



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:39 PM UTC

PDB ID : 7YIH / pdb_00007yih
EMDB ID : EMD-33859
Title : Human KCNH5 open state
Authors : Zhang, M.F.
Deposited on : 2022-07-16
Resolution : 3.50 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.dev132
MolProbity : 4-5-2 with Phenix2.0
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

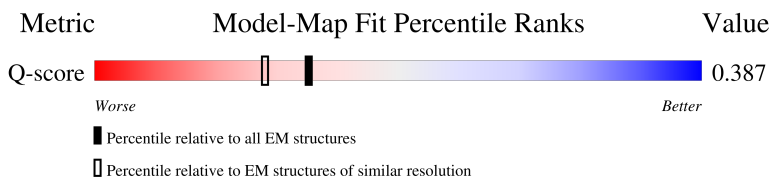
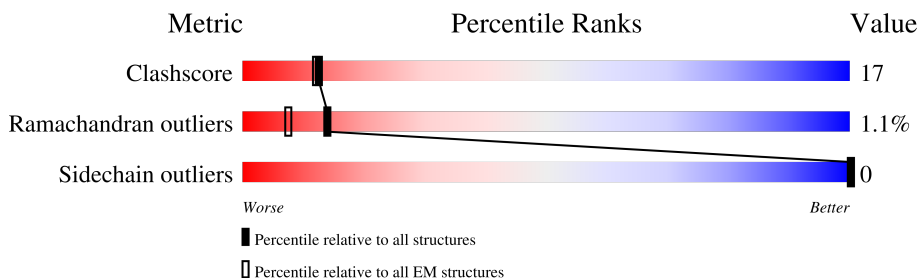
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

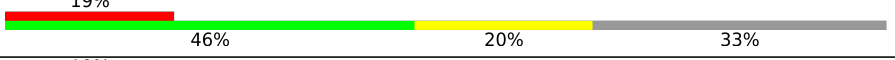
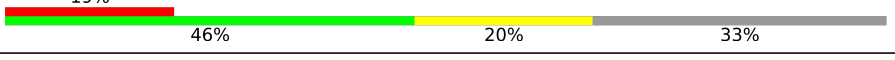
The reported resolution of this entry is 3.50 Å.

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	988	
1	B	988	
1	C	988	
1	D	988	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21321 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 Potassium voltage-gated channel subfamily H member 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	660	Total	C	N	O	S	0	0
			5328	3449	886	961	32		
1	B	660	Total	C	N	O	S	0	0
			5328	3449	886	961	32		
1	C	660	Total	C	N	O	S	0	0
			5328	3449	886	961	32		
1	D	660	Total	C	N	O	S	0	0
			5328	3449	886	961	32		

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	5	Total	K	0
			5	5	

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	O	0
			1	1	
3	B	1	Total	O	0
			1	1	
3	C	1	Total	O	0
			1	1	
3	D	1	Total	O	0
			1	1	

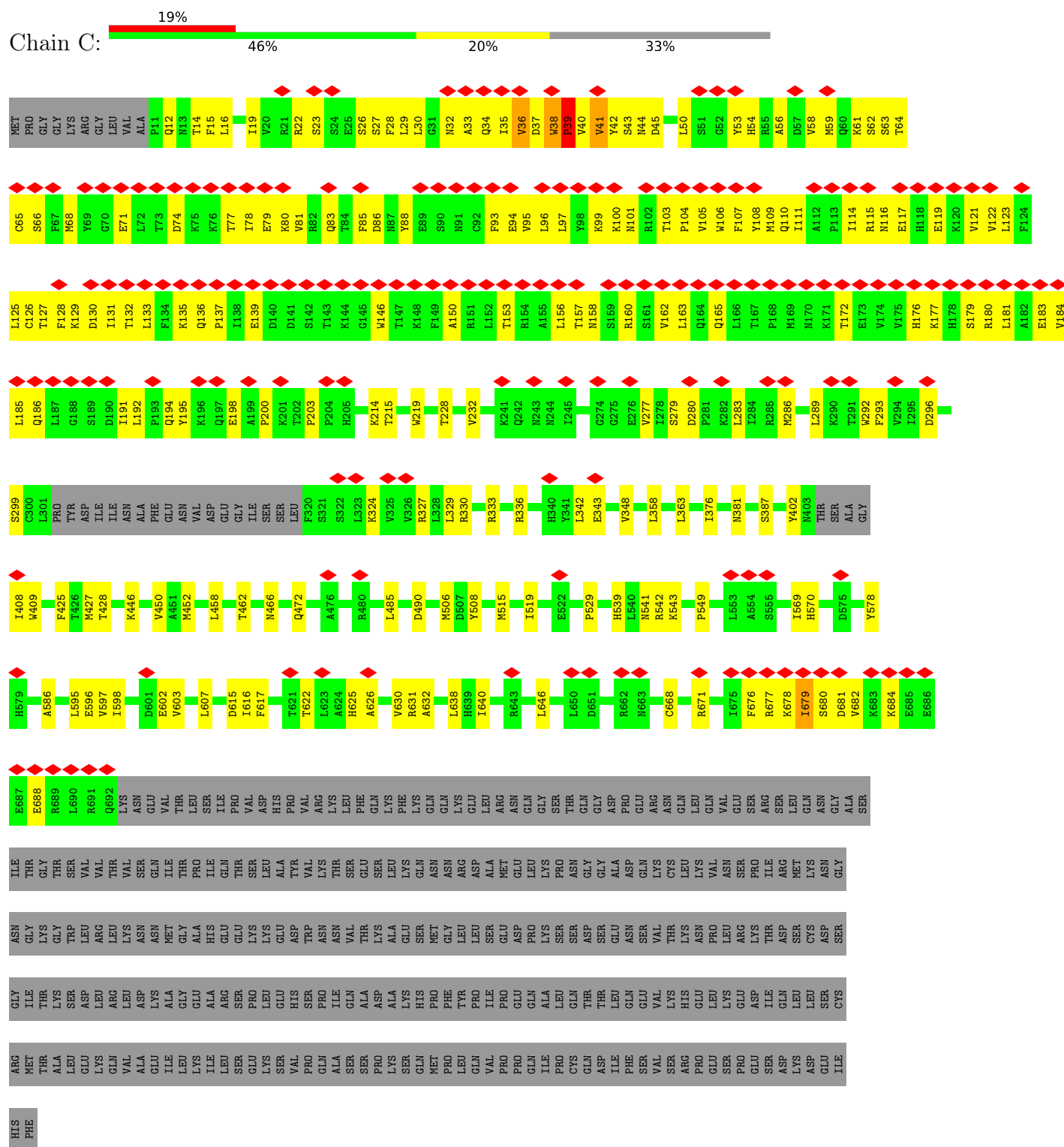
THR	THR
LYS	ALA
SER	LEU
ASP	GLY
LEU	LYS
ARG	GLN
LEU	VAL
LEU	ALA
ASP	GLU
LYS	ILE
ALA	LEU
ALA	LYS
GLY	GLY
GLU	GLU
GLY	LEU
ARG	LYS
ARG	ILE
ALA	LEU
ARG	LEU
PRO	SER
PRO	GLU
GLN	LYS
GLN	VAL
ASP	PRO
ALA	THR
LYS	LEU
LYS	GLN
HIS	VAL
SER	ILE
SER	PRO
PRO	GLN
ILE	ALA
ALA	ILE
GLN	LEU
ASP	GLN
ALA	THR
ALA	THR
LYS	ILE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

