wwPDB EM Validation Summary Report

Nov 10, 2026 – 06:20 PM JST

PDB ID	:	27ZU / pdb_000027zu
EMDB ID	:	EMD-81570
Title	:	Atomic structure of the ASFV virus early transcription factor in DC 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:

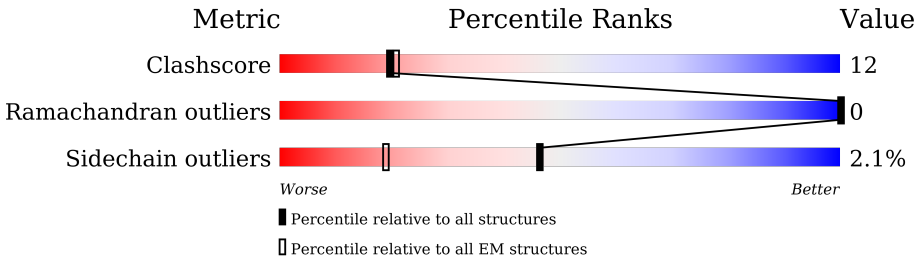
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

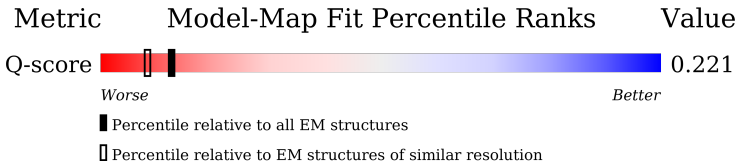
1 Overall quality at a glance (i)

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	B	1141	8% 52% 22% · 25%
2	A	1377	25% 59% 18% 23%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 15583 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
			Total	C	N	O	S		
1	B	857	6860	4404	1181	1247	28	0	0

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	1067	8723	5681	1416	1600	26	0	0

There are 45 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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	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

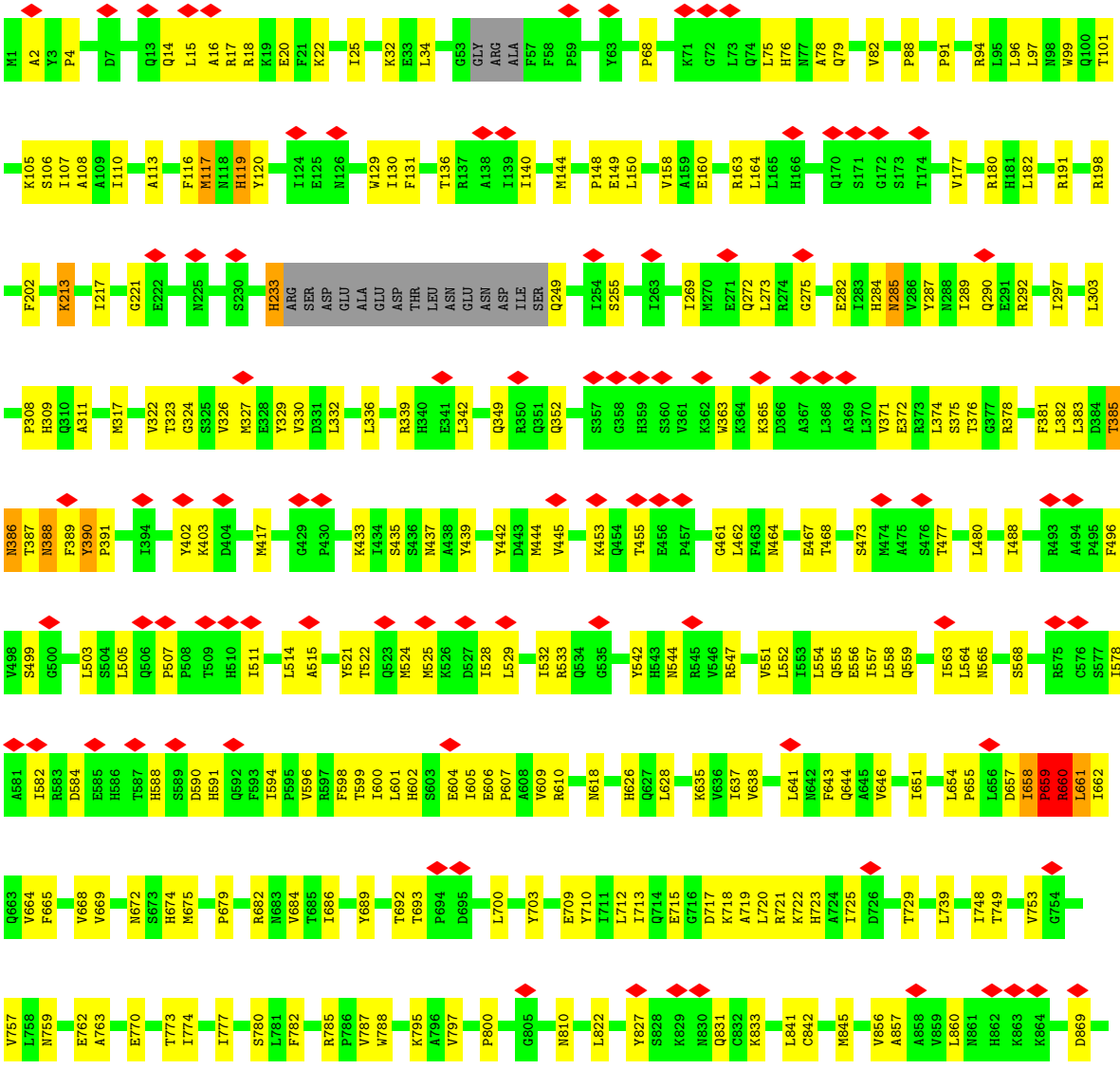
3 Residue-property plots (i)

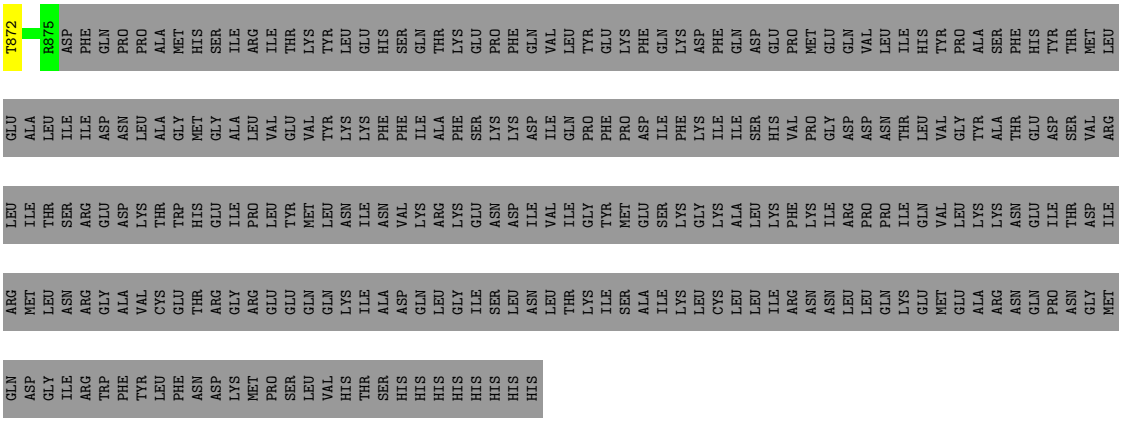
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 B:



