	CA3-CA4-OA6-CA5
64	AM	217	CDL	CB3-CB4-OB6-CB5
64	EA	202	CDL	CA6-CA4-OA6-CA5
64	AM	215	CDL	C14-C15-C16-C17
64	B3	102	CDL	C34-C35-C36-C37
64	N5	603	CDL	C52-C53-C54-C55
63	AM	218	PC1	O21-C21-C22-C23
64	EA	201	CDL	C52-C51-CB5-OB6
63	E8	302	PC1	C35-C36-C37-C38
64	C4	204	CDL	C53-C54-C55-C56
64	AL	304	CDL	C72-C71-CB7-OB8
64	B5	201	CDL	C12-C11-CA5-OA6
64	EA	201	CDL	C72-C71-CB7-OB8
68	N4	505	U10	C2-C3-O3-C3M
67	N4	504	3PE	C2-C1-O11-P
64	AM	217	CDL	C72-C71-CB7-OB8
67	G1	516	3PE	C34-C35-C36-C37
64	AM	215	CDL	C12-C11-CA5-OA6
64	C4	202	CDL	O1-C1-CB2-OB2
63	C4	203	PC1	O31-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
64	C4	202	CDL	OA5-CA3-CA4-CA6
67	N5	607	3PE	O11-C1-C2-C3
64	N4	501	CDL	C34-C35-C36-C37
63	N5	606	PC1	O31-C31-C32-C33
64	A3	201	CDL	OB6-CB4-CB6-OB8
64	AL	302	CDL	OB6-CB4-CB6-OB8
63	AN	301	PC1	C24-C25-C26-C27
63	A1	202	PC1	C33-C34-C35-C36
63	E4	401	PC1	C11-C12-N-C15
65	A9	559	NDP	C2B-O2B-P2B-O2X
64	AM	215	CDL	C52-C51-CB5-OB6
64	E6	431	CDL	C52-C51-CB5-OB6
64	AM	216	CDL	C32-C33-C34-C35
63	N1	702	PC1	O21-C21-C22-C23
67	AN	302	3PE	C2B-C2C-C2D-C2E
65	A9	559	NDP	O4B-C4B-C5B-O5B
63	E8	302	PC1	C38-C39-C3A-C3B
64	B5	201	CDL	C12-C11-CA5-OA7
63	E8	301	PC1	C28-C29-C2A-C2B
63	E4	401	PC1	C11-C12-N-C14
64	N5	608	CDL	C12-C11-CA5-OA7
63	N5	601	PC1	C35-C36-C37-C38
63	E8	302	PC1	C36-C37-C38-C39
63	AL	301	PC1	C27-C28-C29-C2A
63	N5	605	PC1	C33-C34-C35-C36
64	AM	217	CDL	C72-C71-CB7-OB9
64	EA	201	CDL	C52-C51-CB5-OB7
64	EA	201	CDL	C72-C71-CB7-OB9
63	N4	503	PC1	C32-C33-C34-C35
64	C4	202	CDL	C13-C14-C15-C16
63	C4	203	PC1	O32-C31-C32-C33
64	AL	304	CDL	C12-C11-CA5-OA7
64	AL	302	CDL	CB3-CB4-CB6-OB8
63	AM	220	PC1	O21-C21-C22-C23
63	E8	302	PC1	O31-C31-C32-C33
63	E8	303	PC1	O32-C31-C32-C33
63	N1	701	PC1	O22-C21-C22-C23
63	N4	502	PC1	O22-C21-C22-C23
64	AM	215	CDL	C12-C11-CA5-OA7
63	A9	561	PC1	C2-C1-O11-P
64	B5	201	CDL	C1-CA2-OA2-PA1
63	N5	601	PC1	C28-C29-C2A-C2B

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Mol	Chain	Res	Type	Atoms
63	N1	702	PC1	O22-C21-C22-C23
63	N5	605	PC1	O22-C21-C22-C23
64	AL	303	CDL	C12-C11-CA5-OA7
63	AL	301	PC1	C1-O11-P-O14
63	E8	301	PC1	C1-O11-P-O14
63	E8	303	PC1	C11-O13-P-O14
64	AL	303	CDL	CA3-OA5-PA1-OA3
64	AM	216	CDL	CA2-OA2-PA1-OA3
64	AM	216	CDL	CB3-OB5-PB2-OB3
64	B5	201	CDL	CB2-OB2-PB2-OB3
64	N5	603	CDL	CB3-OB5-PB2-OB3
64	N5	608	CDL	CA2-OA2-PA1-OA3
64	N5	608	CDL	CA3-OA5-PA1-OA3
67	G1	516	3PE	C1-O11-P-O12
64	N4	501	CDL	C80-C81-C82-C83
67	N4	504	3PE	O32-C31-C32-C33
63	N4	502	PC1	O31-C31-C32-C33
64	AM	216	CDL	C71-C72-C73-C74
63	AM	218	PC1	O22-C21-C22-C23
64	E6	431	CDL	C52-C51-CB5-OB7
64	N5	603	CDL	C56-C57-C58-C59
67	N5	607	3PE	C2C-C2D-C2E-C2F
64	AL	304	CDL	C72-C71-CB7-OB9
64	E7	301	CDL	C75-C76-C77-C78
67	N5	607	3PE	C3B-C3C-C3D-C3E
64	N4	501	CDL	C59-C60-C61-C62
63	E8	304	PC1	C22-C23-C24-C25
63	A1	202	PC1	C3-C2-O21-C21
63	A9	560	PC1	C3-C2-O21-C21
63	E8	301	PC1	C12-C11-O13-P
64	AM	217	CDL	CA6-CA4-OA6-CA5
64	AM	217	CDL	CB6-CB4-OB6-CB5
64	E6	431	CDL	CB3-CB4-OB6-CB5
64	EA	202	CDL	CA3-CA4-OA6-CA5
66	AB	150	ZMP	O3-C16-C17-C18
67	G1	516	3PE	C12-C11-O13-P
64	EA	202	CDL	O1-C1-CA2-OA2
64	AM	215	CDL	C52-C51-CB5-OB7
64	AM	215	CDL	C72-C71-CB7-OB8
64	EA	202	CDL	C32-C31-CA7-OA8
64	N4	501	CDL	C12-C11-CA5-OA6
64	N5	608	CDL	C52-C51-CB5-OB6

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Mol	Chain	Res	Type	Atoms
64	E7	301	CDL	C12-C11-CA5-OA6
64	E7	301	CDL	C32-C31-CA7-OA8
67	N5	607	3PE	O31-C31-C32-C33
63	AM	218	PC1	C21-C22-C23-C24
64	AM	216	CDL	C1-CB2-OB2-PB2
63	AM	218	PC1	O32-C31-C32-C33
63	E8	302	PC1	O32-C31-C32-C33
67	N5	607	3PE	C23-C24-C25-C26
63	A9	560	PC1	O31-C31-C32-C33
63	AM	218	PC1	O31-C31-C32-C33
63	N3	301	PC1	O21-C21-C22-C23
64	N5	608	CDL	C41-C42-C43-C44
64	E7	301	CDL	C32-C31-CA7-OA9
63	N4	503	PC1	O31-C31-C32-C33
64	EA	202	CDL	C32-C31-CA7-OA9
63	N5	601	PC1	C11-C12-N-C13
63	N1	701	PC1	C23-C24-C25-C26
63	N4	502	PC1	O32-C31-C32-C33
67	N5	607	3PE	O32-C31-C32-C33
63	E8	302	PC1	C3C-C3D-C3E-C3F
67	G1	516	3PE	O31-C31-C32-C33

There are no ring outliers.

33 monomers are involved in 78 short contacts:

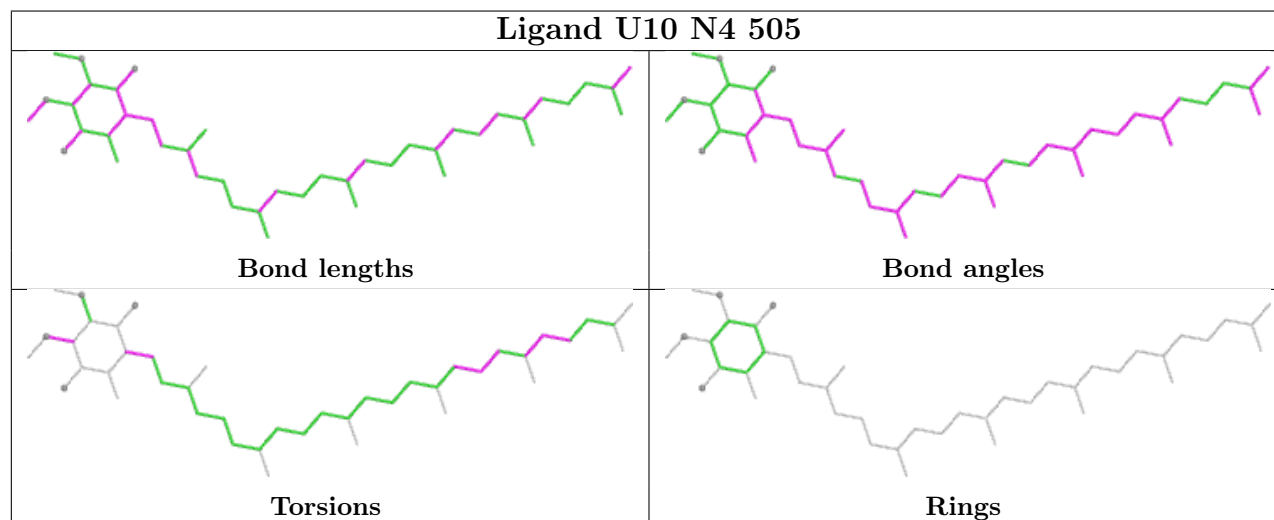
Mol	Chain	Res	Type	Clashes	Symm-Clashes
68	N4	505	U10	5	0
64	B5	201	CDL	1	0
63	N5	601	PC1	1	0
64	AL	303	CDL	2	0
64	C4	202	CDL	1	0
64	EA	202	CDL	1	0
67	G1	516	3PE	2	0
66	AB	150	ZMP	6	0
64	N5	603	CDL	3	0
63	AM	220	PC1	1	0
64	N4	501	CDL	4	0
64	AM	215	CDL	4	0
64	B3	102	CDL	1	0
65	A9	559	NDP	3	0
63	A9	560	PC1	1	0
63	A1	203	PC1	1	0

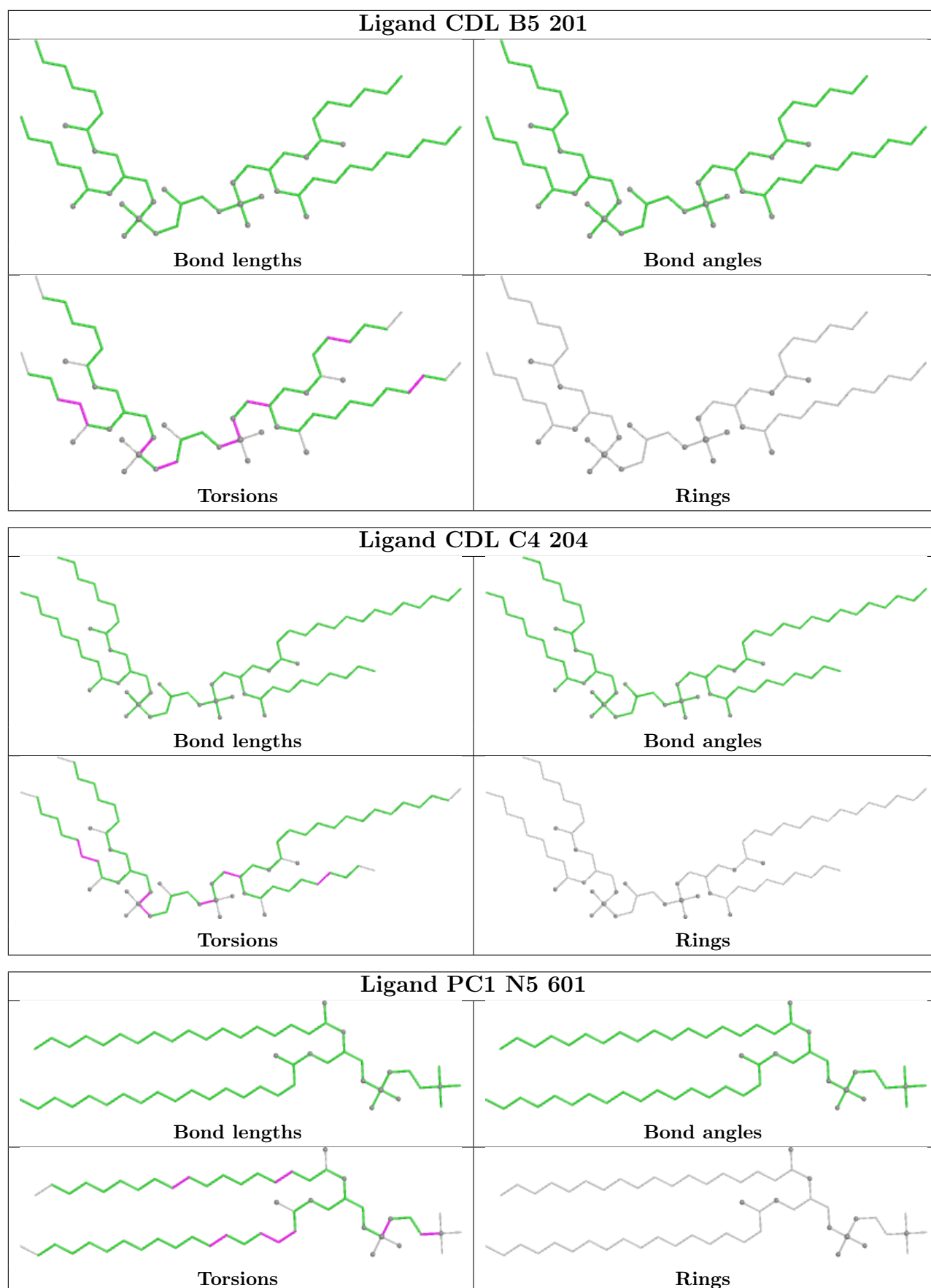
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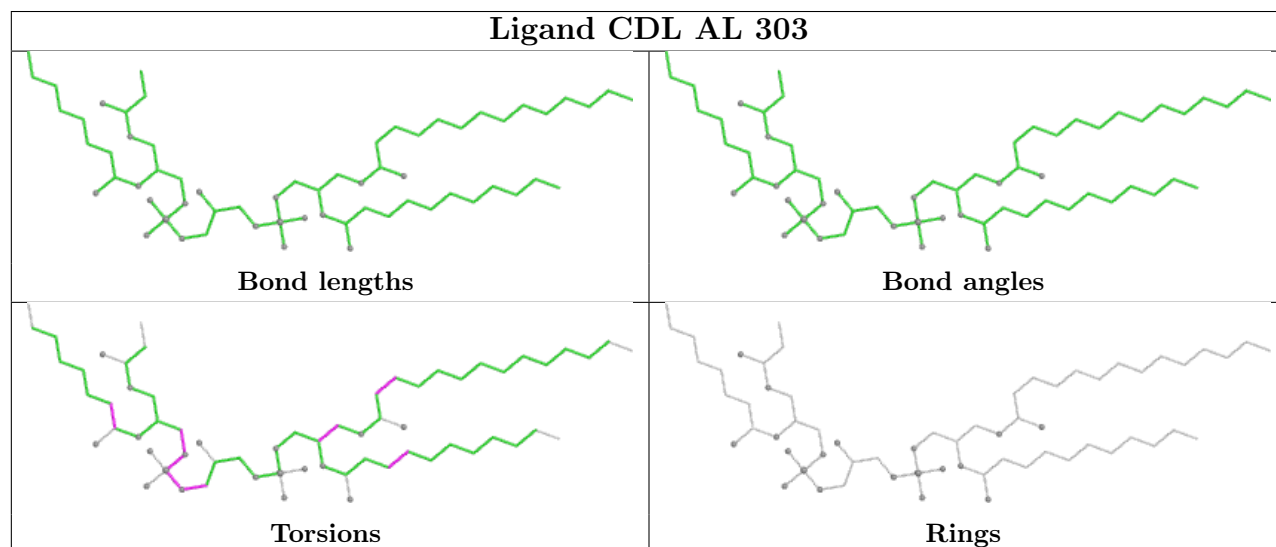
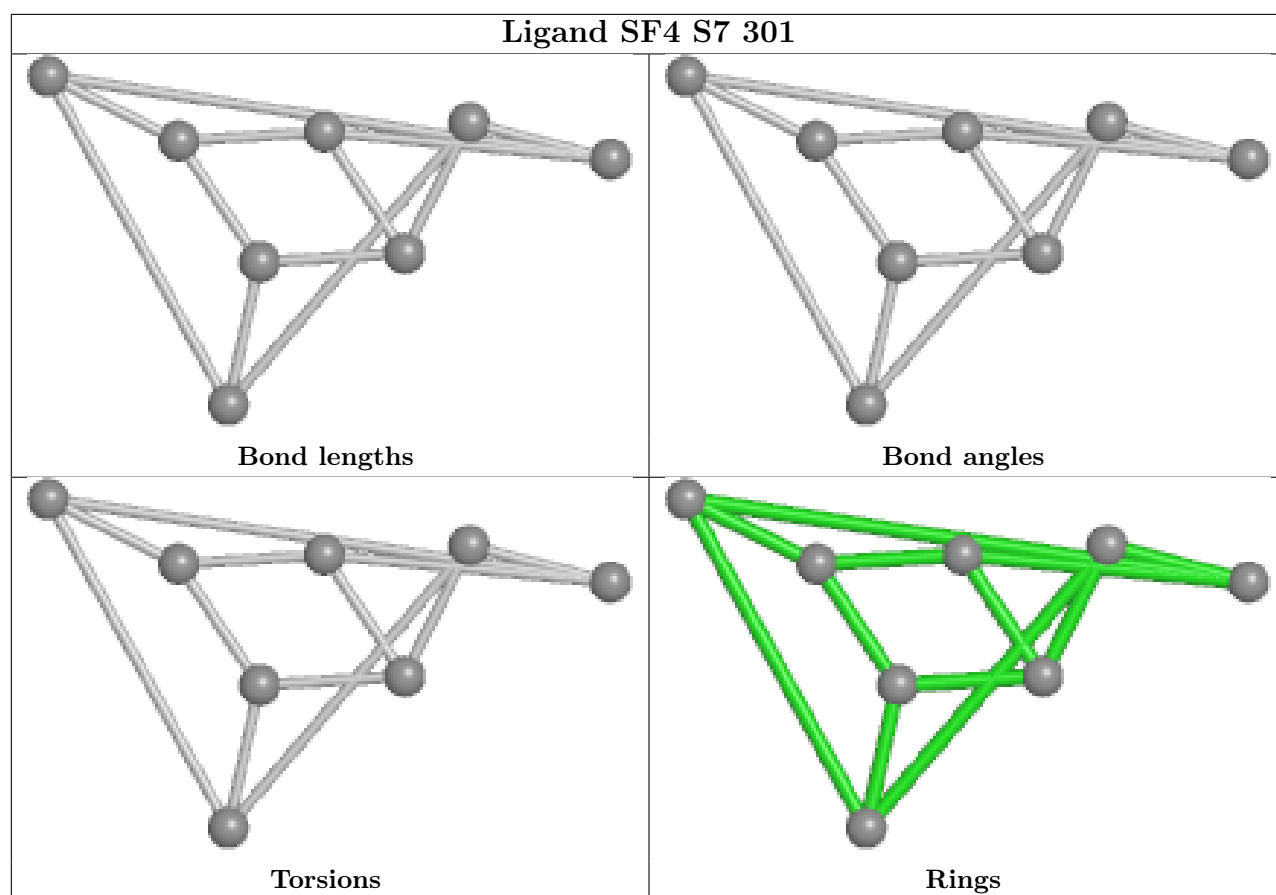
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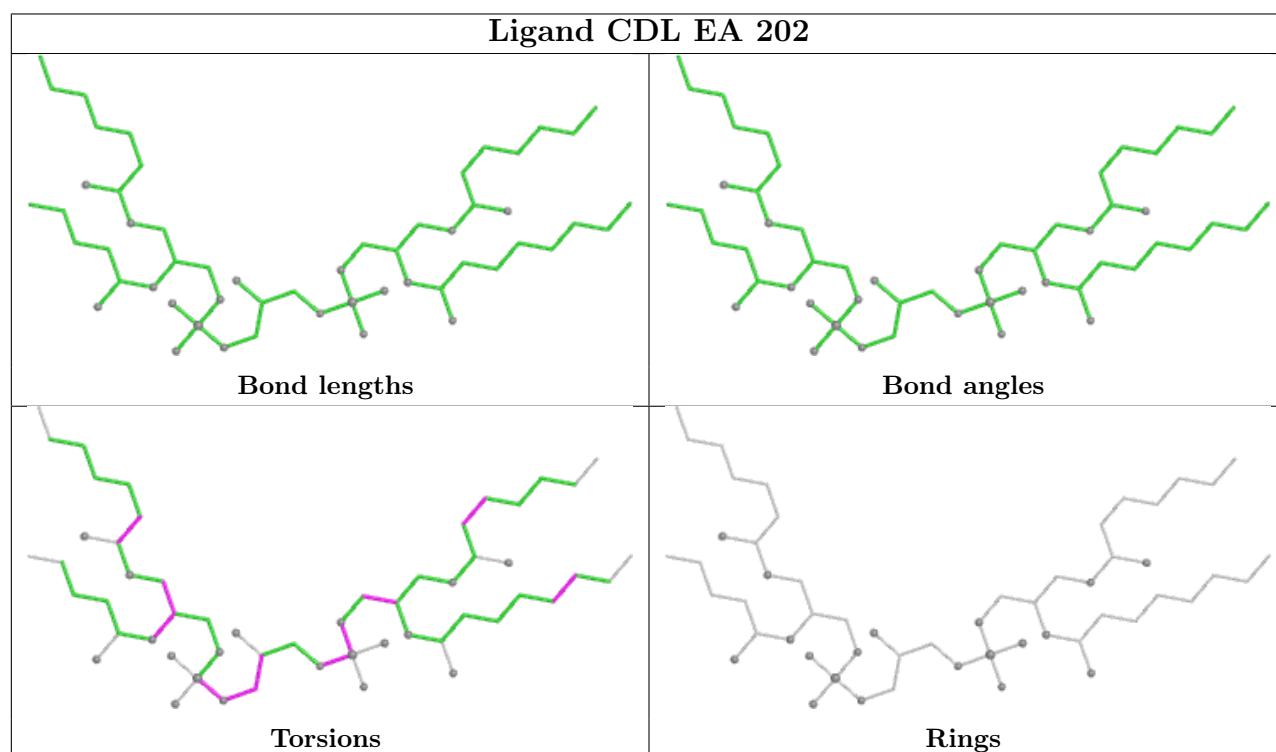
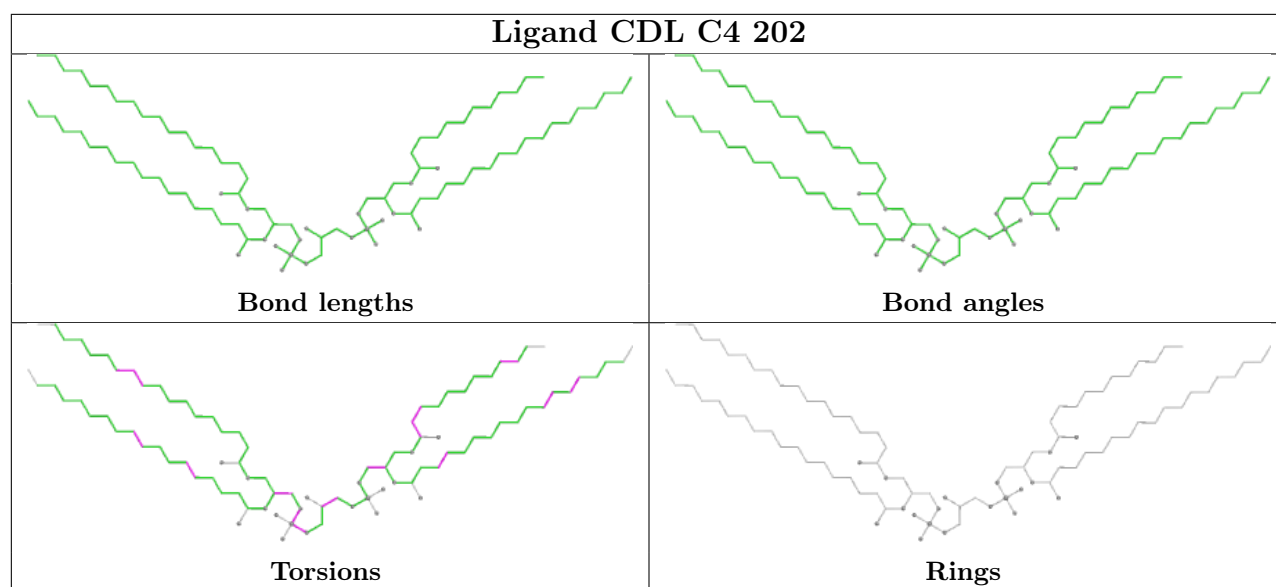
Mol	Chain	Res	Type	Clashes	Symm-Clashes
63	E8	301	PC1	2	0
61	S8	298	SF4	2	0
64	A3	201	CDL	1	0
63	A1	202	PC1	2	0
64	N5	608	CDL	1	0
61	V1	580	SF4	1	0
66	AC	201	ZMP	15	0
67	N5	607	3PE	1	0
63	ED	201	PC1	1	0
63	B5	203	PC1	2	0
64	AM	217	CDL	2	0
63	N2	301	PC1	1	0
64	AM	216	CDL	4	0
61	S8	297	SF4	3	0
63	E8	302	PC1	1	0
63	C4	203	PC1	1	0
63	N4	502	PC1	2	0