● Molecule 1: Potassium voltage-gated channel subfamily H member 5



MET	S66	C126	Q186	I295	W403	E885	ASN	ASP	SER	GLY	ALA
PRO	F67	T127	L187	D296	THR	E886	GLY	ARG	SER	ILE	THR
GLY	M68	F128	G188	S299	ALA	E887	GLY	THR	THR	THR	THR
LYS	Y69	D130	S189	C300	GLY	E888	LYS	THR	SER	THR	THR
ARG	G70	I131	D190	L301	W408	R689	TRP	VAL	SER	VAL	VAL
GLY	E71	T132	L191	PRO	I409	L690	LEU	ARG	ASP	VAL	VAL
LEU	L72	L133	L192	TYR	M427	R691	LEU	GLN	LEU	GLN	VAL
VAL	T73	T134	F193	ILE	K446	Q692	VAL	LEU	VAL	VAL	VAL
ALA	D74	Q135	Q194	ILE	K446	LYS	SER	LEU	SER	SER	ALA
P11	K75	K135	Y195	ASN	V450	D601	ASN	GLY	GLN	GLN	GLY
Q12	K76	Q136	K196	ALA	A451	E602	GLY	VAL	ILE	ILE	GLY
T14	T77	P137	Q197	PHE	M452	V603	THR	THR	THR	THR	ALA
F15	T77	T138	E198	GLU	L458	L607	LEU	LEU	PRO	PRO	LYS
I19	T78	E139	A199	ASN	L458	L607	LEU	LEU	ALA	ALA	ALA
V20	E79	D140	P200	VAL	T462	D615	SER	ILE	GLY	GLY	GLY
R21	K80	D141	K201	ASP	N466	I616	ILE	PRO	GLY	GLY	GLY
R22	V81	T202	T202	GLY	Q472	F617	THR	VAL	THR	THR	THR
S23	R82	S142	P203	ILE	N466	T621	ASP	VAL	SER	SER	SER
S24	Q83	T143	P204	SER	Q472	T622	HIS	THR	THR	THR	THR
E25	T84	K144	H205	LEU	A476	L623	PRO	VAL	VAL	VAL	VAL
S26	F85	G145	K214	ARG	A476	A624	VAL	GLY	GLY	GLY	GLY
S27	D86	W146	S321	SER	R480	H625	THR	LEU	THR	THR	THR
F28	R87	T147	S322	LEU	L485	A626	LYS	LEU	GLY	GLY	GLY
L29	Y88	F148	K323	GLY	D490	V630	LYS	GLY	GLY	GLY	GLY
L30	E89	K148	K324	THR	D490	R631	LYS	LEU	LEU	LEU	LEU
PRO	S90	A150	V326	THR	M506	A632	LYS	GLY	GLY	GLY	GLY
PRO	N91	R151	L327	THR	D507	L638	LYS	LEU	LEU	LEU	LEU
VAL	C92	L152	L328	THR	Y508	H639	GLY	LEU	LEU	LEU	LEU
PRO	F93	T153	L329	THR	M515	I640	GLY	LEU	LEU	LEU	LEU
GLY	I35	R154	R330	THR	I519	R643	GLY	LEU	LEU	LEU	LEU
GLN	V36	A155	R333	THR	E522	L646	GLY	LEU	LEU	LEU	LEU
ILE	D37	L156	R336	THR	P529	L650	GLY	LEU	LEU	LEU	LEU
LEU	W38	L157	K337	THR	H539	D651	GLY	LEU	LEU	LEU	LEU
CTG	P39	T157	L338	THR	N541	R662	GLY	LEU	LEU	LEU	LEU
GLN	V40	K99	D339	THR	R542	N663	GLY	LEU	LEU	LEU	LEU
THR	V41	K100	H340	THR	K543	C668	GLY	LEU	LEU	LEU	LEU
THR	Y42	S159	Y341	THR	P549	R671	GLY	LEU	LEU	LEU	LEU
ILE	S43	R160	L342	THR	L553	I675	GLY	LEU	LEU	LEU	LEU
PHE	N44	S161	E343	THR	A554	F676	GLY	LEU	LEU	LEU	LEU
SER	D45	V162	L376	THR	S555	R677	GLY	LEU	LEU	LEU	LEU
VAL	L50	L163	I381	THR	I569	K678	GLY	LEU	LEU	LEU	LEU
SER	S51	Q165	V348	THR	H570	I679	GLY	LEU	LEU	LEU	LEU
LYS	S52	Q166	L351	THR	D575	S680	GLY	LEU	LEU	LEU	LEU
GLY	Y53	L166	L363	THR	D575	D681	GLY	LEU	LEU	LEU	LEU
ASP	H54	T167	L376	THR	D575	V682	GLY	LEU	LEU	LEU	LEU
GLN	R55	P168	I376	THR	D575	K683	GLY	LEU	LEU	LEU	LEU
ASP	A56	M169	N381	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
LYS	D57	M170	M286	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
ASP	V58	K171	M286	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
LEU	M59	P113	M286	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
SER	P60	I114	L289	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
GLY	K61	R115	E173	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
PRO	S62	N116	E173	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
GLY	S63	E117	E173	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
ASP	T64	H118	H176	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
ASP	C65	E119	K177	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
GLY		K120	E119	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
SER		V121	E119	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
CYS		V122	E119	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
ARG		L123	E119	THR	D575	K684	GLY	LEU	LEU	LEU	LEU
MET		L125	E119	THR	D575	K684	GLY	LEU	LEU	LEU	LEU

• Molecule 1: Potassium voltage-gated channel subfamily H member 5



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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63387	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.386	Depositor
Minimum map value	-1.609	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	339.59998, 339.59998, 339.59998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8489999, 0.8489999, 0.8489999	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.18	0/5451	0.46	2/7396 (0.0%)
1	B	0.18	0/5451	0.46	2/7396 (0.0%)
1	C	0.18	0/5451	0.46	2/7396 (0.0%)
1	D	0.18	0/5451	0.46	2/7396 (0.0%)
All	All	0.18	0/21804	0.46	8/29584 (0.0%)

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	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	39	PRO	N-CA-C	5.62	124.04	112.47
1	B	39	PRO	N-CA-C	5.62	124.04	112.47
1	C	39	PRO	N-CA-C	5.62	124.04	112.47
1	D	39	PRO	N-CA-C	5.62	124.04	112.47
1	A	549	PRO	CA-N-CD	-5.20	104.72	112.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	39	PRO	Peptide
1	A	679	ILE	Peptide
1	B	39	PRO	Peptide
1	B	679	ILE	Peptide
1	C	39	PRO	Peptide

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	5328	0	5364	204	0
1	B	5328	0	5364	209	0
1	C	5328	0	5364	207	0
1	D	5328	0	5364	210	0
2	A	5	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	21321	0	21456	718	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 17.

