wwPDB EM Validation Summary Report

Oct 19, 2026 – 04:21 PM JST

PDB ID	:	27ZK / pdb_000027zk
EMDB ID	:	EMD-81562
Title	:	Atomic structure of the ASFV virus early transcription factor in ER state
Authors	:	Yang, Y.G.; Xin, Y.H.
Deposited on	:	2026-06-18
Resolution	:	4.00 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:

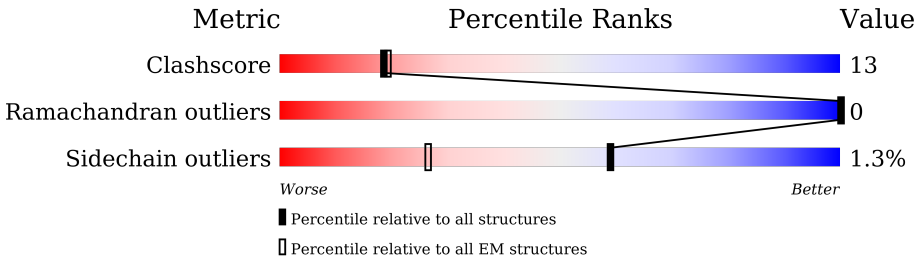
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

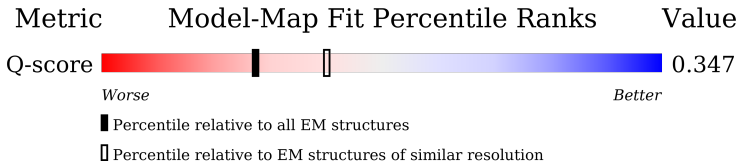
1 Overall quality at a glance (i)

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	1377	17% 60% 24% 16%
2	B	1141	11% 50% 21% • 29%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 15997 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 Early transcription factor large subunit homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1155	Total	C	N	O	S	0	0
			9463	6158	1539	1740	26		

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	initiating methionine	UNP Q65177
A	-27	TRP	-	expression tag	UNP Q65177
A	-26	SER	-	expression tag	UNP Q65177
A	-25	HIS	-	expression tag	UNP Q65177
A	-24	PRO	-	expression tag	UNP Q65177
A	-23	GLN	-	expression tag	UNP Q65177
A	-22	PHE	-	expression tag	UNP Q65177
A	-21	GLU	-	expression tag	UNP Q65177
A	-20	LYS	-	expression tag	UNP Q65177
A	-19	GLY	-	expression tag	UNP Q65177
A	-18	GLY	-	expression tag	UNP Q65177
A	-17	GLY	-	expression tag	UNP Q65177
A	-16	SER	-	expression tag	UNP Q65177
A	-15	GLY	-	expression tag	UNP Q65177
A	-14	GLY	-	expression tag	UNP Q65177
A	-13	GLY	-	expression tag	UNP Q65177
A	-12	SER	-	expression tag	UNP Q65177
A	-11	GLY	-	expression tag	UNP Q65177
A	-10	GLY	-	expression tag	UNP Q65177
A	-9	SER	-	expression tag	UNP Q65177
A	-8	ALA	-	expression tag	UNP Q65177
A	-7	TRP	-	expression tag	UNP Q65177
A	-6	SER	-	expression tag	UNP Q65177
A	-5	HIS	-	expression tag	UNP Q65177
A	-4	PRO	-	expression tag	UNP Q65177
A	-3	GLN	-	expression tag	UNP Q65177
A	-2	PHE	-	expression tag	UNP Q65177
A	-1	GLU	-	expression tag	UNP Q65177

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	LYS	-	expression tag	UNP Q65177
A	20	VAL	ALA	conflict	UNP Q65177
A	62	GLU	LYS	conflict	UNP Q65177
A	91	ARG	SER	conflict	UNP Q65177
A	175	VAL	LEU	conflict	UNP Q65177
A	225	ILE	MET	conflict	UNP Q65177
A	504	VAL	ILE	conflict	UNP Q65177
A	552	THR	ALA	conflict	UNP Q65177
A	906	GLY	GLU	conflict	UNP Q65177
A	965	ILE	VAL	conflict	UNP Q65177
A	1341	HIS	-	expression tag	UNP Q65177
A	1342	HIS	-	expression tag	UNP Q65177
A	1343	HIS	-	expression tag	UNP Q65177
A	1344	HIS	-	expression tag	UNP Q65177
A	1345	HIS	-	expression tag	UNP Q65177
A	1346	HIS	-	expression tag	UNP Q65177
A	1347	HIS	-	expression tag	UNP Q65177
A	1348	HIS	-	expression tag	UNP Q65177

- Molecule 2 is a protein called Early transcription factor large subunit homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	815	Total	C	N	O	S	0	0
			6534	4182	1127	1199	26		

There are 9 discrepancies between the modelled and reference sequences:

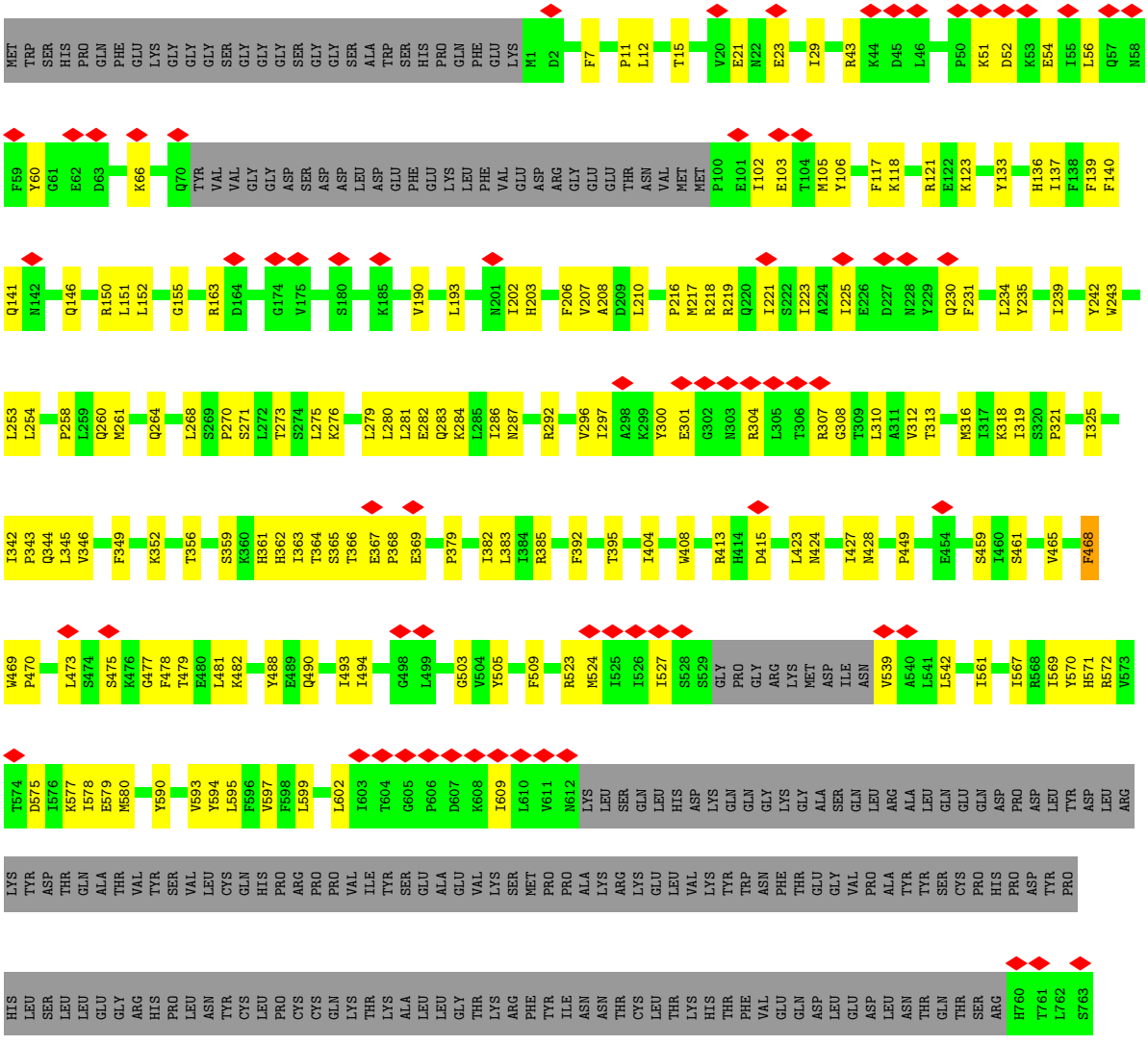
Chain	Residue	Modelled	Actual	Comment	Reference
B	879	PRO	LEU	conflict	UNP Q89525
B	1134	HIS	-	expression tag	UNP Q89525
B	1135	HIS	-	expression tag	UNP Q89525
B	1136	HIS	-	expression tag	UNP Q89525
B	1137	HIS	-	expression tag	UNP Q89525
B	1138	HIS	-	expression tag	UNP Q89525
B	1139	HIS	-	expression tag	UNP Q89525
B	1140	HIS	-	expression tag	UNP Q89525
B	1141	HIS	-	expression tag	UNP Q89525

