



wwPDB EM Validation Summary Report ⓘ

Jun 29, 2025 – 03:01 am BST

PDB ID : 9G02 / pdb_00009g02
EMDB ID : EMD-50907
Title : Structure of carbon monoxide dehydrogenase/acetyl-CoA synthase (CODH/ACS) from Clostridium autoethanogenum (composite structure, semi-extended state)
Authors : Yin, M.D.; Lemaire, O.N.; Wagner, T.; Murphy, B.J.
Deposited on : 2024-07-06
Resolution : 3.29 Å(reported)

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

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

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.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.44

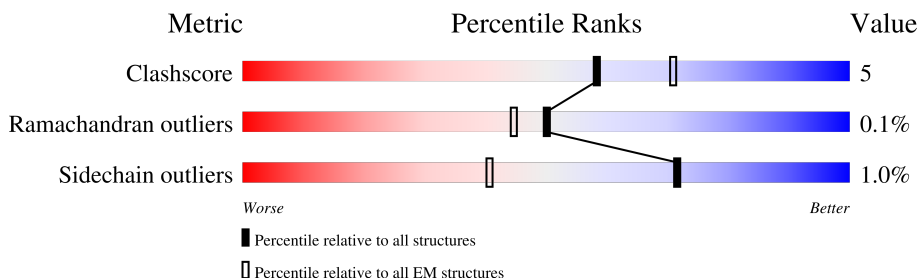
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.29 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	708	
1	D	708	
2	B	630	
2	C	630	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 17018 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.

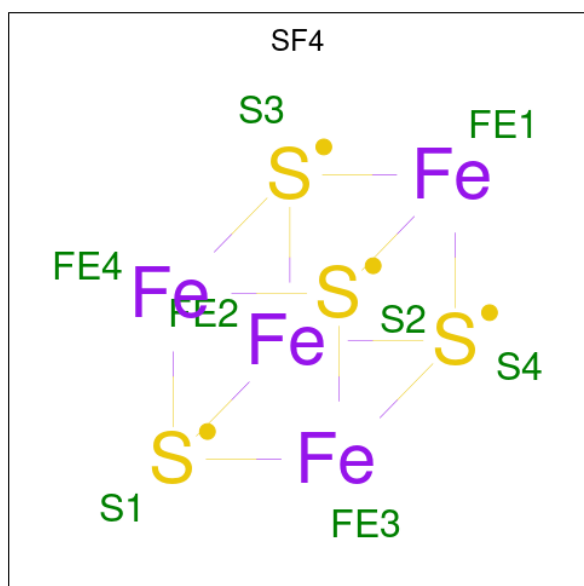
- Molecule 1 is a protein called CO-methylating acetyl-CoA synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	707	Total	C	N	O	S	0	0
			5384	3444	883	1022	35		
1	A	290	Total	C	N	O	S	0	0
			2154	1391	347	409	7		

- Molecule 2 is a protein called Carbon monoxide dehydrogenase/acetyl-CoA synthase beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	628	Total	C	N	O	S	0	0
			4714	2962	813	899	40		
2	C	628	Total	C	N	O	S	0	0
			4714	2962	813	899	40		

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).

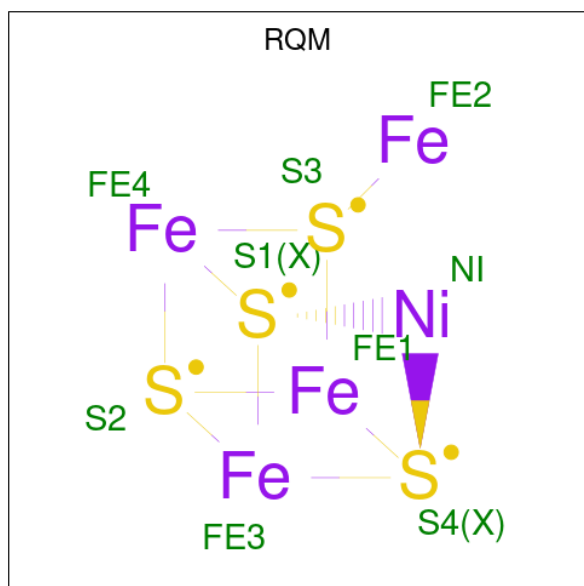


Mol	Chain	Residues	Atoms			AltConf
3	D	1	Total	Fe	S	0
			8	4	4	
3	B	1	Total	Fe	S	0
			8	4	4	
3	B	1	Total	Fe	S	0
			8	4	4	
3	C	1	Total	Fe	S	0
			8	4	4	

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	D	2	Total	Ni	0
			2	2	

- Molecule 5 is Fe(3)-Ni(1)-S(4) cluster (CCD ID: RQM) (formula: Fe₄NiS₄) (labeled as "Ligand of Interest" by depositor).

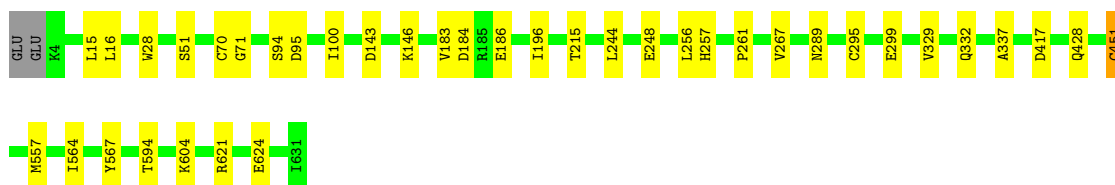


Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	Fe	Ni	S	0
			9	4	1	4	
5	C	1	Total	Fe	Ni	S	0
			9	4	1	4	

GLU	PHE	ASN	LEU	TYR
LEU	GLY	GLU	CYS	ALA
TYR	GLU	THR	GLN	LYS
ASN	LEU	VAL	SER	MET
ASP	ILE	ALA	PHE	LEU
ASN	SER	LYS	ALA	ASP
PHE	MET	ILE	PRO	GLU
ASP	THR	SER	ALA	PHE
ALA	GLY	GLN	HIS	GLY
ASP	GLY	GLY	VAL	SER
MET	GLY	ALA	CYS	VAL
ILE	VAL	VAL	ILE	VAL
CYS	GLN	THR	VAL	ASP
ASP	THR	SER	THR	ASP
GLU	PRO	VAL	PRO	CYS
THR	GLY	THR	GLU	GLY
ILE	PHE	LEU	ARG	VAL
ALA	MET	TYR	LEU	THR
THR	GLY	SER	LEU	ILE
GLU	HIS	ILE	LEU	GLY
SER	GLY	LEU	CYS	THR
GLU	ARG	GLN	GLY	ASP
GLU	GLN	ASP	ALA	PRO
VAL	PHE	PRO	VAL	GLY
VAL	ILE	MET	SER	LYS
LYS	ALA	THR	TRP	ALA
LYS	SER	SER	LEU	GLU
PHE	LYS	CYS	ASP	GLU
GLY	LYS	GLY	ALA	LEU
GLU	PHE	CYS	LYS	GLU
LYS	MET	CYS	ALA	GLY
GLY	LYS	GLU	THR	LYS
HIS	GLY	CYS	LEU	TYR
PRO	GLU	ILE	GLU	ALA
ALA	GLY	THR	LEU	VAL
LEU	GLY	ILE	ASN	PRO
LYS	LEU	ILE	PRO	ARG
MET	GLY	MET	THR	TYR
ASP	ARG	PRO	GLY	LYS
PRO	ILE	GLU	PRO	GLU
ILE	VAL	ALA	CYS	ARG
MET	TRP	ASN	GLN	ASP
	MET	GLY	ALA	ALA
	PRO	VAL	VAL	ARG
	LYS	VAL	PRO	GLU
	GLU	MET	LYS	GLU
	LEU	VAL	GLU	SER
	LYS	ASN	GLY	LEU
	ASP	ARG	VAL	VAL
	PHE	GLU	VAL	VAL
	ALA	PHE	ASP	GLU
	ALA	GLY	GLU	LYS
	GLU	ALA	ASN	VAL
	LYS	THR	LEU	ASP
	LEU	THR	GLY	THR
	ASN	PRO	ILE	PHE
	THR	LEU	TRP	TYR
	LYS	GLY	GLU	SER
	ALA	MET	LYS	CYS
	LYS	THR	VAL	ASN

