



wwPDB EM Validation Summary Report ⓘ

Aug 30, 2023 – 04:33 pm BST

PDB ID : 8BJA
EMDB ID : EMD-16087
Title : Structure of the human UBR5 Dimer.
Authors : Hodakova, Z.; Grishkovskaya, I.; Haselbach, D.
Deposited on : 2022-11-03
Resolution : 3.00 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.dev50
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

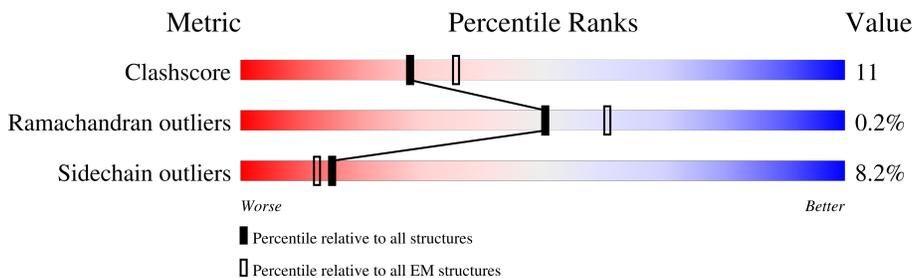
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2830	
1	B	2830	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 25204 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 E3 ubiquitin-protein ligase UBR5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	1638	12897	8178	2239	2384	96	0	0
1	A	1563	12301	7806	2140	2265	90	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	2799	VAL	-	expression tag	UNP O95071
B	2800	GLY	-	expression tag	UNP O95071
B	2801	SER	-	expression tag	UNP O95071
B	2802	ALA	-	expression tag	UNP O95071
B	2803	TRP	-	expression tag	UNP O95071
B	2804	SER	-	expression tag	UNP O95071
B	2805	HIS	-	expression tag	UNP O95071
B	2806	PRO	-	expression tag	UNP O95071
B	2807	GLN	-	expression tag	UNP O95071
B	2808	PHE	-	expression tag	UNP O95071
B	2809	GLU	-	expression tag	UNP O95071
B	2810	LYS	-	expression tag	UNP O95071
B	2811	GLY	-	expression tag	UNP O95071
B	2812	GLY	-	expression tag	UNP O95071
B	2813	GLY	-	expression tag	UNP O95071
B	2814	SER	-	expression tag	UNP O95071
B	2815	GLY	-	expression tag	UNP O95071
B	2816	GLY	-	expression tag	UNP O95071
B	2817	GLY	-	expression tag	UNP O95071
B	2818	SER	-	expression tag	UNP O95071
B	2819	GLY	-	expression tag	UNP O95071
B	2820	GLY	-	expression tag	UNP O95071
B	2821	SER	-	expression tag	UNP O95071
B	2822	ALA	-	expression tag	UNP O95071
B	2823	TRP	-	expression tag	UNP O95071
B	2824	SER	-	expression tag	UNP O95071

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2825	HIS	-	expression tag	UNP O95071
B	2826	PRO	-	expression tag	UNP O95071
B	2827	GLN	-	expression tag	UNP O95071
B	2828	PHE	-	expression tag	UNP O95071
B	2829	GLU	-	expression tag	UNP O95071
B	2830	LYS	-	expression tag	UNP O95071
A	2799	VAL	-	expression tag	UNP O95071
A	2800	GLY	-	expression tag	UNP O95071
A	2801	SER	-	expression tag	UNP O95071
A	2802	ALA	-	expression tag	UNP O95071
A	2803	TRP	-	expression tag	UNP O95071
A	2804	SER	-	expression tag	UNP O95071
A	2805	HIS	-	expression tag	UNP O95071
A	2806	PRO	-	expression tag	UNP O95071
A	2807	GLN	-	expression tag	UNP O95071
A	2808	PHE	-	expression tag	UNP O95071
A	2809	GLU	-	expression tag	UNP O95071
A	2810	LYS	-	expression tag	UNP O95071
A	2811	GLY	-	expression tag	UNP O95071
A	2812	GLY	-	expression tag	UNP O95071
A	2813	GLY	-	expression tag	UNP O95071
A	2814	SER	-	expression tag	UNP O95071
A	2815	GLY	-	expression tag	UNP O95071
A	2816	GLY	-	expression tag	UNP O95071
A	2817	GLY	-	expression tag	UNP O95071
A	2818	SER	-	expression tag	UNP O95071
A	2819	GLY	-	expression tag	UNP O95071
A	2820	GLY	-	expression tag	UNP O95071
A	2821	SER	-	expression tag	UNP O95071
A	2822	ALA	-	expression tag	UNP O95071
A	2823	TRP	-	expression tag	UNP O95071
A	2824	SER	-	expression tag	UNP O95071
A	2825	HIS	-	expression tag	UNP O95071
A	2826	PRO	-	expression tag	UNP O95071
A	2827	GLN	-	expression tag	UNP O95071
A	2828	PHE	-	expression tag	UNP O95071
A	2829	GLU	-	expression tag	UNP O95071
A	2830	LYS	-	expression tag	UNP O95071

