



Full wwPDB EM Validation Report ⓘ

Oct 7, 2024 – 12:11 pm BST

PDB ID : 9ES7
EMDB ID : EMD-19938
Title : Cryo-EM structure of Spinacia oleracea cytochrome b6f complex with water molecules at 1.94 Å resolution
Authors : Pietras, R.; Pintscher, S.; Mielecki, B.; Szwalec, M.; Wojcik-Augustyn, A.; Indyka, P.; Rawski, M.; Koziej, L.; Jaciuk, M.; Wazny, G.; Glatt, S.; Osyczka, A.
Deposited on : 2024-03-25
Resolution : 1.94 Å (reported)
Based on initial model : 7ZYV

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

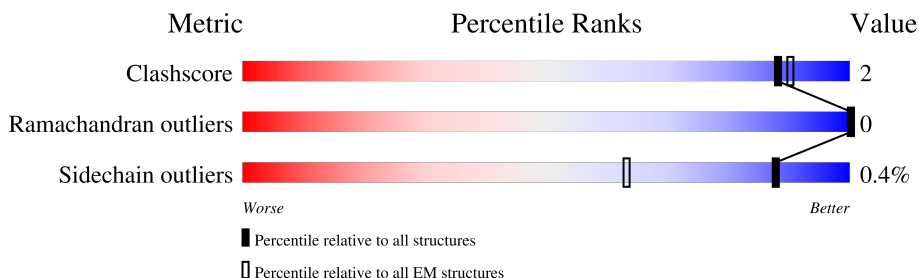
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 1.94 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.



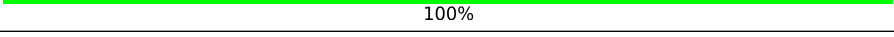
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	A	215	99% .
1	I	215	99% .
2	B	160	99% ..
2	J	160	99% ..
3	C	320	86% . 13%
3	K	320	86% . 13%
4	D	230	70% . 28%

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Mol	Chain	Length	Quality of chain
4	L	230	
5	E	31	
5	M	31	
6	F	131	
6	N	131	
7	G	37	
7	O	37	
8	H	29	
8	P	29	
9	Q	103	
9	R	103	

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	201	X	-	-	-
14	CLA	J	201	X	-	-	-

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 16413 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 Cytochrome b6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	214	Total	C	N	O	S	0	0
			1697	1126	271	289	11		
1	I	214	Total	C	N	O	S	0	0
			1697	1126	271	289	11		

- Molecule 2 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	159	Total	C	N	O	S	0	0
			1226	820	193	209	4		
2	J	159	Total	C	N	O	S	0	0
			1226	820	193	209	4		

- Molecule 3 is a protein called Cytochrome f.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	279	Total	C	N	O	S	0	0
			2168	1396	366	400	6		
3	K	279	Total	C	N	O	S	0	0
			2168	1396	366	400	6		

- Molecule 4 is a protein called Cytochrome b6-f complex iron-sulfur subunit, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	166	Total	C	N	O	S	0	0
			1260	807	212	234	7		
4	L	166	Total	C	N	O	S	0	0
			1260	807	212	234	7		

- Molecule 5 is a protein called Cytochrome b6-f complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	31	Total	C	N	O	S	0	0
			244	167	36	40	1		
5	M	31	Total	C	N	O	S	0	0
			244	167	36	40	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	37	Total	C	N	O	S	1	0
			277	182	45	49	1		
6	N	37	Total	C	N	O	S	1	0
			277	182	45	49	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	34	Total	C	N	O	S	0	0
			270	183	42	44	1		
7	O	34	Total	C	N	O	S	0	0
			270	183	42	44	1		

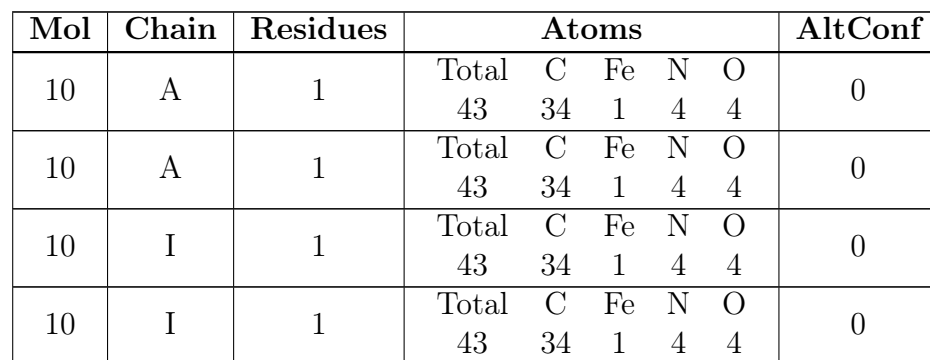
- Molecule 8 is a protein called Cytochrome b6-f complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	29	Total	C	N	O	S	0	0
			223	150	34	37	2		
8	P	29	Total	C	N	O	S	0	0
			223	150	34	37	2		

- Molecule 9 is a protein called Thylakoid soluble phosphoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Q	26	Total	C	N	O	0	0
			219	144	34	41		
9	R	26	Total	C	N	O	0	0
			219	144	34	41		

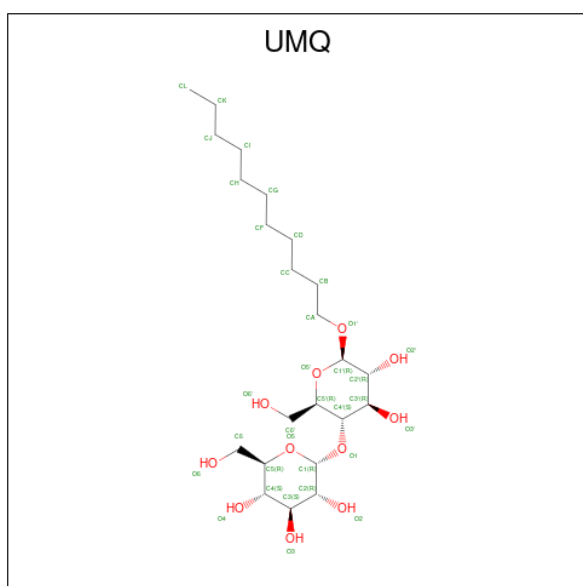
- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



- # HEC
-
- The diagram illustrates the chemical structure of HEC (Hydroxyethylchlorin), a heme derivative. The central iron atom (Fe) is coordinated by four nitrogen atoms (N) in a porphyrin-like ring. The structure is labeled with various atoms and bonds, including side chains and functional groups. Key features include:
- Central Iron (Fe):** The central metal atom, coordinated by four nitrogen atoms.
 - Nitrogen Atoms (N):** Four nitrogen atoms forming the core of the porphyrin ring, labeled NA, NB, NC, and ND.
 - Side Chains and Labels:**
 - Top Left:** O1A, O2A, O1D, O2D, OH, CGA, CGD, CAA, CBA, CAD, CBD.
 - Top Right:** CMA, C3A, C4A, C3B, C4B, C3C, C4C, C3D, C4D, C3E, C4E.
 - Bottom Left:** CMB, C2B, C1B, C4B, C3B, C4B, C3B, C4B, C3B, C4B.
 - Bottom Right:** CMC, C2C, C1C, C4C, C3C, C4C, C3C, C4C, C3C, C4C.
- The structure is highly symmetrical, with the central iron atom coordinated by the four nitrogen atoms. The side chains and labels indicate the specific atoms and bonds within the molecule, including the hydroxyl groups (OH) and the various carbon and oxygen atoms.

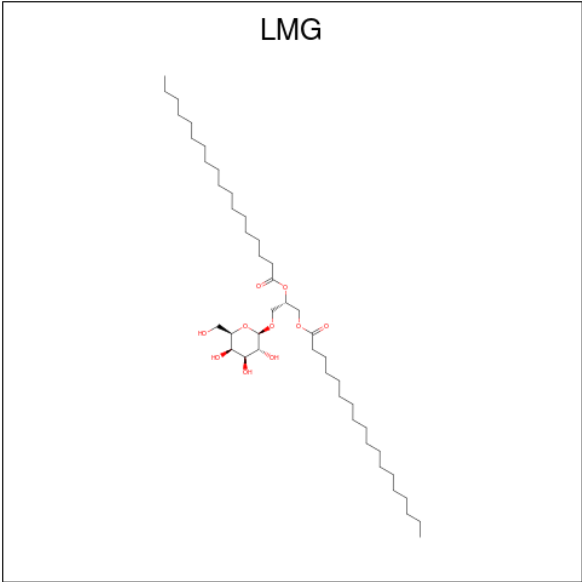
Mol	Chain	Residues	Atoms					AltConf
11	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
11	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
11	I	1	Total 43	C 34	Fe 1	N 4	O 4	0
11	K	1	Total 43	C 34	Fe 1	N 4	O 4	0

- Molecule 12 is UNDECYL-MALTOSIDE (three-letter code: UMQ) (formula: $C_{23}H_{44}O_{11}$).



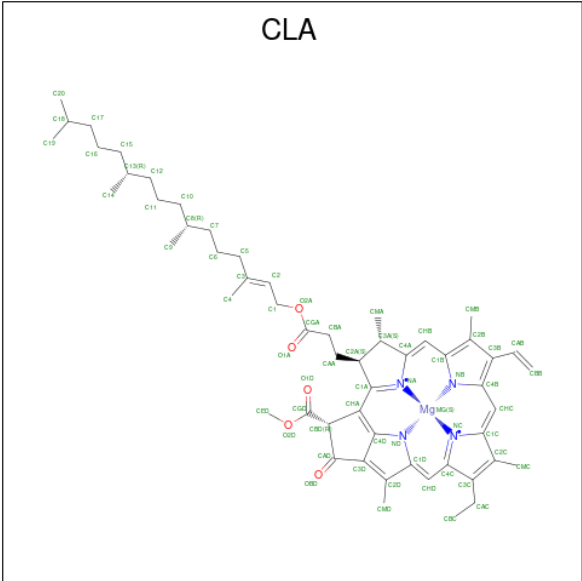
Mol	Chain	Residues	Atoms			AltConf
12	A	1	Total	C	O	0
			34	23	11	
12	H	1	Total	C	O	0
			34	23	11	
12	I	1	Total	C	O	0
			34	23	11	
12	P	1	Total	C	O	0
			34	23	11	

- Molecule 13 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (three-letter code: LMG) (formula: $C_{45}H_{86}O_{10}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
13	A	1	Total	C	O	0
			55	45	10	
13	I	1	Total	C	O	0
			55	45	10	

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



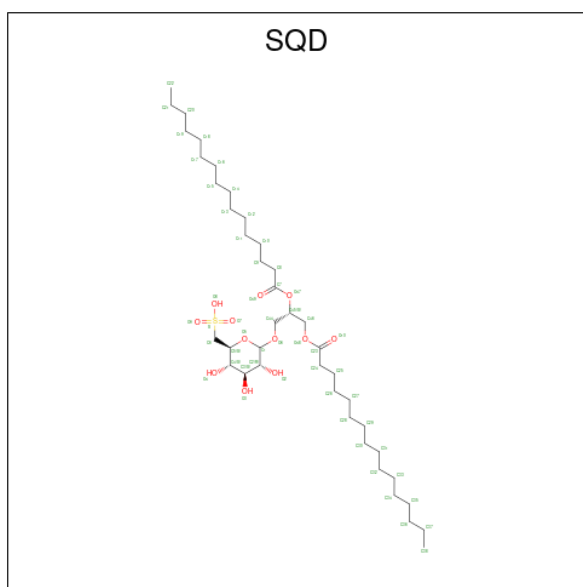
Mol	Chain	Residues	Atoms					AltConf
14	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

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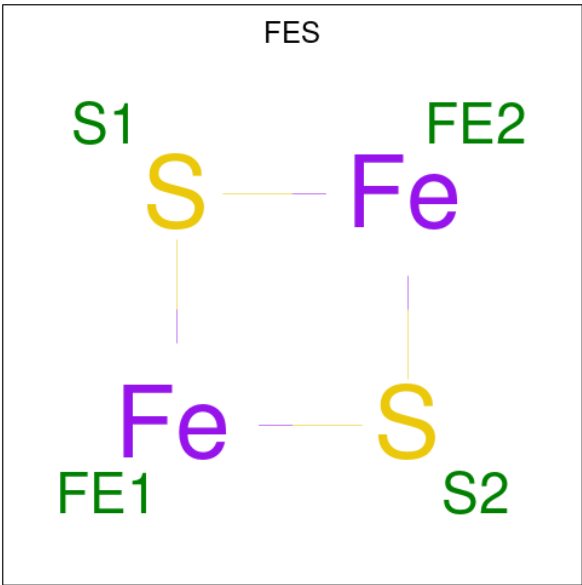
Mol	Chain	Residues	Atoms					AltConf
14	J	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

- Molecule 15 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: $C_{41}H_{78}O_{12}S$) (labeled as "Ligand of Interest" by depositor).



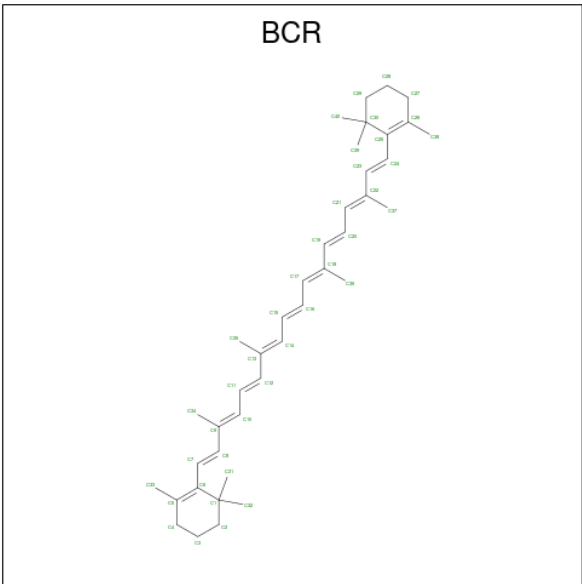
Mol	Chain	Residues	Atoms				AltConf
15	D	1	Total	C	O	S	0
			54	41	12	1	
15	L	1	Total	C	O	S	0
			54	41	12	1	

- Molecule 16 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 17 is BETA-CAROTENE (three-letter code: BCR) (formula: C₄₀H₅₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		AltConf
17	G	1	Total	C	0
			40	40	

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Mol	Chain	Residues	Atoms	AltConf
17	O	1	Total C 40 40	0

- Molecule 18 is water.

Mol	Chain	Residues	Atoms	AltConf
18	A	51	Total O 51 51	0
18	B	33	Total O 33 33	0
18	C	57	Total O 57 57	0
18	D	13	Total O 13 13	0
18	F	1	Total O 1 1	0
18	G	5	Total O 5 5	0
18	H	3	Total O 3 3	0
18	I	51	Total O 51 51	0
18	J	34	Total O 34 34	0
18	K	57	Total O 57 57	0
18	L	13	Total O 13 13	0
18	N	1	Total O 1 1	0
18	O	5	Total O 5 5	0
18	P	3	Total O 3 3	0
18	Q	1	Total O 1 1	0
18	R	1	Total O 1 1	0

3 Residue-property plots [i](#)

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

- Molecule 1: Cytochrome b6

Chain A:  99%



- Molecule 1: Cytochrome b6

Chain I:  99%



- Molecule 2: Cytochrome b6-f complex subunit 4

Chain B:  99%




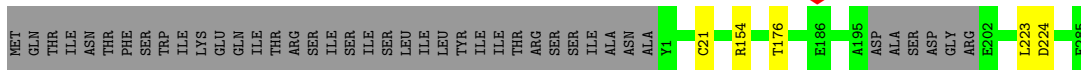
- Molecule 2: Cytochrome b6-f complex subunit 4

Chain J:  99%

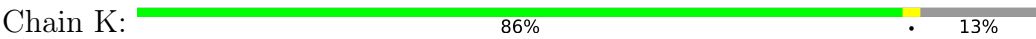


- Molecule 3: Cytochrome f

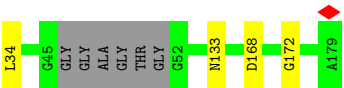
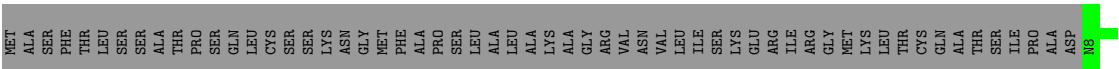
Chain C:  86% 13%



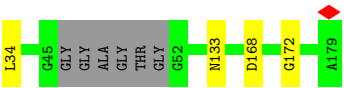
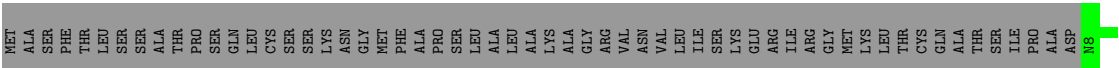
- Molecule 3: Cytochrome f



• Molecule 4: Cytochrome b6-f complex iron-sulfur subunit, chloroplastic



• Molecule 4: Cytochrome b6-f complex iron-sulfur subunit, chloroplastic



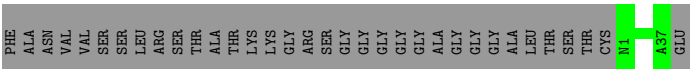
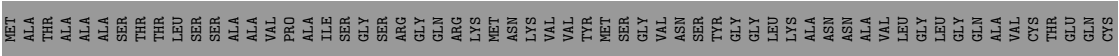
• Molecule 5: Cytochrome b6-f complex subunit 6



• Molecule 5: Cytochrome b6-f complex subunit 6



• Molecule 6: Cytochrome b6-f complex subunit 7



- Molecule 6: Cytochrome b6-f complex subunit 7

Chain N:  28% 72%

MET ALA THR ALA ALA SER THR LEU SER ALA ALA VAL PRO ALA ILE SER GLY SER ARG GLY GLN ARG LYS MET ASN LYS VAL SER TYR MET SER GLY VAL ASN SER TYR GLY GLY LEU LYS ALA ASN ASN ALA VAL LEU GLY LEU GLN ALA VAL CYS THR GLN CYS

PHE ALA ASN VAL VAL SER SER LEU ARG THR THR LYS LYS GLY ARG SER GLY GLY GLY ALA THR THR CYS M1 A37 GLU

- Molecule 7: Cytochrome b6-f complex subunit 5

Chain G:  92% 8%

M1 Q34 LEU ASP LEU

- Molecule 7: Cytochrome b6-f complex subunit 5

Chain O:  92% 8%

M1 Q34 LEU ASP LEU

- Molecule 8: Cytochrome b6-f complex subunit 8

Chain H:  100%

There are no outlier residues recorded for this chain.