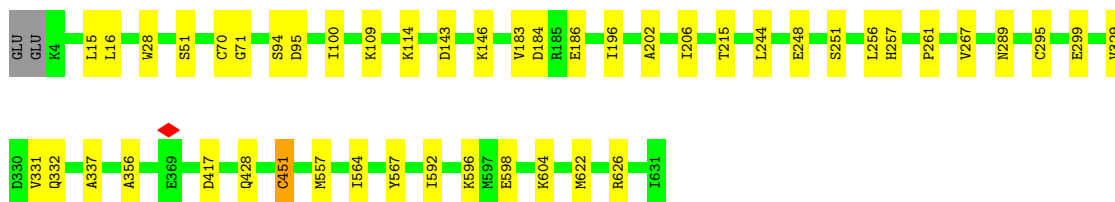
- Molecule 2: Carbon monoxide dehydrogenase/acetyl-CoA synthase beta subunit

Chain B:  94% 6%



- Molecule 2: Carbon monoxide dehydrogenase/acetyl-CoA synthase beta subunit

Chain C:  92% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	649146	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	137.124	Depositor
Minimum map value	-128.563	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.023	Depositor
Recommended contour level	8	Depositor
Map size (Å)	490.56, 490.56, 490.56	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.876, 0.876, 0.876	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: SF4, NI, RQM

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	0.31	0/2185	0.36	0/2970
1	D	0.17	0/5480	0.32	0/7418
2	B	0.38	0/4788	0.45	0/6476
2	C	0.38	0/4788	0.44	0/6476
All	All	0.32	0/17241	0.40	0/23340

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	2154	0	2264	7	0
1	D	5384	0	5480	101	0
2	B	4714	0	4797	24	0
2	C	4714	0	4797	29	0
3	B	16	0	0	1	0
3	C	8	0	0	1	0
3	D	8	0	0	0	0
4	D	2	0	0	0	0
5	B	9	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	9	0	0	1	0
All	All	17018	0	17338	156	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 5.

The worst 5 of 156 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:C:451:CYS:HB3	5:C:702:RQM:S2	2.29	0.72
2:B:451:CYS:HB3	5:B:703:RQM:S2	2.29	0.72
1:D:495:HIS:NE2	1:D:497:CYS:SG	2.64	0.70
1:D:451:LYS:NZ	1:D:454:GLU:OE2	2.24	0.68
1:D:351:ASP:OD1	1:D:352:THR:N	2.27	0.67

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	288/708 (41%)	284 (99%)	4 (1%)	0	100	100
1	D	705/708 (100%)	675 (96%)	30 (4%)	0	100	100
2	B	626/630 (99%)	609 (97%)	16 (3%)	1 (0%)	44	71
2	C	626/630 (99%)	608 (97%)	17 (3%)	1 (0%)	44	71
All	All	2245/2676 (84%)	2176 (97%)	67 (3%)	2 (0%)	50	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	332	GLN

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Mol	Chain	Res	Type
2	B	332	GLN

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	232/583 (40%)	232 (100%)	0	100	100
1	D	582/583 (100%)	568 (98%)	14 (2%)	44	68
2	B	517/519 (100%)	515 (100%)	2 (0%)	89	93
2	C	517/519 (100%)	515 (100%)	2 (0%)	89	93
All	All	1848/2204 (84%)	1830 (99%)	18 (1%)	71	84

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	95	ASP
2	C	451	CYS
2	C	95	ASP
1	D	558	VAL
1	D	703	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	388	ASN
2	C	357	HIS
1	A	287	ASN
1	A	233	ASN
2	B	388	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	SF4	D	801	1,4	0,12,12	-	-	-		
3	SF4	B	702	2	0,12,12	-	-	-		
5	RQM	B	703	2	0,12,12	-	-	-		
3	SF4	B	701	2	0,12,12	-	-	-		
5	RQM	C	702	2	0,12,12	-	-	-		
3	SF4	C	701	2	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
3	SF4	D	801	1,4	-	-	0/6/5/5
3	SF4	B	702	2	-	-	0/6/5/5
5	RQM	B	703	2	-	-	0/4/4/4
3	SF4	B	701	2	-	-	0/6/5/5
5	RQM	C	702	2	-	-	0/4/4/4
3	SF4	C	701	2	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

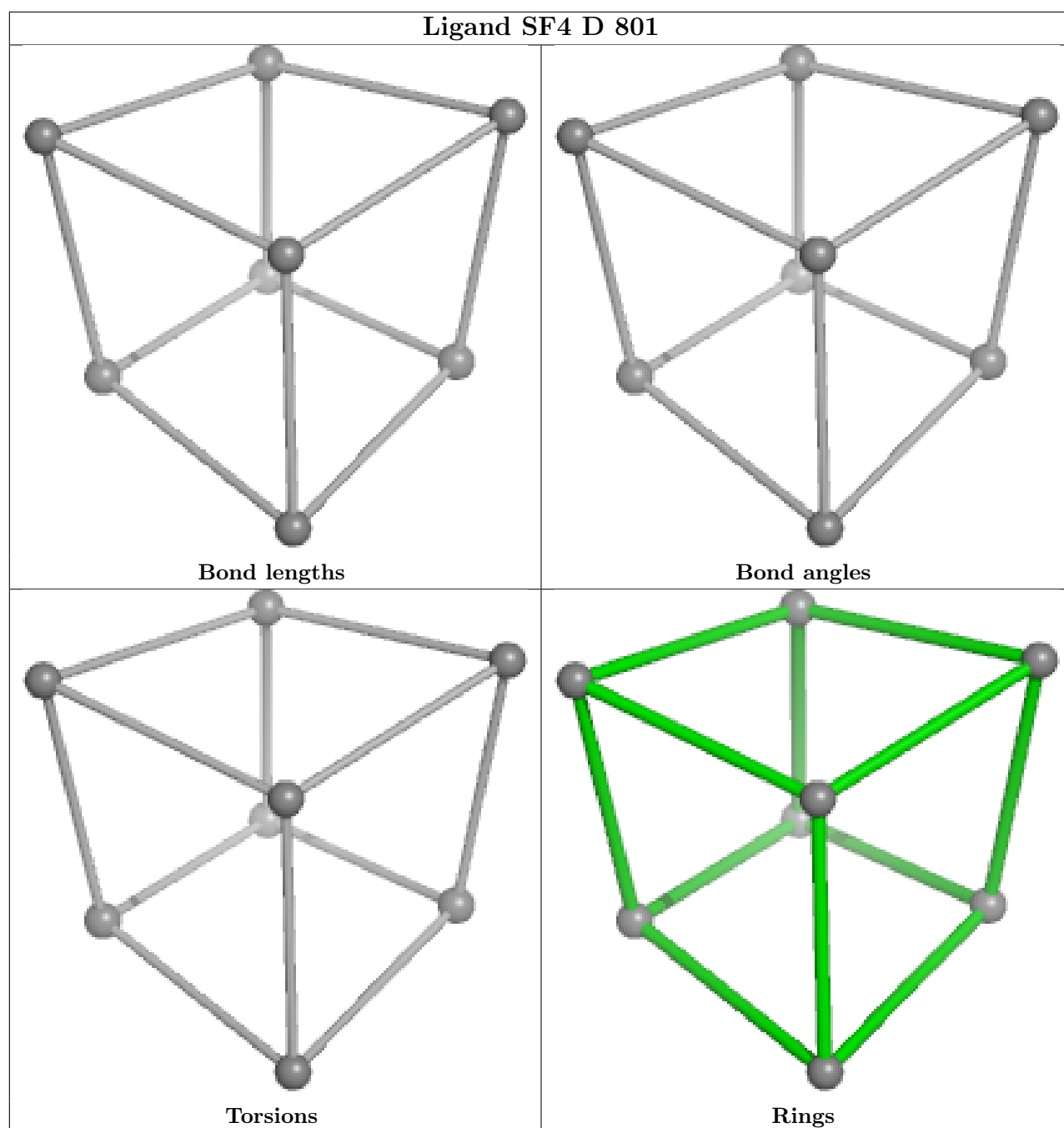
There are no torsion outliers.