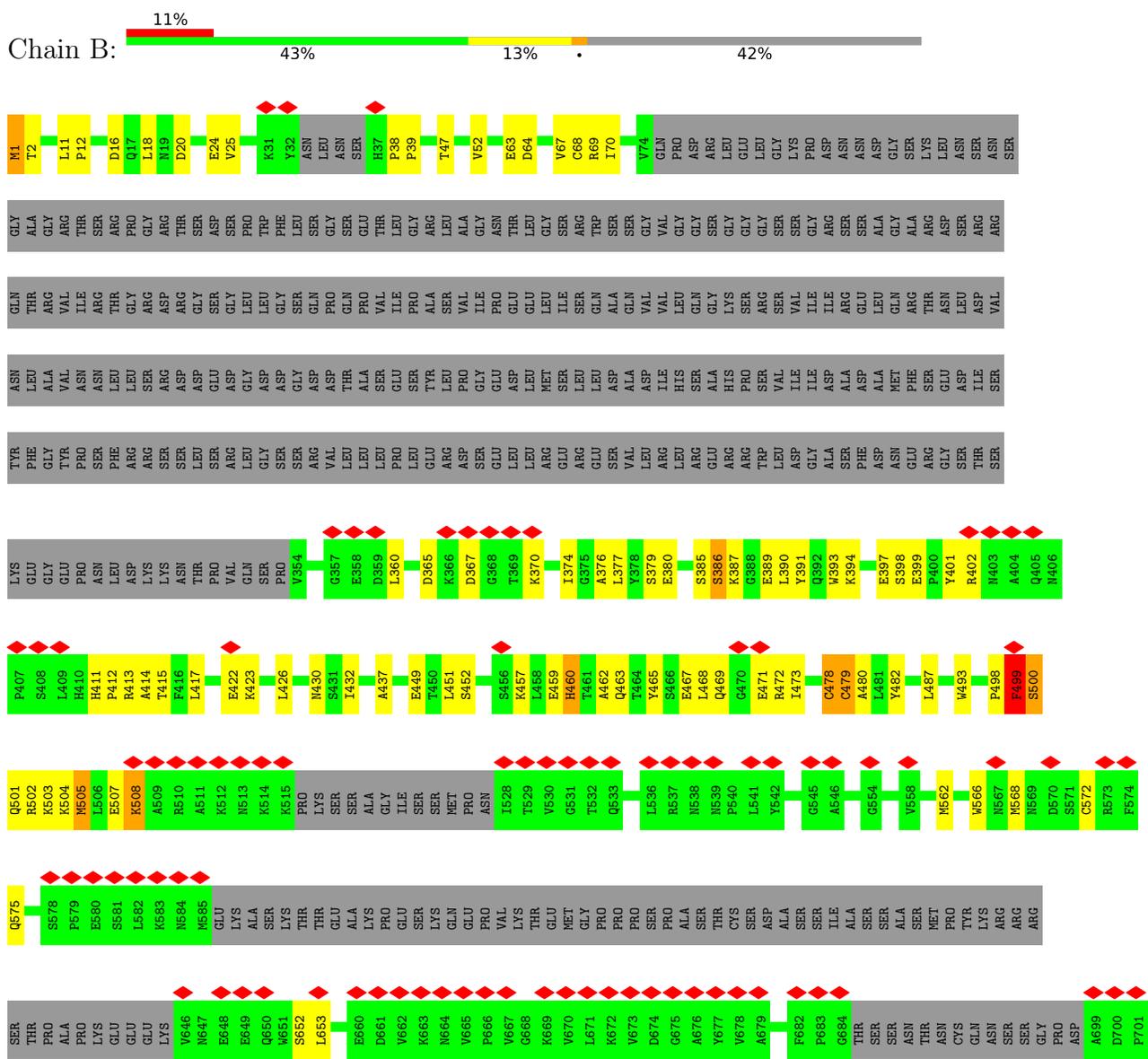
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

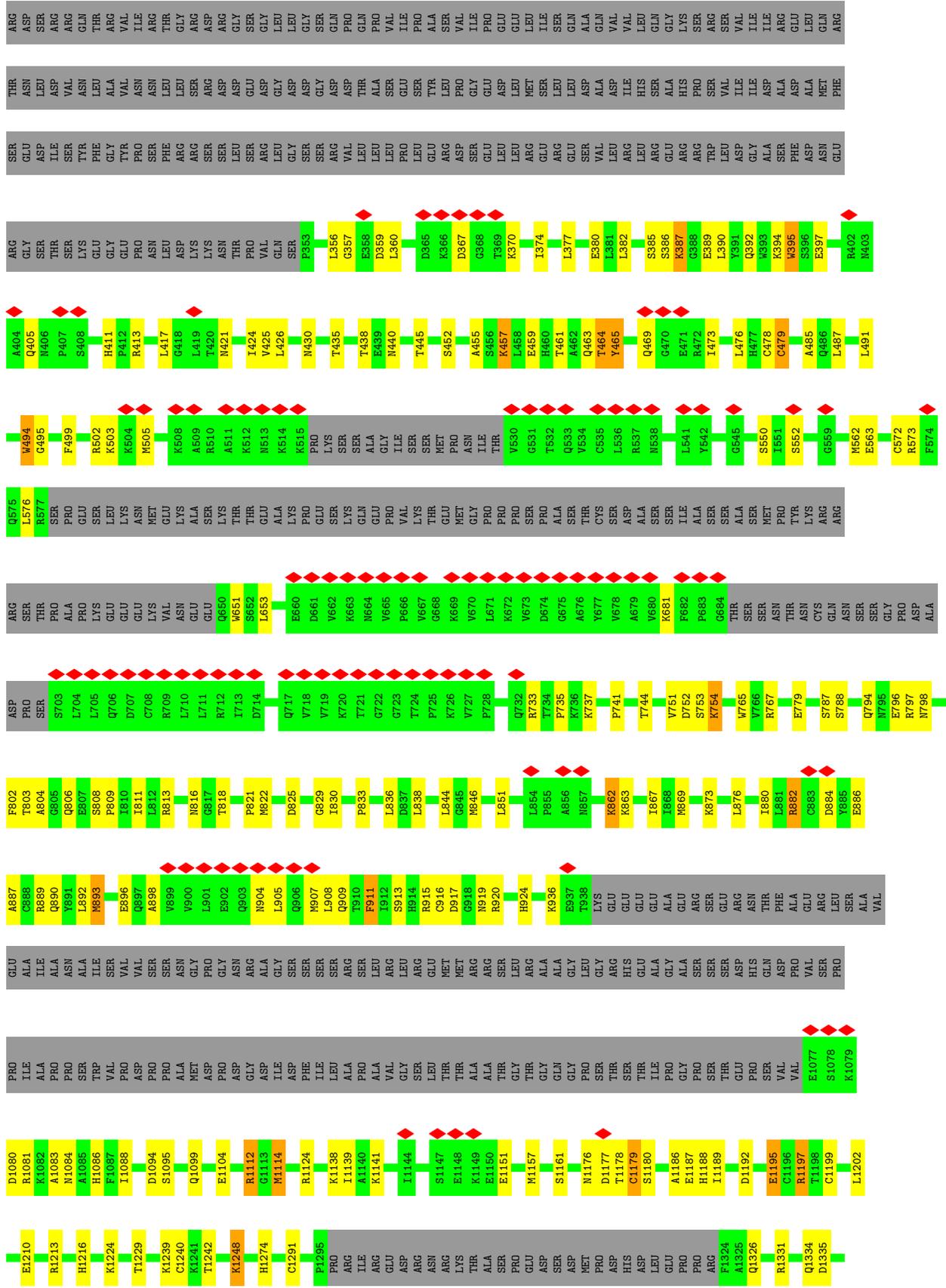
Mol	Chain	Residues	Atoms		AltConf
2	B	3	Total 3	Zn 3	0
2	A	3	Total 3	Zn 3	0

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: E3 ubiquitin-protein ligase UBR5





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	288287	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.330	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.0632	Depositor
Map size (\AA)	446.69998, 446.69998, 446.69998	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.489, 1.489, 1.489	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:
ZN

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	0.29	0/12550	0.55	0/17001
1	B	0.29	0/13155	0.55	0/17813
All	All	0.29	0/25705	0.55	0/34814

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2266	ARG	Sidechain
1	B	2246	ARG	Sidechain
1	B	2248	ARG	Sidechain

