



wwPDB EM Validation Summary Report ⓘ

Feb 10, 2025 – 01:03 pm GMT

PDB ID : 9G02
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.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) : 2.40

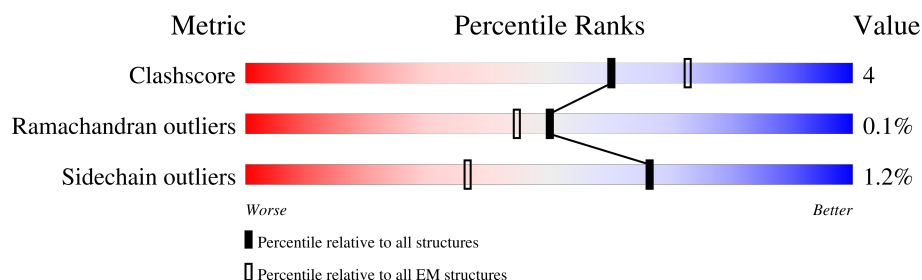
1 Overall quality at a glance

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.

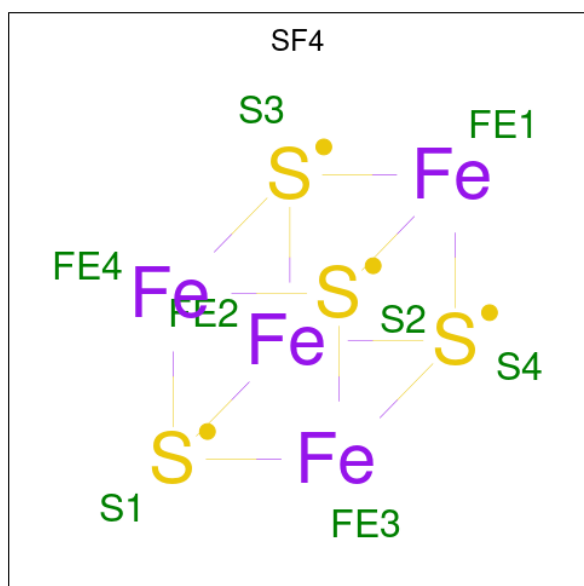
- Molecule 1 is a protein called CO-methylating acetyl-CoA synthase.

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 (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).

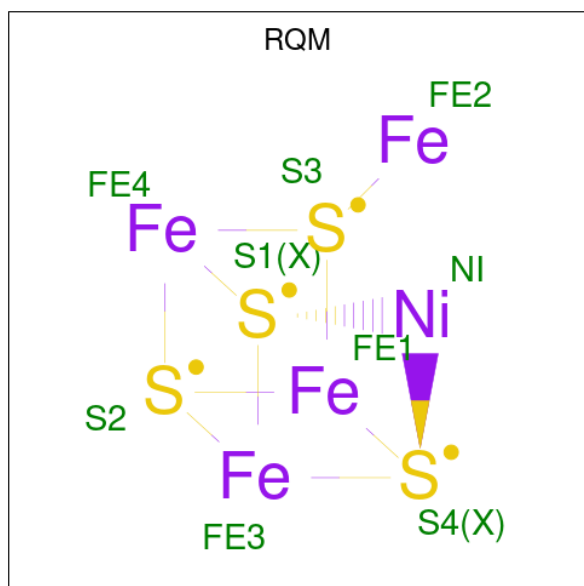


Mol	Chain	Residues	Atoms			AltConf
3	D	1	Total	Fe	S	0
			8	4	4	
3	B	1	Total	Fe	S	0
			8	4	4	
3	B	1	Total	Fe	S	0
			8	4	4	
3	C	1	Total	Fe	S	0
			8	4	4	

- Molecule 4 is NICKEL (II) ION (three-letter code: 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 (three-letter code: RQM) (formula: Fe₄NiS₄) (labeled as "Ligand of Interest" by depositor).

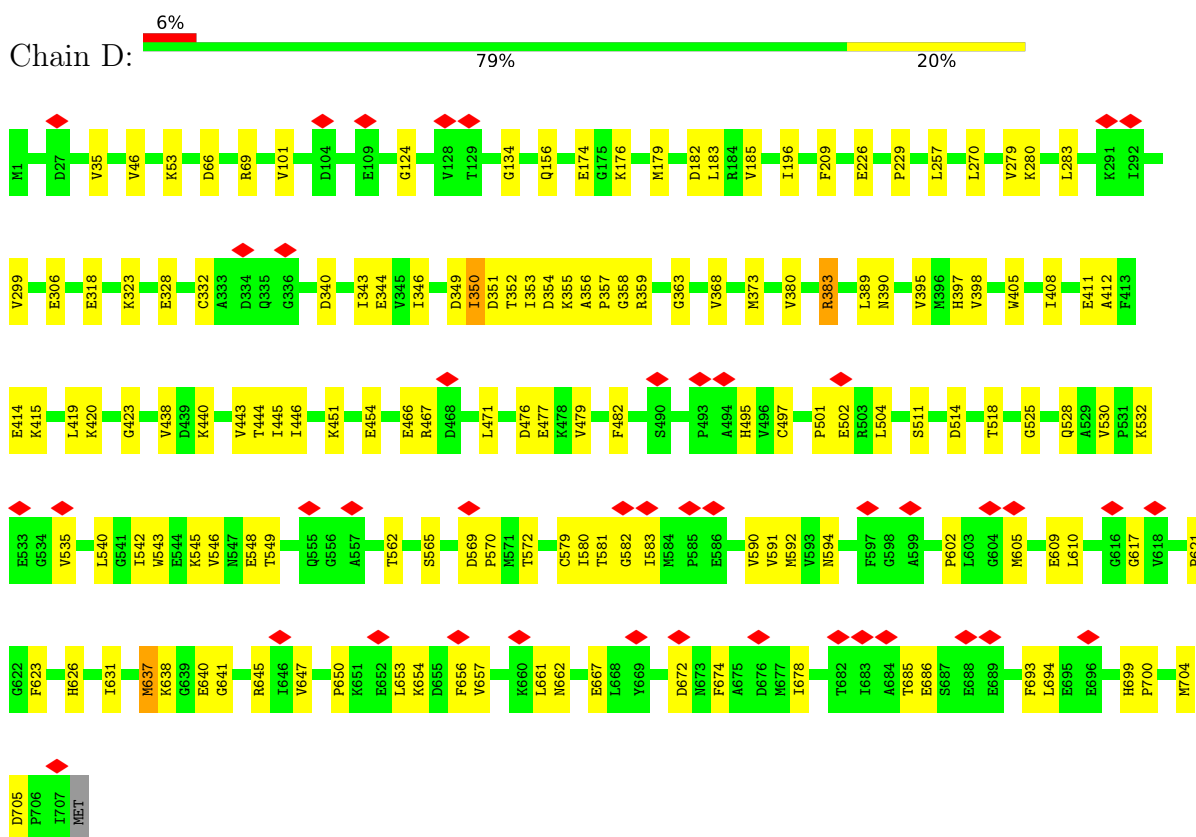


Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	Fe	Ni	S	0
			9	4	1	4	
5	C	1	Total	Fe	Ni	S	0
			9	4	1	4	

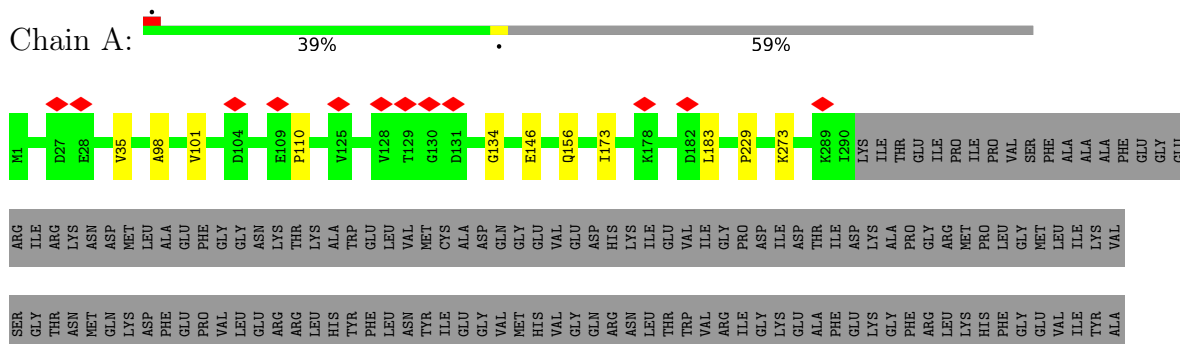
3 Residue-property plots

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: CO-methylating acetyl-CoA synthase



