



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 07:41 PM UTC

PDB ID : 7QSK / pdb_00007qsk
EMDB ID : EMD-14132
Title : Bovine complex I in lipid nanodisc, Active-Q10
Authors : Chung, I.; Bridges, H.R.; Hirst, J.
Deposited on : 2022-01-13
Resolution : 2.84 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

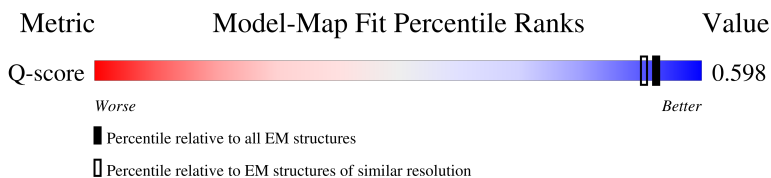
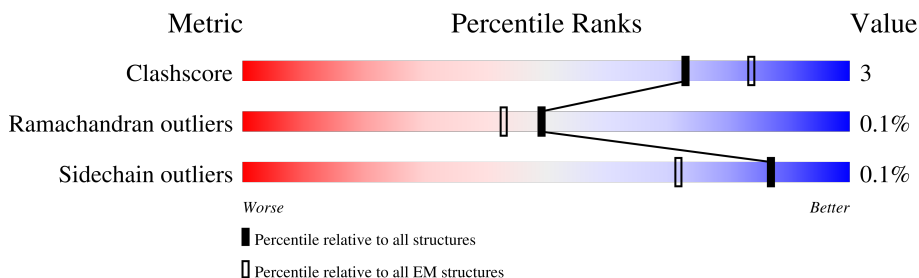
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.84 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	11884 (2.34 - 3.34)

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	

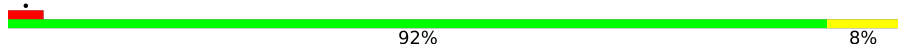
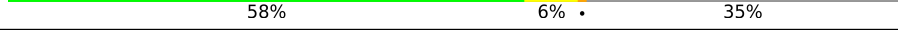
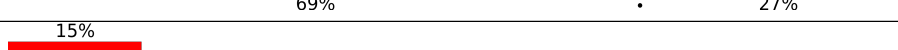
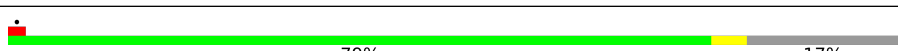
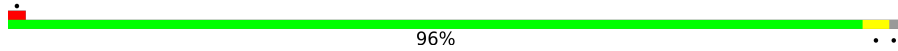
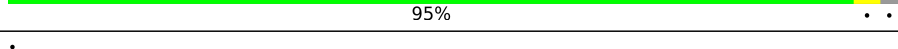
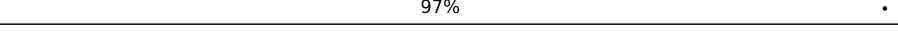
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Mol	Chain	Length	Quality of chain
5	E	249	
6	F	464	
7	G	727	
8	H	318	
9	I	212	
10	J	175	
11	K	98	
12	L	606	
13	M	459	
14	N	347	
15	O	343	
16	P	380	
17	Q	175	
18	R	124	
19	S	99	
20	T	156	
20	U	156	
21	V	116	
22	W	128	
23	X	172	
24	Y	141	
25	Z	144	
26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

There are 60 unique types of molecules in this entry. The entry contains 69986 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	209	Total	C	N	O	S	0	0
			1738	1120	298	317	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	214	Total	C	N	O	S	0	0
			1659	1059	278	312	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	432	Total	C	N	O	S	2	0
			3347	2111	598	618	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	699	Total	C	N	O	S	1	0
			5366	3362	934	1030	40		

- 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	1	0
			2517	1687	386	421	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	175	Total	C	N	O	S	0	0
			1345	906	191	236	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
			4802	3195	737	827	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	342	Total	C	N	O	S	1	0
			2768	1792	489	482	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	129	Total	C	N	O	S	0	0
			1049	659	188	199	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	96	Total	C	N	O	S	0	0
			740	454	140	143	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	87	Total	C	N	O	S	0	0
			700	440	131	127	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	85	Total	C	N	O	S	0	0
			688	444	101	138	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	115	Total	C	N	O	S	0	0
			928	600	157	168	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	115	Total	C	N	O	S	0	0
			976	625	181	166	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	49	Total	C	N	O	0	0
			414	273	70	71		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	120	Total	C	N	O	S	0	0
			999	650	172	172	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	99	Total	C	N	O	S	0	0
			829	523	158	142	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	57	Total	C	N	O	S	0	0
			492	322	86	82	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	100	Total	C	N	O	S	0	0
			839	539	139	157	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	127	Total	C	N	O	S	0	0
			1097	722	191	183	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	71	Total	C	N	O	S	0	0
			597	390	99	107	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	81	Total	C	N	O	S	0	0
			653	427	110	114	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	156	Total	C	N	O	S	0	0
			1314	850	216	240	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	128	Total	C	N	O	S	0	0
			1067	684	188	195			

- 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	122	Total	C	N	O	S	0	0
			1048	653	201	185	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	173	Total	C	N	O	S	0	0
			1453	910	268	267	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		

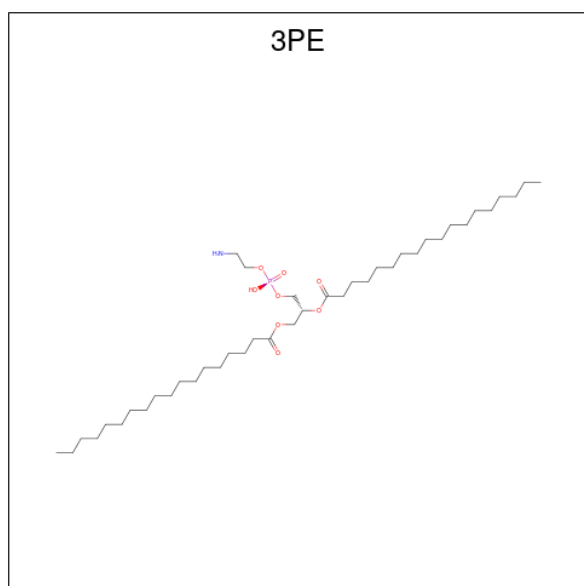
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	95	Total	C	N	O	S	0	0
			776	490	144	139	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	45	Total	C	N	O	S	1	0
			391	244	71	75	1		

- Molecule 45 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



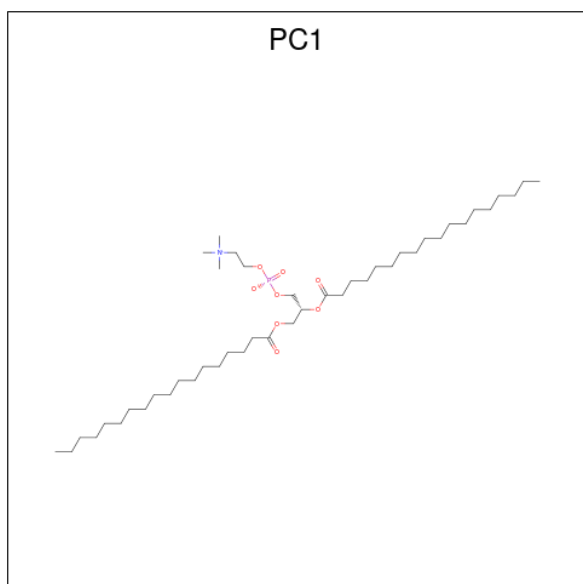
Mol	Chain	Residues	Atoms					AltConf
45	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
45	H	1	Total	C	N	O	P	0
			36	26	1	8	1	
45	K	1	Total	C	N	O	P	0
			44	34	1	8	1	
45	L	1	Total	C	N	O	P	0
			46	36	1	8	1	
45	L	1	Total	C	N	O	P	0
			45	35	1	8	1	
45	L	1	Total	C	N	O	P	0
			44	34	1	8	1	
45	M	1	Total	C	N	O	P	0
			49	39	1	8	1	

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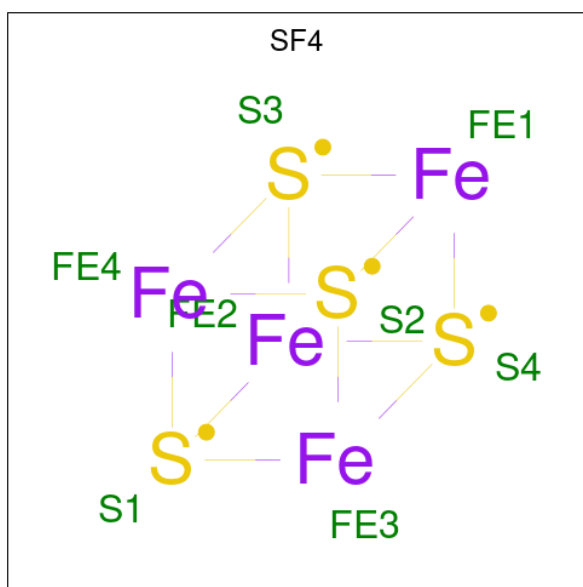
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45	M	1	Total	C	N	O	P	0
			45	35	1	8	1	
45	M	1	Total	C	N	O	P	0
			48	38	1	8	1	
45	N	1	Total	C	N	O	P	0
			51	41	1	8	1	
45	P	1	Total	C	N	O	P	0
			35	25	1	8	1	
45	Y	1	Total	C	N	O	P	0
			31	21	1	8	1	
45	Y	1	Total	C	N	O	P	0
			40	30	1	8	1	
45	Y	1	Total	C	N	O	P	0
			30	20	1	8	1	
45	Y	1	Total	C	N	O	P	0
			33	23	1	8	1	
45	Y	1	Total	C	N	O	P	0
			27	17	1	8	1	
45	d	1	Total	C	N	O	P	0
			49	39	1	8	1	
45	m	1	Total	C	N	O	P	0
			50	40	1	8	1	
45	m	1	Total	C	N	O	P	0
			41	31	1	8	1	

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



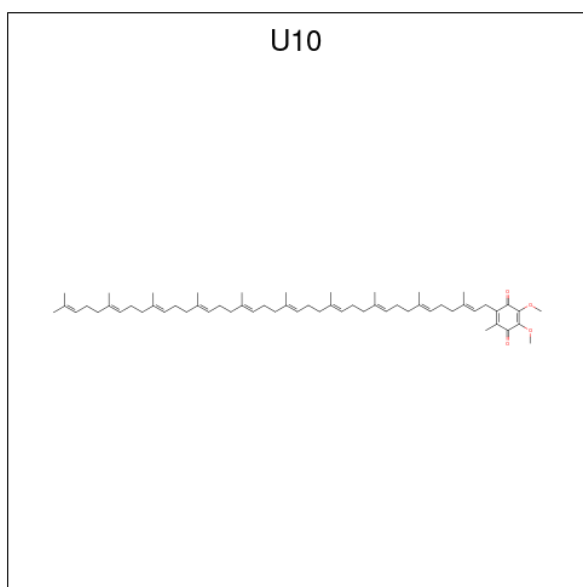
Mol	Chain	Residues	Atoms					AltConf
46	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	A	1	Total	C	N	O	P	0
			33	23	1	8	1	
46	B	1	Total	C	N	O	P	0
			46	36	1	8	1	
46	I	1	Total	C	N	O	P	0
			54	44	1	8	1	
46	I	1	Total	C	N	O	P	0
			44	34	1	8	1	
46	M	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	Y	1	Total	C	N	O	P	0
			46	36	1	8	1	
46	Z	1	Total	C	N	O	P	0
			48	38	1	8	1	
46	d	1	Total	C	N	O	P	0
			39	29	1	8	1	
46	g	1	Total	C	N	O	P	0
			44	34	1	8	1	
46	h	1	Total	C	N	O	P	0
			47	37	1	8	1	
46	q	1	Total	C	N	O	P	0
			48	38	1	8	1	
46	q	1	Total	C	N	O	P	0
			49	39	1	8	1	

- Molecule 47 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



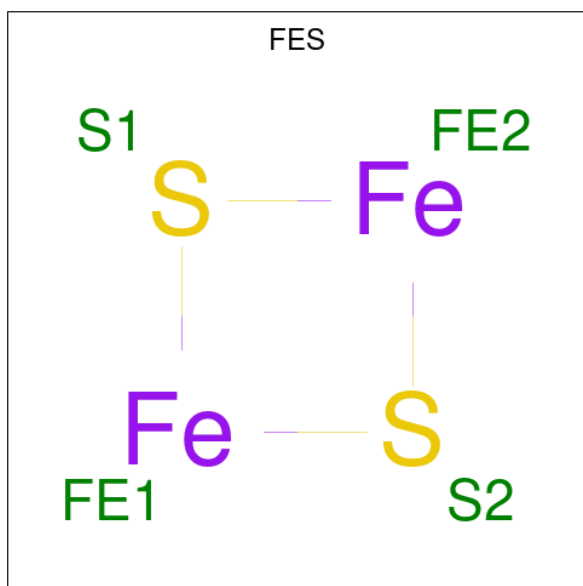
Mol	Chain	Residues	Atoms			AltConf
47	B	1	Total	Fe	S	0
			8	4	4	
47	F	1	Total	Fe	S	
			8	4	4	
47	G	1	Total	Fe	S	
			8	4	4	
47	G	1	Total	Fe	S	0
			8	4	4	
47	I	1	Total	Fe	S	
			8	4	4	
47	I	1	Total	Fe	S	
			8	4	4	

- Molecule 48 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



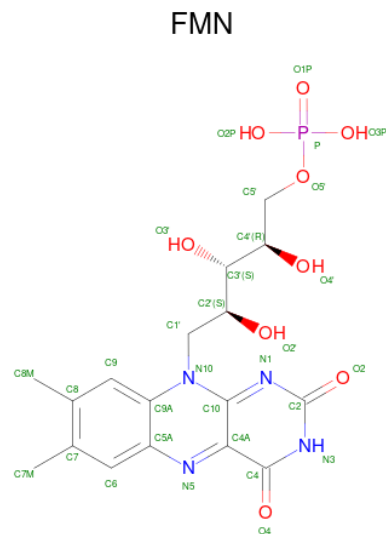
Mol	Chain	Residues	Atoms			AltConf
48	D	1	Total	C	O	0
			63	59	4	

- Molecule 49 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



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

- Molecule 50 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $\text{C}_{17}\text{H}_{21}\text{N}_4\text{O}_9\text{P}$).

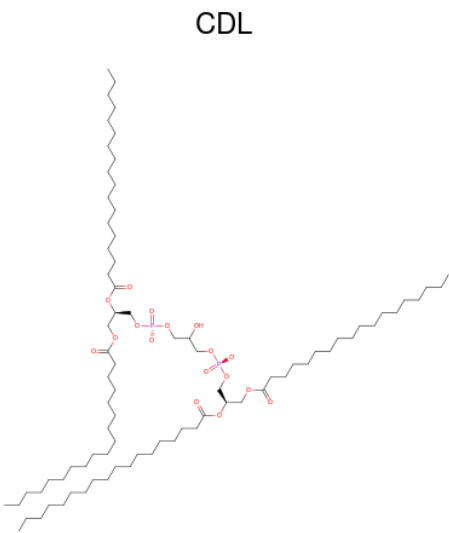


Mol	Chain	Residues	Atoms					AltConf
50	F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 51 is POTASSIUM ION (CCD ID: K) (formula: K).

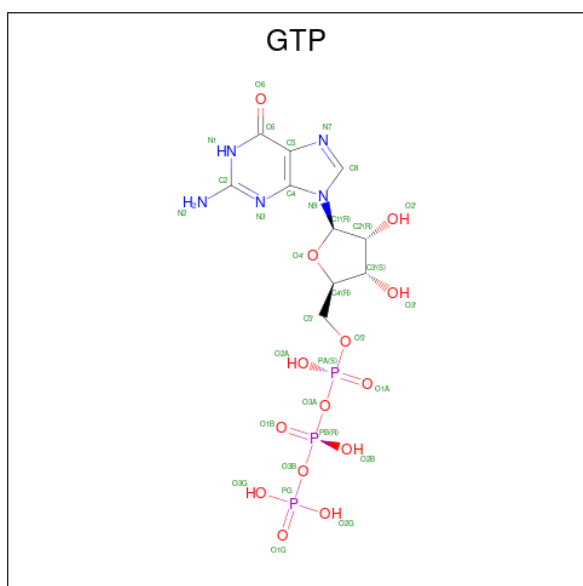
Mol	Chain	Residues	Atoms	AltConf
51	G	1	Total K 1 1	0

- Molecule 52 is CARDIOLIPIN (CCD ID: CDL) (formula: $\text{C}_{81}\text{H}_{156}\text{O}_{17}\text{P}_2$).



Mol	Chain	Residues	Atoms				AltConf
52	H	1	Total	C	O	P	0
			51	32	17	2	
52	L	1	Total	C	O	P	0
			76	57	17	2	
52	N	1	Total	C	O	P	0
			62	43	17	2	
52	X	1	Total	C	O	P	0
			86	67	17	2	
52	d	1	Total	C	O	P	0
			65	46	17	2	
52	h	1	Total	C	O	P	0
			80	61	17	2	
52	r	1	Total	C	O	P	0
			61	42	17	2	

- Molecule 53 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



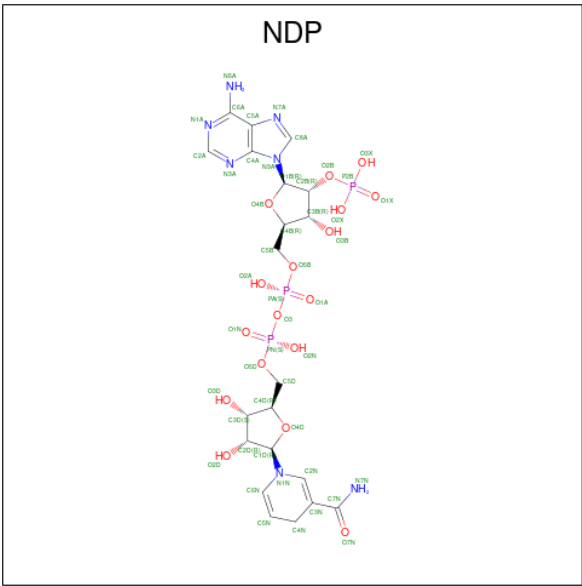
Mol	Chain	Residues	Atoms					AltConf
53	O	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 55 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE

PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).

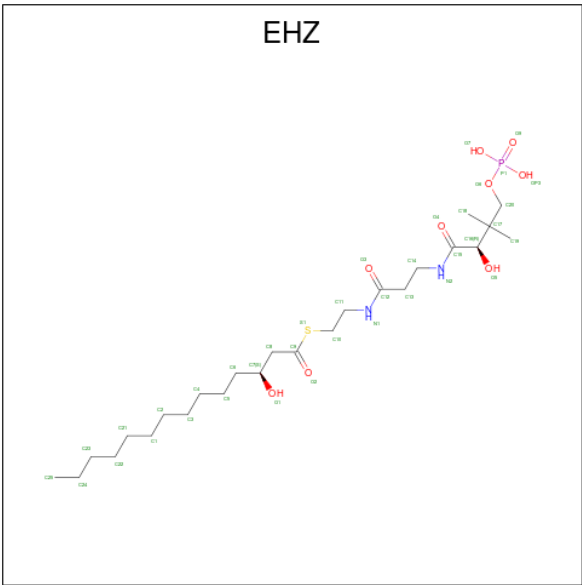


Mol	Chain	Residues	Atoms					AltConf
55	P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

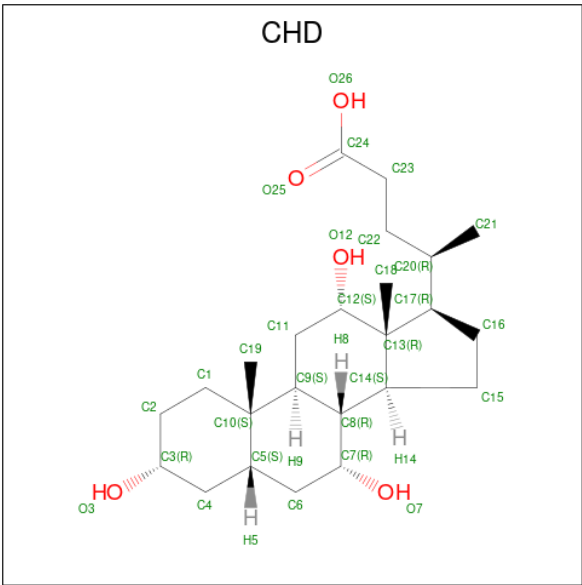
Mol	Chain	Residues	Atoms		AltConf
56	R	1	Total	Zn	0
			1	1	

- Molecule 57 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: C₂₅H₄₉N₂O₉PS).



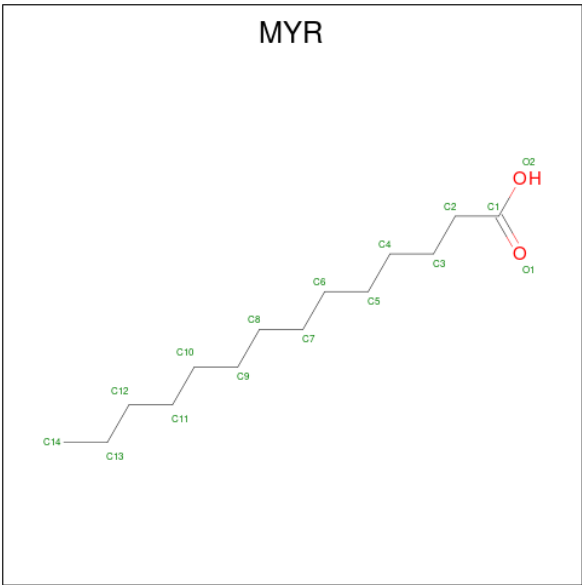
Mol	Chain	Residues	Atoms						AltConf
57	T	1	Total	C	N	O	P	S	0
			37	25	2	8	1	1	
57	U	1	Total	C	N	O	P	S	0
			37	25	2	8	1	1	

- Molecule 58 is CHOLIC ACID (CCD ID: CHD) (formula: C₂₄H₄₀O₅).



Mol	Chain	Residues	Atoms			AltConf
58	i	1	Total	C	O	0
			29	24	5	

- 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	19	Total	O	0
			19	19	
60	B	46	Total	O	0
			46	46	
60	C	42	Total	O	0
			42	42	
60	D	107	Total	O	0
			107	107	
60	E	10	Total	O	0
			10	10	
60	F	42	Total	O	0
			42	42	
60	G	128	Total	O	0
			128	128	
60	H	60	Total	O	0
			60	60	
60	I	52	Total	O	0
			52	52	
60	J	25	Total	O	0
			25	25	
60	K	8	Total	O	0
			8	8	

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Mol	Chain	Residues	Atoms		AltConf
60	L	55	Total 55	O 55	0
60	M	61	Total 61	O 61	0
60	N	38	Total 38	O 38	0
60	O	15	Total 15	O 15	0
60	P	41	Total 41	O 41	0
60	Q	50	Total 50	O 50	0
60	R	11	Total 11	O 11	0
60	T	2	Total 2	O 2	0
60	U	7	Total 7	O 7	0
60	V	5	Total 5	O 5	0
60	W	11	Total 11	O 11	0
60	X	13	Total 13	O 13	0
60	Z	31	Total 31	O 31	0
60	a	14	Total 14	O 14	0
60	b	2	Total 2	O 2	0
60	c	1	Total 1	O 1	0
60	d	13	Total 13	O 13	0
60	e	13	Total 13	O 13	0
60	f	2	Total 2	O 2	0
60	g	8	Total 8	O 8	0
60	h	16	Total 16	O 16	0

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Mol	Chain	Residues	Atoms		AltConf
60	i	4	Total 4	O 4	0
60	j	2	Total 2	O 2	0
60	k	1	Total 1	O 1	0
60	l	10	Total 10	O 10	0
60	m	11	Total 11	O 11	0
60	n	19	Total 19	O 19	0
60	o	5	Total 5	O 5	0
60	p	20	Total 20	O 20	0
60	q	24	Total 24	O 24	0
60	r	13	Total 13	O 13	0
60	s	3	Total 3	O 3	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.