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	12301	0	12343	253	0
1	B	12897	0	12962	251	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
All	All	25204	0	25305	497	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 497 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:2656:LYS:HA	1:A:2659:LEU:HB2	1.54	0.89
1:A:2709:GLN:N	1:A:2709:GLN:HE21	1.71	0.88
1:B:1216:HIS:HD2	1:B:1219:HIS:ND1	1.72	0.85
1:B:1796:SER:HG	1:B:1957:TRP:HD1	1.22	0.84
1:B:1961:MET:HG3	1:B:2171:PRO:HB3	1.60	0.83

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	1533/2830 (54%)	1456 (95%)	75 (5%)	2 (0%)	51 85
1	B	1604/2830 (57%)	1506 (94%)	93 (6%)	5 (0%)	41 76
All	All	3137/5660 (55%)	2962 (94%)	168 (5%)	7 (0%)	50 82

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	462	ALA
1	B	499	PHE
1	B	873	LYS
1	A	41	ASN
1	A	2204	VAL

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	1366/2439 (56%)	1258 (92%)	108 (8%)	12	41
1	B	1438/2439 (59%)	1316 (92%)	122 (8%)	10	38
All	All	2804/4878 (58%)	2574 (92%)	230 (8%)	15	39

5 of 230 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2689	MET
1	A	2673	GLU
1	A	653	LEU
1	A	2656	LYS
1	A	2231	LYS

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	890	GLN
1	A	1870	HIS
1	A	1962	ASN
1	B	411	HIS
1	B	405	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.

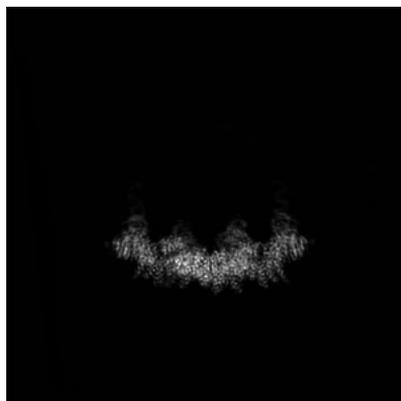
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16087. These allow visual inspection of the internal detail of the map and identification of artifacts.

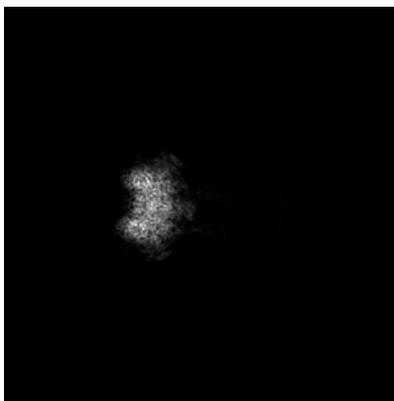
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