- Molecule 8: Cytochrome b6-f complex subunit 8

Chain P:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Thylakoid soluble phosphoprotein

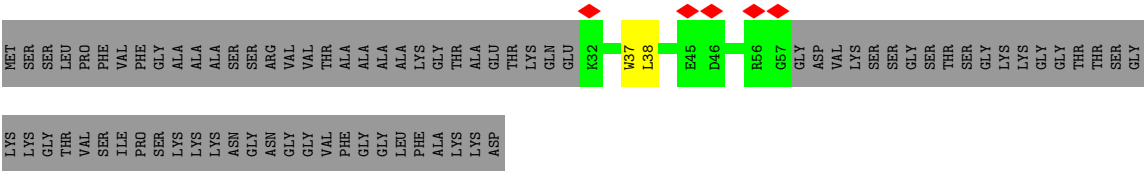
Chain Q:  5% 23% 75%

MET SER LEU PRO PHE VAL PHE GLY ALA ALA SER SER ARG VAL VAL THR ALA ALA ALA LYS GLY THR ALA GLU THR LYS GLN GLU K32 W37 L38 E45 D46 R56 G57 GLY ASP VAL LYS SER SER GLY THR SER GLY LYS LYS GLY THR SER GLY

LYS LYS THR VAL SER ILE PRO SER LYS LYS LYS ASN GLY ASN ARG GLY VAL PHE GLY GLY LEU PHE LYS LYS ASP

- Molecule 9: Thylakoid soluble phosphoprotein

Chain R:  5% 23% 75%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	1320078	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.7	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.567	Depositor
Minimum map value	-0.128	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.044	Depositor
Map size (Å)	440.32, 440.32, 440.32	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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: CLA, SQD, FES, BCR, LMG, HEC, HEM, UMQ

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	0.24	0/1747	0.46	0/2382
1	I	0.24	0/1747	0.45	0/2382
2	B	0.24	0/1263	0.44	0/1733
2	J	0.24	0/1263	0.44	0/1733
3	C	0.24	0/2214	0.46	0/2999
3	K	0.24	0/2214	0.46	0/2999
4	D	0.24	0/1294	0.45	0/1769
4	L	0.24	0/1294	0.45	0/1769
5	E	0.25	0/248	0.41	0/333
5	M	0.25	0/248	0.40	0/333
6	F	0.24	0/282	0.42	0/382
6	N	0.24	0/282	0.42	0/382
7	G	0.26	0/275	0.45	0/372
7	O	0.26	0/275	0.45	0/372
8	H	0.32	0/228	0.54	0/309
8	P	0.32	0/228	0.54	0/309
9	Q	0.26	0/224	0.41	0/301
9	R	0.26	0/224	0.41	0/301
All	All	0.25	0/15550	0.45	0/21160

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1697	0	1724	1	0
1	I	1697	0	1724	1	0
2	B	1226	0	1276	1	0
2	J	1226	0	1276	1	0
3	C	2168	0	2218	7	0
3	K	2168	0	2218	7	0
4	D	1260	0	1232	2	0
4	L	1260	0	1232	2	0
5	E	244	0	268	1	0
5	M	244	0	268	1	0
6	F	277	0	296	0	0
6	N	277	0	296	0	0
7	G	270	0	288	0	0
7	O	270	0	288	0	0
8	H	223	0	234	0	0
8	P	223	0	234	0	0
9	Q	219	0	216	2	0
9	R	219	0	216	2	0
10	A	86	0	60	10	0
10	I	86	0	60	10	0
11	A	43	0	31	2	0
11	C	43	0	31	3	0
11	I	43	0	31	2	0
11	K	43	0	31	3	0
12	A	34	0	44	0	0
12	H	34	0	44	0	0
12	I	34	0	44	0	0
12	P	34	0	44	0	0
13	A	55	0	86	2	0
13	I	55	0	86	2	0
14	B	65	0	72	0	0
14	J	65	0	72	0	0
15	D	54	0	78	0	0
15	L	54	0	78	0	0
16	D	4	0	0	0	0
16	L	4	0	0	0	0
17	G	40	0	56	0	0
17	O	40	0	56	1	0
18	A	51	0	0	1	0
18	B	33	0	0	1	0
18	C	57	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	D	13	0	0	0	0
18	F	1	0	0	0	0
18	G	5	0	0	0	0
18	H	3	0	0	0	0
18	I	51	0	0	1	0
18	J	34	0	0	1	0
18	K	57	0	0	0	0
18	L	13	0	0	0	0
18	N	1	0	0	0	0
18	O	5	0	0	0	0
18	P	3	0	0	0	0
18	Q	1	0	0	0	0
18	R	1	0	0	0	0
All	All	16413	0	16508	59	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 2.

All (59) 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)
10:I:302:HEM:HBC2	10:I:302:HEM:HMC2	1.59	0.84
10:A:302:HEM:HBC2	10:A:302:HEM:HMC2	1.59	0.83
11:I:303:HEC:O1A	18:I:401:HOH:O	1.97	0.81
11:A:303:HEC:O1A	18:A:401:HOH:O	1.97	0.80
10:I:301:HEM:HMB2	10:I:301:HEM:HBB2	1.64	0.79
10:I:301:HEM:HMC1	10:I:301:HEM:HBC2	1.65	0.79
10:A:301:HEM:HMC1	10:A:301:HEM:HBC2	1.65	0.79
10:A:301:HEM:HMB2	10:A:301:HEM:HBB2	1.64	0.77
11:C:301:HEC:HMC1	11:C:301:HEC:HBC3	1.70	0.73
2:J:29:GLU:OE2	18:J:301:HOH:O	2.06	0.73
2:B:29:GLU:OE2	18:B:301:HOH:O	2.06	0.73
11:K:301:HEC:HMC1	11:K:301:HEC:HBC3	1.70	0.71
13:I:305:LMG:O5	13:I:305:LMG:O9	2.09	0.70
10:A:302:HEM:HMB1	10:A:302:HEM:HBB2	1.73	0.70
10:I:302:HEM:HBB2	10:I:302:HEM:HMB1	1.73	0.69
9:R:37:TRP:HE3	9:R:38:LEU:HD22	1.55	0.69
9:Q:37:TRP:HE3	9:Q:38:LEU:HD22	1.55	0.69
13:A:305:LMG:O5	13:A:305:LMG:O9	2.09	0.69
3:K:21:CYS:HB2	11:K:301:HEC:HAB	1.78	0.66
3:C:21:CYS:HB2	11:C:301:HEC:HAB	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Q:37:TRP:CE3	9:Q:38:LEU:HD22	2.34	0.63
9:R:37:TRP:CE3	9:R:38:LEU:HD22	2.34	0.62
10:I:301:HEM:HBB2	10:I:301:HEM:CMB	2.32	0.60
10:A:301:HEM:HBB2	10:A:301:HEM:CMB	2.32	0.59
10:A:301:HEM:HBC2	10:A:301:HEM:CMC	2.33	0.59
10:A:302:HEM:HBC2	10:A:302:HEM:CMC	2.33	0.58
10:I:302:HEM:HBB2	10:I:302:HEM:CMB	2.35	0.57
10:I:301:HEM:HBC2	10:I:301:HEM:CMC	2.33	0.57
10:A:302:HEM:HBB2	10:A:302:HEM:CMB	2.35	0.55
10:I:302:HEM:HBC2	10:I:302:HEM:CMC	2.33	0.52
11:A:303:HEC:HHH	11:A:303:HEC:HBC3	1.92	0.51
11:I:303:HEC:HBC3	11:I:303:HEC:HHH	1.92	0.51
13:I:305:LMG:O5	13:I:305:LMG:O1	2.28	0.51
10:I:302:HEM:HBA1	10:I:302:HEM:HHA	1.94	0.50
10:A:302:HEM:HBA1	10:A:302:HEM:HHA	1.94	0.50
3:K:176:THR:CG2	3:K:223:LEU:HD21	2.42	0.49
3:C:176:THR:CG2	3:C:223:LEU:HD21	2.42	0.49
3:K:176:THR:HG22	3:K:223:LEU:HD21	1.95	0.48
3:C:176:THR:HG22	3:C:223:LEU:HD21	1.95	0.47
3:K:176:THR:HG22	3:K:223:LEU:CD2	2.45	0.47
3:C:176:THR:HG22	3:C:223:LEU:CD2	2.45	0.47
3:C:176:THR:CG2	3:C:223:LEU:CD2	2.94	0.46
3:K:176:THR:CG2	3:K:223:LEU:CD2	2.94	0.45
1:I:103:ARG:NH2	10:I:302:HEM:O2A	2.49	0.45
3:C:224:ASP:OD1	3:C:224:ASP:O	2.35	0.44
3:K:224:ASP:OD1	3:K:224:ASP:O	2.35	0.44
11:K:301:HEC:HMB1	11:K:301:HEC:HBB3	2.00	0.44
5:E:30:LEU:HD13	5:E:30:LEU:O	2.18	0.44
4:D:168:ASP:O	4:D:172:GLY:N	2.49	0.43
5:M:30:LEU:HD13	5:M:30:LEU:O	2.18	0.43
13:A:305:LMG:O5	13:A:305:LMG:O1	2.29	0.43
11:C:301:HEC:HMB1	11:C:301:HEC:HBB3	2.00	0.43
3:C:223:LEU:O	3:C:224:ASP:CG	2.59	0.41
1:A:103:ARG:NH2	10:A:302:HEM:O2A	2.49	0.41
4:L:168:ASP:O	4:L:172:GLY:N	2.49	0.41
3:K:223:LEU:O	3:K:224:ASP:CG	2.59	0.41
4:D:133:ASN:OD1	4:D:133:ASN:C	2.60	0.41
4:L:133:ASN:C	4:L:133:ASN:OD1	2.59	0.40
17:O:101:BCR:H20C	17:O:101:BCR:H361	1.93	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	212/215 (99%)	208 (98%)	4 (2%)	0	100	100
1	I	212/215 (99%)	208 (98%)	4 (2%)	0	100	100
2	B	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
2	J	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
3	C	275/320 (86%)	269 (98%)	6 (2%)	0	100	100
3	K	275/320 (86%)	269 (98%)	6 (2%)	0	100	100
4	D	162/230 (70%)	159 (98%)	3 (2%)	0	100	100
4	L	162/230 (70%)	159 (98%)	3 (2%)	0	100	100
5	E	29/31 (94%)	29 (100%)	0	0	100	100
5	M	29/31 (94%)	29 (100%)	0	0	100	100
6	F	36/131 (28%)	36 (100%)	0	0	100	100
6	N	36/131 (28%)	36 (100%)	0	0	100	100
7	G	32/37 (86%)	32 (100%)	0	0	100	100
7	O	32/37 (86%)	32 (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	Q	24/103 (23%)	24 (100%)	0	0	100	100
9	R	24/103 (23%)	24 (100%)	0	0	100	100
All	All	1908/2512 (76%)	1878 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	185/186 (100%)	184 (100%)	1 (0%)	86	86
1	I	185/186 (100%)	184 (100%)	1 (0%)	86	86
2	B	134/135 (99%)	134 (100%)	0	100	100
2	J	134/135 (99%)	134 (100%)	0	100	100
3	C	238/275 (86%)	237 (100%)	1 (0%)	89	89
3	K	238/275 (86%)	237 (100%)	1 (0%)	89	89
4	D	135/183 (74%)	134 (99%)	1 (1%)	81	79
4	L	135/183 (74%)	134 (99%)	1 (1%)	81	79
5	E	26/26 (100%)	26 (100%)	0	100	100
5	M	26/26 (100%)	26 (100%)	0	100	100
6	F	27/90 (30%)	27 (100%)	0	100	100
6	N	27/90 (30%)	27 (100%)	0	100	100
7	G	28/31 (90%)	28 (100%)	0	100	100
7	O	28/31 (90%)	28 (100%)	0	100	100
8	H	24/24 (100%)	24 (100%)	0	100	100
8	P	24/24 (100%)	24 (100%)	0	100	100
9	Q	24/78 (31%)	24 (100%)	0	100	100
9	R	24/78 (31%)	24 (100%)	0	100	100
All	All	1642/2056 (80%)	1636 (100%)	6 (0%)	88	89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	148	VAL
3	C	154	ARG
4	D	34	LEU
1	I	148	VAL
3	K	154	ARG
4	L	34	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

22 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$
11	HEC	A	303	1	32,50,50	2.28	3 (9%)	24,82,82	1.30	1 (4%)
17	BCR	O	101	-	41,41,41	0.36	0	56,56,56	0.49	0
10	HEM	A	302	1	41,50,50	1.48	3 (7%)	45,82,82	1.42	7 (15%)
16	FES	L	202	4	0,4,4	-	-	-	-	-
14	CLA	B	201	18	65,73,73	1.47	6 (9%)	76,113,113	1.34	7 (9%)
14	CLA	J	201	18	65,73,73	1.47	6 (9%)	76,113,113	1.34	7 (9%)
13	LMG	I	305	-	55,55,55	0.46	0	63,63,63	0.68	1 (1%)
15	SQD	L	201	-	53,54,54	1.51	6 (11%)	62,65,65	1.40	8 (12%)
13	LMG	A	305	-	55,55,55	0.46	0	63,63,63	0.68	1 (1%)
12	UMQ	I	304	-	35,35,35	0.55	0	46,46,46	0.58	0
10	HEM	I	301	1	41,50,50	1.48	3 (7%)	45,82,82	1.49	7 (15%)
12	UMQ	H	101	-	35,35,35	0.55	0	46,46,46	0.57	0
10	HEM	A	301	1	41,50,50	1.49	3 (7%)	45,82,82	1.49	7 (15%)
11	HEC	I	303	1	32,50,50	2.29	3 (9%)	24,82,82	1.29	1 (4%)
15	SQD	D	201	-	53,54,54	1.52	6 (11%)	62,65,65	1.40	8 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	UMQ	A	304	-	35,35,35	0.55	0	46,46,46	0.58	0
12	UMQ	P	101	-	35,35,35	0.55	0	46,46,46	0.57	0
11	HEC	K	301	3	32,50,50	2.18	3 (9%)	24,82,82	1.39	2 (8%)
16	FES	D	202	4	0,4,4	-	-	-	-	-
11	HEC	C	301	3	32,50,50	2.17	3 (9%)	24,82,82	1.38	2 (8%)
17	BCR	G	101	-	41,41,41	0.36	0	56,56,56	0.49	0
10	HEM	I	302	1	41,50,50	1.48	3 (7%)	45,82,82	1.42	7 (15%)

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
11	HEC	A	303	1	-	1/10/54/54	-
17	BCR	O	101	-	-	2/29/63/63	0/2/2/2
10	HEM	A	302	1	-	2/12/54/54	-
16	FES	L	202	4	-	-	0/1/1/1
14	CLA	B	201	18	1/1/15/20	14/37/115/115	-
14	CLA	J	201	18	1/1/15/20	14/37/115/115	-
13	LMG	I	305	-	-	19/50/70/70	0/1/1/1
15	SQD	L	201	-	-	18/49/69/69	0/1/1/1
13	LMG	A	305	-	-	19/50/70/70	0/1/1/1
12	UMQ	I	304	-	-	0/20/60/60	0/2/2/2
10	HEM	I	301	1	-	5/12/54/54	-
12	UMQ	H	101	-	-	3/20/60/60	0/2/2/2
10	HEM	A	301	1	-	5/12/54/54	-
11	HEC	I	303	1	-	1/10/54/54	-
15	SQD	D	201	-	-	18/49/69/69	0/1/1/1
12	UMQ	A	304	-	-	0/20/60/60	0/2/2/2
12	UMQ	P	101	-	-	3/20/60/60	0/2/2/2
11	HEC	K	301	3	-	0/10/54/54	-
16	FES	D	202	4	-	-	0/1/1/1
11	HEC	C	301	3	-	0/10/54/54	-
17	BCR	G	101	-	-	2/29/63/63	0/2/2/2
10	HEM	I	302	1	-	2/12/54/54	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	201	CLA	C4B-NB	7.12	1.41	1.35
14	J	201	CLA	C4B-NB	7.12	1.41	1.35
11	I	303	HEC	C3C-C2C	-7.03	1.33	1.40
11	A	303	HEC	C3C-C2C	-7.01	1.33	1.40
11	A	303	HEC	C2B-C3B	-6.61	1.33	1.40
11	I	303	HEC	C2B-C3B	-6.61	1.33	1.40
11	K	301	HEC	C2B-C3B	-6.47	1.34	1.40
11	C	301	HEC	C2B-C3B	-6.38	1.34	1.40
11	K	301	HEC	C3C-C2C	-6.21	1.34	1.40
11	C	301	HEC	C3C-C2C	-6.19	1.34	1.40
11	C	301	HEC	C3D-C2D	5.42	1.53	1.37
11	I	303	HEC	C3D-C2D	5.41	1.53	1.37
11	A	303	HEC	C3D-C2D	5.39	1.53	1.37
11	K	301	HEC	C3D-C2D	5.38	1.53	1.37
15	D	201	SQD	O48-C23	4.71	1.47	1.33
15	L	201	SQD	O48-C23	4.69	1.47	1.33
10	A	301	HEM	C3C-C2C	-4.38	1.34	1.40
10	A	302	HEM	C3C-C2C	-4.36	1.34	1.40
10	I	301	HEM	C3C-C2C	-4.34	1.34	1.40
10	I	302	HEM	C3C-C2C	-4.33	1.34	1.40
14	B	201	CLA	C1D-ND	3.76	1.42	1.37
14	J	201	CLA	C1D-ND	3.76	1.42	1.37
10	A	301	HEM	C3C-CAC	3.54	1.55	1.47
10	I	301	HEM	C3C-CAC	3.54	1.55	1.47
10	A	302	HEM	C3C-CAC	3.54	1.55	1.47
10	I	302	HEM	C3C-CAC	3.54	1.55	1.47
15	D	201	SQD	O47-C45	-3.47	1.37	1.46
15	L	201	SQD	O47-C45	-3.43	1.38	1.46
15	D	201	SQD	O47-C7	3.27	1.43	1.34
15	L	201	SQD	O47-C7	3.24	1.43	1.34
15	D	201	SQD	O5-C1	3.12	1.49	1.41
14	B	201	CLA	CHC-C1C	3.12	1.43	1.35
14	J	201	CLA	CHC-C1C	3.12	1.43	1.35
15	L	201	SQD	O5-C1	3.11	1.49	1.41
14	B	201	CLA	C4D-ND	-3.03	1.33	1.37
14	J	201	CLA	C4D-ND	-3.03	1.33	1.37
15	D	201	SQD	C24-C23	2.98	1.59	1.50
15	L	201	SQD	C24-C23	2.95	1.59	1.50
10	A	301	HEM	CAB-C3B	2.83	1.55	1.47
10	I	301	HEM	CAB-C3B	2.82	1.55	1.47
10	A	302	HEM	CAB-C3B	2.79	1.55	1.47
10	I	302	HEM	CAB-C3B	2.79	1.55	1.47
14	B	201	CLA	CMB-C2B	-2.37	1.46	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	J	201	CLA	CMB-C2B	-2.35	1.46	1.51
15	L	201	SQD	O9-S	2.07	1.51	1.45
15	D	201	SQD	O9-S	2.06	1.51	1.45
14	B	201	CLA	CMD-C2D	-2.05	1.46	1.50
14	J	201	CLA	CMD-C2D	-2.03	1.46	1.50