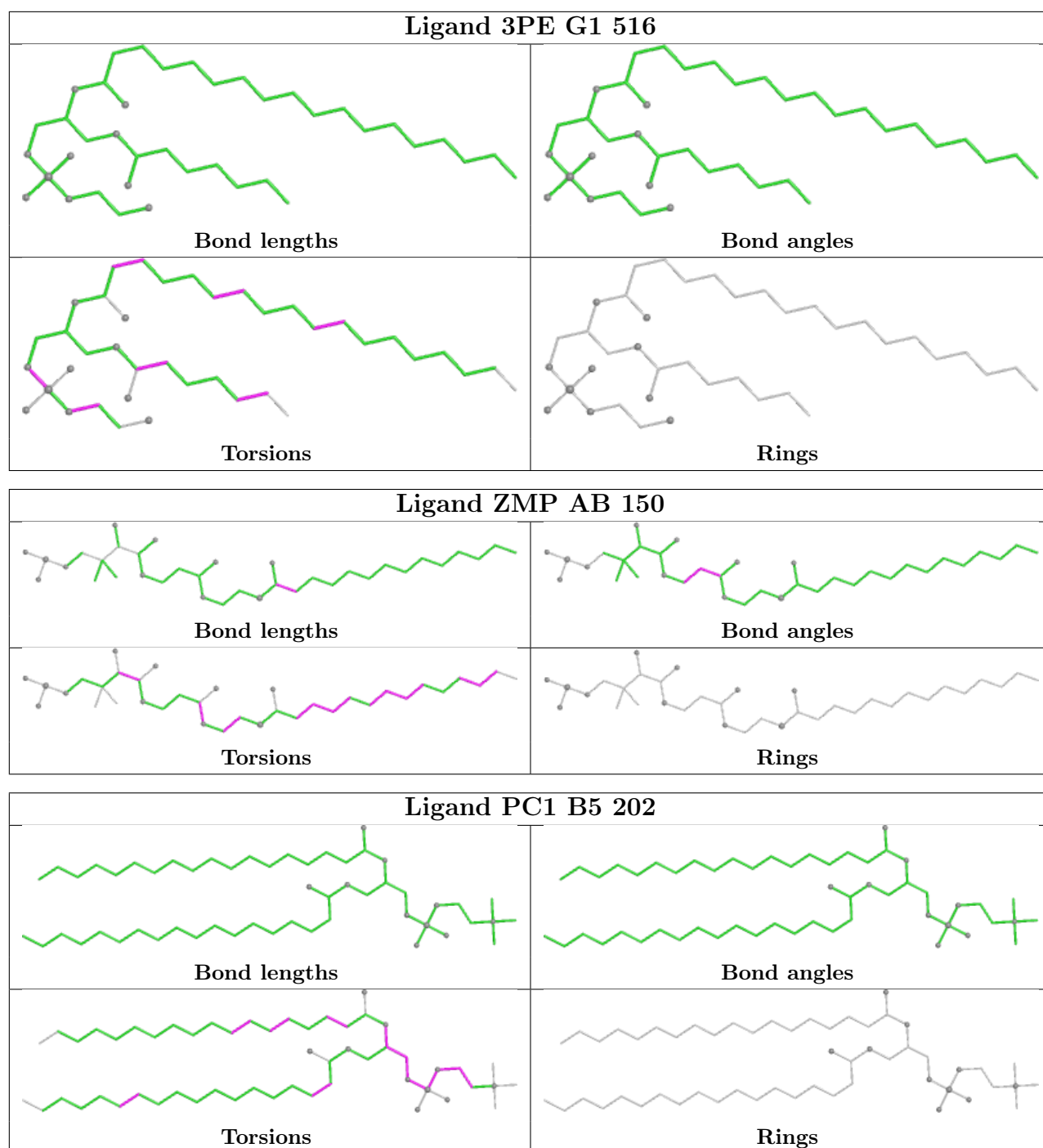
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

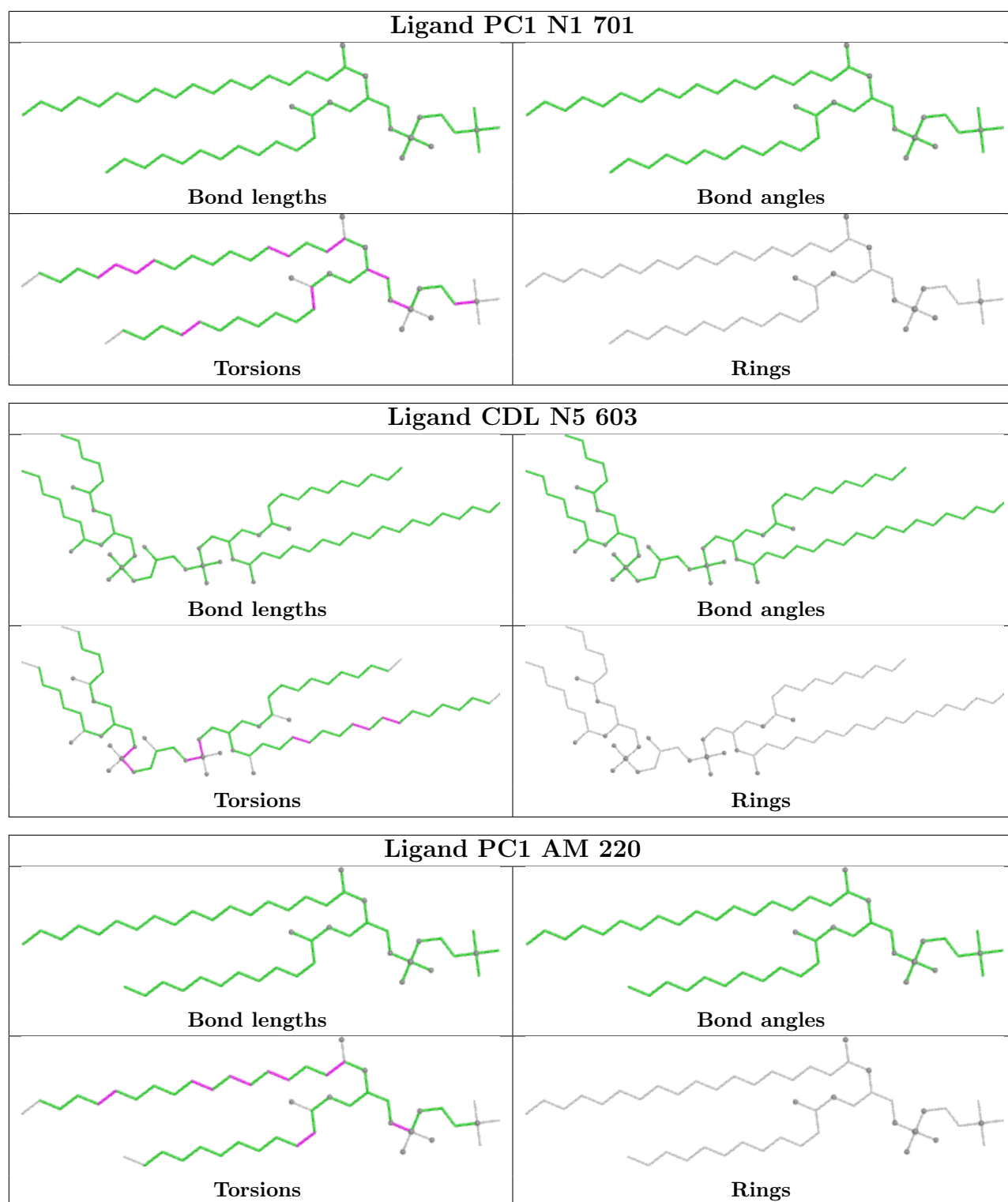


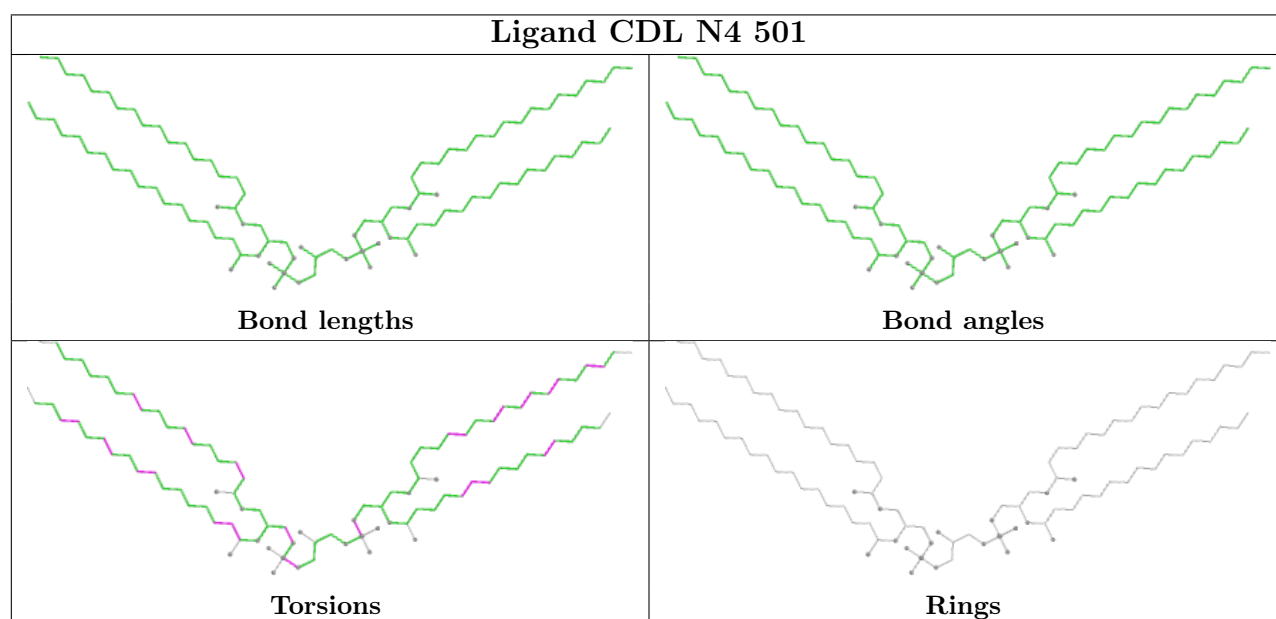
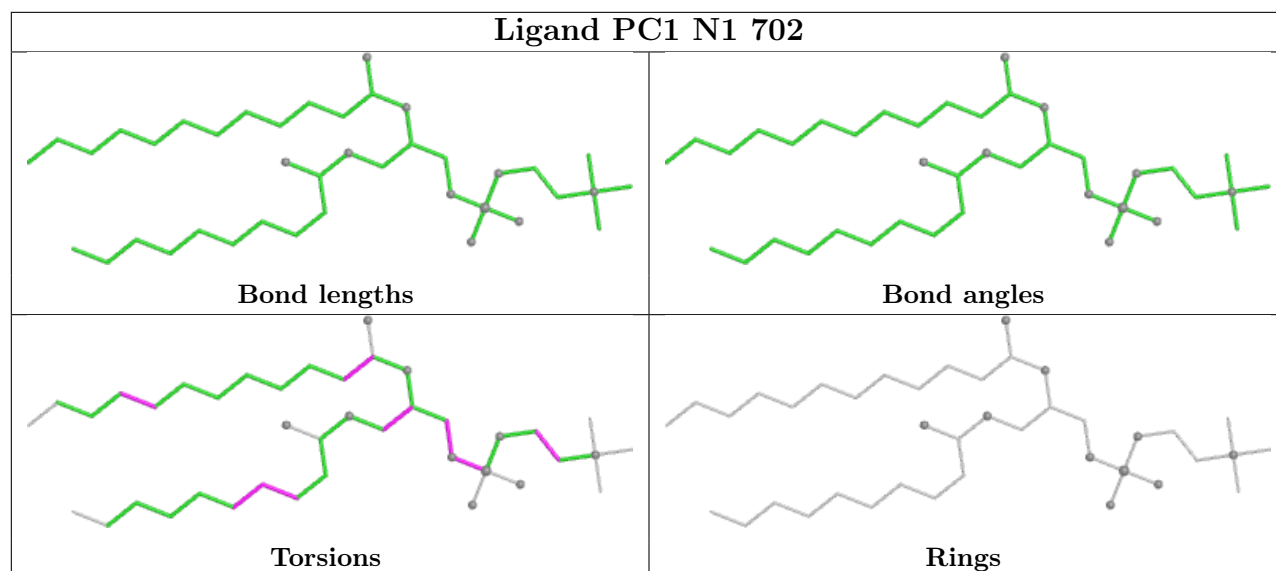
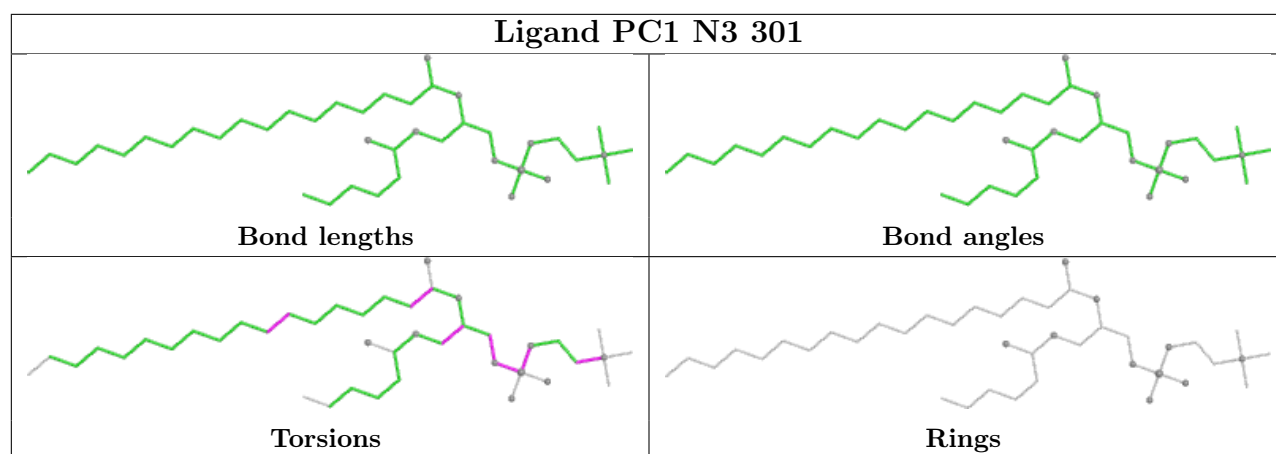


