



# wwPDB EM Validation Summary Report ⓘ

Jun 22, 2023 – 10:35 AM JST

PDB ID : 7W00  
EMDB ID : EMD-32232  
Title : Deactive state CI from Q10 dataset, Subclass 1  
Authors : Gu, J.K.; Yang, M.J.  
Deposited on : 2021-11-17  
Resolution : 3.50 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](mailto: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>.

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

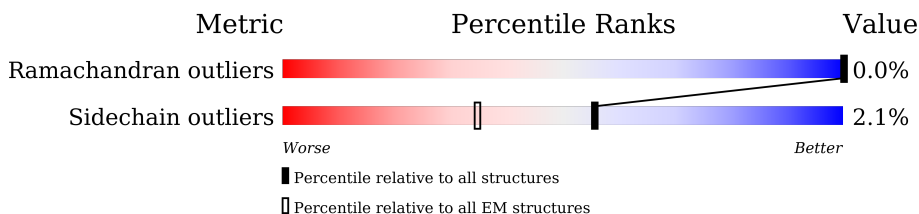
EMDB validation analysis : 0.0.1.dev50  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.33

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	431	99% .
2	B	176	99% .
3	C	156	96% .
4	E	115	6% 97% .
5	F	86	6% 98% .
6	G	88	19% 99% .
6	X	88	6% 98% .
7	H	112	97% .
8	I	112	5% 84% . 13%

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Mol	Chain	Length	Quality of chain
9	J	341	85% 13%
10	K	42	88% 12%
11	L	125	99% 6%
12	M	690	99%
13	N	144	100% 7%
14	O	217	97%
15	P	208	97%
16	Q	430	96%
17	S	70	100%
18	T	96	98% 6%
19	U	83	99%
20	V	140	96%
21	W	142	96%
22	Y	70	99% 11%
23	Z	84	98% 17%
24	a	140	96%
25	b	126	79% 18% 8%
26	c	156	99%
27	d	175	99%
28	e	107	98% 7%
29	f	42	100% 5%
30	g	121	98%
31	h	105	100%
32	i	347	99%
33	j	113	84% 12% 6%

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Mol	Chain	Length	Quality of chain
34	k	98	 98%
35	l	603	 98%
36	m	175	 5% 71% 26%
37	n	56	 14% 98%
38	o	128	 96%
39	p	178	 98%
40	r	459	 99%
41	s	318	 94% 5%
42	u	171	 97%
43	v	124	 9% 95% 5%
44	w	320	 99%

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 66775 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 dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	431	3315	2094	591	610	20	0	0

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	176	1412	887	243	269	13	0	0

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	156	1248	794	227	213	14	0	0

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	115	967	617	179	166	5	0	0

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	86	687	432	128	125	2	0	0

- Molecule 6 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	88	Total	C	N	O	S	0	0
			678	438	102	133	5		
6	X	88	Total	C	N	O	S	0	0
			699	450	103	141	5		

- Molecule 7 is a protein called Complex I subunit B13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	112	Total	C	N	O	S	0	0
			910	588	154	165	3		

- Molecule 8 is a protein called Complex I-B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	97	Total	C	N	O	S	0	0
			780	491	147	139	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	297	Total	C	N	O	S	0	0
			2348	1508	420	412	8		

- Molecule 10 is a protein called Complex I-9kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	42	Total	C	N	O	S	0	0
			355	219	67	68	1		

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	125	Total	C	N	O	S	0	0
			1016	642	181	190	3		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	690	Total	C	N	O	S	0	0
			5293	3319	923	1012	39		

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	144	1204	770	218	212	4	0	0

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	217	1661	1060	279	312	10	0	0

- Molecule 15 is a protein called Complex I-30kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	208	1738	1124	298	314	2	0	0

- Molecule 16 is a protein called Complex I-49kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	419	3377	2162	578	613	24	0	0

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	S	70	567	364	104	94	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	T	96	741	452	140	146	3	0	0

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	83	Total	C	N	O	S	0	0
			643	417	110	115	1		

- Molecule 20 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	140	Total	C	N	O	S	0	0
			1021	651	174	190	6		

- Molecule 21 is a protein called Complex I-B16.6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	142	Total	C	N	O	S	0	0
			1167	752	200	206	9		

- Molecule 22 is a protein called Complex I-AGGG.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	70	Total	C	N	O	S	0	0
			597	392	98	106	1		

- Molecule 23 is a protein called Complex I-B12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Z	84	Total	C	N	O	S	0	0
			674	437	116	120	1		

- Molecule 24 is a protein called Complex I-SGDH.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	140	Total	C	N	O	S	0	0
			1165	762	199	201	3		

- Molecule 25 is a protein called Complex I-B17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	103	Total	C	N	O	S	0	0
			875	571	158	145	1		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	c	156	1299	843	211	237	8	0	0

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	d	175	1461	916	265	272	8	0	0

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	e	107	890	568	145	173	4	0	0

- Molecule 29 is a protein called Complex I-KFYI.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	f	42	344	227	58	59	0	0

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	g	121	1000	650	173	171	6	0	0

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	h	105	867	550	161	150	6	0	0

- Molecule 32 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	i	347	2710	1782	420	462	46	0	0

- Molecule 33 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	99	Total	C	N	O	S	0	0
			797	544	117	131	5		

- Molecule 34 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	k	98	Total	C	N	O	S	0	0
			748	493	113	128	14		

- Molecule 35 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	603	Total	C	N	O	S	0	0
			4783	3172	741	819	51		

- Molecule 36 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	129	Total	C	N	O	S	0	0
			951	637	138	168	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	56	Total	C	N	O	S	0	0
			479	311	88	79	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
38	o	128	Total	C	N	O	0	0
			1062	691	182	189		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	178	Total	C	N	O	S	0	0
			1534	982	279	265	8		

- Molecule 40 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	r	459	3630	2412	572	608	38	0	0

- Molecule 41 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	s	303	2390	1605	369	395	21	0	0

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	u	171	1398	887	250	251	10	0	0

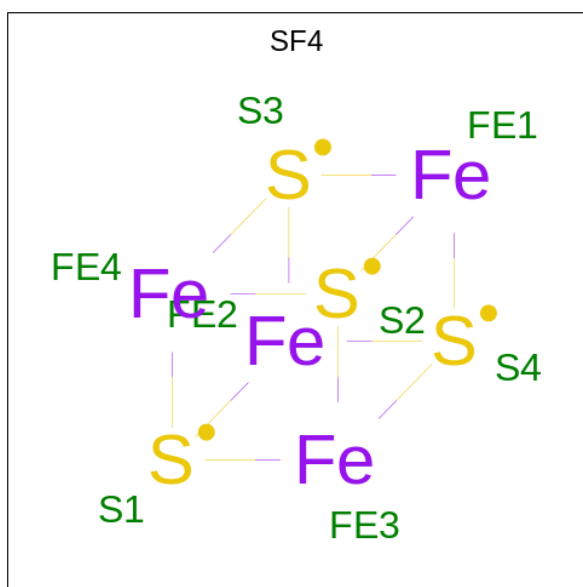
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	v	124	1028	642	195	182	9	0	0

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	w	320	2581	1645	437	489	10	0	0

- Molecule 45 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
45	A	1	8	4	4	0
45	B	1	8	4	4	0
45	B	1	8	4	4	0
45	C	1	8	4	4	0
45	M	1	8	4	4	0
45	M	1	8	4	4	0

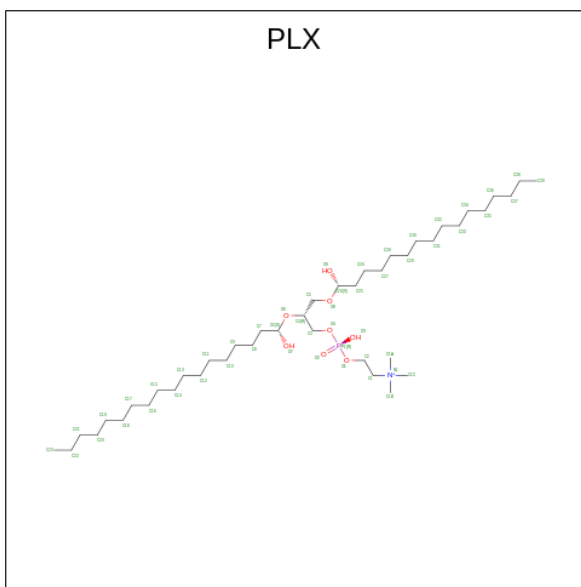
- Molecule 46 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P) (labeled as "Ligand of Interest" by depositor).



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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
47	W	1	Total 41	C 31	N 1	O 8	P 1	0
47	b	1	Total 46	C 36	N 1	O 8	P 1	0
47	i	1	Total 47	C 37	N 1	O 8	P 1	0
47	j	1	Total 51	C 41	N 1	O 8	P 1	0
47	l	1	Total 40	C 30	N 1	O 8	P 1	0
47	l	1	Total 46	C 36	N 1	O 8	P 1	0
47	r	1	Total 51	C 41	N 1	O 8	P 1	0

- Molecule 48 is (9R,11S)-9-({[(1S)-1-HYDROXYHEXADECYL]OXY}METHYL)-2,2-DIMETHYL-5,7,10-TRIOXA-2LAMBDA 5 -AZA-6LAMBDA 5 -PHOSPHAOCTACOSANE-6,6,11-TRIOXOL (three-letter code: PLX) (formula: C<sub>42</sub>H<sub>89</sub>NO<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



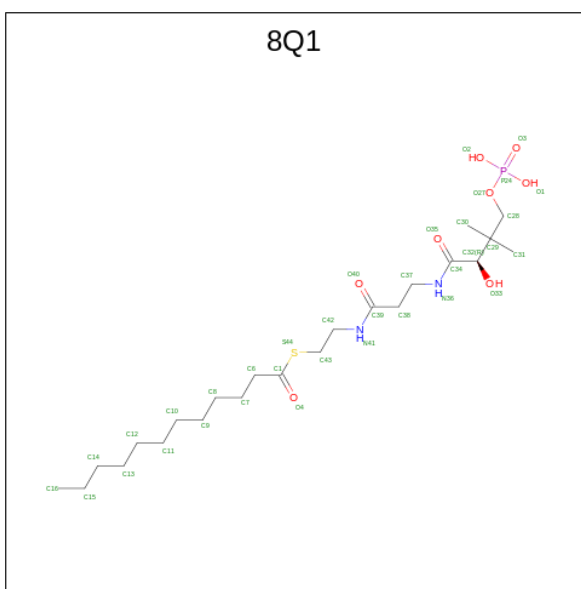
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
48	C	1	Total 52	C 42	N 1	O 8	P 1	0
48	a	1	Total 52	C 42	N 1	O 8	P 1	0
48	g	1	Total 52	C 42	N 1	O 8	P 1	0

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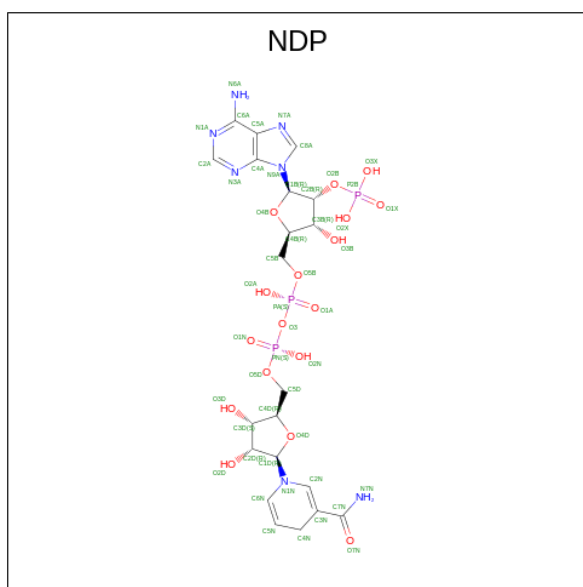
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
48	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	r	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	r	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 49 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: C<sub>23</sub>H<sub>45</sub>N<sub>2</sub>O<sub>8</sub>PS) (labeled as "Ligand of Interest" by depositor).



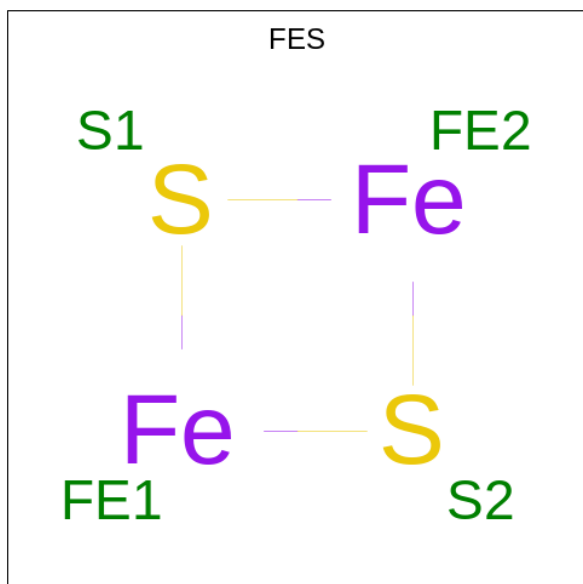
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
49	G	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
49	X	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 50 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 51 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
51	M	1	4	2	2	0
51	O	1	4	2	2	0



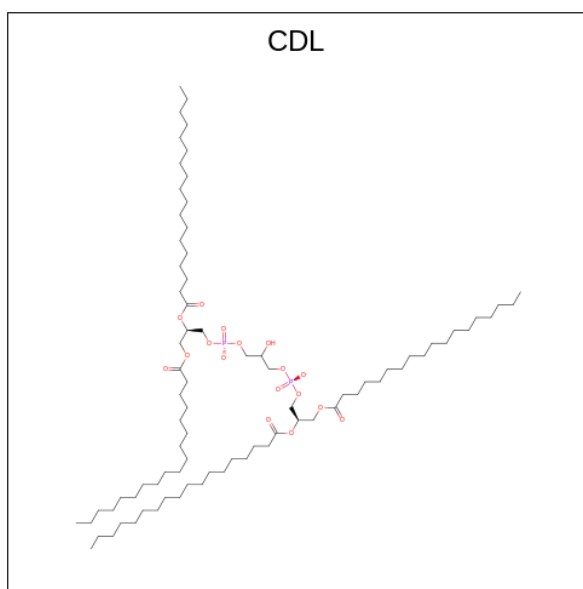
- Molecule 52 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
52	M	1	Total Mg 1 1	0

- Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
53	T	1	Total Zn 1 1	0

- Molecule 54 is CARDIOLIPIN (three-letter code: CDL) (formula: C<sub>81</sub>H<sub>156</sub>O<sub>17</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



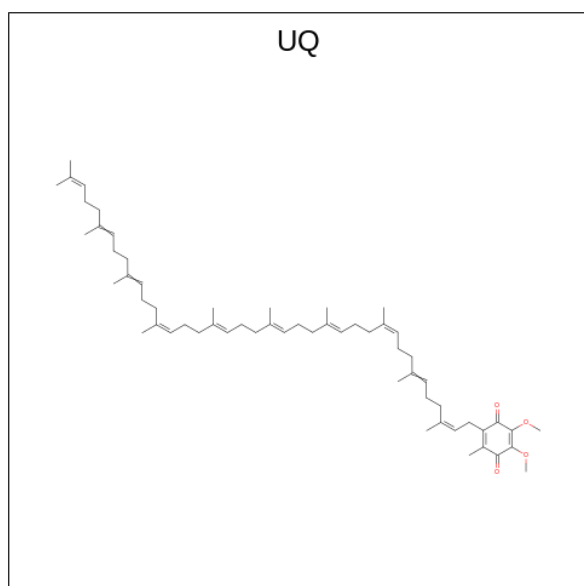
Mol	Chain	Residues	Atoms	AltConf
54	V	1	Total C O P 94 75 17 2	0
54	a	1	Total C O P 91 72 17 2	0
54	i	1	Total C O P 66 47 17 2	0
54	l	1	Total C O P 99 80 17 2	0
54	l	1	Total C O P 100 81 17 2	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
54	o	1	68	49	17	2	0
54	r	1	95	76	17	2	0
54	u	1	78	59	17	2	0

- Molecule 55 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (three-letter code: UQ) (formula: C<sub>59</sub>H<sub>90</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
55	s	1	28	24	4	0

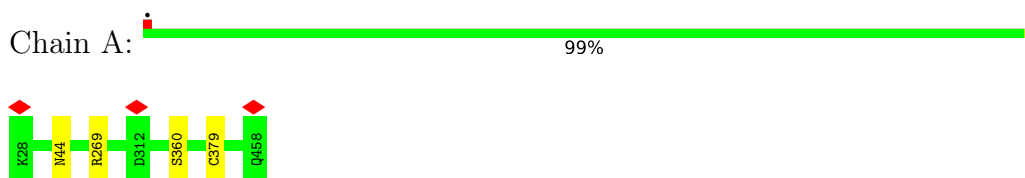
- Molecule 56 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



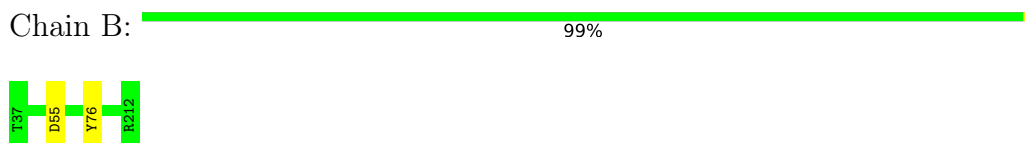
### 3 Residue-property plots [i](#)

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.

