



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:45 AM UTC

PDB ID : 6S6V / pdb_00006s6v
EMDB ID : EMD-10107
Title : Resting state of the E. coli Mre11-Rad50 (SbcCD) head complex bound to ATPgS
Authors : Kaeshammer, L.; Saathoff, J.H.; Gut, F.; Bartho, J.; Alt, A.; Kessler, B.; Lammens, K.; Hopfner, K.P.
Deposited on : 2019-07-03
Resolution : 3.50 Å (reported)
Based on initial models : 4M0V, 3QF7

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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

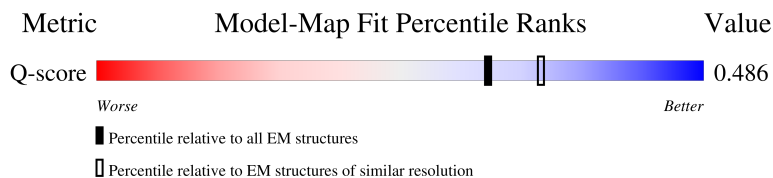
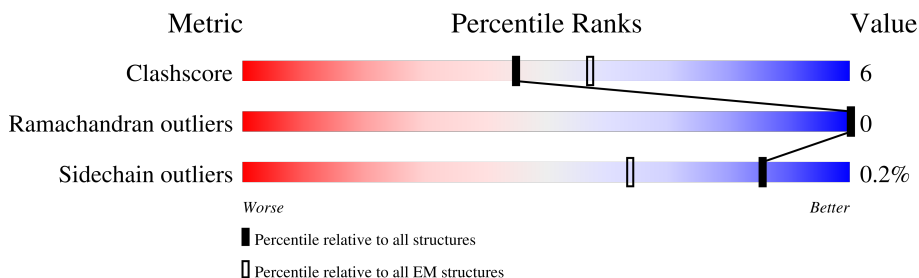
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	407	
1	B	407	
2	C	1048	

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Mol	Chain	Length	Quality of chain
2	D	1048	 A horizontal bar chart showing the quality of chain D. The bar is divided into three segments: a green segment on the left labeled '29%', a yellow segment in the middle labeled '6%', and a grey segment on the right labeled '65%'. The total length of the bar represents 100%.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11820 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 Nuclease SbcCD subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	386	Total	C	N	O	S	0	0
			3047	1921	542	575	9		
1	B	385	Total	C	N	O	S	0	0
			3041	1918	540	574	9		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	401	GLY	-	expression tag	UNP C3TMC7
A	402	HIS	-	expression tag	UNP C3TMC7
A	403	HIS	-	expression tag	UNP C3TMC7
A	404	HIS	-	expression tag	UNP C3TMC7
A	405	HIS	-	expression tag	UNP C3TMC7
A	406	HIS	-	expression tag	UNP C3TMC7
A	407	HIS	-	expression tag	UNP C3TMC7
B	401	GLY	-	expression tag	UNP C3TMC7
B	402	HIS	-	expression tag	UNP C3TMC7
B	403	HIS	-	expression tag	UNP C3TMC7
B	404	HIS	-	expression tag	UNP C3TMC7
B	405	HIS	-	expression tag	UNP C3TMC7
B	406	HIS	-	expression tag	UNP C3TMC7
B	407	HIS	-	expression tag	UNP C3TMC7

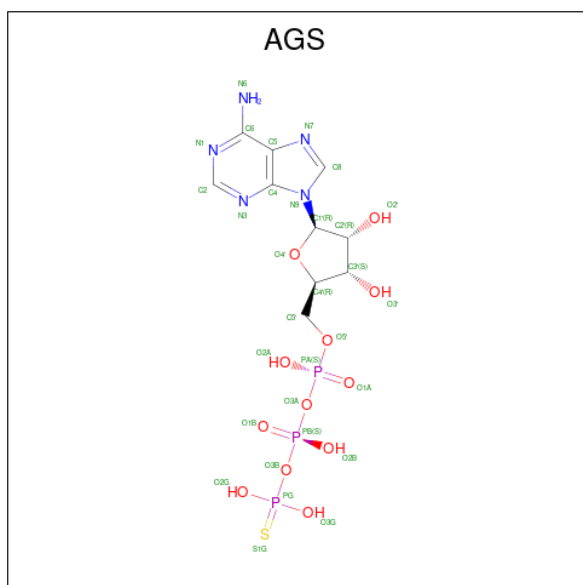
- Molecule 2 is a protein called Nuclease SbcCD subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	364	Total	C	N	O	S	0	0
			2836	1789	494	545	8		
2	D	363	Total	C	N	O	S	0	0
			2828	1785	493	542	8		

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Mn	0
			2	2	
3	B	2	Total	Mn	0
			2	2	

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$).



Mol	Chain	Residues	Atoms						AltConf
4	C	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
4	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
5	C	1	Total	Mg	0
			1	1	
5	D	1	Total	Mg	0
			1	1	

