



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 12:06 AM UTC

PDB ID : 7R42 / pdb_00007r42
EMDB ID : EMD-14256
Title : Bovine complex I in the presence of IM1761092, active class ii (Composite map)
Authors : Bridges, H.R.; Blaza, J.N.; Yin, Z.; Chung, I.; Hirst, J.
Deposited on : 2022-02-08
Resolution : 2.30 Å(reported)

This is a wwPDB EM Validation Summary 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:

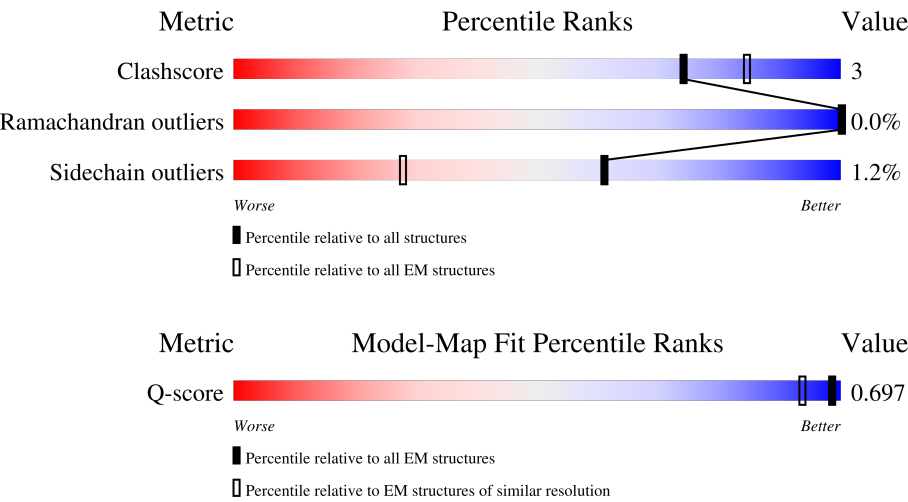
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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.



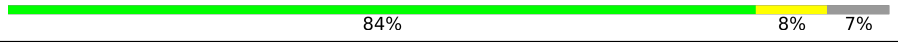
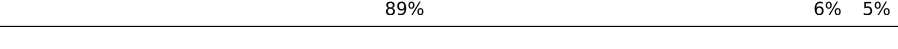
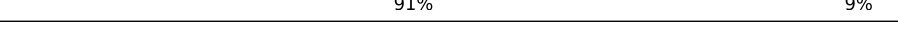
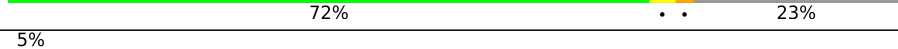
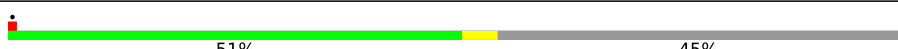
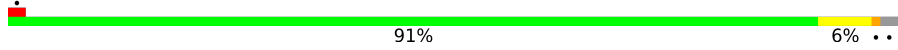
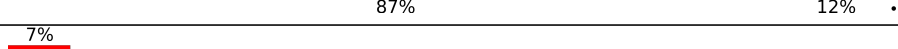
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4254 (1.80 - 2.80)

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	A	115	
2	B	216	
3	C	266	
4	D	463	

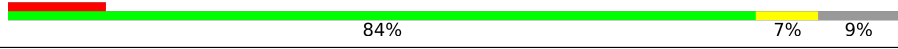
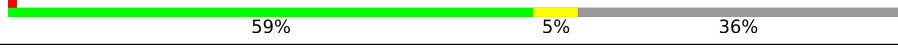
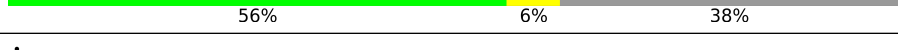
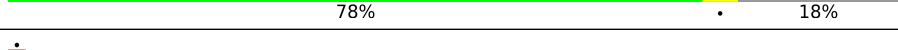
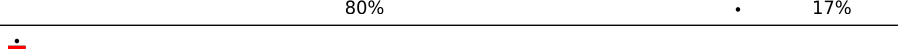
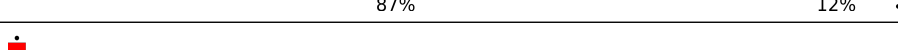
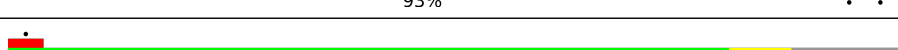
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Mol	Chain	Length	Quality of chain
5	E	249	
6	F	464	
7	G	727	
8	H	318	
9	I	212	
10	J	175	
11	K	98	
12	L	606	
13	M	459	
14	N	347	
15	O	343	
16	P	380	
17	Q	175	
18	R	124	
19	S	99	
20	T	156	
20	U	156	
21	V	116	
22	W	128	
23	X	172	
24	Y	141	
25	Z	144	
26	a	70	
27	b	84	
28	c	76	

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Mol	Chain	Length	Quality of chain
29	d	120	
30	e	106	
31	f	57	
32	g	154	
33	h	189	
34	i	127	
35	j	108	
36	k	98	
37	l	186	
38	m	129	
39	n	179	
40	o	137	
41	p	176	
42	q	145	
43	r	113	
44	s	109	

2 Entry composition [i](#)

There are 60 unique types of molecules in this entry. The entry contains 69480 atoms, of which 0 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 NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	115	Total	C	N	O	S	0	0
			921	622	133	159	7		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	155	Total	C	N	O	S	0	0
			1241	792	224	211	14		

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	207	Total	C	N	O	S	0	0
			1721	1111	296	311	3		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	430	Total	C	N	O	S	0	0
			3459	2209	596	629	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	129	ARG	GLN	variant	UNP P17694

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	213	Total	C	N	O	S	0	0
			1655	1057	277	311	10		

- Molecule 6 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	431	Total	C	N	O	S	0	0
			3319	2091	593	615	20		

- Molecule 7 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	688	Total	C	N	O	S	0	0
			5279	3307	920	1013	39		

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	318	Total	C	N	O	S	0	0
			2509	1681	385	420	23		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	176	Total	C	N	O	S	0	0
			1414	889	243	270	12		

- Molecule 10 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	174	Total	C	N	O	S	0	0
			1337	902	189	234	12		

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	98	Total	C	N	O	S	0	0
			745	486	112	131	16		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	606	Total	C	N	O	S	0	0
			4780	3178	735	824	43		

- Molecule 13 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	459	Total	C	N	O	S	0	0
			3654	2436	570	609	39		

- Molecule 14 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	347	Total	C	N	O	S	0	0
			2733	1817	416	457	43		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	320	Total	C	N	O	S	0	0
			2589	1662	429	488	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	255	LYS	ASN	variant	UNP P34942

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	341	Total	C	N	O	S	0	0
			2747	1777	486	479	5		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	125	Total	C	N	O	S	0	0
			1016	641	181	191	3		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	95	Total	C	N	O	S	0	0
			730	448	137	142	3		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	86	Total	C	N	O	S	0	0
			691	434	129	126	2		

- Molecule 20 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	76	Total	C	N	O	S	0	0
			612	393	90	124	5		
20	U	86	Total	C	N	O	S	0	0
			693	447	102	139	5		

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	114	Total	C	N	O	S	0	0
			923	597	156	167	3		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	114	Total	C	N	O	S	0	0
			971	622	180	165	4		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	171	Total	C	N	O	S	0	0
			1402	887	253	252	10		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	140	Total	C	N	O	S	0	0
			1030	657	176	191	6		

- Molecule 25 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	141	Total	C	N	O	S	0	0
			1152	740	201	202	9		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	70	Total	C	N	O	S	0	0
			569	365	104	95	5		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	83	Total	C	N	O	S	0	0
			651	425	109	115	2		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	c	48	Total	C	N	O	0	0
			405	268	69	68		

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	113	Total	C	N	O	S	0	0
			945	619	161	162	3		

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	97	Total	C	N	O	S	0	0
			819	518	156	139	6		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	52	Total	C	N	O	S	0	0
			451	296	79	75	1		

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	98	Total	C	N	O	S	0	0
			824	529	137	154	4		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	138	Total	C	N	O	S	0	0
			1154	759	196	197	2		

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	104	Total	C	N	O	S	0	0
			898	590	155	152	1		

- Molecule 35 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	67	Total	C	N	O	S	0	0
			580	381	95	103	1		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	80	Total	C	N	O	S	0	0
			644	421	108	113	2		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	155	Total	C	N	O	S	0	0
			1304	844	213	239	8		

- Molecule 38 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	127	Total	C	N	O	S	0	0
			1061	681	187	193			

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	172	Total	C	N	O	S	0	0
			1492	955	273	257	7		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	120	Total	C	N	O	S	0	0
			1035	645	199	183	8		

- Molecule 41 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	171	Total	C	N	O	S	0	0
			1443	904	266	265	8		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	145	Total	C	N	O	S	0	0
			1209	778	216	210	5		

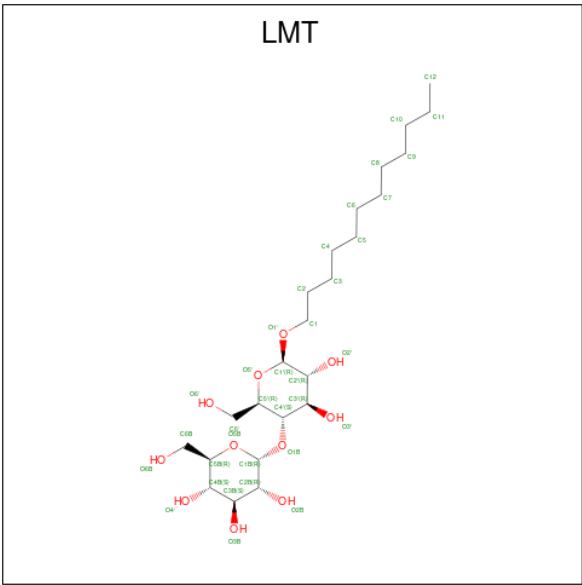
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	94	Total	C	N	O	S	0	0
			767	485	143	136	3		

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	44	Total	C	N	O	S	0	0
			371	233	66	71	1		

- Molecule 45 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



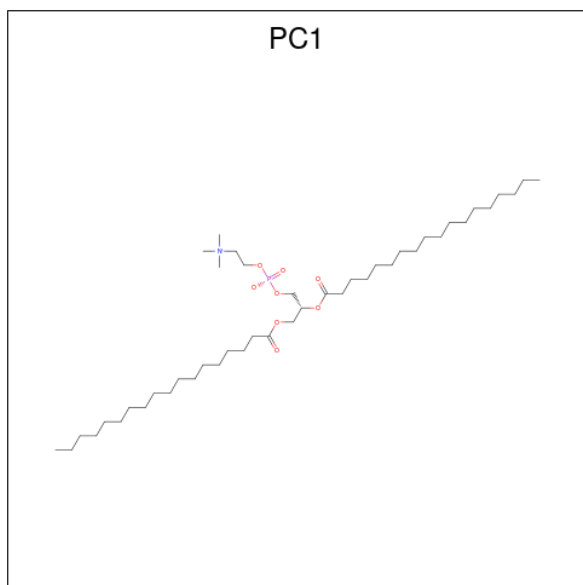
Mol	Chain	Residues	Atoms			AltConf
45	A	1	Total	C	O	0
			35	24	11	
45	A	1	Total	C	O	0
			35	24	11	
45	J	1	Total	C	O	0
			35	24	11	
45	K	1	Total	C	O	0
			35	24	11	
45	L	1	Total	C	O	0
			35	24	11	
45	L	1	Total	C	O	0
			35	24	11	
45	L	1	Total	C	O	0
			35	24	11	

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Mol	Chain	Residues	Atoms			AltConf
45	M	1	Total	C	O	0
			35	24	11	
45	M	1	Total	C	O	0
			35	24	11	
45	M	1	Total	C	O	0
			35	24	11	
45	Y	1	Total	C	O	0
			35	24	11	
45	Y	1	Total	C	O	0
			35	24	11	
45	Y	1	Total	C	O	0
			35	24	11	
45	b	1	Total	C	O	0
			35	24	11	
45	h	1	Total	C	O	0
			35	24	11	
45	j	1	Total	C	O	0
			35	24	11	
45	l	1	Total	C	O	0
			35	24	11	

- Molecule 46 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



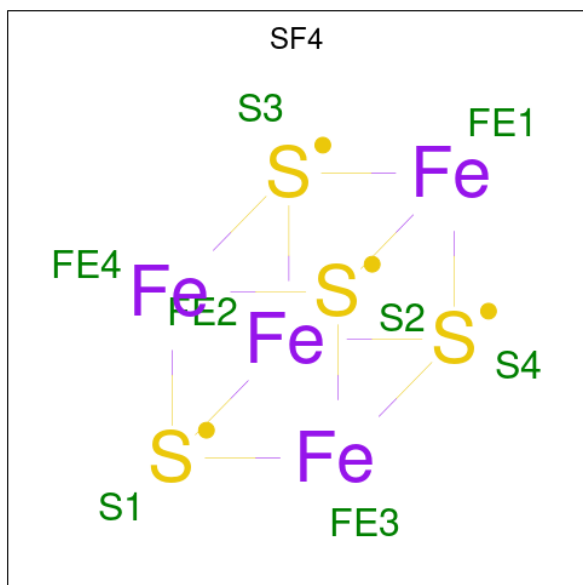
Mol	Chain	Residues	Atoms					AltConf
46	A	1	Total	C	N	O	P	0
			21	11	1	8	1	

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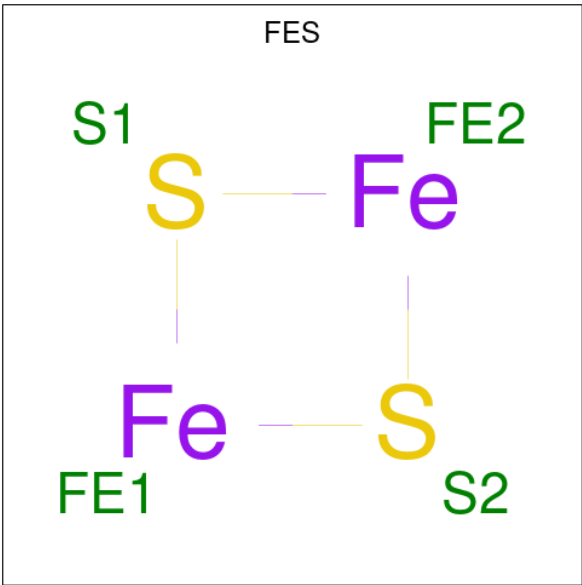
Mol	Chain	Residues	Atoms					AltConf
46	B	1	Total	C	N	O	P	0
			54	44	1	8	1	
46	B	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	L	1	Total	C	N	O	P	0
			49	39	1	8	1	

- Molecule 47 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



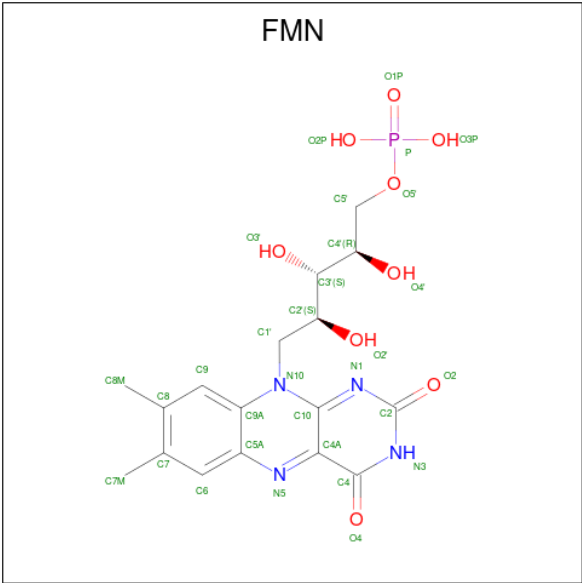
Mol	Chain	Residues	Atoms			AltConf
47	B	1	Total	Fe	S	0
			8	4	4	
47	F	1	Total	Fe	S	0
			8	4	4	
47	G	1	Total	Fe	S	0
			8	4	4	
47	G	1	Total	Fe	S	0
			8	4	4	
47	I	1	Total	Fe	S	0
			8	4	4	
47	I	1	Total	Fe	S	0
			8	4	4	

- Molecule 48 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			AltConf
48	E	1	Total	Fe	S	0
			4	2	2	
48	G	1	Total	Fe	S	0
			4	2	2	

- Molecule 49 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).

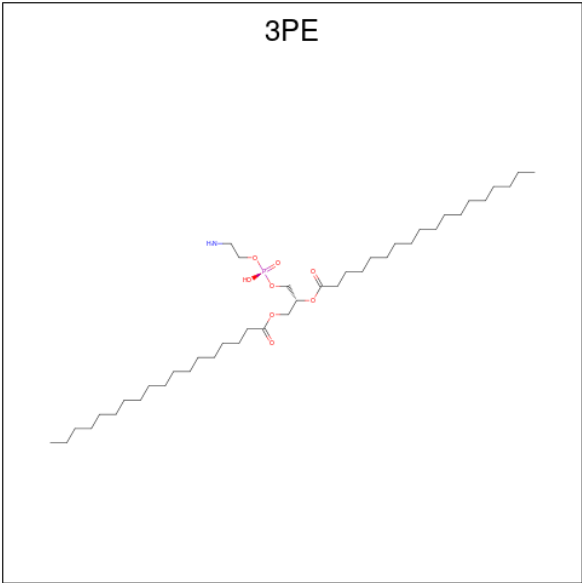


Mol	Chain	Residues	Atoms					AltConf
49	F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 50 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
50	G	1	Total	K	0
			1	1	

- Molecule 51 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



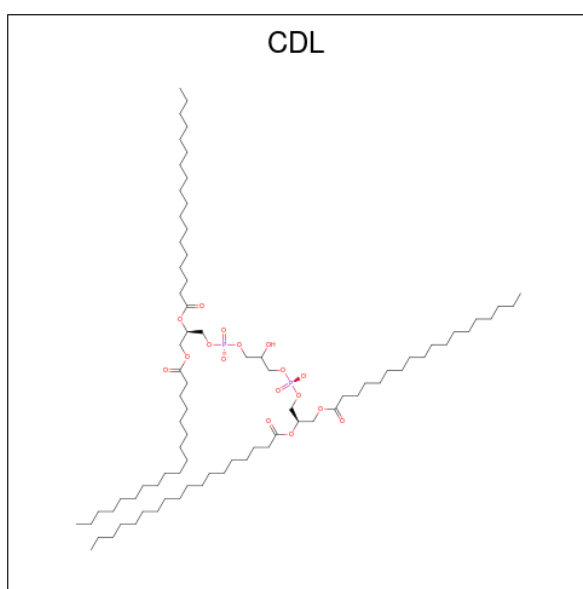
Mol	Chain	Residues	Atoms					AltConf
51	H	1	Total	C	N	O	P	0
			44	34	1	8	1	
51	H	1	Total	C	N	O	P	0
			51	41	1	8	1	
51	H	1	Total	C	N	O	P	0
			34	24	1	8	1	
51	L	1	Total	C	N	O	P	0
			49	39	1	8	1	
51	L	1	Total	C	N	O	P	0
			45	35	1	8	1	
51	M	1	Total	C	N	O	P	0
			46	36	1	8	1	
51	M	1	Total	C	N	O	P	0
			51	41	1	8	1	
51	N	1	Total	C	N	O	P	0
			41	31	1	8	1	
51	N	1	Total	C	N	O	P	0
			29	19	1	8	1	
51	P	1	Total	C	N	O	P	0
			37	27	1	8	1	

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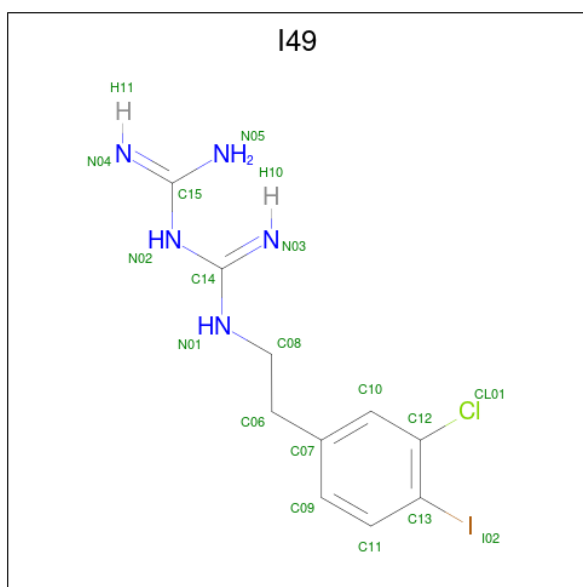
Mol	Chain	Residues	Atoms					AltConf
51	X	1	Total	C	N	O	P	0
			51	41	1	8	1	
51	Y	1	Total	C	N	O	P	0
			35	25	1	8	1	
51	d	1	Total	C	N	O	P	0
			51	41	1	8	1	
51	d	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 52 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



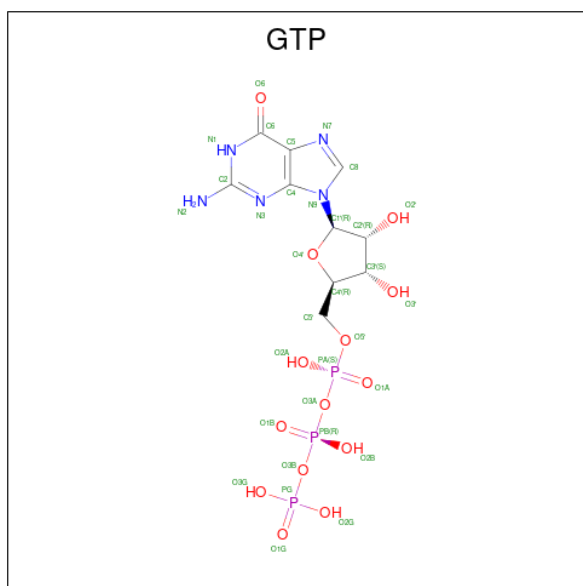
Mol	Chain	Residues	Atoms				AltConf
52	J	1	Total	C	O	P	0
			62	43	17	2	
52	K	1	Total	C	O	P	0
			71	52	17	2	
52	L	1	Total	C	O	P	0
			69	50	17	2	
52	h	1	Total	C	O	P	0
			67	48	17	2	
52	r	1	Total	C	O	P	0
			76	57	17	2	

- Molecule 53 is 1-carbamimidoyl-3-[2-(3-chloranyl-4-iodanyl-phenyl)ethyl]guanidine (CCD ID: I49) (formula: $C_{10}H_{13}ClIN_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
53	N	1	Total	C	Cl	I	N	0
			17	10	1	1	5	

- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

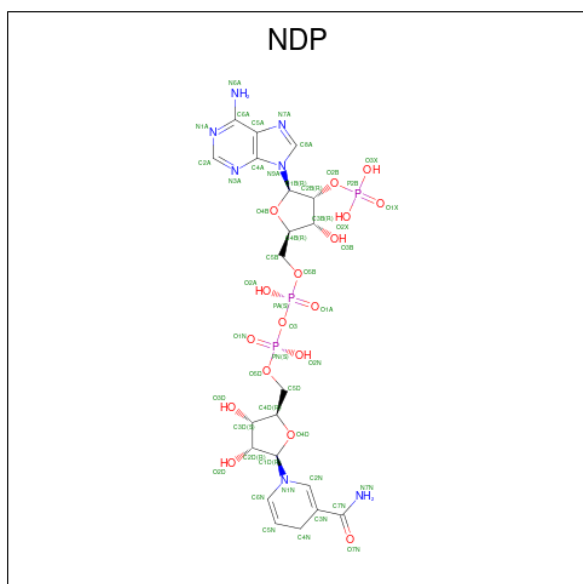


Mol	Chain	Residues	Atoms					AltConf
54	O	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	O	1	Total	Mg	0
			1	1	

- Molecule 56 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).

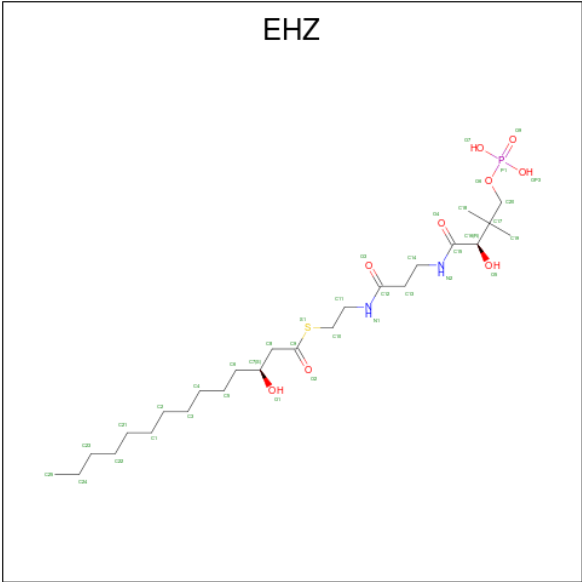


Mol	Chain	Residues	Atoms					AltConf
56	P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

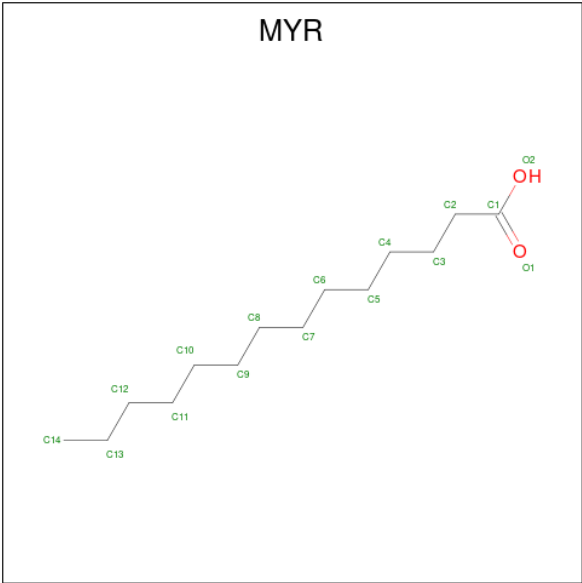
Mol	Chain	Residues	Atoms		AltConf
57	R	1	Total	Zn	0
			1	1	

- Molecule 58 is {S}-[2-[3-[(2 {R})-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] (3 {S})-3-oxidanyltetradecanethioate (CCD ID: EHZ) (formula: $C_{25}H_{49}N_2O_9PS$).