The worst 5 of 718 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:C:36:VAL:HB	1:D:677:ARG:HB3	1.43	1.00
1:A:677:ARG:HB3	1:D:36:VAL:HB	1.43	1.00
1:B:36:VAL:HB	1:C:677:ARG:HB3	1.43	1.00
1:A:36:VAL:HB	1:B:677:ARG:HB3	1.43	0.98
1:B:33:ALA:HA	1:C:680:SER:H	1.32	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	654/988 (66%)	556 (85%)	91 (14%)	7 (1%)	11	43
1	B	654/988 (66%)	556 (85%)	91 (14%)	7 (1%)	11	43
1	C	654/988 (66%)	556 (85%)	91 (14%)	7 (1%)	11	43
1	D	654/988 (66%)	556 (85%)	91 (14%)	7 (1%)	11	43
All	All	2616/3952 (66%)	2224 (85%)	364 (14%)	28 (1%)	14	43

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	VAL
1	A	38	TRP
1	A	39	PRO
1	A	387	SER
1	B	36	VAL

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	595/888 (67%)	595 (100%)	0	100	100
1	B	595/888 (67%)	595 (100%)	0	100	100
1	C	595/888 (67%)	595 (100%)	0	100	100
1	D	595/888 (67%)	595 (100%)	0	100	100
All	All	2380/3552 (67%)	2380 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	391	GLN
1	C	663	ASN
1	D	663	ASN
1	D	287	ASN
1	B	287	ASN

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 5 ligands modelled in this entry, 5 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 ⓘ

There are no chain breaks in this entry.

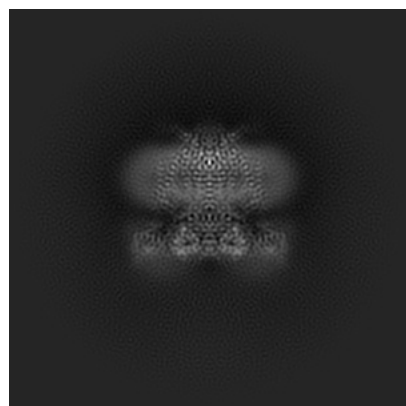
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33859. These allow visual inspection of the internal detail of the map and identification of artifacts.

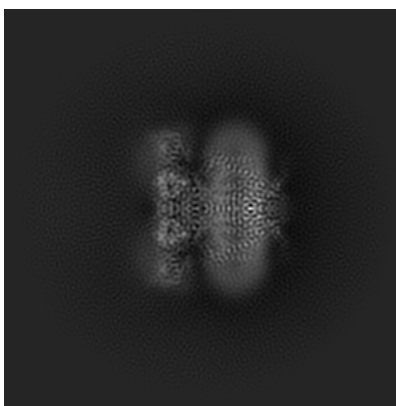
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

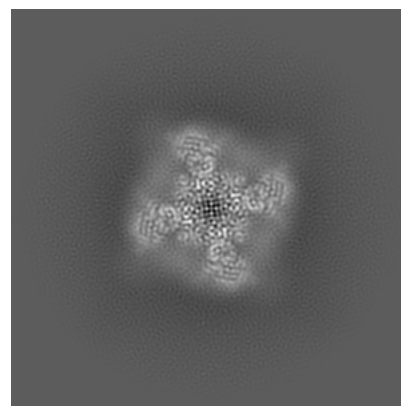
6.1.1 Primary map



X

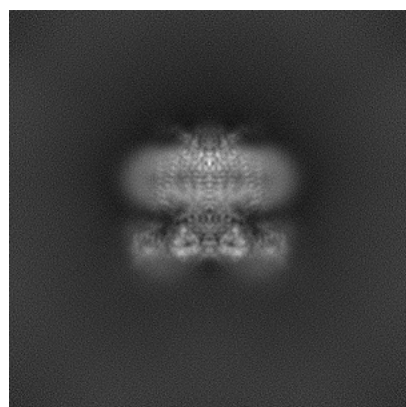


Y

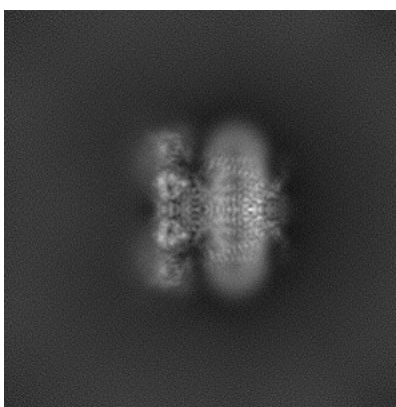


Z

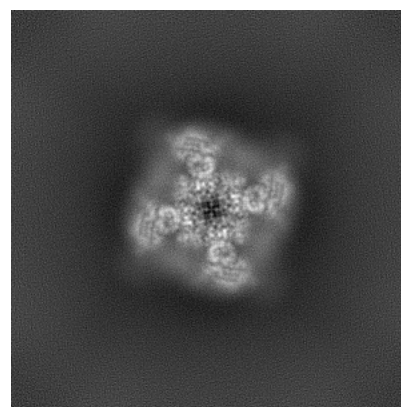
6.1.2 Raw map



X



Y

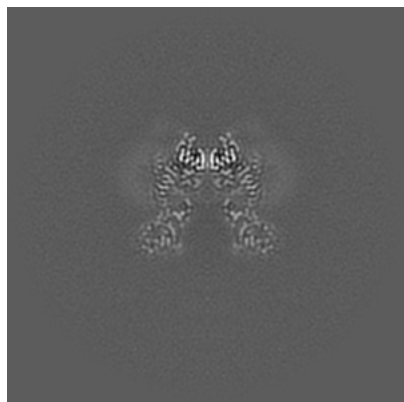


Z

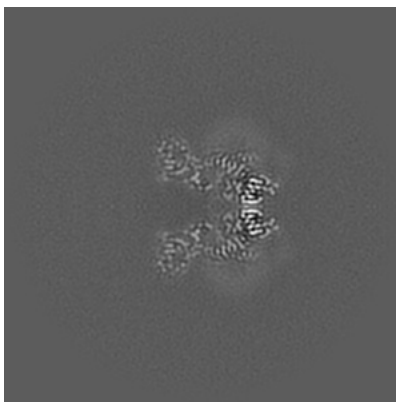
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

