



wwPDB EM Validation Summary Report ⓘ

Jul 16, 2022 – 07:14 am BST

PDB ID : 7R0W
EMDB ID : EMD-14224
Title : 2.8 Angstrom cryo-EM structure of the dimeric cytochrome b6f-PetP complex from *Synechocystis* sp. PCC 6803 with natively bound lipids and plastoquinone molecules
Authors : Farmer, D.F.; Proctor, M.S.; Malone, L.A.; Swainsbury, D.P.K.; Hawkings, F.R.; Hitchcock, A.; Johnson, M.P.
Deposited on : 2022-02-02
Resolution : 2.80 Å (reported)
Based on initial model : 7PPW

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.dev8
Mogul : 1.8.4, 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)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

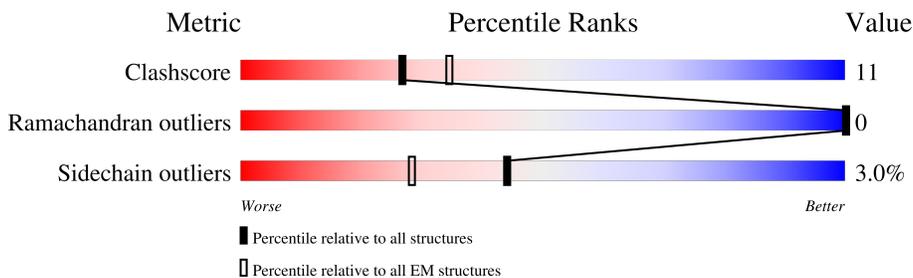
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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)
Clashscore	158937	4297
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 ≥ 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	V	65	6% 51% 43% 5% .
1	X	65	. 54% 40% 5% .
2	A	222	82% 18%
2	I	222	86% 14%
3	B	160	. 82% 16% ..
3	J	160	. 82% 18% .
4	C	328	8% 68% 17% 15%
4	K	328	8% 66% 18% . 15%

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Mol	Chain	Length	Quality of chain
5	E	32	
5	M	32	
6	F	36	
6	N	36	
7	G	38	
7	O	38	
8	H	29	
8	P	29	
9	D	192	
9	L	192	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
14	CLA	B	302	X	-	-	-
14	CLA	J	202	X	-	-	-
16	LMG	N	101	X	-	-	-
17	6PL	H	101	X	-	-	-
17	6PL	P	101	X	-	-	-
19	FES	D	201	-	-	X	-
19	FES	L	202	-	-	X	-

2 Entry composition [i](#)

There are 22 unique types of molecules in this entry. The entry contains 16830 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 Uncharacterized protein Cp097, conserved in cyanobacteria.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	X	64	Total	C	N	O	S	0	0
			500	320	85	94	1		
1	V	64	Total	C	N	O	S	0	0
			500	320	85	94	1		

- Molecule 2 is a protein called Cytochrome b6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	I	222	Total	C	N	O	S	0	0
			1769	1175	283	299	12		
2	A	222	Total	C	N	O	S	0	0
			1769	1175	283	299	12		

- Molecule 3 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	J	159	Total	C	N	O	S	0	0
			1223	820	190	206	7		
3	B	159	Total	C	N	O	S	0	0
			1223	820	190	206	7		

- Molecule 4 is a protein called Cytochrome f.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	K	279	Total	C	N	O	S	0	0
			2115	1356	352	402	5		
4	C	279	Total	C	N	O	S	0	0
			2115	1356	352	402	5		

- Molecule 5 is a protein called Cytochrome B6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	32	Total	C	N	O	S	0	0
			238	165	36	36	1		
5	E	32	Total	C	N	O	S	0	0
			238	165	36	36	1		

- Molecule 6 is a protein called Cytochrome b6-f complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	34	Total	C	N	O	S	0	0
			248	165	38	42	3		
6	F	34	Total	C	N	O	S	0	0
			248	165	38	42	3		

- Molecule 7 is a protein called Cytochrome b6-f complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	32	Total	C	N	O	S	0	0
			242	166	37	38	1		
7	G	32	Total	C	N	O	S	0	0
			242	166	37	38	1		

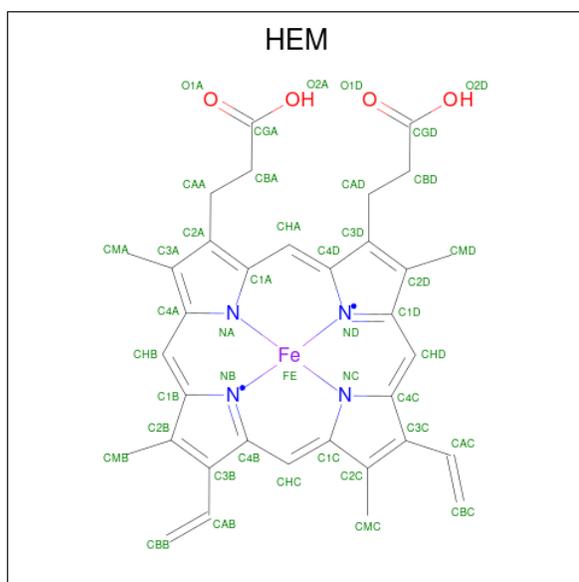
- Molecule 8 is a protein called Cytochrome b6-f complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	29	Total	C	N	O	S	0	0
			234	159	36	37	2		
8	H	29	Total	C	N	O	S	0	0
			234	159	36	37	2		

- Molecule 9 is a protein called Rieske domain, PetC.

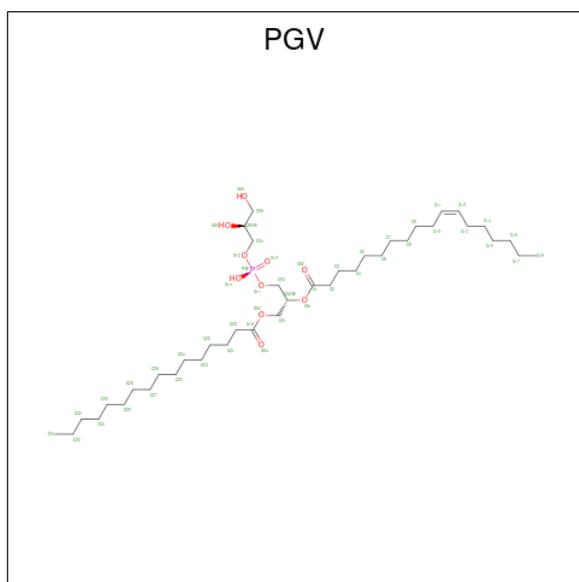
Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	169	Total	C	N	O	S	0	0
			1256	795	215	240	6		
9	L	169	Total	C	N	O	S	0	0
			1256	795	215	240	6		

- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄) (labeled as "Ligand of Interest" by depositor).



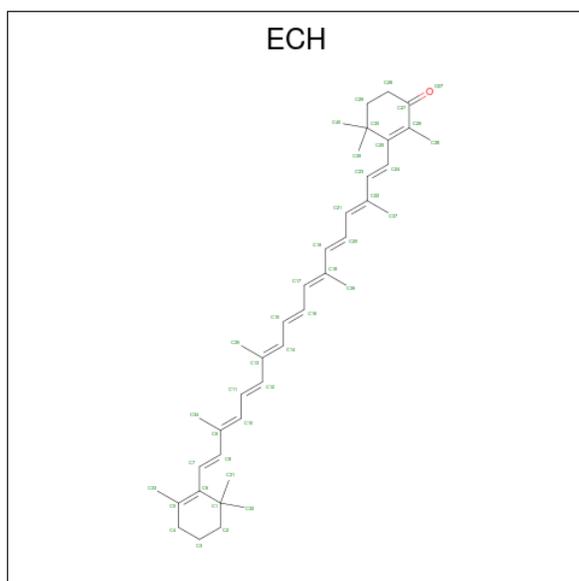
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Fe	N	O	
10	I	1	Total	C	Fe	N	O	0
			129	102	3	12	12	
10	I	1	Total	C	Fe	N	O	0
			129	102	3	12	12	
10	I	1	Total	C	Fe	N	O	0
			129	102	3	12	12	
10	A	1	Total	C	Fe	N	O	0
			86	68	2	8	8	
10	A	1	Total	C	Fe	N	O	0
			86	68	2	8	8	
10	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 11 is (1R)-2-{{[[(2S)-2,3-DIHYDROXYPROPYL]OXY]}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: C₄₀H₇₇O₁₀P).



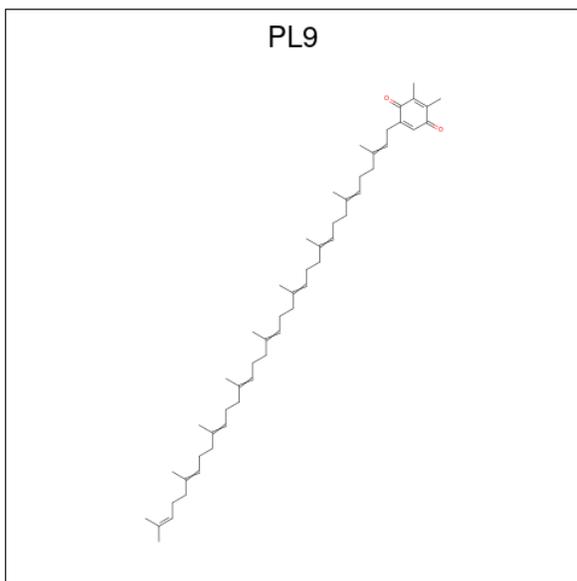
Mol	Chain	Residues	Atoms			AltConf	
			Total	C	O		P
11	I	1	39	28	10	1	0
11	J	1	41	30	10	1	0
11	B	1	51	40	10	1	0
11	C	1	47	36	10	1	0

- Molecule 12 is beta,beta-caroten-4-one (three-letter code: ECH) (formula: $C_{40}H_{54}O$).



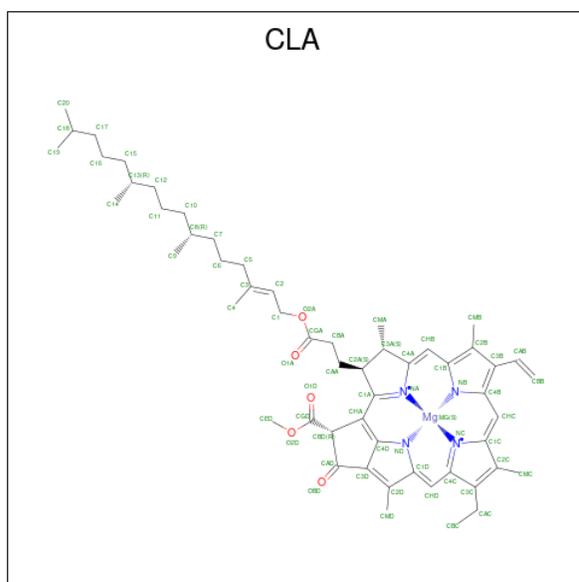
Mol	Chain	Residues	Atoms			AltConf
12	I	1	Total	C	O	0
			41	40	1	
12	A	1	Total	C	O	0
			41	40	1	

- Molecule 13 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (three-letter code: PL9) (formula: $C_{53}H_{80}O_2$).



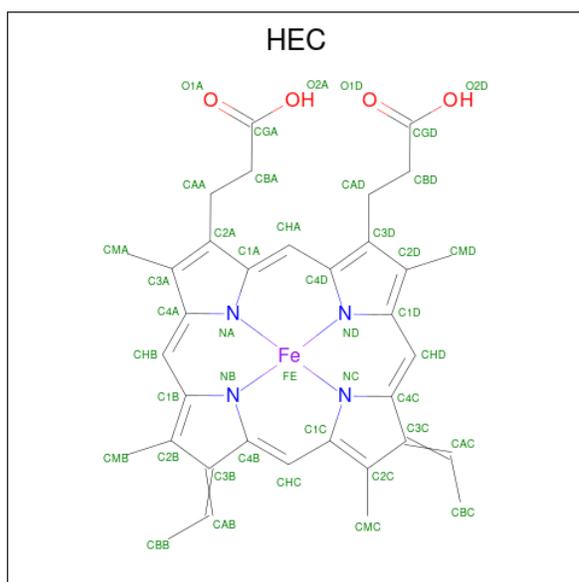
Mol	Chain	Residues	Atoms			AltConf
13	J	1	Total	C	O	0
			55	53	2	
13	A	1	Total	C	O	0
			55	53	2	

- Molecule 14 is CHLOROPHYLL A (three-letter code: CLA) (formula: $C_{55}H_{72}MgN_4O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	Mg	N		O
14	J	1	65	55	1	4	5	0
14	B	1	65	55	1	4	5	0

- Molecule 15 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



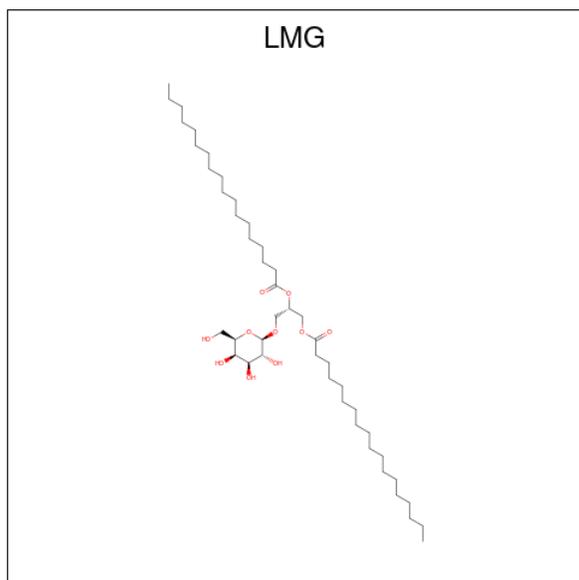
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	Fe	N		O
15	K	1	43	34	1	4	4	0

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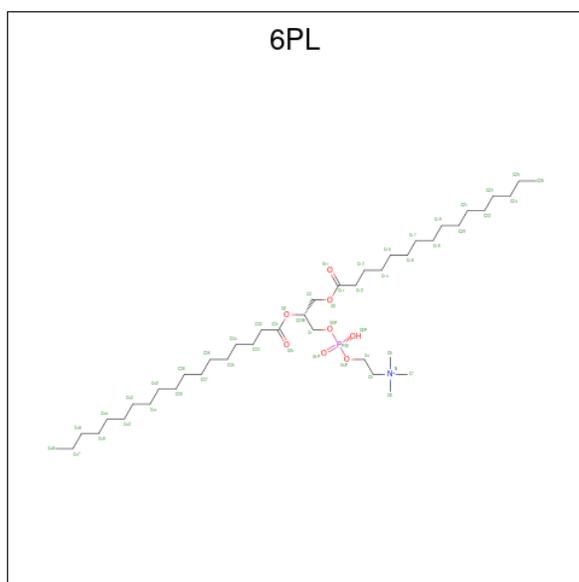
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	Fe	N		O
15	C	1	43	34	1	4	4	0

- Molecule 16 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (three-letter code: LMG) (formula: $C_{45}H_{86}O_{10}$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
16	N	1	55	45	10	0

- Molecule 17 is (4S,7R)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSAN-1-AMINIUM 4-OXIDE (three-letter code: 6PL) (formula: $C_{42}H_{85}NO_8P$).



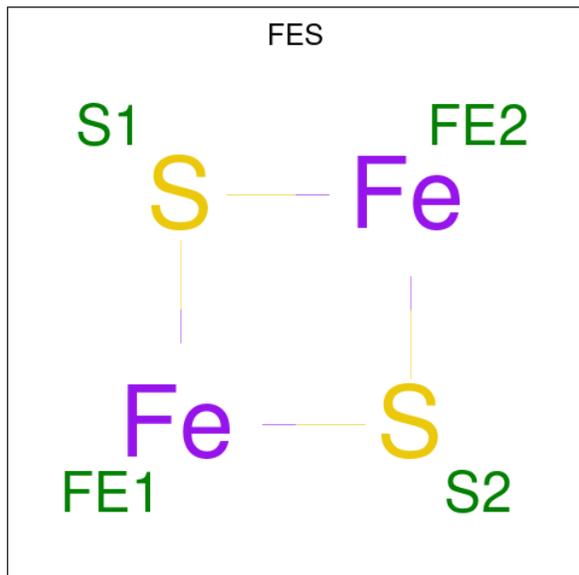
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
17	P	1	51	41	1	8	1	0
17	H	1	52	42	1	8	1	0

- Molecule 18 is (1S,8E)-1-{[(2S)-1-hydroxy-3-{(1S)-1-hydroxypentadecyl]oxy}propan-2-yl]oxy}heptadec-8-en-1-ol (three-letter code: 2WA) (formula: C₃₅H₇₀O₅).