Mol	Chain	Residues	Atoms					AltConf
58	T	1	Total	C	N	O	P	S
			37	25	2	8	1	1
58	U	1	Total	C	N	O	P	S
			37	25	2	8	1	1

- Molecule 59 is MYRISTIC ACID (CCD ID: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			AltConf
59	o	1	Total	C	O	0
			15	14	1	

- Molecule 60 is water.

Mol	Chain	Residues	Atoms		AltConf
60	A	30	Total 30	O 30	0
60	B	65	Total 65	O 65	0
60	C	92	Total 92	O 92	0
60	D	168	Total 168	O 168	0
60	E	15	Total 15	O 15	0
60	F	63	Total 63	O 63	0
60	G	203	Total 203	O 203	0
60	H	70	Total 70	O 70	0
60	I	92	Total 92	O 92	0
60	J	27	Total 27	O 27	0
60	K	18	Total 18	O 18	0
60	L	52	Total 52	O 52	0
60	M	65	Total 65	O 65	0
60	N	52	Total 52	O 52	0
60	O	27	Total 27	O 27	0
60	P	80	Total 80	O 80	0
60	Q	64	Total 64	O 64	0
60	R	44	Total 44	O 44	0
60	S	4	Total 4	O 4	0
60	U	1	Total 1	O 1	0
60	V	17	Total 17	O 17	0
60	W	13	Total 13	O 13	0

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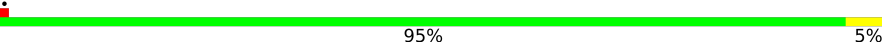
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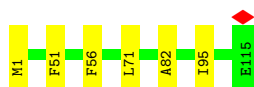
Mol	Chain	Residues	Atoms		AltConf
60	X	28	Total 28	O 28	0
60	Y	2	Total 2	O 2	0
60	Z	22	Total 22	O 22	0
60	a	16	Total 16	O 16	0
60	b	8	Total 8	O 8	0
60	d	17	Total 17	O 17	0
60	e	18	Total 18	O 18	0
60	f	3	Total 3	O 3	0
60	g	5	Total 5	O 5	0
60	h	23	Total 23	O 23	0
60	i	3	Total 3	O 3	0
60	j	2	Total 2	O 2	0
60	k	1	Total 1	O 1	0
60	l	13	Total 13	O 13	0
60	m	11	Total 11	O 11	0
60	n	7	Total 7	O 7	0
60	o	2	Total 2	O 2	0
60	p	16	Total 16	O 16	0
60	q	47	Total 47	O 47	0
60	r	33	Total 33	O 33	0
60	s	6	Total 6	O 6	0

3 Residue-property plots [i](#)

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.

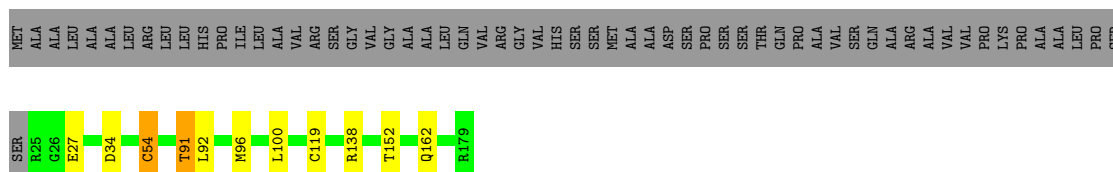
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3

Chain A: 



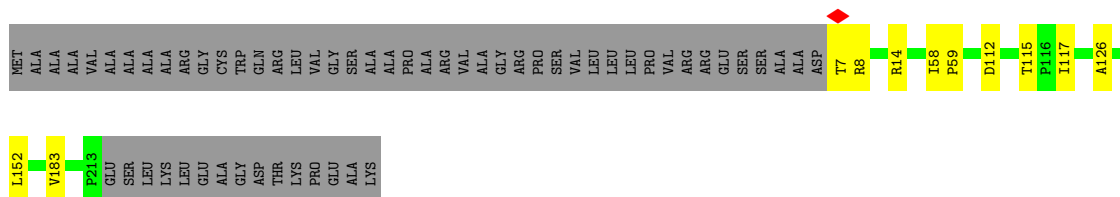
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

Chain B: 



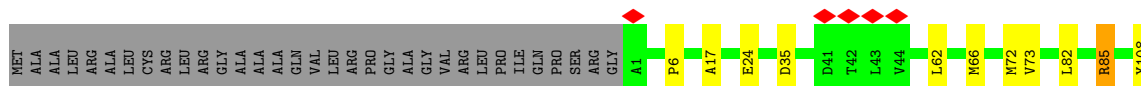
- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial

Chain C: 



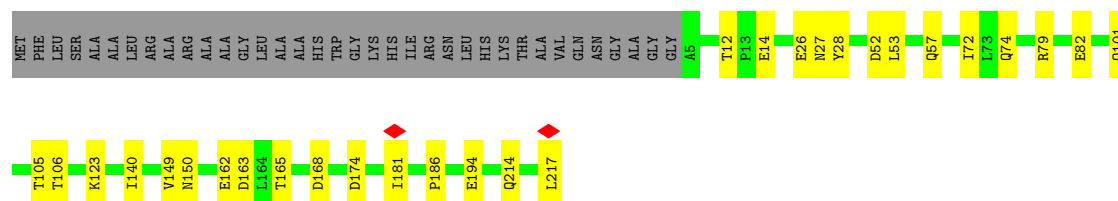
- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

Chain D: 

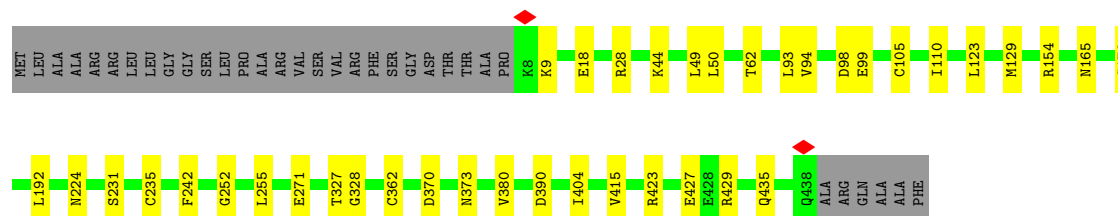
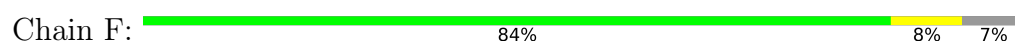




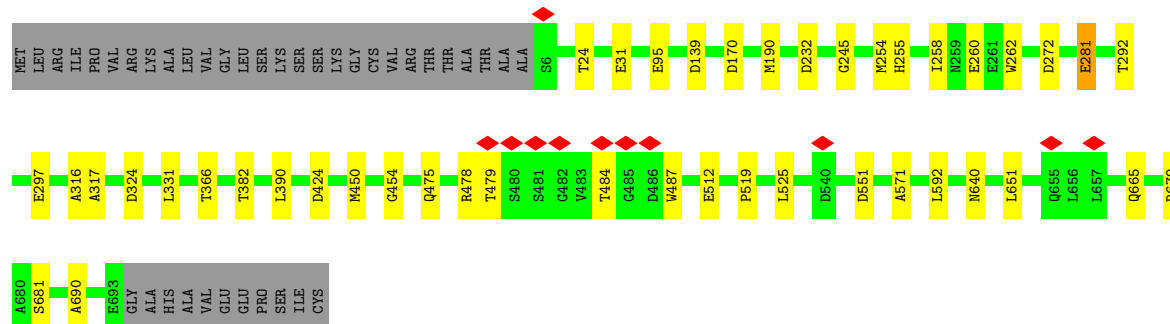
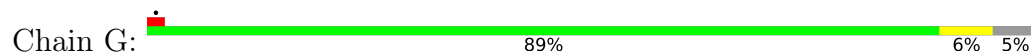
- Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial



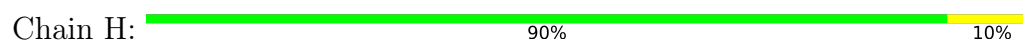
- Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



- Molecule 7: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

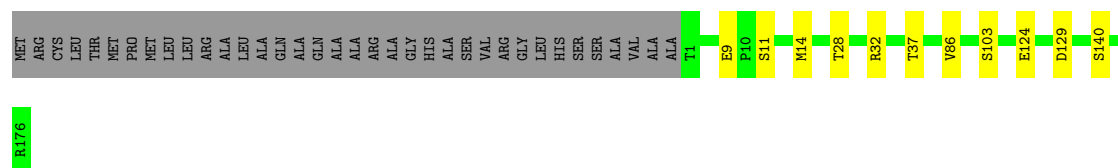


- Molecule 8: NADH-ubiquinone oxidoreductase chain 1



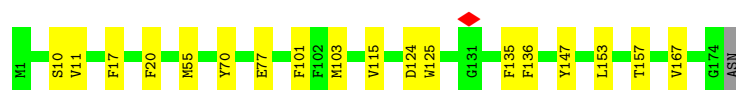
- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial

Chain I:  78% 5% 17%

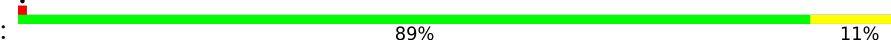


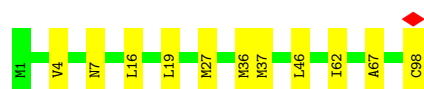
- Molecule 10: NADH-ubiquinone oxidoreductase chain 6

Chain J:  89% 10% .



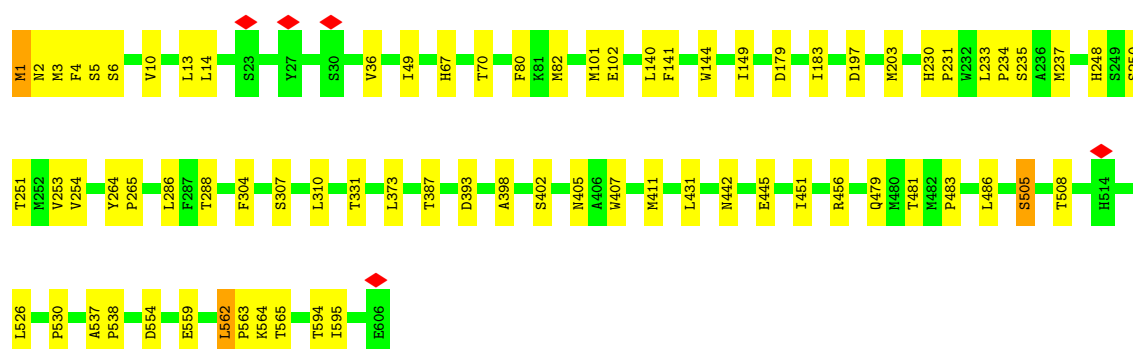
- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

Chain K:  89% 11%

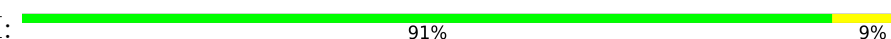


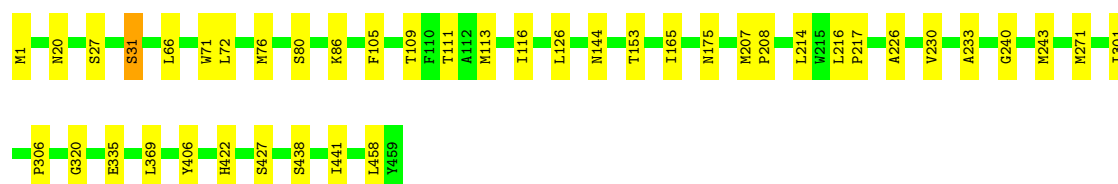
- Molecule 12: NADH-ubiquinone oxidoreductase chain 5

Chain L:  88% 12%



- Molecule 13: NADH-ubiquinone oxidoreductase chain 4

Chain M:  91% 9%



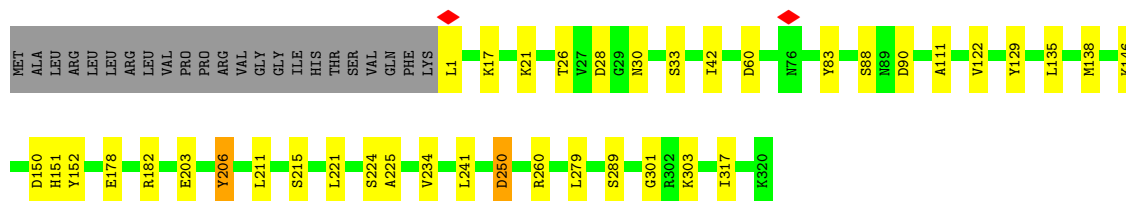
- Molecule 14: NADH-ubiquinone oxidoreductase chain 2

Chain N:  92% 8%



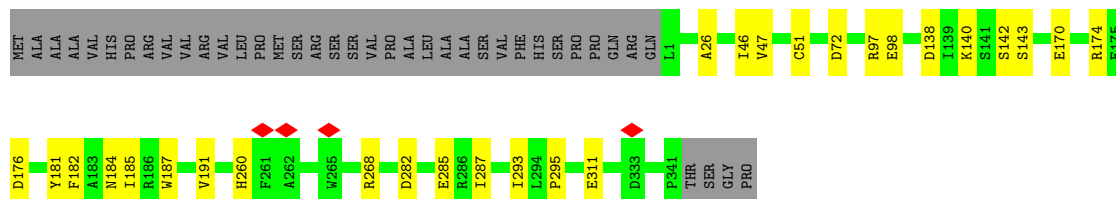
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

Chain O:  82% 11% 7%



- Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial

Chain P:  82% 7% 10%



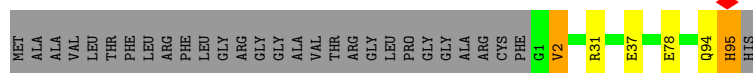
- Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain Q:  69% 29%

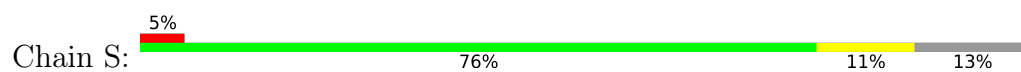


- Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

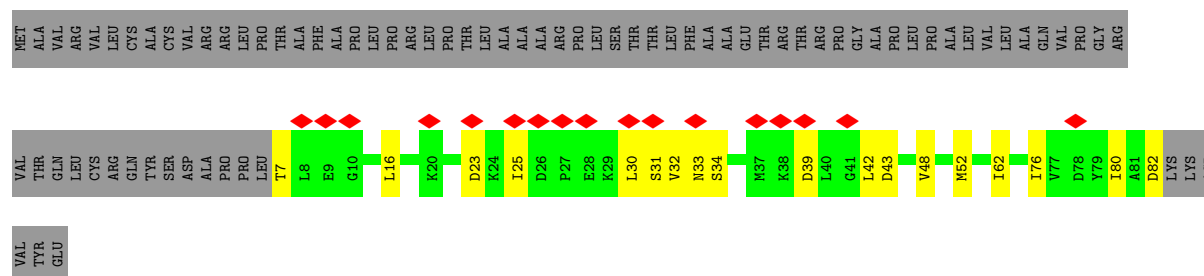
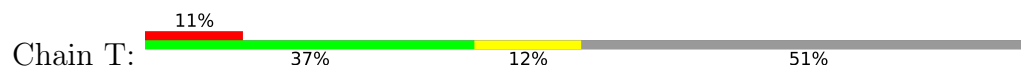
Chain R:  72% 23%



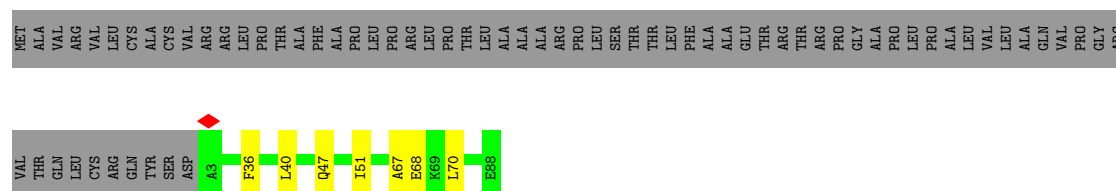
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



- Molecule 20: Acyl carrier protein, mitochondrial



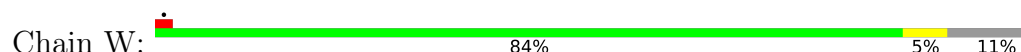
- Molecule 20: Acyl carrier protein, mitochondrial



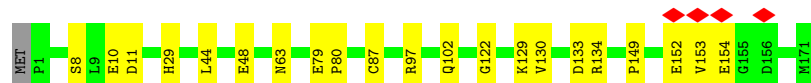
- Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5



- Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



- Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



-
- Diagram illustrating the protein structure with residues A1, K2, T3, R6, T15, H18, Y38, K43, T46, L49, E81, D84, T104, R105, I109, and V140 highlighted in yellow. Red diamonds are placed above each of these highlighted residues.

-
- Number of amino acid mutations
- | Amino Acid | Number of mutations |
|------------|---------------------|
| MET | 1 |
| ALA | 1 |
| ALA | 1 |
| S4 | 2 |
| V13 | 2 |
| Y21 | 1 |
| P26 | 1 |
| R27 | 1 |
| R28 | 1 |
| M35 | 1 |
| L60 | 1 |
| E66 | 1 |
| R81 | 1 |
| M86 | 1 |
| E89 | 1 |
| A95 | 1 |
| N98 | 1 |
| K99 | 1 |
| D100 | 1 |
| V101 | 1 |
| V106 | 1 |
| S109 | 1 |
| L124 | 1 |
| Y125 | 1 |
| G126 | 1 |
| L127 | 1 |
| R128 | 1 |
| T137 | 1 |
| T144 | 1 |

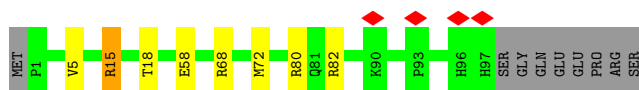
-

-
- Diagram illustrating the locations of 18 genes (A1, E2, R3, V4, N10, V11, W12, A13, K14, T33, T38, L42, R46, D58, N61, M62, V65, L83) across the human genome. The genes are represented by colored blocks (green and yellow) along a horizontal axis. Red diamonds indicate specific genomic regions or features associated with the genes A1, E2, R3, V4, and N61.

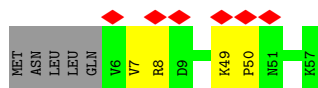
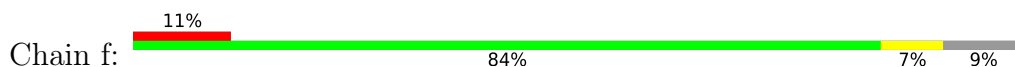
- | | | | | | | | | | |
|-----|----|----|----|-----|-----|-----|-----|-----|-----|----|
| MET | ALA | PRO | SER | ALA | LEU | LEU | ARG | PHE | TRP | LYS | LEU | LEU | ALA | PRO | ALA | ARG | PHE | PRO | SER | SER | SER | ARG | SER | K1 | F2 | E6 | F26 | L27 | W28 | K33 | E37 | L48 | GU |
|-----|----|----|----|-----|-----|-----|-----|-----|-----|----|

- [illegible]

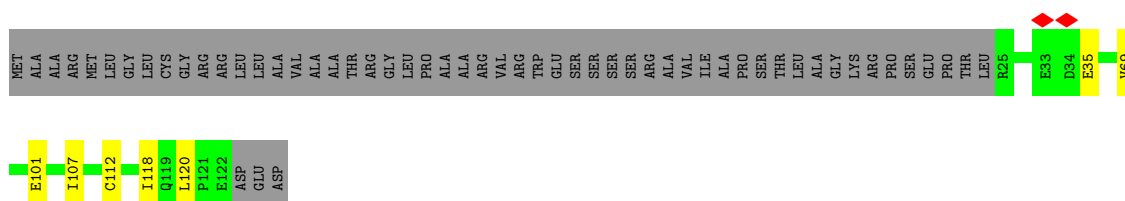
- Chain e: 84% 7% 8%



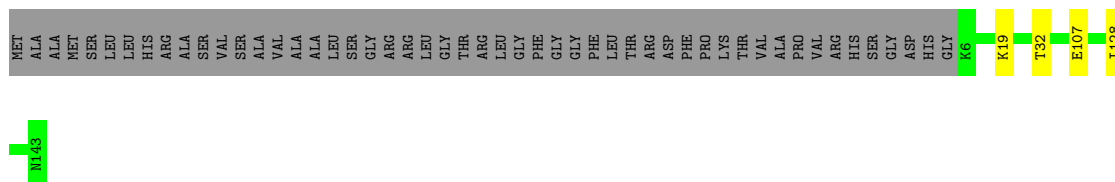
- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



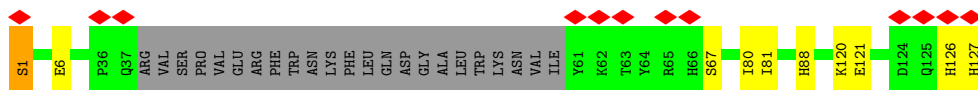
- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



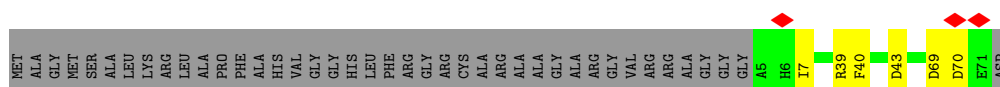
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



- Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

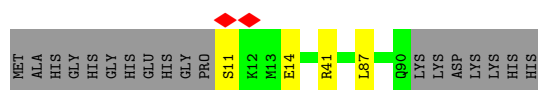


- Molecule 35: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



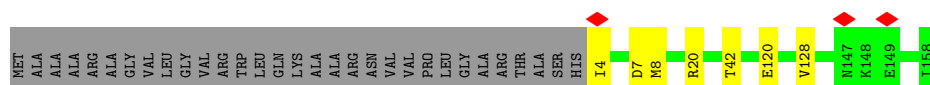
- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

Chain k:  78% 18%



- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

Chain l:  80% 17%



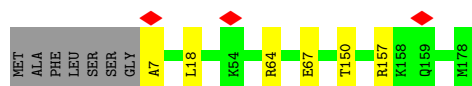
- Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

Chain m:  87% 12%



- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

Chain n:  93%

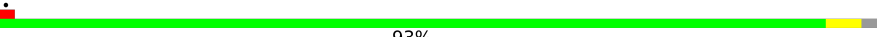


- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain o:  81% 7% 12%



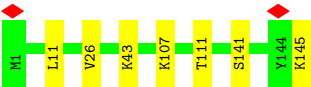
- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

Chain p:  93%

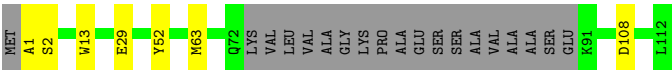


- Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

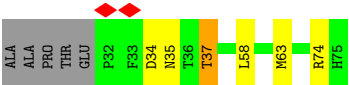
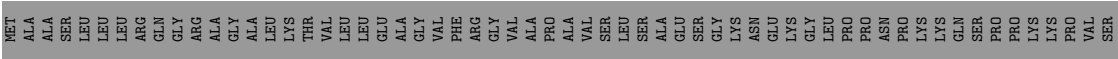
Chain q:  95% 5%



• Molecule 43: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7



• Molecule 44: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53763	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	32.833	Depositor
Minimum map value	-14.121	Depositor
Average map value	0.007	Depositor
Map value standard deviation	1.032	Depositor
Recommended contour level	5	Depositor
Map size ($\text{\AA}$)	482.46, 482.46, 482.46	wwPDB
Map dimensions	660, 660, 660	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.731, 0.731, 0.731	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LMT, MG, K, FME, I49, NDP, 3PE, FES, CDL, FMN, PC1, ZN, MYR, 2MR, EHZ, SF4, AYA, GTP, SAC

