wwPDB EM Validation Summary Report

Oct 28, 2026 – 09:09 pm GMT

PDB ID	:	31JS / pdb_000031js
EMDB ID	:	EMD-58450
Title	:	Oxidized E.coli aerotaxis receptor in MH-cap bound state
Authors	:	Olsthoorn, F.A.; Muok, A.R.; Xu, Y.; Crane, B.R.
Deposited on	:	2026-06-09
Resolution	:	4.00 Å(reported)
Based on initial model	:	.

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:

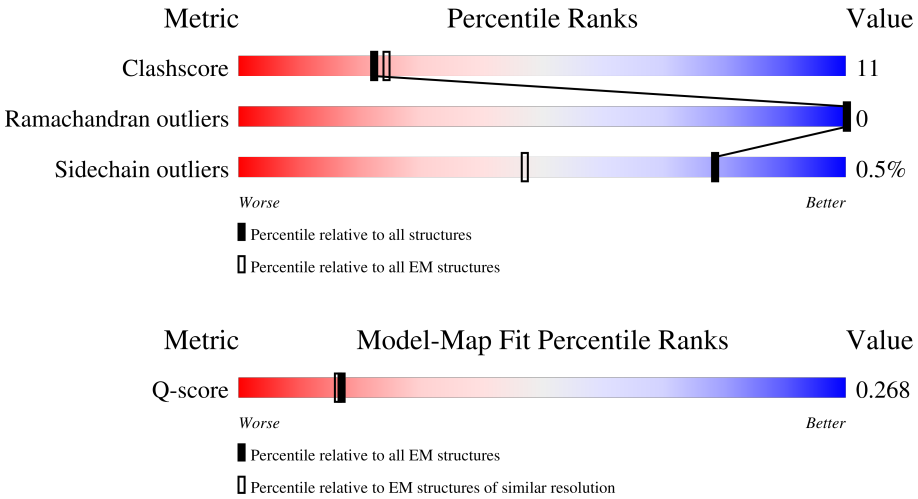
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.51

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 4.00 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	7587 (3.50 - 4.50)

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 <=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	534	12% 48% 14% 38%
1	B	534	11% 48% 14% 38%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10666 atoms, of which 5338 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 Aerotaxis receptor.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	332	Total	C	H	N	O	S	0	0
			5249	1641	2638	474	482	14		
1	B	332	Total	C	H	N	O	S	0	0
			5249	1641	2638	474	482	14		

There are 56 discrepancies between the modelled and reference sequences:

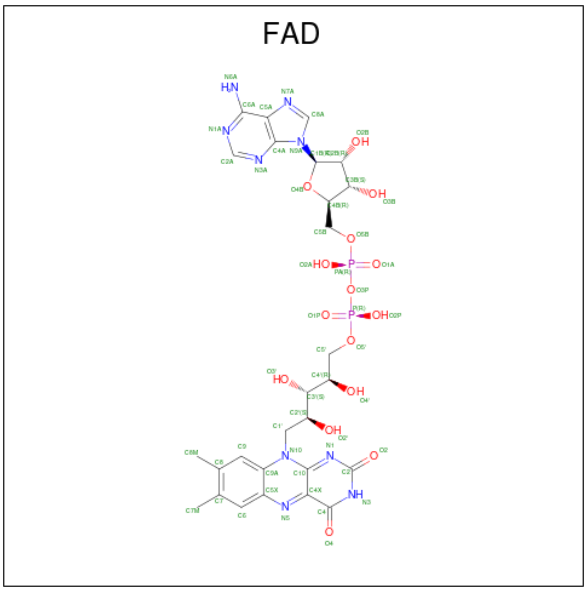
Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	TRP	-	expression tag	UNP P50466
A	-26	SER	-	expression tag	UNP P50466
A	-25	HIS	-	expression tag	UNP P50466
A	-24	PRO	-	expression tag	UNP P50466
A	-23	GLN	-	expression tag	UNP P50466
A	-22	PHE	-	expression tag	UNP P50466
A	-21	GLU	-	expression tag	UNP P50466
A	-20	LYS	-	expression tag	UNP P50466
A	-19	GLY	-	expression tag	UNP P50466
A	-18	GLY	-	expression tag	UNP P50466
A	-17	GLY	-	expression tag	UNP P50466
A	-16	SER	-	expression tag	UNP P50466
A	-15	GLY	-	expression tag	UNP P50466
A	-14	GLY	-	expression tag	UNP P50466
A	-13	GLY	-	expression tag	UNP P50466
A	-12	SER	-	expression tag	UNP P50466
A	-11	GLY	-	expression tag	UNP P50466
A	-10	GLY	-	expression tag	UNP P50466
A	-9	SER	-	expression tag	UNP P50466
A	-8	ALA	-	expression tag	UNP P50466
A	-7	TRP	-	expression tag	UNP P50466
A	-6	SER	-	expression tag	UNP P50466
A	-5	HIS	-	expression tag	UNP P50466
A	-4	PRO	-	expression tag	UNP P50466
A	-3	GLN	-	expression tag	UNP P50466
A	-2	PHE	-	expression tag	UNP P50466

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLU	-	expression tag	UNP P50466
A	0	LYS	-	expression tag	UNP P50466
B	-27	TRP	-	expression tag	UNP P50466
B	-26	SER	-	expression tag	UNP P50466
B	-25	HIS	-	expression tag	UNP P50466
B	-24	PRO	-	expression tag	UNP P50466
B	-23	GLN	-	expression tag	UNP P50466
B	-22	PHE	-	expression tag	UNP P50466
B	-21	GLU	-	expression tag	UNP P50466
B	-20	LYS	-	expression tag	UNP P50466
B	-19	GLY	-	expression tag	UNP P50466
B	-18	GLY	-	expression tag	UNP P50466
B	-17	GLY	-	expression tag	UNP P50466
B	-16	SER	-	expression tag	UNP P50466
B	-15	GLY	-	expression tag	UNP P50466
B	-14	GLY	-	expression tag	UNP P50466
B	-13	GLY	-	expression tag	UNP P50466
B	-12	SER	-	expression tag	UNP P50466
B	-11	GLY	-	expression tag	UNP P50466
B	-10	GLY	-	expression tag	UNP P50466
B	-9	SER	-	expression tag	UNP P50466
B	-8	ALA	-	expression tag	UNP P50466
B	-7	TRP	-	expression tag	UNP P50466
B	-6	SER	-	expression tag	UNP P50466
B	-5	HIS	-	expression tag	UNP P50466
B	-4	PRO	-	expression tag	UNP P50466
B	-3	GLN	-	expression tag	UNP P50466
B	-2	PHE	-	expression tag	UNP P50466
B	-1	GLU	-	expression tag	UNP P50466
B	0	LYS	-	expression tag	UNP P50466

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



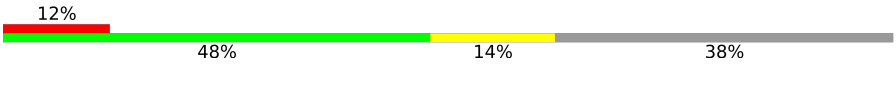
Mol	Chain	Residues	Atoms						AltConf
2	A	1	Total	C	H	N	O	P	0
			84	27	31	9	15	2	
2	B	1	Total	C	H	N	O	P	0
			84	27	31	9	15	2	

