



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 08:35 PM UTC

PDB ID : 9KOU / pdb_00009kou
EMDB ID : EMD-62480
Title : CryoEM structure of osPHT1-11 at pH 5.0
Authors : Du, Z.M.; Guan, Z.Y.; Liu, Z.
Deposited on : 2024-11-21
Resolution : 3.40 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
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

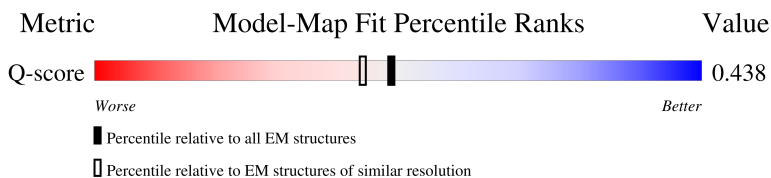
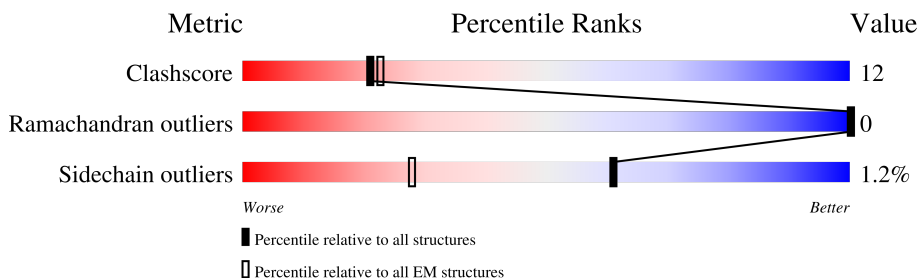
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	584	8% 55% 18% 26%
1	B	584	7% 52% 21% 26%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6672 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 Inorganic phosphate transporter 1-11.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	430	Total	C	N	O	S	0	0
			3331	2205	534	564	28		
1	B	431	Total	C	N	O	S	0	0
			3336	2209	534	565	28		

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	initiating methionine	UNP Q94DB8
A	-27	ASP	-	expression tag	UNP Q94DB8
A	-26	TYR	-	expression tag	UNP Q94DB8
A	-25	LYS	-	expression tag	UNP Q94DB8
A	-24	ASP	-	expression tag	UNP Q94DB8
A	-23	ASP	-	expression tag	UNP Q94DB8
A	-22	ASP	-	expression tag	UNP Q94DB8
A	-21	ASP	-	expression tag	UNP Q94DB8
A	-20	LYS	-	expression tag	UNP Q94DB8
A	-19	GLY	-	expression tag	UNP Q94DB8
A	-18	ASP	-	expression tag	UNP Q94DB8
A	-17	TYR	-	expression tag	UNP Q94DB8
A	-16	LYS	-	expression tag	UNP Q94DB8
A	-15	ASP	-	expression tag	UNP Q94DB8
A	-14	ASP	-	expression tag	UNP Q94DB8
A	-13	ASP	-	expression tag	UNP Q94DB8
A	-12	ASP	-	expression tag	UNP Q94DB8
A	-11	LYS	-	expression tag	UNP Q94DB8
A	-10	ILE	-	expression tag	UNP Q94DB8
A	-9	ASP	-	expression tag	UNP Q94DB8
A	-8	TYR	-	expression tag	UNP Q94DB8
A	-7	LYS	-	expression tag	UNP Q94DB8
A	-6	ASP	-	expression tag	UNP Q94DB8
A	-5	ASP	-	expression tag	UNP Q94DB8
A	-4	ASP	-	expression tag	UNP Q94DB8
A	-3	ASP	-	expression tag	UNP Q94DB8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	LYS	-	expression tag	UNP Q94DB8
A	-1	GLY	-	expression tag	UNP Q94DB8
A	0	SER	-	expression tag	UNP Q94DB8
B	-28	MET	-	initiating methionine	UNP Q94DB8
B	-27	ASP	-	expression tag	UNP Q94DB8
B	-26	TYR	-	expression tag	UNP Q94DB8
B	-25	LYS	-	expression tag	UNP Q94DB8
B	-24	ASP	-	expression tag	UNP Q94DB8
B	-23	ASP	-	expression tag	UNP Q94DB8
B	-22	ASP	-	expression tag	UNP Q94DB8
B	-21	ASP	-	expression tag	UNP Q94DB8
B	-20	LYS	-	expression tag	UNP Q94DB8
B	-19	GLY	-	expression tag	UNP Q94DB8
B	-18	ASP	-	expression tag	UNP Q94DB8
B	-17	TYR	-	expression tag	UNP Q94DB8
B	-16	LYS	-	expression tag	UNP Q94DB8
B	-15	ASP	-	expression tag	UNP Q94DB8
B	-14	ASP	-	expression tag	UNP Q94DB8
B	-13	ASP	-	expression tag	UNP Q94DB8
B	-12	ASP	-	expression tag	UNP Q94DB8
B	-11	LYS	-	expression tag	UNP Q94DB8
B	-10	ILE	-	expression tag	UNP Q94DB8
B	-9	ASP	-	expression tag	UNP Q94DB8
B	-8	TYR	-	expression tag	UNP Q94DB8
B	-7	LYS	-	expression tag	UNP Q94DB8
B	-6	ASP	-	expression tag	UNP Q94DB8
B	-5	ASP	-	expression tag	UNP Q94DB8
B	-4	ASP	-	expression tag	UNP Q94DB8
B	-3	ASP	-	expression tag	UNP Q94DB8
B	-2	LYS	-	expression tag	UNP Q94DB8
B	-1	GLY	-	expression tag	UNP Q94DB8
B	0	SER	-	expression tag	UNP Q94DB8

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P) (labeled as "Ligand of Interest" by depositor).