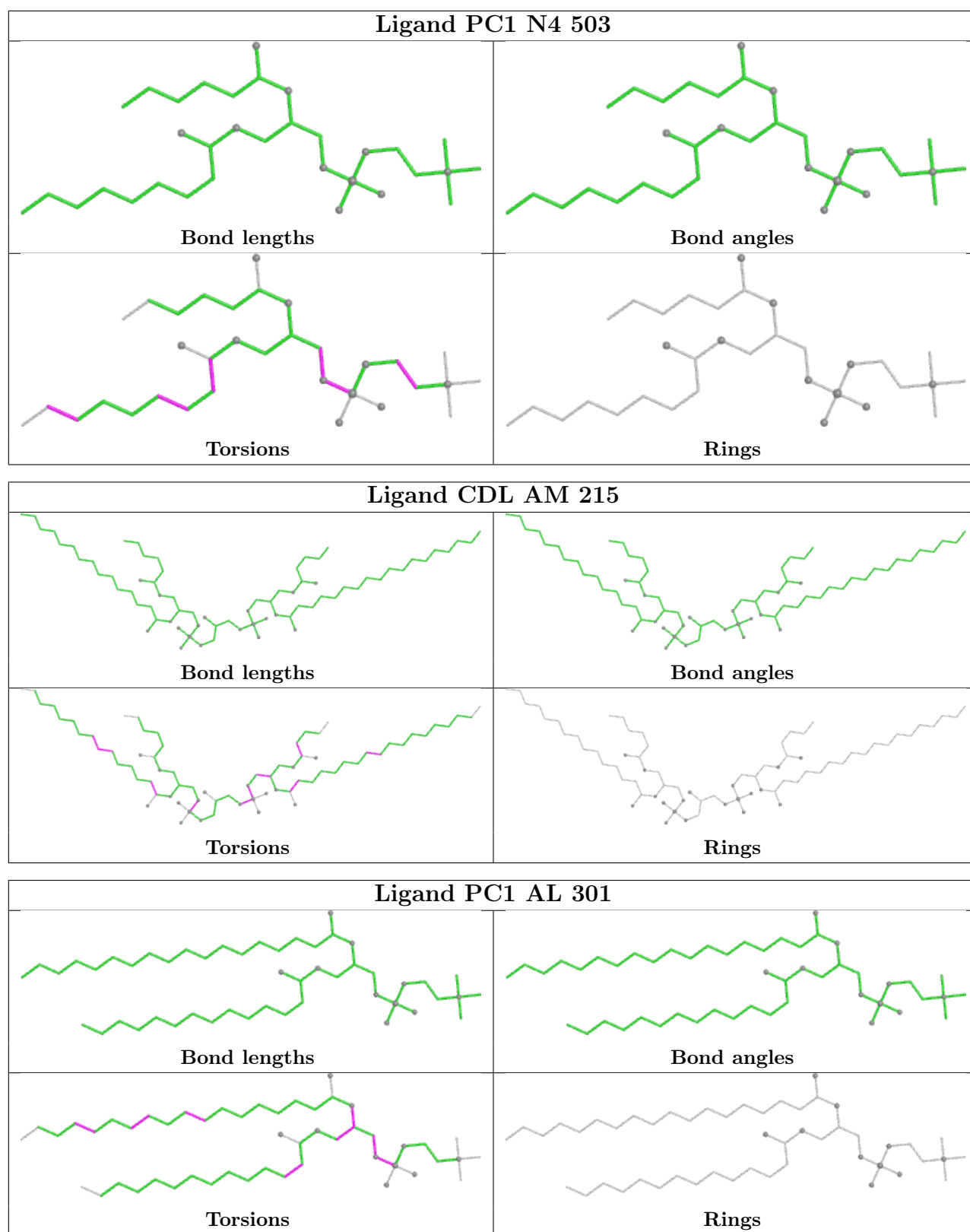


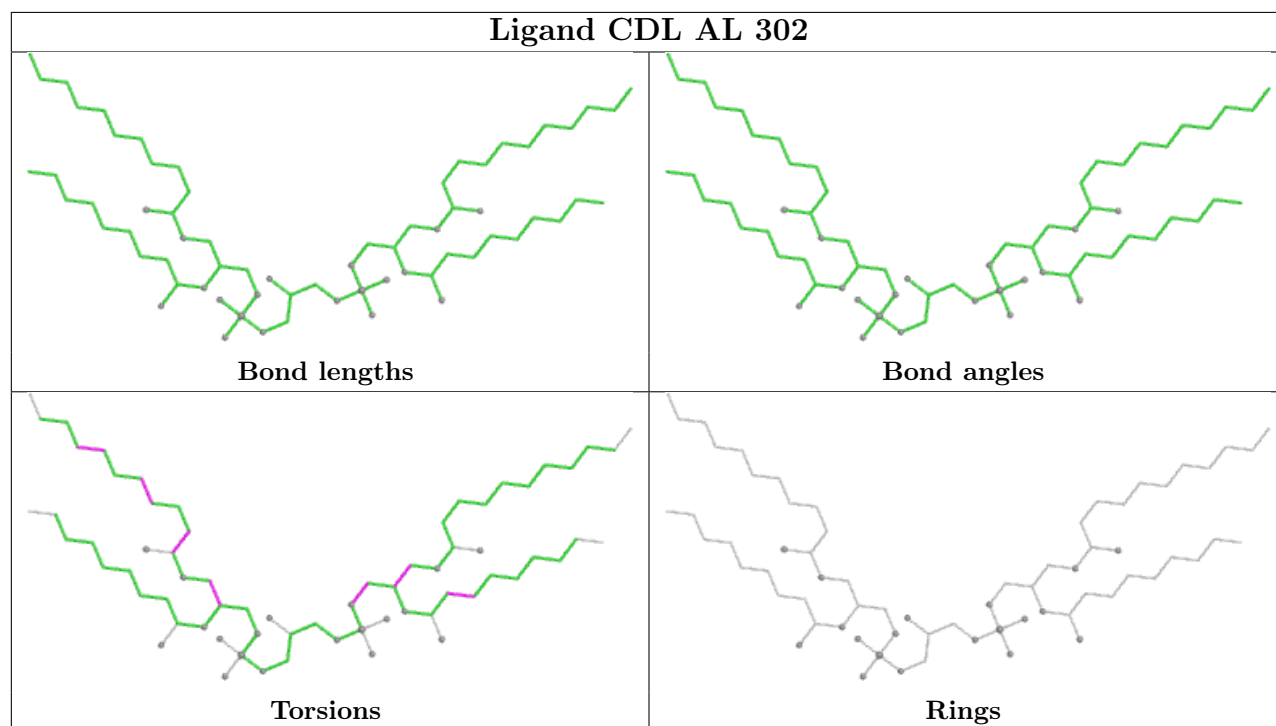
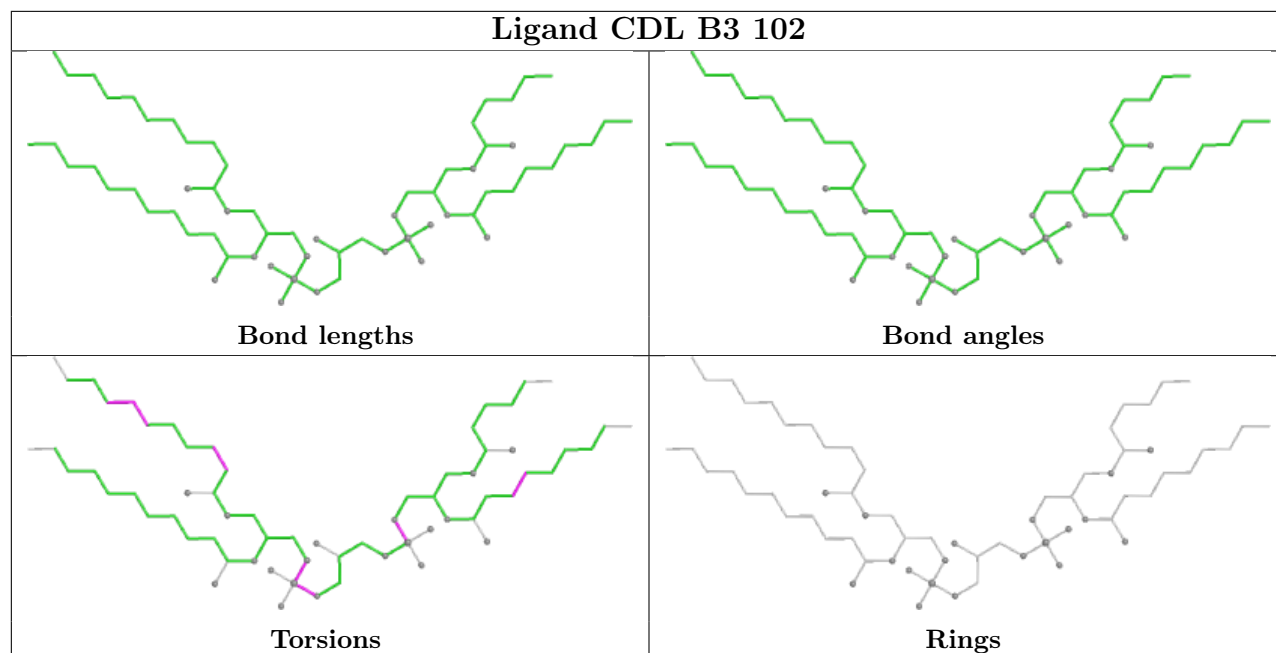




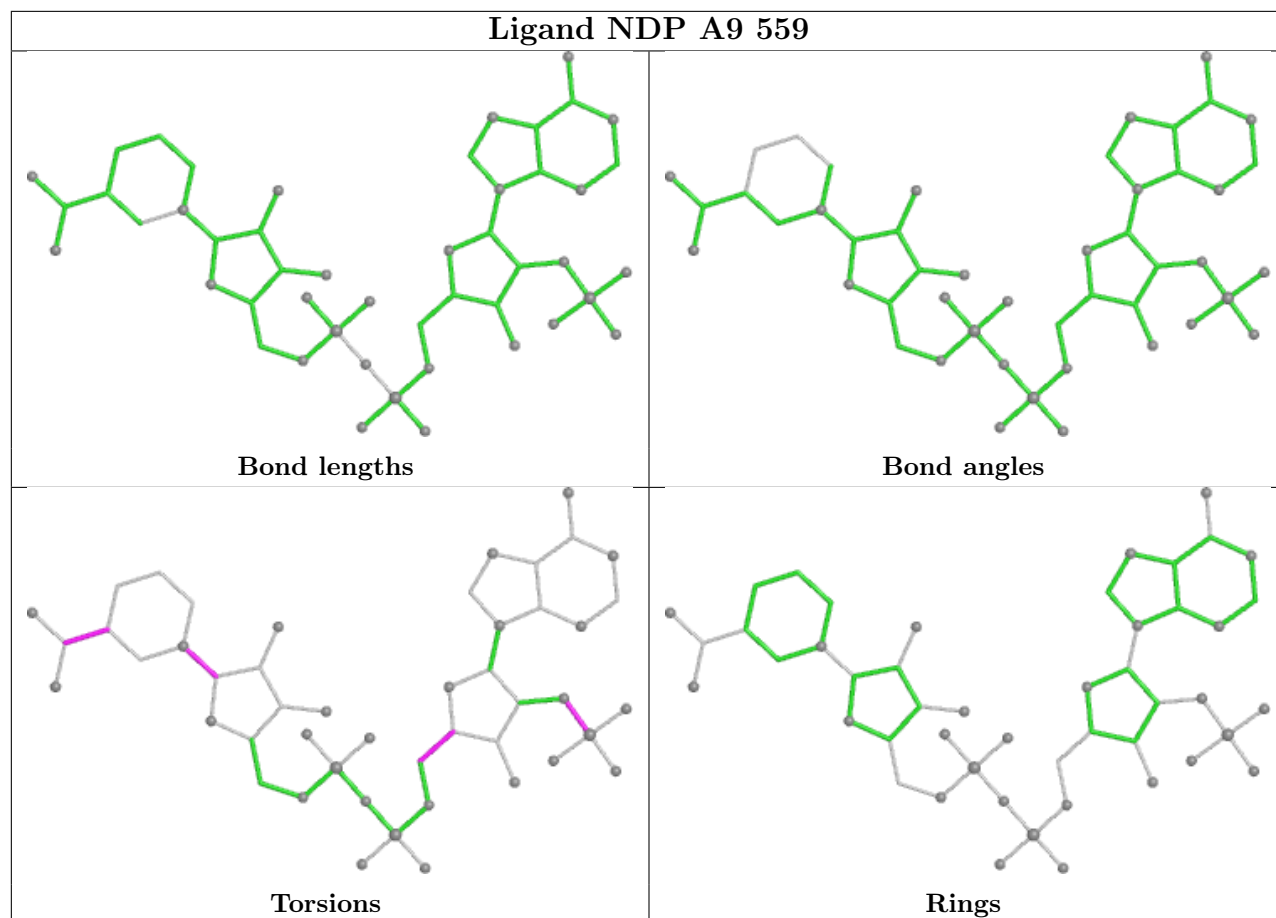




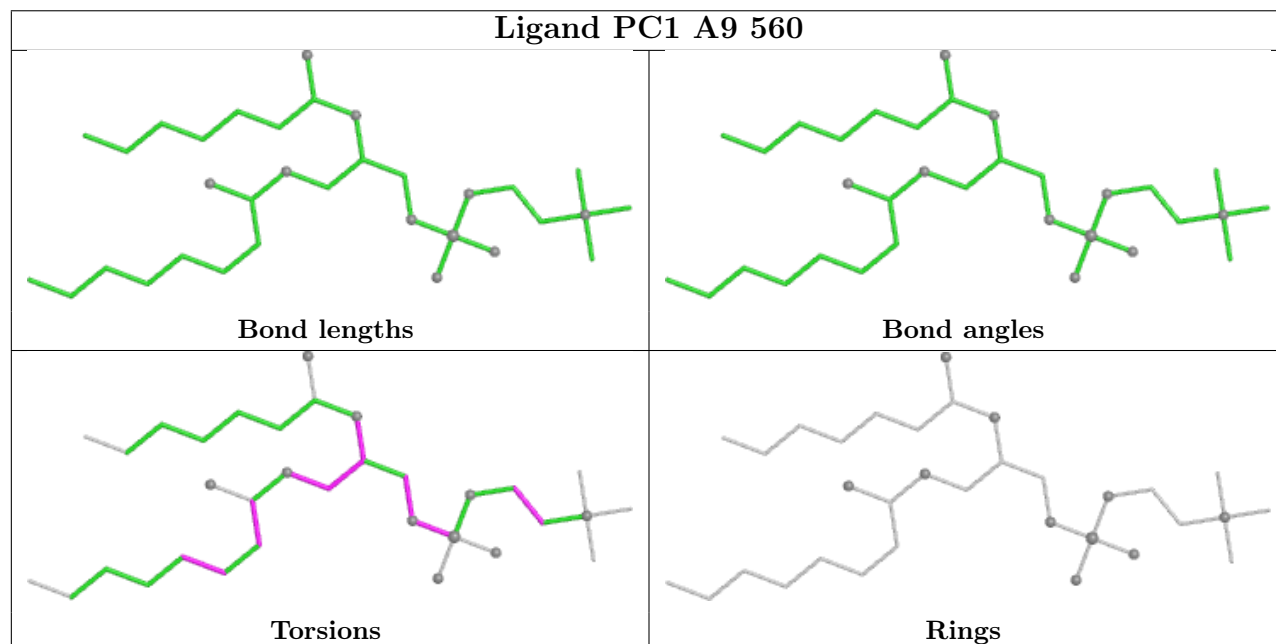


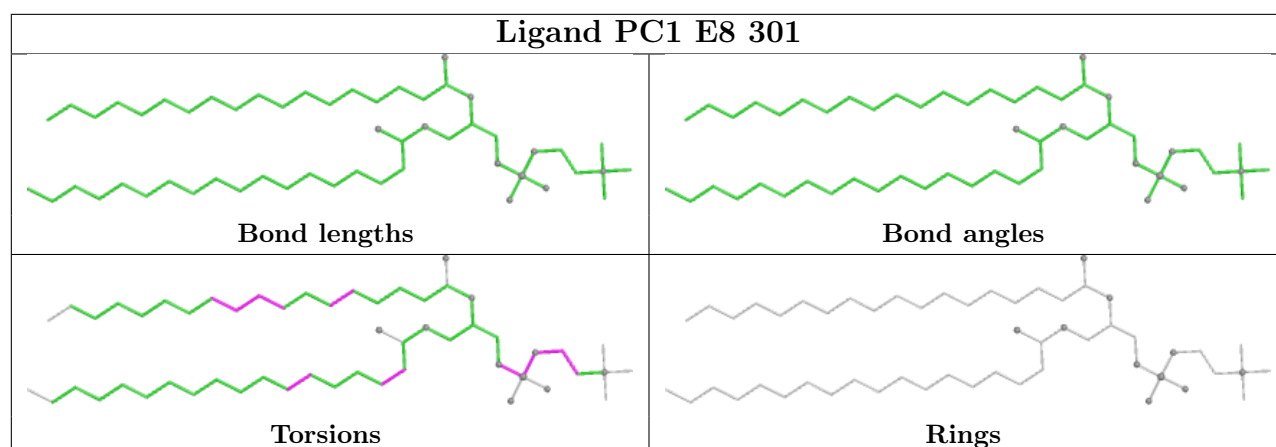
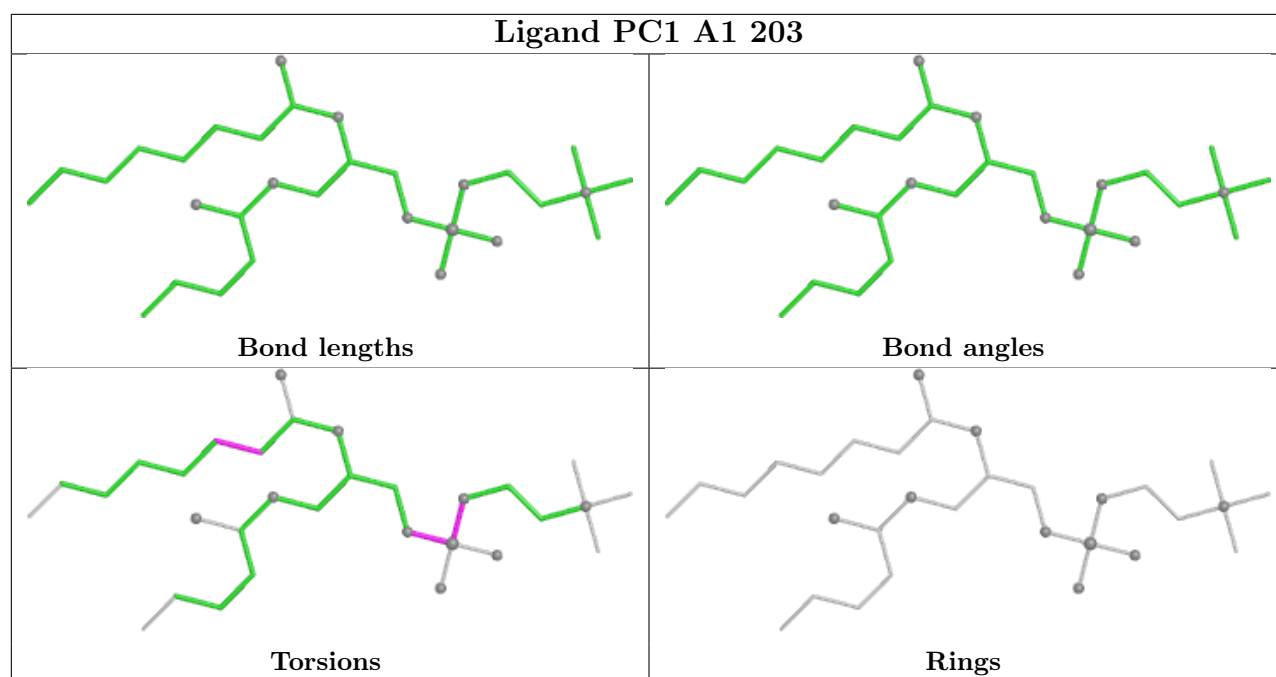


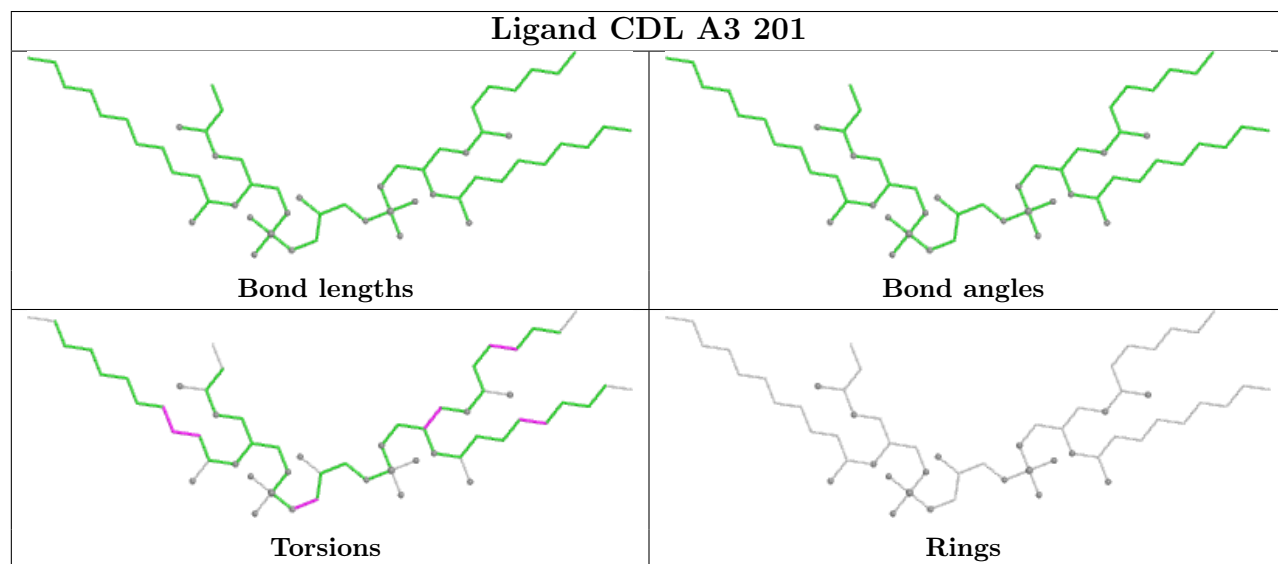
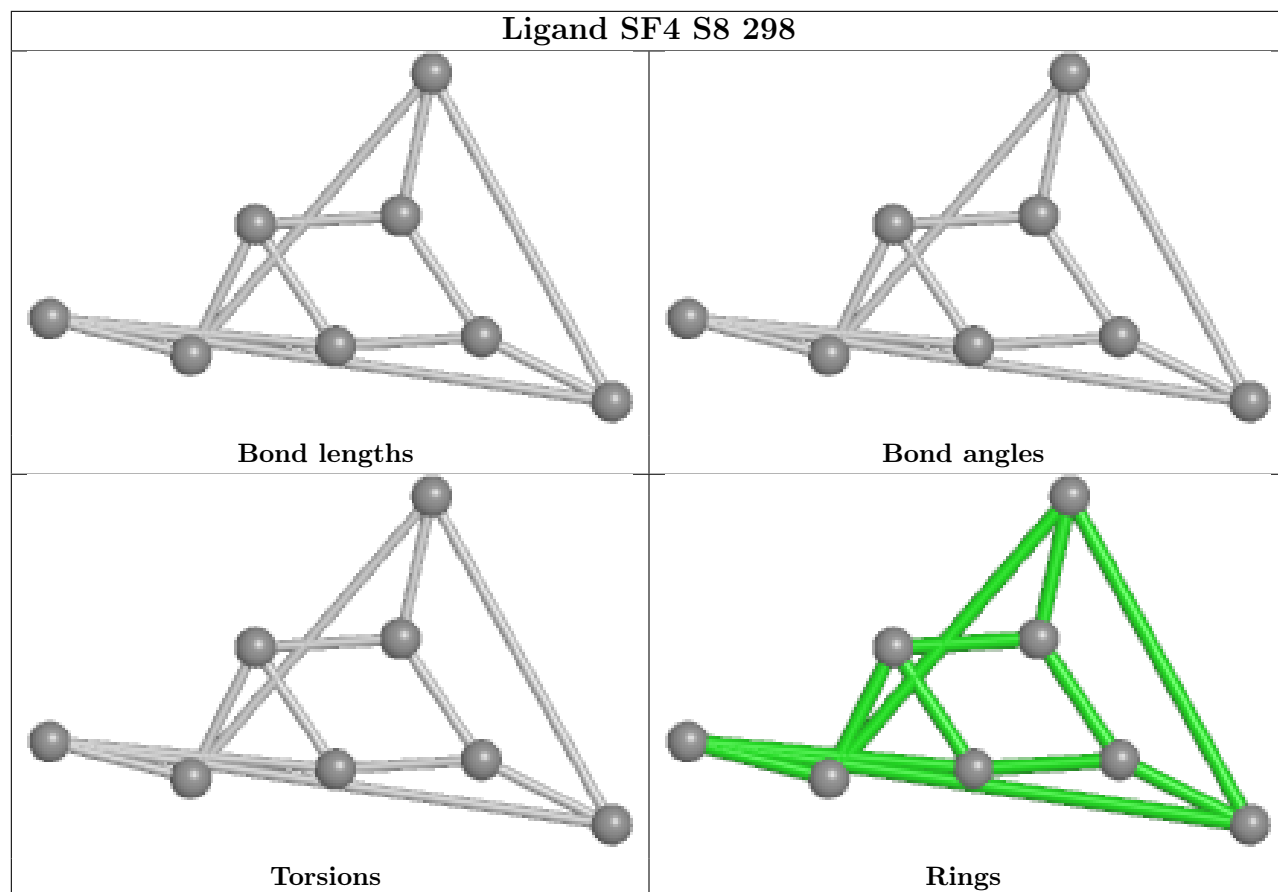
Ligand NDP A9 559