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	B	201	CLA	C4A-NA-C1A	6.53	109.64	106.71
14	J	201	CLA	C4A-NA-C1A	6.52	109.64	106.71
15	L	201	SQD	O9-S-C6	3.98	111.67	106.94
15	D	201	SQD	O9-S-C6	3.98	111.67	106.94
15	L	201	SQD	O7-S-C6	3.92	111.60	106.94
15	D	201	SQD	O7-S-C6	3.92	111.60	106.94
15	D	201	SQD	O9-S-O7	-3.68	101.22	113.95
15	L	201	SQD	O9-S-O7	-3.67	101.24	113.95
15	L	201	SQD	O47-C7-C8	3.63	119.33	111.50
15	D	201	SQD	O47-C7-C8	3.61	119.27	111.50
10	A	301	HEM	C1B-NB-C4B	3.23	108.41	105.07
10	I	301	HEM	C1B-NB-C4B	3.23	108.41	105.07
10	A	302	HEM	C4D-ND-C1D	3.19	108.37	105.07
10	I	302	HEM	C4D-ND-C1D	3.19	108.37	105.07
10	I	302	HEM	C1B-NB-C4B	3.15	108.32	105.07
10	A	302	HEM	C1B-NB-C4B	3.12	108.30	105.07
14	J	201	CLA	CMB-C2B-C1B	-3.03	123.80	128.46
14	B	201	CLA	CMB-C2B-C1B	-3.02	123.82	128.46
10	A	301	HEM	C4C-CHD-C1D	2.93	126.42	122.56
10	I	301	HEM	C4C-CHD-C1D	2.93	126.42	122.56
14	J	201	CLA	O2D-CGD-O1D	-2.92	118.14	123.84
10	A	301	HEM	C4D-ND-C1D	2.92	108.08	105.07
10	I	301	HEM	C4D-ND-C1D	2.92	108.08	105.07
14	B	201	CLA	O2D-CGD-O1D	-2.89	118.19	123.84
15	L	201	SQD	O48-C23-C24	2.71	120.41	111.91
15	D	201	SQD	O48-C23-C24	2.71	120.40	111.91
15	L	201	SQD	O8-S-C6	2.70	110.04	105.74
15	D	201	SQD	O8-S-C6	2.69	110.02	105.74
10	A	302	HEM	C4C-CHD-C1D	2.68	126.09	122.56
10	I	302	HEM	C4C-CHD-C1D	2.68	126.09	122.56
10	I	301	HEM	C4B-CHC-C1C	2.60	125.99	122.56
11	A	303	HEC	CBA-CAA-C2A	-2.59	108.24	112.60
11	I	303	HEC	CBA-CAA-C2A	-2.59	108.24	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	B	201	CLA	CMB-C2B-C3B	2.58	129.50	124.68
10	A	301	HEM	C4B-CHC-C1C	2.57	125.95	122.56
14	J	201	CLA	CMB-C2B-C3B	2.56	129.48	124.68
10	A	302	HEM	C4B-CHC-C1C	2.50	125.85	122.56
10	I	302	HEM	C4B-CHC-C1C	2.50	125.85	122.56
14	B	201	CLA	CHB-C4A-NA	2.48	127.94	124.51
14	J	201	CLA	CHB-C4A-NA	2.45	127.91	124.51
11	K	301	HEC	CBD-CAD-C3D	-2.45	108.44	112.62
11	C	301	HEC	CBD-CAD-C3D	-2.44	108.45	112.62
10	A	301	HEM	C3B-C2B-C1B	2.34	108.22	106.49
10	I	301	HEM	C3B-C2B-C1B	2.34	108.22	106.49
11	C	301	HEC	C1D-C2D-C3D	-2.29	105.40	107.00
15	D	201	SQD	O6-C1-C2	2.28	111.86	108.30
10	A	302	HEM	C3B-C2B-C1B	2.28	108.17	106.49
10	I	302	HEM	C3B-C2B-C1B	2.28	108.17	106.49
11	K	301	HEC	C1D-C2D-C3D	-2.28	105.41	107.00
14	B	201	CLA	C1B-CHB-C4A	-2.27	125.62	130.12
14	J	201	CLA	C1B-CHB-C4A	-2.27	125.62	130.12
10	A	302	HEM	C3D-C4D-ND	-2.27	107.64	110.17
10	I	302	HEM	C3D-C4D-ND	-2.27	107.64	110.17
10	A	301	HEM	C3D-C4D-ND	-2.25	107.66	110.17
10	I	301	HEM	C3D-C4D-ND	-2.25	107.66	110.17
15	L	201	SQD	O6-C1-C2	2.23	111.79	108.30
14	J	201	CLA	O2A-CGA-O1A	-2.14	118.19	123.59
13	A	305	LMG	C7-O1-C1	2.14	117.92	113.74
14	B	201	CLA	O2A-CGA-O1A	-2.13	118.20	123.59
13	I	305	LMG	C7-O1-C1	2.13	117.91	113.74
10	A	301	HEM	C4A-C3A-C2A	2.11	108.47	107.00
10	I	301	HEM	C4A-C3A-C2A	2.11	108.47	107.00
10	I	302	HEM	C4A-C3A-C2A	2.10	108.46	107.00
15	D	201	SQD	C1-O5-C5	-2.09	109.59	113.69
10	A	302	HEM	C4A-C3A-C2A	2.05	108.42	107.00
15	L	201	SQD	C1-O5-C5	-2.05	109.67	113.69

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
14	B	201	CLA	ND
14	J	201	CLA	ND

All (128) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	302	HEM	C1A-C2A-CAA-CBA
10	A	302	HEM	C3A-C2A-CAA-CBA
10	I	302	HEM	C1A-C2A-CAA-CBA
10	I	302	HEM	C3A-C2A-CAA-CBA
13	A	305	LMG	O6-C1-O1-C7
13	A	305	LMG	O9-C10-O7-C8
13	I	305	LMG	O6-C1-O1-C7
13	I	305	LMG	O9-C10-O7-C8
14	B	201	CLA	C1A-C2A-CAA-CBA
14	J	201	CLA	C1A-C2A-CAA-CBA
15	D	201	SQD	O47-C45-C46-O48
15	L	201	SQD	O47-C45-C46-O48
15	D	201	SQD	O10-C23-O48-C46
15	L	201	SQD	O10-C23-O48-C46
14	B	201	CLA	O1A-CGA-O2A-C1
14	J	201	CLA	O1A-CGA-O2A-C1
14	B	201	CLA	CBA-CGA-O2A-C1
14	J	201	CLA	CBA-CGA-O2A-C1
15	D	201	SQD	C24-C23-O48-C46
15	L	201	SQD	C24-C23-O48-C46
13	A	305	LMG	C11-C10-O7-C8
13	I	305	LMG	C11-C10-O7-C8
10	A	301	HEM	C2A-CAA-CBA-CGA
10	I	301	HEM	C2A-CAA-CBA-CGA
13	A	305	LMG	O6-C5-C6-O5
13	I	305	LMG	O6-C5-C6-O5
14	B	201	CLA	C16-C17-C18-C20
14	J	201	CLA	C16-C17-C18-C20
15	L	201	SQD	C10-C11-C12-C13
15	D	201	SQD	C10-C11-C12-C13
14	B	201	CLA	C16-C17-C18-C19
14	J	201	CLA	C16-C17-C18-C19
14	B	201	CLA	C3A-C2A-CAA-CBA
14	J	201	CLA	C3A-C2A-CAA-CBA
13	A	305	LMG	C40-C41-C42-C43
13	I	305	LMG	C40-C41-C42-C43
15	D	201	SQD	C31-C32-C33-C34
15	L	201	SQD	C11-C10-C9-C8
15	L	201	SQD	C31-C32-C33-C34
15	D	201	SQD	C11-C10-C9-C8
15	D	201	SQD	C24-C25-C26-C27
15	L	201	SQD	C24-C25-C26-C27
15	L	201	SQD	C29-C30-C31-C32

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Mol	Chain	Res	Type	Atoms
15	D	201	SQD	C29-C30-C31-C32
14	B	201	CLA	C4-C3-C5-C6
14	J	201	CLA	C4-C3-C5-C6
14	B	201	CLA	C2-C3-C5-C6
14	J	201	CLA	C2-C3-C5-C6
12	H	101	UMQ	O1'-CA-CB-CC
12	P	101	UMQ	O1'-CA-CB-CC
13	I	305	LMG	C35-C36-C37-C38
13	A	305	LMG	C35-C36-C37-C38
13	A	305	LMG	C2-C1-O1-C7
13	I	305	LMG	C2-C1-O1-C7
13	A	305	LMG	C13-C14-C15-C16
13	I	305	LMG	C13-C14-C15-C16
14	B	201	CLA	C6-C7-C8-C9
14	J	201	CLA	C6-C7-C8-C9
15	D	201	SQD	C26-C27-C28-C29
15	L	201	SQD	C26-C27-C28-C29
13	A	305	LMG	C15-C16-C17-C18
13	I	305	LMG	C15-C16-C17-C18
12	H	101	UMQ	CG-CH-CI-CJ
12	P	101	UMQ	CG-CH-CI-CJ
14	B	201	CLA	C6-C7-C8-C10
14	J	201	CLA	C6-C7-C8-C10
13	I	305	LMG	C22-C23-C24-C25
13	A	305	LMG	C22-C23-C24-C25
14	B	201	CLA	C2A-CAA-CBA-CGA
14	J	201	CLA	C2A-CAA-CBA-CGA
15	D	201	SQD	C16-C17-C18-C19
15	L	201	SQD	C16-C17-C18-C19
15	D	201	SQD	C44-C45-C46-O48
15	L	201	SQD	C44-C45-C46-O48
13	A	305	LMG	O1-C7-C8-O7
13	I	305	LMG	O1-C7-C8-O7
15	D	201	SQD	C25-C26-C27-C28
15	L	201	SQD	C25-C26-C27-C28
15	L	201	SQD	C11-C12-C13-C14
15	D	201	SQD	C11-C12-C13-C14
13	A	305	LMG	C9-C8-O7-C10
13	I	305	LMG	C9-C8-O7-C10
14	B	201	CLA	C2-C1-O2A-CGA
14	J	201	CLA	C2-C1-O2A-CGA
13	A	305	LMG	C37-C38-C39-C40

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Mol	Chain	Res	Type	Atoms
13	I	305	LMG	C37-C38-C39-C40
10	I	301	HEM	CAD-CBD-CGD-O1D
17	G	101	BCR	C11-C10-C9-C34
17	O	101	BCR	C11-C10-C9-C34
15	L	201	SQD	C33-C34-C35-C36
10	A	301	HEM	CAD-CBD-CGD-O1D
15	D	201	SQD	C33-C34-C35-C36
13	A	305	LMG	C7-C8-O7-C10
13	I	305	LMG	C7-C8-O7-C10
17	G	101	BCR	C11-C10-C9-C8
17	O	101	BCR	C11-C10-C9-C8
15	L	201	SQD	C27-C28-C29-C30
15	D	201	SQD	C27-C28-C29-C30
13	A	305	LMG	C12-C13-C14-C15
13	I	305	LMG	C12-C13-C14-C15
15	L	201	SQD	C45-C46-O48-C23
12	H	101	UMQ	CC-CD-CF-CG
12	P	101	UMQ	CC-CD-CF-CG
11	A	303	HEC	C3D-CAD-CBD-CGD
11	I	303	HEC	C3D-CAD-CBD-CGD
10	A	301	HEM	CAD-CBD-CGD-O2D
10	I	301	HEM	CAD-CBD-CGD-O2D
13	A	305	LMG	O1-C7-C8-C9
13	I	305	LMG	O1-C7-C8-C9
13	I	305	LMG	C4-C5-C6-O5
15	D	201	SQD	C18-C19-C20-C21
15	D	201	SQD	C45-C46-O48-C23
13	I	305	LMG	C18-C19-C20-C21
13	A	305	LMG	C18-C19-C20-C21
15	L	201	SQD	C17-C18-C19-C20
15	D	201	SQD	C17-C18-C19-C20
13	A	305	LMG	C4-C5-C6-O5
15	L	201	SQD	C18-C19-C20-C21
10	A	301	HEM	CAA-CBA-CGA-O2A
14	B	201	CLA	C15-C16-C17-C18
14	J	201	CLA	C15-C16-C17-C18
10	I	301	HEM	CAA-CBA-CGA-O2A
10	A	301	HEM	CAA-CBA-CGA-O1A
10	I	301	HEM	CAA-CBA-CGA-O1A
13	A	305	LMG	O8-C28-C29-C30
13	I	305	LMG	O8-C28-C29-C30
14	B	201	CLA	CAA-CBA-CGA-O2A

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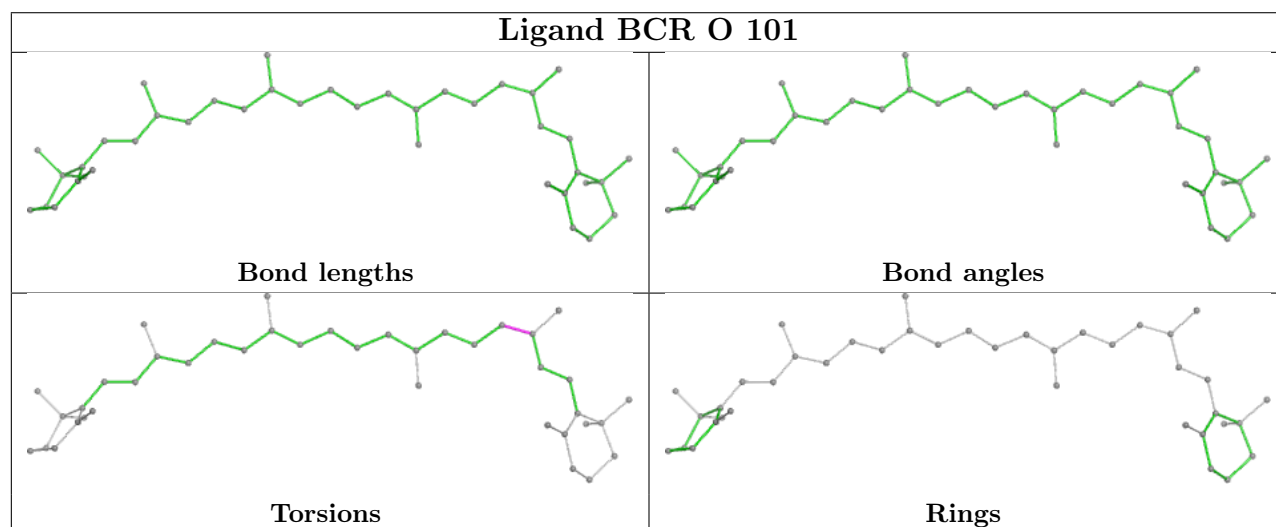
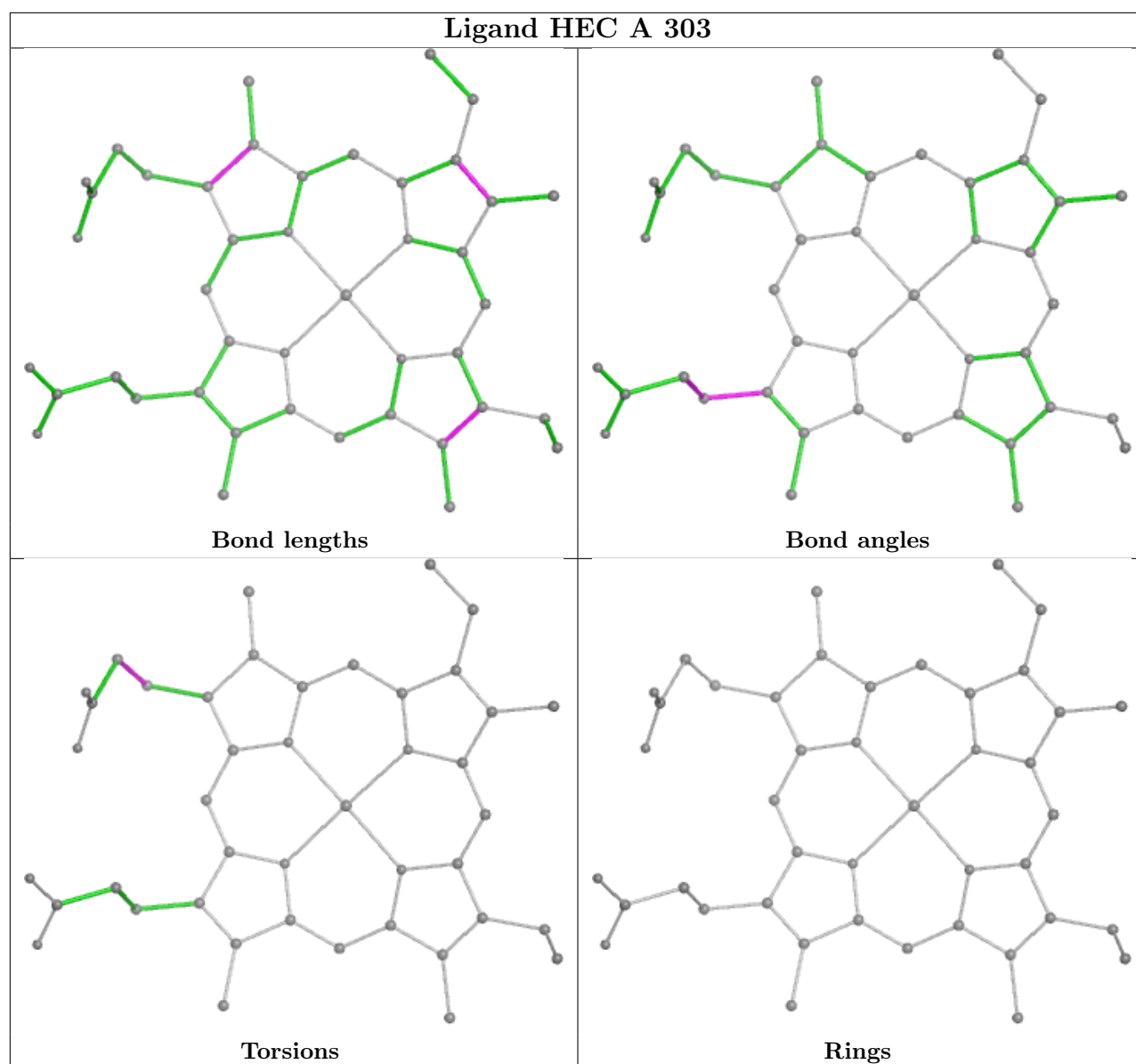
Mol	Chain	Res	Type	Atoms
14	J	201	CLA	CAA-CBA-CGA-O2A

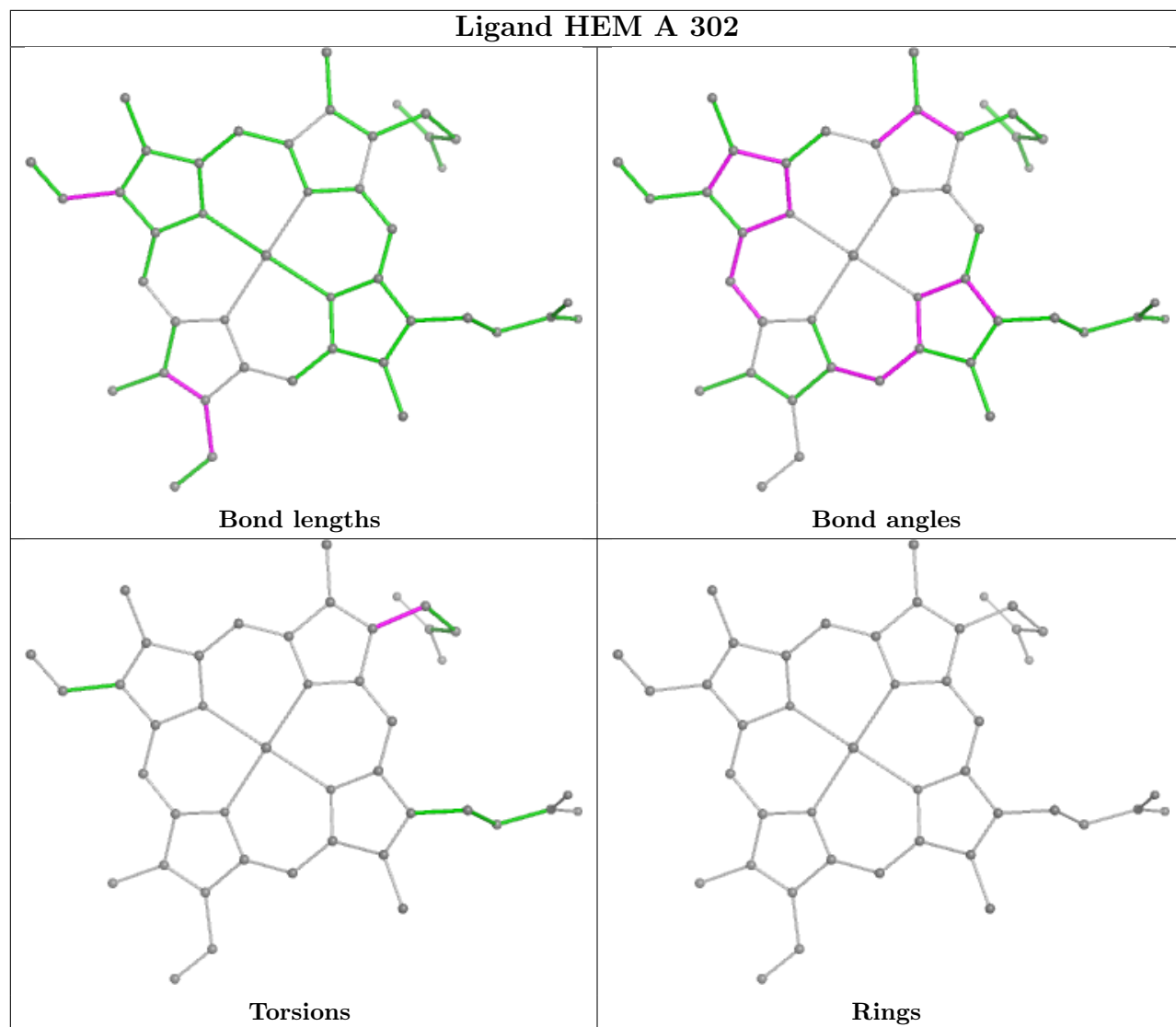
There are no ring outliers.