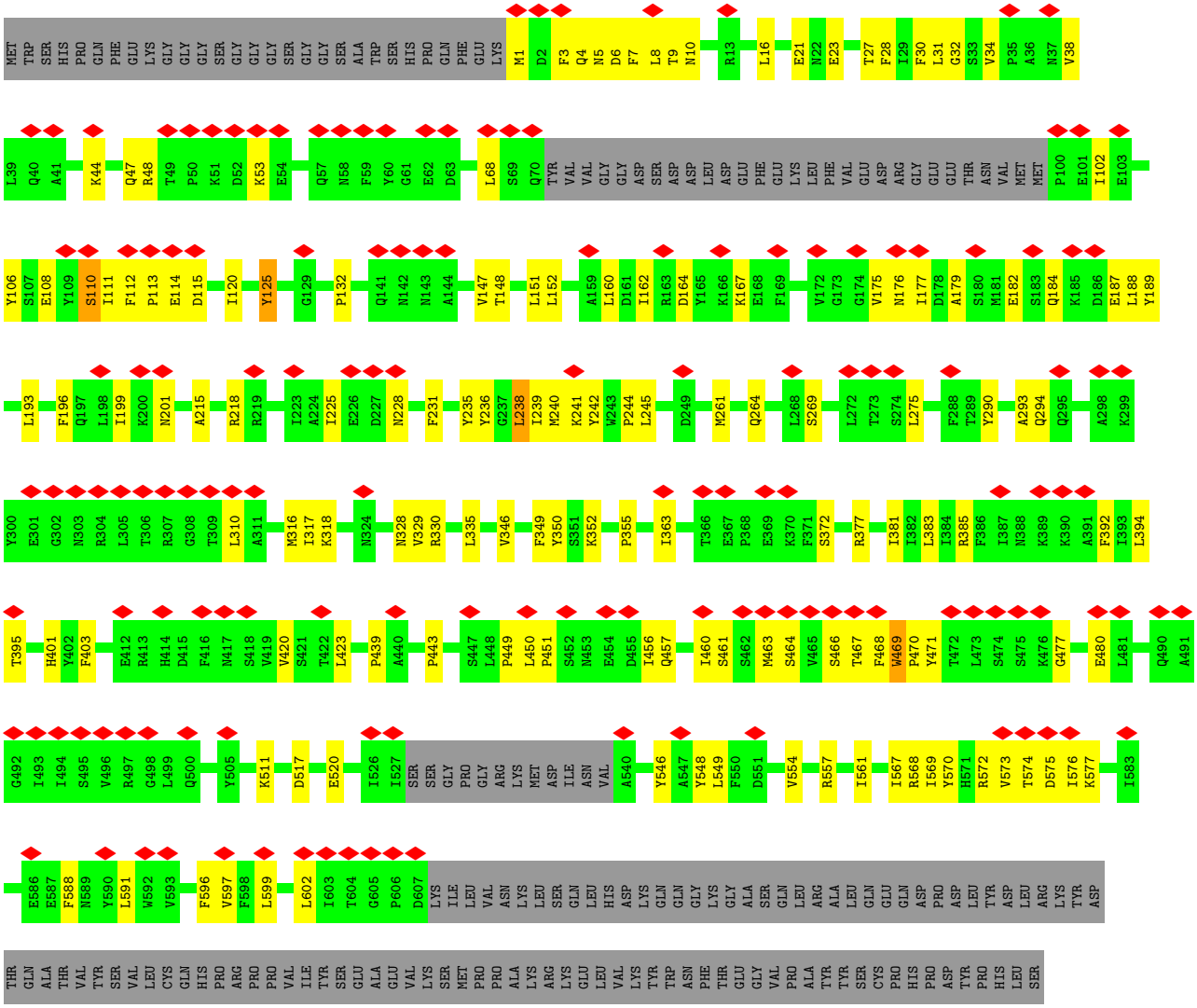


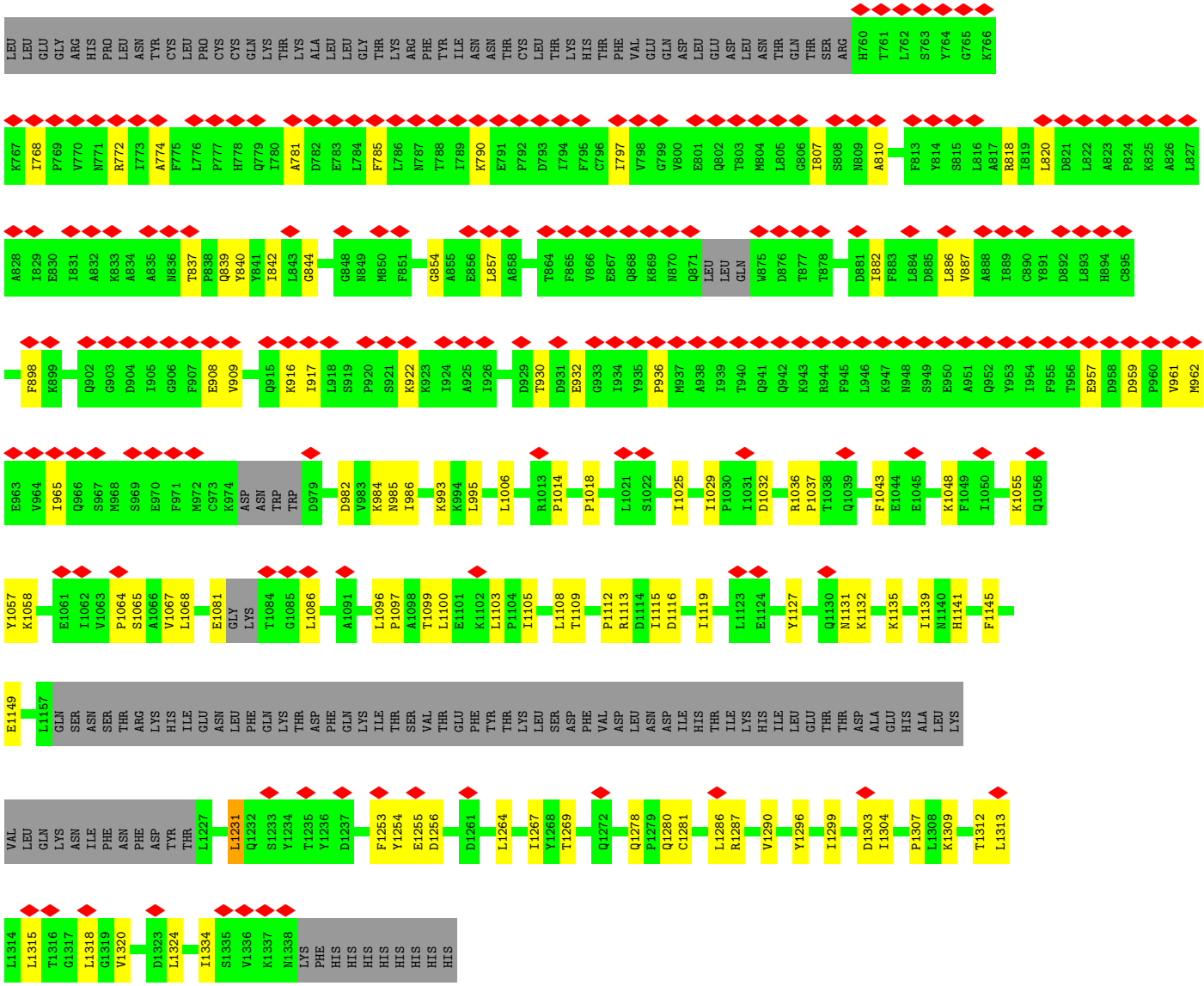


• Molecule 2: Early transcription factor large subunit homolog

Chain A:






LEU LEU GLU GLY ARG HIS PRO LEU ASN TYR CYS LEU PRO CYS CYS GLN LYS THR LYS ALA LEU LEU GLY THR LYS ARG PHE TYR ILE ASN ASN THR CYS LEU THR LYS HIS THR PHE VAL GLU GLN ASP LEU GLU ASP LEU ASN THR GLN THR SER ARG H760 T761 L762 S763 Y764 G765 K766
K767 I768 P769 V770 N771 R772 I773 A774 F775 L776 P777 H778 Q779 I780 A781 D782 E783 L784 F785 L786 N787 T788 I789 K790 E791 P792 D793 I794 F795 C796 I797 V798 G799 V800 E801 Q802 T803 M804 L805 G806 I807 S808 N809 A810 F813 Y814 S815 L816 A817 R818 I819 L820 D821 L822 A823 P824 K825 A826 L827
A828 I829 E830 I831 A832 K833 A834 A835 N836 T837 P838 Q839 Y840 Y841 I842 L843 G844 G848 N849 M850 F851 G854 A855 E856 L857 A858 T864 F865 V866 E867 Q868 K869 N870 Q871 LEU LEU GLN W875 D876 T877 T878 D881 I882 F883 L884 D885 L886 V887 A888 I889 C890 Y891 D892 L893 H894 C895
F898 K899 Q902 G903 D904 I905 G906 F907 E908 V909 Q915 K916 I917 L918 S919 P920 S921 K922 K923 I924 A925 I926 D929 T930 D931 E932 G933 I934 Y935 P936 M937 A938 I939 T940 Q941 Q942 K943 R944 F945 L946 K947 N948 S949 E950 A951 Q952 Y953 I954 F955 T956 E957 D958 D959 P960 V961 M962
E963 V964 I965 Q966 S967 M968 S969 E970 F971 M972 C973 K974 ASP ASN TRP TRP D979 D982 V983 K984 N985 I986 K993 K994 L995 L1006 R1013 P1014 P1018 L1021 S1022 I1025 I1029 P1030 I1031 D1032 R1036 P1037 T1038 Q1039 F1043 E1044 E1045 K1048 F1049 I1050 K1055 Q1056
Y1057 K1058 E1061 I1062 V1063 P1064 S1065 A1066 V1067 L1068 E1081 GLY LYS T1084 G1085 L1086 A1091 L1096 P1097 A1098 T1099 L1100 E1101 K1102 L1103 P1104 I1105 L1108 T1109 P1112 R1113 D1114 I1115 D1116 I1119 L1123 E1124 Y1127 Q1130 N1131 K1132 K1135 I1139 N1140 H1141 F1145
E1149 L1157 GLN SER ASN SER THR ARG LYS HIS ILE GLU ASN LEU PHE GLN LYS THR ASP PHE GLN LYS ILE THR SER VAL THR GLU PHE TYR THR LYS LEU SER ASP PHE VAL ASP LEU ASN ASP ILE HIS THR ILE LYS HIS ILE LEU GLU THR THR ASP ALA GLU HIS ALA LEU LYS
VAL LEU GLN LYS ASN ILE PHE ASN PHE ASP TYR THR L1227 L1231 Q1232 S1233 Y1234 T1235 Y1236 D1237 F1253 Y1254 E1255 D1256 D1261 L1264 I1267 Y1268 T1269 Q1272 Q1278 P1279 Q1280 C1281 L1286 R1287 V1290 Y1296 I1299 D1303 I1304 P1307 L1308 K1309 T1312 L1313
L1314 L1315 T1316 G1317 L1318 G1319 V1320 D1323 L1324 I1334 S1335 V1336 K1337 N1338 LYS PHE 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	73062	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	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.618	Depositor
Minimum map value	-0.975	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	266.24, 266.24, 266.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

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	B	0.28	0/7022	0.60	6/9514 (0.1%)
2	A	0.20	0/8937	0.52	3/12130 (0.0%)
All	All	0.24	0/15959	0.56	9/21644 (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	B	0	1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	468	PHE	CA-C-N	12.80	141.91	121.17
2	A	468	PHE	C-N-CA	12.80	141.91	121.17
1	B	390	TYR	CB-CA-C	-6.24	99.17	109.15
1	B	660	ARG	N-CA-C	-5.89	105.19	112.38
1	B	659	PRO	CA-CB-CG	-5.36	94.33	104.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	660	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	B	6860	0	6910	211	0
2	A	8723	0	8722	188	0
All	All	15583	0	15632	389	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 389 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:563:ILE:O	1:B:598:PHE:HE2	1.29	1.12
1:B:376:THR:HG23	1:B:723:HIS:CB	1.80	1.11
1:B:762:GLU:HG3	2:A:1139:ILE:HG22	1.21	1.11
2:A:114:GLU:HG2	2:A:290:TYR:CD2	1.85	1.10
2:A:10:ASN:HB2	2:A:111:ILE:HD12	1.42	1.00

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	B	851/1141 (75%)	781 (92%)	70 (8%)	0	100	100
2	A	1051/1377 (76%)	963 (92%)	88 (8%)	0	100	100
All	All	1902/2518 (76%)	1744 (92%)	158 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	B	758/1016 (75%)	741 (98%)	17 (2%)	45	65
2	A	970/1252 (78%)	951 (98%)	19 (2%)	48	66
All	All	1728/2268 (76%)	1692 (98%)	36 (2%)	46	65

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	561	ILE
2	A	1324	LEU
2	A	567	ILE
2	A	1127	TYR
1	B	659	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	985	ASN
2	A	1134	ASN
2	A	1241	GLN
2	A	1131	ASN
1	B	559	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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.

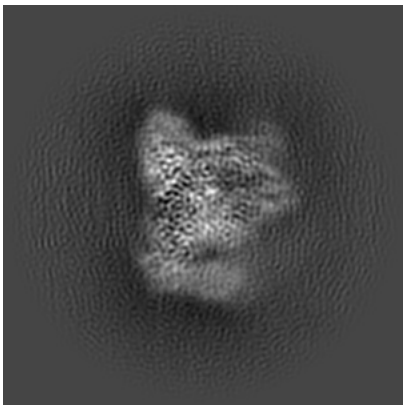
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-81570. These allow visual inspection of the internal detail of the map and identification of artifacts.