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	A	0.23	0/936	0.28	0/1281
2	B	0.27	0/1272	0.37	0/1720
3	C	0.25	0/1772	0.32	0/2413
4	D	0.26	0/3537	0.33	0/4794
5	E	0.22	0/1695	0.31	0/2307
6	F	0.23	0/3393	0.30	0/4584
7	G	0.24	0/5367	0.32	0/7274
8	H	0.27	0/2571	0.35	0/3513
9	I	0.27	0/1445	0.35	0/1956
10	J	0.24	0/1362	0.31	0/1848
11	K	0.24	0/745	0.28	0/1008
12	L	0.26	0/4896	0.30	0/6663
13	M	0.27	0/3738	0.31	0/5097
14	N	0.26	0/2792	0.30	0/3800
15	O	0.24	0/2651	0.29	0/3587
16	P	0.23	0/2824	0.32	0/3831
17	Q	0.24	0/1039	0.32	0/1404
18	R	0.26	0/742	0.33	0/999
19	S	0.22	0/702	0.31	0/945
20	T	0.18	0/621	0.31	0/837
20	U	0.28	0/705	0.30	0/952
21	V	0.21	0/943	0.27	0/1277
22	W	0.24	0/995	0.31	0/1337
23	X	0.24	0/1439	0.33	0/1942
24	Y	0.19	0/1042	0.29	0/1414
25	Z	0.23	0/1181	0.29	0/1592
26	a	0.25	0/584	0.32	0/786
27	b	0.22	0/672	0.31	0/923
28	c	0.22	0/418	0.28	0/567
29	d	0.24	0/975	0.31	0/1319
30	e	0.23	0/840	0.36	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	f	0.22	0/464	0.33	0/626
32	g	0.23	0/850	0.29	0/1154
33	h	0.25	0/1188	0.31	0/1607
34	i	0.25	0/920	0.34	0/1251
35	j	0.25	0/607	0.29	0/833
36	k	0.24	0/663	0.30	0/895
37	l	0.25	0/1358	0.30	0/1858
38	m	0.26	0/1088	0.31	0/1472
39	n	0.25	0/1545	0.29	0/2092
40	o	0.26	0/1060	0.34	0/1420
41	p	0.27	0/1476	0.28	0/1990
42	q	0.23	0/1250	0.32	0/1698
43	r	0.22	0/780	0.31	0/1056
44	s	0.20	0/383	0.28	0/518
All	All	0.25	0/67526	0.31	0/91563

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	275	TYR	Peptide
4	D	85	2MR	Mainchain

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	A	921	0	952	5	0
2	B	1241	0	1251	8	0
3	C	1721	0	1675	8	0
4	D	3459	0	3404	32	0
5	E	1655	0	1661	18	0
6	F	3319	0	3274	24	0
7	G	5279	0	5301	28	0
8	H	2509	0	2621	18	0
9	I	1414	0	1370	8	0
10	J	1337	0	1346	17	0
11	K	745	0	785	10	0
12	L	4780	0	4926	46	0
13	M	3654	0	3852	26	0
14	N	2733	0	2912	20	0
15	O	2589	0	2565	22	0
16	P	2747	0	2766	18	0
17	Q	1016	0	1014	3	0
18	R	730	0	707	4	0
19	S	691	0	706	4	0
20	T	612	0	604	9	0
20	U	693	0	688	4	0
21	V	923	0	964	5	0
22	W	971	0	989	4	0
23	X	1402	0	1385	14	0
24	Y	1030	0	1039	5	0
25	Z	1152	0	1151	18	0
26	a	569	0	568	5	0
27	b	651	0	662	8	0
28	c	405	0	409	6	0
29	d	945	0	932	9	0
30	e	819	0	821	6	0
31	f	451	0	453	2	0
32	g	824	0	772	6	0
33	h	1154	0	1168	3	0
34	i	898	0	907	7	0
35	j	580	0	519	3	0
36	k	644	0	626	1	0
37	l	1304	0	1203	9	0
38	m	1061	0	1059	14	0
39	n	1492	0	1438	6	0
40	o	1035	0	1004	7	0
41	p	1443	0	1415	6	0
42	q	1209	0	1182	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	r	767	0	776	6	0
44	s	371	0	344	5	0
45	A	70	0	92	2	0
45	J	35	0	46	2	0
45	K	35	0	46	0	0
45	L	105	0	138	0	0
45	M	105	0	138	6	0
45	Y	105	0	138	1	0
45	b	35	0	46	0	0
45	h	35	0	46	1	0
45	j	35	0	46	0	0
45	l	35	0	46	0	0
46	A	21	0	18	1	0
46	B	89	0	132	4	0
46	L	49	0	75	3	0
47	B	8	0	0	0	0
47	F	8	0	0	0	0
47	G	16	0	0	0	0
47	I	16	0	0	0	0
48	E	4	0	0	0	0
48	G	4	0	0	0	0
49	F	31	0	19	1	0
50	G	1	0	0	0	0
51	H	129	0	194	0	0
51	L	94	0	142	2	0
51	M	97	0	151	4	0
51	N	70	0	88	0	0
51	P	37	0	48	0	0
51	X	51	0	82	2	0
51	Y	35	0	44	1	0
51	d	102	0	164	0	0
52	J	62	0	68	1	0
52	K	71	0	86	0	0
52	L	69	0	82	0	0
52	h	67	0	81	2	0
52	r	76	0	96	1	0
53	N	17	0	0	4	0
54	O	32	0	12	3	0
55	O	1	0	0	0	0
56	P	48	0	26	1	0
57	R	1	0	0	0	0
58	T	37	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	U	37	0	0	0	0
59	o	15	0	27	0	0
60	A	30	0	0	0	0
60	B	65	0	0	3	0
60	C	92	0	0	2	0
60	D	168	0	0	7	0
60	E	15	0	0	1	0
60	F	63	0	0	4	0
60	G	203	0	0	8	0
60	H	70	0	0	0	0
60	I	92	0	0	1	0
60	J	27	0	0	1	0
60	K	18	0	0	0	0
60	L	52	0	0	1	0
60	M	65	0	0	3	0
60	N	52	0	0	2	0
60	O	27	0	0	5	0
60	P	80	0	0	4	0
60	Q	64	0	0	1	0
60	R	44	0	0	1	0
60	S	4	0	0	0	0
60	U	1	0	0	0	0
60	V	17	0	0	2	0
60	W	13	0	0	0	0
60	X	28	0	0	2	0
60	Y	2	0	0	0	0
60	Z	22	0	0	1	0
60	a	16	0	0	1	0
60	b	8	0	0	0	0
60	d	17	0	0	0	0
60	e	18	0	0	0	0
60	f	3	0	0	0	0
60	g	5	0	0	0	0
60	h	23	0	0	2	0
60	i	3	0	0	0	0
60	j	2	0	0	0	0
60	k	1	0	0	0	0
60	l	13	0	0	1	0
60	m	11	0	0	2	0
60	n	7	0	0	0	0
60	o	2	0	0	0	0
60	p	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	q	47	0	0	0	0
60	r	33	0	0	2	0
60	s	6	0	0	0	0
All	All	69480	0	68583	434	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 3.

The worst 5 of 434 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)
53:N:703:I49:I02	29:d:82:MET:HB3	2.31	1.01
53:N:703:I49:I02	29:d:82:MET:O	2.57	0.92
16:P:51:CYS:O	60:P:601:HOH:O	1.93	0.85
16:P:98:GLU:OE1	60:P:602:HOH:O	1.97	0.81
52:J:701:CDL:OB4	60:J:801:HOH:O	1.97	0.81

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	A	113/115 (98%)	109 (96%)	4 (4%)	0	100	100
2	B	153/216 (71%)	147 (96%)	6 (4%)	0	100	100
3	C	205/266 (77%)	200 (98%)	5 (2%)	0	100	100
4	D	427/463 (92%)	409 (96%)	18 (4%)	0	100	100
5	E	211/249 (85%)	204 (97%)	7 (3%)	0	100	100
6	F	429/464 (92%)	419 (98%)	10 (2%)	0	100	100
7	G	686/727 (94%)	673 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	316/318 (99%)	305 (96%)	11 (4%)	0	100	100
9	I	174/212 (82%)	170 (98%)	4 (2%)	0	100	100
10	J	172/175 (98%)	160 (93%)	12 (7%)	0	100	100
11	K	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
12	L	604/606 (100%)	582 (96%)	21 (4%)	1 (0%)	43	55
13	M	457/459 (100%)	450 (98%)	7 (2%)	0	100	100
14	N	345/347 (99%)	339 (98%)	6 (2%)	0	100	100
15	O	318/343 (93%)	312 (98%)	6 (2%)	0	100	100
16	P	339/380 (89%)	330 (97%)	9 (3%)	0	100	100
17	Q	123/175 (70%)	123 (100%)	0	0	100	100
18	R	93/124 (75%)	90 (97%)	3 (3%)	0	100	100
19	S	84/99 (85%)	81 (96%)	3 (4%)	0	100	100
20	T	74/156 (47%)	72 (97%)	2 (3%)	0	100	100
20	U	84/156 (54%)	83 (99%)	1 (1%)	0	100	100
21	V	112/116 (97%)	110 (98%)	2 (2%)	0	100	100
22	W	112/128 (88%)	110 (98%)	2 (2%)	0	100	100
23	X	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
24	Y	138/141 (98%)	134 (97%)	4 (3%)	0	100	100
25	Z	139/144 (96%)	136 (98%)	3 (2%)	0	100	100
26	a	68/70 (97%)	68 (100%)	0	0	100	100
27	b	81/84 (96%)	77 (95%)	4 (5%)	0	100	100
28	c	46/76 (60%)	45 (98%)	1 (2%)	0	100	100
29	d	111/120 (92%)	111 (100%)	0	0	100	100
30	e	95/106 (90%)	94 (99%)	1 (1%)	0	100	100
31	f	50/57 (88%)	50 (100%)	0	0	100	100
32	g	96/154 (62%)	91 (95%)	5 (5%)	0	100	100
33	h	136/189 (72%)	135 (99%)	1 (1%)	0	100	100
34	i	100/127 (79%)	97 (97%)	3 (3%)	0	100	100
35	j	65/108 (60%)	63 (97%)	2 (3%)	0	100	100
36	k	78/98 (80%)	77 (99%)	1 (1%)	0	100	100
37	l	153/186 (82%)	150 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	m	125/129 (97%)	119 (95%)	6 (5%)	0	100	100
39	n	170/179 (95%)	167 (98%)	3 (2%)	0	100	100
40	o	118/137 (86%)	113 (96%)	5 (4%)	0	100	100
41	p	169/176 (96%)	168 (99%)	1 (1%)	0	100	100
42	q	143/145 (99%)	141 (99%)	2 (1%)	0	100	100
43	r	90/113 (80%)	86 (96%)	4 (4%)	0	100	100
44	s	42/109 (38%)	40 (95%)	2 (5%)	0	100	100
All	All	8109/9212 (88%)	7899 (97%)	209 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	562	LEU

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	A	100/100 (100%)	100 (100%)	0	100	100
2	B	131/175 (75%)	128 (98%)	3 (2%)	44	63
3	C	188/228 (82%)	187 (100%)	1 (0%)	81	90
4	D	370/392 (94%)	368 (100%)	2 (0%)	81	90
5	E	183/205 (89%)	181 (99%)	2 (1%)	65	81
6	F	345/368 (94%)	339 (98%)	6 (2%)	53	72
7	G	578/608 (95%)	573 (99%)	5 (1%)	70	84
8	H	274/274 (100%)	273 (100%)	1 (0%)	84	92
9	I	151/175 (86%)	148 (98%)	3 (2%)	48	67
10	J	140/141 (99%)	139 (99%)	1 (1%)	76	87
11	K	85/85 (100%)	84 (99%)	1 (1%)	63	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	L	528/533 (99%)	520 (98%)	8 (2%)	57	75
13	M	412/412 (100%)	407 (99%)	5 (1%)	63	79
14	N	315/315 (100%)	314 (100%)	1 (0%)	86	93
15	O	283/303 (93%)	275 (97%)	8 (3%)	38	56
16	P	295/327 (90%)	293 (99%)	2 (1%)	76	87
17	Q	112/153 (73%)	112 (100%)	0	100	100
18	R	78/97 (80%)	76 (97%)	2 (3%)	40	59
19	S	76/82 (93%)	73 (96%)	3 (4%)	28	43
20	T	70/135 (52%)	67 (96%)	3 (4%)	26	39
20	U	79/135 (58%)	79 (100%)	0	100	100
21	V	101/102 (99%)	100 (99%)	1 (1%)	68	82
22	W	107/114 (94%)	106 (99%)	1 (1%)	70	84
23	X	154/155 (99%)	153 (99%)	1 (1%)	78	89
24	Y	101/102 (99%)	101 (100%)	0	100	100
25	Z	120/121 (99%)	119 (99%)	1 (1%)	73	86
26	a	59/59 (100%)	59 (100%)	0	100	100
27	b	71/72 (99%)	69 (97%)	2 (3%)	38	56
28	c	44/68 (65%)	43 (98%)	1 (2%)	44	63
29	d	101/105 (96%)	101 (100%)	0	100	100
30	e	88/96 (92%)	86 (98%)	2 (2%)	44	63
31	f	49/54 (91%)	49 (100%)	0	100	100
32	g	89/131 (68%)	88 (99%)	1 (1%)	65	81
33	h	121/158 (77%)	120 (99%)	1 (1%)	73	86
34	i	99/120 (82%)	97 (98%)	2 (2%)	48	67
35	j	61/84 (73%)	59 (97%)	2 (3%)	33	50
36	k	62/76 (82%)	59 (95%)	3 (5%)	23	35
37	l	139/159 (87%)	139 (100%)	0	100	100
38	m	113/115 (98%)	113 (100%)	0	100	100
39	n	156/161 (97%)	155 (99%)	1 (1%)	78	89
40	o	109/120 (91%)	107 (98%)	2 (2%)	51	70
41	p	155/157 (99%)	153 (99%)	2 (1%)	61	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	q	131/131 (100%)	126 (96%)	5 (4%)	29	44
43	r	84/97 (87%)	84 (100%)	0	100	100
44	s	43/92 (47%)	42 (98%)	1 (2%)	44	63
All	All	7150/7892 (91%)	7064 (99%)	86 (1%)	61	79

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	V	57	MET
35	j	40	PHE
23	X	154	GLU
30	e	15	ARG
39	n	150	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
14	N	268	GLN
40	o	42	GLN
16	P	8	HIS
39	n	77	GLN
44	s	43	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

11 non-standard protein/DNA/RNA residues are 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
10	FME	J	1	10	8,9,10	0.95	0	8,9,11	1.01	0
12	FME	L	1	12	8,9,10	1.04	1 (12%)	8,9,11	0.92	0
1	FME	A	1	1	8,9,10	0.95	0	8,9,11	1.04	1 (12%)
43	AYA	r	1	43	6,7,8	1.89	2 (33%)	6,8,10	1.28	1 (16%)
24	AYA	Y	1	24	6,7,8	1.83	2 (33%)	6,8,10	1.43	1 (16%)
34	SAC	i	1	34	7,8,9	0.99	0	7,9,11	1.82	2 (28%)
4	2MR	D	85	4	10,12,13	2.71	4 (40%)	5,13,15	1.19	1 (20%)
14	FME	N	1	14	8,9,10	1.01	0	8,9,11	0.95	0
8	FME	H	1	8	8,9,10	1.07	1 (12%)	8,9,11	0.92	0
13	FME	M	1	13	8,9,10	1.02	1 (12%)	8,9,11	0.94	0
11	FME	K	1	11	8,9,10	0.95	0	8,9,11	0.84	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
10	FME	J	1	10	-	3/7/9/11	-
12	FME	L	1	12	-	2/7/9/11	-
1	FME	A	1	1	-	3/7/9/11	-
43	AYA	r	1	43	-	0/5/6/8	-
24	AYA	Y	1	24	-	1/5/6/8	-
34	SAC	i	1	34	-	6/7/8/10	-
4	2MR	D	85	4	-	0/10/13/15	-
14	FME	N	1	14	-	5/7/9/11	-
8	FME	H	1	8	-	3/7/9/11	-
13	FME	M	1	13	-	0/7/9/11	-
11	FME	K	1	11	-	1/7/9/11	-

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	85	2MR	CZ-NH2	5.21	1.44	1.33
4	D	85	2MR	CZ-NE	4.58	1.44	1.34
4	D	85	2MR	O-C	4.12	1.35	1.20
43	r	1	AYA	CT-N	3.48	1.45	1.34
24	Y	1	AYA	CT-N	3.33	1.45	1.34

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	i	1	SAC	C-CA-N	3.17	115.61	109.50
4	D	85	2MR	NE-CZ-NH2	-2.41	117.27	119.48
24	Y	1	AYA	CM-CT-N	2.40	120.10	116.12
43	r	1	AYA	CM-CT-N	2.34	120.00	116.12
1	A	1	FME	C-CA-N	2.20	113.75	109.50

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	C-CA-CB-CG
1	A	1	FME	O-C-CA-CB
8	H	1	FME	O-C-CA-CB
10	J	1	FME	O1-CN-N-CA
12	L	1	FME	O1-CN-N-CA

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	L	1	FME	2	0
34	i	1	SAC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 58 ligands modelled in this entry, 3 are monoatomic - leaving 55 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
51	3PE	Y	802	-	34,34,50	1.07	4 (11%)	37,39,55	1.21	2 (5%)
47	SF4	G	801	7	0,12,12	-	-	-	-	-
53	I49	N	703	-	15,17,17	0.81	1 (6%)	17,22,22	1.89	5 (29%)
51	3PE	H	403	-	33,33,50	1.30	4 (12%)	34,37,55	1.25	2 (5%)
51	3PE	L	701	-	48,48,50	0.91	4 (8%)	51,53,55	1.15	2 (3%)
47	SF4	B	201	2	0,12,12	-	-	-	-	-
51	3PE	H	401	-	43,43,50	0.95	3 (6%)	46,48,55	1.11	2 (4%)
51	3PE	X	401	-	50,50,50	0.86	4 (8%)	53,55,55	1.15	2 (3%)
58	EHZ	U	101	20	31,36,37	1.56	5 (16%)	36,44,47	1.54	5 (13%)
45	LMT	h	1002	-	36,36,36	1.16	2 (5%)	47,47,47	0.94	3 (6%)
52	CDL	r	201	-	75,75,99	1.01	6 (8%)	81,87,111	1.12	4 (4%)
56	NDP	P	501	-	51,52,52	2.23	5 (9%)	71,80,80	1.50	18 (25%)
45	LMT	l	201	-	36,36,36	1.23	3 (8%)	47,47,47	1.15	3 (6%)
46	PC1	L	707	-	48,48,53	0.99	4 (8%)	54,56,61	1.08	2 (3%)
51	3PE	H	402	-	50,50,50	0.89	4 (8%)	53,55,55	1.07	3 (5%)
46	PC1	B	202	-	53,53,53	0.94	3 (5%)	59,61,61	1.06	2 (3%)
52	CDL	K	502	-	70,70,99	1.05	6 (8%)	76,82,111	1.09	4 (5%)
52	CDL	L	703	-	68,68,99	1.05	6 (8%)	74,80,111	1.11	4 (5%)
45	LMT	K	501	-	36,36,36	1.19	3 (8%)	47,47,47	1.02	0
45	LMT	A	302	-	36,36,36	1.23	2 (5%)	47,47,47	1.10	3 (6%)
45	LMT	j	101	-	36,36,36	1.21	3 (8%)	47,47,47	0.98	2 (4%)
52	CDL	J	701	-	61,61,99	1.08	7 (11%)	67,73,111	1.27	5 (7%)
51	3PE	P	502	-	36,36,50	1.04	4 (11%)	39,41,55	1.17	2 (5%)
45	LMT	A	301	-	36,36,36	1.13	2 (5%)	47,47,47	1.14	3 (6%)
51	3PE	N	701	-	40,40,50	0.98	4 (10%)	43,45,55	1.10	2 (4%)
58	EHZ	T	101	20	31,36,37	1.55	5 (16%)	36,44,47	1.72	6 (16%)
45	LMT	b	101	-	36,36,36	1.16	2 (5%)	47,47,47	1.18	3 (6%)
51	3PE	d	1201	-	50,50,50	0.87	4 (8%)	53,55,55	1.11	2 (3%)
45	LMT	M	604	-	36,36,36	1.23	4 (11%)	47,47,47	0.97	0
51	3PE	L	705	-	44,44,50	0.92	3 (6%)	47,49,55	1.08	2 (4%)
46	PC1	B	203	-	34,34,53	1.19	4 (11%)	40,42,61	1.13	2 (5%)
46	PC1	A	303	-	20,20,53	1.78	3 (15%)	24,27,61	1.19	1 (4%)
54	GTP	O	401	55	33,34,34	3.25	15 (45%)	50,54,54	1.83	13 (26%)
45	LMT	L	704	-	36,36,36	1.23	3 (8%)	47,47,47	0.93	0
48	FES	E	301	5	0,4,4	-	-	-	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
45	LMT	Y	803	-	36,36,36	1.17	3 (8%)	47,47,47	1.02	2 (4%)
52	CDL	h	1001	-	66,66,99	1.07	8 (12%)	72,78,111	1.24	4 (5%)
45	LMT	M	603	-	36,36,36	1.15	2 (5%)	47,47,47	0.99	1 (2%)
45	LMT	M	602	-	36,36,36	1.13	2 (5%)	47,47,47	1.03	2 (4%)
45	LMT	L	702	-	36,36,36	1.18	2 (5%)	47,47,47	0.92	0
45	LMT	J	702	-	36,36,36	1.21	3 (8%)	47,47,47	1.12	2 (4%)
47	SF4	F	502	6	0,12,12	-	-	-		
47	SF4	I	201	9	0,12,12	-	-	-		
51	3PE	N	702	-	28,28,50	1.15	3 (10%)	31,33,55	1.17	2 (6%)
51	3PE	M	601	-	45,45,50	0.92	4 (8%)	48,50,55	0.99	2 (4%)
45	LMT	Y	801	-	36,36,36	1.15	3 (8%)	47,47,47	1.16	4 (8%)
45	LMT	Y	804	-	36,36,36	1.19	3 (8%)	47,47,47	1.08	2 (4%)
47	SF4	I	202	9	0,12,12	-	-	-		
49	FMN	F	501	-	33,33,33	1.09	2 (6%)	48,50,50	1.30	6 (12%)
47	SF4	G	802	7	0,12,12	-	-	-		
59	MYR	o	201	40	13,14,15	0.95	0	12,13,15	0.57	0
45	LMT	L	706	-	36,36,36	1.19	2 (5%)	47,47,47	1.14	4 (8%)
51	3PE	M	605	-	50,50,50	0.88	3 (6%)	53,55,55	1.13	2 (3%)
48	FES	G	803	7	0,4,4	-	-	-		
51	3PE	d	1202	-	50,50,50	0.83	3 (6%)	53,55,55	1.20	4 (7%)

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
51	3PE	Y	802	-	-	17/38/38/54	-
47	SF4	G	801	7	-	-	0/6/5/5
53	I49	N	703	-	-	5/10/10/10	0/1/1/1
51	3PE	H	403	-	-	18/36/36/54	-
51	3PE	L	701	-	-	24/52/52/54	-
51	3PE	X	401	-	-	24/54/54/54	-
51	3PE	H	401	-	-	23/47/47/54	-
58	EHZ	U	101	20	-	8/42/44/45	-
47	SF4	B	201	2	-	-	0/6/5/5
45	LMT	h	1002	-	-	6/21/61/61	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	CDL	r	201	-	-	31/86/86/110	-
56	NDP	P	501	-	-	4/34/77/77	0/5/5/5
45	LMT	l	201	-	-	6/21/61/61	0/2/2/2
46	PC1	L	707	-	-	25/52/52/57	-
51	3PE	H	402	-	-	17/54/54/54	-
46	PC1	B	202	-	-	22/57/57/57	-
52	CDL	K	502	-	-	31/81/81/110	-
52	CDL	L	703	-	-	31/79/79/110	-
45	LMT	K	501	-	-	10/21/61/61	0/2/2/2
45	LMT	A	302	-	-	14/21/61/61	0/2/2/2
45	LMT	j	101	-	-	9/21/61/61	0/2/2/2
52	CDL	J	701	-	-	29/71/71/110	-
51	3PE	P	502	-	-	22/40/40/54	-
45	LMT	A	301	-	-	1/21/61/61	0/2/2/2
51	3PE	N	701	-	-	19/44/44/54	-
58	EHZ	T	101	20	-	10/42/44/45	-
45	LMT	b	101	-	-	3/21/61/61	0/2/2/2
51	3PE	d	1201	-	-	27/54/54/54	-
45	LMT	M	604	-	-	11/21/61/61	0/2/2/2
51	3PE	L	705	-	-	14/48/48/54	-
46	PC1	B	203	-	-	13/38/38/57	-
46	PC1	A	303	-	-	8/22/22/57	-
54	GTP	O	401	55	-	3/22/38/38	0/3/3/3
45	LMT	L	704	-	-	8/21/61/61	0/2/2/2
48	FES	E	301	5	-	-	0/1/1/1
45	LMT	Y	803	-	-	11/21/61/61	0/2/2/2
52	CDL	h	1001	-	-	34/77/77/110	-
45	LMT	M	603	-	-	10/21/61/61	0/2/2/2
45	LMT	M	602	-	-	7/21/61/61	0/2/2/2
45	LMT	L	702	-	-	9/21/61/61	0/2/2/2
45	LMT	J	702	-	-	9/21/61/61	0/2/2/2
51	3PE	N	702	-	-	18/32/32/54	-
47	SF4	F	502	6	-	-	0/6/5/5
47	SF4	I	201	9	-	-	0/6/5/5
51	3PE	M	601	-	-	17/49/49/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	LMT	Y	801	-	-	8/21/61/61	0/2/2/2
45	LMT	Y	804	-	-	8/21/61/61	0/2/2/2
49	FMN	F	501	-	-	2/18/18/18	0/3/3/3
47	SF4	I	202	9	-	-	0/6/5/5
47	SF4	G	802	7	-	-	0/6/5/5
59	MYR	o	201	40	-	9/12/12/13	-
45	LMT	L	706	-	-	8/21/61/61	0/2/2/2
51	3PE	M	605	-	-	22/54/54/54	-
48	FES	G	803	7	-	-	0/1/1/1
51	3PE	d	1202	-	-	16/54/54/54	-

The worst 5 of 175 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	P	501	NDP	P2B-O2B	12.81	1.82	1.59
54	O	401	GTP	O6-C6	8.65	1.40	1.23
54	O	401	GTP	C5-N7	6.70	1.52	1.39
46	A	303	PC1	O21-C2	-5.11	1.40	1.46
54	O	401	GTP	PA-O3A	4.93	1.64	1.59

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	O	401	GTP	C8-N9-C4	7.52	120.12	106.03
58	T	101	EHZ	C8-C9-S1	6.43	121.68	113.56
58	U	101	EHZ	C8-C9-S1	5.96	121.08	113.56
51	H	403	3PE	O21-C21-O22	-5.27	118.94	125.70
52	h	1001	CDL	OB6-CB5-C51	4.78	121.83	111.48

There are no chirality outliers.