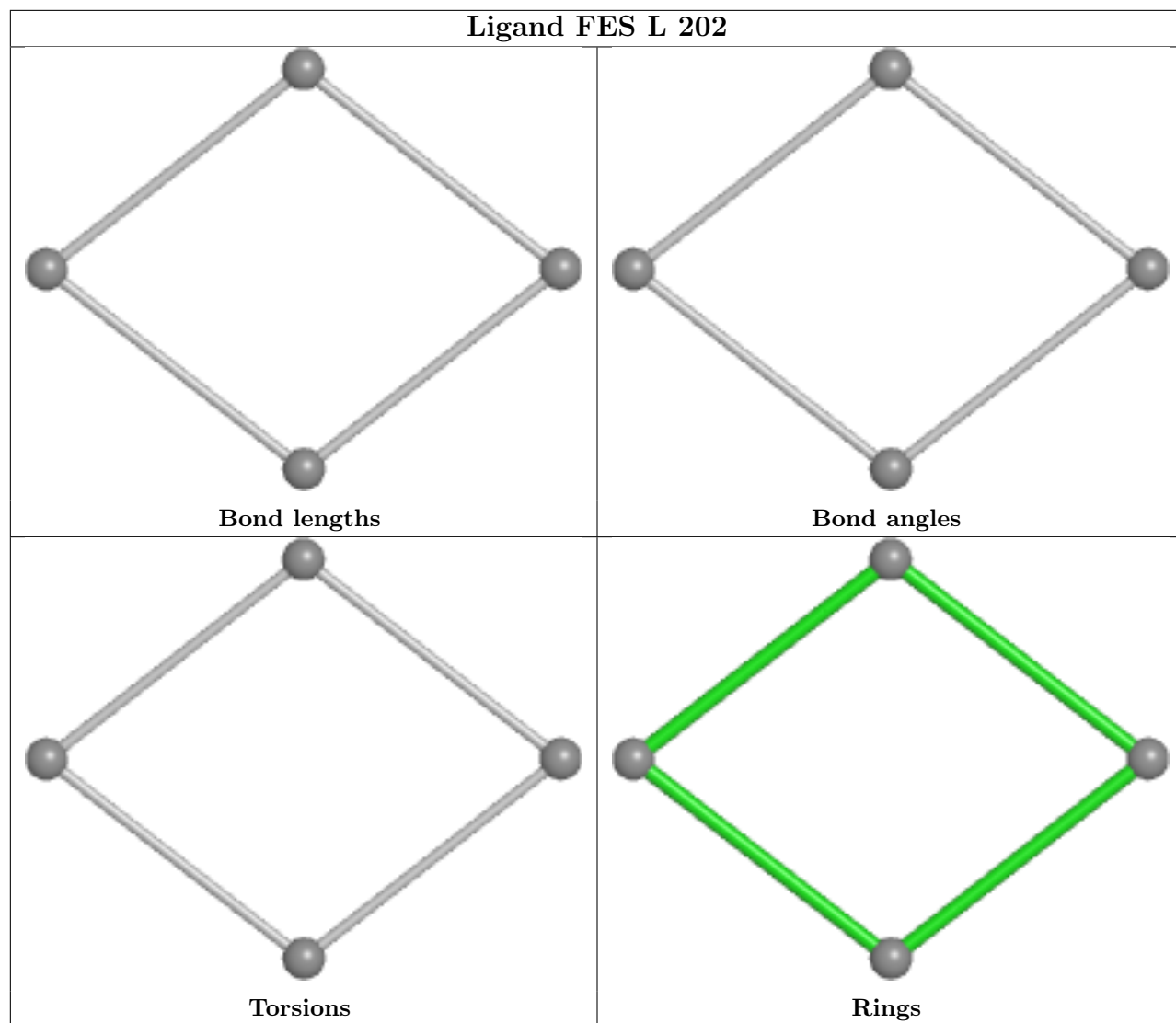
11 monomers are involved in 35 short contacts:

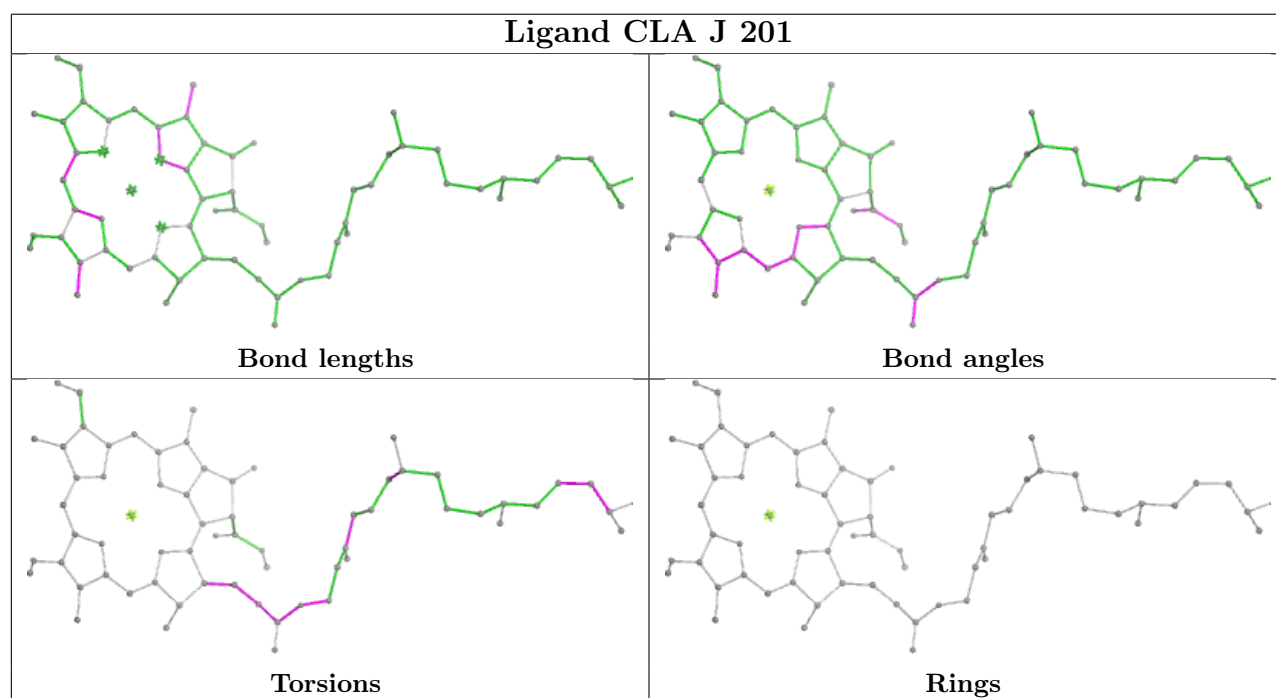
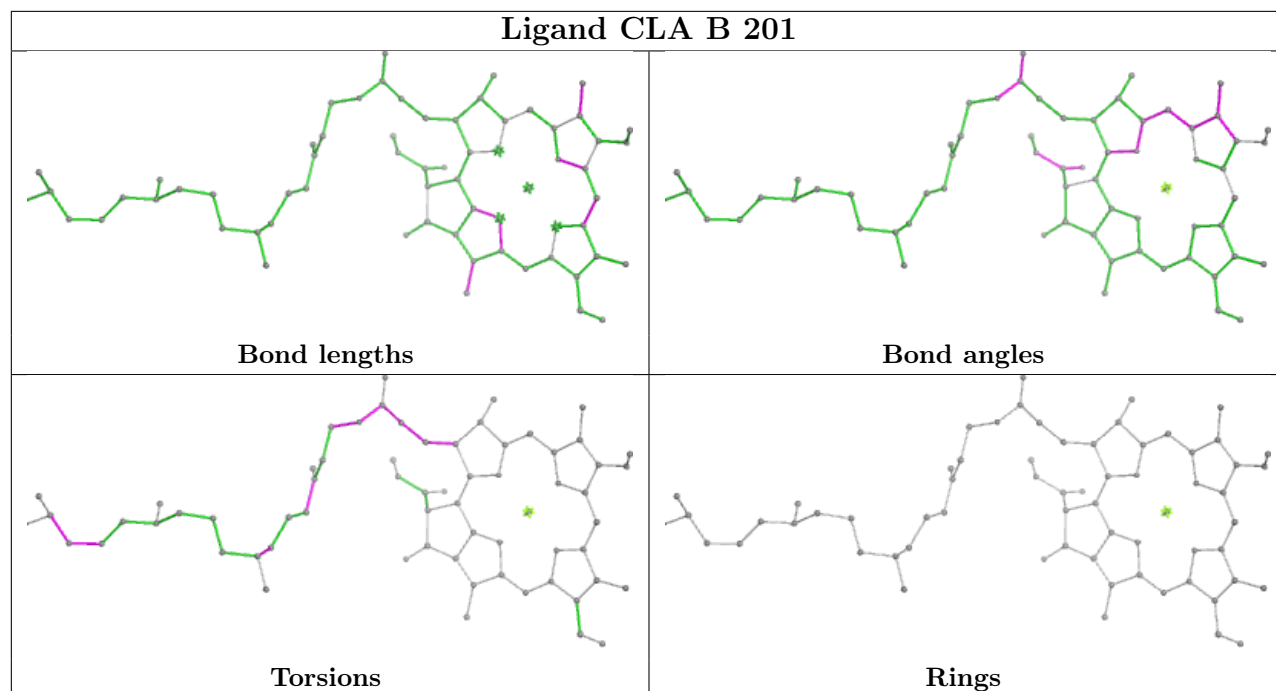
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	303	HEC	2	0
17	O	101	BCR	1	0
10	A	302	HEM	6	0
13	I	305	LMG	2	0
13	A	305	LMG	2	0
10	I	301	HEM	4	0
10	A	301	HEM	4	0
11	I	303	HEC	2	0
11	K	301	HEC	3	0
11	C	301	HEC	3	0
10	I	302	HEM	6	0

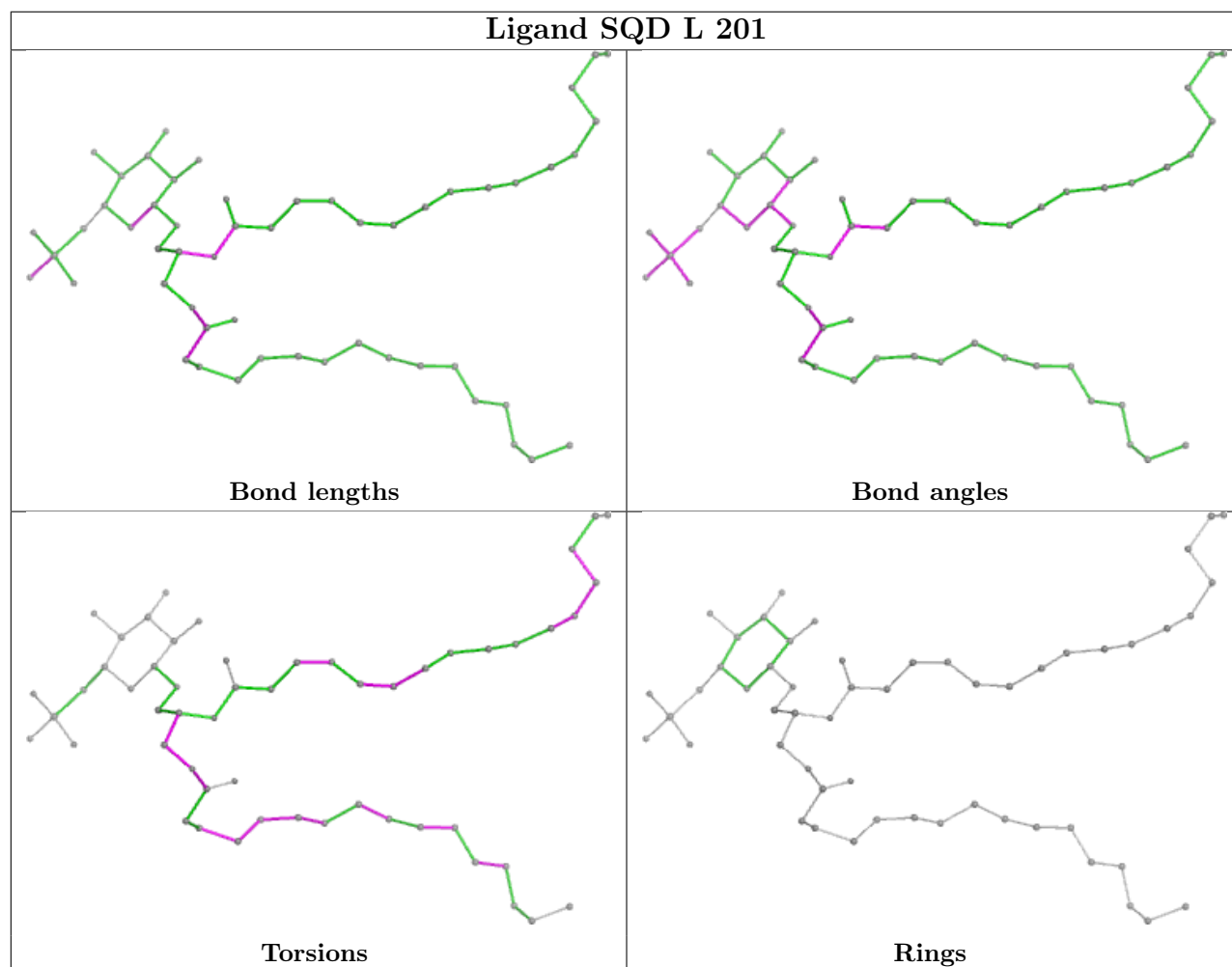
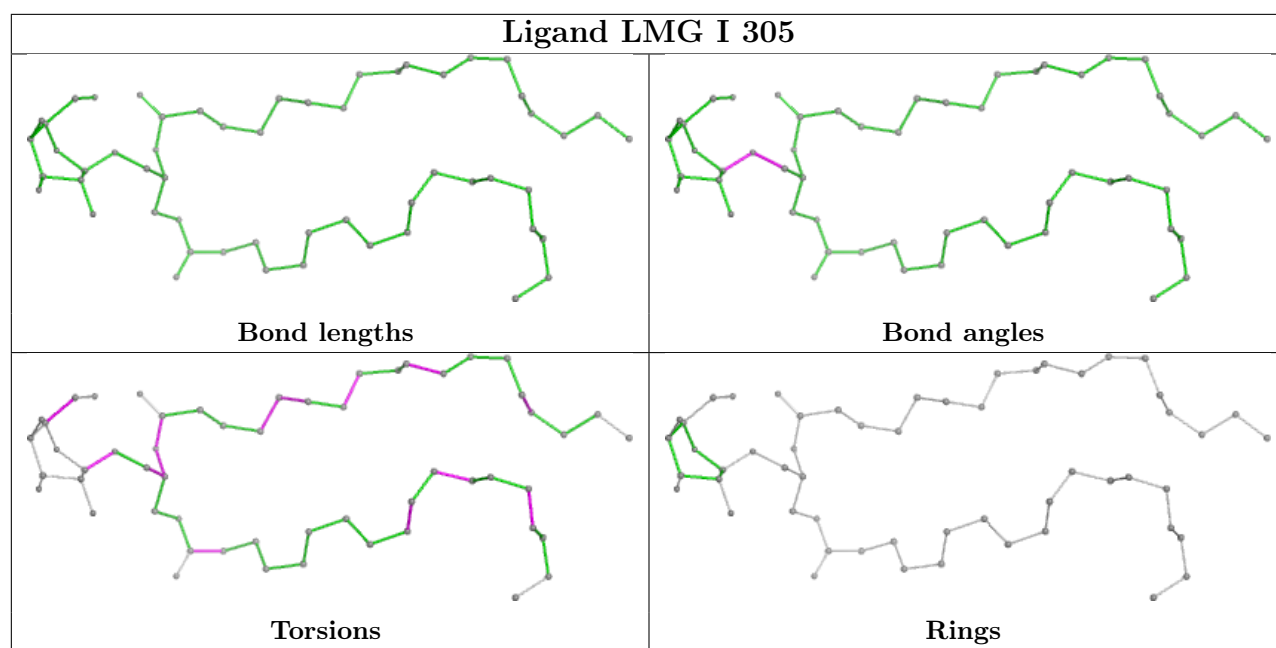
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