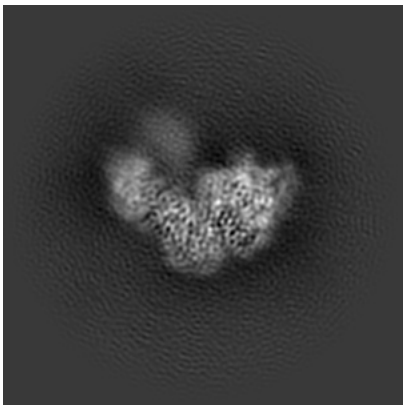
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

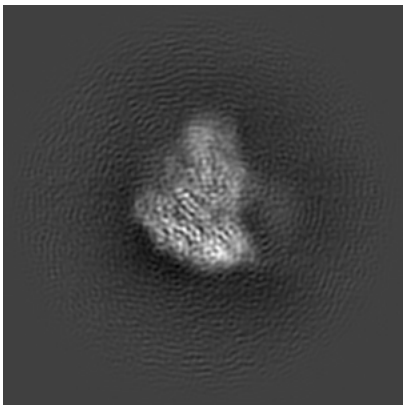
6.1.1 Primary map



X

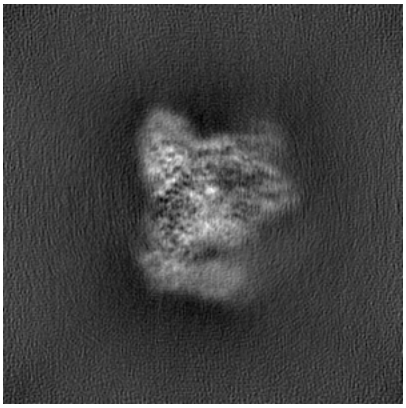


Y

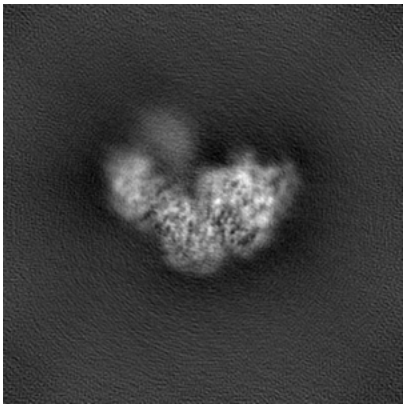


Z

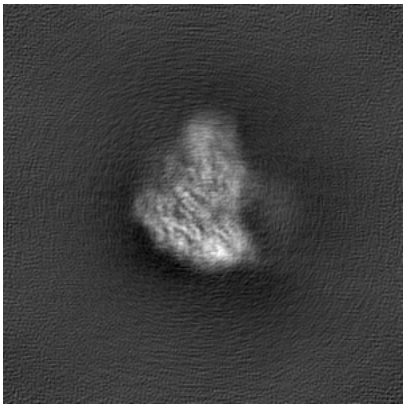
6.1.2 Raw map



X



Y

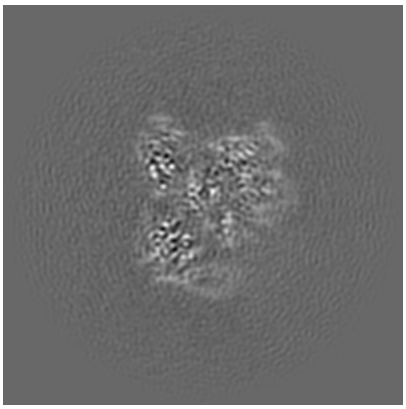


Z

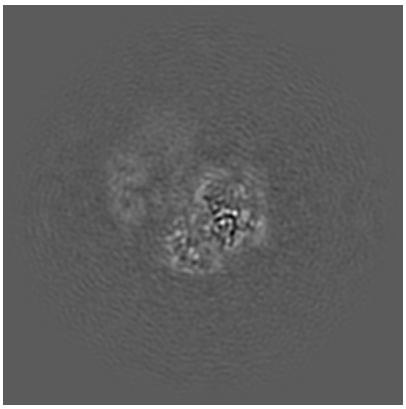
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

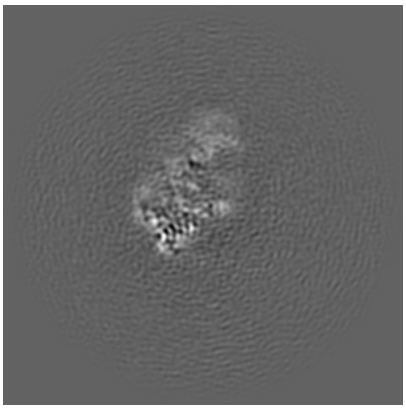
6.2.1 Primary map



X Index: 128

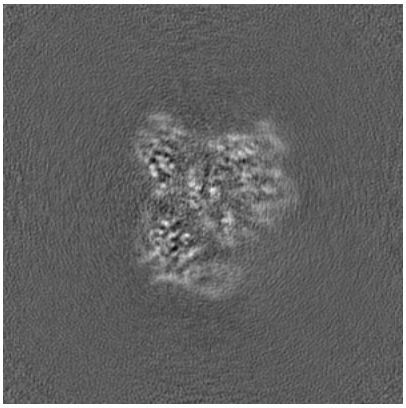


Y Index: 128

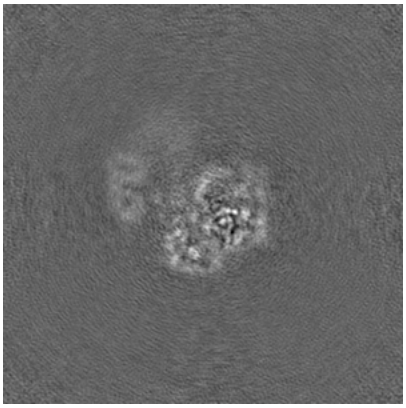


Z Index: 128

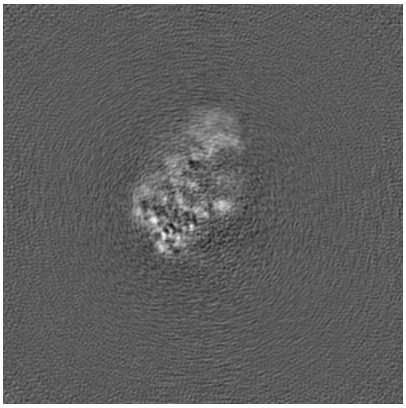
6.2.2 Raw map



X Index: 128



Y Index: 128

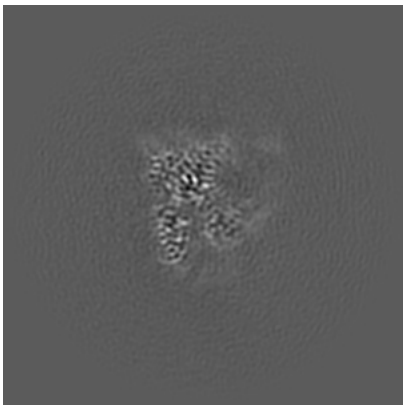


Z Index: 128

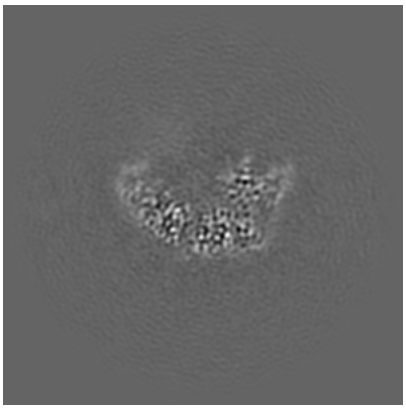
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