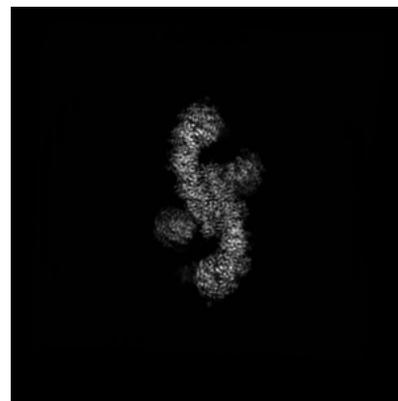
6.1.1 Primary map



X

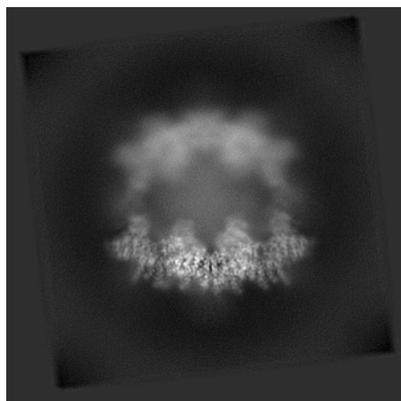


Y

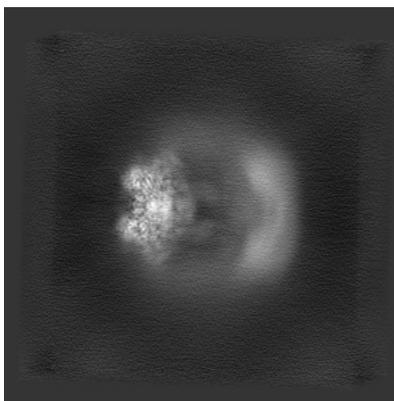


Z

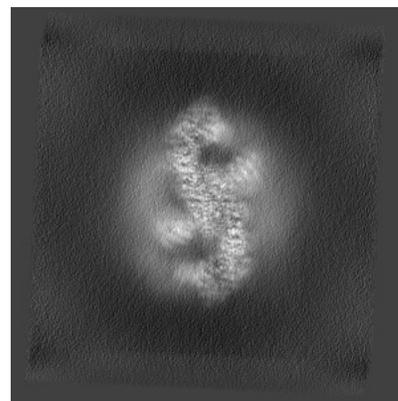
6.1.2 Raw map



X



Y

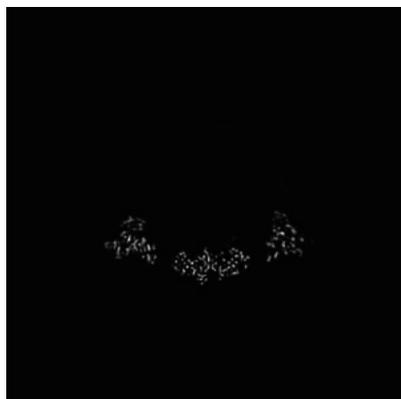


Z

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

6.2 Central slices [i](#)

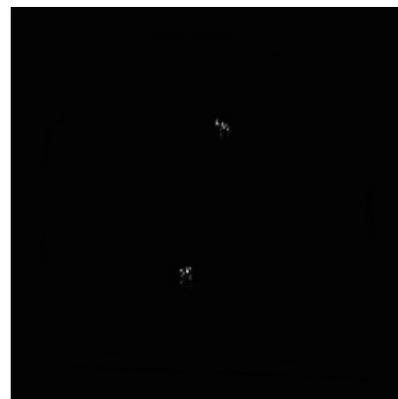
6.2.1 Primary map



X Index: 150

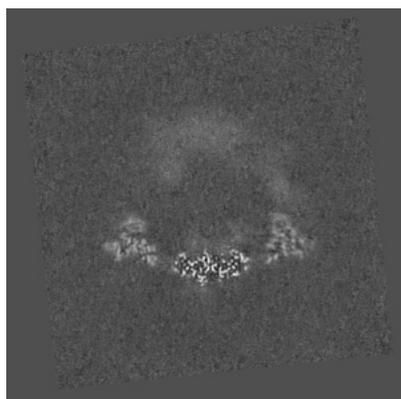


Y Index: 150

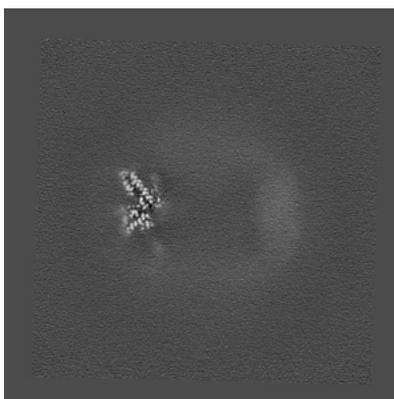


Z Index: 150

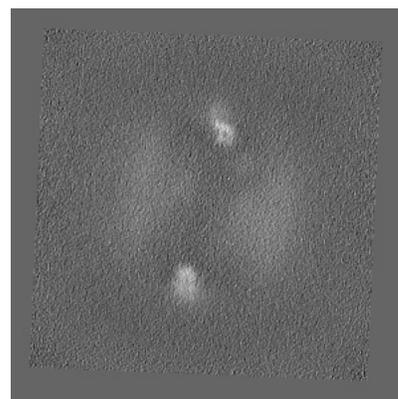
6.2.2 Raw map



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: 135

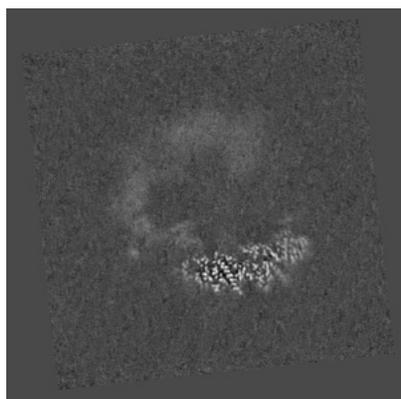


Y Index: 172

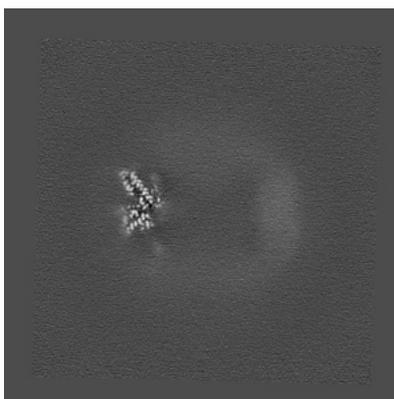


Z Index: 107

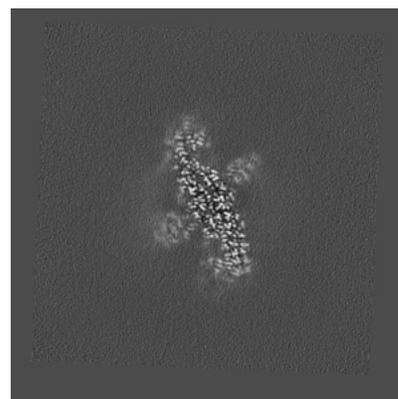
6.3.2 Raw map



X Index: 137



Y Index: 150

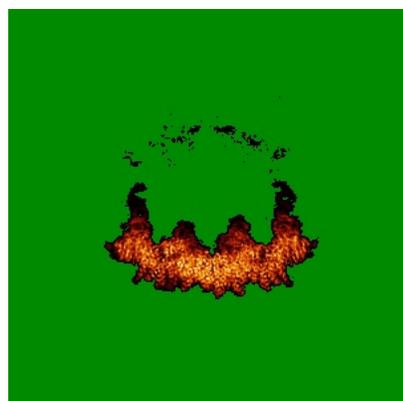


Z Index: 107

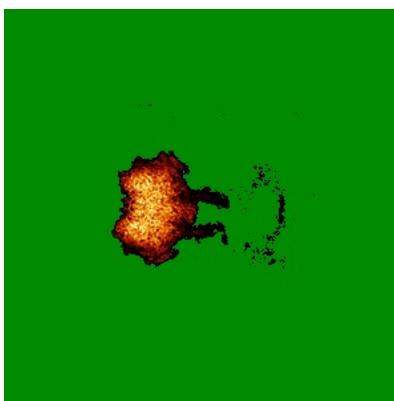
The images above show the largest variance slices of the map in three orthogonal directions.

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

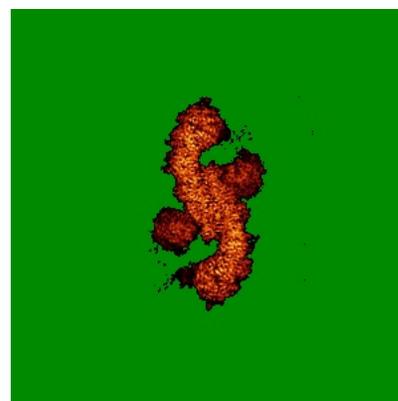
6.4.1 Primary map



X

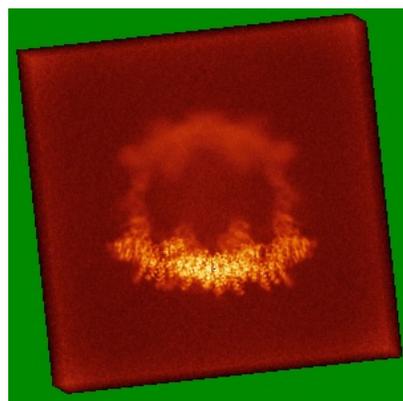


Y

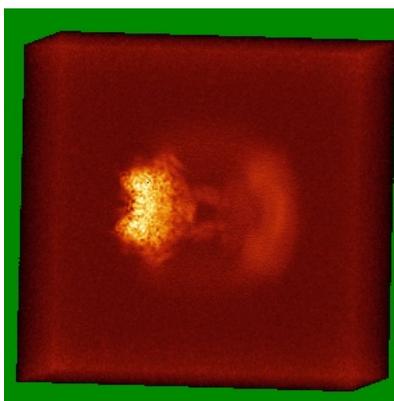


Z

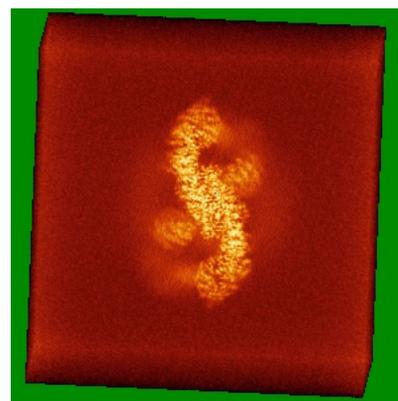
6.4.2 Raw map



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.