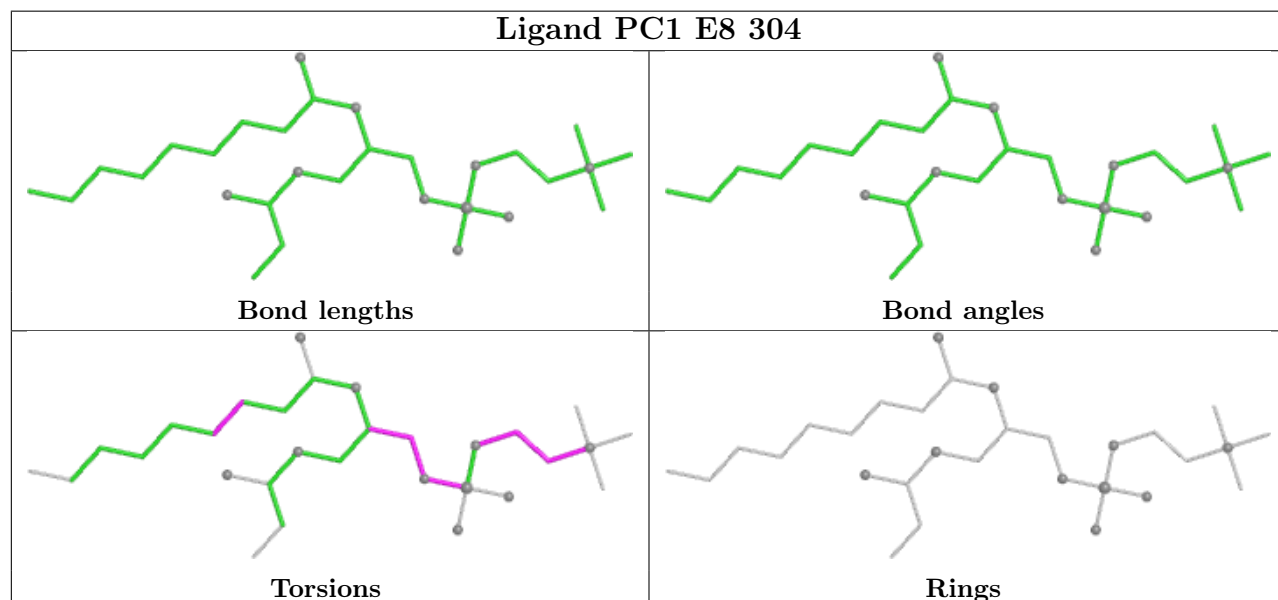
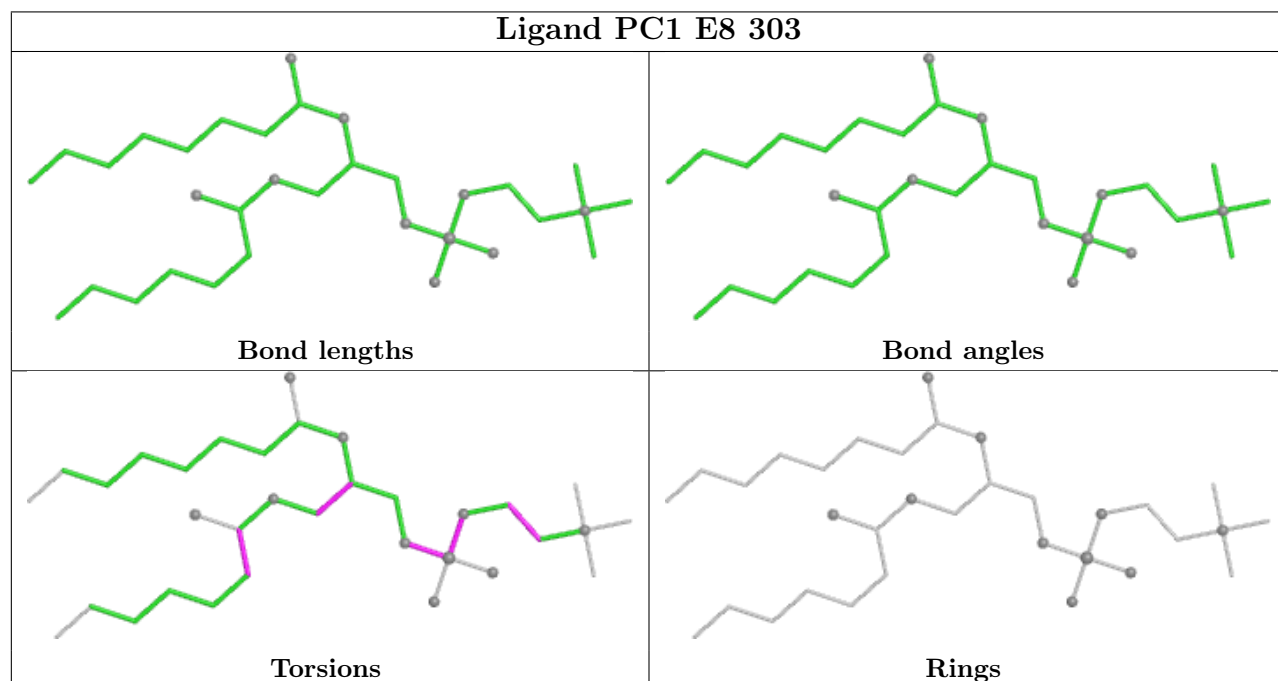
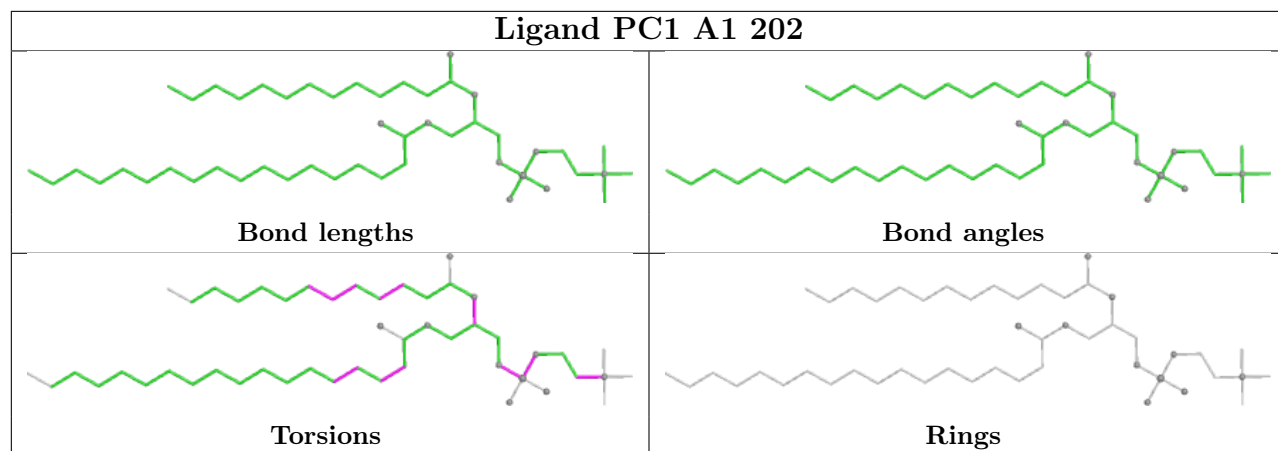


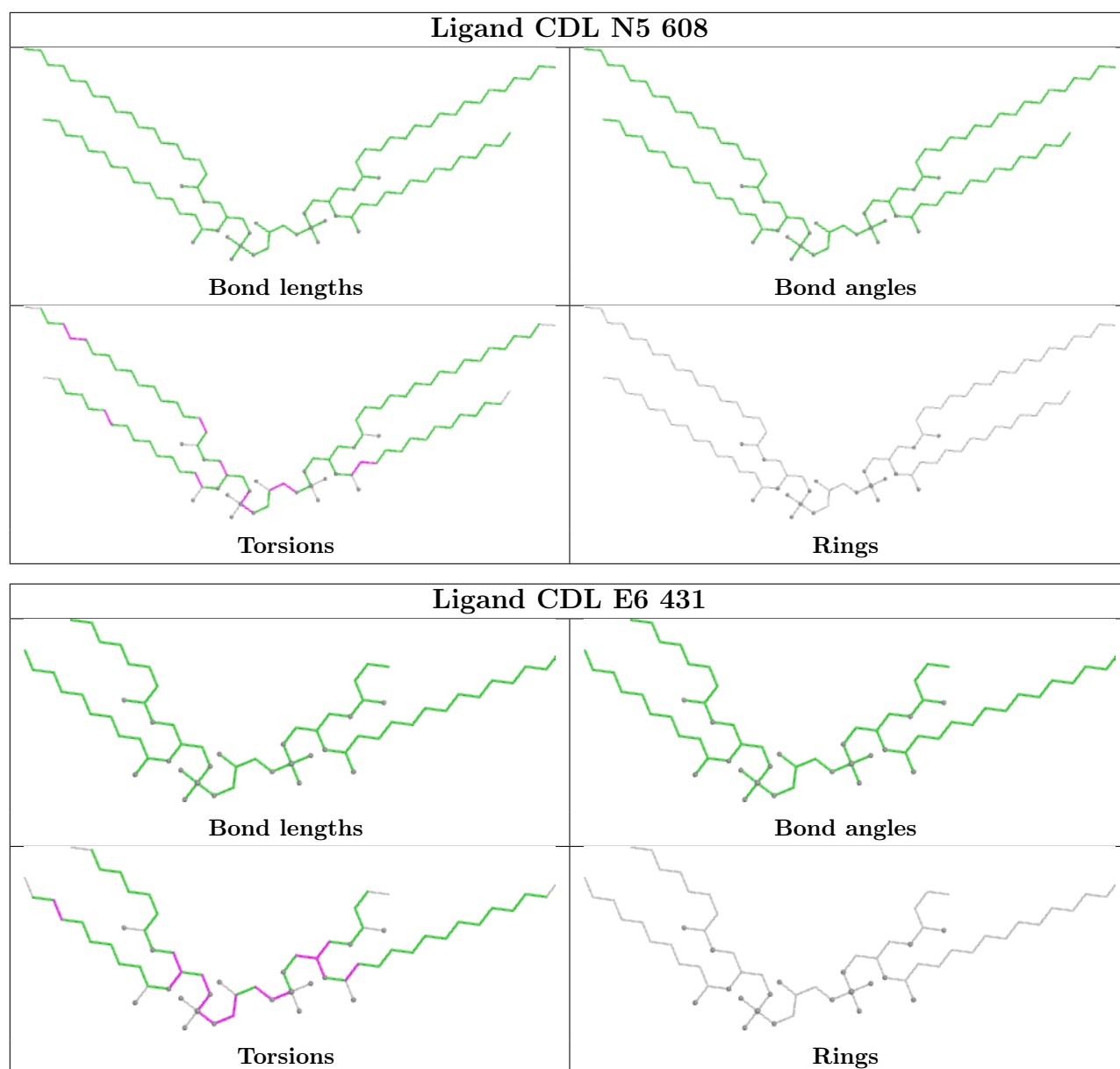
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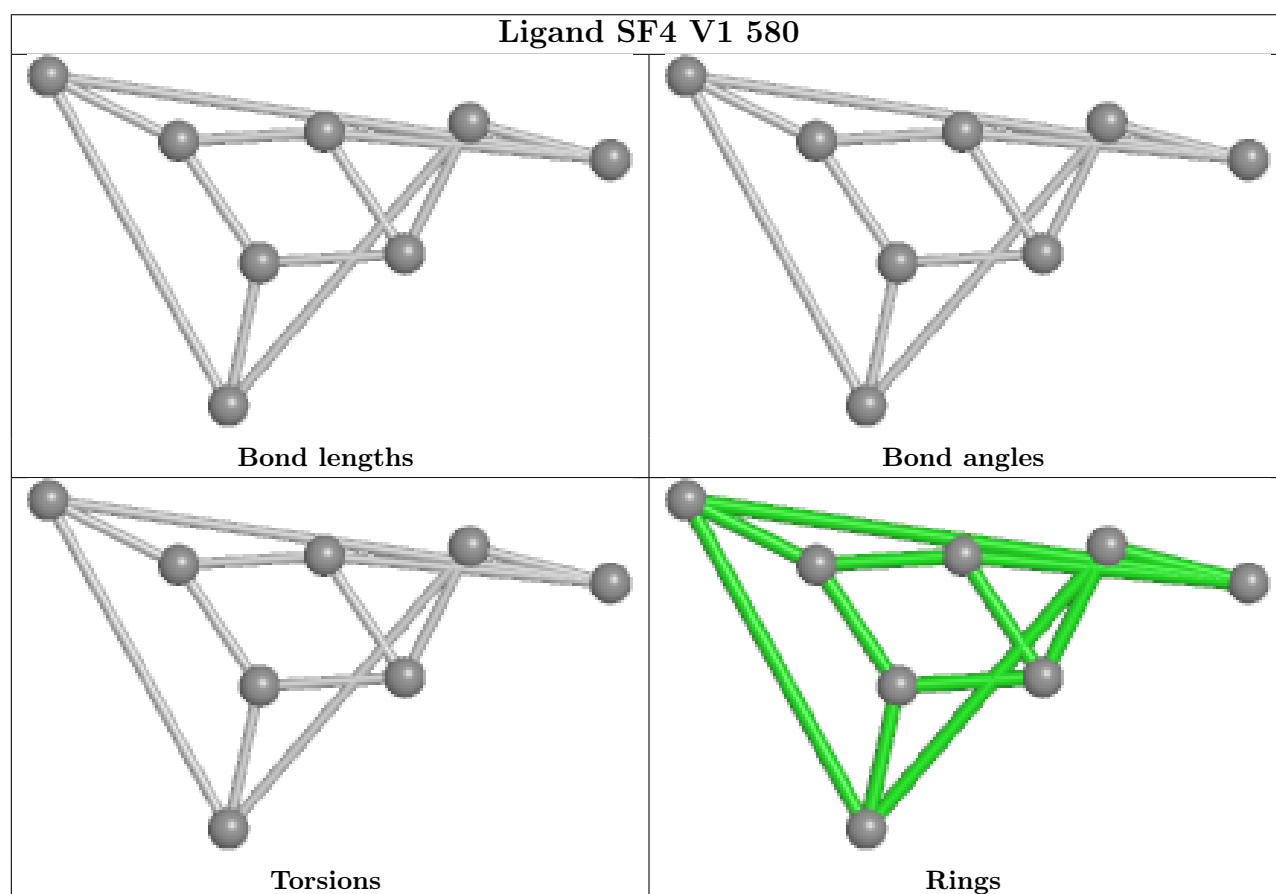
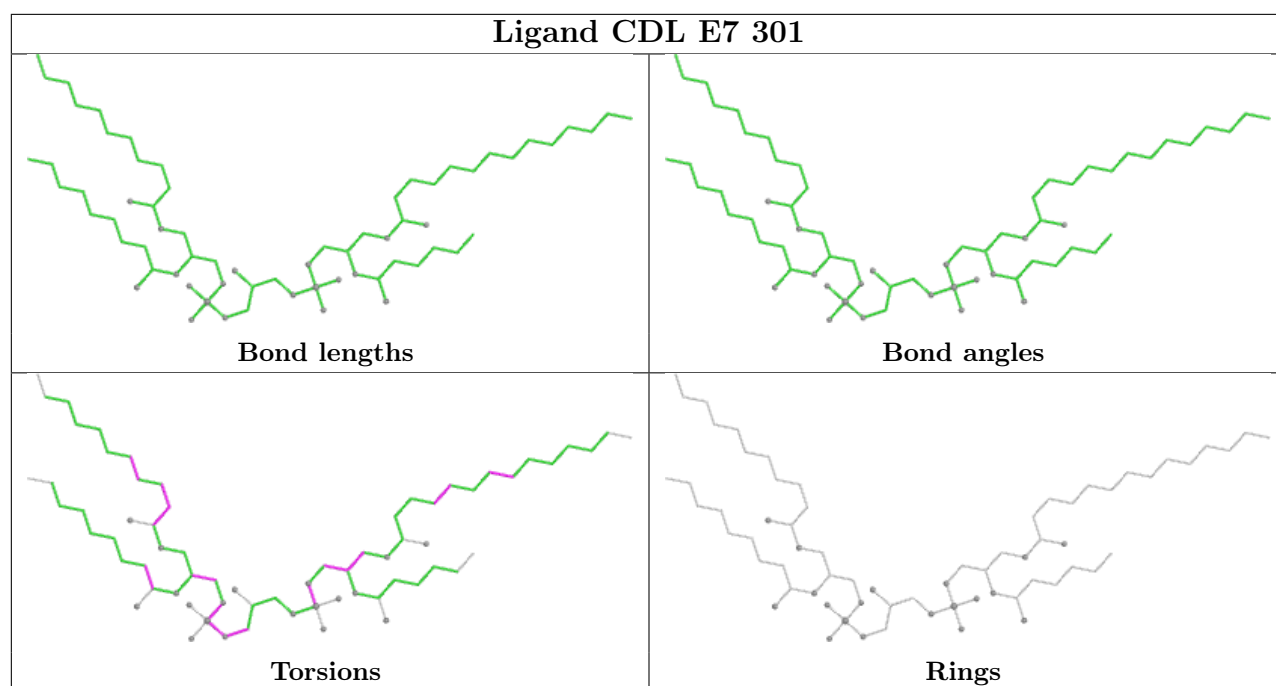