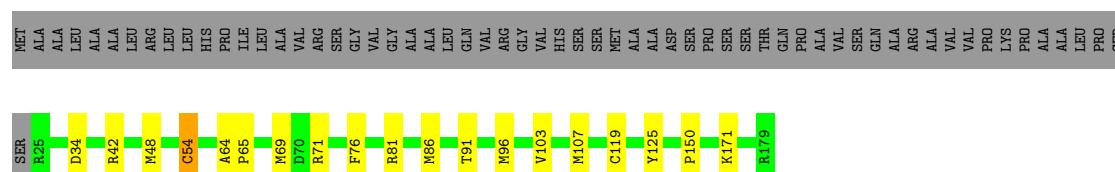
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3

Chain A: 



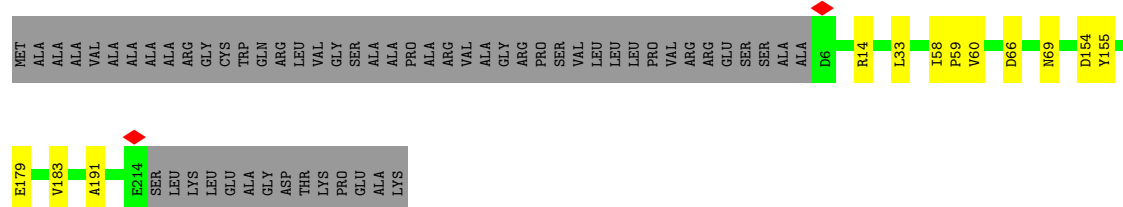
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

Chain B: 



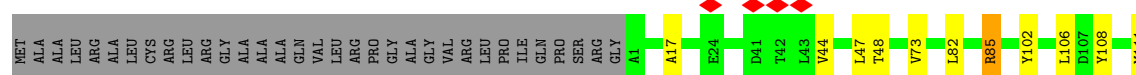
- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial

Chain C: 

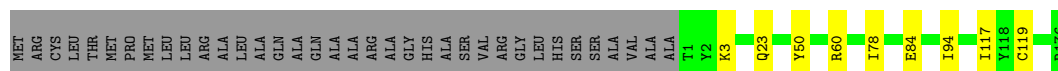


- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

Chain D: 



Chain I:  79% 17%



- Molecule 10: NADH-ubiquinone oxidoreductase chain 6

Chain J:  91% 9%



- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

Chain K:  86% 14%

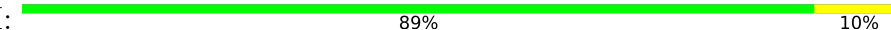


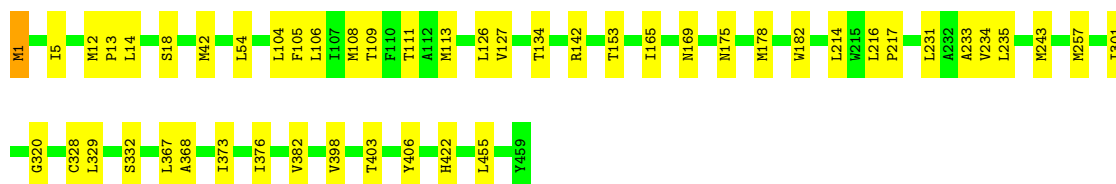
- Molecule 12: NADH-ubiquinone oxidoreductase chain 5

Chain L:  89% 11%

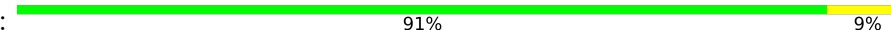


- Molecule 13: NADH-ubiquinone oxidoreductase chain 4

Chain M:  89% 10%



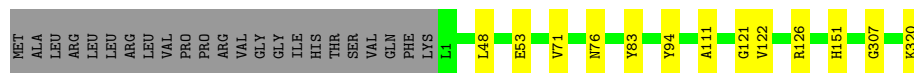
- Molecule 14: NADH-ubiquinone oxidoreductase chain 2

Chain N:  91% 9%



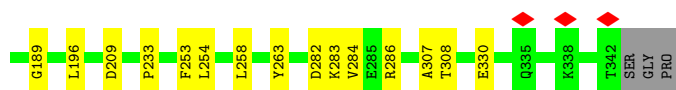
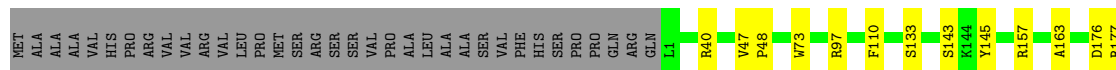
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

Chain O: 90% 7%



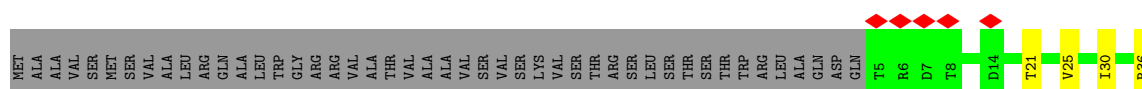
- Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial

Chain P: 83% 7% 10%



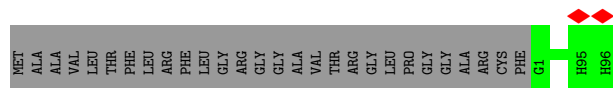
- Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain Q: 68% 6% 26%



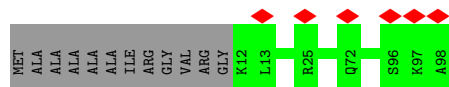
- Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

Chain R: 77% 23%

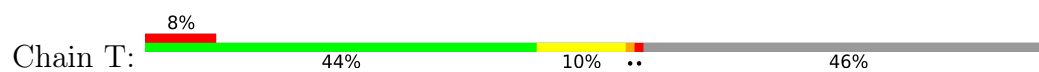


- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

Chain S: 6% 88% 12%



- Molecule 20: Acyl carrier protein, mitochondrial



MET ALA VAL ARG VAL CYS ALA VAL ARG LEU PRO THR PHE ALA PRO LEU PRO ARG LEU PRO THR LEU ALA ALA ARG PRO LEU SER THR LEU PHE ALA ALA GLU THR THR ARG ARG PRO GLY ALA PRO LEU PRO ALA VAL VAL ALA VAL PRO GLY ARG

VAL THR GLN LEU ARG CYS GLN TYR ASP ALA P4 P5 L6 E9 D13 R14 V15 L19 D23 K24 I25 D26 D27 E28 K29 L30 S31 S32 N33 S34 K37 K38 D39 S44 L45 D46 M52 E61 I65 E68 K64 Y67 E68

- Molecule 20: Acyl carrier protein, mitochondrial



MET ALA VAL ARG VAL CYS ALA VAL ARG LEU PRO THR PHE ALA PRO LEU PRO ARG LEU PRO THR LEU ALA ALA ARG PRO LEU SER THR THR LEU PHE ALA ALA GLU THR THR ARG ARG PRO GLY ALA PRO LEU PRO ALA VAL VAL ALA VAL PRO GLY ARG

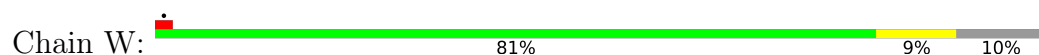
VAL THR GLN LEU ARG CYS GLN TYR ASP A3 P4 P5 V15 L16 Y17 V18 L19 K20 L21 P27 E28 K29 L30 S31 V32 N33 S34 K37 S44 M52 E57 E61 D64 I65 D66 A67 E68 E68

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



MET A1 G2 L3 Q49 I50 E53 M57 R70 Q82 I115

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



MET ALA SER GLY LEU ARG GLN ALA VAL ALA S14 R33 W39 Y40 R41 H48 R64 I73 V79 G86 V96 T101 R114 P115 K116 D127 P128

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



MET P1 E16 N39 M43 W47 M63 C87 C99 D120 L121 D156 M171

- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



MET A1 E2 T3 V4 L5 R6 D10 I11 F48 V52 T104 V140

- Molecule 25: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

Chain Z:  87% 11% .



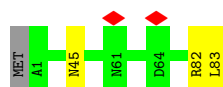
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

Chain a:  97% .



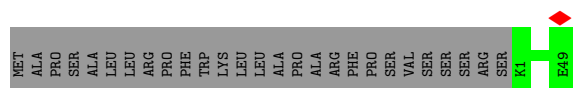
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

Chain b:  95% . .



- Molecule 28: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

Chain c:  64% 36%



- Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain d:  92% 8%



- Molecule 30: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

Chain e:  86% 8% 7%

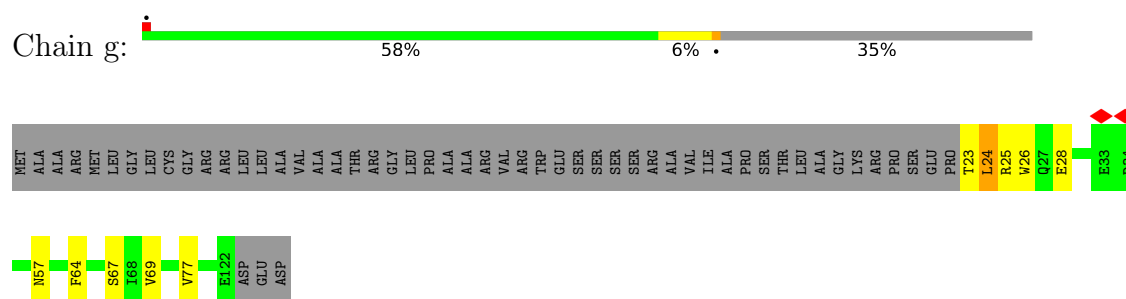


- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1

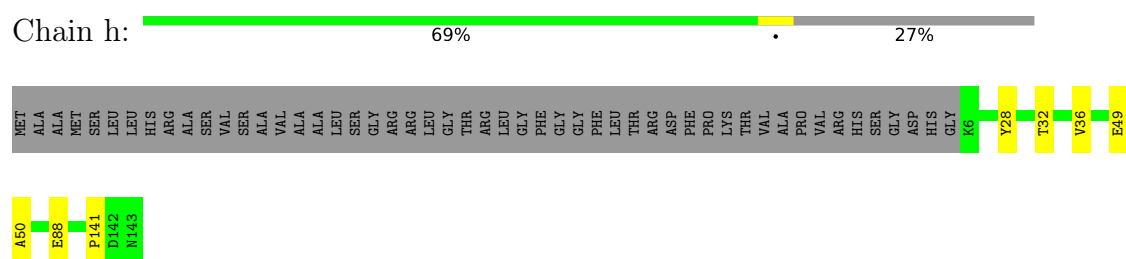
Chain f:  18% 86% 14%



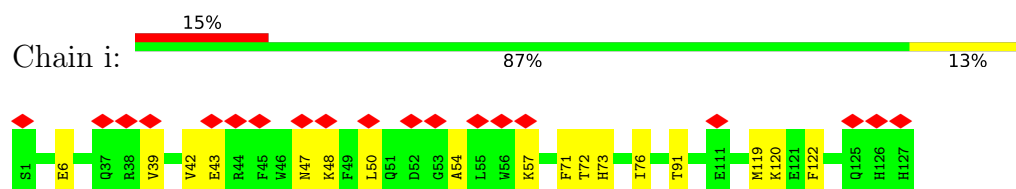
- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



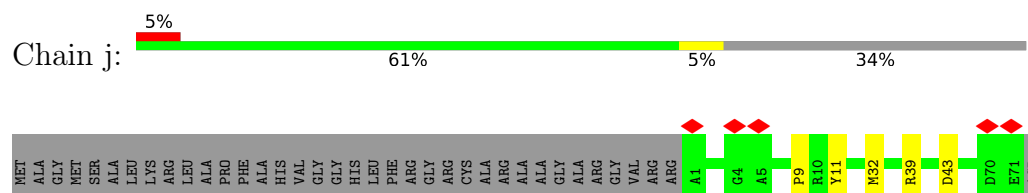
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



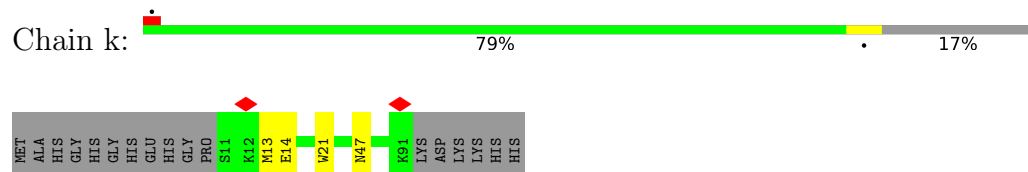
- Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6



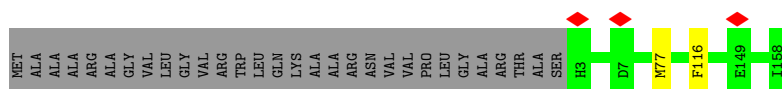
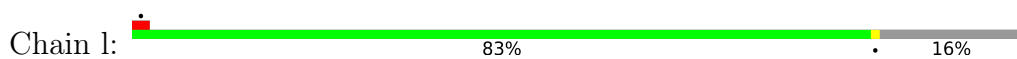
- Molecule 35: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



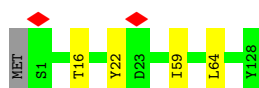
- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



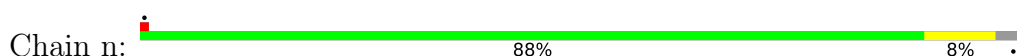
- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



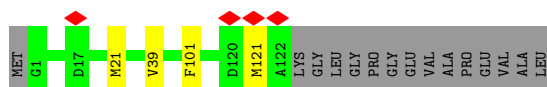
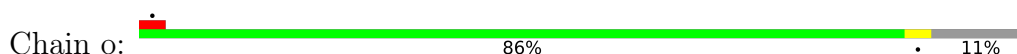
- Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



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



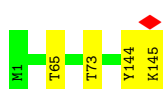
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



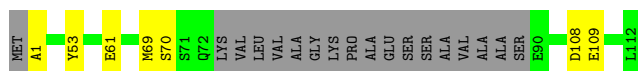
- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



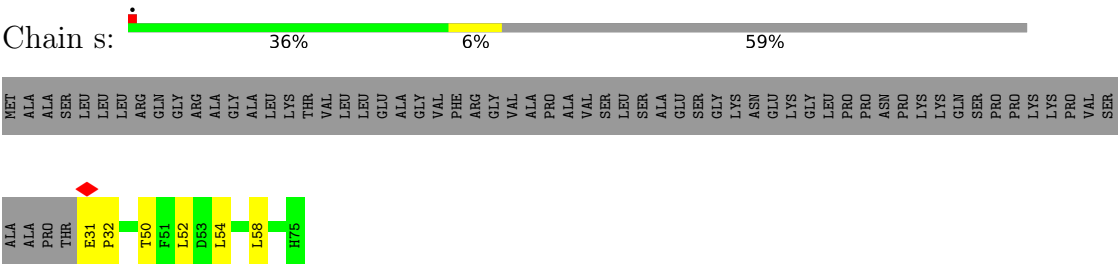
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



- 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, C1	Depositor
Number of particles used	23449	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 ($e^-/\text{\AA}^2$)	40.5	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	31.499	Depositor
Minimum map value	-14.518	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.943	Depositor
Recommended contour level	5	Depositor
Map size (Å)	479.744, 479.744, 479.744	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7496, 0.7496, 0.7496	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAC, AME, GTP, ZN, U10, K, NDP, FES, PC1, FME, 3PE, MG, FMN, CDL, 2MR, CHD, AYA, MYR, SF4, EH2

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	0.28	0/936	0.29	0/1281
2	B	0.31	0/1272	0.40	1/1720 (0.1%)
3	C	0.28	0/1789	0.31	0/2436
4	D	0.29	0/3537	0.30	0/4794
5	E	0.25	0/1699	0.32	0/2312
6	F	0.25	0/3424	0.30	0/4627
7	G	0.27	0/5457	0.33	0/7397
8	H	0.33	0/2579	0.37	0/3524
9	I	0.30	0/1445	0.33	0/1956
10	J	0.25	0/1370	0.29	0/1859
11	K	0.28	0/745	0.33	0/1008
12	L	0.26	0/4920	0.29	0/6694
13	M	0.29	0/3738	0.32	0/5097
14	N	0.28	0/2792	0.31	0/3800
15	O	0.24	0/2651	0.27	0/3587
16	P	0.26	0/2847	0.31	0/3864
17	Q	0.26	0/1072	0.31	0/1449
18	R	0.26	0/753	0.29	0/1014
19	S	0.22	0/711	0.29	0/956
20	T	0.29	0/700	0.63	1/944 (0.1%)
20	U	0.36	0/705	0.68	1/952 (0.1%)
21	V	0.25	0/948	0.26	0/1284
22	W	0.25	0/1000	0.31	0/1344
23	X	0.25	0/1439	0.33	0/1942
24	Y	0.23	0/1042	0.28	0/1414
25	Z	0.26	0/1181	0.30	0/1592
26	a	0.26	0/584	0.31	0/786
27	b	0.23	0/672	0.33	0/923
28	c	0.23	0/427	0.27	0/579
29	d	0.26	0/1018	0.32	0/1375
30	e	0.23	0/850	0.36	0/1136

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	f	0.23	0/505	0.39	0/681
32	g	0.31	0/865	0.41	1/1175 (0.1%)
33	h	0.26	0/1188	0.30	0/1607
34	i	0.23	0/1127	0.39	1/1534 (0.1%)
35	j	0.22	0/624	0.27	0/855
36	k	0.20	0/672	0.27	0/906
37	l	0.24	0/1369	0.32	0/1873
38	m	0.25	0/1094	0.29	0/1480
39	n	0.24	0/1545	0.30	0/2092
40	o	0.25	0/1073	0.34	0/1437
41	p	0.24	0/1486	0.30	0/2004
42	q	0.25	0/1250	0.31	0/1698
43	r	0.25	0/789	0.31	0/1068
44	s	0.20	0/403	0.27	0/545
All	All	0.27	0/68293	0.32	5/92601 (0.0%)

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	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	U	28	GLU	CA-CB-CG	6.21	126.51	114.10
20	T	28	GLU	CA-CB-CG	6.19	126.47	114.10
2	B	54	CYS	CA-CB-SG	5.50	127.05	114.40
32	g	57	ASN	N-CA-C	-5.12	106.54	112.89
34	i	39	VAL	CG1-CB-CG2	5.08	121.97	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
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	19	0
2	B	1241	0	1251	20	0
3	C	1738	0	1685	9	0
4	D	3459	0	3405	32	0
5	E	1659	0	1664	9	0
6	F	3347	0	3297	24	0
7	G	5366	0	5378	41	0
8	H	2517	0	2631	33	0
9	I	1414	0	1370	10	0
10	J	1345	0	1352	14	0
11	K	745	0	785	14	0
12	L	4802	0	4960	44	0
13	M	3654	0	3852	37	0
14	N	2733	0	2912	24	0
15	O	2589	0	2566	7	0
16	P	2768	0	2782	24	0
17	Q	1049	0	1045	10	0
18	R	740	0	714	0	0
19	S	700	0	719	0	0
20	T	688	0	684	13	0
20	U	693	0	688	18	0
21	V	928	0	972	4	0
22	W	976	0	991	13	0
23	X	1402	0	1381	7	0
24	Y	1030	0	1039	5	0
25	Z	1152	0	1151	16	0
26	a	569	0	568	2	0
27	b	651	0	662	2	0
28	c	414	0	415	0	0
29	d	999	0	988	6	0
30	e	829	0	829	7	0
31	f	492	0	501	7	0
32	g	839	0	790	8	0
33	h	1154	0	1168	6	0
34	i	1097	0	1108	12	0
35	j	597	0	536	4	0
36	k	653	0	639	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	l	1314	0	1210	2	0
38	m	1067	0	1067	4	0
39	n	1492	0	1438	12	0
40	o	1048	0	1018	3	0
41	p	1453	0	1425	5	0
42	q	1209	0	1182	2	0
43	r	776	0	782	5	0
44	s	391	0	361	4	0
45	A	47	0	71	0	0
45	H	36	0	46	0	0
45	K	44	0	62	0	0
45	L	135	0	201	2	0
45	M	142	0	212	2	0
45	N	51	0	82	7	0
45	P	35	0	44	0	0
45	Y	161	0	195	1	0
45	d	49	0	75	0	0
45	m	91	0	136	2	0
46	A	103	0	128	1	0
46	B	46	0	66	0	0
46	I	98	0	150	1	0
46	M	35	0	44	0	0
46	Y	46	0	66	0	0
46	Z	48	0	73	7	0
46	d	39	0	52	0	0
46	g	44	0	65	0	0
46	h	47	0	71	1	0
46	q	97	0	145	1	0
47	B	8	0	0	1	0
47	F	8	0	0	0	0
47	G	16	0	0	0	0
47	I	16	0	0	0	0
48	D	63	0	90	2	0
49	E	4	0	0	0	0
49	G	4	0	0	0	0
50	F	31	0	19	0	0
51	G	1	0	0	0	0
52	H	51	0	46	0	0
52	L	76	0	99	0	0
52	N	62	0	68	0	0
52	X	86	0	125	1	0
52	d	65	0	77	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	h	80	0	104	1	0
52	r	61	0	66	0	0
53	O	32	0	12	1	0
54	O	1	0	0	0	0
55	P	48	0	26	3	0
56	R	1	0	0	0	0
57	T	37	0	0	2	0
57	U	37	0	0	2	0
58	i	29	0	37	1	0
59	o	15	0	27	0	0
60	A	19	0	0	2	0
60	B	46	0	0	1	0
60	C	42	0	0	0	0
60	D	107	0	0	1	0
60	E	10	0	0	0	0
60	F	42	0	0	2	0
60	G	128	0	0	3	0
60	H	60	0	0	3	0
60	I	52	0	0	1	0
60	J	25	0	0	0	0
60	K	8	0	0	0	0
60	L	55	0	0	2	0
60	M	61	0	0	2	0
60	N	38	0	0	3	0
60	O	15	0	0	0	0
60	P	41	0	0	3	0
60	Q	50	0	0	3	0
60	R	11	0	0	0	0
60	T	2	0	0	1	0
60	U	7	0	0	0	0
60	V	5	0	0	0	0
60	W	11	0	0	1	0
60	X	13	0	0	0	0
60	Z	31	0	0	1	0
60	a	14	0	0	0	0
60	b	2	0	0	0	0
60	c	1	0	0	0	0
60	d	13	0	0	0	0
60	e	13	0	0	0	0
60	f	2	0	0	0	0
60	g	8	0	0	0	0
60	h	16	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	i	4	0	0	0	0
60	j	2	0	0	0	0
60	k	1	0	0	0	0
60	l	10	0	0	0	0
60	m	11	0	0	0	0
60	n	19	0	0	0	0
60	o	5	0	0	0	0
60	p	20	0	0	1	0
60	q	24	0	0	0	0
60	r	13	0	0	1	0
60	s	3	0	0	0	0
All	All	69986	0	69693	460	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 460 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)
1:A:67:LEU:HD11	11:K:68:ALA:HB3	1.44	0.96
20:U:31:SER:HG	20:U:34:SER:HG	1.06	0.95
14:N:263:LYS:HG3	60:N:522:HOH:O	1.68	0.94
7:G:190:MET:HE3	7:G:695:ALA:HB2	1.50	0.93
7:G:433:ALA:O	7:G:476:LYS:NZ	2.02	0.91

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	A	113/115 (98%)	108 (96%)	5 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	153/216 (71%)	146 (95%)	7 (5%)	0	100	100
3	C	207/266 (78%)	203 (98%)	4 (2%)	0	100	100
4	D	427/463 (92%)	411 (96%)	16 (4%)	0	100	100
5	E	212/249 (85%)	204 (96%)	8 (4%)	0	100	100
6	F	432/464 (93%)	420 (97%)	12 (3%)	0	100	100
7	G	698/727 (96%)	669 (96%)	27 (4%)	2 (0%)	36	55
8	H	317/318 (100%)	305 (96%)	12 (4%)	0	100	100
9	I	174/212 (82%)	170 (98%)	4 (2%)	0	100	100
10	J	173/175 (99%)	164 (95%)	8 (5%)	1 (1%)	21	39
11	K	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
12	L	604/606 (100%)	581 (96%)	22 (4%)	1 (0%)	43	62
13	M	457/459 (100%)	452 (99%)	5 (1%)	0	100	100
14	N	345/347 (99%)	333 (96%)	12 (4%)	0	100	100
15	O	318/343 (93%)	315 (99%)	3 (1%)	0	100	100
16	P	341/380 (90%)	332 (97%)	9 (3%)	0	100	100
17	Q	127/175 (73%)	124 (98%)	3 (2%)	0	100	100
18	R	94/124 (76%)	91 (97%)	3 (3%)	0	100	100
19	S	85/99 (86%)	81 (95%)	4 (5%)	0	100	100
20	T	83/156 (53%)	80 (96%)	3 (4%)	0	100	100
20	U	84/156 (54%)	80 (95%)	4 (5%)	0	100	100
21	V	113/116 (97%)	110 (97%)	3 (3%)	0	100	100
22	W	113/128 (88%)	106 (94%)	7 (6%)	0	100	100
23	X	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
24	Y	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
25	Z	139/144 (96%)	134 (96%)	5 (4%)	0	100	100
26	a	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
27	b	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
28	c	47/76 (62%)	47 (100%)	0	0	100	100
29	d	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
30	e	97/106 (92%)	95 (98%)	2 (2%)	0	100	100
31	f	55/57 (96%)	52 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	g	98/154 (64%)	94 (96%)	3 (3%)	1 (1%)	12	24
33	h	136/189 (72%)	133 (98%)	3 (2%)	0	100	100
34	i	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
35	j	69/108 (64%)	67 (97%)	2 (3%)	0	100	100
36	k	79/98 (81%)	76 (96%)	3 (4%)	0	100	100
37	l	154/186 (83%)	148 (96%)	6 (4%)	0	100	100
38	m	126/129 (98%)	119 (94%)	7 (6%)	0	100	100
39	n	170/179 (95%)	168 (99%)	2 (1%)	0	100	100
40	o	120/137 (88%)	115 (96%)	5 (4%)	0	100	100
41	p	171/176 (97%)	169 (99%)	2 (1%)	0	100	100
42	q	143/145 (99%)	141 (99%)	2 (1%)	0	100	100
43	r	91/113 (80%)	87 (96%)	4 (4%)	0	100	100
44	s	44/109 (40%)	42 (96%)	2 (4%)	0	100	100
All	All	8204/9212 (89%)	7947 (97%)	252 (3%)	5 (0%)	49	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	590	PRO
10	J	24	PRO
12	L	562	LEU
7	G	540	ASP
32	g	24	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%)	131 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	190/228 (83%)	190 (100%)	0	100	100
4	D	370/392 (94%)	370 (100%)	0	100	100
5	E	183/205 (89%)	183 (100%)	0	100	100
6	F	348/368 (95%)	348 (100%)	0	100	100
7	G	587/608 (96%)	587 (100%)	0	100	100
8	H	275/274 (100%)	275 (100%)	0	100	100
9	I	151/175 (86%)	151 (100%)	0	100	100
10	J	141/141 (100%)	141 (100%)	0	100	100
11	K	85/85 (100%)	85 (100%)	0	100	100
12	L	533/533 (100%)	533 (100%)	0	100	100
13	M	412/412 (100%)	412 (100%)	0	100	100
14	N	315/315 (100%)	315 (100%)	0	100	100
15	O	283/303 (93%)	283 (100%)	0	100	100
16	P	297/327 (91%)	297 (100%)	0	100	100
17	Q	116/153 (76%)	116 (100%)	0	100	100
18	R	79/97 (81%)	79 (100%)	0	100	100
19	S	77/82 (94%)	77 (100%)	0	100	100
20	T	79/135 (58%)	74 (94%)	5 (6%)	16	34
20	U	79/135 (58%)	74 (94%)	5 (6%)	16	34
21	V	101/102 (99%)	101 (100%)	0	100	100
22	W	107/114 (94%)	107 (100%)	0	100	100
23	X	154/155 (99%)	154 (100%)	0	100	100
24	Y	101/102 (99%)	101 (100%)	0	100	100
25	Z	120/121 (99%)	120 (100%)	0	100	100
26	a	59/59 (100%)	59 (100%)	0	100	100
27	b	71/72 (99%)	71 (100%)	0	100	100
28	c	45/68 (66%)	45 (100%)	0	100	100
29	d	105/105 (100%)	105 (100%)	0	100	100
30	e	89/96 (93%)	89 (100%)	0	100	100
31	f	54/54 (100%)	54 (100%)	0	100	100
32	g	91/131 (70%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	121/158 (77%)	121 (100%)	0	100	100
34	i	120/120 (100%)	120 (100%)	0	100	100
35	j	61/84 (73%)	61 (100%)	0	100	100
36	k	63/76 (83%)	63 (100%)	0	100	100
37	l	140/159 (88%)	140 (100%)	0	100	100
38	m	114/115 (99%)	114 (100%)	0	100	100
39	n	156/161 (97%)	156 (100%)	0	100	100
40	o	110/120 (92%)	110 (100%)	0	100	100
41	p	155/157 (99%)	155 (100%)	0	100	100
42	q	131/131 (100%)	131 (100%)	0	100	100
43	r	85/97 (88%)	85 (100%)	0	100	100
44	s	45/92 (49%)	45 (100%)	0	100	100
All	All	7229/7892 (92%)	7219 (100%)	10 (0%)	87	96