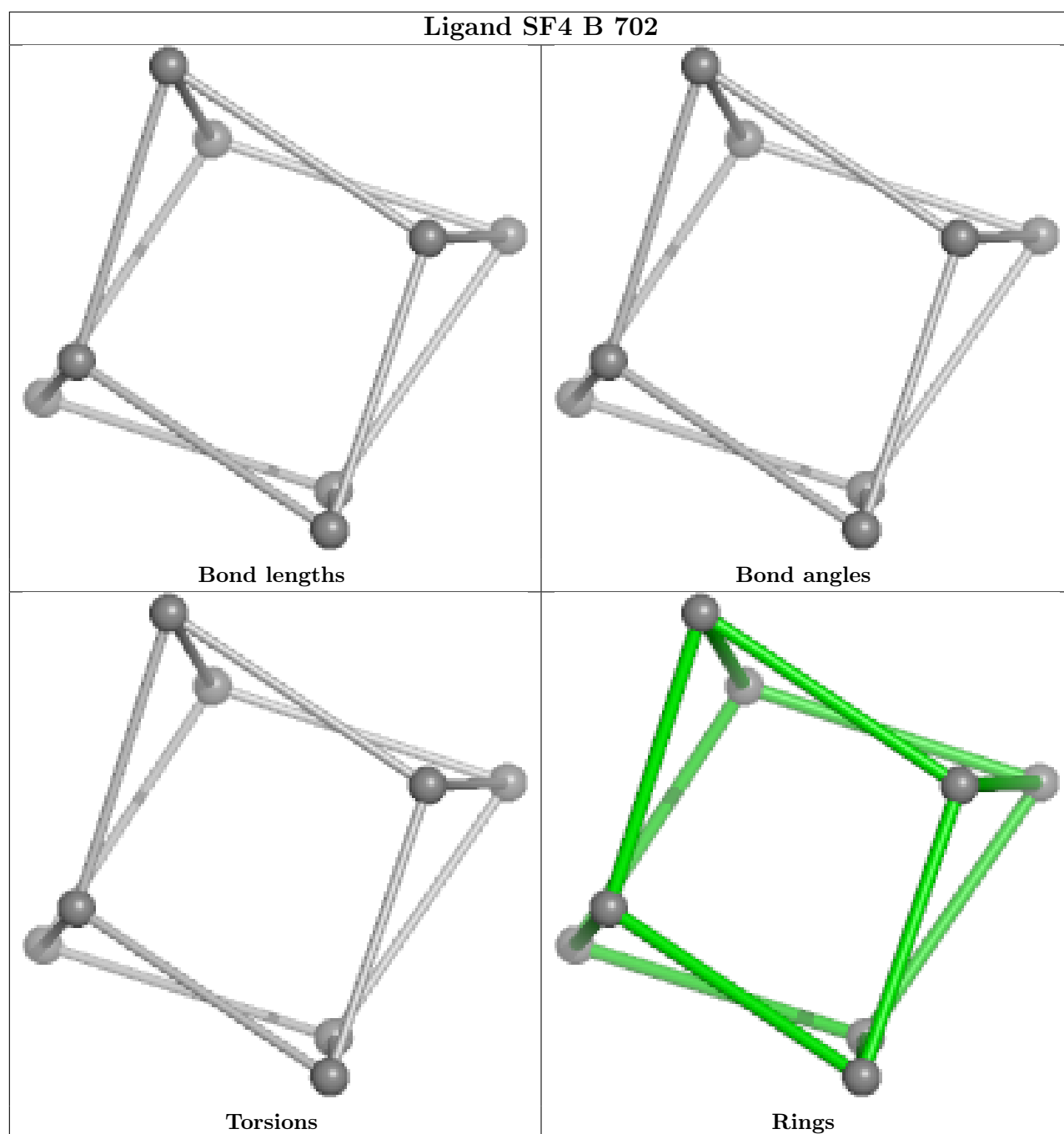
There are no ring outliers.

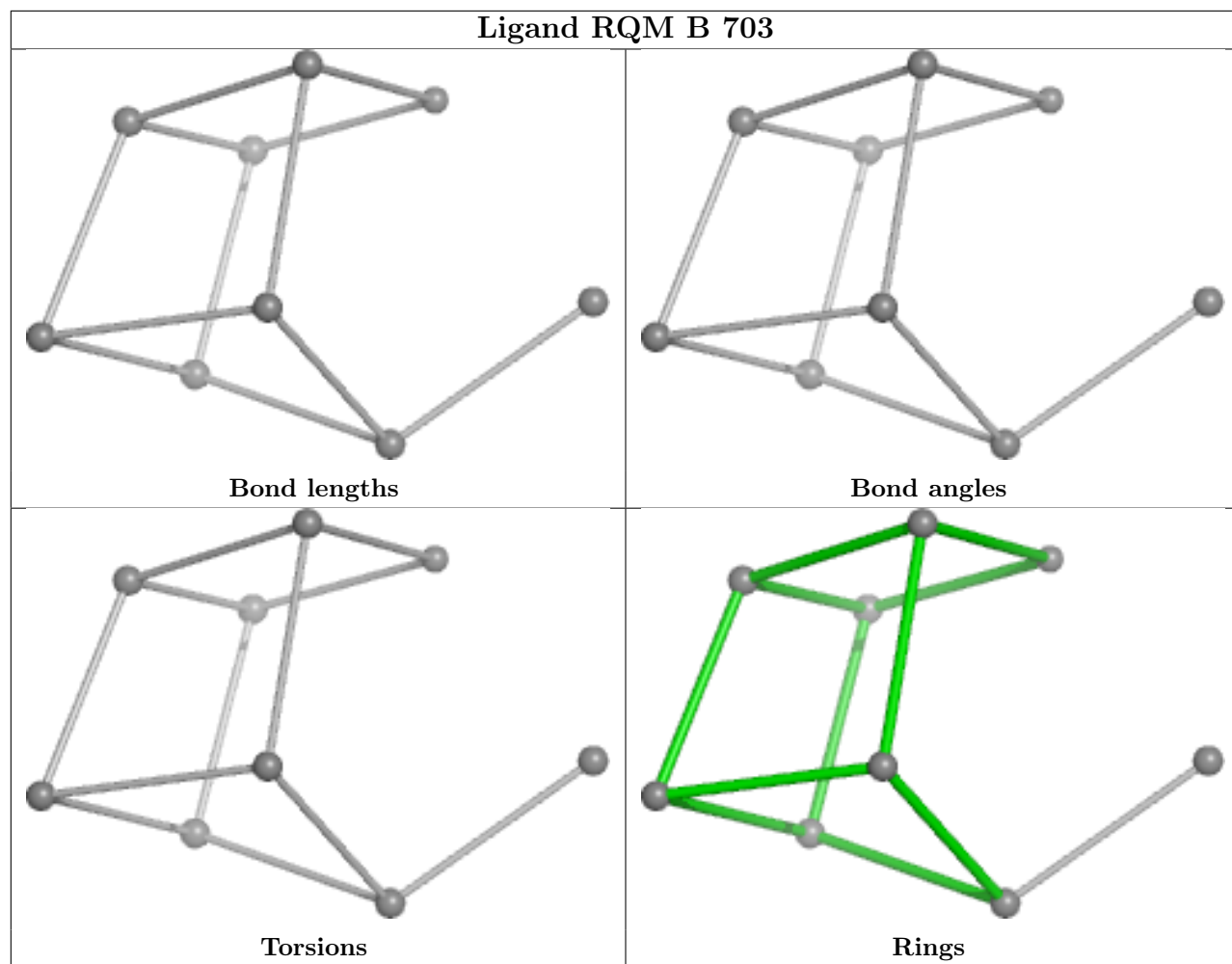
4 monomers are involved in 4 short contacts:

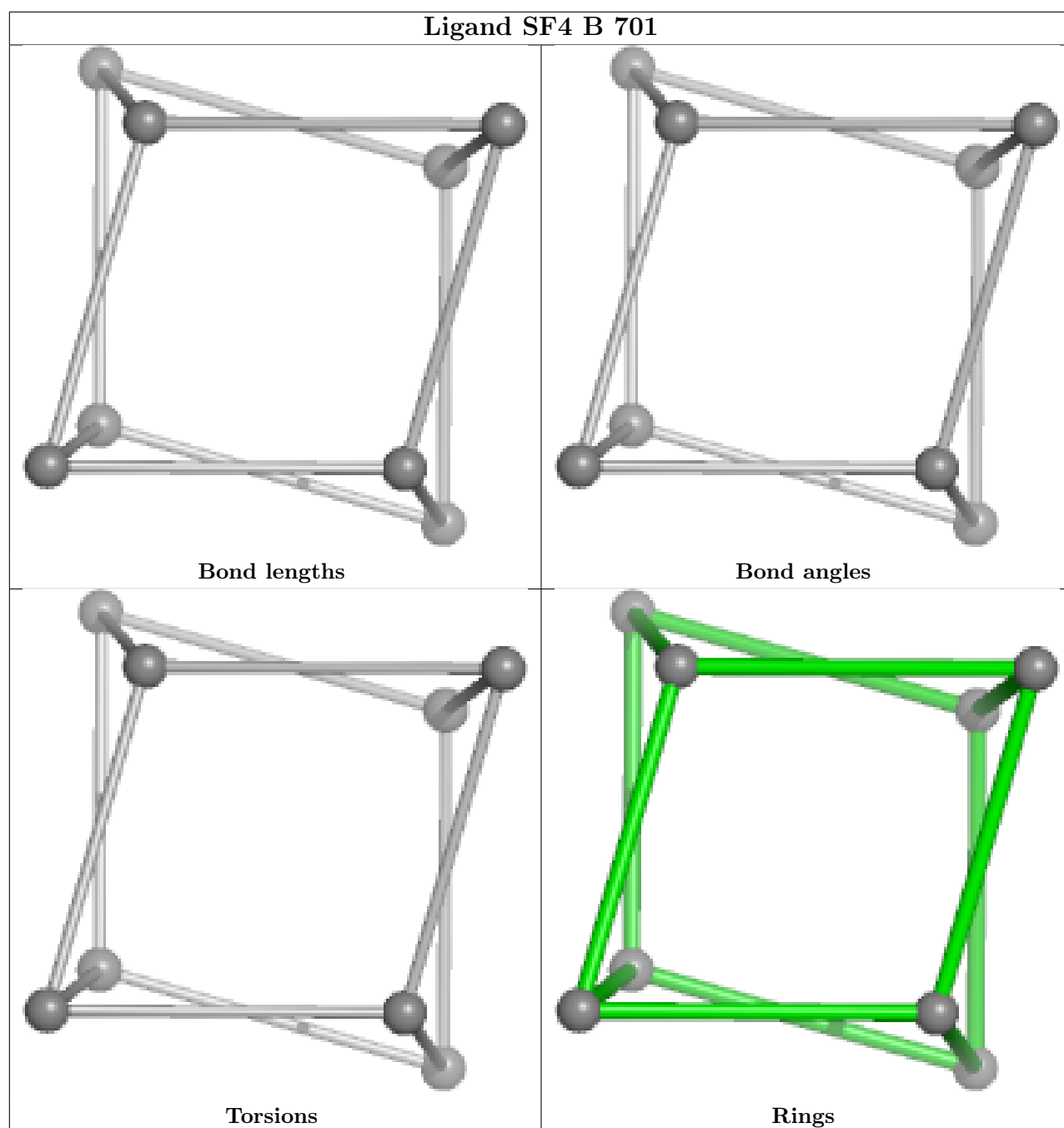
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	702	SF4	1	0
5	B	703	RQM	1	0
5	C	702	RQM	1	0
3	C	701	SF4	1	0

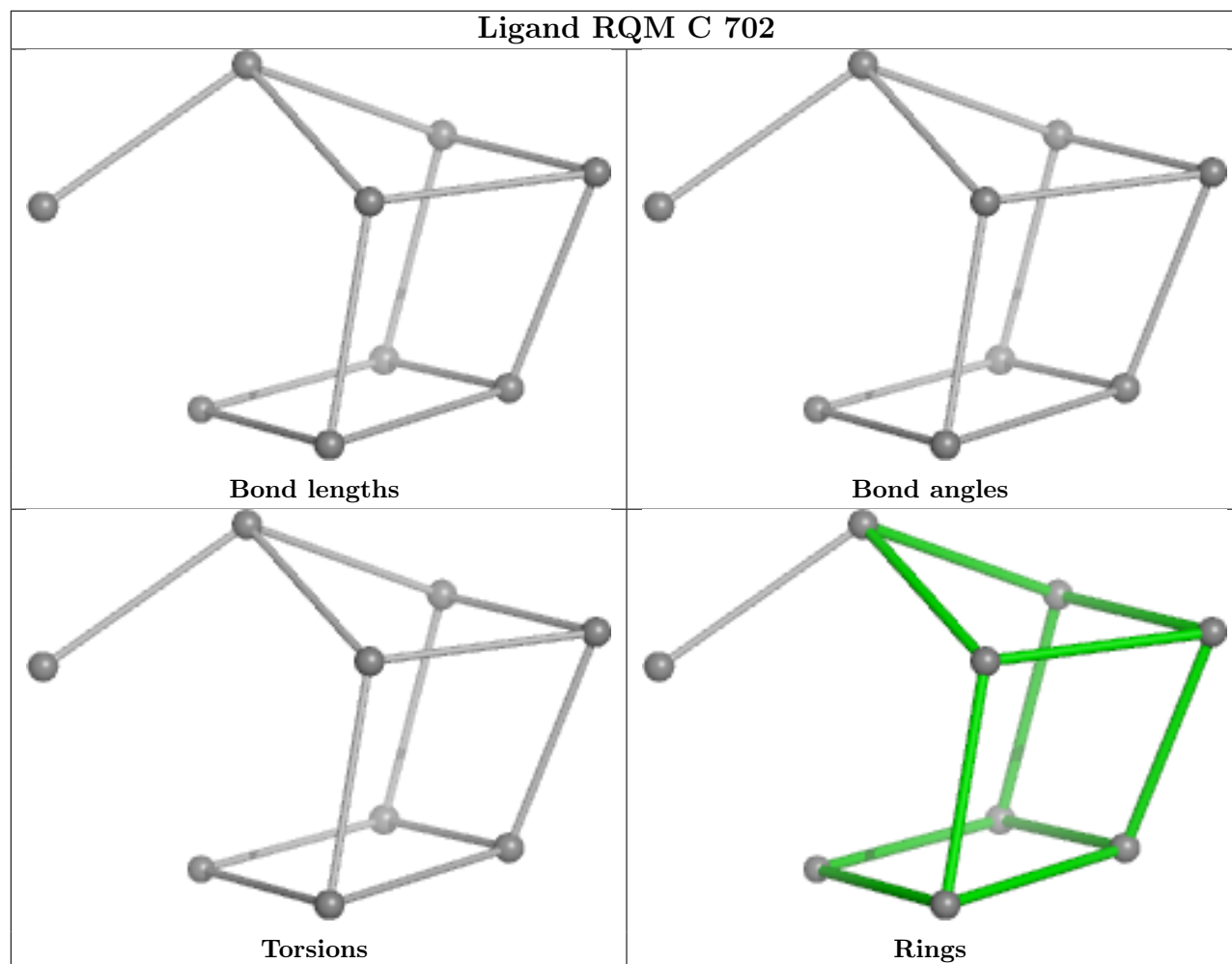
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