5 of 681 torsion outliers are listed below:

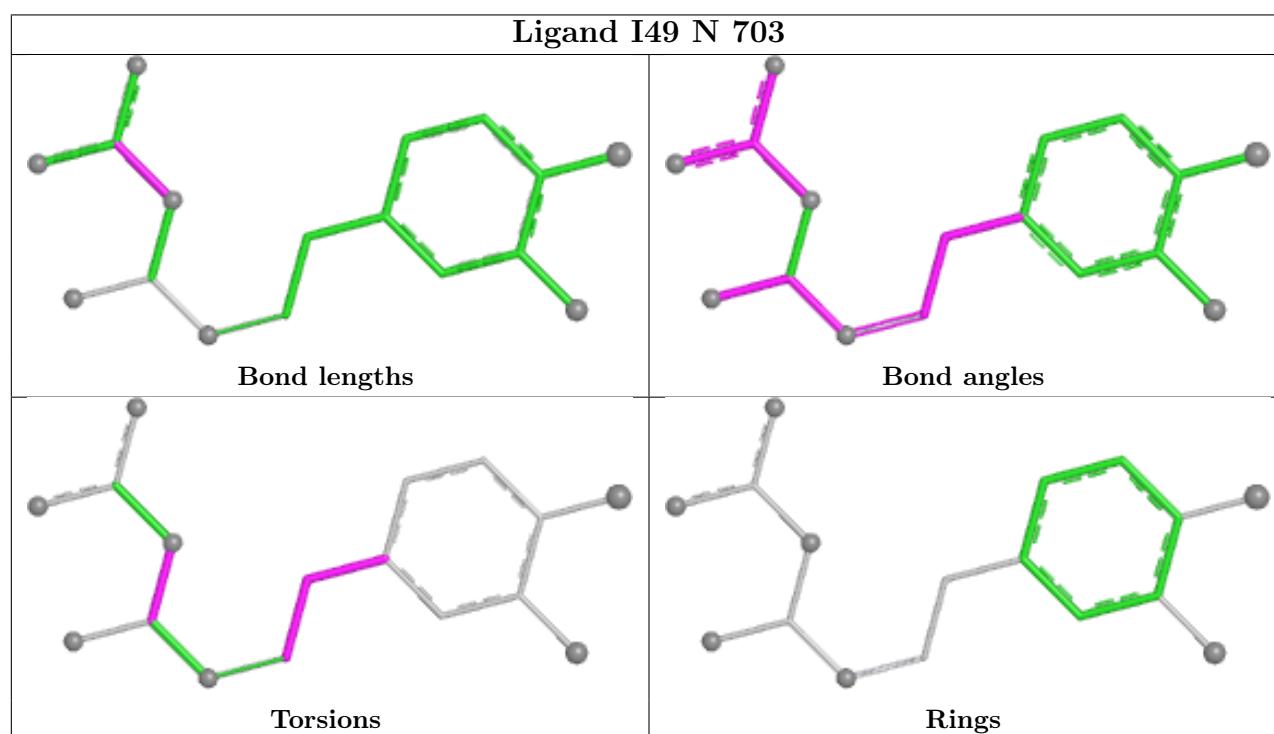
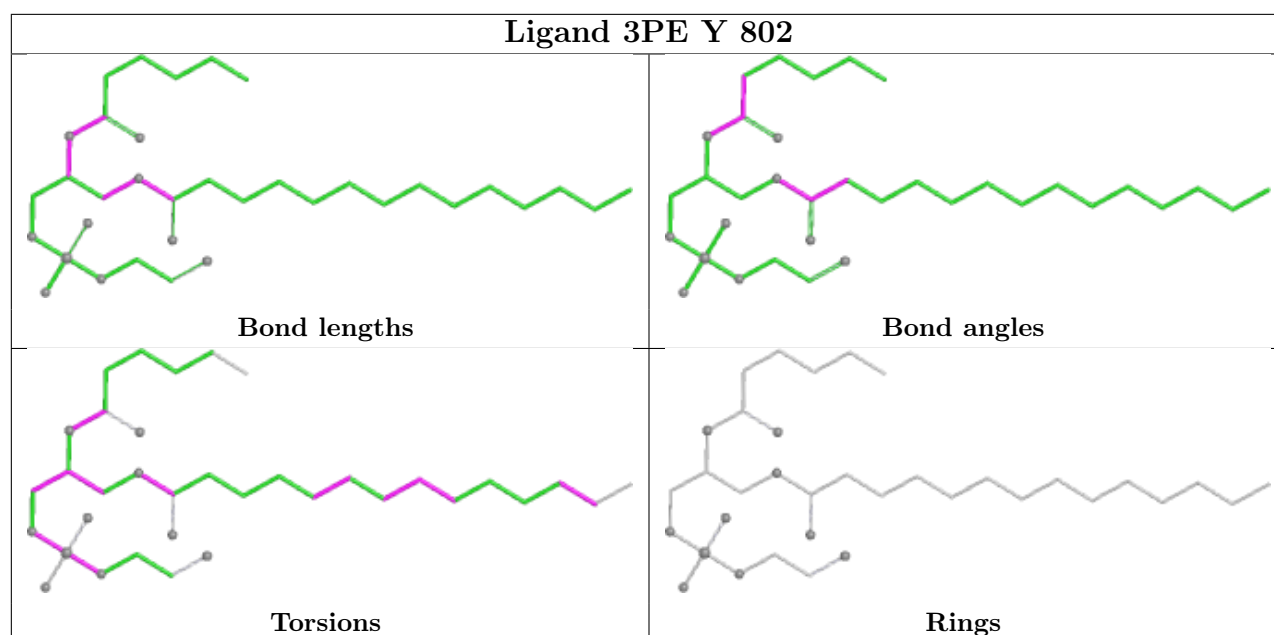
Mol	Chain	Res	Type	Atoms
45	A	302	LMT	O5'-C1'-O1'-C1
45	L	702	LMT	C2'-C1'-O1'-C1
45	L	702	LMT	O5'-C1'-O1'-C1
45	L	706	LMT	O5'-C1'-O1'-C1
45	M	603	LMT	C2'-C1'-O1'-C1

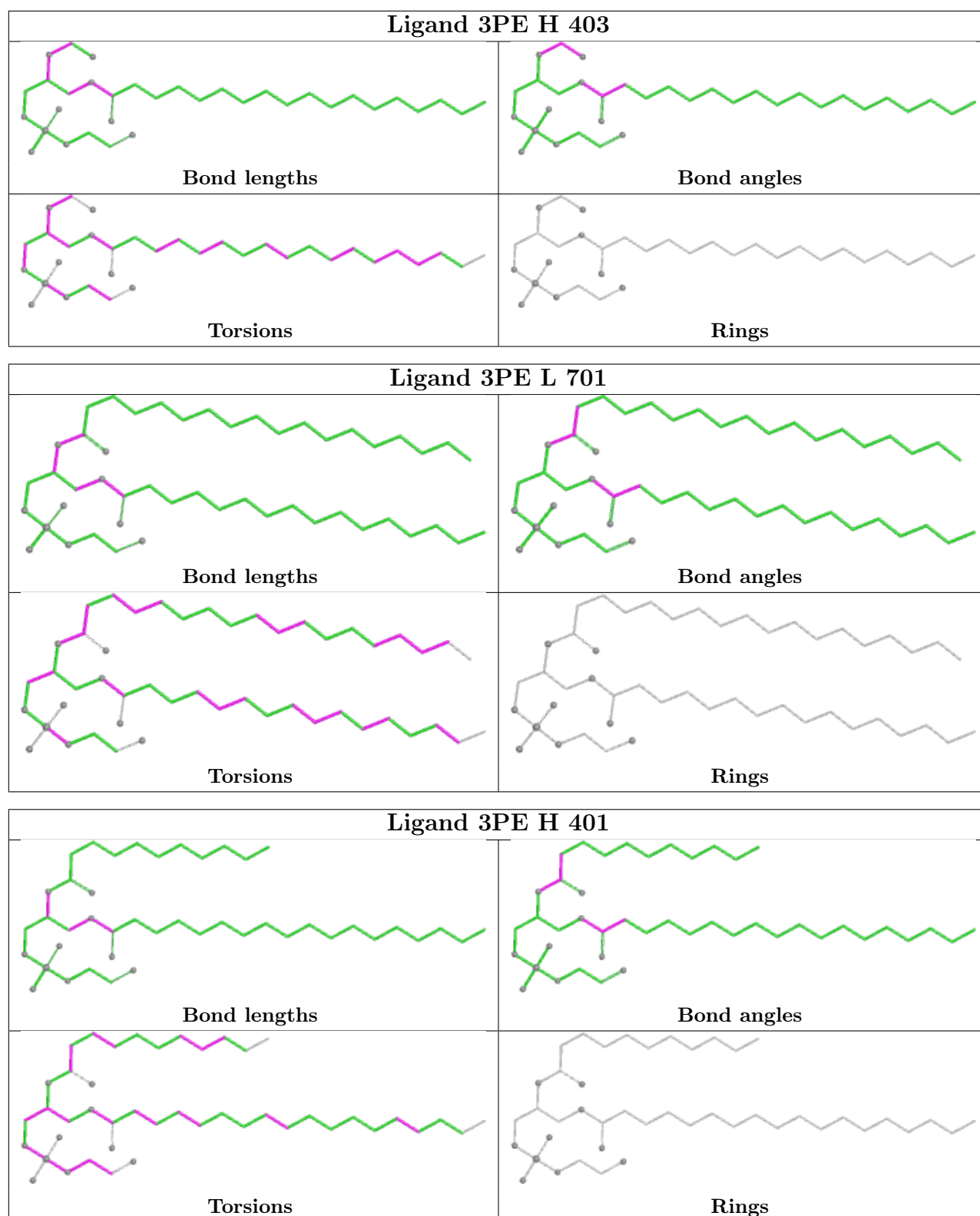
There are no ring outliers.

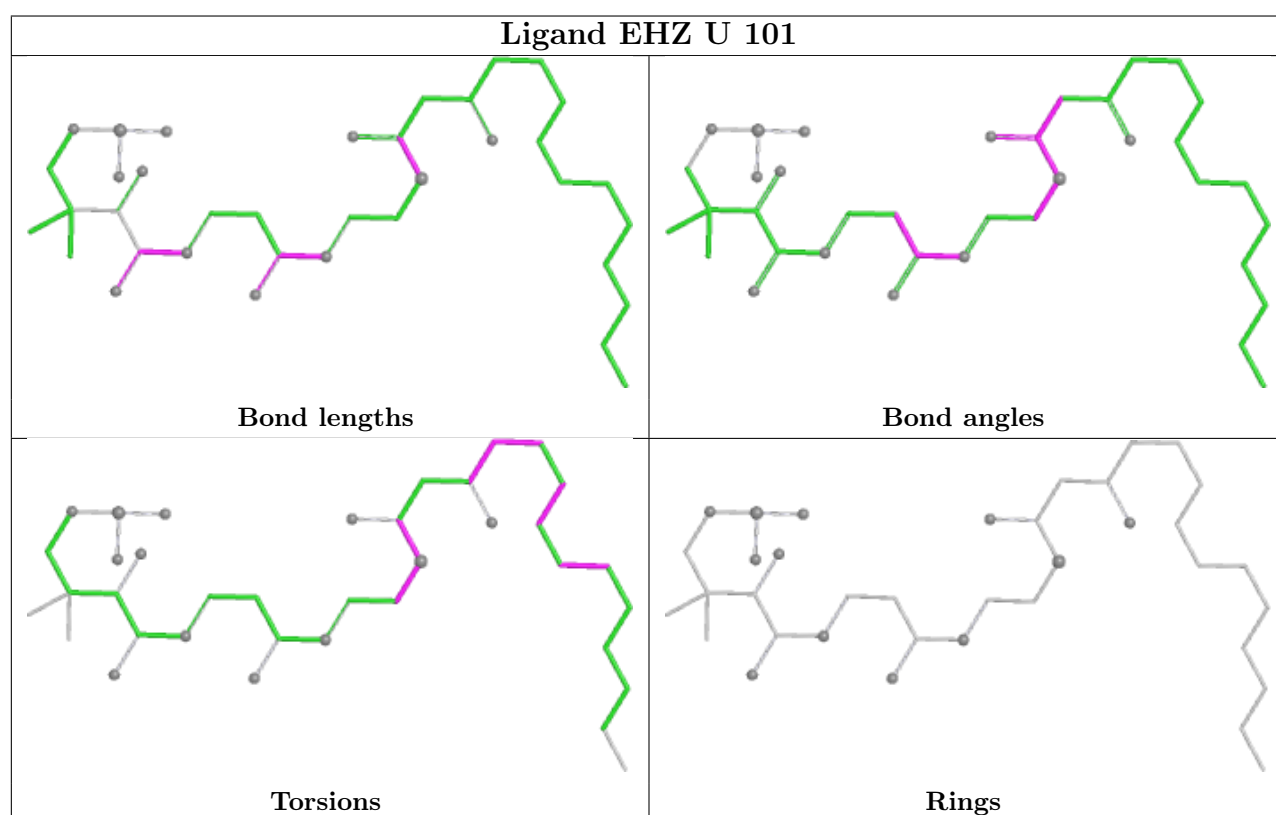
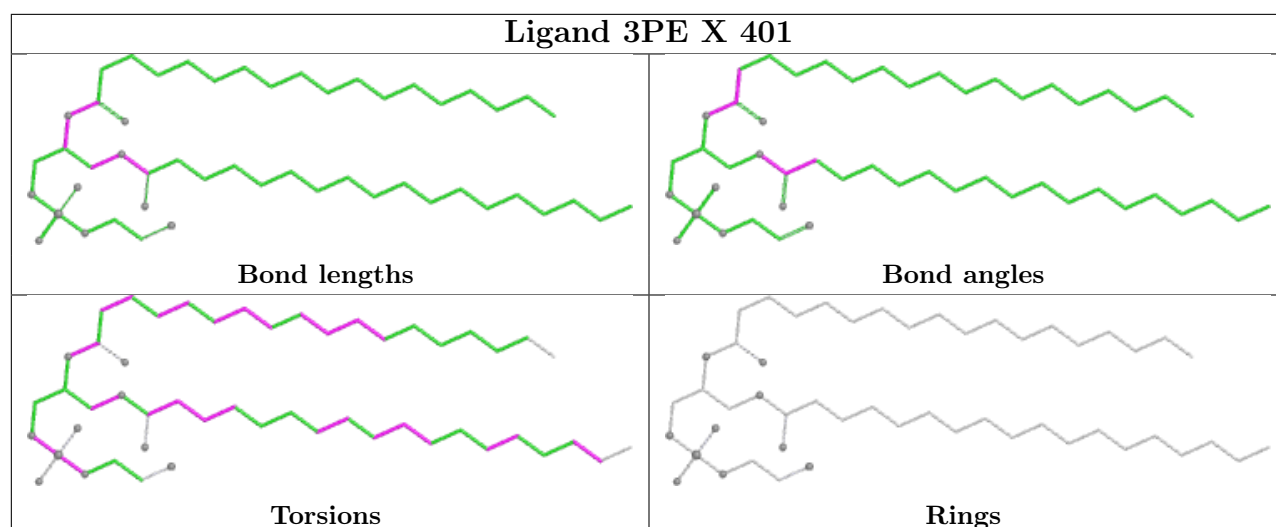
23 monomers are involved in 39 short contacts:

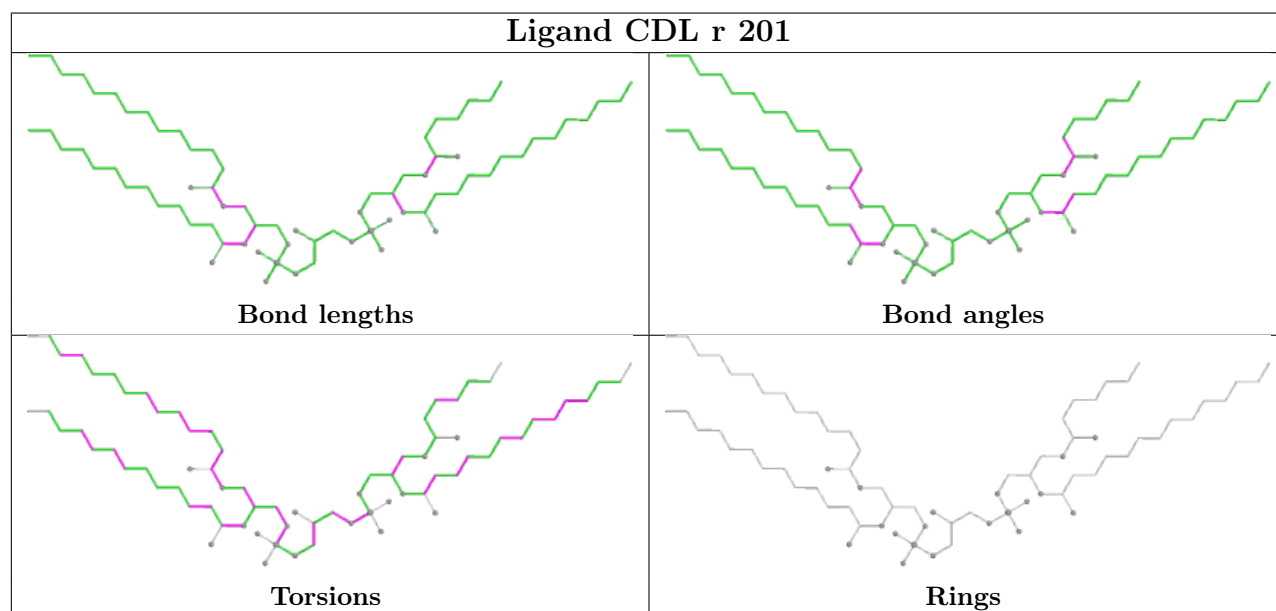
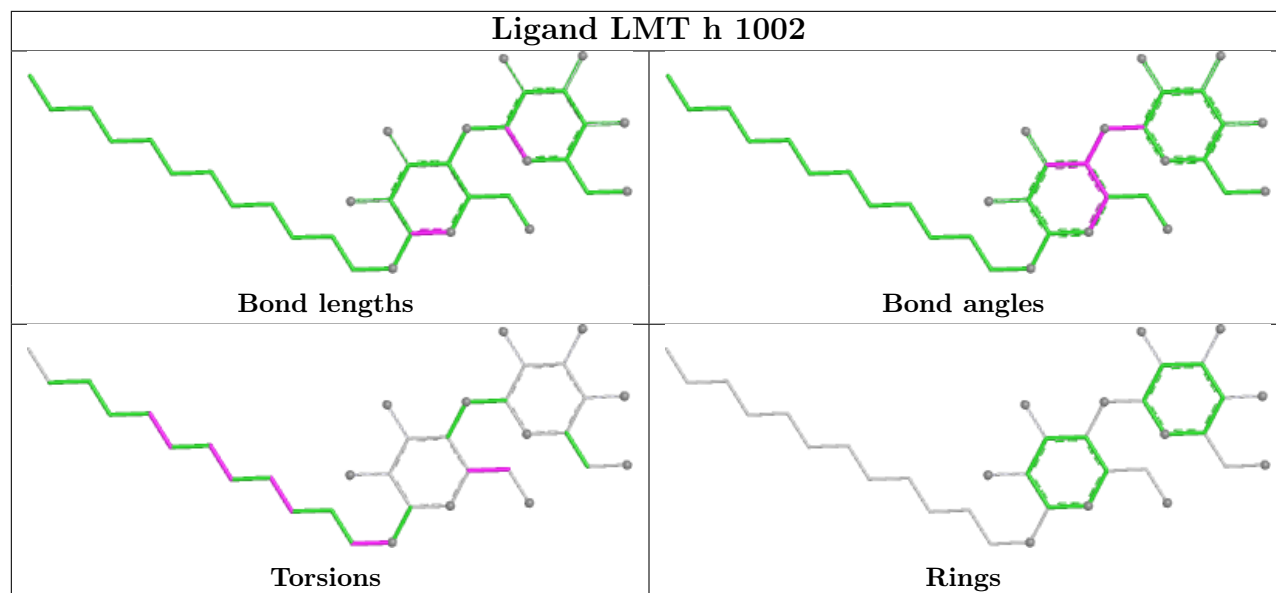
Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	Y	802	3PE	1	0
53	N	703	I49	4	0
51	X	401	3PE	2	0
45	h	1002	LMT	1	0
52	r	201	CDL	1	0
56	P	501	NDP	1	0
46	L	707	PC1	3	0
46	B	202	PC1	2	0
52	J	701	CDL	1	0
45	A	301	LMT	2	0
58	T	101	EHZ	1	0
51	L	705	3PE	2	0
46	B	203	PC1	2	0
46	A	303	PC1	1	0
54	O	401	GTP	3	0
52	h	1001	CDL	2	0
45	M	603	LMT	1	0
45	M	602	LMT	5	0
45	J	702	LMT	2	0
51	M	601	3PE	2	0
45	Y	804	LMT	1	0
49	F	501	FMN	1	0
51	M	605	3PE	2	0

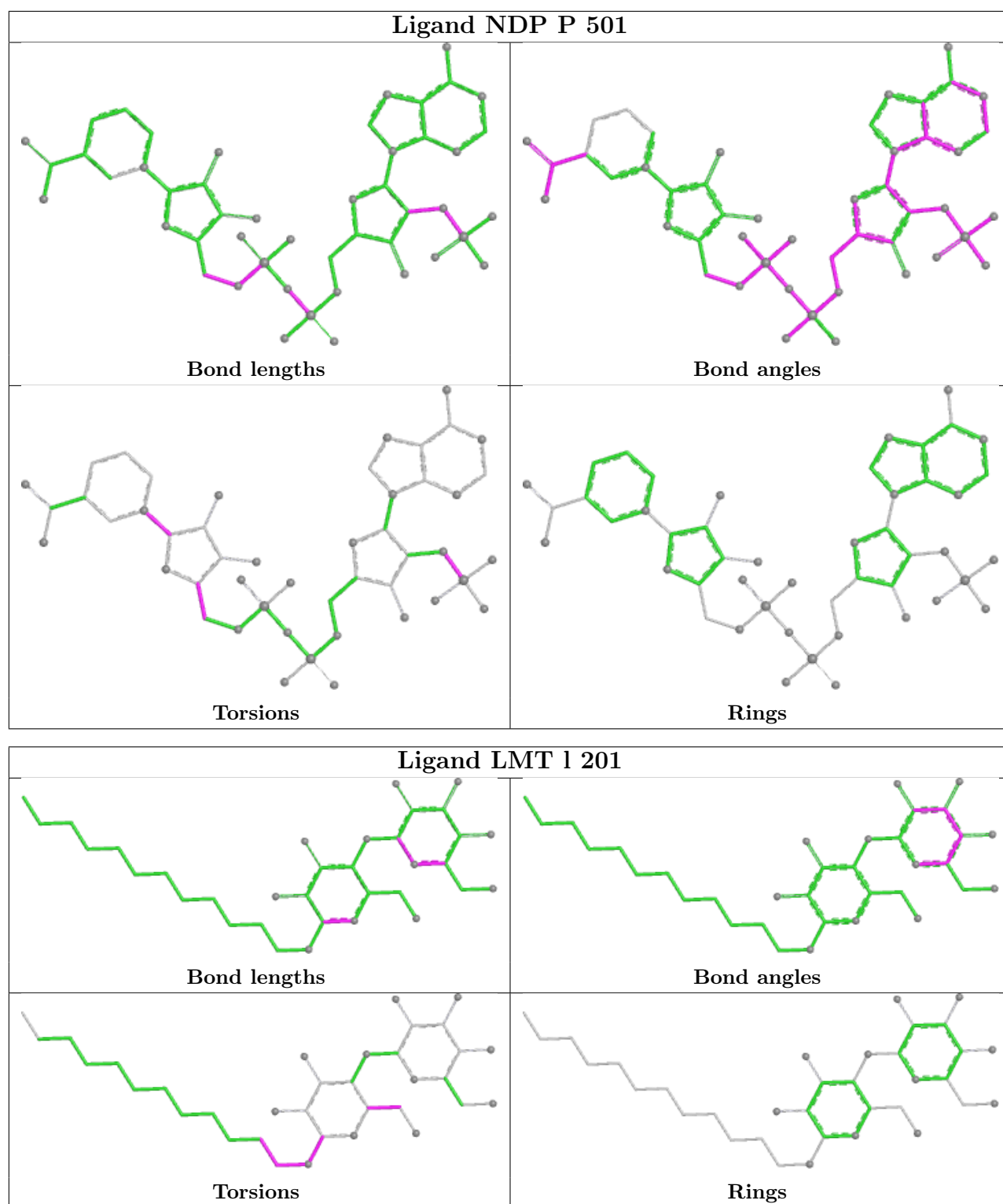
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