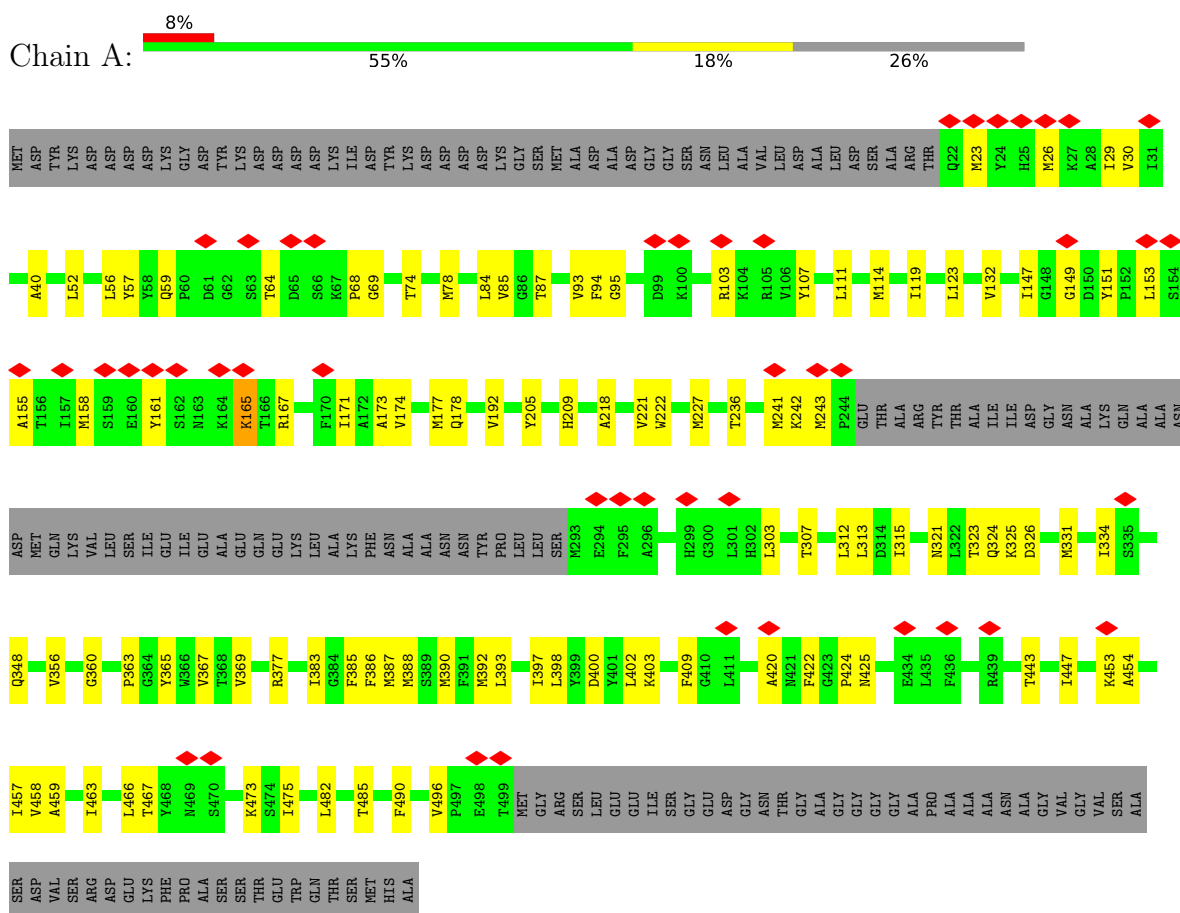


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
2	A	1	5	4	1	0

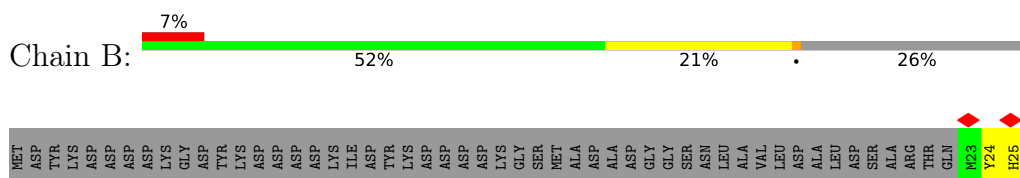
3 Residue-property plots

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: Inorganic phosphate transporter 1-11



- Molecule 1: Inorganic phosphate transporter 1-11



THR	GLY	ALA	GLY	GLY	GLY	ALA	PRO	ALA	ALA	ALA	ASN	ALA	VAL	SER	SER	ALA	SER	ASP	ASP	VAL	SER	ARG	ASP	GLU	LYS	PHE	PRO	ALA	ALA	SER	SER	THR	SER	SER	THR	TRP	GLN	THR	SER	SER	HIS	ALA									
N421	F422	G423	P424	N425	L431	F432	A433	E434	L435	F436	R441	S442	T443	K453	A456	I457	V458	G462	N469	S470	Q471	K477	I481	L482	S483	N486	M487	L488	G489	F490	F491	V496	P497	E498	T499	MET	GLY	ARG	SER	LEU	GLU	ILE	SER	GLY	GLU	ASP	ASN				
L313	D314	Y318	S319	Q320	N321	L322	G332	L333	I334	S335	G336	A337	A338	K342	L343	T344	E345	M346	T349	P363	V367	T368	D373	M379	I380	Q381	G384	F385	F386	M387	M388	S389	M390	F391	M392	M395	L398	L402	L408	F409	F417	F418	F419	A420							
M243	P244	GLU	THR	ALA	ARG	THR	ALA	ILE	ILE	ASP	GLY	ASN	ALA	LYS	GLN	ALA	ALA	ASN	ASP	MET	GLN	LYS	VAL	LEU	SER	ILE	GLU	ILE	GLU	ALA	GLU	GLN	LYS	LEU	ALA	ALA	ASN	ASN	TYR	PRO	LEU	L291	S292	M293	E294	F295	L301	H302	L303	I304	W310
F36	F37	T38	Y41	D42	V49	L52	L53	G54	R55	L56	Y57	Y58	T54	K67	P68	M78	V82	A83	L84	T87	L88	M89	L92	V93	F94	G95	Y96	F97	G98	D99	K100	L101	G102	R103	K104	R105	V106	Y107	T110	M114	I119	L123	S124	V132							
W142	L143	G144	F145	G146	I147	G148	G149	Y151	P152	L153	S154	S159	E160	Y161	S162	N163	K164	K165	T166	R167	G168	A169	F170	V174	M177	Q178	G179	I183	V188	I191	N200	K201	Y205	K206	G207	M215	V221	L226	M227	L234	W239	R240	M241	K242							

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	333051	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.757	Depositor
Minimum map value	-2.023	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.45	Depositor
Map size ($\text{\AA}$)	299.6, 299.6, 299.6	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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: PO4

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	0.16	0/3417	0.40	0/4617
1	B	0.17	0/3422	0.48	1/4624 (0.0%)
All	All	0.17	0/6839	0.45	1/9241 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	106	VAL	N-CA-C	-5.87	107.03	112.43

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	3331	0	3399	72	0
1	B	3336	0	3407	89	0
2	A	5	0	0	0	0
All	All	6672	0	6806	160	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 12.

The worst 5 of 160 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:30:VAL:HG13	1:B:177:MET:HE2	1.60	0.83
1:B:388:MET:HB3	1:B:486:ASN:HD22	1.45	0.80
1:B:101:LEU:HD12	1:B:105:ARG:HB3	1.65	0.77
1:A:111:LEU:HD21	1:A:236:THR:HG22	1.66	0.77
1:A:114:MET:HE2	1:A:147:ILE:HD13	1.73	0.70

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	426/584 (73%)	403 (95%)	23 (5%)	0	100	100
1	B	427/584 (73%)	387 (91%)	40 (9%)	0	100	100
All	All	853/1168 (73%)	790 (93%)	63 (7%)	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	345/461 (75%)	343 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	346/461 (75%)	340 (98%)	6 (2%)	53	67
All	All	691/922 (75%)	683 (99%)	8 (1%)	61	72

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	498	GLU
1	B	443	THR
1	B	301	LEU
1	B	88	LEU
1	B	395	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	59	GLN
1	B	381	GLN
1	B	464	GLN
1	A	381	GLN
1	A	348	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](#)

1 ligand is 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	PO4	A	601	-	4,4,4	1.53	1 (25%)	6,6,6	0.49	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	PO4	P-O1	2.66	1.56	1.50

There are no bond angle outliers.