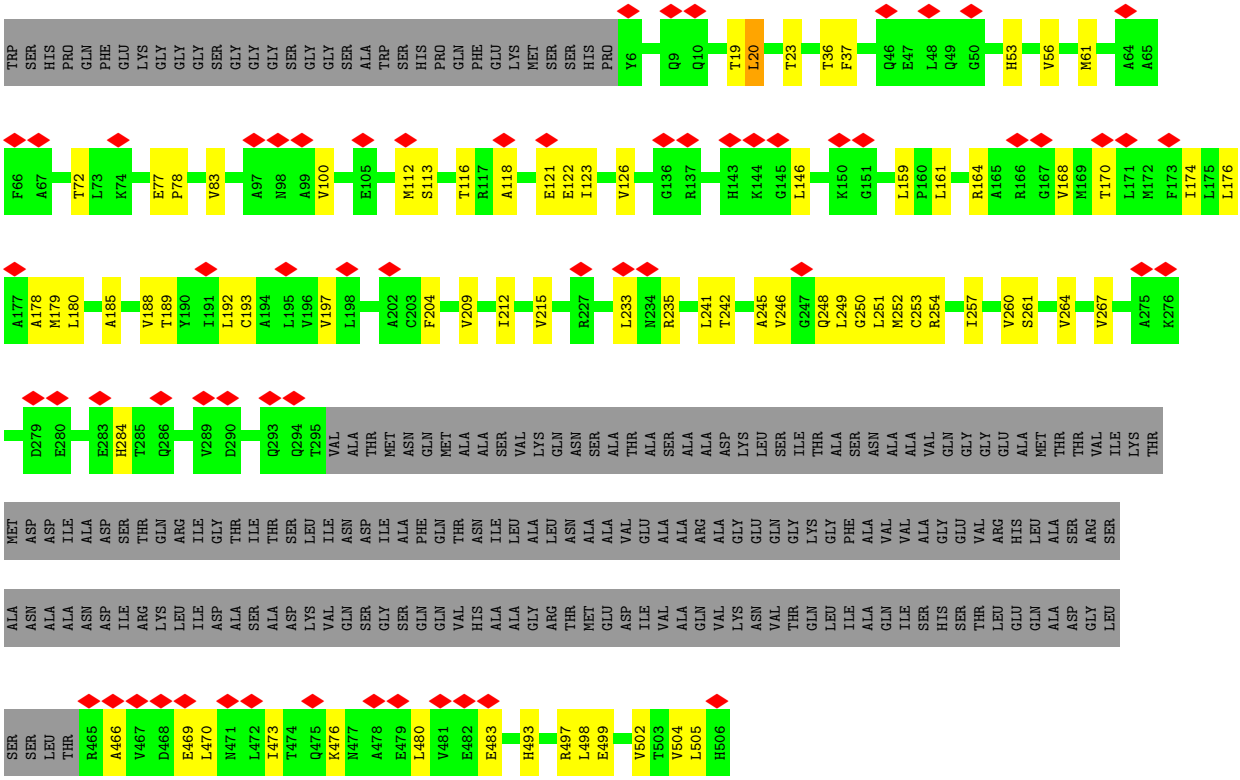
3 Residue-property plots (i)

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: Aerotaxis receptor

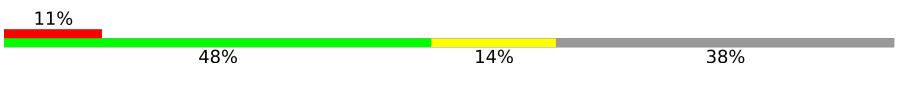
Chain A:

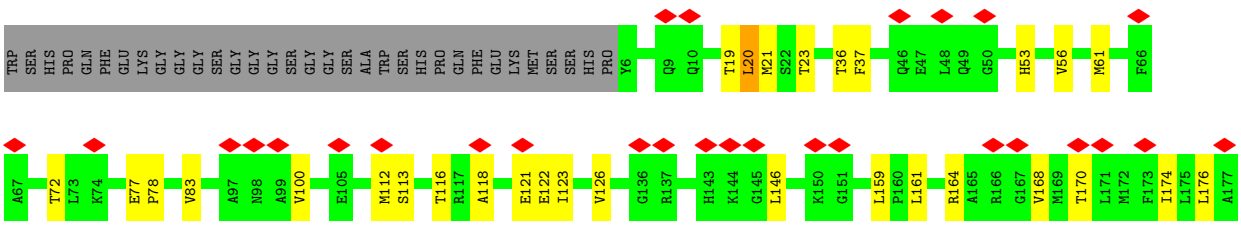


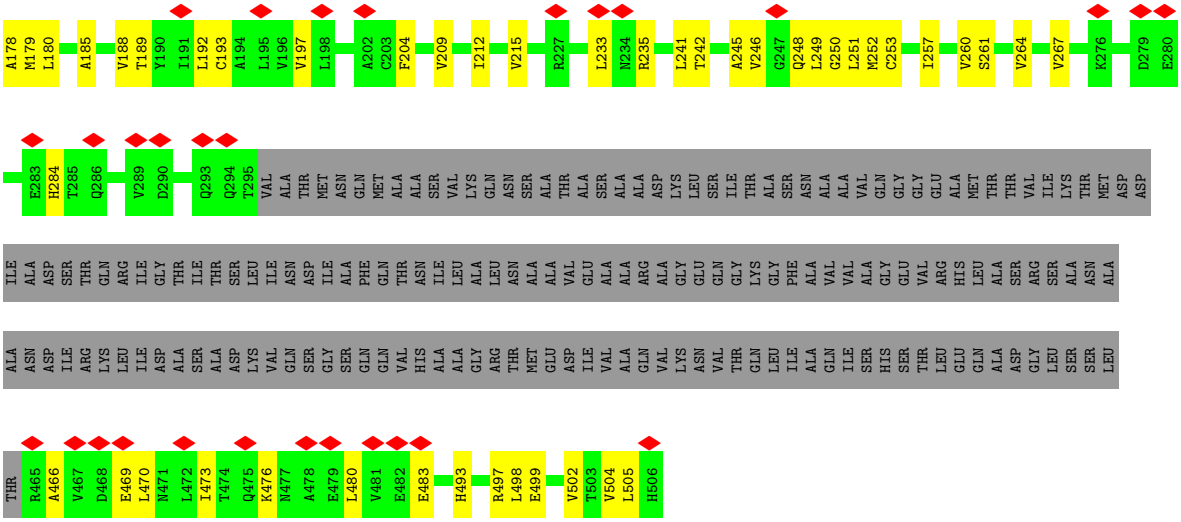


• Molecule 1: Aerotaxis receptor

Chain B:






A178 M179 L180 A185 V188 T189 Y190 I191 L192 C193 A194 L195 V196 V197 L198 A202 C203 F204 V209 I212 V215 R227 L233 N234 R235 L241 T242 A245 V246 G247 Q248 L249 G250 L251 M252 C253 I257 V260 S261 V264 V267 K276 D279 E280
E283 H284 T285 Q286 V289 D290 Q293 Q294 T295 VAL ALA THR MET ASN GLN MET ALA ALA SER VAL LYS GLN ASN SER ALA THR ALA SER ALA ALA ASP LYS LEU SER ILE THR ALA SER ASN ALA ALA VAL GLN GLY GLY GLU ALA MET THR THR VAL ILE LYS THR MET ASP ASP
ILE ALA ASP SER THR GLN ARG ILE GLY THR ILE THR SER LEU ILE ASN ASP ILE ALA PHE GLN THR ASN ILE LEU ALA LEU ASN ALA ALA VAL GLU ALA ALA ARG ALA GLY GLN GLY LYS GLY PHE ALA VAL VAL ALA GLY GLU VAL ARG HIS LEU ALA SER ARG SER ALA ASN ALA
ALA ASN ASP ILE ARG LYS LEU ILE ASP ALA SER ALA ASP LYS VAL GLN SER GLY SER GLN GLN VAL HIS ALA ALA GLY ARG THR MET GLU ASP ILE VAL ALA GLN VAL LYS ASN VAL THR GLN LEU ILE ALA GLN ILE SER HIS SER THR LEU GLU GLN ALA ASP GLY LEU SER SER LEU
THR R465 A466 V467 D468 E469 L470 N471 L472 I473 T474 Q475 K476 N477 A478 E479 L480 V481 E482 E483 H493 R497 L498 E499 V502 T503 V504 L505 H506

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	14486	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.145	Depositor
Minimum map value	-0.066	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0515	Depositor
Map size (Å)	249.59999, 249.59999, 249.59999	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAD

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	0.17	0/2659	0.34	0/3608
1	B	0.16	0/2659	0.33	0/3608
All	All	0.16	0/5318	0.33	0/7216

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

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	2611	2638	2636	73	0
1	B	2611	2638	2636	72	0
2	A	53	31	31	2	0
2	B	53	31	31	2	0
All	All	5328	5338	5334	121	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 11.