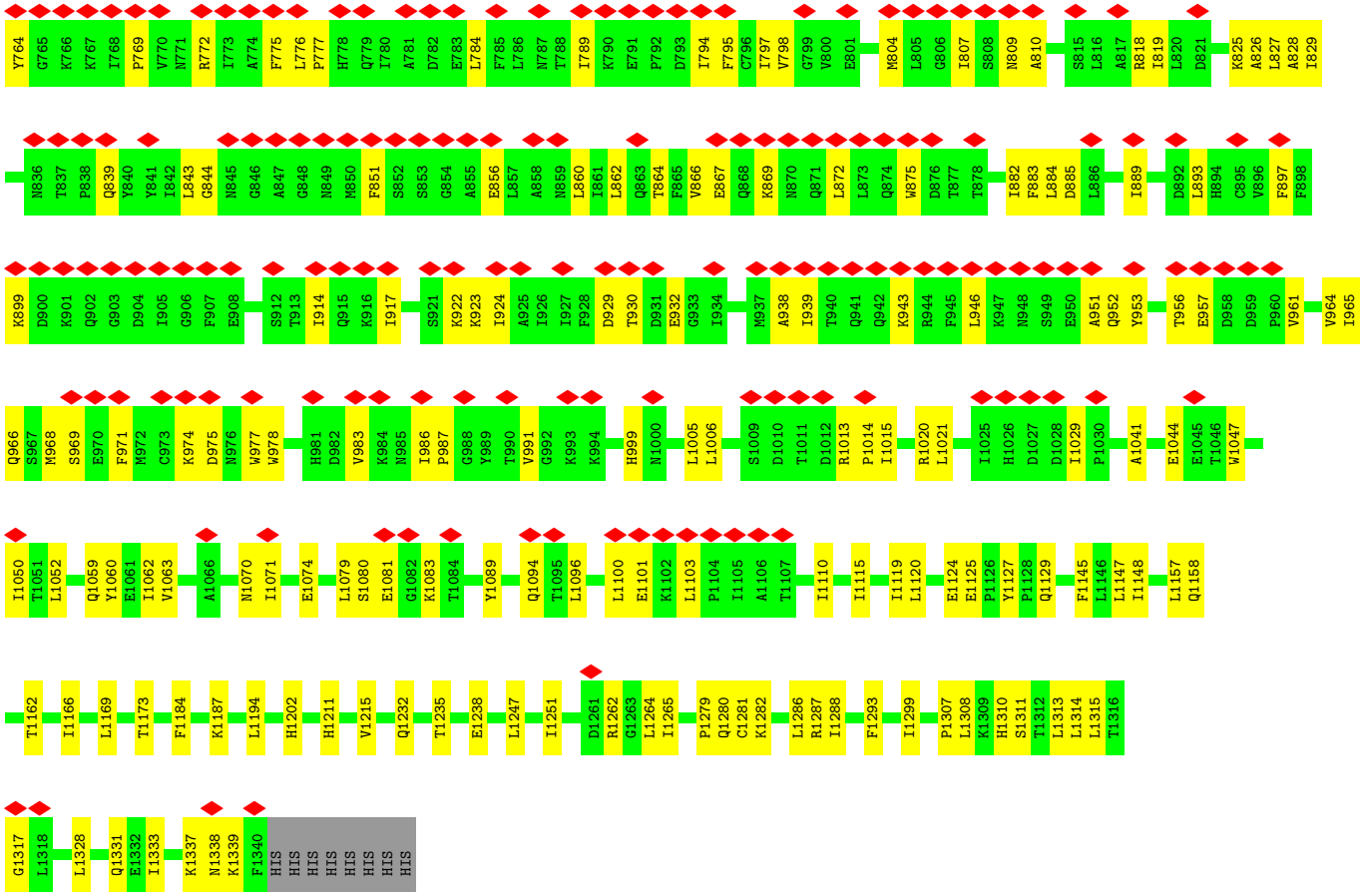
3 Residue-property plots (i)

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.

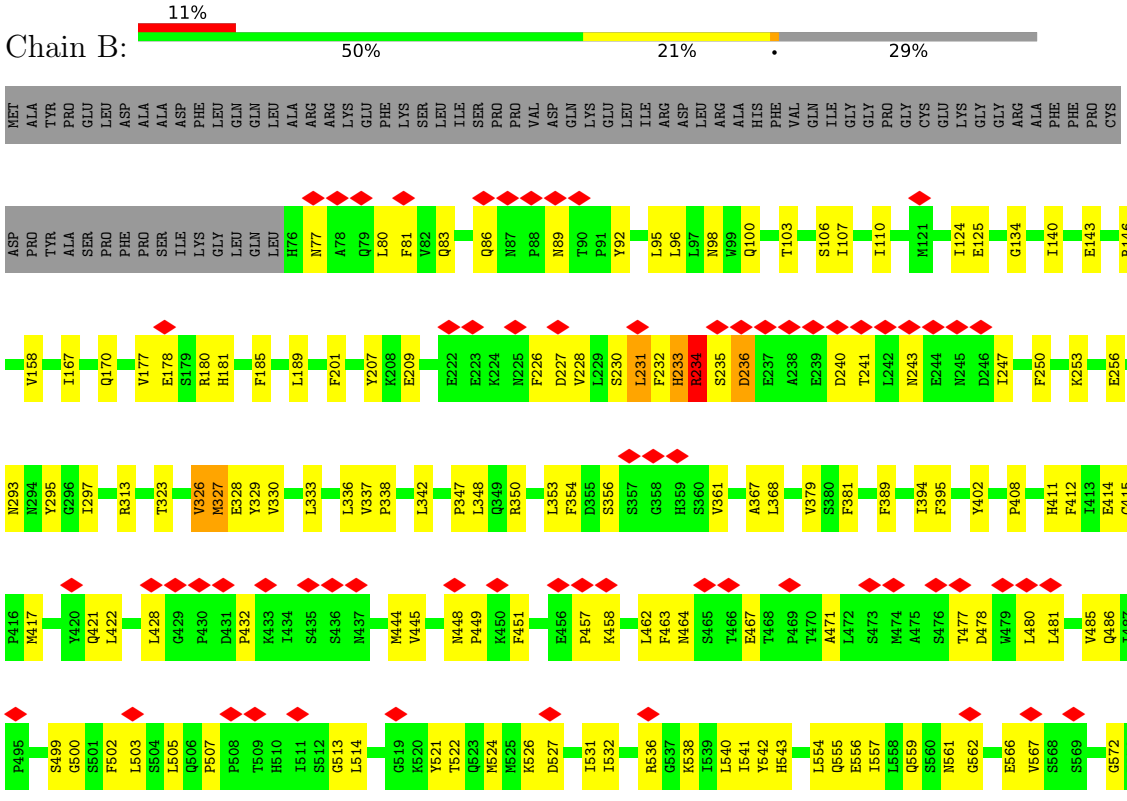
- Molecule 1: Early transcription factor large subunit homolog