- Molecule 1: CO-methylating acetyl-CoA synthase



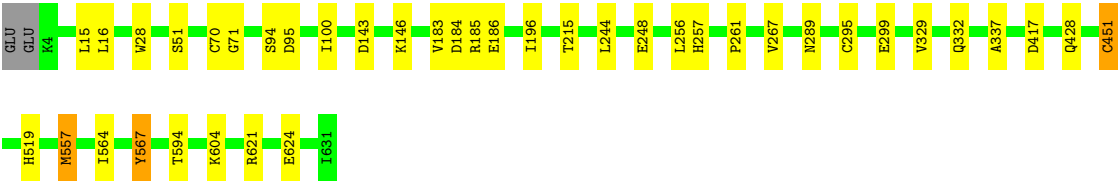
LYS	GLN	THR	GLU	TYR
MET	SER	VAL	LEU	ASN
LEU	PHE	SER	ALA	ILE
ASP	ALA	LYS	SER	ASP
GLU	PRO	ILE	ASN	PHE
PHE	ALA	SER	THR	ALA
GLY	HIS	GLN	GLY	ASP
SER	VAL	GLY	GLY	MET
VAL	CYS	ILE	VAL	ILE
ASP	VAL	THR	GLN	CYS
LYS	THR	SER	THR	ASP
CYS	PRO	VAL	GLU	GLY
GLU	GLU	THR	GLY	THR
VAL	ARG	LEU	PHE	ILE
THR	LEU	SER	ALA	THR
ILE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

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

Chain B:

93%

6%

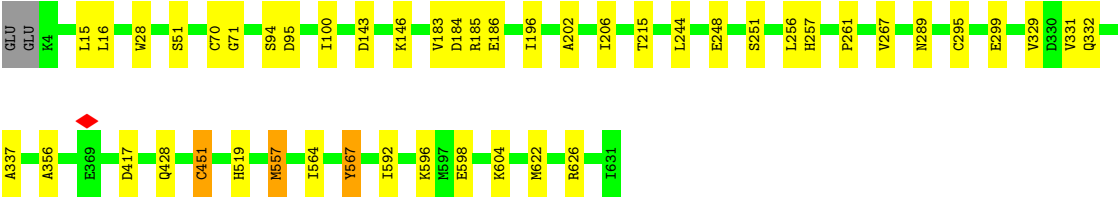


● Molecule 2: Carbon monoxide dehydrogenase/acetyl-CoA synthase beta subunit

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	0.43	0/2185	0.51	0/2970
1	D	0.29	0/5480	0.49	0/7418
2	B	0.48	0/4788	0.56	0/6476
2	C	0.48	0/4788	0.55	0/6476
All	All	0.42	0/17241	0.53	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	6	0
1	D	5384	0	5480	95	0
2	B	4714	0	4797	24	0
2	C	4714	0	4797	28	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	148	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 4.

The worst 5 of 148 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%)	231 (100%)	1 (0%)	89	93
1	D	582/583 (100%)	572 (98%)	10 (2%)	56	74
2	B	517/519 (100%)	511 (99%)	6 (1%)	67	80
2	C	517/519 (100%)	511 (99%)	6 (1%)	67	80
All	All	1848/2204 (84%)	1825 (99%)	23 (1%)	66	80

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	519	HIS
2	C	95	ASP
2	B	567	TYR
2	C	185	ARG
1	D	656	PHE

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

Mol	Chain	Res	Type
1	D	402	ASN

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 [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	$\# Z > 2$
5	RQM	C	702	2	0,12,12	-	-	-		
3	SF4	C	701	2	0,12,12	-	-	-		
3	SF4	D	801	1,4	0,12,12	-	-	-		
3	SF4	B	701	2	0,12,12	-	-	-		
5	RQM	B	703	2	0,12,12	-	-	-		
3	SF4	B	702	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
5	RQM	C	702	2	-	-	0/4/4/4
3	SF4	C	701	2	-	-	0/6/5/5
3	SF4	D	801	1,4	-	-	0/6/5/5
3	SF4	B	701	2	-	-	0/6/5/5
5	RQM	B	703	2	-	-	0/4/4/4
3	SF4	B	702	2	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

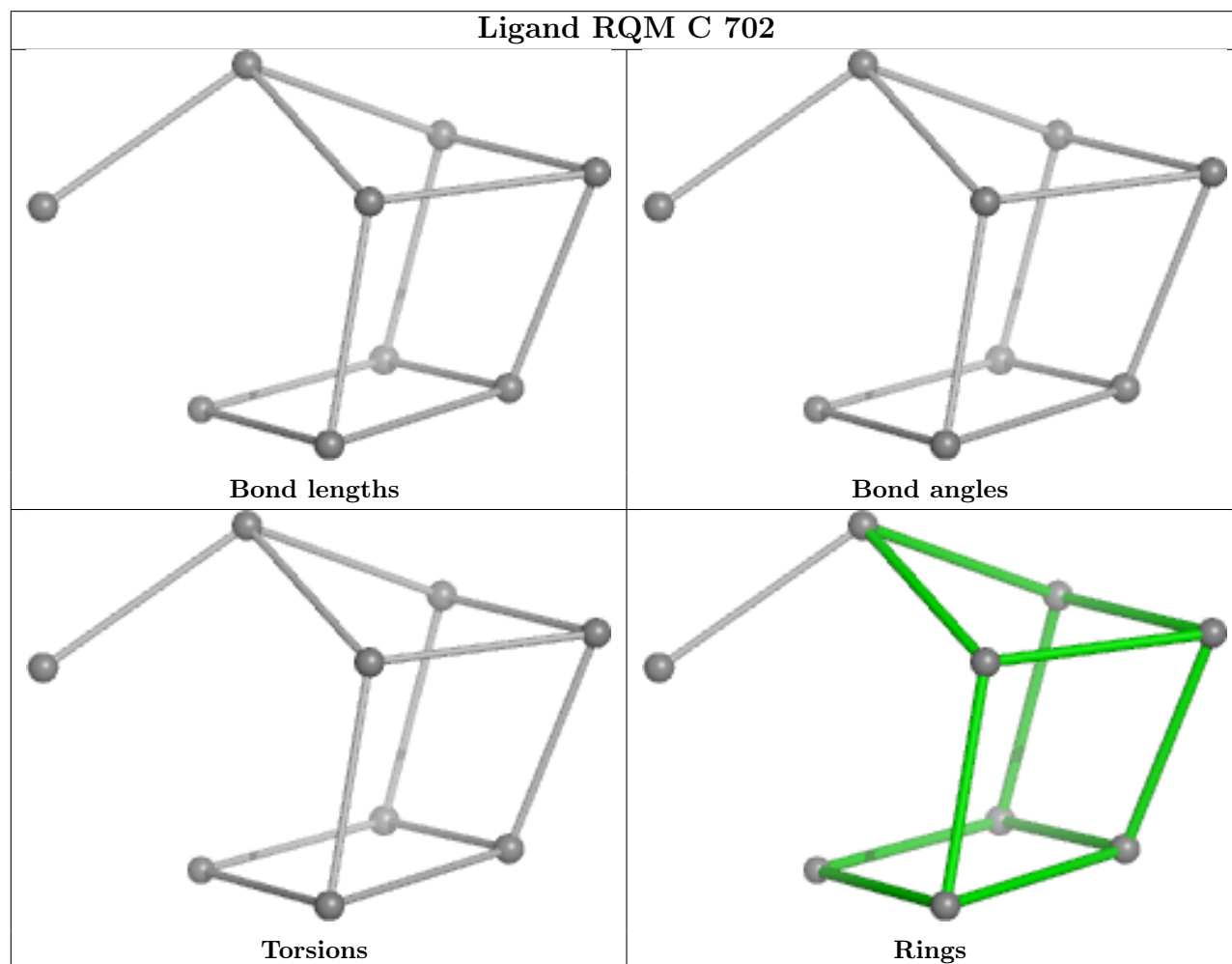
There are no torsion outliers.