The worst 5 of 121 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:A:249:LEU:HD13	1:B:249:LEU:HD13	1.59	0.83
1:A:23:THR:HG21	1:A:504:VAL:HG13	1.71	0.72
1:B:23:THR:HG21	1:B:504:VAL:HG13	1.71	0.71
1:B:23:THR:CG2	1:B:504:VAL:HG13	2.25	0.67
1:A:23:THR:CG2	1:A:504:VAL:HG13	2.25	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	328/534 (61%)	315 (96%)	13 (4%)	0	100	100
1	B	328/534 (61%)	315 (96%)	13 (4%)	0	100	100
All	All	656/1068 (61%)	630 (96%)	26 (4%)	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	283/434 (65%)	282 (100%)	1 (0%)	84	84
1	B	283/434 (65%)	281 (99%)	2 (1%)	76	79
All	All	566/868 (65%)	563 (100%)	3 (0%)	78	82

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

Mol	Chain	Res	Type
1	A	20	LEU
1	B	20	LEU
1	B	21	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	217	HIS
1	B	228	ASN
1	B	232	HIS
1	A	228	ASN
1	A	217	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

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	$\#\|Z\|>2$
2	FAD	A	601	-	56,58,58	0.84	1 (1%)	81,89,89	0.73	1 (1%)
2	FAD	B	601	-	56,58,58	0.83	1 (1%)	81,89,89	0.73	1 (1%)

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
2	FAD	A	601	-	-	12/34/50/50	0/6/6/6
2	FAD	B	601	-	-	12/34/50/50	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FAD	C5X-N5	-2.33	1.35	1.39
2	B	601	FAD	C5X-N5	-2.27	1.35	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	FAD	C9-C9A-N10	2.17	124.77	121.84
2	B	601	FAD	C9-C9A-N10	2.13	124.72	121.84

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	FAD	C5B-O5B-PA-O2A
2	A	601	FAD	C5B-O5B-PA-O3P
2	A	601	FAD	C1'-C2'-C3'-O3'
2	A	601	FAD	C1'-C2'-C3'-C4'
2	A	601	FAD	O2'-C2'-C3'-O3'

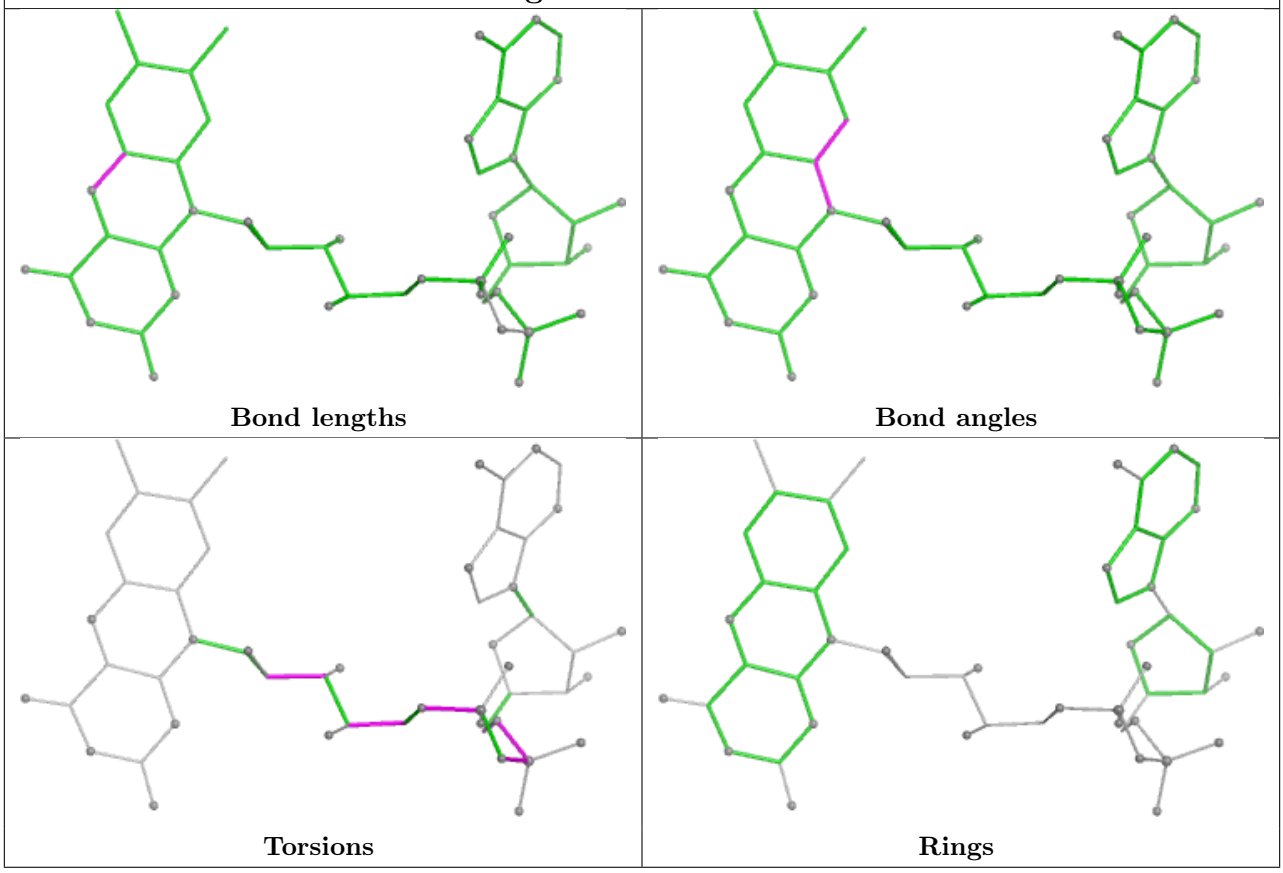
There are no ring outliers.

2 monomers are involved in 4 short contacts:

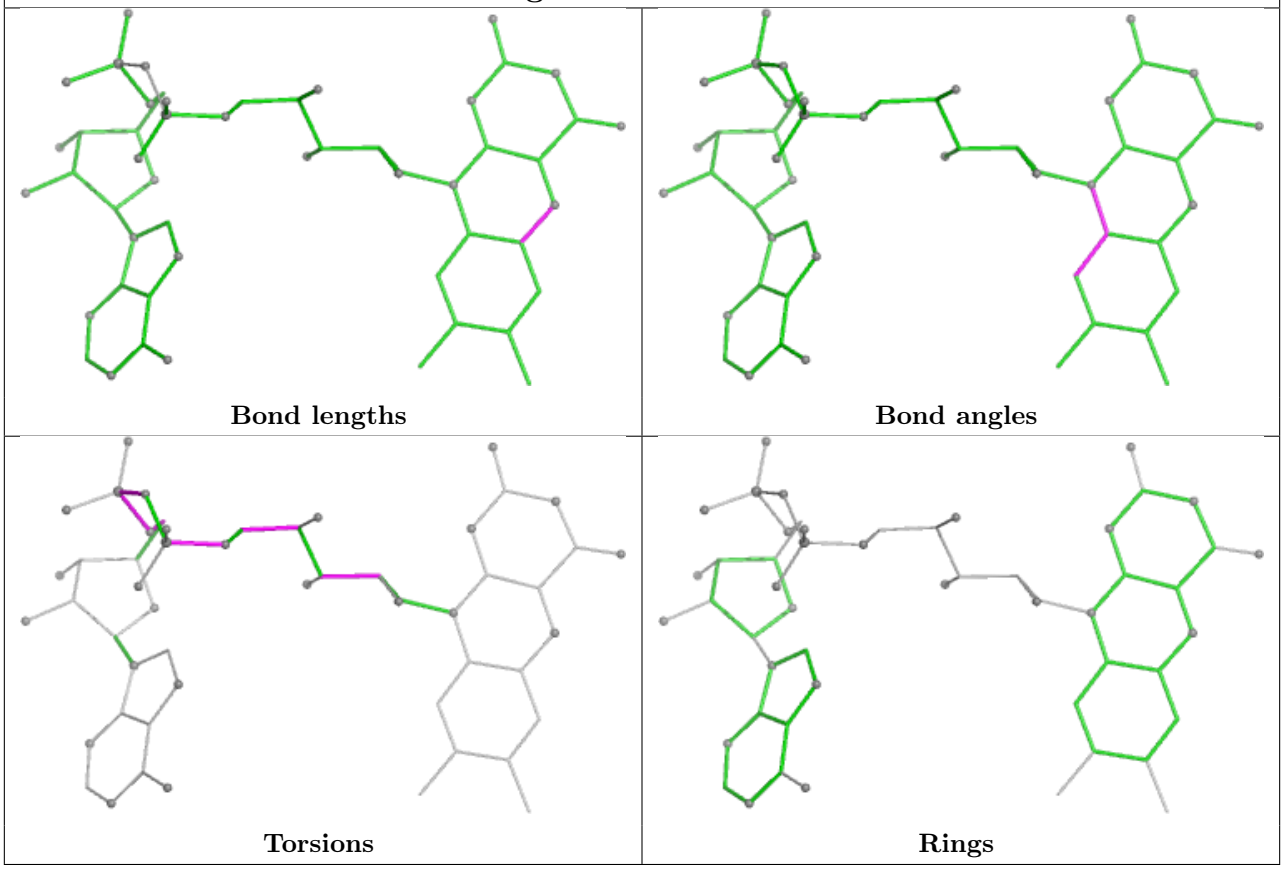
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FAD	2	0
2	B	601	FAD	2	0

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 then 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.