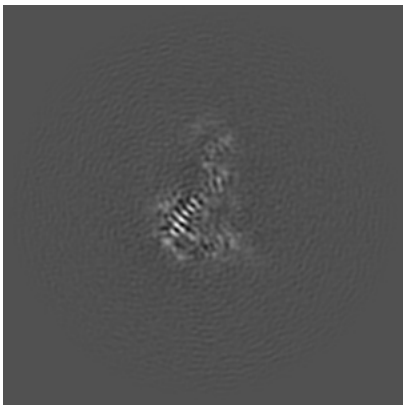
6.3.1 Primary map



X Index: 116

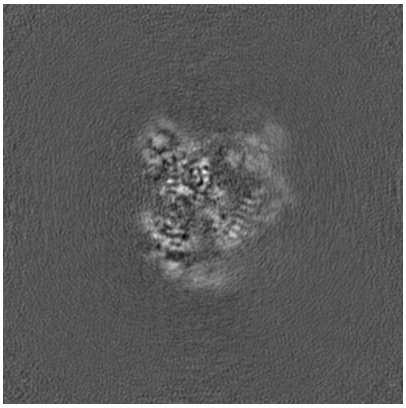


Y Index: 110

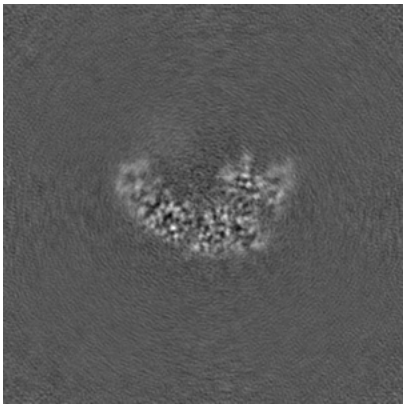


Z Index: 143

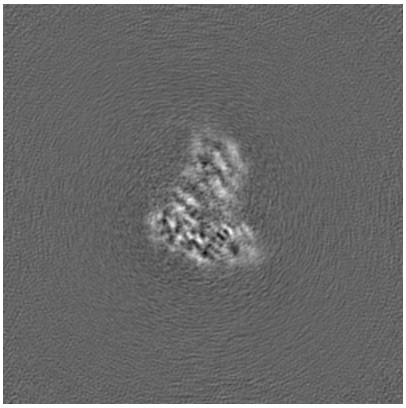
6.3.2 Raw map



X Index: 122



Y Index: 109

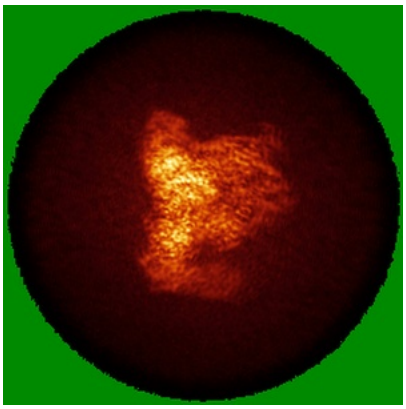


Z Index: 155

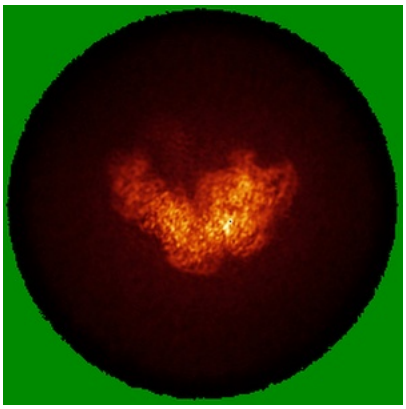
The images above show the largest variance slices of the map in three orthogonal directions.

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

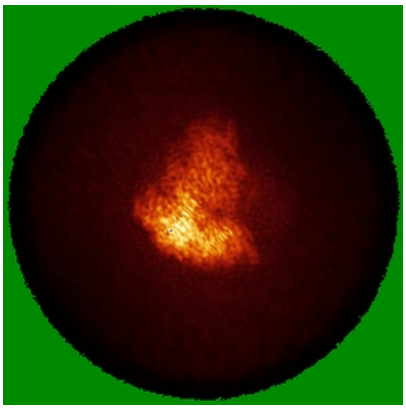
6.4.1 Primary map



X

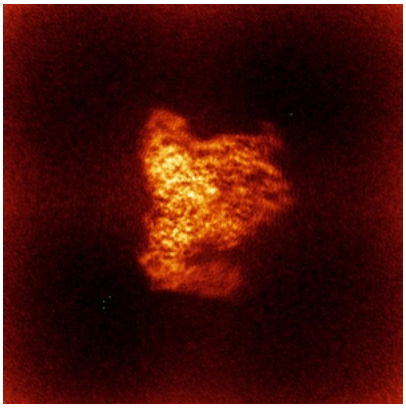


Y

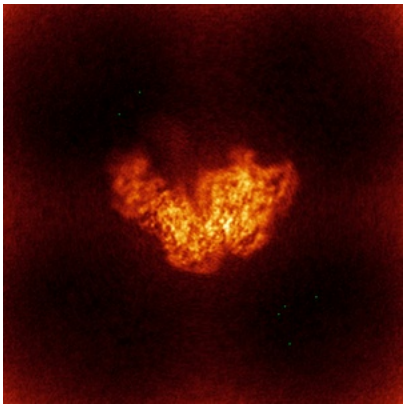


Z

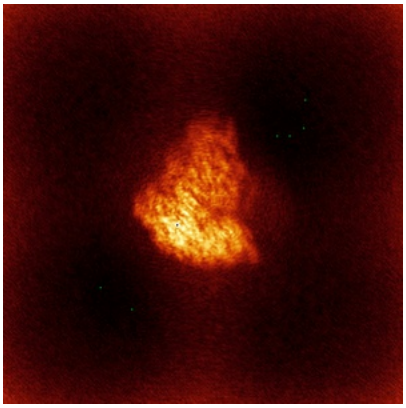
6.4.2 Raw map



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 0.11. 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.

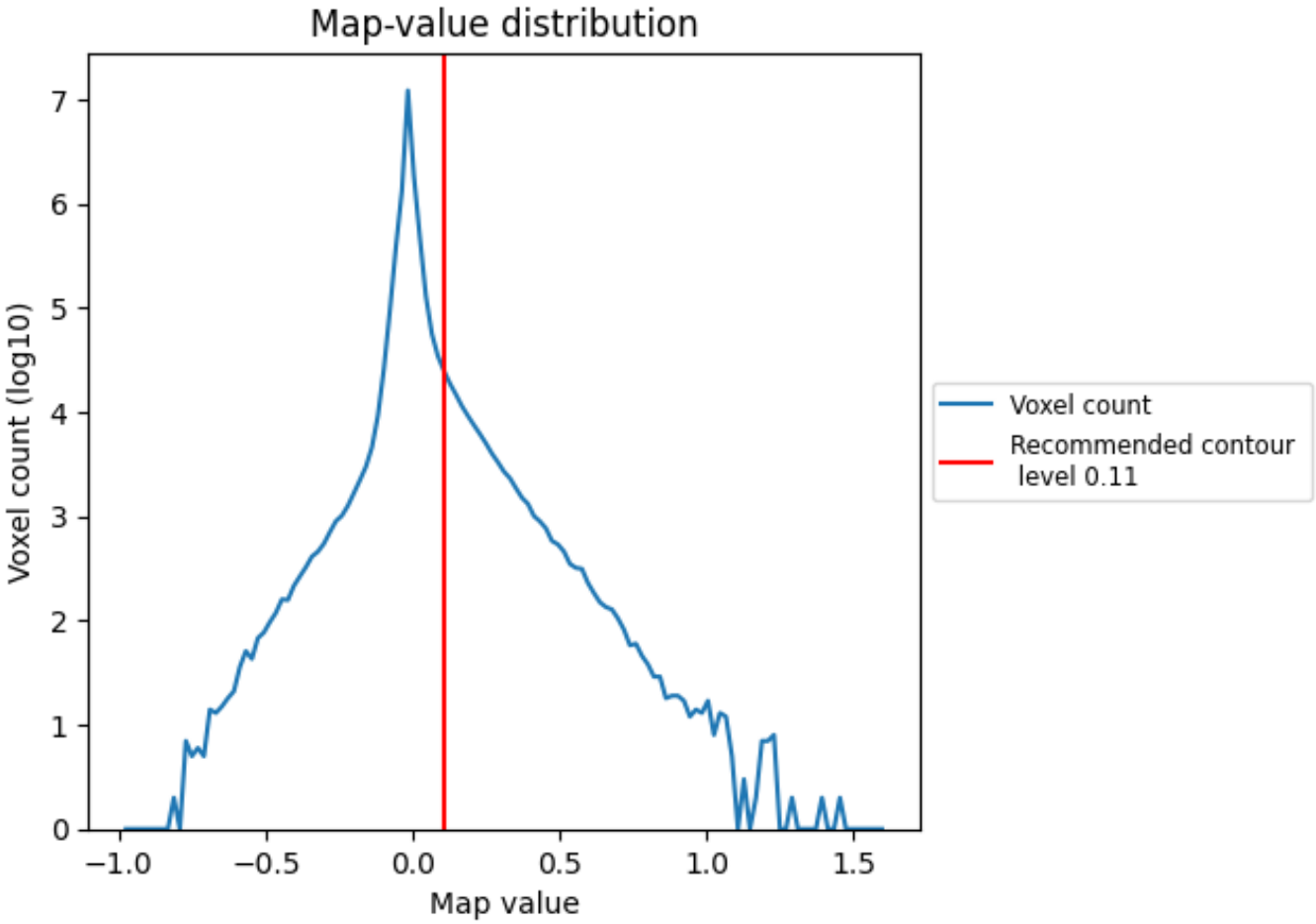
6.6 Mask visualisation (i)