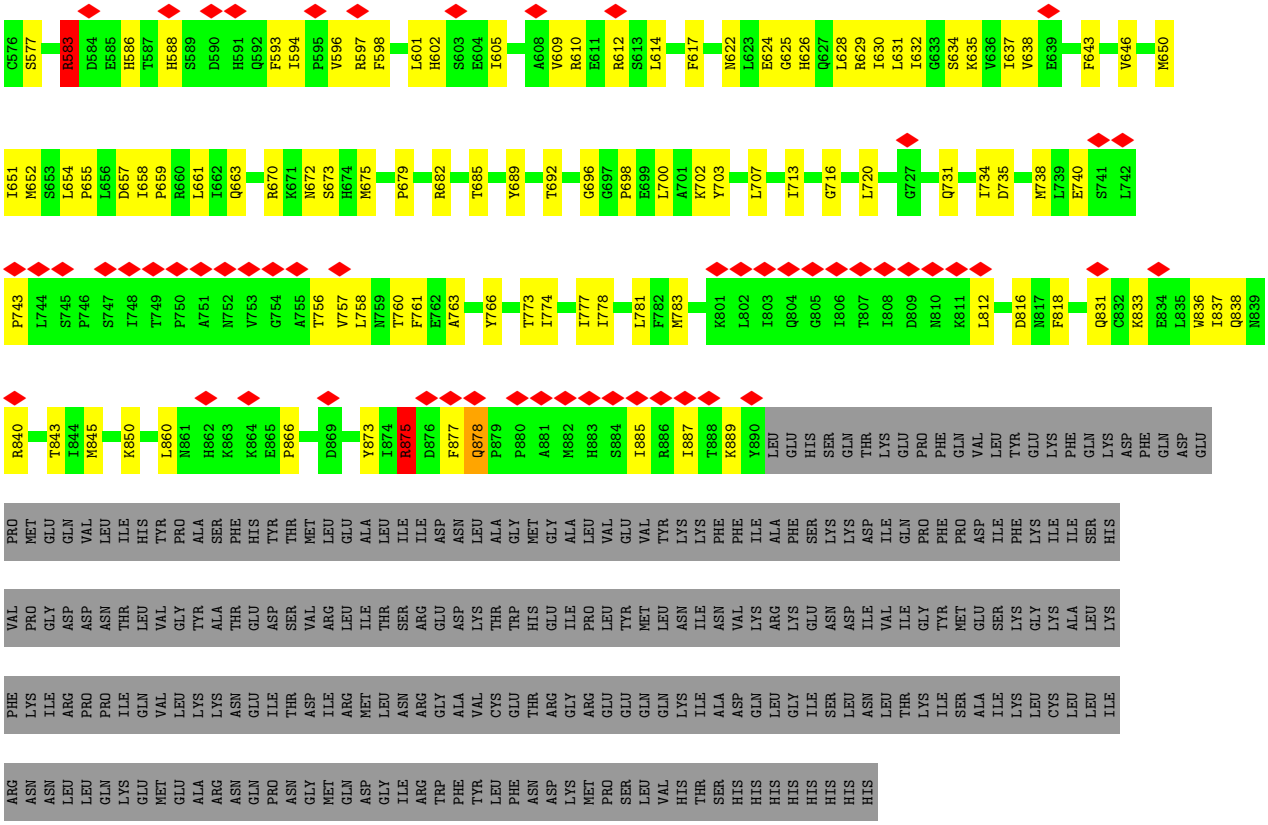
Chain A:





• Molecule 2: Early transcription factor large subunit homolog




C576 S577 R583 D584 E585 H586 T587 H588 S589 D590 H591 Q592 F593 I594 P595 V596 R597 F598 L601 H602 S603 E604 I605 A608 V609 R610 E611 R612 S613 L614 F617 N622 L623 E624 G625 H626 Q627 L628 R629 I630 L631 I632 G633 S634 K635 V636 I637 V638 E639 F643 V646 M650
I651 M652 S653 L654 P655 L656 D657 I658 P659 R660 L661 I662 Q663 R670 K671 N672 S673 H674 M675 P679 R682 T685 Y689 T692 G696 G697 P698 E699 L700 A701 K702 Y703 L707 I713 G716 L720 G727 Q731 I734 D735 M738 L739 E740 S741 L742
P743 L744 S745 P746 S747 I748 T749 P750 A751 N752 V753 G754 A755 T756 V757 L758 N759 T760 F761 E762 A763 Y766 T773 I774 I777 I778 L781 F782 M783 K801 L802 I803 Q804 G805 I806 T807 I808 D809 N810 K811 L812 D816 N817 F818 Q831 C832 K833 E834 L835 W836 I837 Q838 N839
R840 T843 I844 M845 K850 L860 N861 H862 K863 K864 E865 P866 D869 Y873 I874 R875 D876 F877 Q878 P879 P880 A881 M882 H883 S884 I885 R886 I887 T888 K889 Y890 LEU GLU HIS SER GLN THR LYS GLU PRO PHE GLN VAL LEU TYR GLU LYS PHE GLN LYS ASP PHE GLN ASP GLU
PRO MET GLU GLN VAL LEU ILE HIS TYR PRO ALA SER PHE HIS TYR THR MET LEU GLU ALA LEU ILE ILE ASP ASN LEU ALA GLY MET GLY ALA LEU VAL GLU VAL TYR LYS LYS PHE PHE ILE ALA PHE SER LYS LYS ASP ILE GLN PRO PHE PRO ASP ILE PHE LYS ILE ILE SER HIS
VAL PRO GLY ASP ASP ASN THR LEU VAL GLY TYR ALA THR GLU ASP SER VAL ARG LEU ILE THR SER ARG GLU ASP LYS THR TRP HIS GLU ILE PRO LEU TYR MET LEU ASN ILE ILE ASN VAL LYS ARG LYS GLU ASN ASP ILE VAL ILE GLY TYR MET GLU SER LYS GLY LYS ALA LEU LYS
PHE LYS ILE ARG PRO PRO ILE GLN VAL LEU LYS LYS ASN GLU ILE THR ASP ILE ARG MET LEU ASN ARG GLY ALA VAL CYS GLU THR ARG GLY ARG GLU GLU GLN GLN LYS ILE ALA ASP GLN LEU GLY ILE SER LEU ASN LEU THR LYS ILE SER ALA ILE LYS LEU CYS LEU LEU ILE
ARG ASN ASN LEU LEU GLN LYS GLU MET GLU ALA ARG ASN GLN PRO ASN GLY MET GLN ASP GLY ILE ARG TRP PHE TYR LEU PHE ASN ASP LYS MET PRO SER LEU VAL HIS THR SER HIS HIS HIS HIS HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	108829	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.558	Depositor
Minimum map value	-0.372	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0506	Depositor
Map size (Å)	298.88, 298.88, 298.88	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.934, 0.934, 0.934	Depositor

5 Model quality

5.1 Standard geometry

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	0.15	0/9698	0.36	0/13167
2	B	0.22	0/6686	0.42	0/9064
All	All	0.18	0/16384	0.39	0/22231

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
2	B	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
2	B	234	ARG	Sidechain
2	B	583	ARG	Sidechain
2	B	875	ARG	Sidechain

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	9463	0	9462	248	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	6534	0	6563	185	0
All	All	15997	0	16025	417	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 13.