Ligand FAD A 601



Ligand FAD B 601



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.

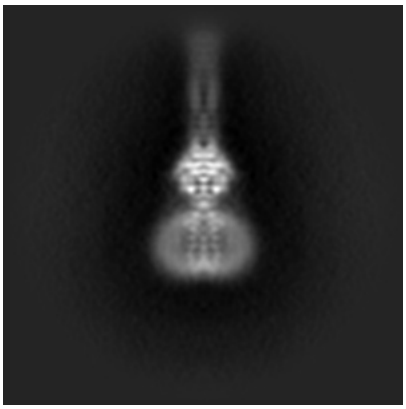
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-58450. These allow visual inspection of the internal detail of the map and identification of artifacts.

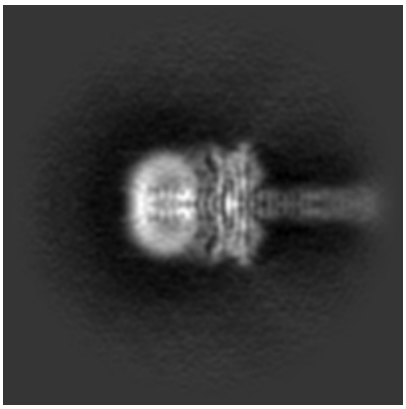
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

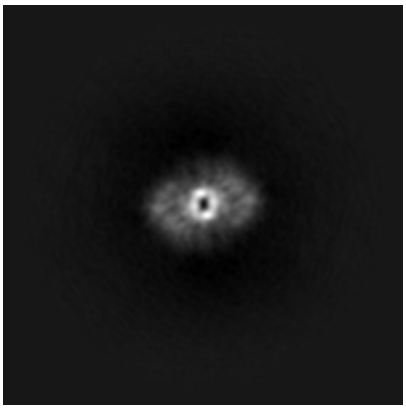
6.1.1 Primary map



X

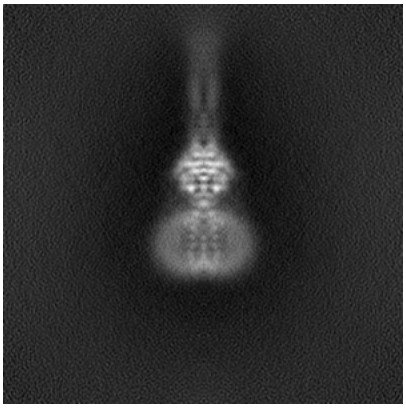


Y

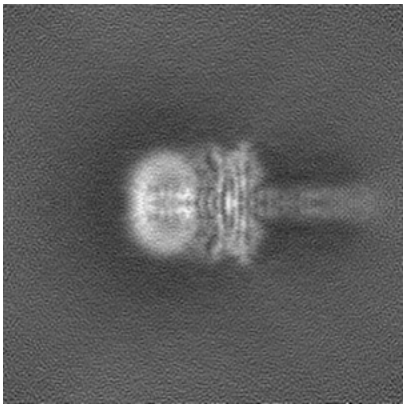


Z

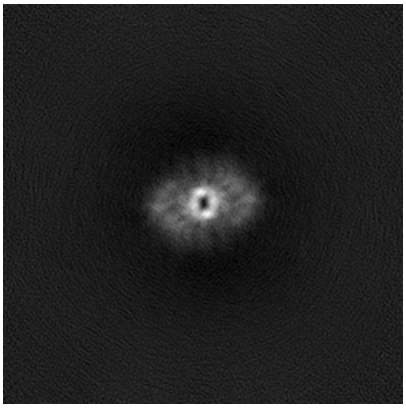
6.1.2 Raw map



X



Y

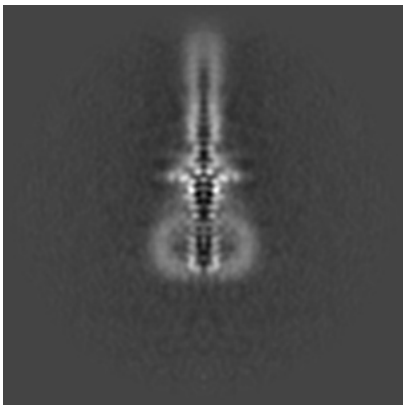


Z

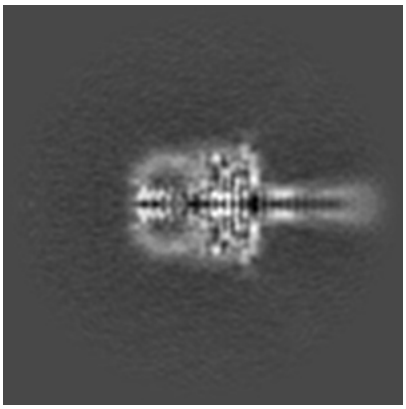
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

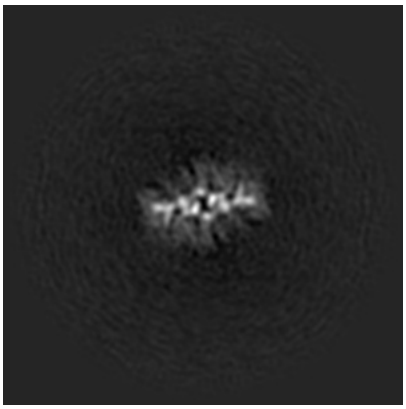
6.2.1 Primary map



X Index: 120

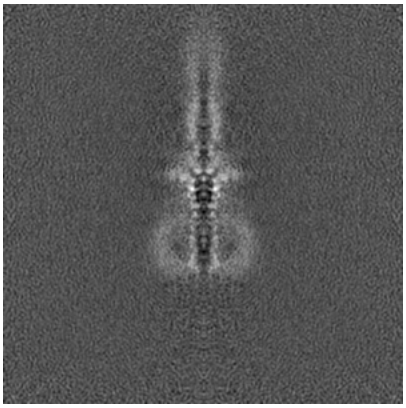


Y Index: 120

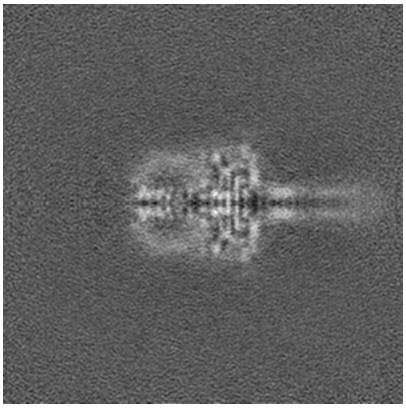


Z Index: 120

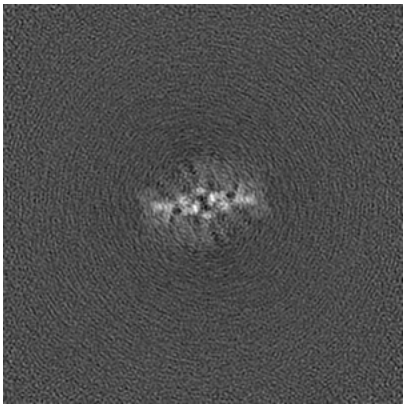
6.2.2 Raw map



X Index: 120



Y Index: 120

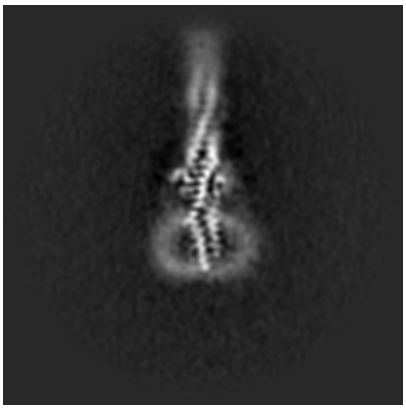


Z Index: 120

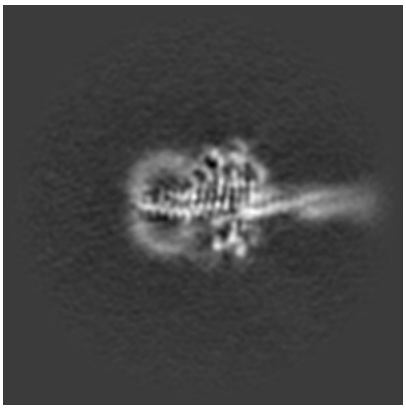
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

