wwPDB EM Validation Summary Report (i)

Oct 31, 2026 – 09:07 am GMT

PDB ID	:	9TGR / pdb_00009tgr
EMDB ID	:	EMD-55909
Title	:	Cryo-EM structure of tail-fully-disengaged TamAB complex
Authors	:	Dong, H.; Tang, X.; Luo, Q.; Zerang, Z.
Deposited on	:	2025-12-02
Resolution	:	6.42 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 (i) 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 (i)) were used in the production of this report:

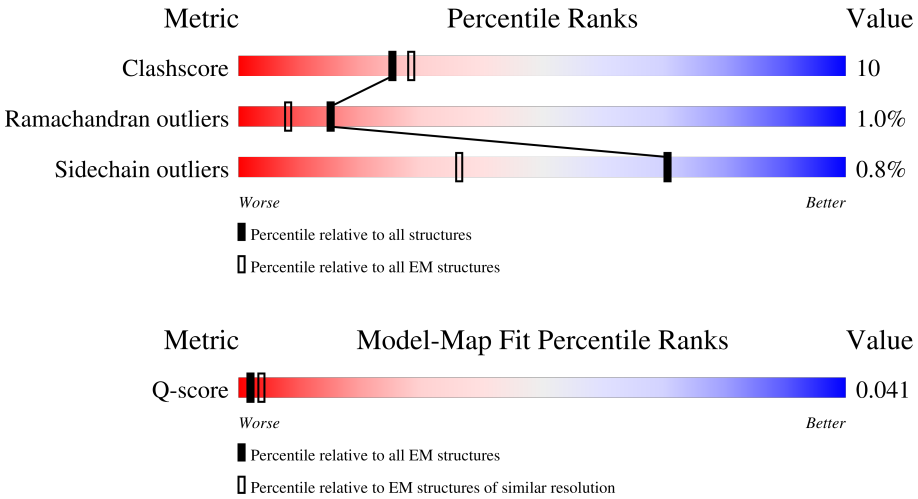
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & 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 6.42 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	502 (5.92 - 6.91)

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	577	10% 70% 25%
2	B	1259	8% 38% 8% 54%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8851 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 Translocation and assembly module subunit TamA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	556	4427	2815	769	838	5	0	0

