



wwPDB EM Validation Summary Report ⓘ

Sep 22, 2022 – 06:10 pm BST

PDB ID : 7Z0T
EMDB ID : EMD-14430
Title : Structure of the Escherichia coli formate hydrogenlyase complex (aerobic preparation, composite structure)
Authors : Steinhilper, R.; Murphy, B.J.
Deposited on : 2022-02-23
Resolution : 3.40 Å(reported)

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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.dev8
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.30

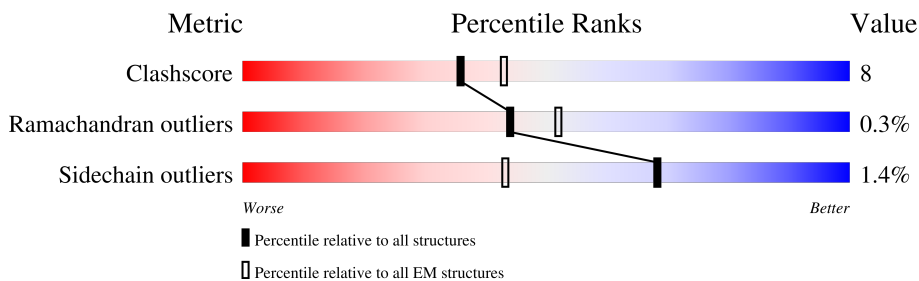
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	C	608	
2	E	581	
3	B	203	
4	G	255	
5	F	180	
6	D	307	
7	A	715	

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
10	SF4	A	800	-	-	X	-

2 Entry composition i

There are 13 unique types of molecules in this entry. The entry contains 20634 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 Formate hydrogenlyase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	C	603	4469	2955	738	741	35	0	0

- Molecule 2 is a protein called Formate hydrogenlyase subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	532	4244	2689	746	782	27	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	82B	HIS	-	insertion	UNP P16431
E	82C	HIS	-	insertion	UNP P16431
E	82D	HIS	-	insertion	UNP P16431
E	82E	HIS	-	insertion	UNP P16431
E	82F	HIS	-	insertion	UNP P16431
E	82G	HIS	-	insertion	UNP P16431
E	82H	HIS	-	insertion	UNP P16431
E	82I	HIS	-	insertion	UNP P16431
E	82J	HIS	-	insertion	UNP P16431
E	82K	HIS	-	insertion	UNP P16431
E	82L	GLY	-	insertion	UNP P16431
E	82M	SER	-	insertion	UNP P16431

- Molecule 3 is a protein called Formate hydrogenlyase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	170	1254	775	227	232	20	0	0

- Molecule 4 is a protein called Formate hydrogenlyase subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	G	249	1703	1069	311	311	12	0	0

- Molecule 5 is a protein called Formate hydrogenlyase subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	136	1075	664	196	201	14	1	0

- Molecule 6 is a protein called Formate hydrogenlyase subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	D	287	2152	1430	345	366	11	0	0

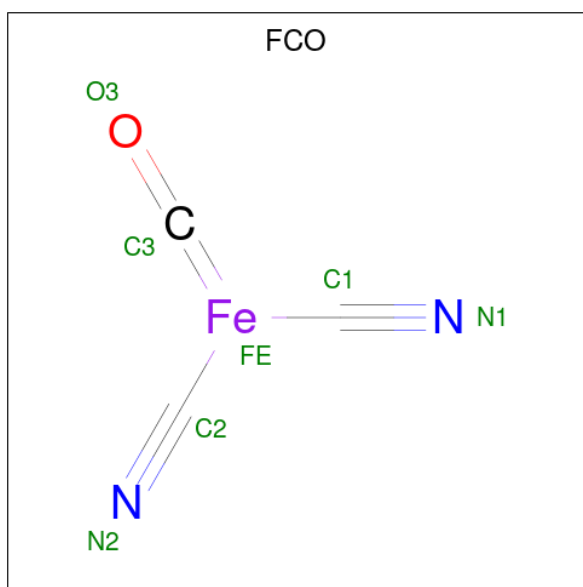
- Molecule 7 is a protein called Formate dehydrogenase H.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	S	Se		
7	A	714	5569	3505	972	1058	33	1	0	0

- Molecule 8 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

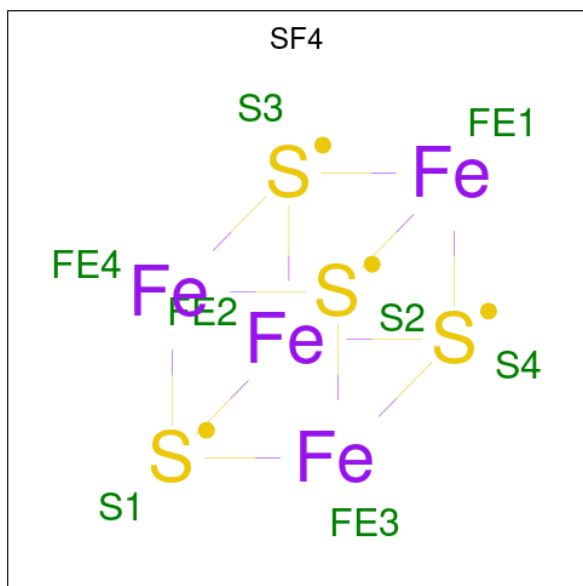
Mol	Chain	Residues	Atoms		AltConf
			Total	Ni	
8	E	1	1	1	0

- Molecule 9 is CARBONMONOXIDE-(DICYANO) IRON (three-letter code: FCO) (formula: C₃FeN₂O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	Fe	N	O	
9	E	1	7	3	1	2	1	0

- Molecule 10 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
10	B	1	32	16	16	0
10	B	1	32	16	16	0

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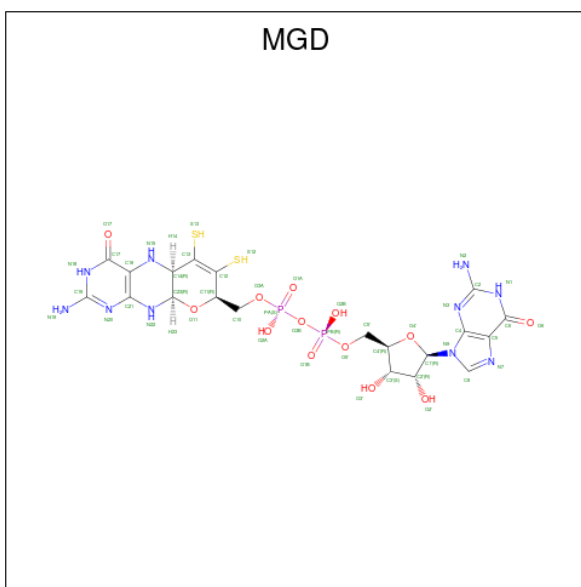
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Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
10	B	1	32	16	16	0
10	B	1	32	16	16	0
10	G	1	8	4	4	0
10	F	1	16	8	8	0
10	F	1	16	8	8	0
10	A	1	8	4	4	0

- Molecule 11 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Fe	
11	F	1	1	1	0

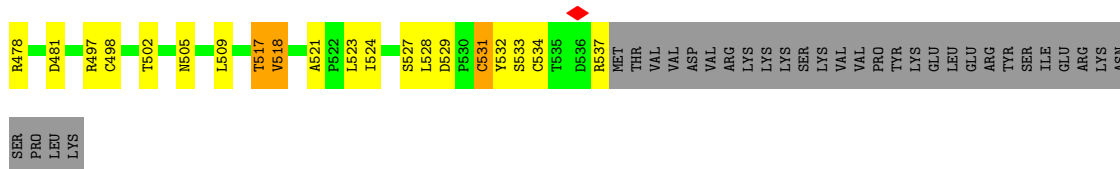
- Molecule 12 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂) (labeled as "Ligand of Interest" by depositor).



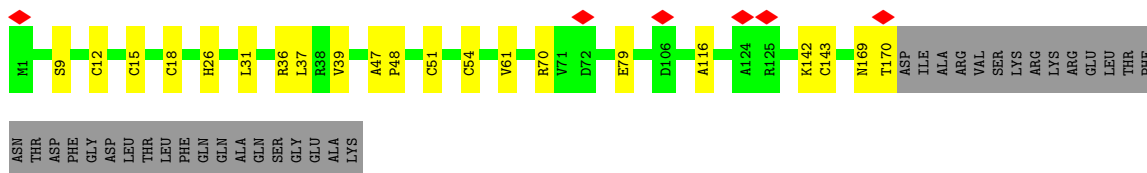
Mol	Chain	Residues	Atoms						AltConf
12	A	1	Total	C	N	O	P	S	0
			94	40	20	26	4	4	
12	A	1	Total	C	N	O	P	S	0
			94	40	20	26	4	4	

- Molecule 13 is MOLYBDENUM(VI) ION (three-letter code: 6MO) (formula: Mo) (labeled as "Ligand of Interest" by depositor).

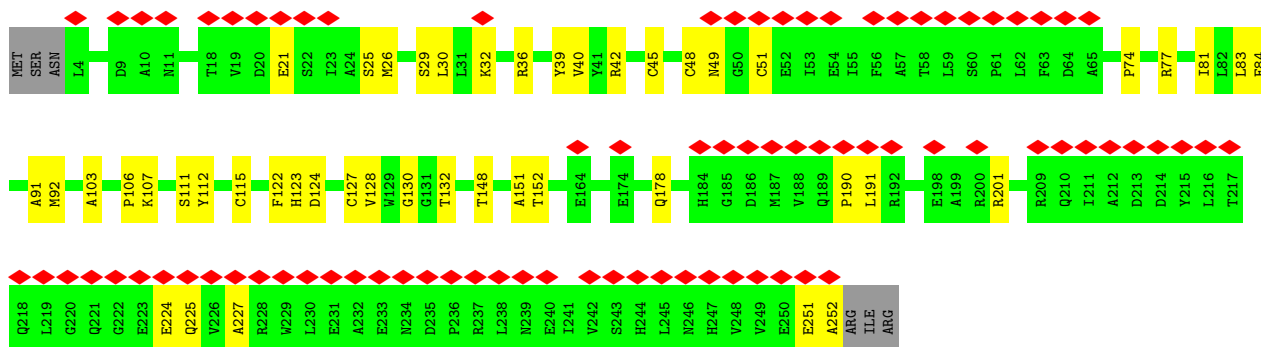
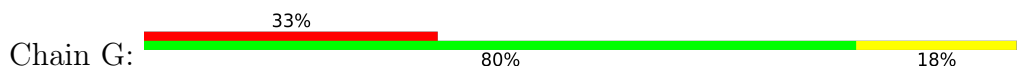
Mol	Chain	Residues	Atoms		AltConf
13	A	1	Total	Mo	0
			1	1	