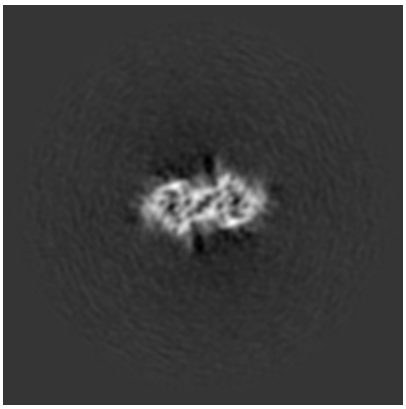
6.3.1 Primary map



X Index: 115

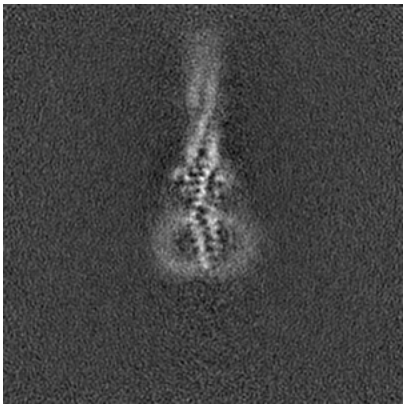


Y Index: 126

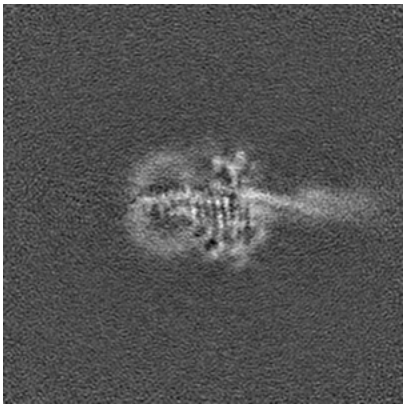


Z Index: 144

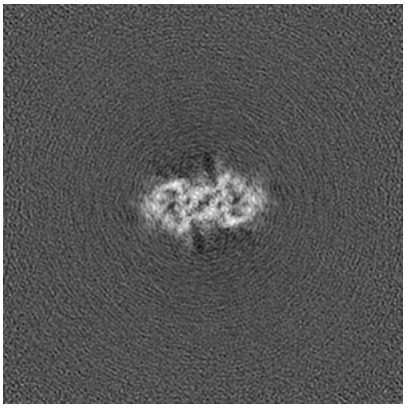
6.3.2 Raw map



X Index: 115



Y Index: 114

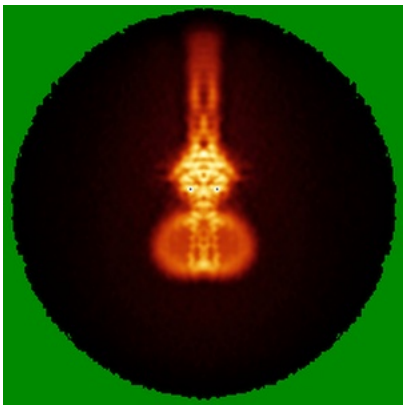


Z Index: 144

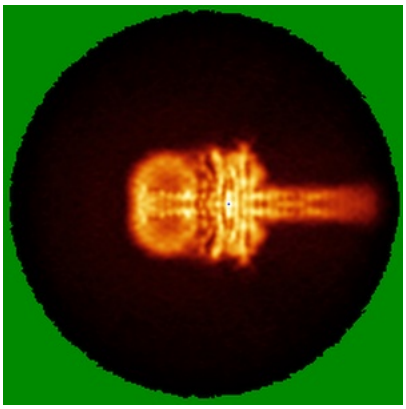
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

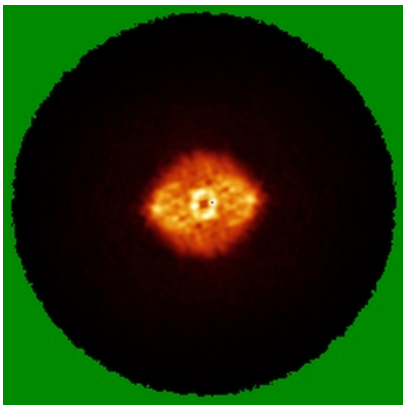
6.4.1 Primary map



X

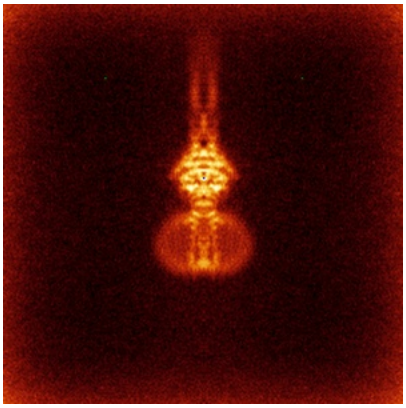


Y

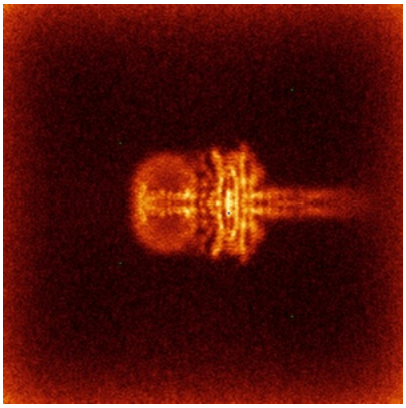


Z

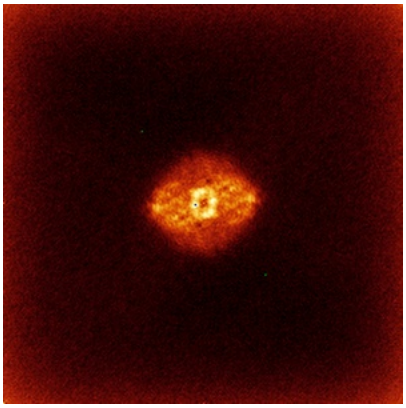
6.4.2 Raw map



X



Y

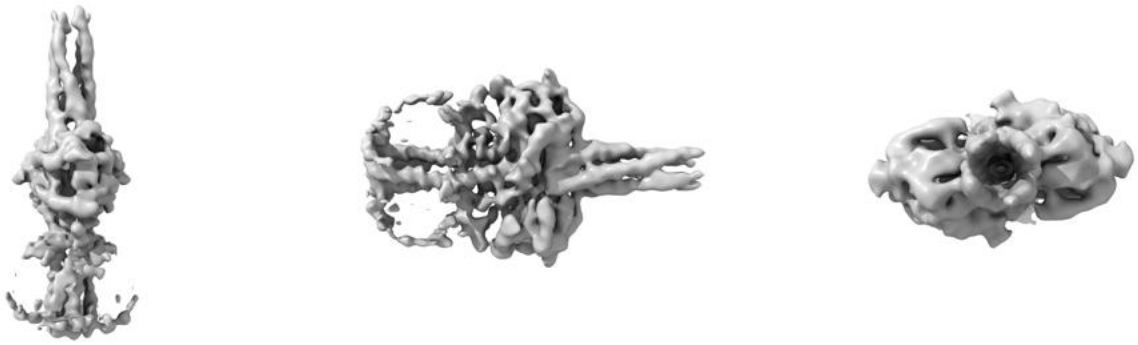


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0515. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

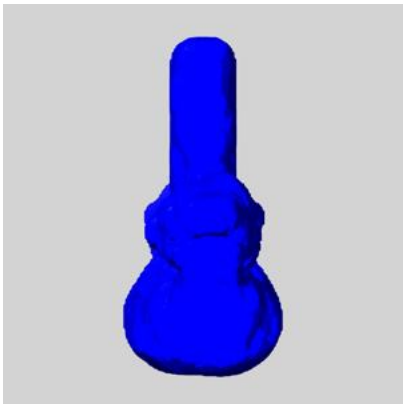
6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

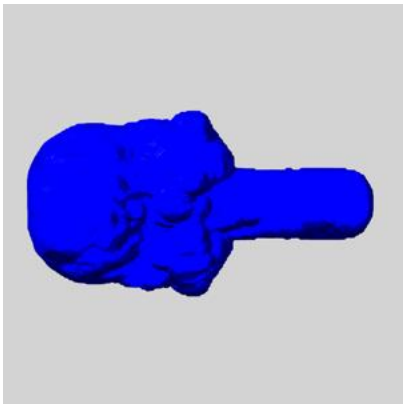
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