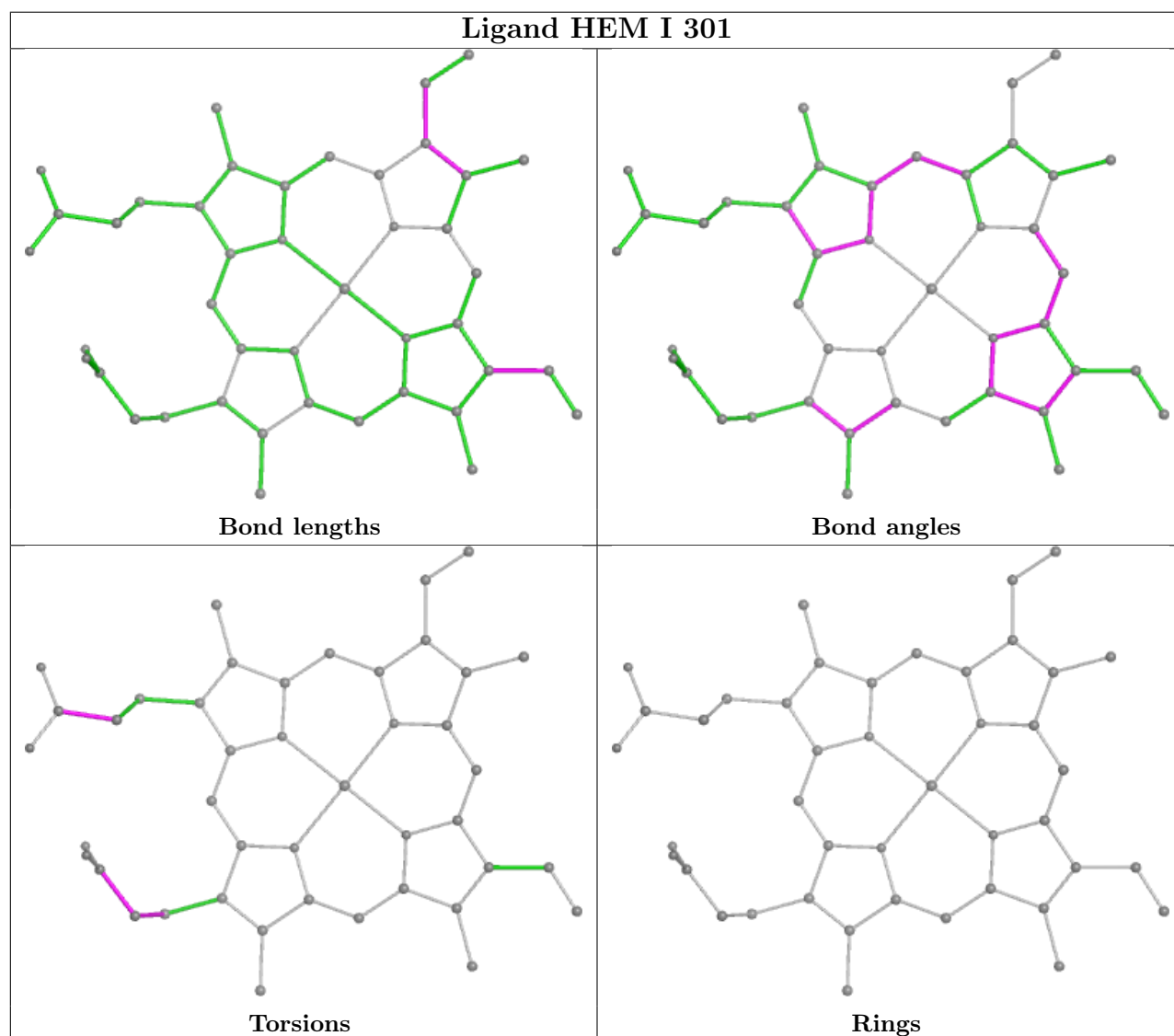
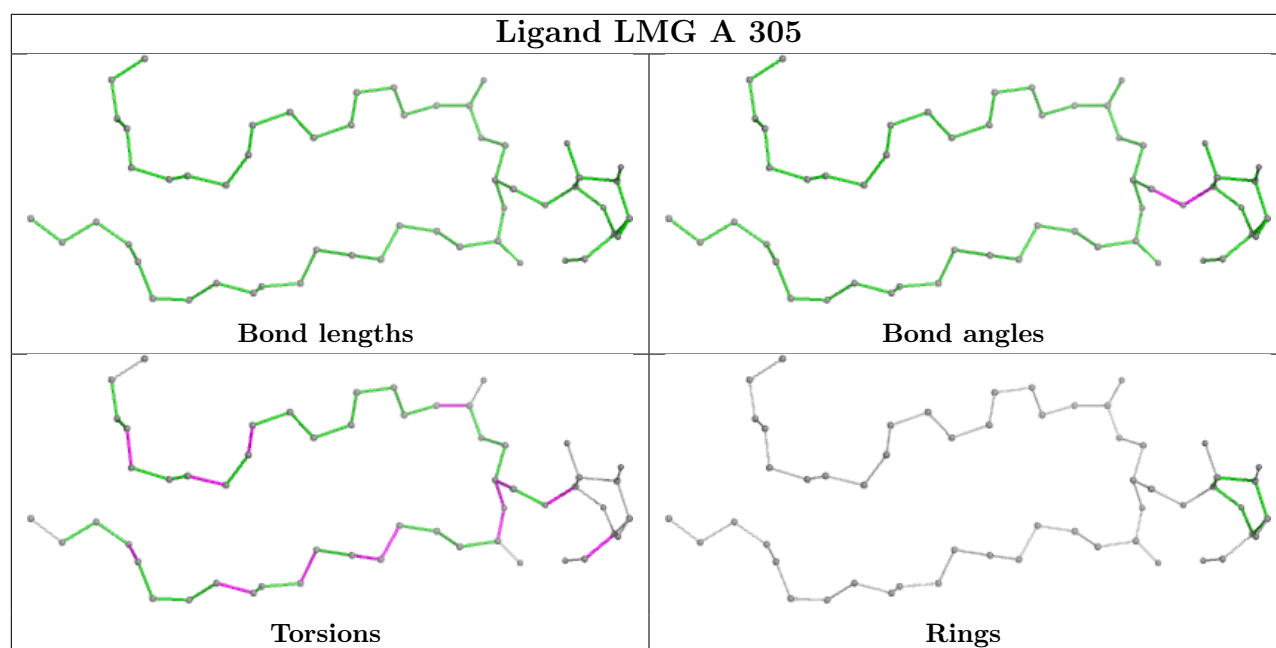


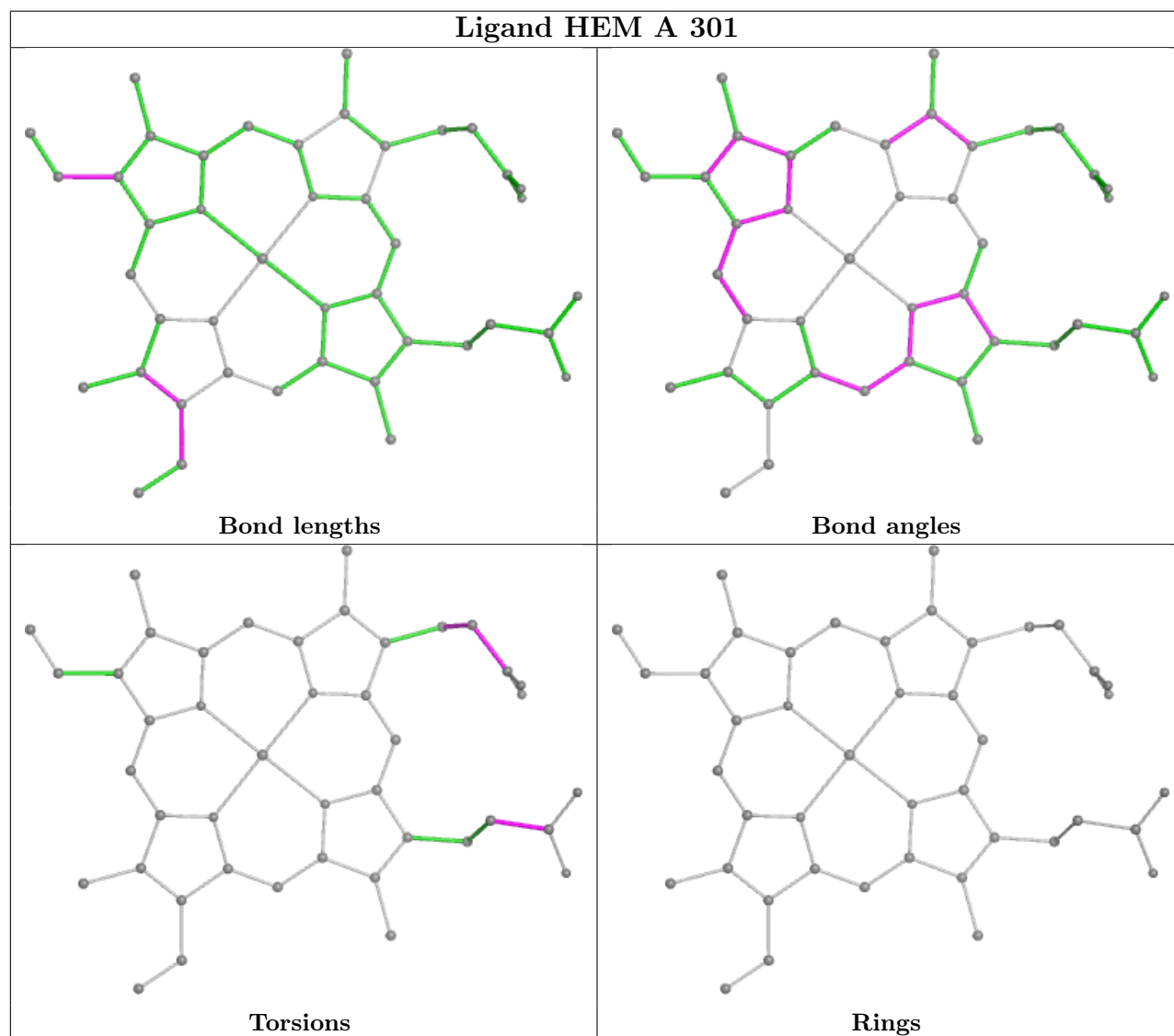
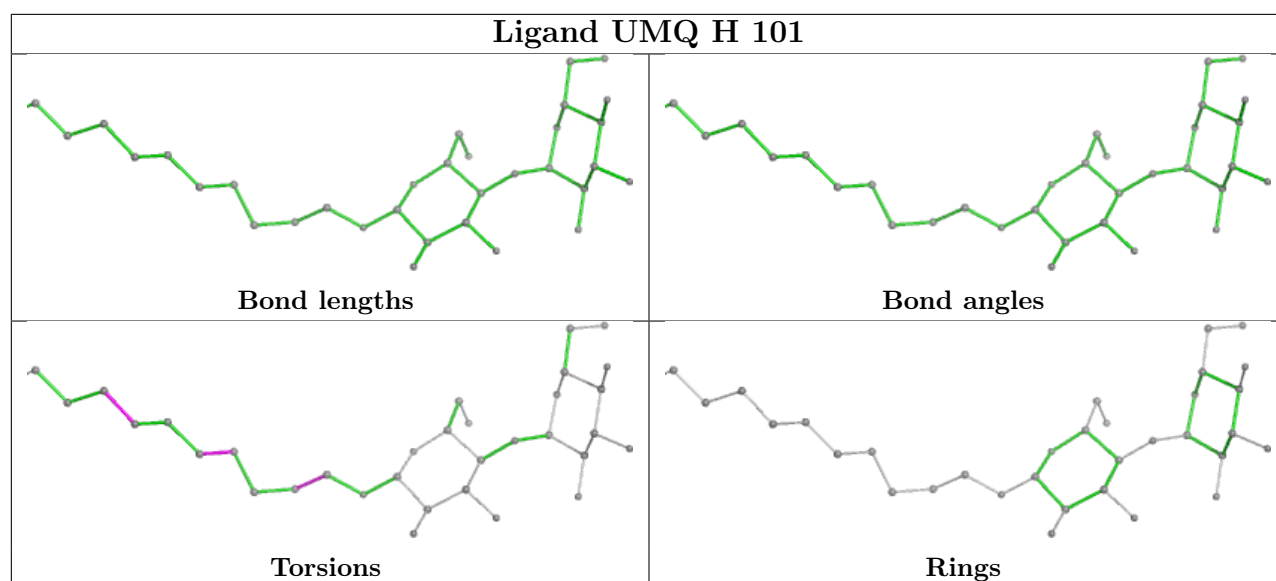