The worst 5 of 417 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)
2:B:185:PHE:CE1	2:B:189:LEU:HD11	1.83	1.12
1:A:346:VAL:HG22	1:A:359:SER:HB2	1.36	1.03
1:A:481:LEU:HD11	1:A:602:LEU:HD11	1.44	0.99
2:B:185:PHE:CE1	2:B:189:LEU:CD1	2.59	0.86
2:B:124:ILE:HG23	2:B:201:PHE:HZ	1.43	0.82

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	1147/1377 (83%)	1068 (93%)	79 (7%)	0	100	100
2	B	813/1141 (71%)	742 (91%)	71 (9%)	0	100	100
All	All	1960/2518 (78%)	1810 (92%)	150 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM

entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1056/1252 (84%)	1049 (99%)	7 (1%)	76 79
2	B	725/1016 (71%)	708 (98%)	17 (2%)	44 64
All	All	1781/2268 (78%)	1757 (99%)	24 (1%)	59 72

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	326	VAL
2	B	415	CYS
2	B	328	GLU
2	B	463	PHE
1	A	1337	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	243	ASN
2	B	592	GLN
2	B	561	ASN
2	B	602	HIS
1	A	966	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)

There are no ligands in this entry.

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.

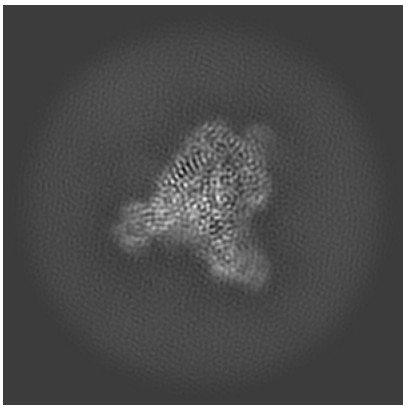
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-81562. These allow visual inspection of the internal detail of the map and identification of artifacts.

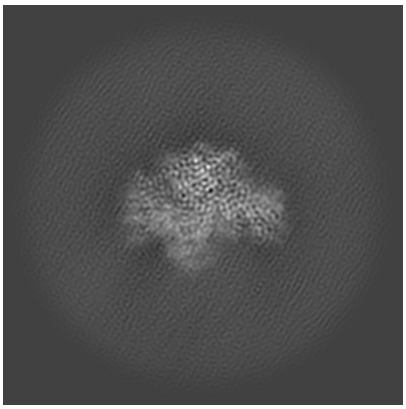
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

6.1.1 Primary map



X



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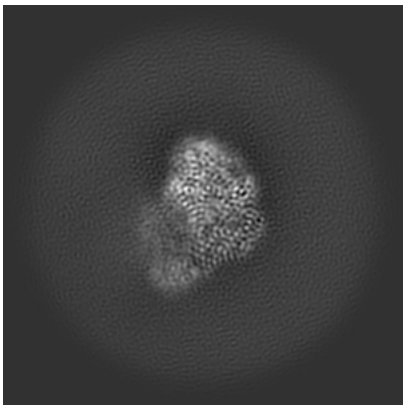
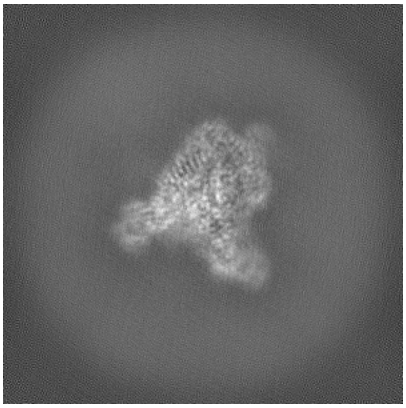


Z

6.1.2 Raw map



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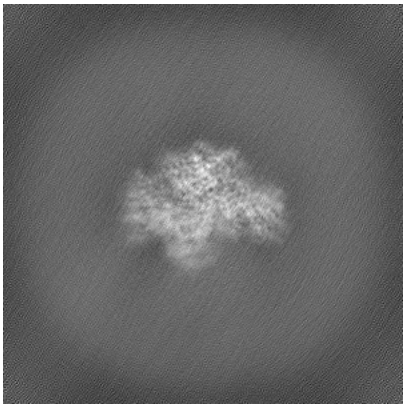
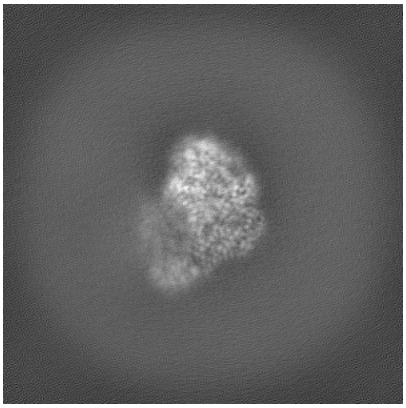


Y

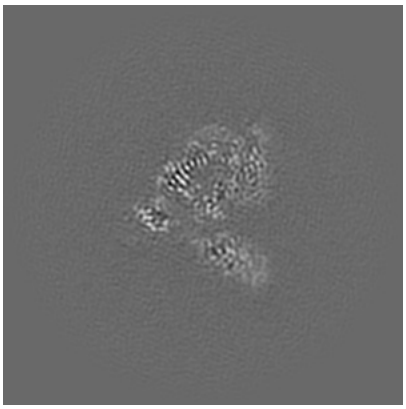


Z

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

6.2 Central slices (i)

6.2.1 Primary map



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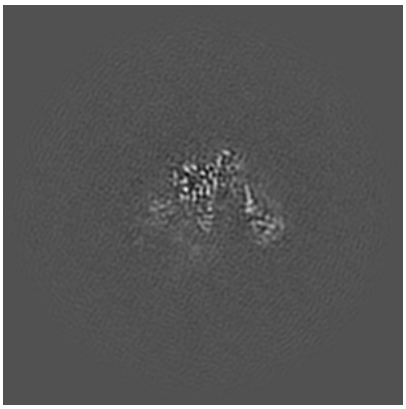

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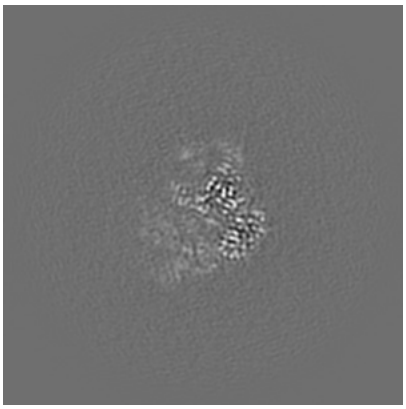
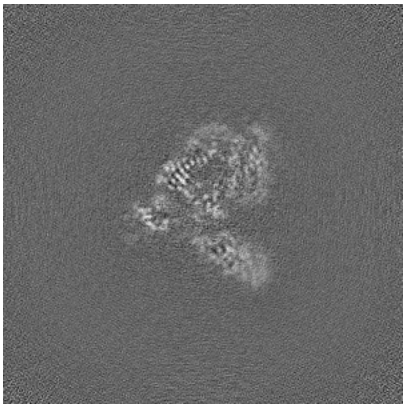
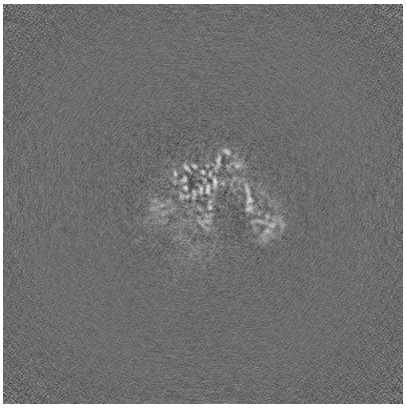