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	U	61	GLU
20	U	65	ILE
20	U	68	GLU
20	T	65	ILE
20	T	68	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
29	d	6	GLN
41	p	143	HIS
30	e	26	HIS
35	j	58	GLN
42	q	72	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 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$
12	FME	L	1	12	8,9,10	0.98	0	8,9,11	0.72	0
43	AYA	r	1	43	6,7,8	1.26	1 (16%)	6,8,10	0.95	0
13	FME	M	1	13	8,9,10	1.01	0	8,9,11	0.95	1 (12%)
10	FME	J	1	10	8,9,10	1.01	0	8,9,11	0.84	0
1	FME	A	1	1	8,9,10	0.98	0	8,9,11	1.11	1 (12%)
34	SAC	i	1	34	7,8,9	0.97	0	7,9,11	1.09	0
14	FME	N	1	14	8,9,10	0.96	0	8,9,11	1.13	0
8	FME	H	1	8	8,9,10	0.98	0	8,9,11	1.03	0
11	FME	K	1	11	8,9,10	0.97	0	8,9,11	0.86	0
24	AYA	Y	1	24	6,7,8	1.30	1 (16%)	6,8,10	1.19	1 (16%)
29	AME	d	1	29	9,10,11	1.51	2 (22%)	9,11,13	1.39	1 (11%)
4	2MR	D	85	4	10,12,13	2.76	4 (40%)	5,13,15	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
12	FME	L	1	12	-	2/7/9/11	-
43	AYA	r	1	43	-	0/5/6/8	-
13	FME	M	1	13	-	1/7/9/11	-
10	FME	J	1	10	-	4/7/9/11	-
1	FME	A	1	1	-	5/7/9/11	-
34	SAC	i	1	34	-	1/7/8/10	-
14	FME	N	1	14	-	3/7/9/11	-
8	FME	H	1	8	-	3/7/9/11	-
11	FME	K	1	11	-	4/7/9/11	-
24	AYA	Y	1	24	-	1/5/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	AME	d	1	29	-	5/9/10/12	-
4	2MR	D	85	4	-	0/10/13/15	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	85	2MR	CZ-NH2	5.14	1.44	1.33
4	D	85	2MR	CZ-NE	4.84	1.44	1.34
4	D	85	2MR	O-C	4.27	1.36	1.20
29	d	1	AME	CT1-N	3.40	1.45	1.34
24	Y	1	AYA	CA-N	-2.59	1.43	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	Y	1	AYA	CB-CA-N	2.61	112.63	109.68
1	A	1	FME	C-CA-N	2.23	113.80	109.50
13	M	1	FME	C-CA-N	2.03	113.42	109.50
29	d	1	AME	CT2-CT1-N	2.00	119.44	116.12

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	M	1	FME	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 59 ligands modelled in this entry, 3 are monoatomic - leaving 56 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
45	3PE	H	601	-	35,35,50	1.04	4 (11%)	38,40,55	1.08	2 (5%)
46	PC1	q	202	-	48,48,53	0.99	4 (8%)	54,56,61	1.04	2 (3%)
52	CDL	H	602	-	50,50,99	1.21	8 (16%)	56,62,111	1.21	4 (7%)
52	CDL	X	201	-	85,85,99	0.94	8 (9%)	91,97,111	1.05	4 (4%)
45	3PE	M	901	-	48,48,50	0.88	4 (8%)	51,53,55	1.04	2 (3%)
46	PC1	d	202	-	38,38,53	1.15	4 (10%)	44,46,61	1.10	2 (4%)
50	FMN	F	501	-	33,33,33	1.08	2 (6%)	48,50,50	1.20	6 (12%)
46	PC1	A	202	-	34,34,53	1.19	4 (11%)	40,42,61	1.09	2 (5%)
47	SF4	B	201	2	0,12,12	-	-	-	-	-
45	3PE	d	201	-	48,48,50	0.89	4 (8%)	51,53,55	1.05	2 (3%)
49	FES	E	301	5	0,4,4	-	-	-	-	-
53	GTP	O	401	54	33,34,34	3.29	14 (42%)	50,54,54	1.87	15 (30%)
45	3PE	m	401	-	49,49,50	0.88	4 (8%)	52,54,55	1.11	2 (3%)
46	PC1	I	204	-	43,43,53	1.06	4 (9%)	49,51,61	1.07	2 (4%)
45	3PE	A	201	-	46,46,50	0.90	4 (8%)	49,51,55	1.07	2 (4%)
46	PC1	q	201	-	47,47,53	1.03	4 (8%)	53,55,61	1.05	2 (3%)
45	3PE	Y	804	-	32,32,50	1.06	4 (12%)	35,37,55	1.07	2 (5%)
46	PC1	Y	806	-	45,45,53	1.03	4 (8%)	51,53,61	1.01	2 (3%)
47	SF4	F	502	6	0,12,12	-	-	-	-	-
57	EHZ	U	101	20	31,36,37	1.52	5 (16%)	36,44,47	2.72	8 (22%)
58	CHD	i	201	-	32,32,32	3.29	10 (31%)	51,51,51	3.34	25 (49%)
45	3PE	P	502	-	34,34,50	1.04	4 (11%)	37,39,55	1.24	2 (5%)
45	3PE	Y	802	-	39,39,50	0.97	4 (10%)	42,44,55	1.10	2 (4%)
57	EHZ	T	101	20	31,36,37	1.51	5 (16%)	36,44,47	2.72	8 (22%)
45	3PE	L	701	-	45,45,50	0.92	4 (8%)	48,50,55	1.10	2 (4%)
45	3PE	m	402	-	40,40,50	0.97	4 (10%)	43,45,55	1.16	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
45	3PE	M	903	-	47,47,50	0.90	4 (8%)	50,52,55	1.07	2 (4%)
47	SF4	G	801	7	0,12,12	-	-	-		
45	3PE	L	704	-	43,43,50	0.94	4 (9%)	46,48,55	1.10	2 (4%)
52	CDL	N	402	-	61,61,99	1.11	8 (13%)	67,73,111	1.24	4 (5%)
55	NDP	P	501	-	51,52,52	2.25	7 (13%)	71,80,80	1.58	15 (21%)
45	3PE	L	703	-	44,44,50	0.91	4 (9%)	47,49,55	1.06	2 (4%)
47	SF4	I	202	9	0,12,12	-	-	-		
46	PC1	M	904	-	34,34,53	1.19	4 (11%)	40,42,61	1.08	2 (5%)
46	PC1	A	203	-	34,34,53	1.19	4 (11%)	40,42,61	1.08	2 (5%)
52	CDL	L	702	-	75,75,99	1.02	8 (10%)	81,87,111	1.06	4 (4%)
45	3PE	Y	803	-	29,29,50	1.12	4 (13%)	32,34,55	1.20	2 (6%)
47	SF4	I	203	9	0,12,12	-	-	-		
59	MYR	o	201	40	13,14,15	0.99	0	12,13,15	0.56	0
47	SF4	G	802	7	0,12,12	-	-	-		
52	CDL	d	203	-	64,64,99	1.08	7 (10%)	70,76,111	1.07	4 (5%)
46	PC1	Z	201	-	47,47,53	0.47	0	53,55,61	0.61	2 (3%)
46	PC1	h	202	-	46,46,53	1.03	4 (8%)	52,54,61	1.06	2 (3%)
45	3PE	M	902	-	44,44,50	0.92	4 (9%)	47,49,55	1.09	2 (4%)
46	PC1	I	201	-	53,53,53	0.96	4 (7%)	59,61,61	1.00	2 (3%)
48	U10	D	701	-	63,63,63	2.74	17 (26%)	78,79,79	1.93	21 (26%)
45	3PE	Y	805	-	26,26,50	1.19	4 (15%)	29,31,55	1.16	2 (6%)
46	PC1	B	202	-	45,45,53	1.04	4 (8%)	51,53,61	1.00	2 (3%)
46	PC1	g	201	-	43,43,53	1.06	4 (9%)	49,51,61	1.09	2 (4%)
49	FES	G	803	7	0,4,4	-	-	-		
52	CDL	h	201	-	79,79,99	0.98	8 (10%)	85,91,111	1.11	4 (4%)
52	CDL	r	201	-	60,60,99	1.12	8 (13%)	66,72,111	1.17	4 (6%)
45	3PE	Y	801	-	30,30,50	1.10	4 (13%)	33,35,55	1.07	2 (6%)
45	3PE	K	101	-	43,43,50	0.93	4 (9%)	46,48,55	1.16	3 (6%)
46	PC1	A	204	-	32,32,53	1.26	5 (15%)	38,40,61	1.17	2 (5%)
45	3PE	N	401	-	50,50,50	0.84	4 (8%)	53,55,55	1.08	2 (3%)

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
45	3PE	H	601	-	-	19/39/39/54	-
46	PC1	q	202	-	-	19/52/52/57	-
52	CDL	H	602	-	-	28/61/61/110	-
52	CDL	X	201	-	-	44/96/96/110	-
45	3PE	M	901	-	-	23/52/52/54	-
46	PC1	d	202	-	-	18/42/42/57	-
50	FMN	F	501	-	-	2/18/18/18	0/3/3/3
46	PC1	A	202	-	-	22/38/38/57	-
47	SF4	B	201	2	-	-	0/6/5/5
45	3PE	d	201	-	-	21/52/52/54	-
53	GTP	O	401	54	-	5/22/38/38	0/3/3/3
49	FES	E	301	5	-	-	0/1/1/1
45	3PE	m	401	-	-	23/53/53/54	-
46	PC1	I	204	-	-	18/47/47/57	-
45	3PE	A	201	-	-	24/50/50/54	-
46	PC1	q	201	-	-	14/51/51/57	-
45	3PE	Y	804	-	-	16/36/36/54	-
46	PC1	Y	806	-	-	16/49/49/57	-
57	EHZ	U	101	20	-	13/42/44/45	-
58	CHD	i	201	-	-	2/9/74/74	0/4/4/4
47	SF4	F	502	6	-	-	0/6/5/5
45	3PE	P	502	-	-	16/38/38/54	-
45	3PE	Y	802	-	-	21/43/43/54	-
57	EHZ	T	101	20	-	13/42/44/45	-
45	3PE	L	701	-	-	21/49/49/54	-
45	3PE	m	402	-	-	26/44/44/54	-
45	3PE	M	903	-	-	20/51/51/54	-
52	CDL	N	402	-	-	37/71/71/110	-
45	3PE	L	704	-	-	15/47/47/54	-
47	SF4	G	801	7	-	-	0/6/5/5
55	NDP	P	501	-	-	7/34/77/77	0/5/5/5
45	3PE	L	703	-	-	21/48/48/54	-
47	SF4	I	202	9	-	-	0/6/5/5
46	PC1	M	904	-	-	18/38/38/57	-
46	PC1	A	203	-	-	15/38/38/57	-
52	CDL	L	702	-	-	31/86/86/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	3PE	Y	803	-	-	9/33/33/54	-
59	MYR	o	201	40	-	6/12/12/13	-
47	SF4	I	203	9	-	-	0/6/5/5
52	CDL	d	203	-	-	21/75/75/110	-
47	SF4	G	802	7	-	-	0/6/5/5
46	PC1	Z	201	-	-	17/51/51/57	-
46	PC1	h	202	-	-	24/50/50/57	-
45	3PE	M	902	-	-	18/48/48/54	-
46	PC1	I	201	-	-	20/57/57/57	-
48	U10	D	701	-	-	30/63/87/87	0/1/1/1
45	3PE	Y	805	-	-	10/30/30/54	-
46	PC1	B	202	-	-	11/49/49/57	-
46	PC1	g	201	-	-	16/47/47/57	-
52	CDL	h	201	-	-	31/90/90/110	-
49	FES	G	803	7	-	-	0/1/1/1
52	CDL	r	201	-	-	20/71/71/110	-
45	3PE	Y	801	-	-	25/34/34/54	-
45	3PE	K	101	-	-	22/47/47/54	-
46	PC1	A	204	-	-	12/36/36/57	-
45	3PE	N	401	-	-	30/54/54/54	-

The worst 5 of 244 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	P	501	NDP	P2B-O2B	12.65	1.81	1.59
58	i	201	CHD	C11-C12	8.74	1.67	1.53
53	O	401	GTP	O6-C6	8.73	1.40	1.23
58	i	201	CHD	C16-C15	7.04	1.73	1.54
53	O	401	GTP	C5-N7	6.69	1.52	1.39

The worst 5 of 193 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	T	101	EHZ	C14-N2-C15	10.06	140.61	122.55
58	i	201	CHD	C4-C5-C10	10.05	123.36	112.66
57	U	101	EHZ	C14-N2-C15	10.03	140.56	122.55
57	T	101	EHZ	C11-N1-C12	8.53	138.71	122.82
57	U	101	EHZ	C11-N1-C12	8.48	138.61	122.82

There are no chirality outliers.

5 of 910 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
45	A	201	3PE	C1-O11-P-O12
45	A	201	3PE	C1-O11-P-O13
45	A	201	3PE	C1-O11-P-O14
45	A	201	3PE	C11-O13-P-O11
45	A	201	3PE	C11-O13-P-O12

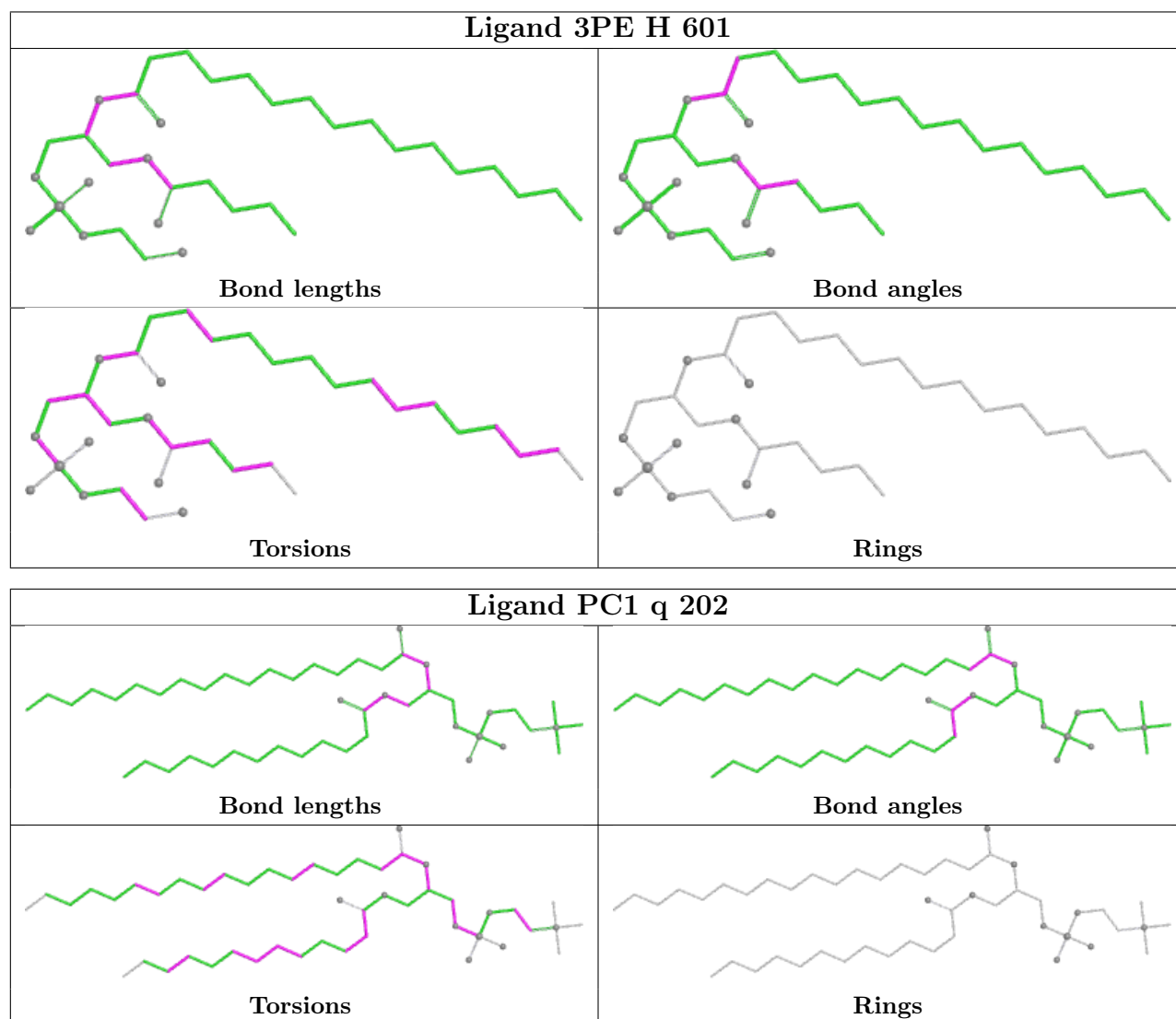
There are no ring outliers.

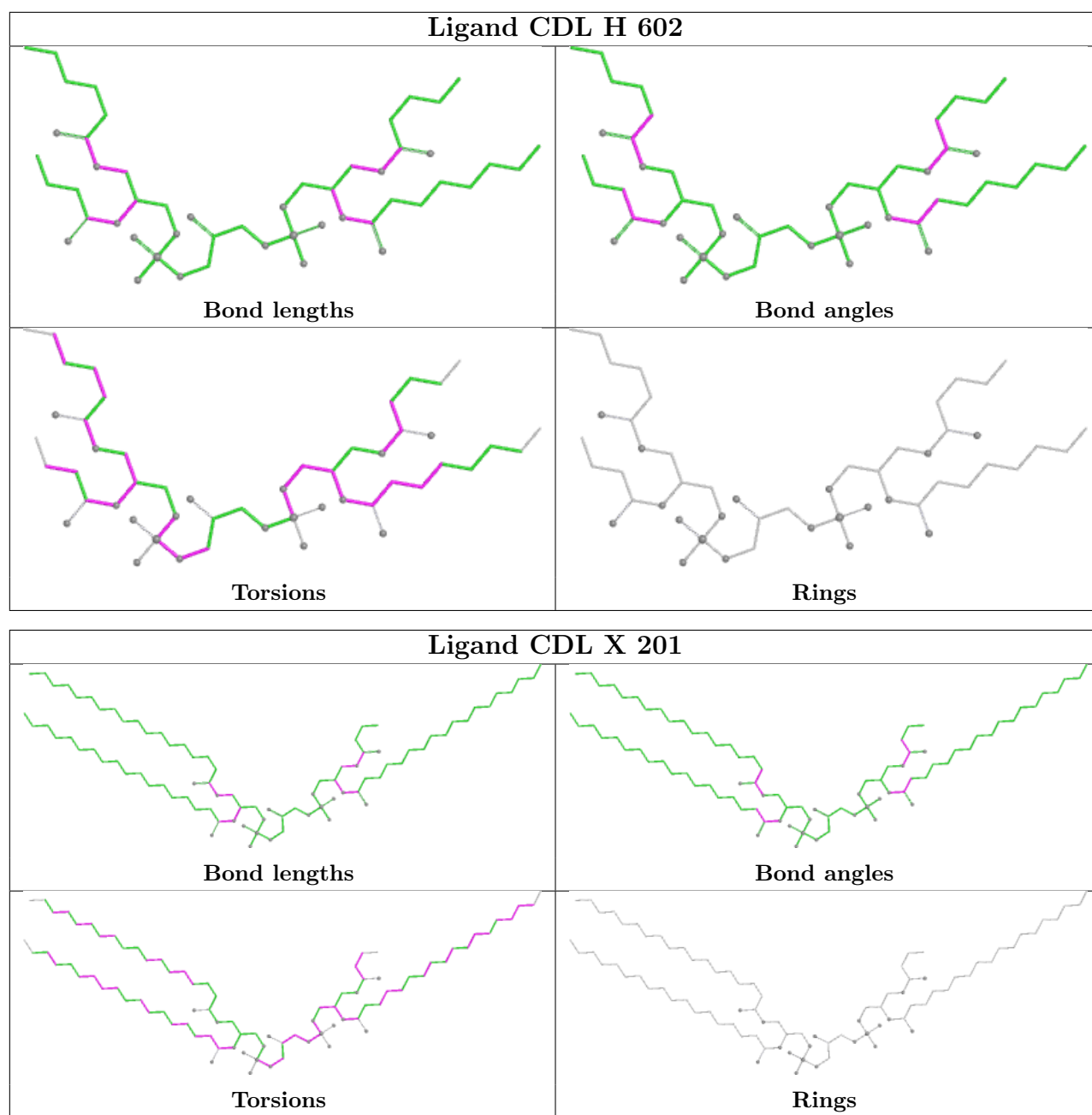
23 monomers are involved in 41 short contacts:

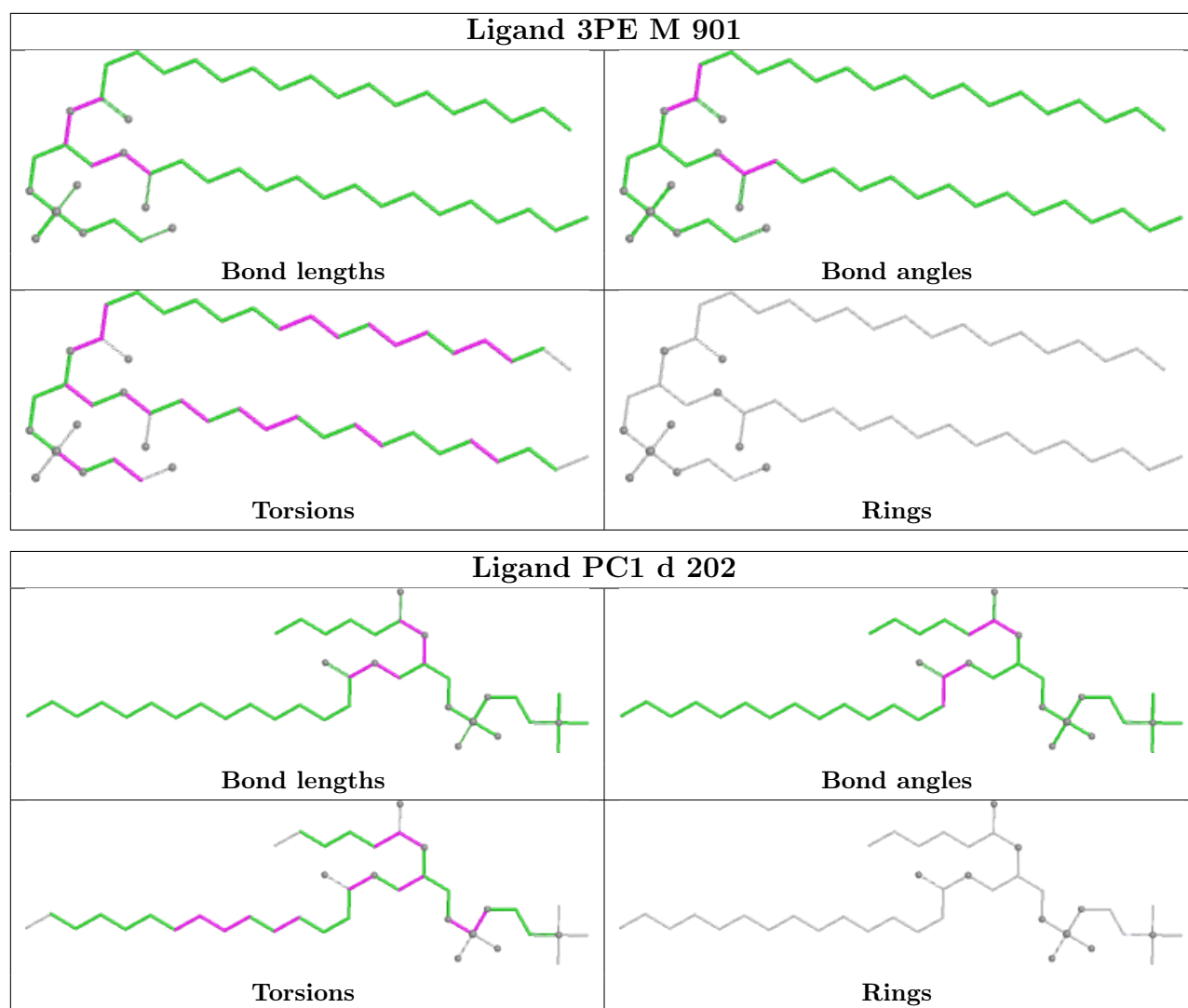
Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	X	201	CDL	1	0
46	A	202	PC1	1	0
47	B	201	SF4	1	0
53	O	401	GTP	1	0
45	m	401	3PE	1	0
46	q	201	PC1	1	0
57	U	101	EHZ	2	0
58	i	201	CHD	1	0
57	T	101	EHZ	2	0
45	L	701	3PE	1	0
45	m	402	3PE	1	0
45	M	903	3PE	1	0
45	L	704	3PE	1	0
55	P	501	NDP	3	0
45	Y	803	3PE	1	0
52	d	203	CDL	2	0
46	Z	201	PC1	7	0
46	h	202	PC1	1	0
45	M	902	3PE	1	0
46	I	201	PC1	1	0
48	D	701	U10	2	0
52	h	201	CDL	1	0
45	N	401	3PE	7	0