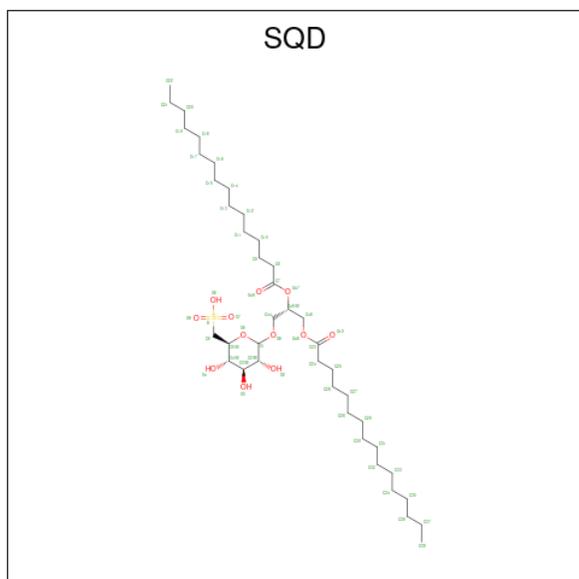
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
18	B	1	40	35	5	0

- Molecule 19 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



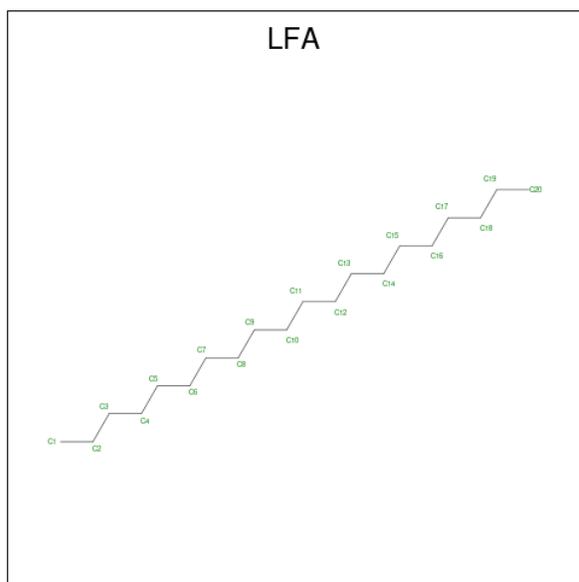
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
19	D	1	4	2	2	0
19	L	1	4	2	2	0

- Molecule 20 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: C₄₁H₇₈O₁₂S).



Mol	Chain	Residues	Atoms				AltConf
20	D	1	Total	C	O	S	0
			54	41	12	1	
20	L	1	Total	C	O	S	0
			54	41	12	1	

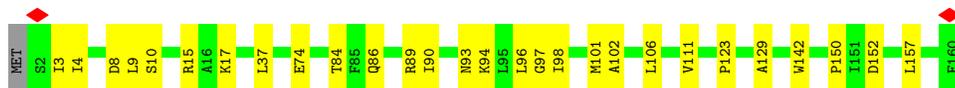
- Molecule 21 is EICOSANE (three-letter code: LFA) (formula: $C_{20}H_{42}$).



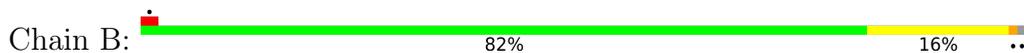
Mol	Chain	Residues	Atoms		AltConf
21	E	1	Total	C	0
			20	20	

- Molecule 22 is water.

Mol	Chain	Residues	Atoms		AltConf
22	I	1	Total	O	0
			1	1	
22	B	1	Total	O	0
			1	1	



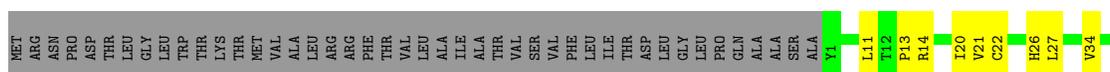
• Molecule 3: Cytochrome b6-f complex subunit 4



• Molecule 4: Cytochrome f



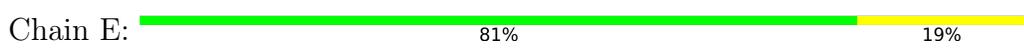
• Molecule 4: Cytochrome f



• Molecule 5: Cytochrome B6

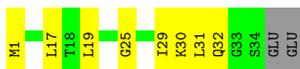


• Molecule 5: Cytochrome B6





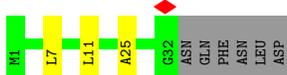
- Molecule 6: Cytochrome b6-f complex subunit 7



- Molecule 6: Cytochrome b6-f complex subunit 7



- Molecule 7: Cytochrome b6-f complex subunit 5



- Molecule 7: Cytochrome b6-f complex subunit 5



- Molecule 8: Cytochrome b6-f complex subunit 8

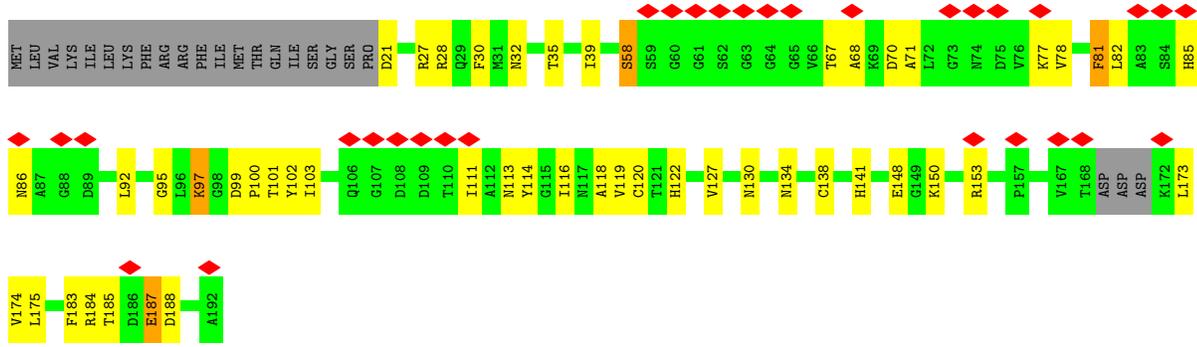


- Molecule 8: Cytochrome b6-f complex subunit 8

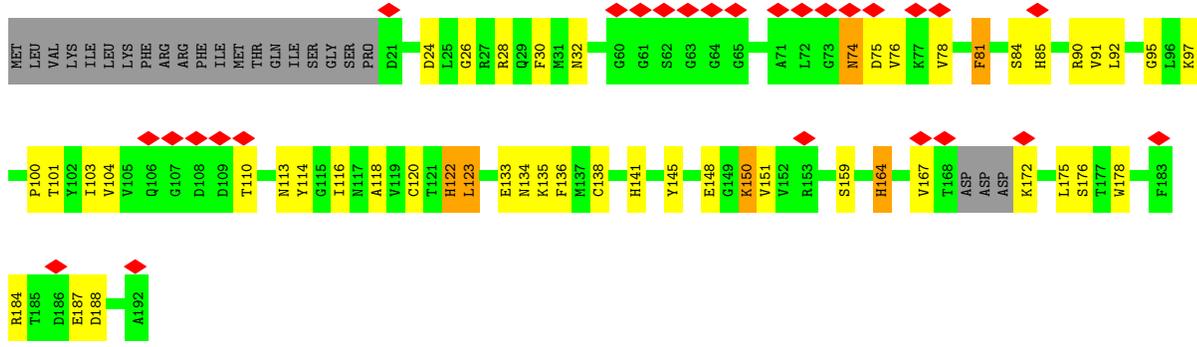


- Molecule 9: Rieske domain, PetC





• Molecule 9: Rieske domain, PetC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	152860	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)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.986	Depositor
Minimum map value	-0.270	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.132	Depositor
Map size (Å)	211.99998, 211.99998, 211.99998	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: FES, ECH, LFA, PGV, 6PL, CLA, 2WA, PL9, SQD, HEM, LMG, HEC

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	V	0.32	0/507	0.67	0/679
1	X	0.37	0/507	0.71	0/679
2	A	0.29	0/1821	0.49	0/2480
2	I	0.30	0/1821	0.50	0/2480
3	B	0.28	0/1261	0.48	0/1721
3	J	0.28	0/1261	0.50	0/1721
4	C	0.27	0/2158	0.51	0/2935
4	K	0.28	0/2158	0.50	0/2935
5	E	0.34	0/242	0.57	0/326
5	M	0.33	0/242	0.59	0/326
6	F	0.33	0/251	0.51	0/337
6	N	0.38	0/251	0.60	0/337
7	G	0.32	0/246	0.52	0/334
7	O	0.30	0/246	0.52	0/334
8	H	0.30	0/241	0.47	0/329
8	P	0.32	0/241	0.54	0/329
9	D	0.28	0/1286	0.56	1/1757 (0.1%)
9	L	0.28	0/1286	0.54	0/1757
All	All	0.29	0/16026	0.53	1/21796 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D	97	LYS	CA-CB-CG	5.42	125.34	113.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V	500	0	513	29	0
1	X	500	0	513	26	0
2	A	1769	0	1799	33	0
2	I	1769	0	1799	24	0
3	B	1223	0	1268	19	0
3	J	1223	0	1268	22	0
4	C	2115	0	2133	38	0
4	K	2115	0	2133	48	0
5	E	238	0	264	7	0
5	M	238	0	264	10	0
6	F	248	0	268	6	0
6	N	248	0	268	8	0
7	G	242	0	274	9	0
7	O	242	0	274	2	0
8	H	234	0	240	6	0
8	P	234	0	240	9	0
9	D	1256	0	1220	44	0
9	L	1256	0	1219	38	0
10	A	86	0	60	5	0
10	B	43	0	30	3	0
10	I	129	0	90	12	0
11	B	51	0	76	0	0
11	C	47	0	65	0	0
11	I	39	0	47	0	0
11	J	41	0	50	2	0
12	A	41	0	54	5	0
12	I	41	0	54	2	0
13	A	55	0	80	0	0
13	J	55	0	80	4	0
14	B	65	0	71	4	0
14	J	65	0	71	2	0
15	C	43	0	32	6	0
15	K	43	0	31	6	0
16	N	55	0	85	0	0
17	H	52	0	83	1	0
17	P	51	0	78	1	0
18	B	40	0	70	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	D	4	0	0	2	0
19	L	4	0	0	2	0
20	D	54	0	78	3	0
20	L	54	0	78	2	0
21	E	20	0	42	0	0
22	B	1	0	0	0	0
22	I	1	0	0	0	0
All	All	16830	0	17362	375	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 11.

The worst 5 of 375 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)
2:I:42:CYS:SG	10:I:302:HEM:HAB	1.91	1.11
2:I:42:CYS:SG	10:I:302:HEM:CAB	2.40	1.09
2:I:42:CYS:HG	10:I:302:HEM:CAB	1.65	1.09
2:A:42:CYS:SG	10:B:301:HEM:HAB	2.02	1.00
1:V:52:ARG:O	1:V:52:ARG:NH1	2.05	0.90

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	V	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
1	X	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
2	A	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
2	I	220/222 (99%)	213 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
3	J	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
4	C	275/328 (84%)	266 (97%)	9 (3%)	0	100	100
4	K	275/328 (84%)	258 (94%)	17 (6%)	0	100	100
5	E	30/32 (94%)	29 (97%)	1 (3%)	0	100	100
5	M	30/32 (94%)	29 (97%)	1 (3%)	0	100	100
6	F	32/36 (89%)	32 (100%)	0	0	100	100
6	N	32/36 (89%)	32 (100%)	0	0	100	100
7	G	30/38 (79%)	30 (100%)	0	0	100	100
7	O	30/38 (79%)	30 (100%)	0	0	100	100
8	H	27/29 (93%)	27 (100%)	0	0	100	100
8	P	27/29 (93%)	27 (100%)	0	0	100	100
9	D	165/192 (86%)	160 (97%)	5 (3%)	0	100	100
9	L	165/192 (86%)	159 (96%)	6 (4%)	0	100	100
All	All	1996/2204 (91%)	1932 (97%)	64 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	V	54/55 (98%)	49 (91%)	5 (9%)	9	26
1	X	54/55 (98%)	51 (94%)	3 (6%)	21	51
2	A	192/192 (100%)	189 (98%)	3 (2%)	62	88
2	I	192/192 (100%)	190 (99%)	2 (1%)	76	93
3	B	127/128 (99%)	125 (98%)	2 (2%)	62	88
3	J	127/128 (99%)	125 (98%)	2 (2%)	62	88
4	C	226/266 (85%)	225 (100%)	1 (0%)	91	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	K	226/266 (85%)	222 (98%)	4 (2%)	59	86
5	E	23/23 (100%)	22 (96%)	1 (4%)	29	62
5	M	23/23 (100%)	22 (96%)	1 (4%)	29	62
6	F	25/27 (93%)	25 (100%)	0	100	100
6	N	25/27 (93%)	25 (100%)	0	100	100
7	G	25/31 (81%)	25 (100%)	0	100	100
7	O	25/31 (81%)	25 (100%)	0	100	100
8	H	26/26 (100%)	23 (88%)	3 (12%)	5	17
8	P	26/26 (100%)	24 (92%)	2 (8%)	13	35
9	D	132/154 (86%)	124 (94%)	8 (6%)	18	48
9	L	132/154 (86%)	120 (91%)	12 (9%)	9	27
All	All	1660/1804 (92%)	1611 (97%)	49 (3%)	44	75

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	11	TYR
9	L	114	TYR
8	H	1	MET
9	L	32	ASN
9	L	122	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
9	D	86	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

27 ligands 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
19	FES	L	202	9	0,4,4	-	-	-		
12	ECH	I	305	-	42,42,42	0.36	0	55,58,58	0.78	2 (3%)
11	PGV	B	304	-	50,50,50	0.49	0	53,56,56	0.63	1 (1%)
10	HEM	I	302	22	41,50,50	1.48	3 (7%)	45,82,82	1.32	5 (11%)
10	HEM	A	301	2	41,50,50	1.47	3 (7%)	45,82,82	1.28	4 (8%)
17	6PL	P	101	-	50,50,51	0.49	0	56,58,59	1.21	4 (7%)
11	PGV	C	301	-	46,46,50	0.51	0	48,52,56	0.55	0
14	CLA	J	202	-	65,73,73	1.51	6 (9%)	76,113,113	1.59	12 (15%)
15	HEC	K	301	4	32,50,50	2.29	4 (12%)	24,82,82	1.39	3 (12%)
13	PL9	A	303	-	55,55,55	0.97	4 (7%)	68,69,69	1.47	7 (10%)
10	HEM	I	303	2	41,50,50	1.46	3 (7%)	45,82,82	1.34	4 (8%)
14	CLA	B	302	-	65,73,73	1.54	6 (9%)	76,113,113	1.45	13 (17%)
18	2WA	B	303	-	39,39,39	0.53	1 (2%)	39,41,41	0.86	3 (7%)
19	FES	D	201	9	0,4,4	-	-	-		
10	HEM	B	301	22	41,50,50	1.47	3 (7%)	45,82,82	1.36	4 (8%)
11	PGV	I	304	-	38,38,50	0.57	0	41,44,56	0.51	0
16	LMG	N	101	-	55,55,55	0.91	1 (1%)	63,63,63	1.58	10 (15%)
20	SQD	D	202	-	53,54,54	1.58	8 (15%)	62,65,65	1.27	5 (8%)
11	PGV	J	203	-	40,40,50	0.56	0	42,46,56	0.80	2 (4%)
17	6PL	H	101	-	51,51,51	0.49	0	57,59,59	1.23	5 (8%)
21	LFA	E	101	-	19,19,19	0.32	0	18,18,18	0.59	0
15	HEC	C	302	4	32,50,50	2.30	3 (9%)	24,82,82	1.40	4 (16%)
12	ECH	A	304	-	42,42,42	0.33	0	55,58,58	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	SQD	L	201	-	53,54,54	1.56	7 (13%)	62,65,65	1.81	10 (16%)
10	HEM	I	301	2	41,50,50	1.46	3 (7%)	45,82,82	1.34	5 (11%)
10	HEM	A	302	2	41,50,50	1.46	3 (7%)	45,82,82	1.34	6 (13%)
13	PL9	J	201	-	55,55,55	0.94	2 (3%)	68,69,69	1.48	11 (16%)