Z Index: 160

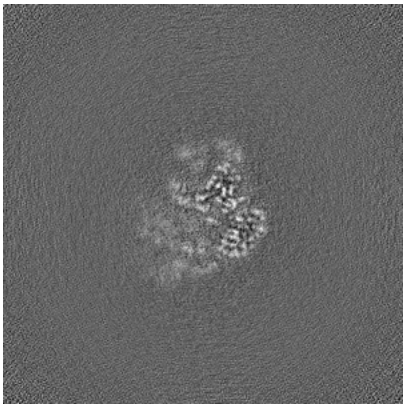
6.2.2 Raw map



X Index: 160



Y Index: 160

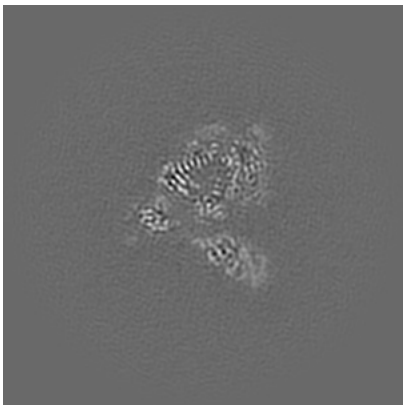


Z Index: 160

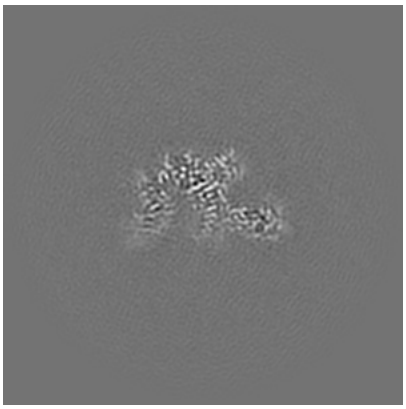
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

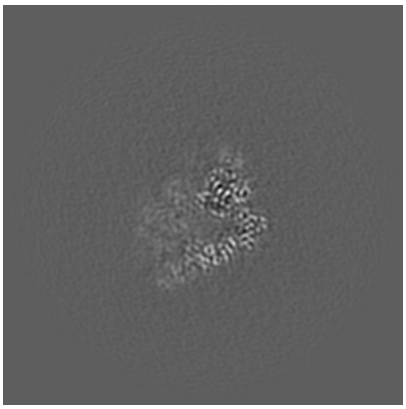
6.3.1 Primary map



X Index: 159

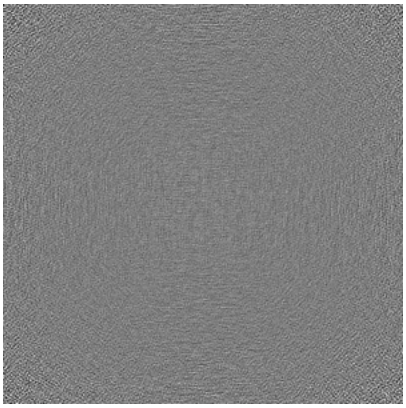


Y Index: 172

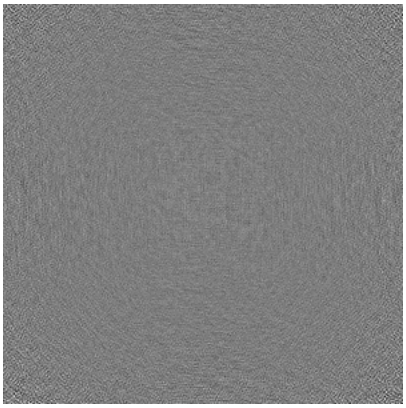


Z Index: 155

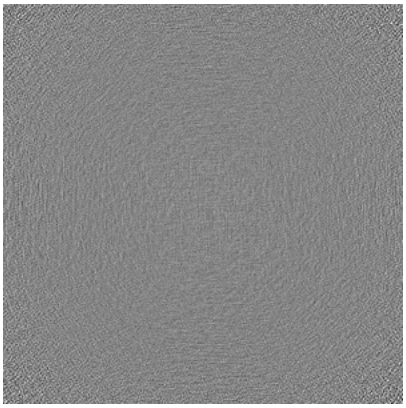
6.3.2 Raw map



X Index: 0



Y Index: 0

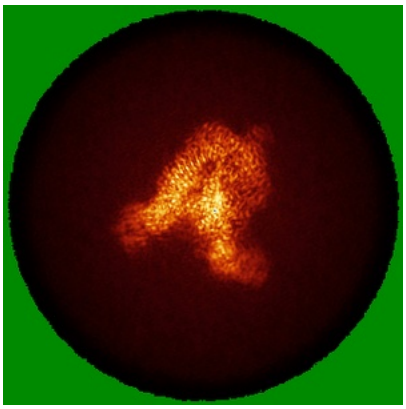


Z Index: 319

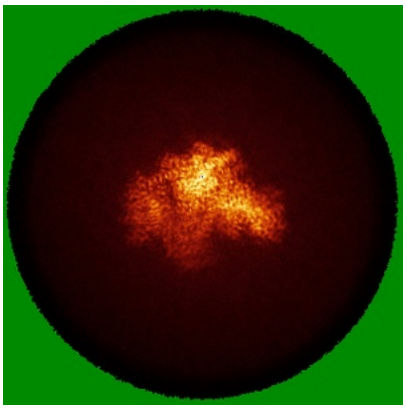
The images above show the largest variance slices of the map in three orthogonal directions.

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

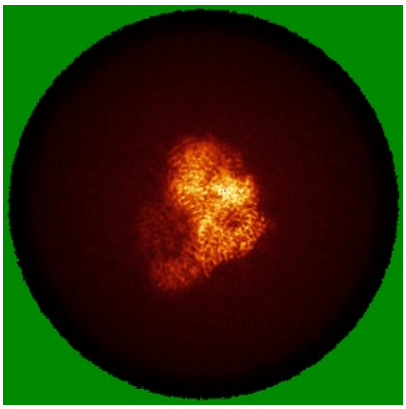
6.4.1 Primary map



X

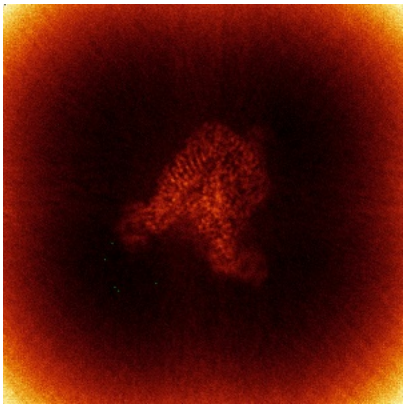


Y

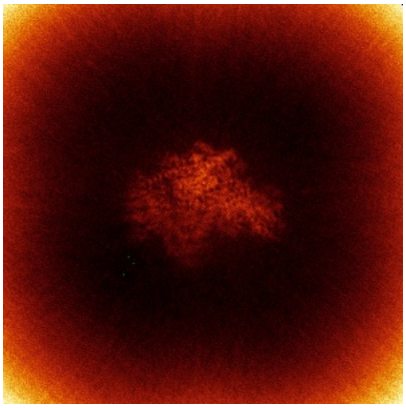


Z

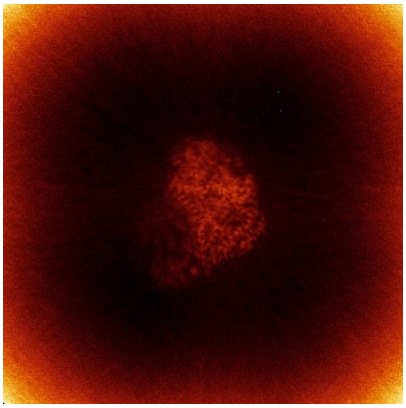
6.4.2 Raw map



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 0.0506. 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.