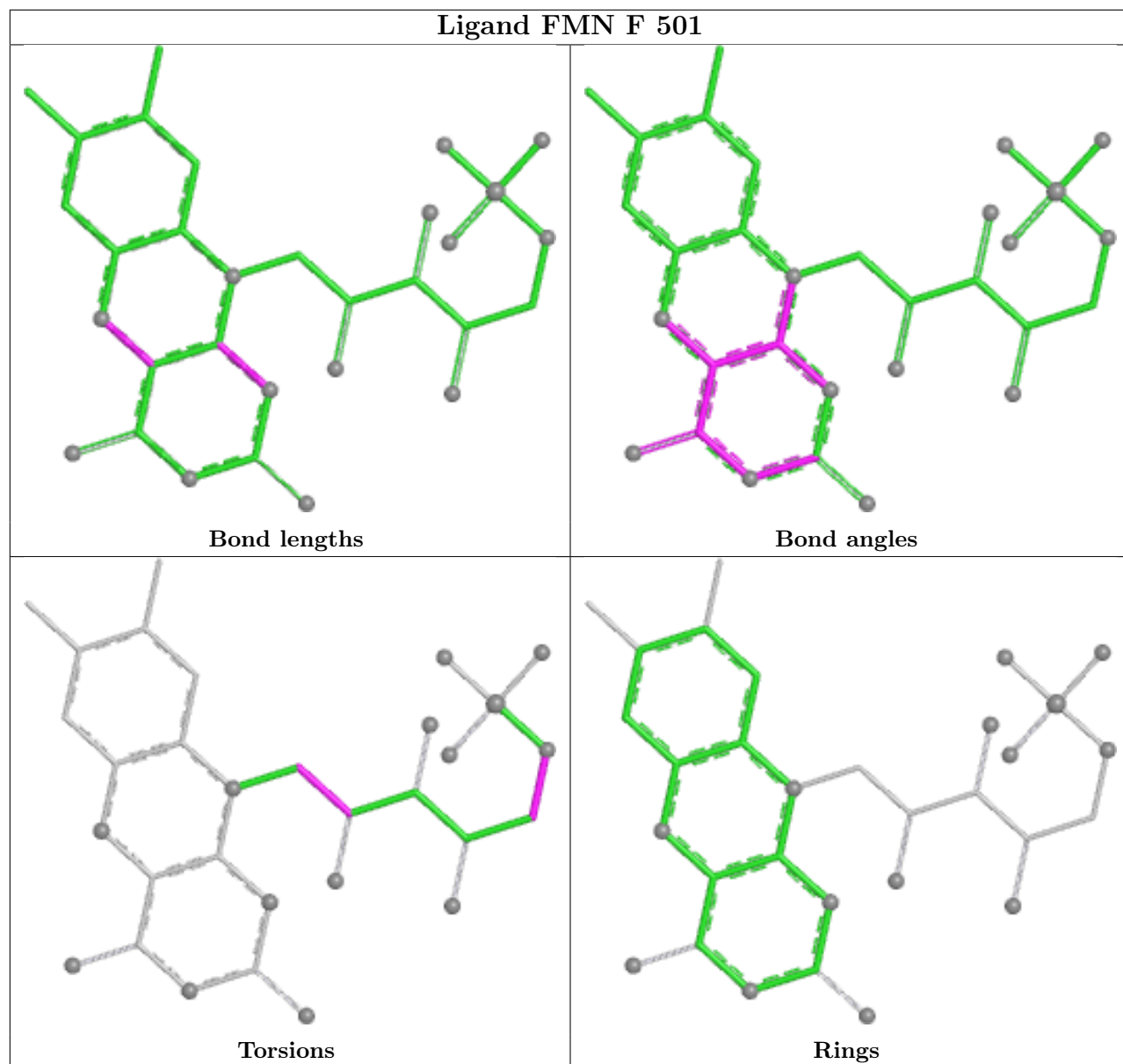
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

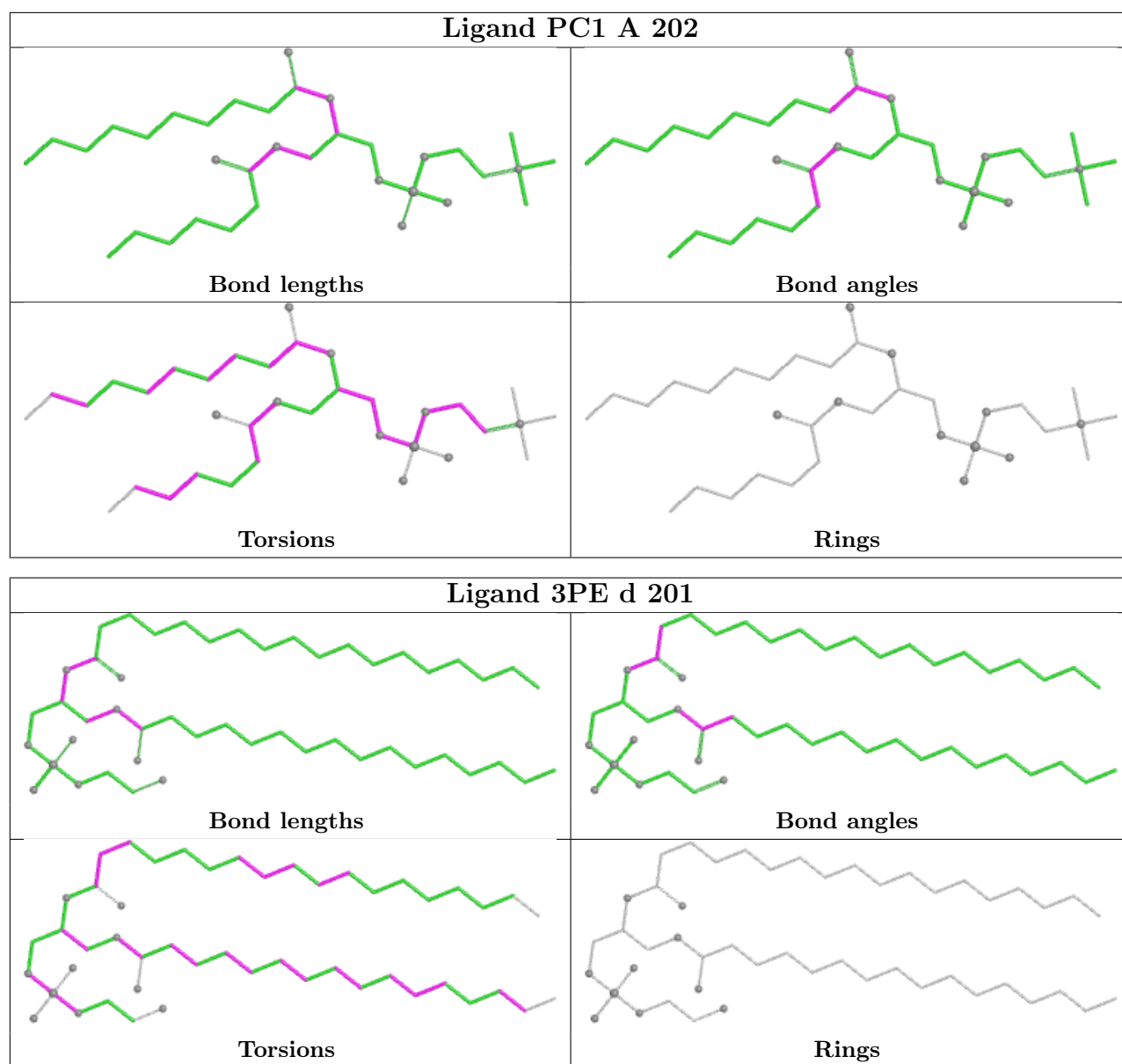
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

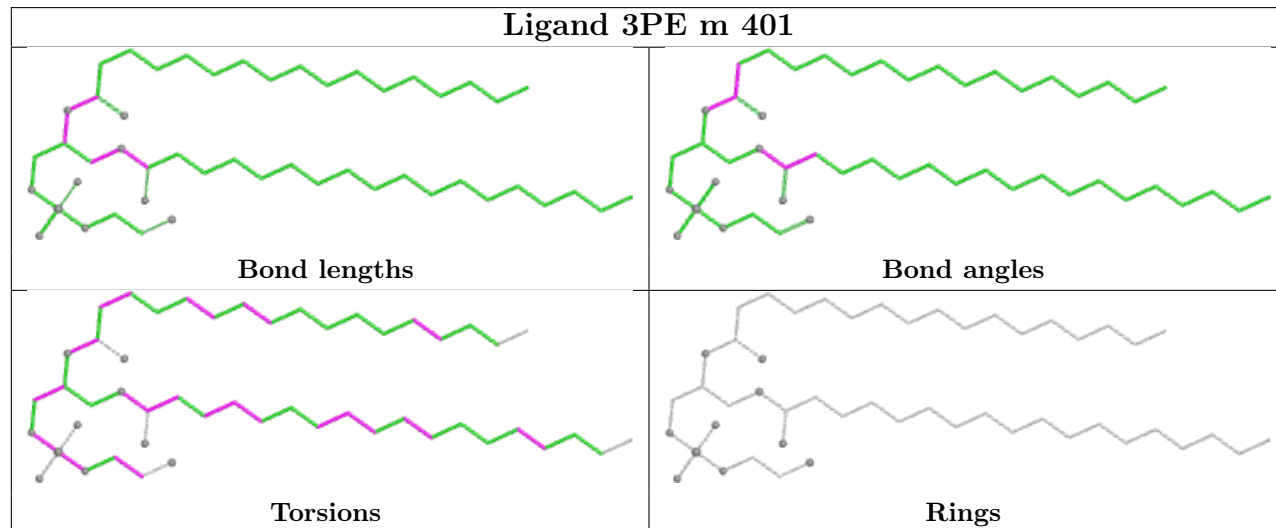
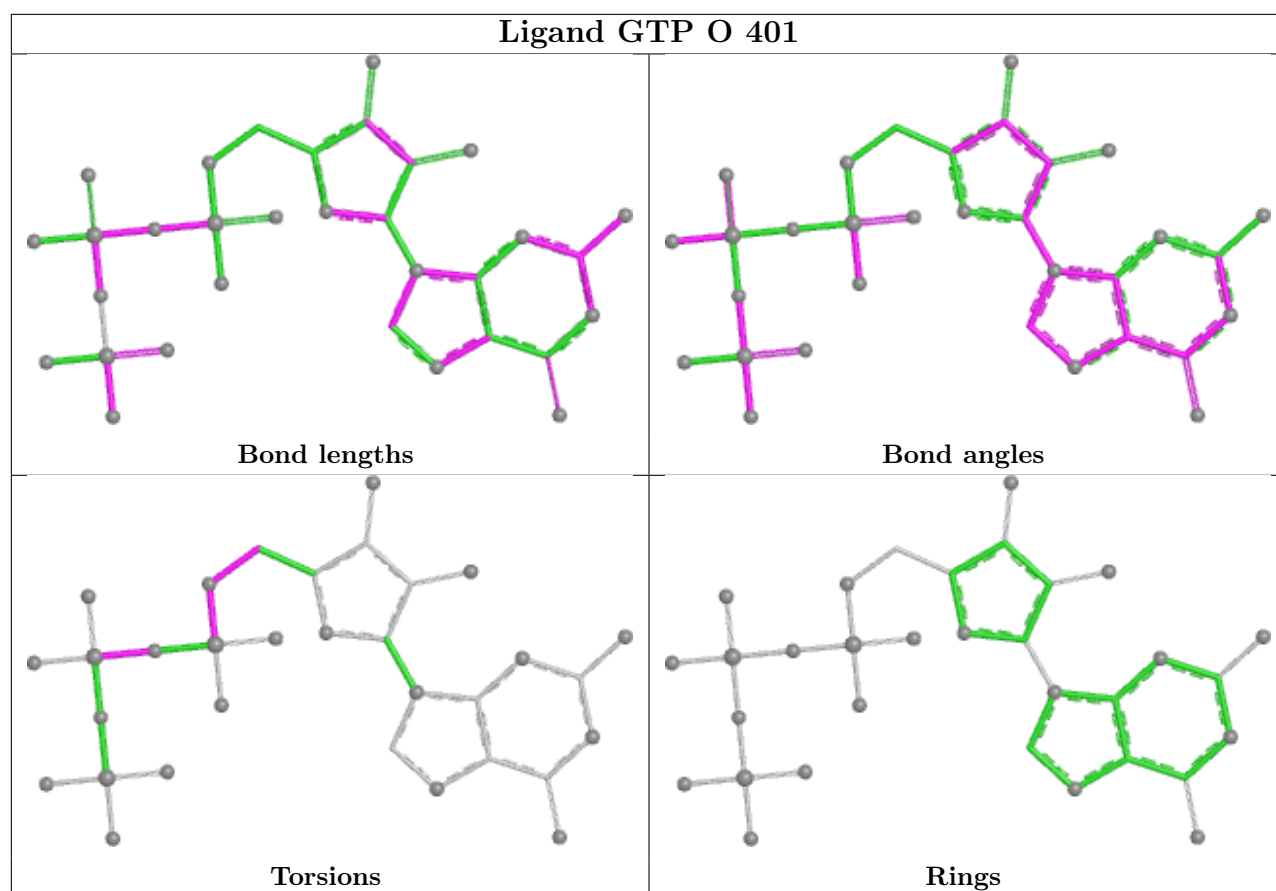


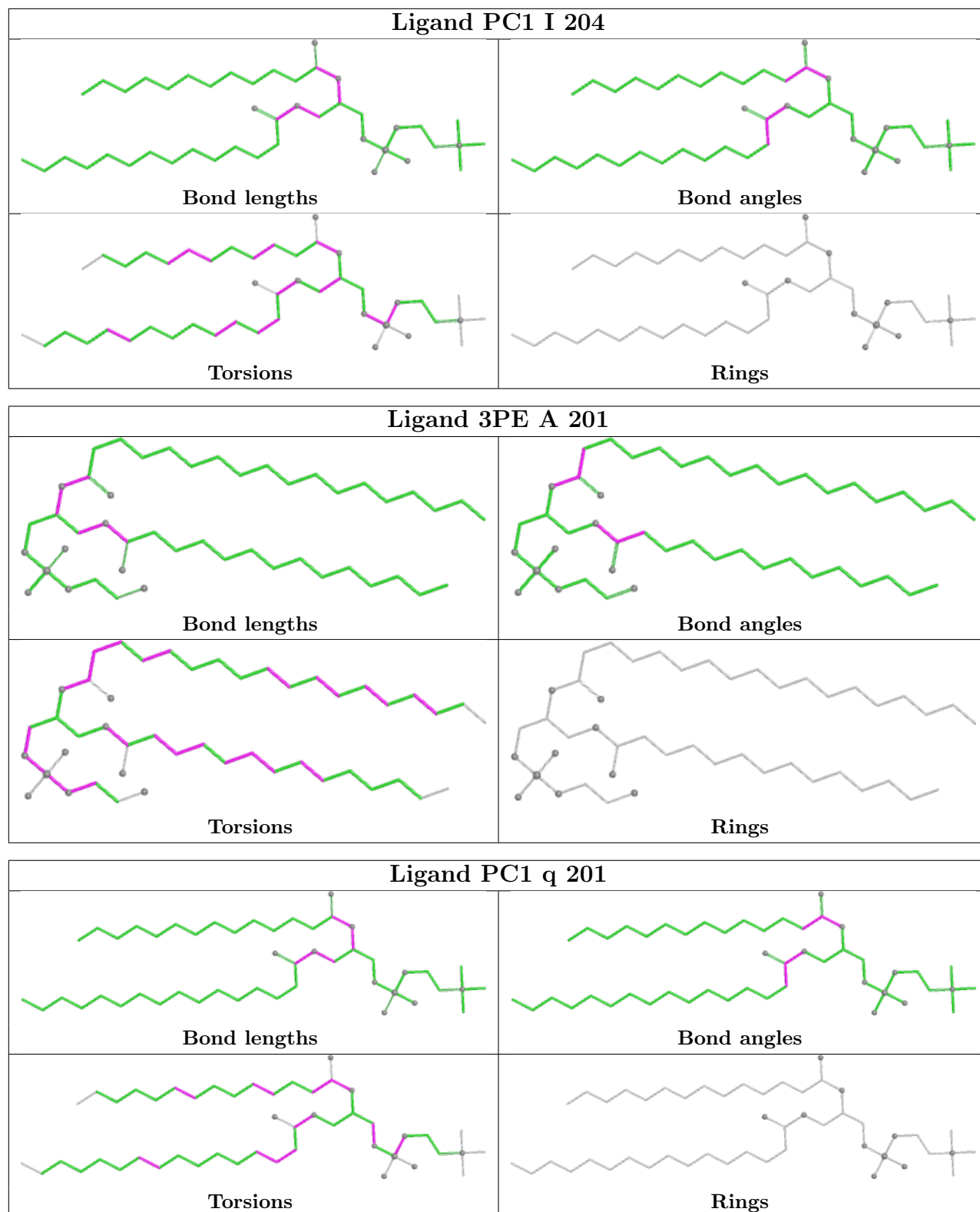


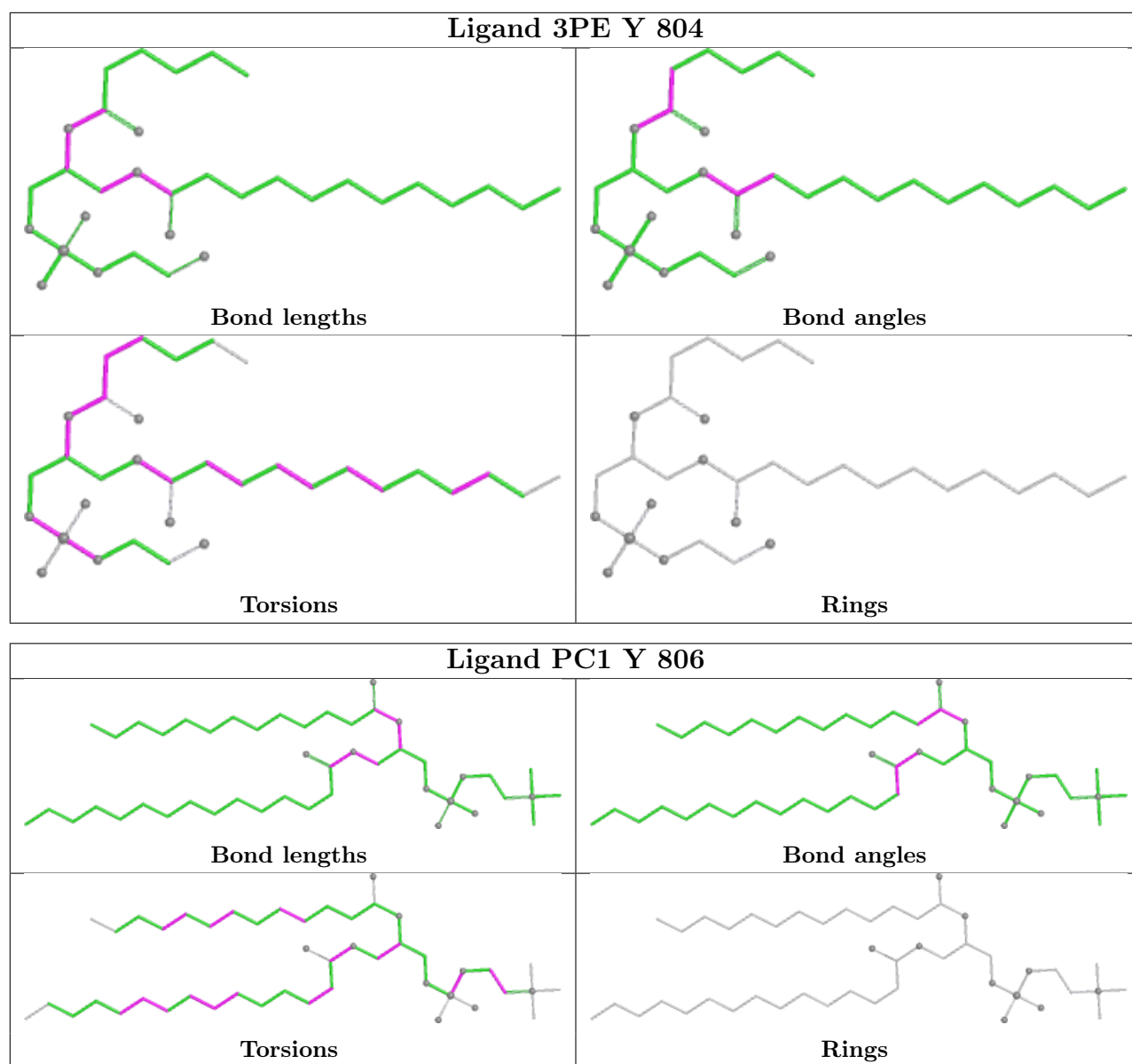


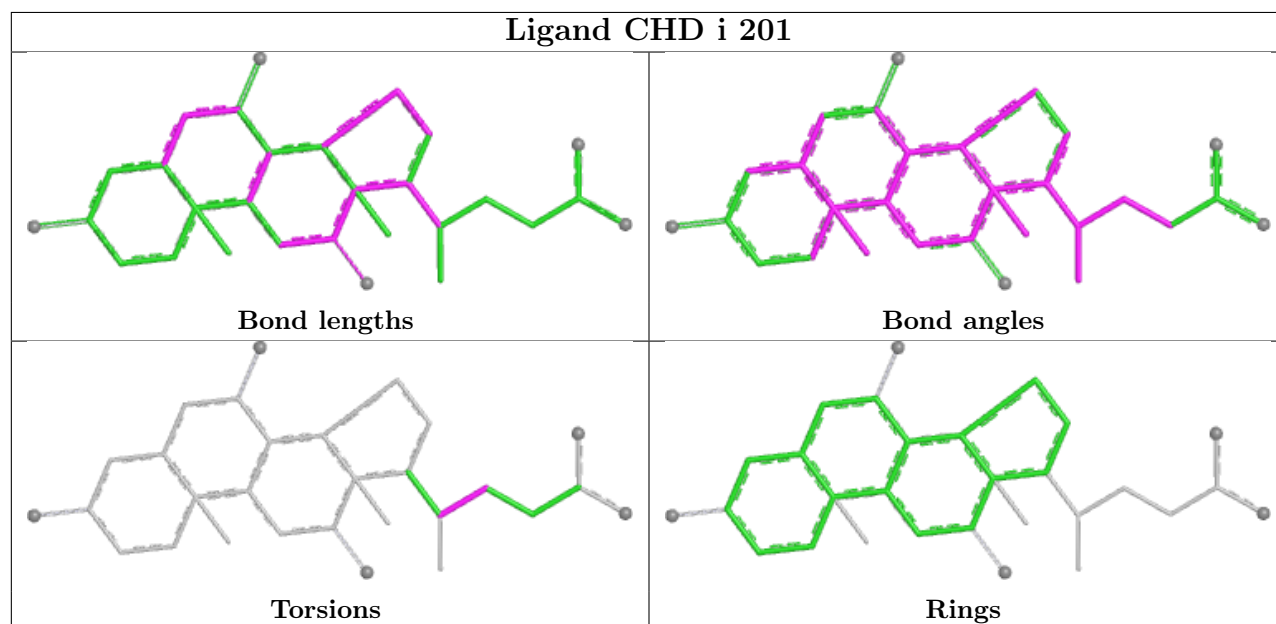
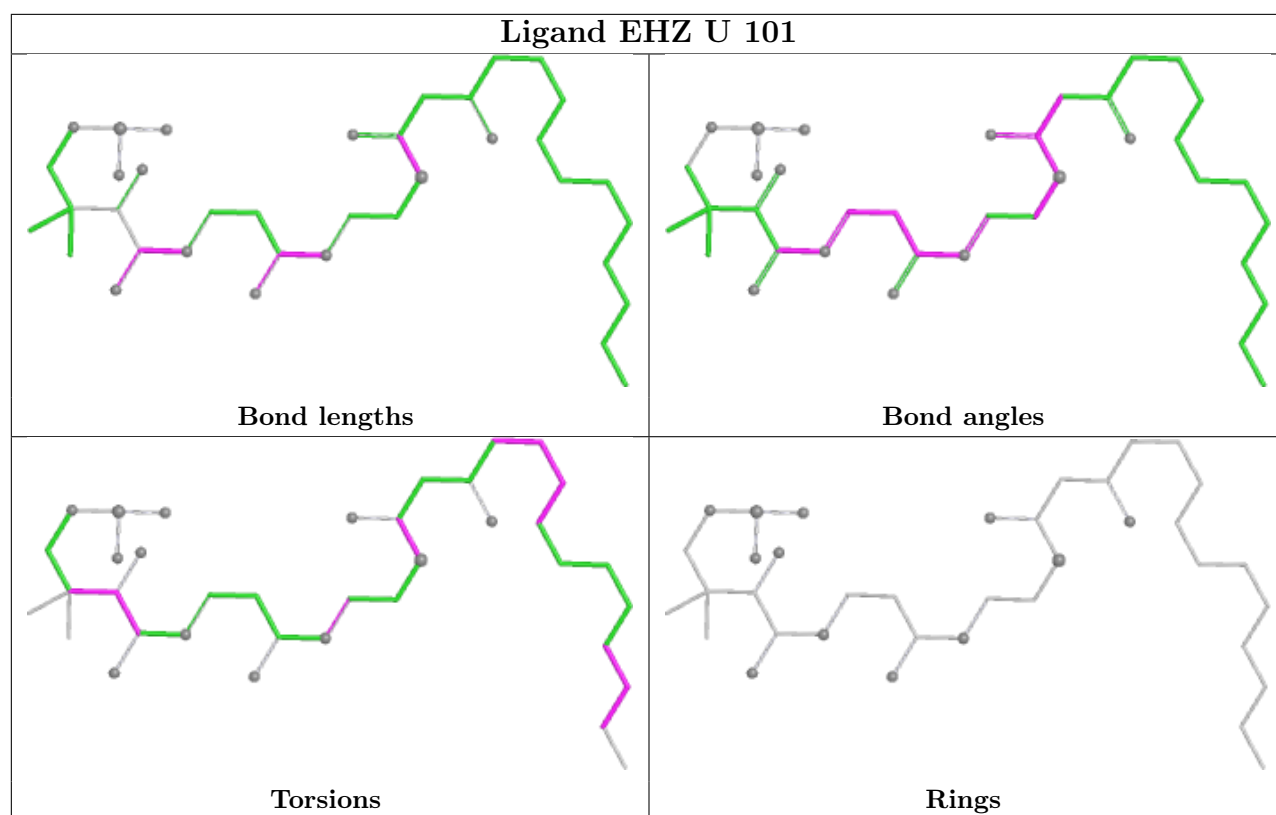