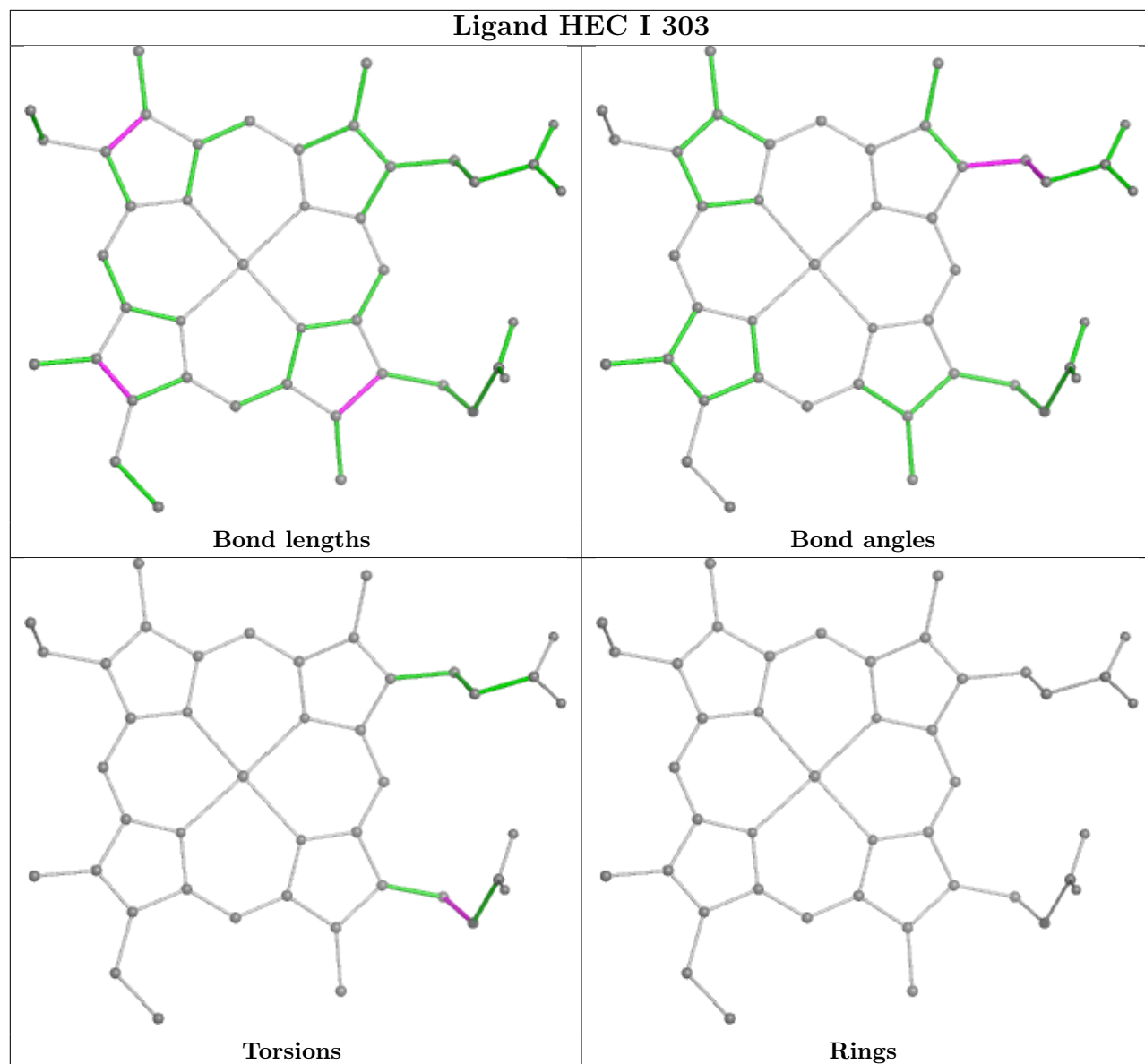


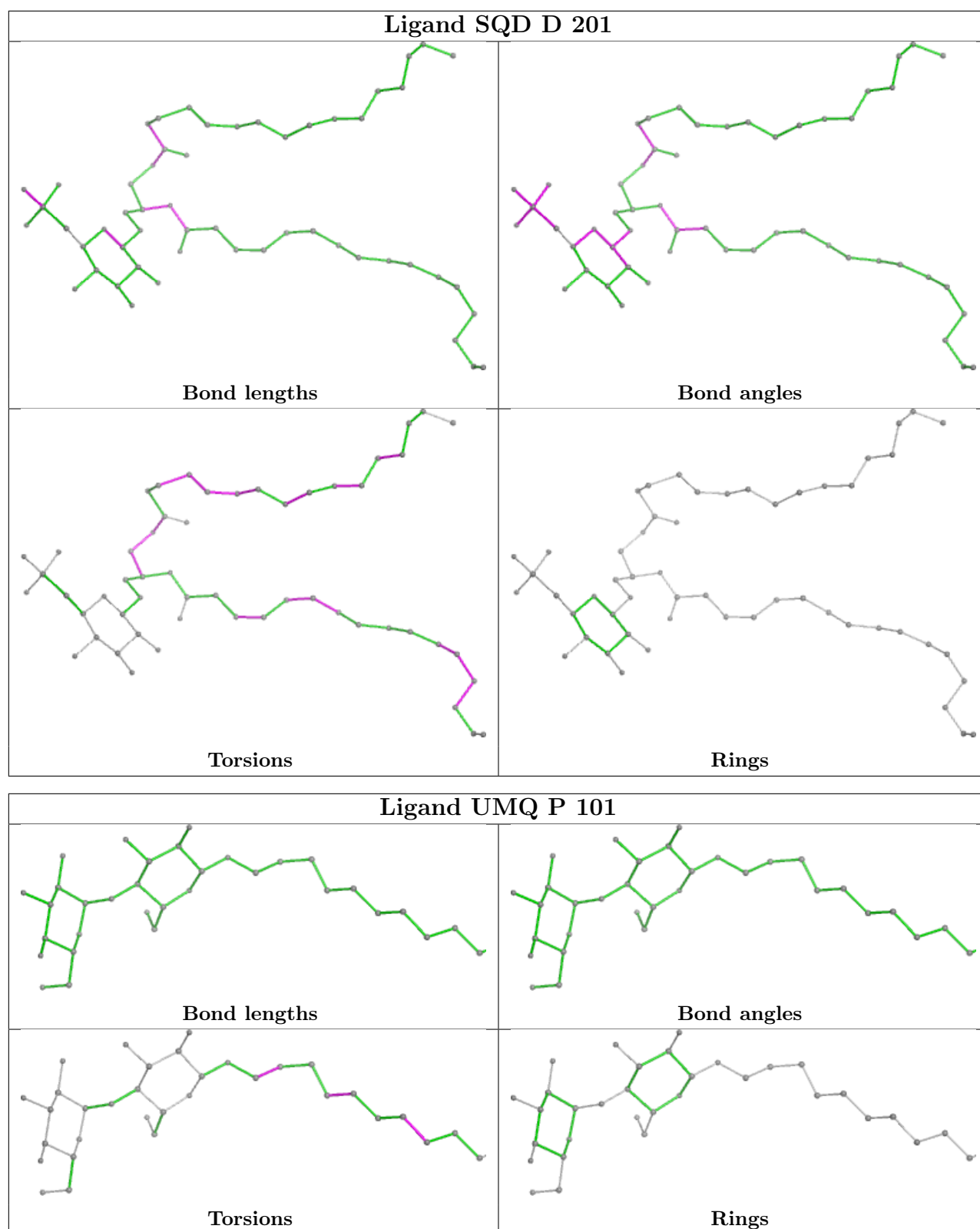


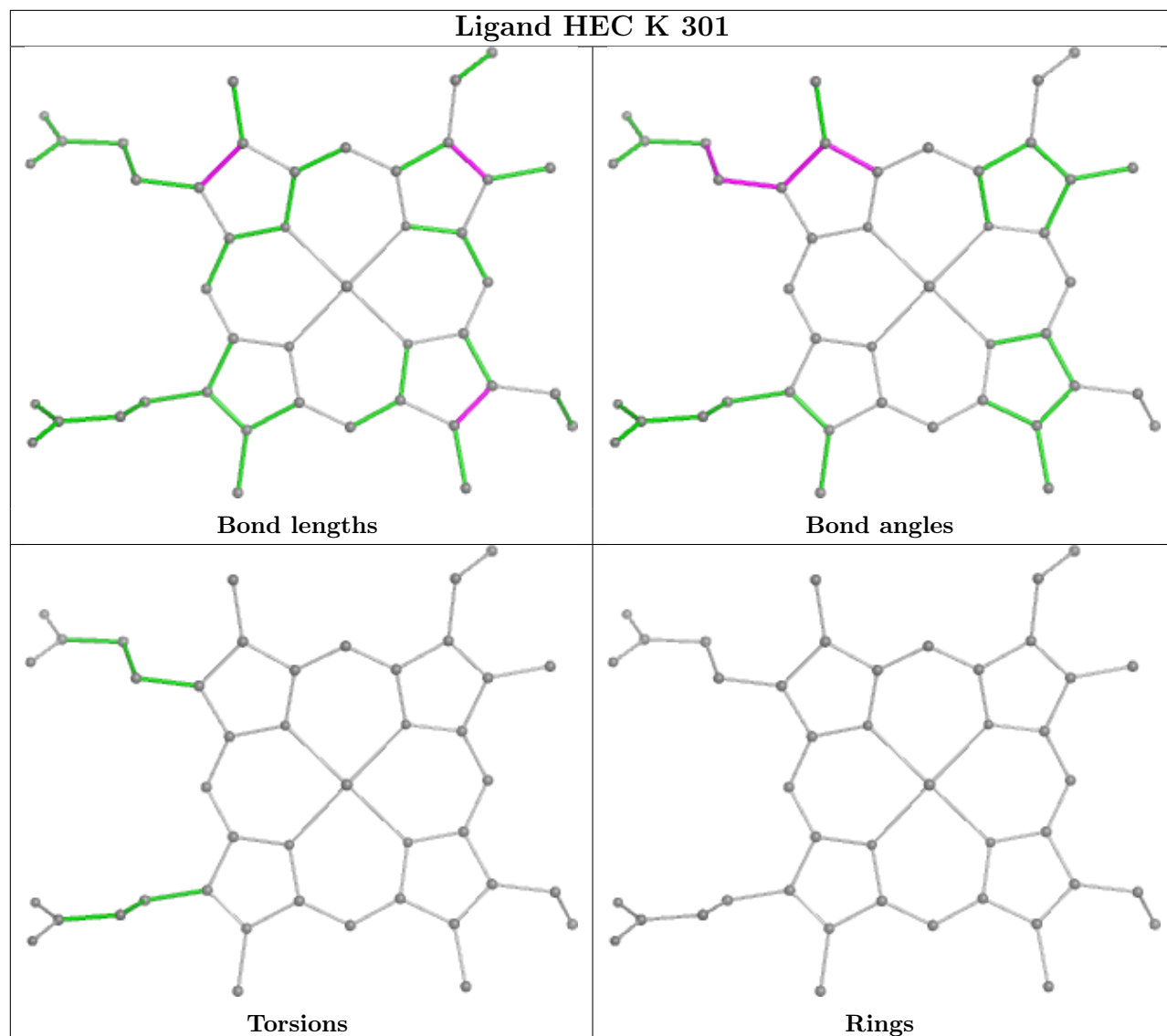


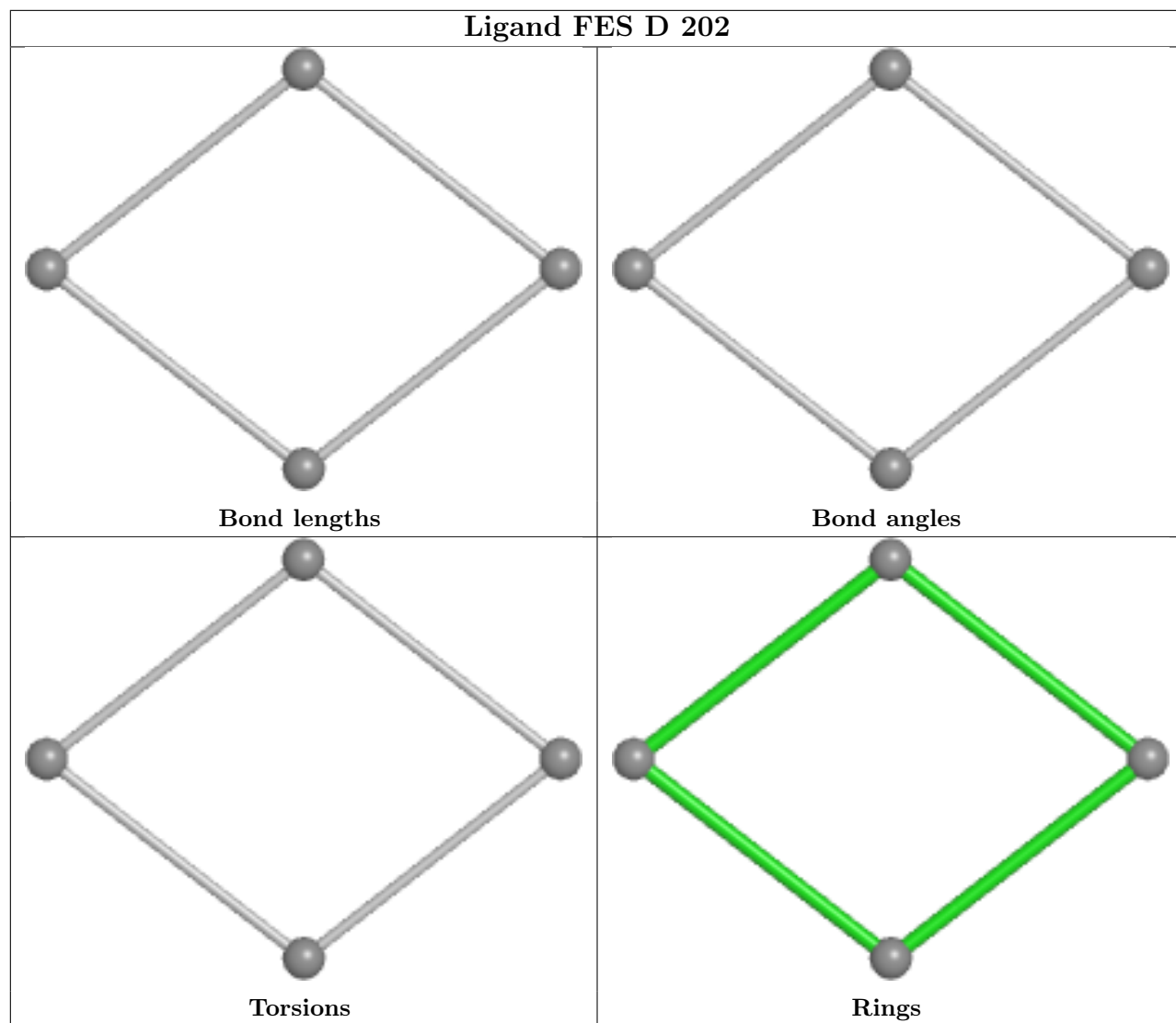


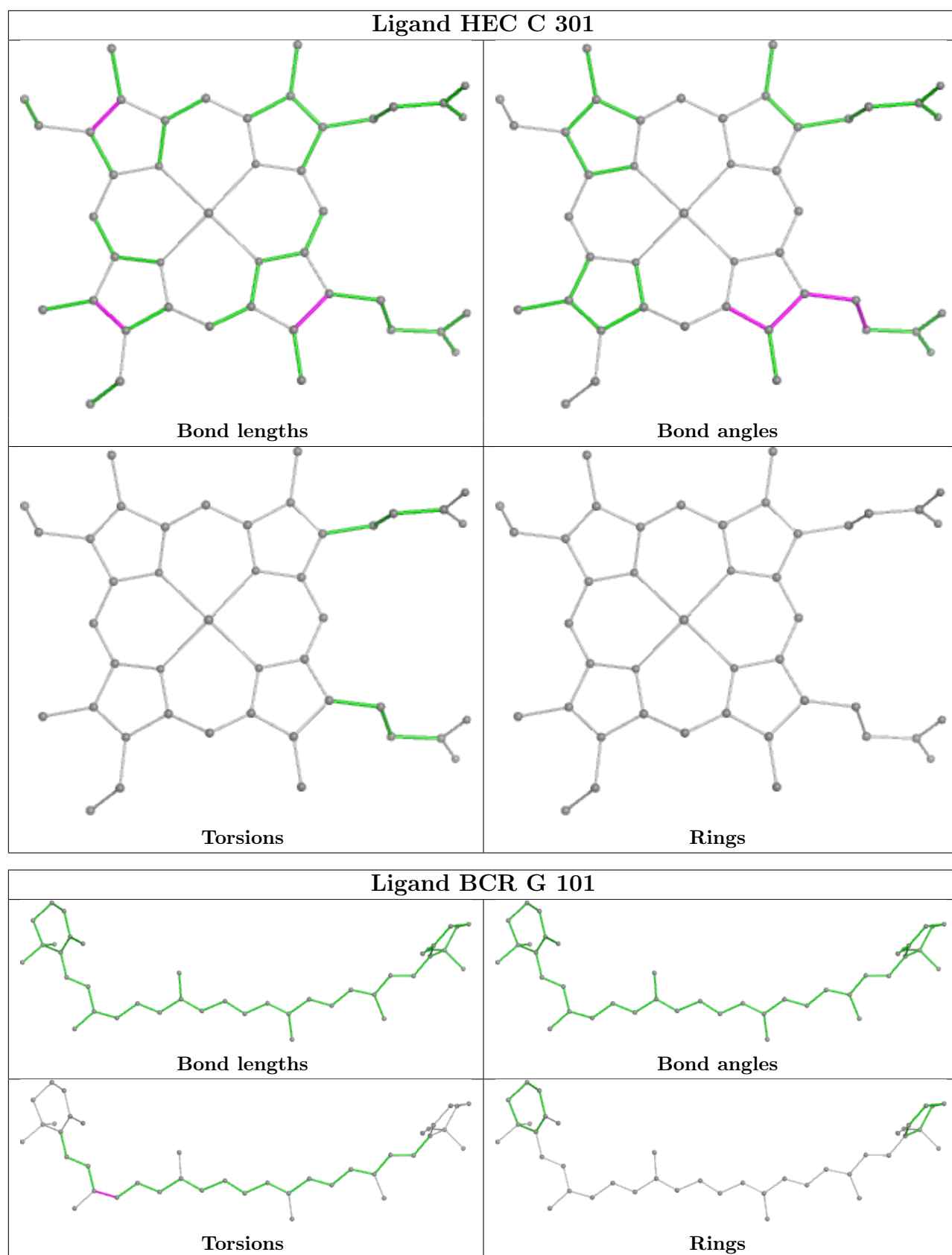
Ligand HEC I 303

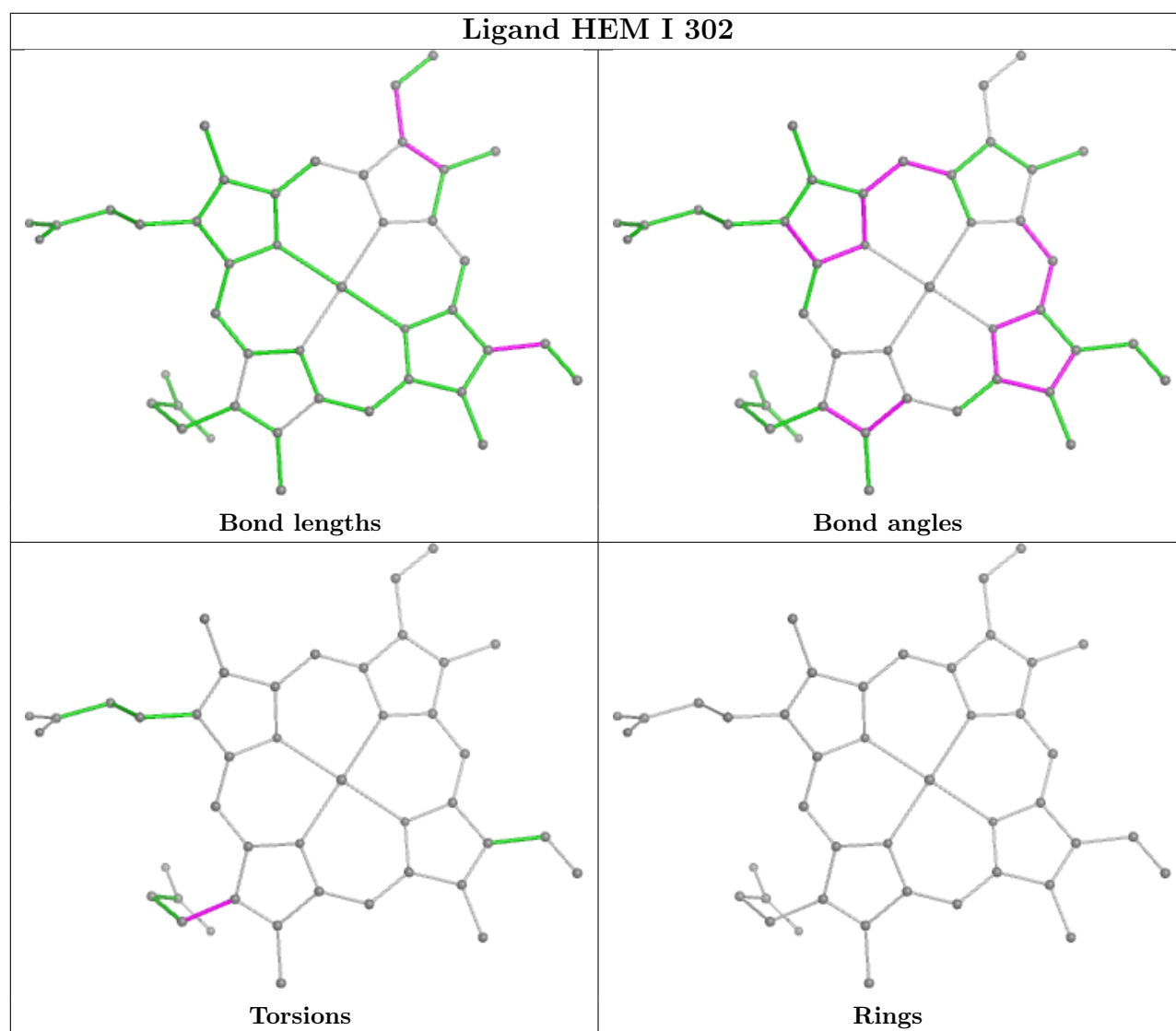












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

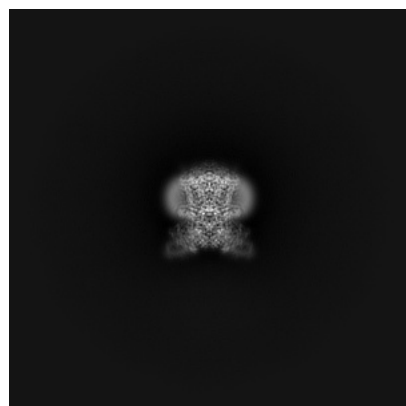
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19938. These allow visual inspection of the internal detail of the map and identification of artifacts.

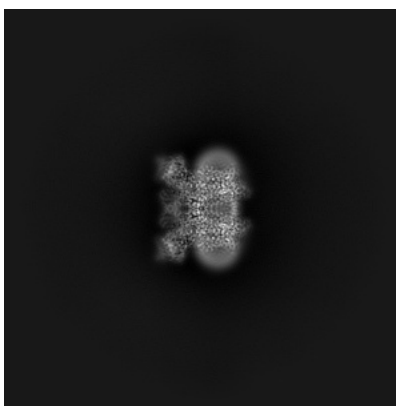
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

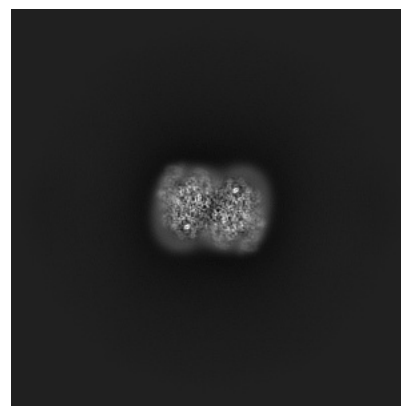
6.1.1 Primary map



X

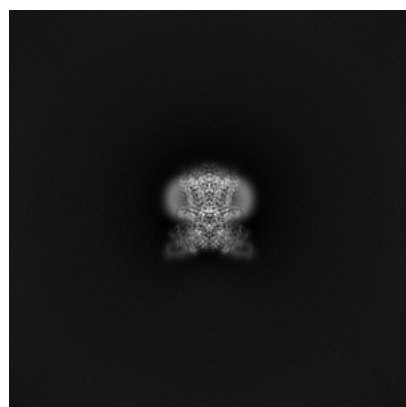


Y

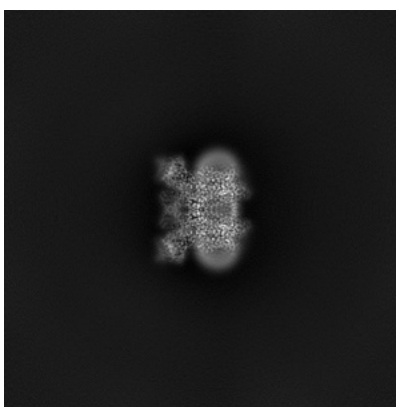


Z

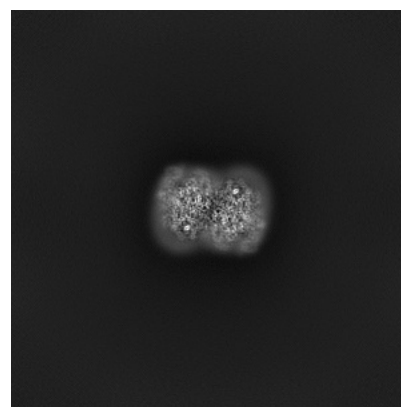
6.1.2 Raw map



X



Y

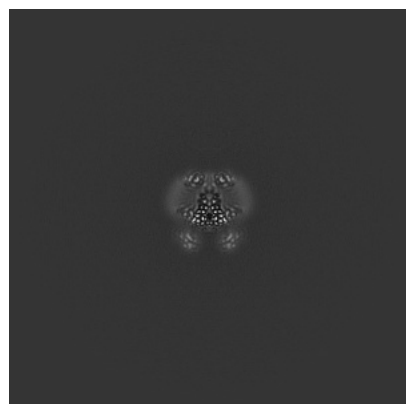


Z

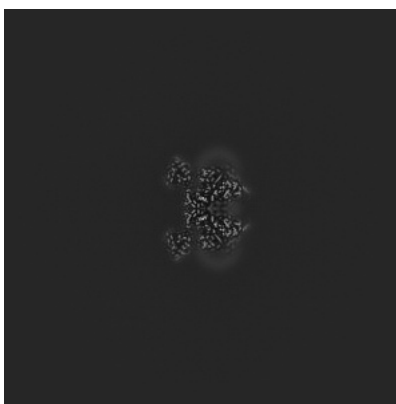
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

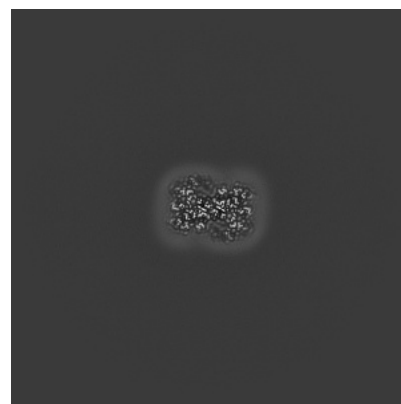
6.2.1 Primary map



X Index: 256

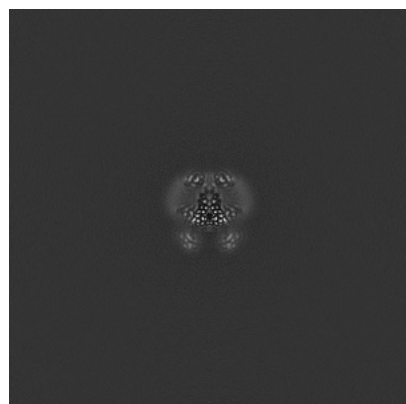


Y Index: 256

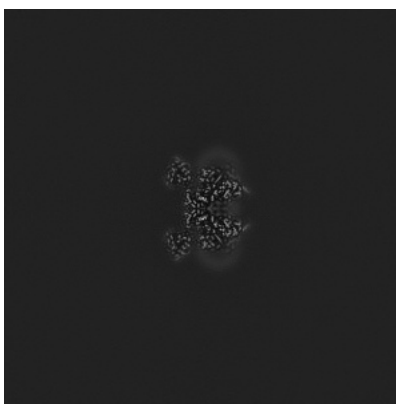


Z Index: 256

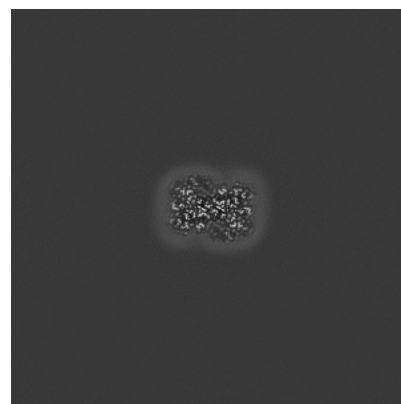
6.2.2 Raw map



X Index: 256



Y Index: 256

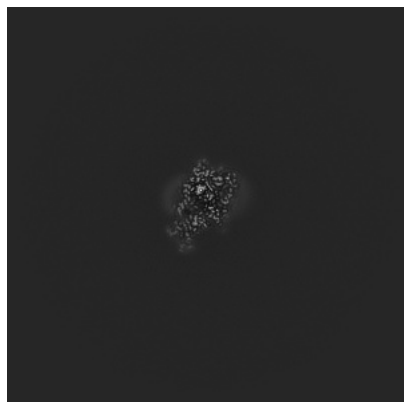


Z Index: 256

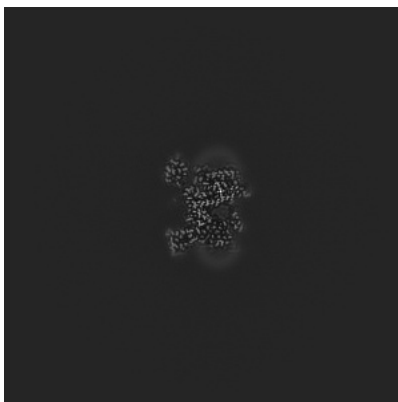
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