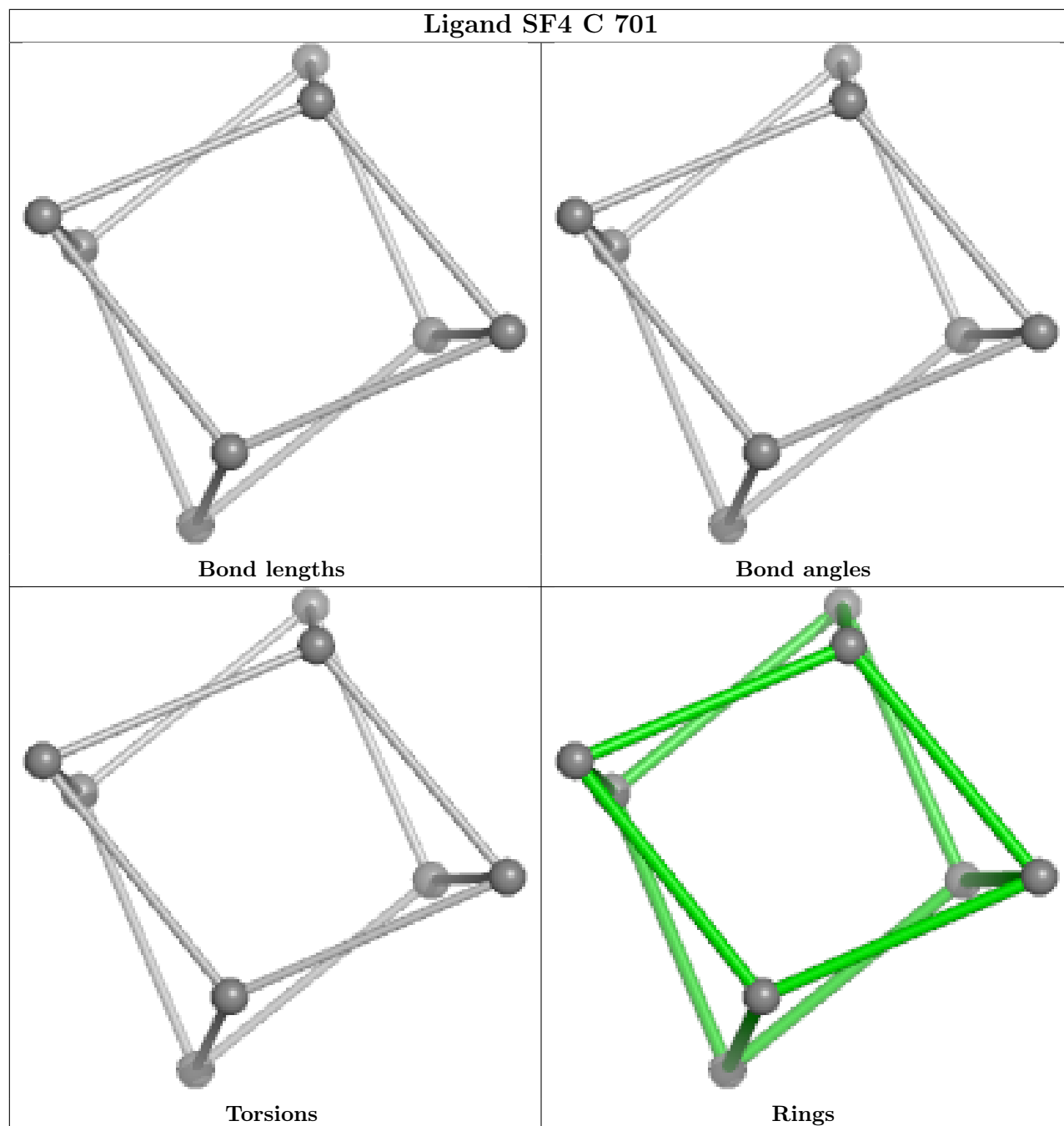
There are no ring outliers.

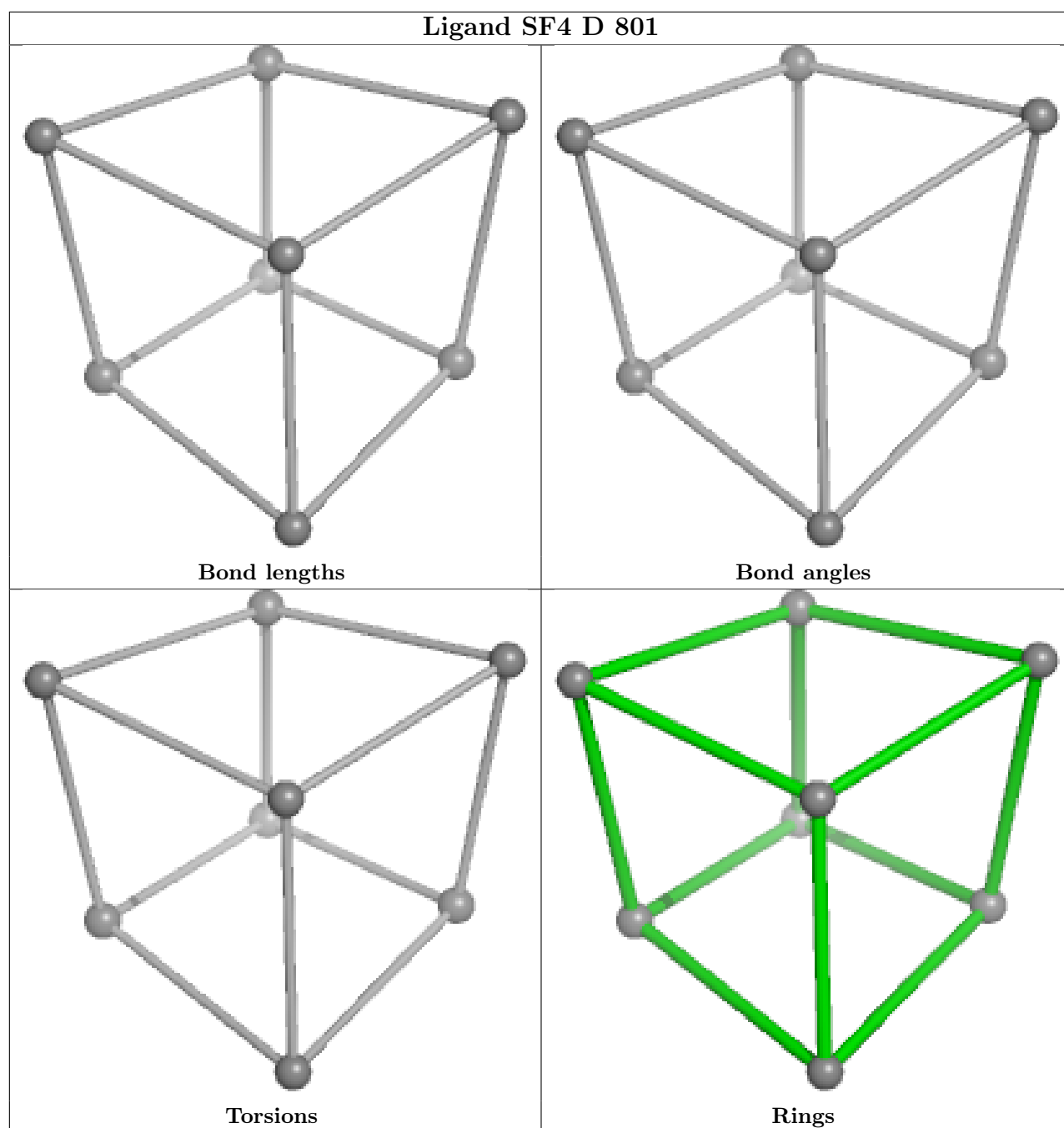
4 monomers are involved in 4 short contacts:

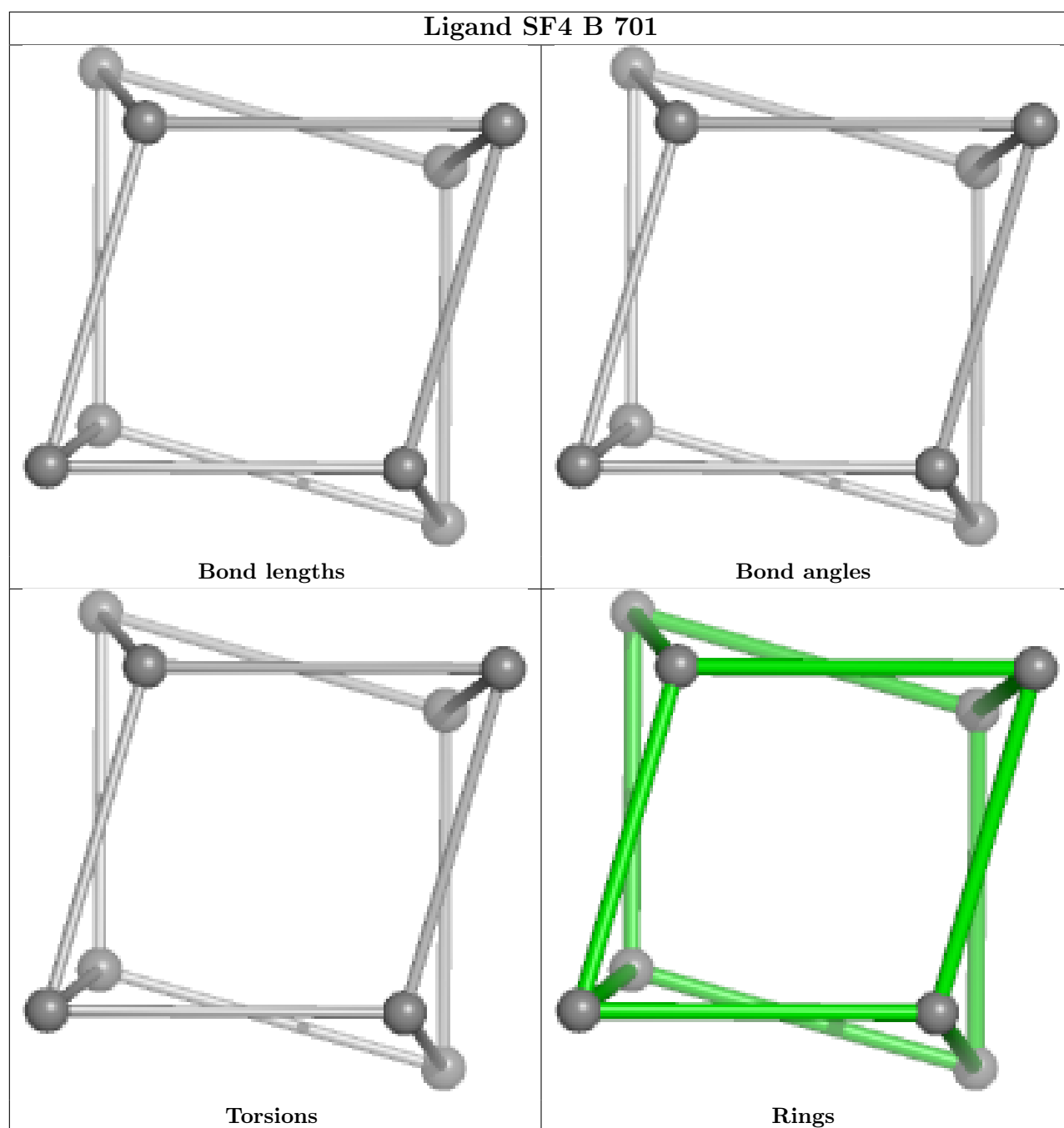
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	702	RQM	1	0
3	C	701	SF4	1	0
5	B	703	RQM	1	0
3	B	702	SF4	1	0

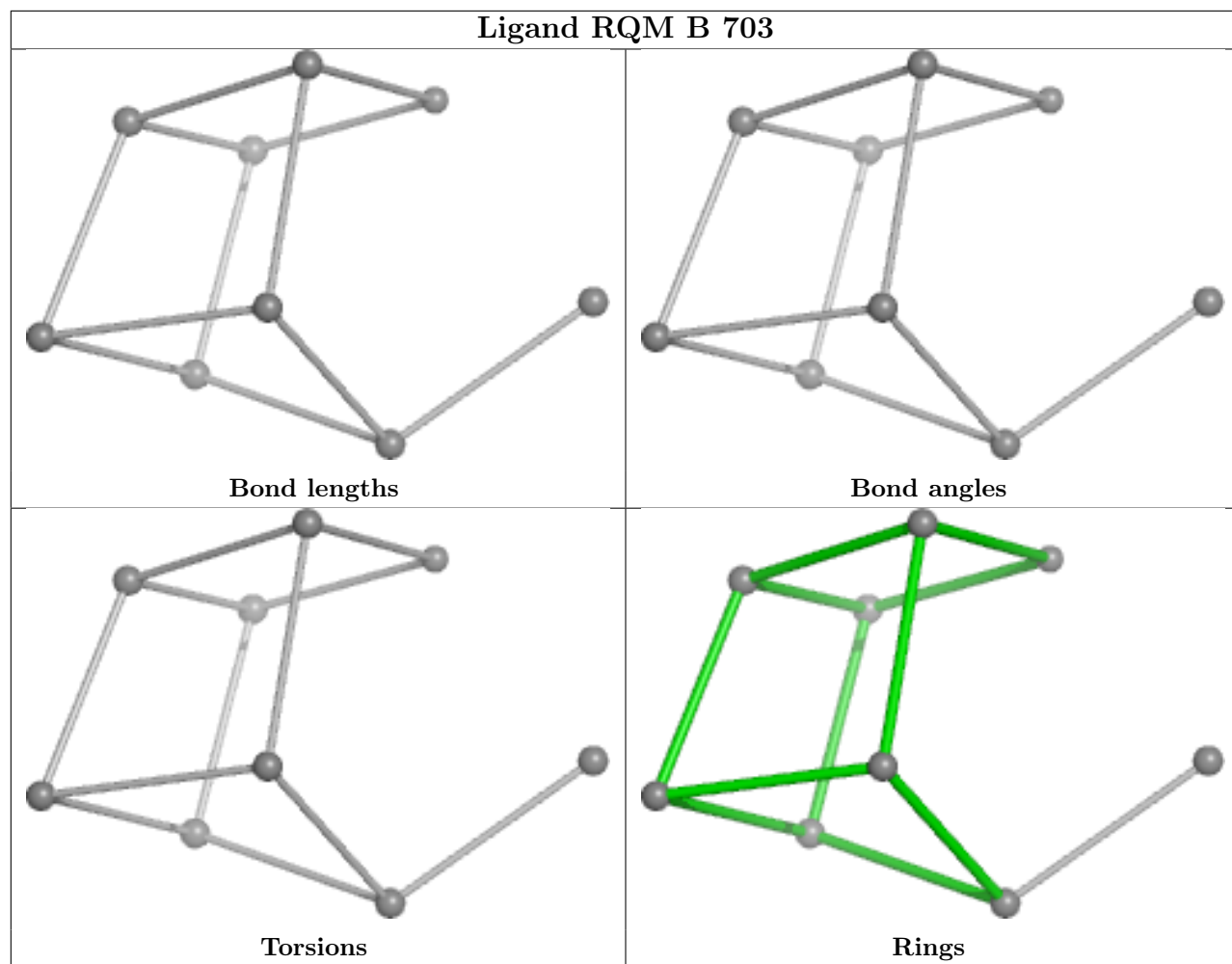
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