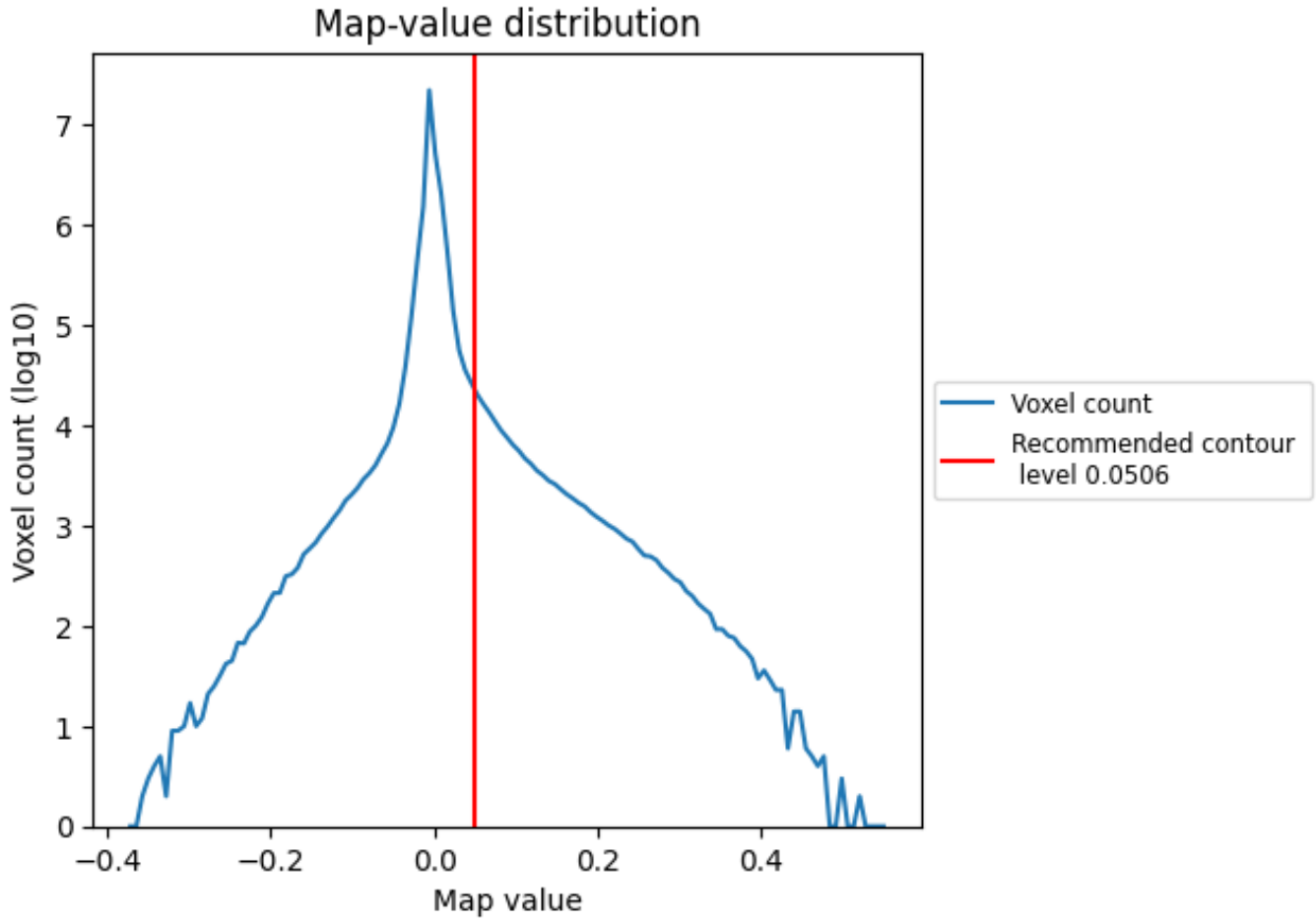
6.6 Mask visualisation (i)

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

7 Map analysis

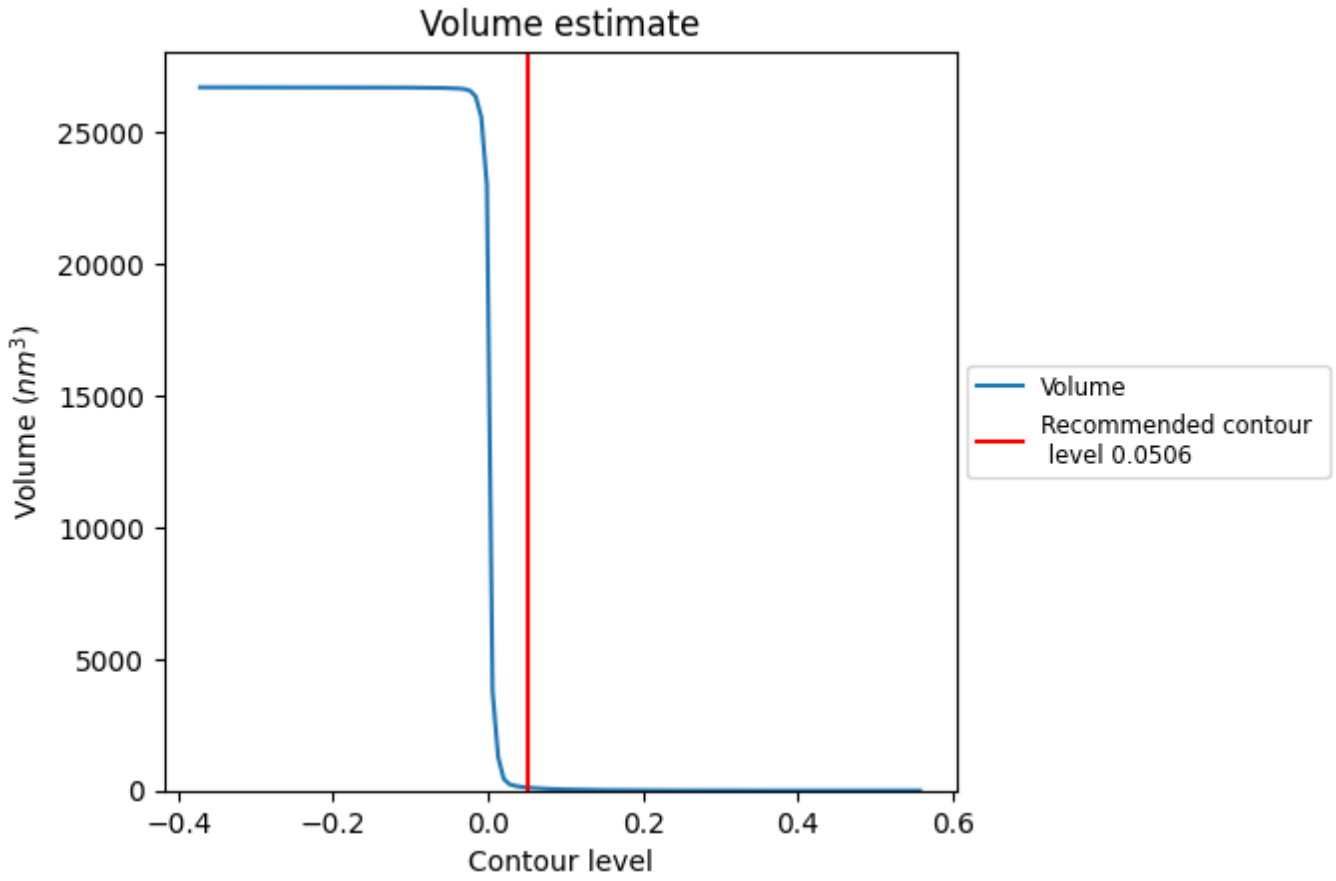
This section contains the results of statistical analysis of the map.

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.