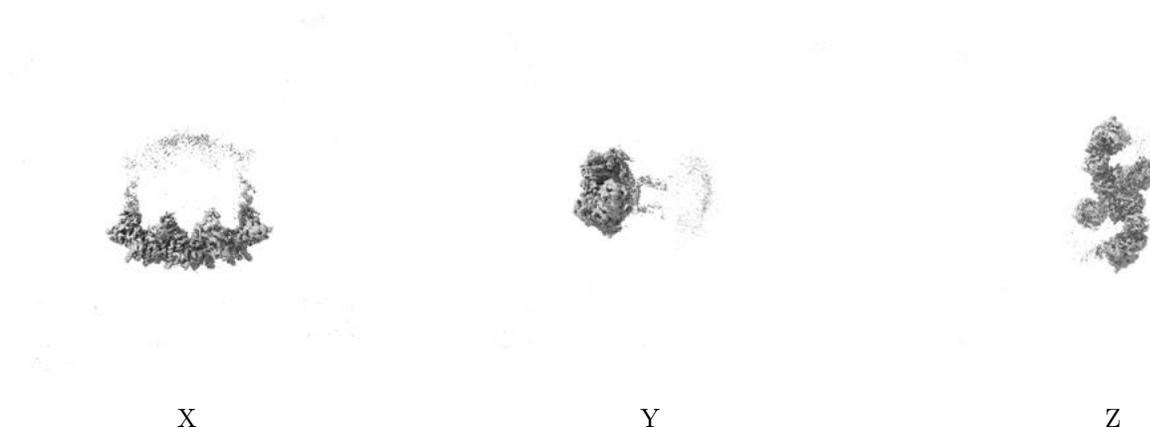
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0632. 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



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.

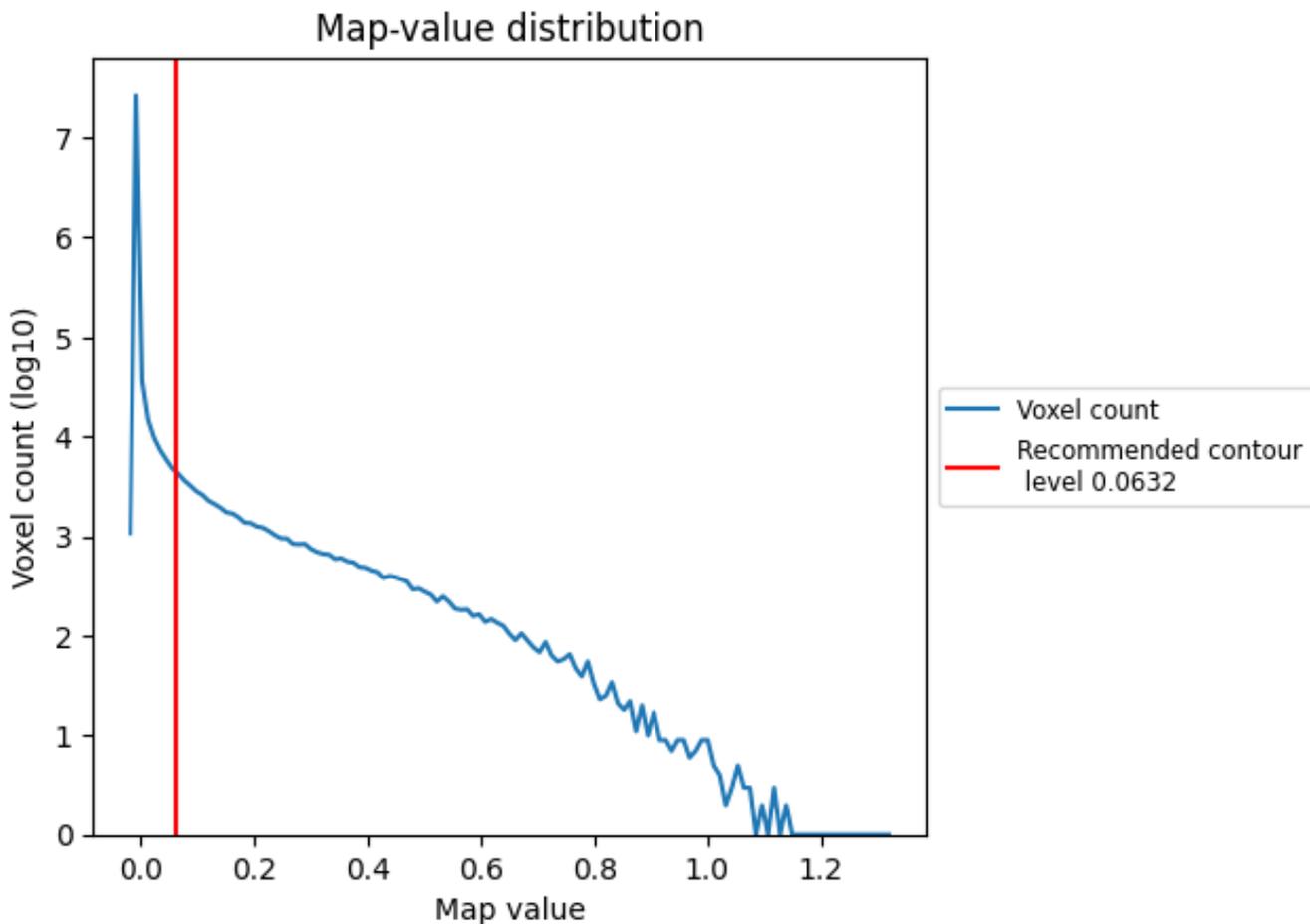
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