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
19	FES	L	202	9	-	-	0/1/1/1
12	ECH	I	305	-	-	16/29/66/66	0/2/2/2
11	PGV	B	304	-	-	29/55/55/55	-
10	HEM	I	302	22	-	5/12/54/54	-
10	HEM	A	301	2	-	3/12/54/54	-
17	6PL	P	101	-	1/1/5/5	30/54/54/55	-
11	PGV	C	301	-	-	30/51/51/55	-
14	CLA	J	202	-	2/2/15/20	17/37/115/115	-
15	HEC	K	301	4	-	1/10/54/54	-
13	PL9	A	303	-	-	18/53/73/73	0/1/1/1
10	HEM	I	303	2	-	4/12/54/54	-
14	CLA	B	302	-	2/2/15/20	15/37/115/115	-
18	2WA	B	303	-	-	20/41/41/41	-
19	FES	D	201	9	-	-	0/1/1/1
10	HEM	B	301	22	-	7/12/54/54	-
11	PGV	I	304	-	-	21/43/43/55	-
16	LMG	N	101	-	1/1/8/8	19/50/70/70	0/1/1/1
20	SQD	D	202	-	-	35/49/69/69	0/1/1/1
11	PGV	J	203	-	-	33/45/45/55	-
17	6PL	H	101	-	1/1/5/5	26/55/55/55	-
21	LFA	E	101	-	-	8/17/17/17	-
15	HEC	C	302	4	-	3/10/54/54	-
12	ECH	A	304	-	-	10/29/66/66	0/2/2/2
20	SQD	L	201	-	-	25/49/69/69	0/1/1/1
10	HEM	I	301	2	-	4/12/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	HEM	A	302	2	-	5/12/54/54	-
13	PL9	J	201	-	-	28/53/73/73	0/1/1/1

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	302	CLA	C4B-NB	8.13	1.42	1.35
14	J	202	CLA	C4B-NB	7.99	1.42	1.35
15	C	302	HEC	C3C-C2C	-7.09	1.33	1.40
15	K	301	HEC	C3C-C2C	-6.84	1.33	1.40
15	K	301	HEC	C2B-C3B	-6.79	1.33	1.40

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	L	201	SQD	O6-C1-C2	7.55	120.09	108.30
17	P	101	6PL	C1-C2-C3	6.74	127.74	111.79
16	N	101	LMG	O6-C5-C4	6.16	120.88	109.69
13	A	303	PL9	C7-C3-C4	5.71	121.52	116.88
14	J	202	CLA	C4A-NA-C1A	5.43	109.15	106.71

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
14	J	202	CLA	C8
14	J	202	CLA	ND
14	B	302	CLA	C8
14	B	302	CLA	ND
16	N	101	LMG	C5

5 of 412 torsion outliers are listed below:

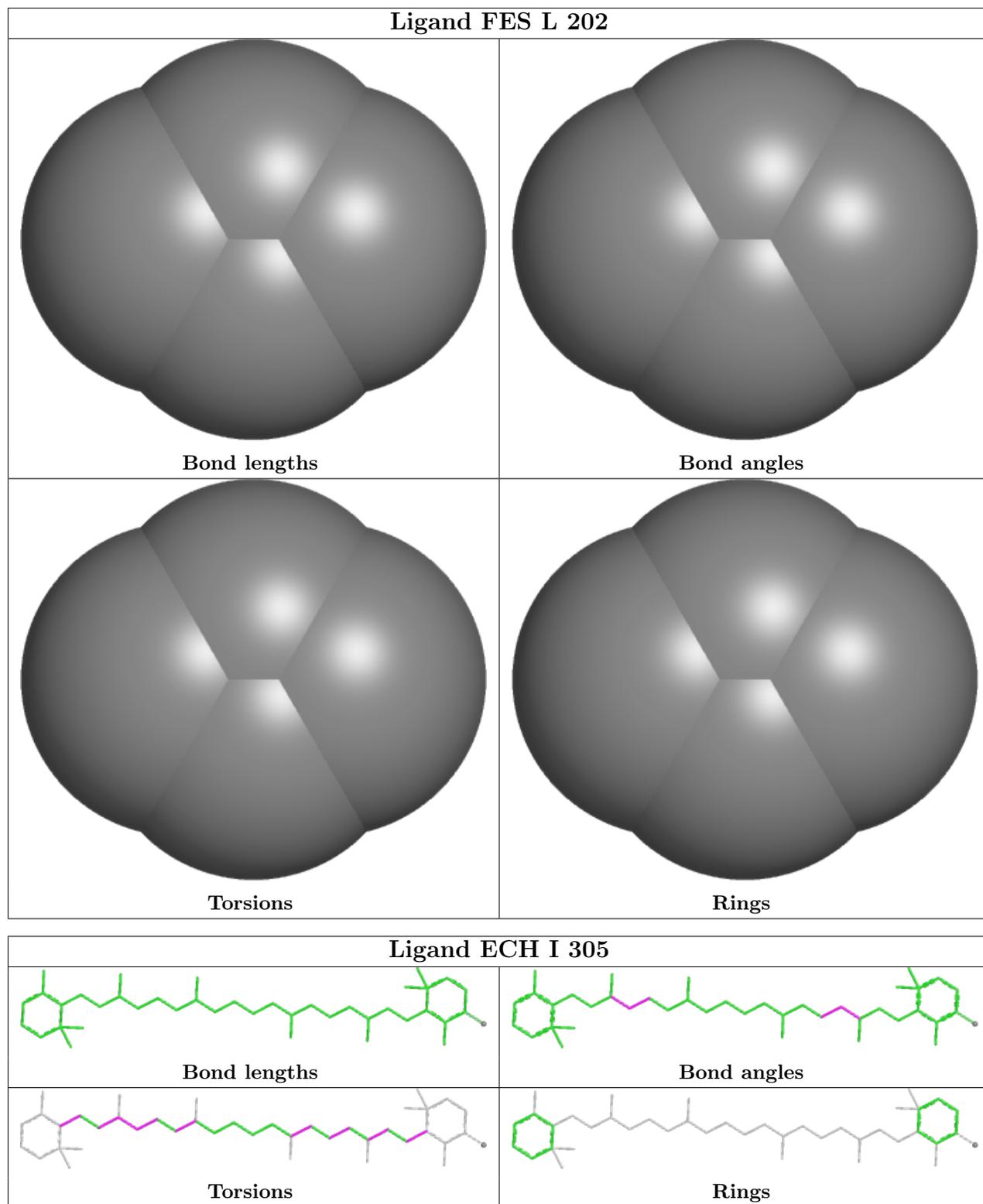
Mol	Chain	Res	Type	Atoms
10	I	302	HEM	C2B-C3B-CAB-CBB
10	I	303	HEM	C1A-C2A-CAA-CBA
10	A	301	HEM	C2A-CAA-CBA-CGA
10	B	301	HEM	C2B-C3B-CAB-CBB
11	I	304	PGV	C03-O11-P-O14

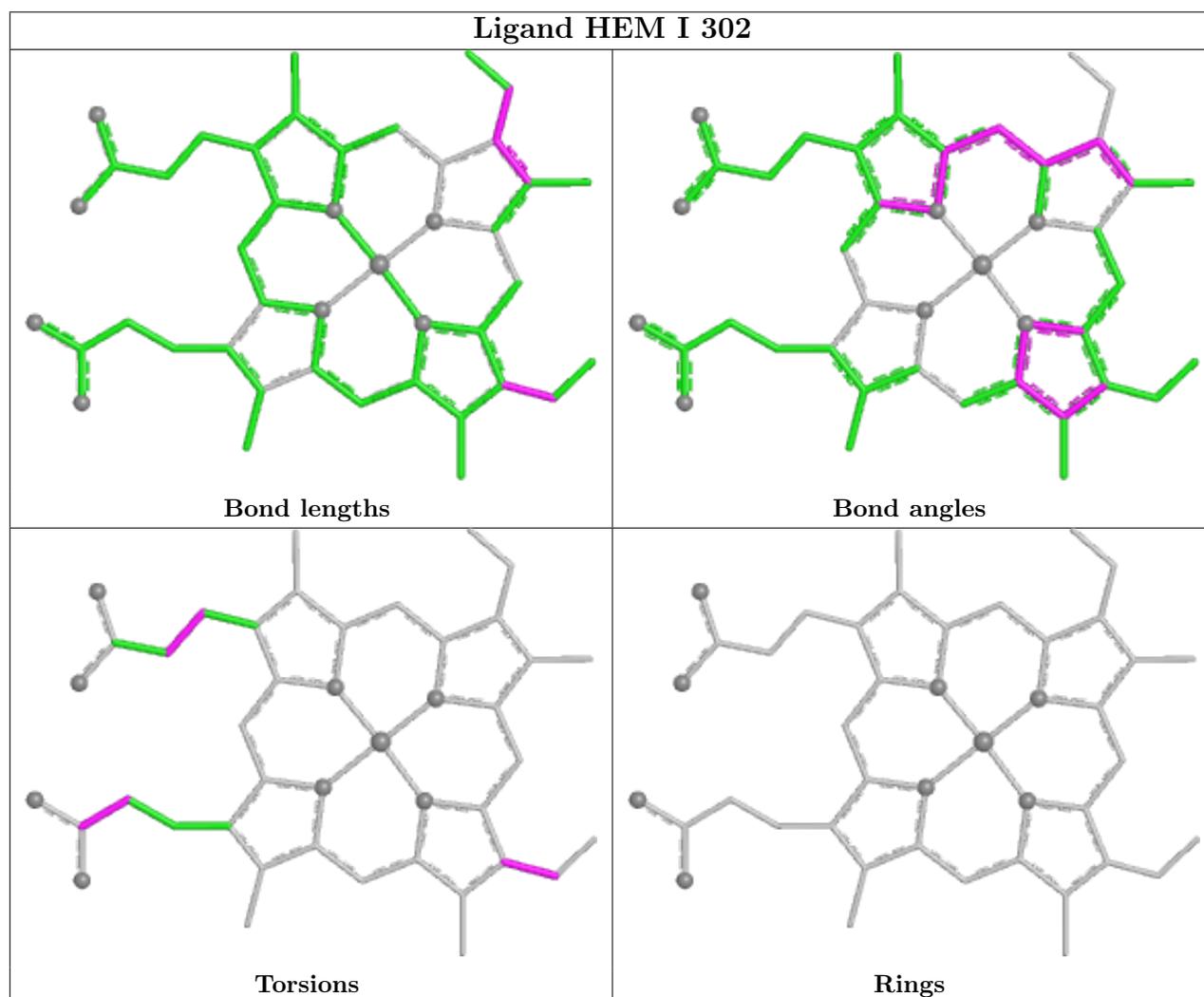
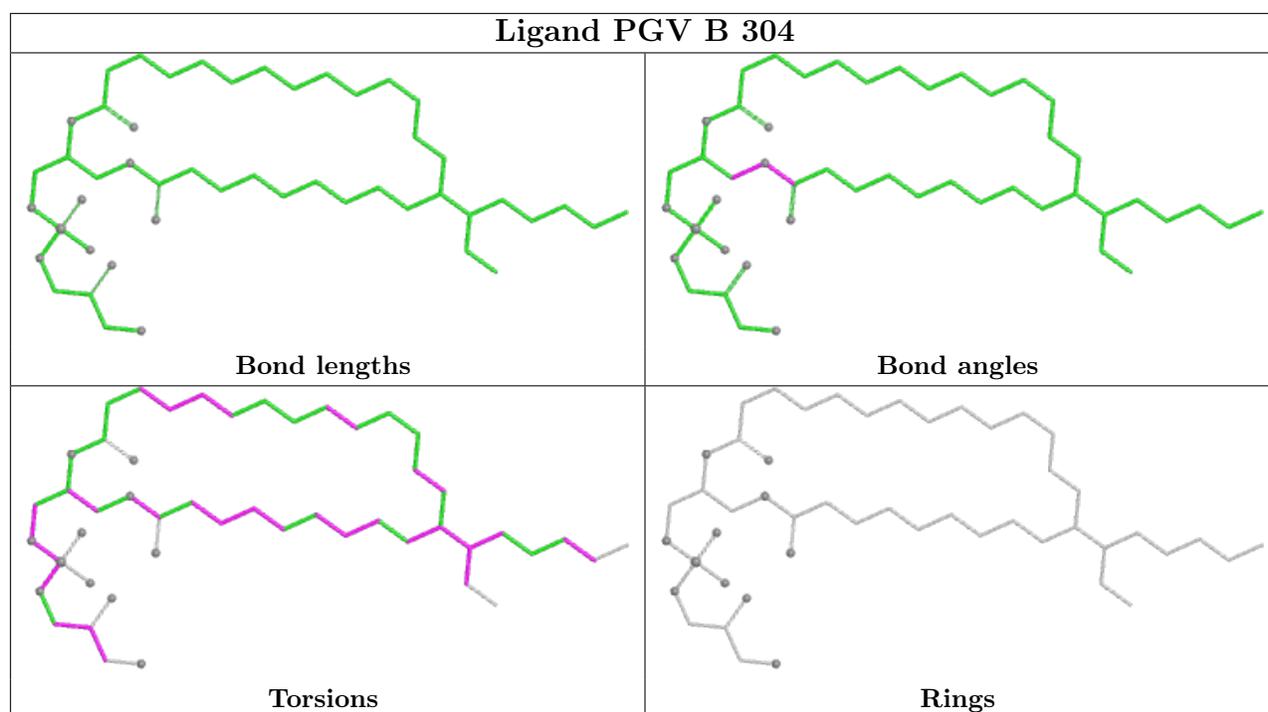
There are no ring outliers.

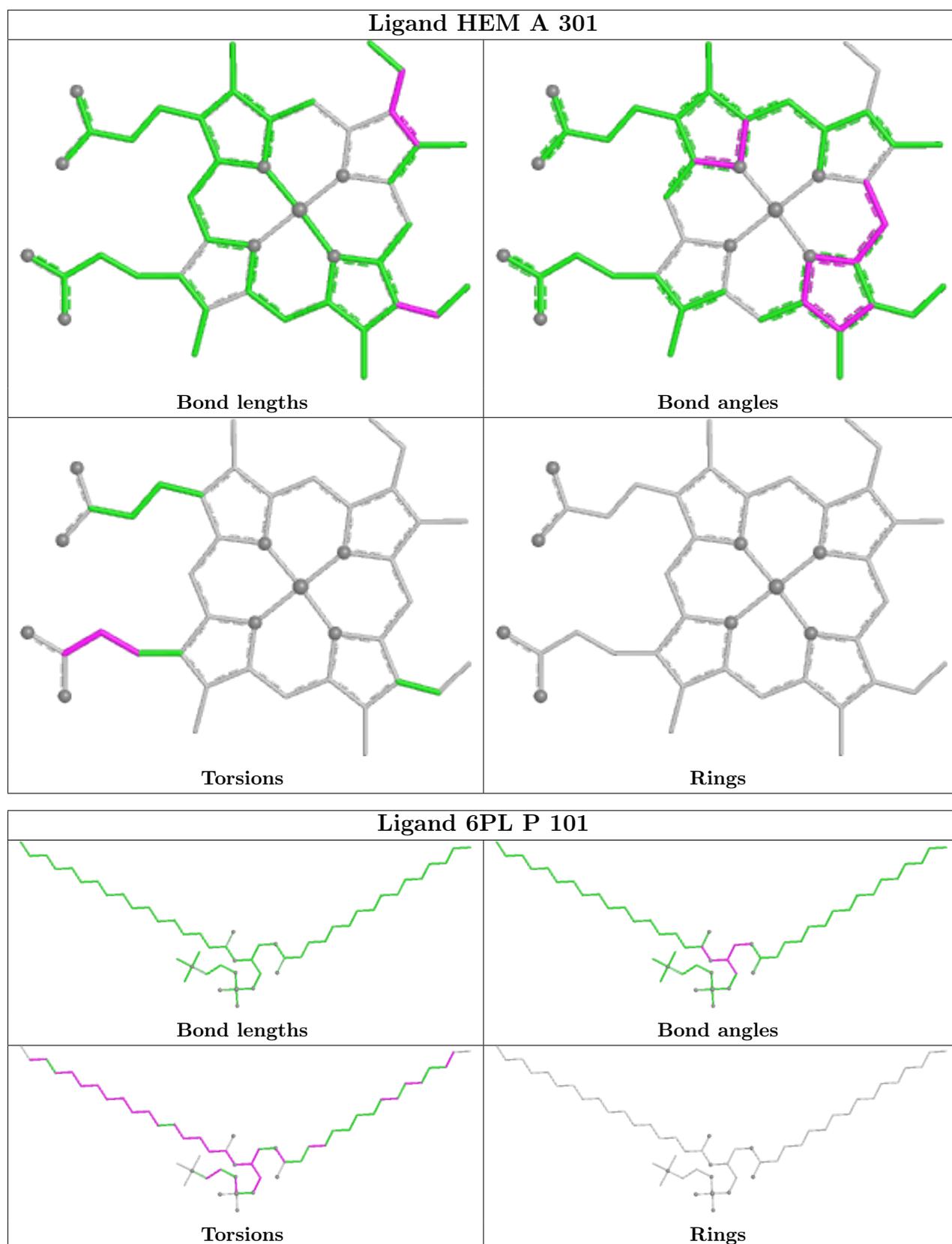
21 monomers are involved in 64 short contacts:

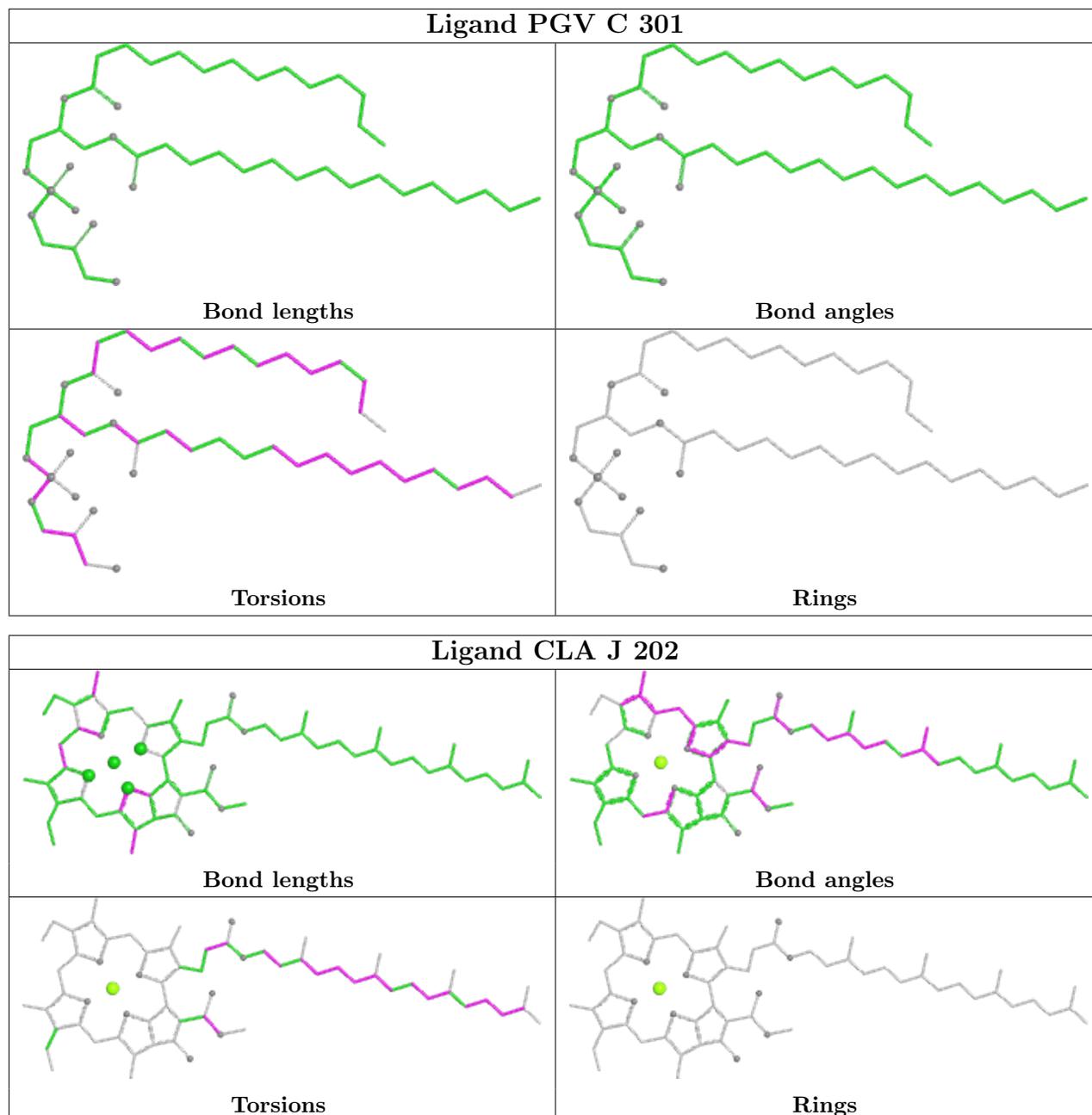
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	L	202	FES	2	0
12	I	305	ECH	2	0
10	I	302	HEM	4	0
10	A	301	HEM	4	0
17	P	101	6PL	1	0
14	J	202	CLA	2	0
15	K	301	HEC	6	0
10	I	303	HEM	5	0
14	B	302	CLA	4	0
18	B	303	2WA	2	0
19	D	201	FES	2	0
10	B	301	HEM	3	0
20	D	202	SQD	3	0
11	J	203	PGV	2	0
17	H	101	6PL	1	0
15	C	302	HEC	6	0
12	A	304	ECH	5	0
20	L	201	SQD	2	0
10	I	301	HEM	3	0
10	A	302	HEM	1	0
13	J	201	PL9	4	0

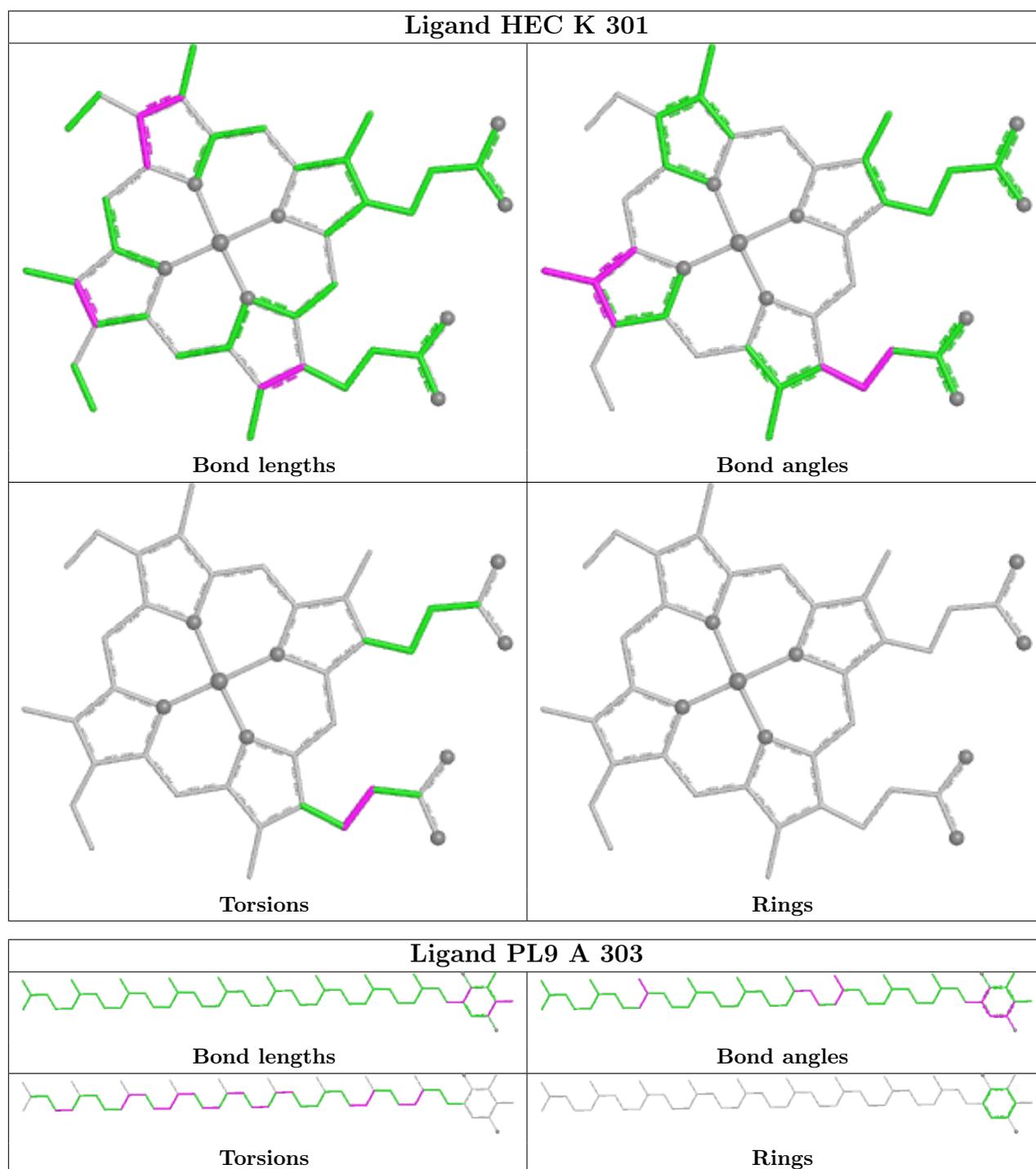
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

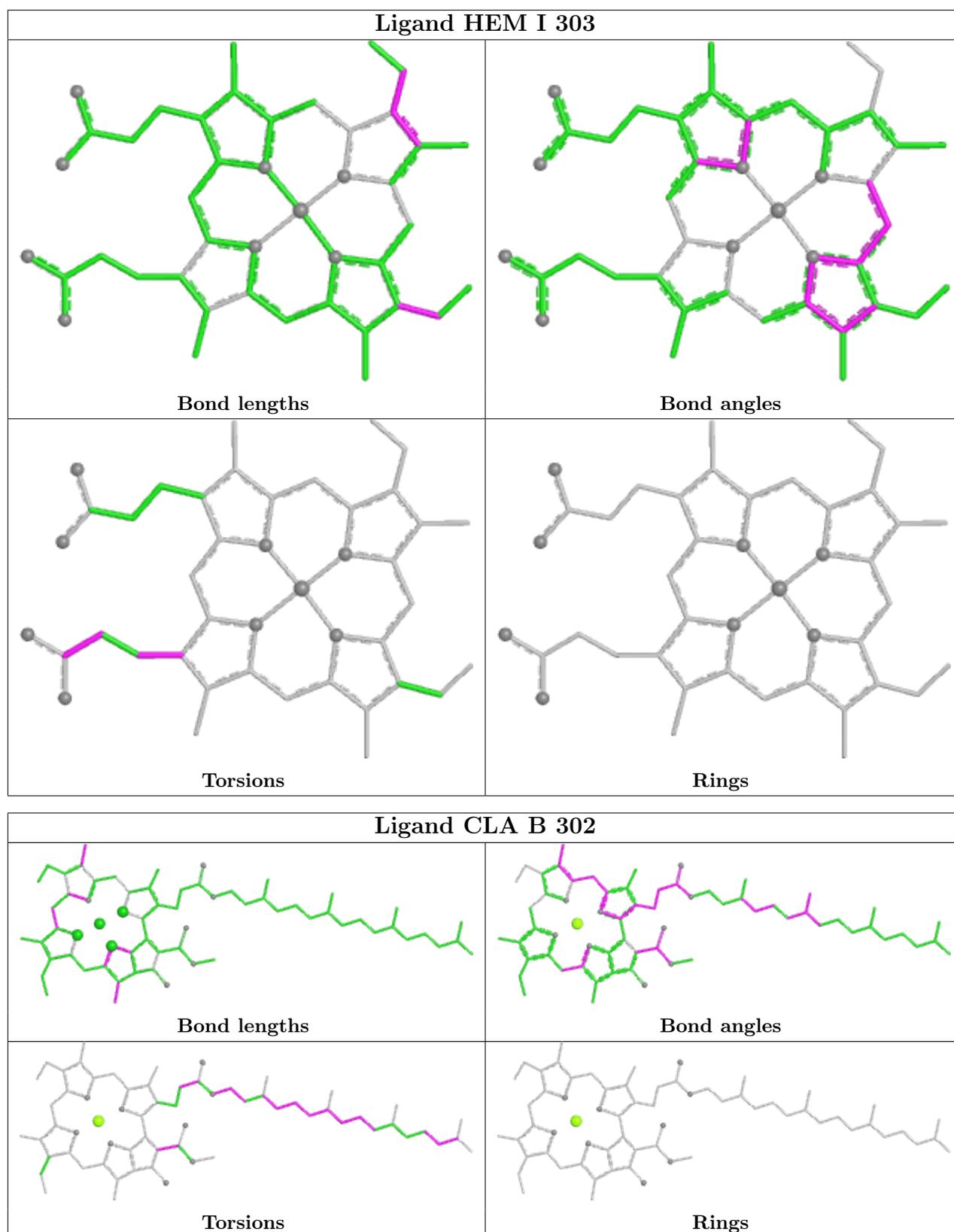


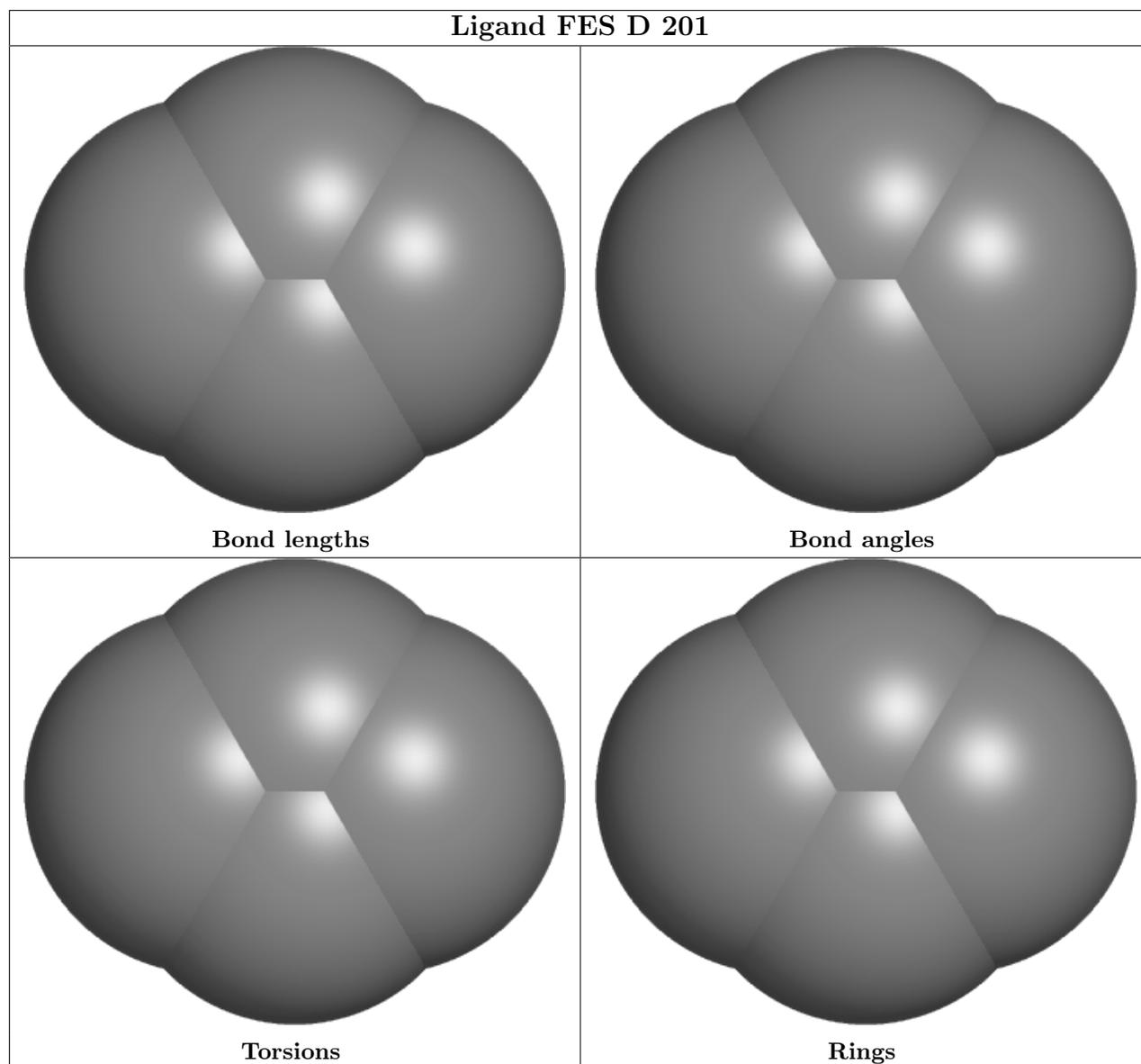
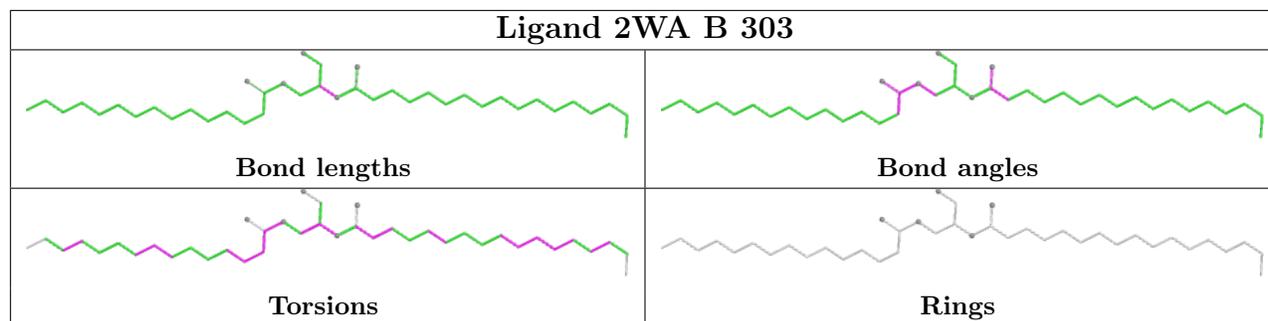