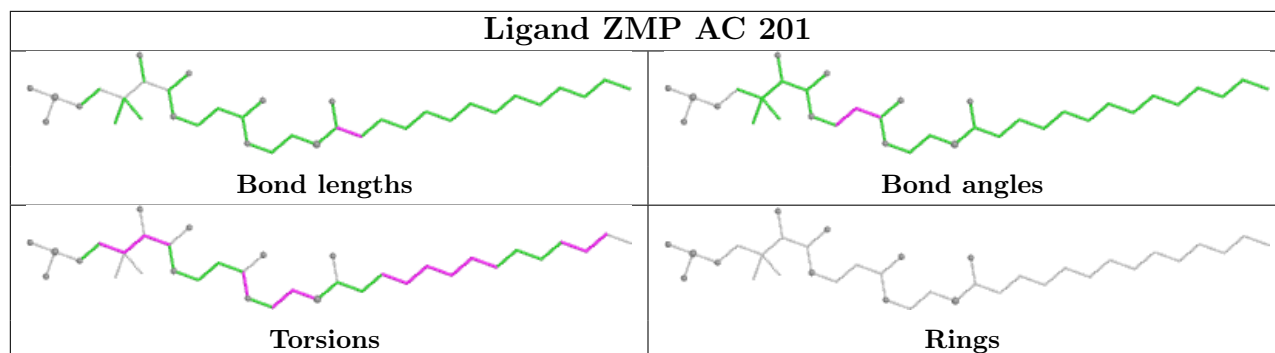




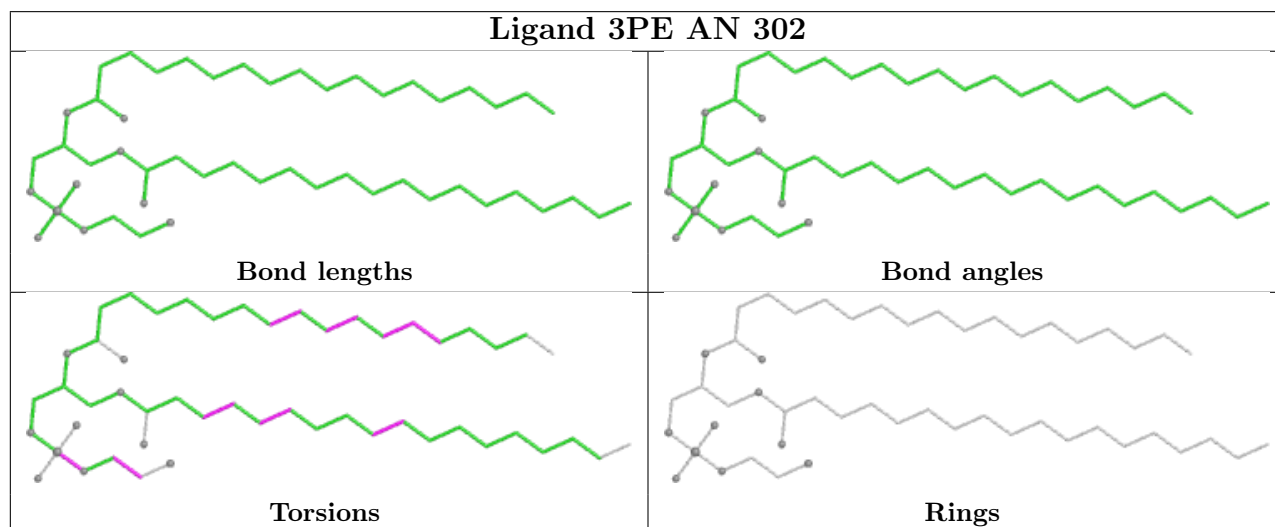




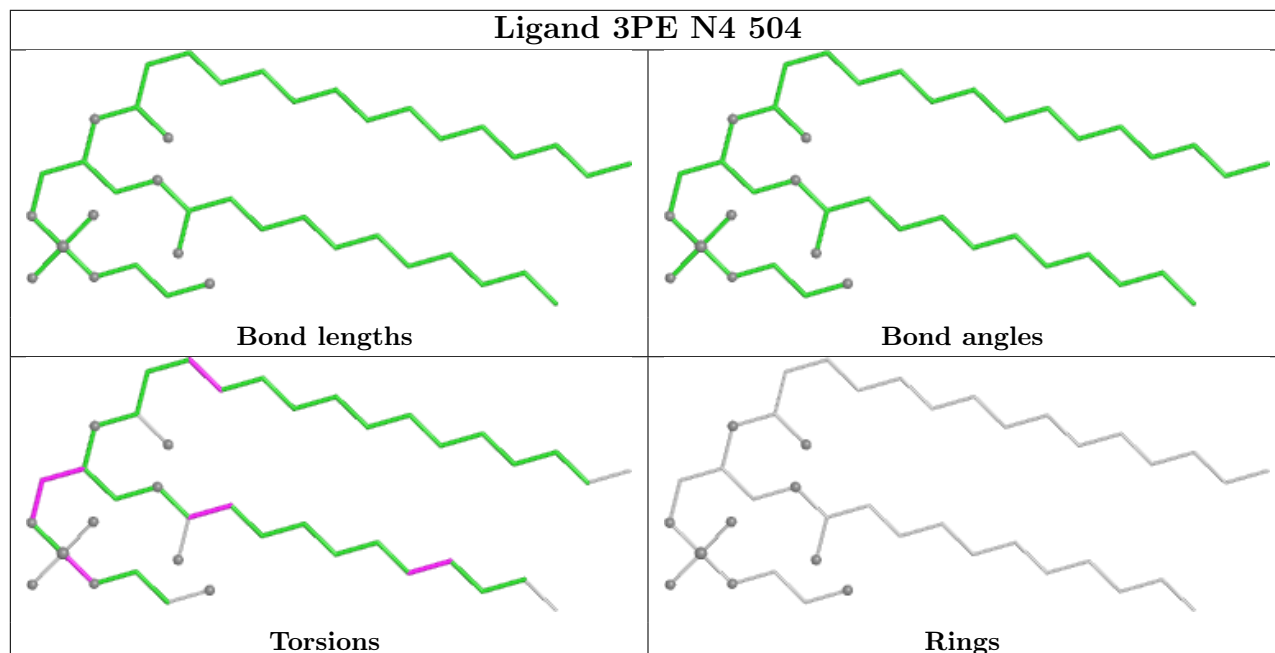
Ligand ZMP AC 201

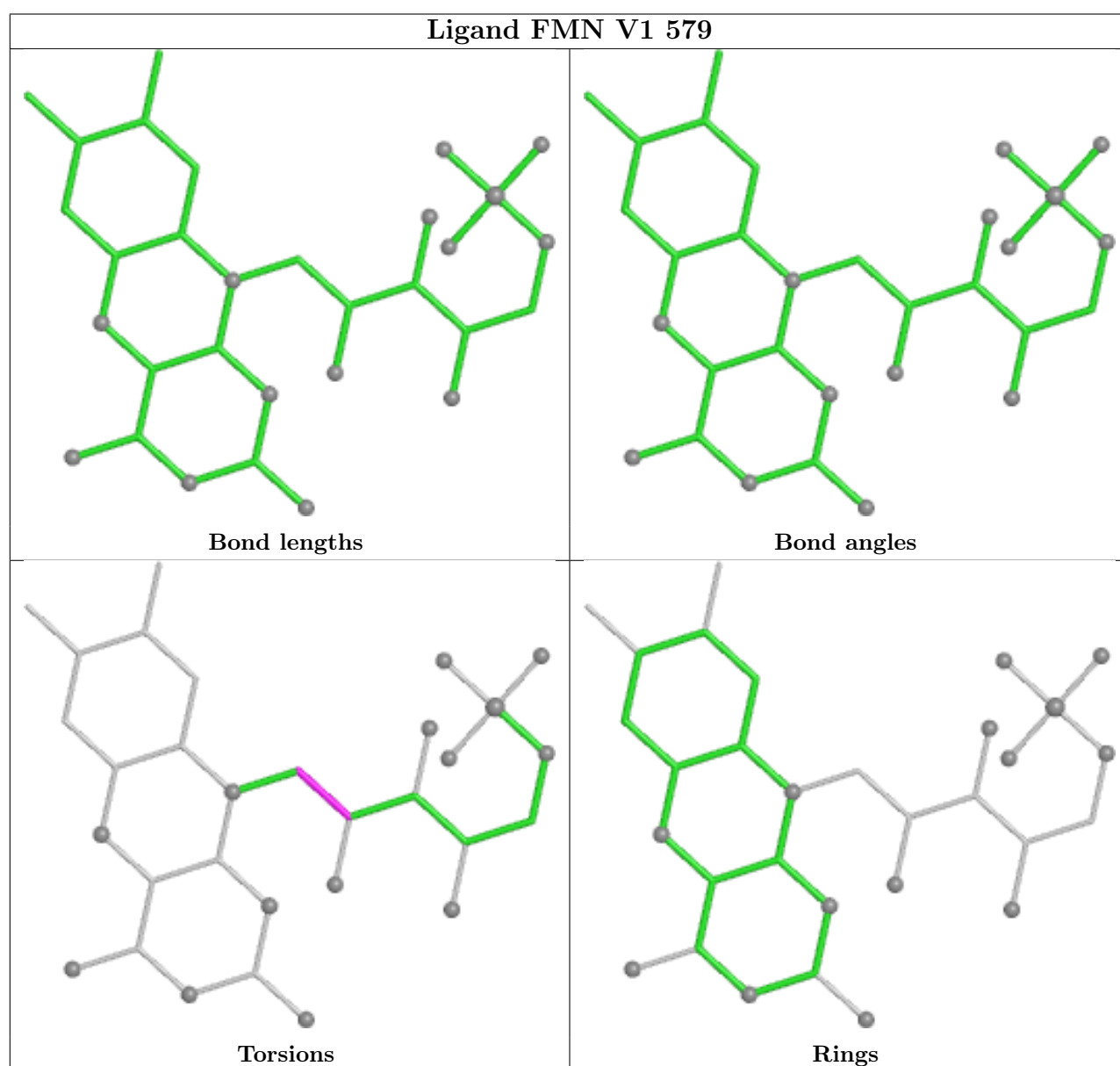
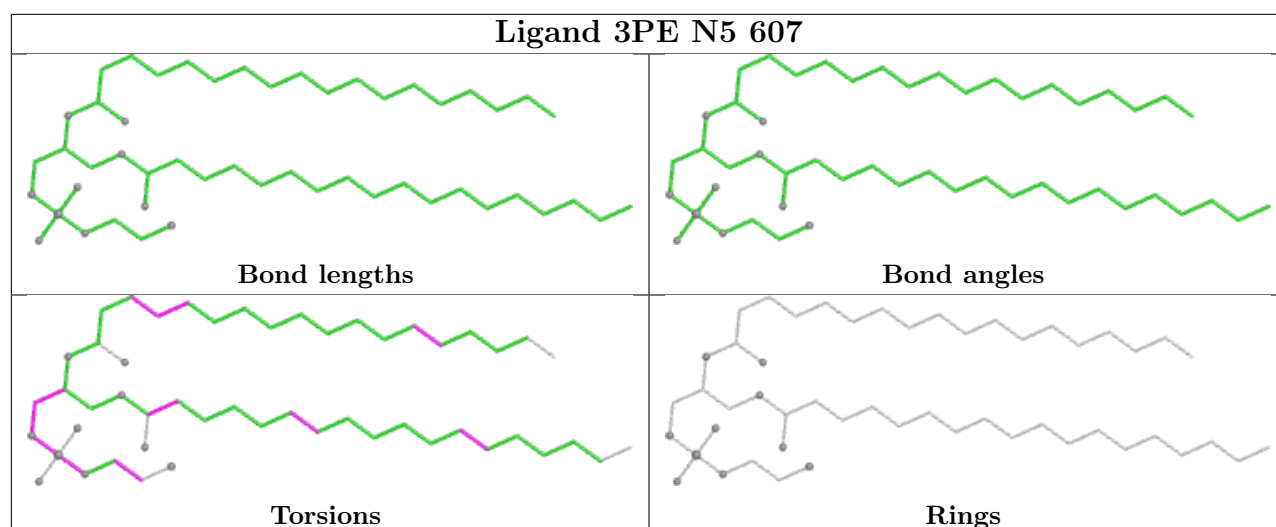


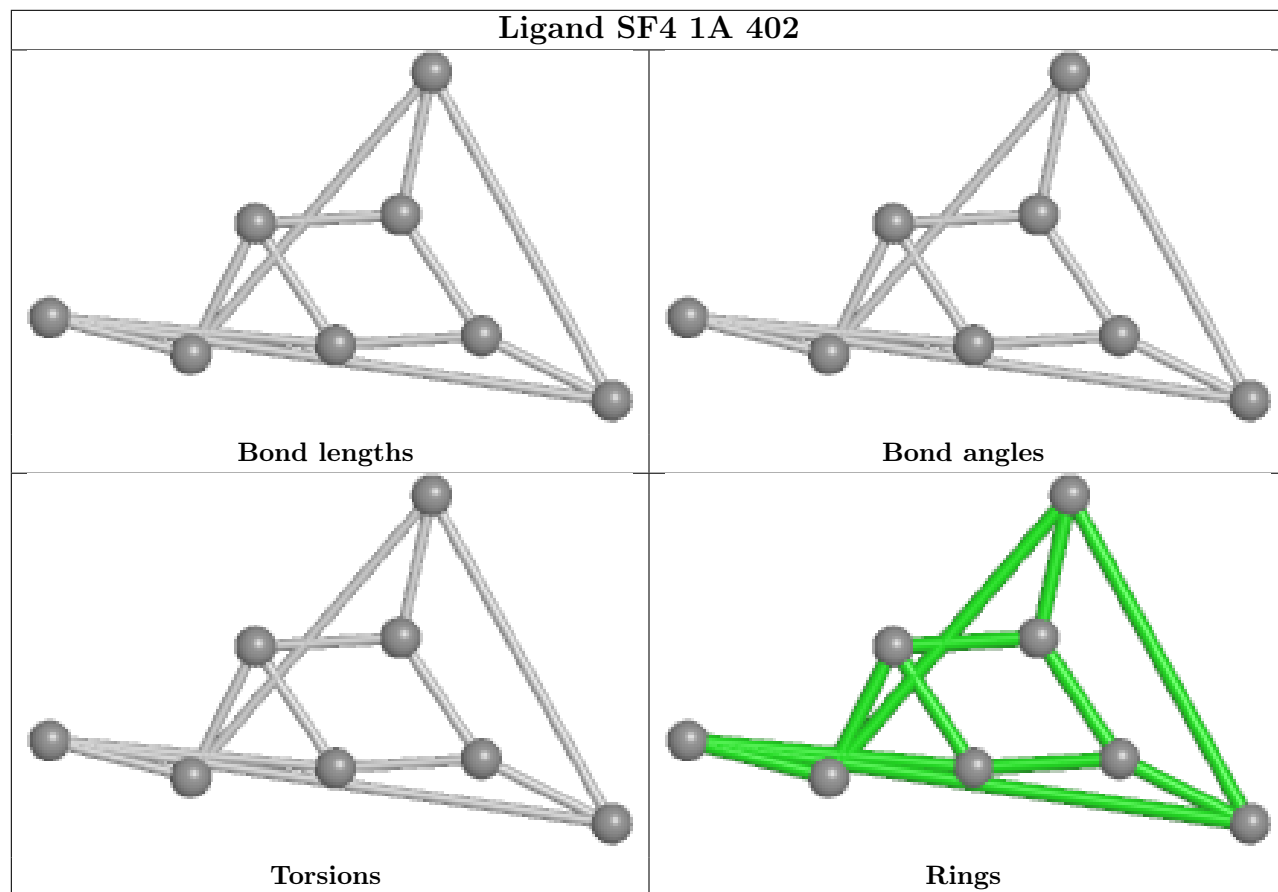
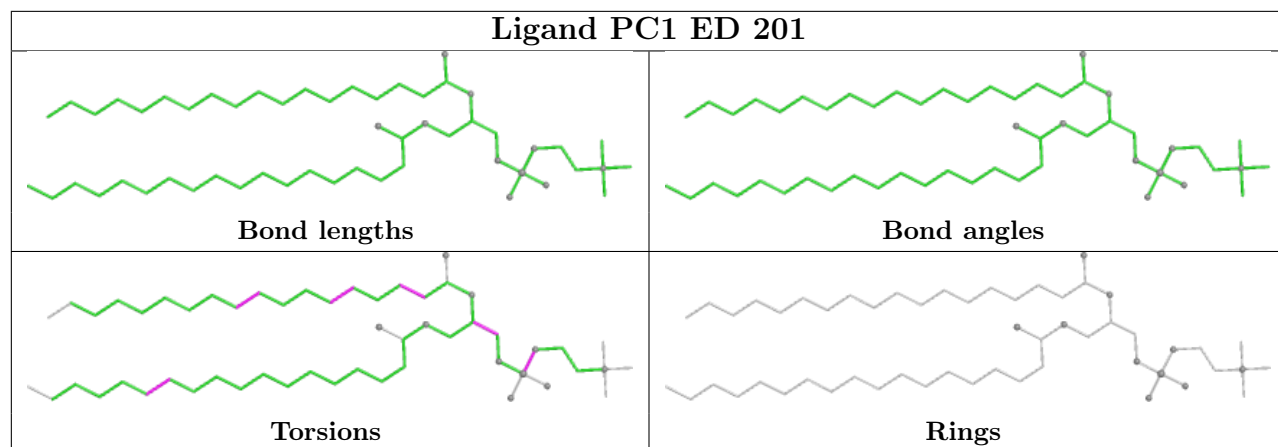
Ligand 3PE AN 302