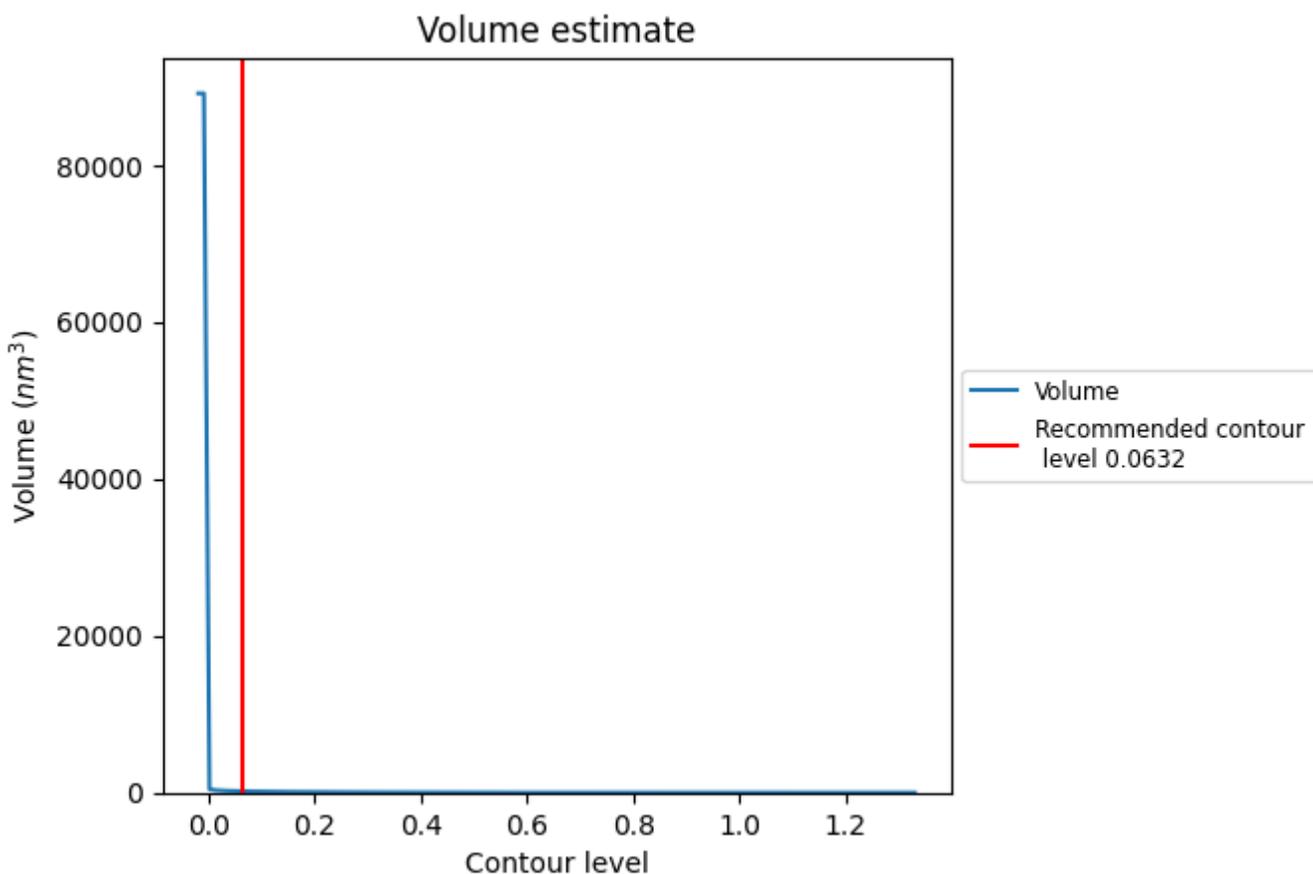
This section contains the results of statistical analysis of the map.

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.

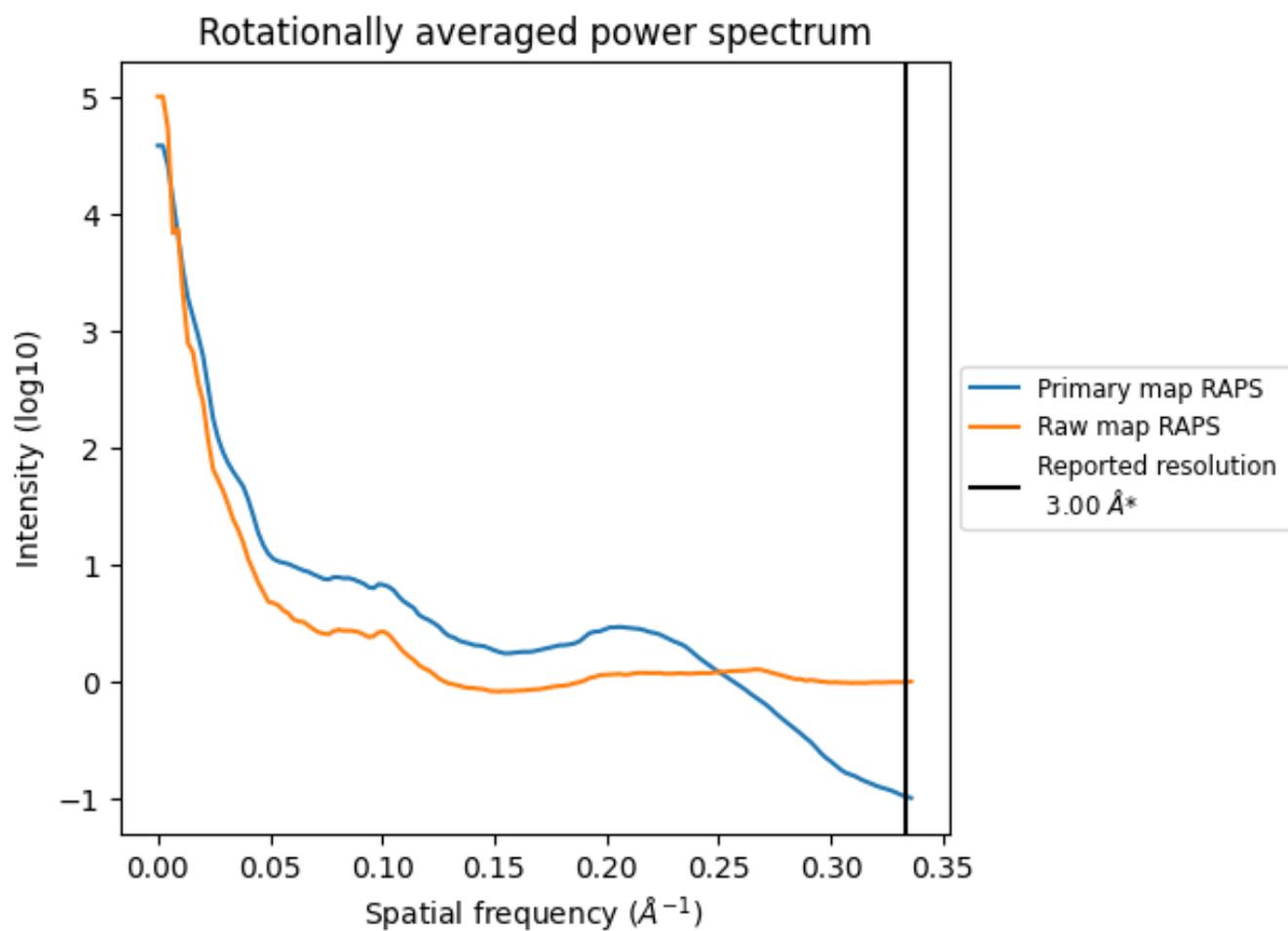
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm^3 ; this corresponds to an approximate mass of 162 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](#)