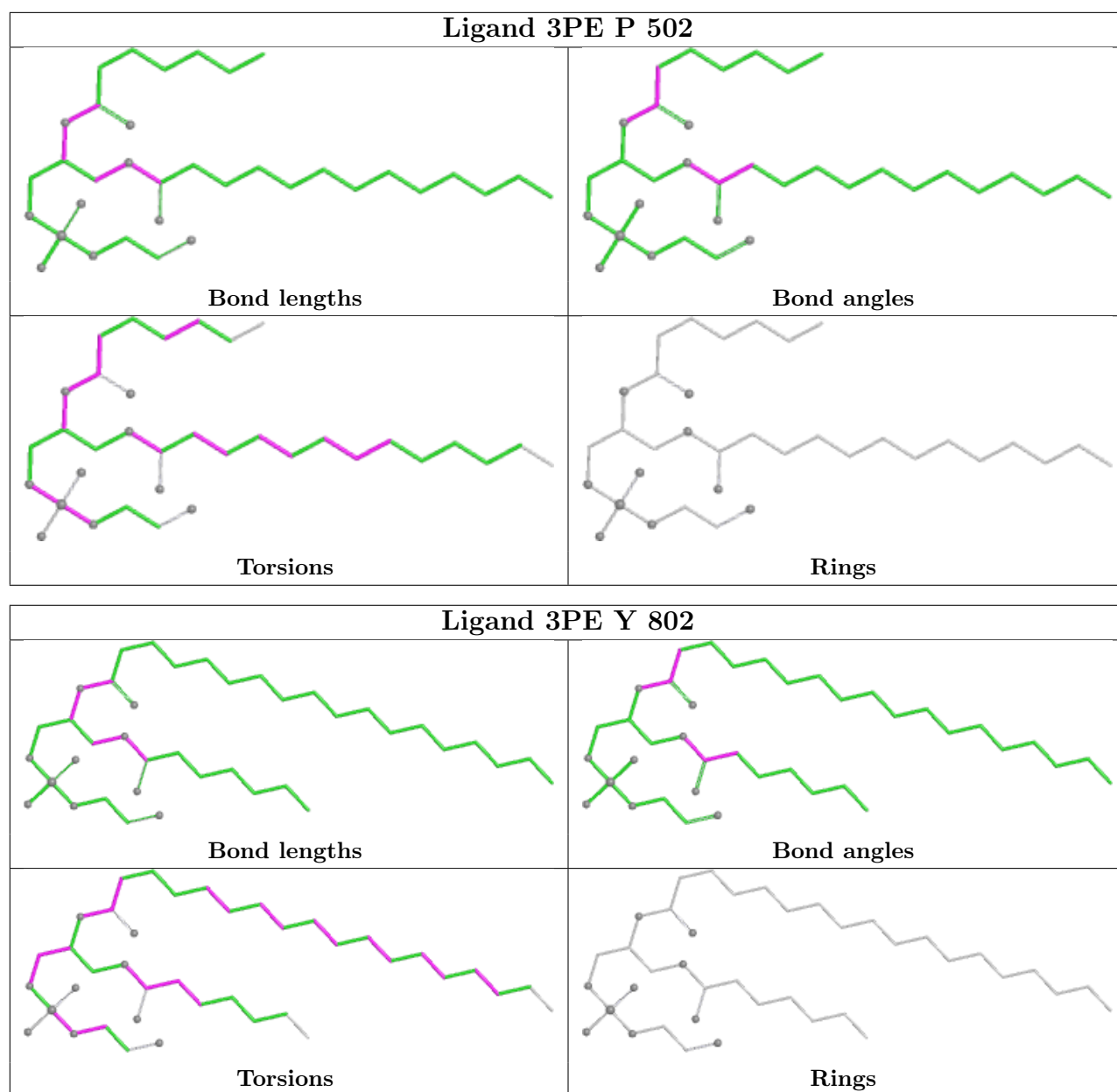


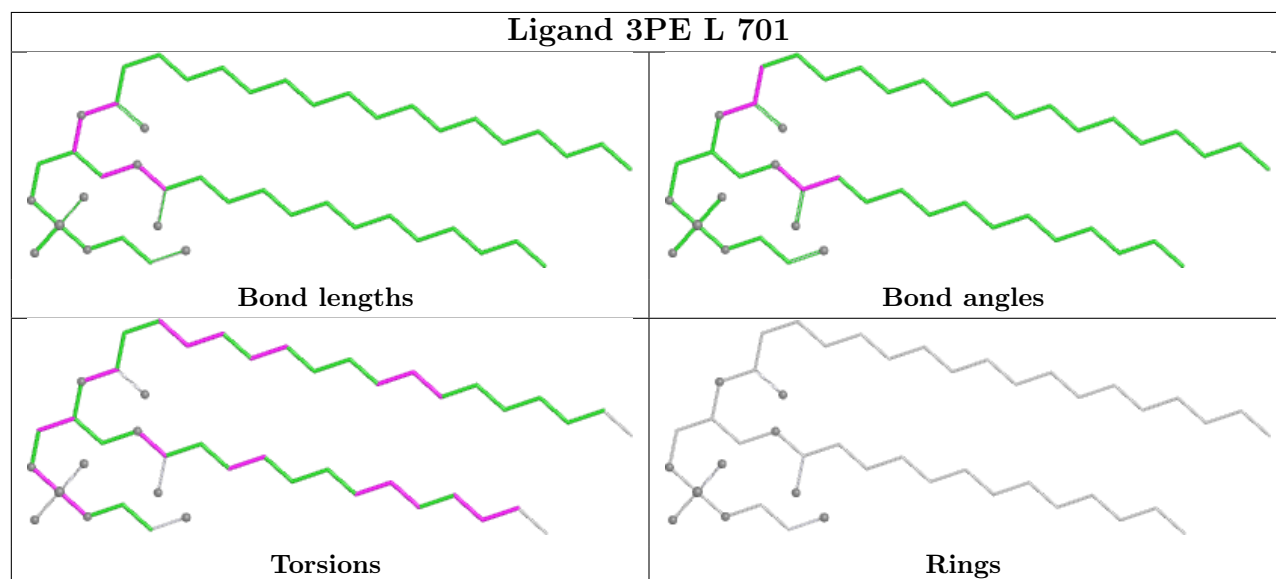
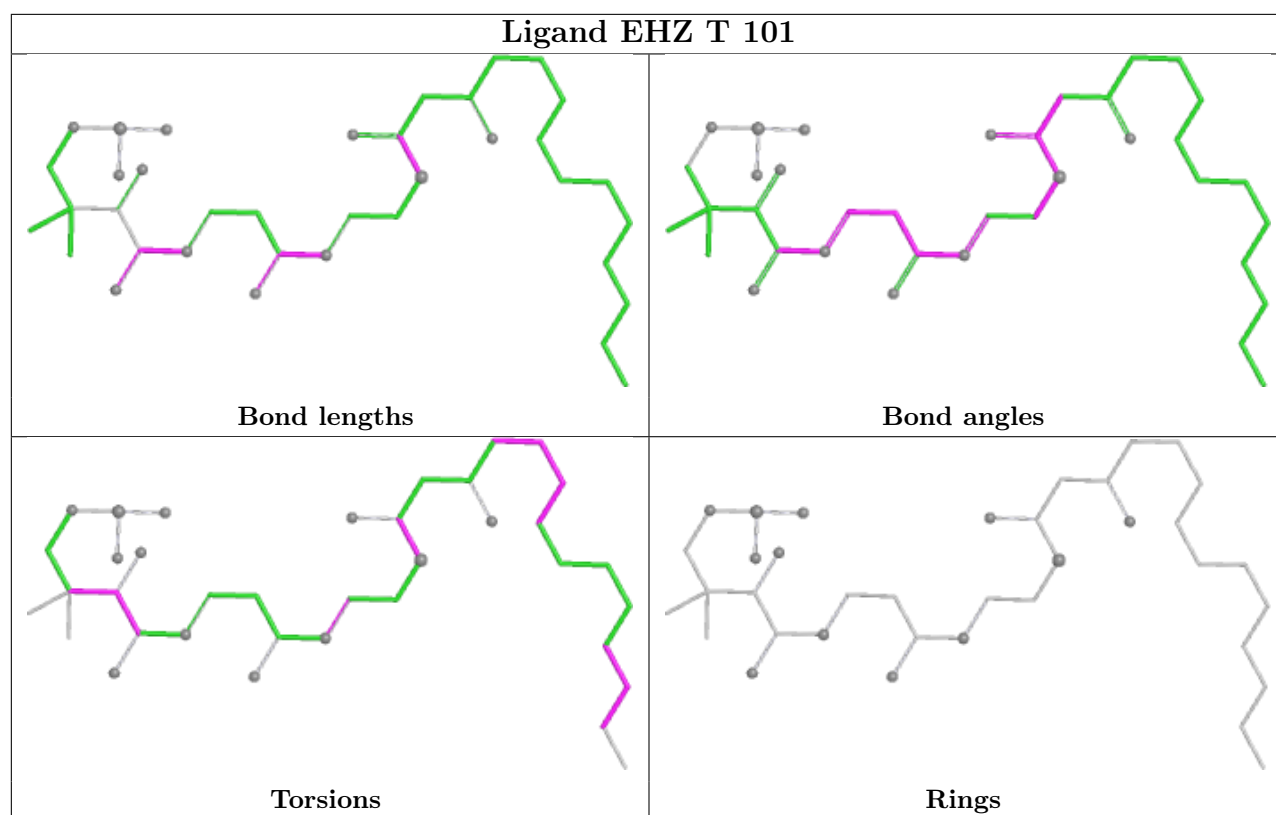


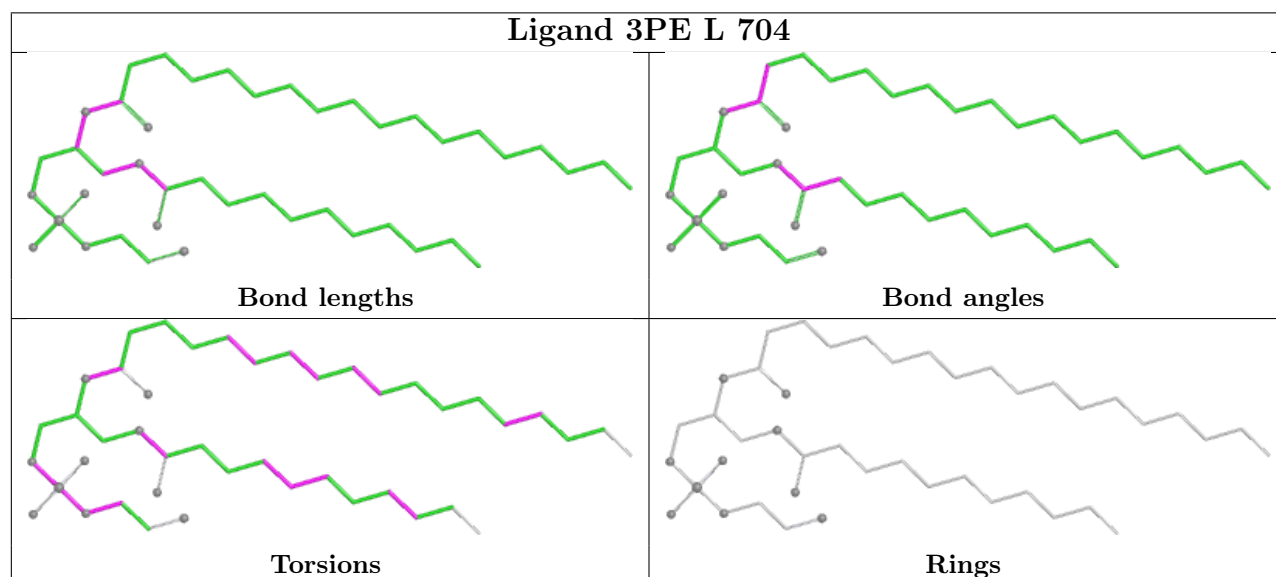
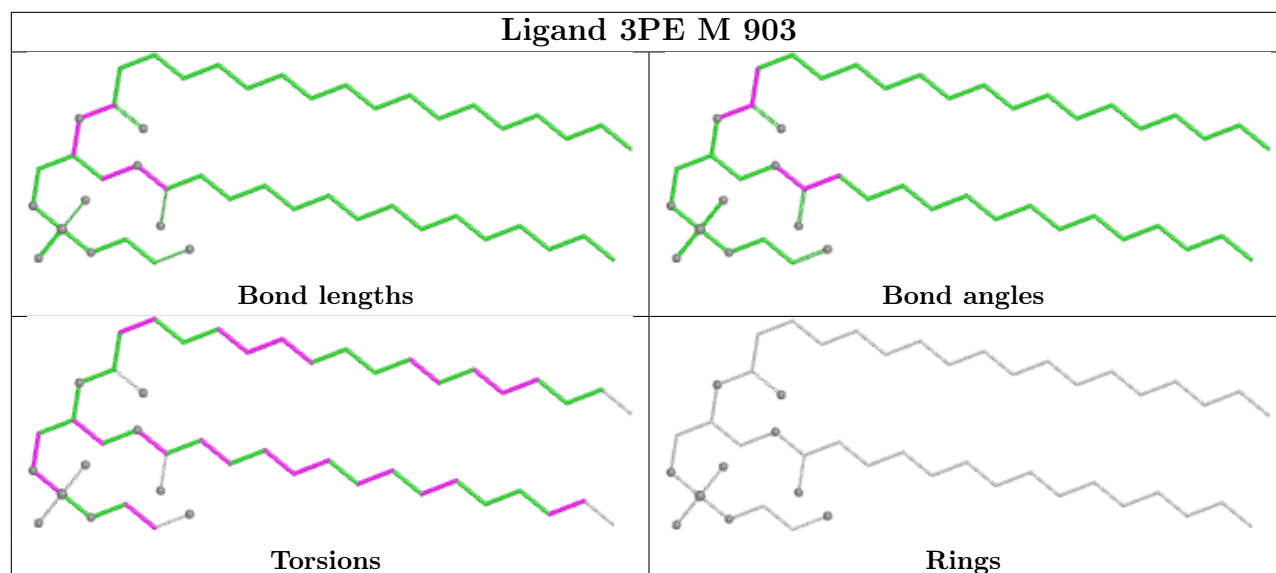
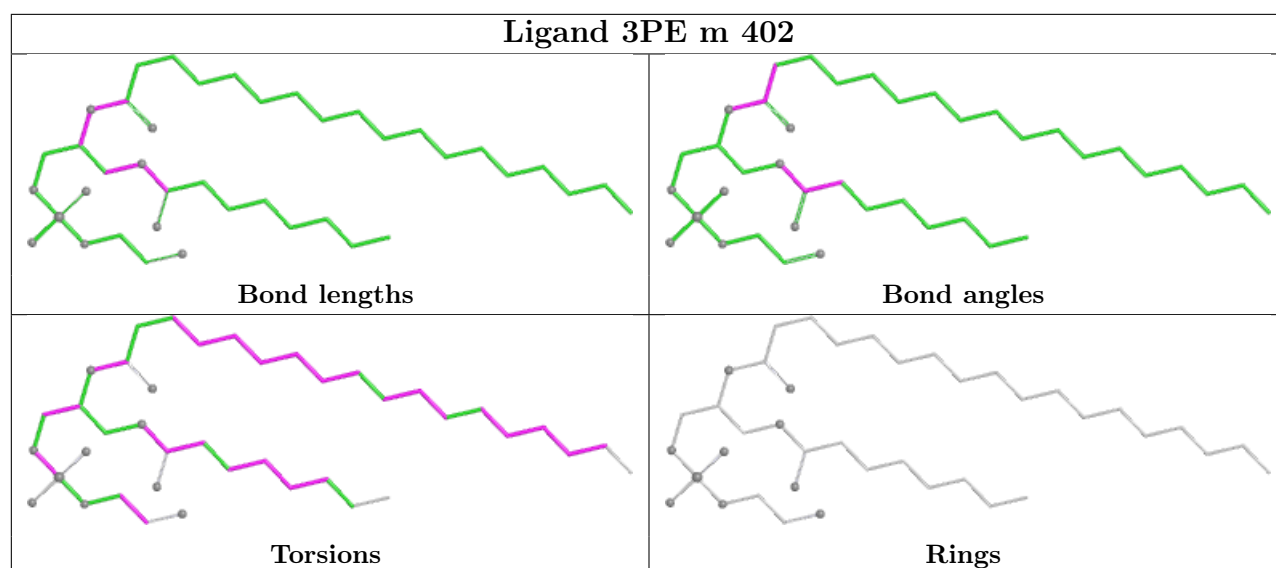


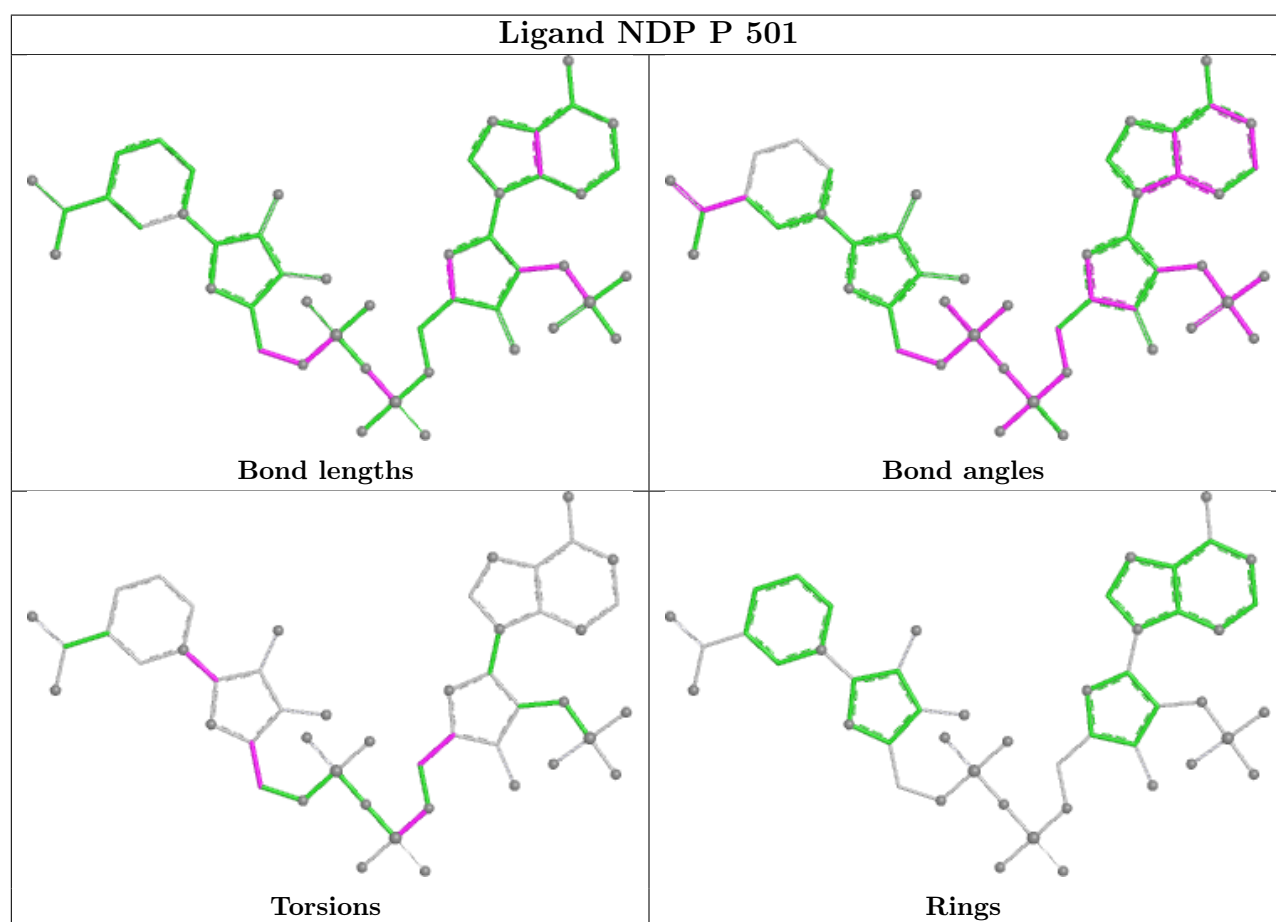
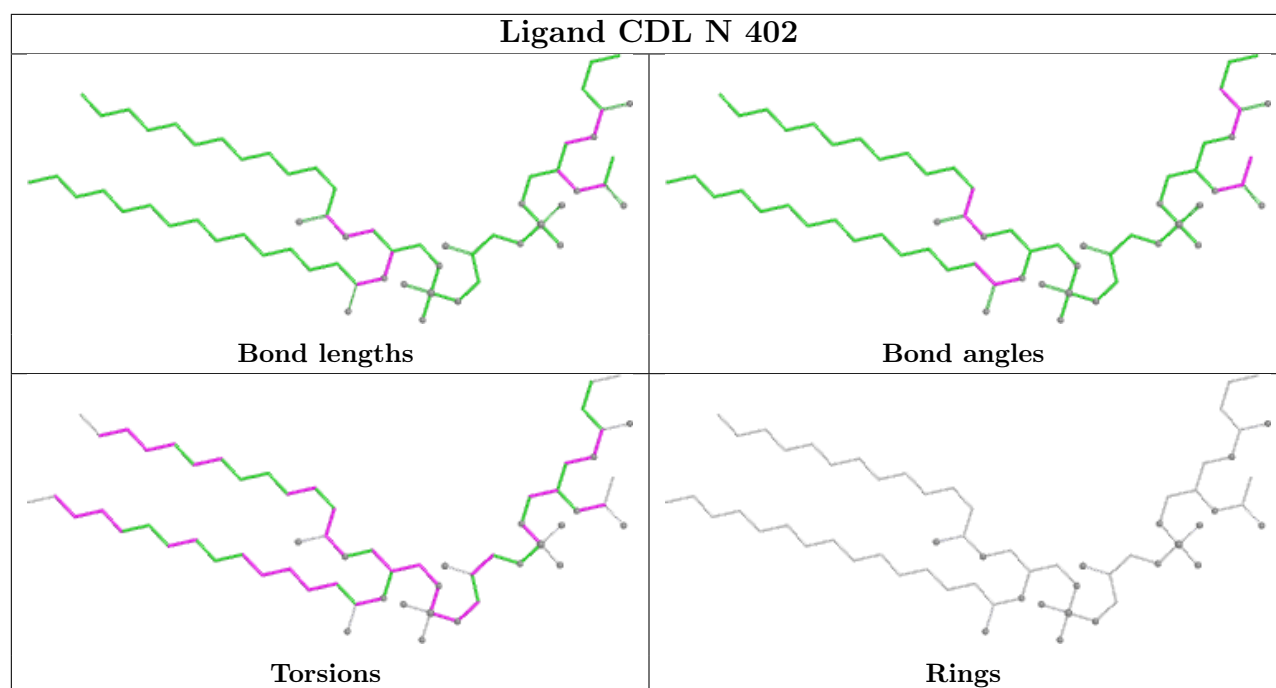


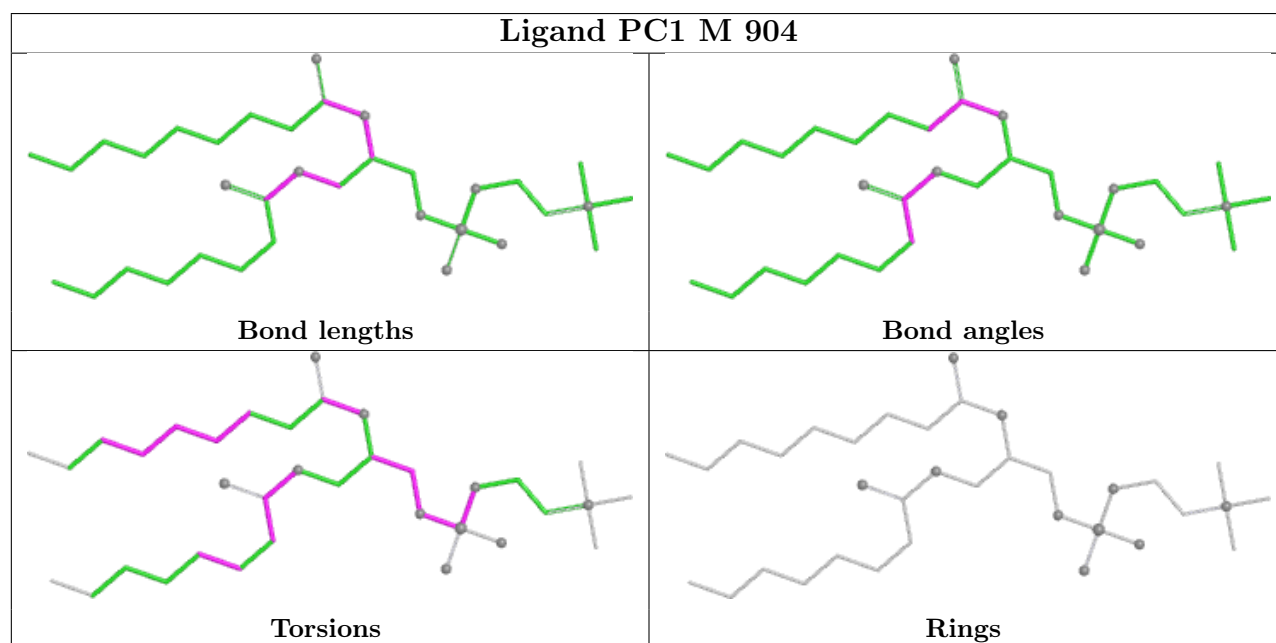
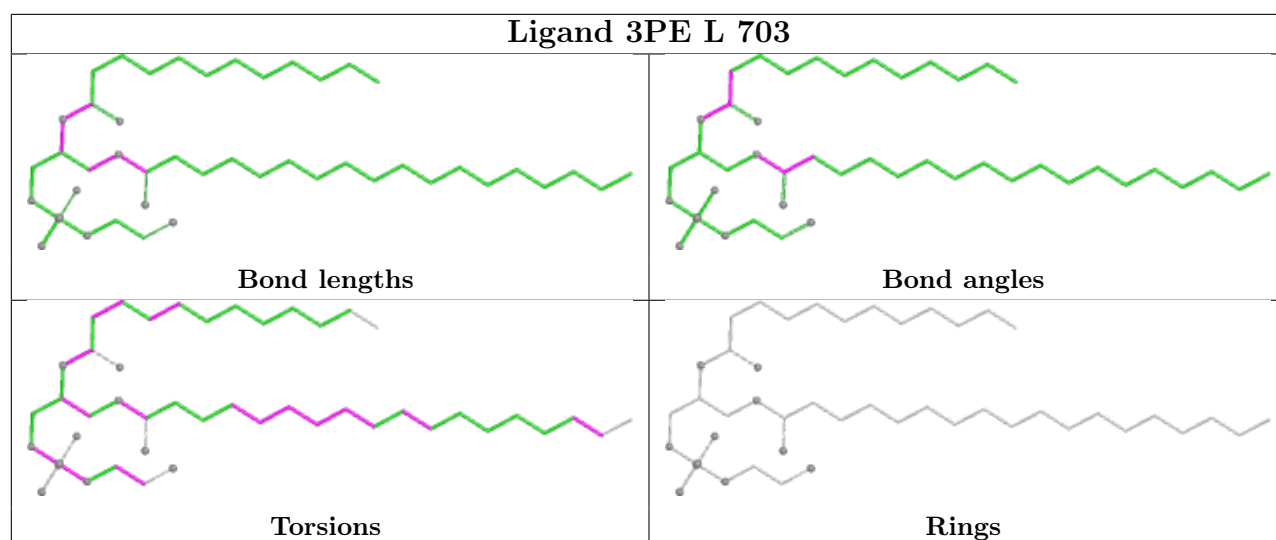


