



wwPDB EM Validation Summary Report ⓘ

Dec 12, 2022 – 06:57 PM EST

PDB ID : 3JBT
EMDB ID : EMD-6480
Title : Atomic structure of the Apaf-1 apoptosome
Authors : Zhou, M.; Li, Y.; Hu, Q.; Bai, X.; Huang, W.; Yan, C.; Scheres, S.H.W.; Shi, Y.
Deposited on : 2015-10-15
Resolution : 3.80 Å (reported)
Based on initial models : 3J2T, 4RSZ

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

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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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

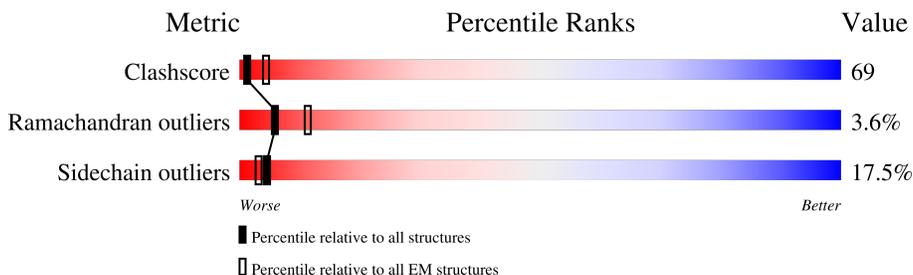
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



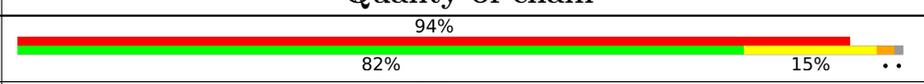
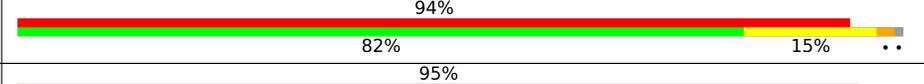
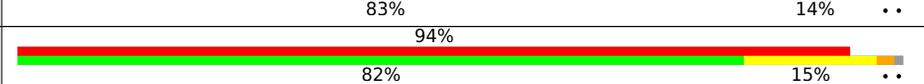
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	A	1260	
1	C	1260	
1	E	1260	
1	G	1260	
1	I	1260	
1	K	1260	
1	M	1260	
2	B	105	

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Mol	Chain	Length	Quality of chain
2	D	105	
2	F	105	
2	H	105	
2	J	105	
2	L	105	
2	N	105	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 70252 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 Apoptotic protease-activating factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1144	9139	5789	1569	1720	61	0	0
1	C	1144	9139	5789	1569	1720	61	0	0
1	E	1144	9139	5789	1569	1720	61	0	0
1	G	1144	9139	5789	1569	1720	61	0	0
1	I	1144	9139	5789	1569	1720	61	0	0
1	K	1144	9139	5789	1569	1720	61	0	0
1	M	1144	9139	5789	1569	1720	61	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1249	LEU	-	expression tag	UNP O14727
A	1250	GLU	-	expression tag	UNP O14727
A	1251	HIS	-	expression tag	UNP O14727
A	1252	HIS	-	expression tag	UNP O14727
A	1253	HIS	-	expression tag	UNP O14727
A	1254	HIS	-	expression tag	UNP O14727
A	1255	HIS	-	expression tag	UNP O14727
A	1256	HIS	-	expression tag	UNP O14727
A	1257	HIS	-	expression tag	UNP O14727
A	1258	HIS	-	expression tag	UNP O14727
A	1259	HIS	-	expression tag	UNP O14727
A	1260	HIS	-	expression tag	UNP O14727
C	1249	LEU	-	expression tag	UNP O14727
C	1250	GLU	-	expression tag	UNP O14727
C	1251	HIS	-	expression tag	UNP O14727
C	1252	HIS	-	expression tag	UNP O14727

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1253	HIS	-	expression tag	UNP O14727
C	1254	HIS	-	expression tag	UNP O14727
C	1255	HIS	-	expression tag	UNP O14727
C	1256	HIS	-	expression tag	UNP O14727
C	1257	HIS	-	expression tag	UNP O14727
C	1258	HIS	-	expression tag	UNP O14727
C	1259	HIS	-	expression tag	UNP O14727
C	1260	HIS	-	expression tag	UNP O14727
E	1249	LEU	-	expression tag	UNP O14727
E	1250	GLU	-	expression tag	UNP O14727
E	1251	HIS	-	expression tag	UNP O14727
E	1252	HIS	-	expression tag	UNP O14727
E	1253	HIS	-	expression tag	UNP O14727
E	1254	HIS	-	expression tag	UNP O14727
E	1255	HIS	-	expression tag	UNP O14727
E	1256	HIS	-	expression tag	UNP O14727
E	1257	HIS	-	expression tag	UNP O14727
E	1258	HIS	-	expression tag	UNP O14727
E	1259	HIS	-	expression tag	UNP O14727
E	1260	HIS	-	expression tag	UNP O14727
G	1249	LEU	-	expression tag	UNP O14727
G	1250	GLU	-	expression tag	UNP O14727
G	1251	HIS	-	expression tag	UNP O14727
G	1252	HIS	-	expression tag	UNP O14727
G	1253	HIS	-	expression tag	UNP O14727
G	1254	HIS	-	expression tag	UNP O14727
G	1255	HIS	-	expression tag	UNP O14727
G	1256	HIS	-	expression tag	UNP O14727
G	1257	HIS	-	expression tag	UNP O14727
G	1258	HIS	-	expression tag	UNP O14727
G	1259	HIS	-	expression tag	UNP O14727
G	1260	HIS	-	expression tag	UNP O14727
I	1249	LEU	-	expression tag	UNP O14727
I	1250	GLU	-	expression tag	UNP O14727
I	1251	HIS	-	expression tag	UNP O14727
I	1252	HIS	-	expression tag	UNP O14727
I	1253	HIS	-	expression tag	UNP O14727
I	1254	HIS	-	expression tag	UNP O14727
I	1255	HIS	-	expression tag	UNP O14727
I	1256	HIS	-	expression tag	UNP O14727
I	1257	HIS	-	expression tag	UNP O14727
I	1258	HIS	-	expression tag	UNP O14727

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Chain	Residue	Modelled	Actual	Comment	Reference
I	1259	HIS	-	expression tag	UNP O14727
I	1260	HIS	-	expression tag	UNP O14727
K	1249	LEU	-	expression tag	UNP O14727
K	1250	GLU	-	expression tag	UNP O14727
K	1251	HIS	-	expression tag	UNP O14727
K	1252	HIS	-	expression tag	UNP O14727
K	1253	HIS	-	expression tag	UNP O14727
K	1254	HIS	-	expression tag	UNP O14727
K	1255	HIS	-	expression tag	UNP O14727
K	1256	HIS	-	expression tag	UNP O14727
K	1257	HIS	-	expression tag	UNP O14727
K	1258	HIS	-	expression tag	UNP O14727
K	1259	HIS	-	expression tag	UNP O14727
K	1260	HIS	-	expression tag	UNP O14727
M	1249	LEU	-	expression tag	UNP O14727
M	1250	GLU	-	expression tag	UNP O14727
M	1251	HIS	-	expression tag	UNP O14727
M	1252	HIS	-	expression tag	UNP O14727
M	1253	HIS	-	expression tag	UNP O14727
M	1254	HIS	-	expression tag	UNP O14727
M	1255	HIS	-	expression tag	UNP O14727
M	1256	HIS	-	expression tag	UNP O14727
M	1257	HIS	-	expression tag	UNP O14727
M	1258	HIS	-	expression tag	UNP O14727
M	1259	HIS	-	expression tag	UNP O14727
M	1260	HIS	-	expression tag	UNP O14727

- Molecule 2 is a protein called Cytochrome c.

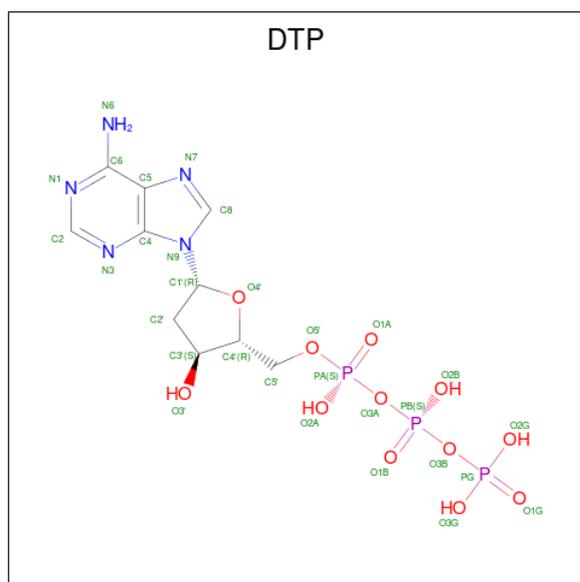
Mol	Chain	Residues	Atoms				AltConf	Trace	
2	B	104	Total	C	N	O	S	0	0
			823	524	144	151	4		
2	D	104	Total	C	N	O	S	0	0
			823	524	144	151	4		
2	F	104	Total	C	N	O	S	0	0
			823	524	144	151	4		
2	H	104	Total	C	N	O	S	0	0
			823	524	144	151	4		
2	J	104	Total	C	N	O	S	0	0
			823	524	144	151	4		
2	L	104	Total	C	N	O	S	0	0
			823	524	144	151	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	N	104	Total 823	C 524	N 144	O 151	S 4	0	0

- Molecule 3 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	A	1	Total 30	C 10	N 5	O 12	P 3	0
3	C	1	Total 30	C 10	N 5	O 12	P 3	0
3	E	1	Total 30	C 10	N 5	O 12	P 3	0
3	G	1	Total 30	C 10	N 5	O 12	P 3	0
3	I	1	Total 30	C 10	N 5	O 12	P 3	0
3	K	1	Total 30	C 10	N 5	O 12	P 3	0
3	M	1	Total 30	C 10	N 5	O 12	P 3	0

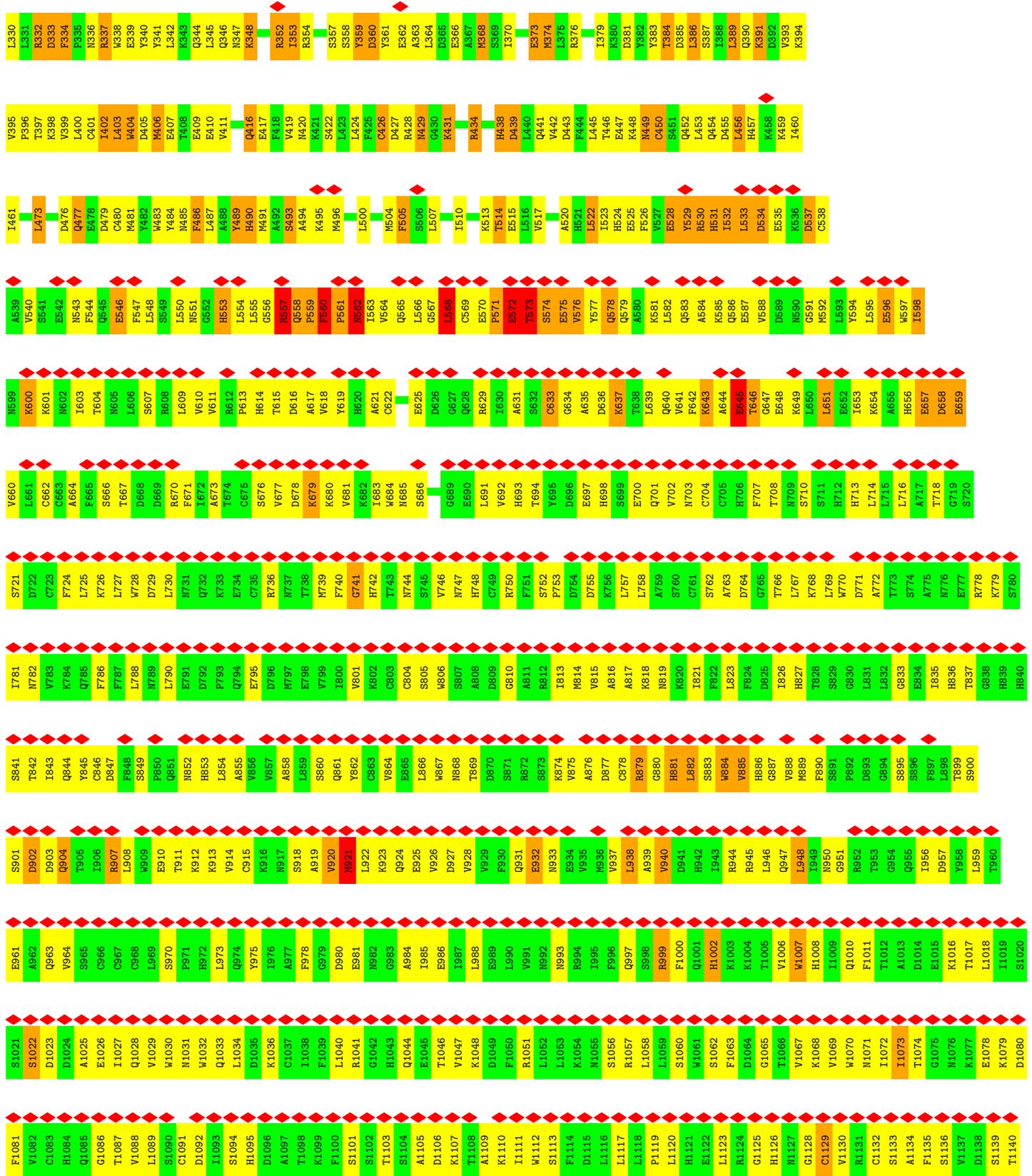
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
4	A	1	Total 1	Mg 1	0