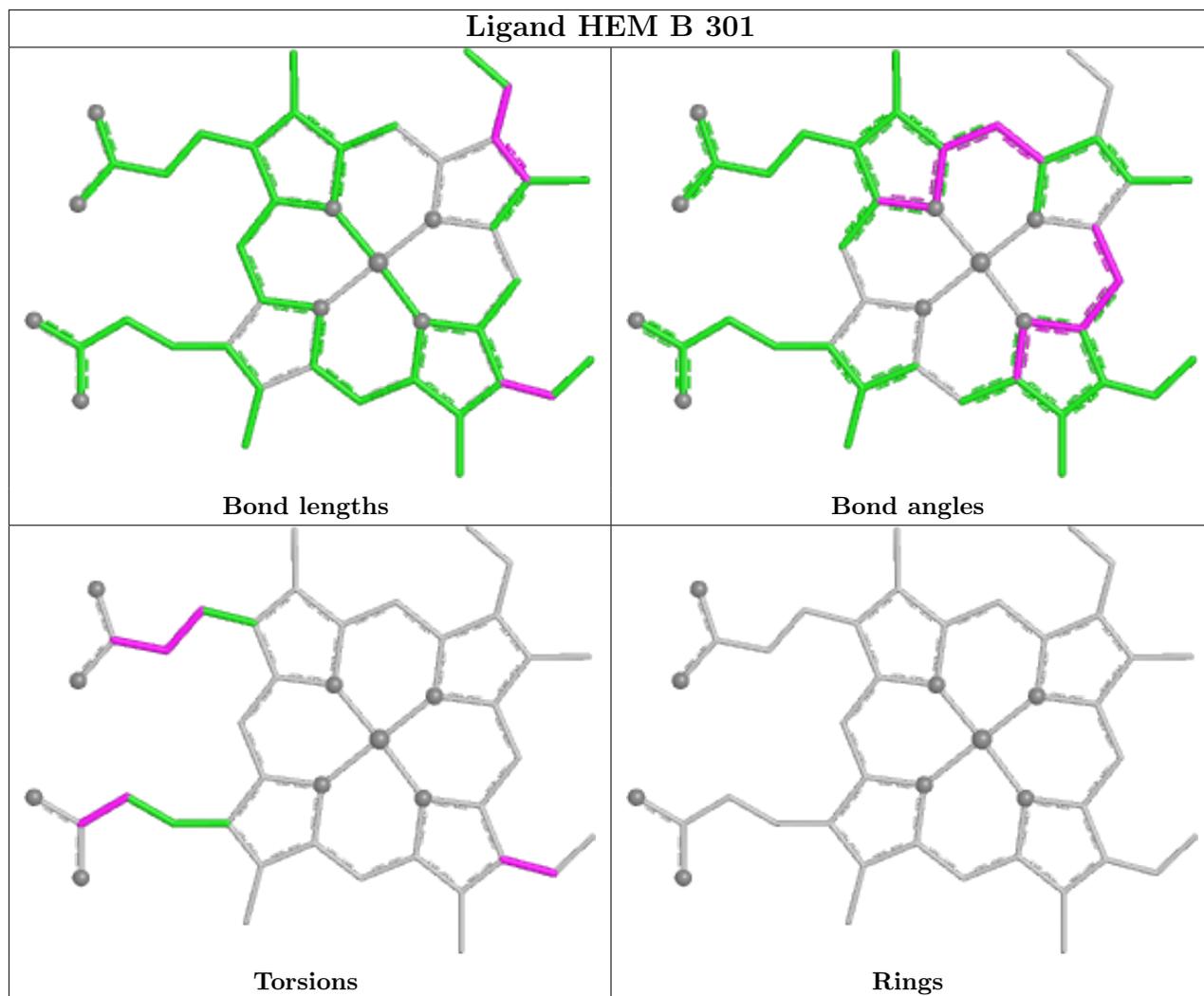


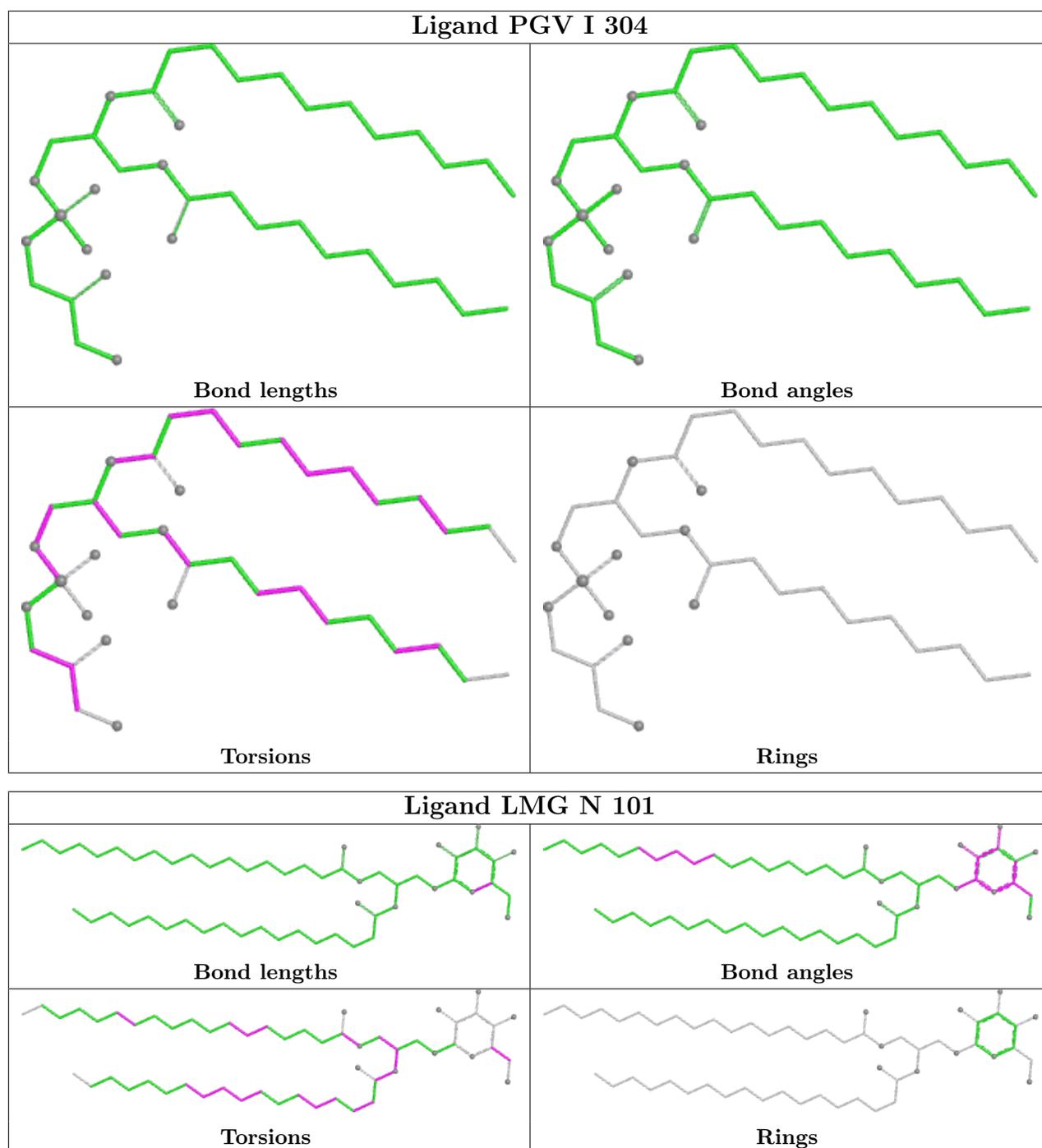


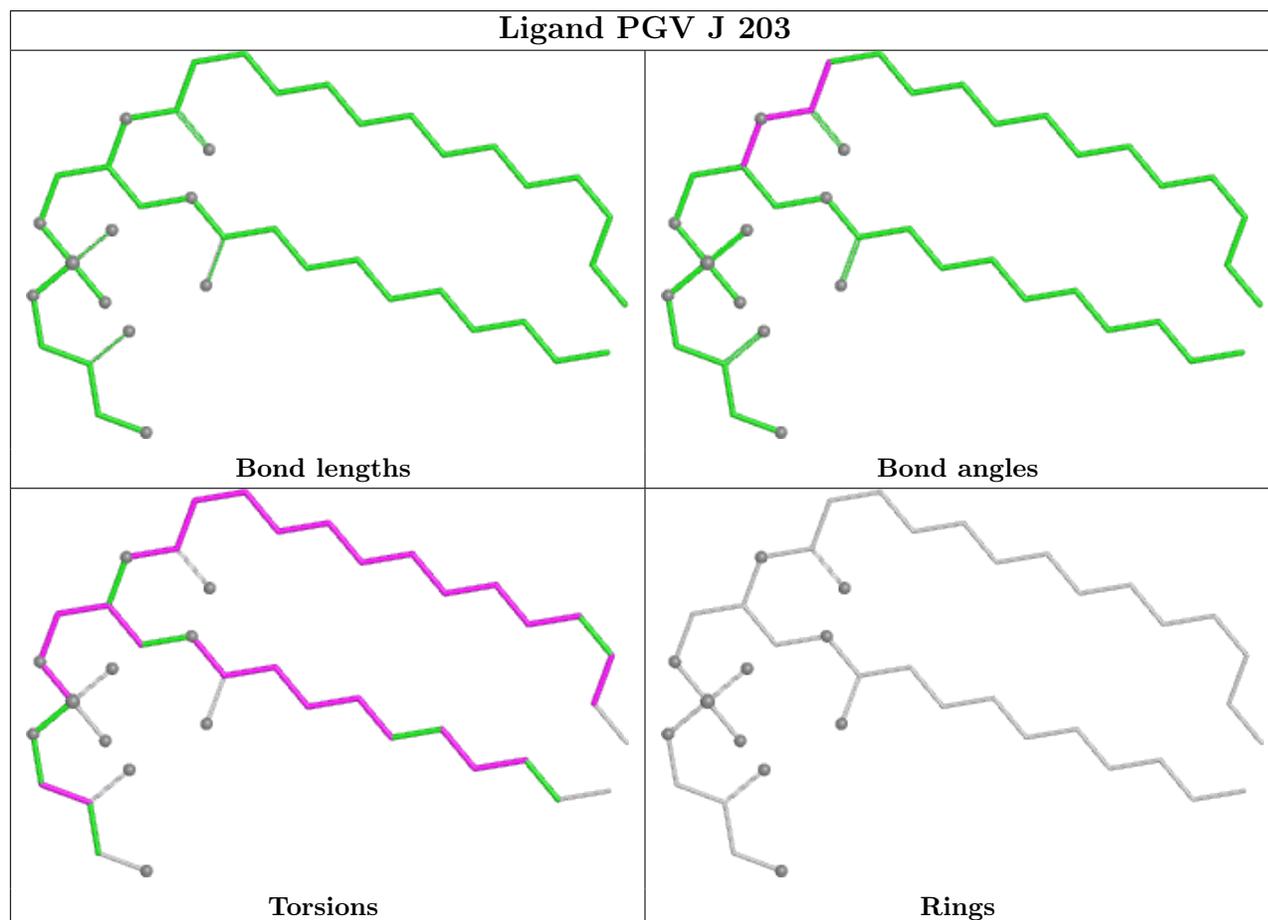
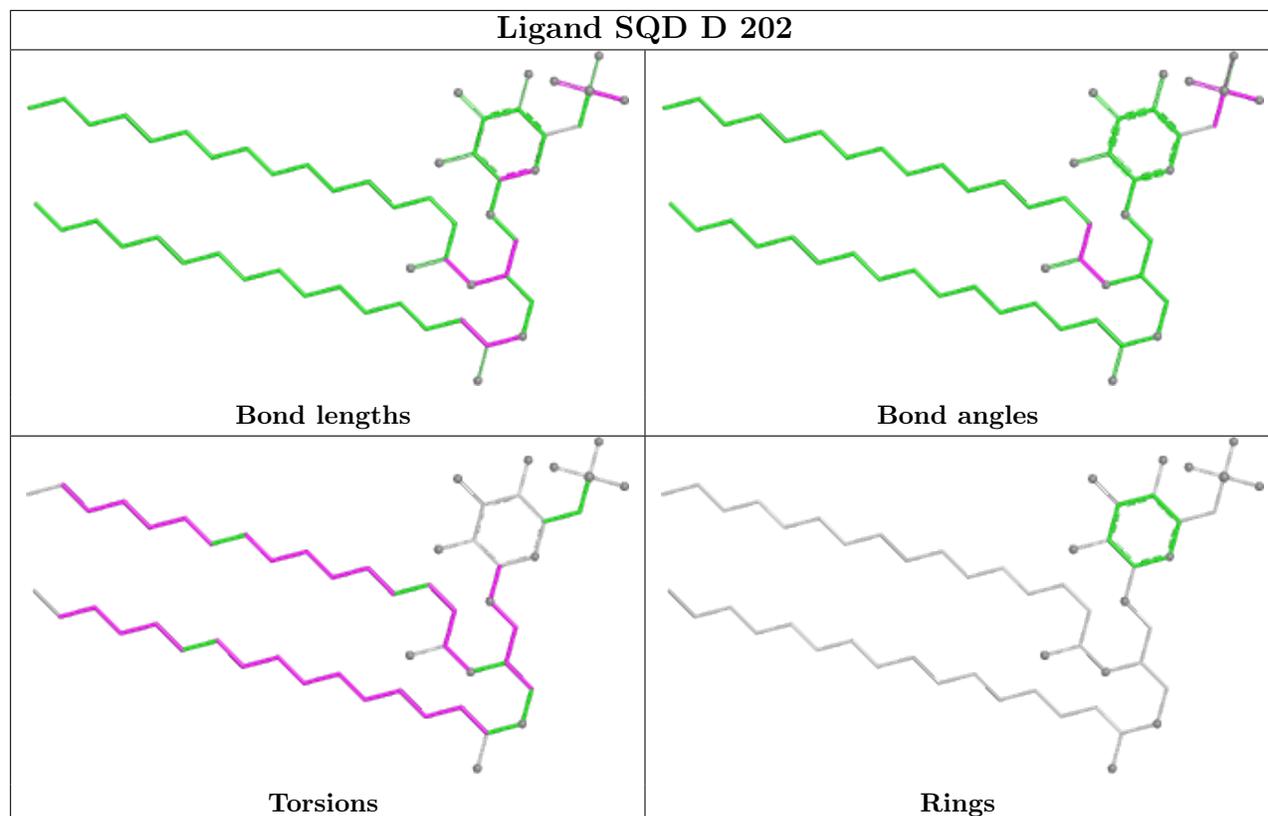