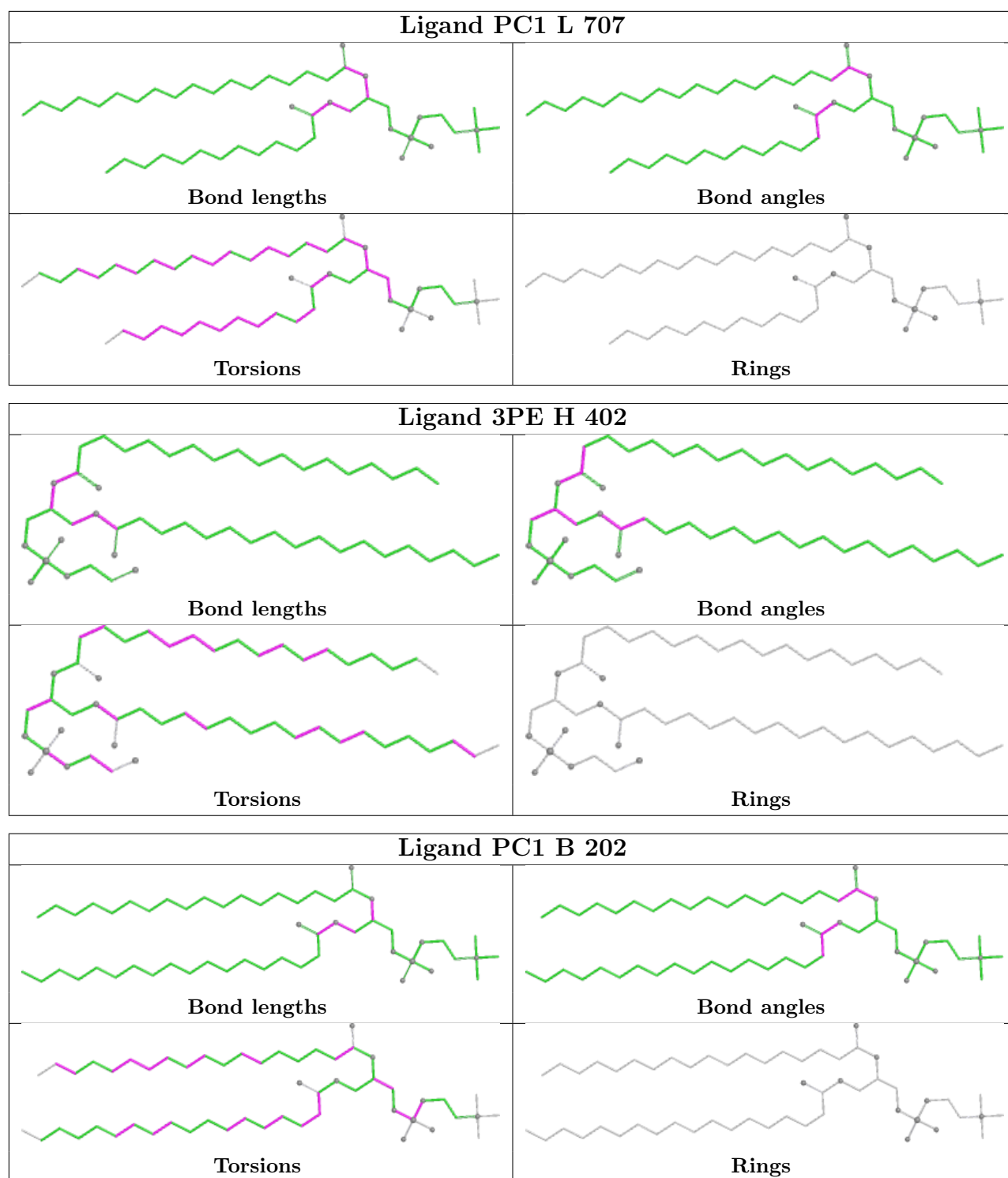


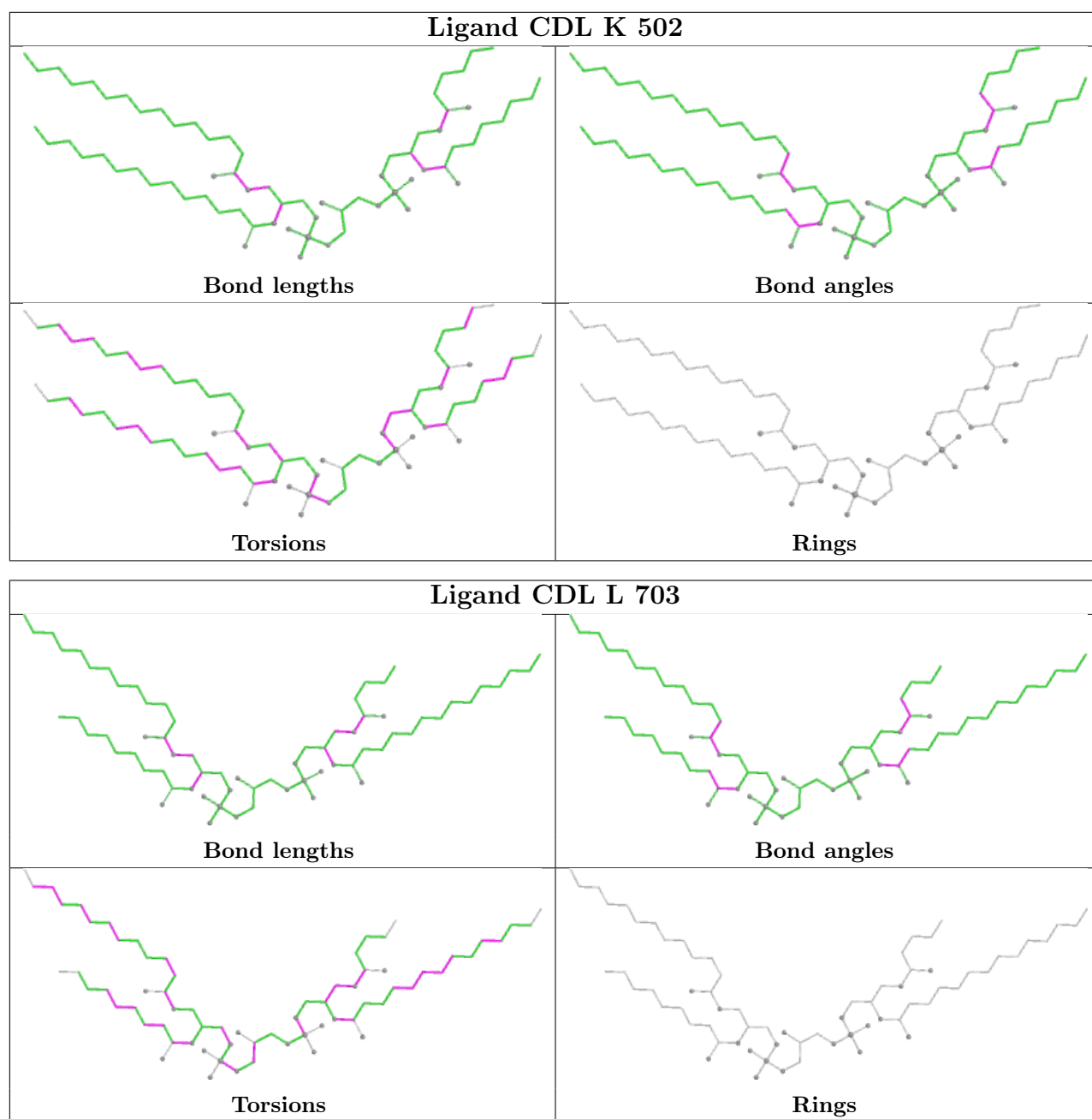


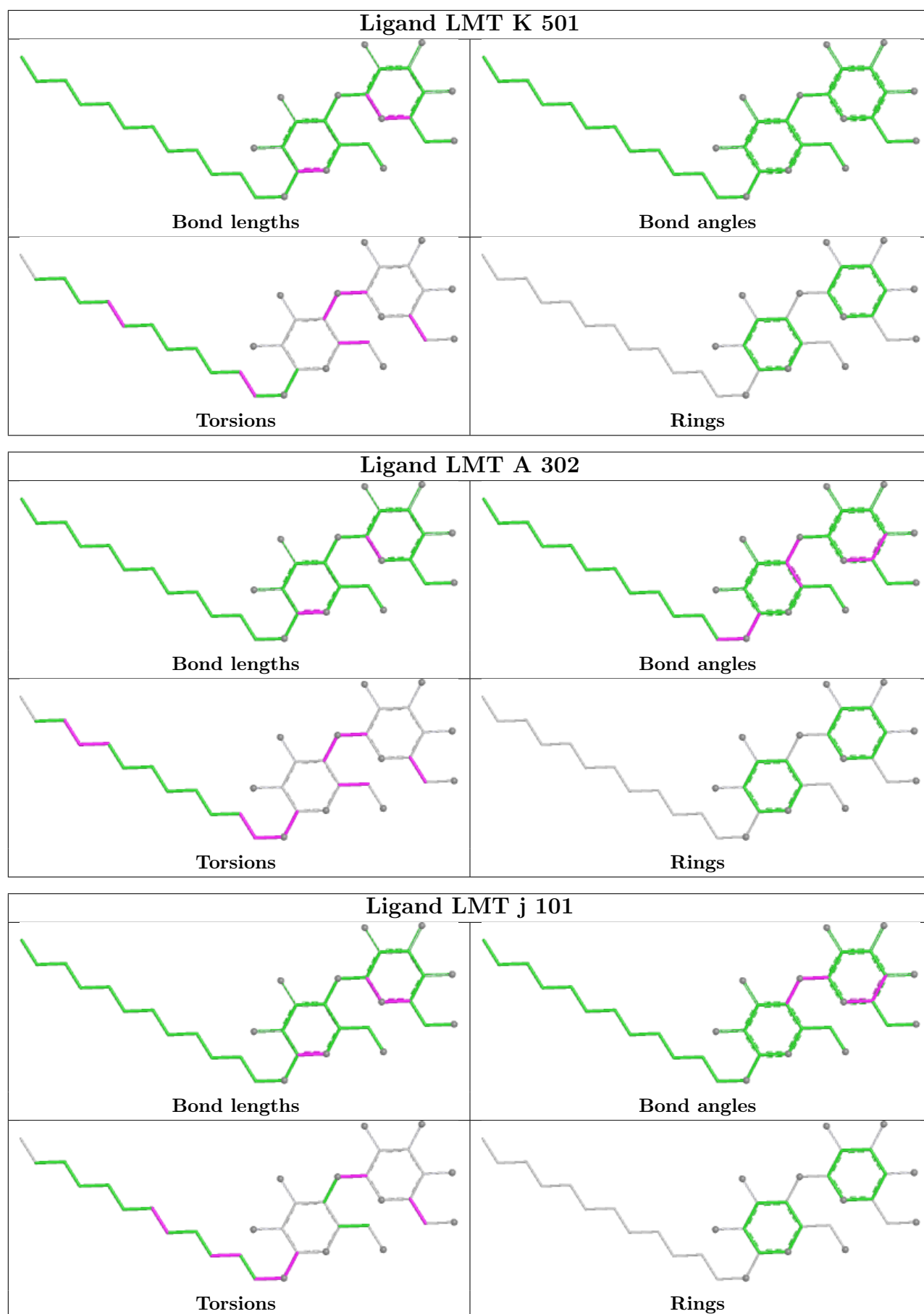


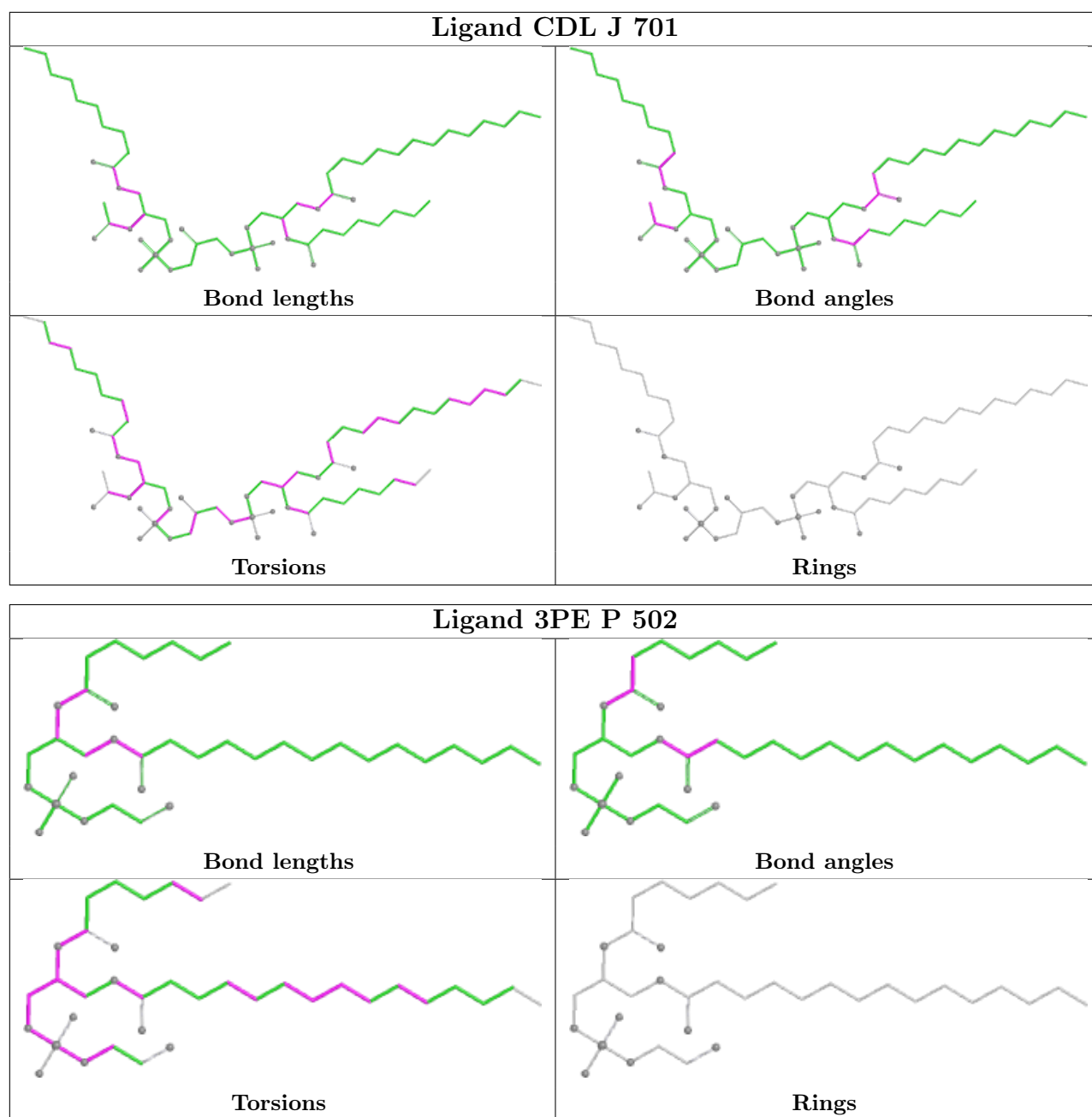


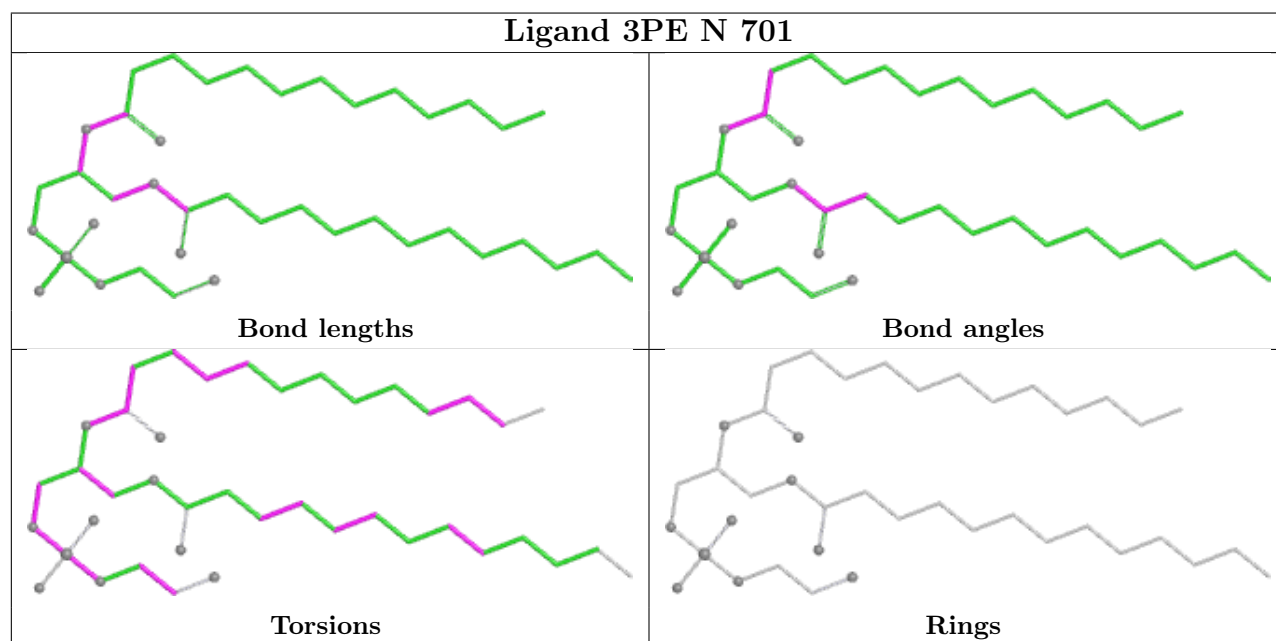
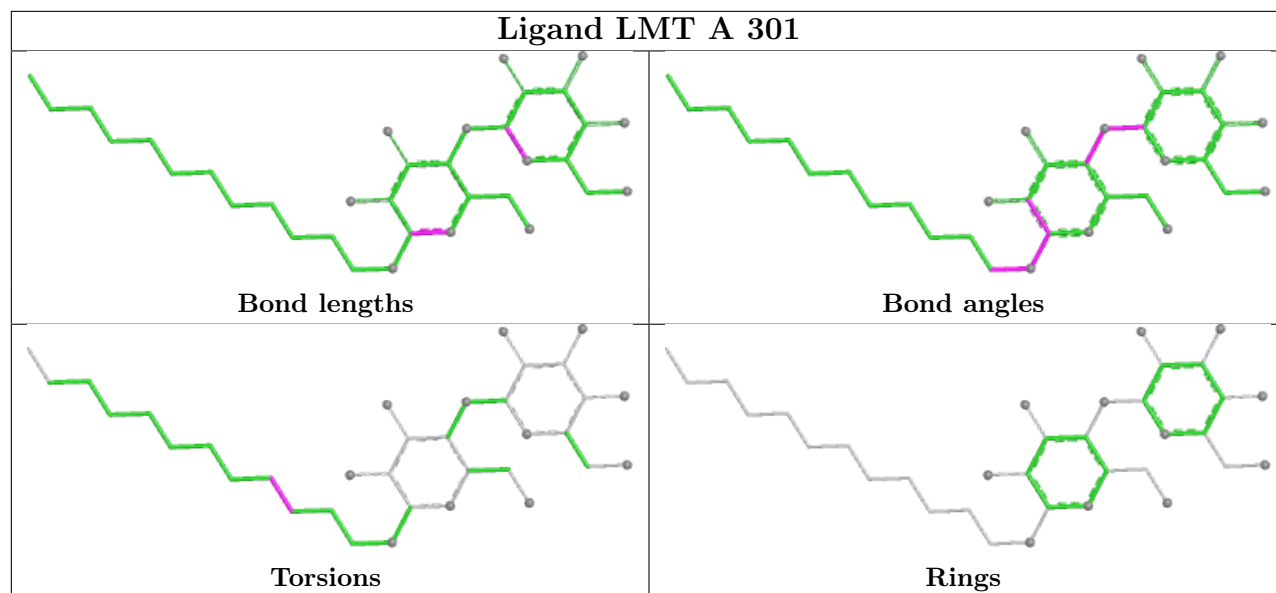


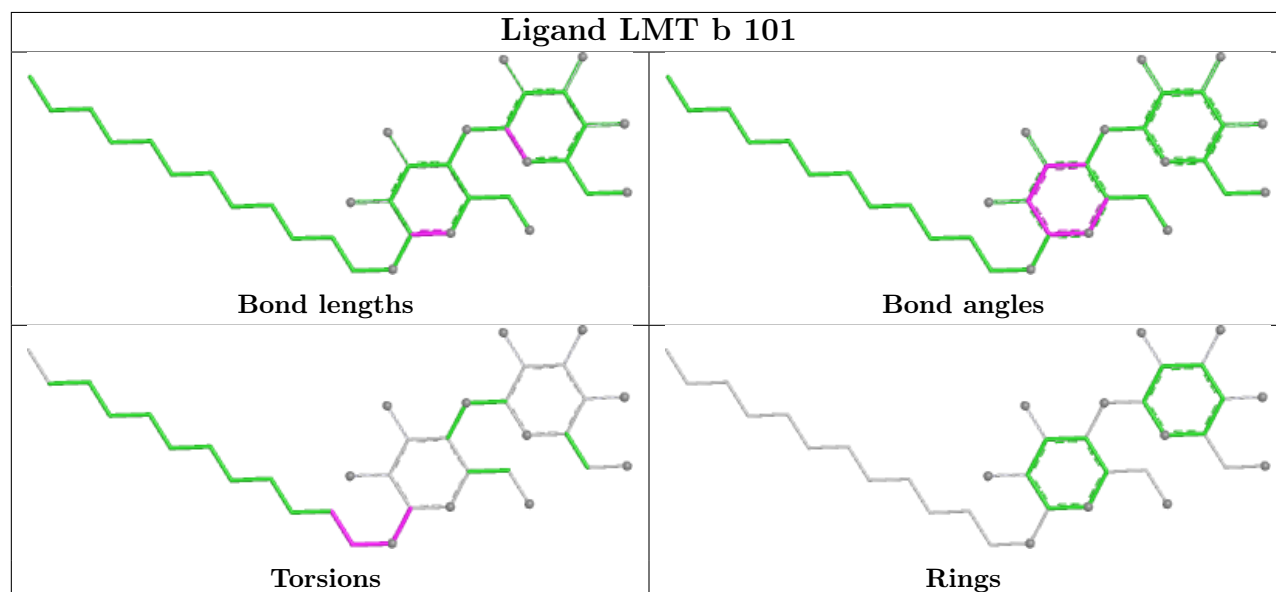
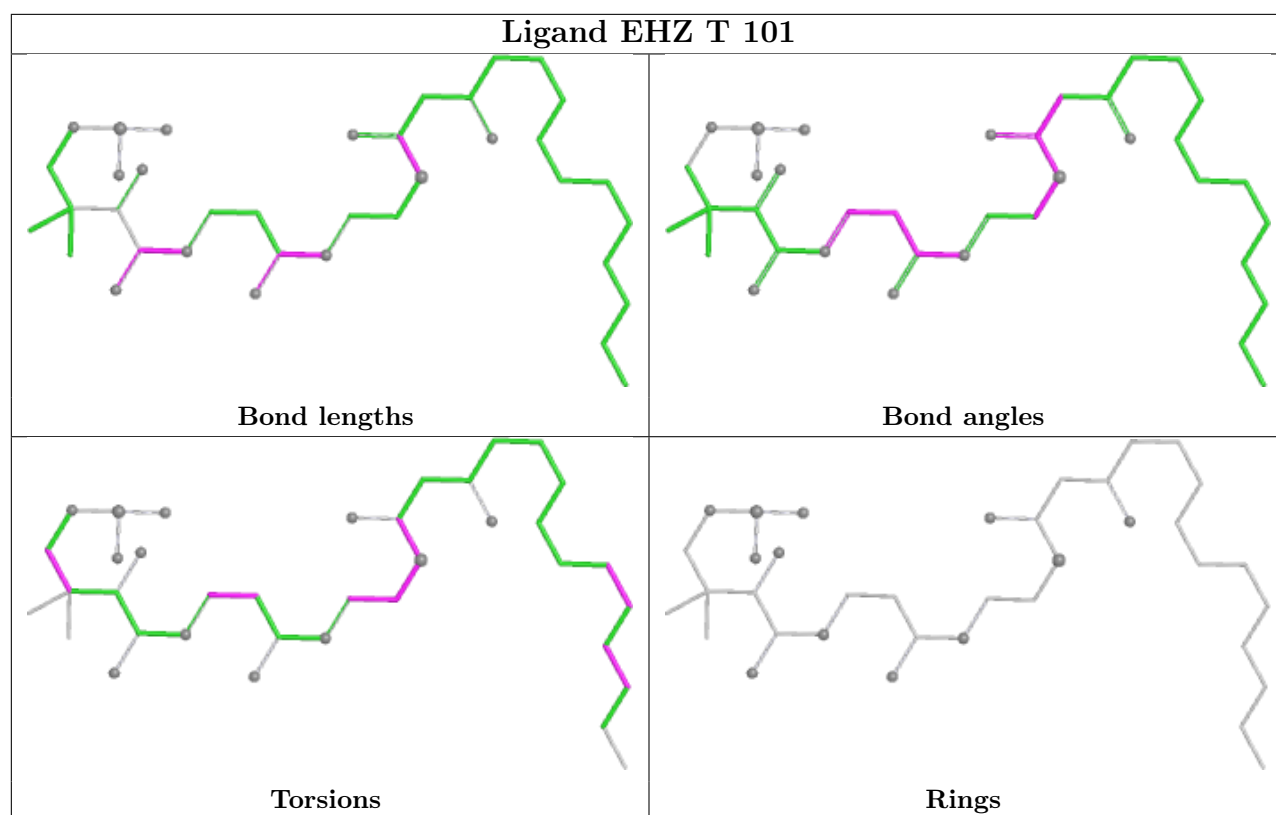