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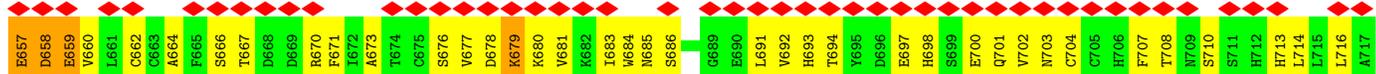
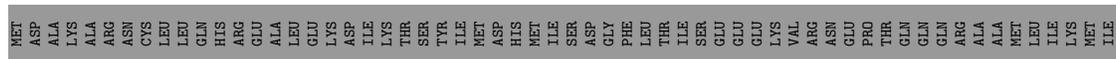
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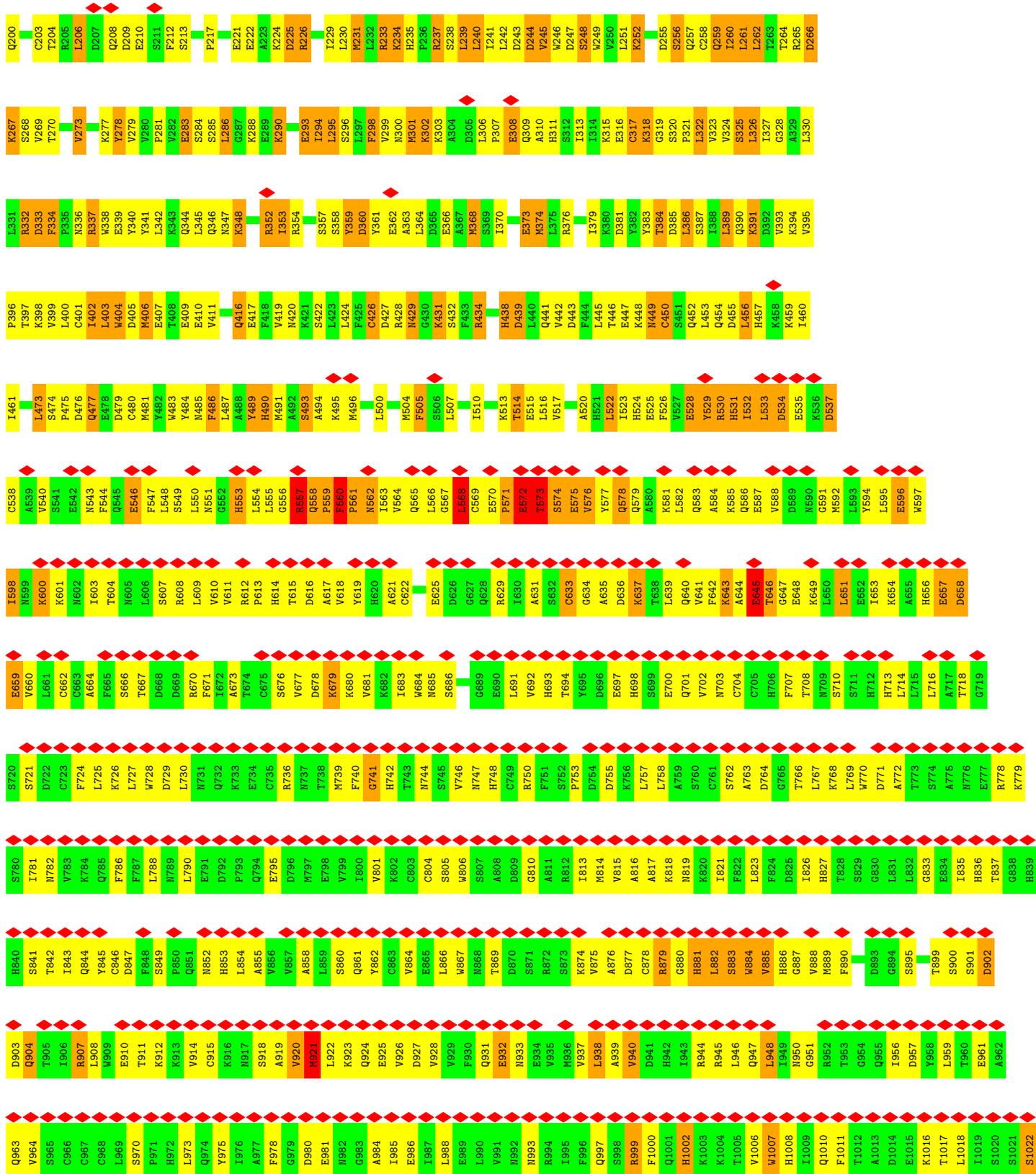
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Fe	N	O	
5	L	1	43	34	1	4	4	0
5	N	1	43	34	1	4	4	0

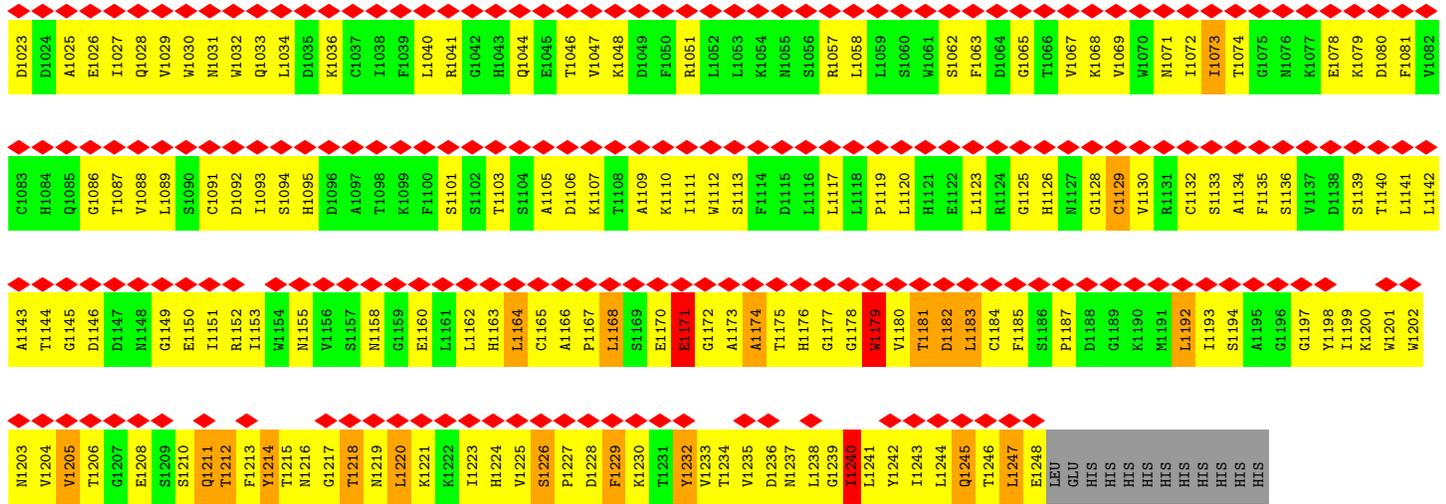




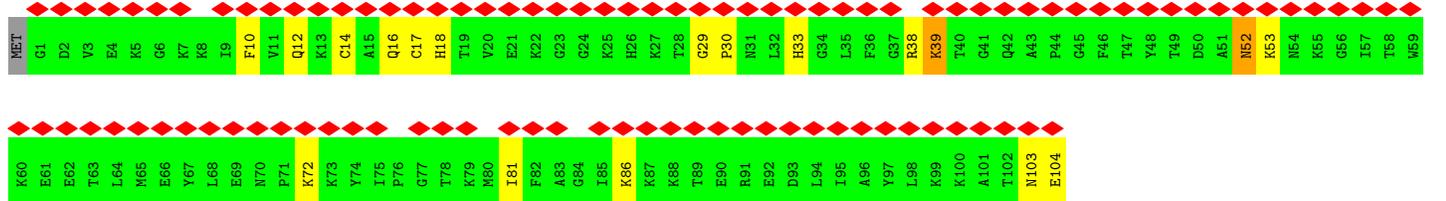
• Molecule 1: Apoptotic protease-activating factor 1



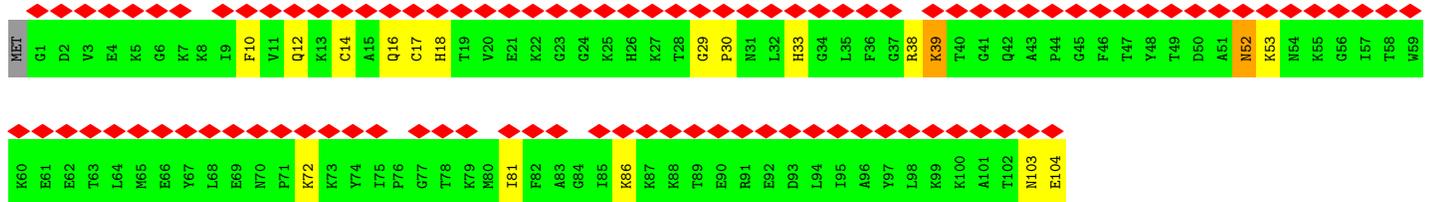
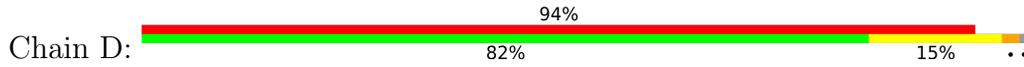




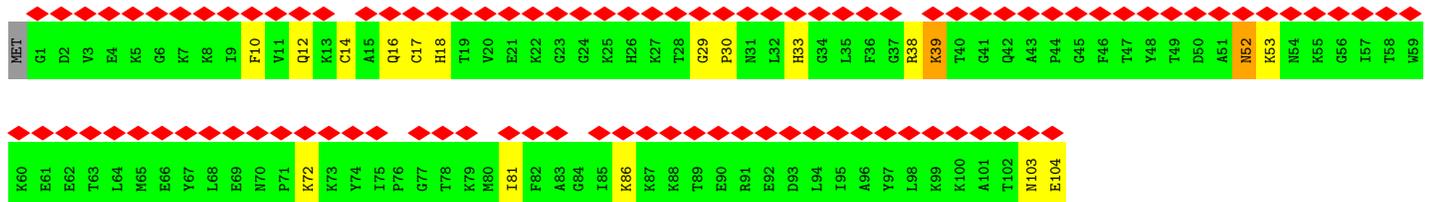
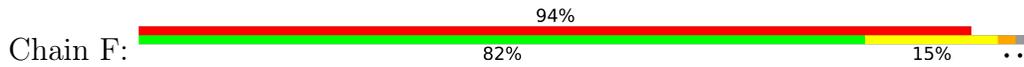
• Molecule 2: Cytochrome c



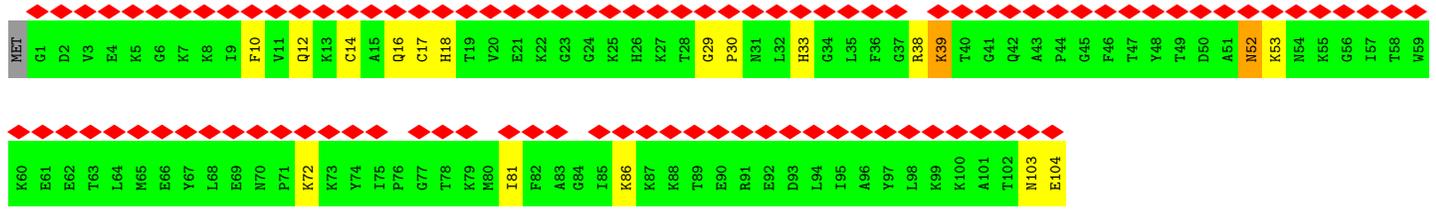
• Molecule 2: Cytochrome c



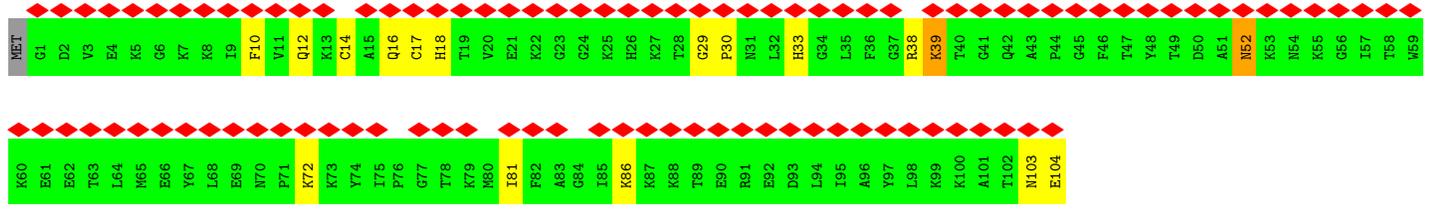
• Molecule 2: Cytochrome c



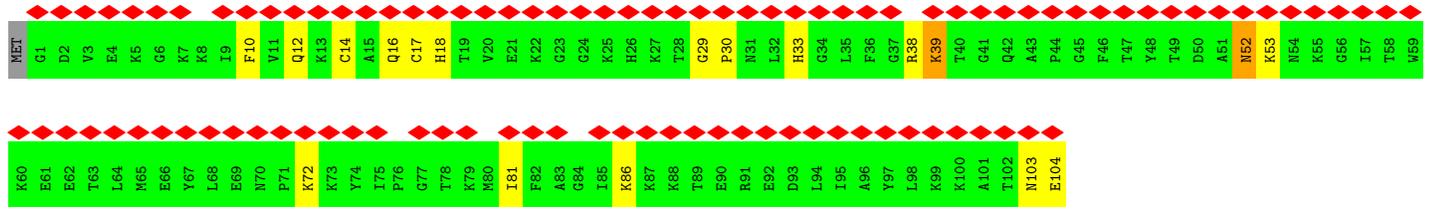
• Molecule 2: Cytochrome c



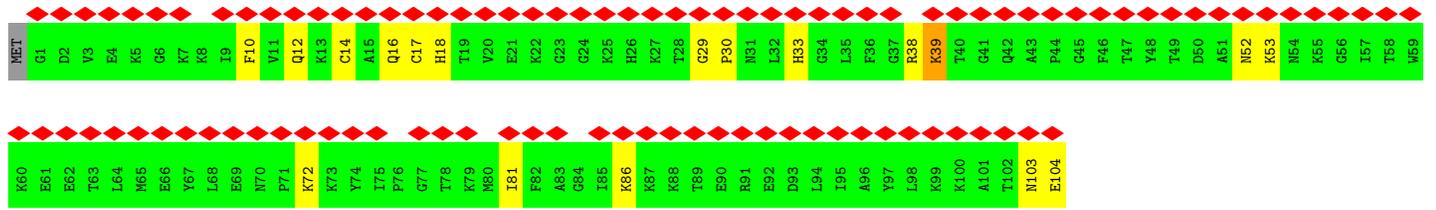
• Molecule 2: Cytochrome c



• Molecule 2: Cytochrome c



• Molecule 2: Cytochrome c



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	134919	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.351	Depositor
Minimum map value	-0.239	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.32, 1.32, 1.32	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: DTP, MG, HEM

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	0.30	0/9337	0.51	2/12636 (0.0%)
1	C	0.30	0/9337	0.51	2/12636 (0.0%)
1	E	0.30	0/9337	0.51	2/12636 (0.0%)
1	G	0.30	0/9337	0.51	2/12636 (0.0%)
1	I	0.30	0/9337	0.51	2/12636 (0.0%)
1	K	0.30	0/9337	0.51	2/12636 (0.0%)
1	M	0.30	0/9337	0.51	2/12636 (0.0%)
2	B	0.65	0/839	0.73	0/1118
2	D	0.65	0/839	0.73	0/1118
2	F	0.65	0/839	0.73	0/1118
2	H	0.65	0/839	0.73	0/1118
2	J	0.65	0/839	0.73	0/1118
2	L	0.65	0/839	0.73	0/1118
2	N	0.65	0/839	0.73	0/1118
All	All	0.34	0/71232	0.53	14/96278 (0.0%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	880	GLY	N-CA-C	5.73	127.43	113.10
1	I	880	GLY	N-CA-C	5.73	127.43	113.10
1	K	880	GLY	N-CA-C	5.73	127.43	113.10
1	M	880	GLY	N-CA-C	5.73	127.42	113.10
1	E	880	GLY	N-CA-C	5.72	127.41	113.10

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	A	9139	0	9005	1372	0
1	C	9139	0	9005	1371	0
1	E	9139	0	9005	1360	0
1	G	9139	0	9005	1382	0
1	I	9139	0	9005	1358	0
1	K	9139	0	9005	1357	0
1	M	9139	0	9005	1366	0
2	B	823	0	849	31	0
2	D	823	0	849	33	0
2	F	823	0	849	30	0
2	H	823	0	849	34	0
2	J	823	0	849	32	0
2	L	823	0	849	33	0
2	N	823	0	849	31	0
3	A	30	0	12	6	0
3	C	30	0	12	6	0
3	E	30	0	12	6	0
3	G	30	0	12	6	0
3	I	30	0	12	7	0
3	K	30	0	12	6	0
3	M	30	0	12	6	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
4	K	1	0	0	0	0
4	M	1	0	0	0	0
5	B	43	0	30	15	0
5	D	43	0	30	16	0
5	F	43	0	30	14	0
5	H	43	0	30	16	0
5	J	43	0	30	15	0
5	L	43	0	30	15	0
5	N	43	0	30	13	0
All	All	70252	0	69272	9596	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 69.