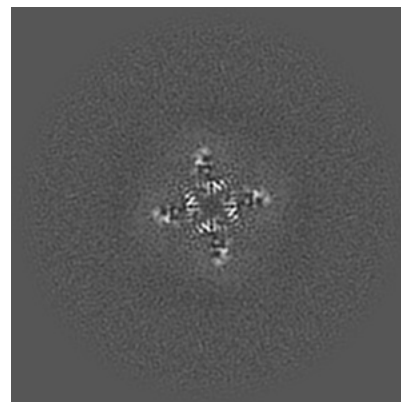
6.2.1 Primary map



X Index: 200

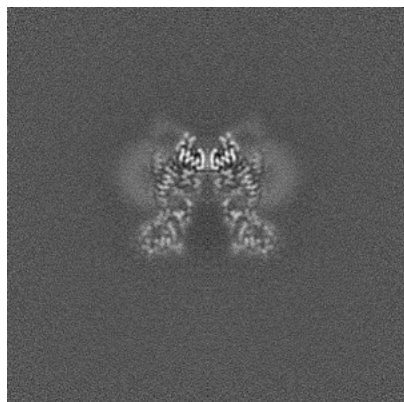


Y Index: 200

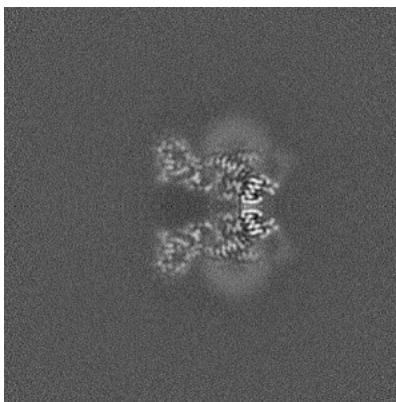


Z Index: 200

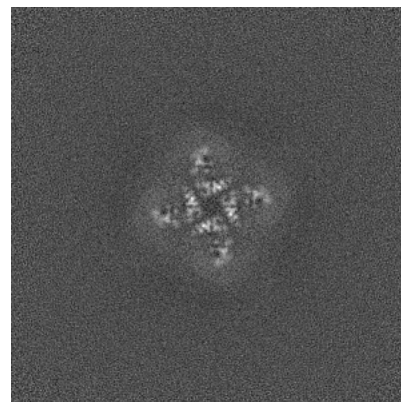
6.2.2 Raw map



X Index: 200



Y Index: 200

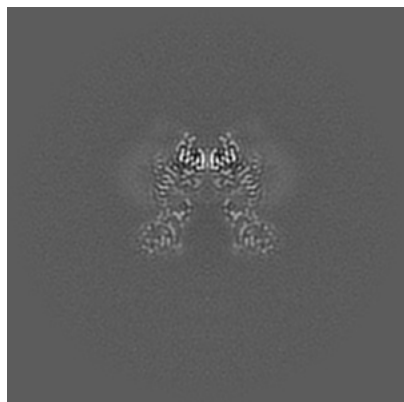


Z Index: 200

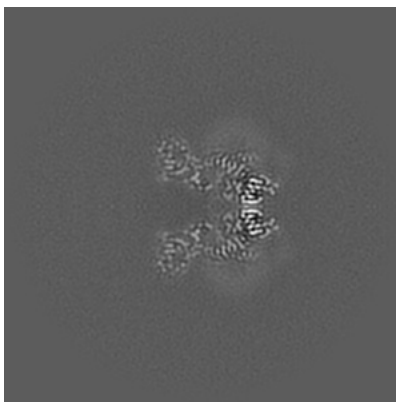
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

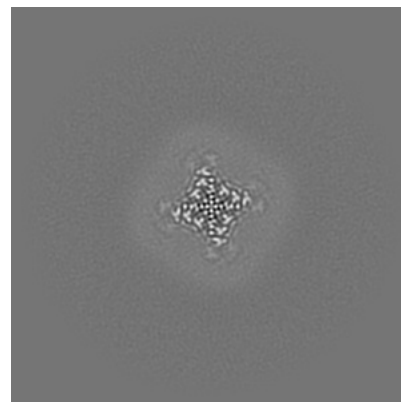
6.3.1 Primary map



X Index: 200

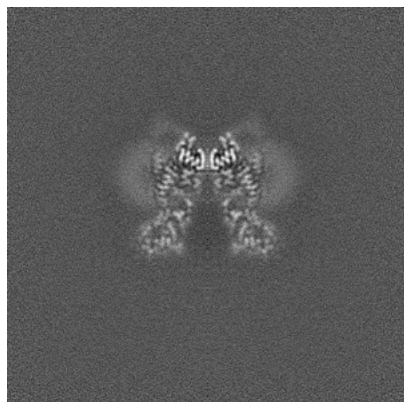


Y Index: 200

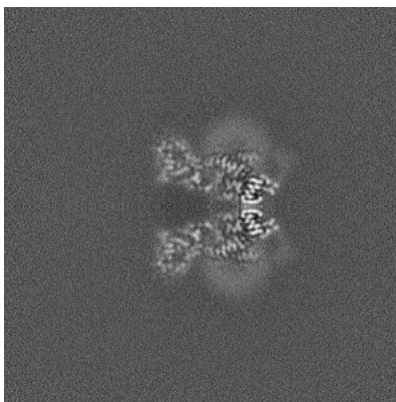


Z Index: 247

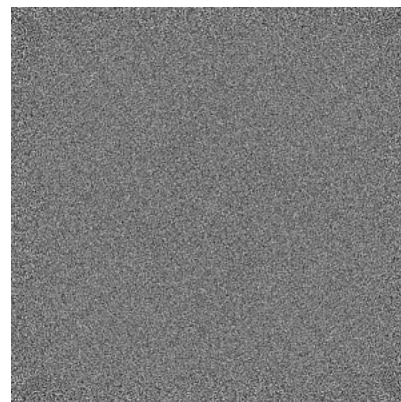
6.3.2 Raw map



X Index: 200



Y Index: 200

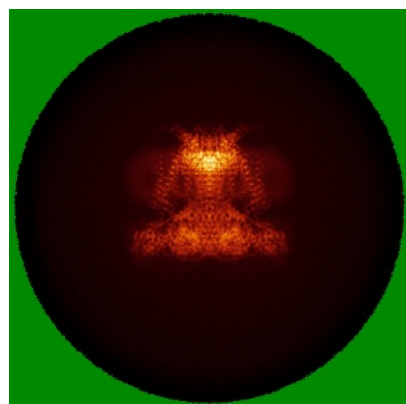


Z Index: 0

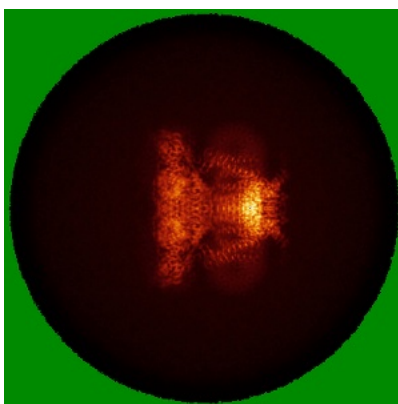
The images above show the largest variance slices of the map in three orthogonal directions.