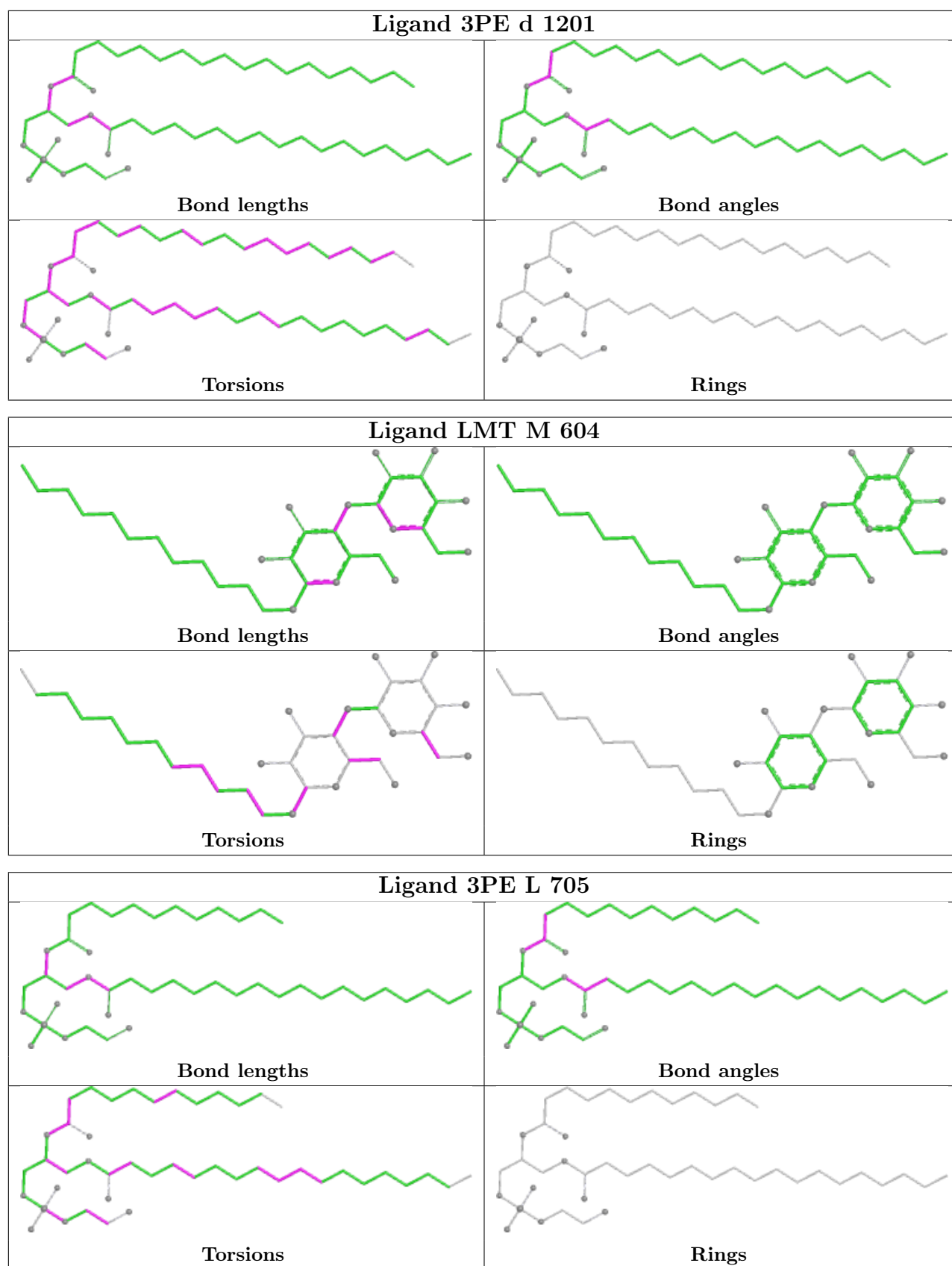


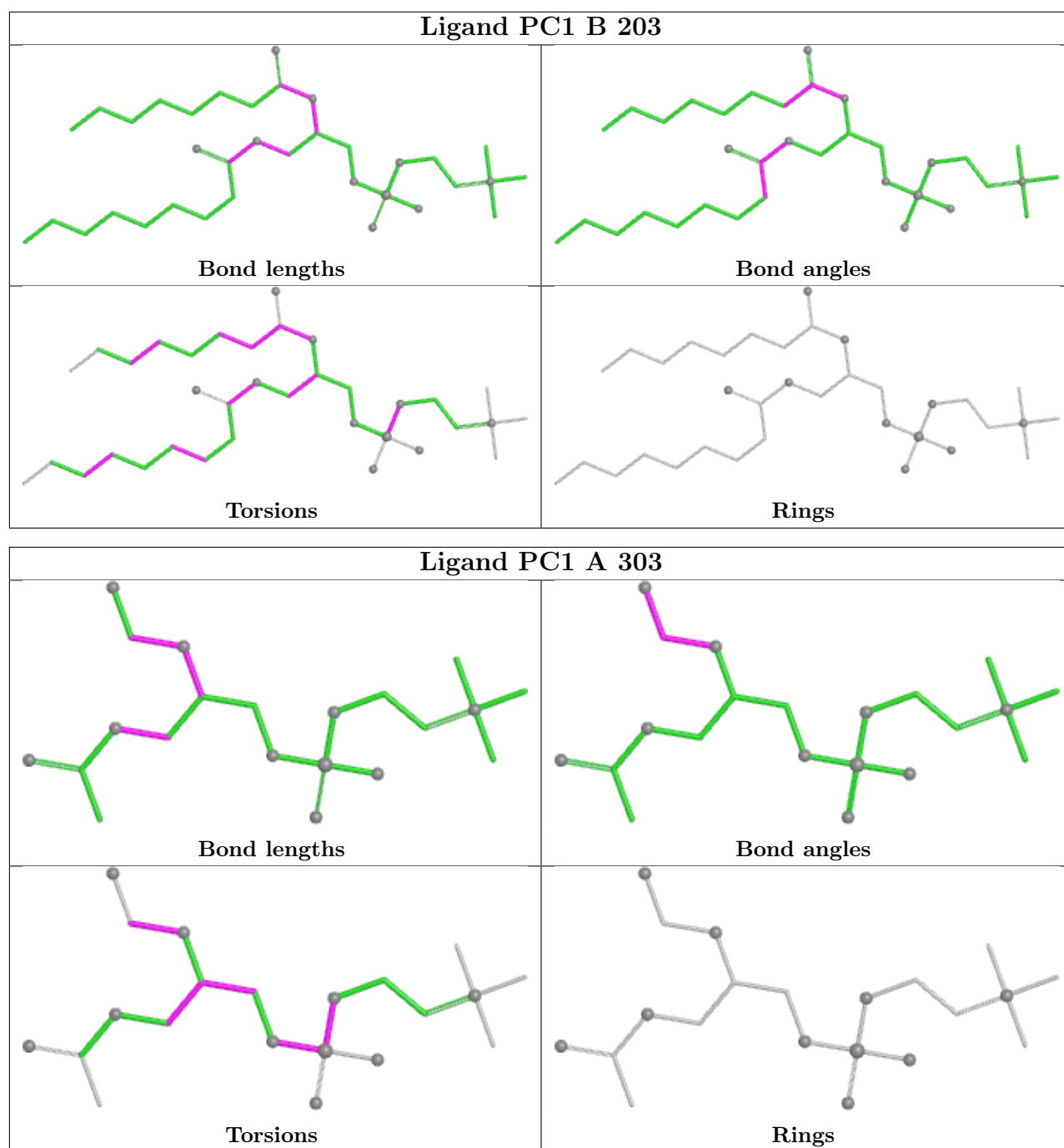


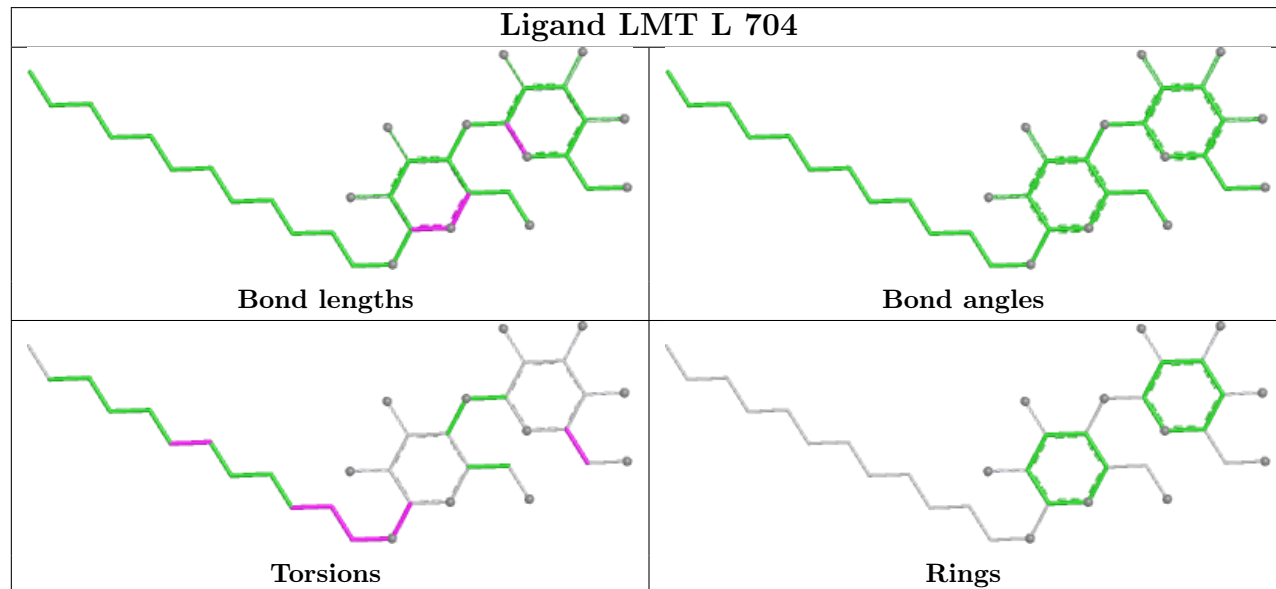
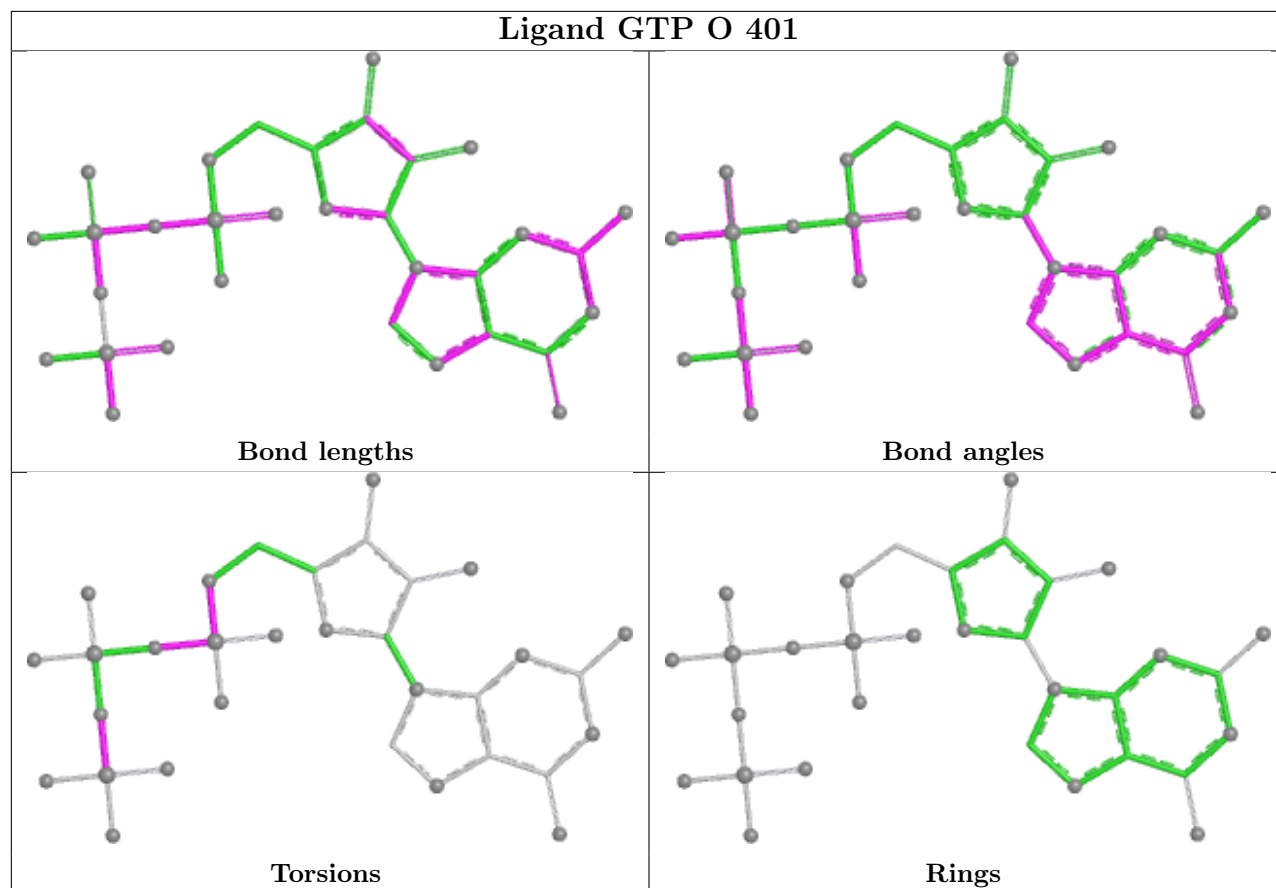


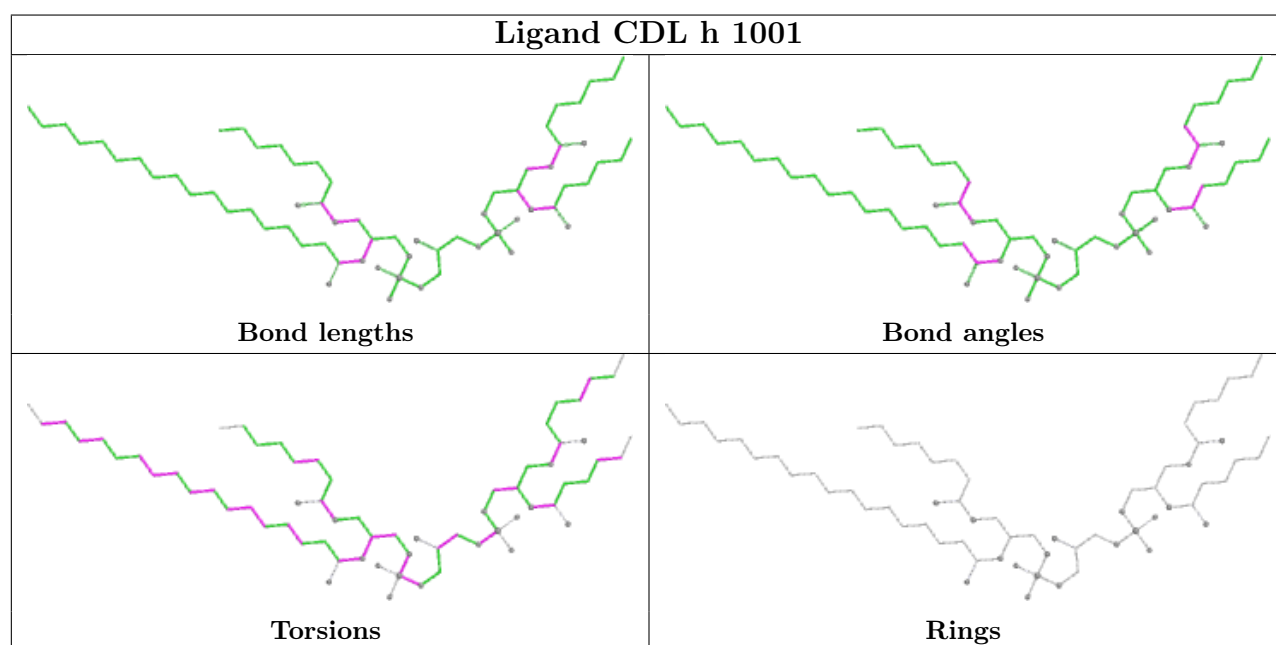
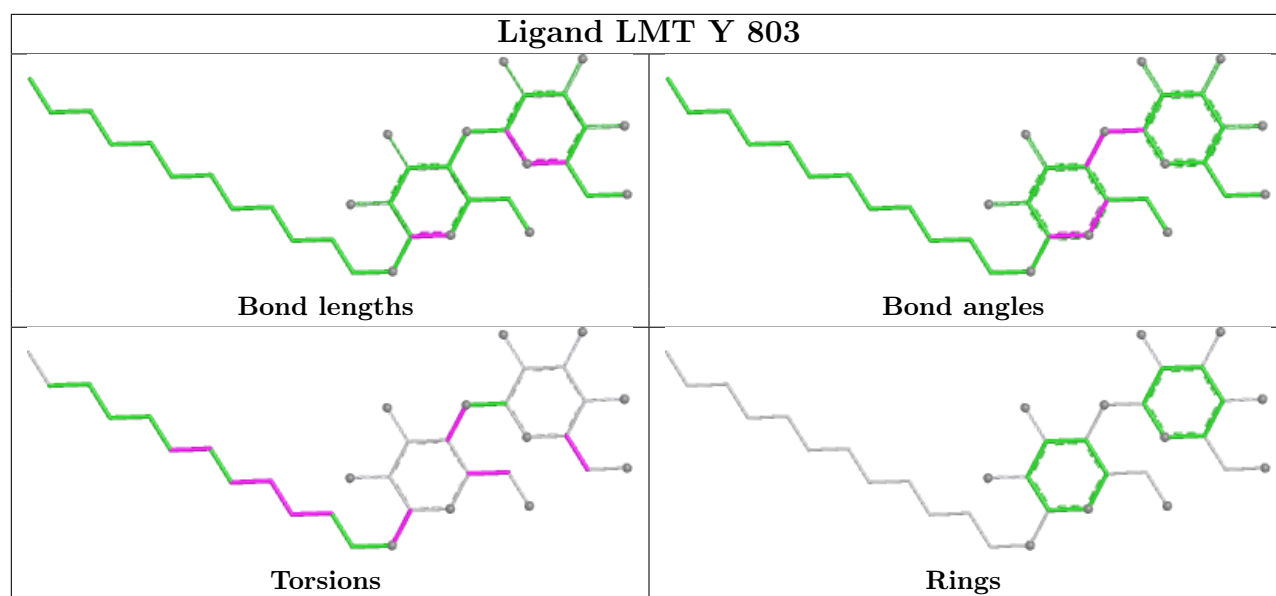