- Molecule 2: Nuclease SbcCD subunit C



LEU	ASP	LEU	GLY	SER	TLE	ASP	H103	H1
ASP	ALA	ALA	ILE	GLN	GLU	GLU	R194	L4
ILE	GLN	VAL	VAL	THR	VAL	GLN	ALA	L11
THR	ALA	PRO	PRO	SER	ASN	GLN	ARG	L14
LYS	ALA	GLN	GLN	ASP	THR	GLU	THR	L14
GLN	GLN	GLN	LYS	ARG	ARG	ALA	GLU	D21
LEU	LEU	LEU	ARG	GLN	GLN	SER	GLU	L14
GLN	GLN	GLN	GLN	HIS	GLN	ARG	LYS	D21
ARG	ALA	ALA	LEU	LEU	SER	ARG	LYS	D21
ASP	GLY	ALA	ALA	ARG	THR	GLN	GLN	R24
GLU	GLN	GLN	GLN	GLN	THR	GLN	GLN	R24
ASN	PRO	PRO	LEU	TRP	ALA	ALA	ALA	S29
GLU	CYS	CYS	GLN	GLN	LEU	LEU	GLN	N30
ALA	PRO	VAL	VAL	GLN	ARG	GLN	ALA	N30
GLN	GLN	ALA	ALA	LEU	ALA	GLN	SER	I35
SER	CYS	ILE	ILE	LEU	SER	ALA	GLY	I35
LEU	GLY	ASN	GLN	THR	ILE	LEU	VAL	K43
ARG	SER	ASN	GLN	HIS	ARG	ALA	THR	K43
GLN	THR	VAL	VAL	ALA	HIS	GLU	LEU	L47
ASP	SER	THR	THR	GLU	HIS	GLU	LEU	L47
GLU	HIS	GLN	GLN	ALA	GLN	GLU	THR	L71
GLN	PRO	GLN	GLN	LYS	ALA	LYS	PRO	M72
ALA	ALA	GLN	GLN	LEU	LYS	ALA	GLU	T73
LEU	VAL	THR	THR	ASN	GLN	GLN	GLN	T73
THR	GLU	GLN	ARG	LEU	SER	PRO	VAL	R74
GLN	ALA	ALA	ARG	ALA	GLN	GLN	GLN	D75
GLN	TYR	ASN	ASN	ALA	GLU	LEU	SER	T76
TRP	GLN	ALA	ALA	ALA	LEU	ALA	LEU	C79
GLN	ALA	ALA	ALA	ILE	GLN	ALA	THR	C79
ALA	LEU	LEU	LEU	THR	GLN	SER	ALA	E86
VAL	GLU	ASN	ASN	GLU	GLN	LEU	ALA	V87
THR	PRO	GLU	GLU	THR	GLN	LEU	SER	V87
ALA	ALA	GLY	MET	THR	GLN	ALA	GLN	R93
SER	VAL	VAL	ARG	THR	GLN	GLN	VAL	R93
LEU	ASN	GLN	GLN	ALA	LEU	PRO	LEU	A101
ASN	GLN	ARG	ARG	ASP	ASN	ALA	THR	A101
ILE	ILE	TYR	TYR	GLU	THR	ARG	ASP	P105
THR	THR	SER	ARG	VAL	TRP	ASN	GLU	P105
LEU	LEU	GLU	GLU	LEU	LEU	LEU	GLU	N108
GLN	LEU	LYS	LYS	THR	GLN	ARG	LYS	N108
PRO	ALA	THR	THR	ALA	GLU	PRO	GLN	E115
LEU	LEU	GLN	GLN	LEU	HIS	HIS	LEU	E115
ASP	GLU	GLN	GLN	ALA	ASP	TRP	ILE	A126
THR	ASN	LEU	LEU	ARG	GLN	ARG	THR	A126
ILE	GLU	ALA	ALA	HIS	PHE	GLU	ALA	L135
GLN	VAL	VAL	ASP	ALA	ARG	ILE	GLN	L135
PRO	LYS	VAL	VAL	GLU	GLN	ALA	GLN	L142
TRP	LYS	LYS	THR	GLN	TRP	GLU	GLN	L142
LEU	LEU	THR	THR	ASN	ASN	HIS	GLU	G145
ASP	GLY	ILE	ILE	PRO	ASN	SER	GLN	R146
ALA	ALA	GLU	CYS	LEU	GLU	ALA	GLN	R146
GLN	GLU	GLU	GLU	ARG	PRO	ALA	SER	R149
ASP	GLY	GLN	GLN	GLN	ALA	LEU	LEU	S150
GLU	ALA	ALA	GLU	HIS	GLY	ALA	ASN	M151
HIS	THR	ALA	ALA	LEU	TRP	HIS	TRP	M151
GLU	LEU	ARG	ARG	VAL	ARG	ILE	LEU	L173
ARG	ARG	ILE	ILE	ALA	ALA	THR	THR	L173
GLN	GLY	LYS	THR	LEU	GLN	GLN	ARG	S186
LEU	THR	THR	THR	HIS	PHE	GLN	GLN	S186

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	142229	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 ($e^-/\text{\AA}^2$)	68	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.235	Depositor
Minimum map value	-0.074	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0109	Depositor
Map size (Å)	317.99997, 317.99997, 317.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: AGS, MG, MN

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	0.35	0/3112	0.50	0/4238
1	B	0.35	0/3106	0.50	0/4230
2	C	0.42	0/2877	0.53	0/3880
2	D	0.43	0/2869	0.57	0/3869
All	All	0.38	0/11964	0.52	0/16217

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	3047	0	3011	30	0
1	B	3041	0	3004	47	0
2	C	2836	0	2871	38	0
2	D	2828	0	2866	39	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	C	31	0	11	2	0
4	D	31	0	11	1	0
5	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	1	0	0	0	0
All	All	11820	0	11774	147	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 6.

The worst 5 of 147 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:B:5:HIS:CE1	1:B:219:ALA:HB1	1.71	1.24
1:B:5:HIS:CE1	1:B:219:ALA:CB	2.45	1.00
1:B:5:HIS:NE2	1:B:219:ALA:HB1	1.96	0.80
2:D:1041:LEU:HD12	2:D:1042:GLU:N	1.97	0.78
1:A:125:VAL:O	1:A:179:ILE:HA	1.88	0.72

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	380/407 (93%)	351 (92%)	29 (8%)	0	100	100
1	B	379/407 (93%)	350 (92%)	29 (8%)	0	100	100
2	C	360/1048 (34%)	332 (92%)	28 (8%)	0	100	100
2	D	359/1048 (34%)	330 (92%)	29 (8%)	0	100	100
All	All	1478/2910 (51%)	1363 (92%)	115 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	334/350 (95%)	333 (100%)	1 (0%)	86	83
1	B	333/350 (95%)	333 (100%)	0	100	100
2	C	304/897 (34%)	304 (100%)	0	100	100
2	D	303/897 (34%)	301 (99%)	2 (1%)	76	78
All	All	1274/2494 (51%)	1271 (100%)	3 (0%)	85	85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	333	VAL
2	D	76	THR
2	D	87	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	914	GLN
2	D	914	GLN
2	D	1005	ASN
2	D	925	GLN
1	B	25	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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
4	AGS	C	1101	5	32,33,33	1.04	3 (9%)	45,52,52	0.71	1 (2%)
4	AGS	D	1101	5	32,33,33	0.85	2 (6%)	45,52,52	0.70	1 (2%)