The worst 5 of 9596 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:544:PHE:CE1	1:E:576:VAL:HG13	1.28	1.68
1:G:544:PHE:CE1	1:G:576:VAL:HG13	1.28	1.67
1:C:544:PHE:CE1	1:C:576:VAL:HG13	1.28	1.65
1:C:862:TYR:CD1	1:C:885:VAL:HG12	1.26	1.64
1:A:544:PHE:CE1	1:A:576:VAL:HG13	1.28	1.64

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1142/1260 (91%)	999 (88%)	98 (9%)	45 (4%)	3	28
1	C	1142/1260 (91%)	999 (88%)	98 (9%)	45 (4%)	3	28
1	E	1142/1260 (91%)	999 (88%)	98 (9%)	45 (4%)	3	28
1	G	1142/1260 (91%)	999 (88%)	98 (9%)	45 (4%)	3	28
1	I	1142/1260 (91%)	999 (88%)	98 (9%)	45 (4%)	3	28
1	K	1142/1260 (91%)	999 (88%)	97 (8%)	46 (4%)	3	28
1	M	1142/1260 (91%)	999 (88%)	97 (8%)	46 (4%)	3	28
2	B	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
2	D	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
2	F	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
2	H	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
2	J	102/105 (97%)	100 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	L	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
2	N	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
All	All	8708/9555 (91%)	7693 (88%)	698 (8%)	317 (4%)	6	30

5 of 317 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	PRO
1	A	557	ARG
1	A	560	PHE
1	A	562	ASN
1	A	645	GLU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
1	C	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
1	E	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
1	G	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
1	I	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
1	K	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
1	M	1027/1131 (91%)	838 (82%)	189 (18%)	1	11
2	B	86/87 (99%)	80 (93%)	6 (7%)	15	46
2	D	86/87 (99%)	80 (93%)	6 (7%)	15	46
2	F	86/87 (99%)	80 (93%)	6 (7%)	15	46
2	H	86/87 (99%)	80 (93%)	6 (7%)	15	46
2	J	86/87 (99%)	81 (94%)	5 (6%)	20	51
2	L	86/87 (99%)	80 (93%)	6 (7%)	15	46
2	N	86/87 (99%)	80 (93%)	6 (7%)	15	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7791/8526 (91%)	6427 (82%)	1364 (18%)	4 13

5 of 1364 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	633	CYS
1	K	1170	GLU
1	I	1171	GLU
1	I	619	TYR
1	K	332	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 208 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	1237	ASN
1	I	1126	HIS
1	M	840	HIS
1	I	138	GLN
1	I	457	HIS

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](#)

Of 21 ligands modelled in this entry, 7 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DTP	C	1301	4	26,32,32	0.86	1 (3%)	30,50,50	1.56	4 (13%)
5	HEM	N	201	2	41,50,50	1.31	6 (14%)	45,82,82	1.74	6 (13%)
5	HEM	L	201	2	41,50,50	1.32	6 (14%)	45,82,82	1.73	6 (13%)
5	HEM	F	201	2	41,50,50	1.31	5 (12%)	45,82,82	1.73	6 (13%)
3	DTP	E	1301	4	26,32,32	0.87	1 (3%)	30,50,50	1.56	4 (13%)
3	DTP	M	1301	4	26,32,32	0.86	1 (3%)	30,50,50	1.56	4 (13%)
5	HEM	D	201	2	41,50,50	1.31	6 (14%)	45,82,82	1.73	6 (13%)
5	HEM	J	201	2	41,50,50	1.32	6 (14%)	45,82,82	1.73	6 (13%)
5	HEM	B	201	2	41,50,50	1.31	6 (14%)	45,82,82	1.73	6 (13%)
3	DTP	G	1301	4	26,32,32	0.87	1 (3%)	30,50,50	1.56	4 (13%)
3	DTP	K	1301	4	26,32,32	0.86	1 (3%)	30,50,50	1.56	4 (13%)
3	DTP	A	1301	4	26,32,32	0.86	1 (3%)	30,50,50	1.56	4 (13%)
5	HEM	H	201	2	41,50,50	1.32	6 (14%)	45,82,82	1.73	6 (13%)
3	DTP	I	1301	4	26,32,32	0.86	1 (3%)	30,50,50	1.56	4 (13%)

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
3	DTP	C	1301	4	-	5/18/34/34	0/3/3/3
5	HEM	N	201	2	-	7/12/54/54	-
5	HEM	L	201	2	-	7/12/54/54	-
5	HEM	F	201	2	-	7/12/54/54	-
3	DTP	E	1301	4	-	5/18/34/34	0/3/3/3
3	DTP	M	1301	4	-	5/18/34/34	0/3/3/3
5	HEM	D	201	2	-	7/12/54/54	-
5	HEM	J	201	2	-	7/12/54/54	-
5	HEM	B	201	2	-	7/12/54/54	-
3	DTP	G	1301	4	-	5/18/34/34	0/3/3/3
3	DTP	K	1301	4	-	5/18/34/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DTP	A	1301	4	-	5/18/34/34	0/3/3/3
5	HEM	H	201	2	-	7/12/54/54	-
3	DTP	I	1301	4	-	5/18/34/34	0/3/3/3

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	201	HEM	C1B-NB	-3.40	1.34	1.40
5	H	201	HEM	C1B-NB	-3.38	1.34	1.40
5	L	201	HEM	C1B-NB	-3.37	1.34	1.40
5	N	201	HEM	C1B-NB	-3.37	1.34	1.40
5	F	201	HEM	C1B-NB	-3.35	1.34	1.40

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	201	HEM	CHC-C4B-NB	4.71	129.54	124.43
5	N	201	HEM	CHC-C4B-NB	4.70	129.53	124.43
5	L	201	HEM	CHC-C4B-NB	4.69	129.52	124.43
5	H	201	HEM	CHC-C4B-NB	4.67	129.51	124.43
5	D	201	HEM	CHC-C4B-NB	4.65	129.49	124.43

There are no chirality outliers.

5 of 84 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1301	DTP	C5'-O5'-PA-O2A
3	A	1301	DTP	C5'-O5'-PA-O3A
3	C	1301	DTP	C5'-O5'-PA-O2A
3	C	1301	DTP	C5'-O5'-PA-O3A
3	E	1301	DTP	C5'-O5'-PA-O2A

There are no ring outliers.

14 monomers are involved in 147 short contacts:

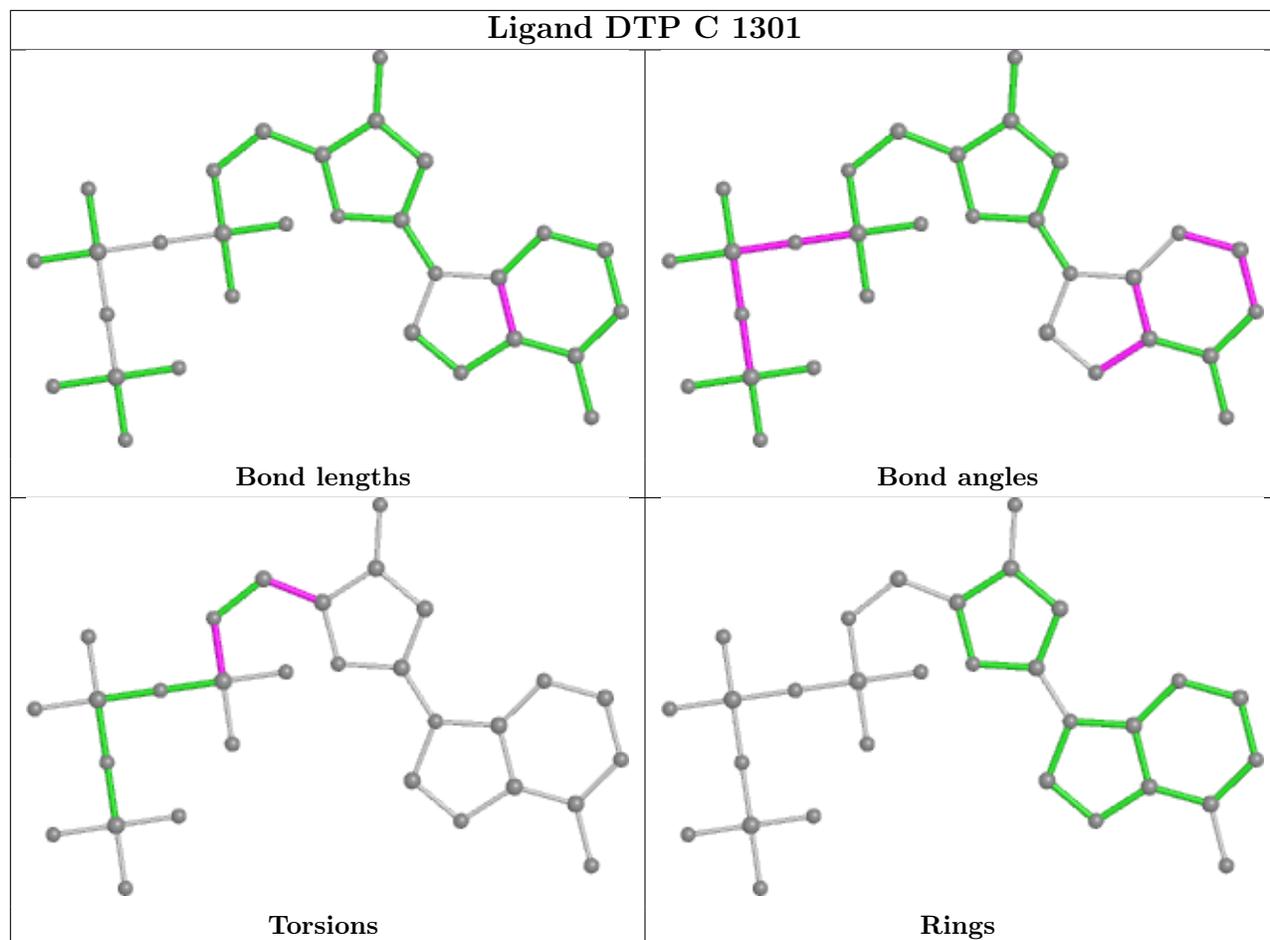
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1301	DTP	6	0
5	N	201	HEM	13	0
5	L	201	HEM	15	0
5	F	201	HEM	14	0