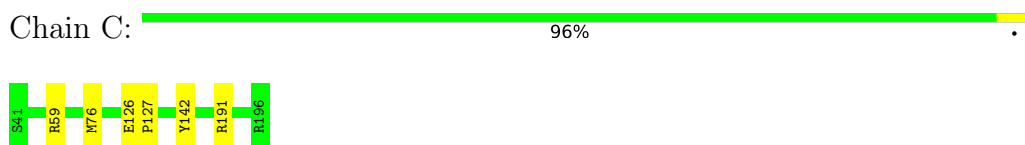
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



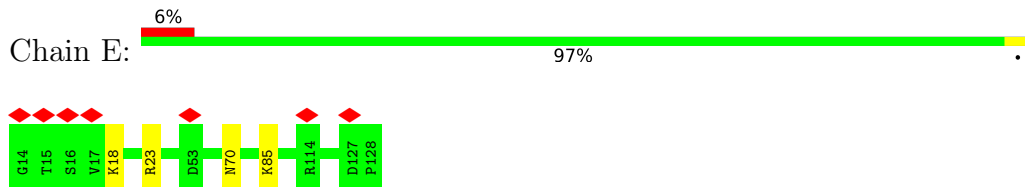
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial



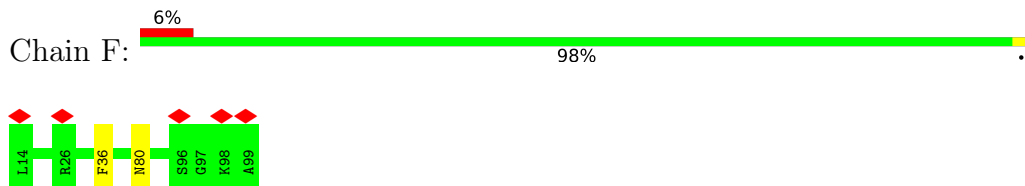
- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial



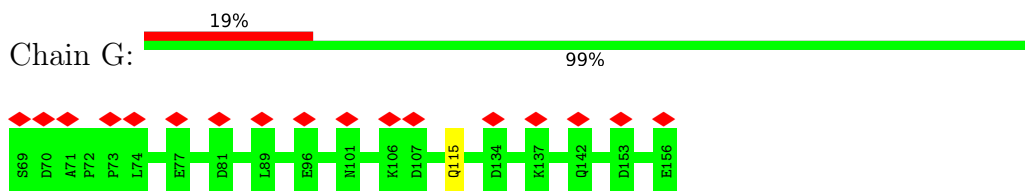
- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



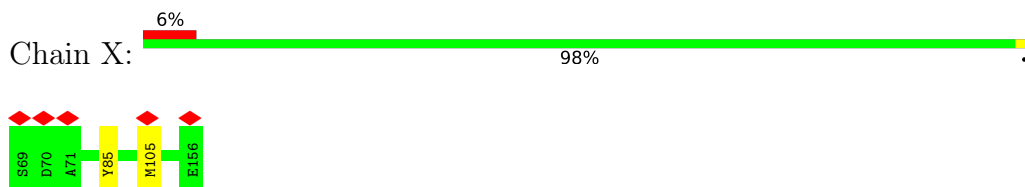
- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



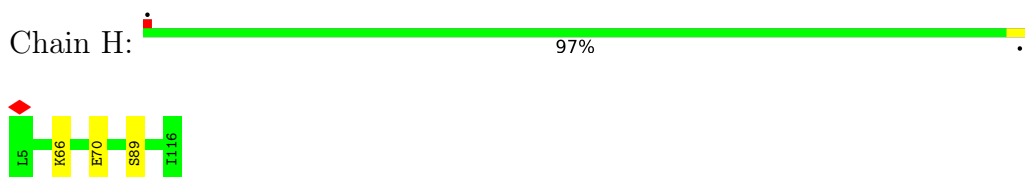
- Molecule 6: Acyl carrier protein



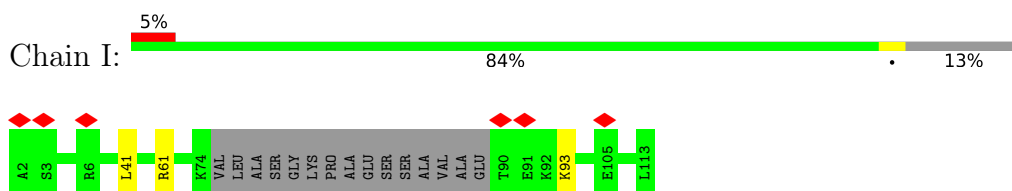
- Molecule 6: Acyl carrier protein



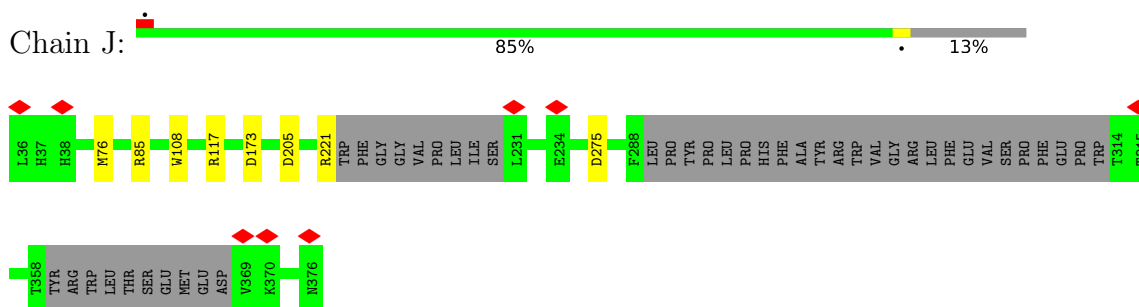
- Molecule 7: Complex I subunit B13



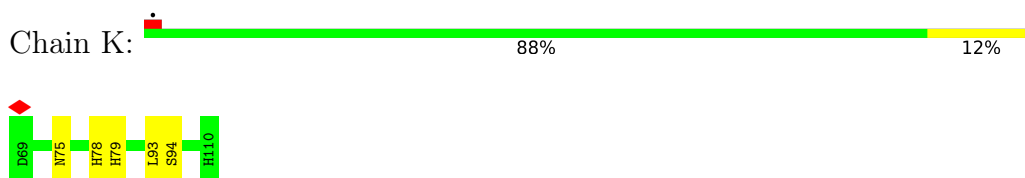
- Molecule 8: Complex I-B14.5a



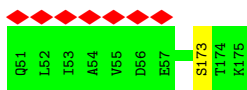
- Molecule 9: NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 9, mitochondrial



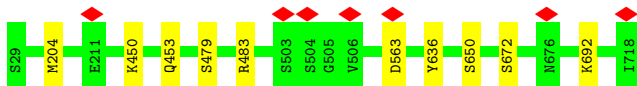
- Molecule 10: Complex I-9kD



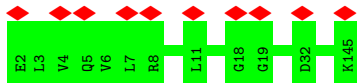
- Molecule 11: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



- Molecule 12: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial



- Molecule 13: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



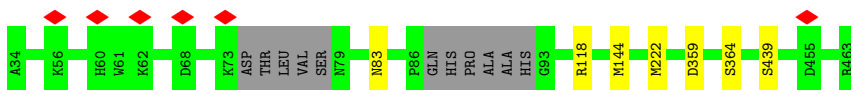
- Molecule 14: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial



- Molecule 15: Complex I-30kD



- Molecule 16: Complex I-49kD

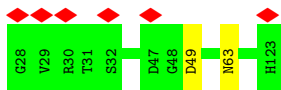


- Molecule 17: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

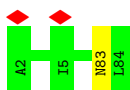




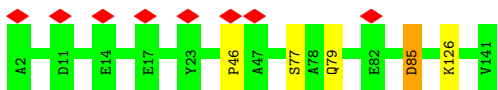
- Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3



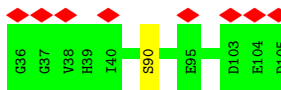
- Molecule 20: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



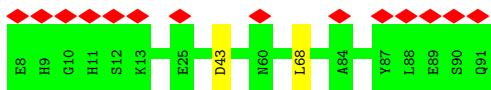
- Molecule 21: Complex I-B16.6



- Molecule 22: Complex I-AGGG



- Molecule 23: Complex I-B12




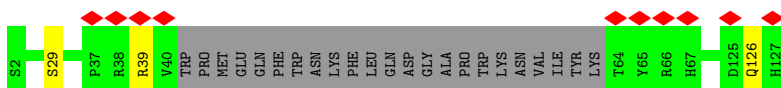
- Molecule 24: Complex I-SGDH

Chain a:  96%



- Molecule 25: Complex I-B17

Chain b:  8% 79% 18%



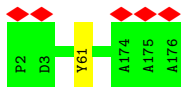
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

Chain c:  99%



- Molecule 27: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

Chain d:  99%



- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial

Chain e:  7% 98%



- Molecule 29: Complex I-KFYI

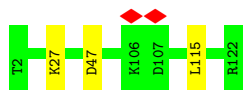
Chain f:  5% 100%



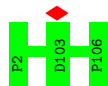
- Molecule 30: NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain g:  98%





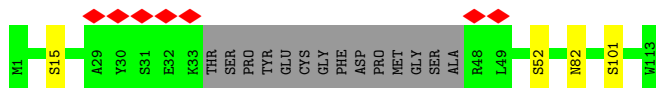
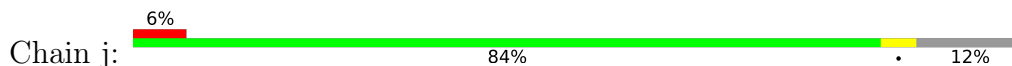
- Molecule 31: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5



- Molecule 32: NADH-ubiquinone oxidoreductase chain 2



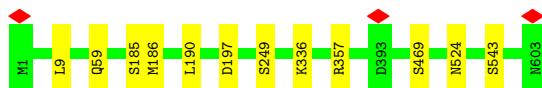
- Molecule 33: NADH-ubiquinone oxidoreductase chain 3



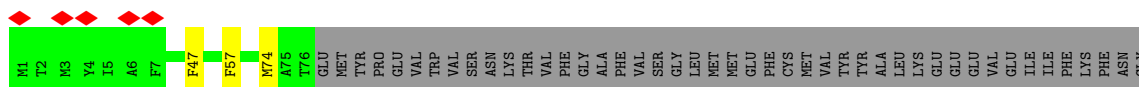
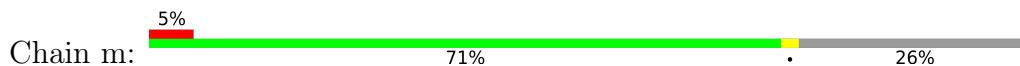
- Molecule 34: NADH-ubiquinone oxidoreductase chain 4L

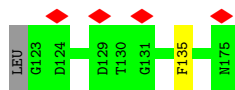


- Molecule 35: NADH-ubiquinone oxidoreductase chain 5

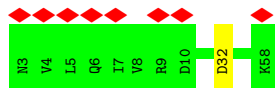


- Molecule 36: NADH-ubiquinone oxidoreductase chain 6





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



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



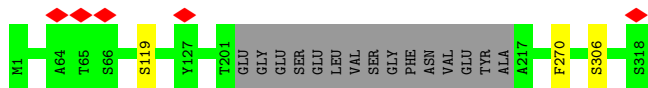
- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



- Molecule 40: NADH-ubiquinone oxidoreductase chain 4



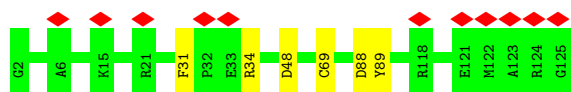
- Molecule 41: NADH-ubiquinone oxidoreductase chain 1



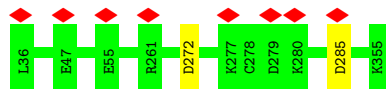
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



- Molecule 43: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



- Molecule 44: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	88543	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.256	Depositor
Minimum map value	-0.090	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0204	Depositor
Map size (Å)	354.48602, 354.48602, 354.48602	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 8Q1, PEE, FMN, 2MR, CDL, FES, NDP, UQ, MG, ADP, SF4, ZN, PLX

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	0.25	0/3390	0.49	0/4580
2	B	0.26	0/1443	0.51	0/1952
3	C	0.26	0/1279	0.61	1/1730 (0.1%)
4	E	0.26	0/991	0.55	0/1335
5	F	0.26	0/698	0.59	0/940
6	G	0.26	0/689	0.52	0/935
6	X	0.25	0/711	0.42	0/963
7	H	0.24	0/929	0.44	0/1258
8	I	0.25	0/798	0.53	0/1079
9	J	0.25	0/2400	0.49	0/3241
10	K	0.24	0/365	0.57	1/493 (0.2%)
11	L	0.25	0/1039	0.51	0/1403
12	M	0.25	0/5381	0.50	0/7291
13	N	0.25	0/1245	0.49	0/1694
14	O	0.25	0/1701	0.46	0/2316
15	P	0.26	0/1789	0.50	0/2436
16	Q	0.26	0/3451	0.48	0/4672
17	S	0.25	0/582	0.48	0/783
18	T	0.25	0/755	0.51	0/1018
19	U	0.25	0/664	0.43	0/912
20	V	0.26	0/1042	0.48	1/1411 (0.1%)
21	W	0.25	0/1198	0.49	0/1617
22	Y	0.25	0/623	0.45	0/853
23	Z	0.26	0/695	0.54	1/939 (0.1%)
24	a	0.27	0/1199	0.48	0/1623
25	b	0.26	0/902	0.53	0/1227
26	c	0.27	0/1355	0.48	0/1857
27	d	0.26	0/1494	0.51	0/2015
28	e	0.25	0/916	0.49	0/1246
29	f	0.24	0/353	0.41	0/477
30	g	0.26	0/1031	0.49	1/1394 (0.1%)
31	h	0.25	0/889	0.48	0/1190

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	i	0.25	0/2773	0.45	0/3768
33	j	0.26	0/816	0.48	0/1113
34	k	0.26	0/759	0.44	0/1029
35	l	0.26	0/4912	0.45	0/6680
36	m	0.27	0/973	0.48	0/1320
37	n	0.24	0/491	0.50	0/663
38	o	0.27	0/1092	0.53	1/1481 (0.1%)
39	p	0.27	0/1590	0.53	0/2155
40	r	0.25	0/3722	0.44	0/5077
41	s	0.26	0/2460	0.46	0/3364
42	u	0.25	0/1436	0.49	1/1938 (0.1%)
43	v	0.28	0/1052	0.58	0/1411
44	w	0.26	0/2641	0.47	0/3577
All	All	0.26	0/66714	0.49	7/90456 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	126	GLU	C-N-CD	-12.02	94.16	120.60
10	K	93	LEU	CA-CB-CG	5.95	128.99	115.30
23	Z	43	ASP	CB-CG-OD1	5.53	123.28	118.30
20	V	85	ASP	CB-CG-OD1	5.46	123.22	118.30
38	o	84	PRO	CA-N-CD	-5.39	103.95	111.50

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [\(i\)](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	429/431 (100%)	417 (97%)	12 (3%)	0	100	100
2	B	174/176 (99%)	173 (99%)	1 (1%)	0	100	100
3	C	154/156 (99%)	148 (96%)	5 (3%)	1 (1%)	25	64
4	E	113/115 (98%)	110 (97%)	3 (3%)	0	100	100
5	F	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
6	G	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
6	X	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
7	H	110/112 (98%)	103 (94%)	7 (6%)	0	100	100
8	I	93/112 (83%)	82 (88%)	11 (12%)	0	100	100
9	J	289/341 (85%)	280 (97%)	9 (3%)	0	100	100
10	K	40/42 (95%)	40 (100%)	0	0	100	100
11	L	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
12	M	688/690 (100%)	669 (97%)	19 (3%)	0	100	100
13	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
14	O	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
15	P	206/208 (99%)	194 (94%)	12 (6%)	0	100	100
16	Q	412/430 (96%)	399 (97%)	13 (3%)	0	100	100
17	S	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
18	T	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
19	U	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
20	V	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	22	61
21	W	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
22	Y	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
23	Z	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
24	a	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
25	b	99/126 (79%)	97 (98%)	2 (2%)	0	100	100
26	c	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
27	d	173/175 (99%)	169 (98%)	4 (2%)	0	100	100
28	e	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
29	f	40/42 (95%)	40 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	g	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
31	h	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
32	i	345/347 (99%)	331 (96%)	14 (4%)	0	100	100
33	j	95/113 (84%)	90 (95%)	5 (5%)	0	100	100
34	k	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
35	l	601/603 (100%)	573 (95%)	28 (5%)	0	100	100
36	m	125/175 (71%)	113 (90%)	12 (10%)	0	100	100
37	n	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
38	o	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
39	p	176/178 (99%)	168 (96%)	7 (4%)	1 (1%)	25	64
40	r	457/459 (100%)	443 (97%)	14 (3%)	0	100	100
41	s	299/318 (94%)	289 (97%)	10 (3%)	0	100	100
42	u	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
43	v	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
44	w	318/320 (99%)	303 (95%)	15 (5%)	0	100	100
All	All	8029/8308 (97%)	7721 (96%)	305 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	127	PRO
39	p	175	ARG
20	V	46	PRO

### 5.3.2 Protein sidechains [i](#)

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	344/345 (100%)	340 (99%)	4 (1%)	71	87
2	B	151/151 (100%)	149 (99%)	2 (1%)	69	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	132/132 (100%)	128 (97%)	4 (3%)	41	71
4	E	106/107 (99%)	102 (96%)	4 (4%)	33	65
5	F	75/76 (99%)	73 (97%)	2 (3%)	44	73
6	G	72/81 (89%)	71 (99%)	1 (1%)	67	85
6	X	78/81 (96%)	76 (97%)	2 (3%)	46	74
7	H	99/99 (100%)	96 (97%)	3 (3%)	41	71
8	I	87/97 (90%)	84 (97%)	3 (3%)	37	68
9	J	252/295 (85%)	244 (97%)	8 (3%)	39	69
10	K	41/41 (100%)	37 (90%)	4 (10%)	8	33
11	L	113/113 (100%)	112 (99%)	1 (1%)	78	90
12	M	579/580 (100%)	569 (98%)	10 (2%)	60	82
13	N	130/130 (100%)	130 (100%)	0	100	100
14	O	180/183 (98%)	174 (97%)	6 (3%)	38	68
15	P	190/190 (100%)	183 (96%)	7 (4%)	34	65
16	Q	361/370 (98%)	355 (98%)	6 (2%)	60	82
17	S	58/58 (100%)	58 (100%)	0	100	100
18	T	79/79 (100%)	77 (98%)	2 (2%)	47	75
19	U	69/69 (100%)	68 (99%)	1 (1%)	67	85
20	V	101/101 (100%)	97 (96%)	4 (4%)	31	64
21	W	122/123 (99%)	117 (96%)	5 (4%)	30	63
22	Y	62/63 (98%)	61 (98%)	1 (2%)	62	83
23	Z	65/65 (100%)	64 (98%)	1 (2%)	65	84
24	a	122/122 (100%)	117 (96%)	5 (4%)	30	63
25	b	97/119 (82%)	94 (97%)	3 (3%)	40	70
26	c	137/141 (97%)	136 (99%)	1 (1%)	84	93
27	d	155/155 (100%)	154 (99%)	1 (1%)	86	94
28	e	99/99 (100%)	97 (98%)	2 (2%)	55	79
29	f	36/38 (95%)	36 (100%)	0	100	100
30	g	108/108 (100%)	106 (98%)	2 (2%)	57	80
31	h	93/93 (100%)	93 (100%)	0	100	100
32	i	311/311 (100%)	307 (99%)	4 (1%)	69	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	j	87/99 (88%)	83 (95%)	4 (5%)	27	61
34	k	85/85 (100%)	83 (98%)	2 (2%)	49	76
35	l	536/537 (100%)	524 (98%)	12 (2%)	52	78
36	m	99/141 (70%)	95 (96%)	4 (4%)	31	64
37	n	53/53 (100%)	52 (98%)	1 (2%)	57	80
38	o	113/113 (100%)	109 (96%)	4 (4%)	36	67
39	p	159/159 (100%)	156 (98%)	3 (2%)	57	80
40	r	409/410 (100%)	405 (99%)	4 (1%)	76	88
41	s	262/275 (95%)	259 (99%)	3 (1%)	73	88
42	u	153/153 (100%)	148 (97%)	5 (3%)	38	68
43	v	104/111 (94%)	98 (94%)	6 (6%)	20	53
44	w	281/283 (99%)	279 (99%)	2 (1%)	84	93
All	All	7045/7234 (97%)	6896 (98%)	149 (2%)	56	79

5 of 149 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	l	524	ASN
43	v	48	ASP
36	m	74	MET
40	r	248	THR
14	O	223	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
14	O	69	ASN
18	T	63	ASN
40	r	169	ASN
35	l	541	ASN
12	M	260	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
16	2MR	Q	118	16	10,12,13	1.93	1 (10%)	5,13,15	6.10	3 (60%)

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
16	2MR	Q	118	16	-	3/10/13/15	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	Q	118	2MR	CZ-NE	5.54	1.46	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	118	2MR	NE-CZ-NH2	12.51	130.95	119.48
16	Q	118	2MR	CD-NE-CZ	4.47	131.79	123.41
16	Q	118	2MR	CQ2-NH2-CZ	2.92	130.32	123.86