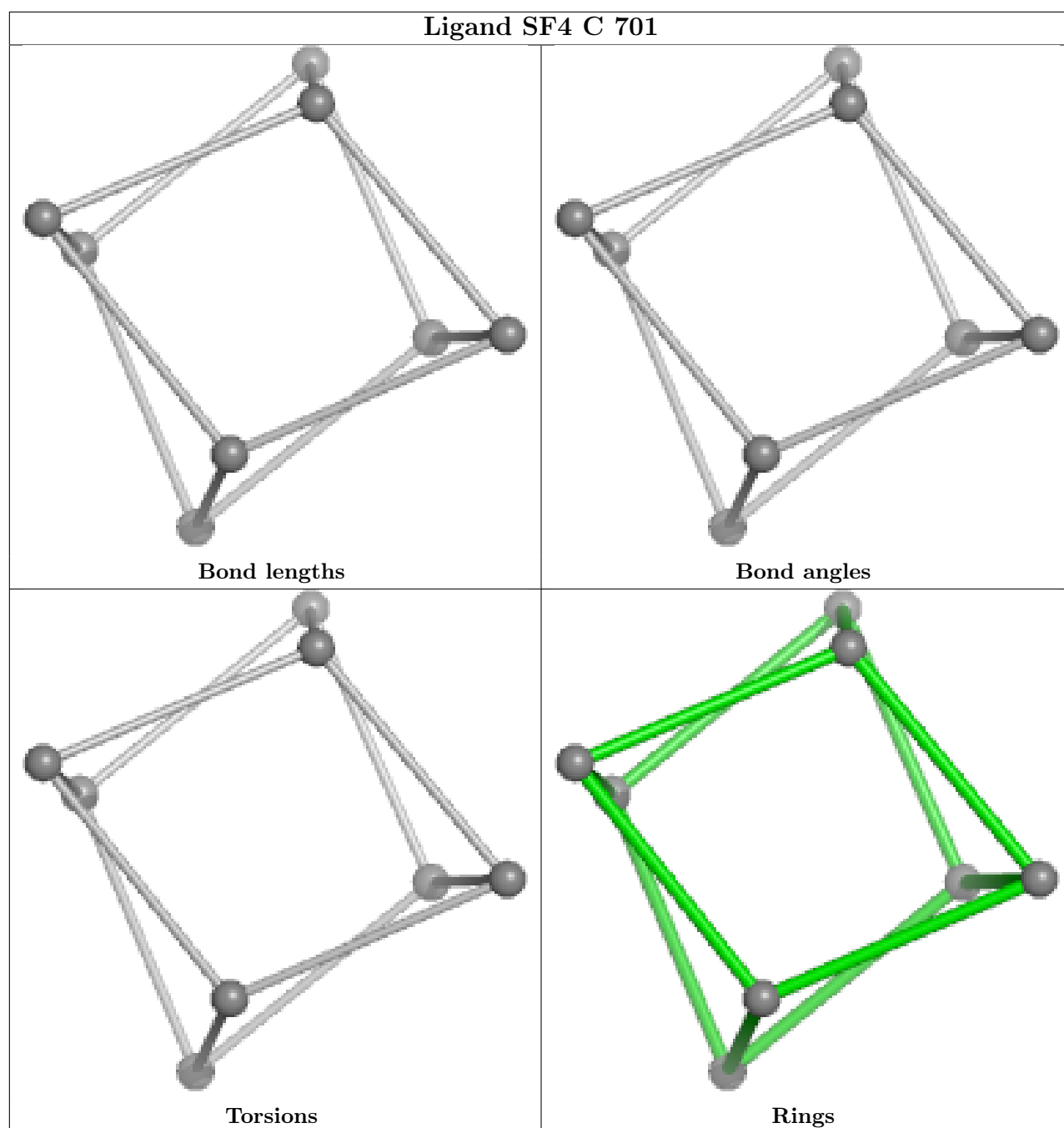












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

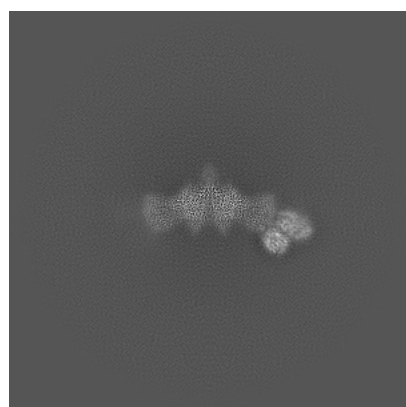
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50907. These allow visual inspection of the internal detail of the map and identification of artifacts.

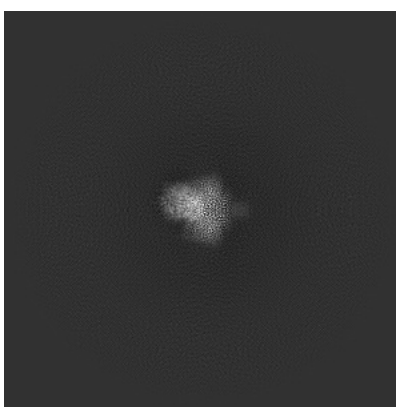
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

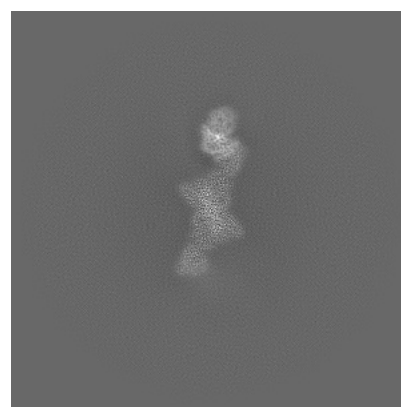
6.1.1 Primary map



X



Y



Z

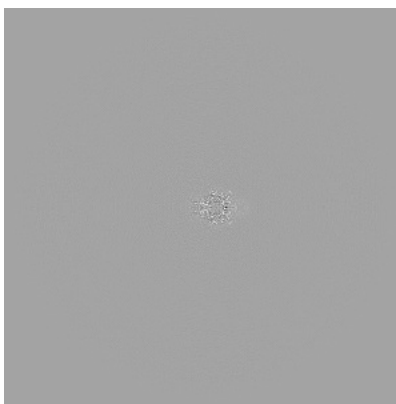
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

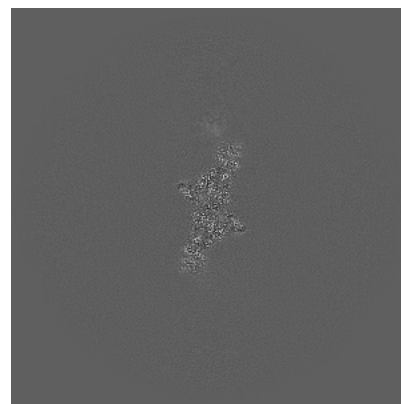
6.2.1 Primary map



X Index: 280



Y Index: 280

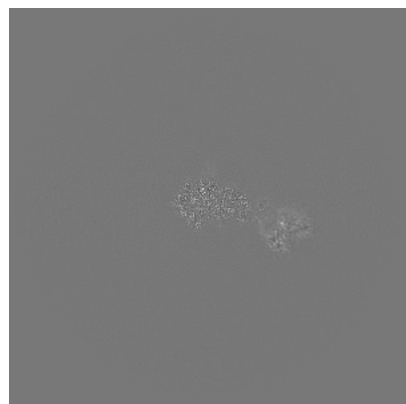


Z Index: 280

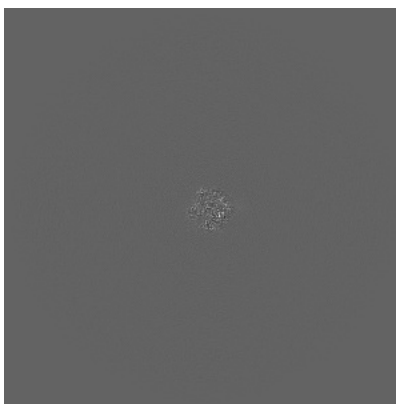
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

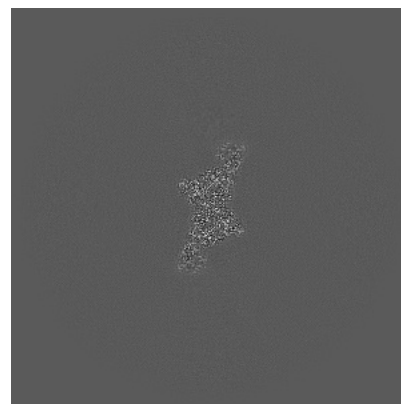
6.3.1 Primary map



X Index: 288



Y Index: 290



Z Index: 287

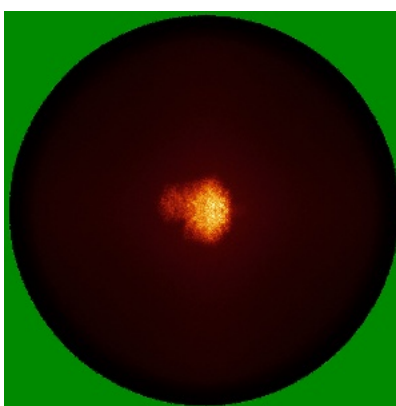
The images above show the largest variance slices of the map in three orthogonal directions.