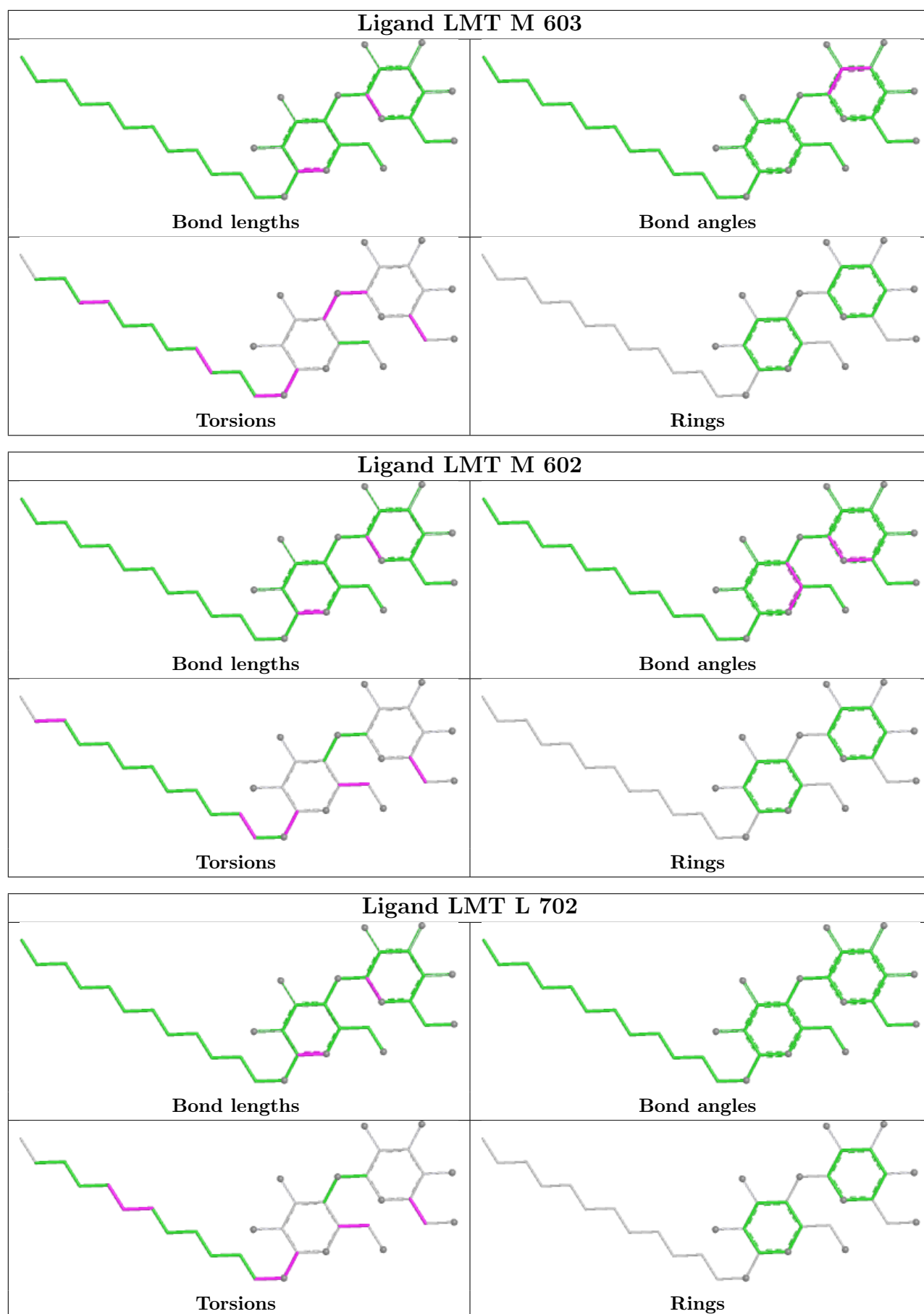


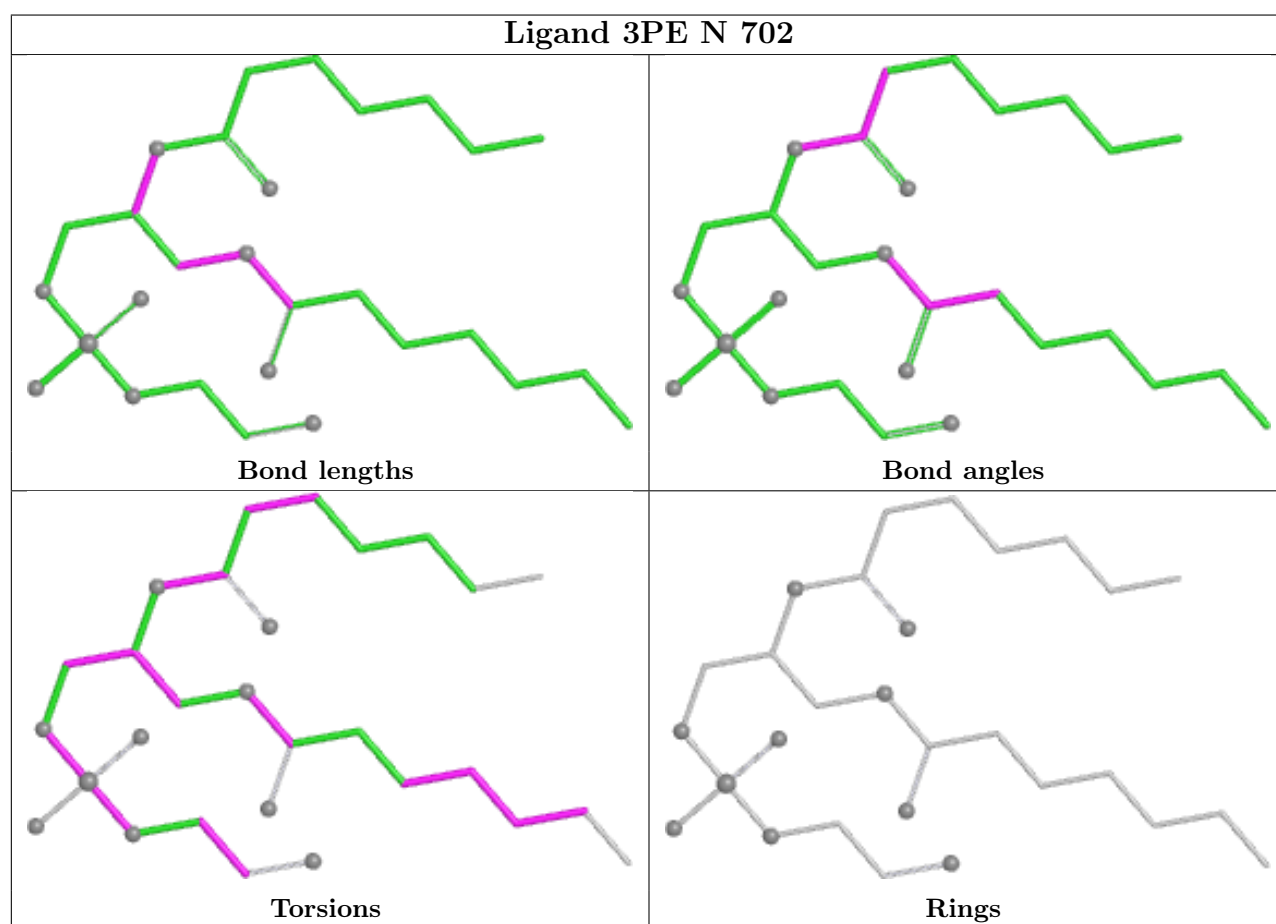
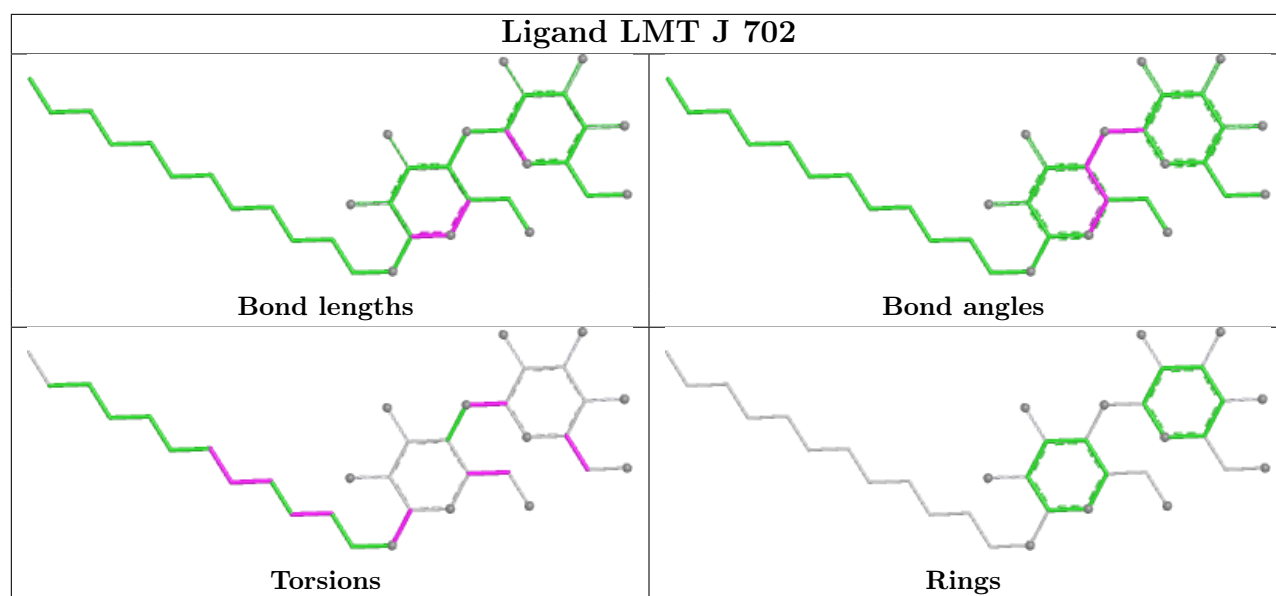


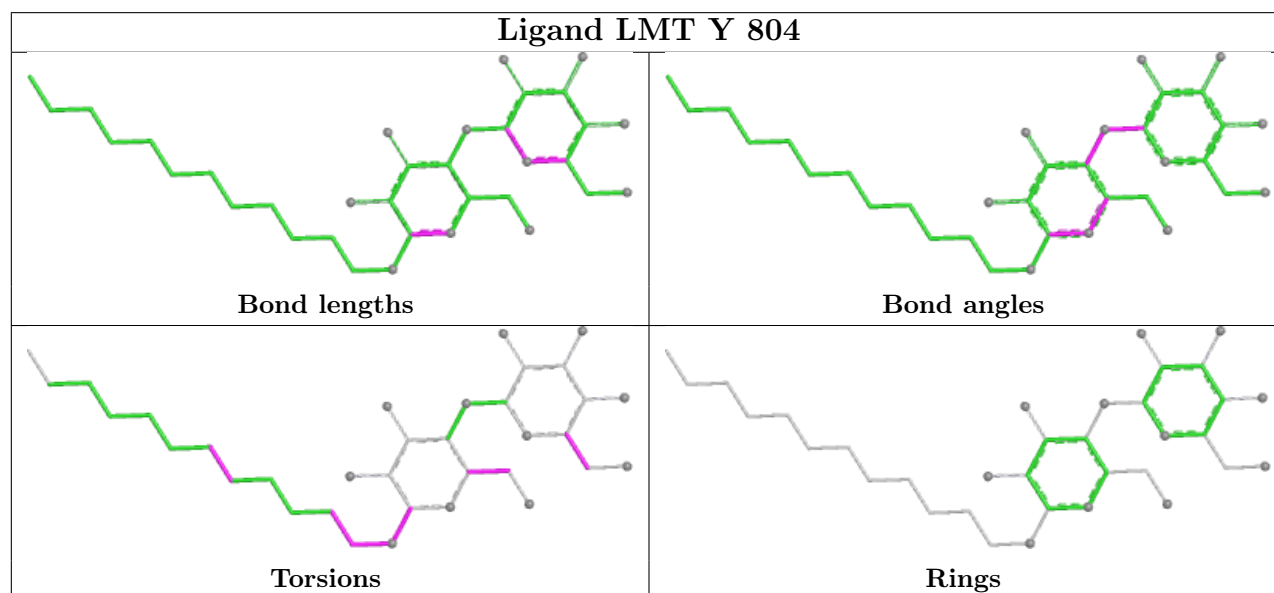
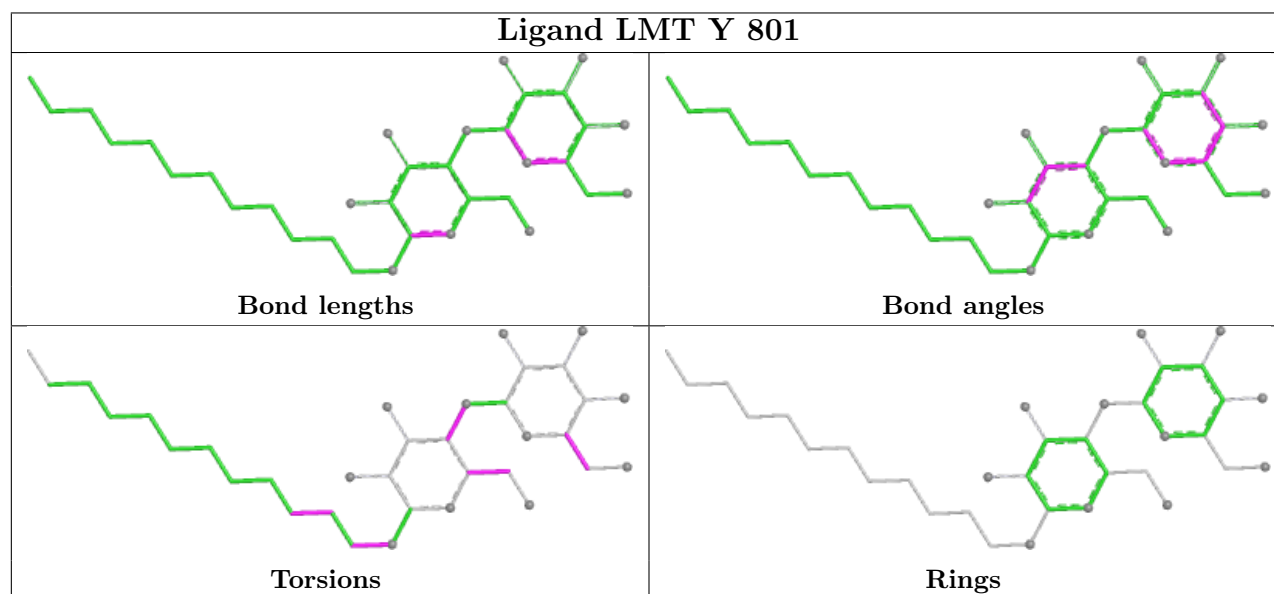
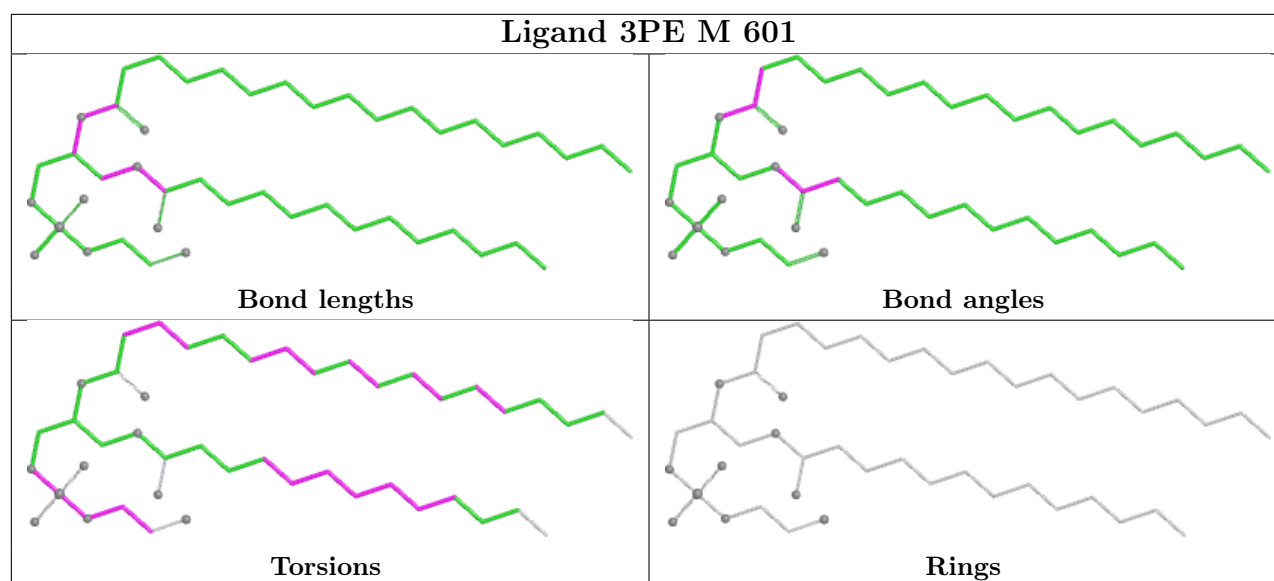


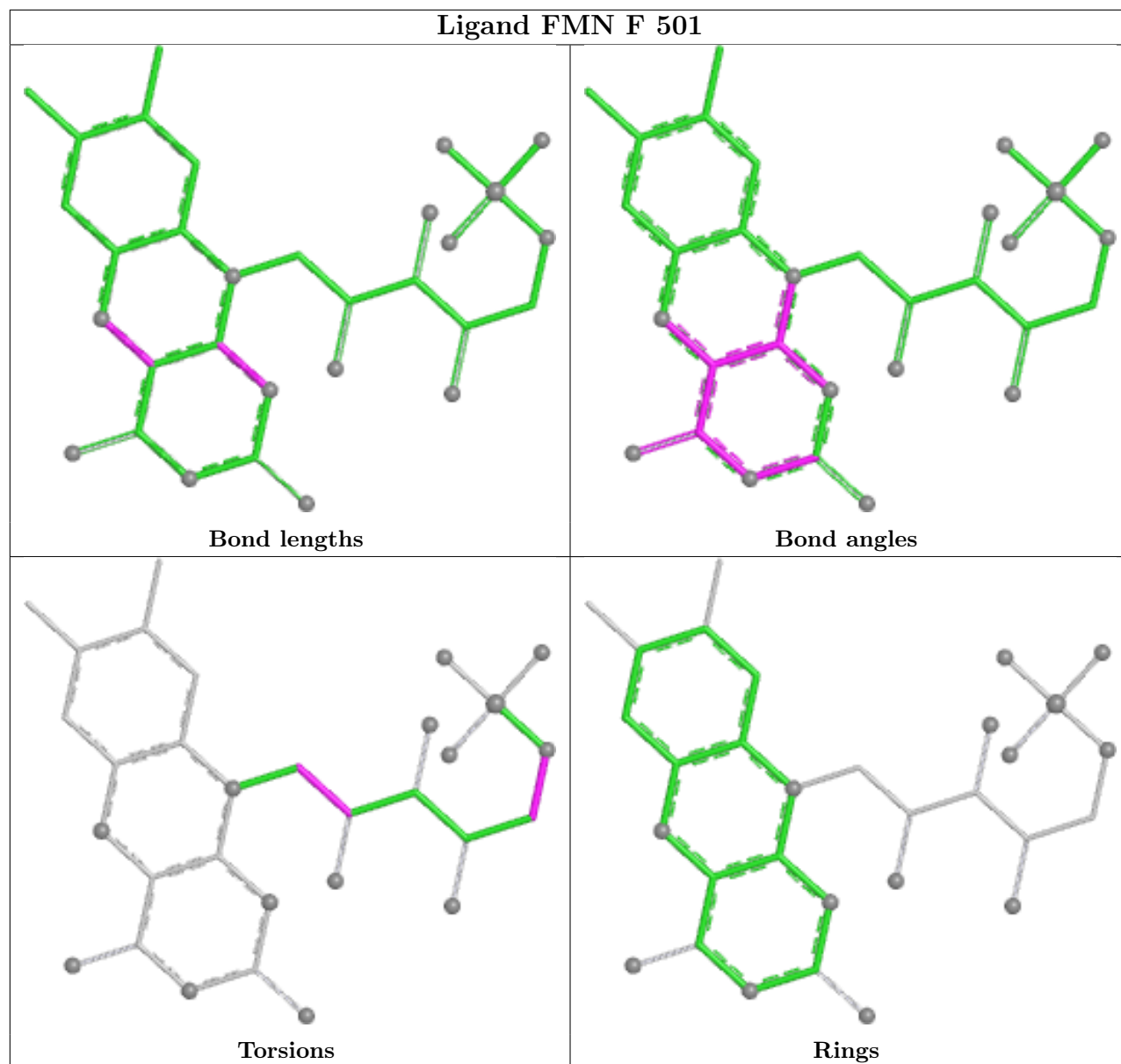


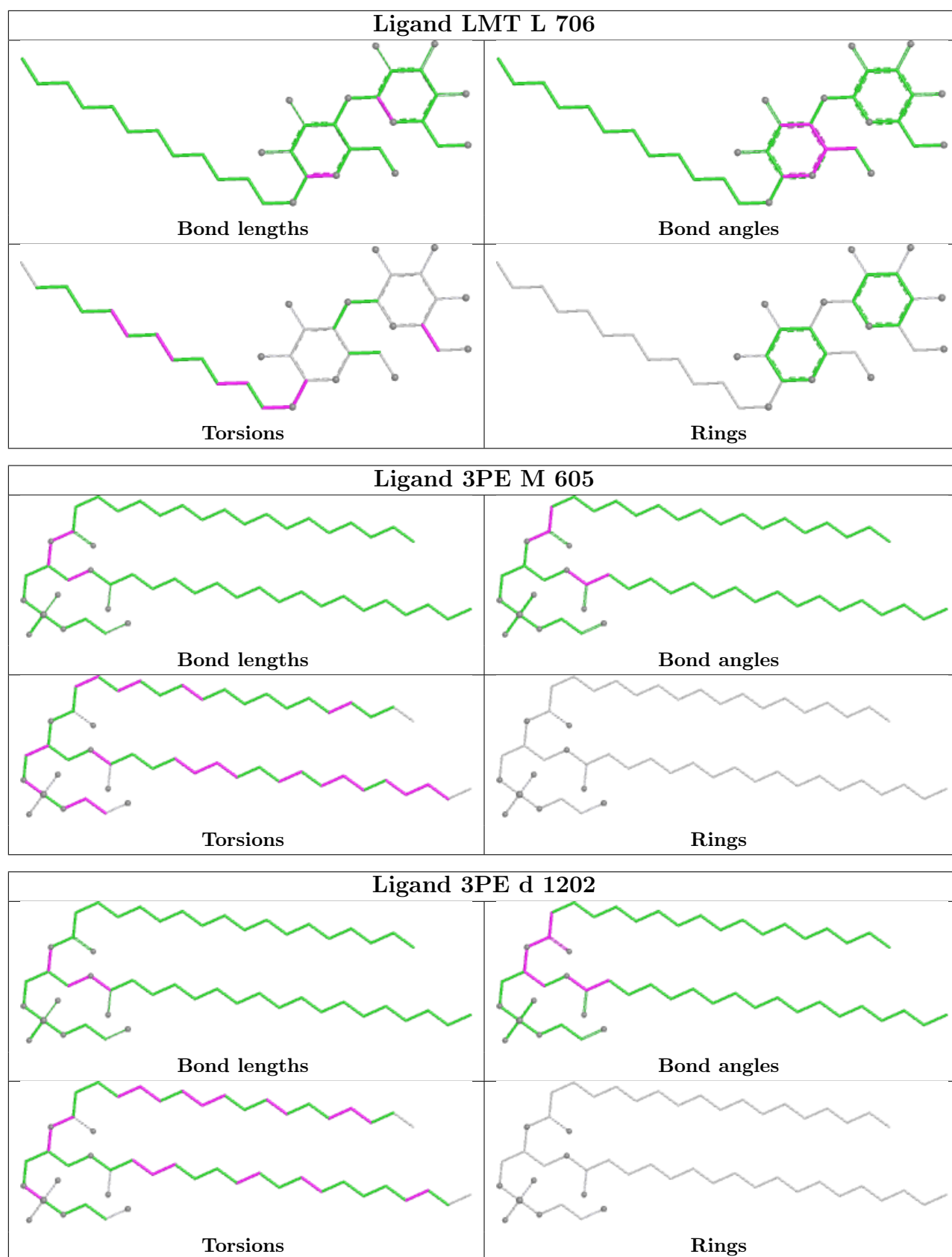












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

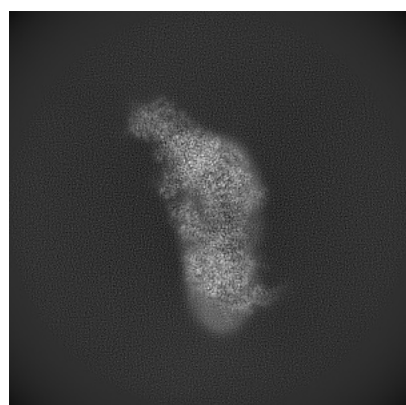
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14256. These allow visual inspection of the internal detail of the map and identification of artifacts.

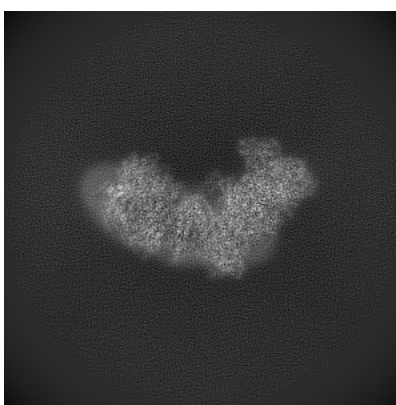
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

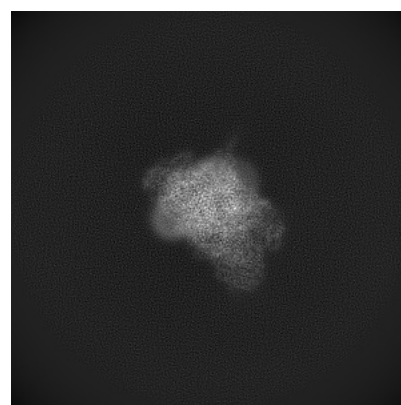
6.1.1 Primary map



X



Y

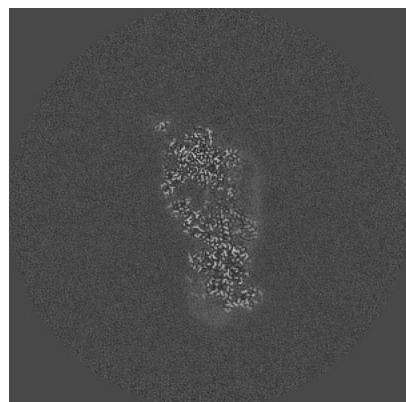


Z

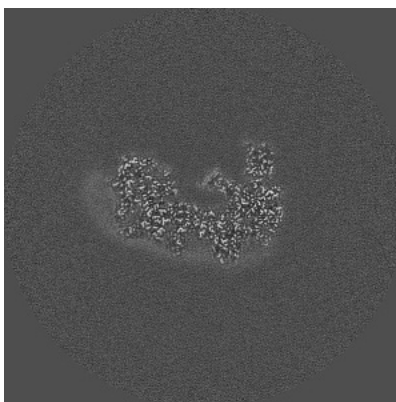
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

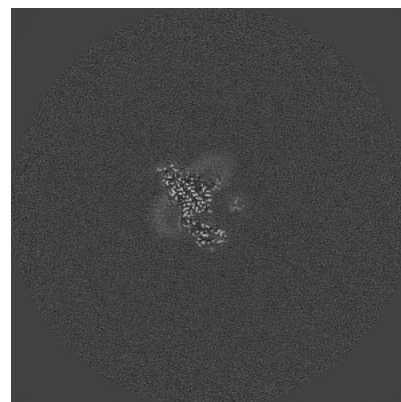
6.2.1 Primary map



X Index: 330



Y Index: 330

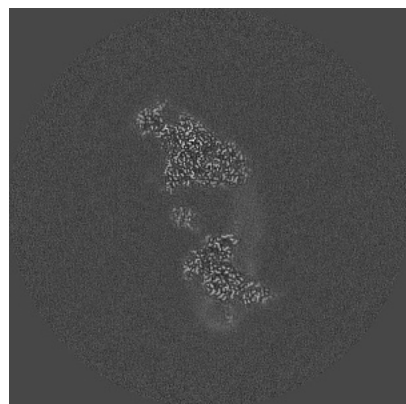


Z Index: 330

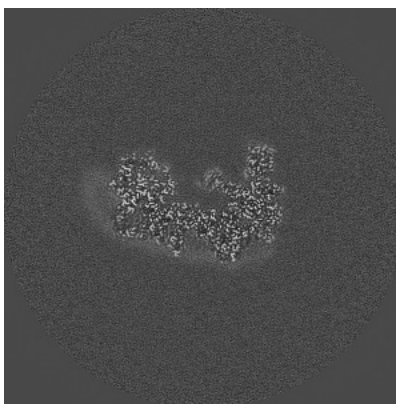
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

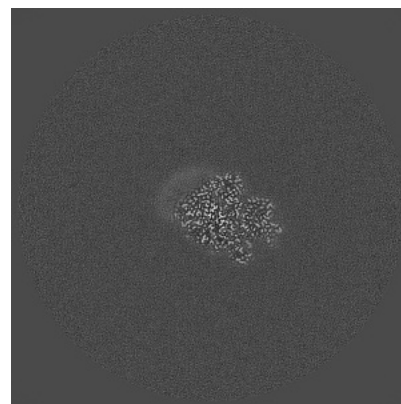
6.3.1 Primary map



X Index: 353



Y Index: 333

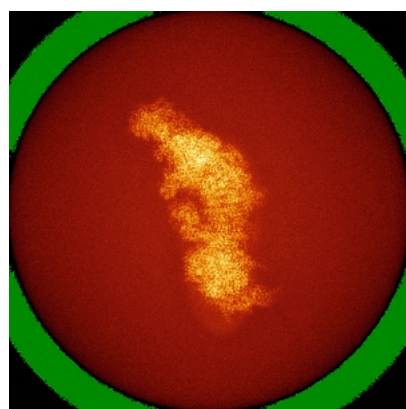


Z Index: 421

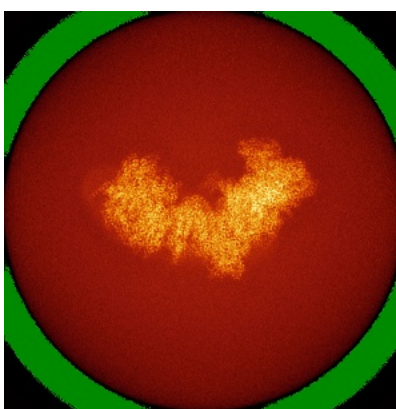
The images above show the largest variance slices of the map in three orthogonal directions.