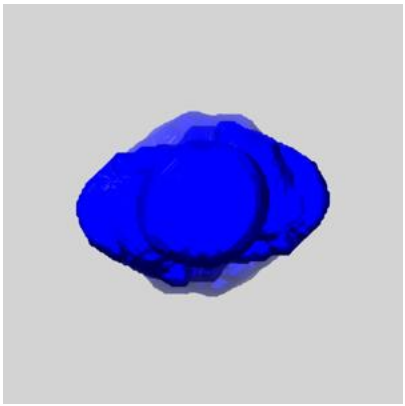
6.6.1 emd_58450_msk_1.map



X



Y

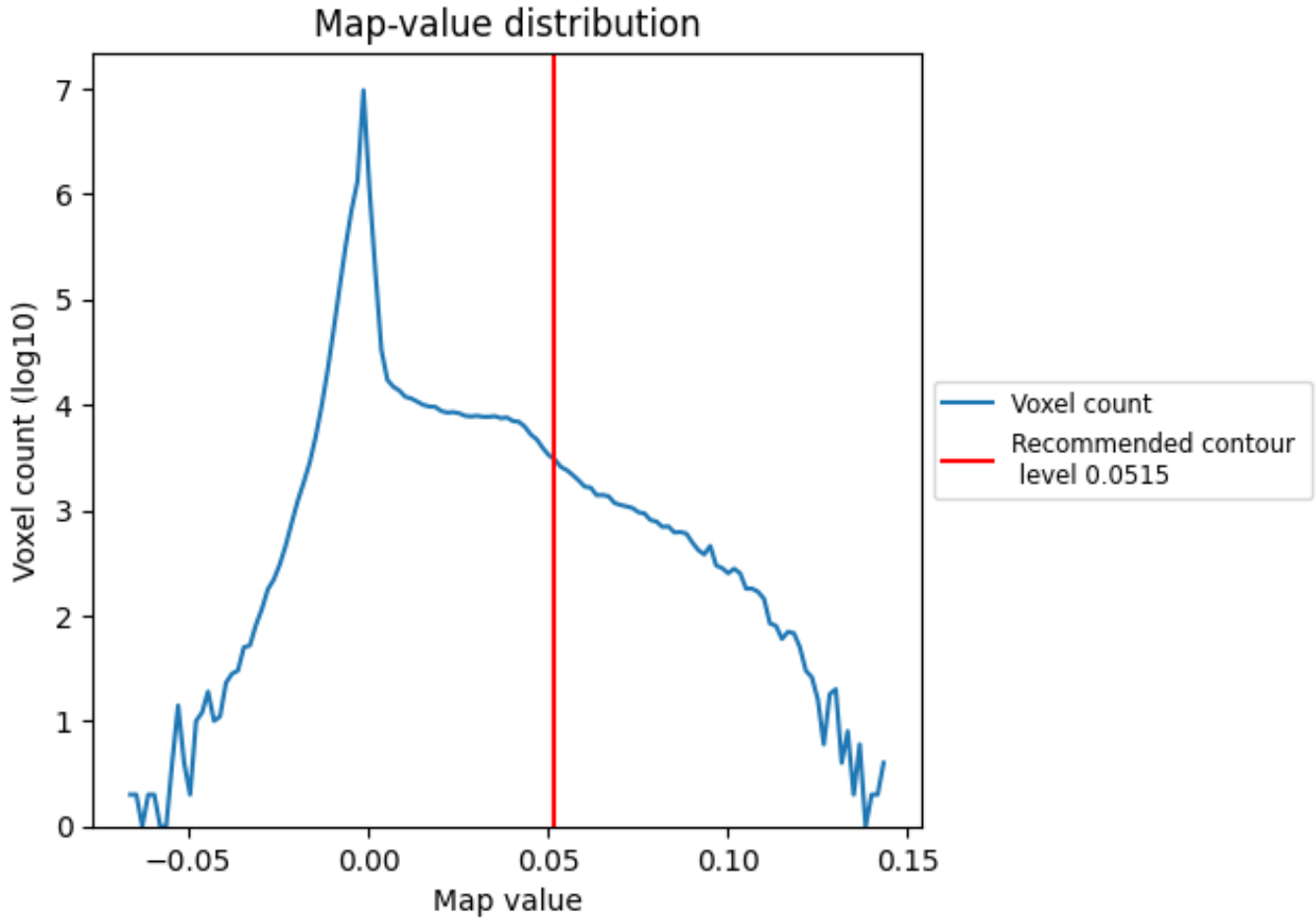


Z

7 Map analysis

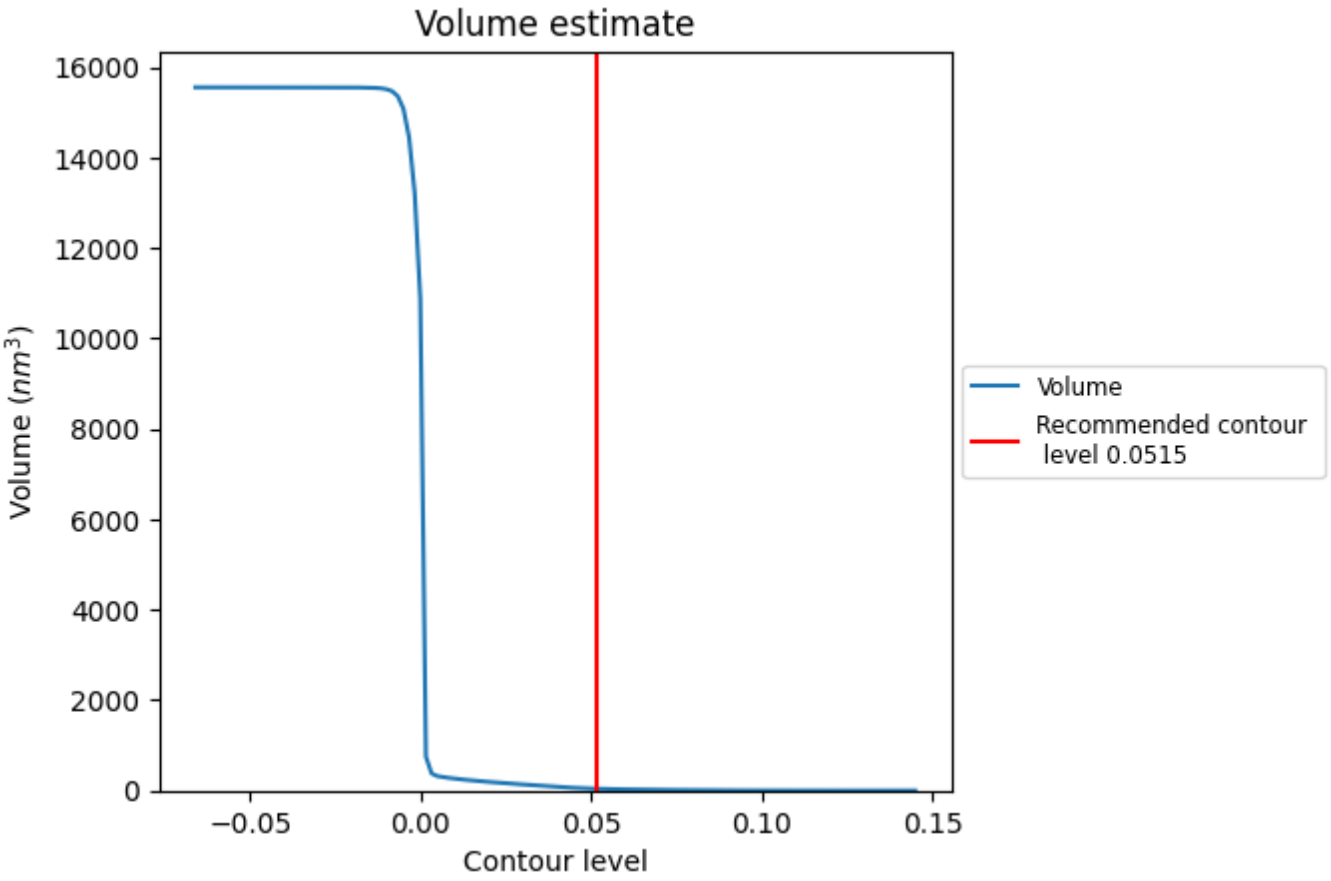
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