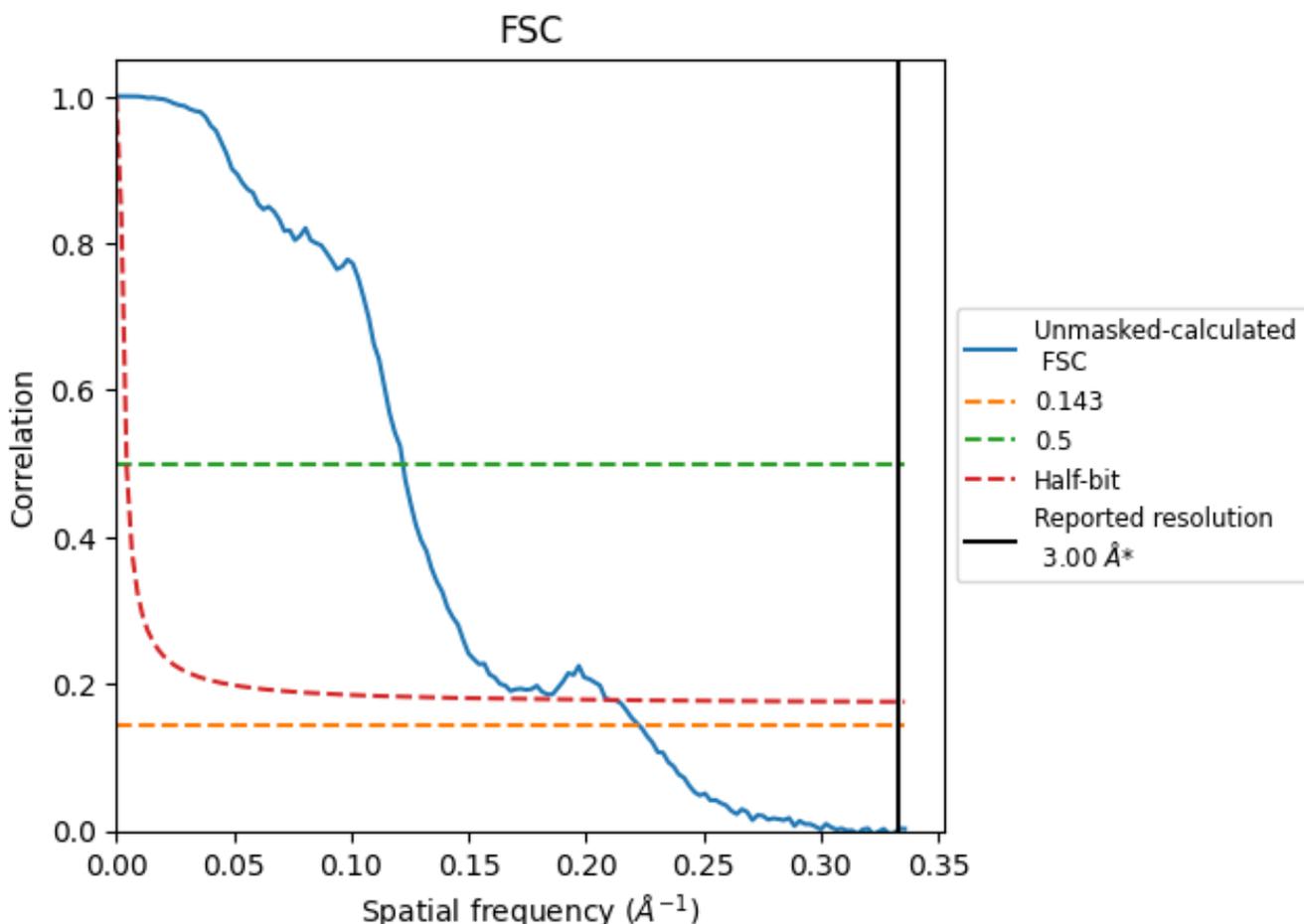


*Reported resolution corresponds to spatial frequency of 0.333\AA^{-1}

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.333\AA^{-1}

8.2 Resolution estimates [i](#)

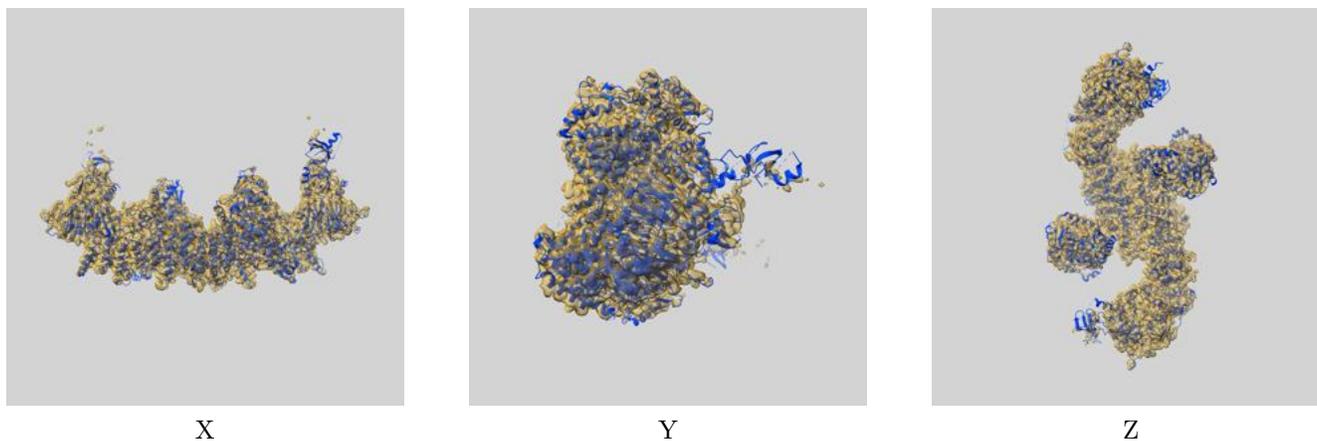
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	3.00	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.49	8.20	4.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.5 CUT-OFF 8.20 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