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

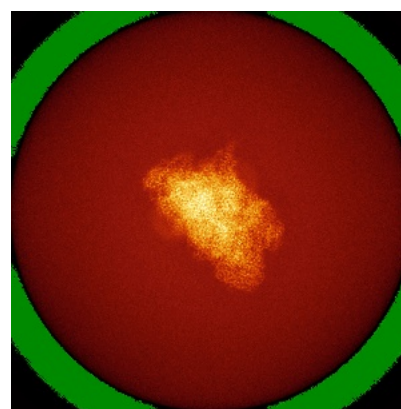
6.4.1 Primary map



X



Y

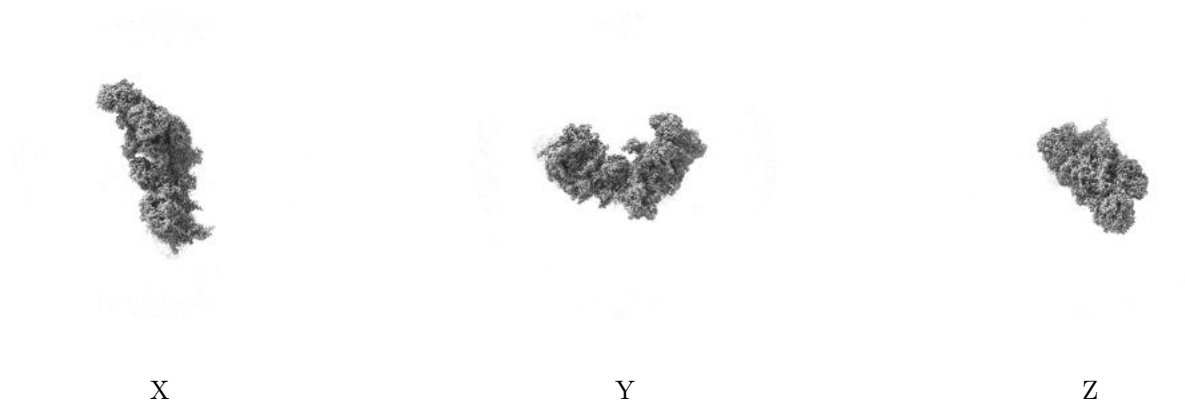


Z

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.

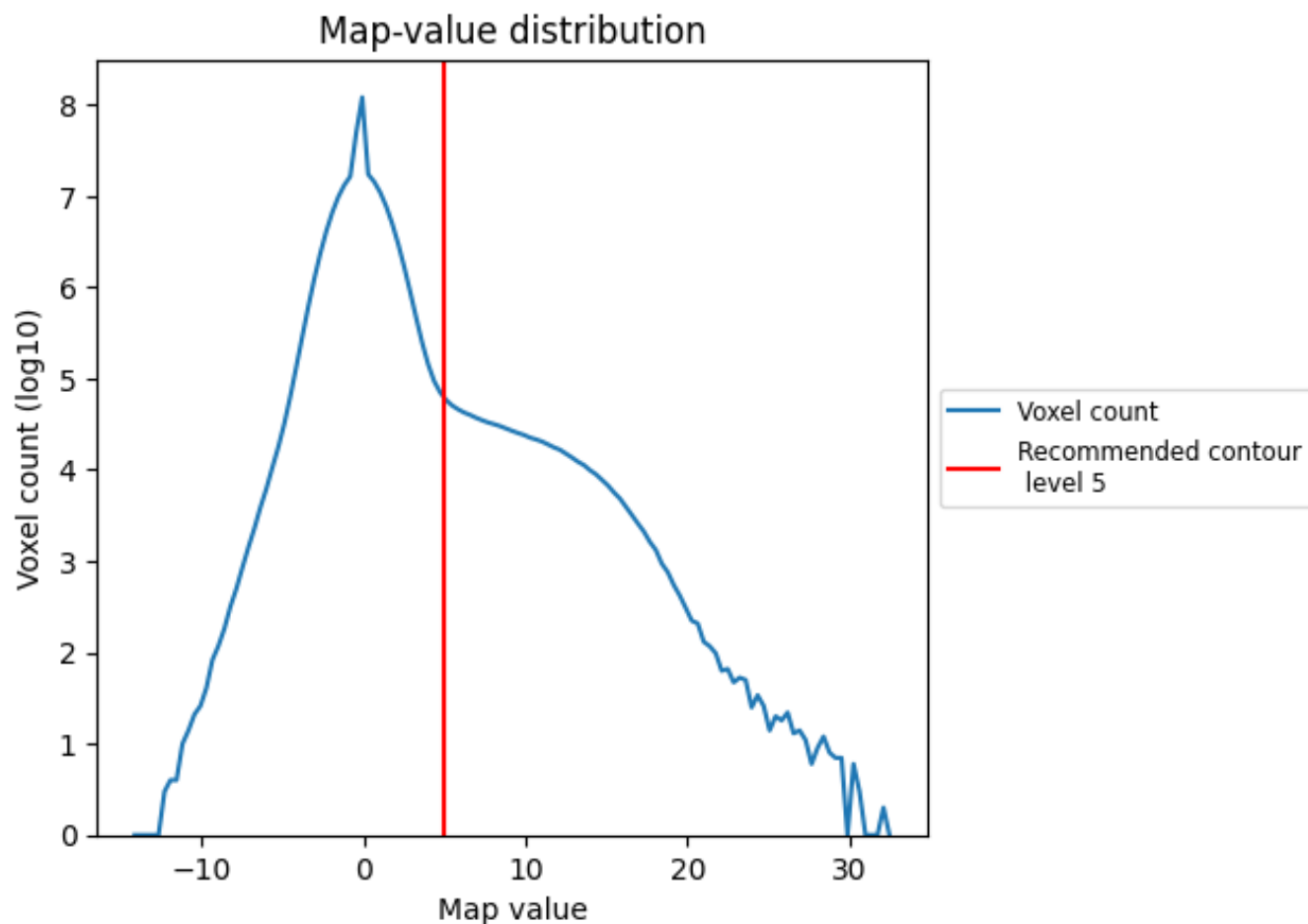
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

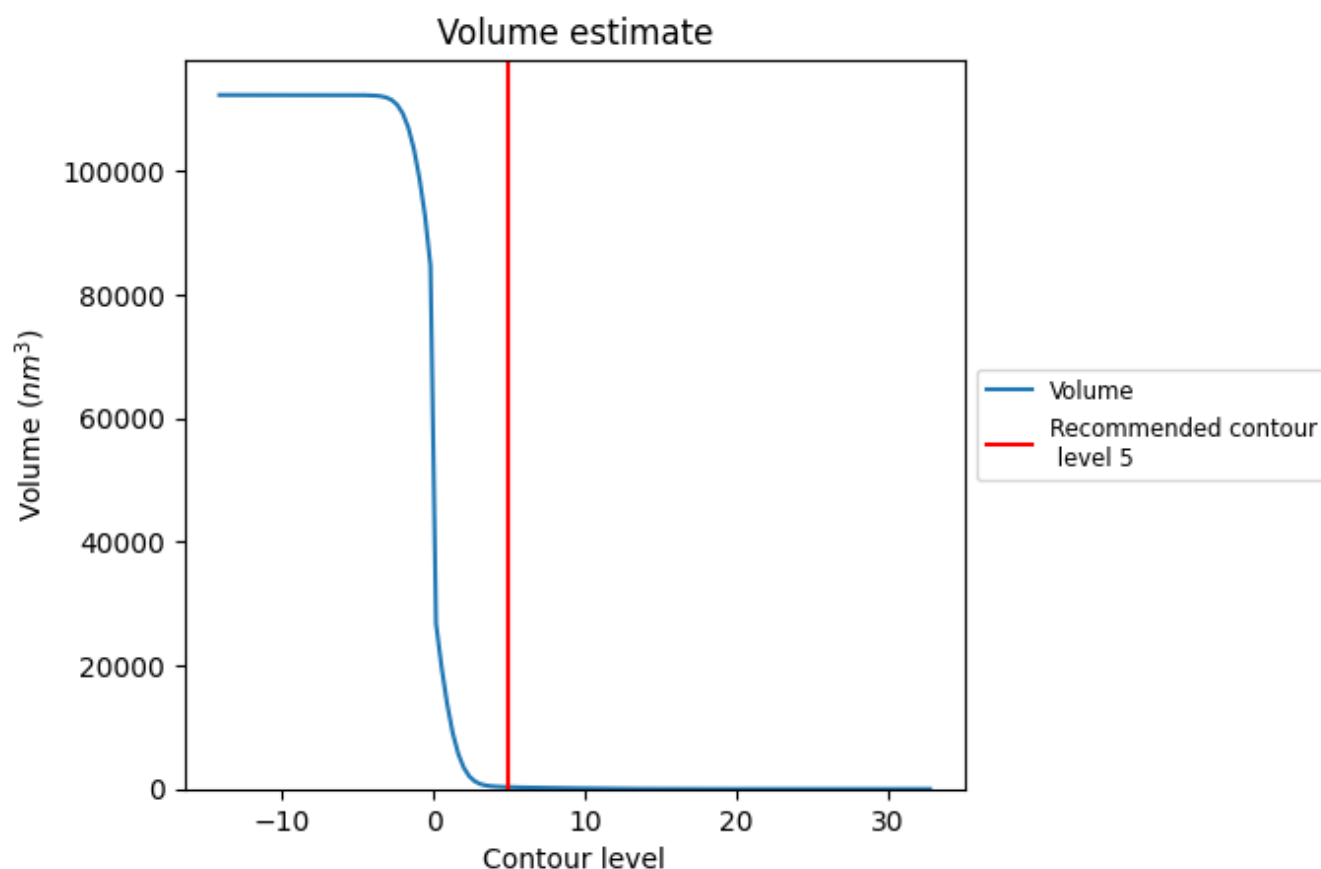
This section contains the results of statistical analysis of the map.

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.

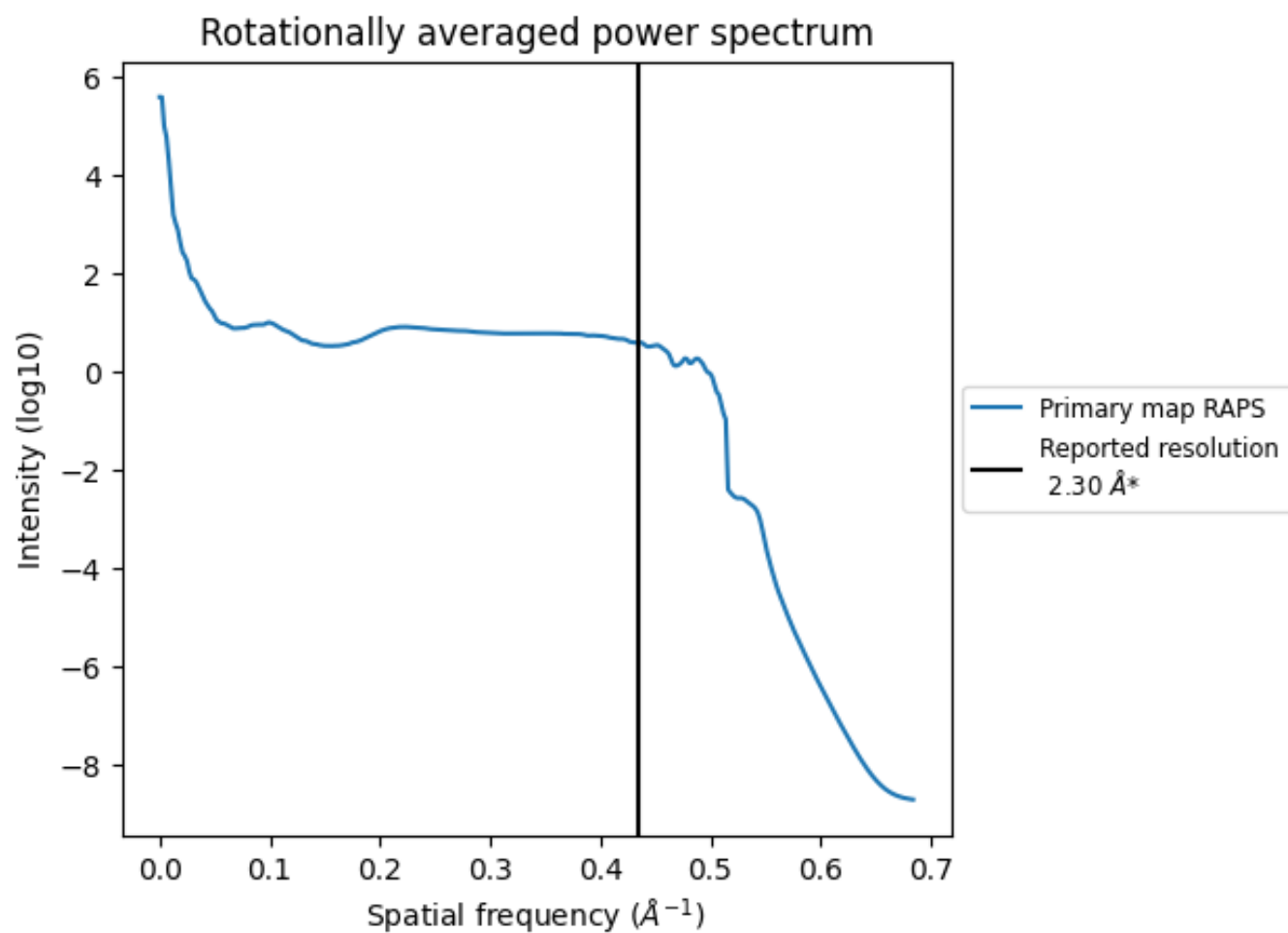
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 297 nm^3 ; this corresponds to an approximate mass of 269 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 0.435 Å⁻¹

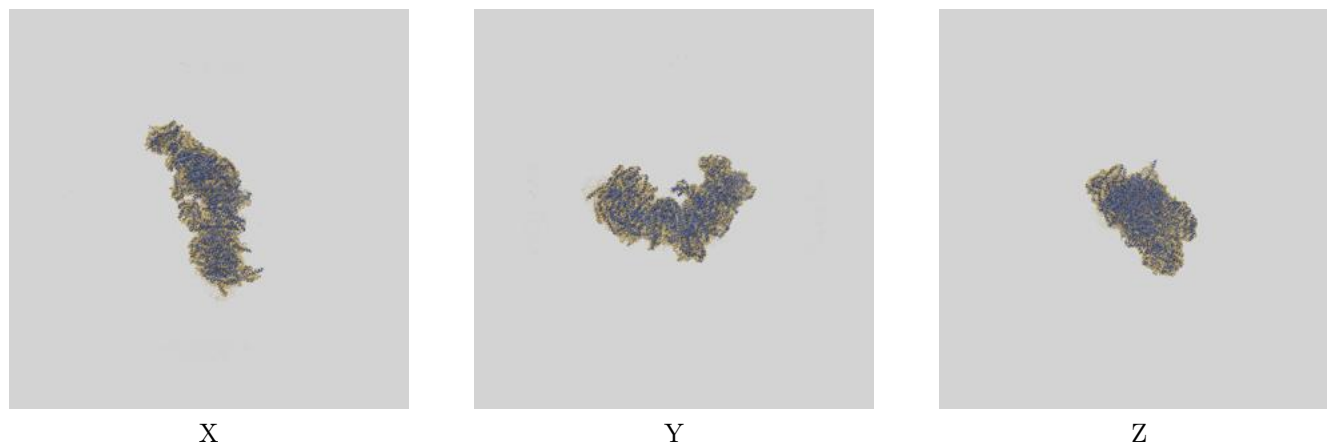
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

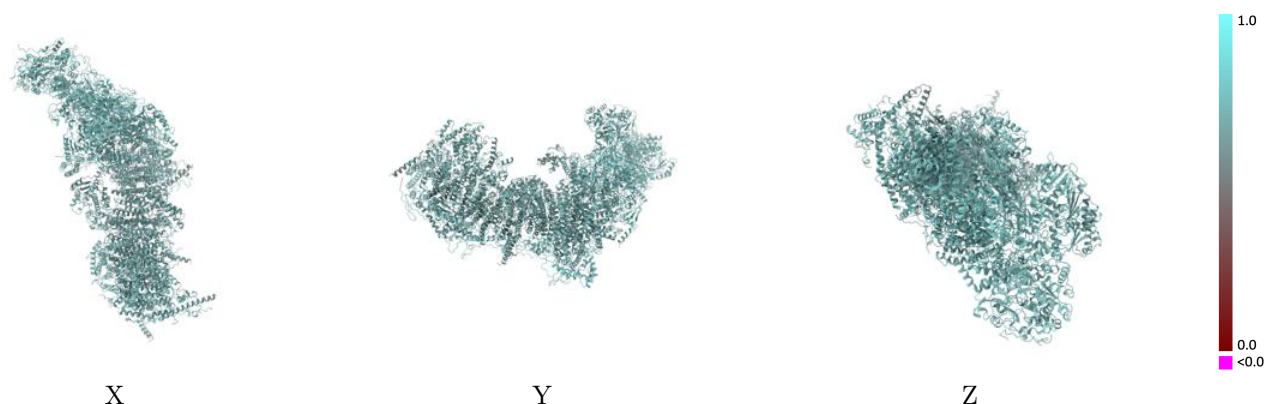
This section contains information regarding the fit between EMDB map EMD-14256 and PDB model 7R42. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

9.1 Map-model overlay [i](#)



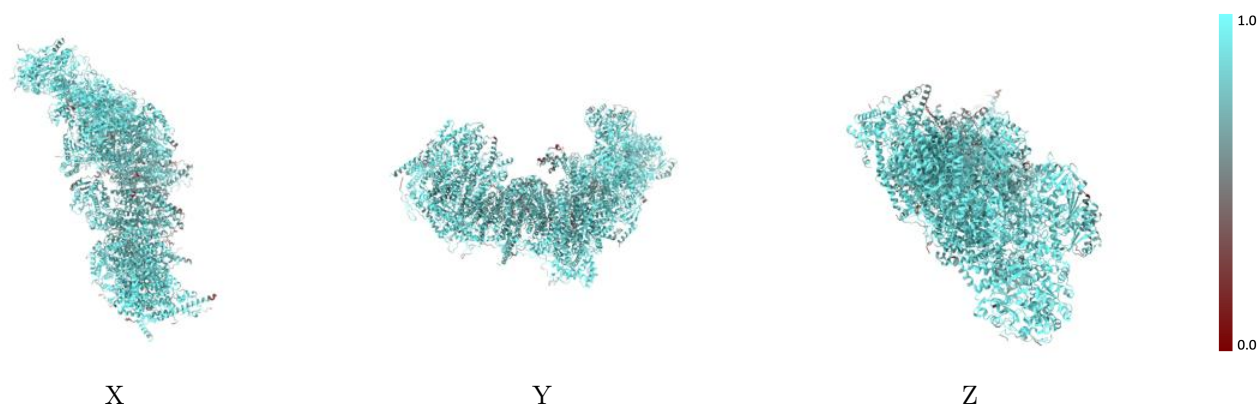
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



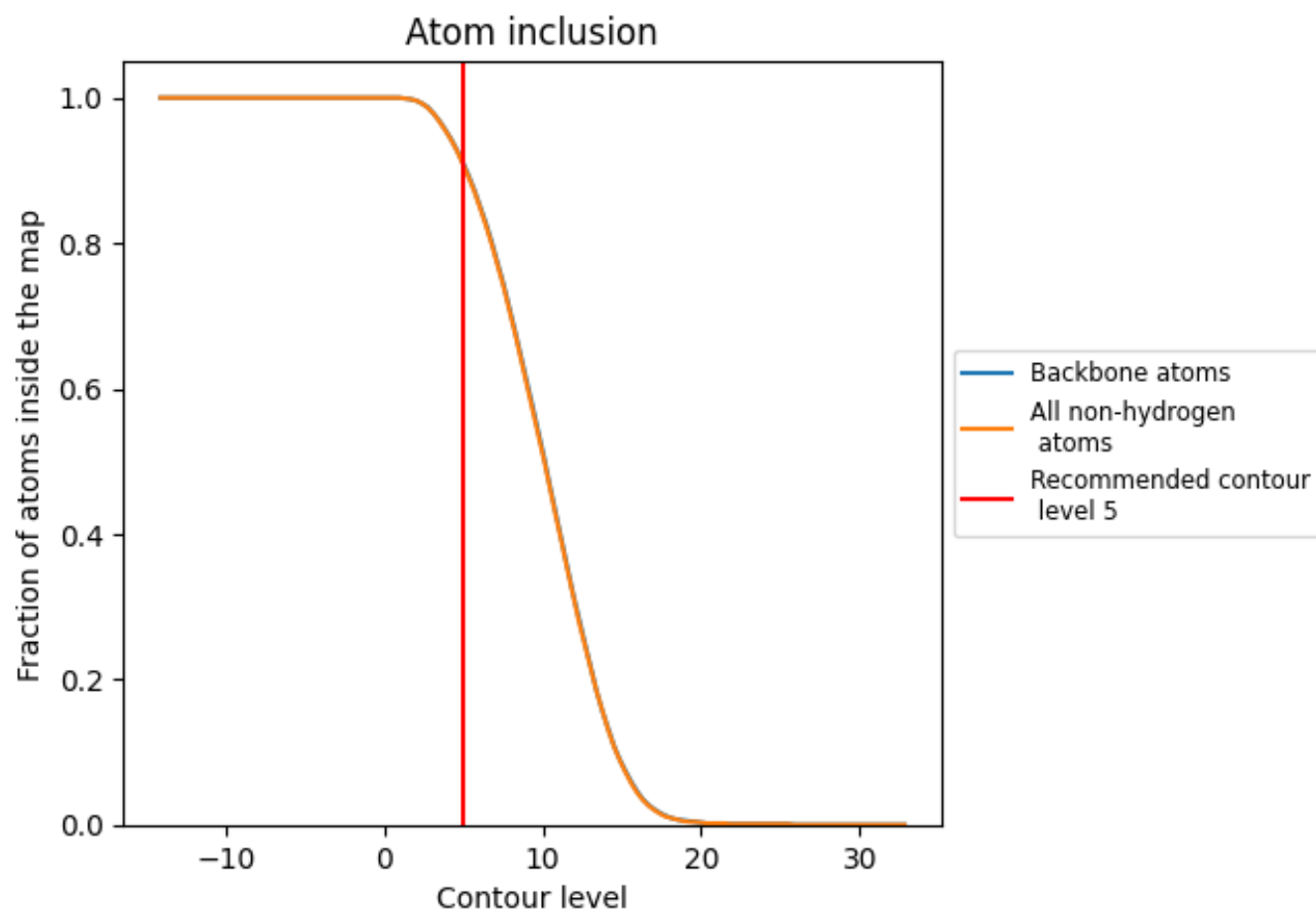
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 91% of all backbone atoms, 91% 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	 0.9070	 0.6970
A	 0.9030	 0.7040
B	 0.9640	 0.7340
C	 0.9610	 0.7350
D	 0.9550	 0.7320
E	 0.8870	 0.6830
F	 0.9340	 0.7000
G	 0.9170	 0.7090
H	 0.9710	 0.7220
I	 0.9740	 0.7400
J	 0.8920	 0.6930
K	 0.9050	 0.7070
L	 0.9380	 0.6860
M	 0.9570	 0.7060
N	 0.9700	 0.7160
O	 0.8990	 0.6840
P	 0.8950	 0.7030
Q	 0.9220	 0.7200
R	 0.9170	 0.7140
S	 0.8270	 0.6730
T	 0.6150	 0.6110
U	 0.9100	 0.6740
V	 0.8780	 0.7050
W	 0.8850	 0.7030
X	 0.8910	 0.6780
Y	 0.7100	 0.6520
Z	 0.8880	 0.6850
a	 0.9400	 0.7020
b	 0.8200	 0.6560
c	 0.8430	 0.6530
d	 0.8880	 0.6870
e	 0.8580	 0.6780
f	 0.8130	 0.6630
g	 0.8880	 0.6830
h	 0.9220	 0.6910



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Chain	Atom inclusion	Q-score
i	 0.8210	 0.6530
j	 0.8570	 0.6470
k	 0.8900	 0.6460
l	 0.8960	 0.6760
m	 0.8730	 0.6750
n	 0.9010	 0.6810
o	 0.8610	 0.6520
p	 0.9030	 0.6810
q	 0.9060	 0.7090
r	 0.8870	 0.7070
s	 0.8540	 0.6780