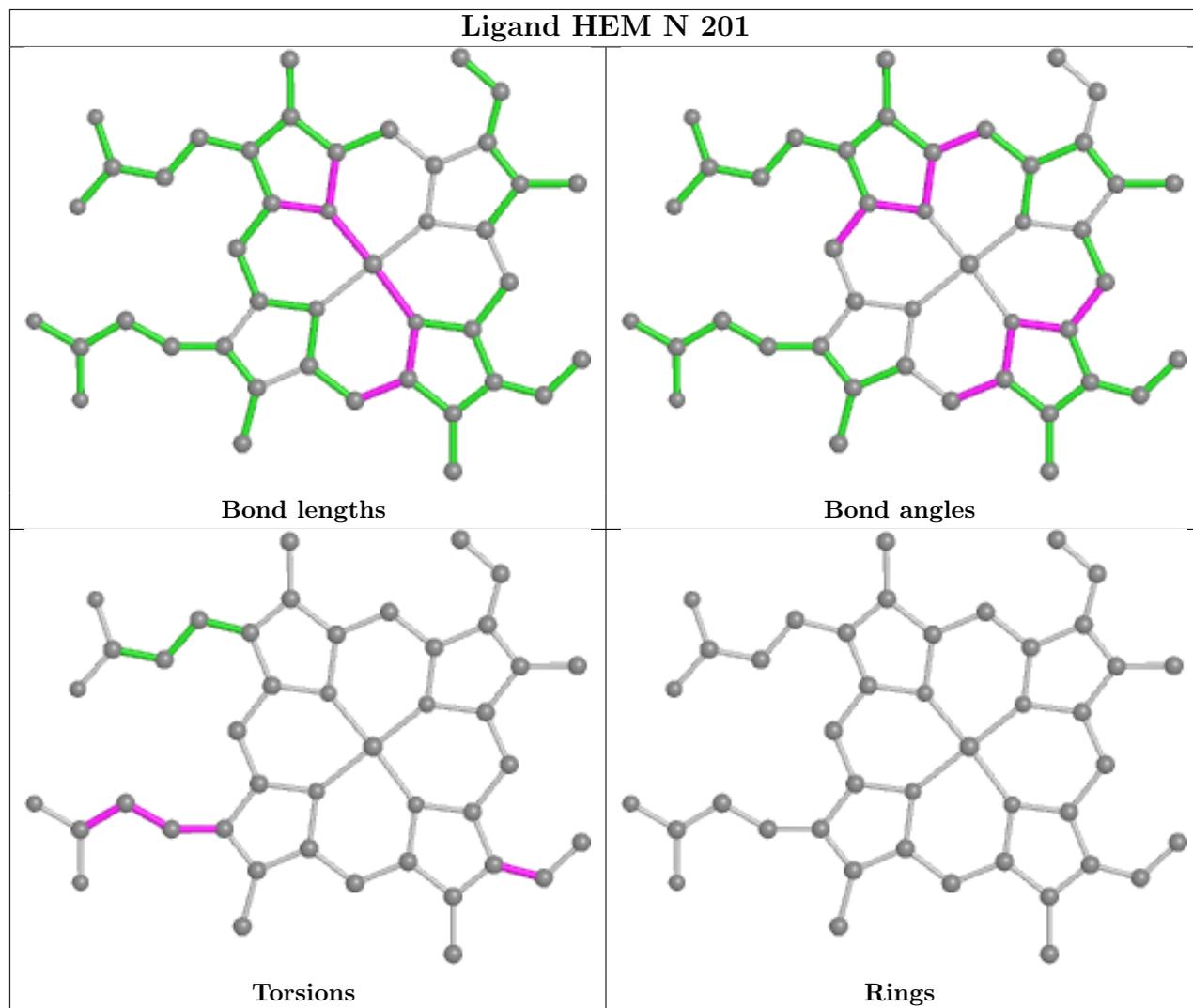
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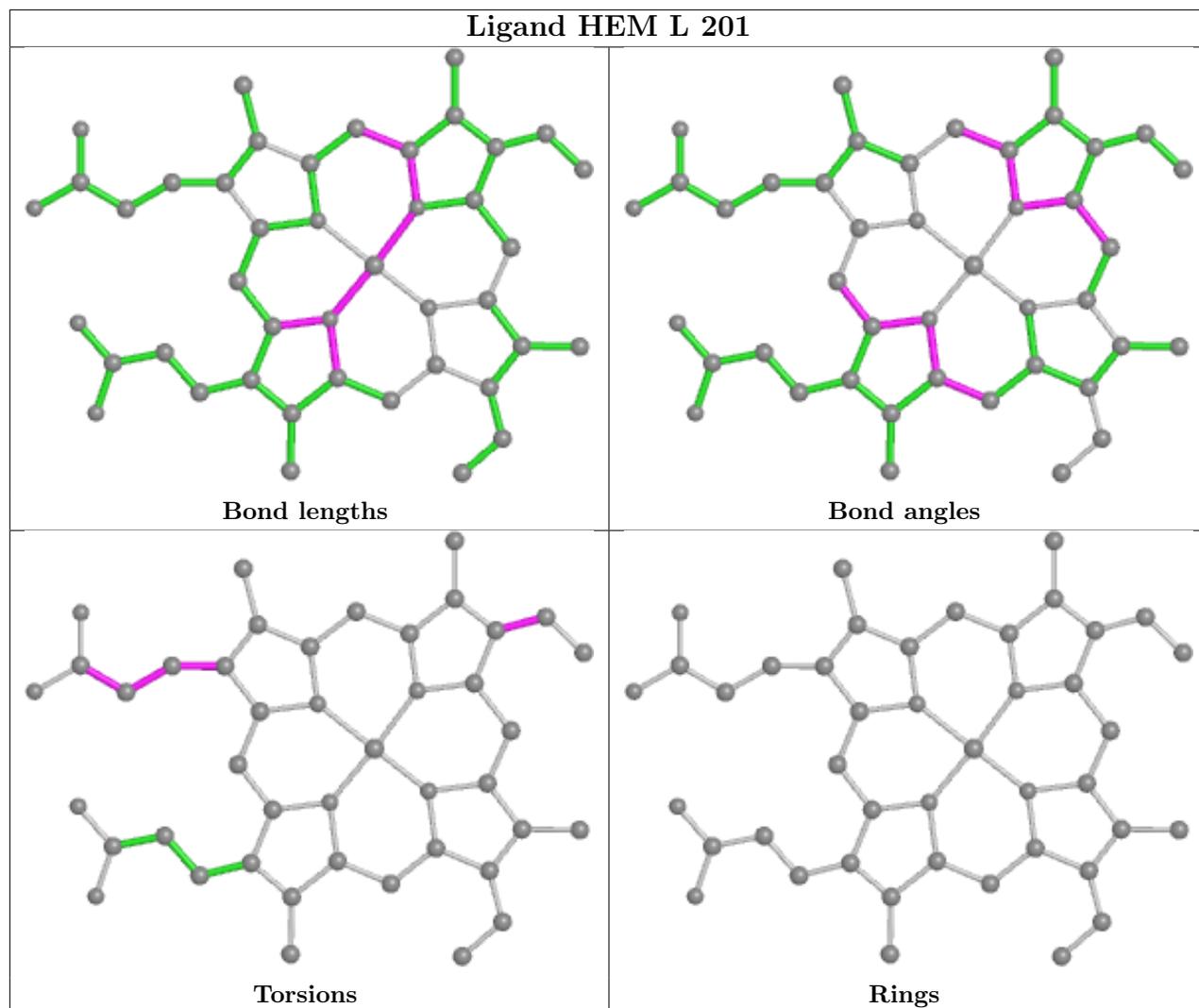
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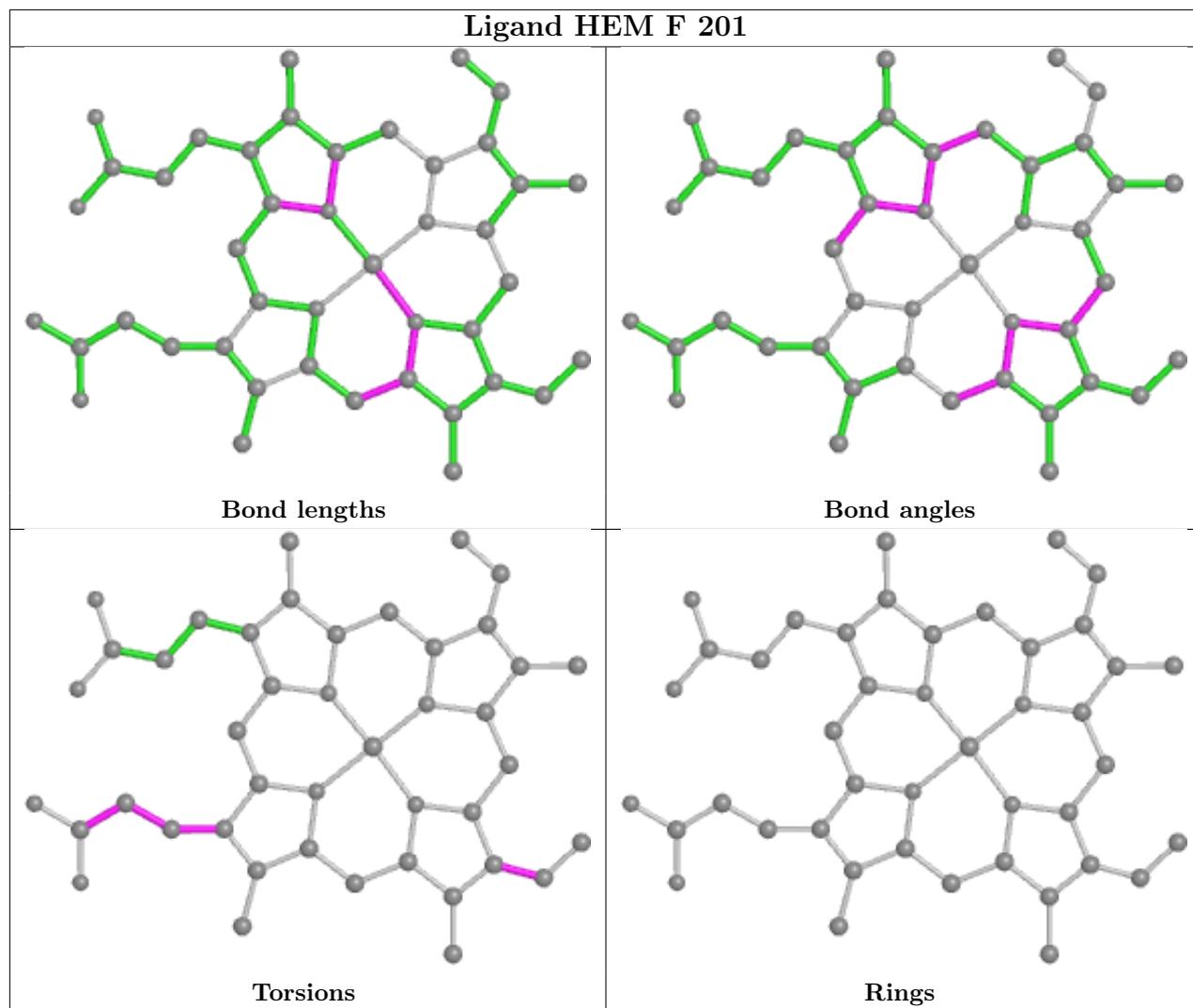
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1301	DTP	6	0
3	M	1301	DTP	6	0
5	D	201	HEM	16	0
5	J	201	HEM	15	0
5	B	201	HEM	15	0
3	G	1301	DTP	6	0
3	K	1301	DTP	6	0
3	A	1301	DTP	6	0
5	H	201	HEM	16	0
3	I	1301	DTP	7	0

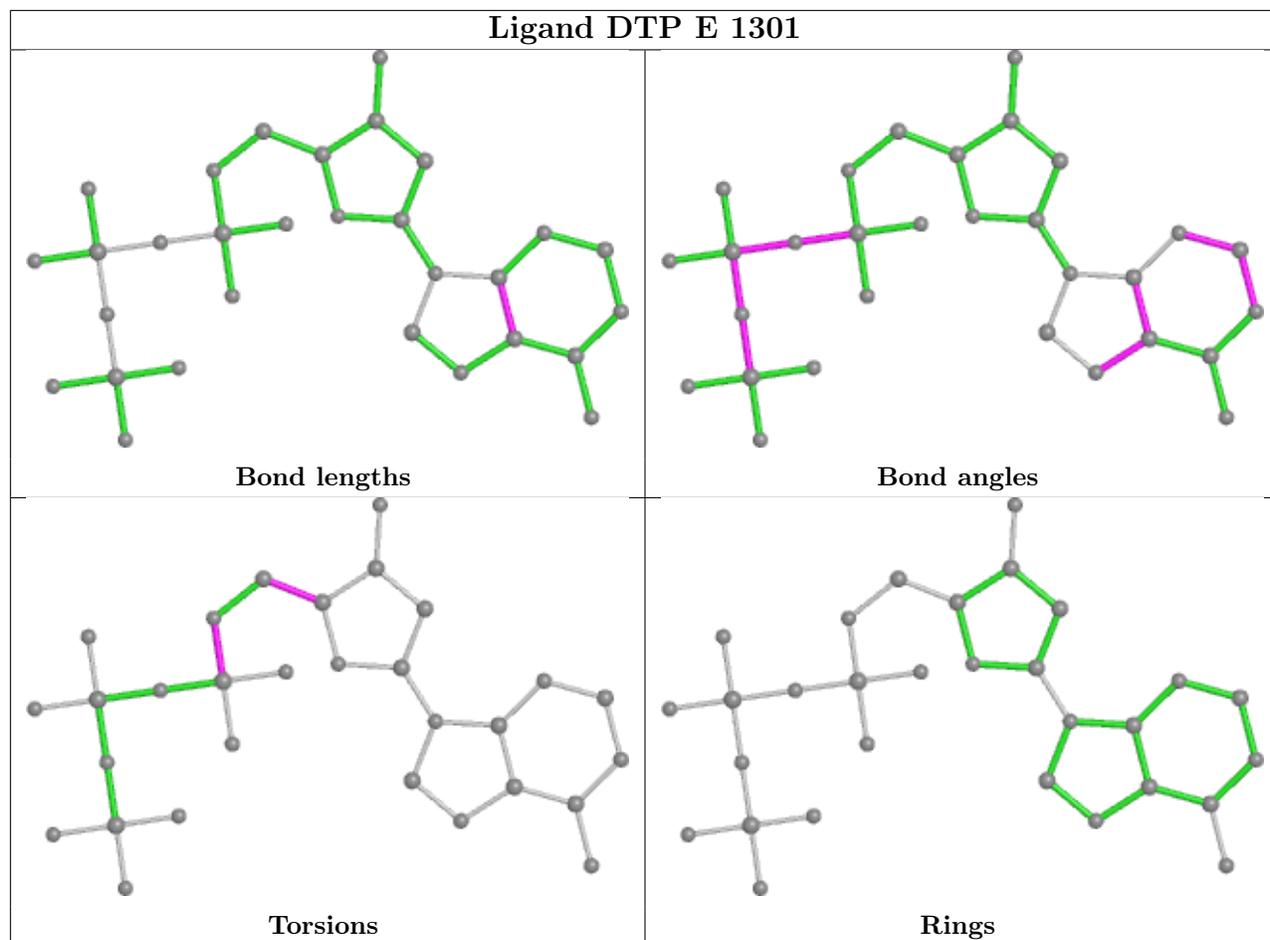
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