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
4	AGS	C	1101	5	-	6/21/38/38	0/3/3/3
4	AGS	D	1101	5	-	10/21/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1101	AGS	PB-O3A	-3.15	1.56	1.59
4	C	1101	AGS	PB-O3B	-2.94	1.56	1.59
4	D	1101	AGS	PB-O3A	-2.74	1.56	1.59
4	C	1101	AGS	PA-O3A	-2.34	1.57	1.59
4	D	1101	AGS	PB-O3B	-2.08	1.57	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1101	AGS	PB-O3B-PG	-3.18	121.55	133.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1101	AGS	PB-O3B-PG	-3.10	121.82	133.17

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

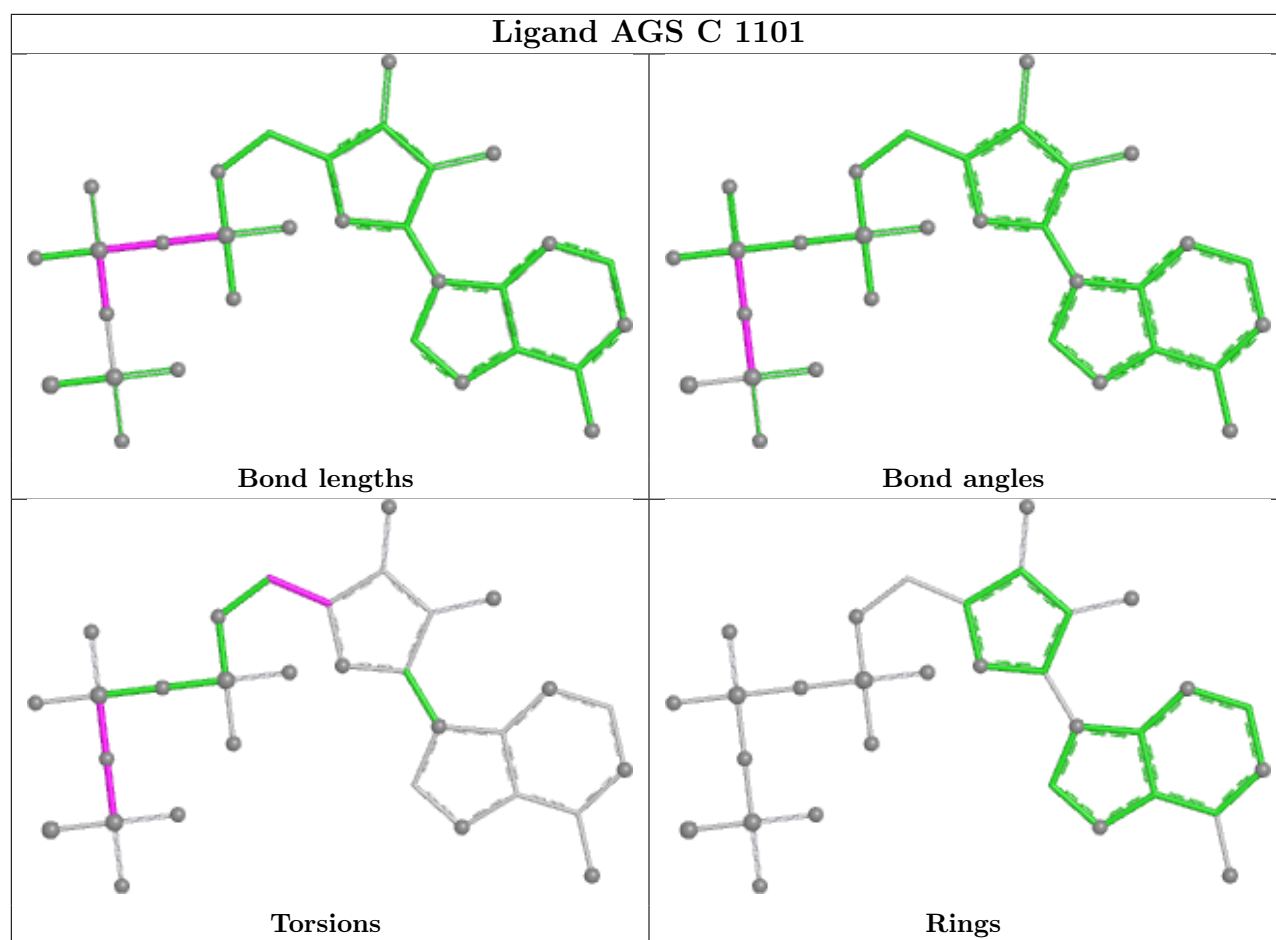
Mol	Chain	Res	Type	Atoms
4	C	1101	AGS	PB-O3B-PG-O2G
4	D	1101	AGS	PB-O3B-PG-O3G
4	D	1101	AGS	C5'-O5'-PA-O1A
4	D	1101	AGS	C5'-O5'-PA-O3A
4	D	1101	AGS	O4'-C4'-C5'-O5'