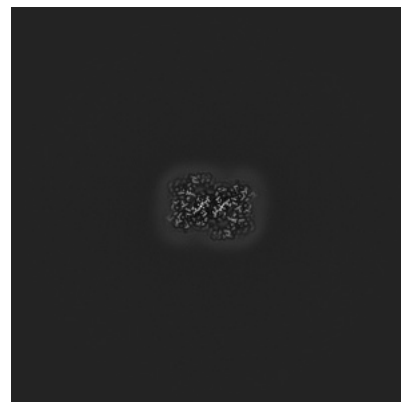
6.3.1 Primary map



X Index: 276

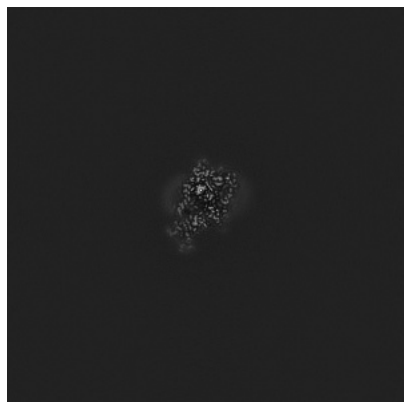


Y Index: 248

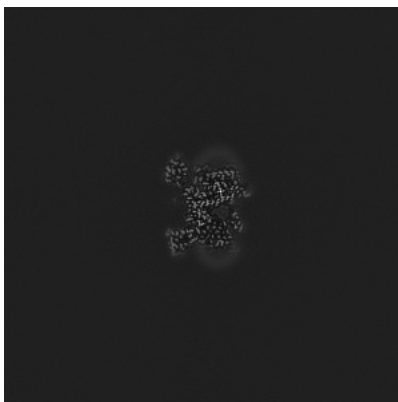


Z Index: 254

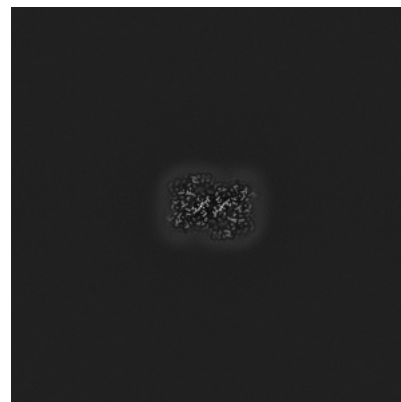
6.3.2 Raw map



X Index: 276



Y Index: 248

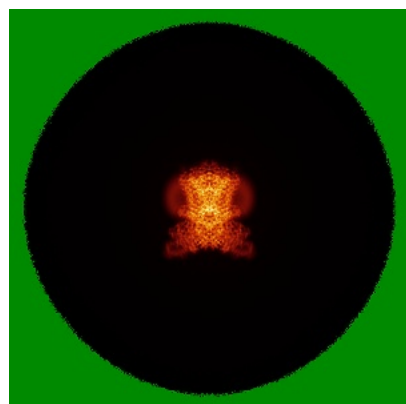


Z Index: 254

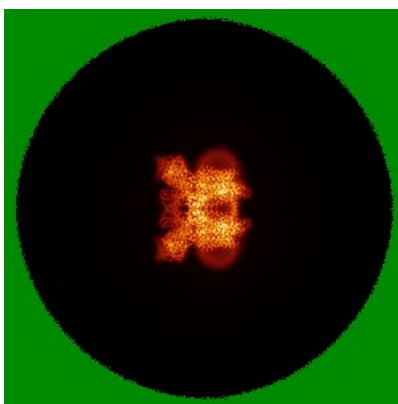
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

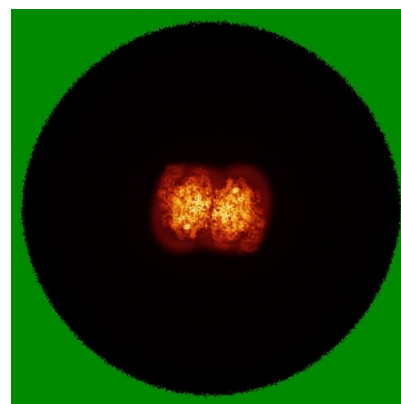
6.4.1 Primary map



X

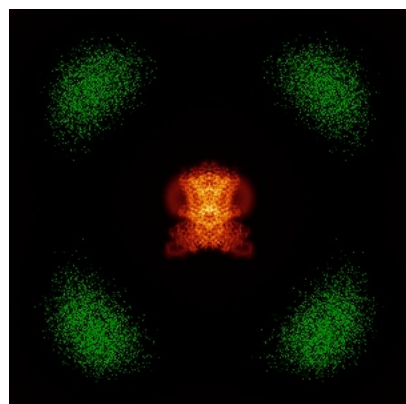


Y

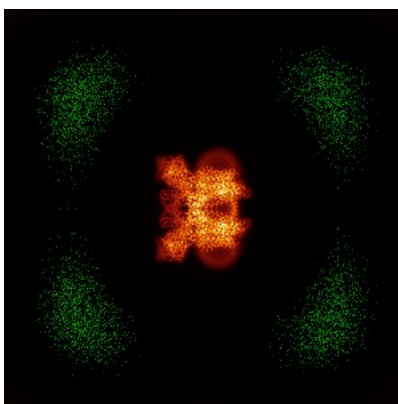


Z

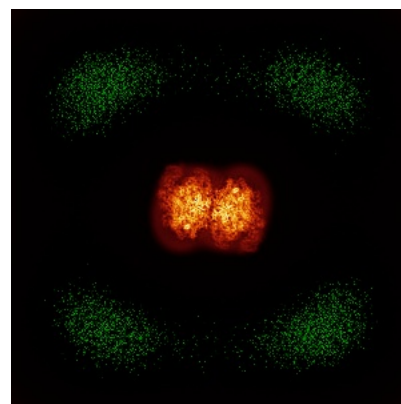
6.4.2 Raw map



X



Y

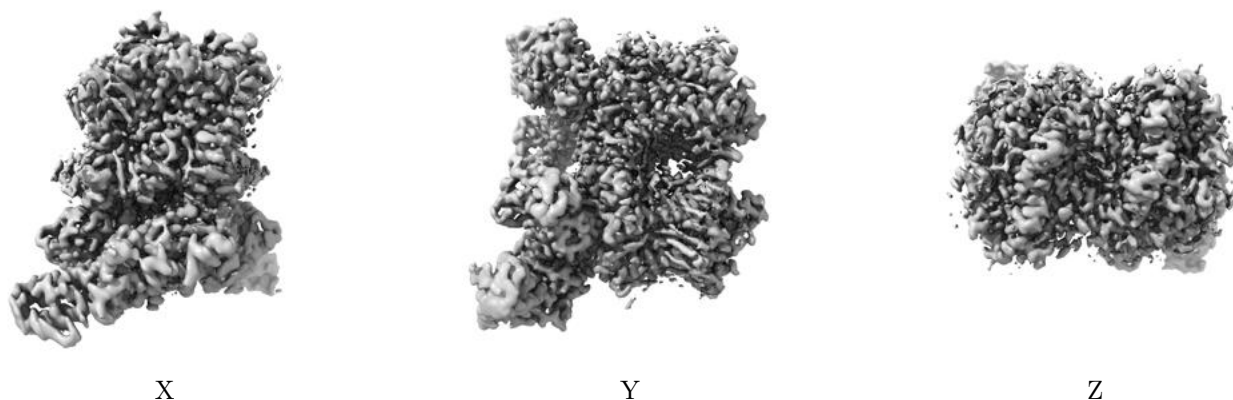


Z

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

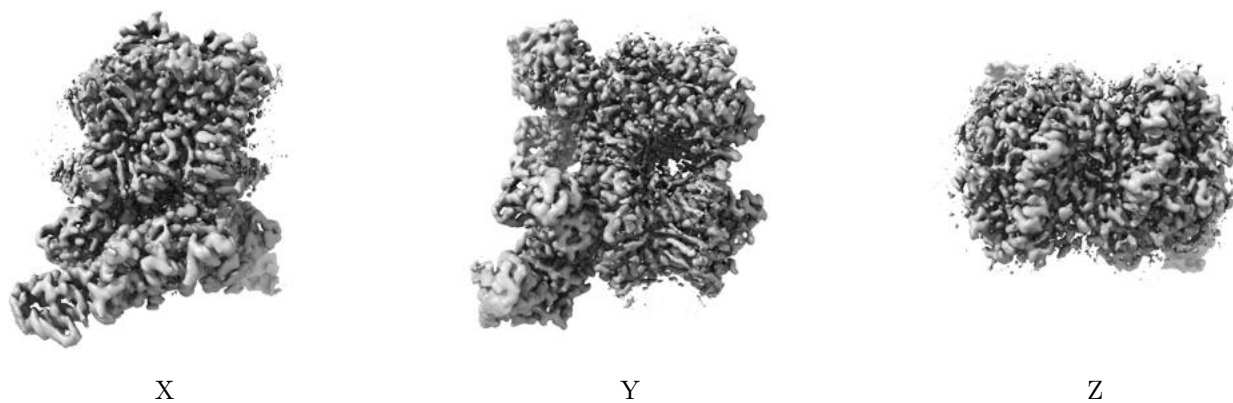
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.044. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

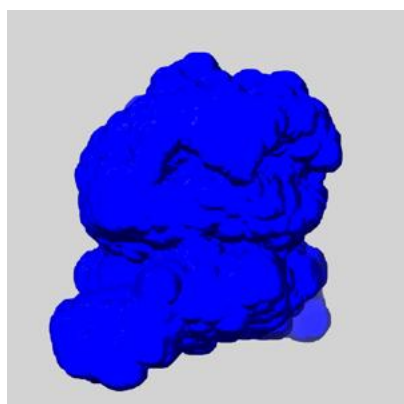
6.6 Mask visualisation [i](#)

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

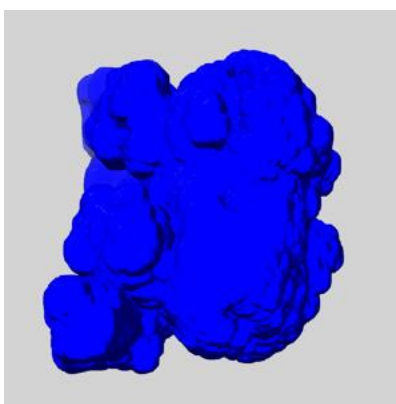
A mask typically either:

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

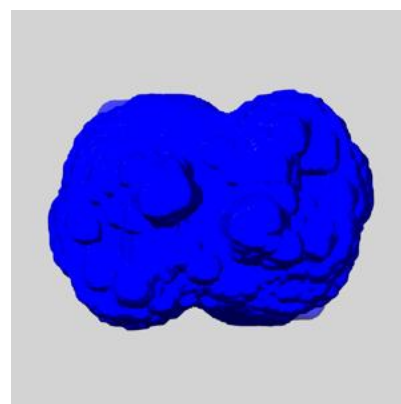
6.6.1 emd_19938_msk_1.map [i](#)



X

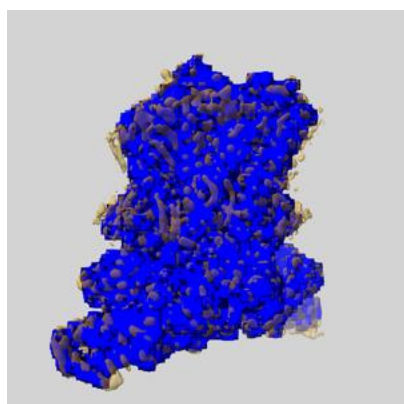


Y

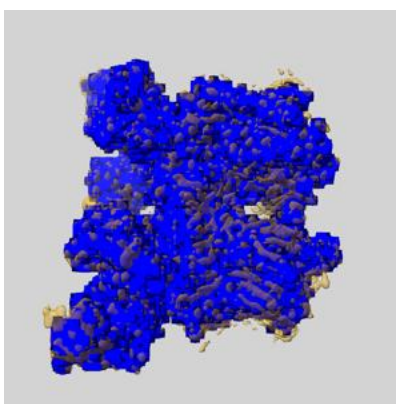


Z

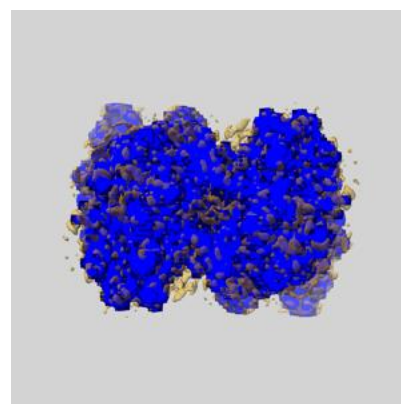
6.6.2 emd_19938_msk_2.map [i](#)



X



Y

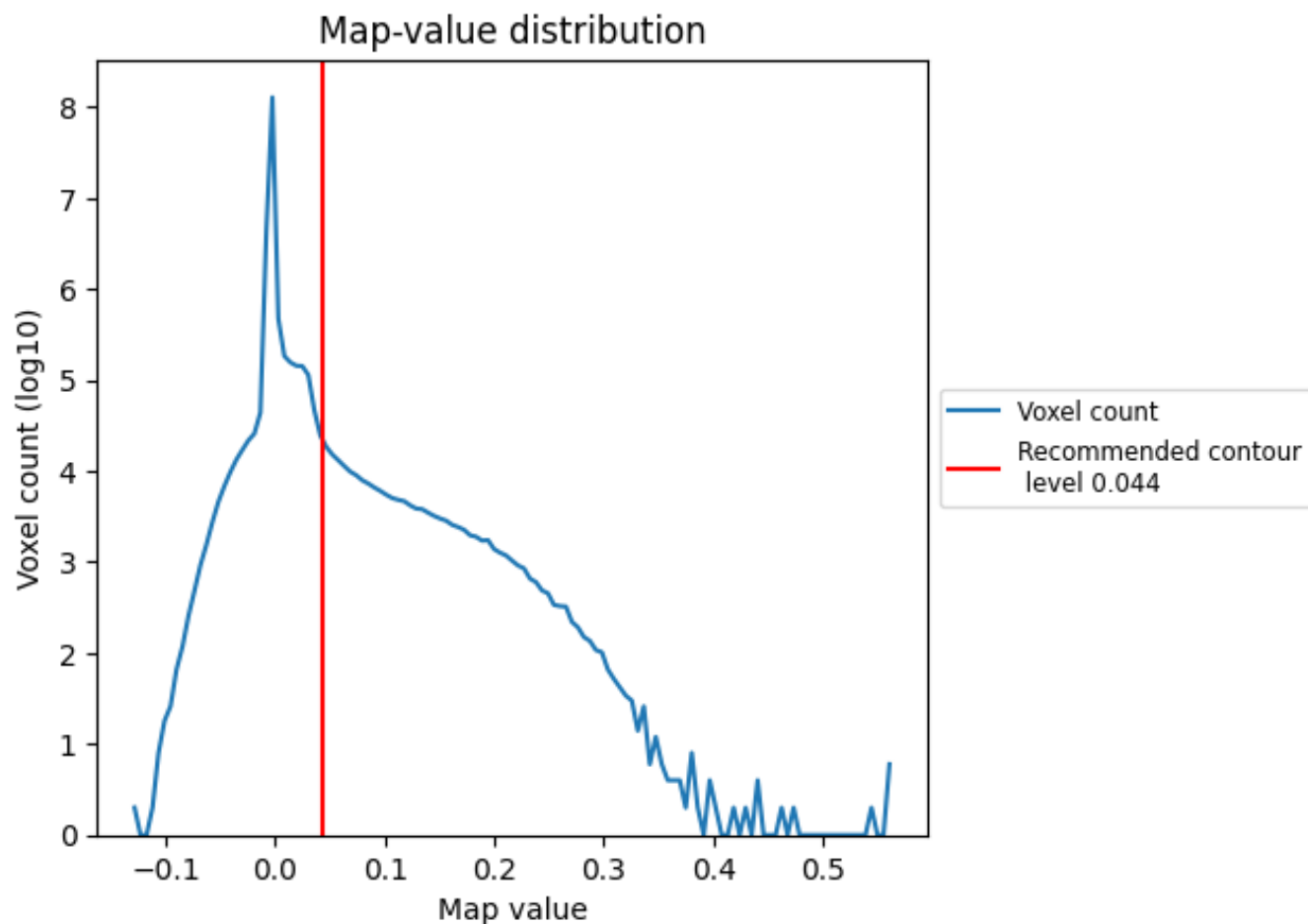


Z

7 Map analysis [i](#)

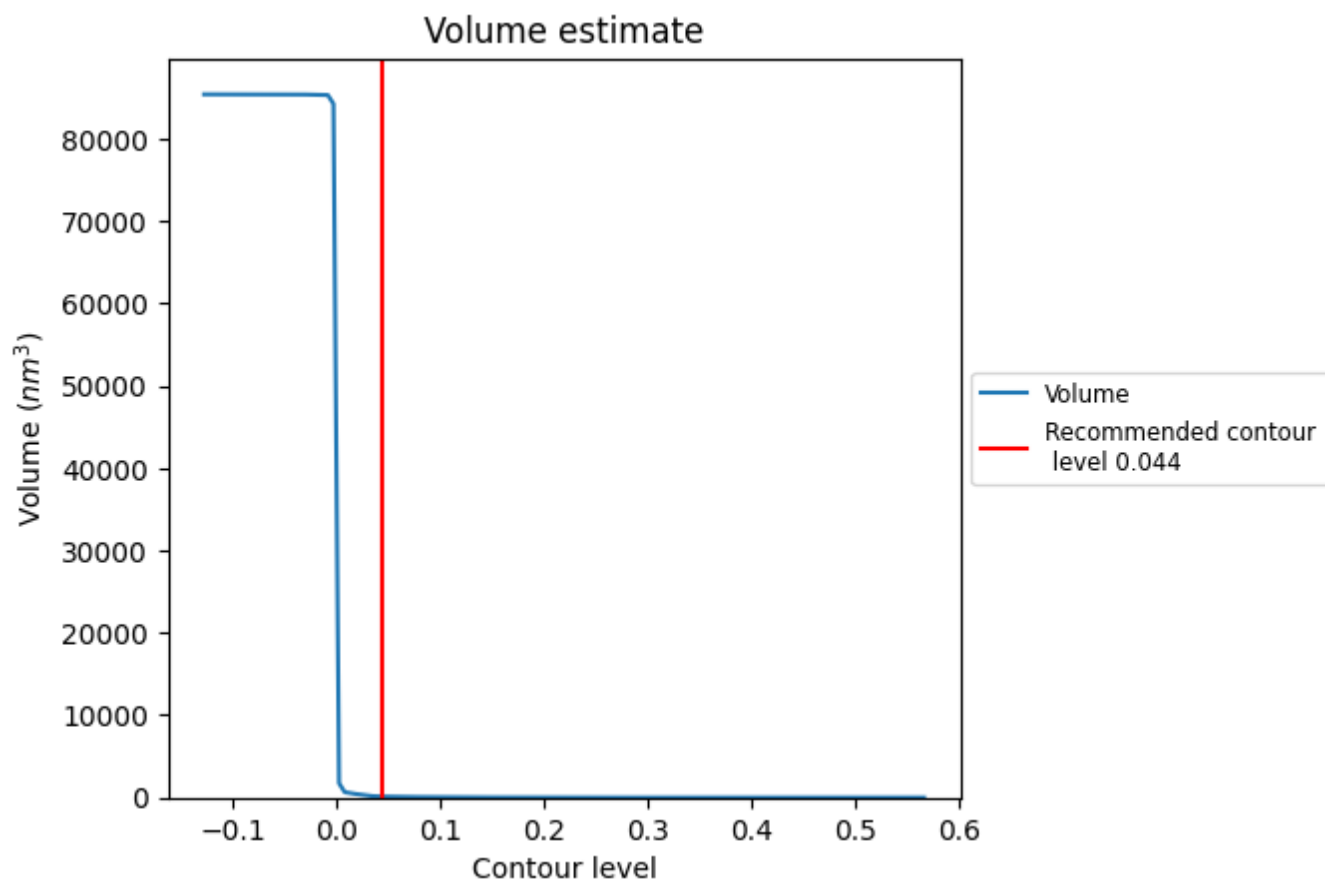
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