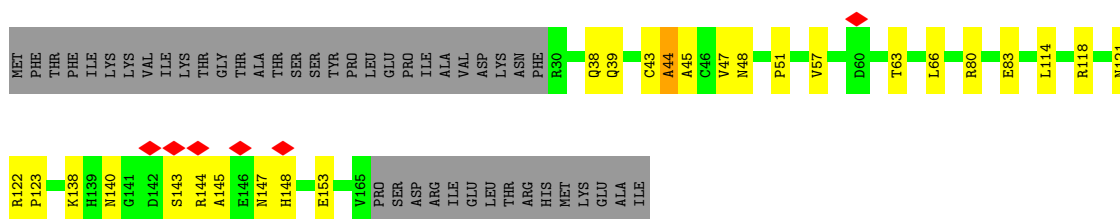
• Molecule 3: Formate hydrogenlyase subunit 2



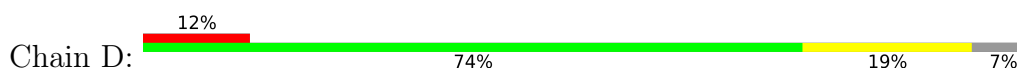
• Molecule 4: Formate hydrogenlyase subunit 7

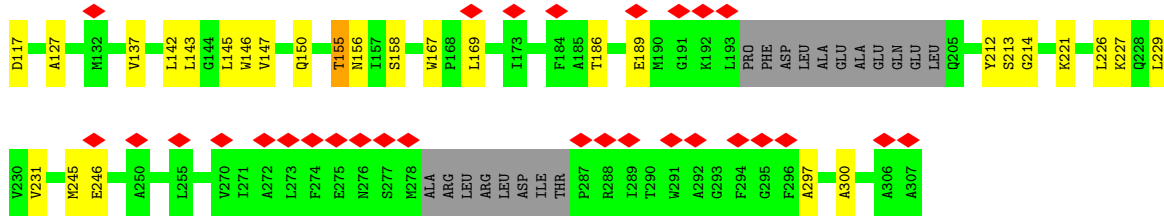


• Molecule 5: Formate hydrogenlyase subunit 6

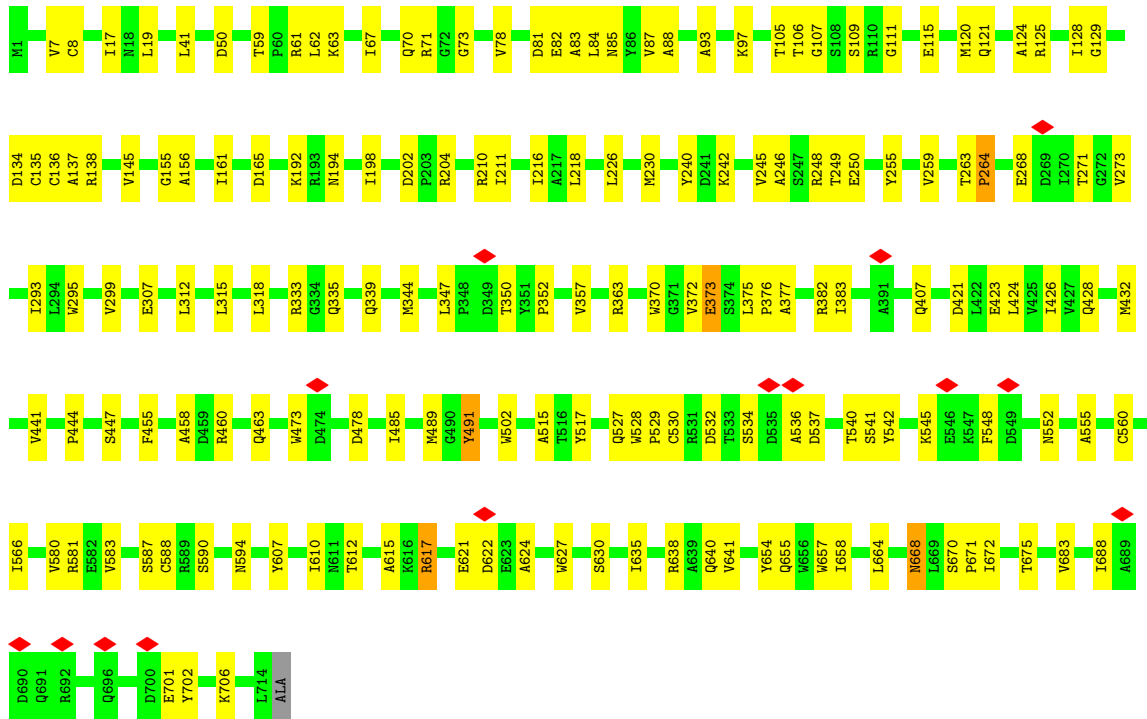
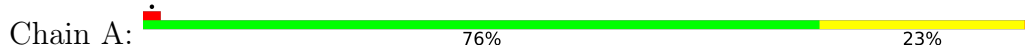


• Molecule 6: Formate hydrogenlyase subunit 4





• Molecule 7: Formate dehydrogenase H



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90459	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	72	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	69.052	Depositor
Minimum map value	-27.956	Depositor
Average map value	0.002	Depositor
Map value standard deviation	1.105	Depositor
Recommended contour level	8.0	Depositor
Map size (\AA)	397.44, 397.44, 397.44	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.828, 0.828, 0.828	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FCO, SF4, NI, FE, SEC, 6MO, MGD

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	C	0.32	1/4573 (0.0%)	0.62	3/6238 (0.0%)
2	E	0.39	1/4345 (0.0%)	0.78	9/5898 (0.2%)
3	B	0.27	0/1281	0.59	1/1748 (0.1%)
4	G	0.44	0/1736	0.72	1/2369 (0.0%)
5	F	0.47	0/1095	0.77	0/1479
6	D	0.31	0/2201	0.62	2/3003 (0.1%)
7	A	0.41	1/5684 (0.0%)	0.77	11/7712 (0.1%)
All	All	0.38	3/20915 (0.0%)	0.71	27/28447 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	E	0	1
5	F	0	4
7	A	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	264	PRO	N-CD	-9.45	1.34	1.47
2	E	362	VAL	C-O	5.82	1.34	1.23
1	C	366	PRO	N-CD	-5.18	1.40	1.47

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	517	THR	N-CA-C	15.26	152.19	111.00
2	E	518	VAL	N-CA-CB	12.54	139.08	111.50
7	A	81	ASP	CB-CA-C	-12.11	86.17	110.40
6	D	156	ASN	CB-CA-C	-8.63	93.15	110.40
2	E	517	THR	CB-CA-C	-8.01	89.97	111.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	A	268	GLU	Mainchain
2	E	360	VAL	Mainchain
5	F	121	ASN	Mainchain
5	F	122[A]	ARG	Mainchain
5	F	122[B]	ARG	Mainchain

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	C	4469	0	4723	63	0
2	E	4244	0	4145	81	0
3	B	1254	0	1235	14	0
4	G	1703	0	1551	29	0
5	F	1075	0	1032	18	0
6	D	2152	0	2239	47	0
7	A	5569	0	5448	120	0
8	E	1	0	0	0	0
9	E	7	0	0	1	0
10	A	8	0	0	2	0
10	B	32	0	0	0	0
10	F	16	0	0	0	0
10	G	8	0	0	0	0
11	F	1	0	0	0	0
12	A	94	0	44	3	0
13	A	1	0	0	0	0
All	All	20634	0	20417	349	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 8.

The worst 5 of 349 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:204:GLU:HG3	2:E:517:THR:O	1.55	1.07
2:E:145:LEU:HD11	2:E:153:MET:HB3	1.55	0.88
7:A:529:PRO:HD2	7:A:540:THR:HB	1.57	0.87
7:A:622:ASP:OD1	7:A:622:ASP:O	1.95	0.84
7:A:156:ALA:HA	7:A:333:ARG:HH21	1.46	0.80

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	C	601/608 (99%)	572 (95%)	29 (5%)	0	100	100
2	E	528/581 (91%)	493 (93%)	29 (6%)	6 (1%)	14	44
3	B	168/203 (83%)	165 (98%)	3 (2%)	0	100	100
4	G	247/255 (97%)	237 (96%)	10 (4%)	0	100	100
5	F	135/180 (75%)	129 (96%)	4 (3%)	2 (2%)	10	36
6	D	281/307 (92%)	275 (98%)	6 (2%)	0	100	100
7	A	711/715 (99%)	673 (95%)	38 (5%)	0	100	100
All	All	2671/2849 (94%)	2544 (95%)	119 (4%)	8 (0%)	44	72

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	334	ARG
2	E	367	PRO

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Mol	Chain	Res	Type
2	E	518	VAL
5	F	44	ALA
2	E	323	LYS

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	C	461/464 (99%)	455 (99%)	6 (1%)	69	84
2	E	454/505 (90%)	442 (97%)	12 (3%)	46	72
3	B	142/170 (84%)	142 (100%)	0	100	100
4	G	146/207 (70%)	140 (96%)	6 (4%)	30	59
5	F	117/156 (75%)	114 (97%)	3 (3%)	46	72
6	D	225/246 (92%)	225 (100%)	0	100	100
7	A	584/584 (100%)	581 (100%)	3 (0%)	88	94
All	All	2129/2332 (91%)	2099 (99%)	30 (1%)	68	83

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	365	SER
7	A	491	TYR
2	E	531	CYS
7	A	672	ILE
5	F	39	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
6	D	156	ASN
7	A	104	GLN
2	E	282	HIS
2	E	368	ASN

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Mol	Chain	Res	Type
5	F	147	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 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
10	SF4	F	201	5	0,12,12	-	-	-		
9	FCO	E	602	2	0,6,6	-	-	-		
10	SF4	B	302	3	0,12,12	-	-	-		
10	SF4	B	303	3	0,12,12	-	-	-		
10	SF4	G	301	4	0,12,12	-	-	-		
10	SF4	A	800	7	0,12,12	-	-	-		
12	MGD	A	802	13	41,52,52	0.98	4 (9%)	40,81,81	1.15	3 (7%)
10	SF4	B	304	3	0,12,12	-	-	-		
12	MGD	A	801	13	41,52,52	0.95	3 (7%)	40,81,81	0.97	3 (7%)
10	SF4	B	301	3	0,12,12	-	-	-		
10	SF4	F	202	5	0,12,12	-	-	-		

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
10	SF4	F	201	5	-	-	0/6/5/5
10	SF4	B	302	3	-	-	0/6/5/5
10	SF4	B	303	3	-	-	0/6/5/5
10	SF4	G	301	4	-	-	0/6/5/5
10	SF4	A	800	7	-	-	0/6/5/5
12	MGD	A	802	13	-	3/18/66/66	0/6/6/6
10	SF4	B	304	3	-	-	0/6/5/5
12	MGD	A	801	13	-	5/18/66/66	0/6/6/6
10	SF4	B	301	3	-	-	0/6/5/5
10	SF4	F	202	5	-	-	0/6/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A	801	MGD	C5-C6	-3.18	1.41	1.47
12	A	802	MGD	C5-C6	-2.65	1.42	1.47
12	A	801	MGD	C5-C4	-2.39	1.37	1.43
12	A	801	MGD	C8-N7	-2.29	1.31	1.35
12	A	802	MGD	C8-N7	-2.23	1.31	1.35