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	Q	118	2MR	NE-CD-CG-CB
16	Q	118	2MR	CA-CB-CG-CD
16	Q	118	2MR	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 39 ligands modelled in this entry, 2 are monoatomic - leaving 37 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
54	CDL	a	201	-	90,90,99	1.14	8 (8%)	96,102,111	0.92	4 (4%)
48	PLX	a	202	-	51,51,51	1.14	4 (7%)	55,59,59	0.62	1 (1%)
45	SF4	B	301	2	0,12,12	-	-	-		
54	CDL	l	702	-	98,98,99	1.09	8 (8%)	104,110,111	0.89	4 (3%)
48	PLX	j	202	-	51,51,51	1.15	4 (7%)	55,59,59	0.59	1 (1%)
49	8Q1	G	201	6	31,34,34	1.71	6 (19%)	40,43,43	1.54	6 (15%)
54	CDL	u	201	-	77,77,99	1.21	8 (10%)	83,89,111	0.96	4 (4%)
47	PEE	C	302	-	46,46,50	1.21	6 (13%)	49,51,55	0.96	2 (4%)
47	PEE	i	402	-	46,46,50	1.20	6 (13%)	49,51,55	0.98	2 (4%)
45	SF4	A	501	1	0,12,12	-	-	-		
54	CDL	V	201	-	93,93,99	1.12	8 (8%)	99,105,111	0.86	4 (4%)
48	PLX	r	502	-	51,51,51	1.14	4 (7%)	55,59,59	0.62	1 (1%)
47	PEE	W	201	-	40,40,50	1.15	5 (12%)	43,45,55	0.99	2 (4%)
45	SF4	M	802	12	0,12,12	-	-	-		
55	UQ	s	401	-	28,28,63	3.28	8 (28%)	34,37,79	2.76	11 (32%)
48	PLX	g	201	-	51,51,51	1.15	4 (7%)	55,59,59	0.60	1 (1%)
51	FES	O	301	14	0,4,4	-	-	-		
47	PEE	b	201	-	45,45,50	1.22	6 (13%)	48,50,55	0.98	2 (4%)
47	PEE	j	201	-	50,50,50	1.16	6 (12%)	53,55,55	0.95	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
47	PEE	l	701	-	39,39,50	1.31	6 (15%)	41,44,55	1.05	2 (4%)
54	CDL	l	703	-	99,99,99	1.10	9 (9%)	105,111,111	0.84	4 (3%)
47	PEE	r	501	-	50,50,50	1.16	6 (12%)	53,55,55	0.97	2 (3%)
49	8Q1	X	201	6	31,34,34	1.70	6 (19%)	40,43,43	1.57	6 (15%)
48	PLX	r	503	-	51,51,51	1.15	4 (7%)	55,59,59	0.59	1 (1%)
45	SF4	M	801	12	0,12,12	-	-	-	-	-
54	CDL	r	504	-	94,94,99	1.11	9 (9%)	100,106,111	0.87	4 (4%)
54	CDL	o	201	-	67,67,99	1.26	8 (11%)	73,79,111	1.02	4 (5%)
51	FES	M	803	12	0,4,4	-	-	-	-	-
45	SF4	B	302	2	0,12,12	-	-	-	-	-
54	CDL	i	401	-	65,65,99	1.28	9 (13%)	71,77,111	1.01	4 (5%)
47	PEE	l	704	-	45,45,50	1.23	6 (13%)	48,50,55	0.99	2 (4%)
50	NDP	J	401	-	45,52,52	4.58	20 (44%)	53,80,80	1.93	7 (13%)
45	SF4	C	301	16,3	0,12,12	-	-	-	-	-
46	FMN	A	502	-	33,33,33	1.07	2 (6%)	48,50,50	1.20	8 (16%)
56	ADP	w	401	-	24,29,29	3.12	6 (25%)	29,45,45	1.44	4 (13%)
47	PEE	B	303	-	50,50,50	1.16	6 (12%)	53,55,55	1.00	2 (3%)
48	PLX	C	303	-	51,51,51	1.14	4 (7%)	55,59,59	0.61	1 (1%)

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
54	CDL	a	201	-	-	47/101/101/110	-
48	PLX	a	202	-	-	22/55/55/55	-
45	SF4	B	301	2	-	-	0/6/5/5
54	CDL	l	702	-	-	56/109/109/110	-
48	PLX	j	202	-	-	27/55/55/55	-
49	8Q1	G	201	6	-	12/41/41/41	-
54	CDL	u	201	-	-	36/88/88/110	-
47	PEE	C	302	-	-	19/50/50/54	-
47	PEE	i	402	-	-	20/50/50/54	-
54	CDL	V	201	-	-	57/104/104/110	-
45	SF4	A	501	1	-	-	0/6/5/5
48	PLX	r	502	-	-	24/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	PEE	W	201	-	-	19/44/44/54	-
45	SF4	M	802	12	-	-	0/6/5/5
55	UQ	s	401	-	-	10/21/45/87	0/1/1/1
48	PLX	g	201	-	-	25/55/55/55	-
51	FES	O	301	14	-	-	0/1/1/1
47	PEE	b	201	-	-	31/49/49/54	-
47	PEE	j	201	-	-	30/54/54/54	-
47	PEE	l	701	-	-	32/43/43/54	-
54	CDL	l	703	-	-	58/110/110/110	-
47	PEE	r	501	-	-	30/54/54/54	-
49	8Q1	X	201	6	-	16/41/41/41	-
48	PLX	r	503	-	-	36/55/55/55	-
45	SF4	M	801	12	-	-	0/6/5/5
54	CDL	r	504	-	-	58/105/105/110	-
54	CDL	o	201	-	-	45/78/78/110	-
51	FES	M	803	12	-	-	0/1/1/1
45	SF4	B	302	2	-	-	0/6/5/5
54	CDL	i	401	-	-	37/76/76/110	-
47	PEE	l	704	-	-	22/49/49/54	-
50	NDP	J	401	-	-	6/30/77/77	0/4/5/5
45	SF4	C	301	16,3	-	-	0/6/5/5
46	FMN	A	502	-	-	6/18/18/18	0/3/3/3
56	ADP	w	401	-	-	4/12/32/32	0/3/3/3
47	PEE	B	303	-	-	23/54/54/54	-
48	PLX	C	303	-	-	26/55/55/55	-

The worst 5 of 192 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	J	401	NDP	C3B-C2B	-13.06	1.23	1.52
50	J	401	NDP	C6N-C5N	12.36	1.55	1.33
50	J	401	NDP	O4D-C4D	10.71	1.68	1.45
50	J	401	NDP	C3D-C4D	-9.83	1.27	1.53
55	s	401	UQ	C13-C14	9.31	1.55	1.33

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	s	401	UQ	C7-C8-C9	-9.42	111.10	126.79
50	J	401	NDP	C3N-C2N-N1N	-7.64	112.19	123.10
50	J	401	NDP	C1D-N1N-C2N	-7.08	109.33	121.11
49	X	201	8Q1	C6-C1-S44	6.16	120.62	113.46
55	s	401	UQ	C12-C13-C14	-5.79	113.72	127.66

There are no chirality outliers.

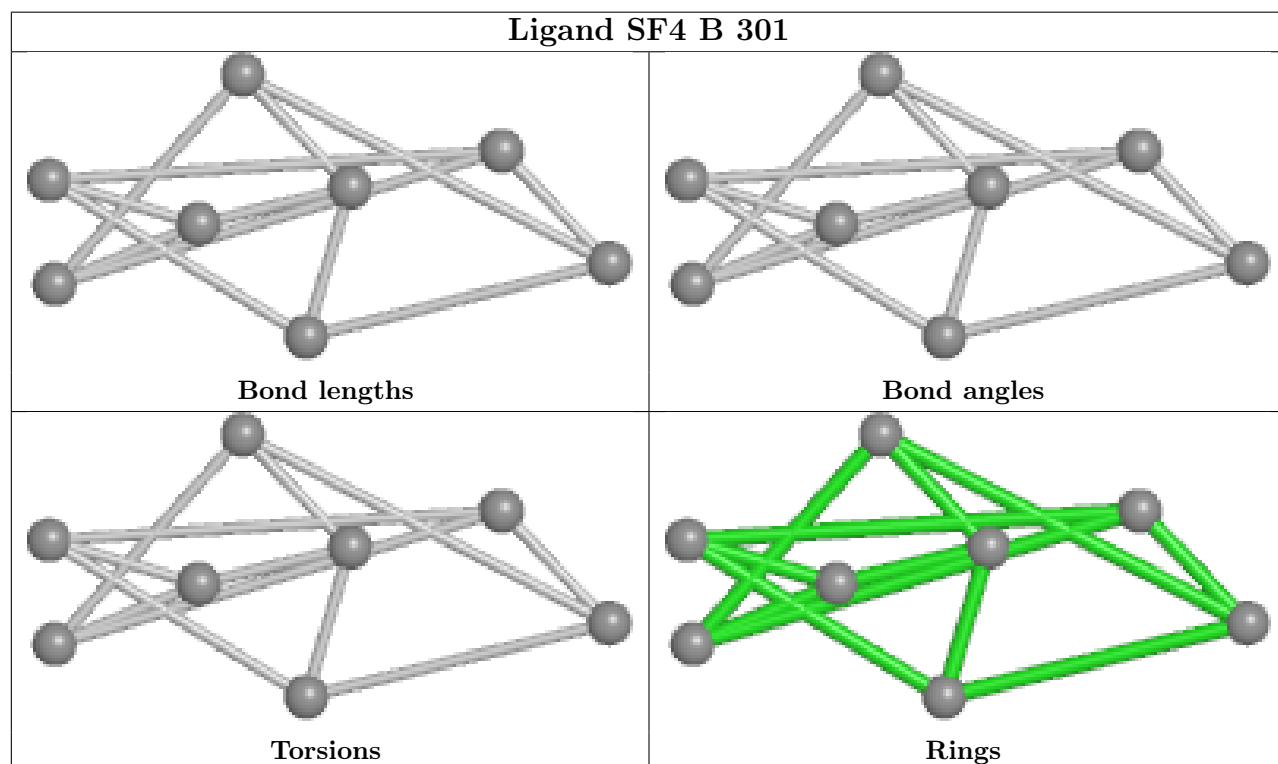
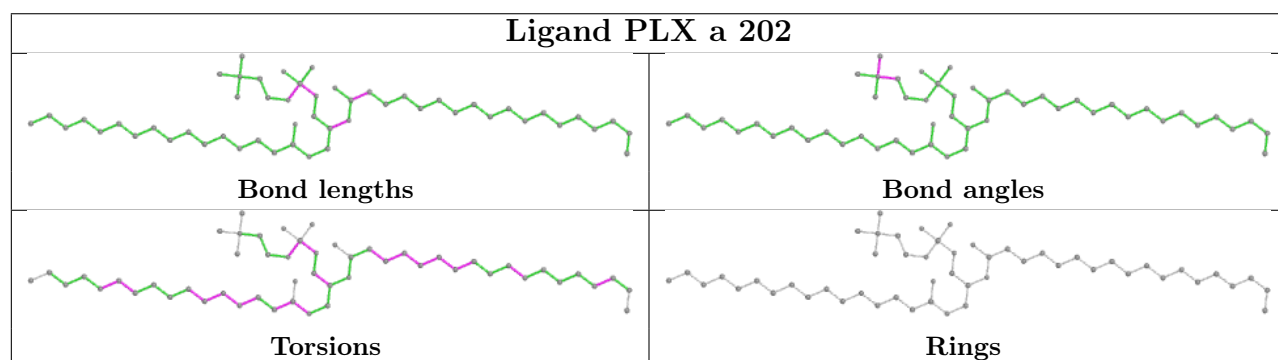
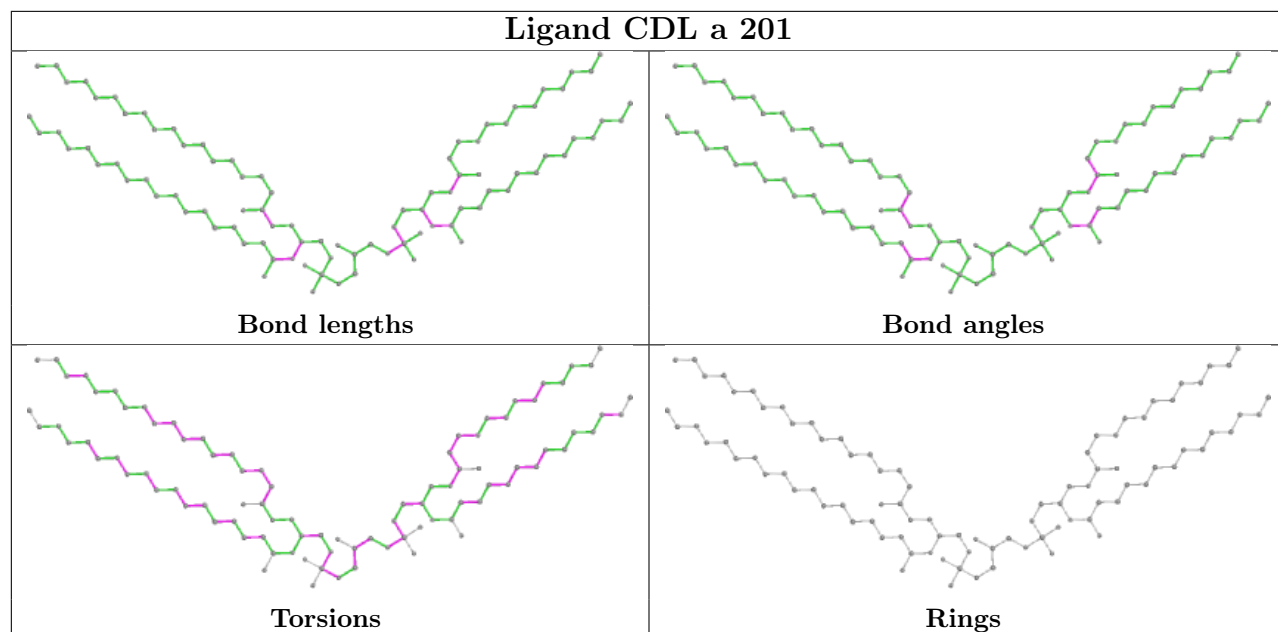
5 of 834 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	A	502	FMN	N10-C1'-C2'-O2'
46	A	502	FMN	N10-C1'-C2'-C3'
46	A	502	FMN	C1'-C2'-C3'-O3'
46	A	502	FMN	C1'-C2'-C3'-C4'
47	B	303	PEE	C37-C38-C39-C40

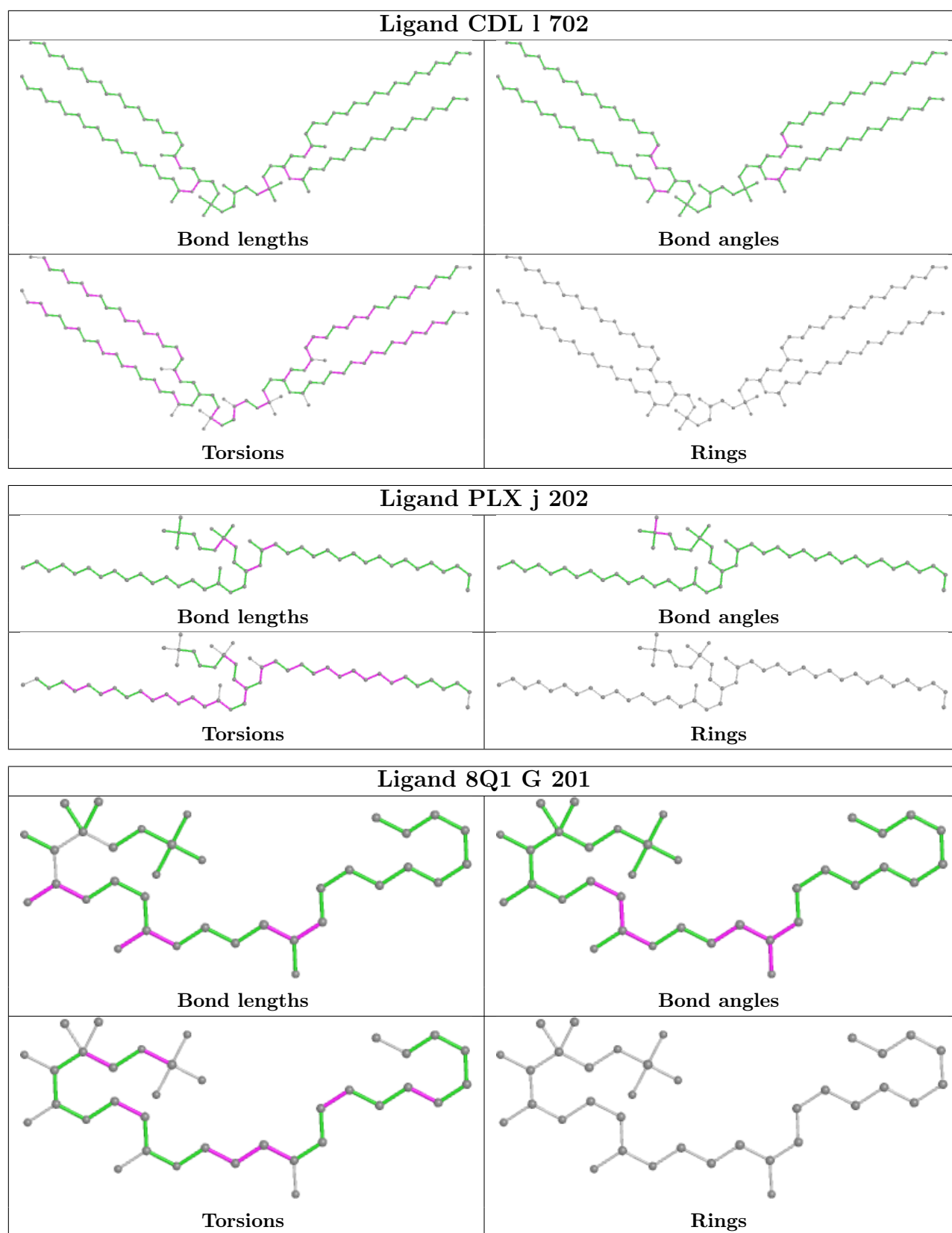
There are no ring outliers.