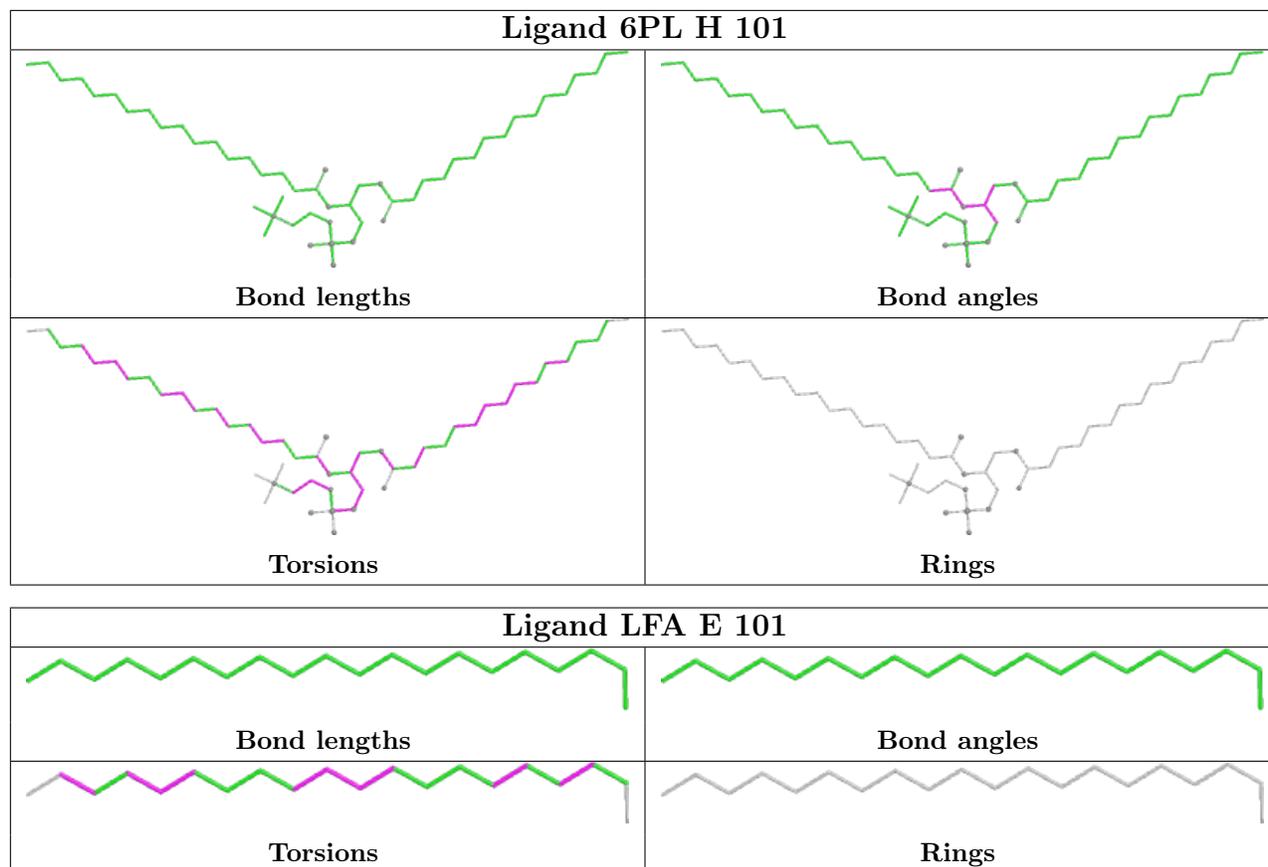


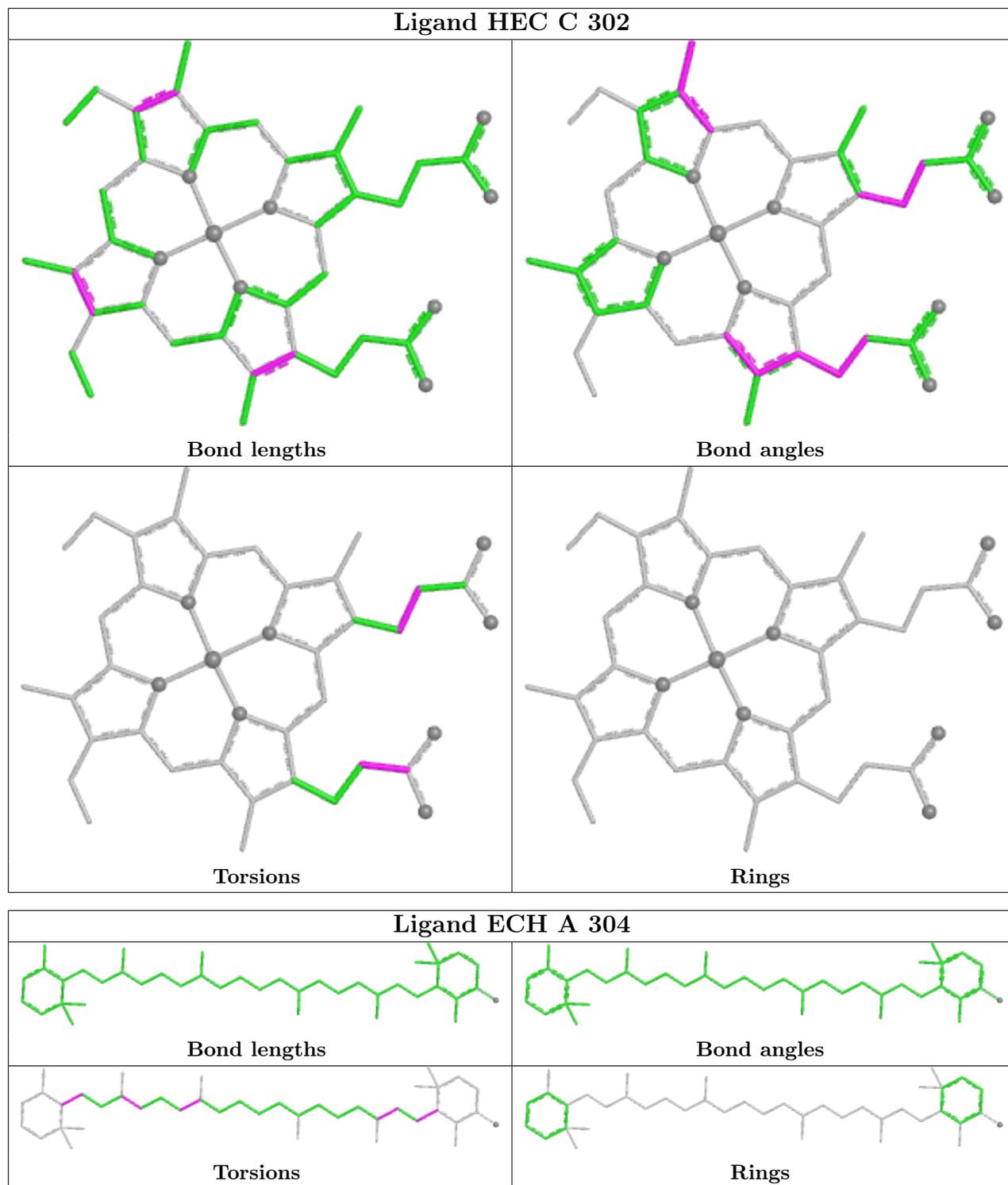


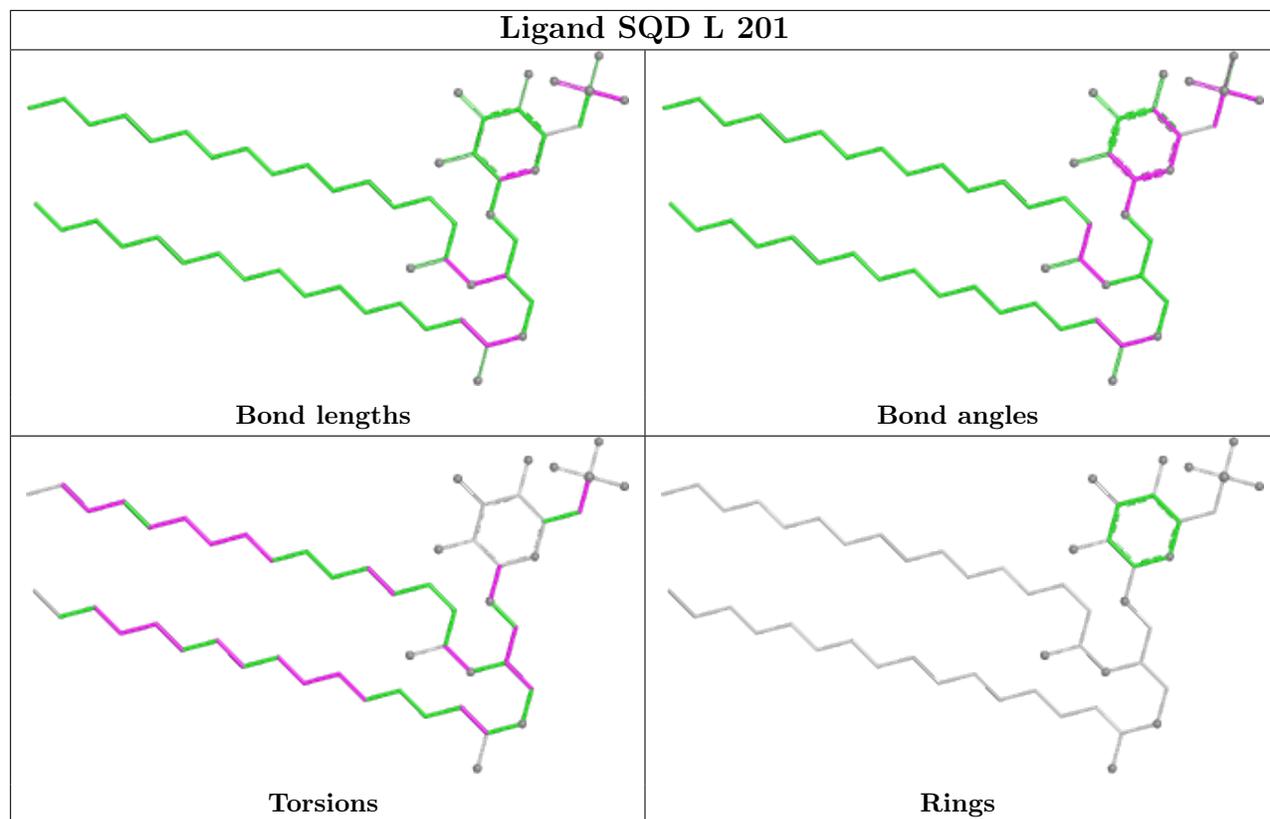


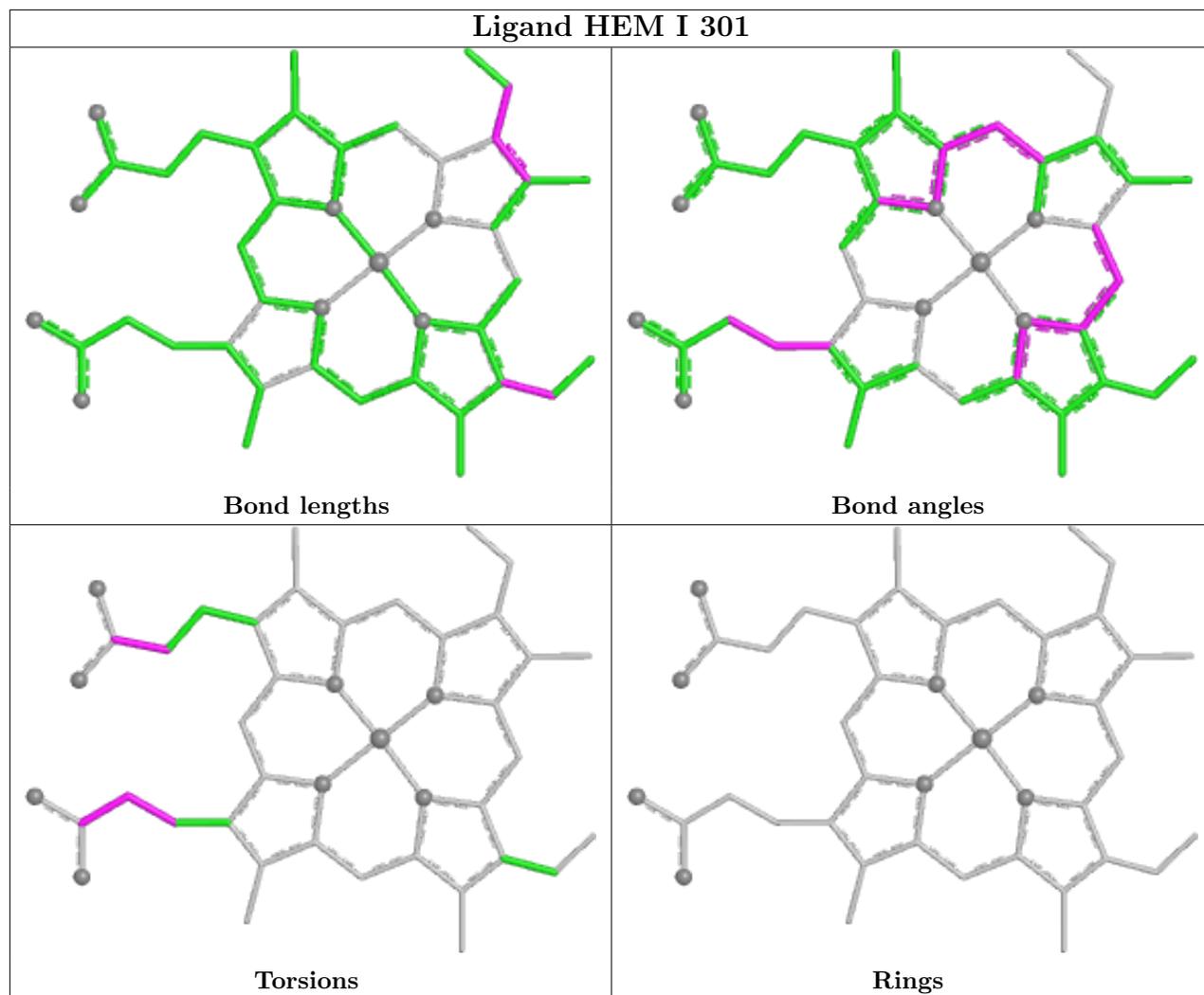


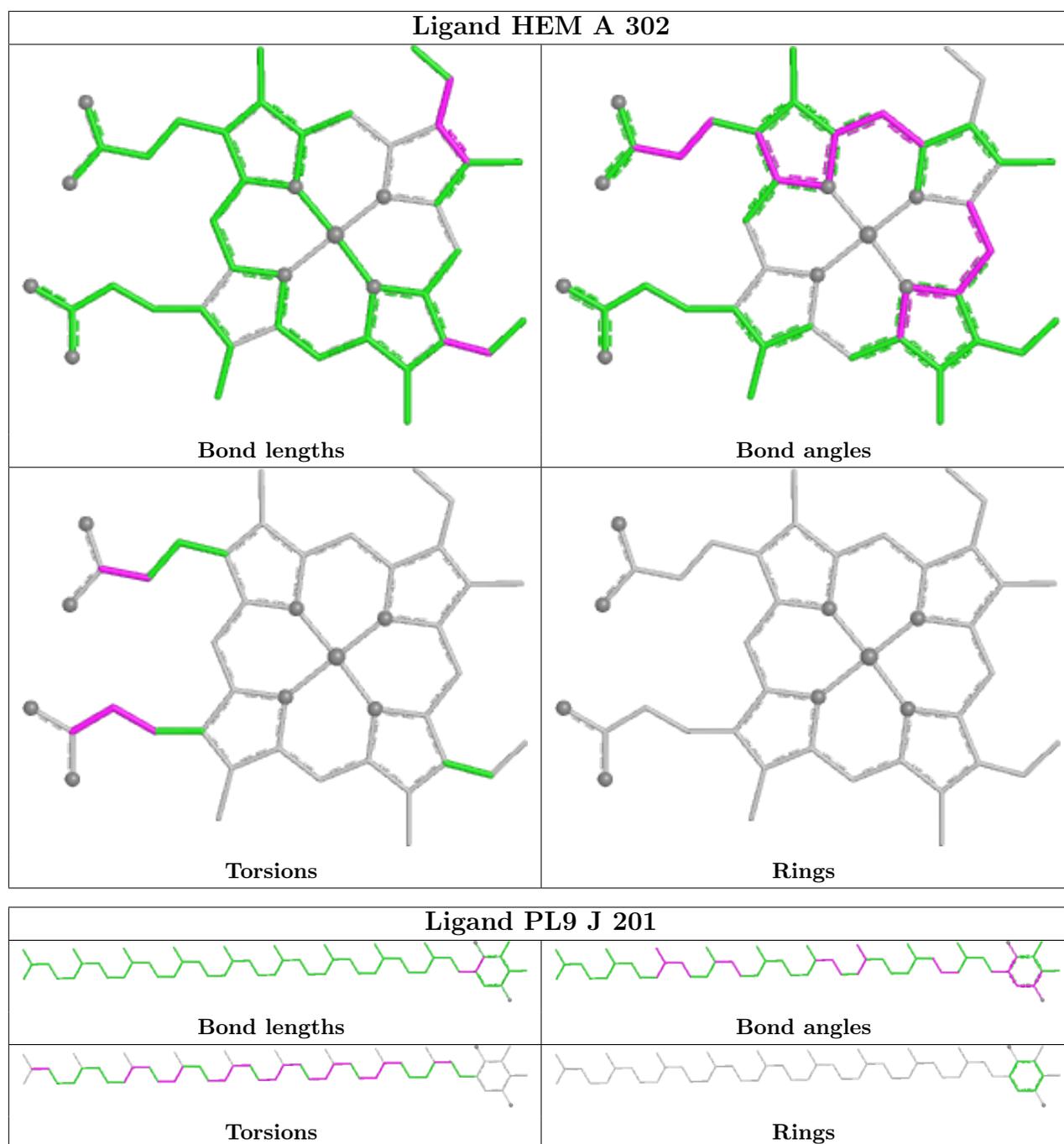












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

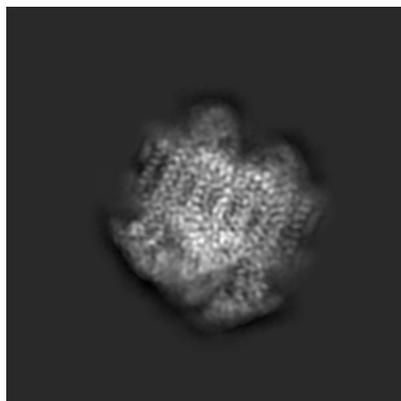
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14224. These allow visual inspection of the internal detail of the map and identification of artifacts.