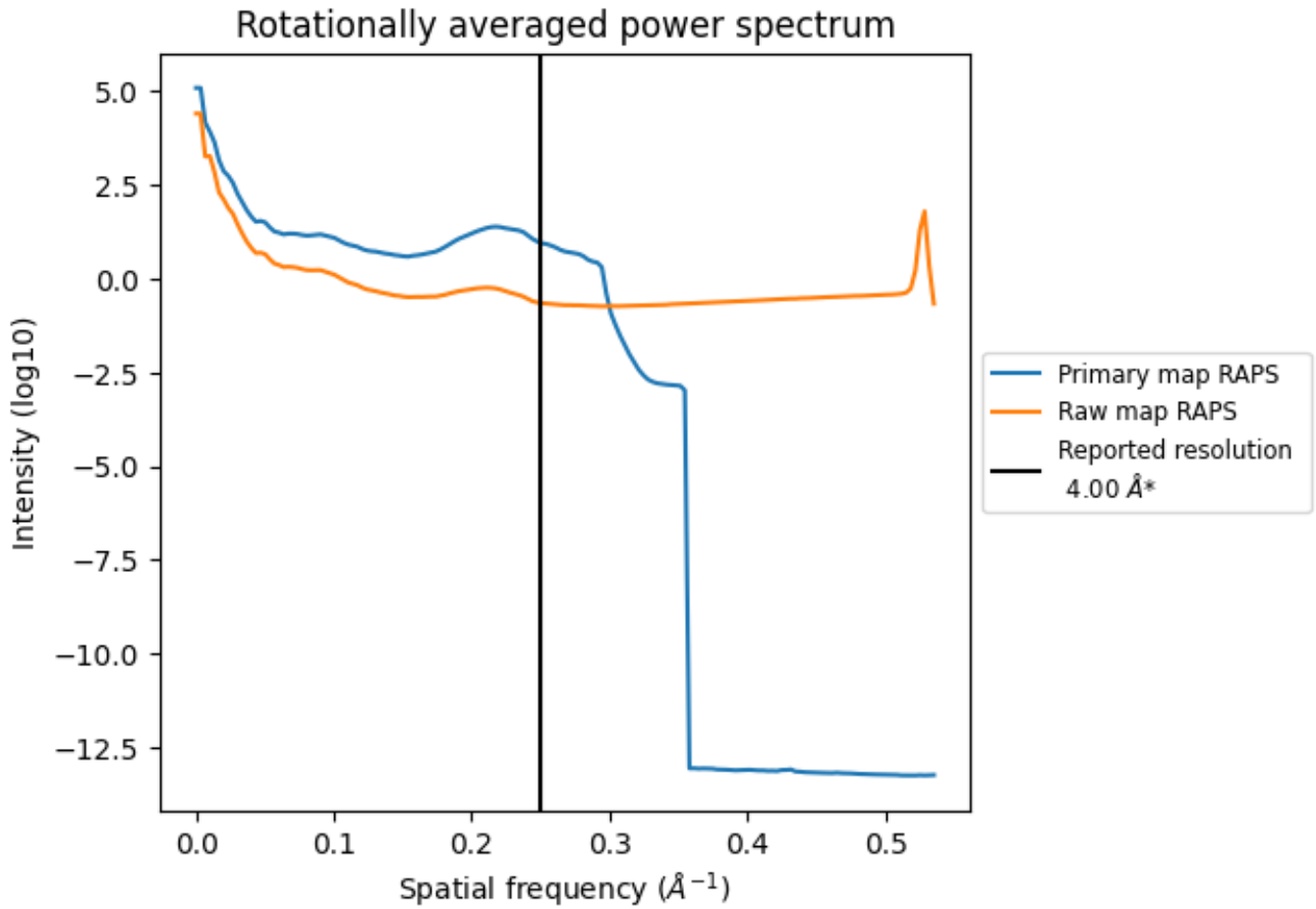
7.2 Volume estimate (i)



The volume at the recommended contour level is 115 nm^3; this corresponds to an approximate mass of 104 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)

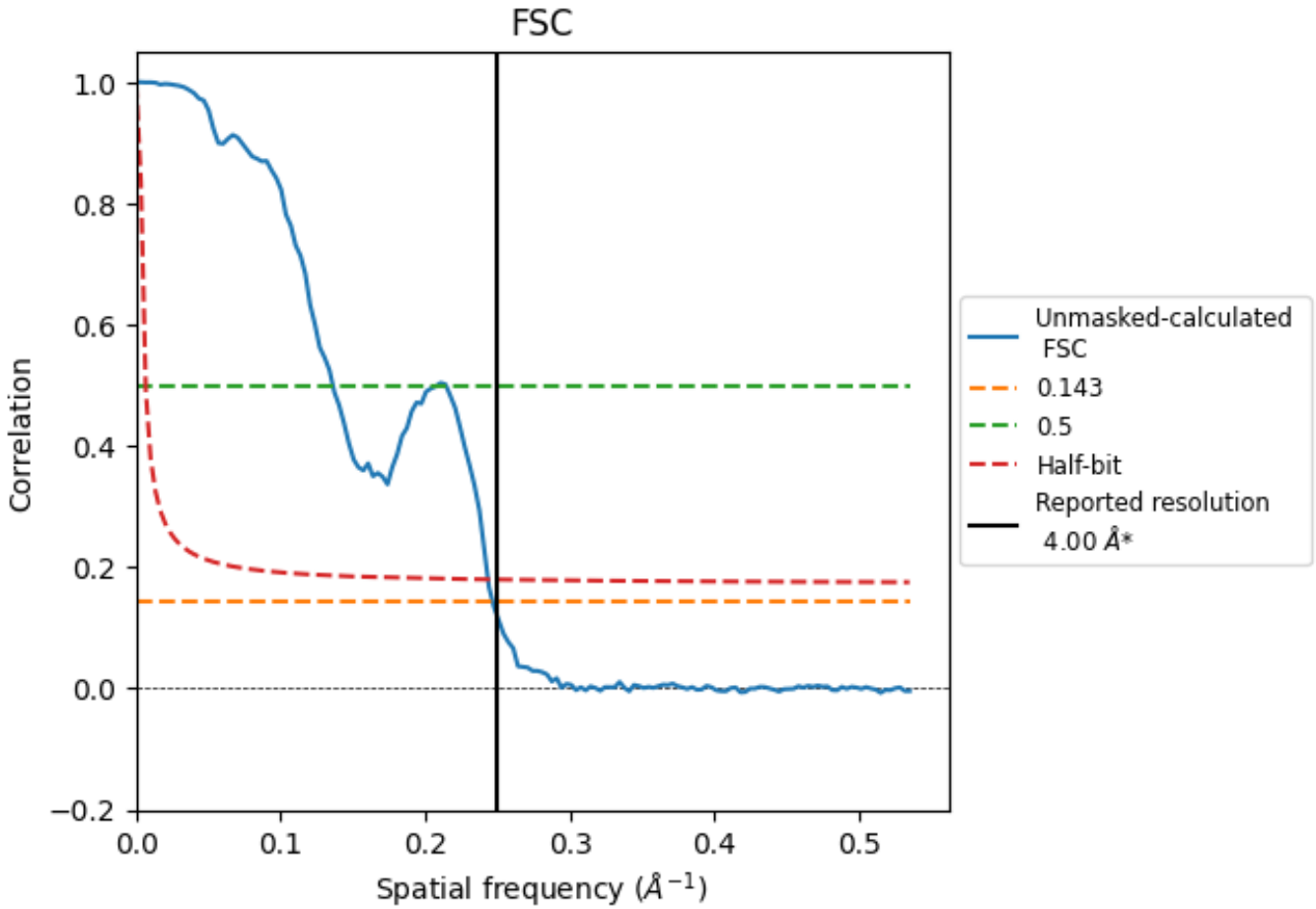


*Reported resolution corresponds to spatial frequency of 0.250 $Å^{-1}$

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)

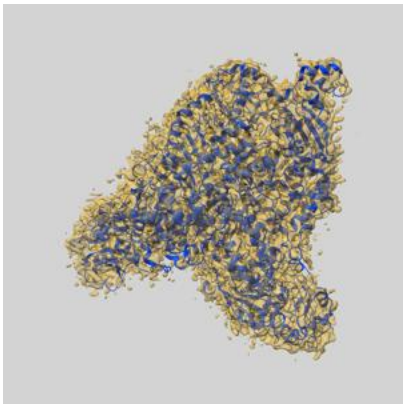
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.05	7.35	4.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

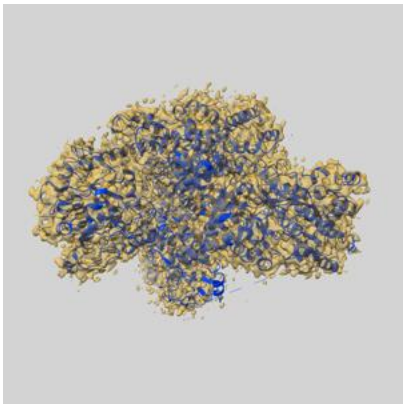
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-81562 and PDB model 27ZK. Per-residue inclusion information can be found in section 3 on page 5.