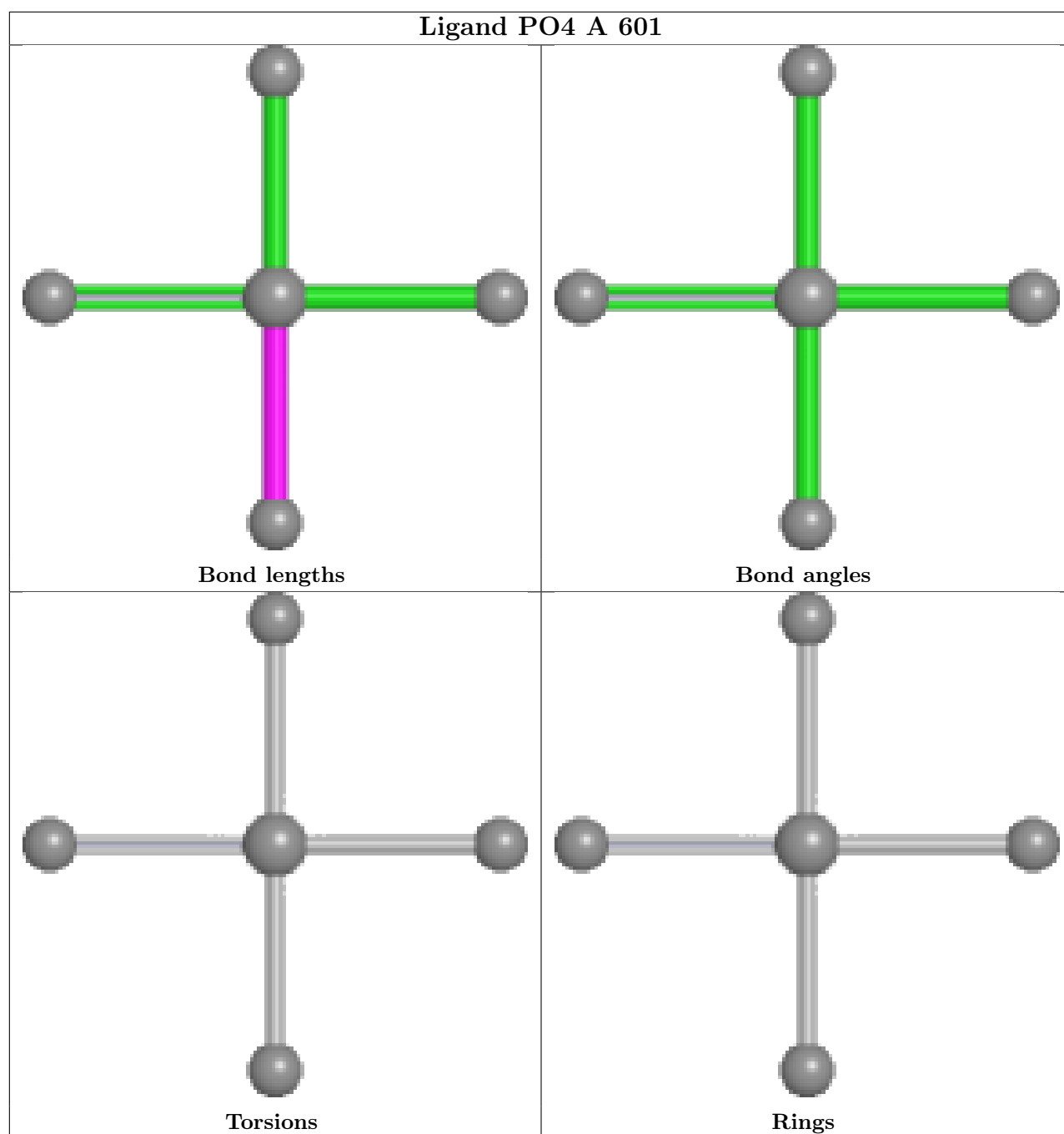
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

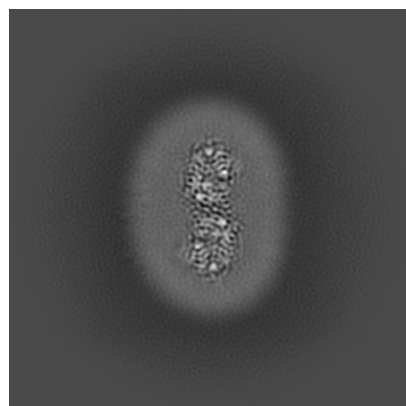
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62480. These allow visual inspection of the internal detail of the map and identification of artifacts.

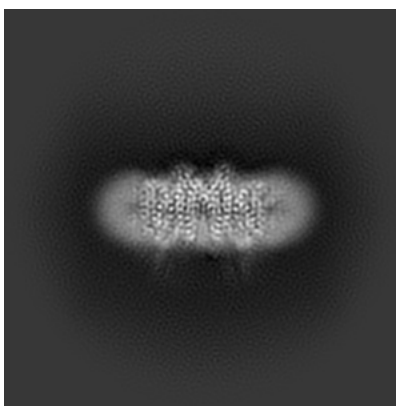
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

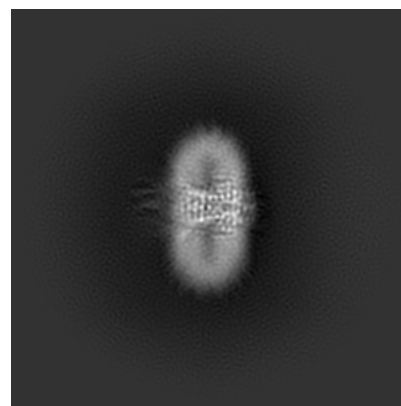
6.1.1 Primary map



X

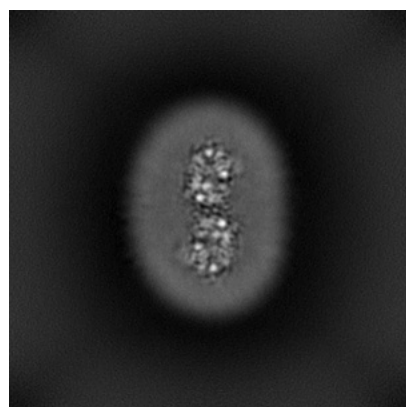


Y

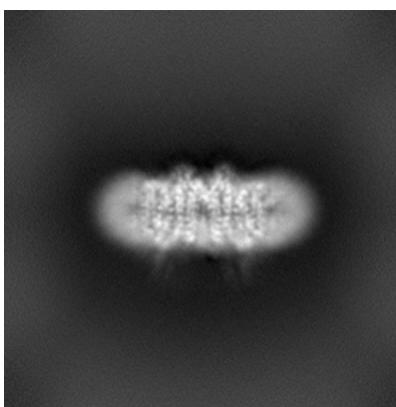


Z

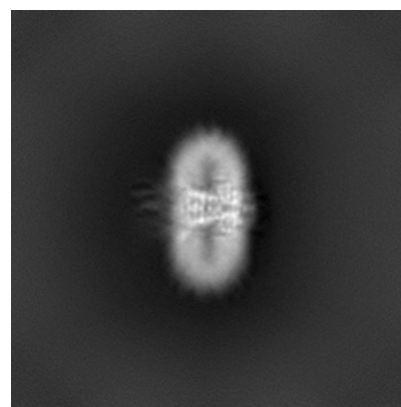
6.1.2 Raw map



X



Y

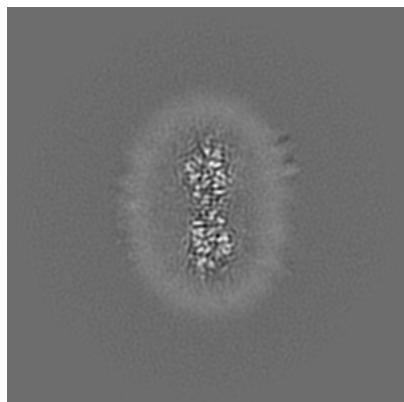


Z

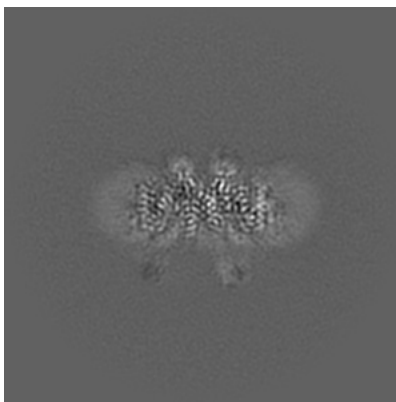
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