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	802	MGD	C19-N20-C21	3.14	119.11	113.43
12	A	801	MGD	C19-N20-C21	2.91	118.69	113.43
12	A	802	MGD	O4'-C1'-C2'	-2.90	102.69	106.93
12	A	802	MGD	O6-C6-C5	2.16	128.59	124.37
12	A	801	MGD	PB-O5'-C5'	-2.11	109.29	121.68

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

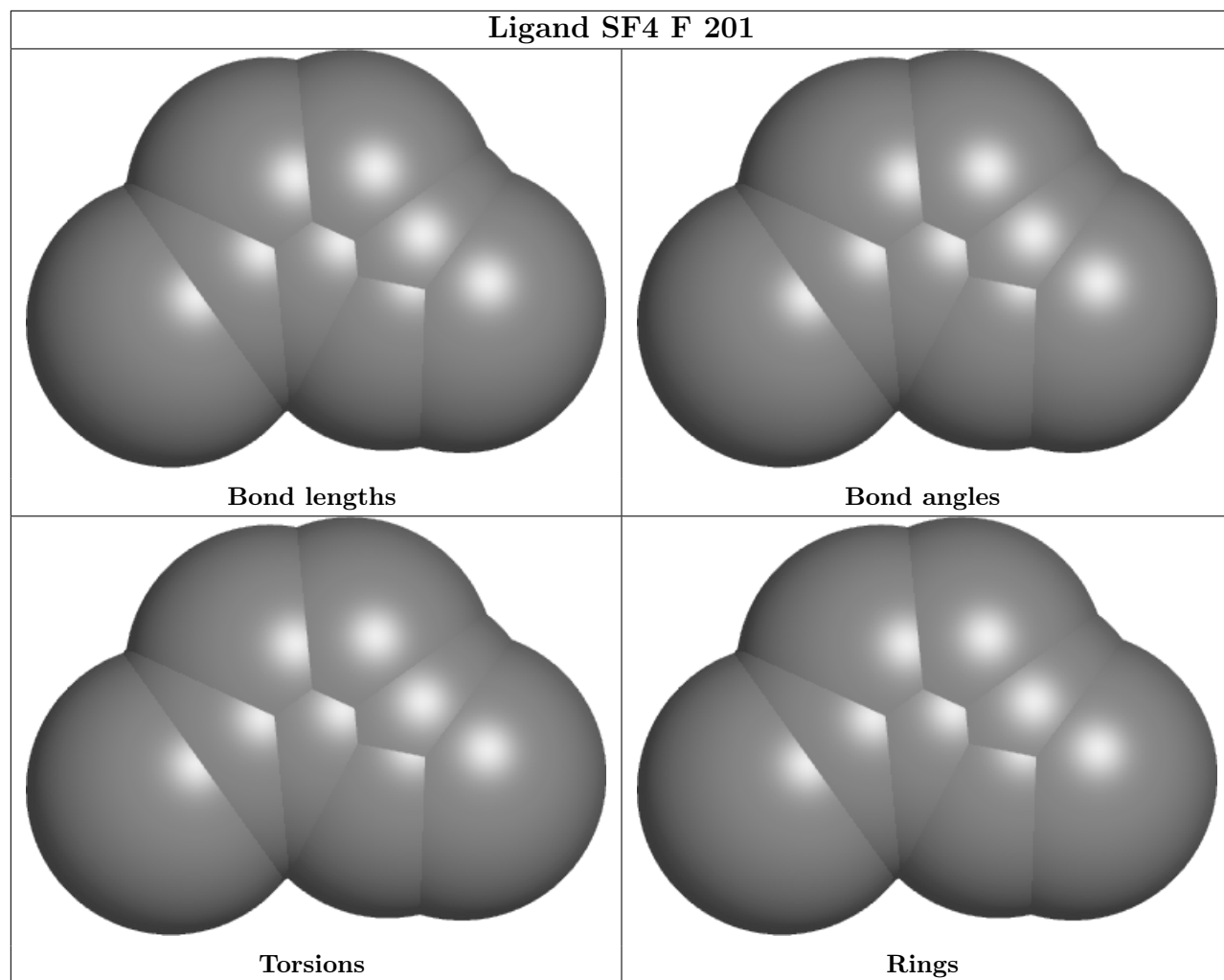
Mol	Chain	Res	Type	Atoms
12	A	801	MGD	C5'-O5'-PB-O1B
12	A	801	MGD	C5'-O5'-PB-O2B
12	A	802	MGD	O3A-C10-C11-O11
12	A	801	MGD	O4'-C4'-C5'-O5'
12	A	801	MGD	C3'-C4'-C5'-O5'

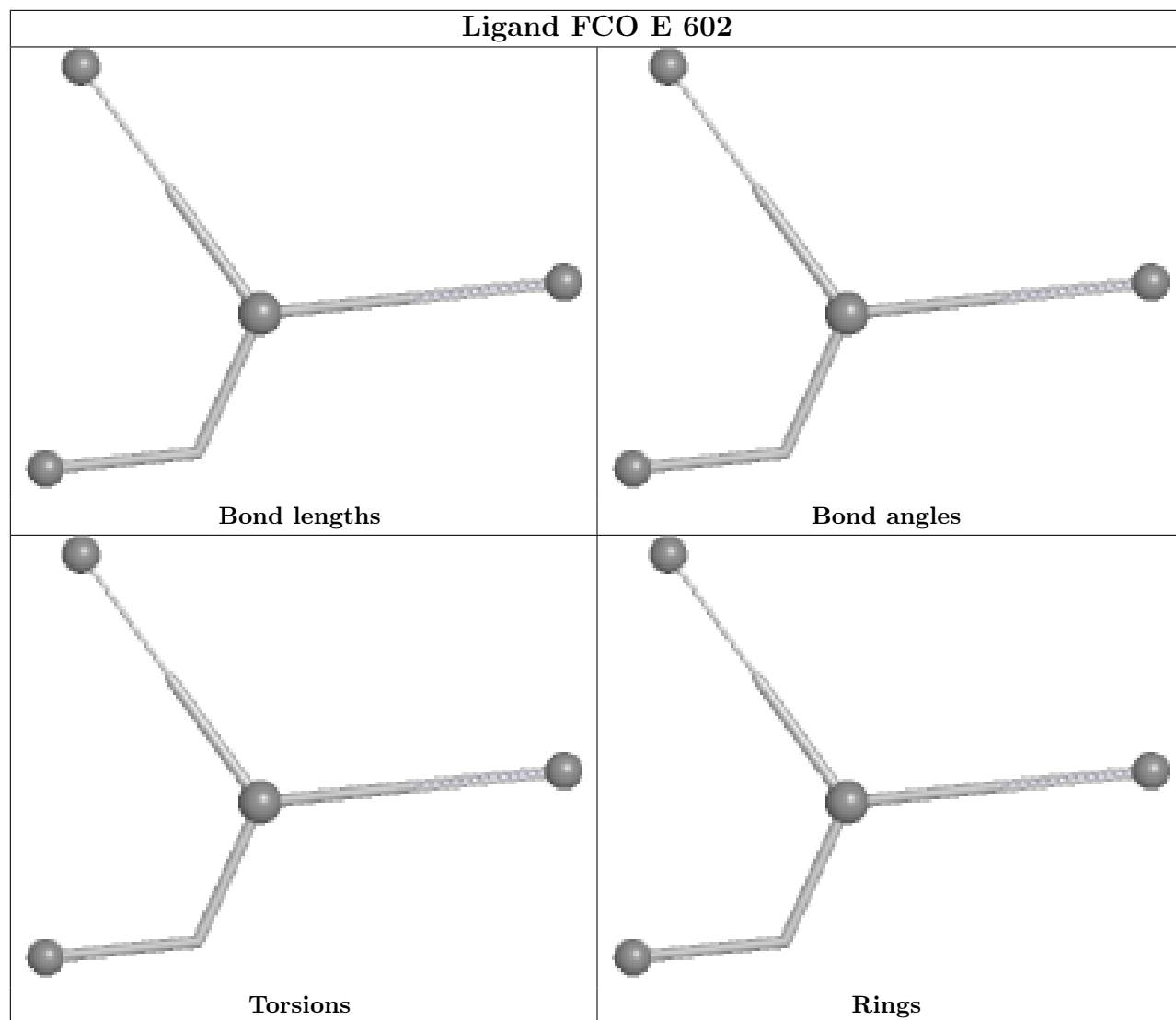
There are no ring outliers.

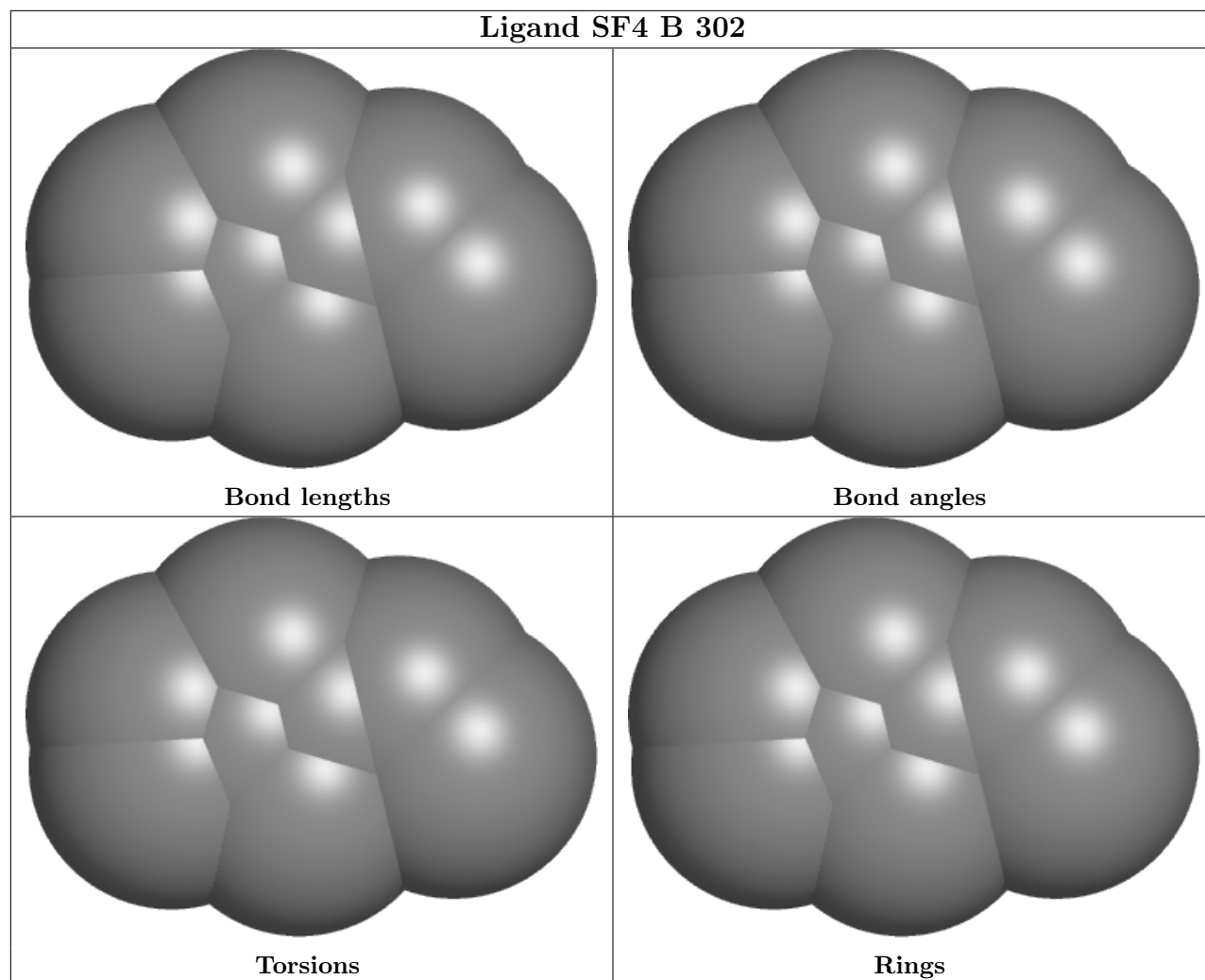
4 monomers are involved in 6 short contacts:

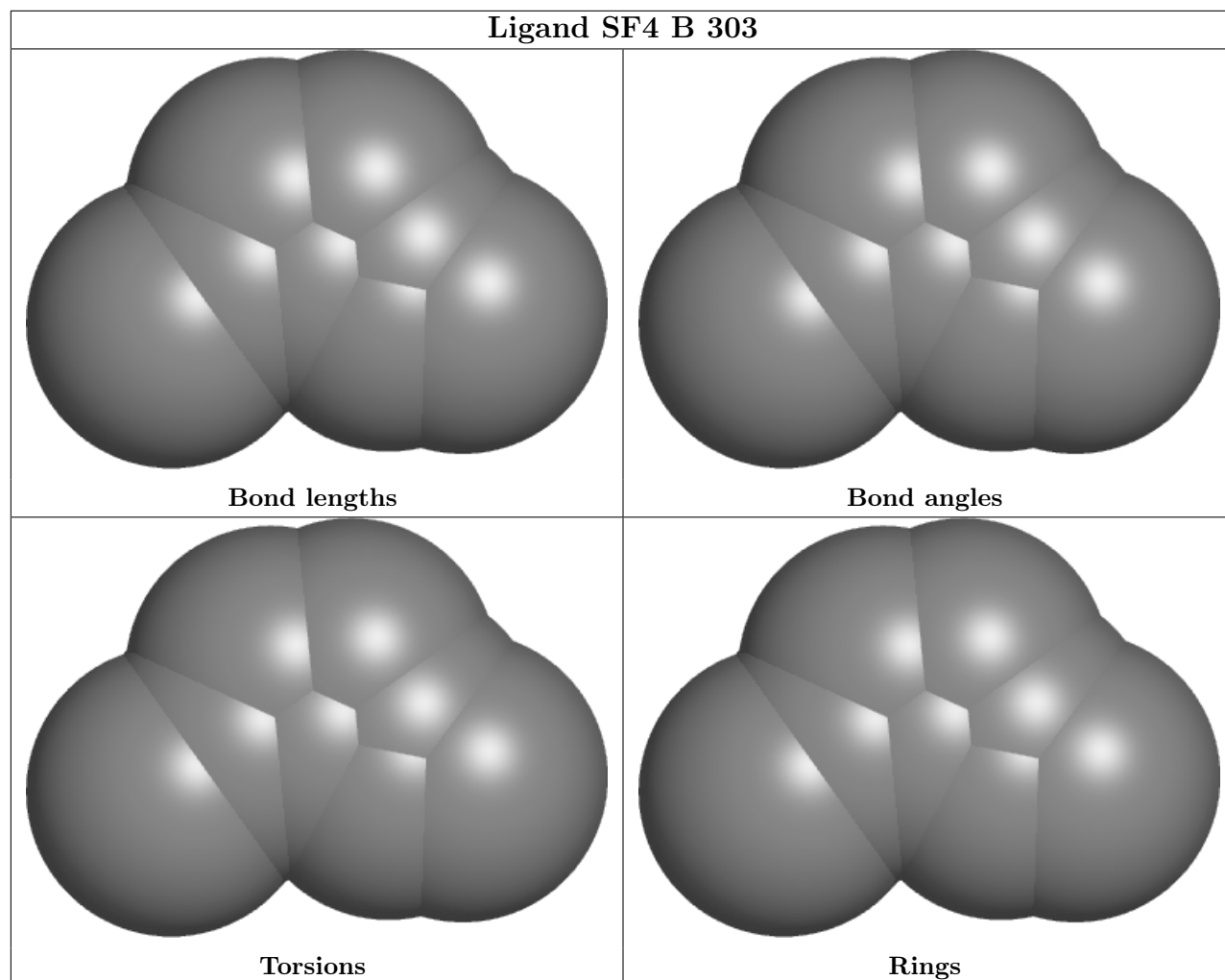
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	602	FCO	1	0
10	A	800	SF4	2	0
12	A	802	MGD	2	0
12	A	801	MGD	1	0

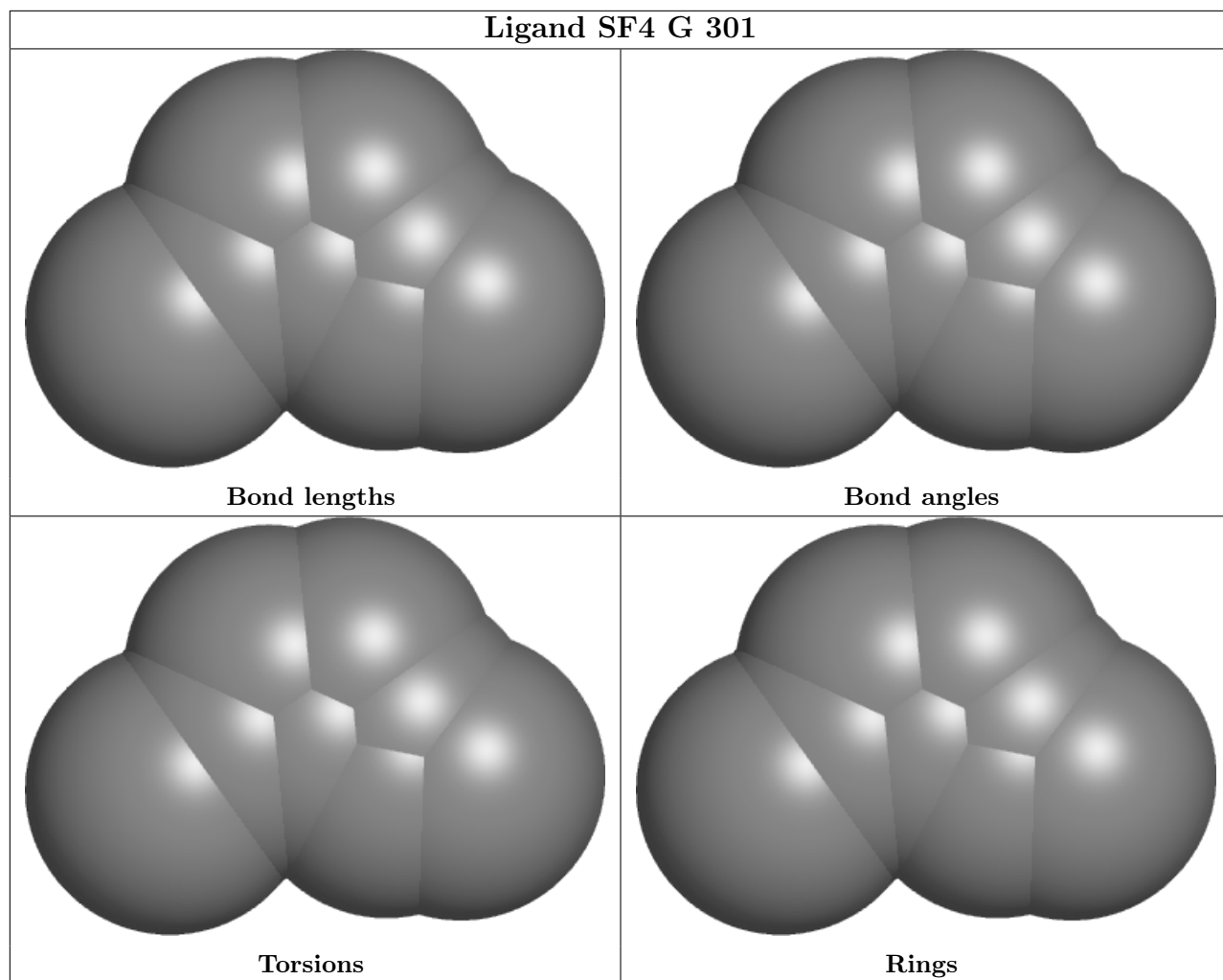
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