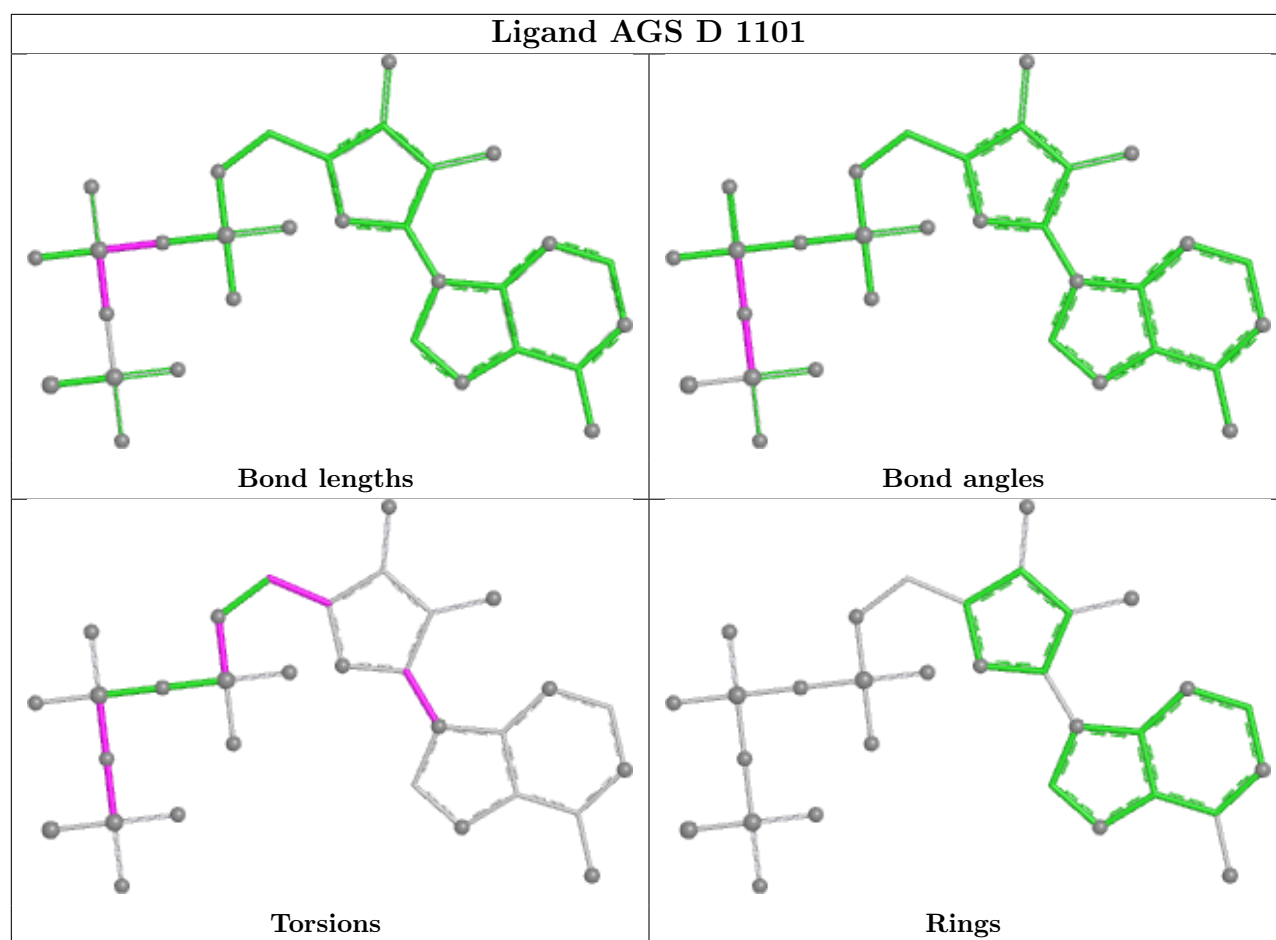
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1101	AGS	2	0
4	D	1101	AGS	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.

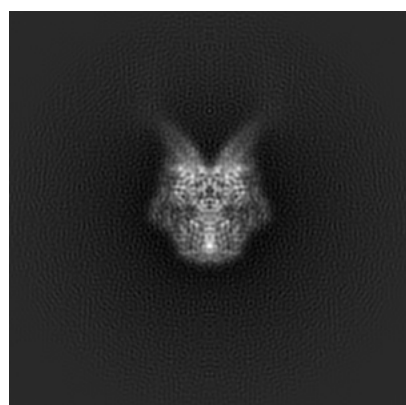
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10107. These allow visual inspection of the internal detail of the map and identification of artifacts.

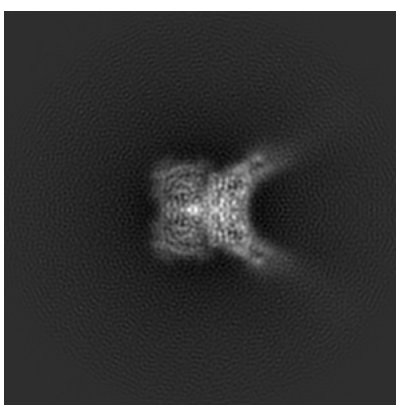
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

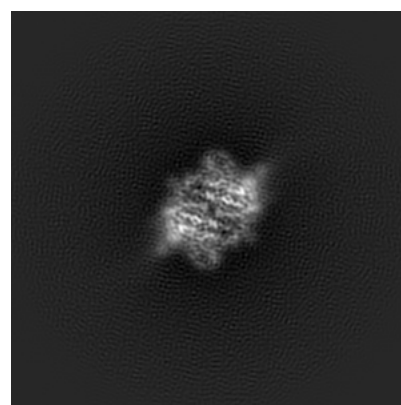
6.1.1 Primary map



X



Y

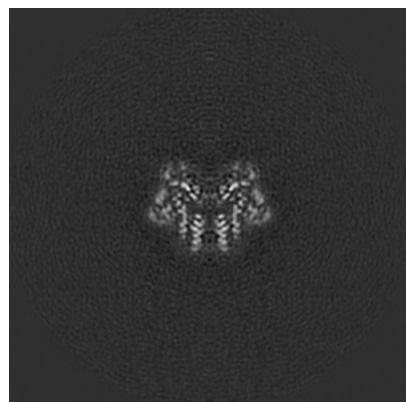


Z

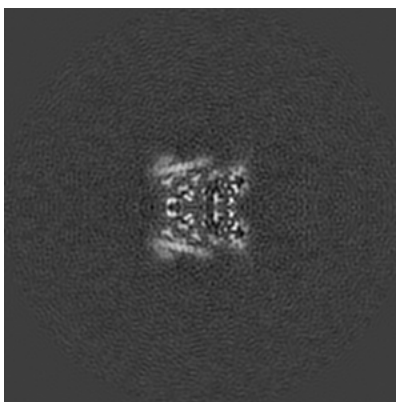
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