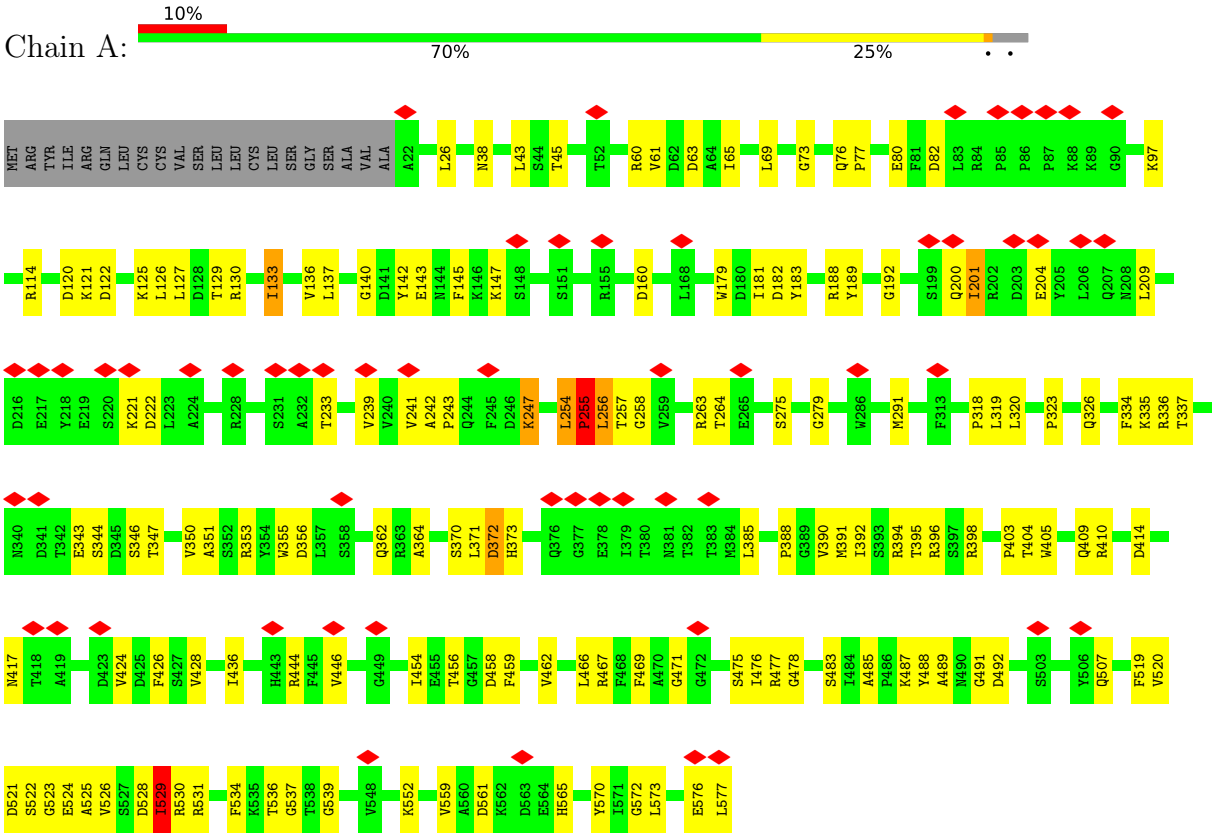
- Molecule 2 is a protein called Translocation and assembly module subunit TamB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	581	4424	2775	776	857	16	0	0

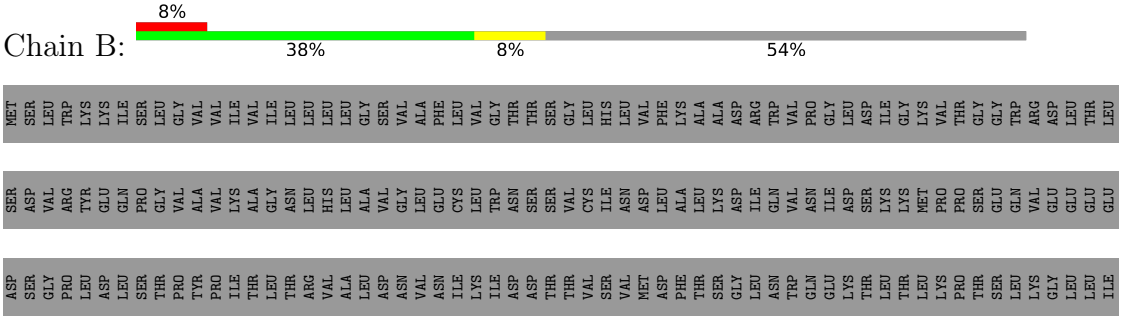
3 Residue-property plots (i)