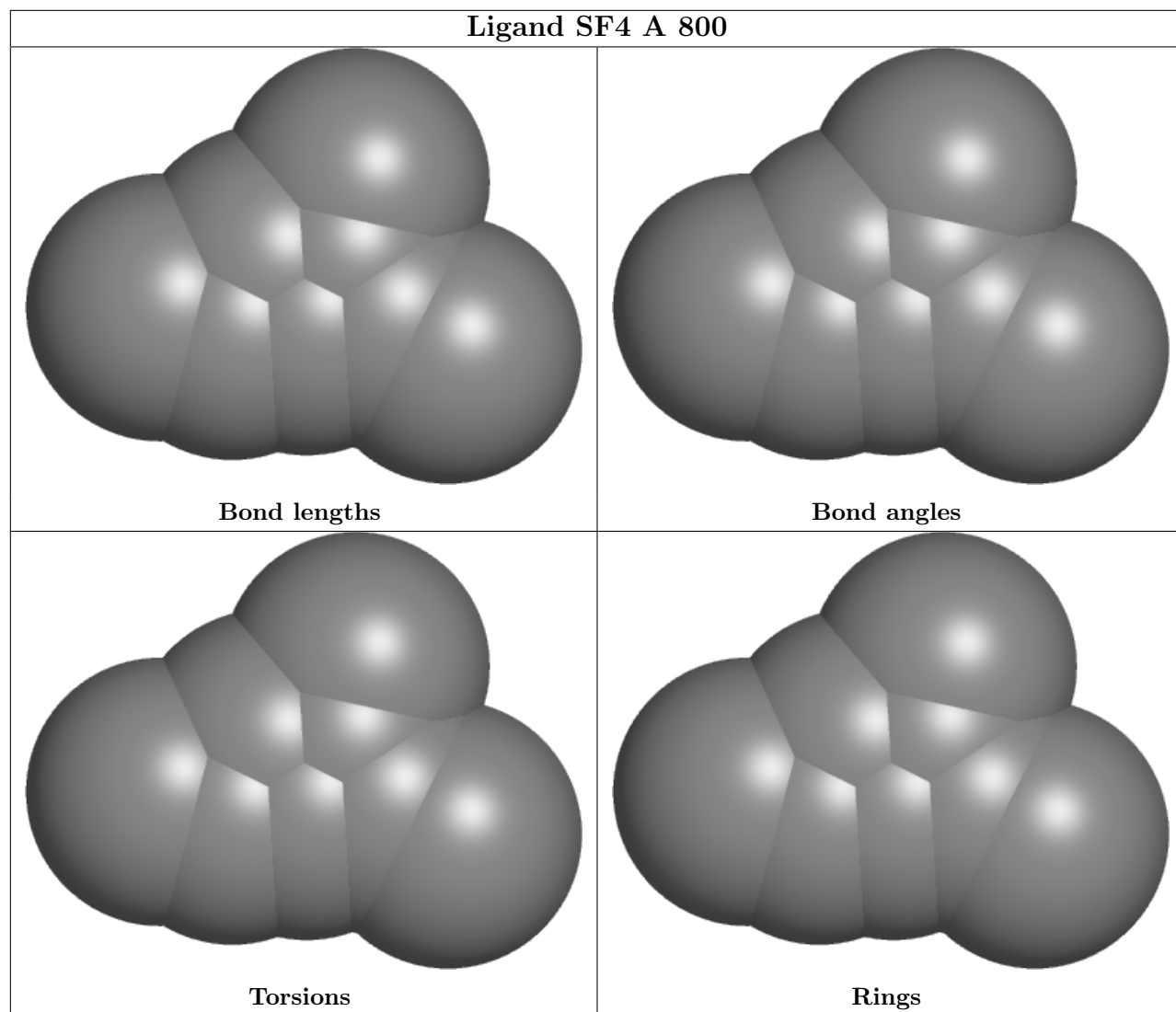


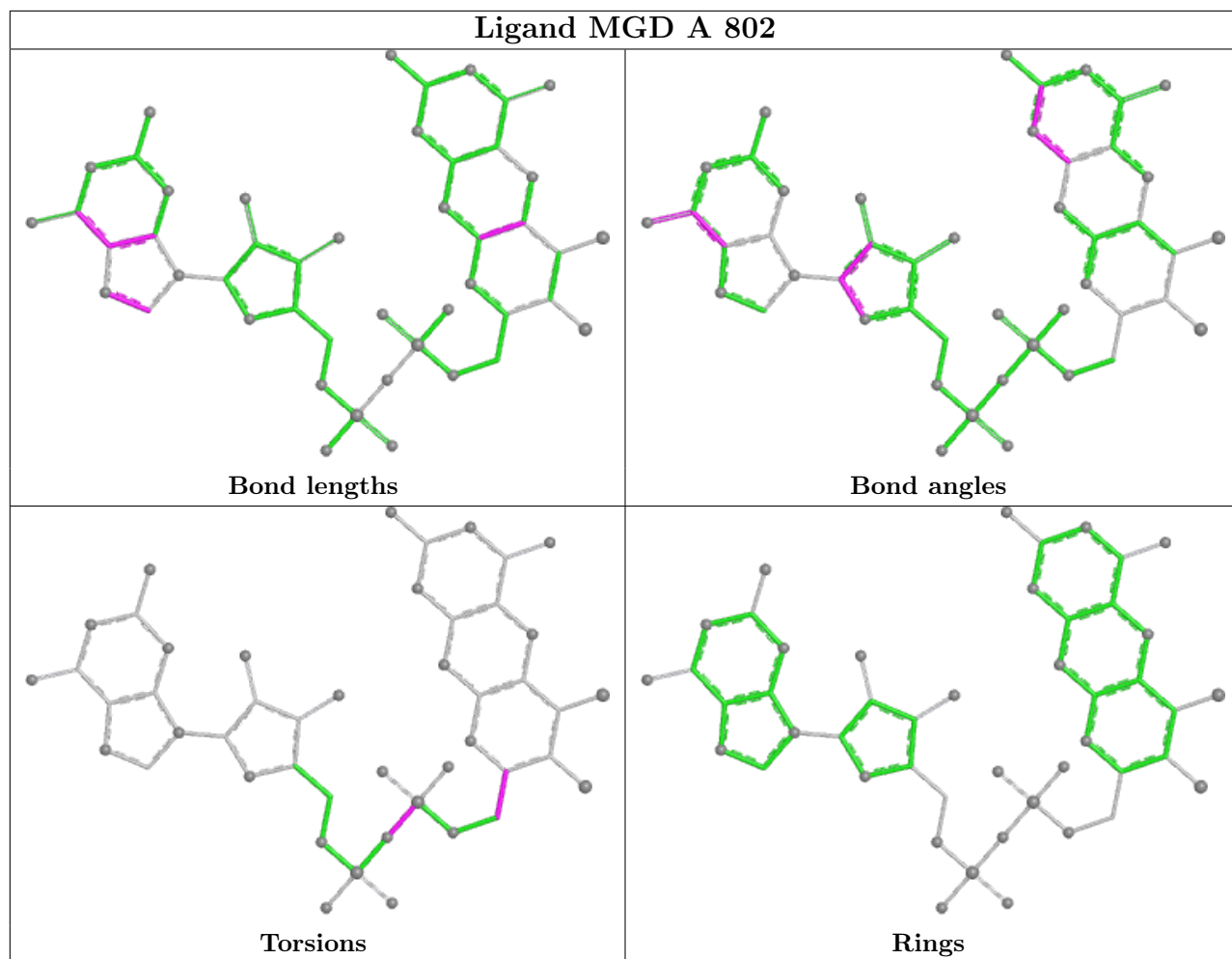


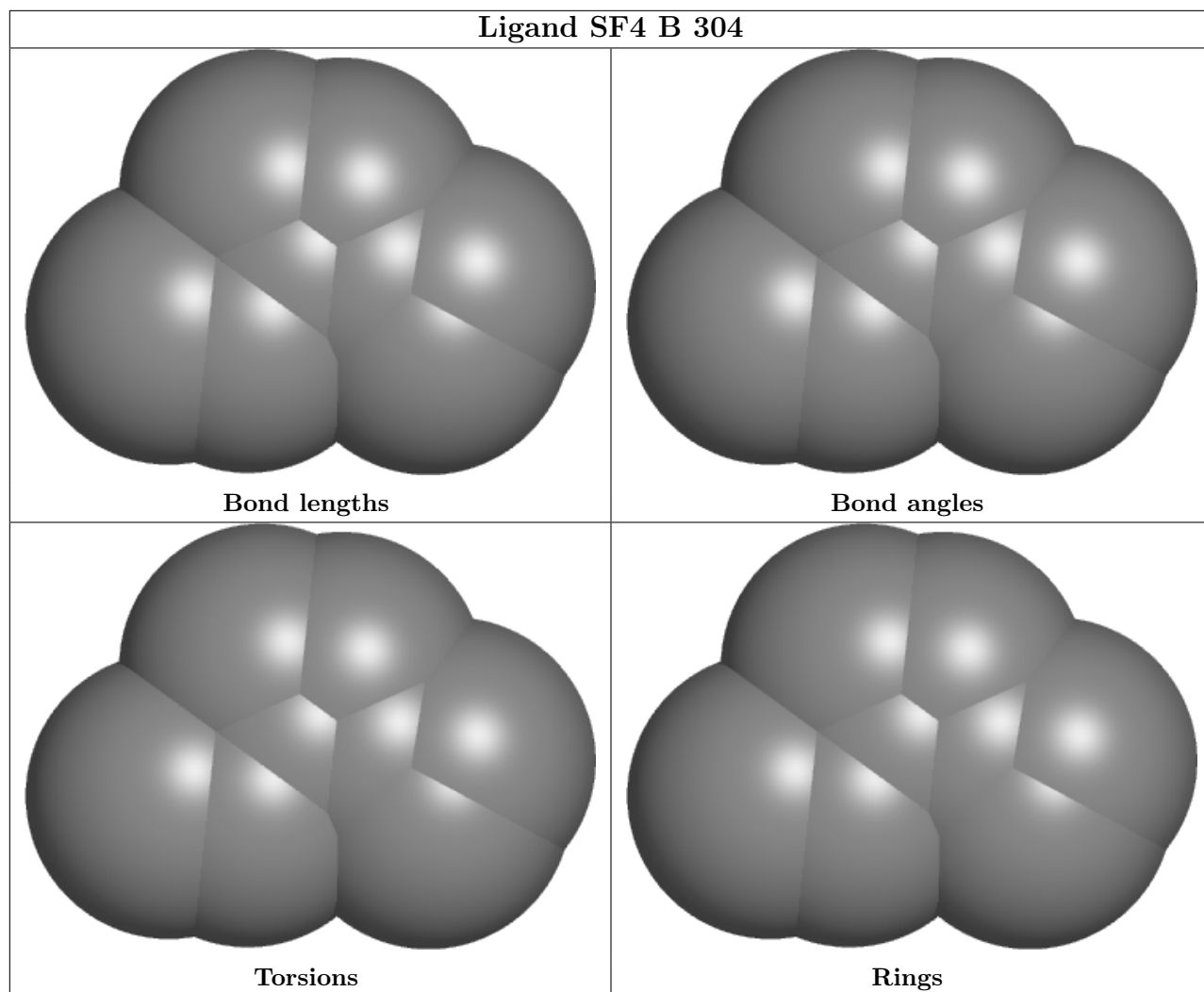


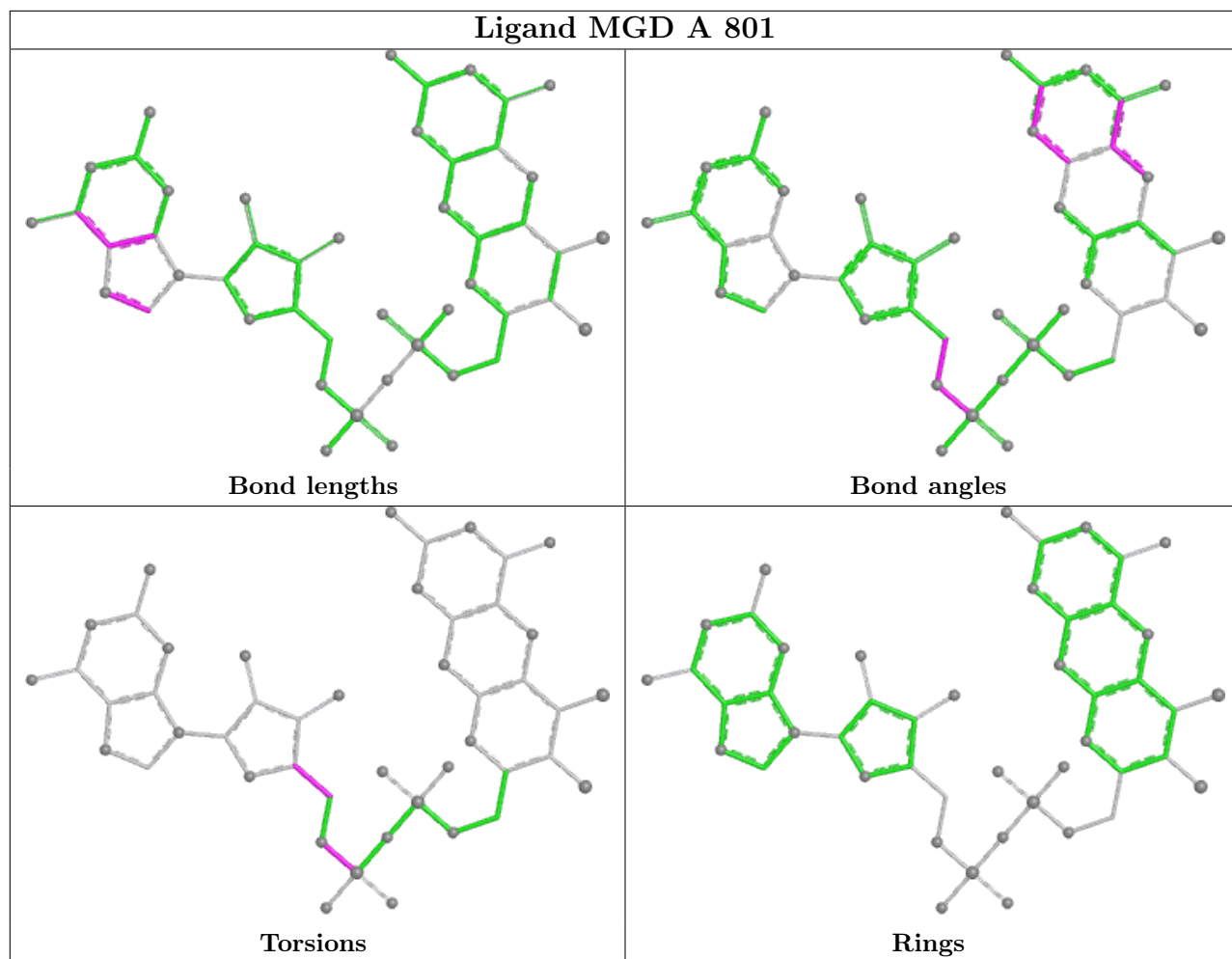


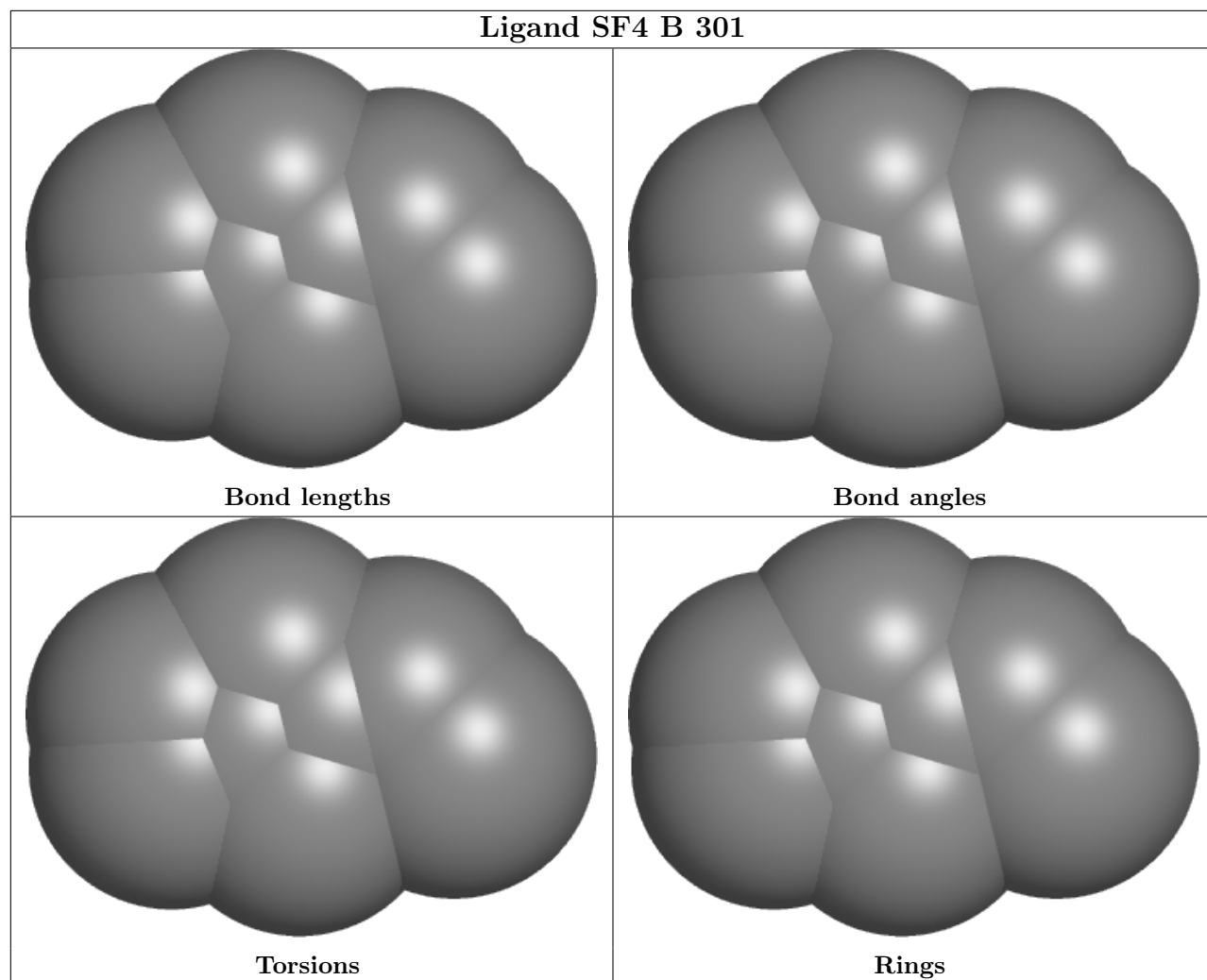