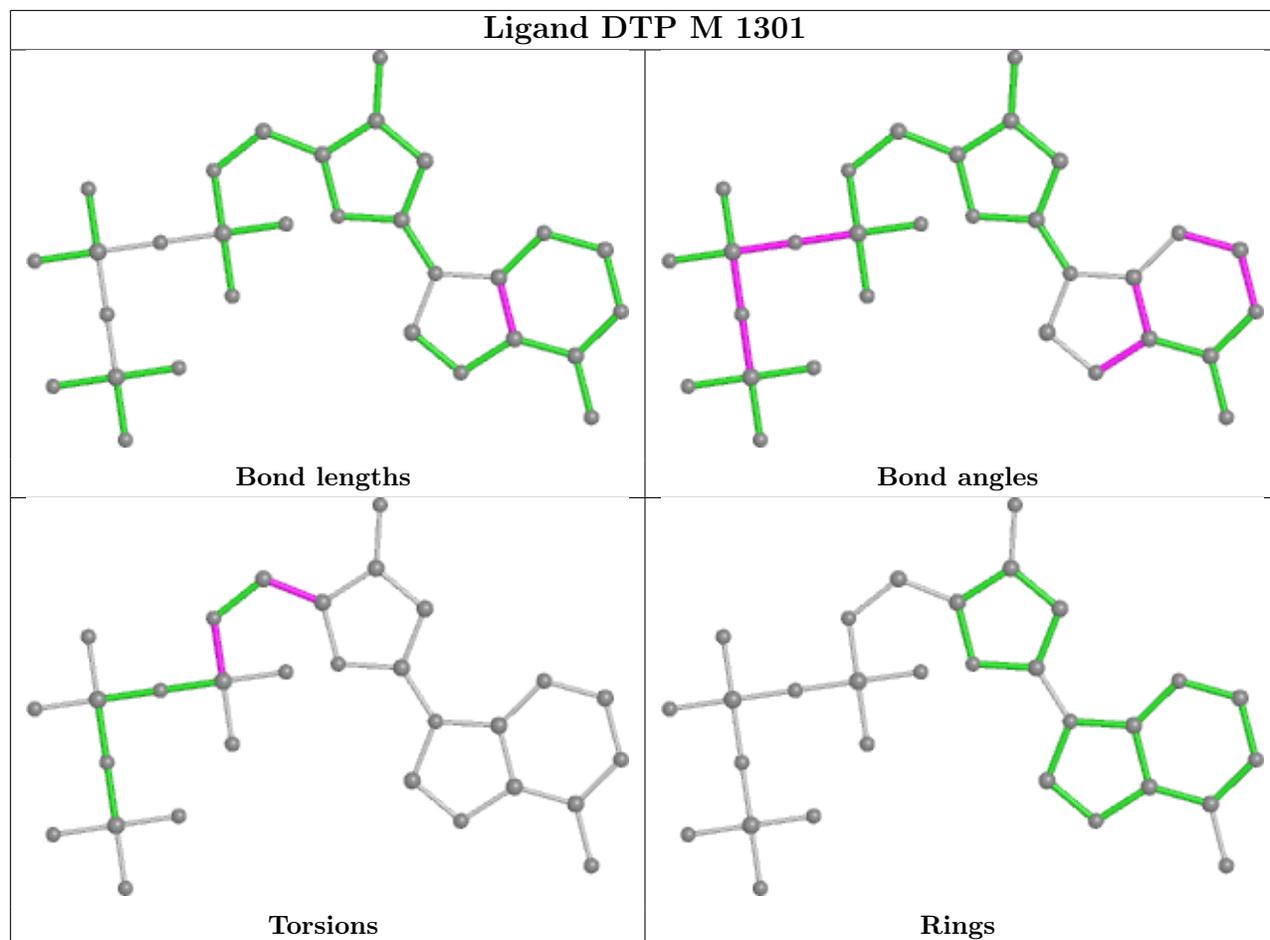


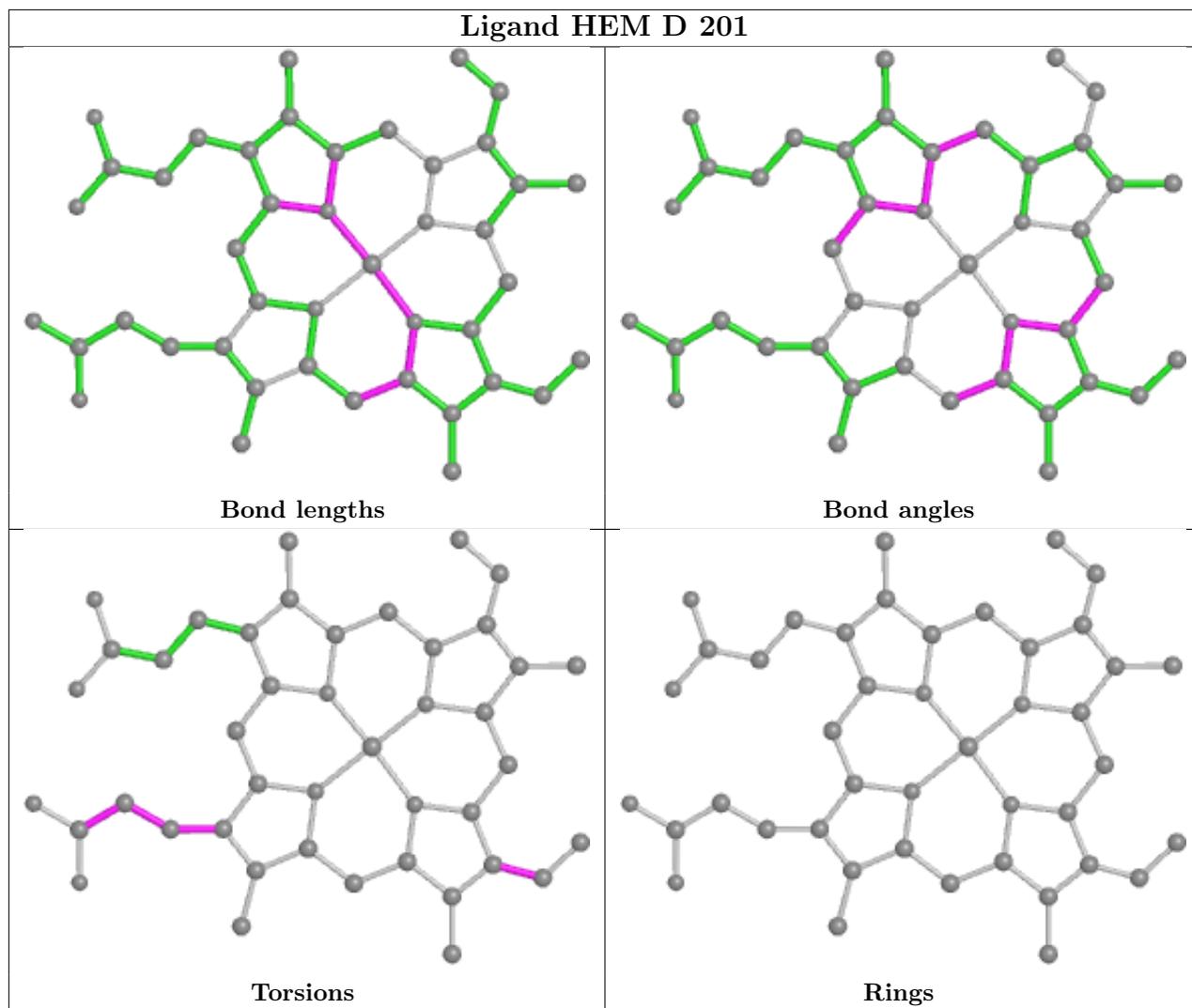


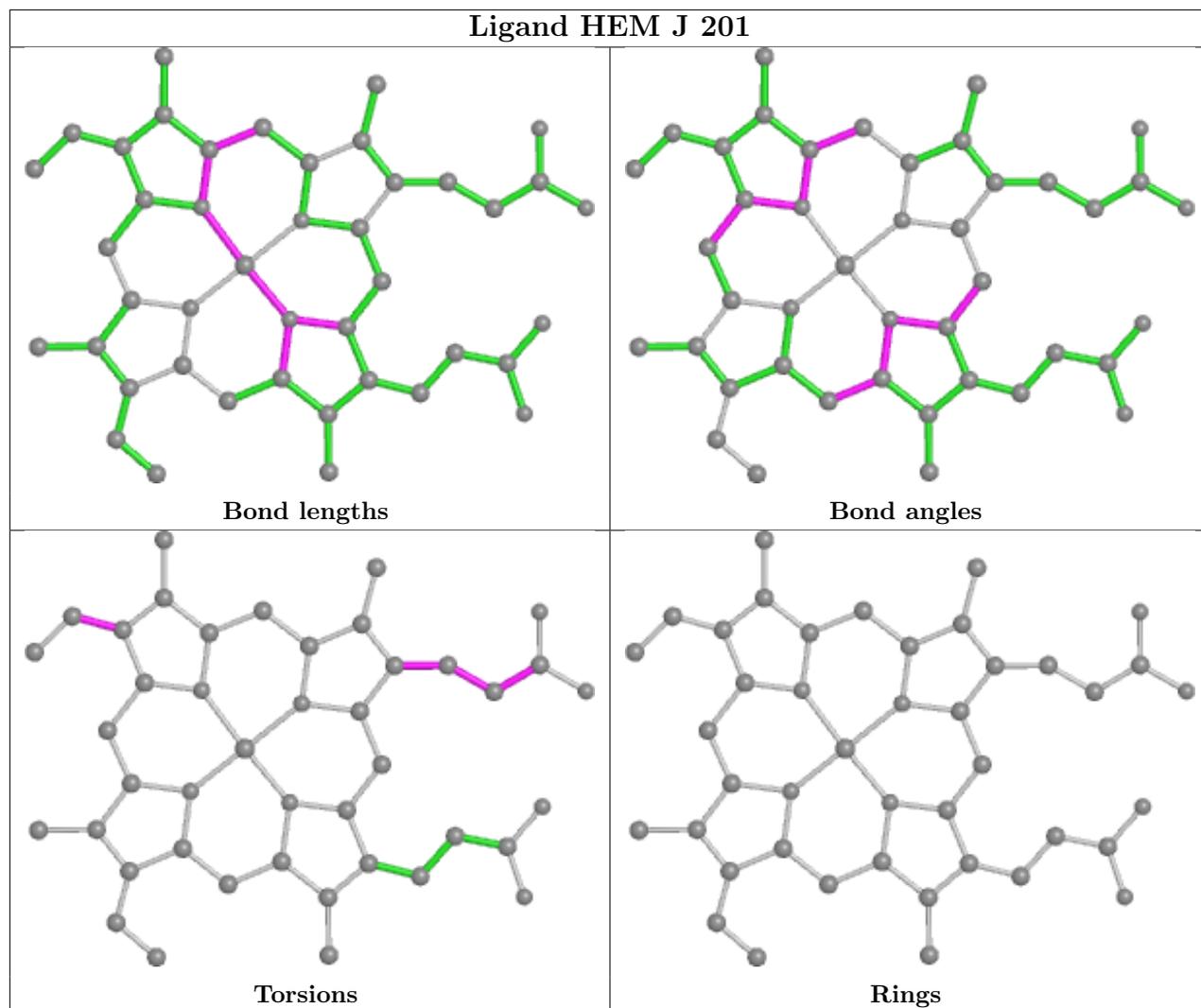


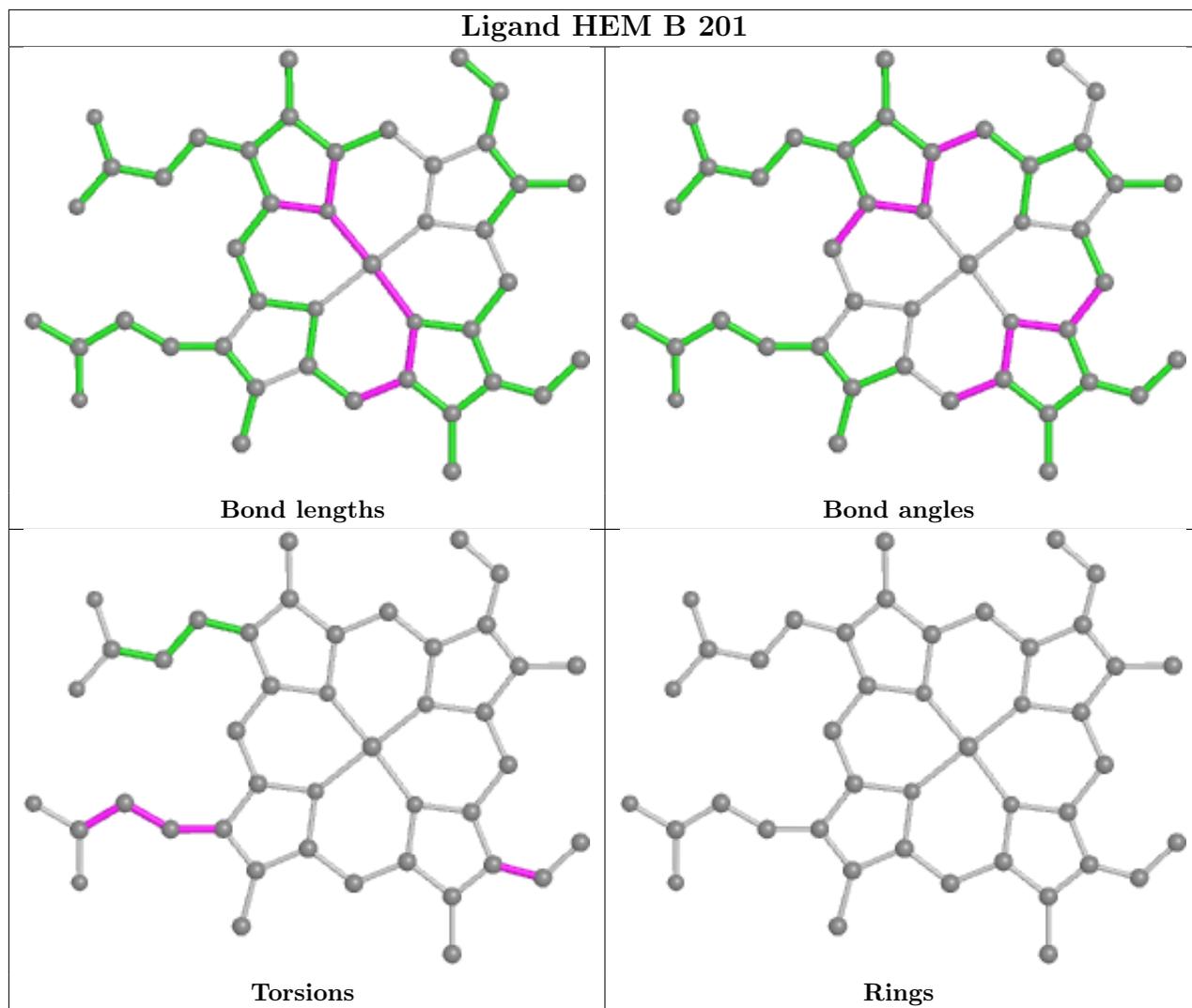


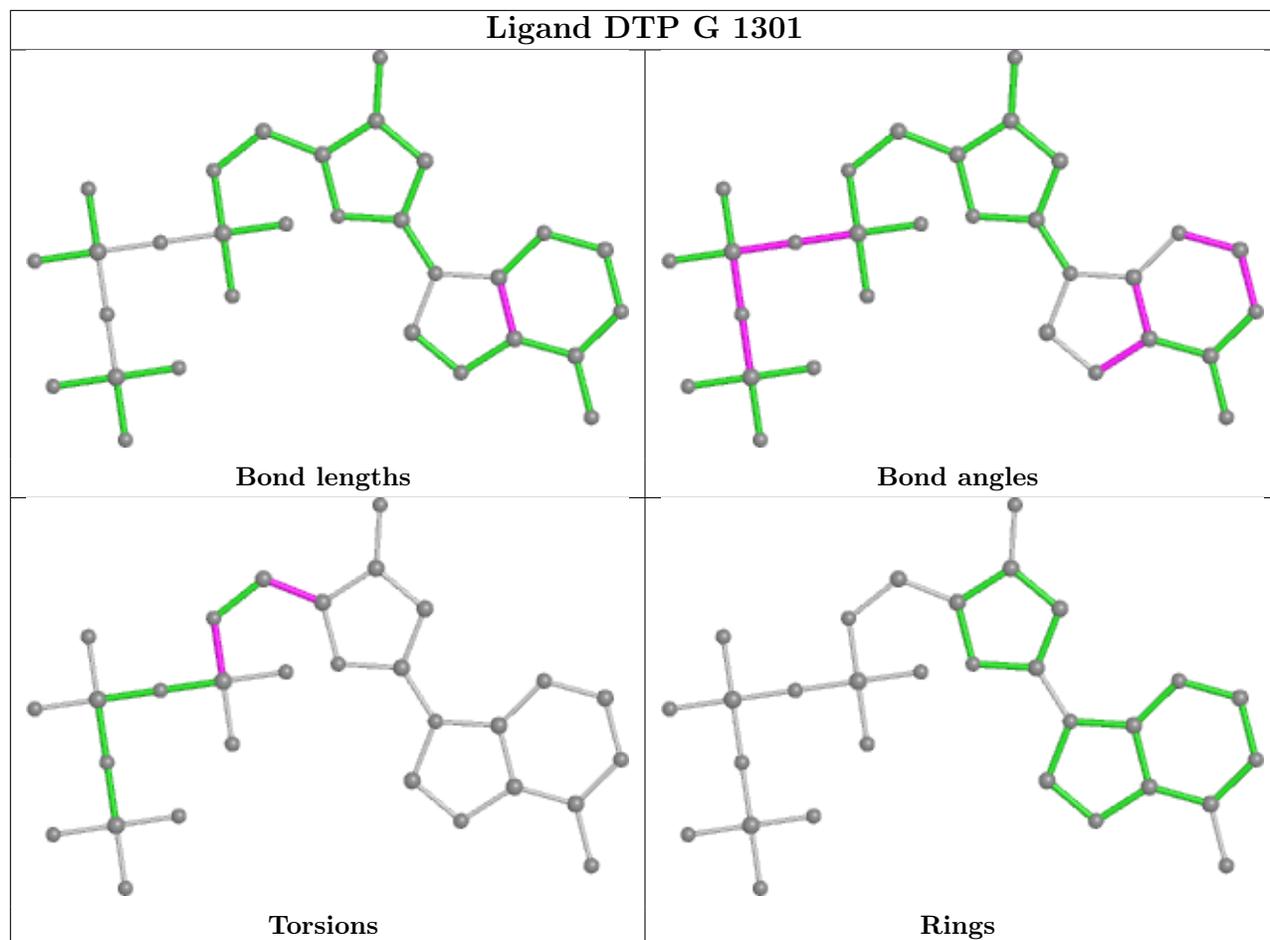


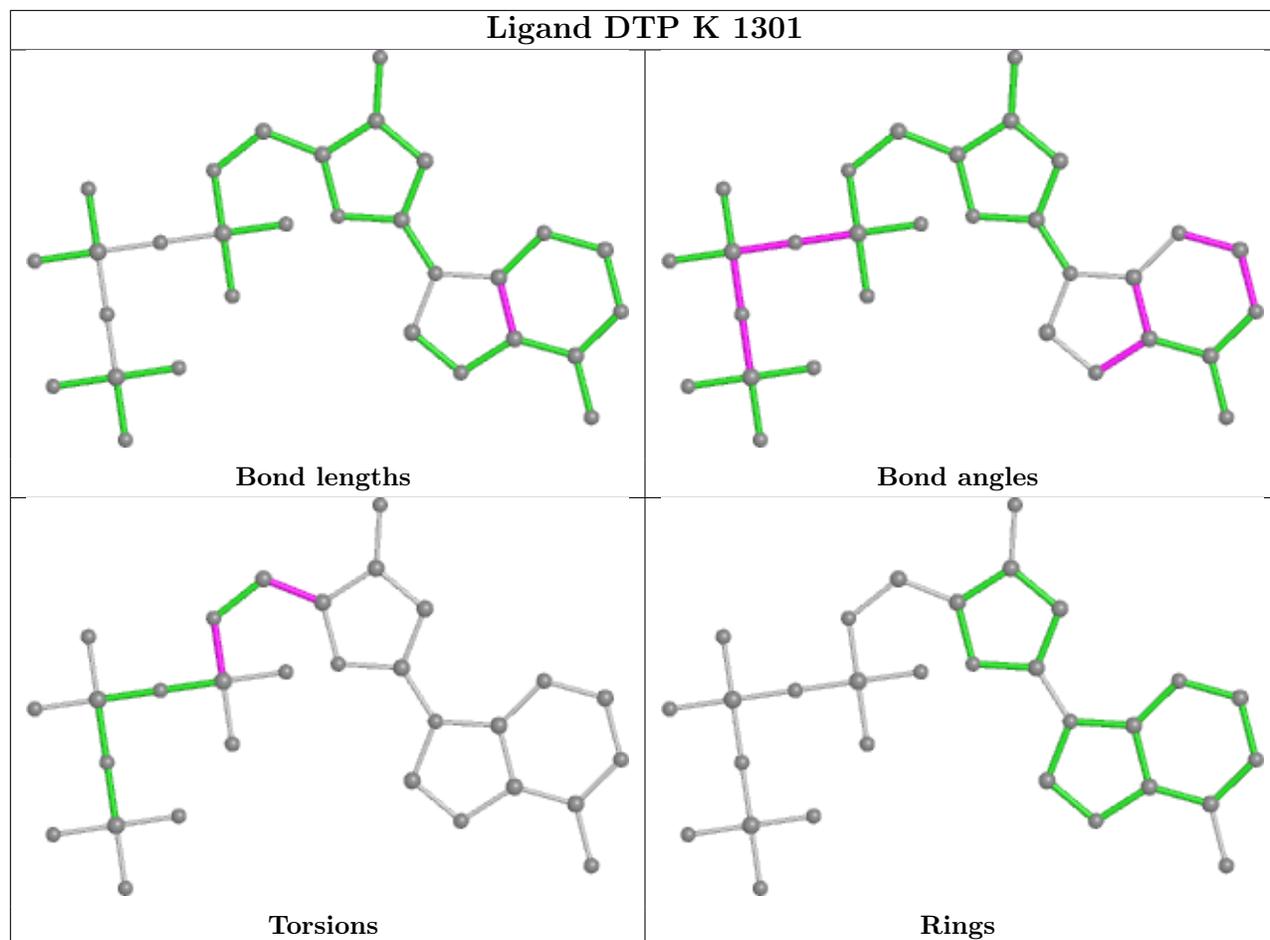


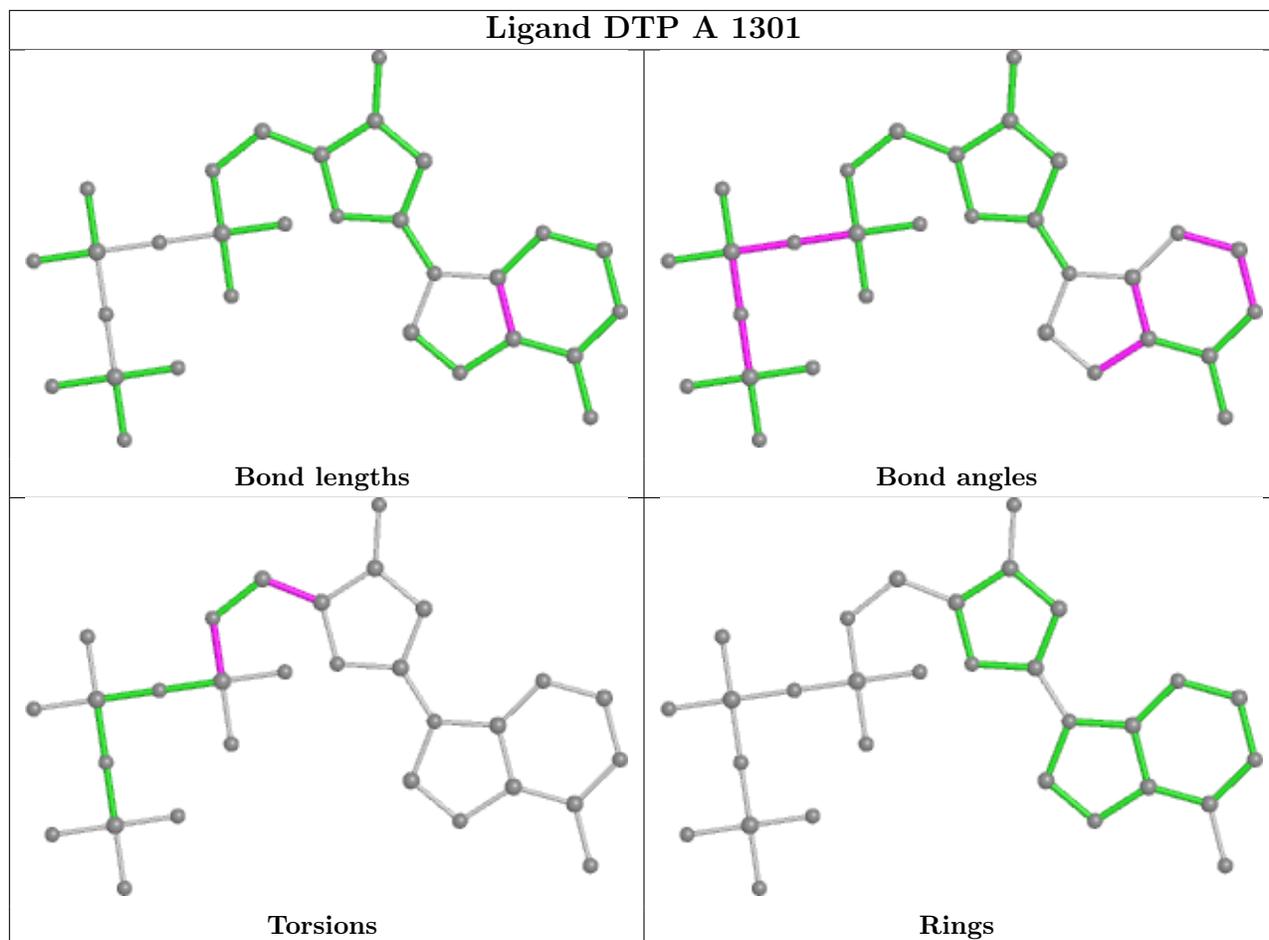


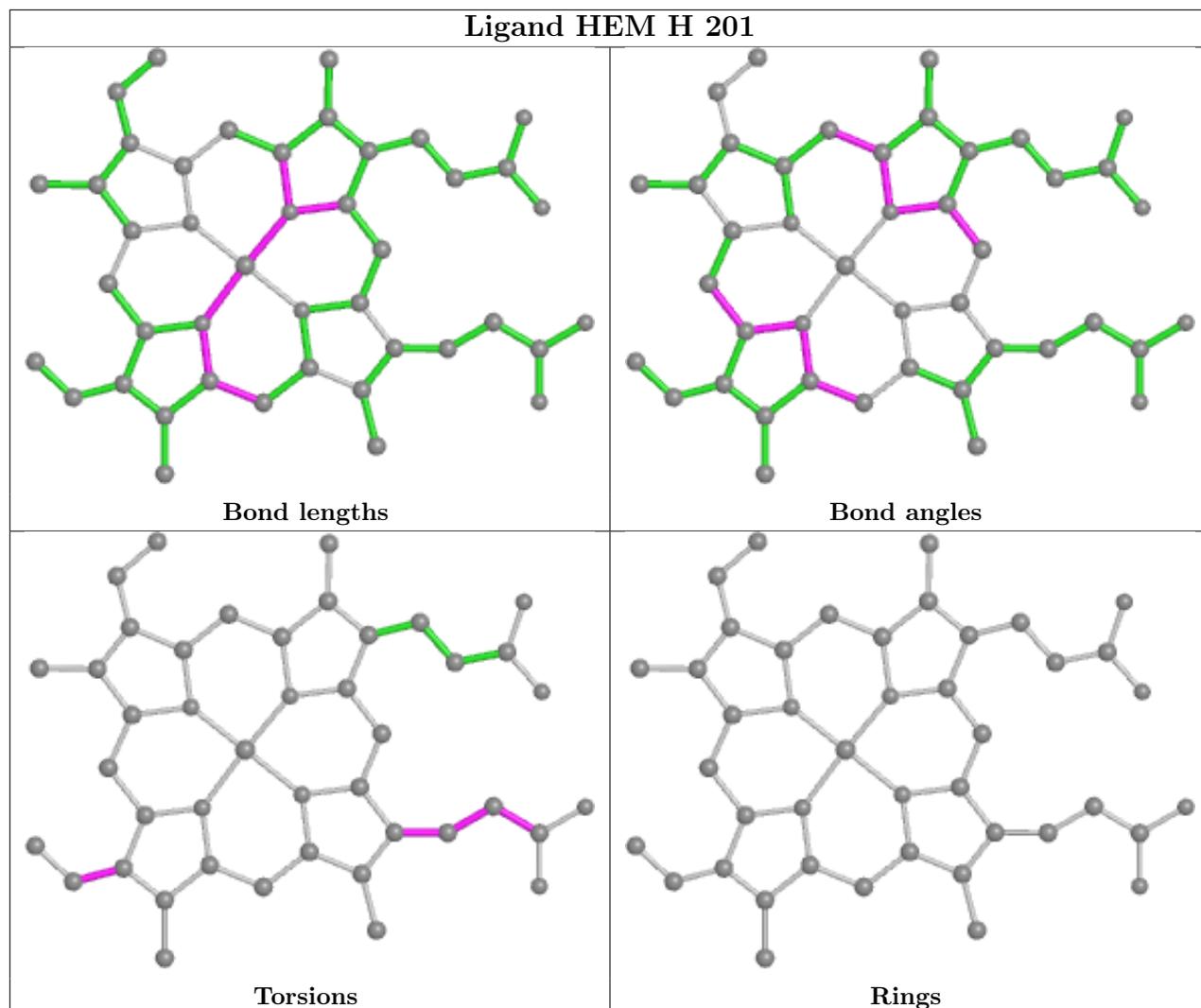


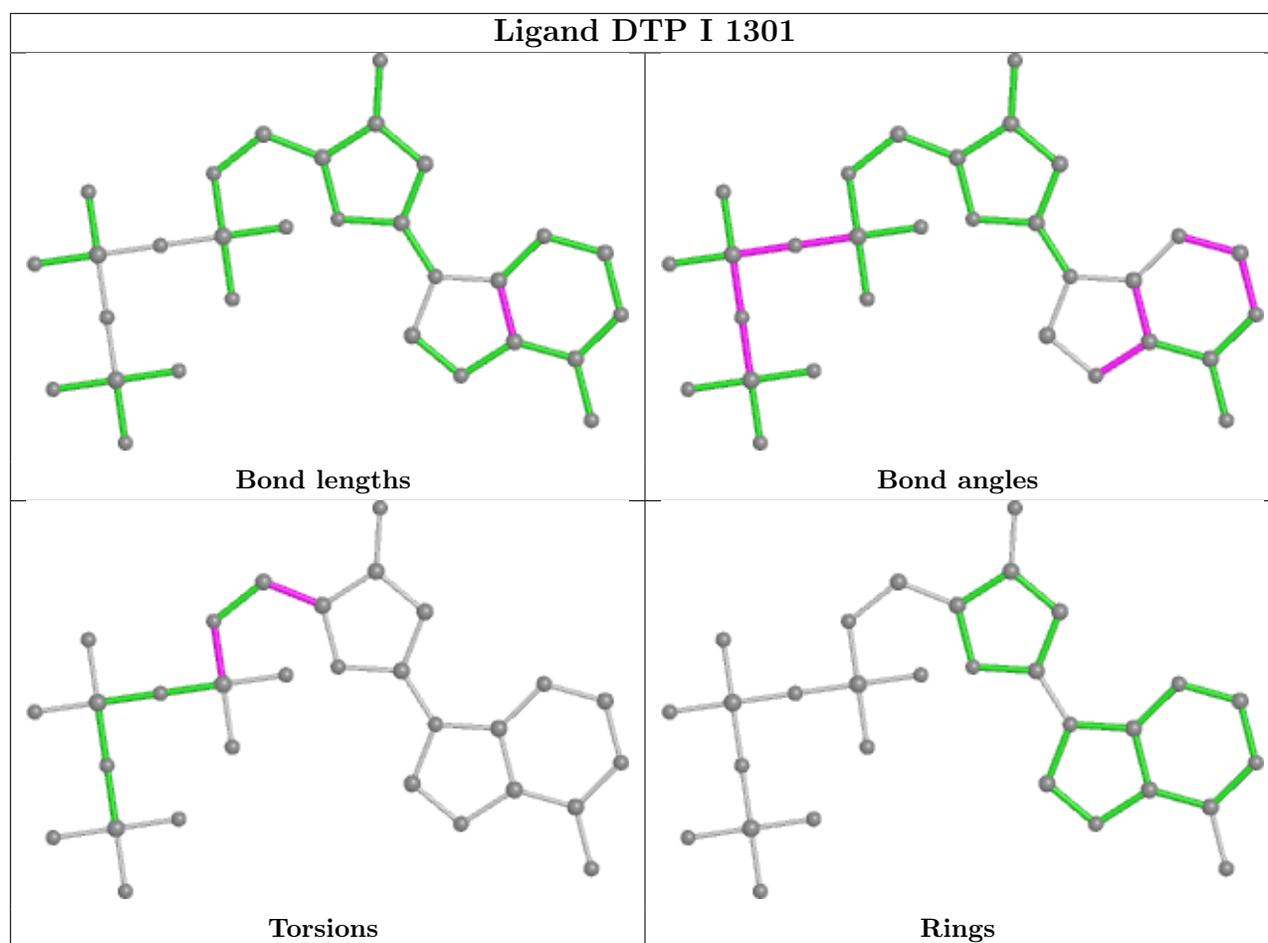












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

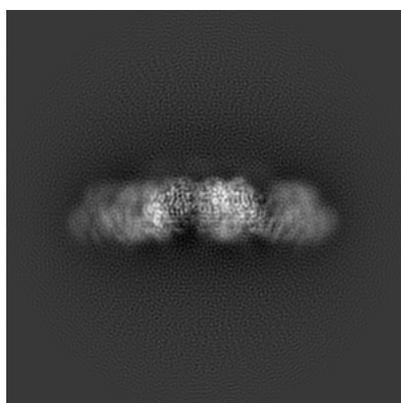
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6480. These allow visual inspection of the internal detail of the map and identification of artifacts.