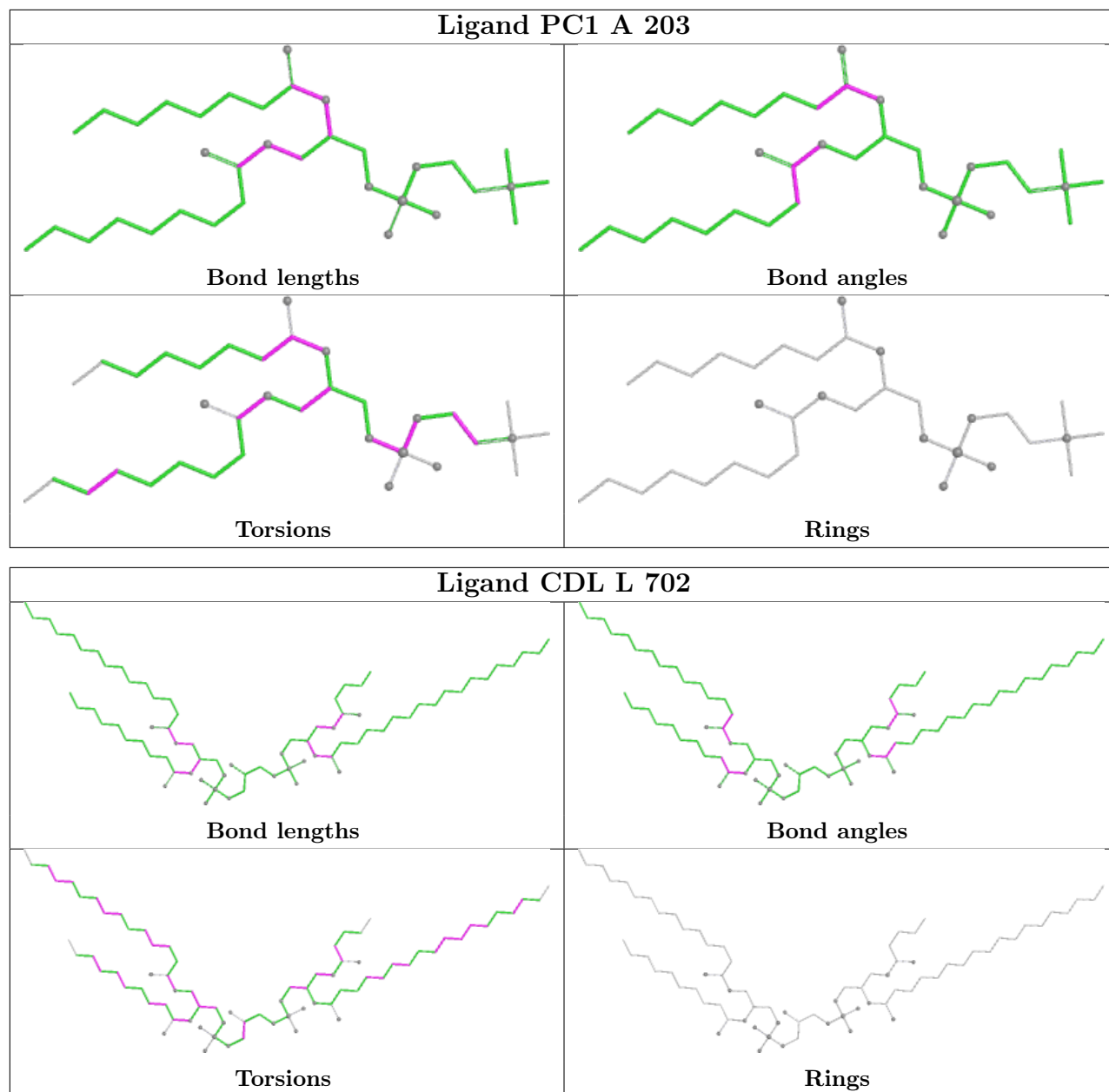


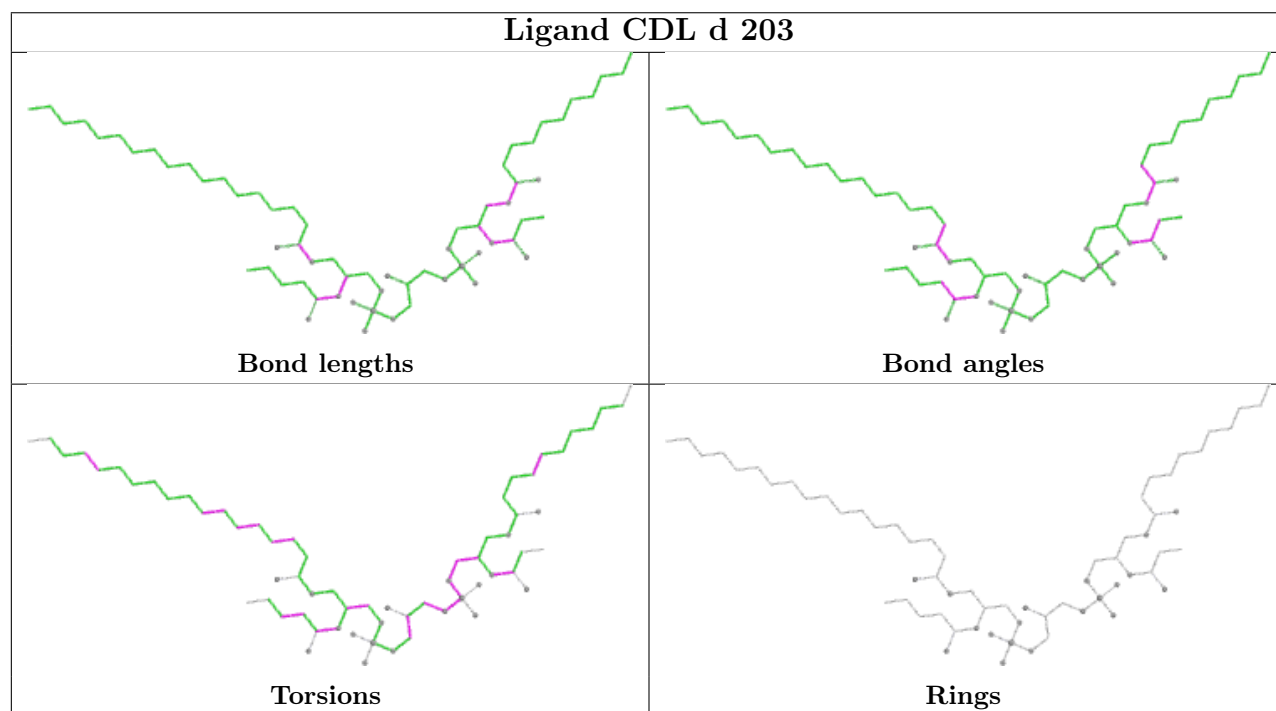
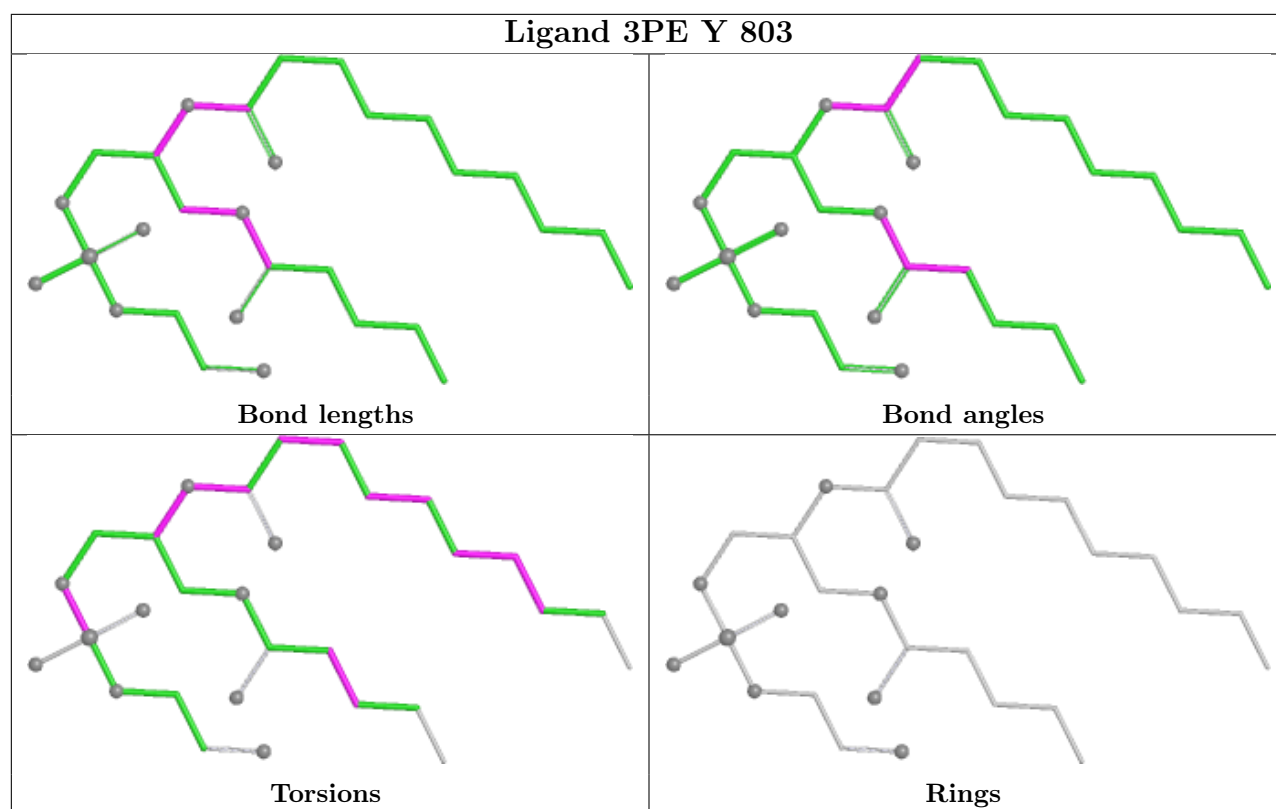


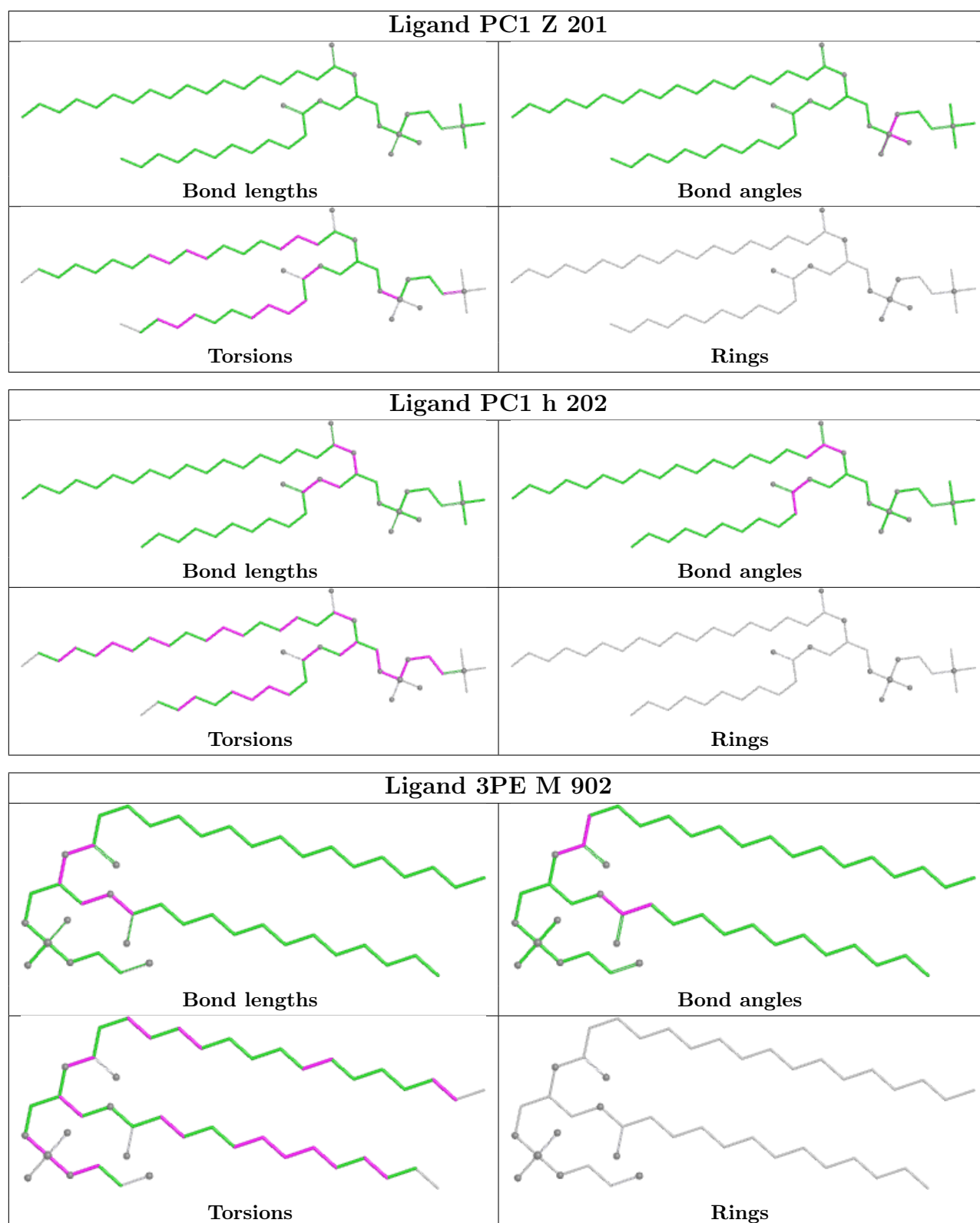


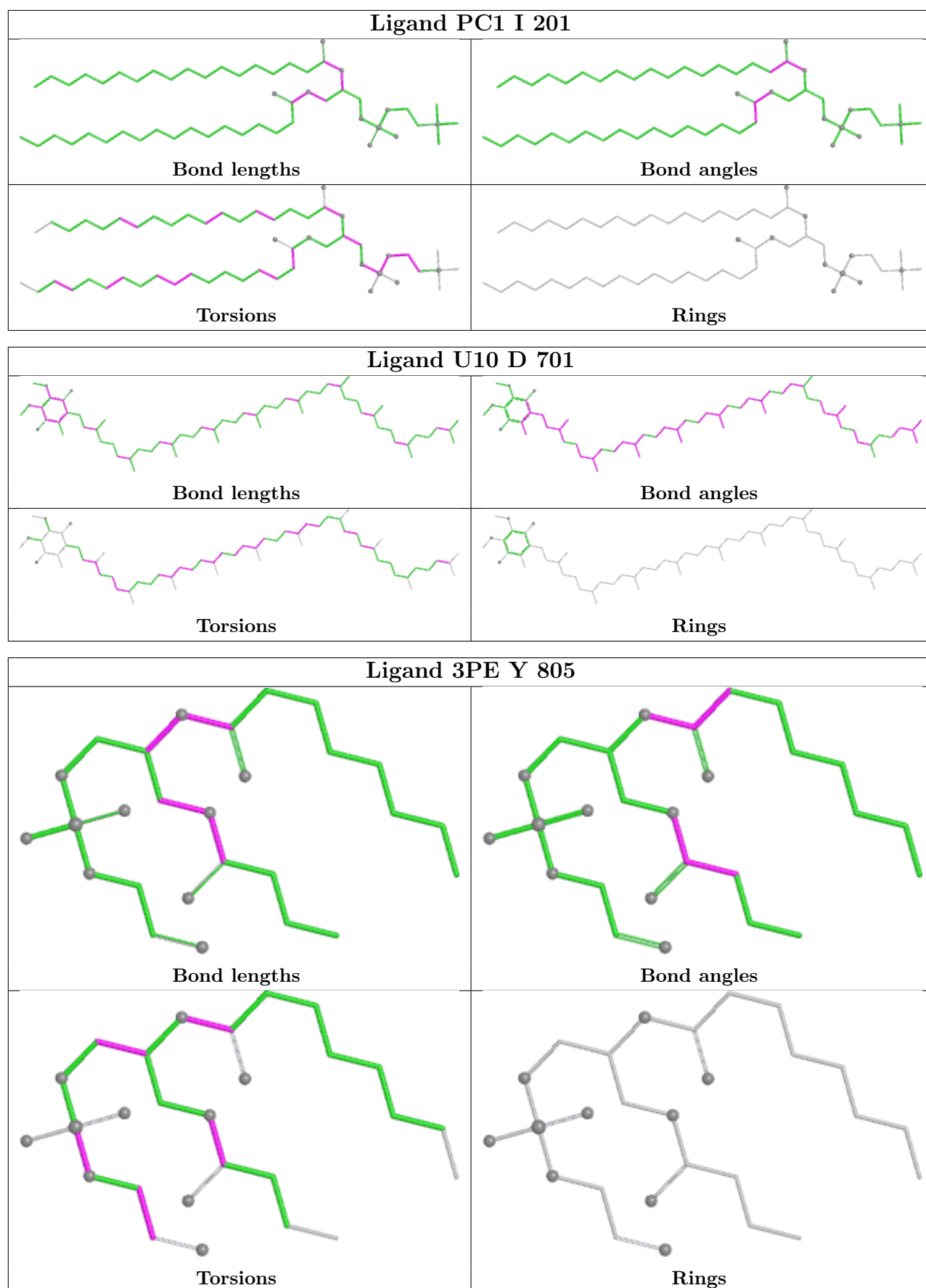


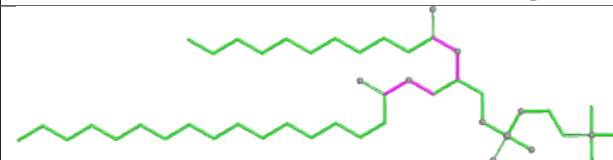
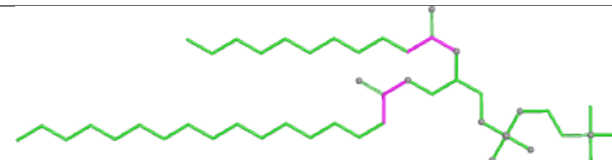
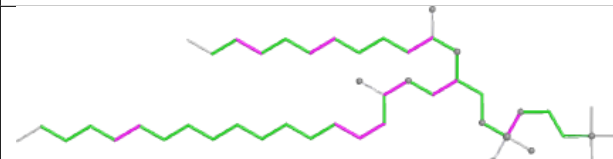
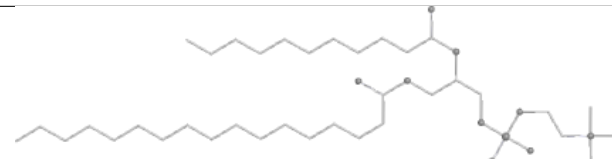


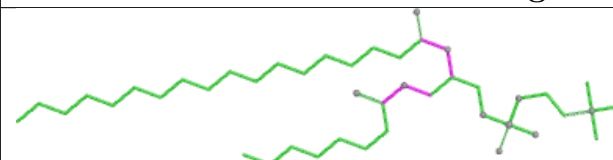
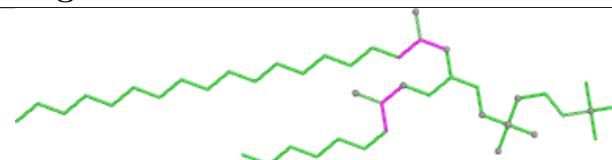
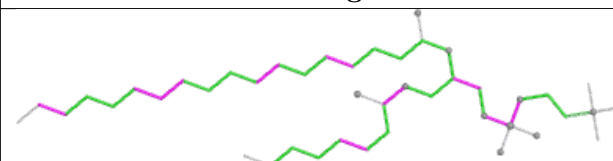
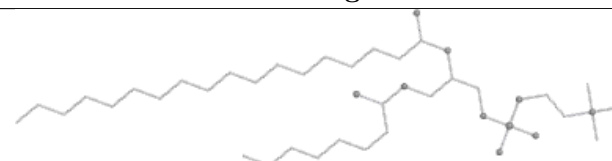


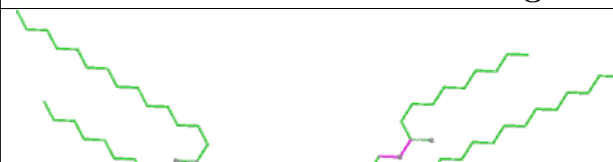
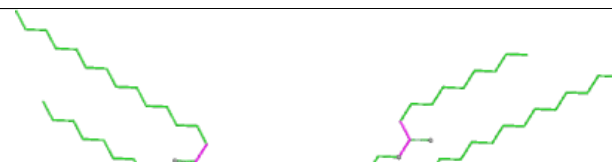
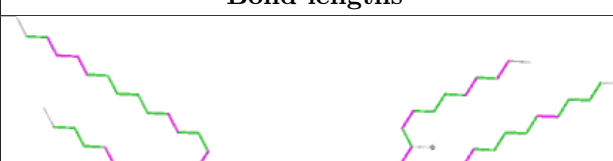


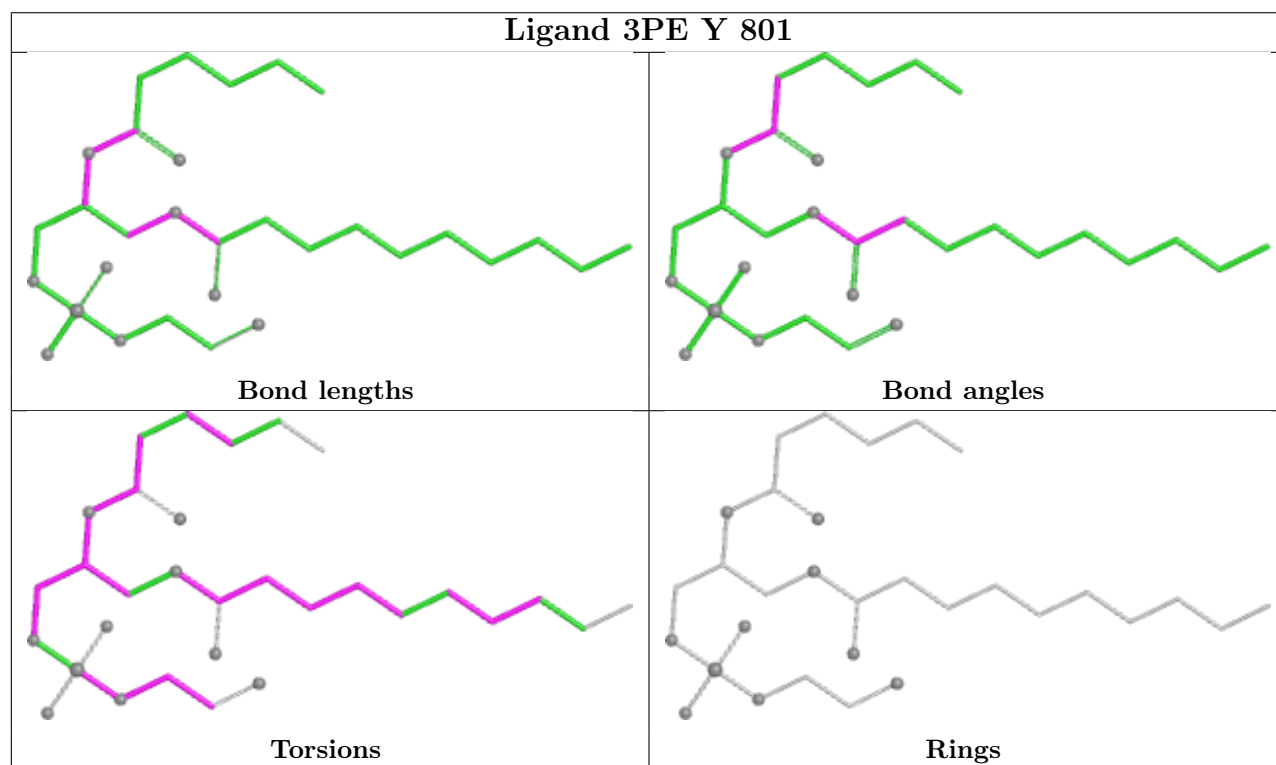
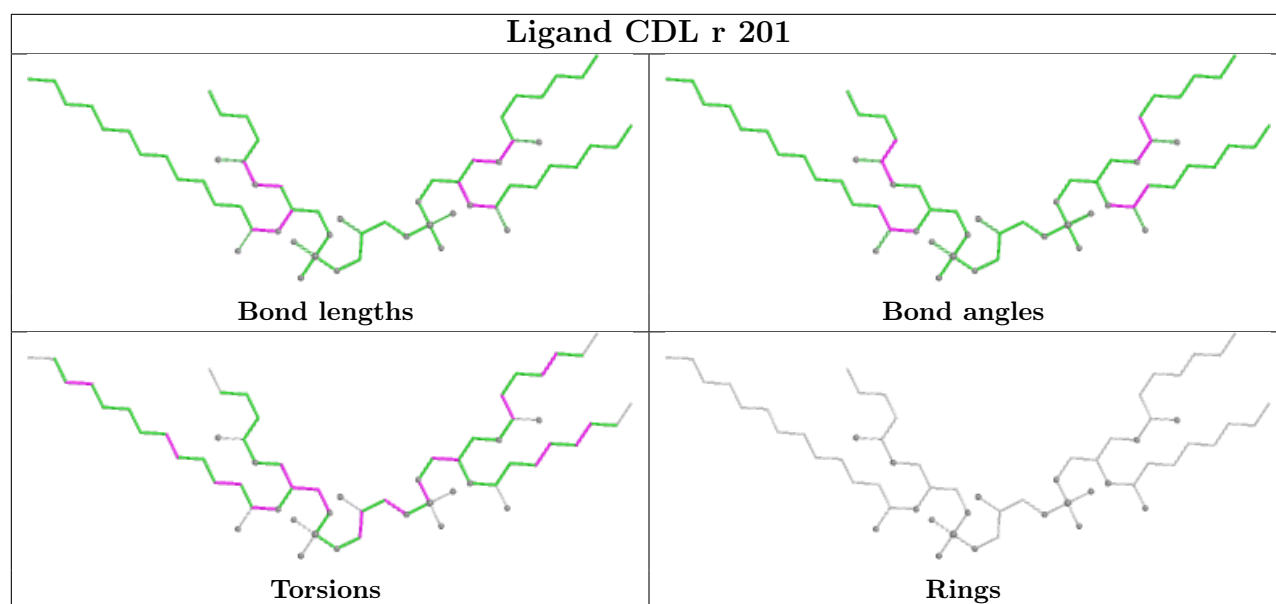