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

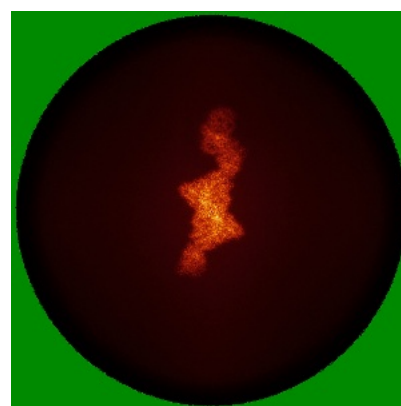
6.4.1 Primary map



X



Y

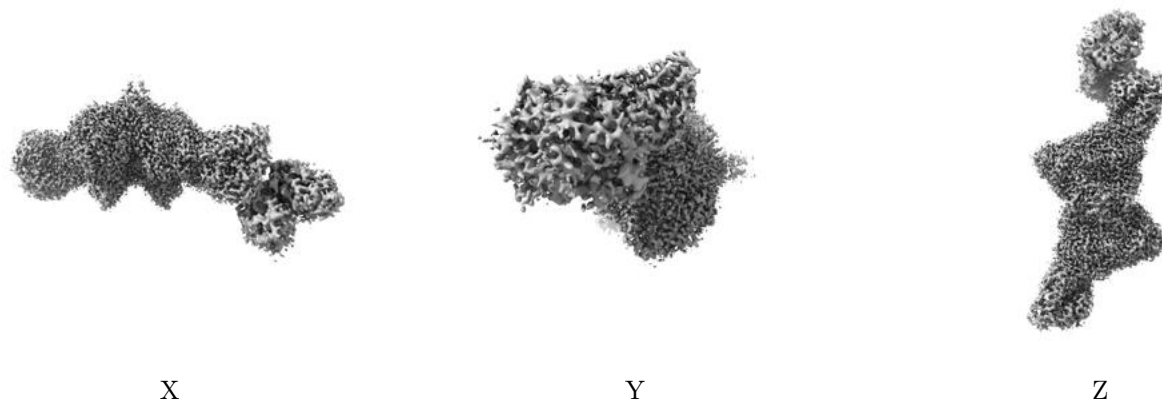


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 8.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

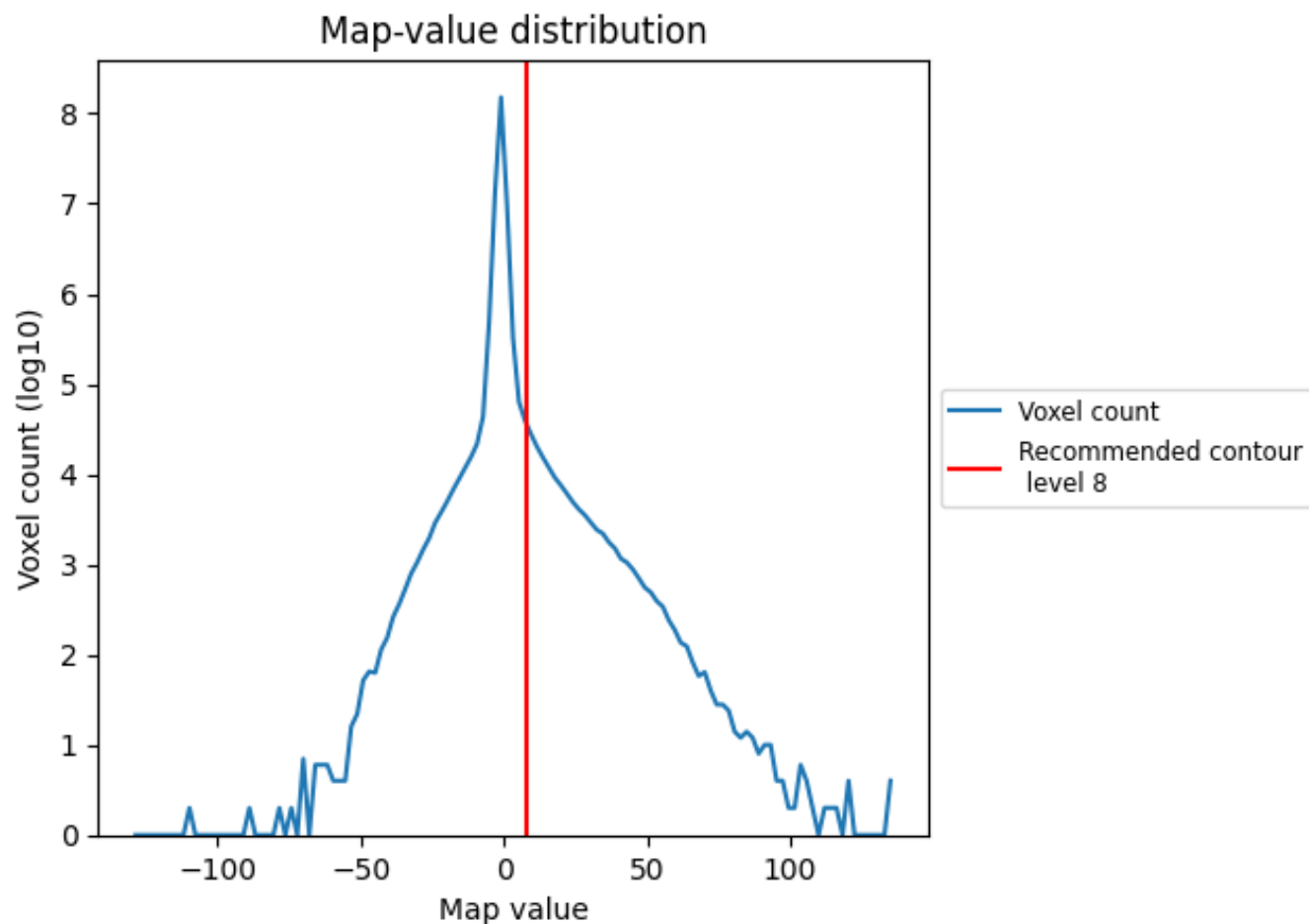
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