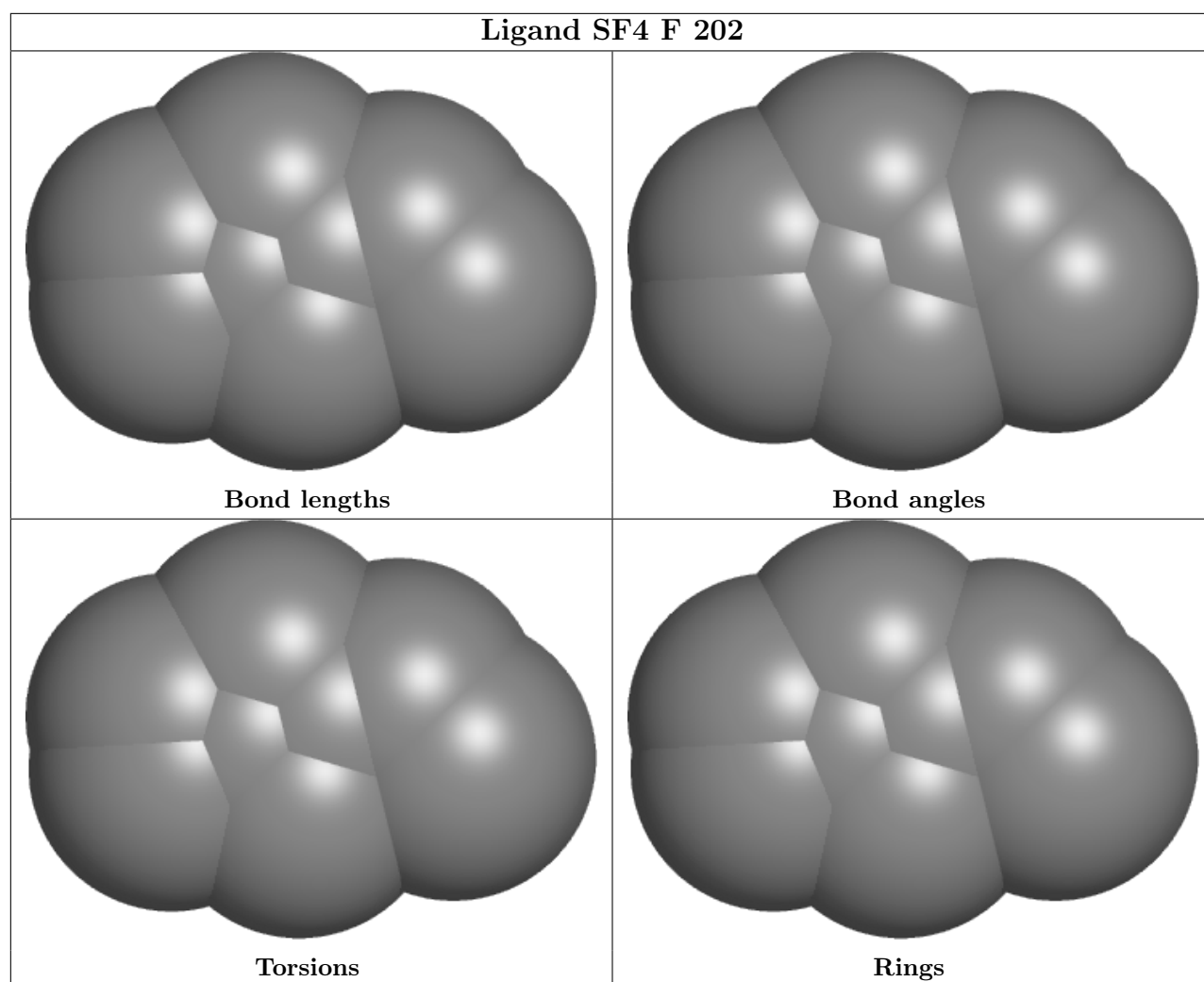












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

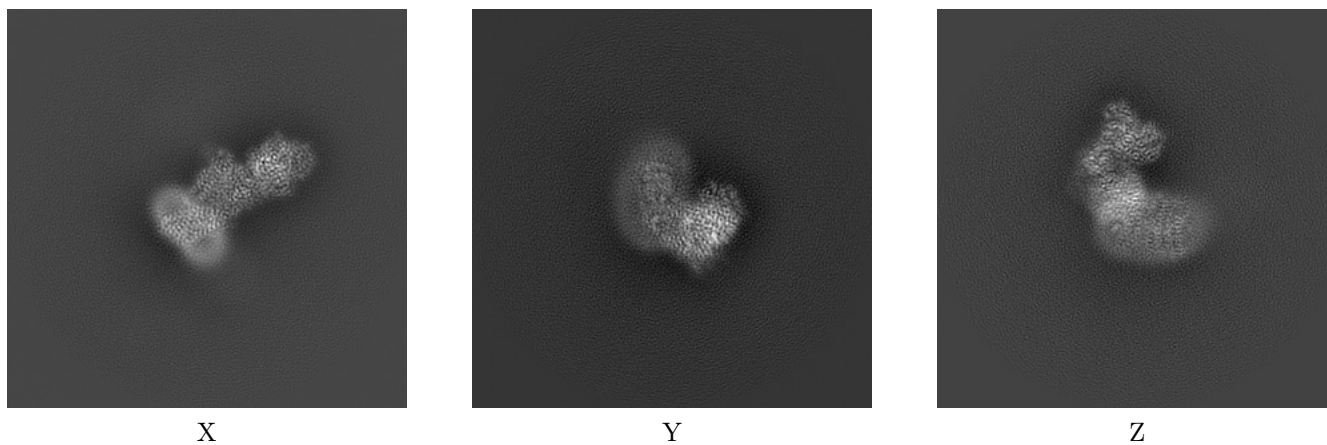
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14430. 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](#)