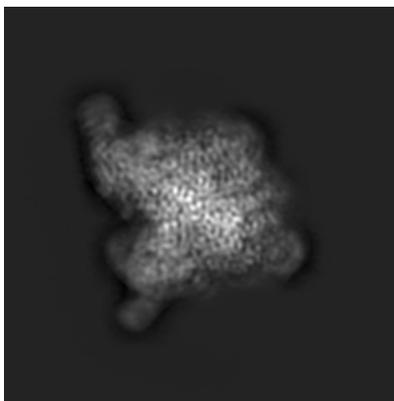
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

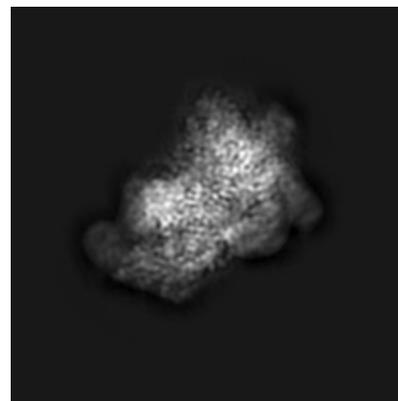
6.1.1 Primary map



X

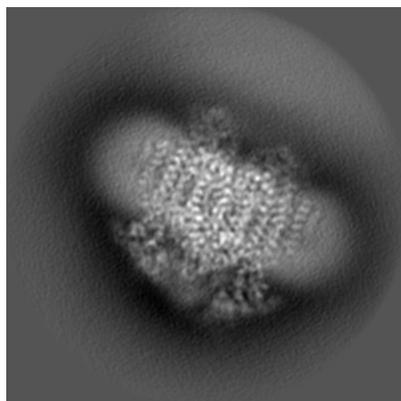


Y

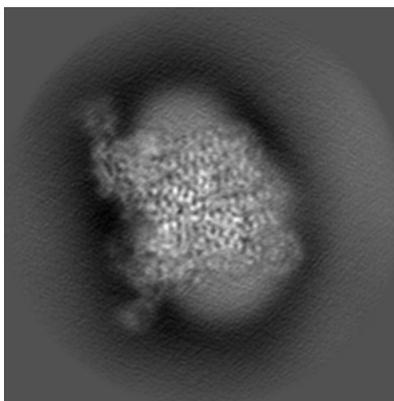


Z

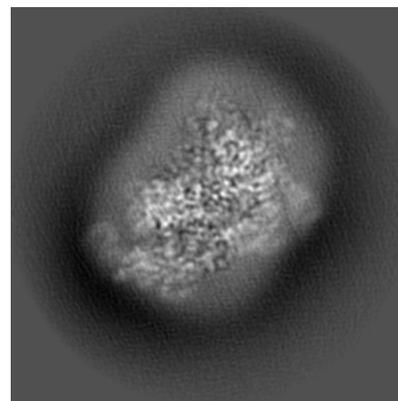
6.1.2 Raw map



X



Y

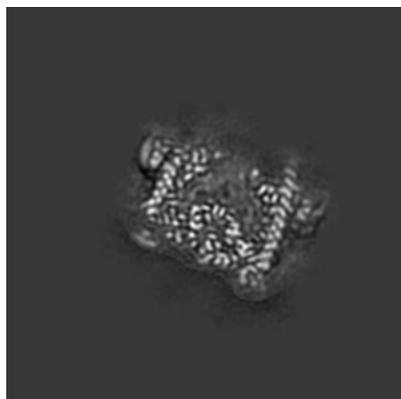


Z

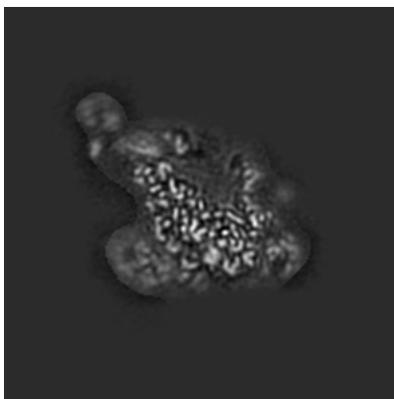
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

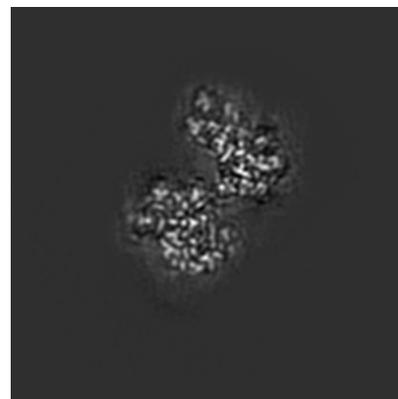
6.2.1 Primary map



X Index: 100

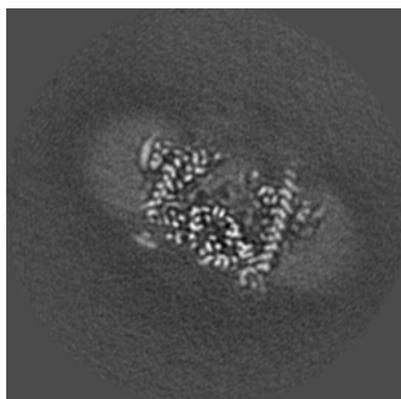


Y Index: 100

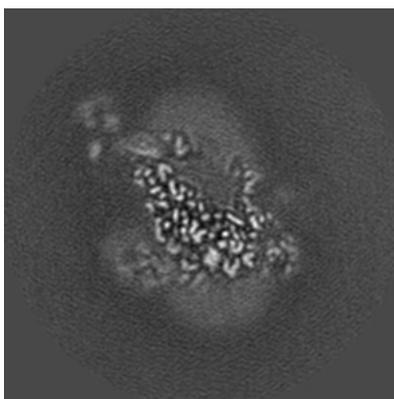


Z Index: 100

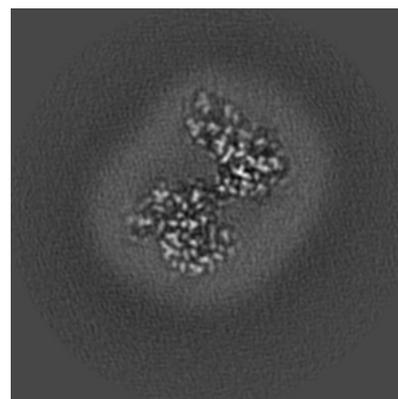
6.2.2 Raw map



X Index: 100



Y Index: 100

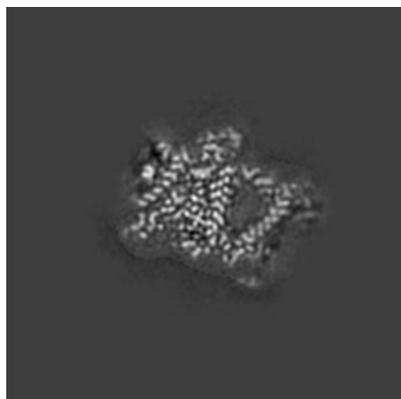


Z Index: 100

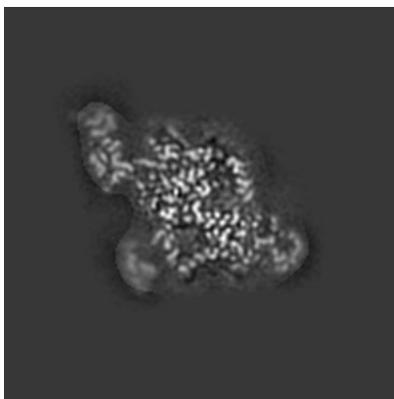
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

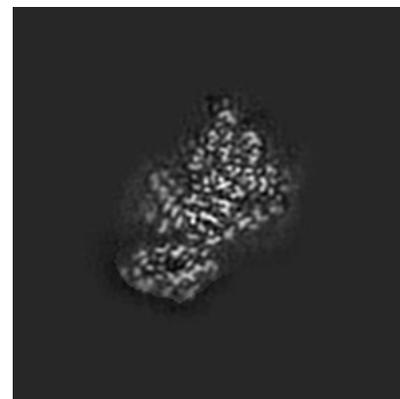
6.3.1 Primary map



X Index: 93

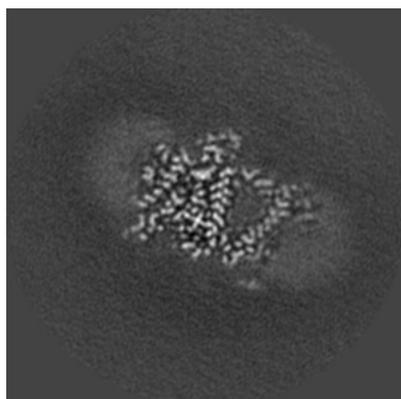


Y Index: 108

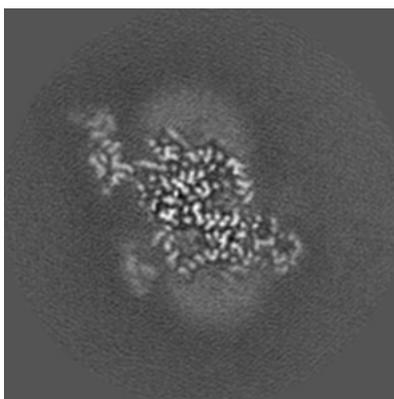


Z Index: 85

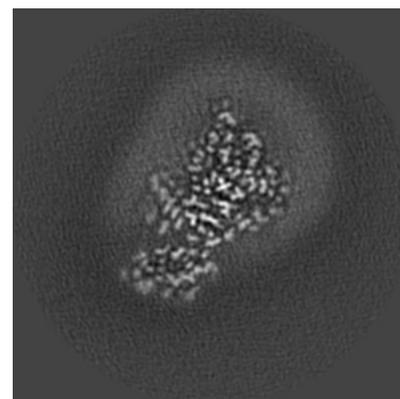
6.3.2 Raw map



X Index: 93



Y Index: 108

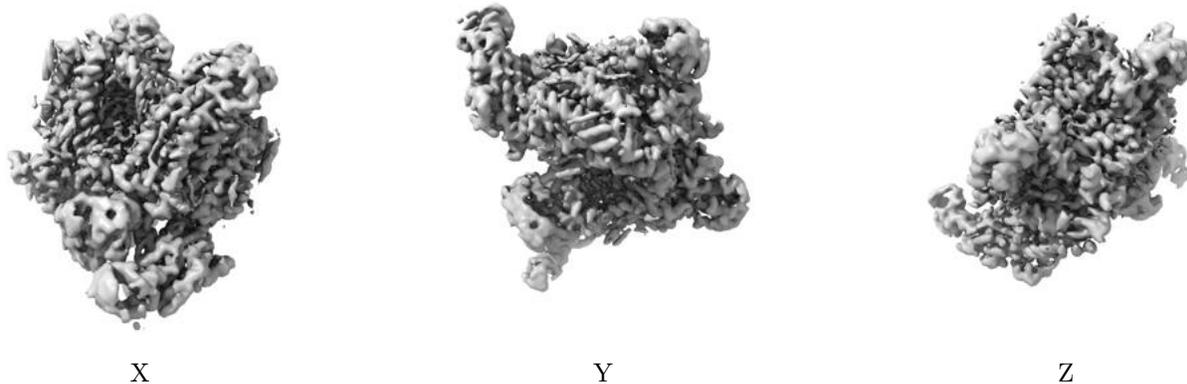


Z Index: 85

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.132. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

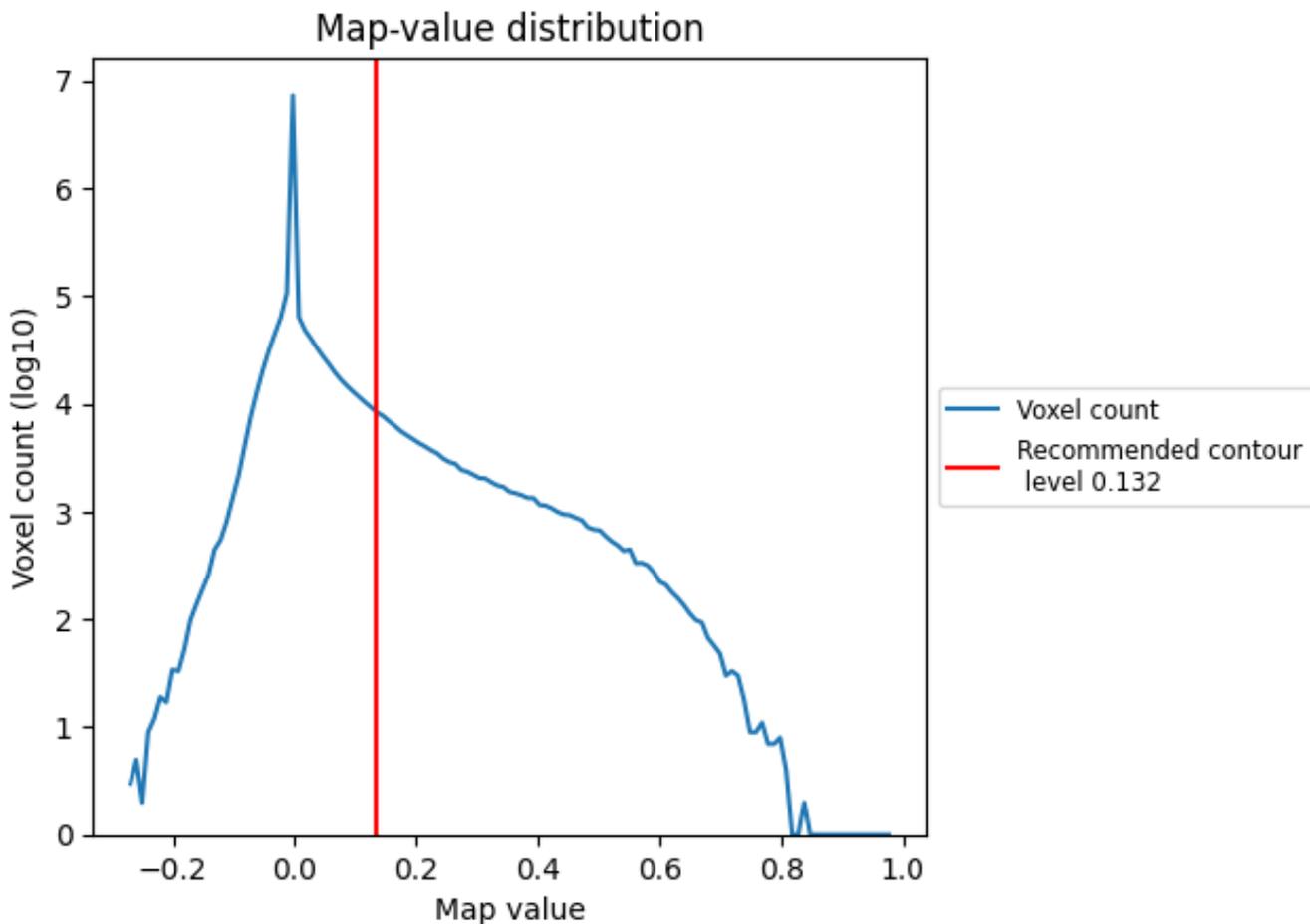
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