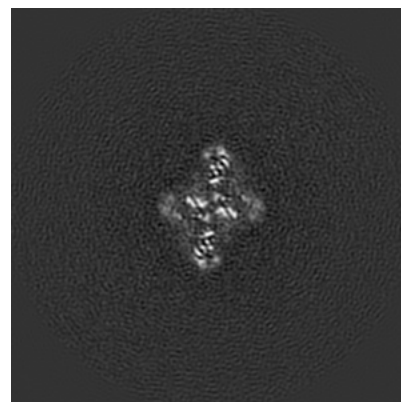
6.2.1 Primary map



X Index: 150



Y Index: 150

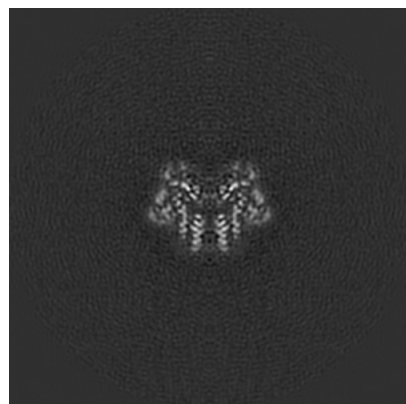


Z Index: 150

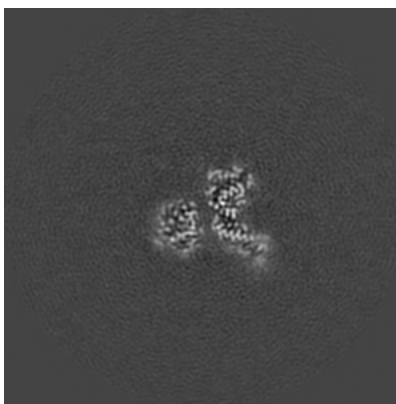
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

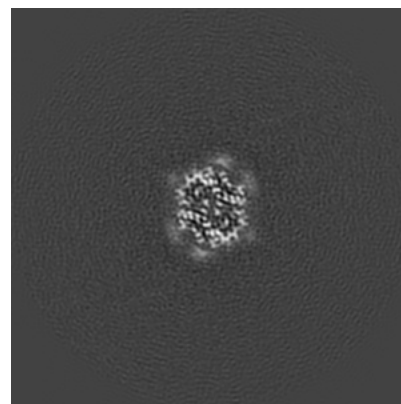
6.3.1 Primary map



X Index: 150



Y Index: 137

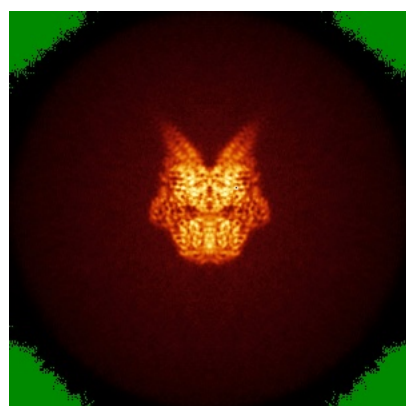


Z Index: 167

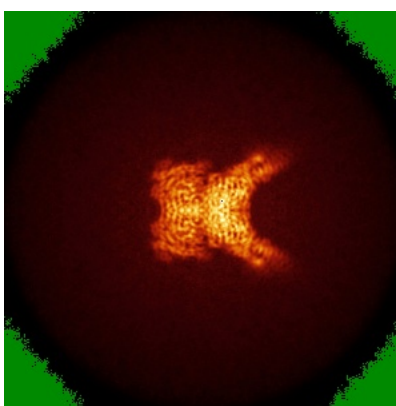
The images above show the largest variance slices of the map in three orthogonal directions.

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

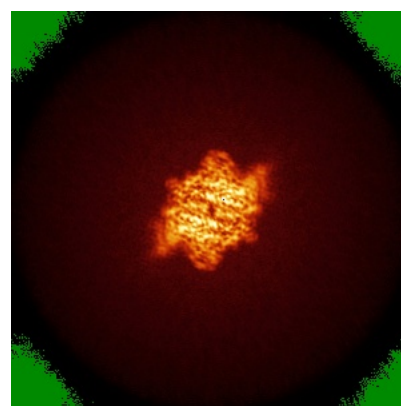
6.4.1 Primary map



X



Y

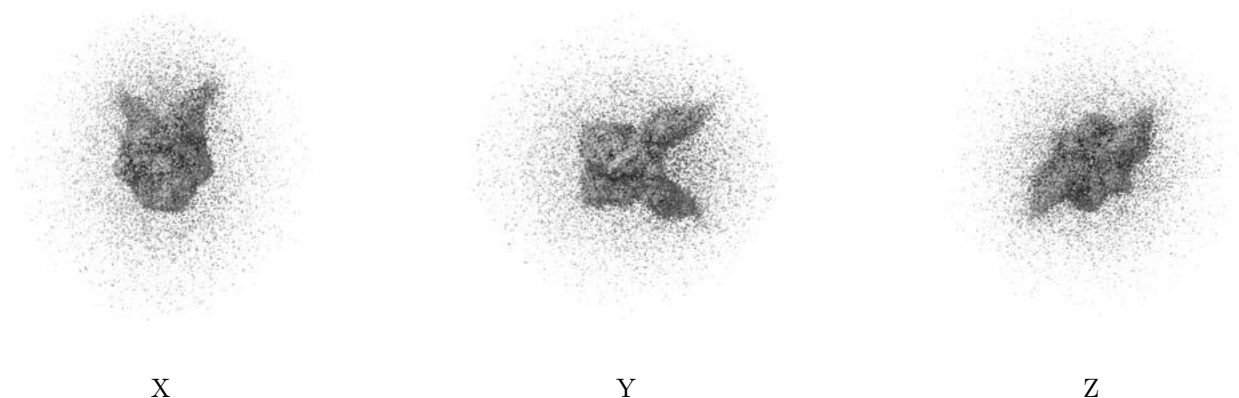


Z

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 0.0109. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