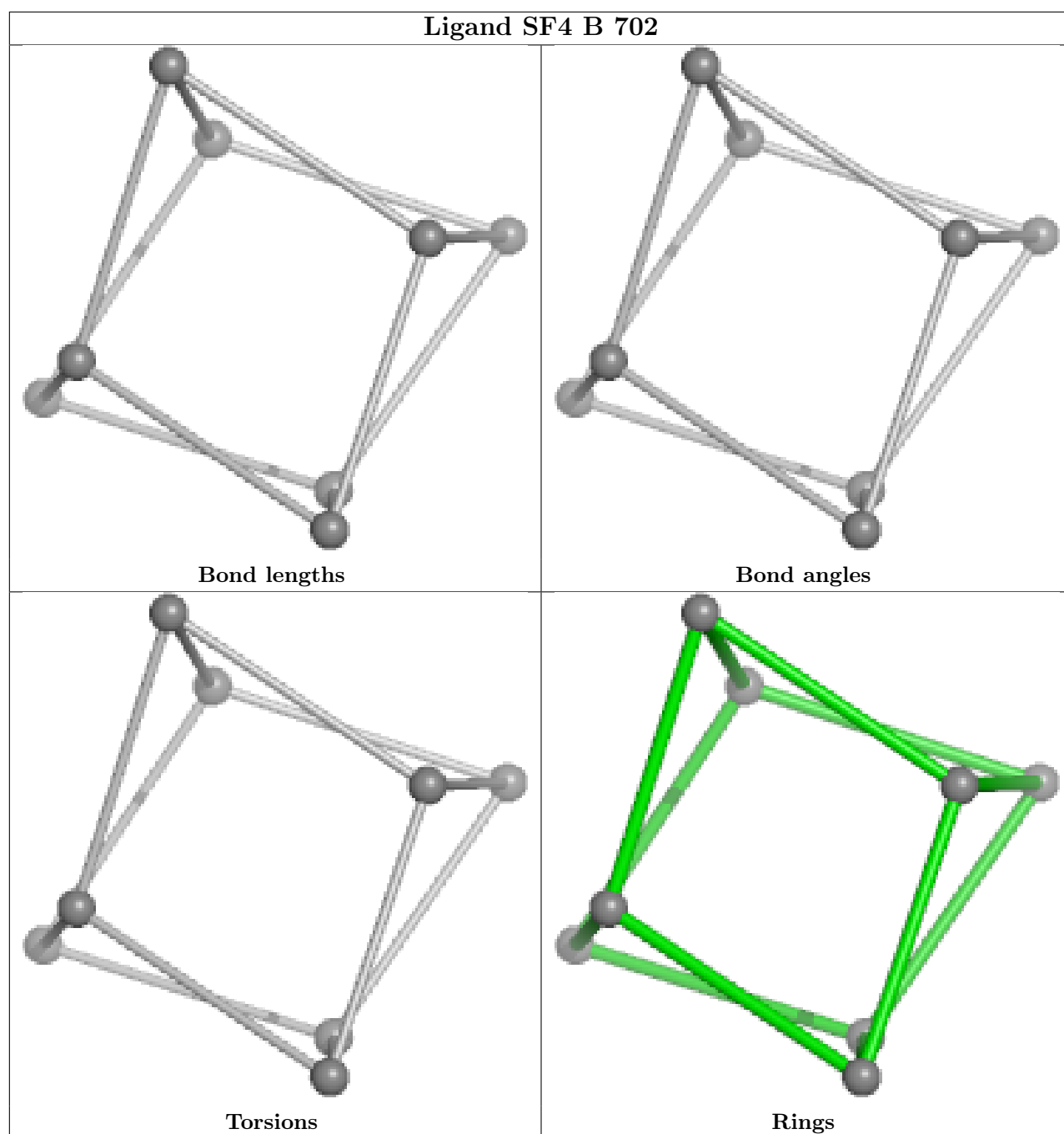












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

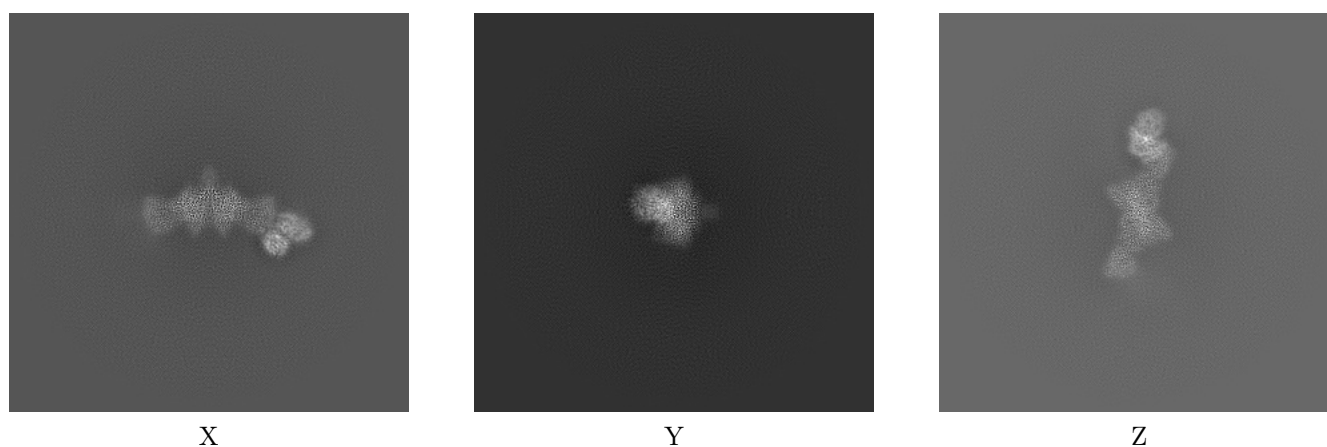
6 Map visualisation [i](#)

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](#)

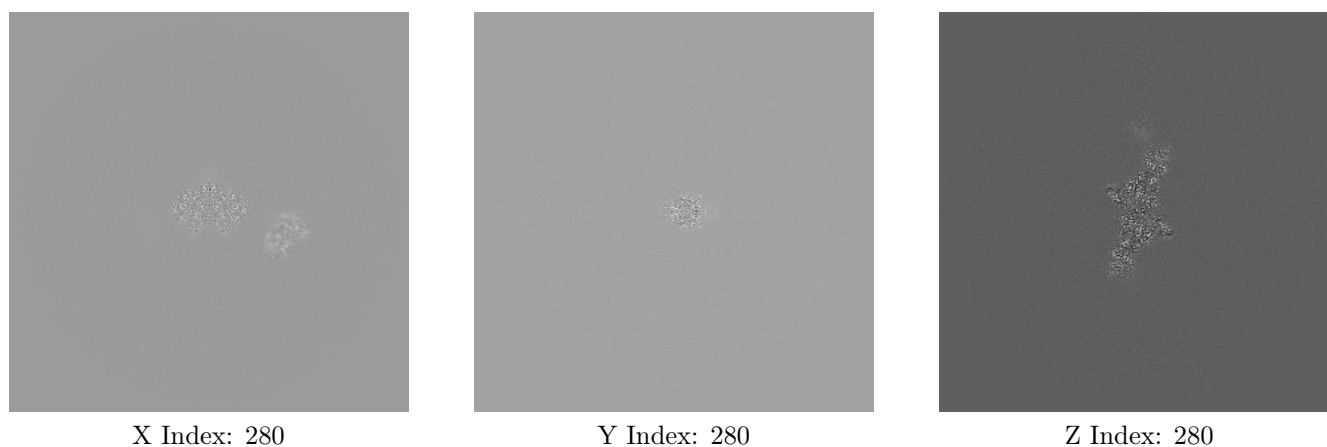
6.1.1 Primary map



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

6.2 Central slices [i](#)

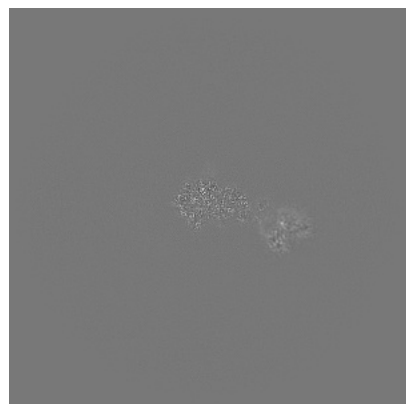
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

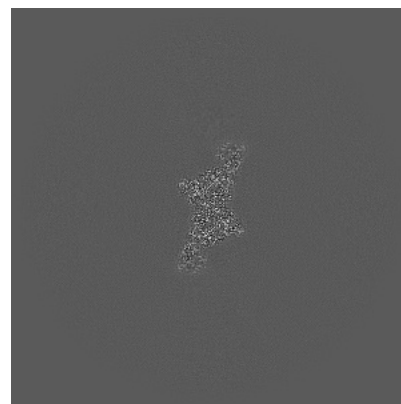
6.3.1 Primary map



X Index: 288



Y Index: 290



Z Index: 287

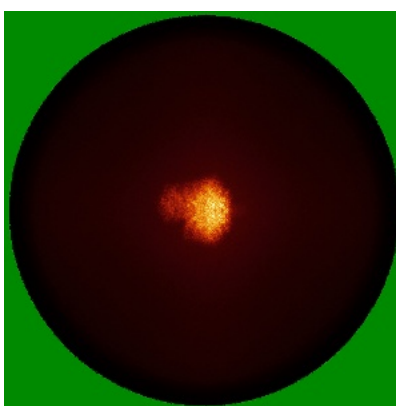
The images above show the largest variance slices of the map in three orthogonal directions.