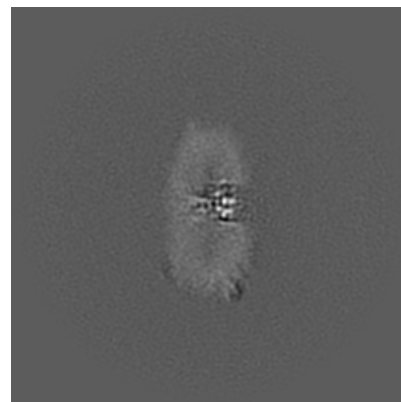
6.2.1 Primary map



X Index: 140

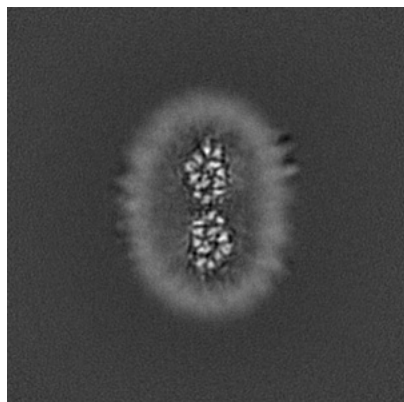


Y Index: 140

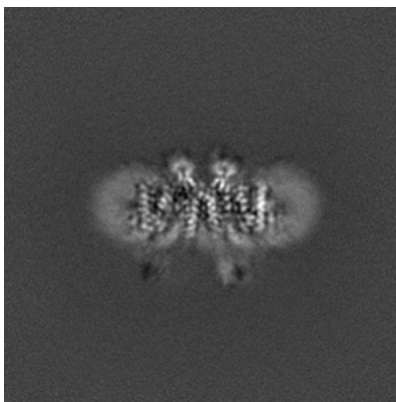


Z Index: 140

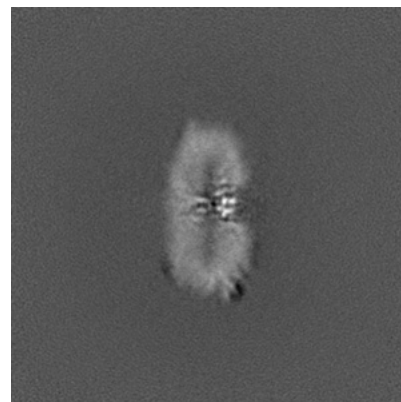
6.2.2 Raw map



X Index: 140



Y Index: 140

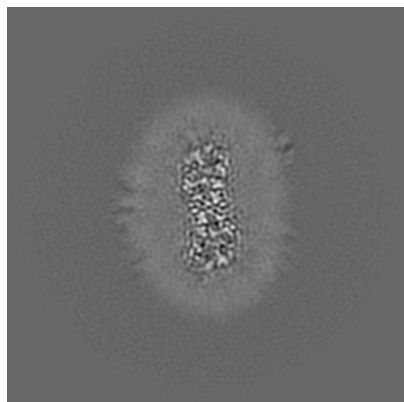


Z Index: 140

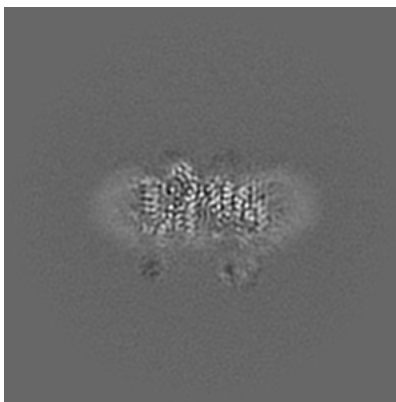
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

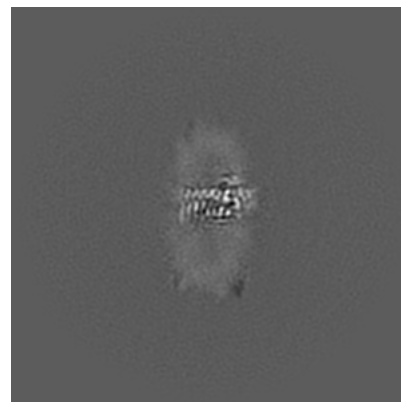
6.3.1 Primary map



X Index: 147

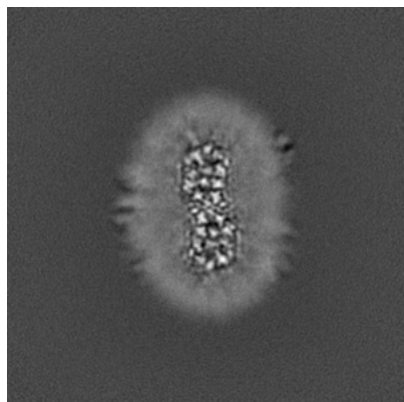


Y Index: 148

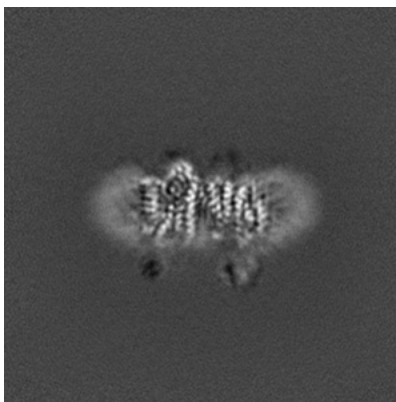


Z Index: 130

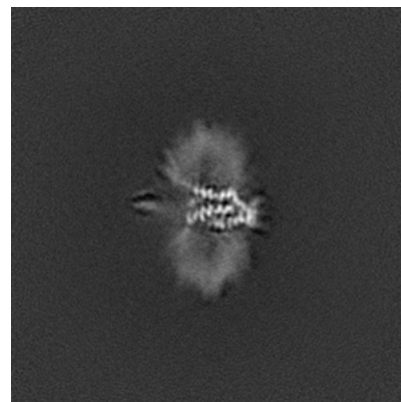
6.3.2 Raw map



X Index: 147



Y Index: 148

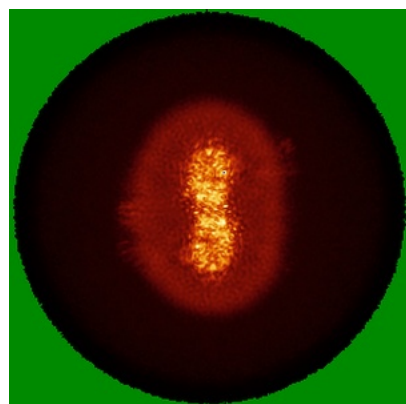


Z Index: 156

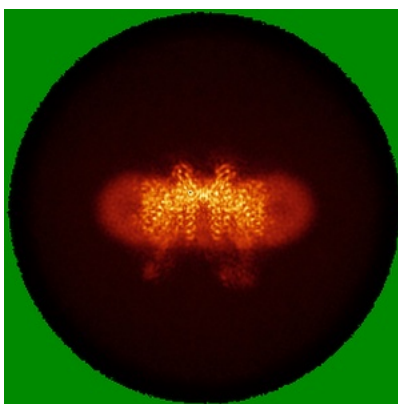
The images above show the largest variance slices of the map in three orthogonal directions.