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

7 Map analysis

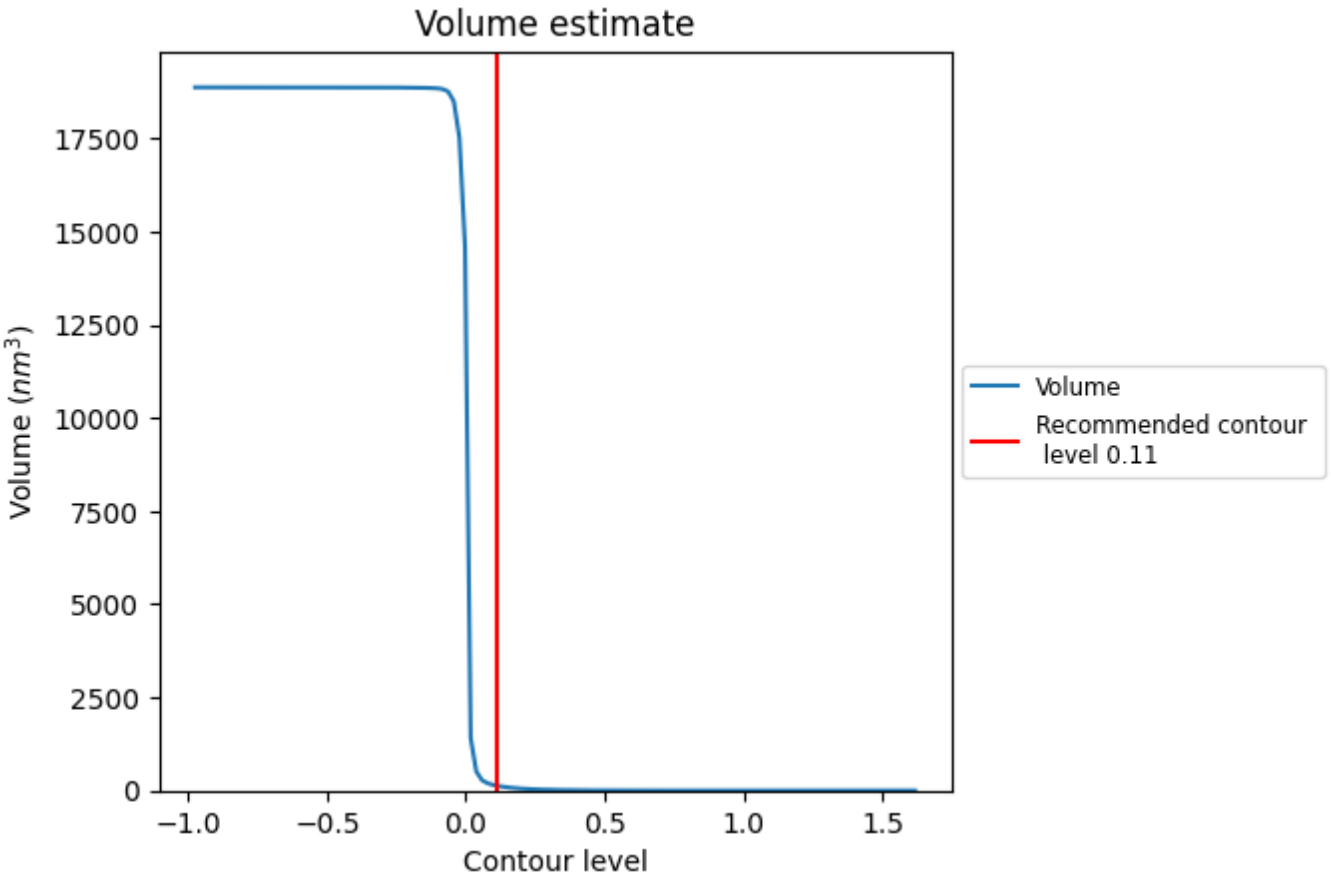
This section contains the results of statistical analysis of the map.

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.