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

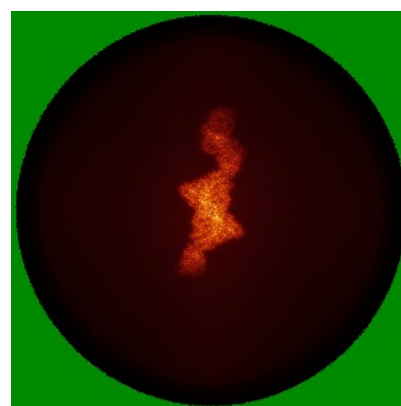
6.4.1 Primary map



X



Y

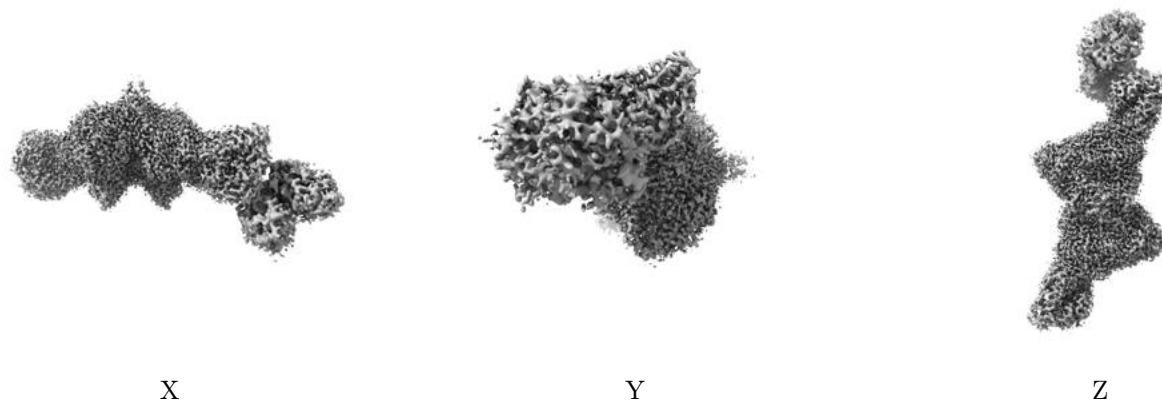


Z

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.

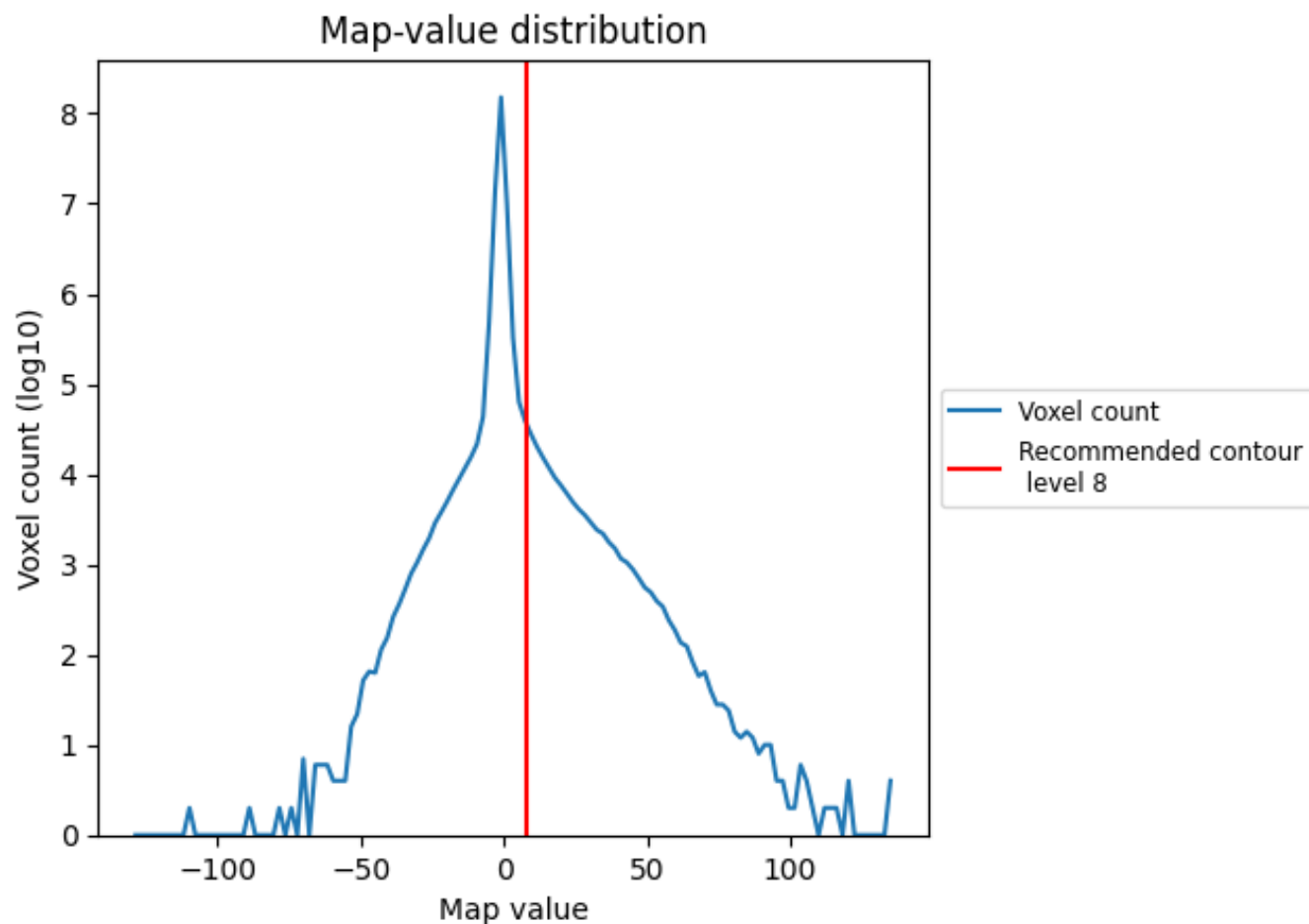
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