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

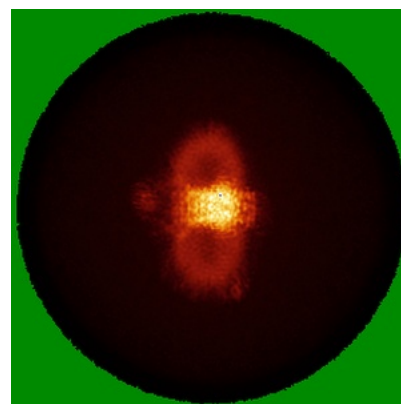
6.4.1 Primary map



X

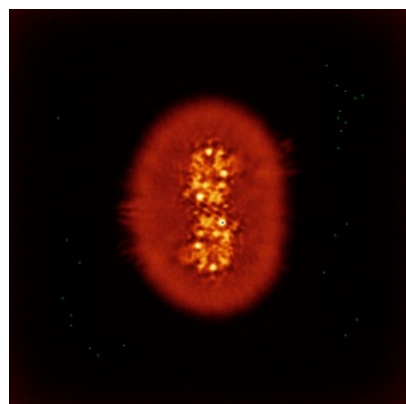


Y

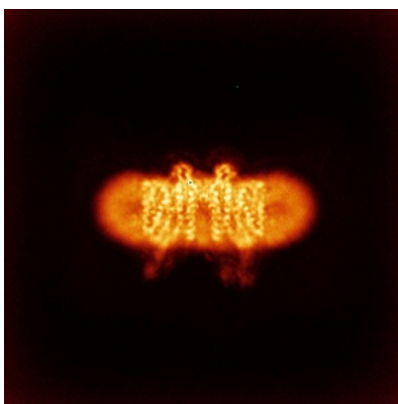


Z

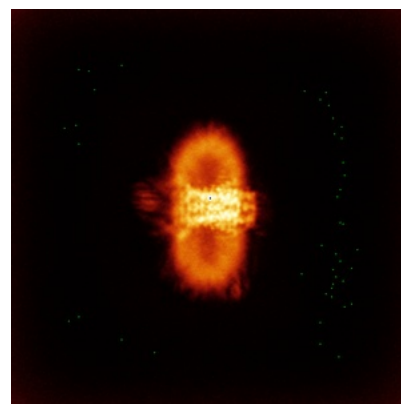
6.4.2 Raw map



X



Y

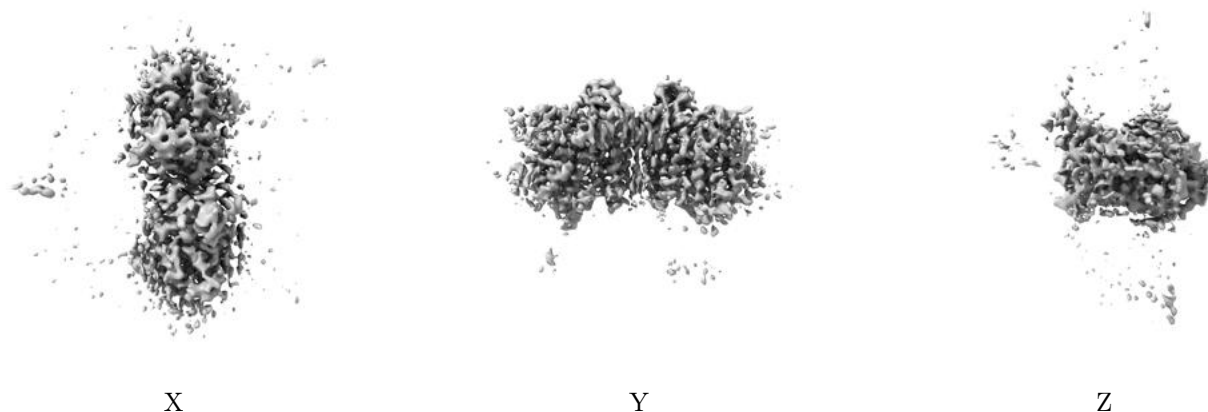


Z

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

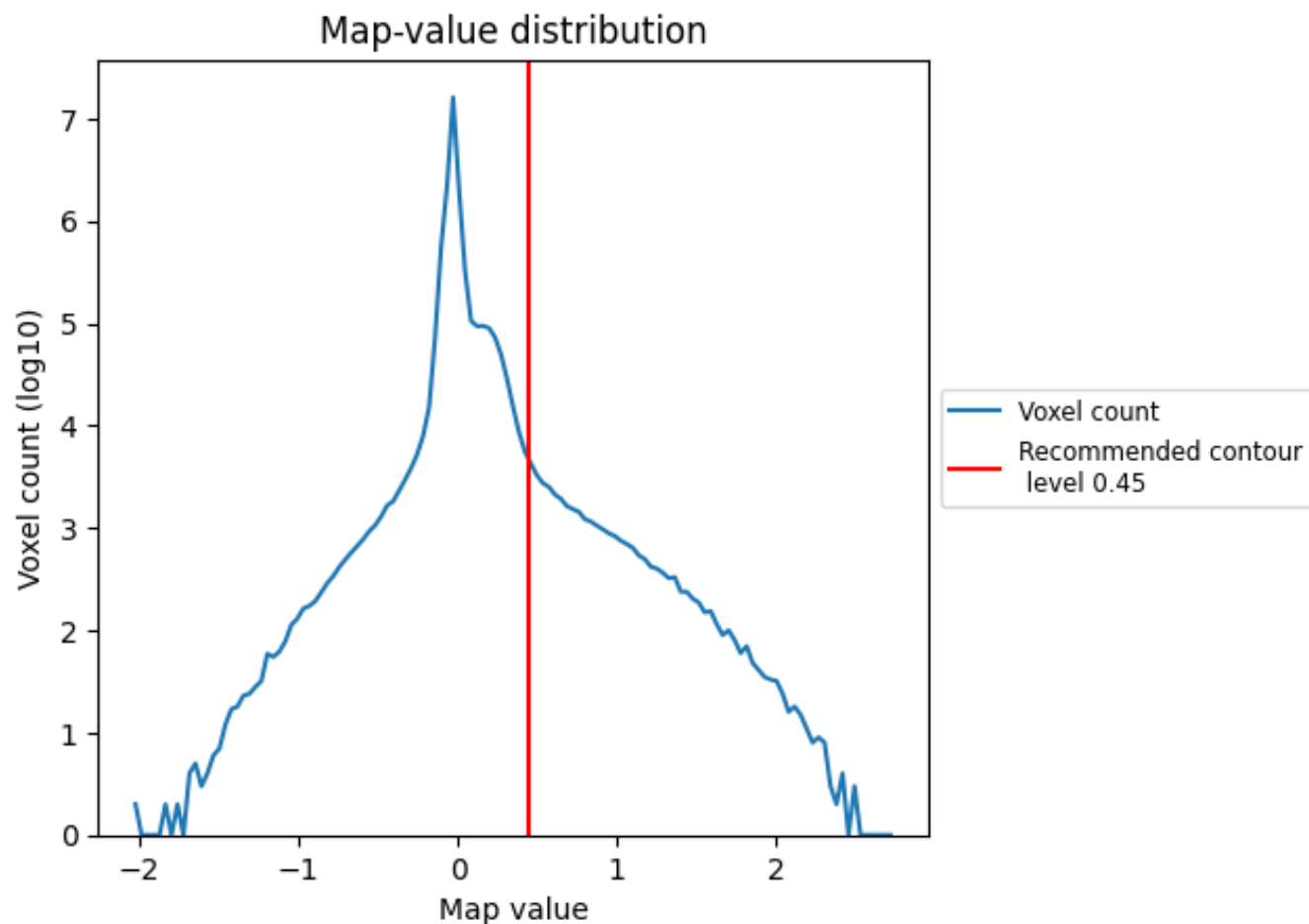
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