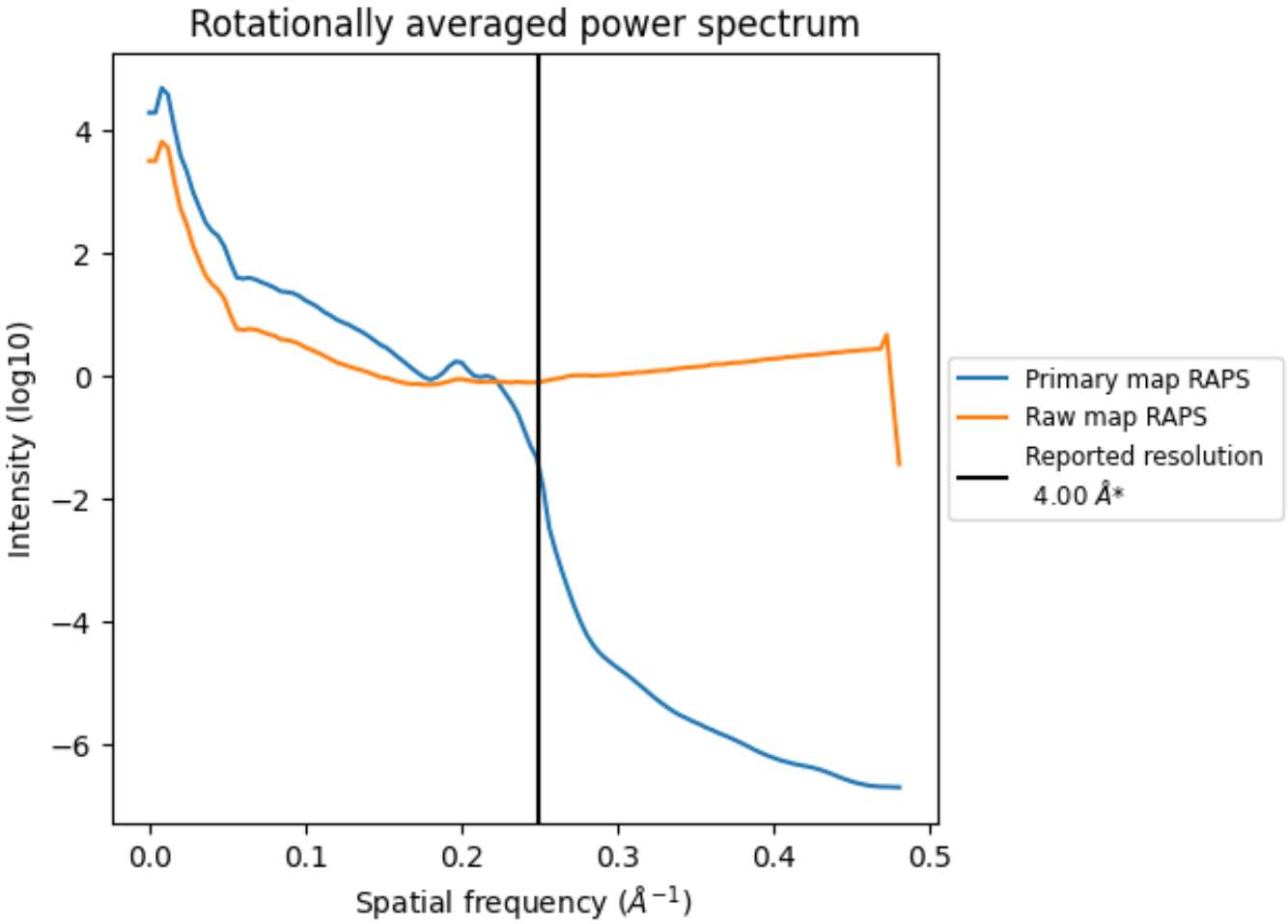
7.2 Volume estimate (i)



The volume at the recommended contour level is 40 nm^3; this corresponds to an approximate mass of 36 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)

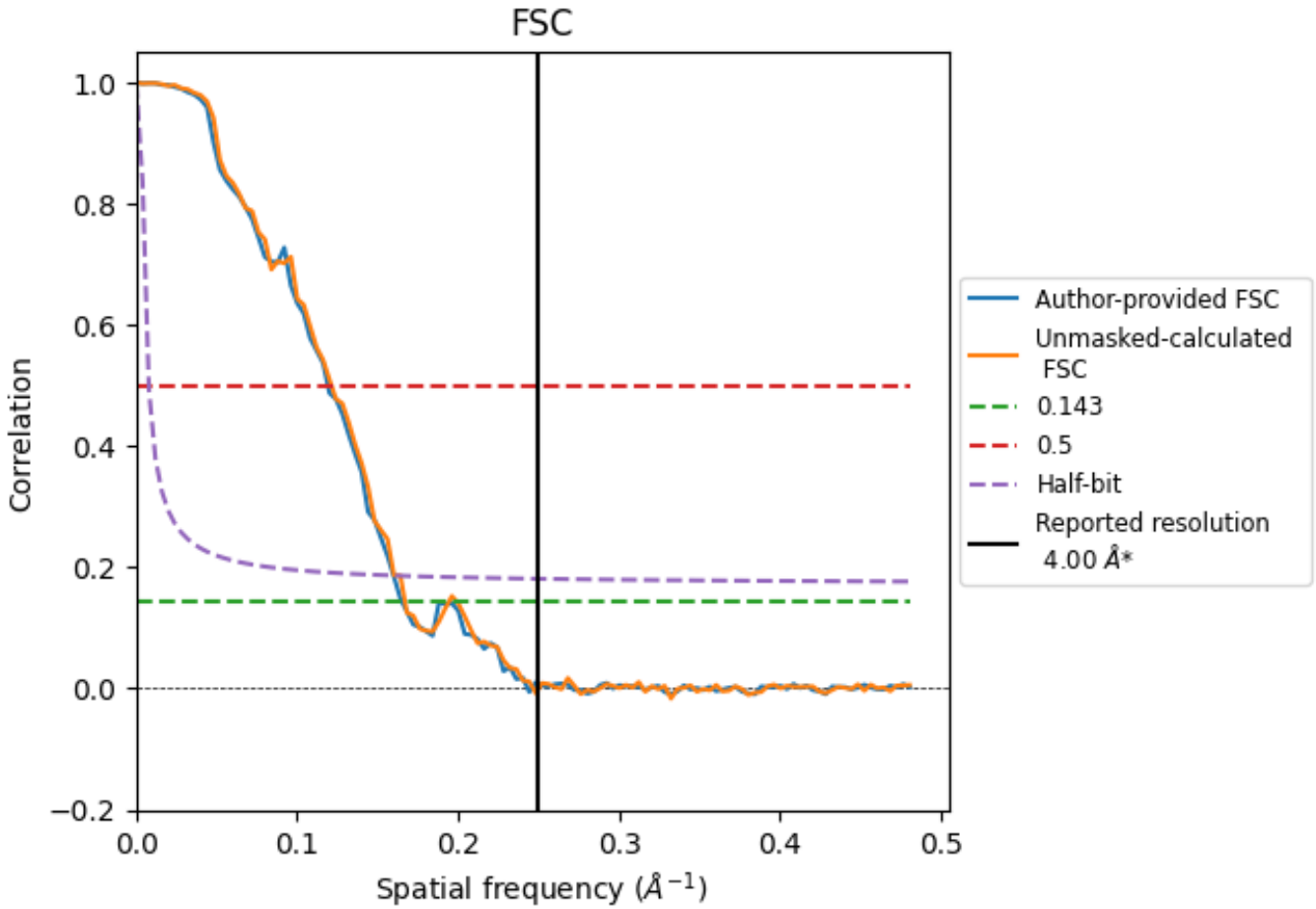


*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	6.05	8.39	6.25
Unmasked-calculated*	5.98	8.24	6.09

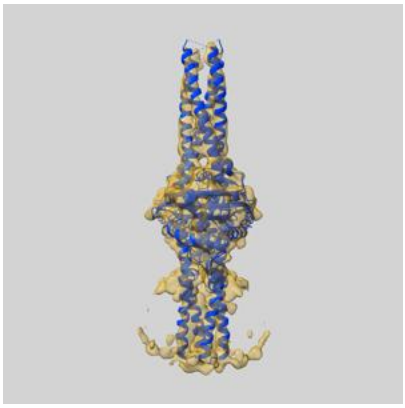
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.05 differs from the reported value 4.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.98 differs from the reported value 4.0 by more than 10 %

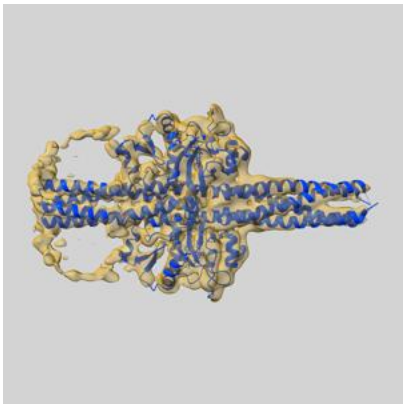
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-58450 and PDB model 31JS. Per-residue inclusion information can be found in section 3 on page 6.