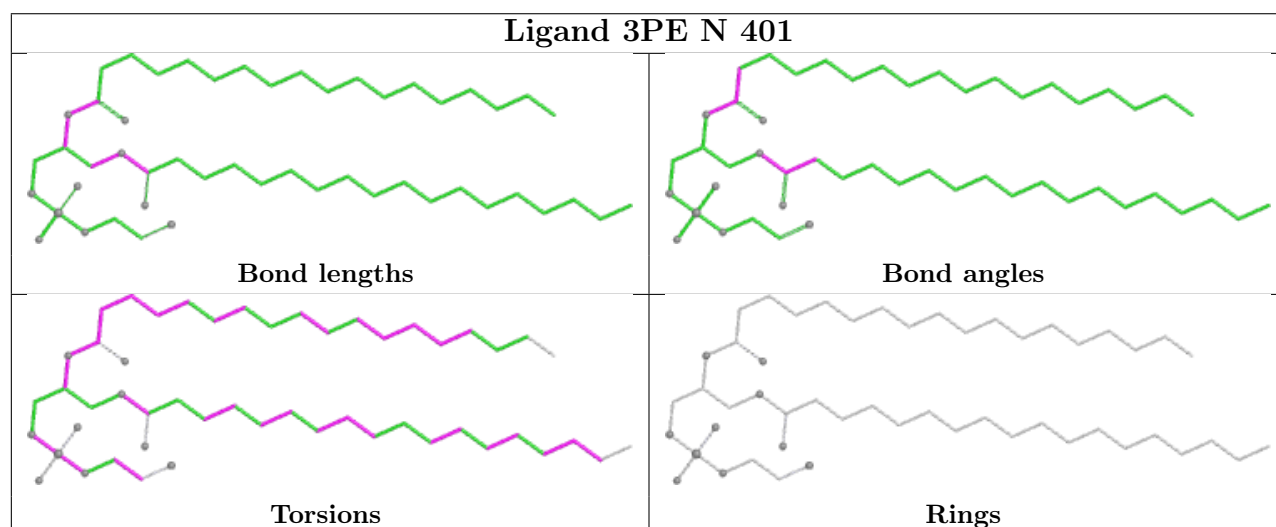
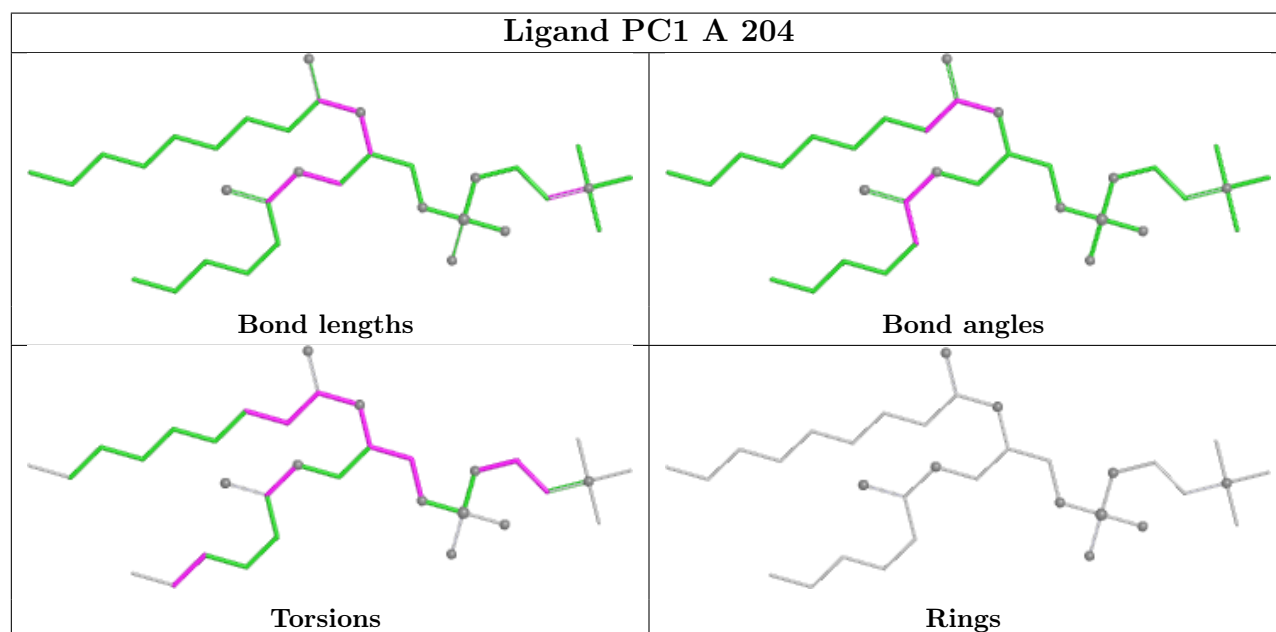
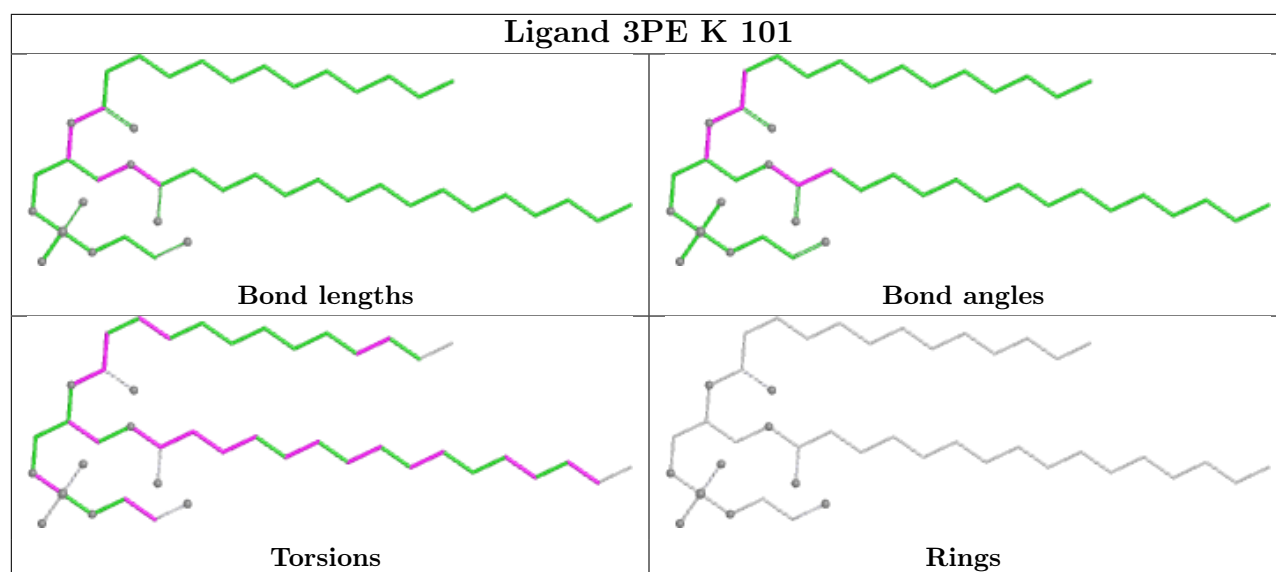


Ligand PC1 B 202	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PC1 g 201	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CDL h 201	
	
Bond lengths	Bond angles
	
Torsions	Rings





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.

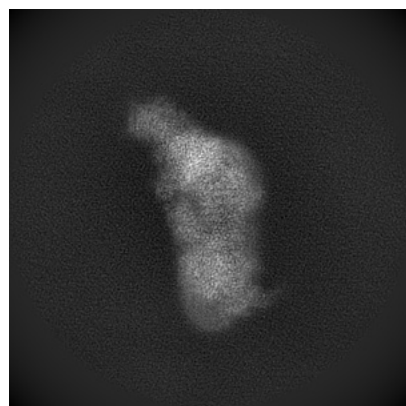
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14132. These allow visual inspection of the internal detail of the map and identification of artifacts.

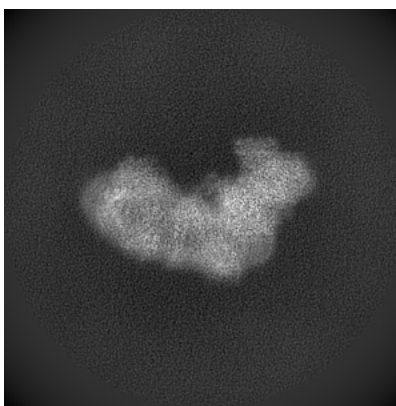
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

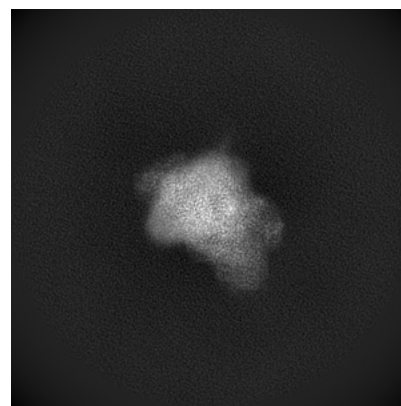
6.1.1 Primary map



X

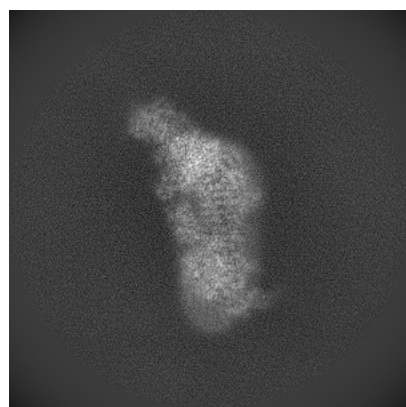


Y

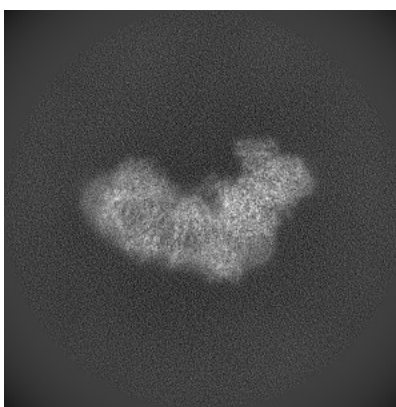


Z

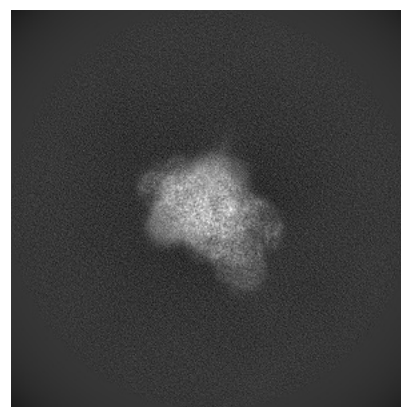
6.1.2 Raw map



X



Y

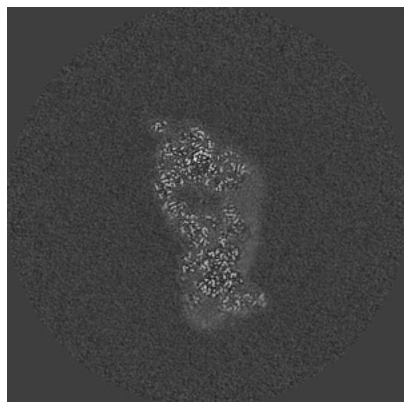


Z

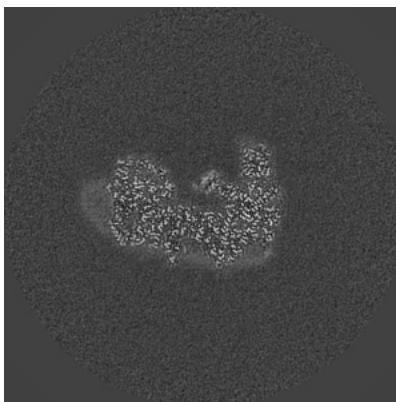
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

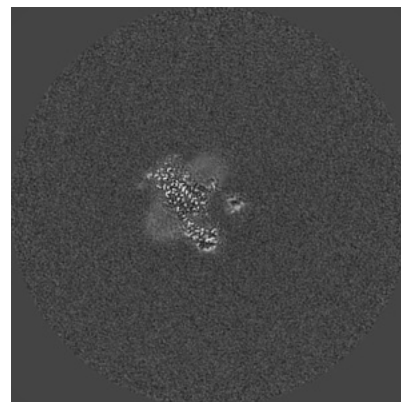
6.2.1 Primary map



X Index: 320

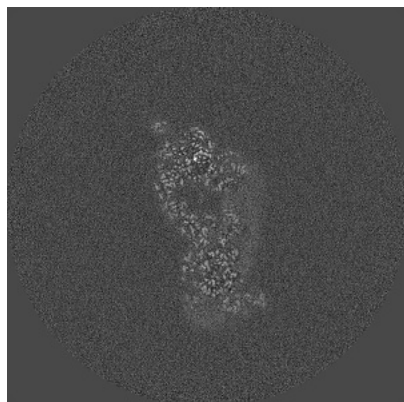


Y Index: 320

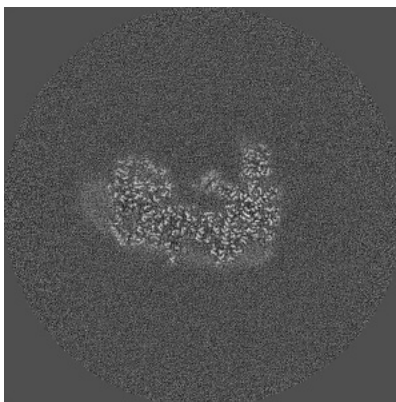


Z Index: 320

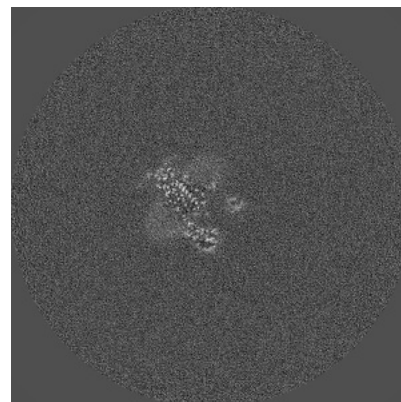
6.2.2 Raw map



X Index: 320



Y Index: 320

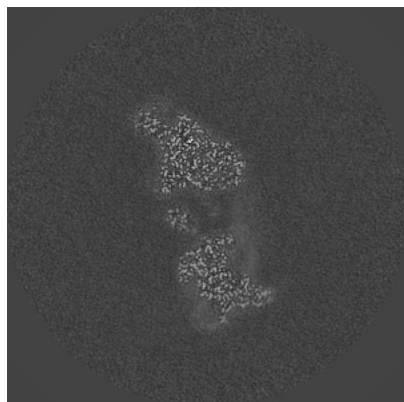


Z Index: 320

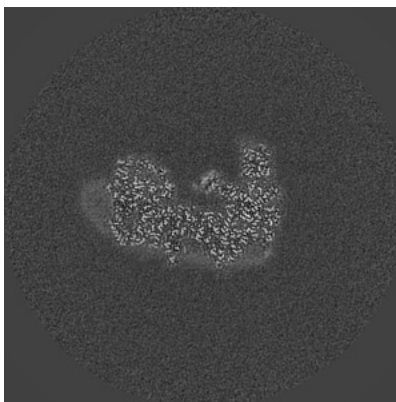
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

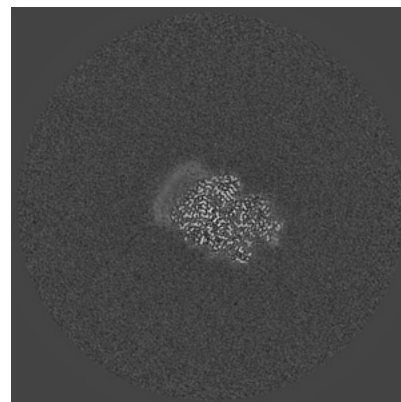
6.3.1 Primary map



X Index: 339

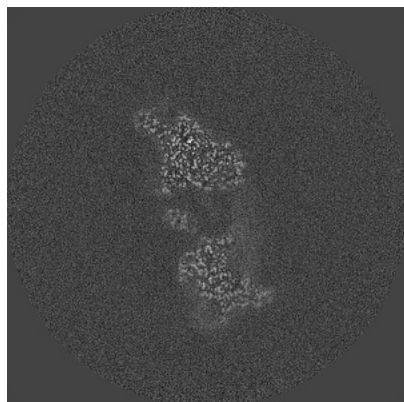


Y Index: 320

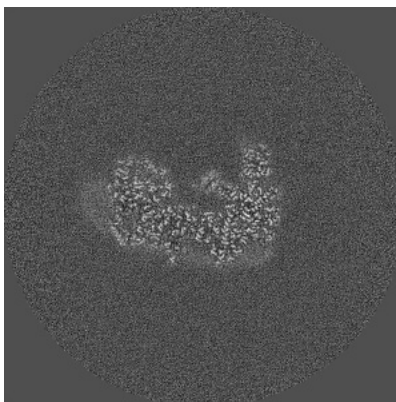


Z Index: 405

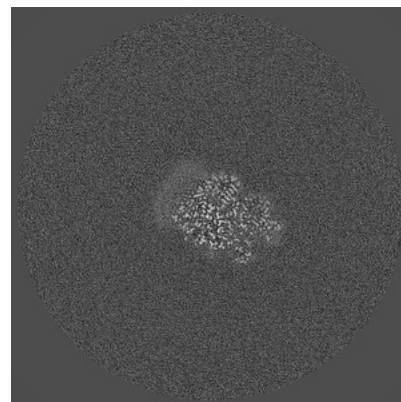
6.3.2 Raw map



X Index: 339



Y Index: 320

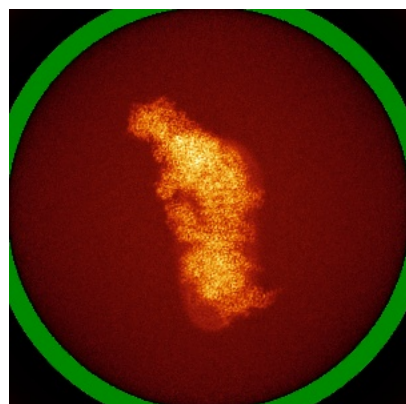


Z Index: 404

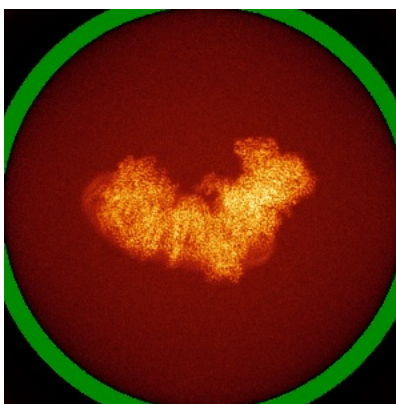
The images above show the largest variance slices of the map in three orthogonal directions.

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

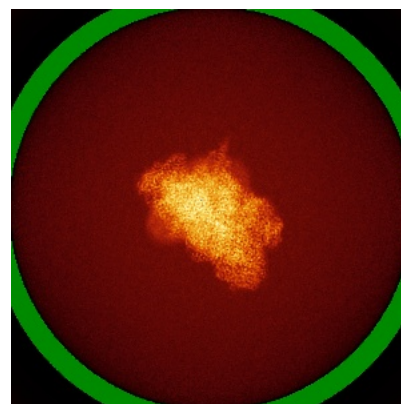
6.4.1 Primary map



X

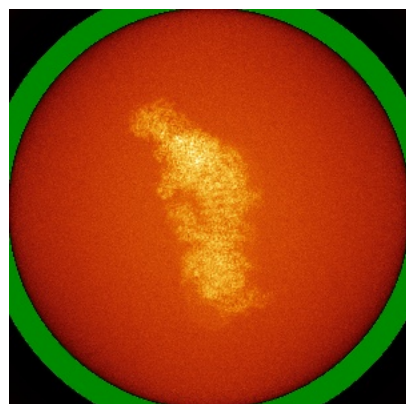


Y

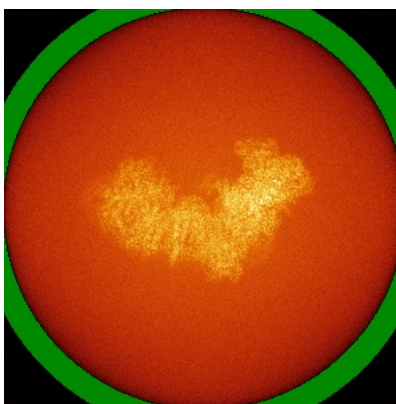


Z

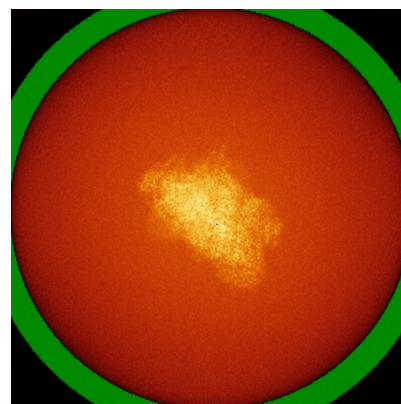
6.4.2 Raw map



X



Y

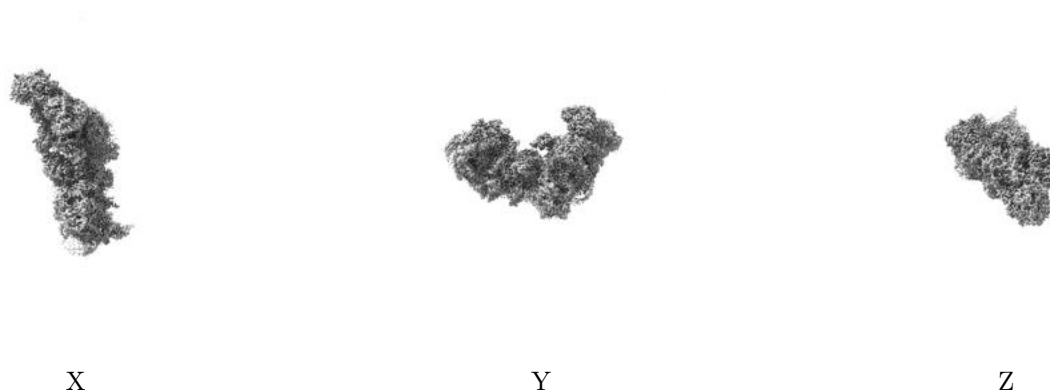


Z

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.

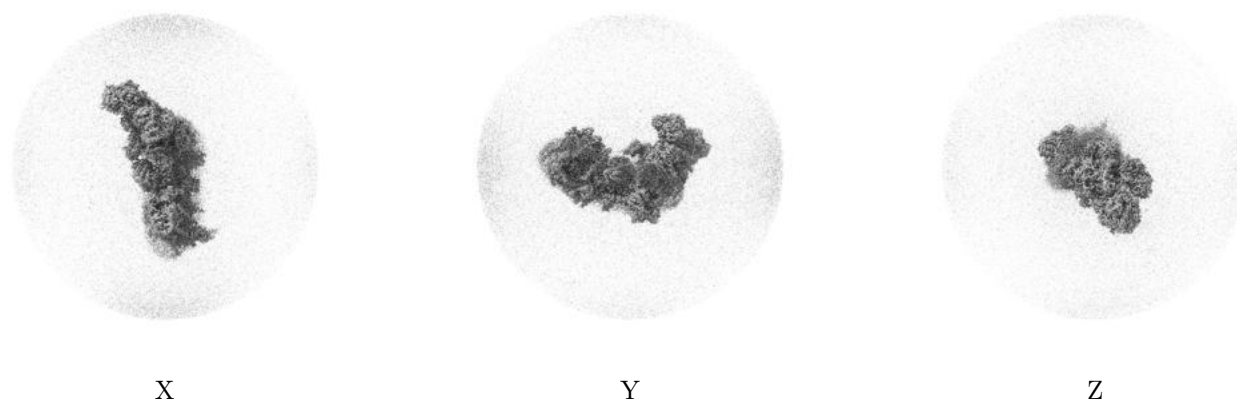
6.5 Orthogonal surface views [i](#)

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.