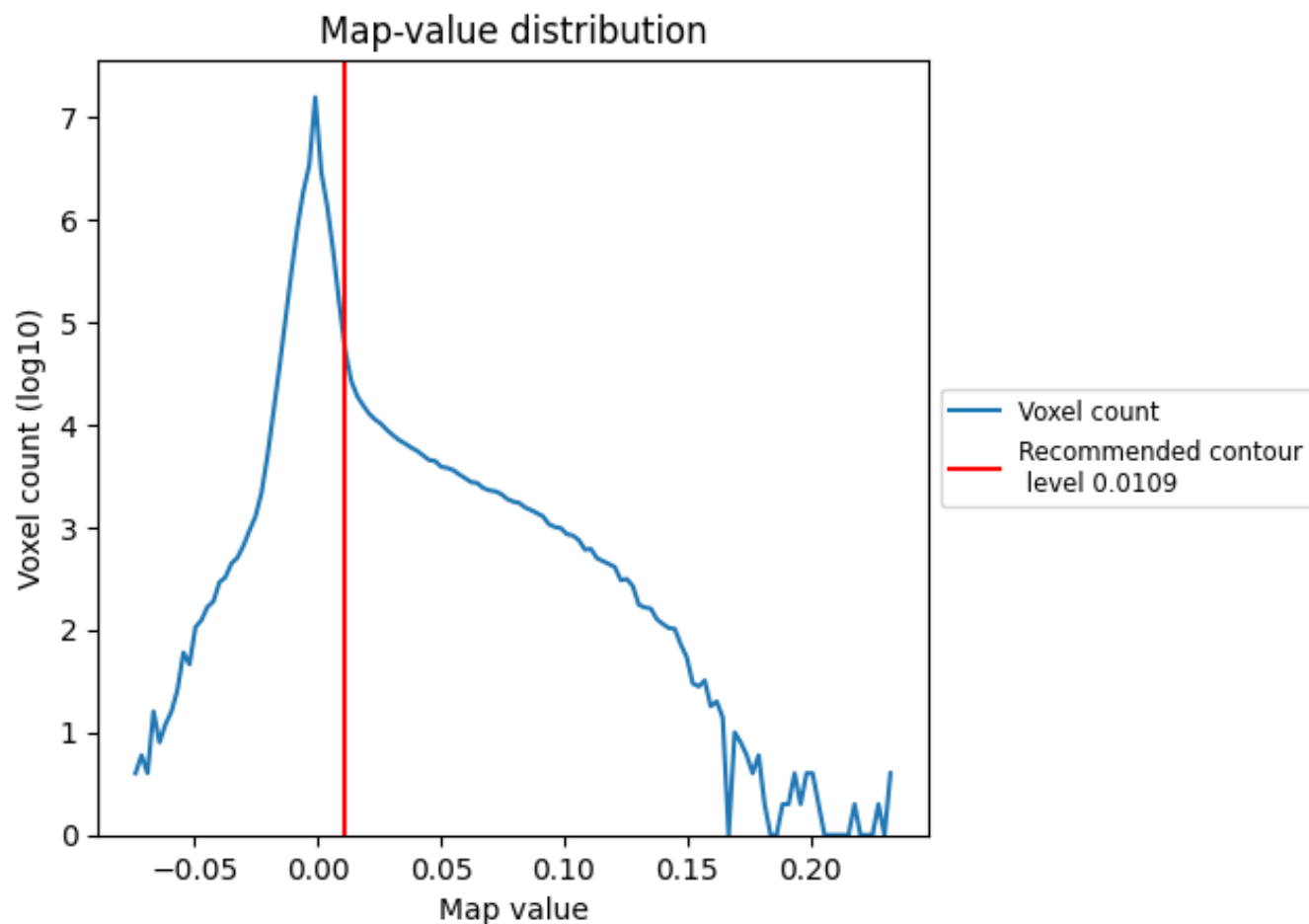
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

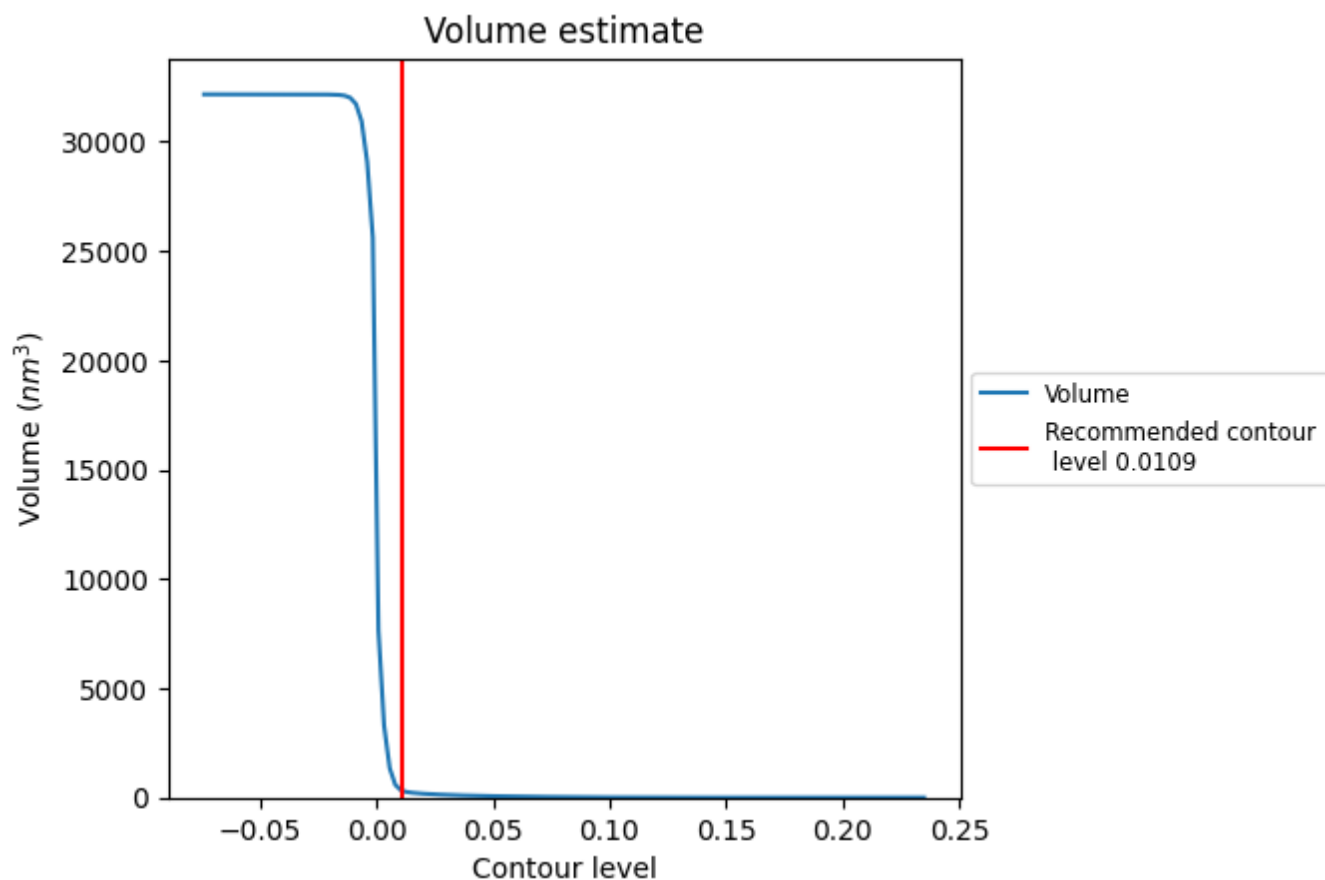
This section contains the results of statistical analysis of the map.