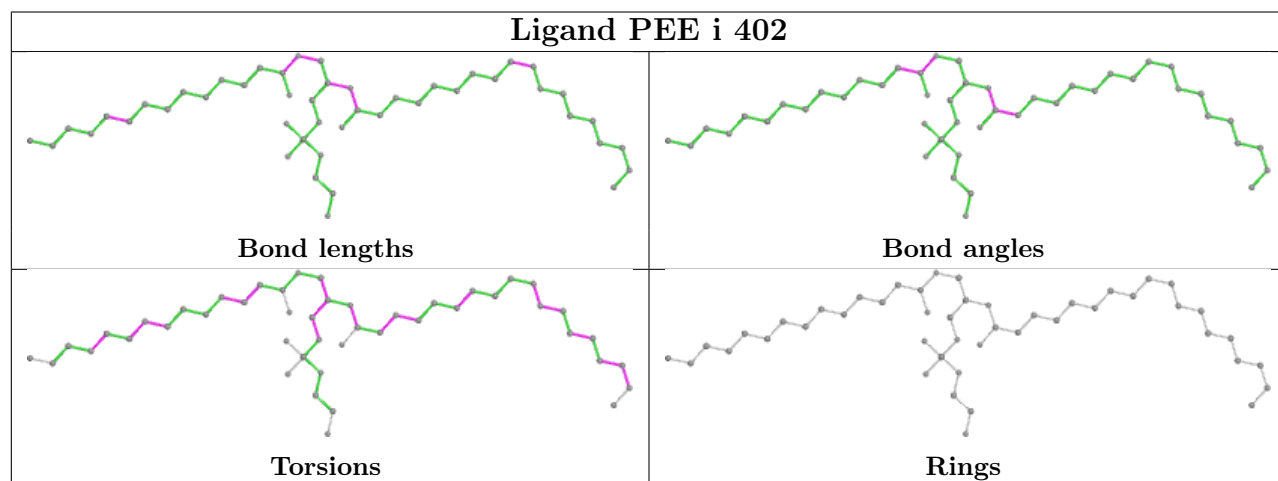
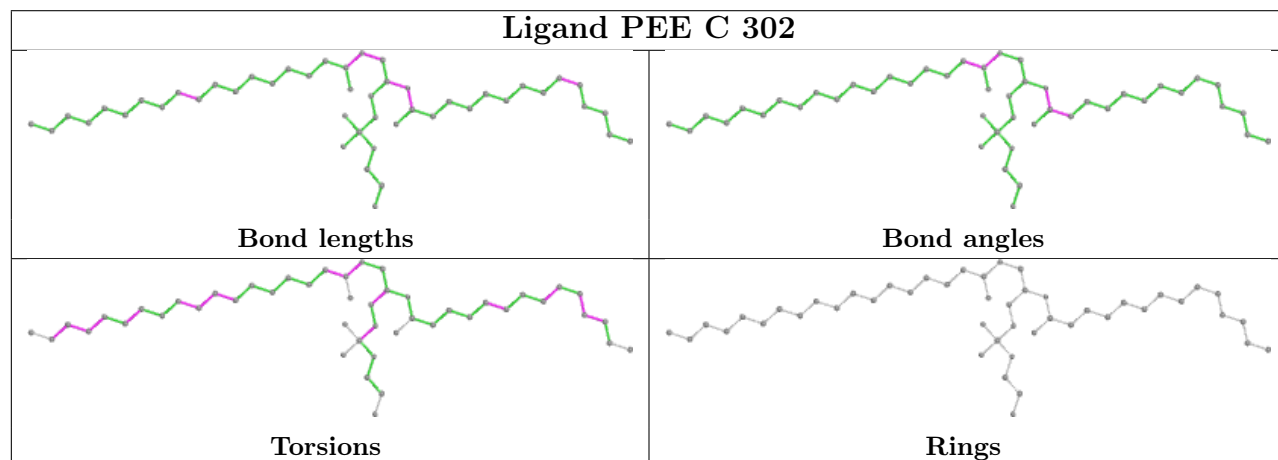
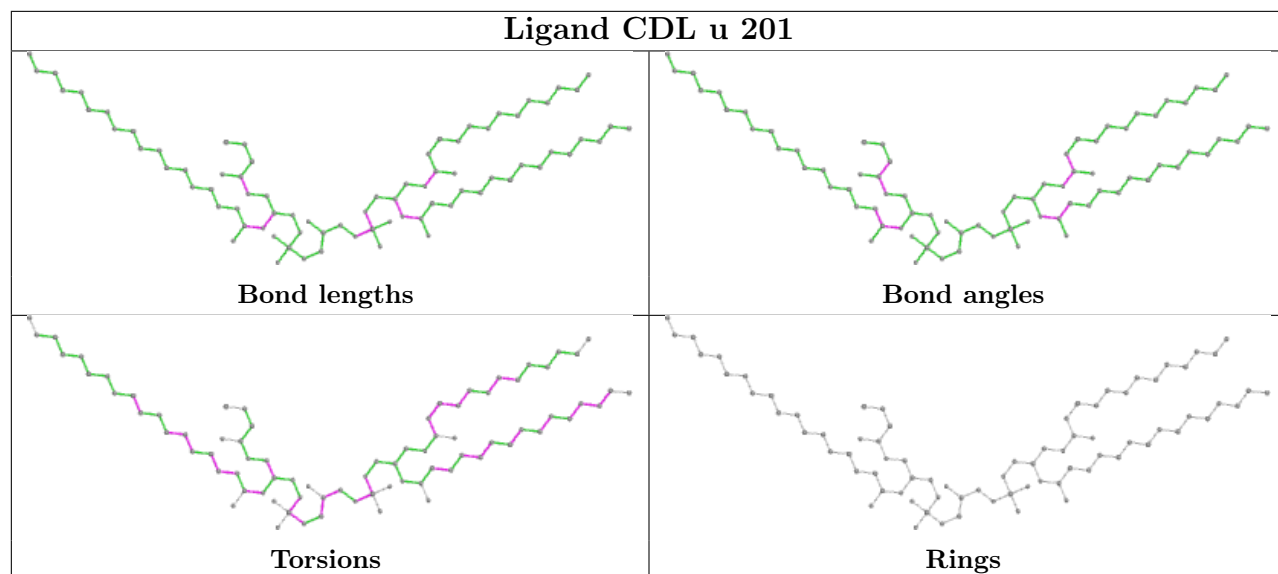
No monomer is involved in short contacts.

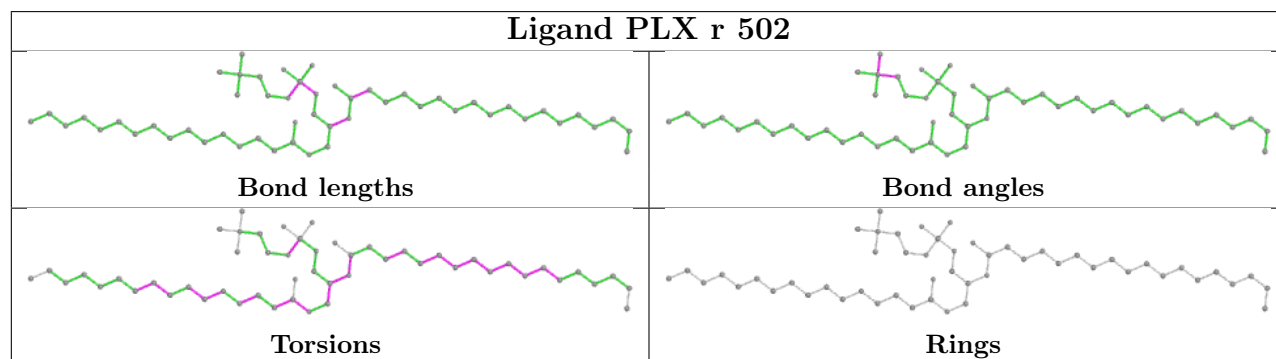
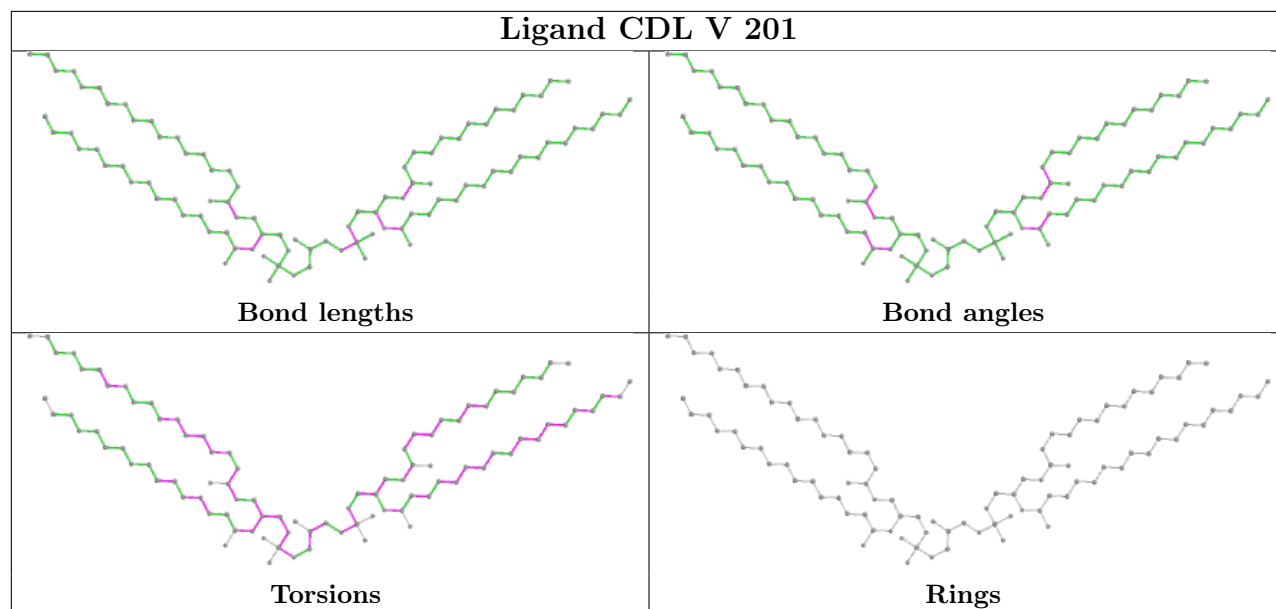
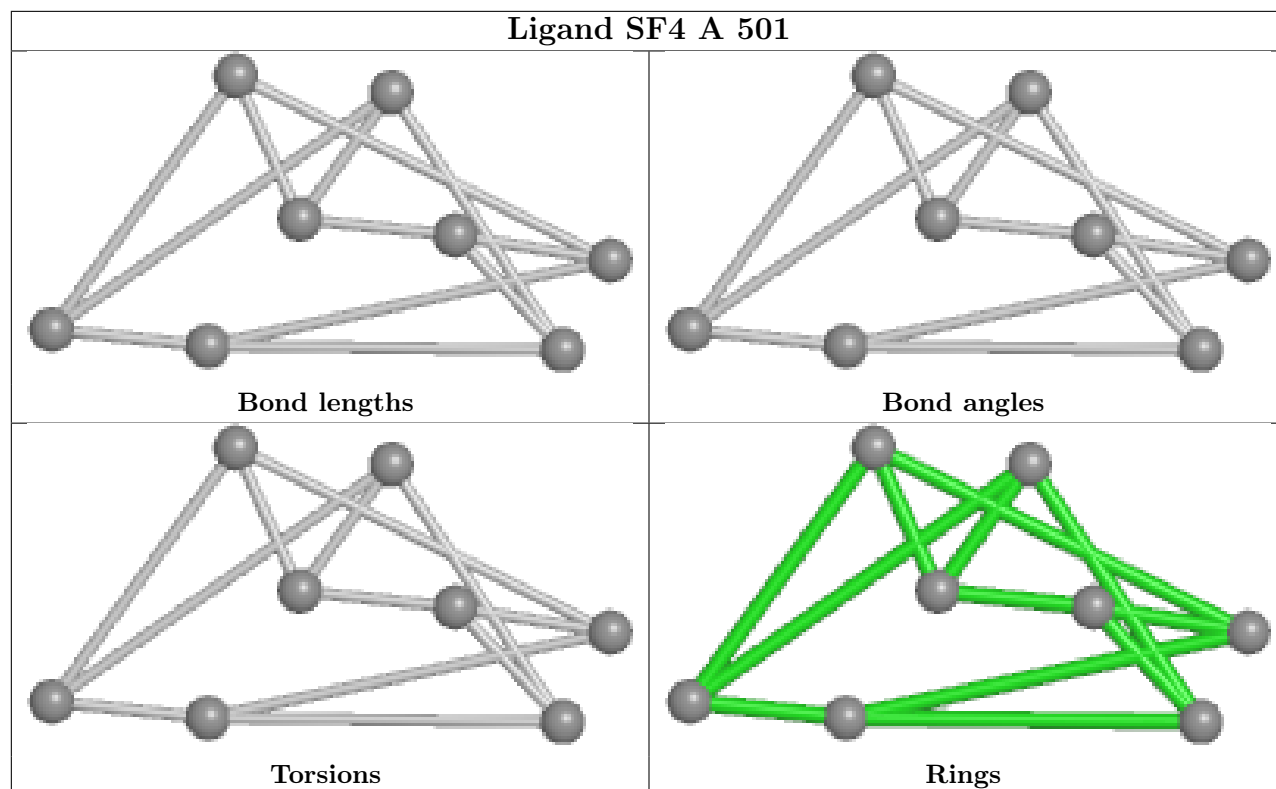
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

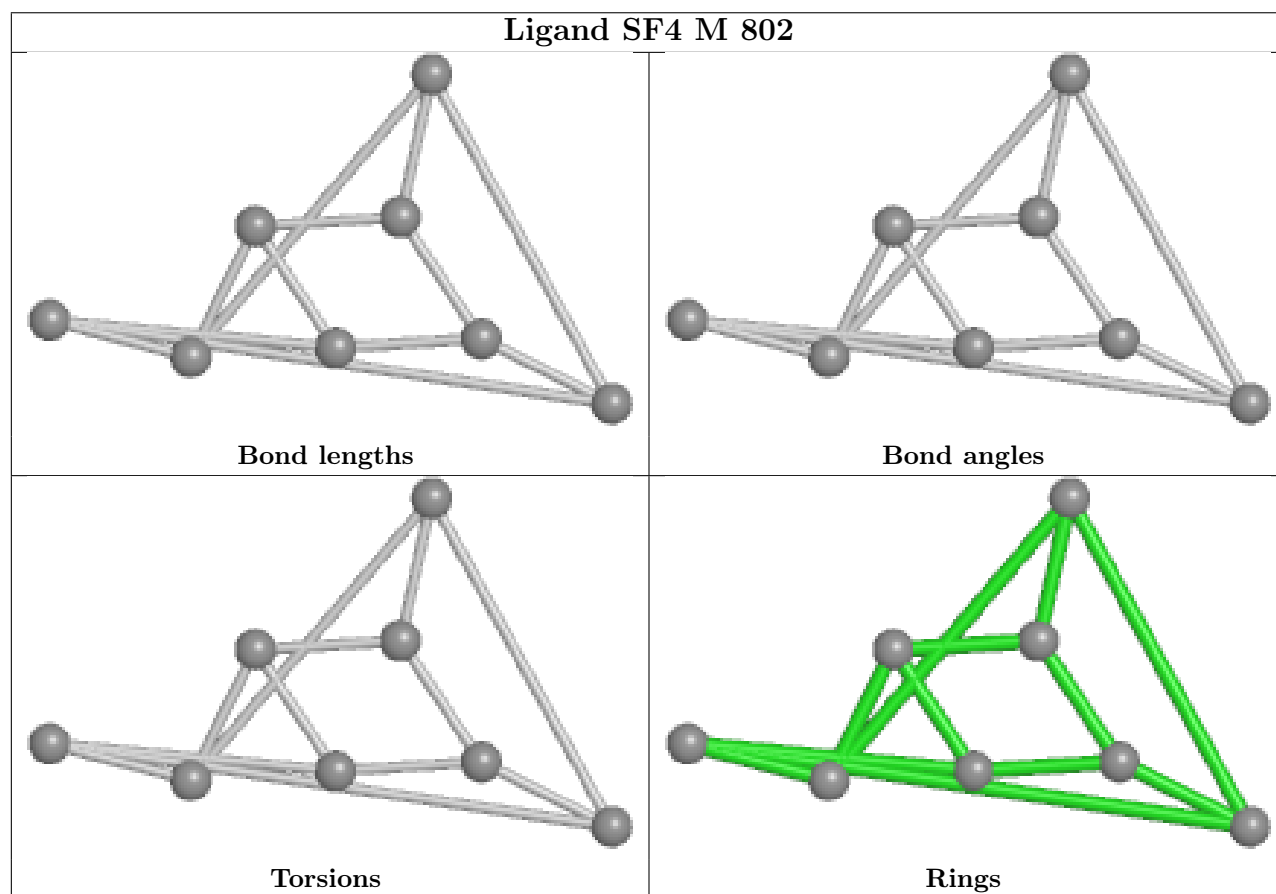
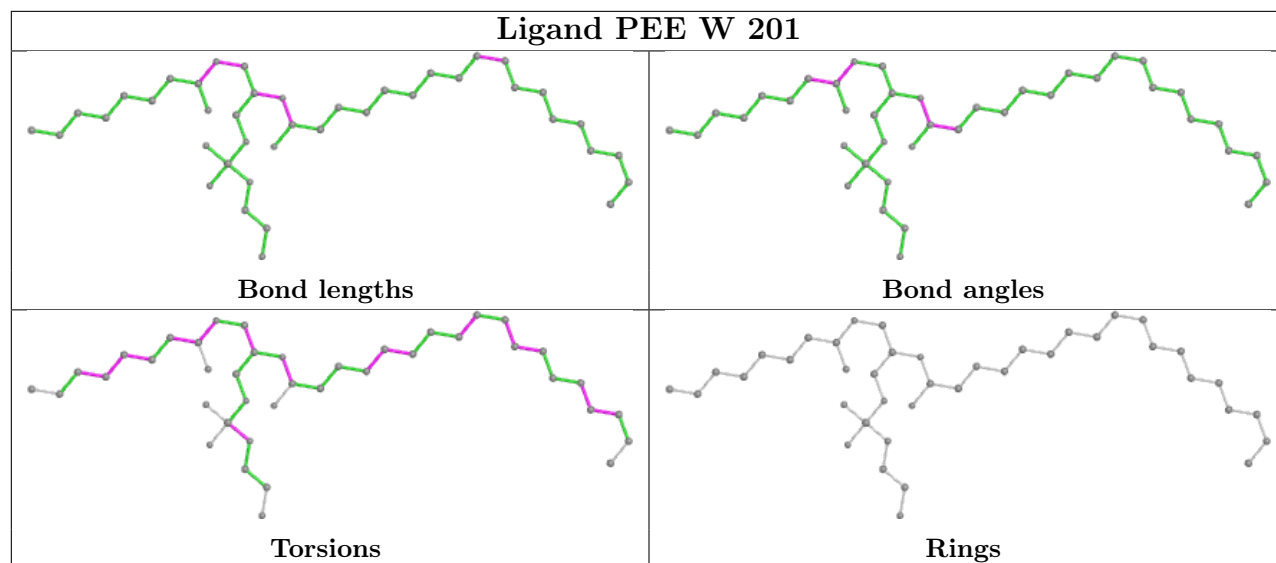