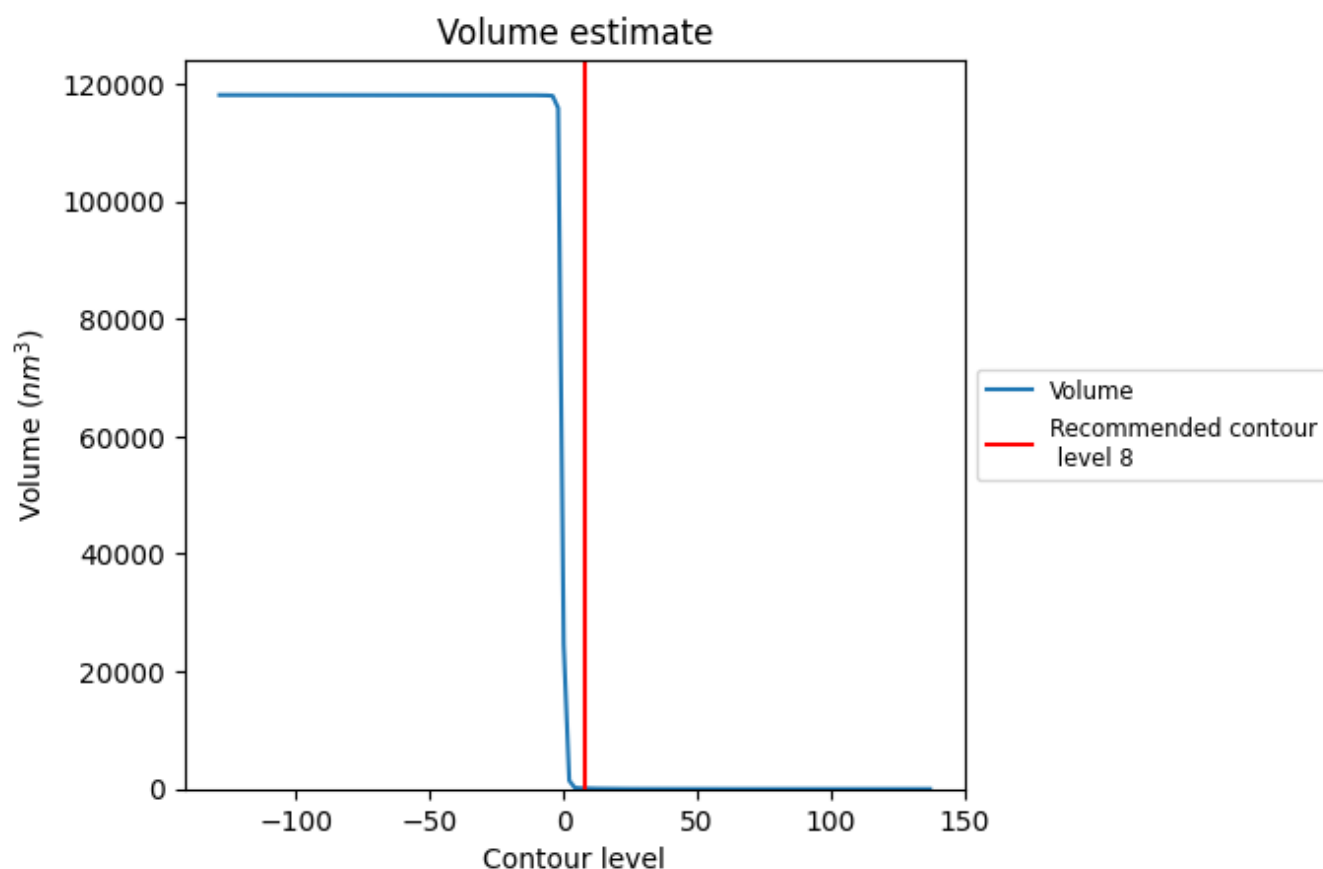
This section contains the results of statistical analysis of the map.

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.

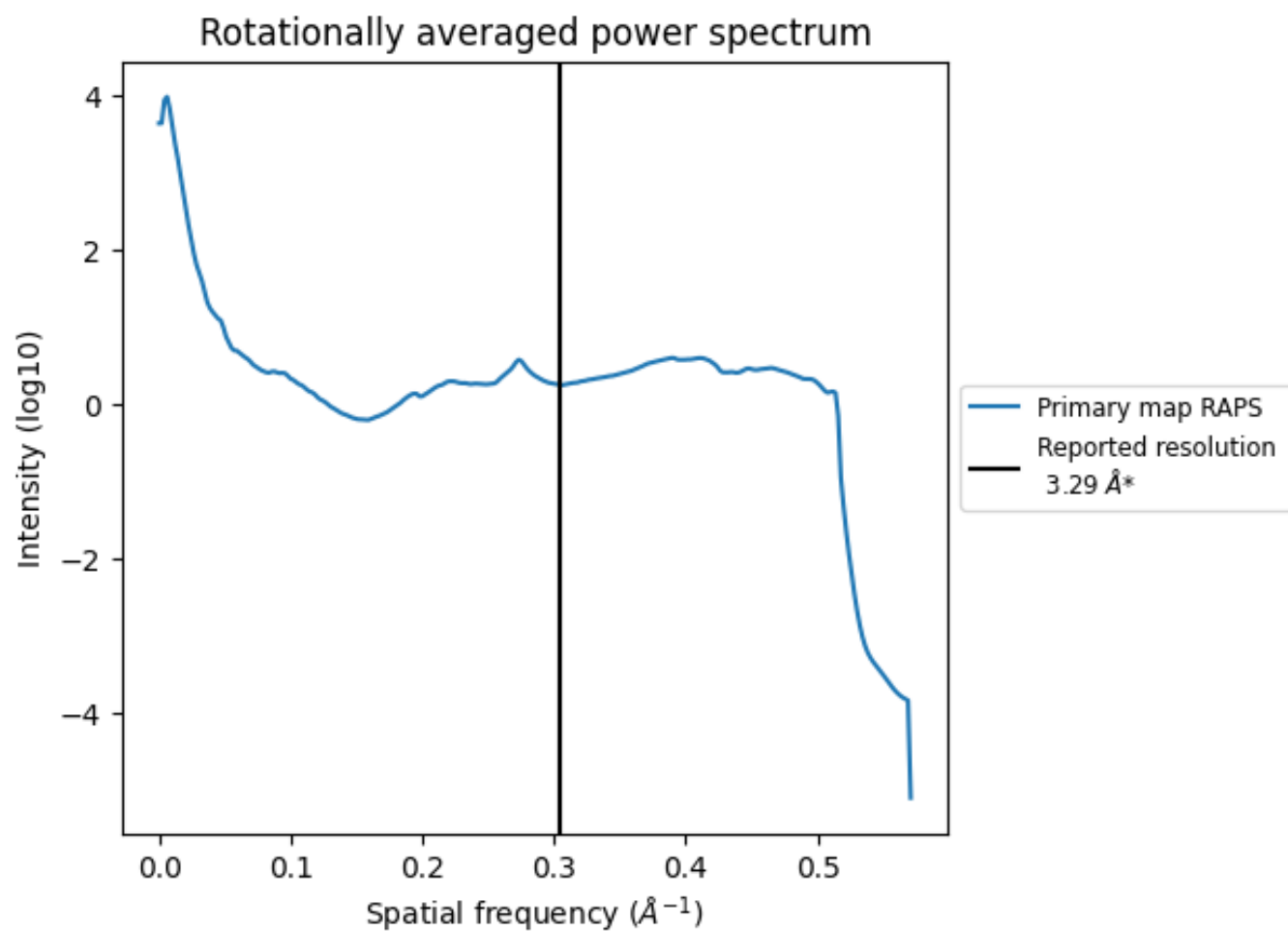
7.2 Volume estimate [i](#)



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

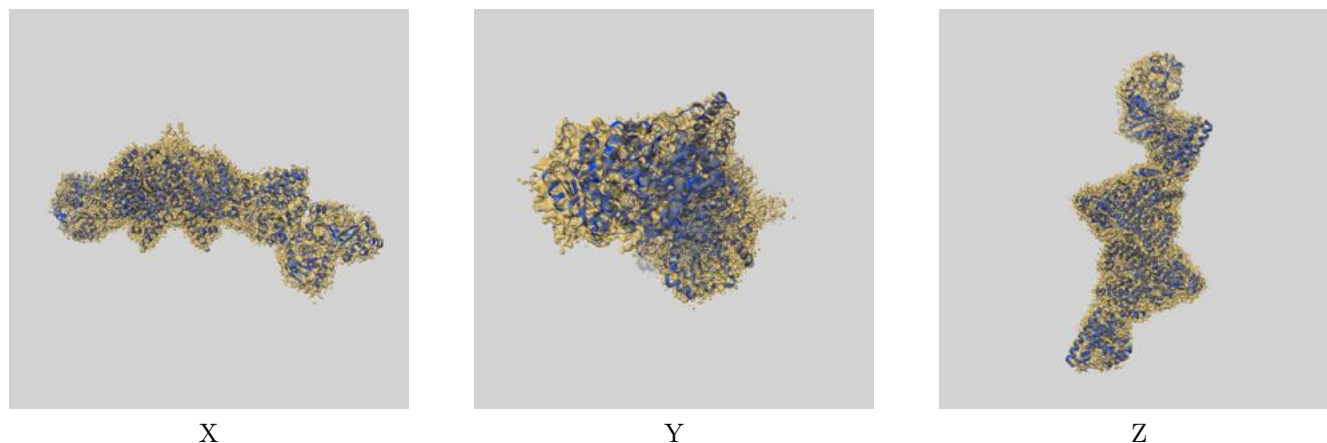
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