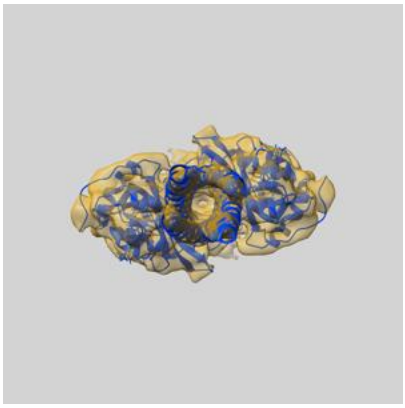
9.1 Map-model overlay



X



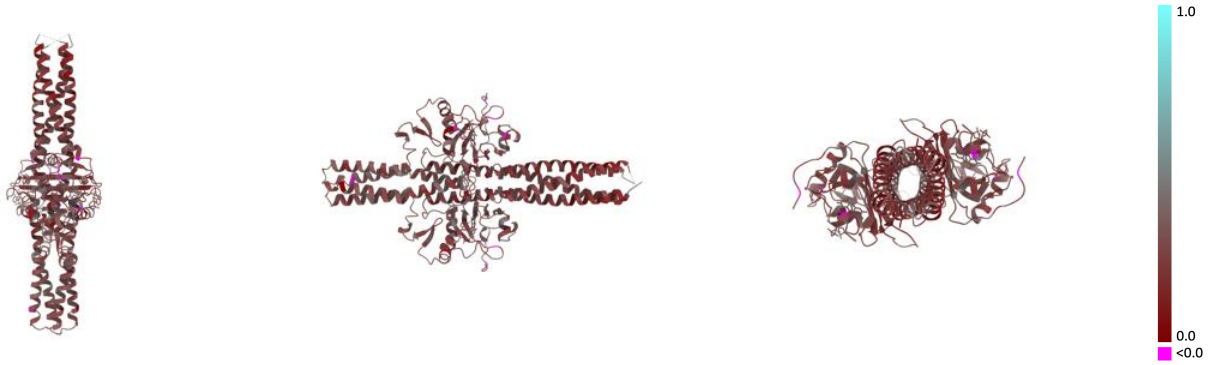
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0515 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.

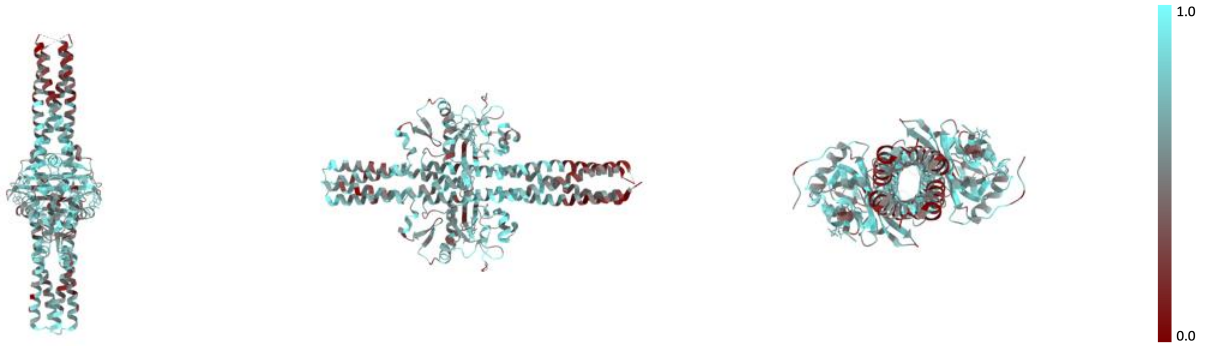
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

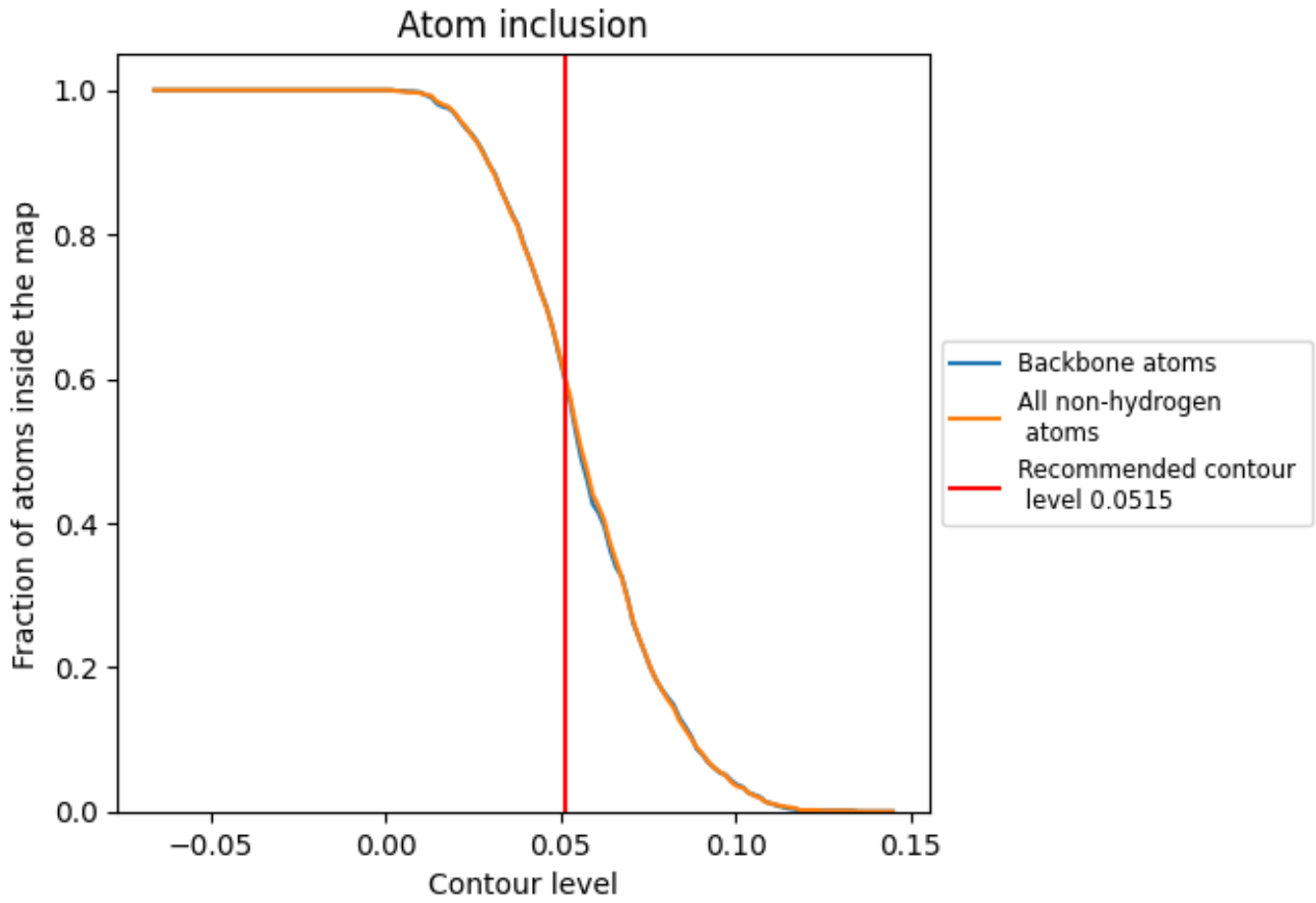
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0515).

9.4 Atom inclusion (i)



At the recommended contour level, 60% of all backbone atoms, 60% 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 (0.0515) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.5970	0.2680
A	0.6110	0.2680
B	0.6150	0.2690