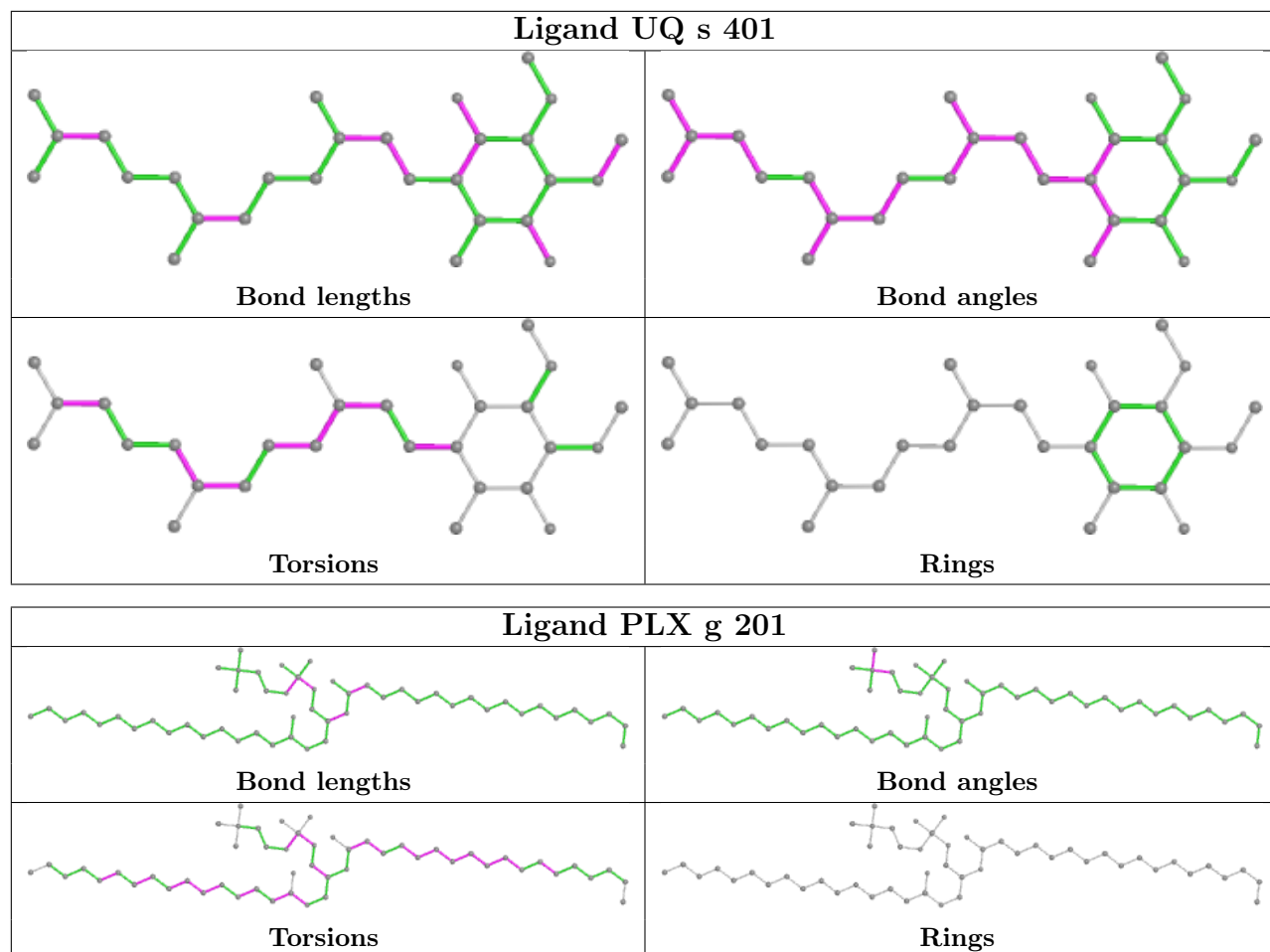


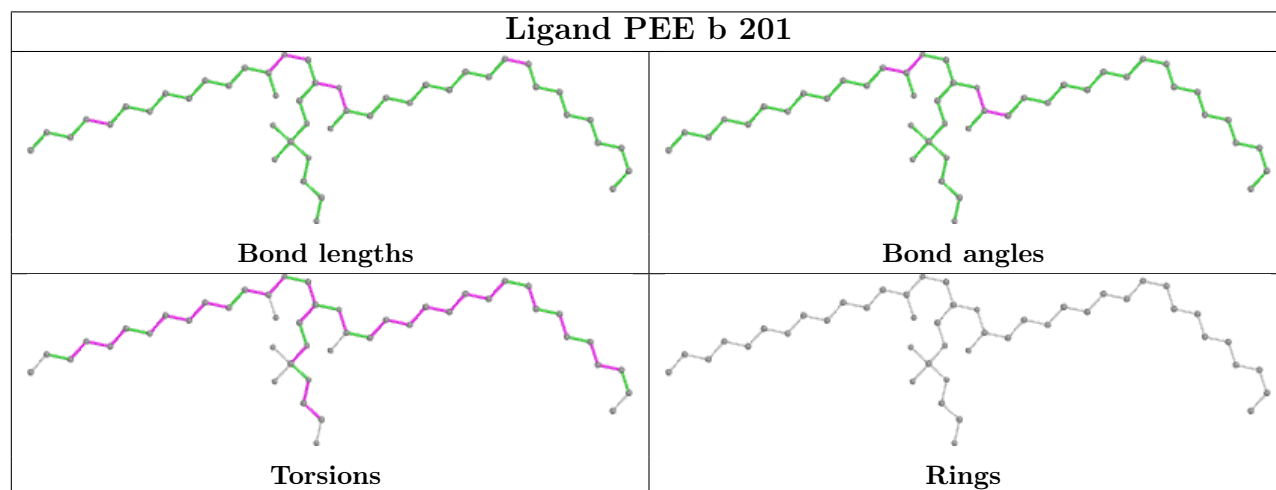
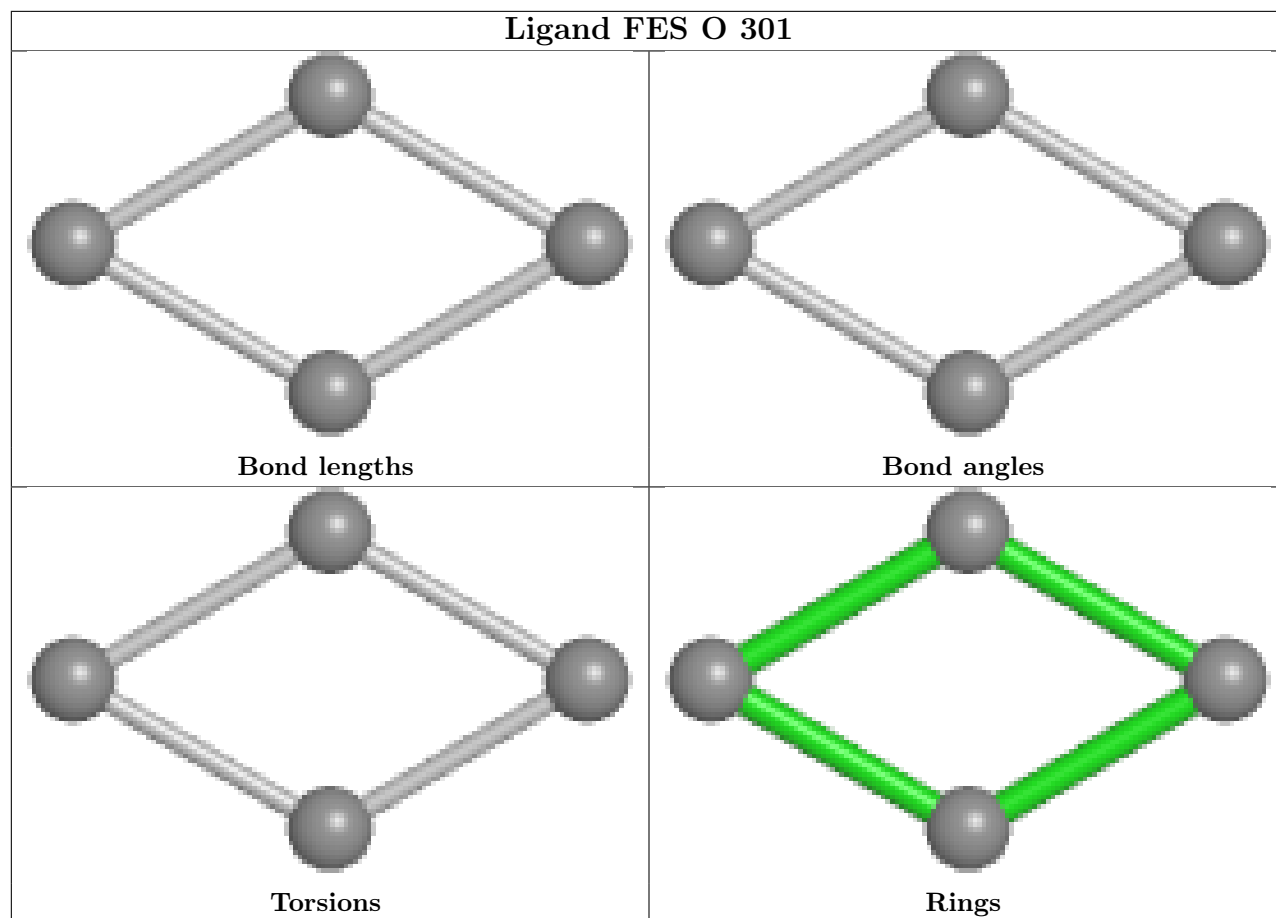


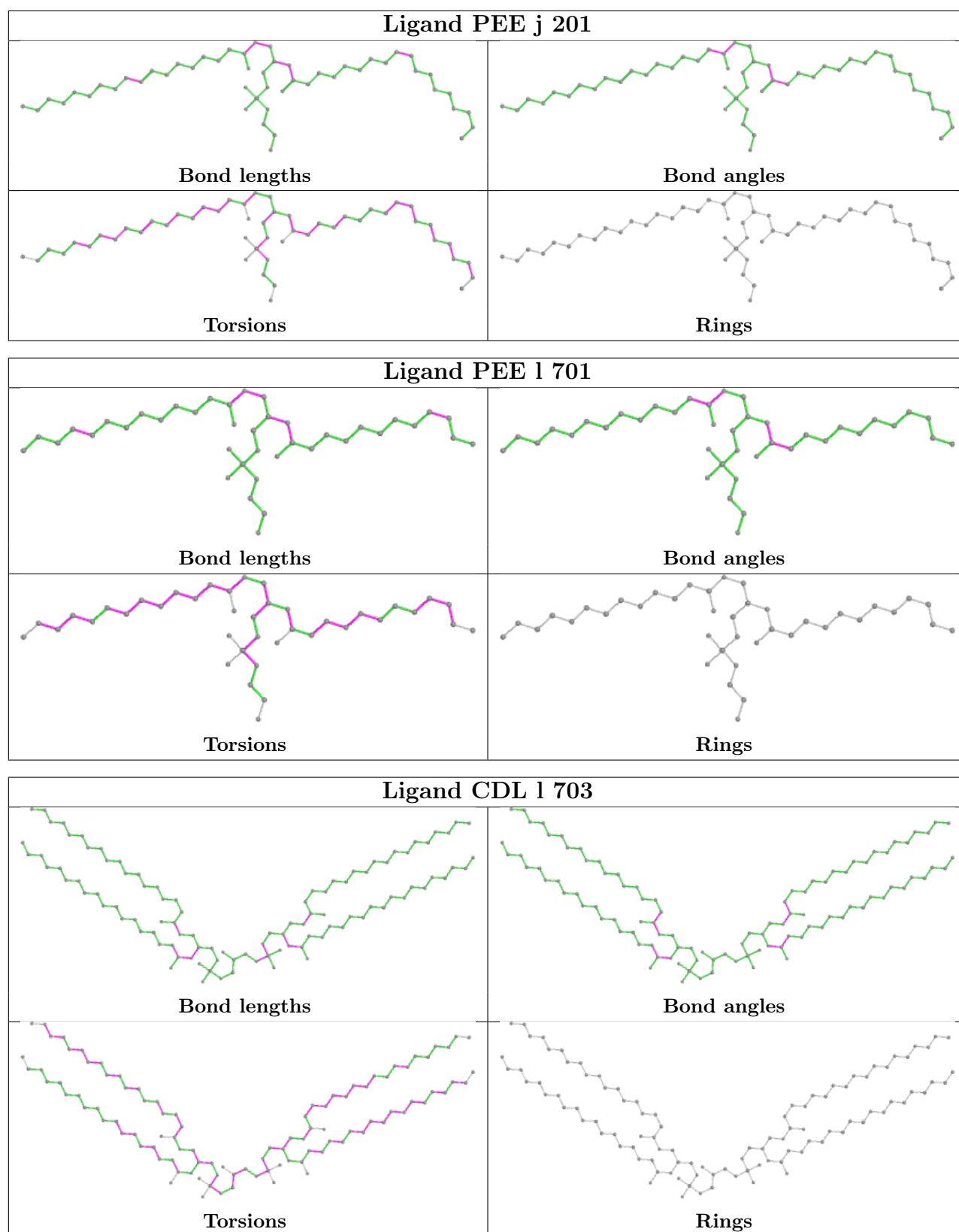


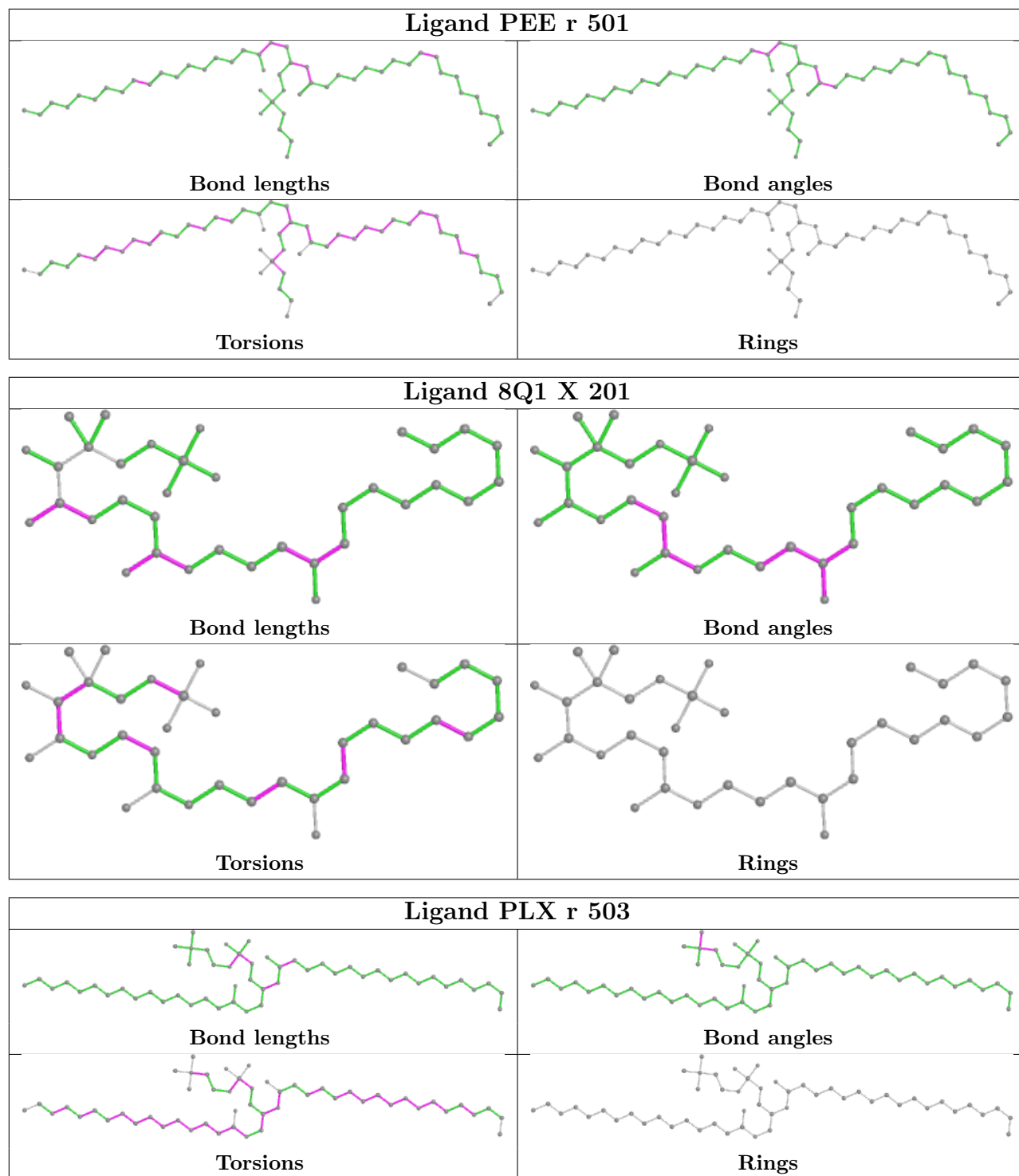




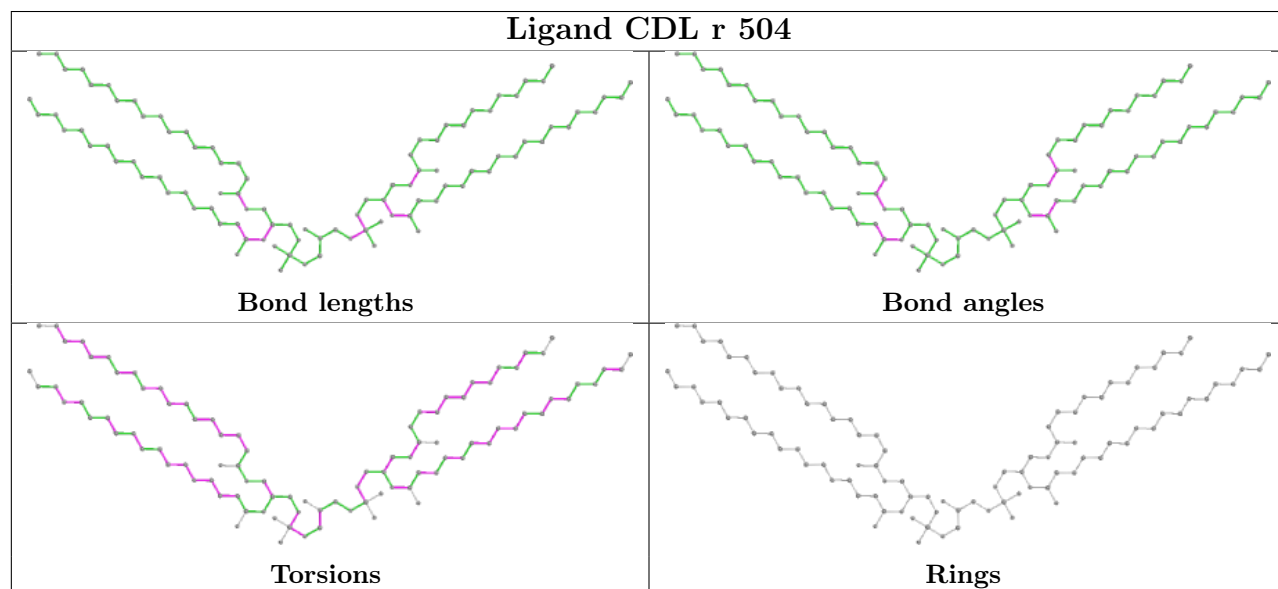
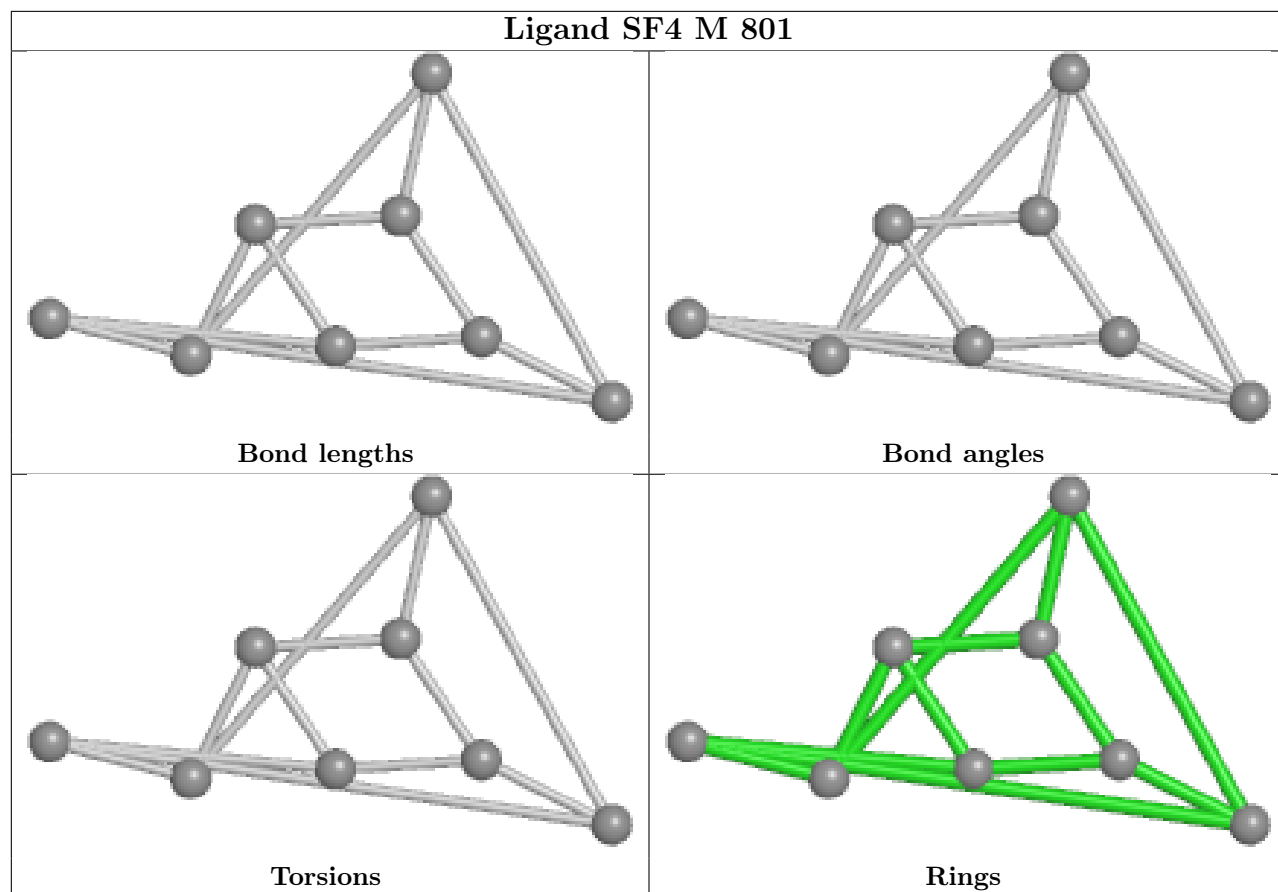