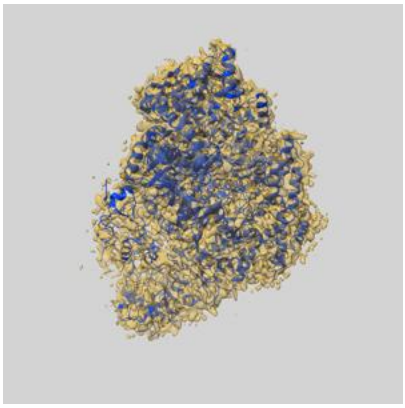
9.1 Map-model overlay



X



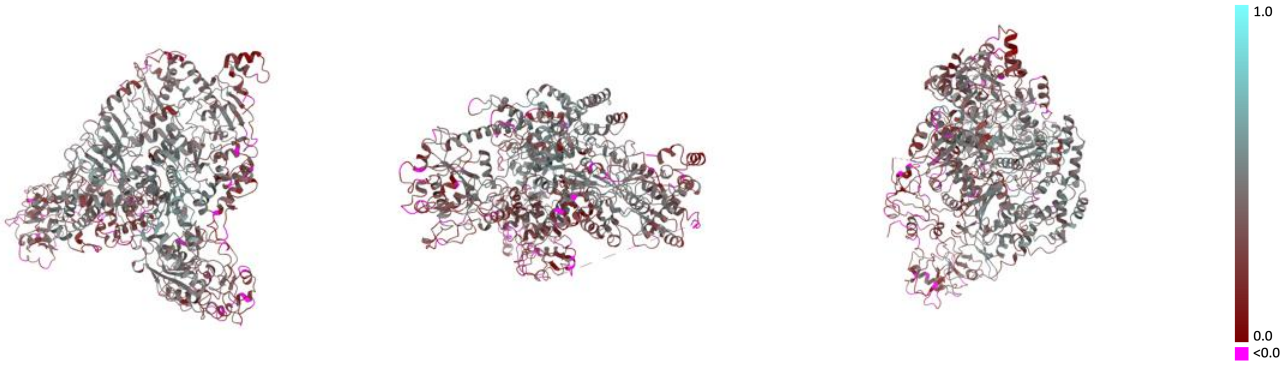
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0506 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.

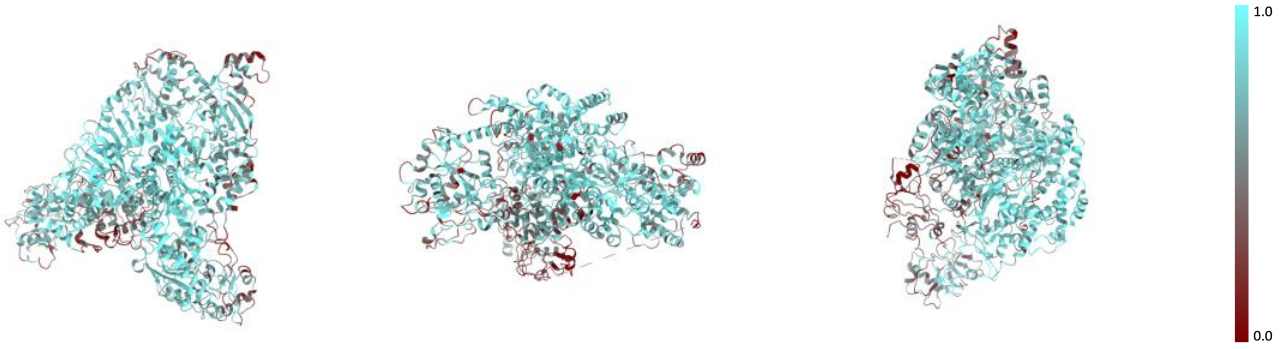
9.2 Q-score mapped to coordinate model (i)



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.

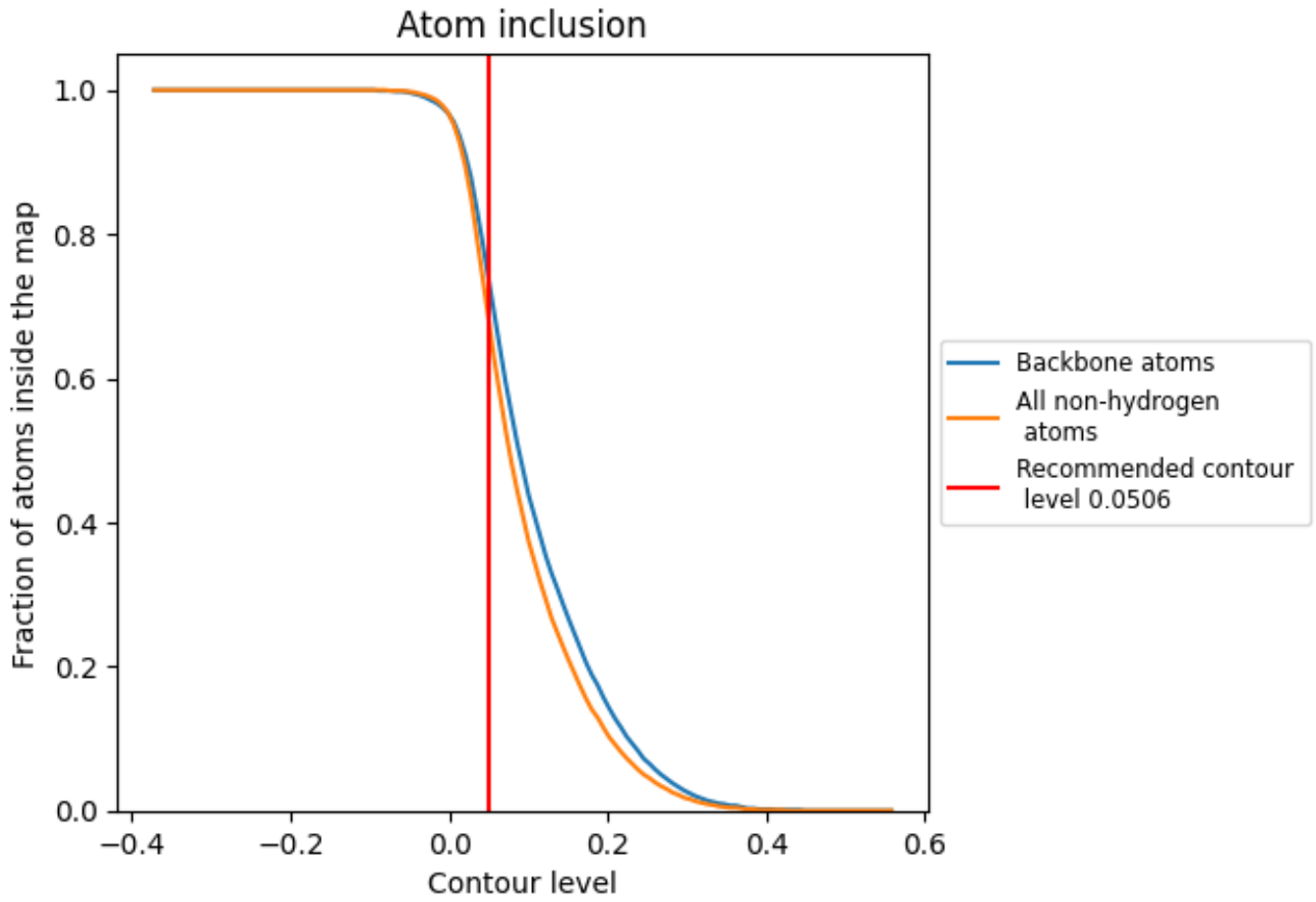
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0506).

9.4 Atom inclusion (i)



At the recommended contour level, 73% of all backbone atoms, 68% 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 (0.0506) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6760	0.3470
A	0.6550	0.3370
B	0.7050	0.3610