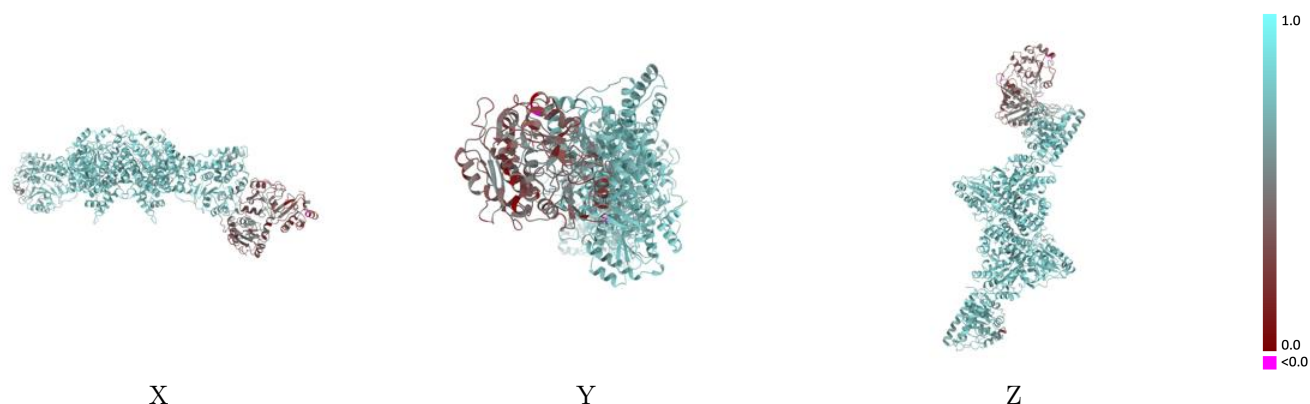
This section contains information regarding the fit between EMDB map EMD-50907 and PDB model 9G02. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



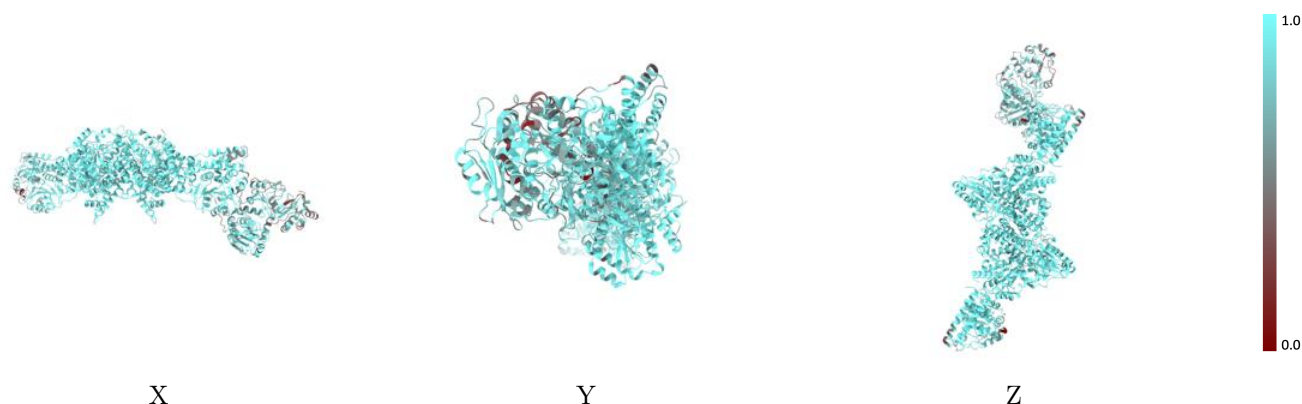
The images above show the 3D surface view of the map at the recommended contour level 8.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



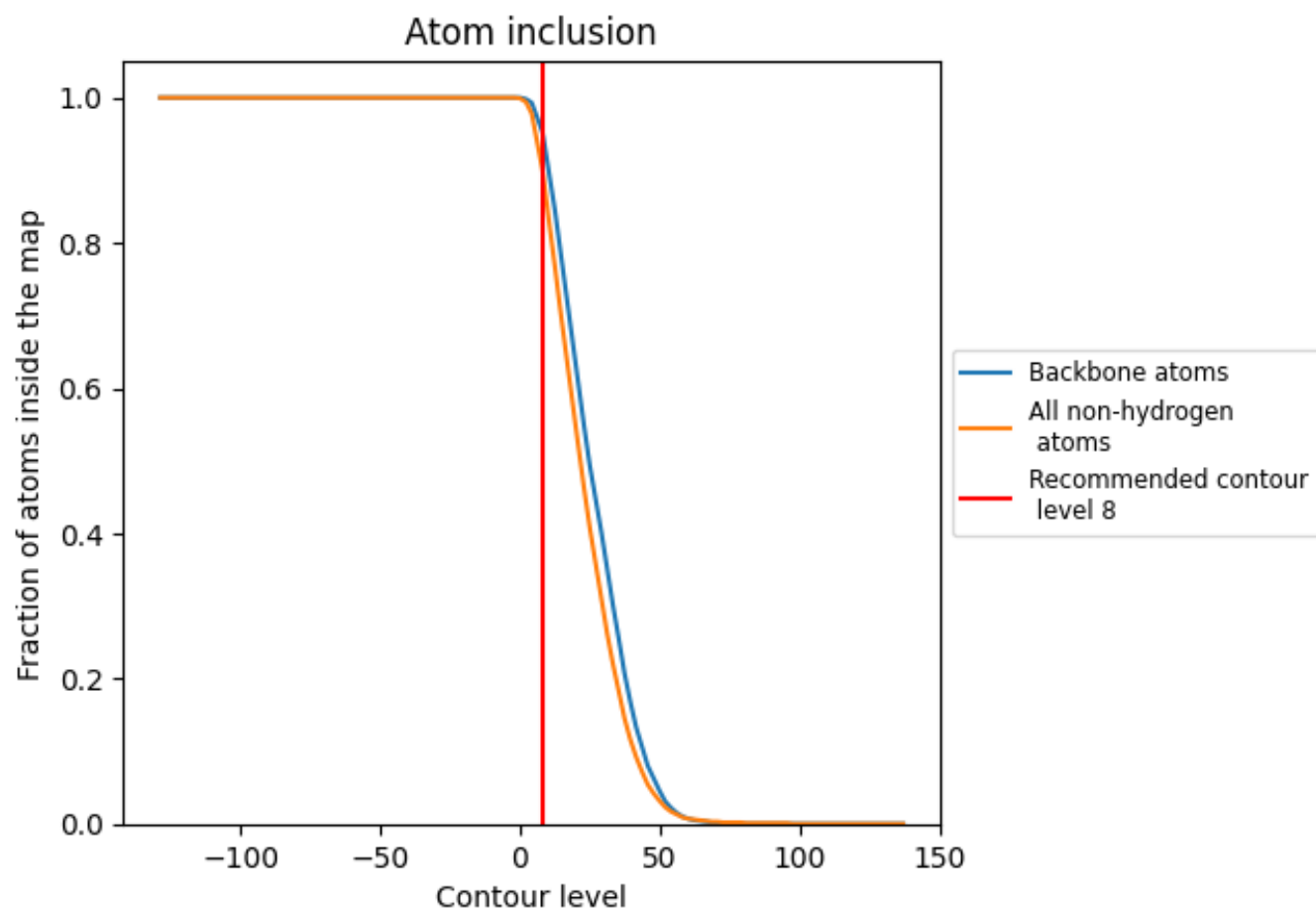
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