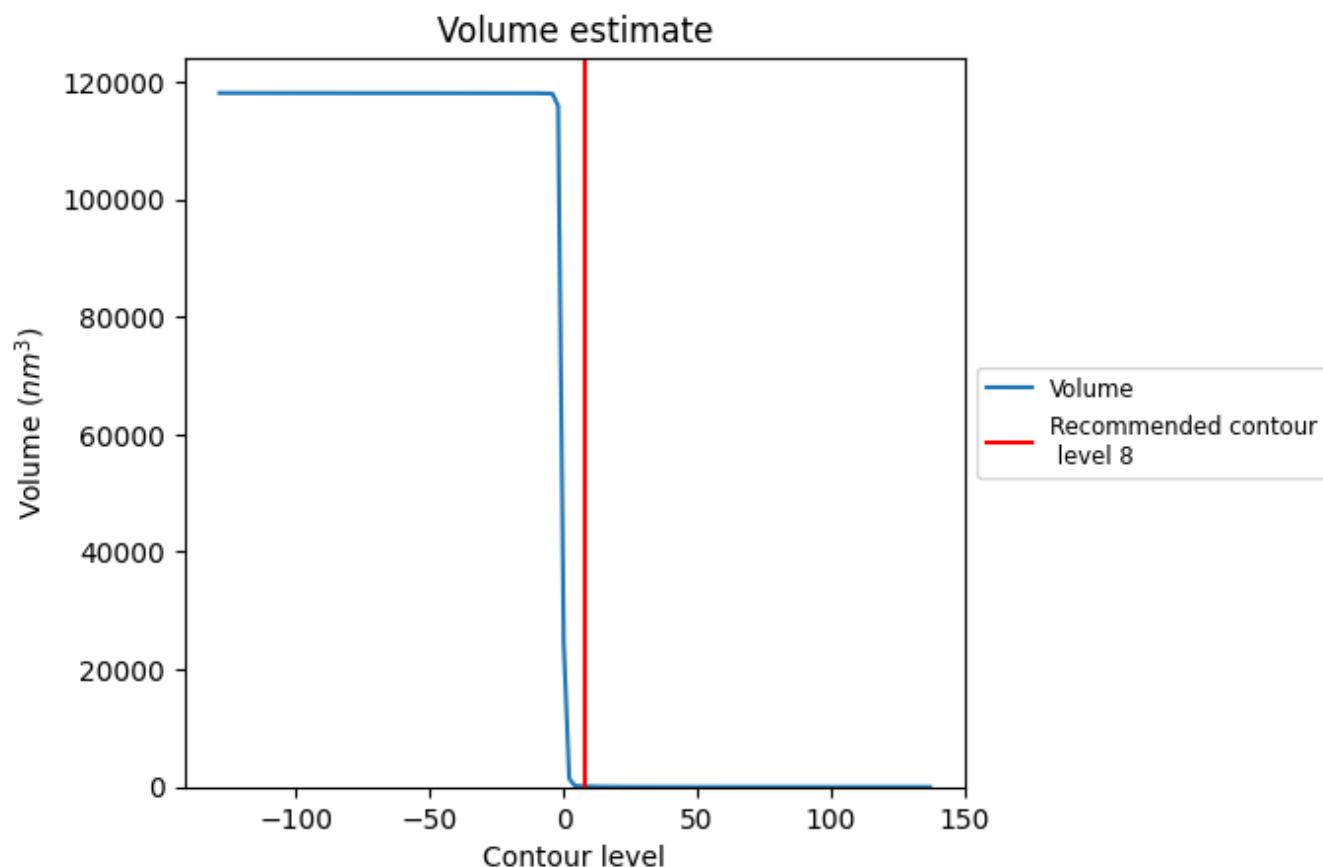
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

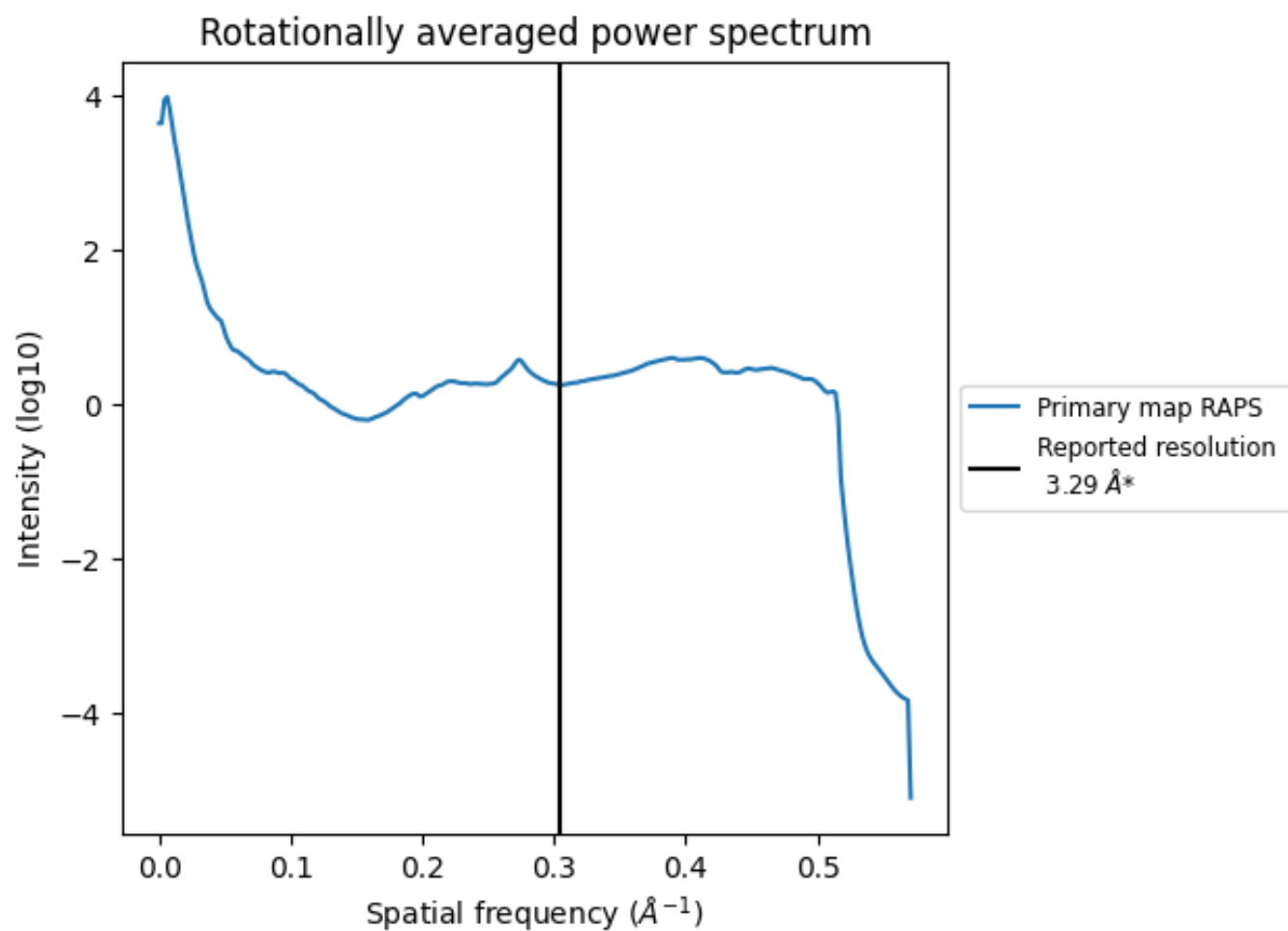
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 105 nm³; this corresponds to an approximate mass of 95 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 0.304 Å⁻¹

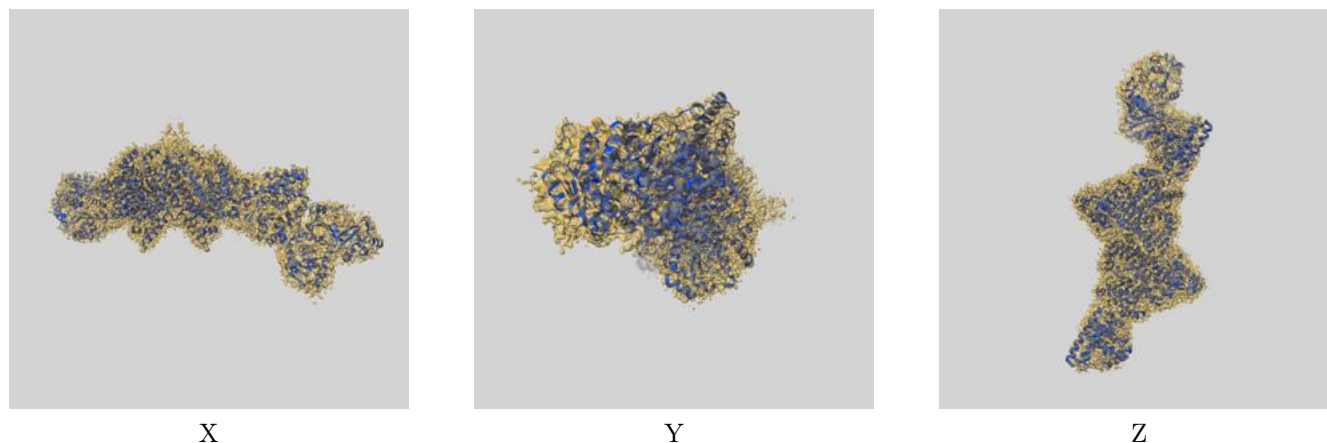
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