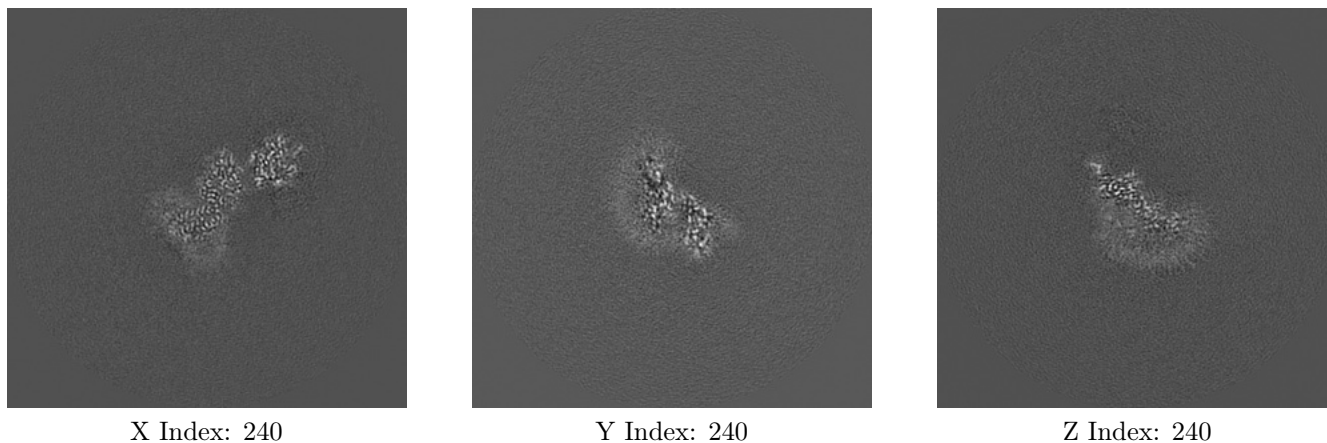
6.1.1 Primary map



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

6.2 Central slices [i](#)

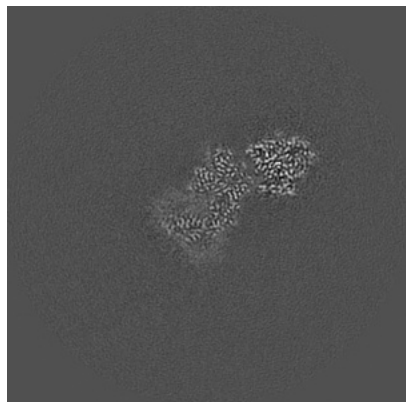
6.2.1 Primary map



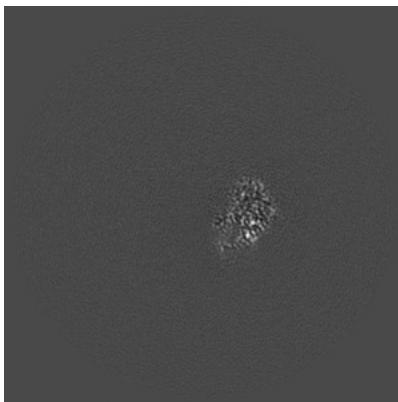
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

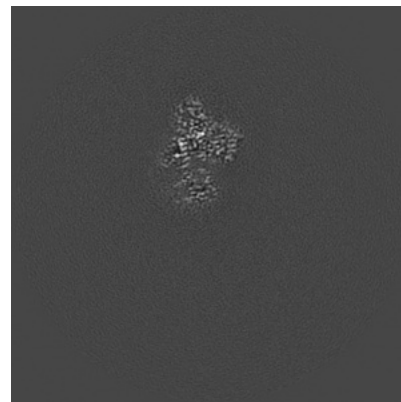
6.3.1 Primary map



X Index: 225



Y Index: 314



Z Index: 291

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

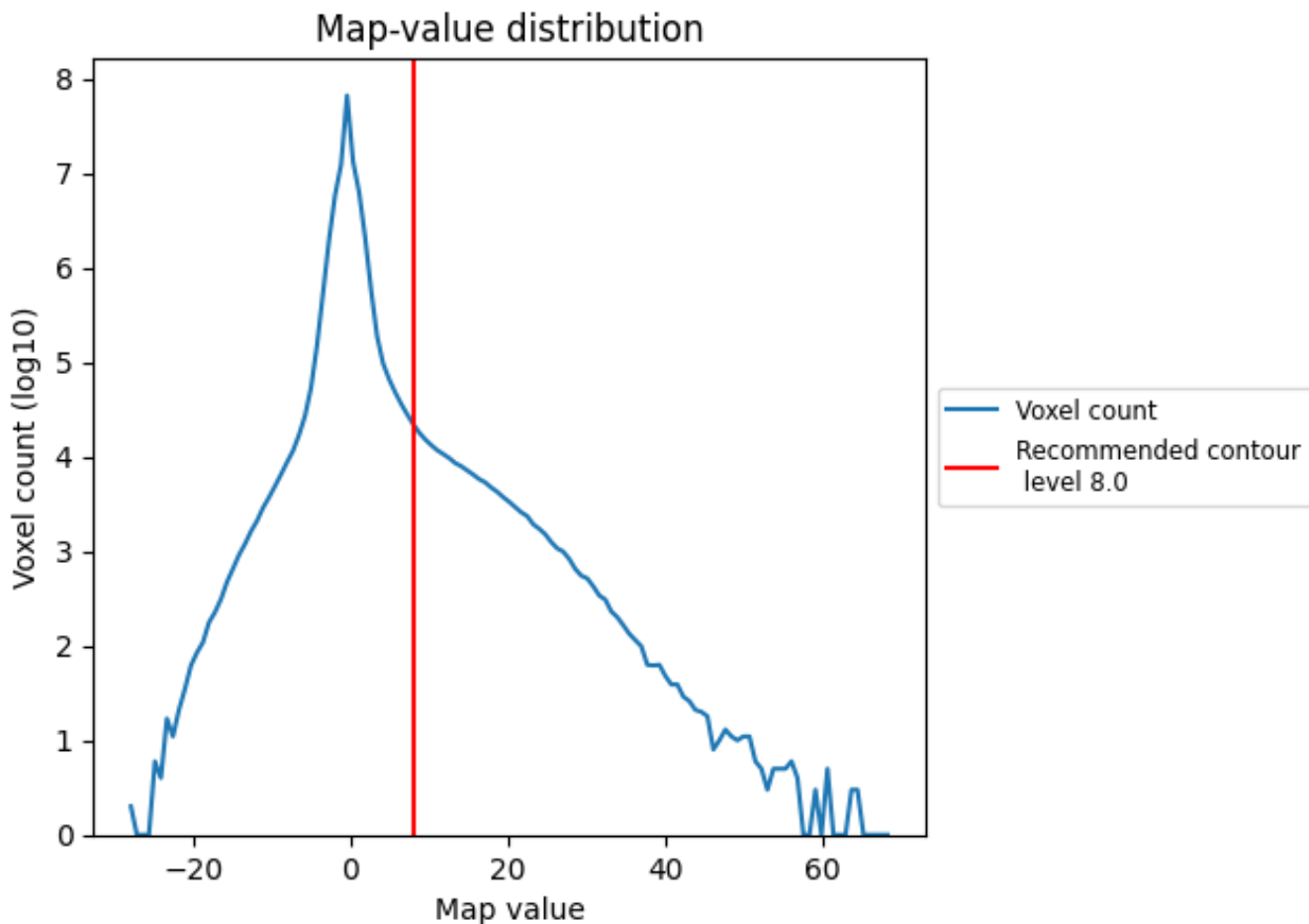
6.5 Mask visualisation

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

7 Map analysis [i](#)

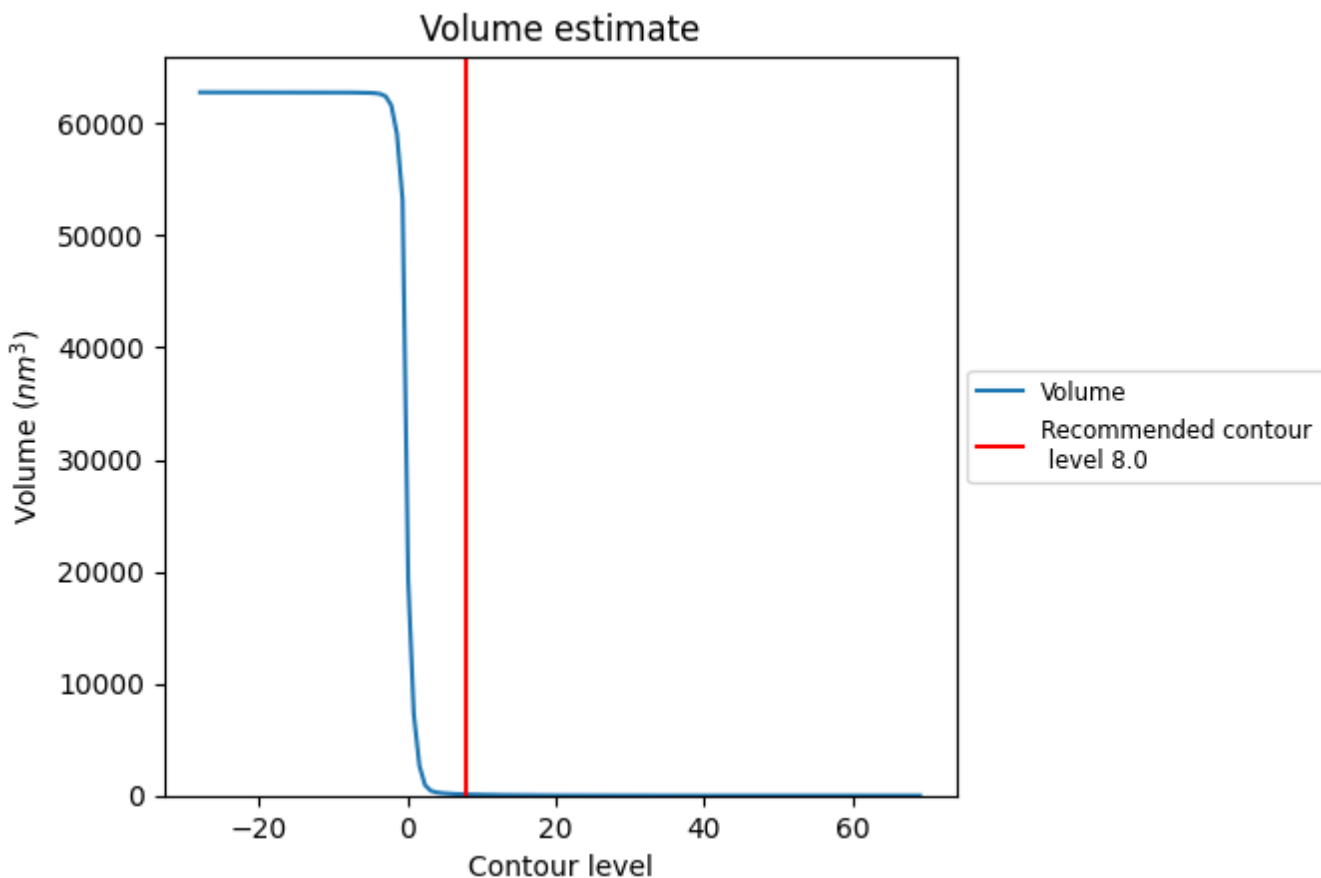
This section contains the results of statistical analysis of the map.