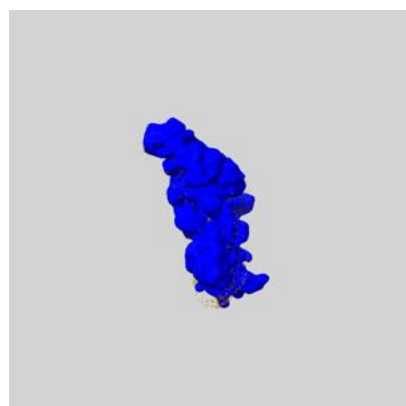
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

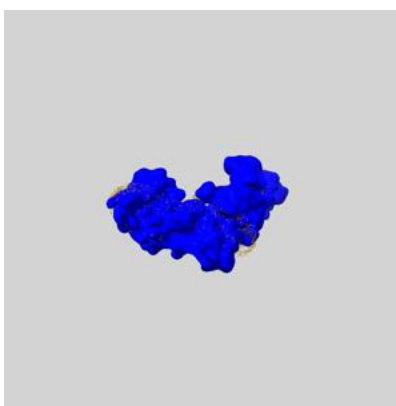
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

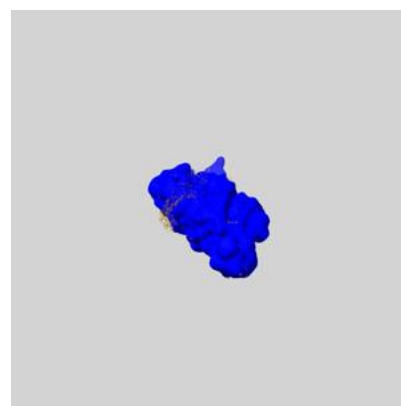
6.6.1 emd_14132_msk_1.map [i](#)



X



Y

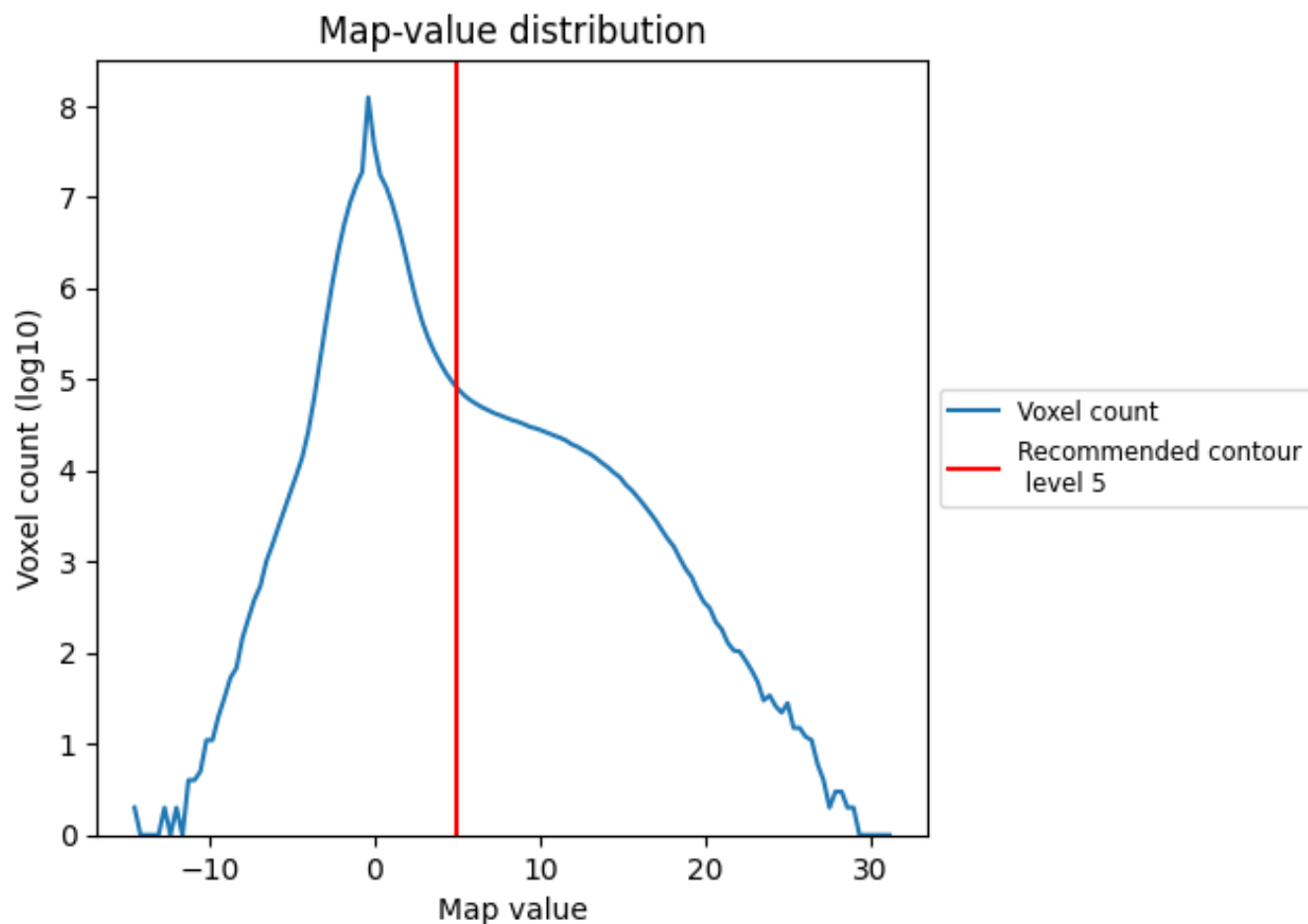


Z

7 Map analysis [i](#)

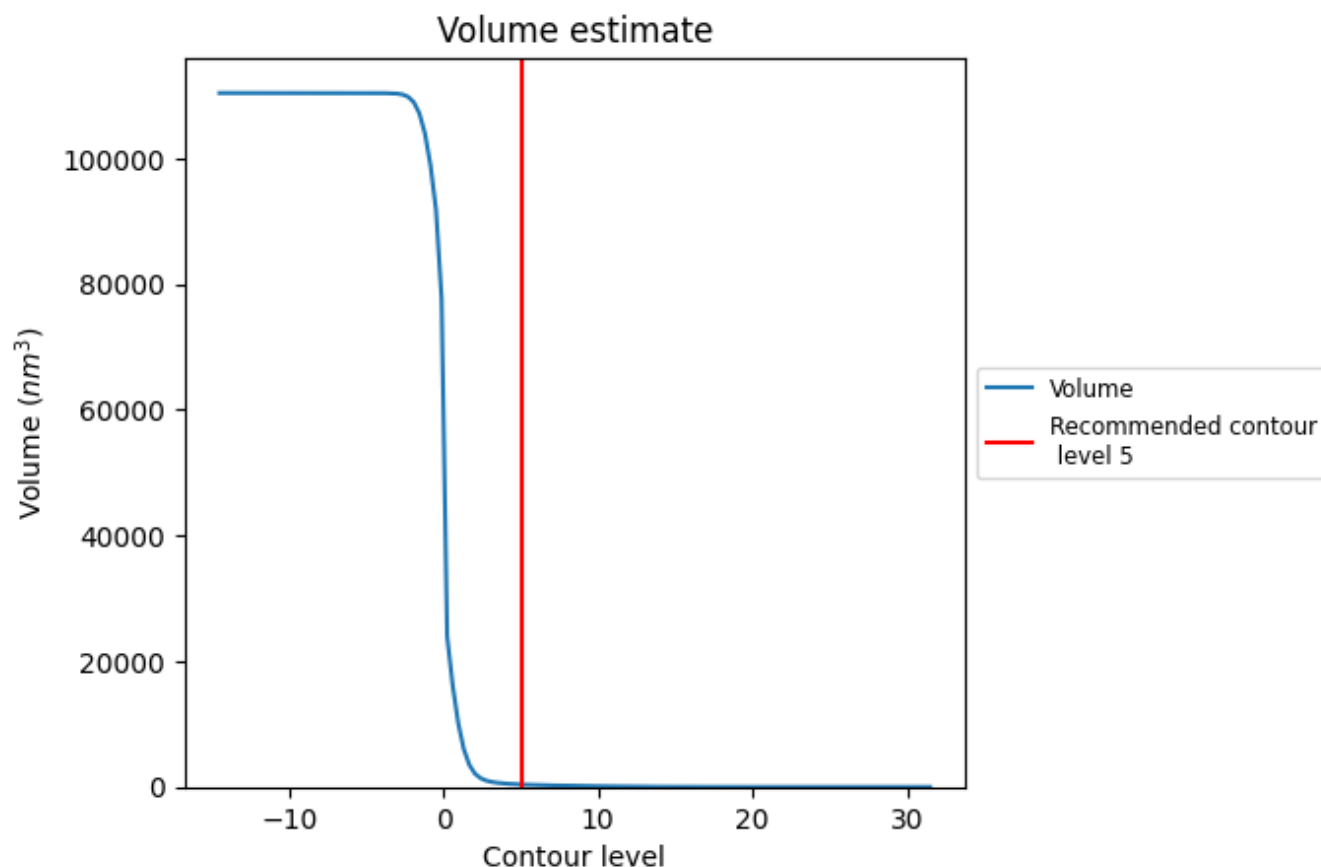
This section contains the results of statistical analysis of the map.

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.

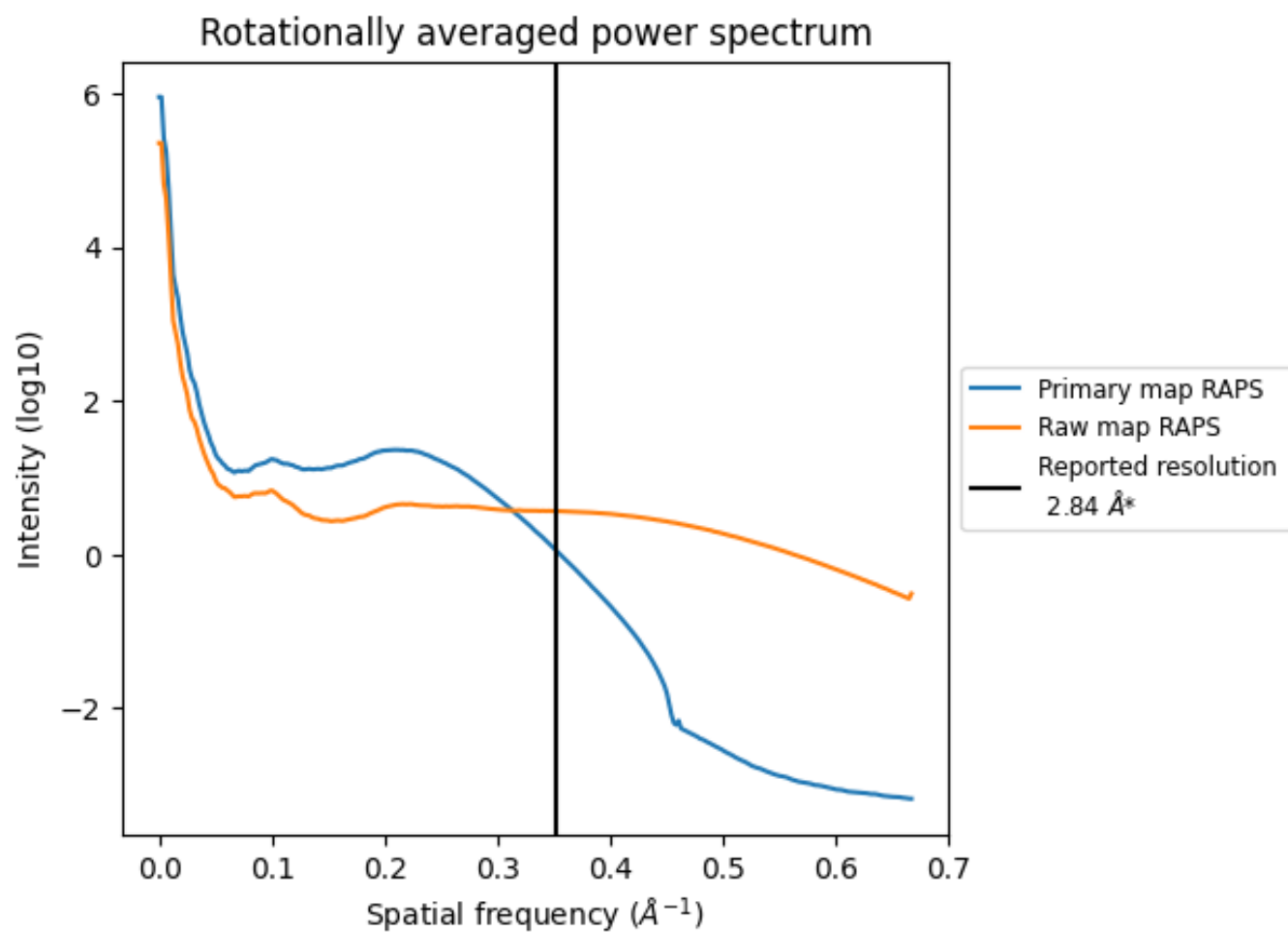
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 393 nm^3 ; this corresponds to an approximate mass of 355 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 ⓘ

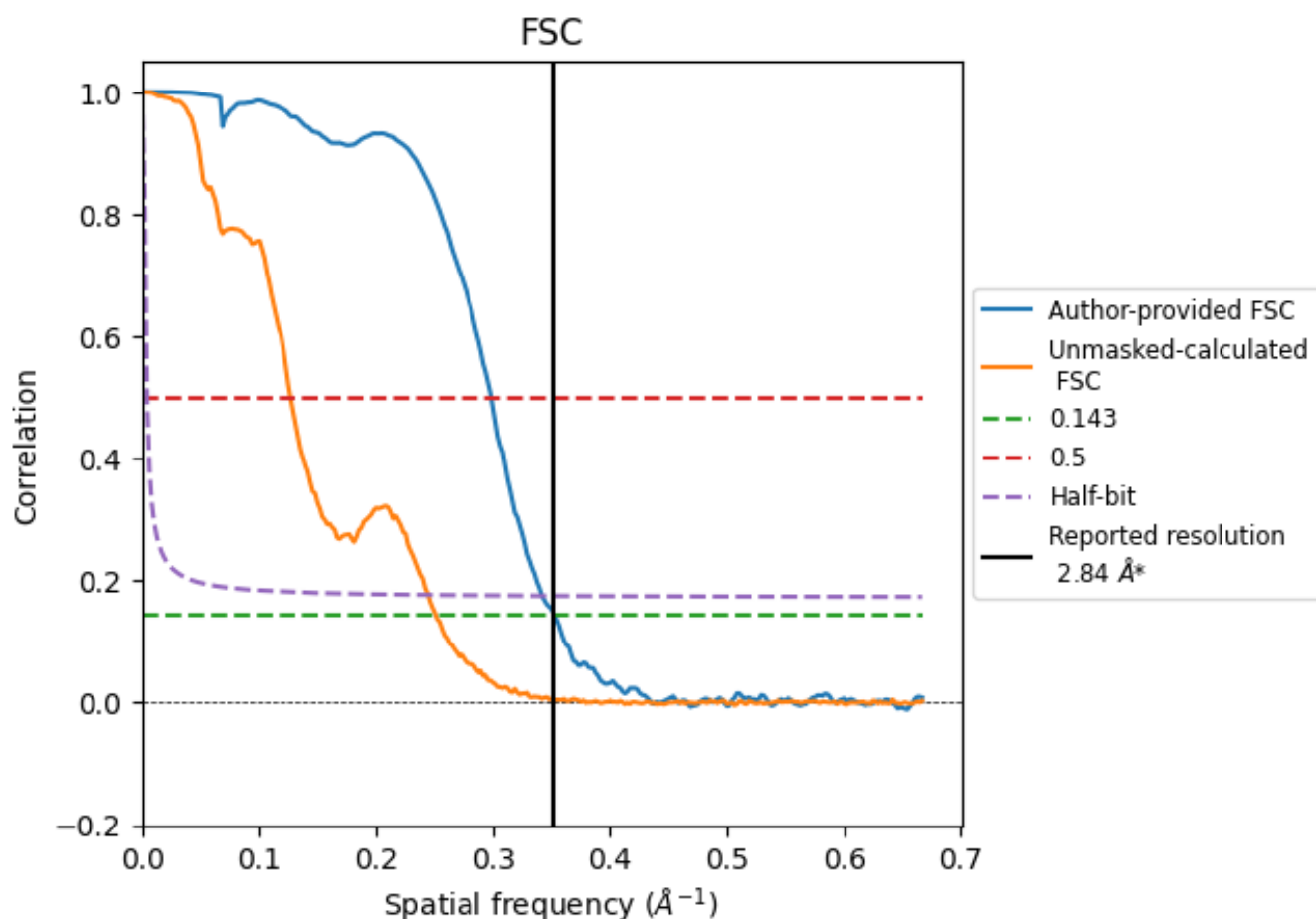


*Reported resolution corresponds to spatial frequency of 0.352 $\text{\AA}^{-1}$

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 $0.352 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

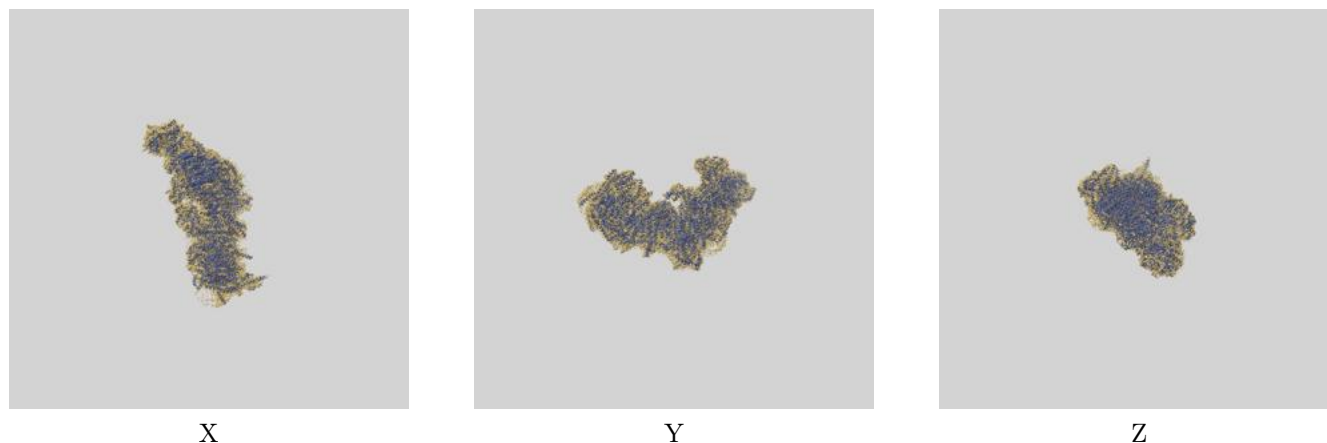
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.35	2.92
Unmasked-calculated*	3.98	7.88	4.10

*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 3.98 differs from the reported value 2.84 by more than 10 %

9 Map-model fit [i](#)

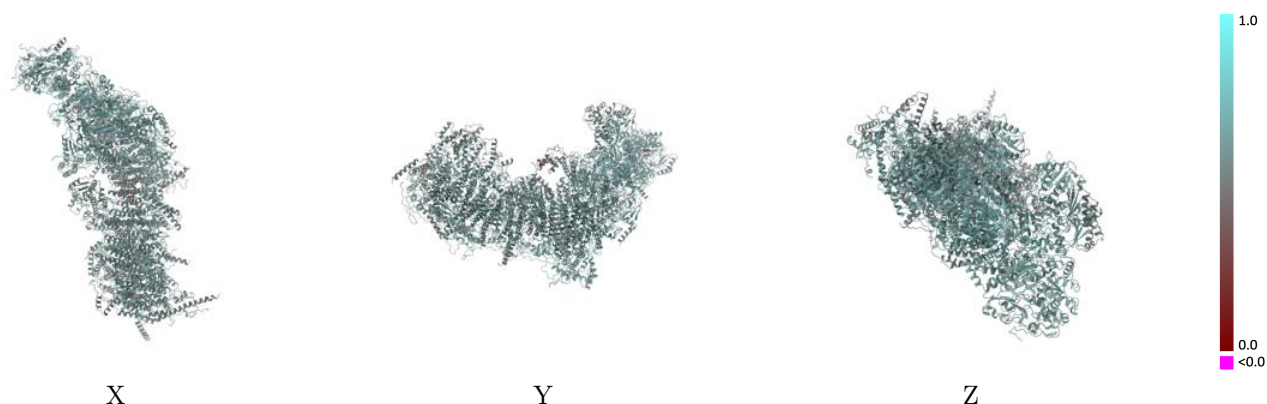
This section contains information regarding the fit between EMDB map EMD-14132 and PDB model 7QSK. Per-residue inclusion information can be found in section 3 on page 24.

9.1 Map-model overlay [i](#)



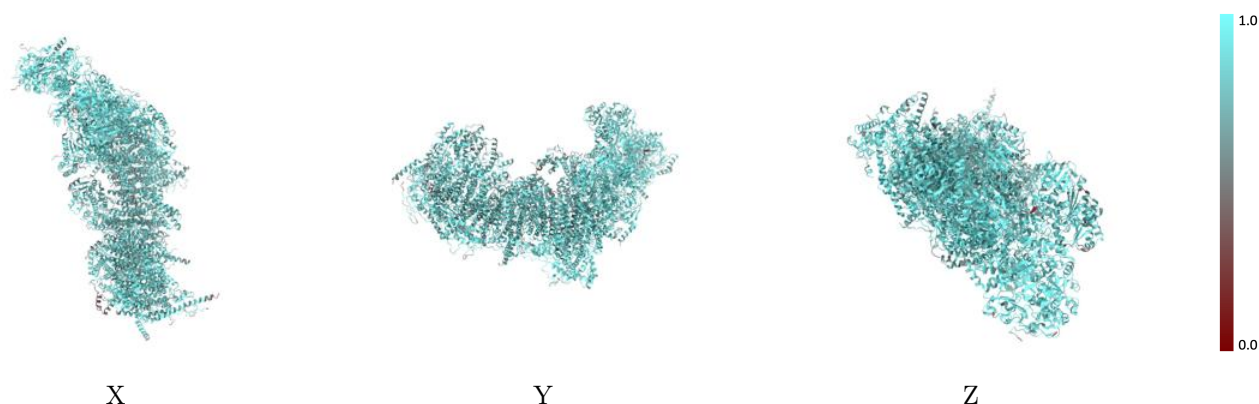
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



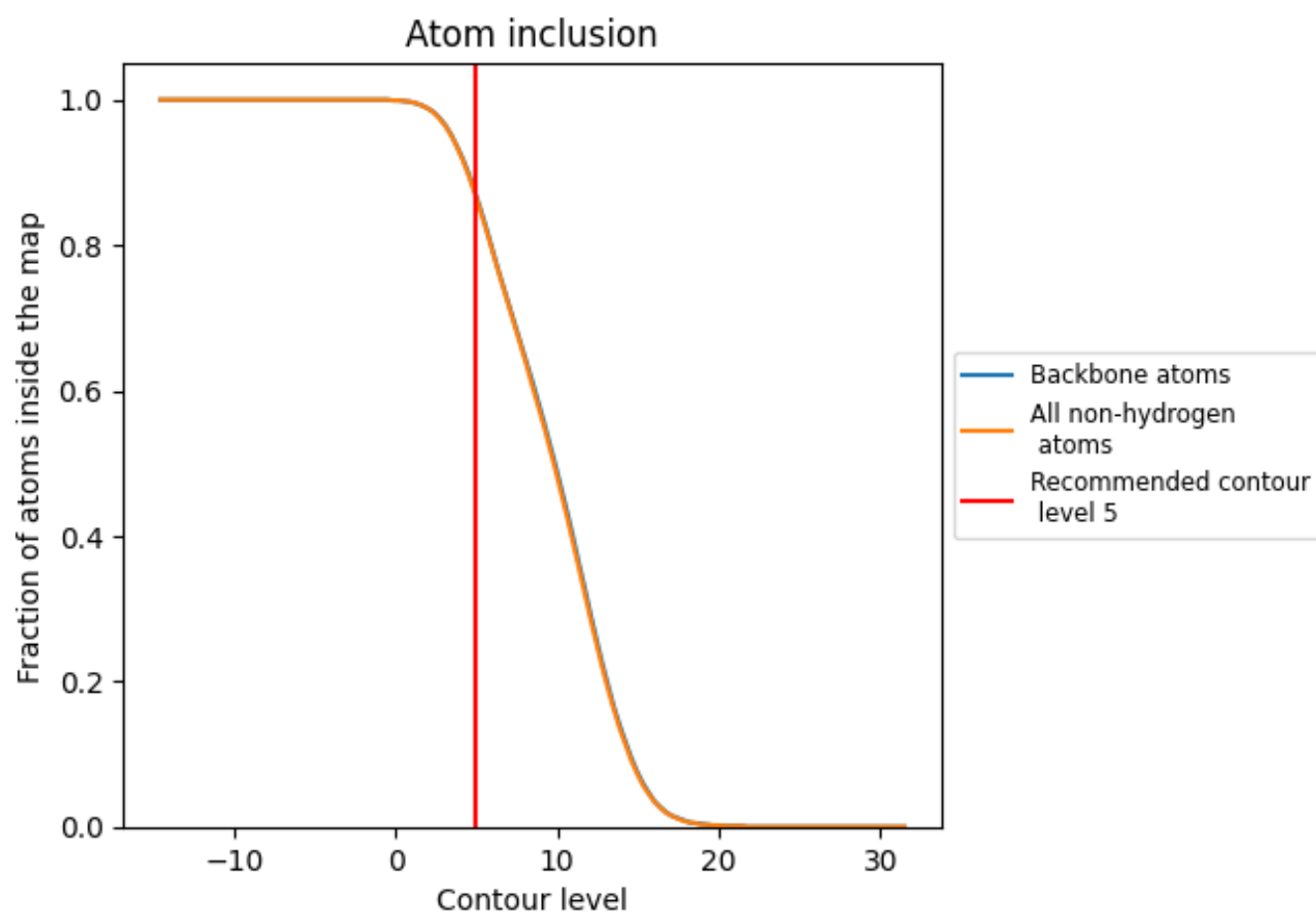
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 87% of all backbone atoms, 87% 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	 0.8660	 0.5980
A	 0.8670	 0.6110
B	 0.9500	 0.6440
C	 0.9250	 0.6380
D	 0.9250	 0.6350
E	 0.8710	 0.5840
F	 0.8980	 0.6010
G	 0.8870	 0.6060
H	 0.9230	 0.6320
I	 0.9440	 0.6500
J	 0.8680	 0.6000
K	 0.8930	 0.6180
L	 0.8660	 0.5970
M	 0.9150	 0.6240
N	 0.9380	 0.6310
O	 0.8430	 0.5820
P	 0.8740	 0.6050
Q	 0.8850	 0.6200
R	 0.8740	 0.6160
S	 0.7970	 0.5480
T	 0.6220	 0.4120
U	 0.7490	 0.5180
V	 0.8190	 0.5940
W	 0.8460	 0.5990
X	 0.8530	 0.5890
Y	 0.7890	 0.5670
Z	 0.8800	 0.6000
a	 0.9220	 0.6080
b	 0.8270	 0.5760
c	 0.7950	 0.5620
d	 0.8470	 0.5960
e	 0.8520	 0.5890
f	 0.7100	 0.5210
g	 0.8230	 0.5720
h	 0.8820	 0.6080



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.7080	 0.5220
j	 0.7970	 0.5410
k	 0.7770	 0.5260
l	 0.8440	 0.5760
m	 0.8010	 0.5730
n	 0.8210	 0.5760
o	 0.7840	 0.5240
p	 0.8440	 0.5760
q	 0.8720	 0.6130
r	 0.8780	 0.5970
s	 0.8490	 0.5760