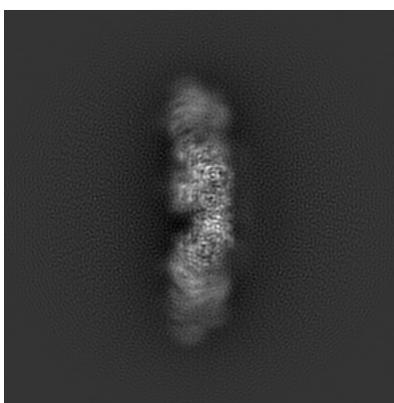
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

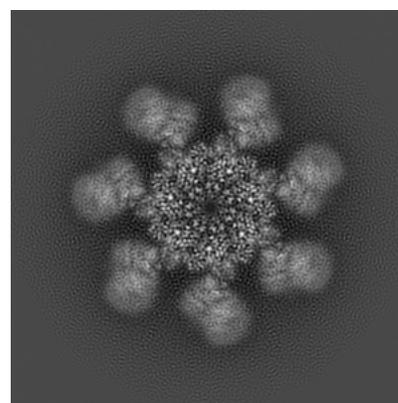
6.1.1 Primary map



X



Y

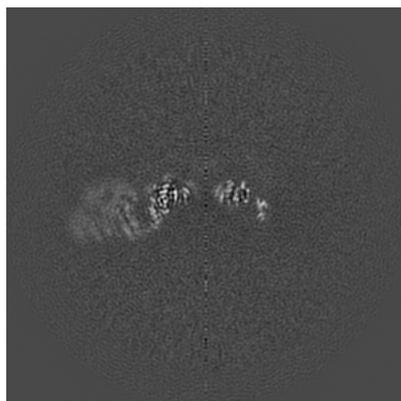


Z

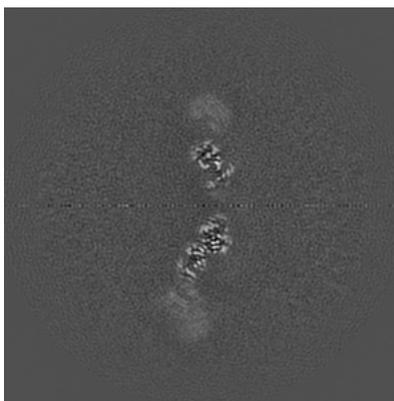
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

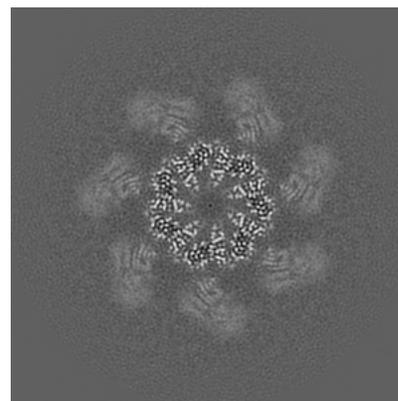
6.2.1 Primary map



X Index: 160



Y Index: 160



Z Index: 160

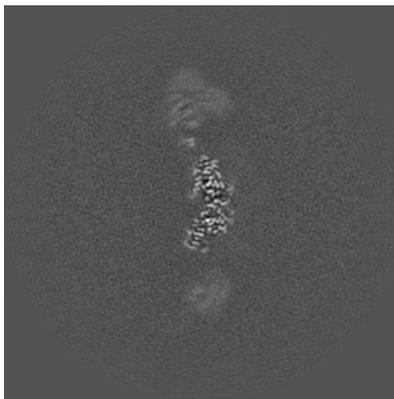
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