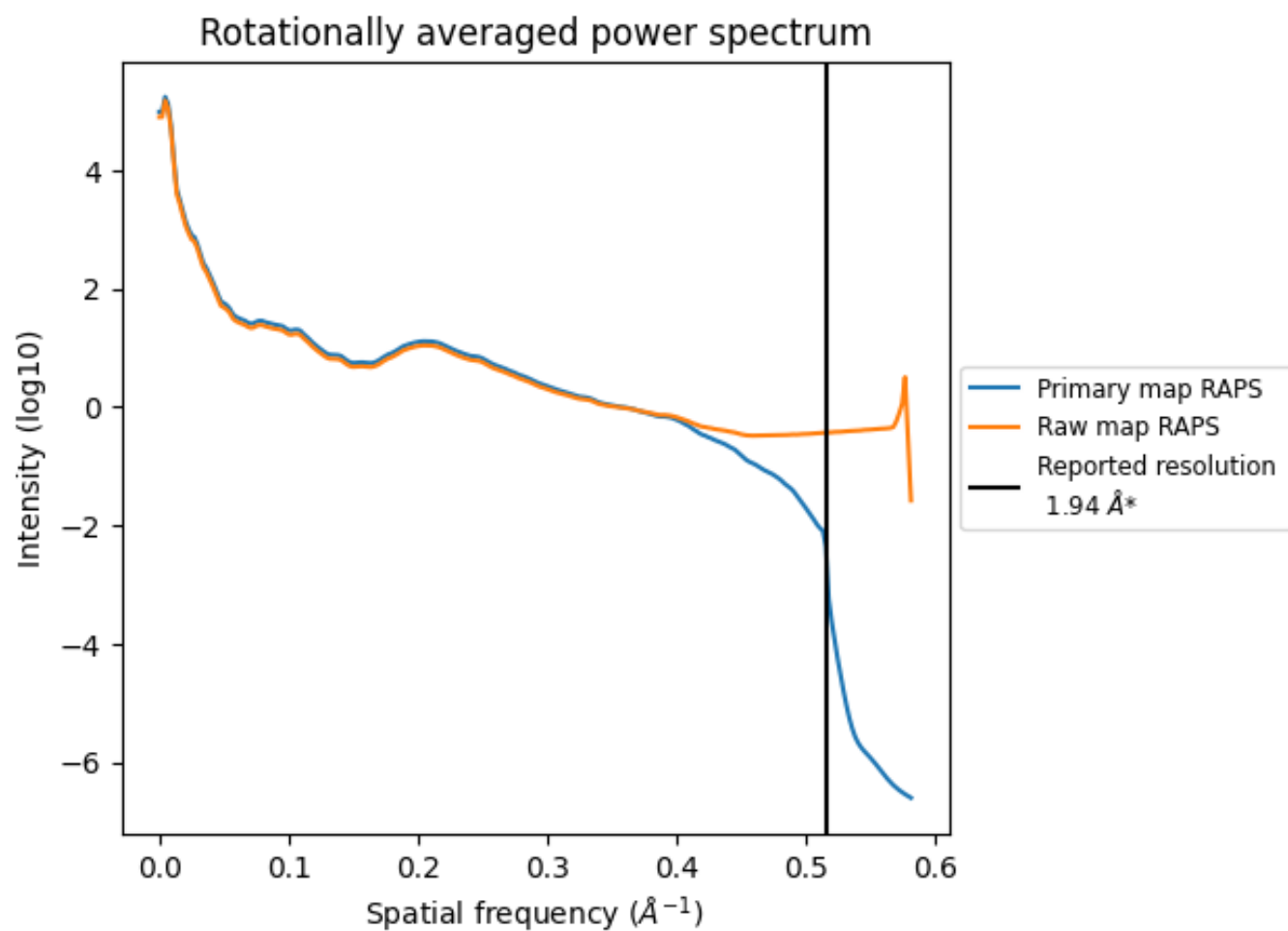
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 119 nm^3 ; this corresponds to an approximate mass of 108 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

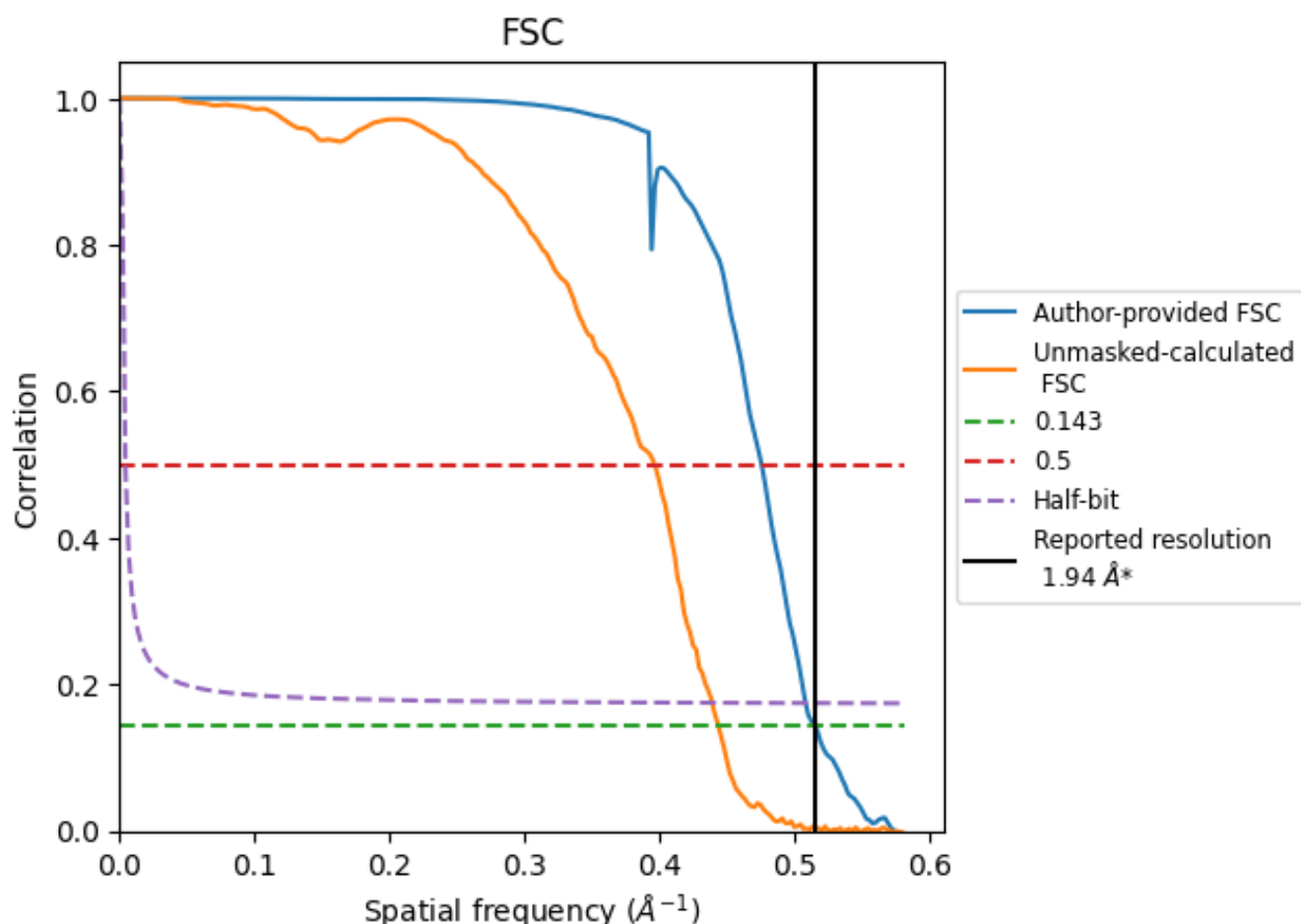


*Reported resolution corresponds to spatial frequency of 0.515 Å⁻¹

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 0.515 Å⁻¹

8.2 Resolution estimates [i](#)

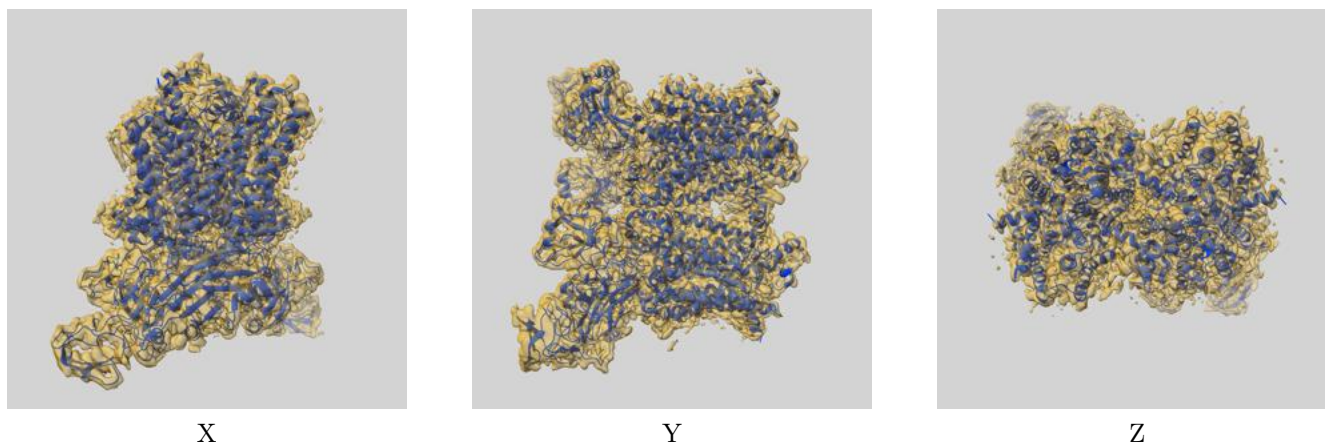
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.94	-	-
Author-provided FSC curve	1.94	2.10	1.97
Unmasked-calculated*	2.26	2.53	2.28

*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 2.26 differs from the reported value 1.94 by more than 10 %

9 Map-model fit [i](#)

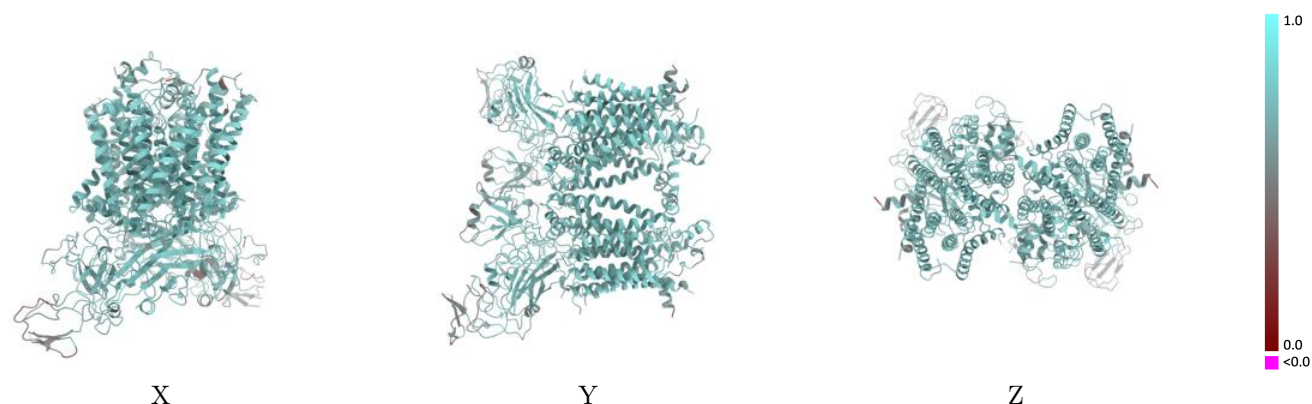
This section contains information regarding the fit between EMDB map EMD-19938 and PDB model 9ES7. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



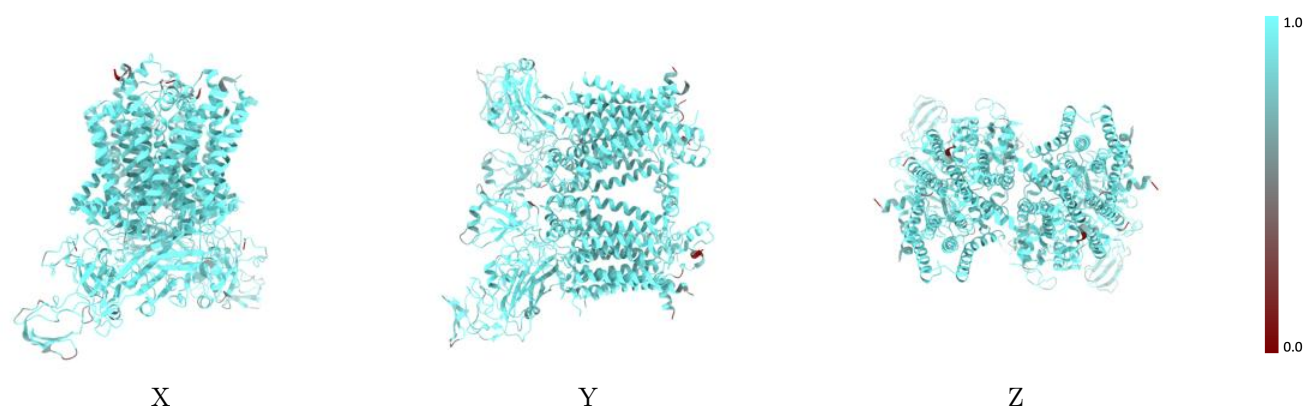
The images above show the 3D surface view of the map at the recommended contour level 0.044 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



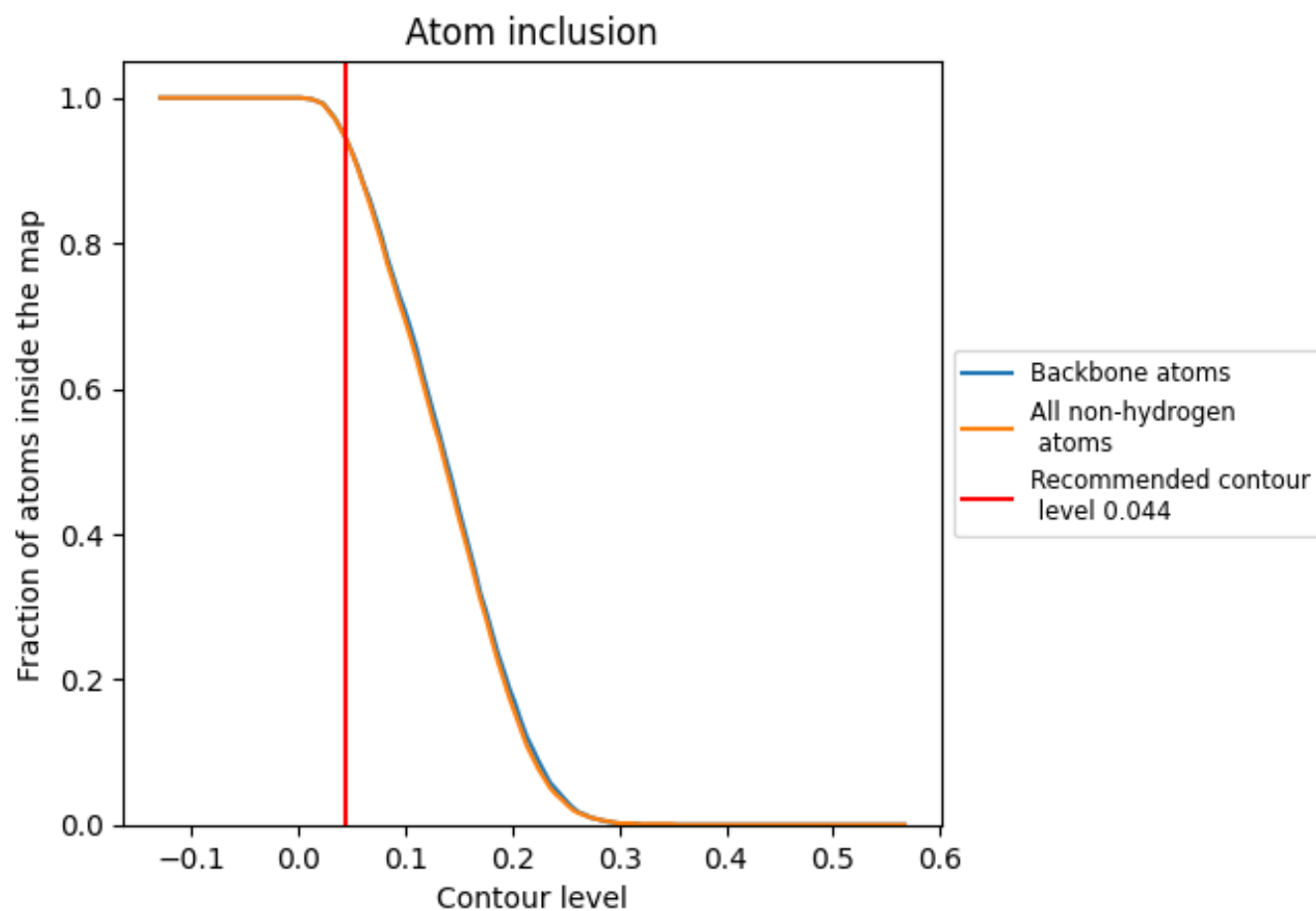
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.044).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.044) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.6820
A	 0.9780	 0.7260
B	 0.9740	 0.7040
C	 0.9350	 0.6480
D	 0.9270	 0.6550
E	 0.9710	 0.6870
F	 0.9470	 0.6870
G	 0.9280	 0.6970
H	 0.9880	 0.7250
I	 0.9780	 0.7270
J	 0.9740	 0.7030
K	 0.9350	 0.6480
L	 0.9270	 0.6540
M	 0.9710	 0.6860
N	 0.9470	 0.6850
O	 0.9240	 0.6980
P	 0.9880	 0.7280
Q	 0.7210	 0.5860
R	 0.7400	 0.5770