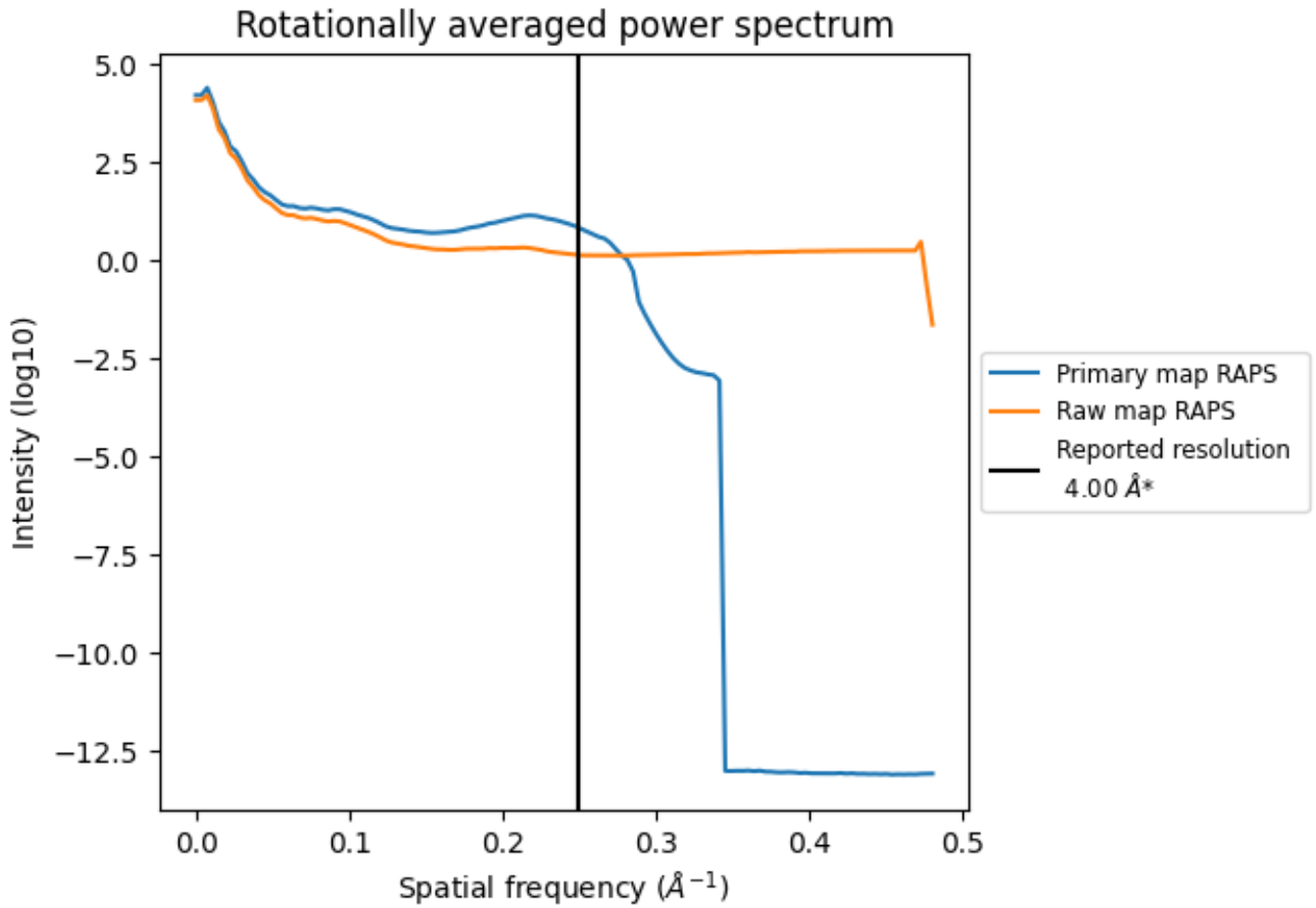
7.2 Volume estimate (i)



The volume at the recommended contour level is 134 nm^3; this corresponds to an approximate mass of 121 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)

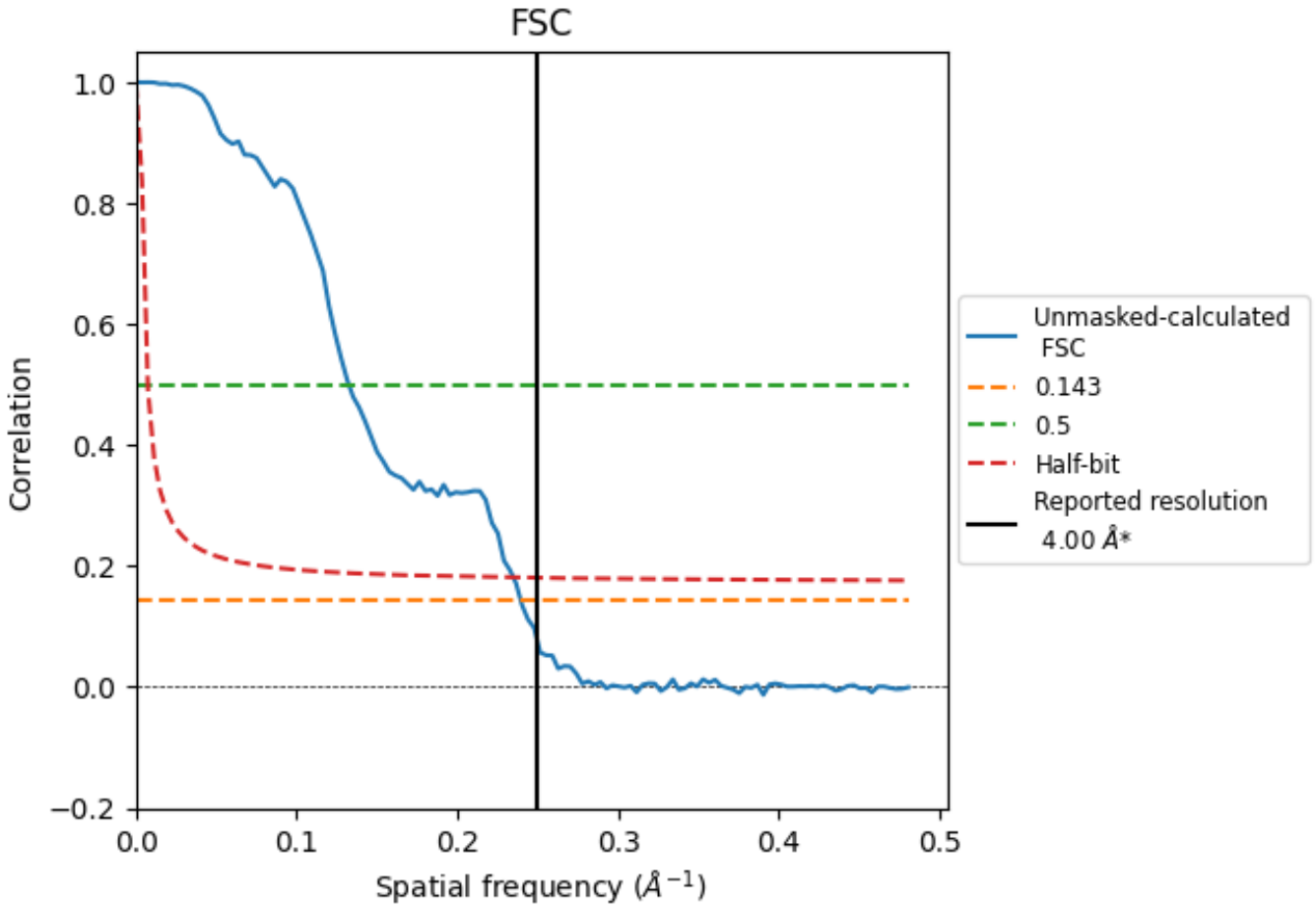


*Reported resolution corresponds to spatial frequency of 0.250 $Å^{-1}$

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)

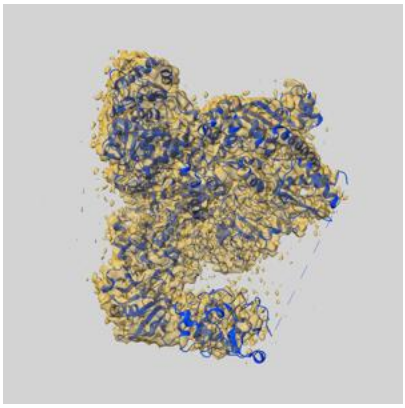
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.17	7.55	4.26

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

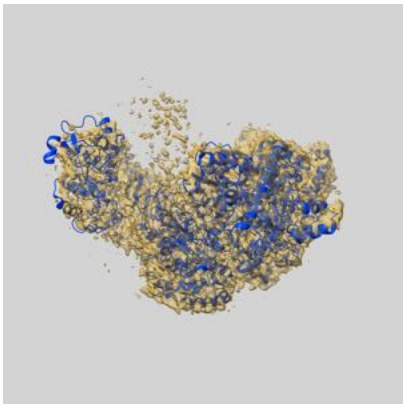
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-81570 and PDB model 27ZU. Per-residue inclusion information can be found in section 3 on page 5.