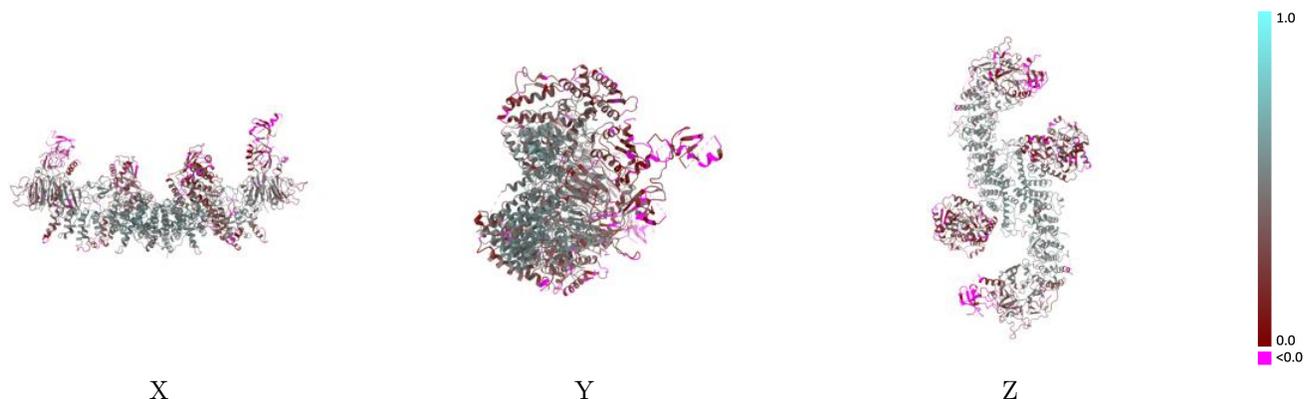
This section contains information regarding the fit between EMDB map EMD-16087 and PDB model 8BJA. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



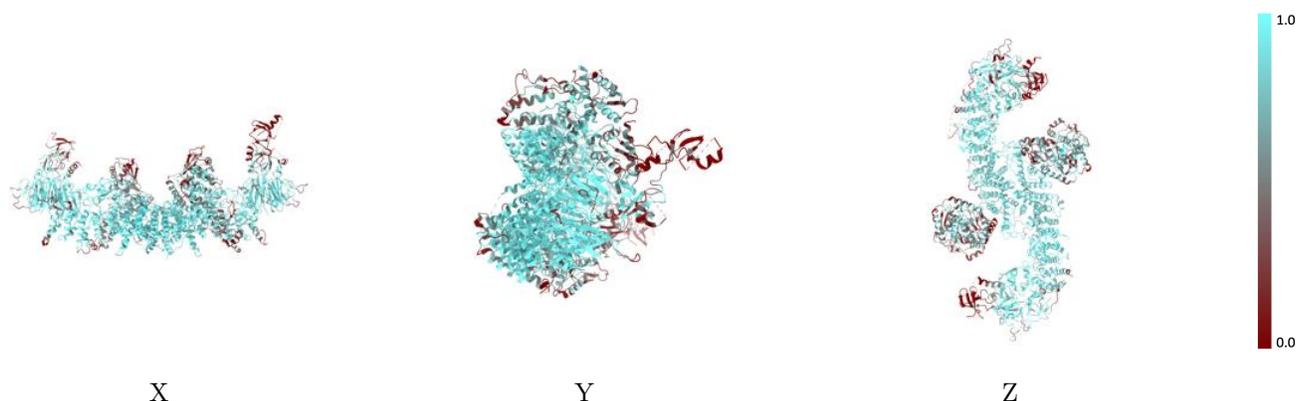
The images above show the 3D surface view of the map at the recommended contour level 0.0632 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



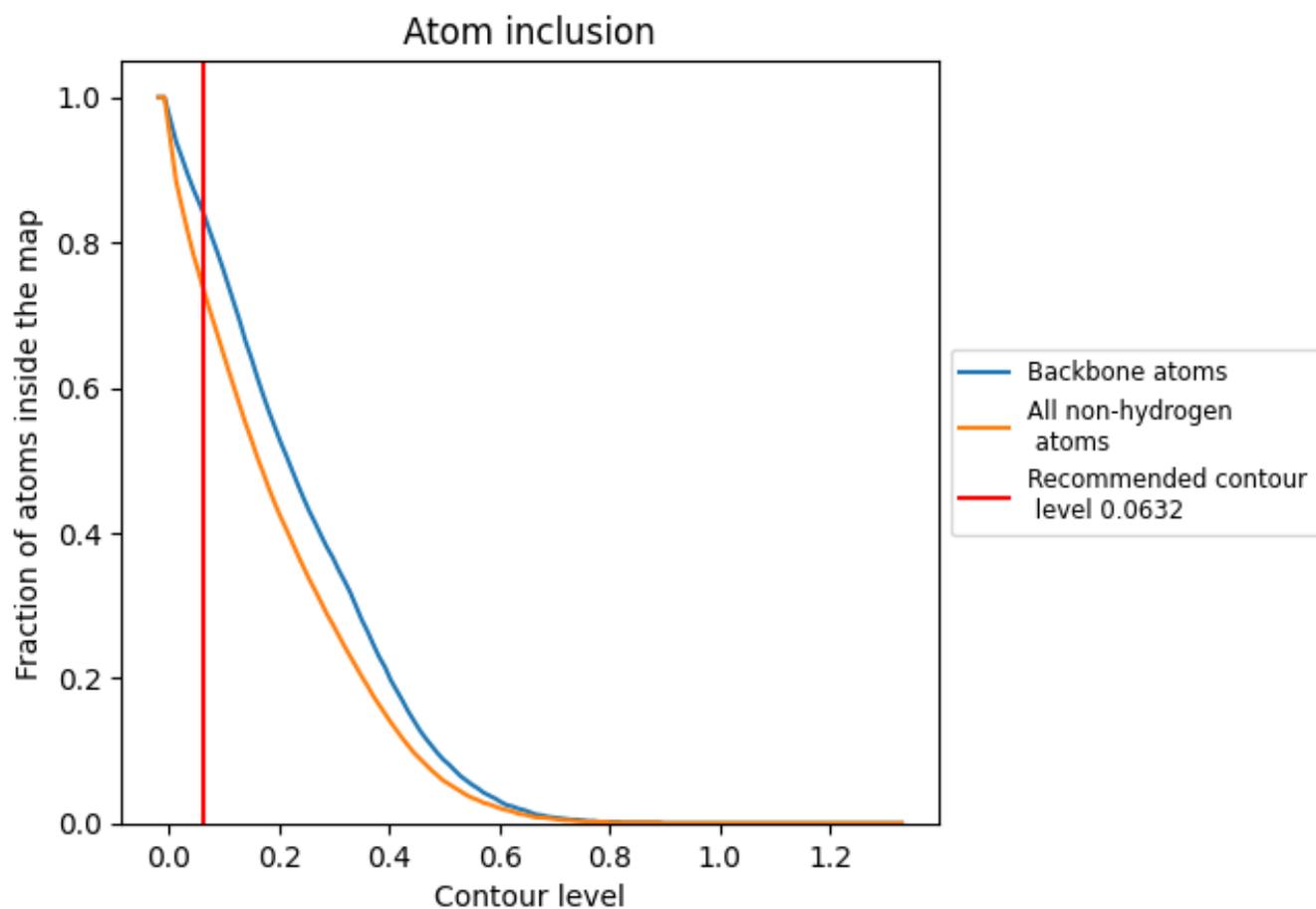
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0632).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.0632) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7350	 0.3630
A	 0.7500	 0.3700
B	 0.7200	 0.3570