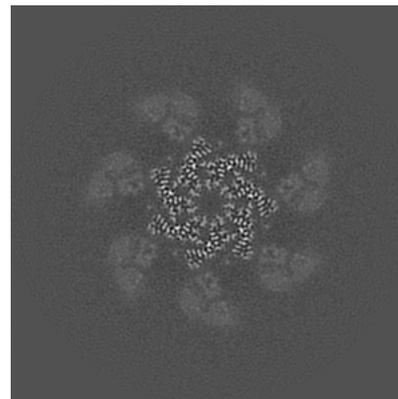
6.3.1 Primary map



X Index: 185



Y Index: 190

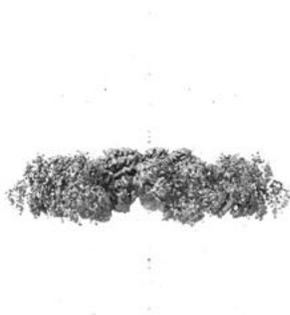


Z Index: 164

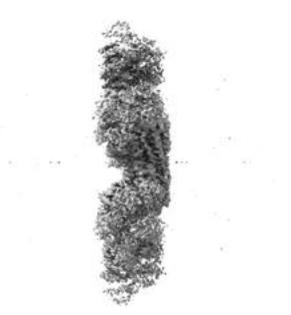
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

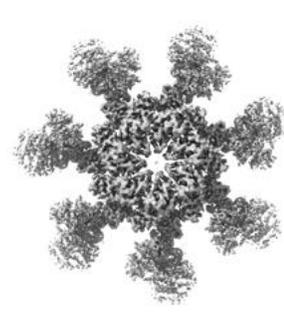
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

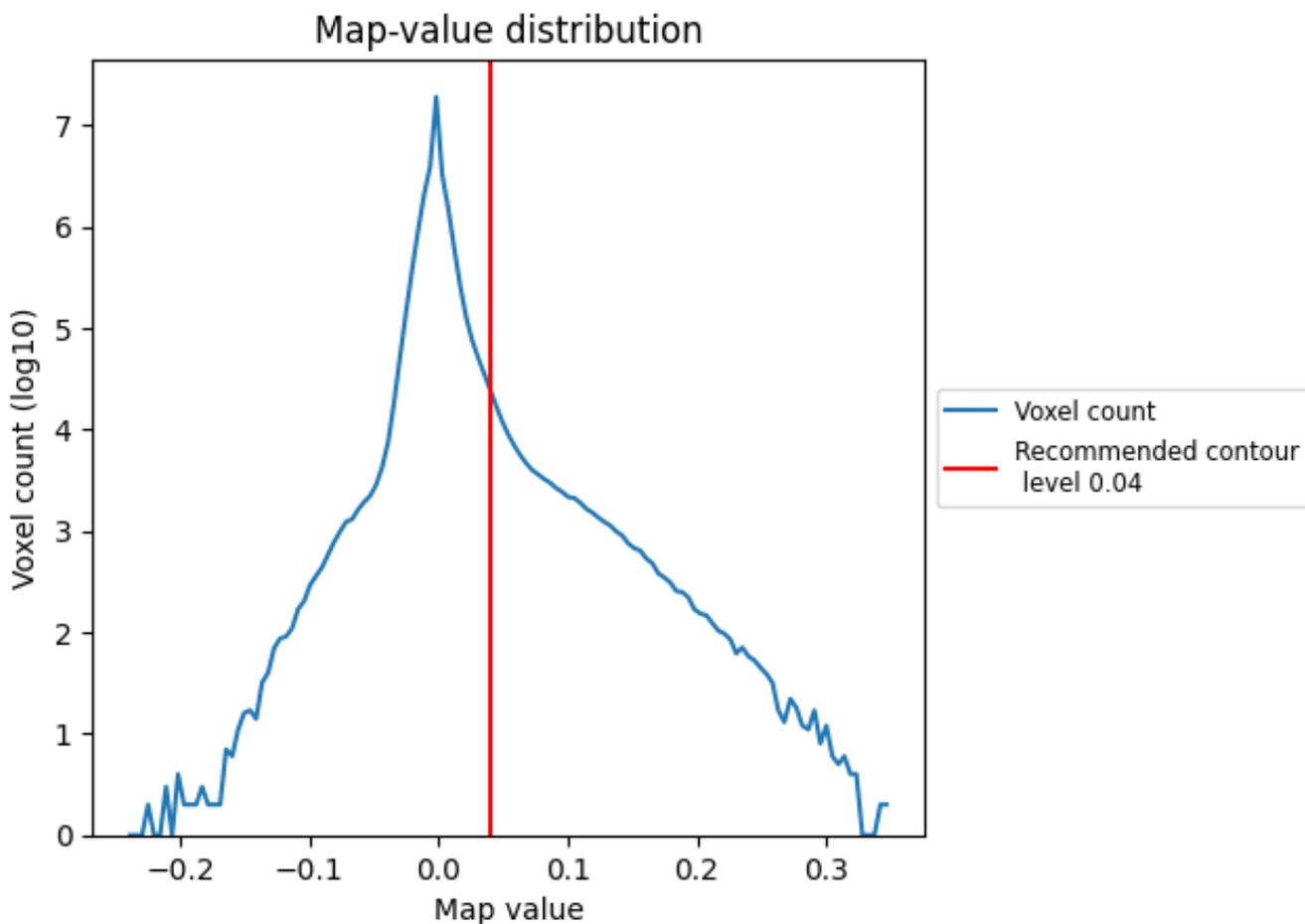
6.5 Mask visualisation

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

7 Map analysis [i](#)

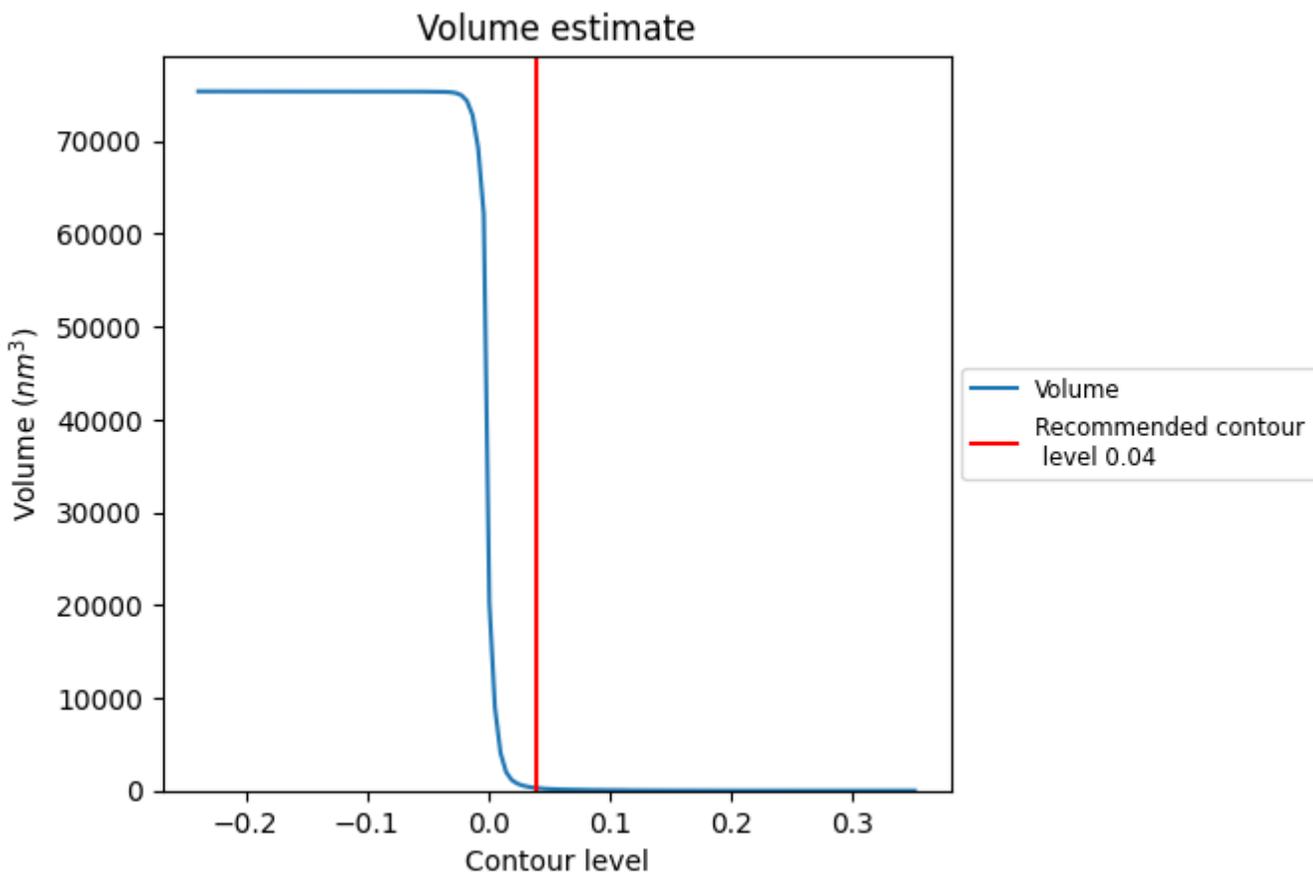
This section contains the results of statistical analysis of the map.