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

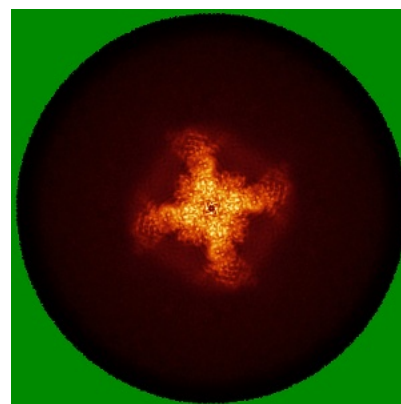
6.4.1 Primary map



X

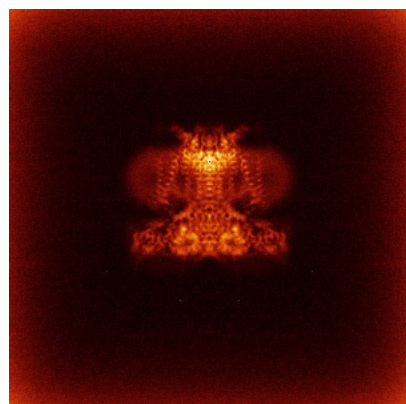


Y

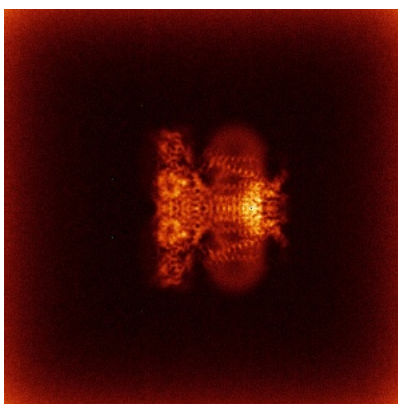


Z

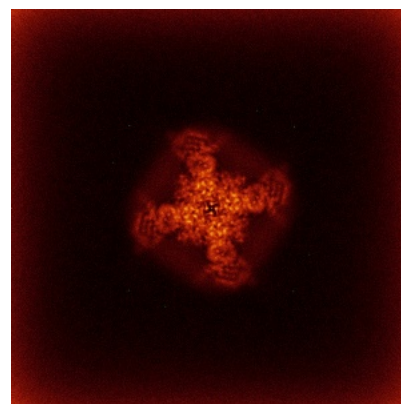
6.4.2 Raw map



X



Y

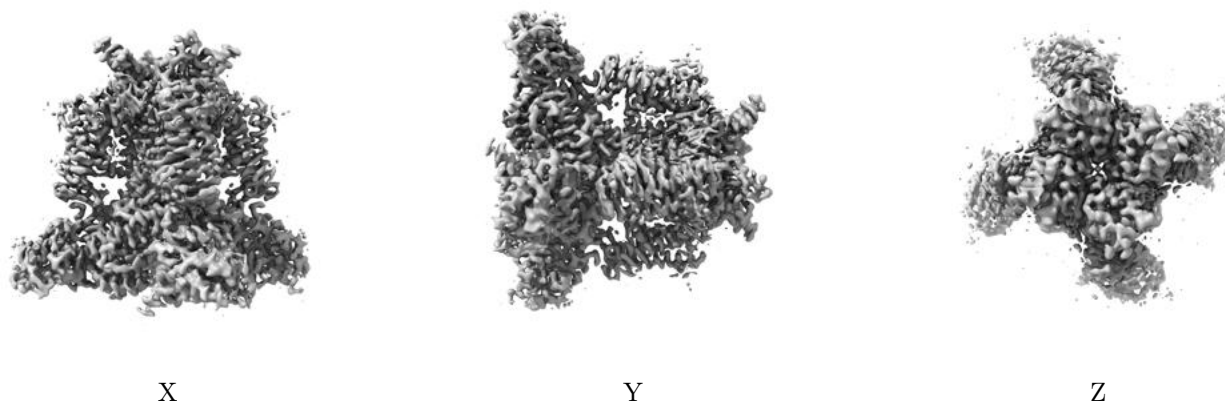


Z

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.

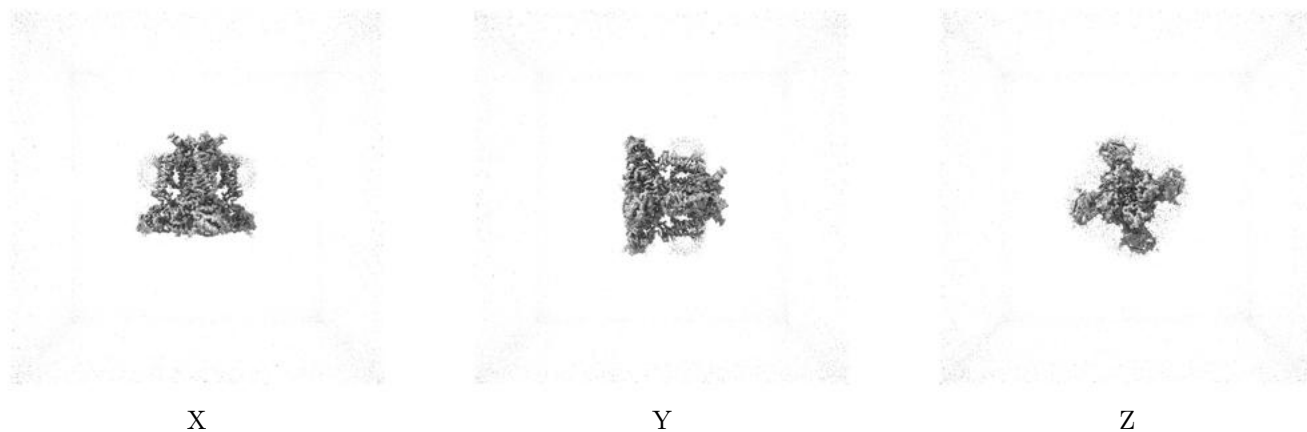
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

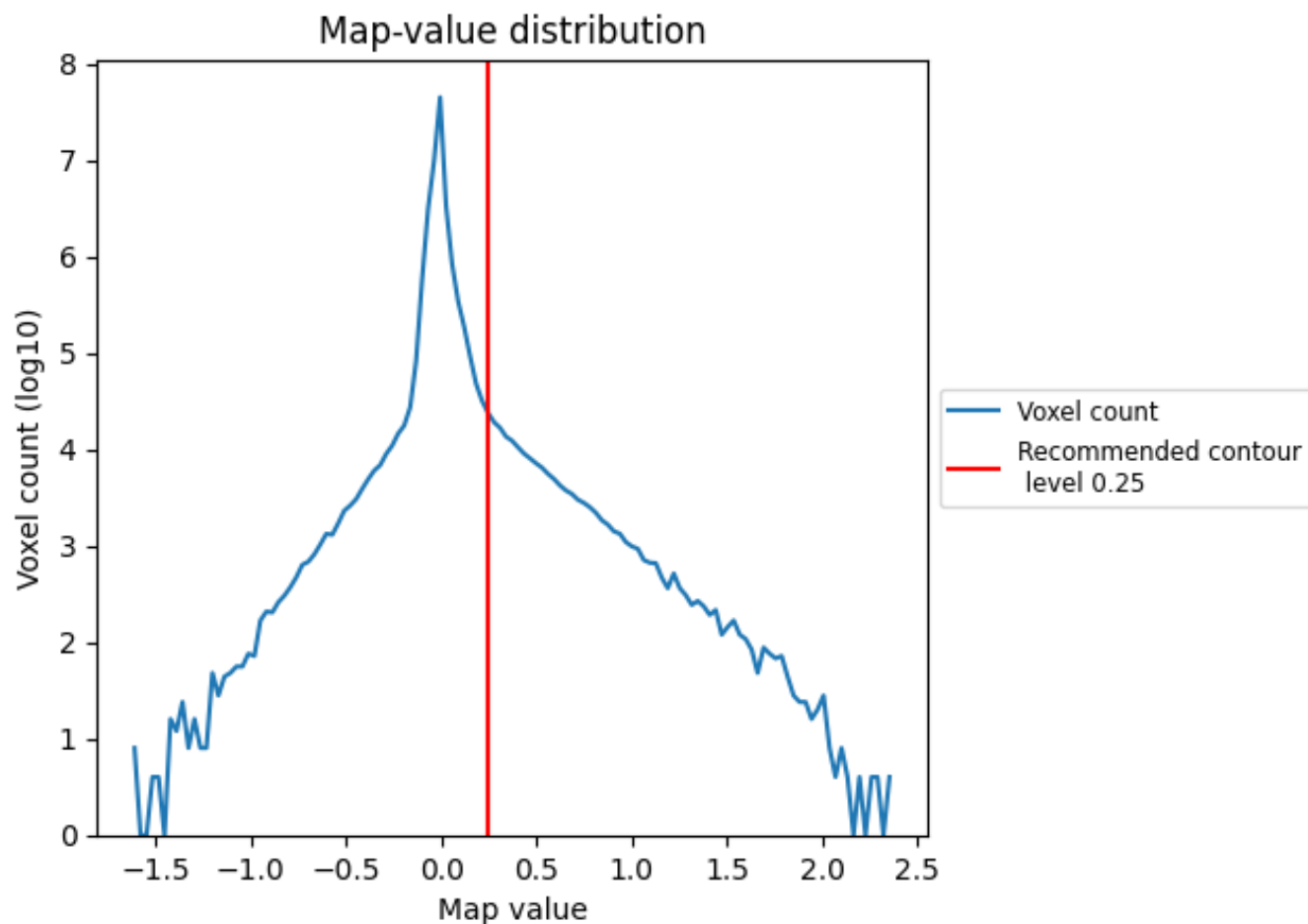
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