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.

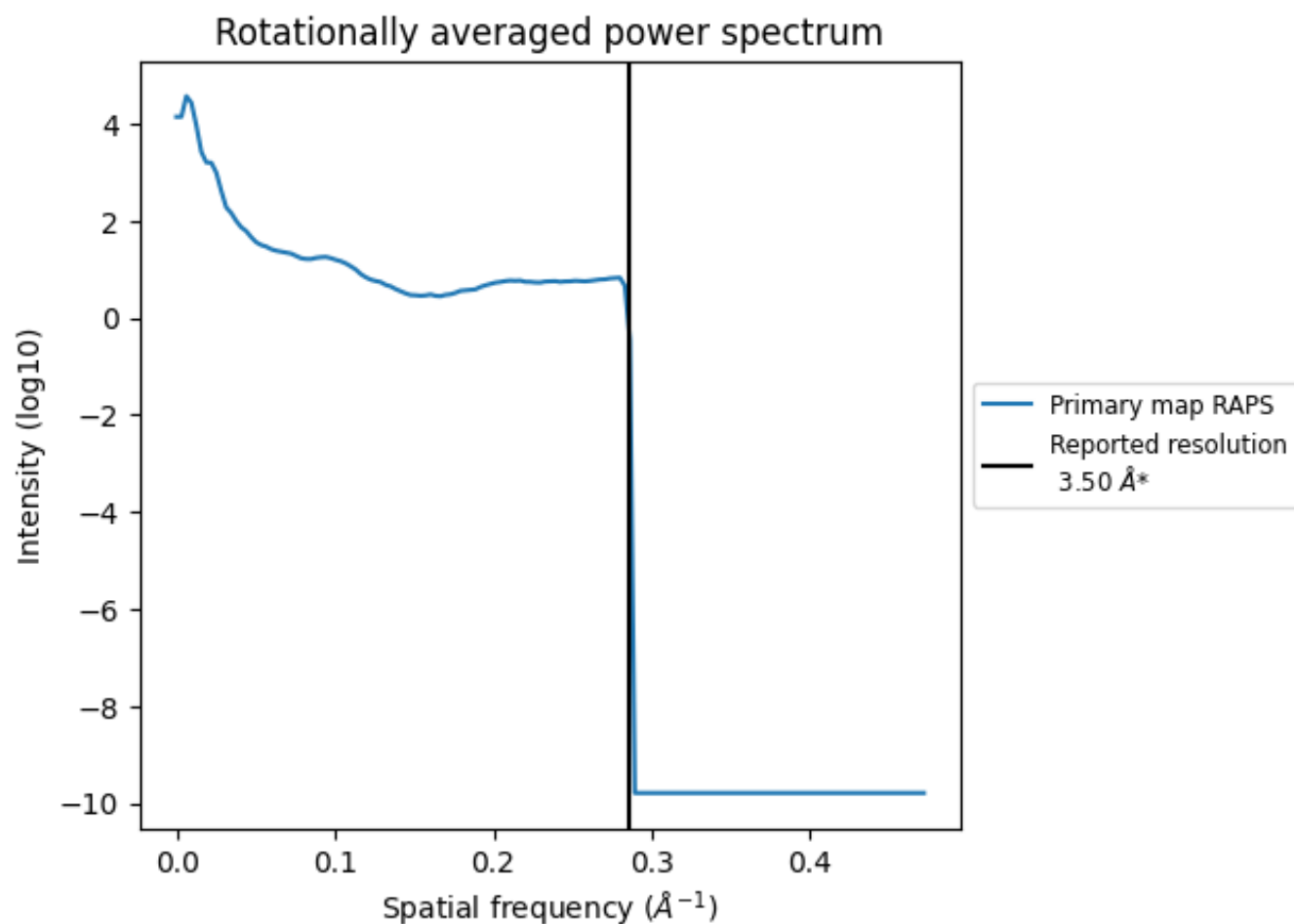
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 324 nm^3 ; this corresponds to an approximate mass of 293 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 0.286 Å⁻¹

8 Fourier-Shell correlation

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

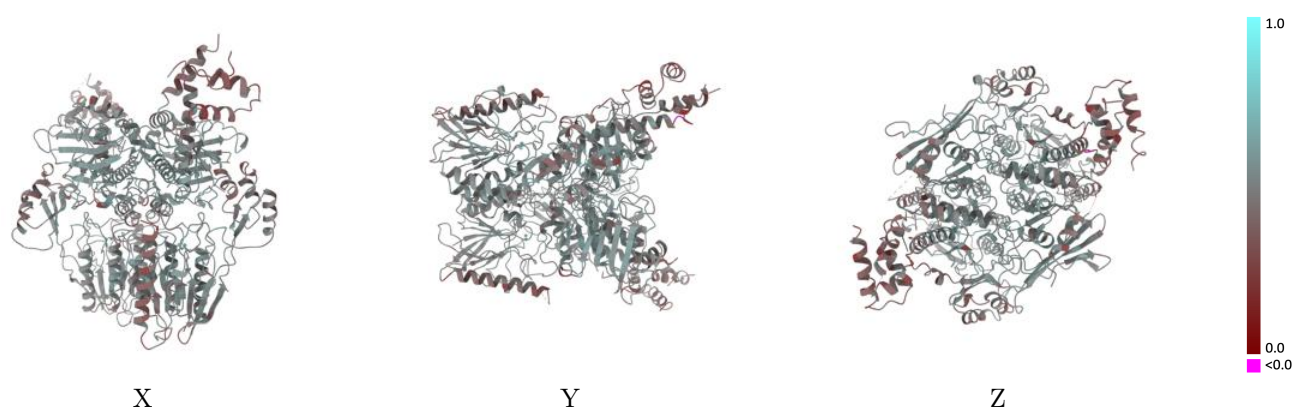
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10107 and PDB model 6S6V. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