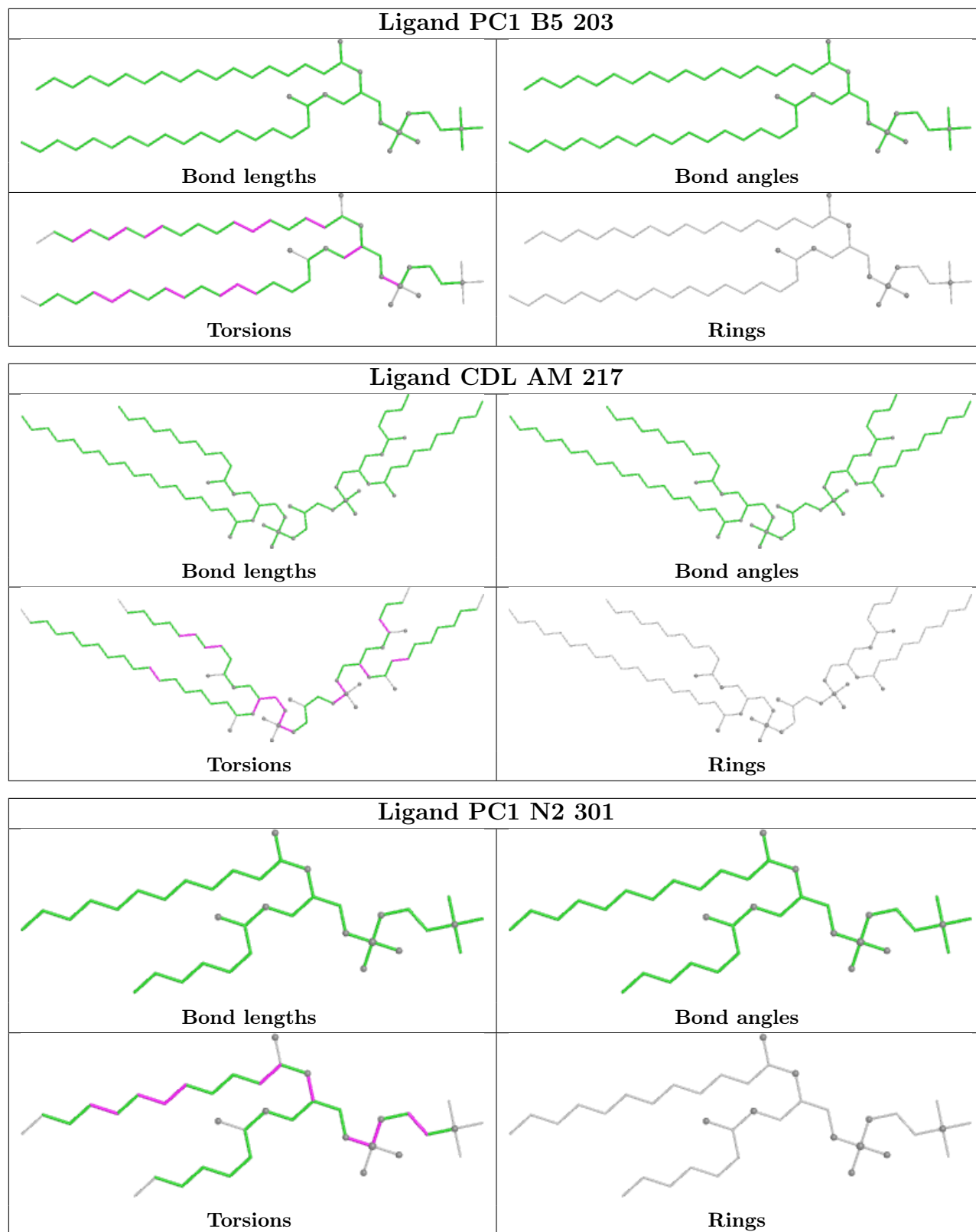


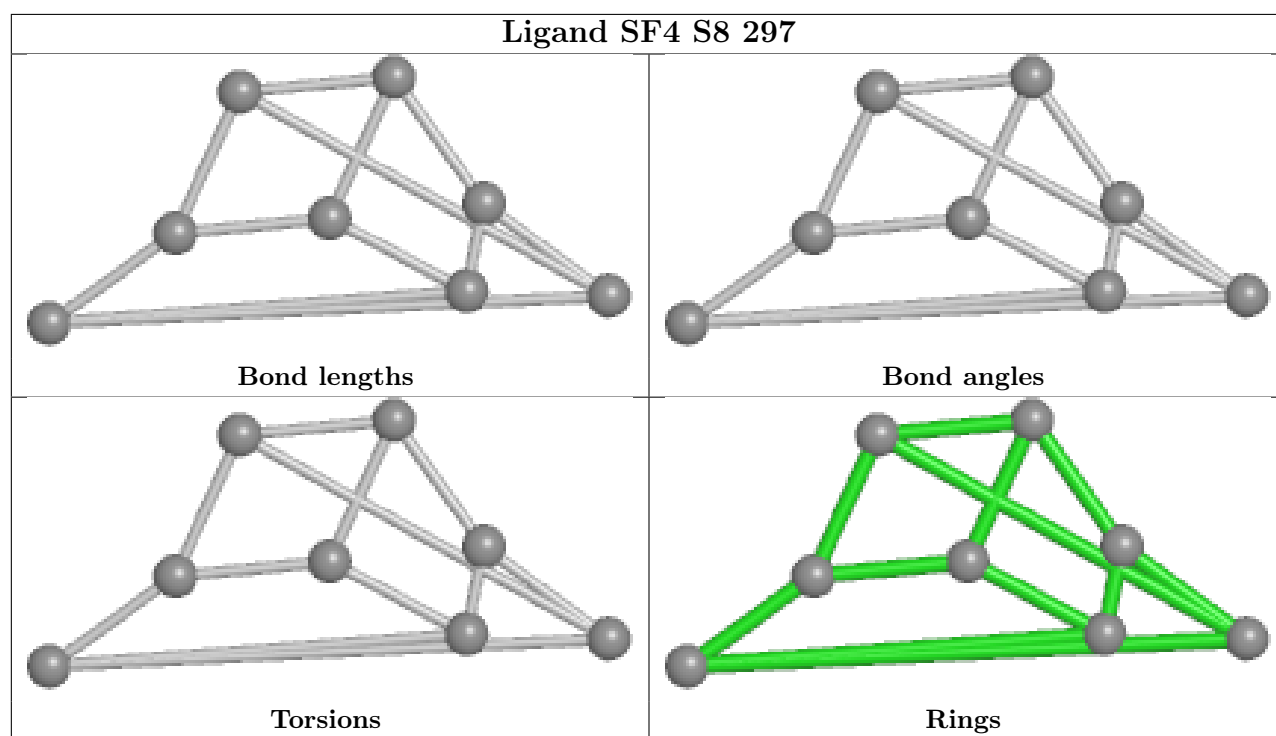
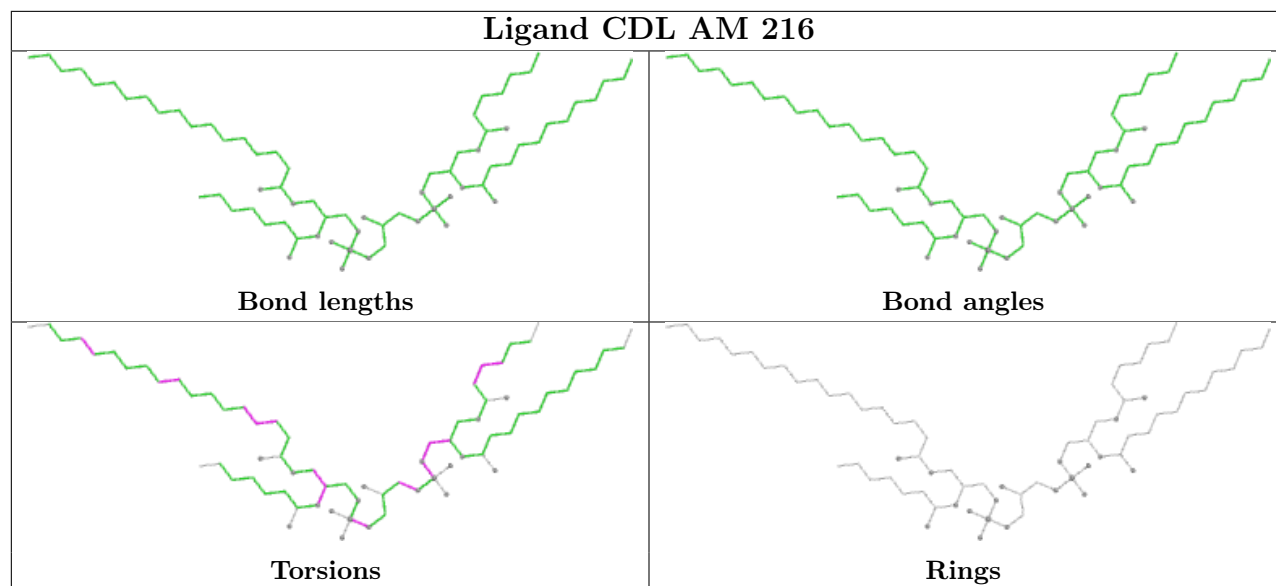
Ligand 3PE N4 504

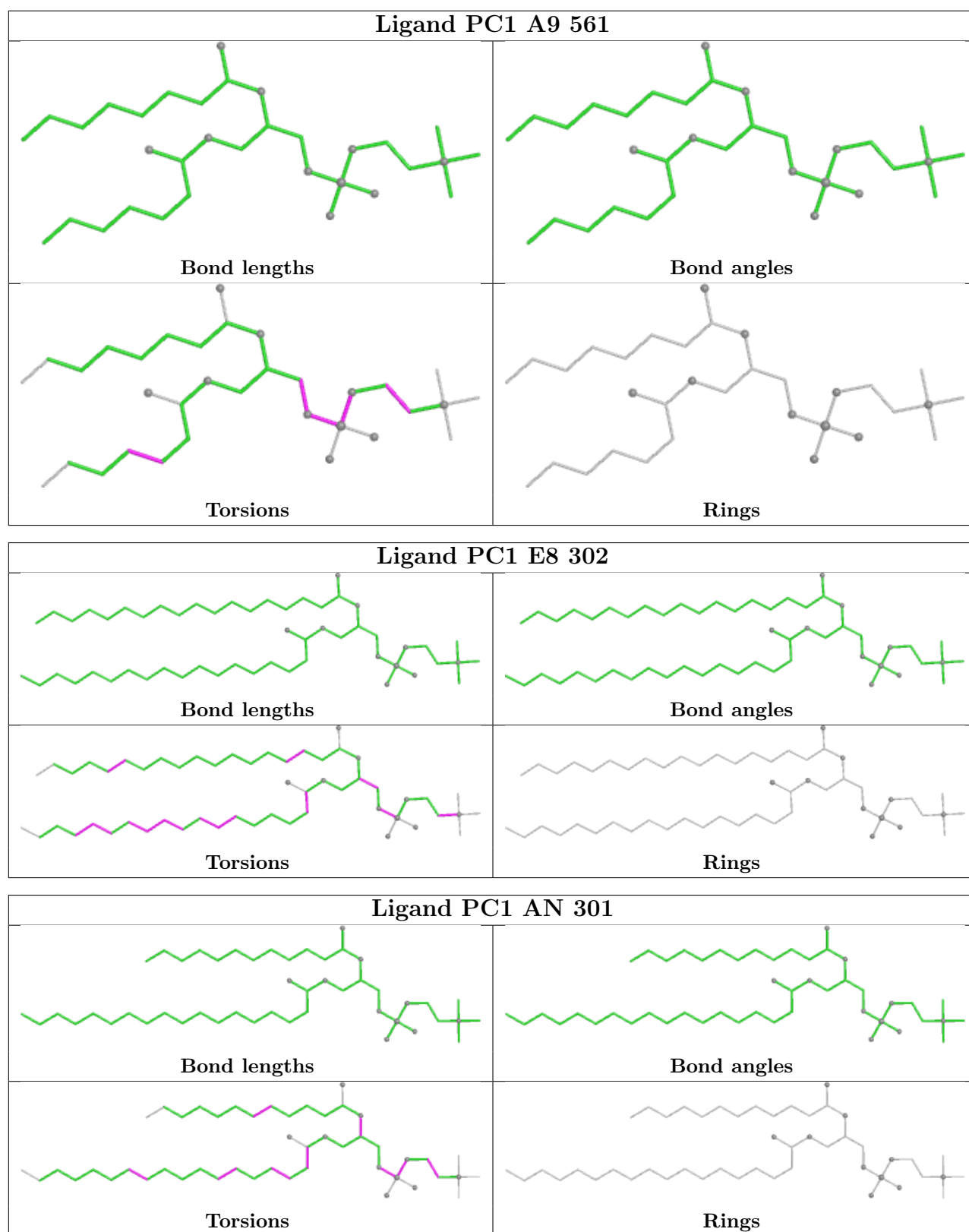


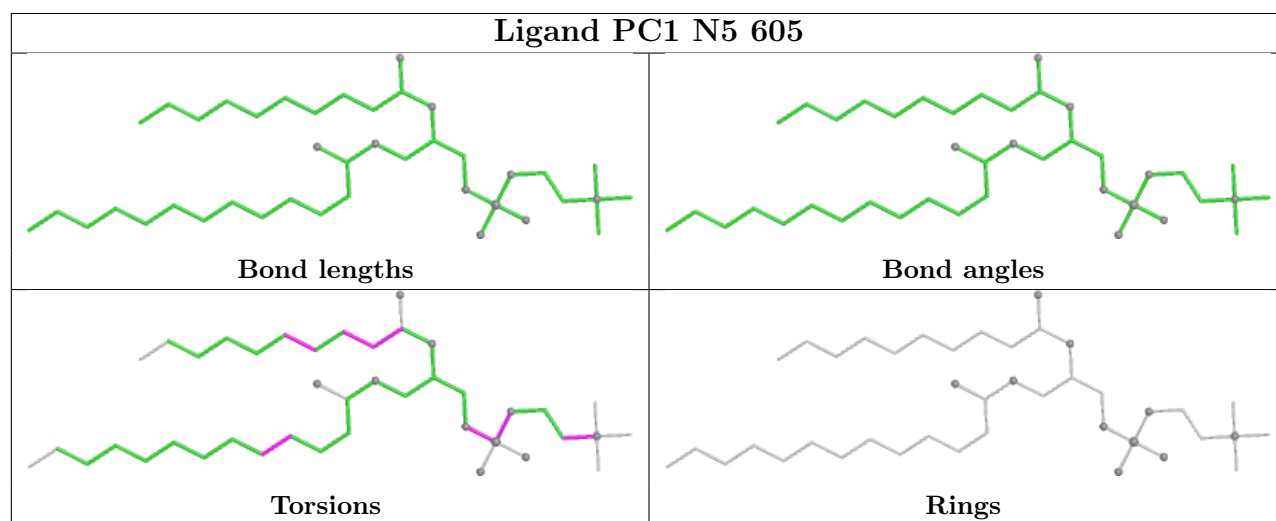
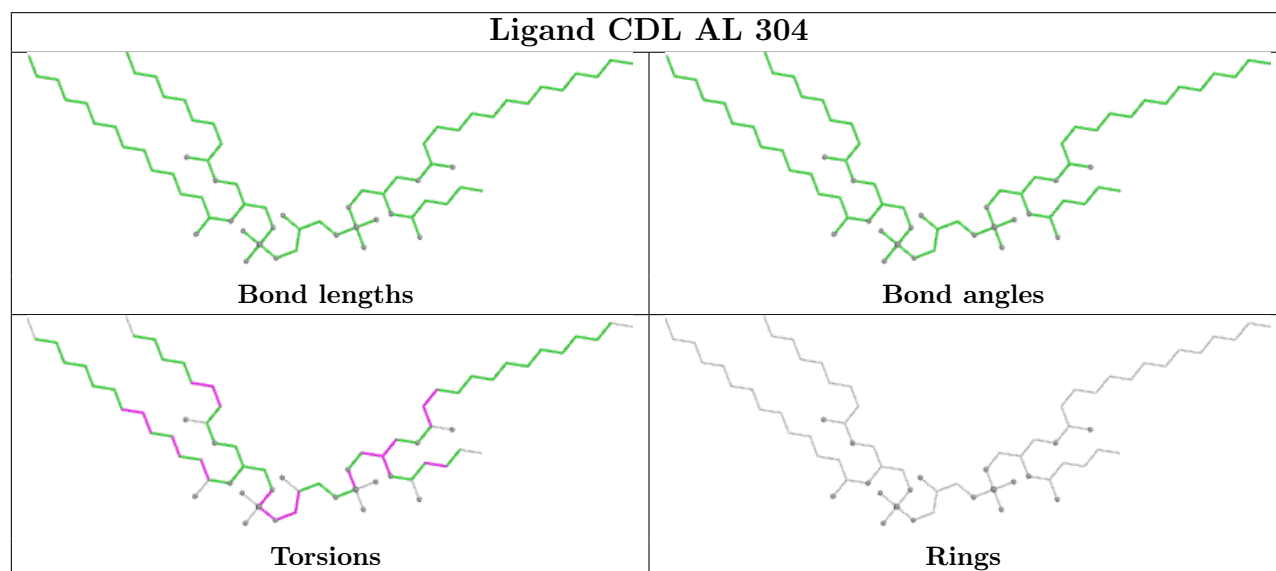
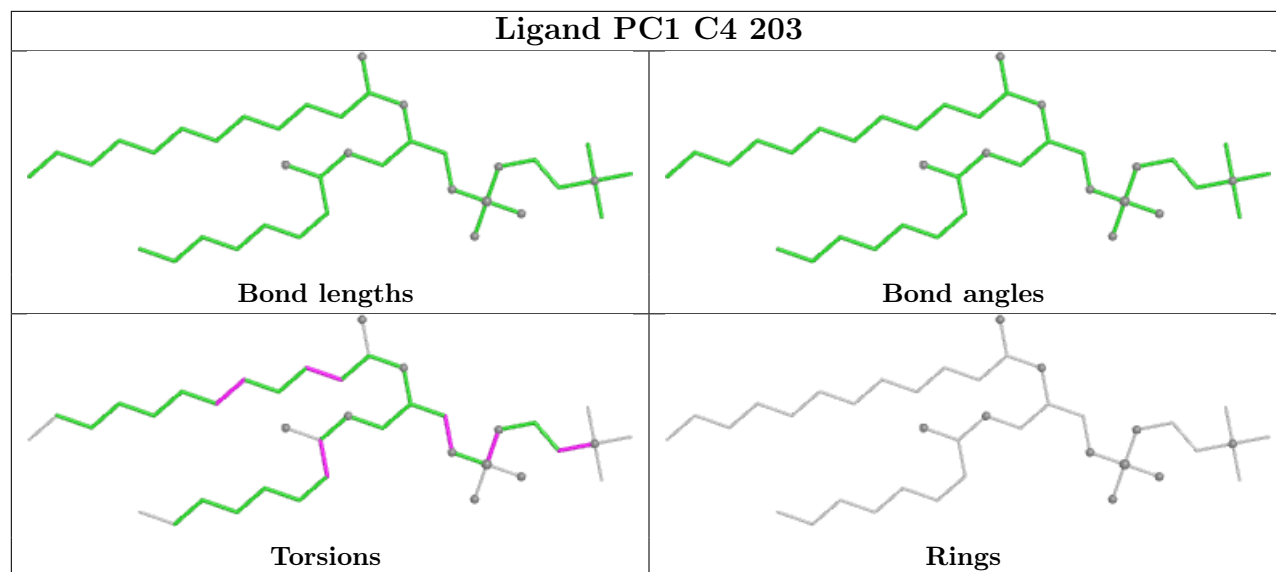