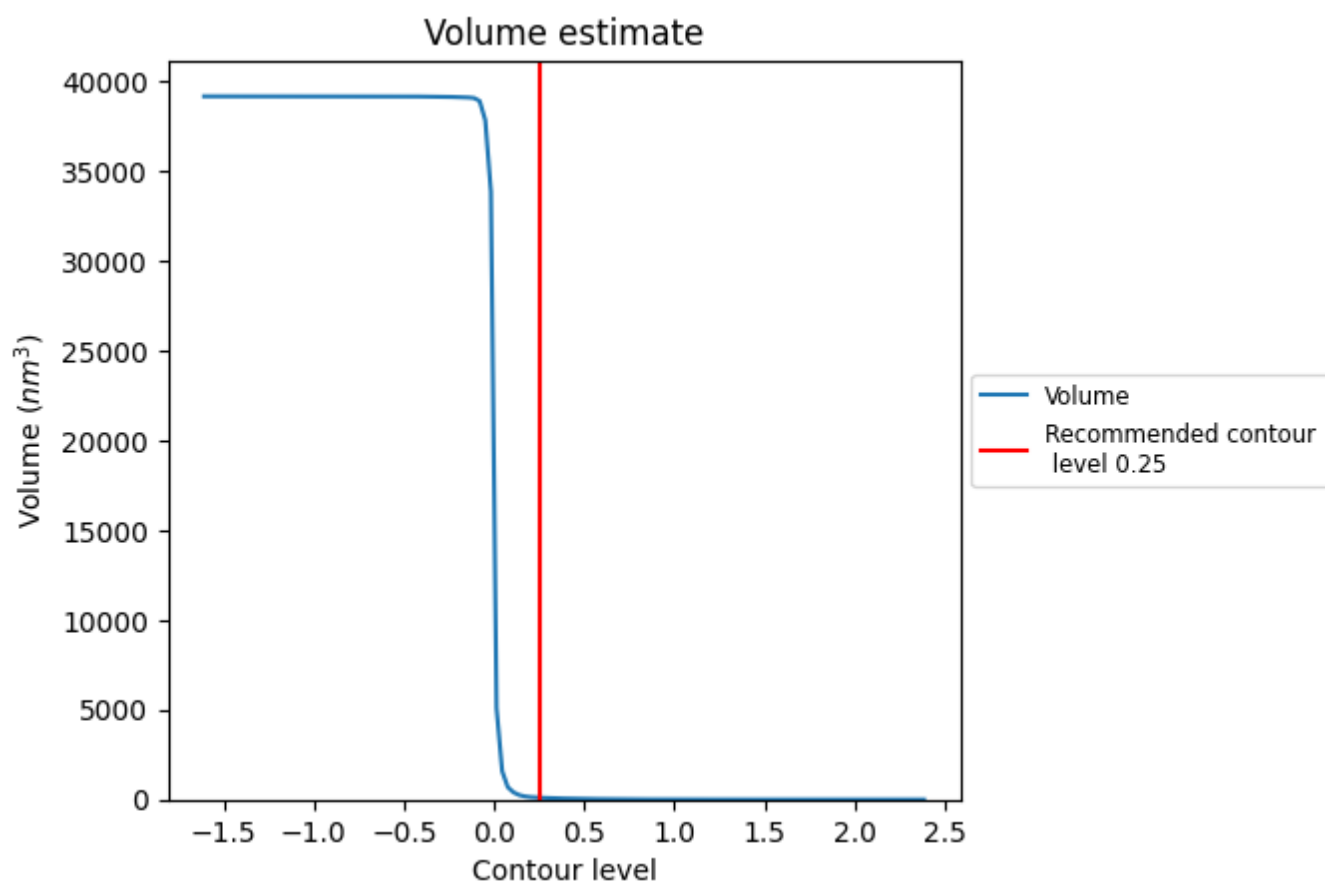
This section contains the results of statistical analysis of the map.

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.

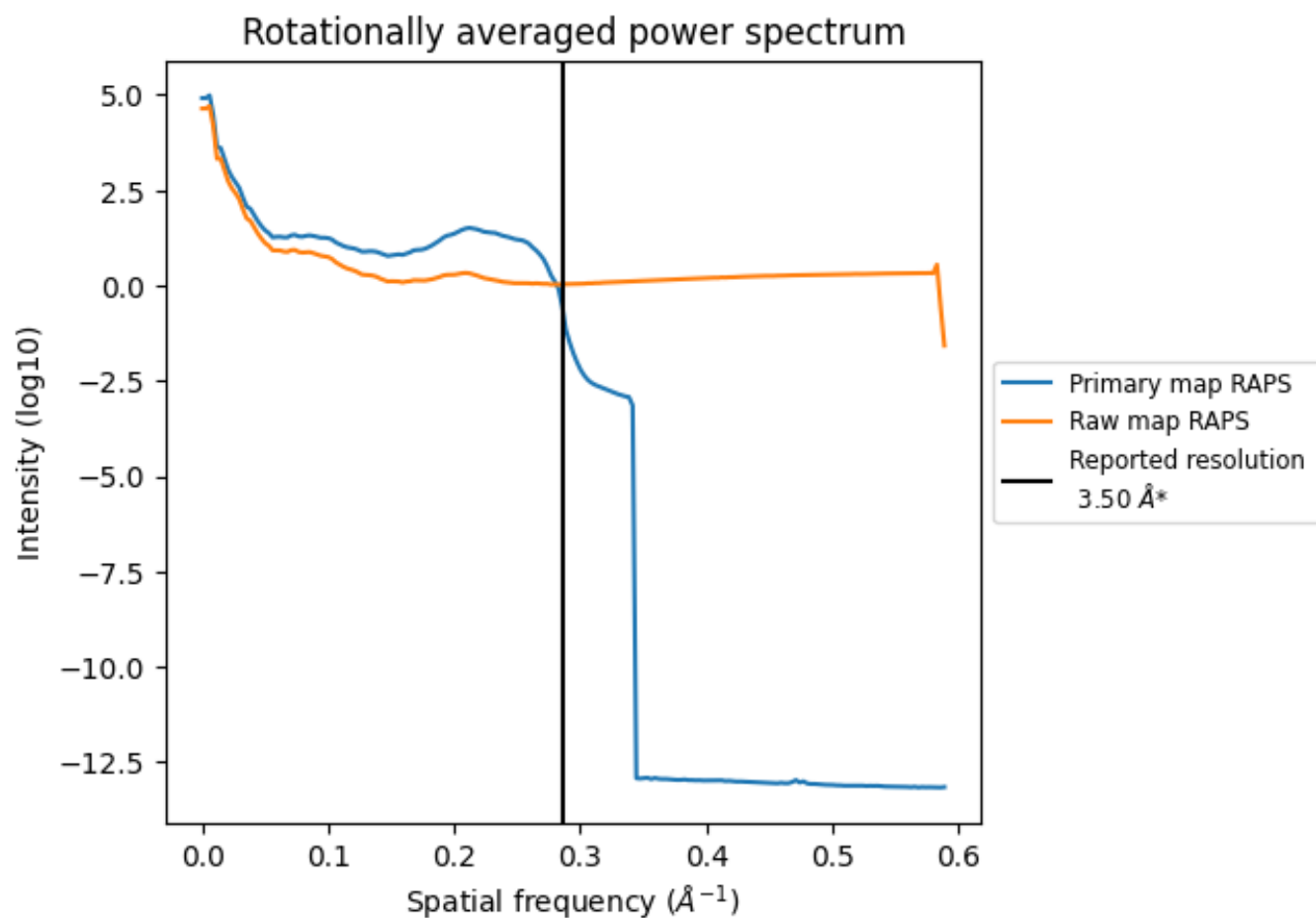
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 106 nm^3 ; this corresponds to an approximate mass of 96 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 ⓘ