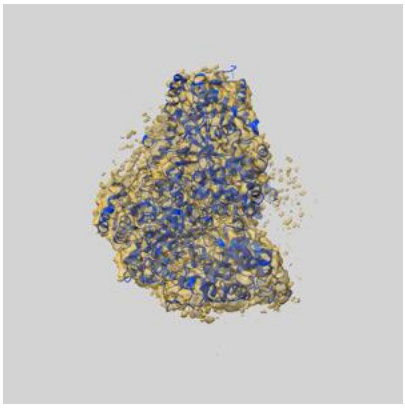
9.1 Map-model overlay



X



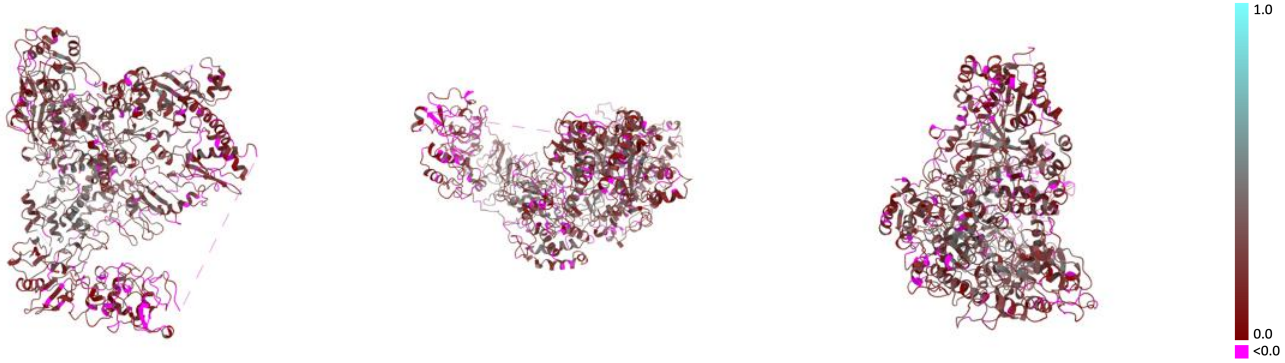
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11 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.

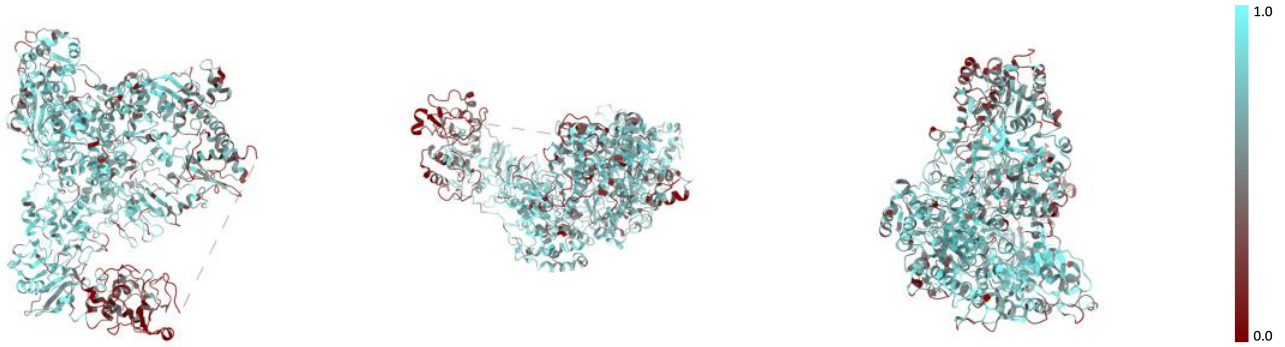
9.2 Q-score mapped to coordinate model (i)



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.

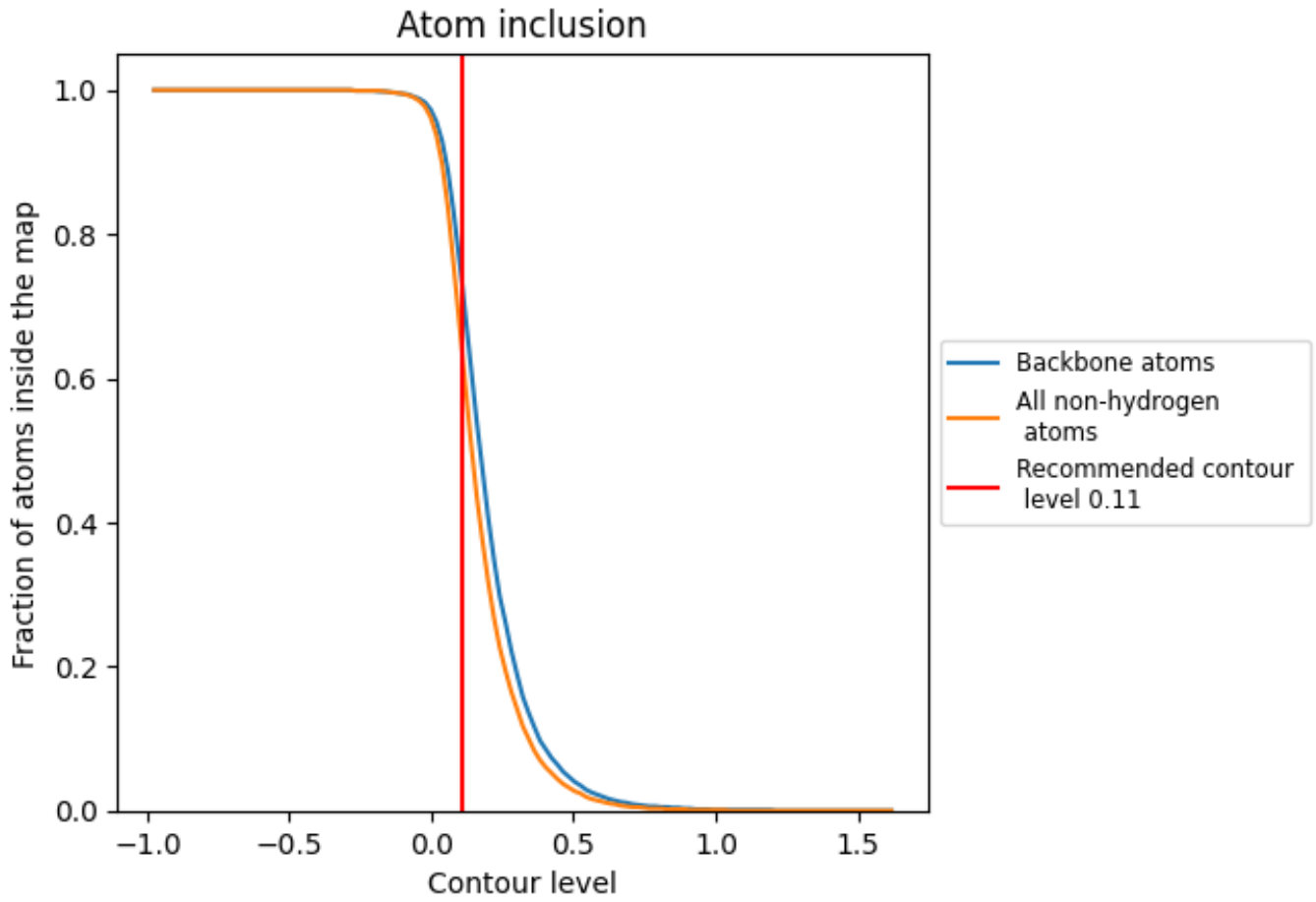
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.11).

9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 63% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6280	0.2210
A	0.5550	0.1850
B	0.7210	0.2670