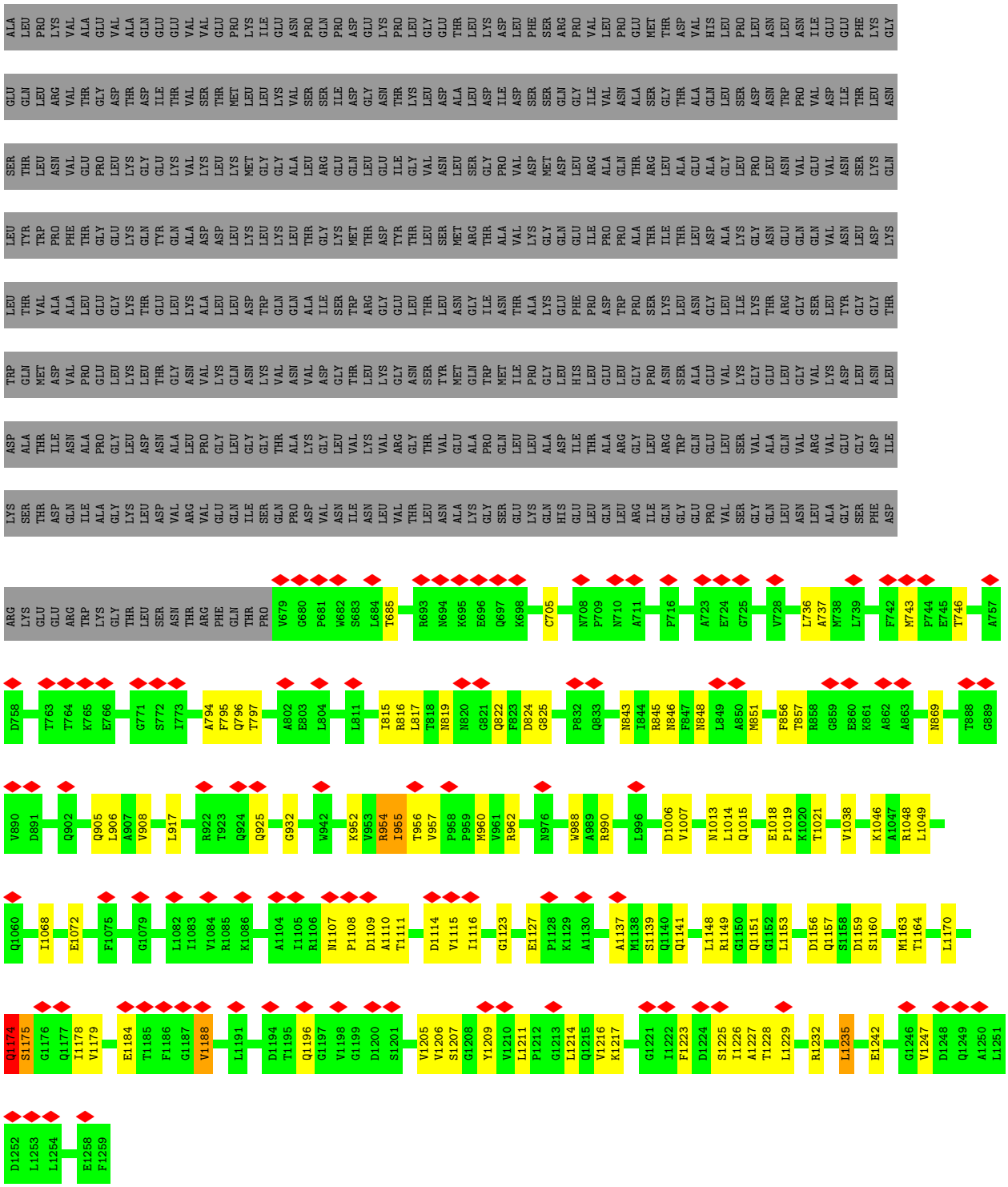
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