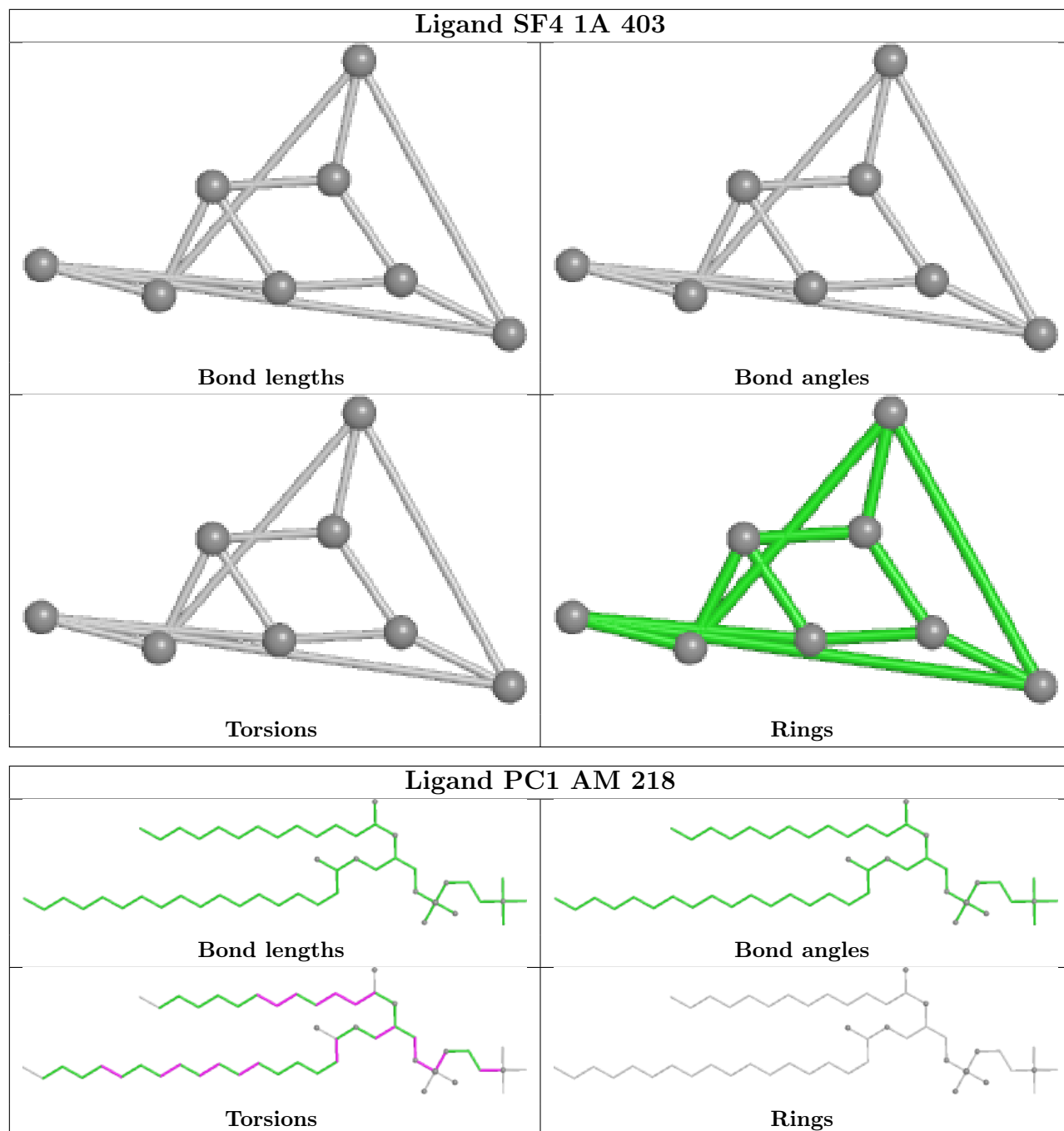


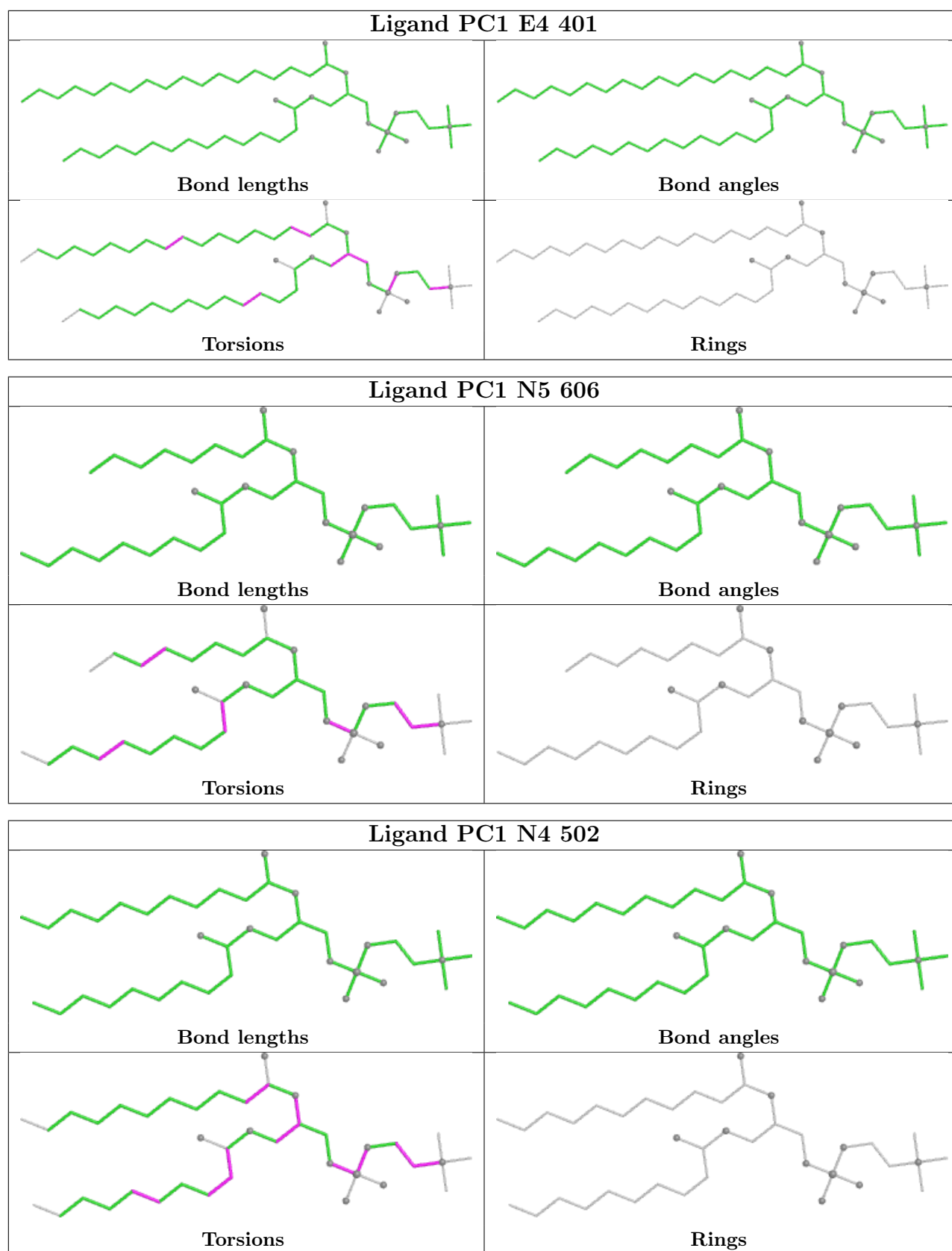


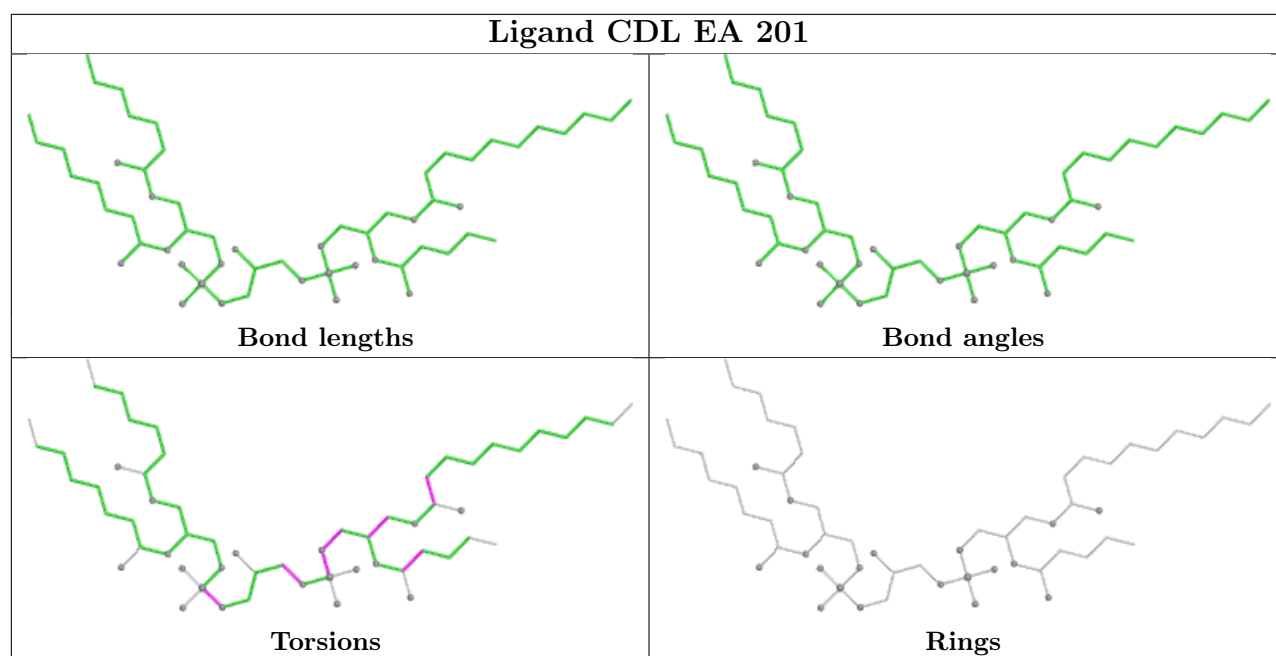












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

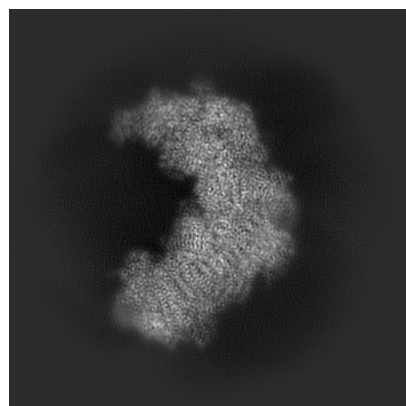
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36107. These allow visual inspection of the internal detail of the map and identification of artifacts.

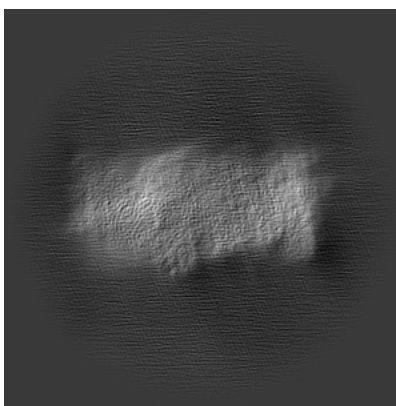
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

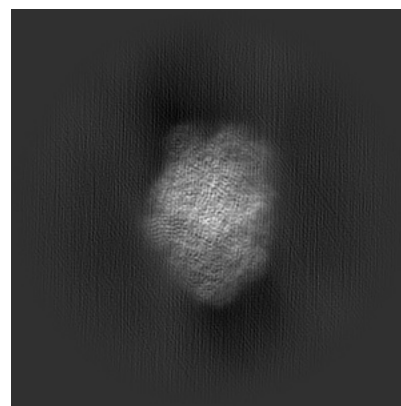
6.1.1 Primary map



X

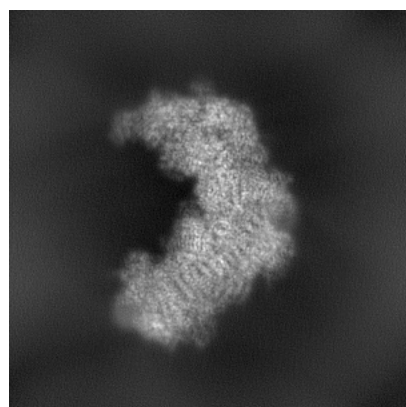


Y

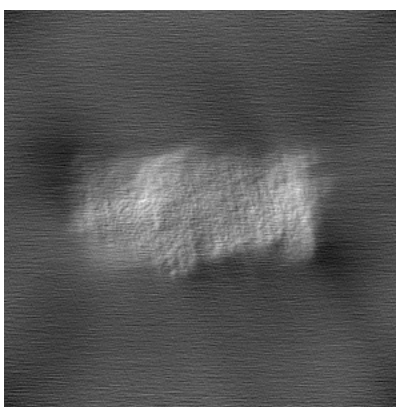


Z

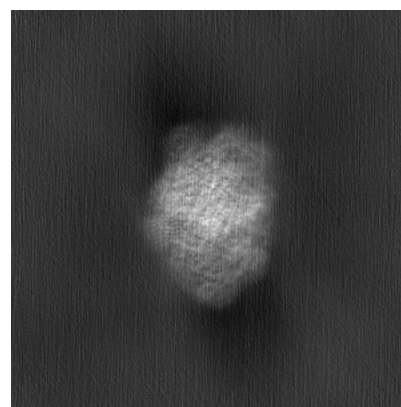
6.1.2 Raw map



X



Y

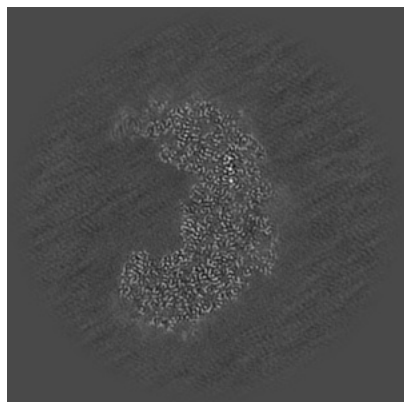


Z

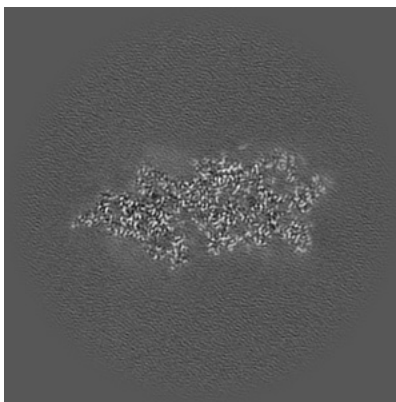
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

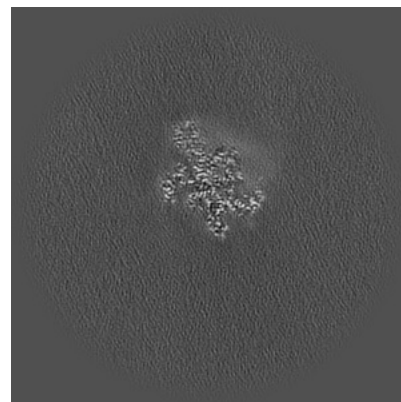
6.2.1 Primary map



X Index: 240



Y Index: 240

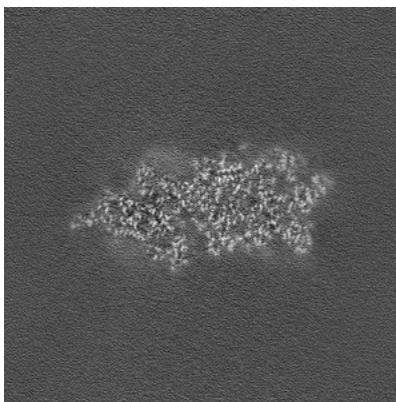


Z Index: 240

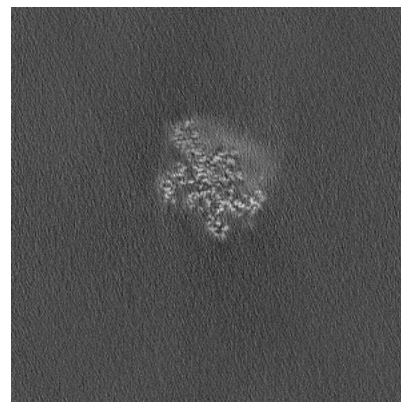
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

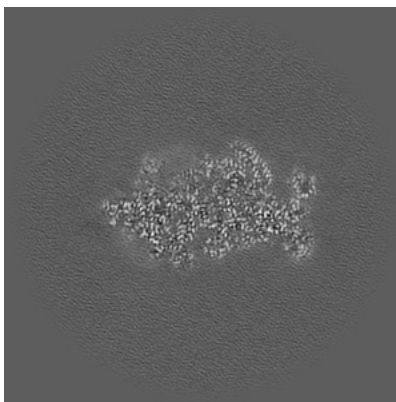
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

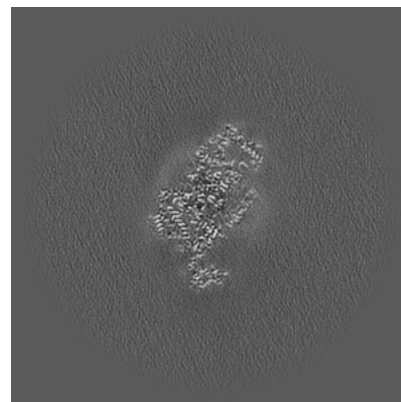
6.3.1 Primary map



X Index: 241



Y Index: 255

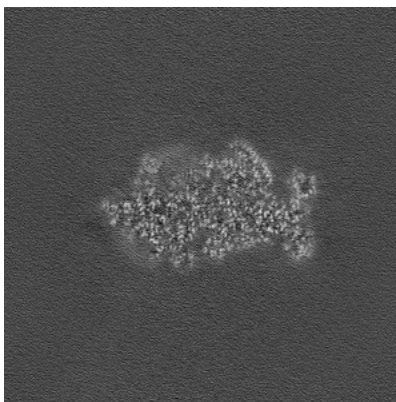


Z Index: 183

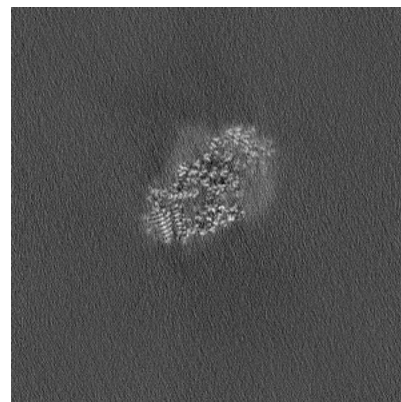
6.3.2 Raw map



X Index: 243



Y Index: 255

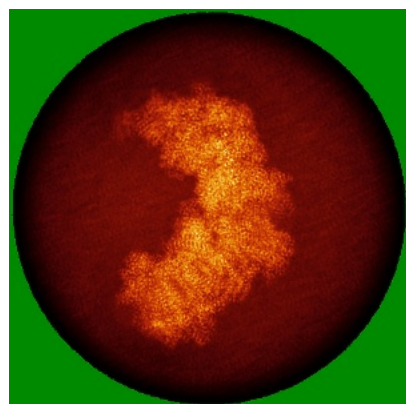


Z Index: 210

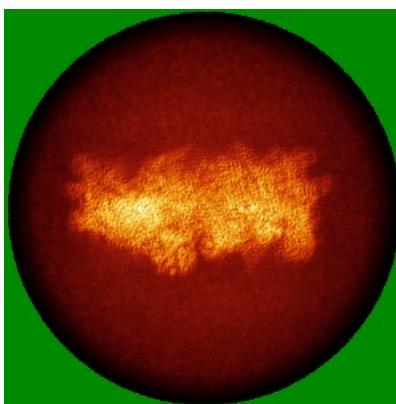
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

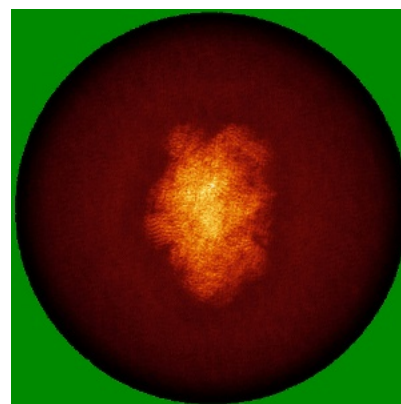
6.4.1 Primary map



X

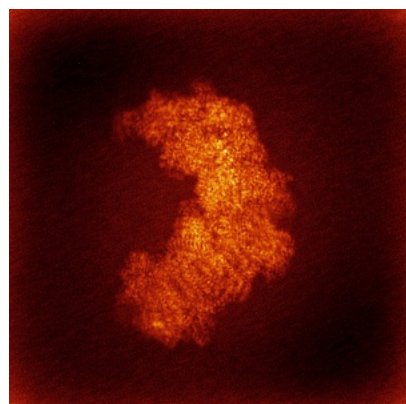


Y

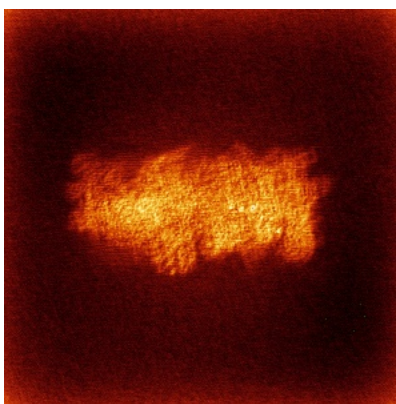


Z

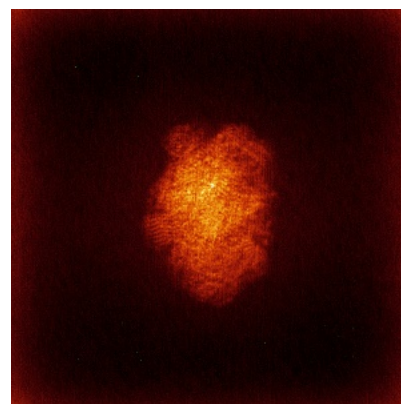
6.4.2 Raw map



X



Y

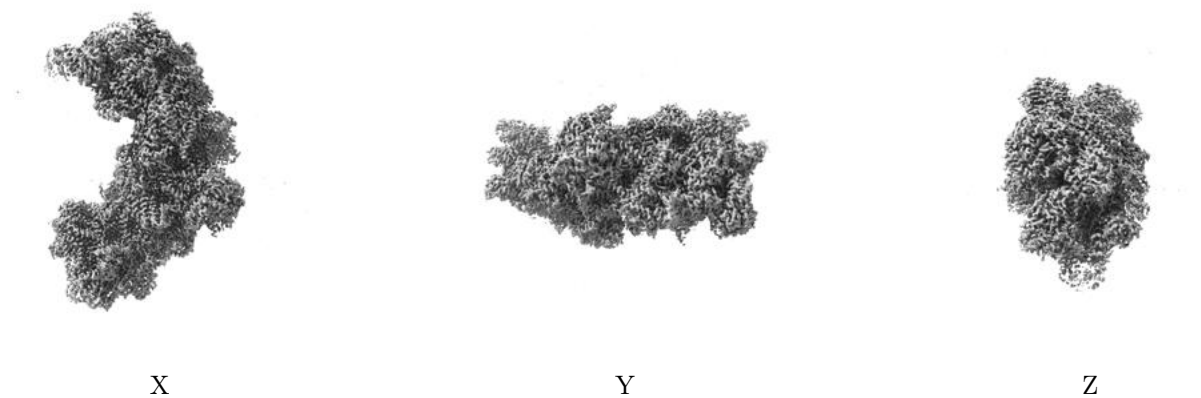


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

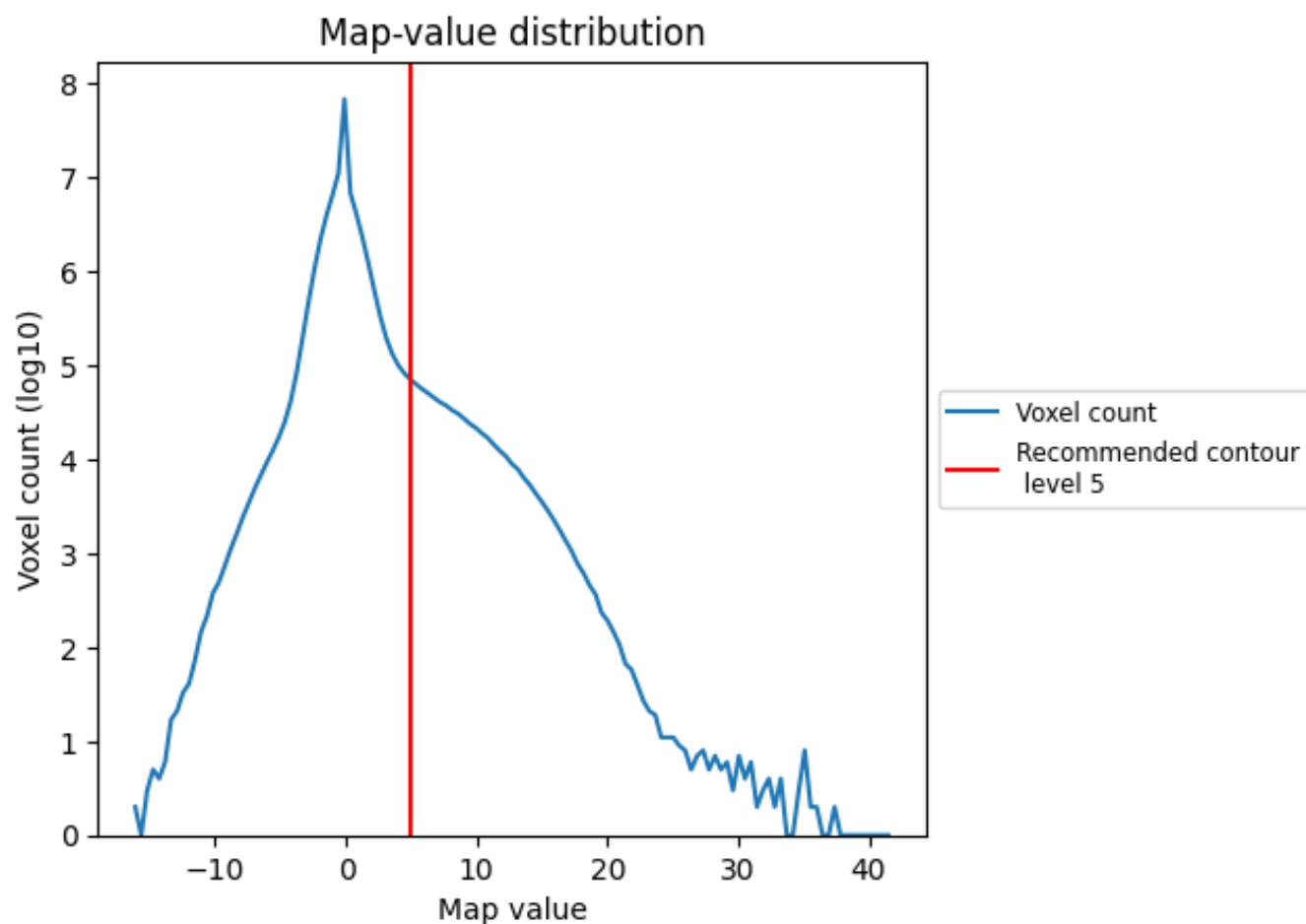
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