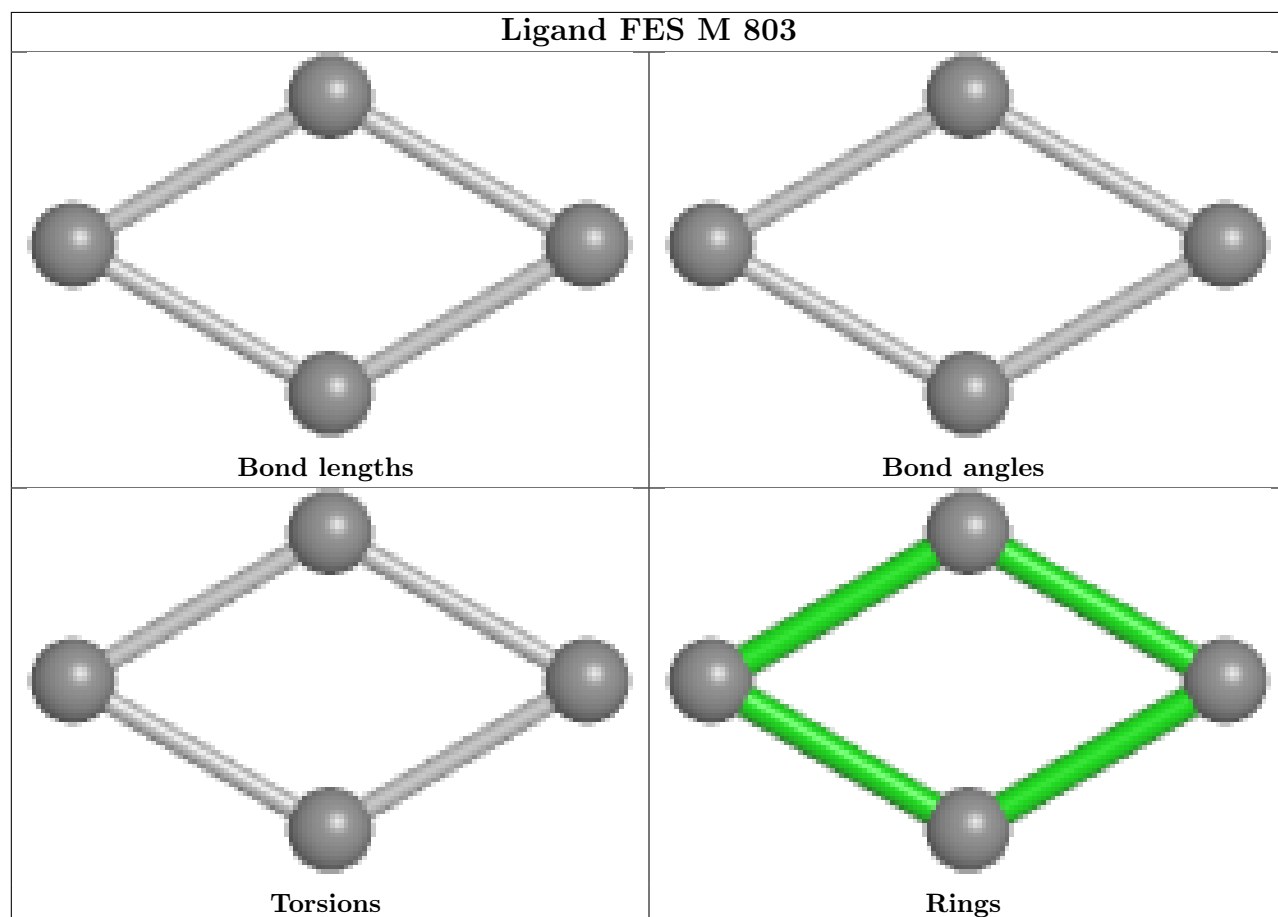
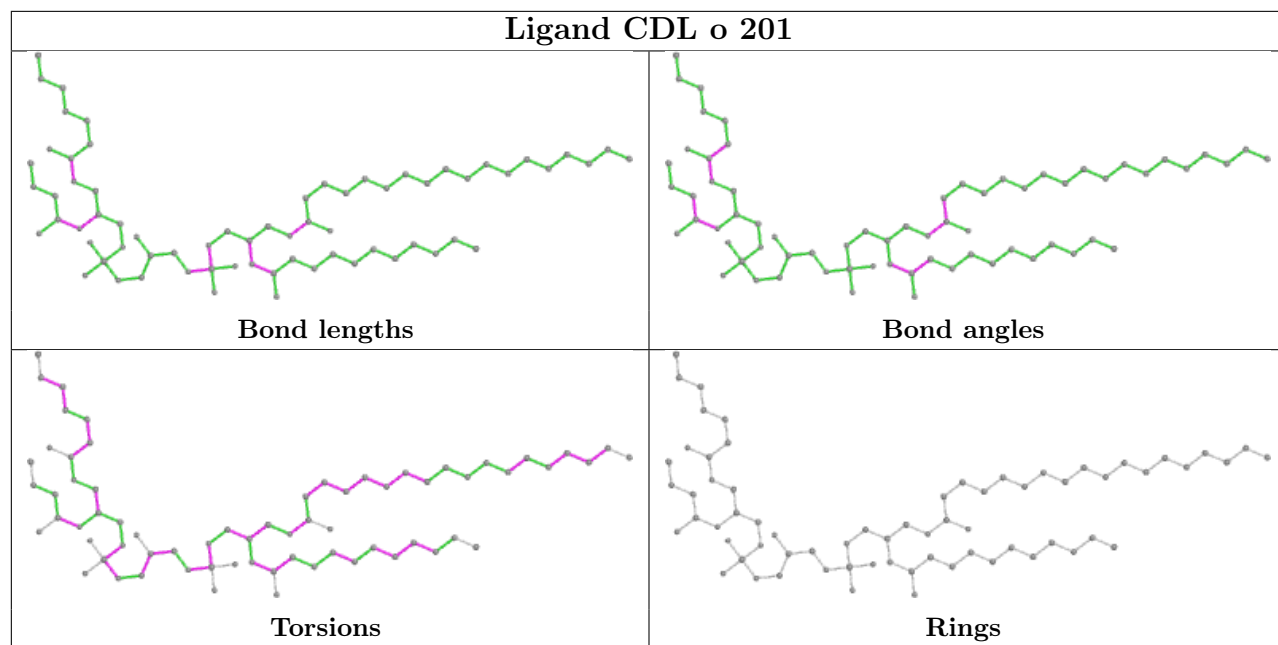


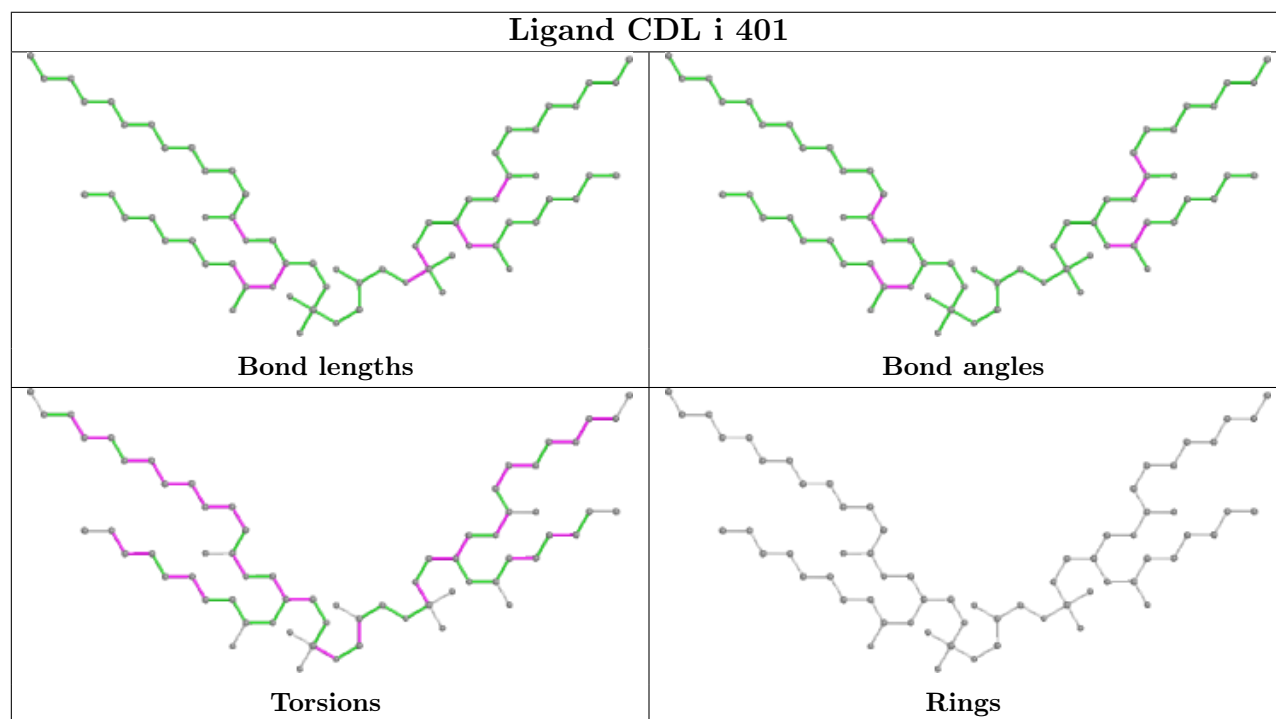
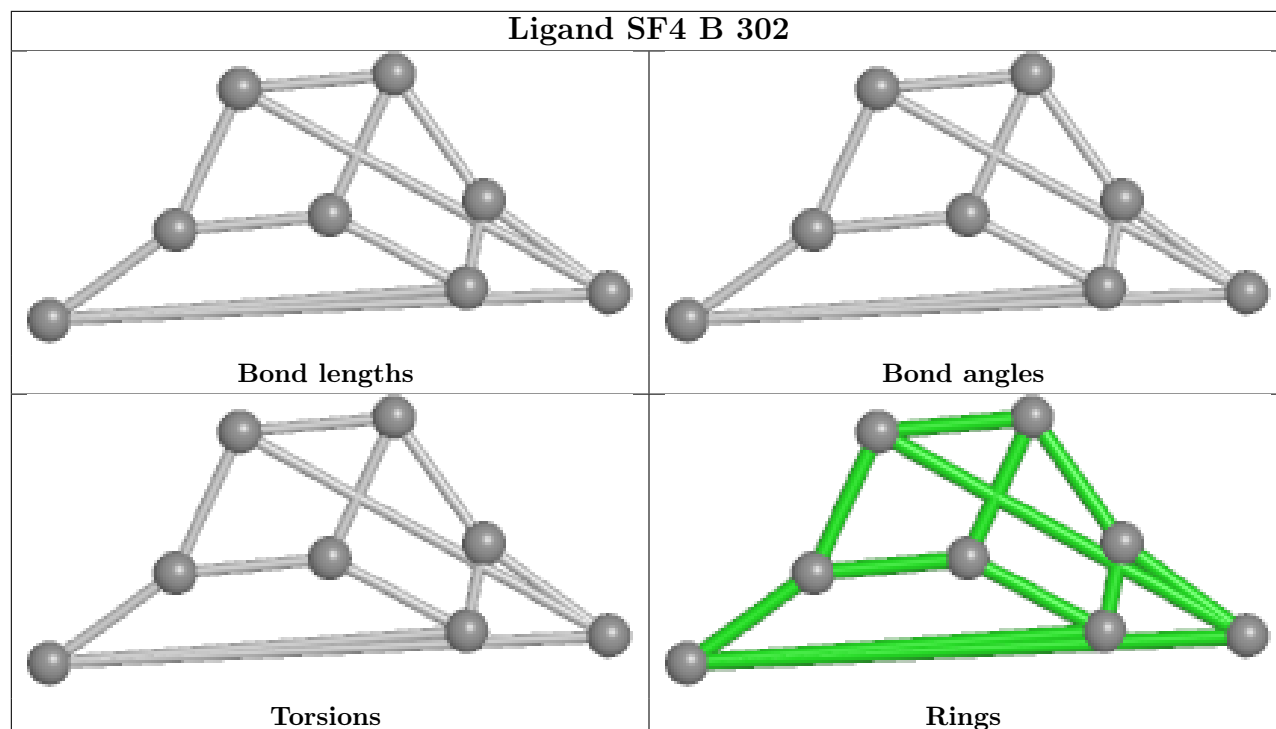


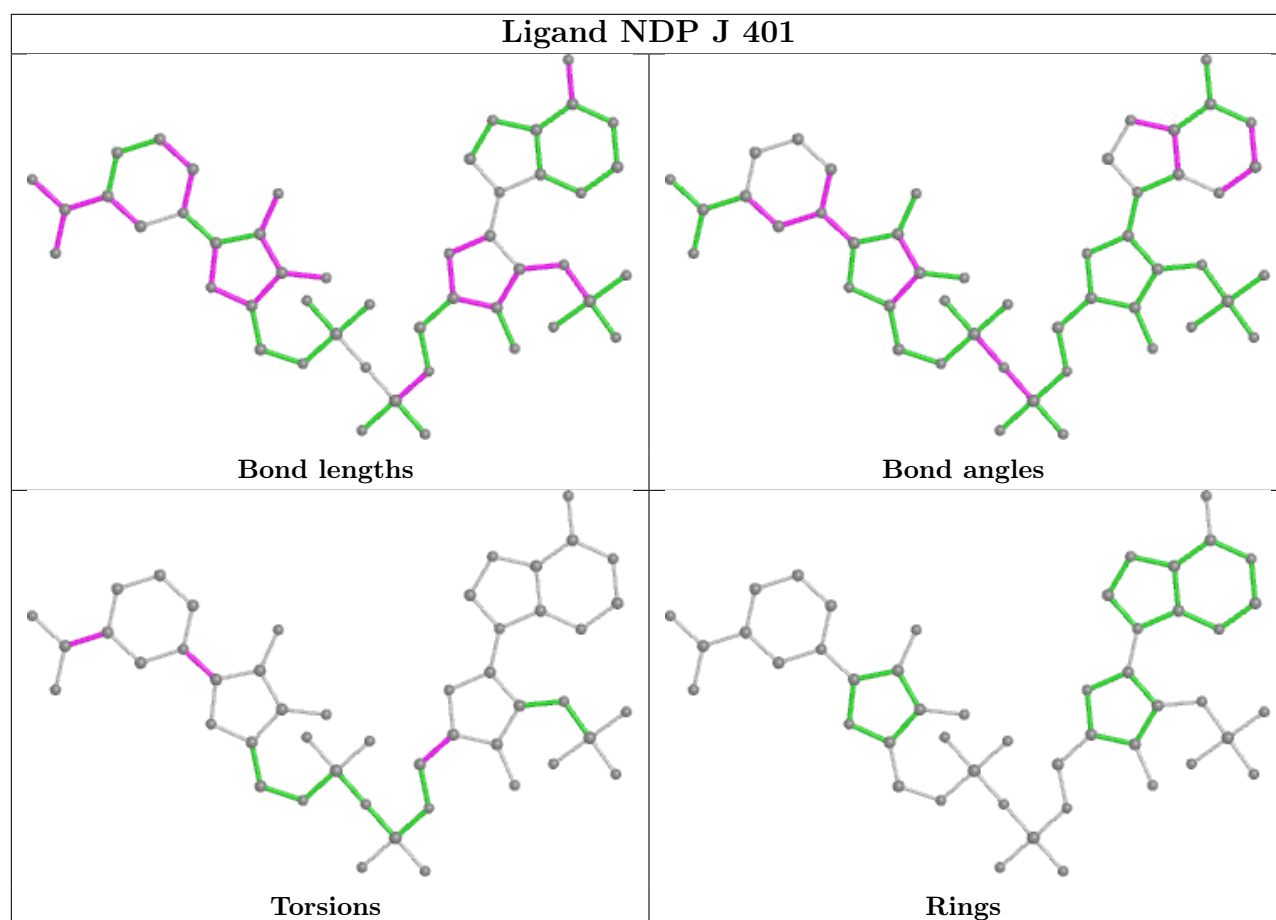
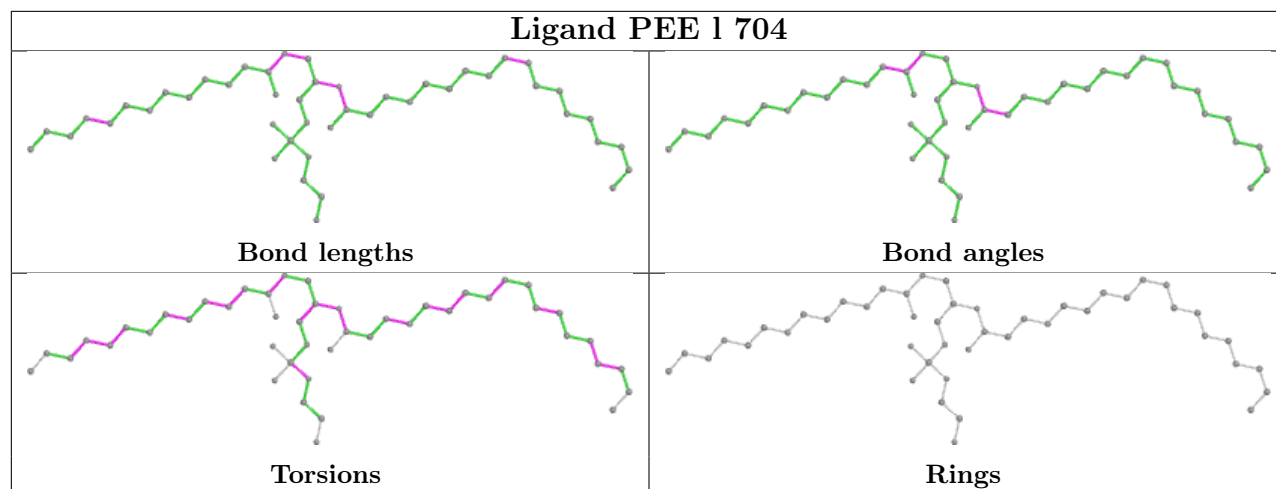