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.

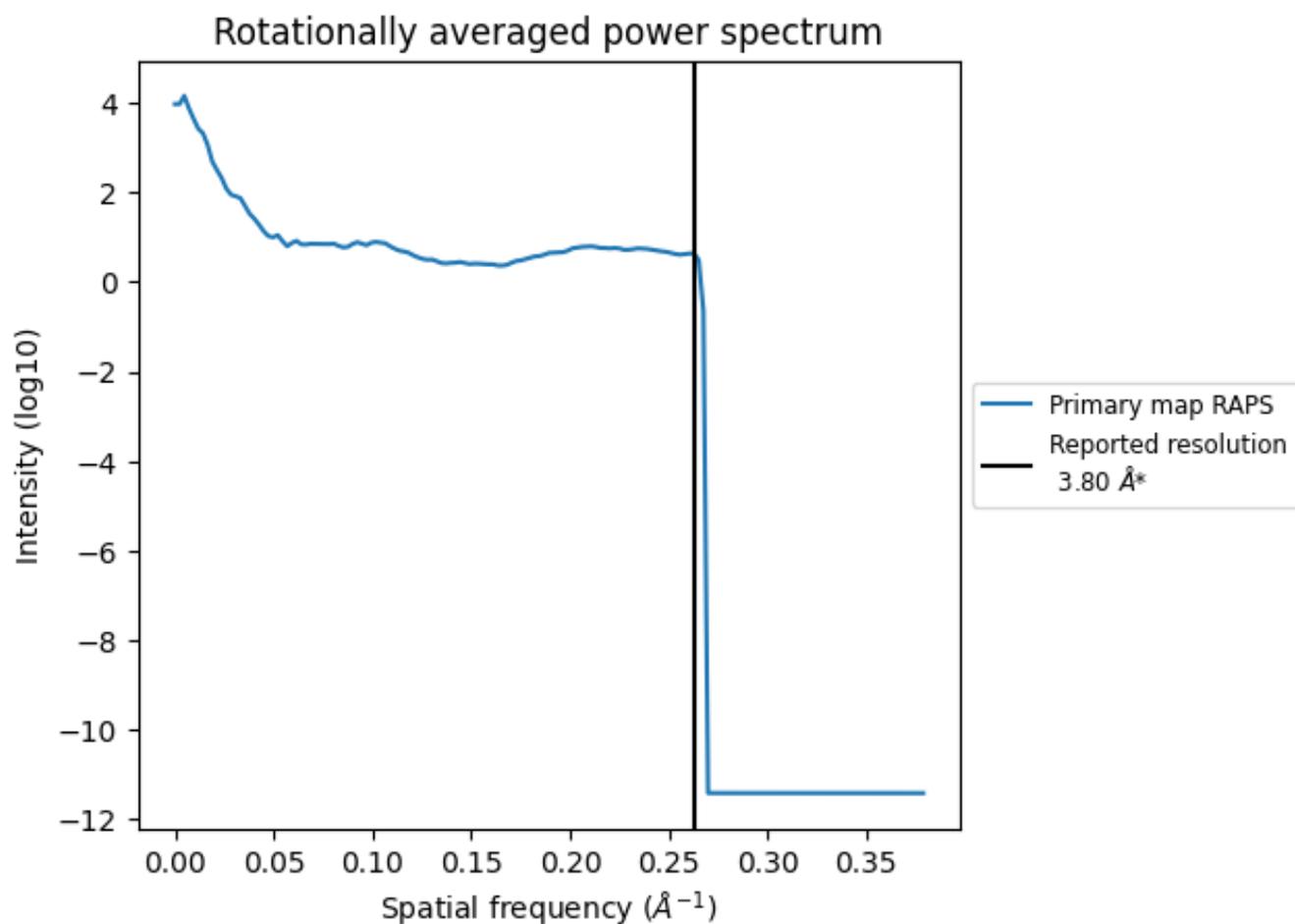
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 276 nm³; this corresponds to an approximate mass of 249 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 0.263 Å⁻¹

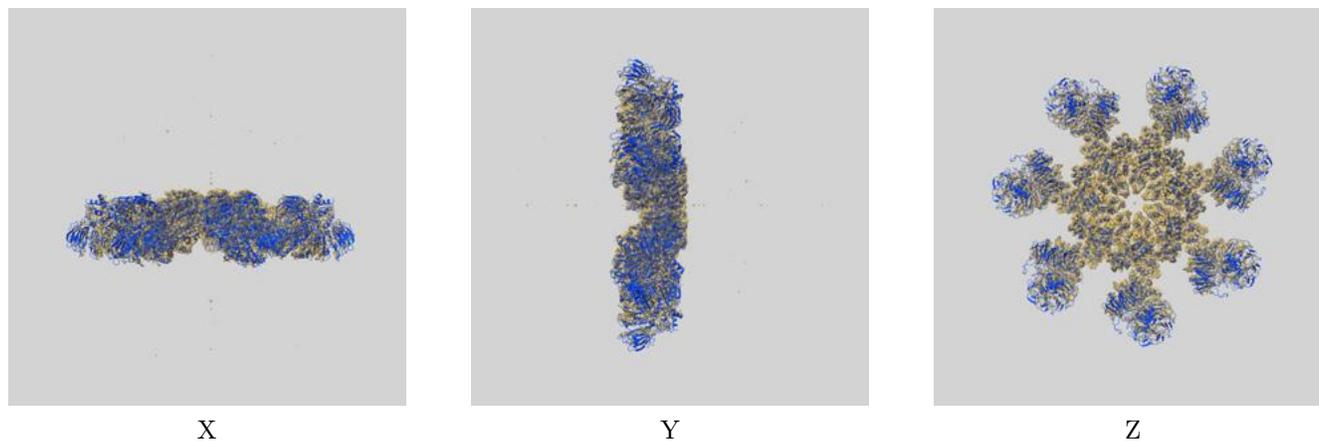
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

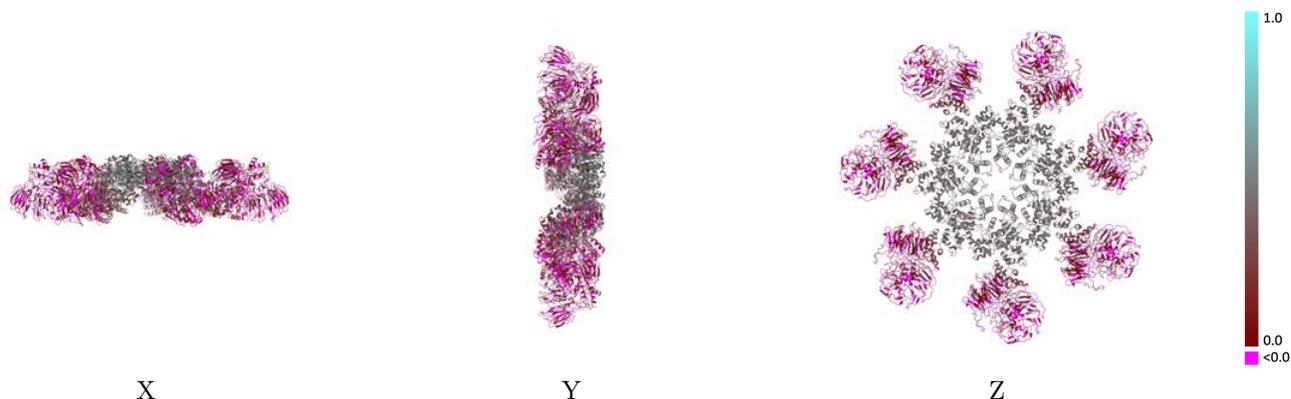
This section contains information regarding the fit between EMDB map EMD-6480 and PDB model 3JBT. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



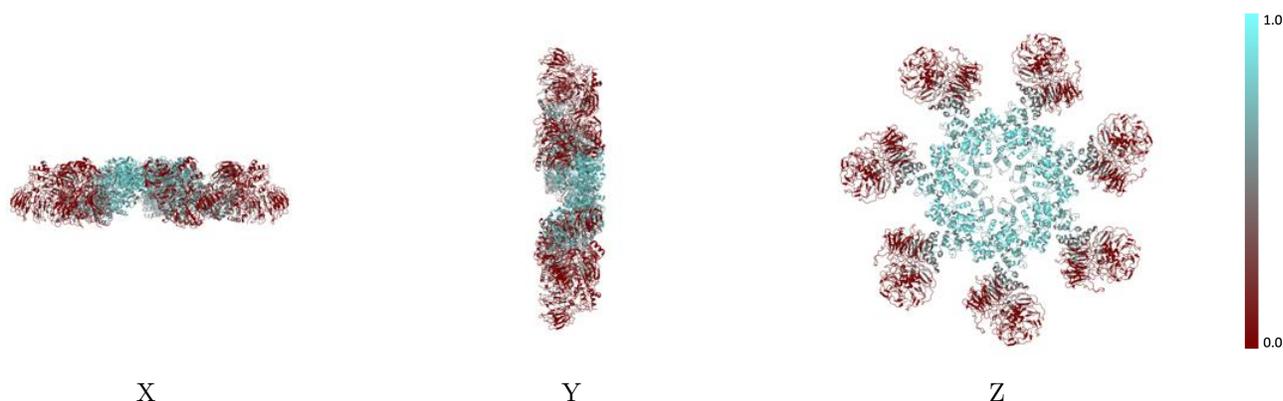
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



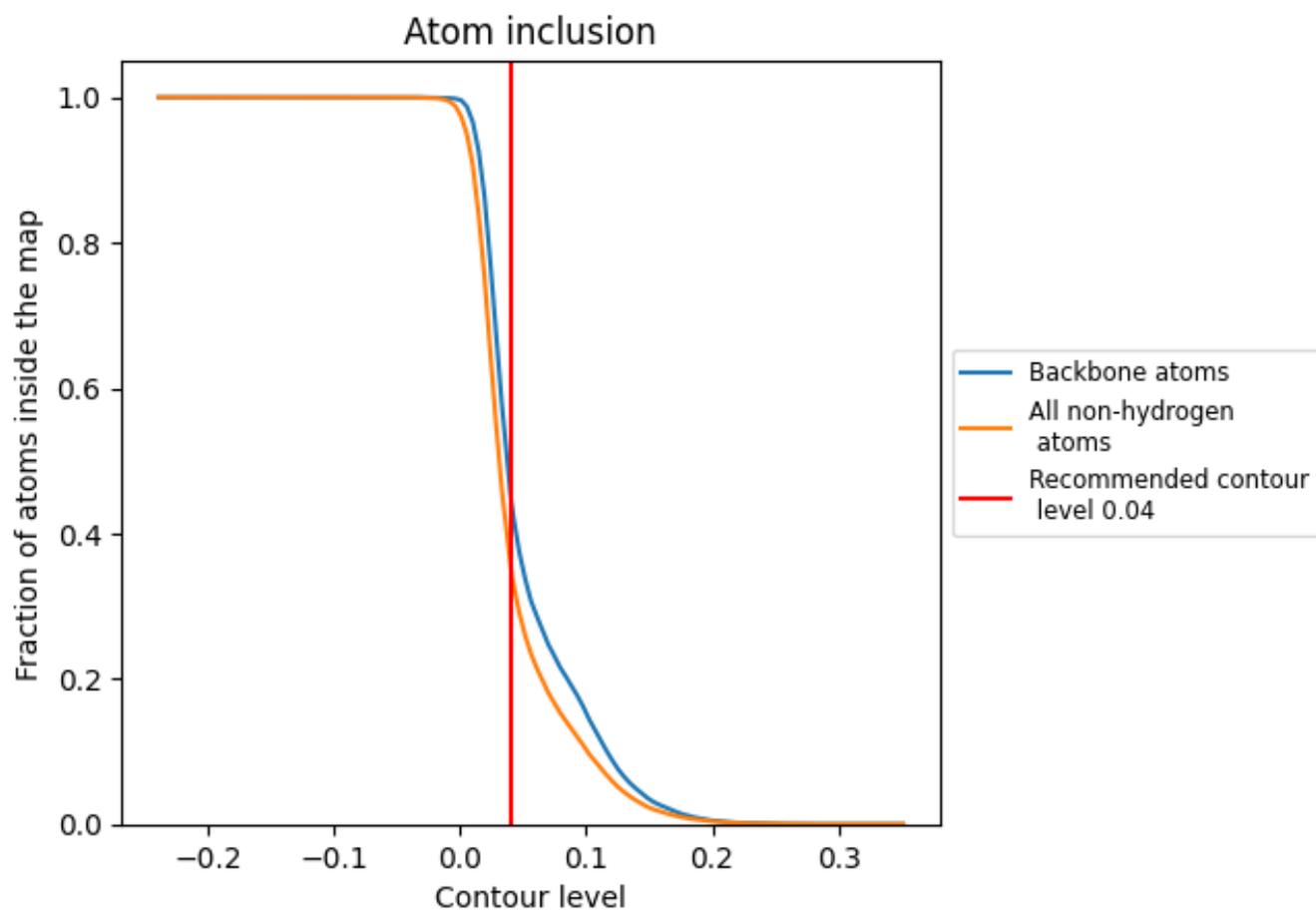
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 45% of all backbone atoms, 35% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3547	 0.2010
A	 0.3790	 0.2120
B	 0.0961	 0.0860
C	 0.3784	 0.2120
D	 0.0938	 0.0880
E	 0.3796	 0.2120
F	 0.0985	 0.0840
G	 0.3785	 0.2110
H	 0.0985	 0.0830
I	 0.3779	 0.2110
J	 0.1032	 0.0870
K	 0.3790	 0.2110
L	 0.1008	 0.0900
M	 0.3801	 0.2110
N	 0.0973	 0.0860