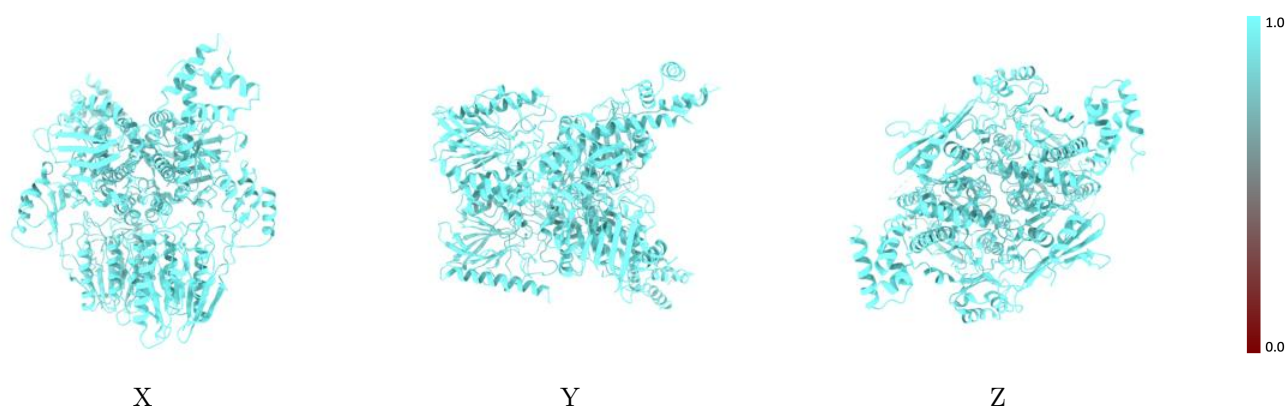
This section was not generated.

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



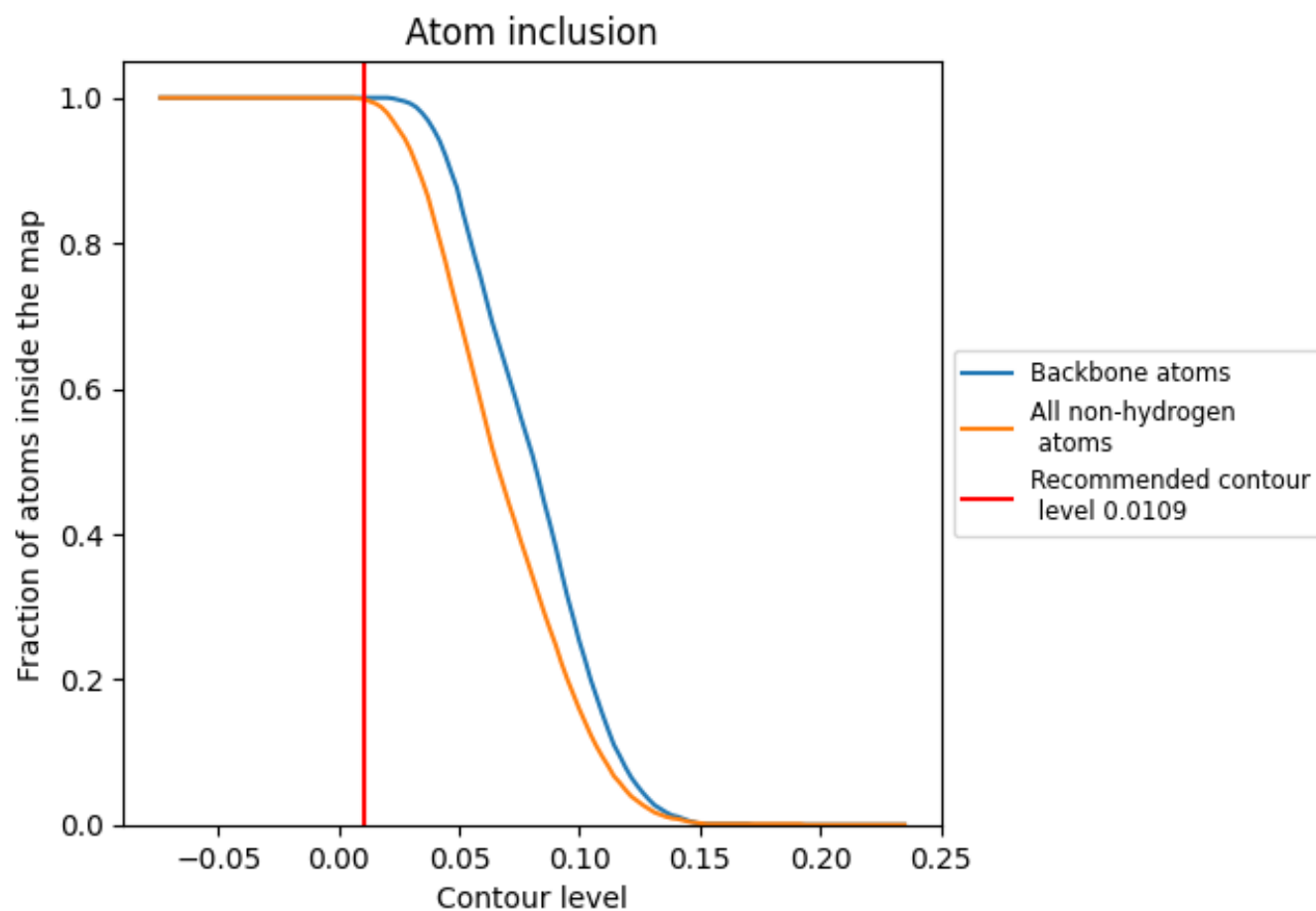
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0109).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0109) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9980	0.4860
A	0.9980	0.4680
B	0.9980	0.4690
C	0.9970	0.5050
D	0.9980	0.5010