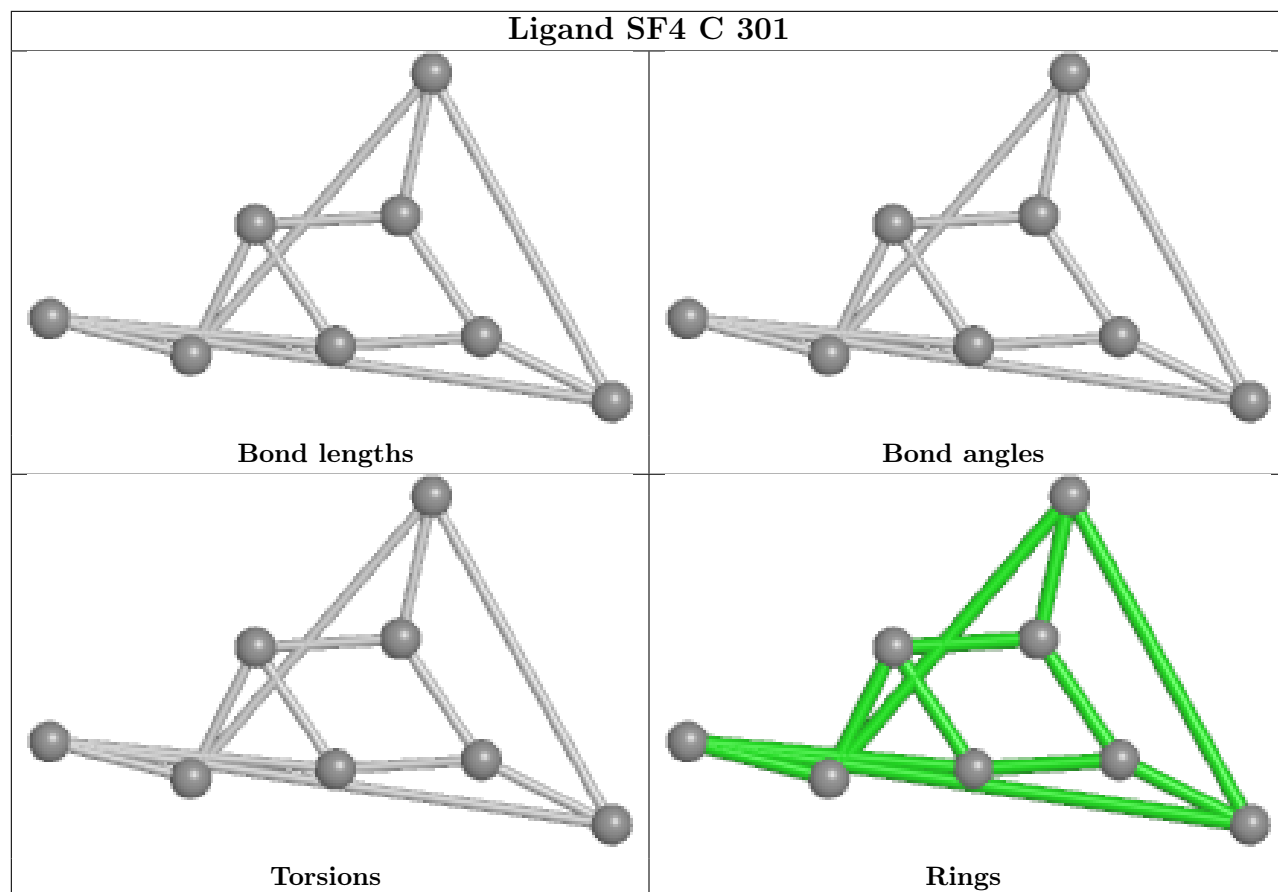


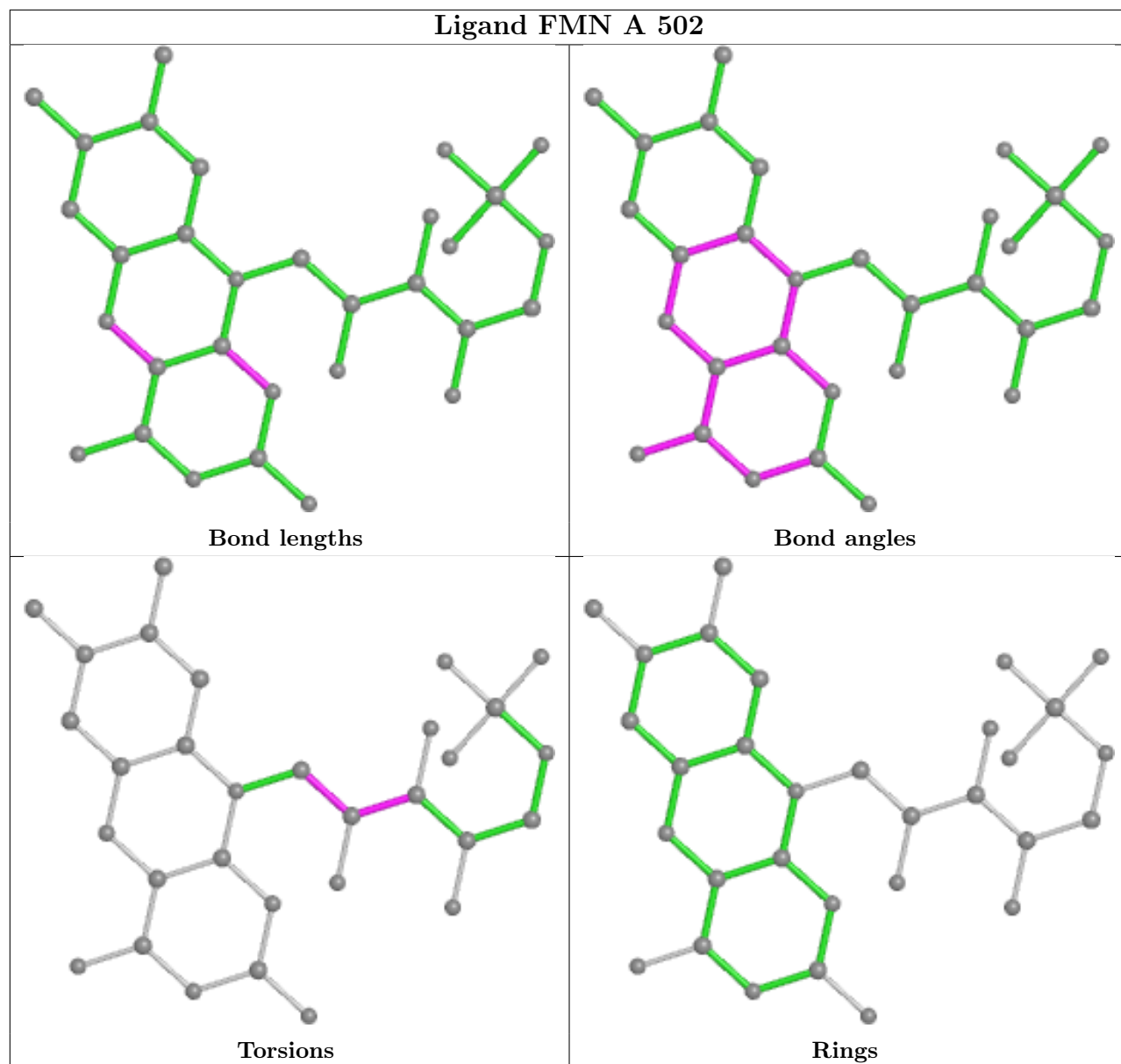


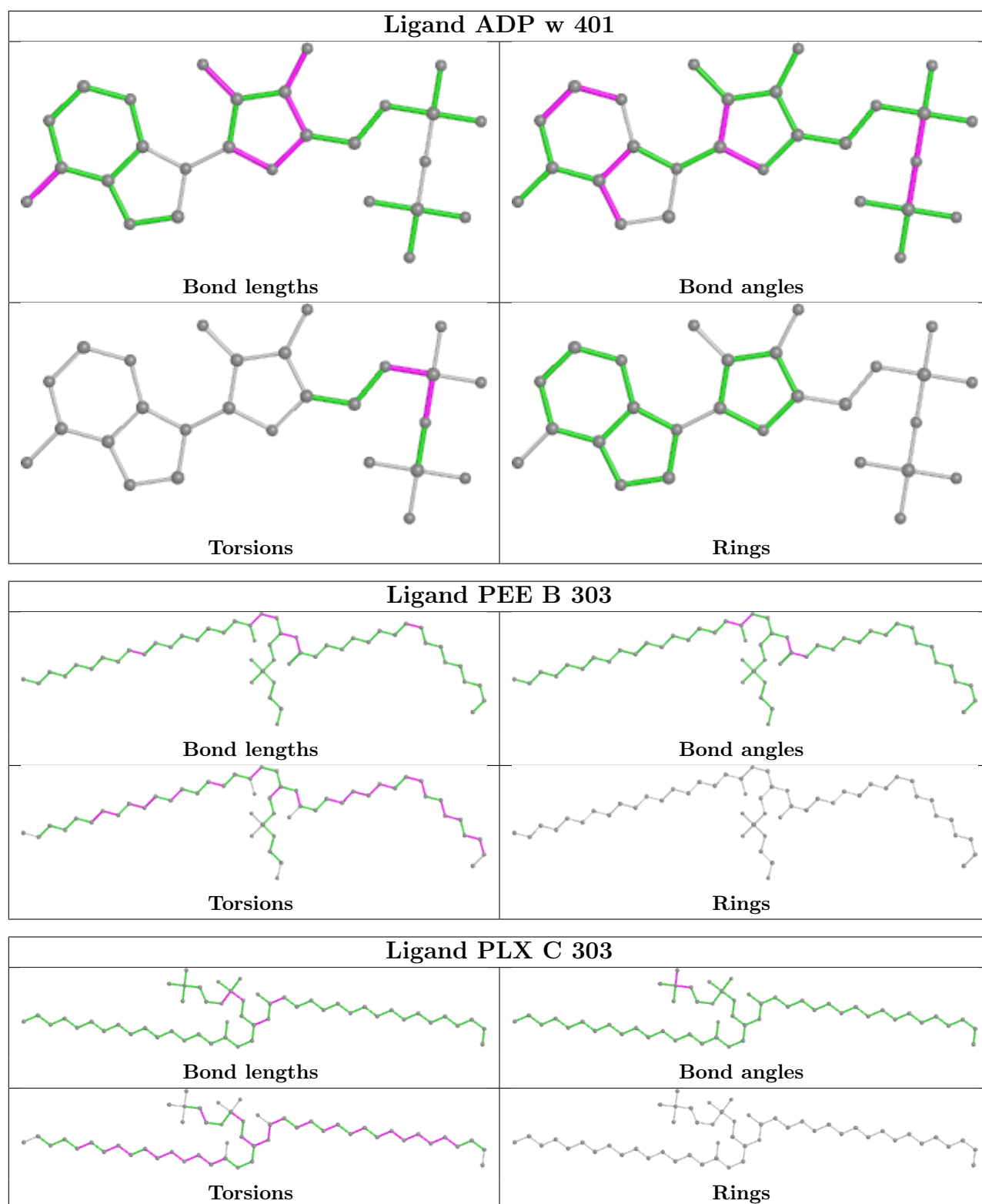












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



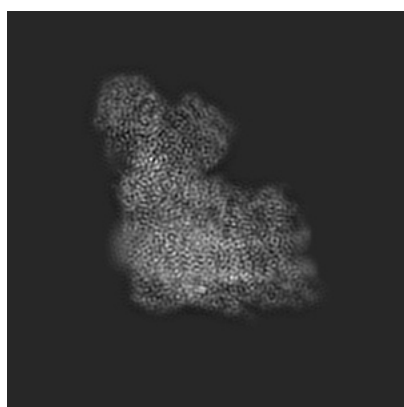
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32232. These allow visual inspection of the internal detail of the map and identification of artifacts.

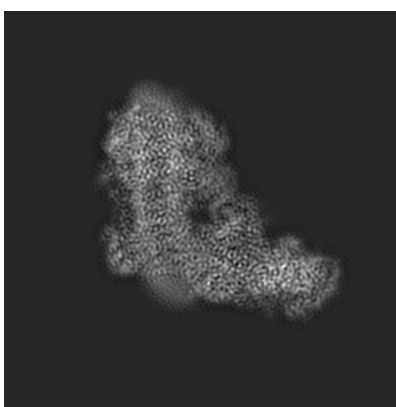
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

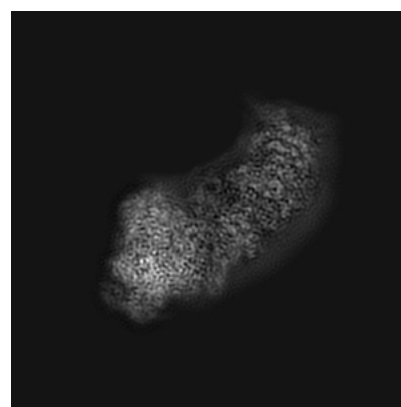
#### 6.1.1 Primary map



X



Y

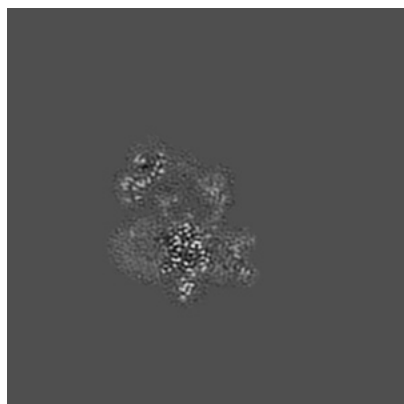


Z

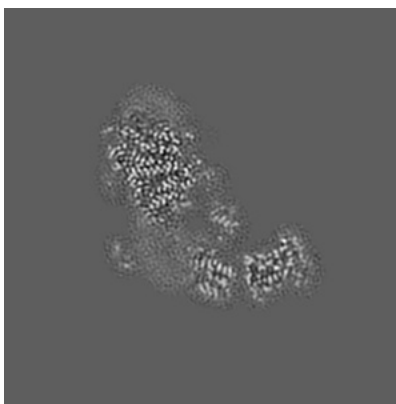
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

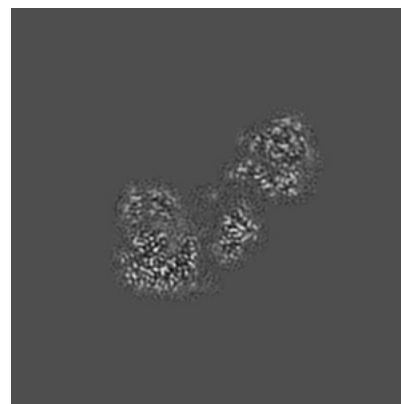
#### 6.2.1 Primary map



X Index: 165



Y Index: 165

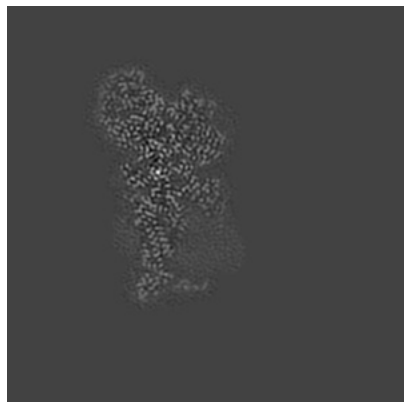


Z Index: 165

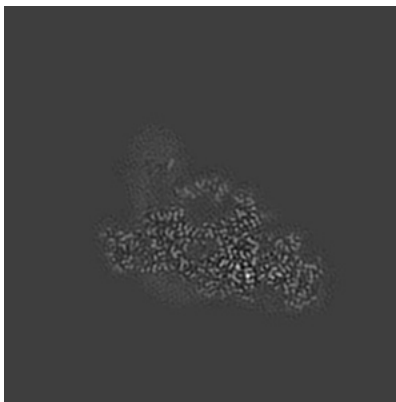
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

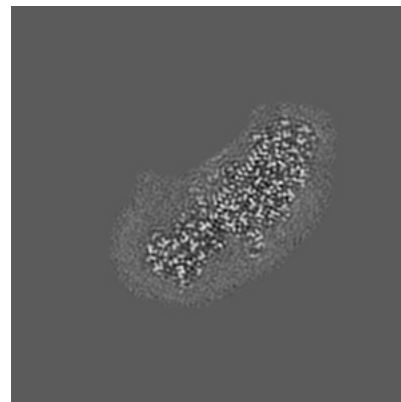
### 6.3.1 Primary map



X Index: 115



Y Index: 123

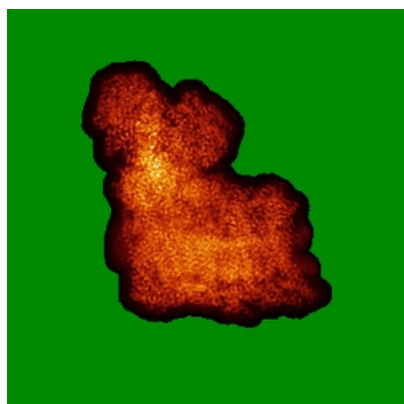


Z Index: 137

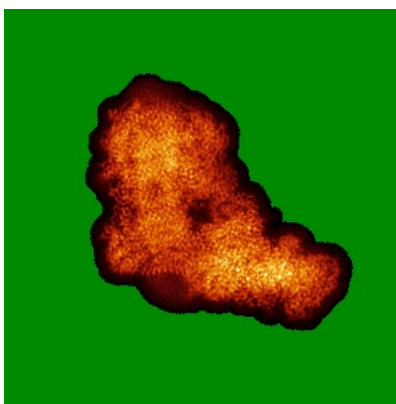
The images above show the largest variance slices of the map in three orthogonal directions.

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

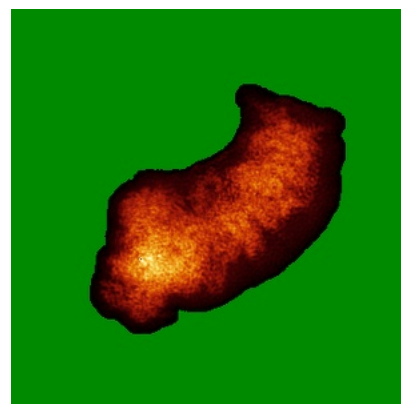
### 6.4.1 Primary map



X



Y

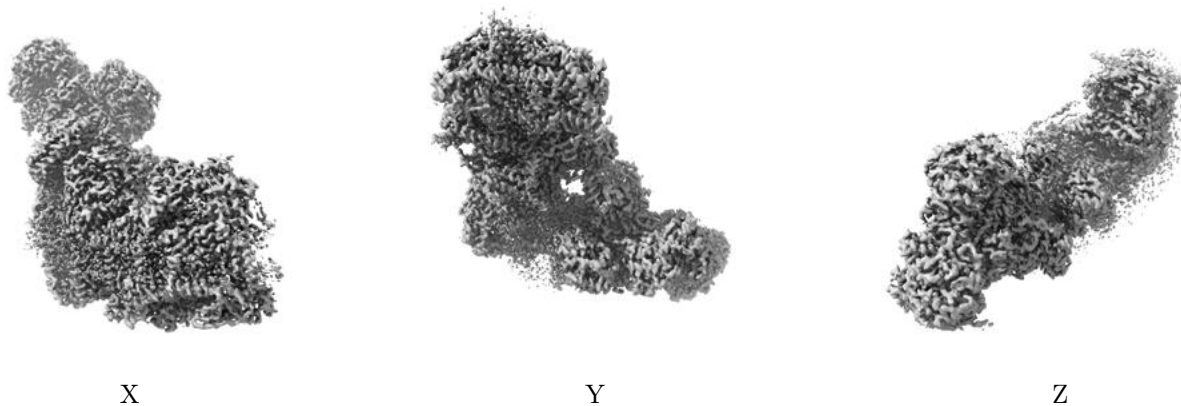


Z

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 0.0204. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

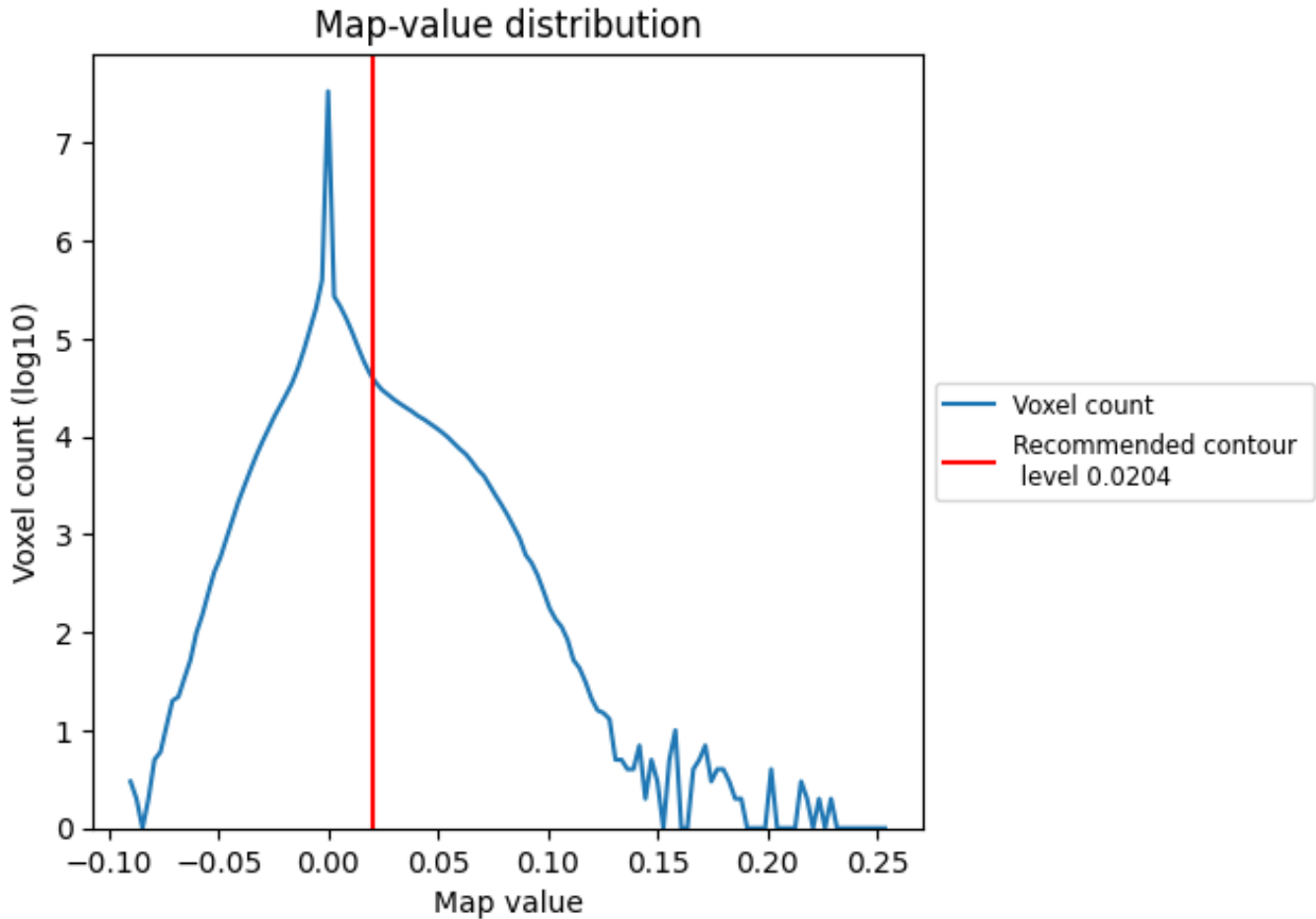
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