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.

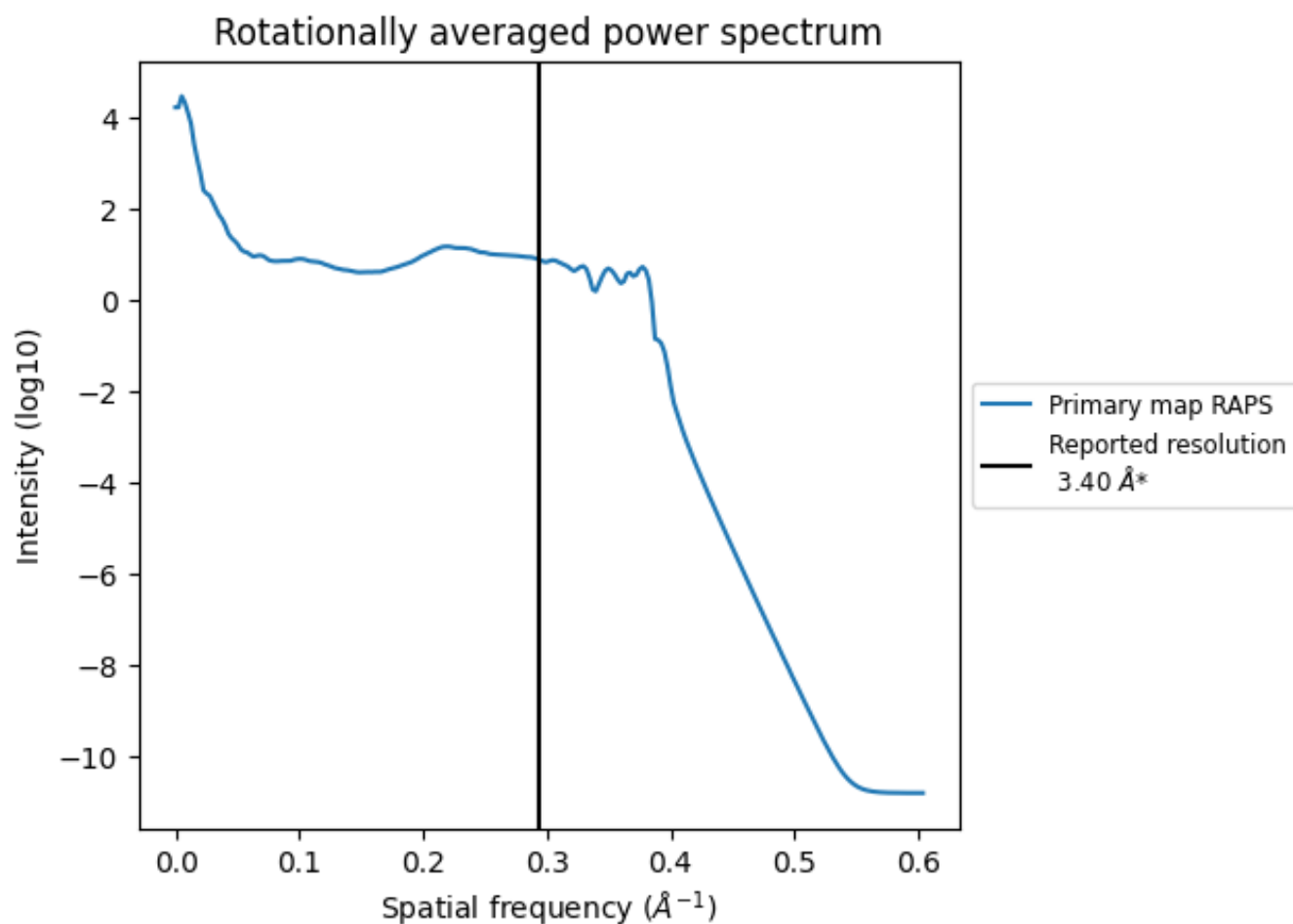
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 102 nm³; this corresponds to an approximate mass of 92 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 0.294\AA^{-1}

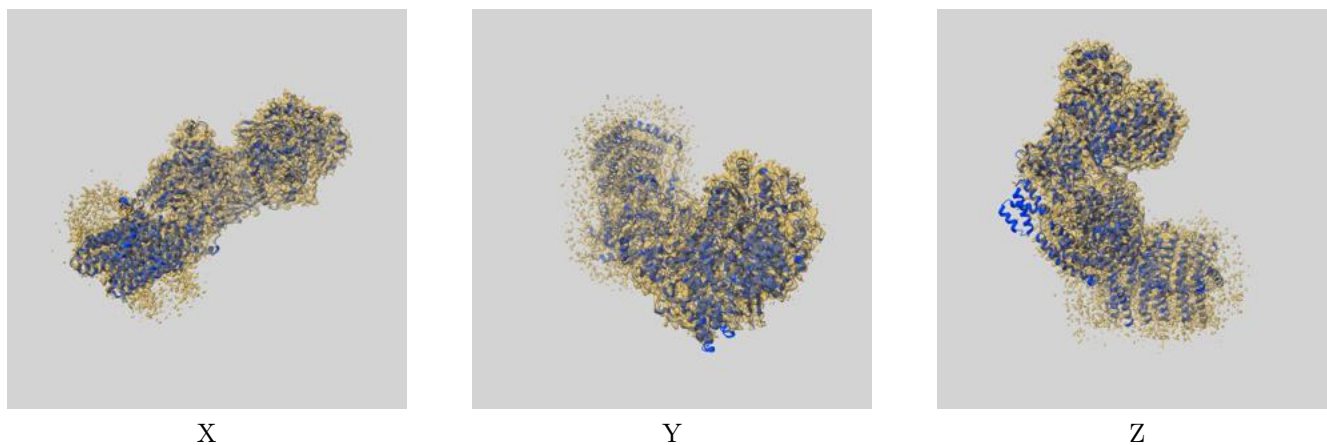
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

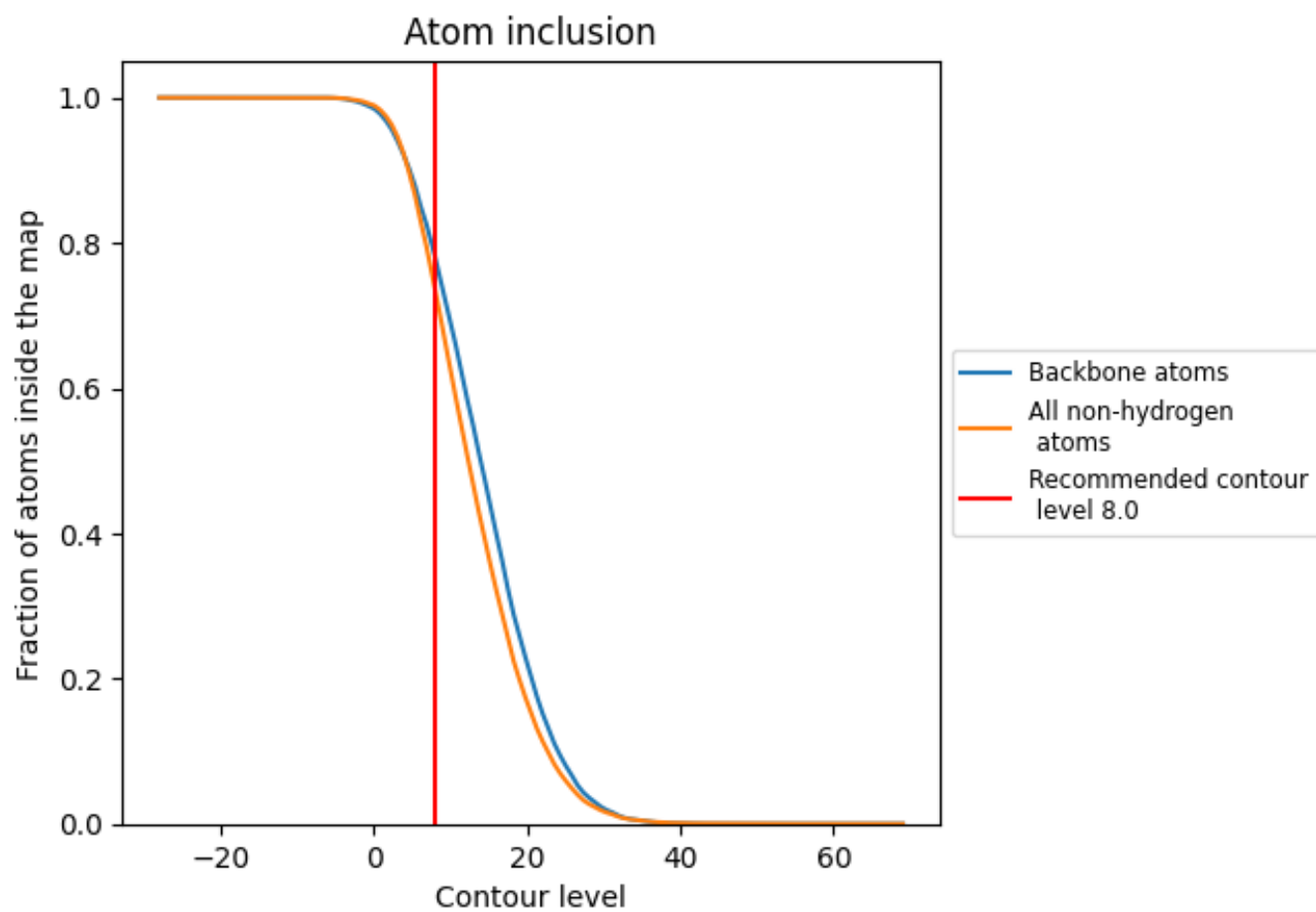
This section contains information regarding the fit between EMDB map EMD-14430 and PDB model 7Z0T. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 8.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.