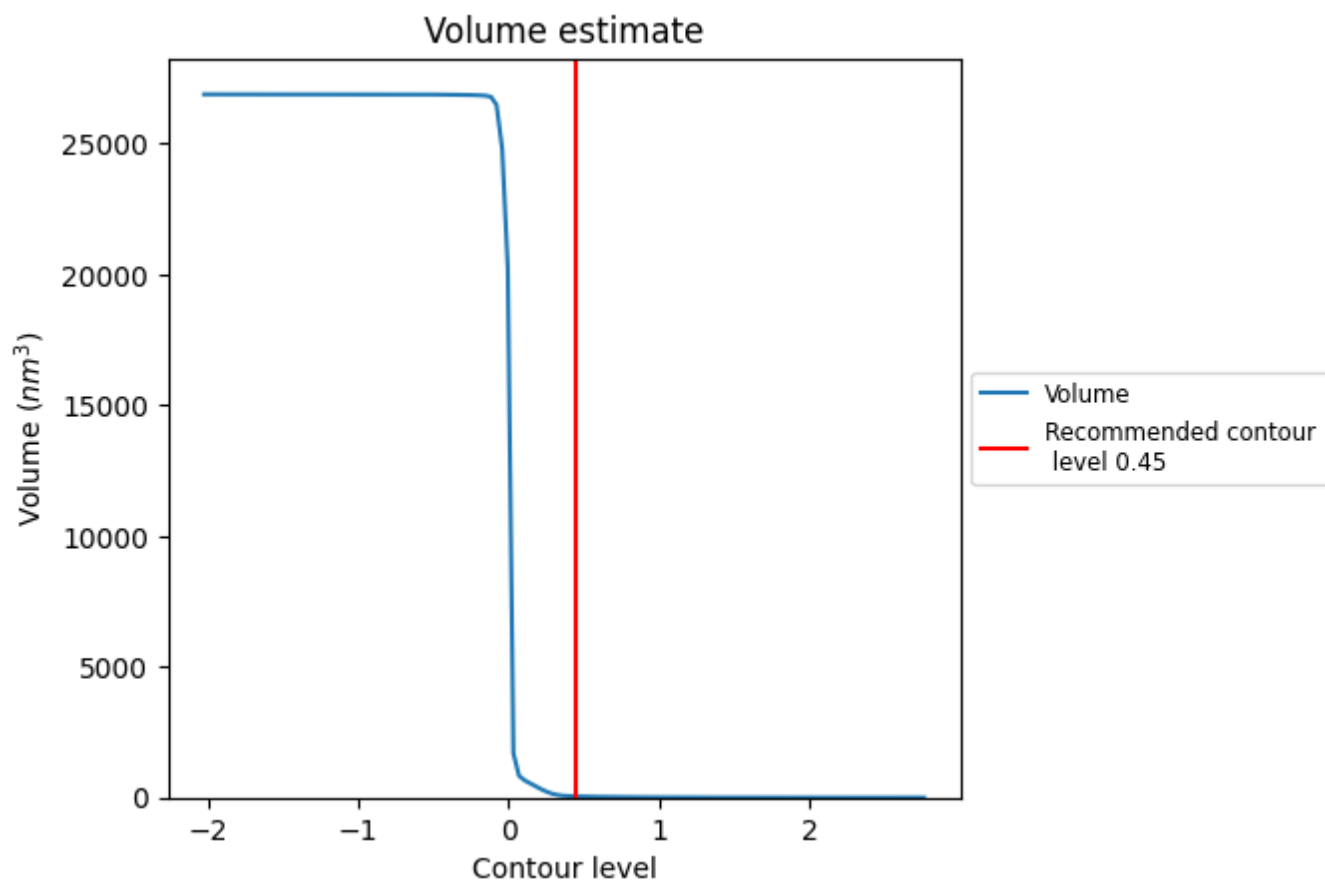
This section contains the results of statistical analysis of the map.

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.

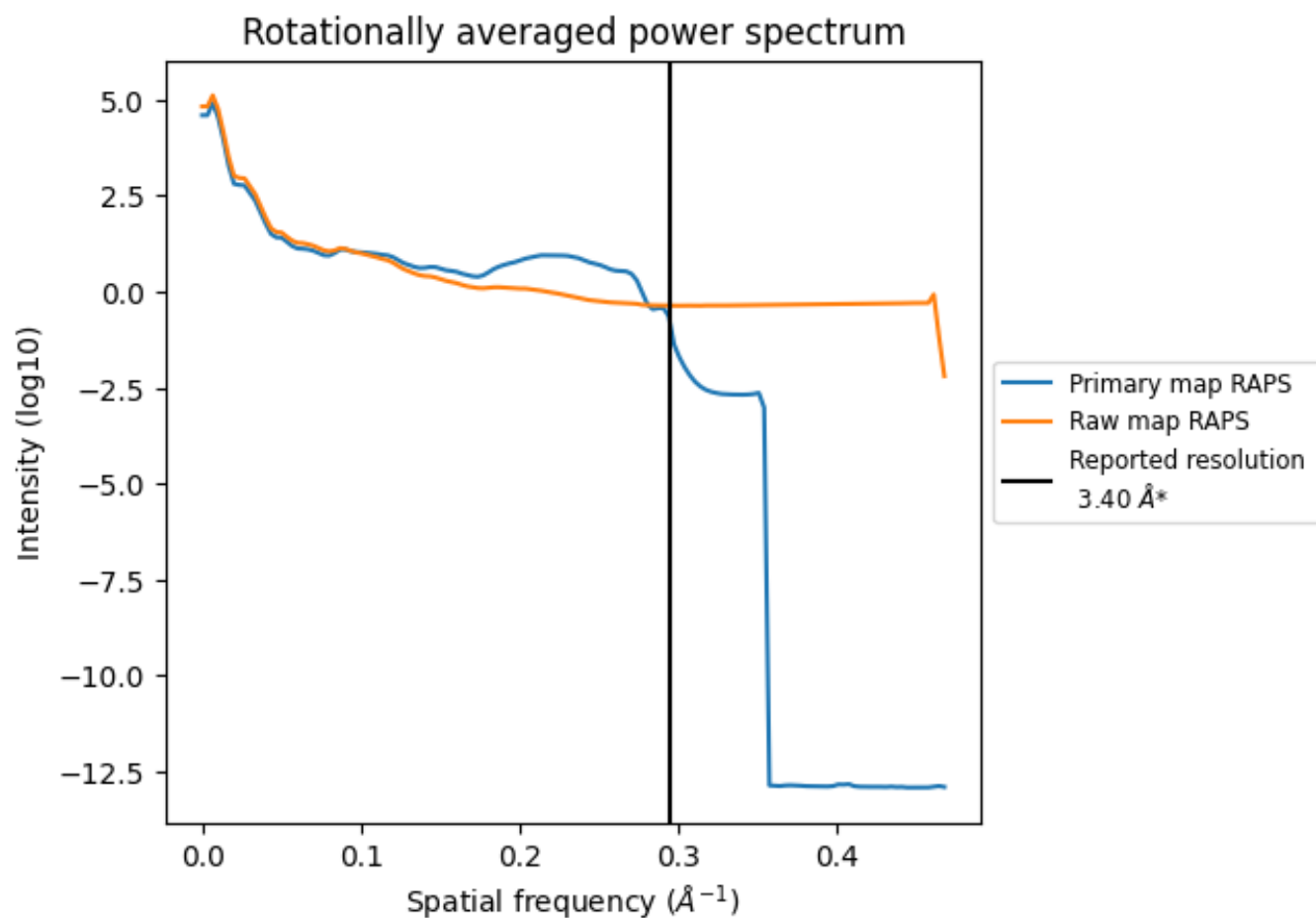
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 44 nm³; this corresponds to an approximate mass of 40 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 ⓘ