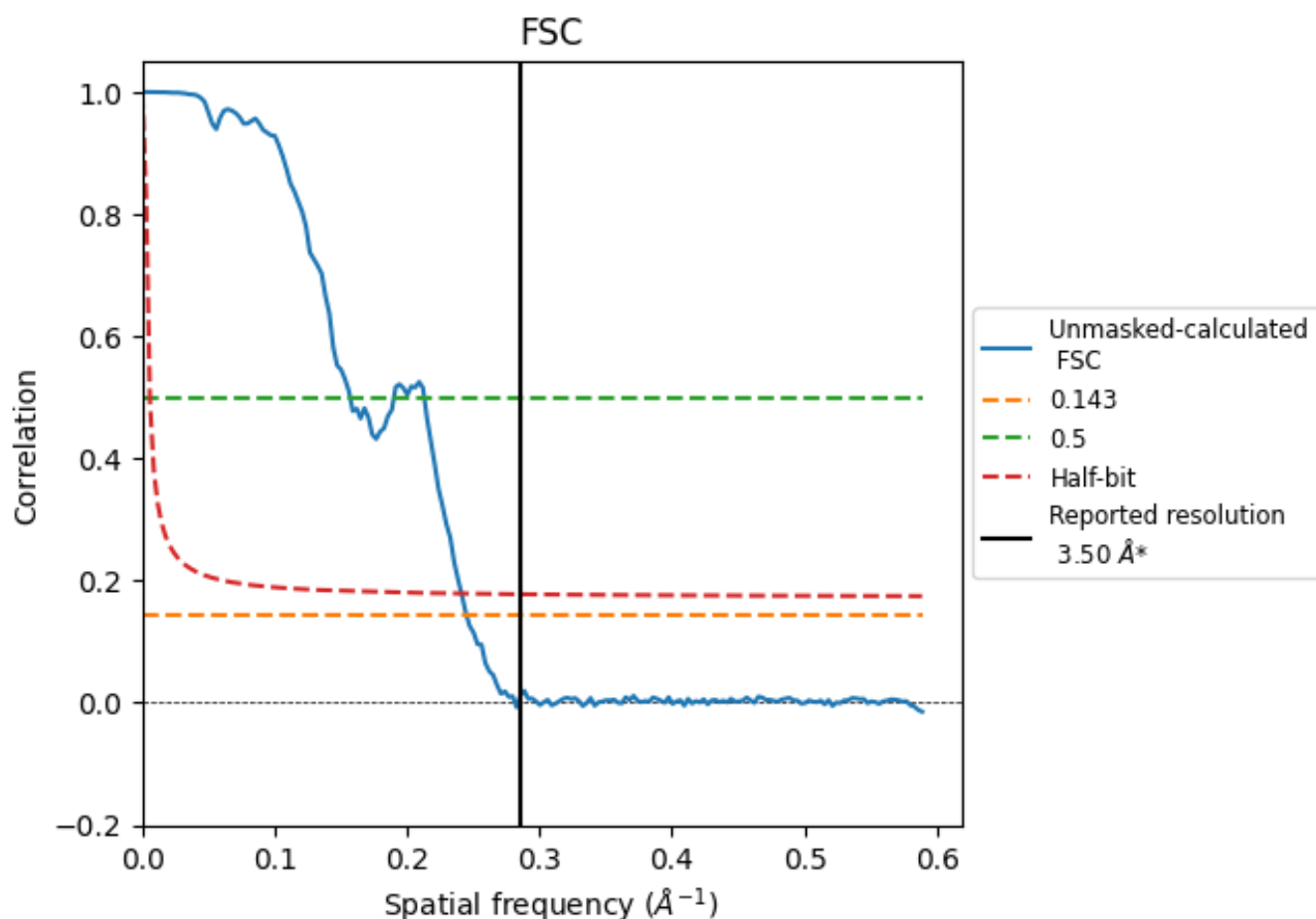


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

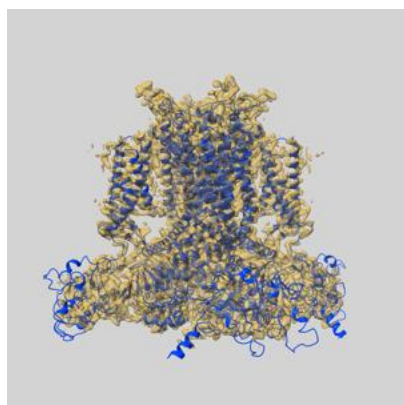
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.08	6.37	4.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.08 differs from the reported value 3.5 by more than 10 %

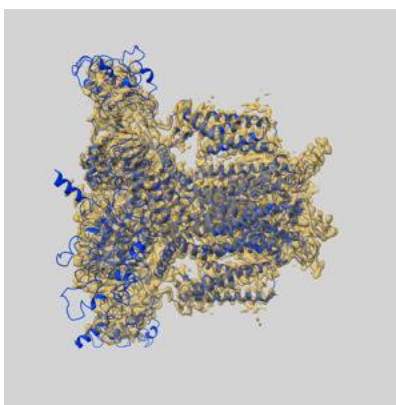
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33859 and PDB model 7YIH. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

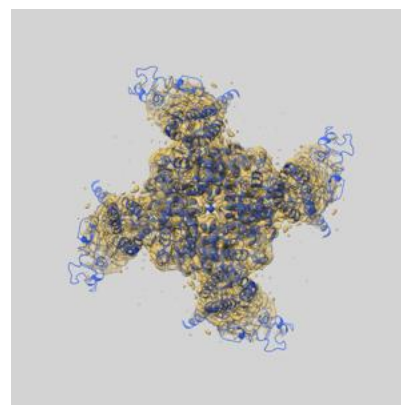
9.1 Map-model overlay [i](#)