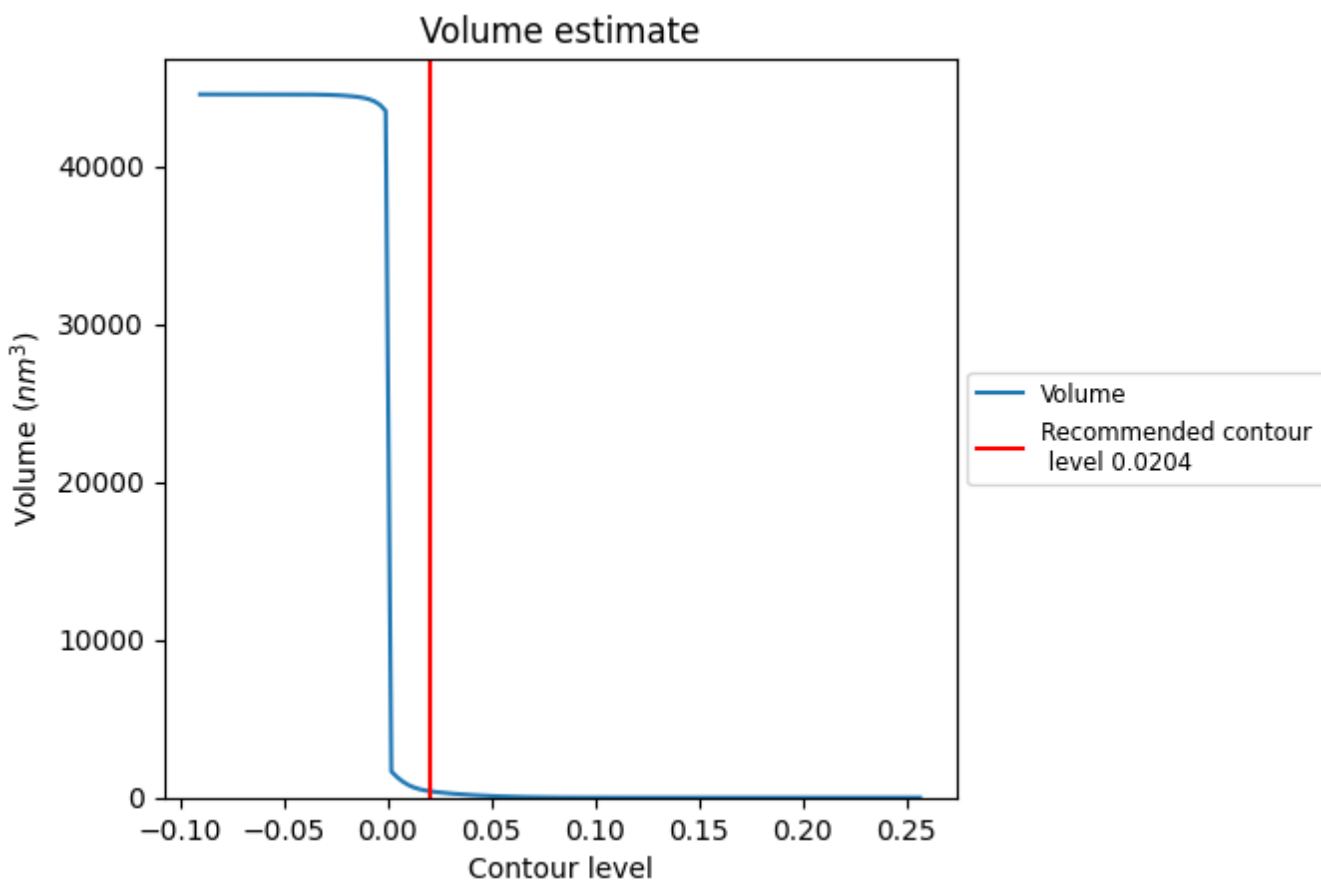
This section contains the results of statistical analysis of the map.

### 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.

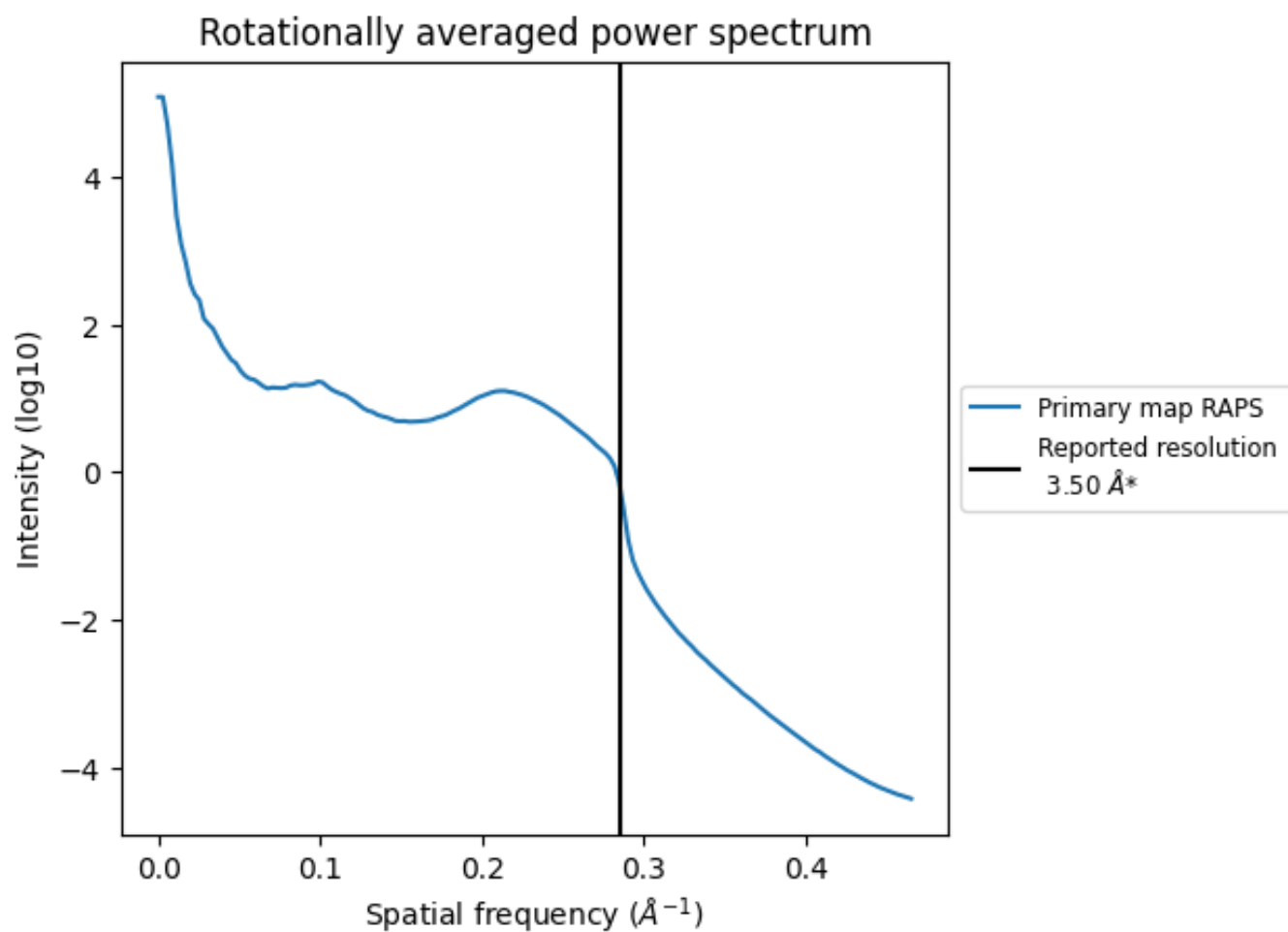
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 404 nm<sup>3</sup>; this corresponds to an approximate mass of 365 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 [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.286 \text{\AA}^{-1}$

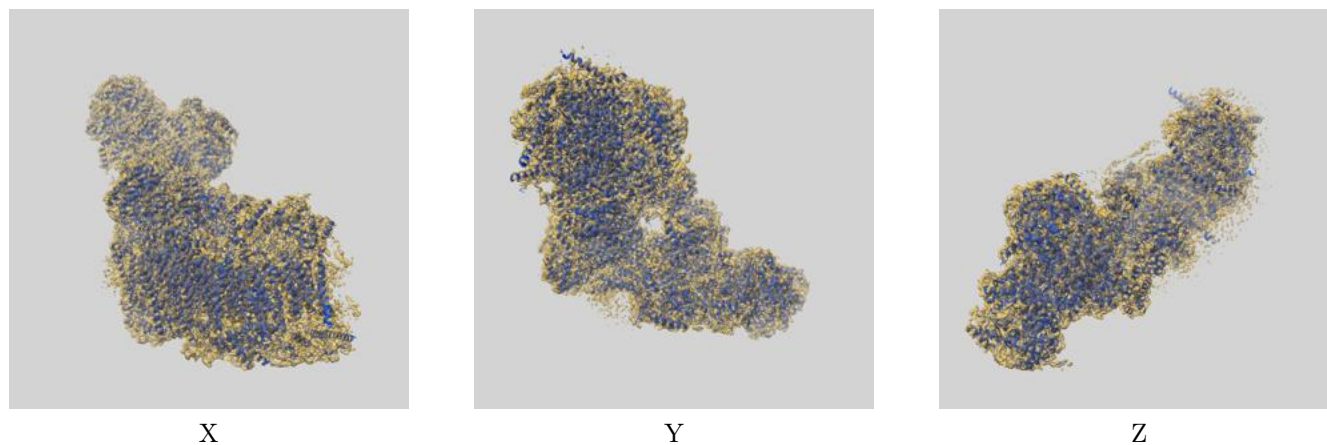
## 8 Fourier-Shell correlation

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-32232 and PDB model 7W00. Per-residue inclusion information can be found in section 3 on page 20.

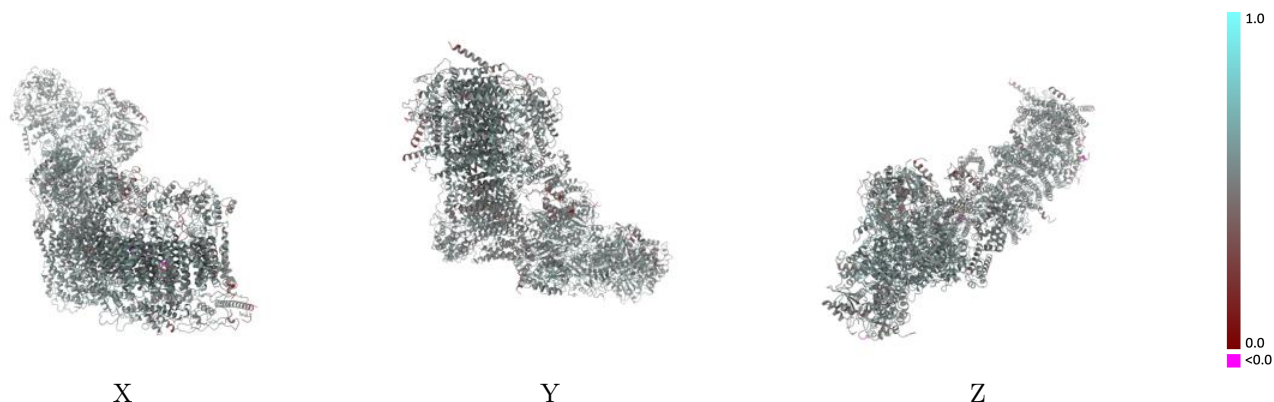
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0204 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.

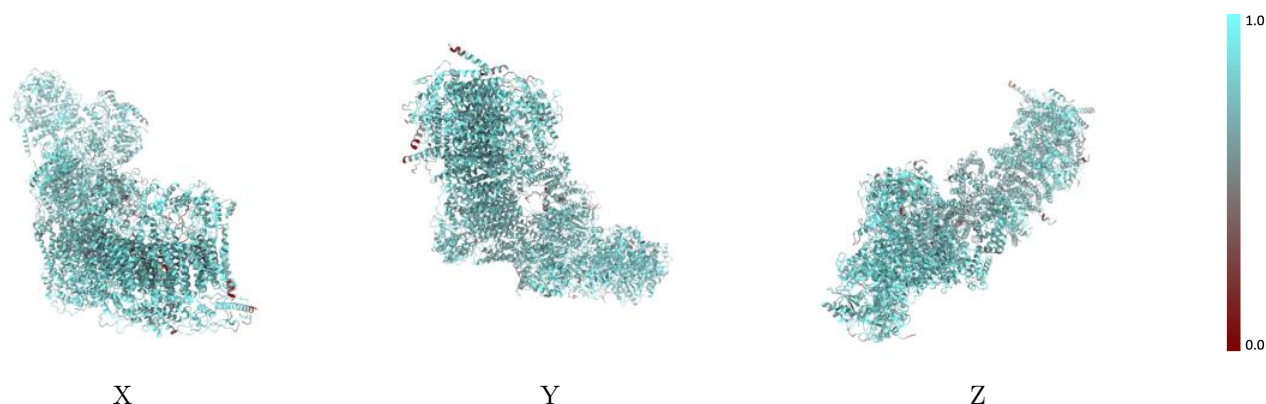


## 9.2 Q-score mapped to coordinate model [i](#)



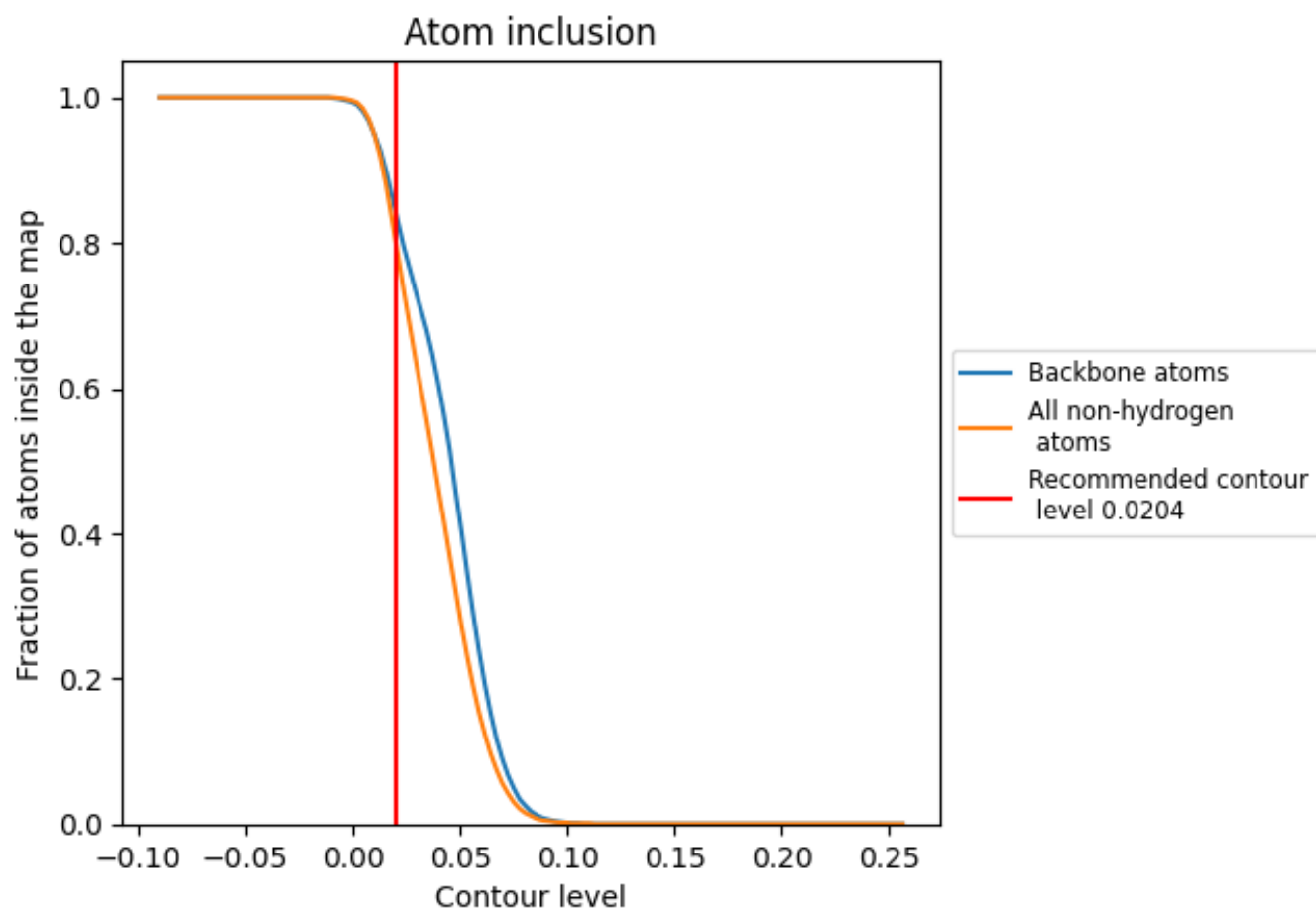
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0204).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% 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 (0.0204) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7940	 0.5190
A	 0.8060	 0.5150
B	 0.8750	 0.5500
C	 0.8280	 0.5390
E	 0.7760	 0.5180
F	 0.7430	 0.4770
G	 0.6310	 0.4170
H	 0.7900	 0.5050
I	 0.7750	 0.5290
J	 0.7770	 0.5140
K	 0.7940	 0.5110
L	 0.7960	 0.5270
M	 0.8260	 0.5290
N	 0.7490	 0.5180
O	 0.7770	 0.5040
P	 0.8510	 0.5490
Q	 0.8380	 0.5420
S	 0.8480	 0.5290
T	 0.7940	 0.5360
U	 0.7920	 0.5120
V	 0.6590	 0.4780
W	 0.8130	 0.5260
X	 0.7430	 0.4880
Y	 0.7580	 0.4820
Z	 0.6670	 0.4490
a	 0.8070	 0.5390
b	 0.7190	 0.4870
c	 0.8040	 0.5260
d	 0.7820	 0.5060
e	 0.7500	 0.5020
f	 0.7530	 0.4940
g	 0.8220	 0.5300
h	 0.8010	 0.5270
i	 0.8300	 0.5360
j	 0.6940	 0.4960



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Chain	Atom inclusion	Q-score
k	 0.7560	 0.5150
l	 0.7960	 0.5260
m	 0.7490	 0.4970
n	 0.7000	 0.4940
o	 0.7610	 0.5180
p	 0.8070	 0.5170
r	 0.8140	 0.5360
s	 0.8130	 0.5220
u	 0.8200	 0.5260
v	 0.7540	 0.4850
w	 0.7840	 0.5110