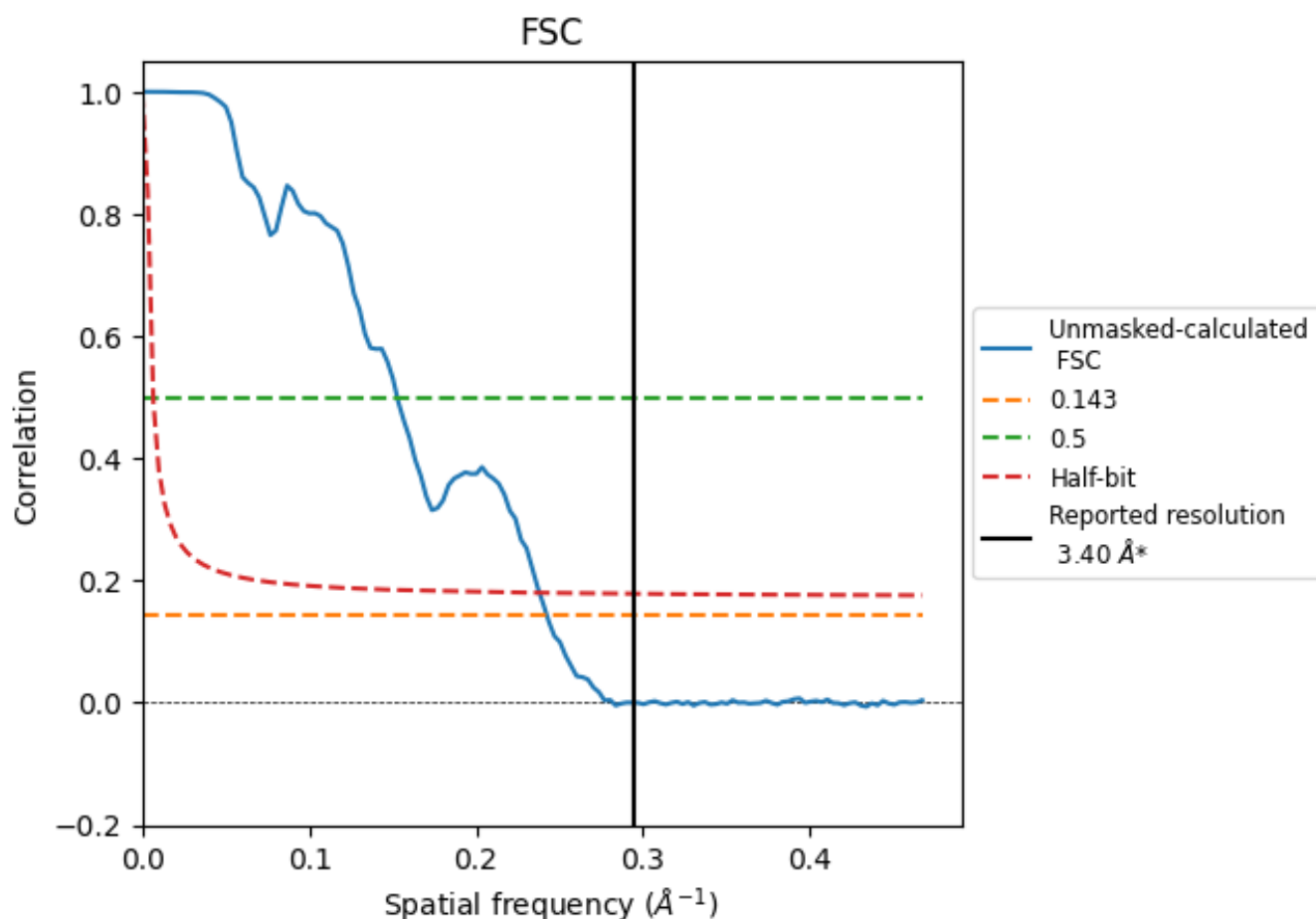


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

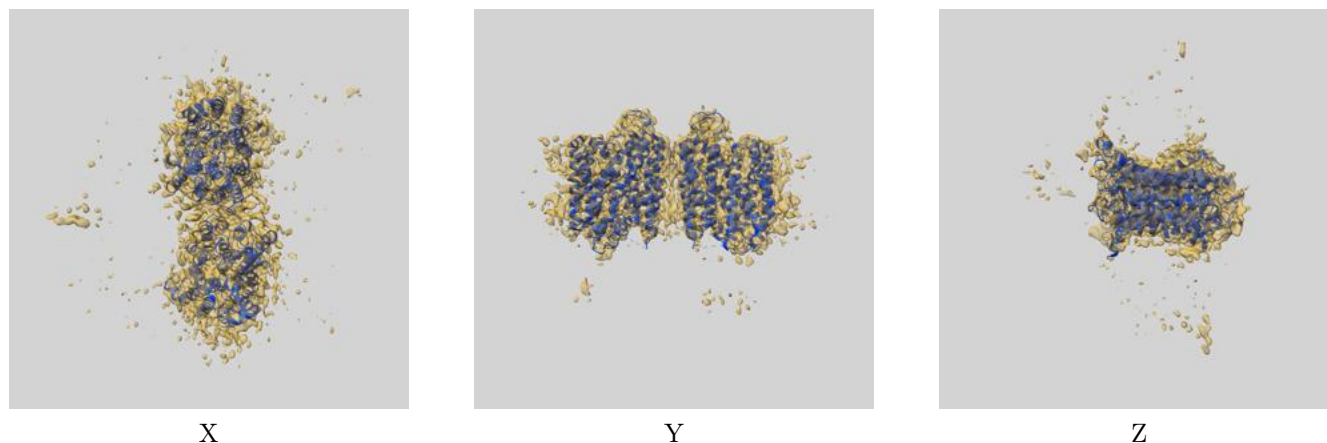
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.13	6.54	4.20

*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 4.13 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