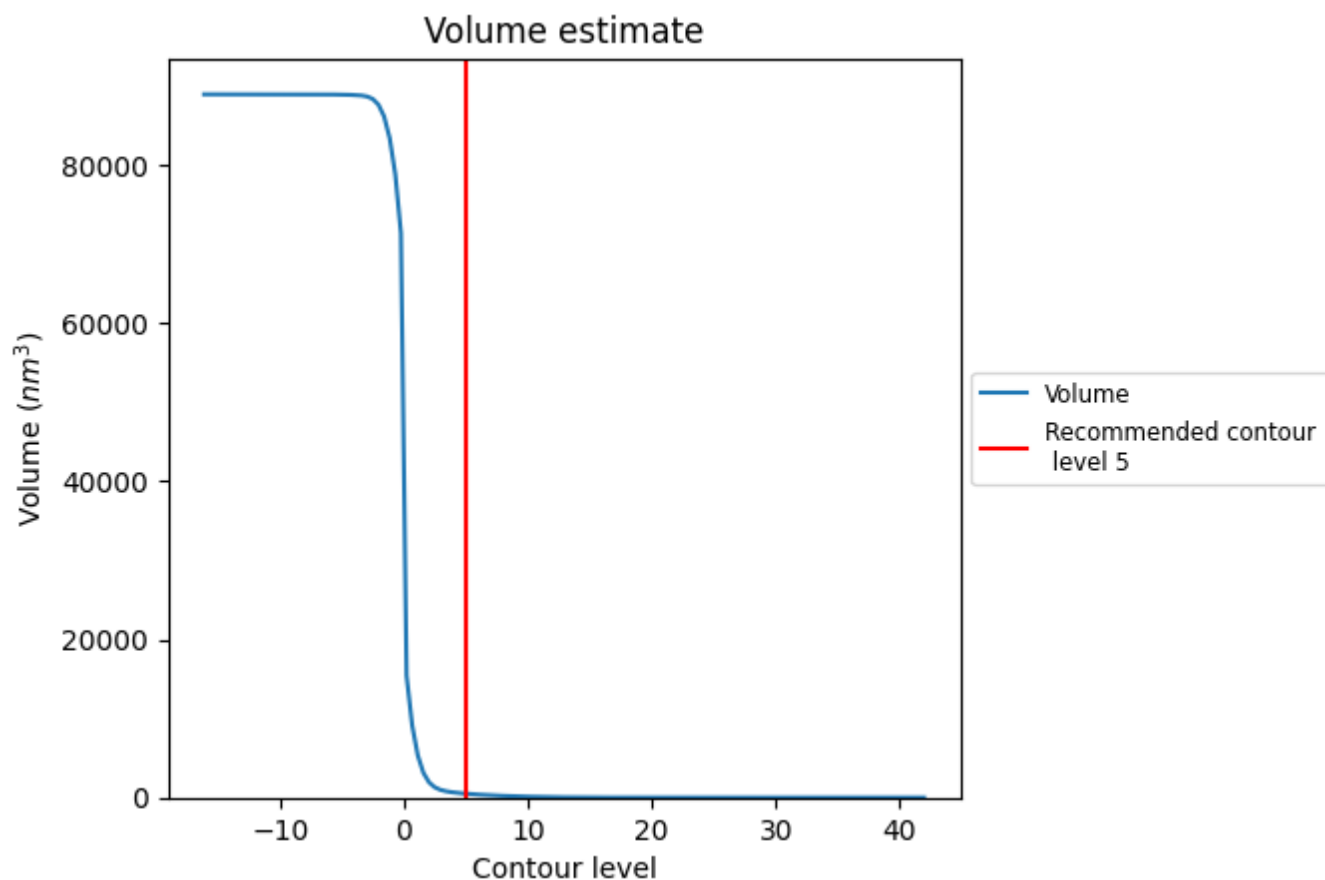
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

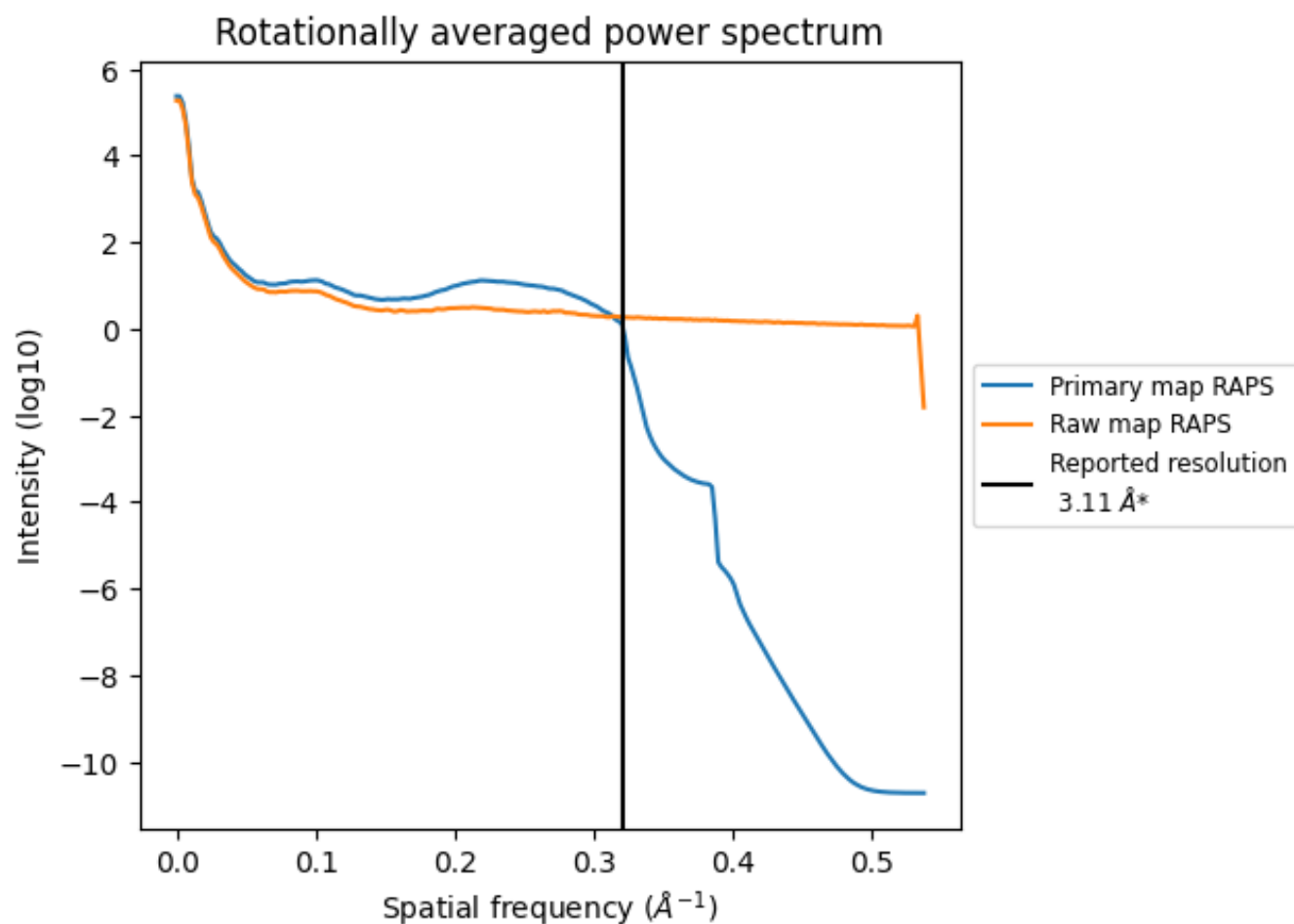
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 492 nm^3 ; this corresponds to an approximate mass of 445 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

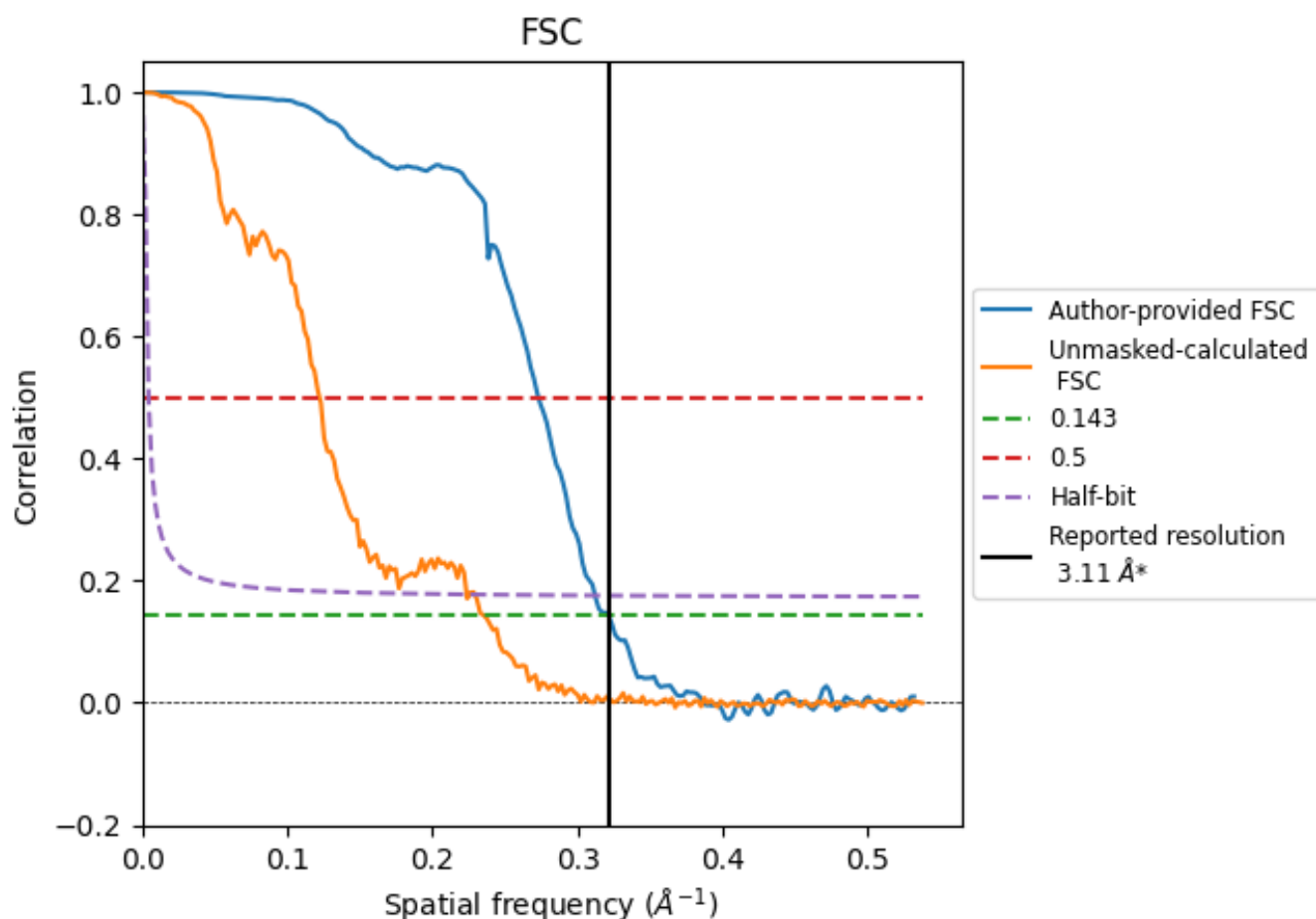


*Reported resolution corresponds to spatial frequency of 0.322 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.322 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

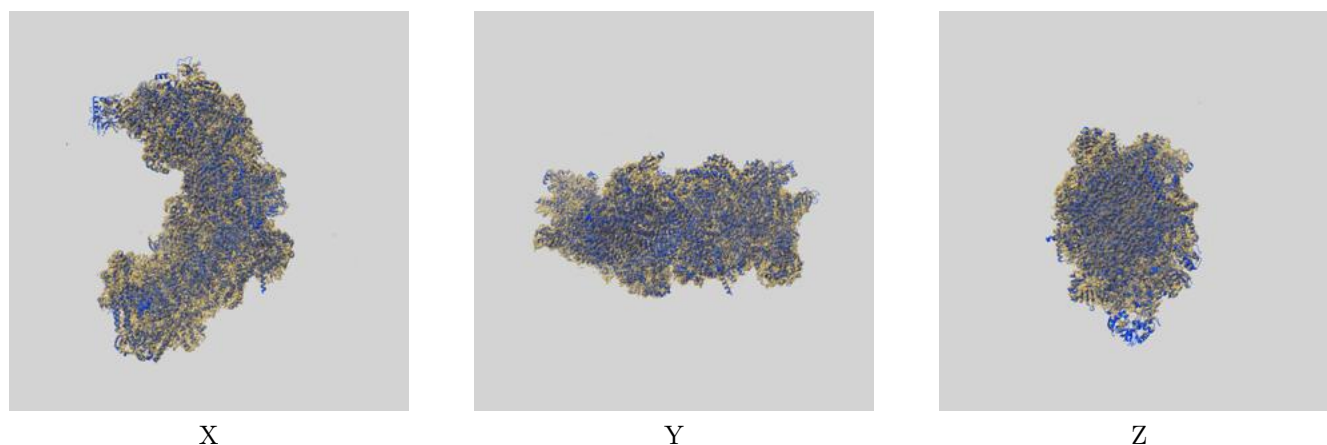
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.11	-	-
Author-provided FSC curve	3.11	3.66	3.20
Unmasked-calculated*	4.25	8.18	4.47

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.25 differs from the reported value 3.11 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36107 and PDB model 8J9H. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

9.1 Map-model overlay [i](#)



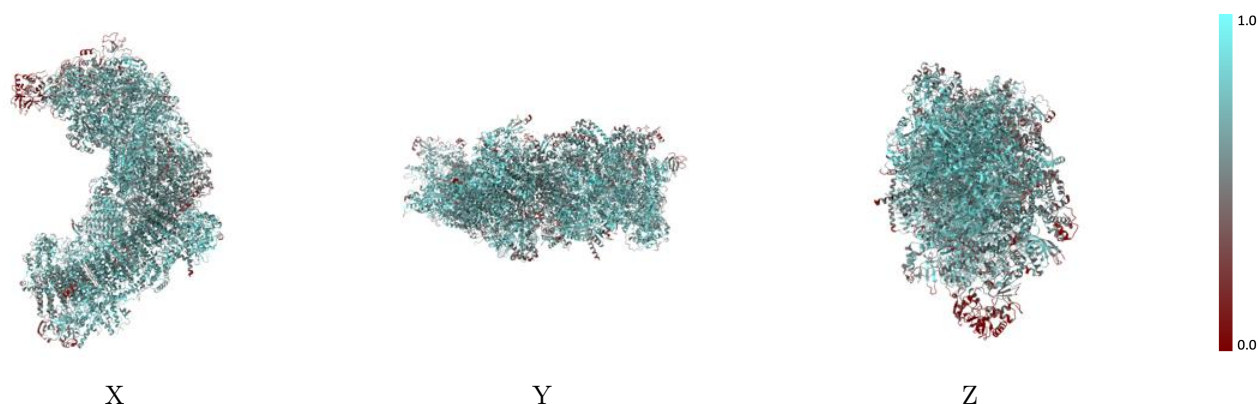
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



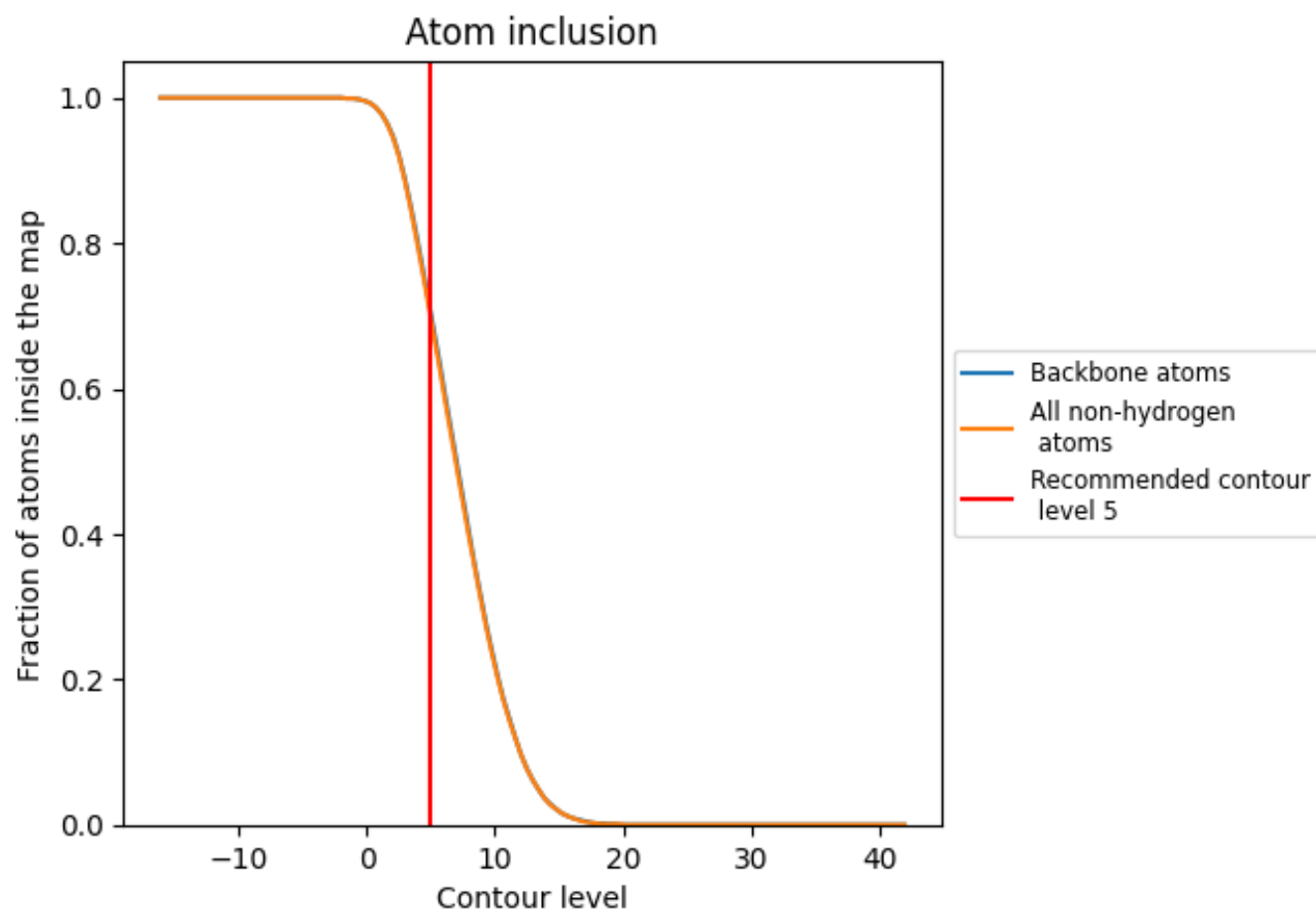
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6960	 0.5280
1A	 0.7610	 0.5470
1B	 0.7450	 0.5450
2B	 0.7580	 0.5480
4L	 0.7770	 0.5510
A1	 0.6470	 0.5160
A2	 0.6960	 0.5400
A3	 0.7050	 0.5380
A5	 0.7070	 0.5210
A6	 0.6010	 0.5050
A7	 0.7700	 0.5480
A8	 0.7400	 0.5270
A9	 0.7160	 0.5320
AB	 0.6660	 0.5280
AC	 0.7030	 0.5440
AL	 0.6980	 0.5340
AM	 0.6620	 0.5160
AN	 0.6990	 0.5280
B2	 0.7240	 0.5380
B3	 0.6950	 0.5310
B4	 0.7480	 0.5450
B5	 0.7350	 0.5270
B6	 0.7300	 0.5370
B7	 0.7620	 0.5290
B8	 0.7890	 0.5470
B9	 0.7620	 0.5520
BL	 0.7490	 0.5370
BM	 0.7280	 0.5400
C4	 0.6920	 0.5320
E1	 0.6710	 0.5130
E2	 0.6260	 0.5010
E3	 0.6040	 0.5050
E4	 0.6490	 0.5310
E5	 0.2050	 0.3270
E6	 0.6120	 0.5020



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Chain	Atom inclusion	Q-score
E7	 0.5100	 0.4620
E8	 0.6260	 0.5000
EA	 0.7720	 0.5550
EB	 0.7180	 0.5230
EC	 0.5870	 0.5080
ED	 0.6320	 0.5100
FX	 0.7710	 0.5550
G1	 0.7410	 0.5510
G2	 0.6850	 0.5280
G3	 0.7170	 0.5330
N1	 0.7090	 0.5360
N2	 0.7710	 0.5510
N3	 0.6980	 0.5420
N4	 0.7570	 0.5410
N5	 0.7310	 0.5320
N6	 0.6690	 0.5210
S2	 0.7950	 0.5550
S3	 0.7990	 0.5530
S4	 0.7350	 0.5510
S5	 0.7240	 0.5220
S6	 0.7780	 0.5520
S7	 0.7600	 0.5480
S8	 0.7980	 0.5540
U1	 0.5170	 0.4690
U2	 0.6170	 0.5230
V1	 0.7360	 0.5310
V2	 0.7490	 0.5310