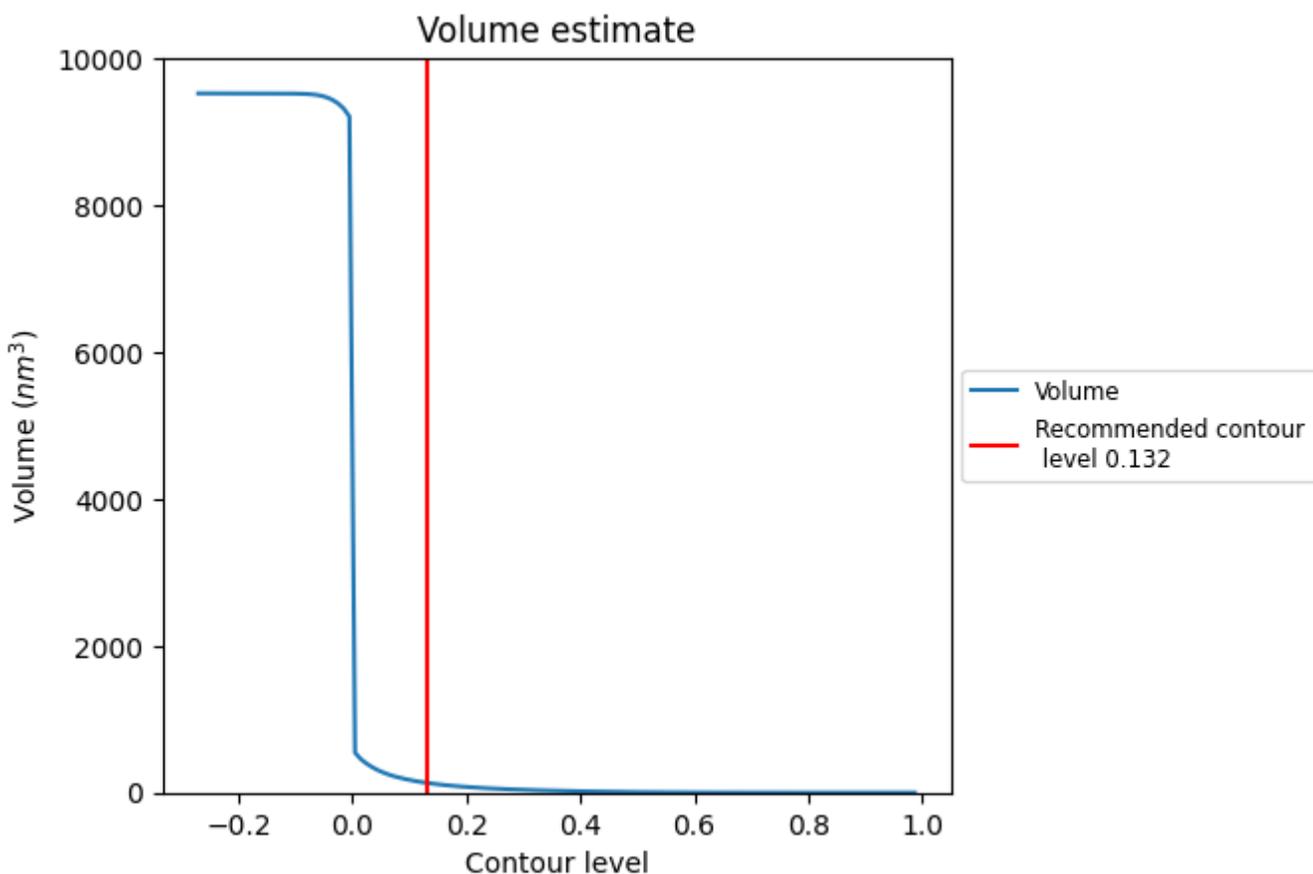
This section contains the results of statistical analysis of the map.

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.

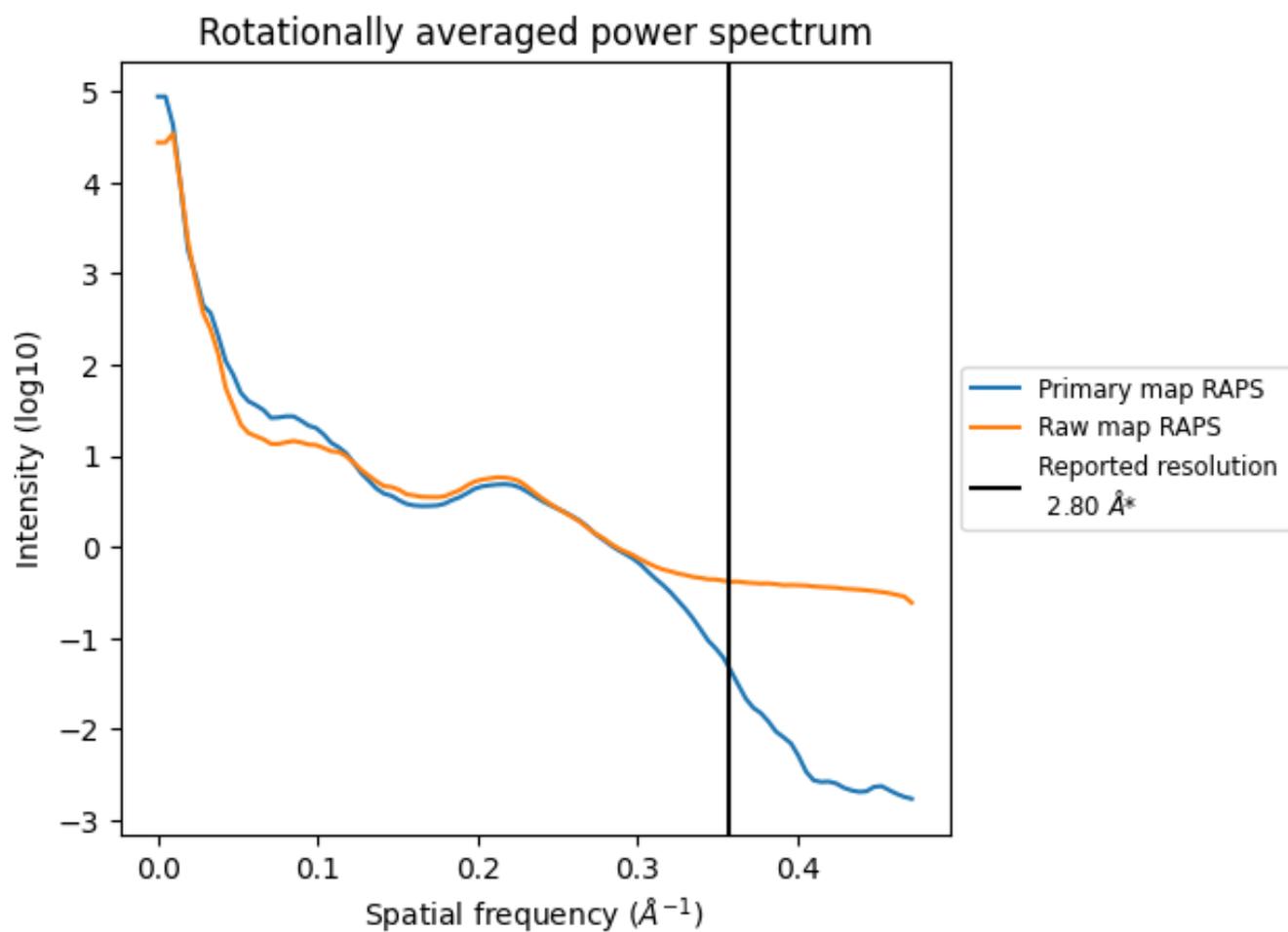
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 131 nm³; this corresponds to an approximate mass of 118 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](#)

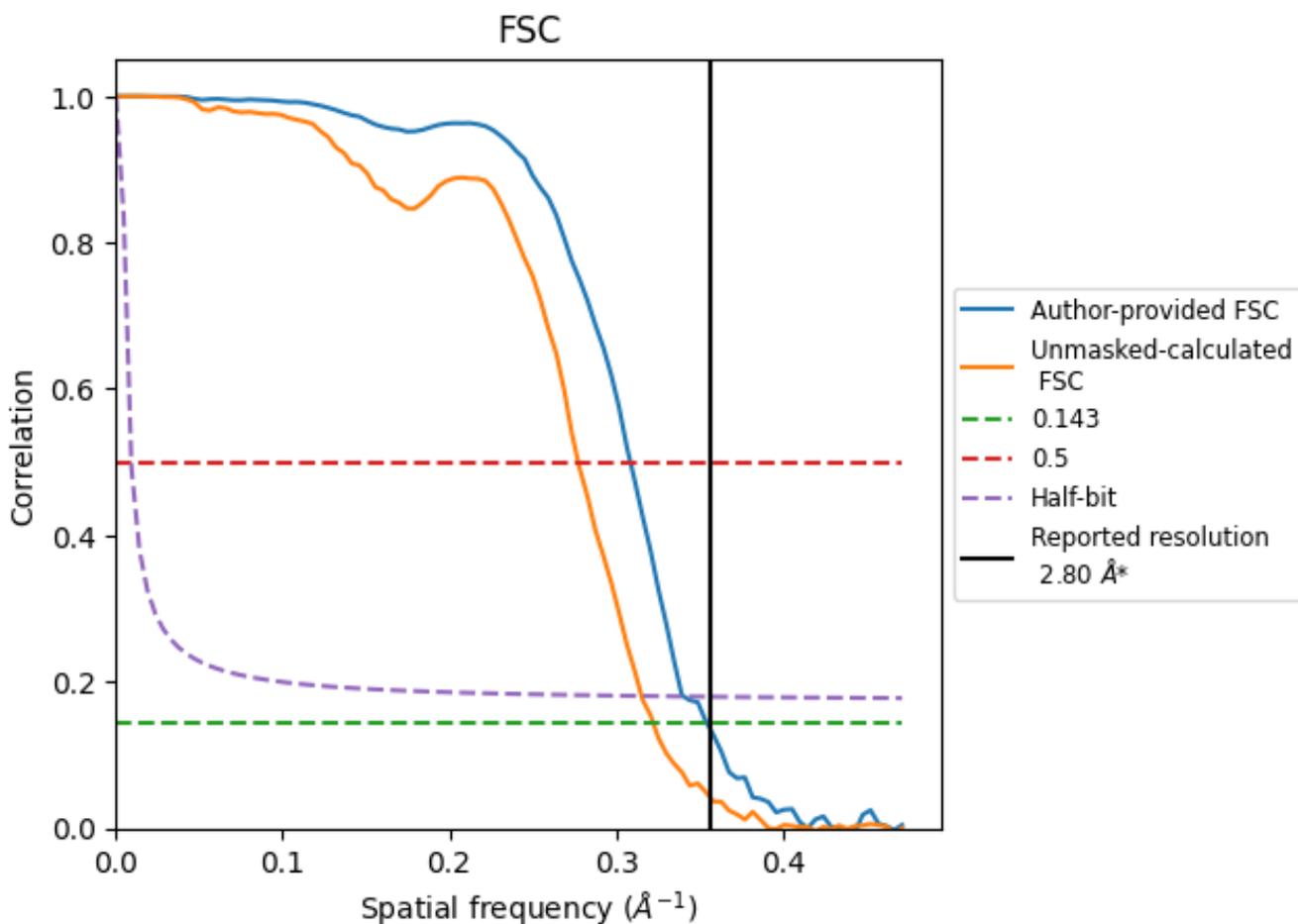


*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

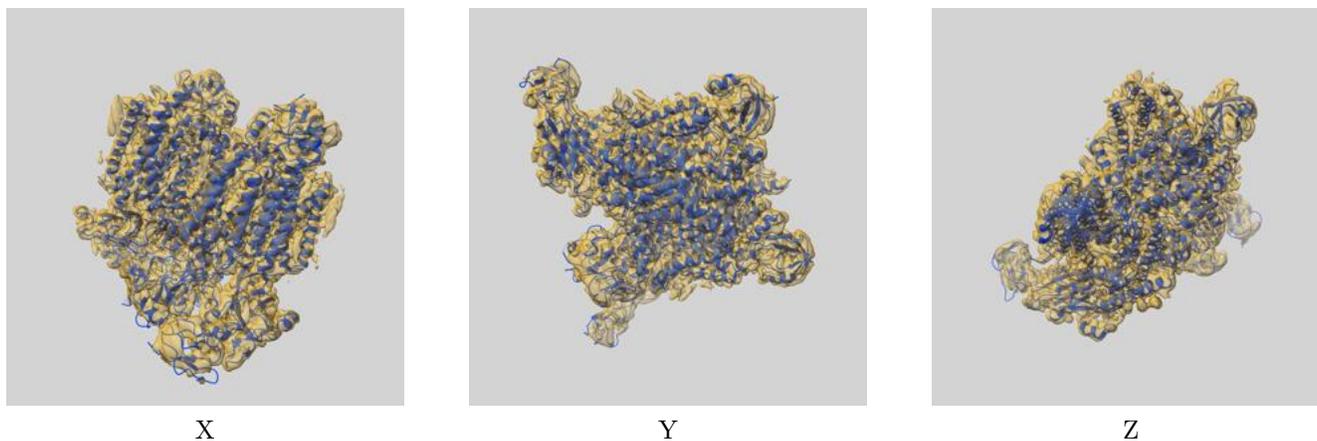
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.82	3.24	2.94
Unmasked-calculated*	3.10	3.60	3.17

*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 3.10 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

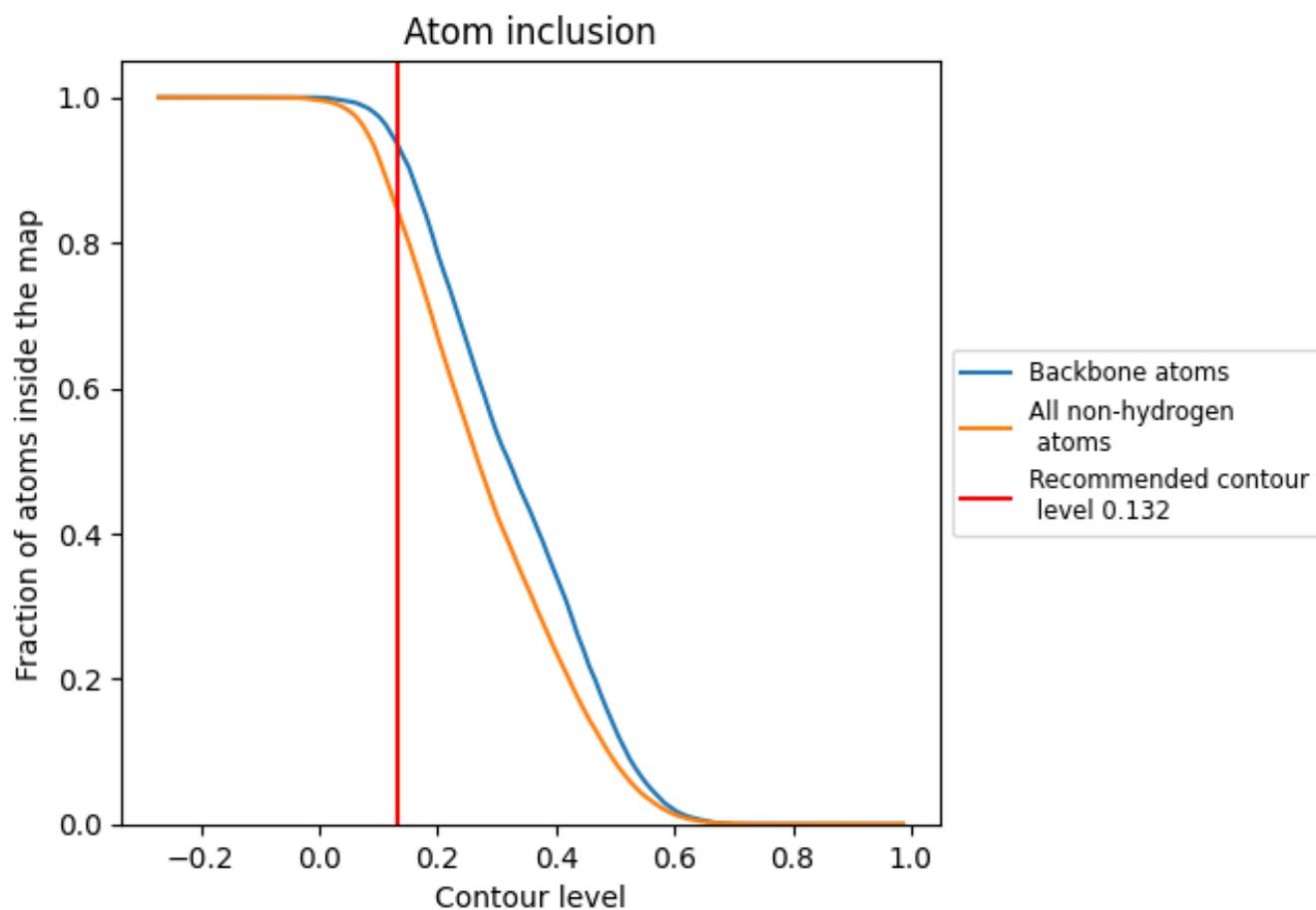
This section contains information regarding the fit between EMDB map EMD-14224 and PDB model 7R0W. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.132 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 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.