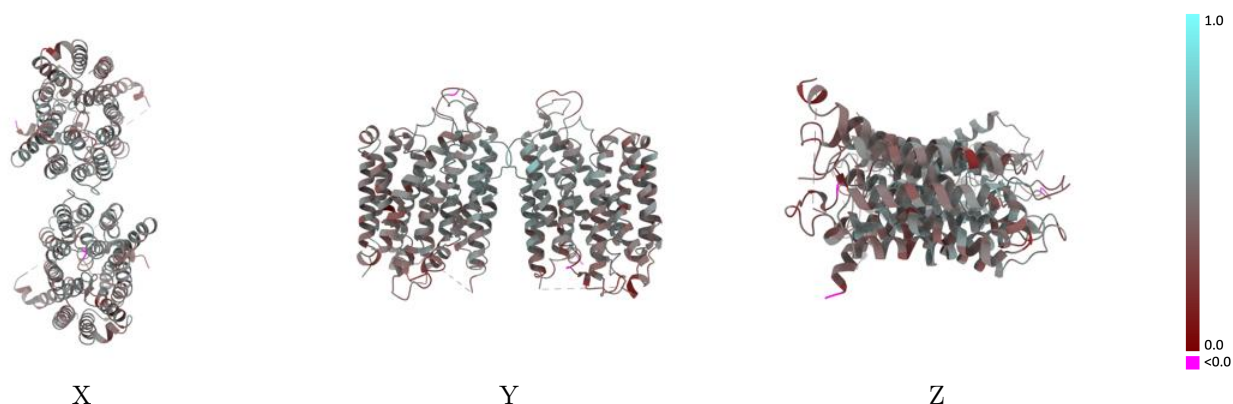
This section contains information regarding the fit between EMDB map EMD-62480 and PDB model 9KOU. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



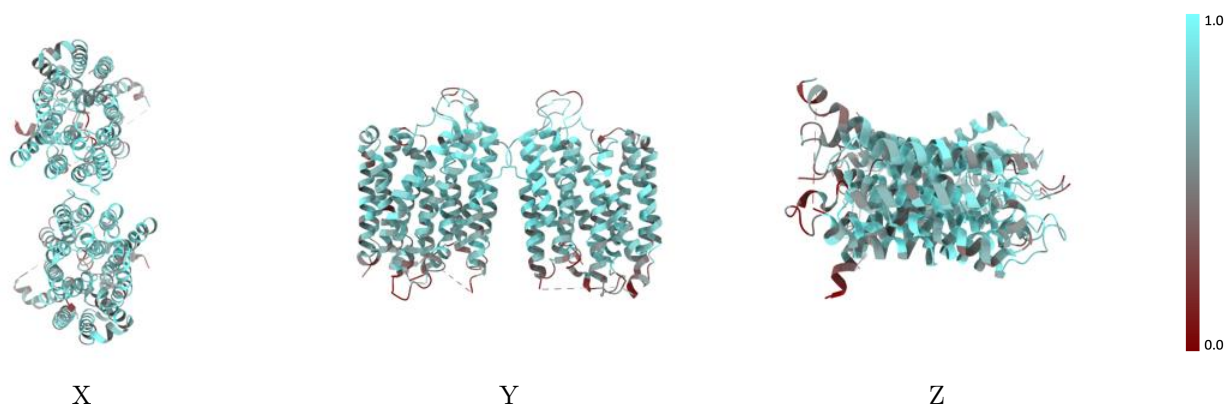
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



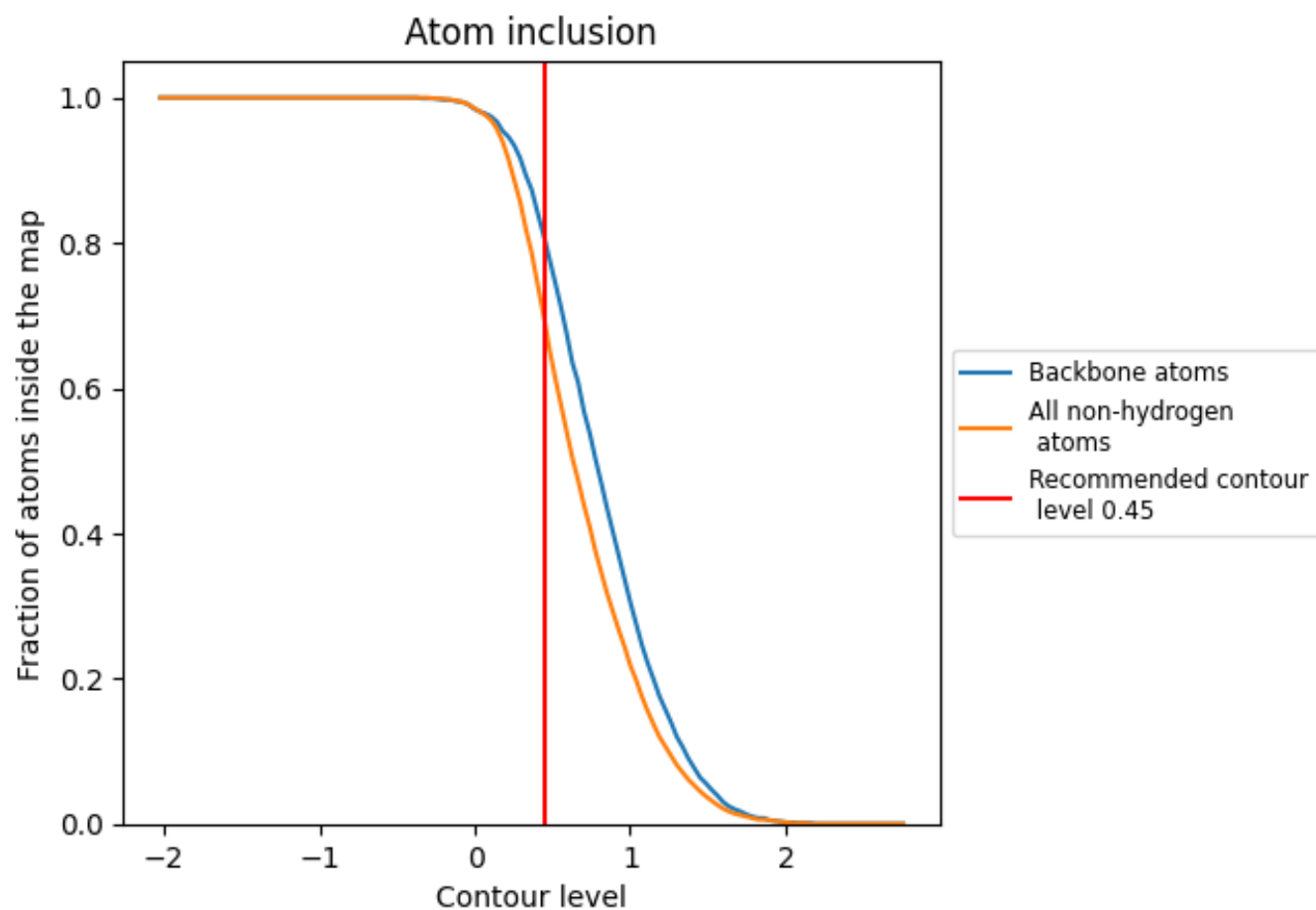
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 69% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6920	0.4380
A	0.6930	0.4350
B	0.6910	0.4410