X



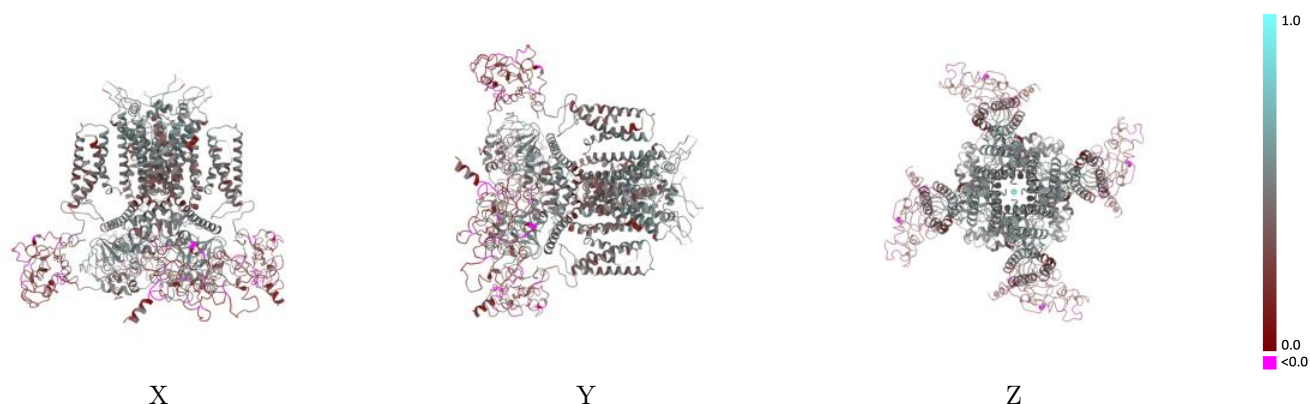
Y



Z

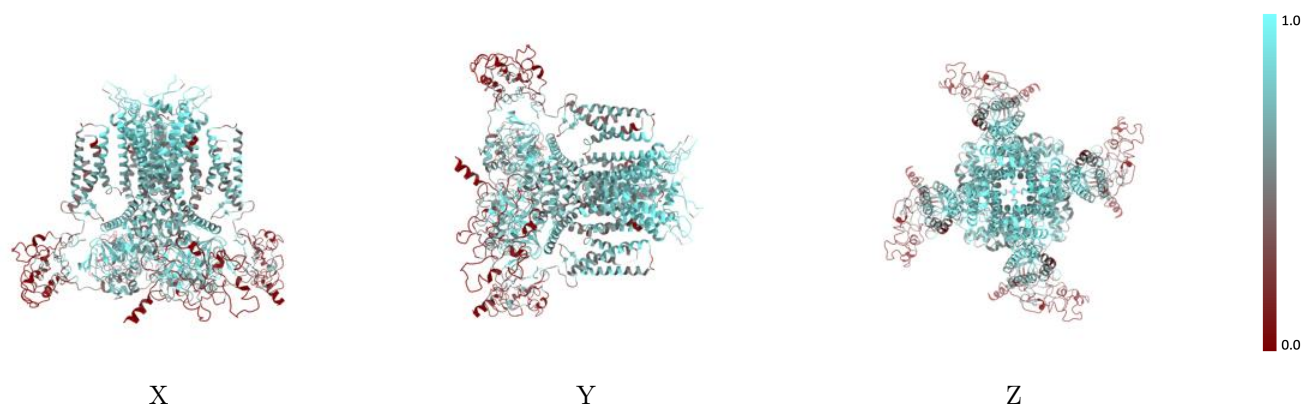
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



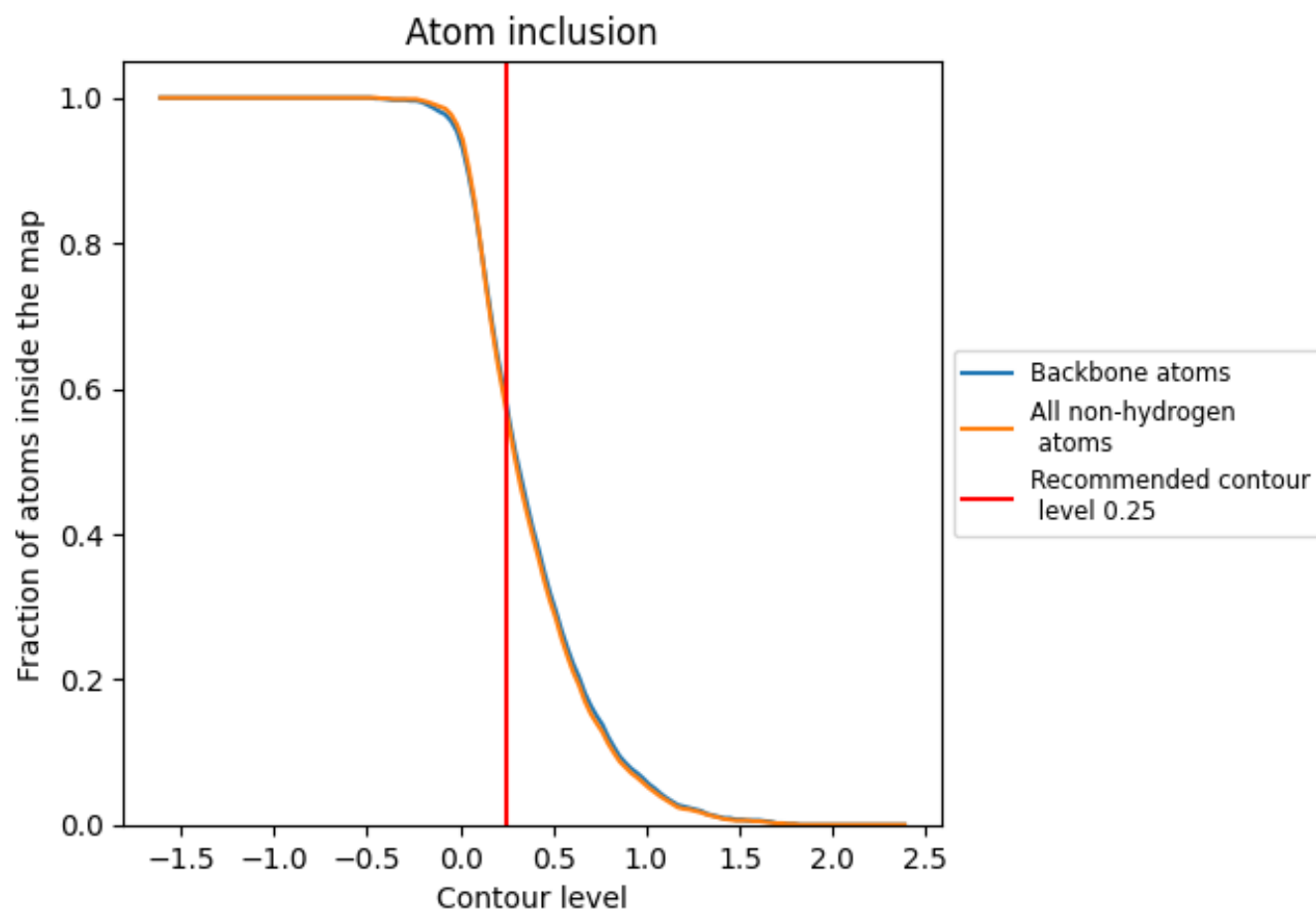
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 57% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5670	0.3870
A	0.5740	0.3880
B	0.5730	0.3870
C	0.5730	0.3860
D	0.5730	0.3860