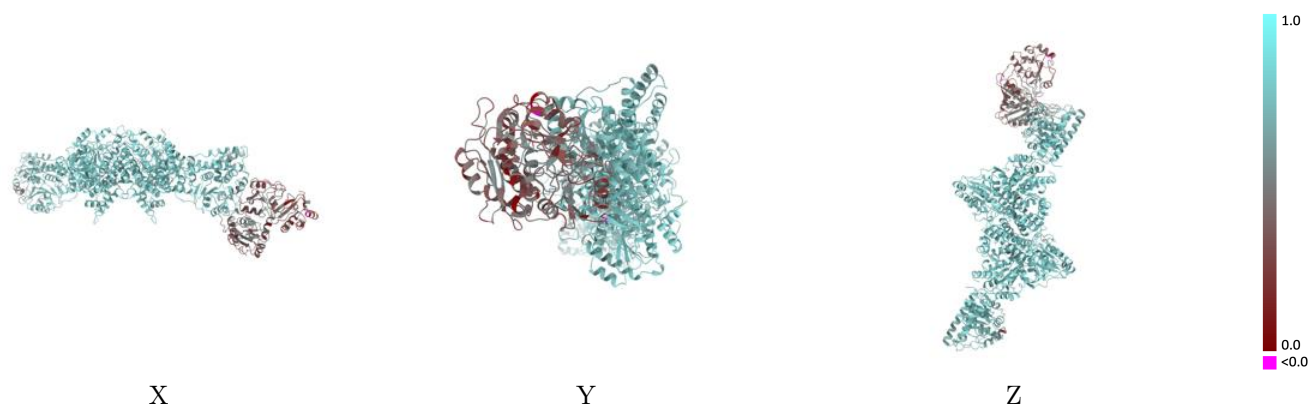
This section contains information regarding the fit between EMDB map EMD-50907 and PDB model 9G02. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



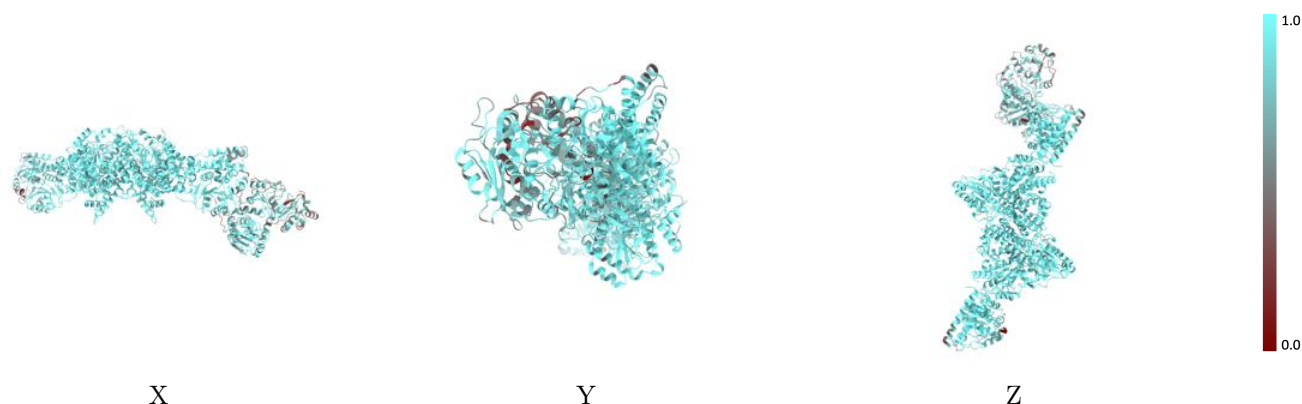
The images above show the 3D surface view of the map at the recommended contour level 8.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



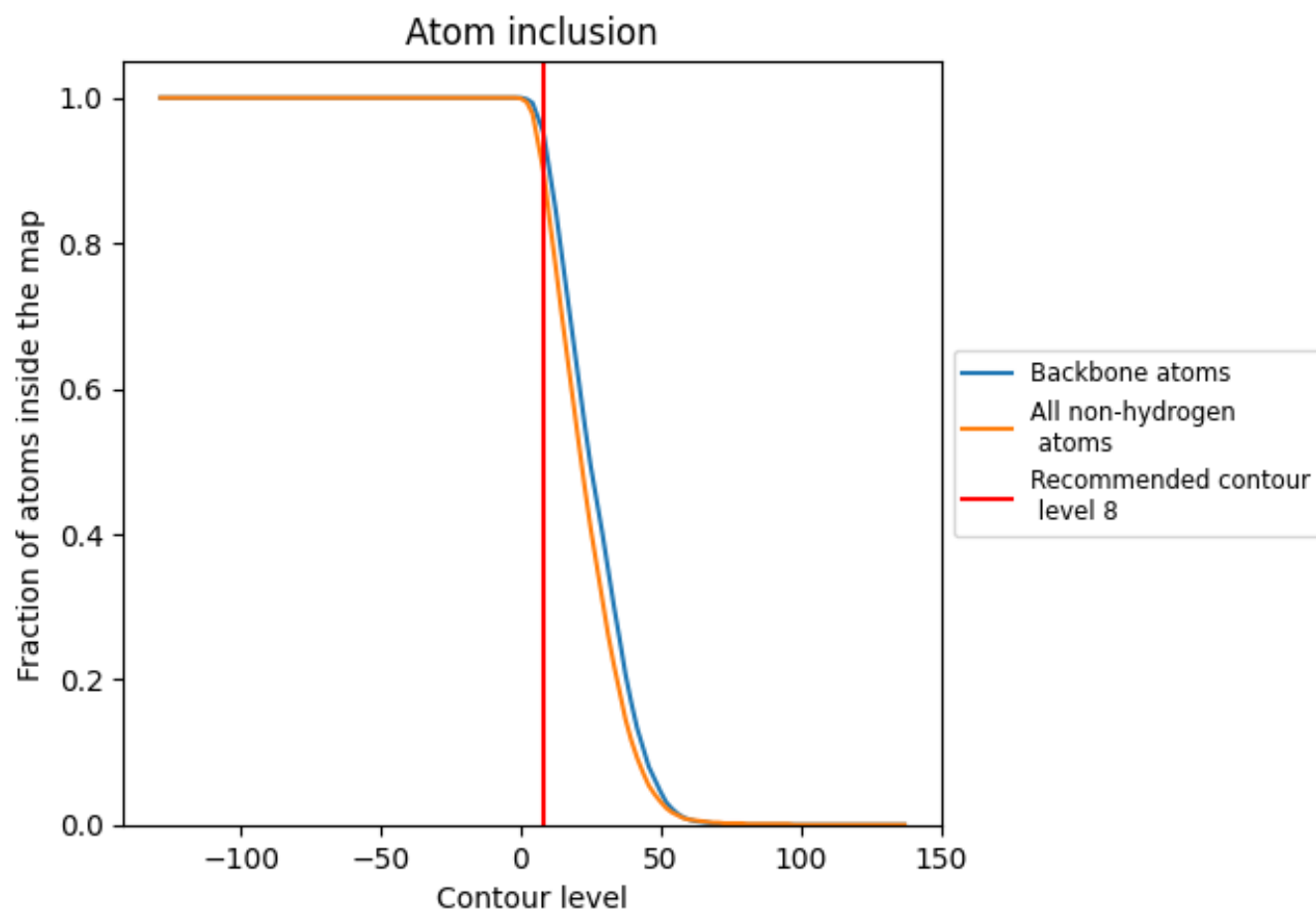
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 90% 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 (8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9030	<div></div> 0.6720
A	<div></div> 0.8840	<div></div> 0.6960
B	<div></div> 0.9680	<div></div> 0.7610
C	<div></div> 0.9680	<div></div> 0.7610
D	<div></div> 0.7970	<div></div> 0.5070