• Molecule 2: Translocation and assembly module subunit TamB




ALA LEU PRO LYS VAL ALA GLU VAL ALA GLN GLU GLU VAL VAL GLU PRO LYS ILE GLU ASN PRO GLN PRO ASP GLU LYS PRO LEU GLY GLU THR LEU LYS ASP LEU PHE SER ARG PRO VAL LEU PRO GLU MET THR ASP VAL HIS LEU PRO LEU ASN LEU ASN ILE GLU GLU GLU PHE LYS GLY
GLU GLN LEU ARG VAL THR GLY ASP THR ASP ILE THR VAL SER THR MET LEU LEU LYS VAL ALA SER SER ILE ASP GLY ASN THR LYS LEU ASP ALA LEU ASP ILE ASP SER SER GLN GLY ILE VAL ASN ALA SER GLY THR ALA GLN LEU SER ASP ASN TRP PRO VAL ASP ILE THR LEU ASN
SER THR LEU ASN VAL GLU PRO LEU LYS GLY GLU LYS VAL LYS ALA LEU ARG GLU GLN LEU GLU ILE GLY VAL ASN LEU SER GLY PRO VAL ASP MET ASP LEU GLN GLU VAL ASN SER LYS GLN
LEU TYR TRP PRO PHE THR GLY GLU LYS GLN TYR GLN ALA ASP ASP LEU LYS LEU LYS LEU THR GLY LYS MET THR ASP TYR THR LEU SER MET ARG THR ALA VAL LYS GLY GLN GLU ILE PRO PRO ALA THR ILE THR LEU ASP ALA LYS GLY GLN GLU VAL ASN ASN LEU ASP ASP
LEU THR VAL ALA ALA LEU GLU GLY LYS THR GLU LEU LYS ALA ALA LEU LEU ASP TRP GLN GLN ALA ALA ILE SER TRP ARG GLY GLU LEU THR LEU ASN THR LEU ASN GLY LYS GLU LEU PHE PRO ASP PRO ALA TRP PRO SER LYS LEU ASN GLY LEU ILE LYS GLY GLU GLU LEU GLY VAL LEU ASN SER
TRP GLN MET ASP VAL PRO GLU LEU LYS LEU THR GLY ASN VAL LYS GLN ASN LYS VAL ASN VAL ASP GLY THR LEU LYS GLY ASN SER TYR MET GLN TRP MET ILE PRO GLY LEU HIS LEU GLU GLU LEU GLY PRO ASN SER ALA GLU VAL LYS GLY GLU LEU GLY VAL LYS ASP LEU ASN LEU
ASP ALA THR ILE ASN PRO GLY LEU ASP ASN ALA LEU PRO GLY LEU ASP ASN ALA LEU VAL LYS VAL ARG GLY VAL GLU GLN ILE SER GLN PRO ASP VAL ASN ILE ASN LEU VAL THR LEU ASN ALA LYS GLY SER GLU LYS GLN HIS GLU LEU GLN LEU ARG ILE GLN GLY GLU PRO VAL SER GLY GLN LEU ASN LEU ALA GLY SER PHE ASP
ARG LYS GLU GLU ARG TRP LYS GLY THR LEU SER ASN THR ARG PHE GLN THR PRO V679 G680 P681 W682 S683 L684 T685 R693 N694 K695 E696 Q697 K698 C705 N708 P709 N710 A711 P716 A723 E724 G725 V728 L736 A737 M738 L739 F742 M743 P744 E745 T746 A757
D758 T763 T764 K765 E766 G771 S772 I773 A794 F795 Q796 T797 A802 E803 L804 L811 I815 R816 L817 T818 N819 N820 G821 Q822 F823 D824 G825 P832 Q833 N843 I844 R845 N846 F847 N848 L849 A850 M851 F856 T857 R858 G859 E860 K861 A862 A863 N869 T888 G889
V890 D891 Q902 Q905 L906 A907 V908 L917 R922 T923 Q924 Q925 G932 W942 K952 V953 R954 I955 T956 V957 P958 P959 M960 V961 R962 N976 W988 A989 R990 L996 D1006 V1007 N1013 L1014 Q1015 E1018 P1019 K1020 T1021 V1038 K1046 A1047 R1048 L1049
Q1060 I1068 E1072 F1075 G1079 L1082 I1083 V1084 R1085 K1086 A1104 I1105 R1106 N1107 P1108 D1109 A1110 T1111 D1114 V1115 I1116 G1123 E1127 P1128 K1129 A1130 A1137 M1138 S1139 Q1140 Q1141 L1148 R1149 G1150 Q1151 G1152 L1153 D1156 Q1157 S1158 D1159 S1160 M1163 T1164 L1170
Q1174 S1175 G1176 Q1177 I1178 V1179 E1184 T1185 F1186 G1187 V1188 L1191 D1194 T1195 Q1196 G1197 V1198 G1199 D1200 S1201 V1205 V1206 S1207 G1208 Y1209 V1210 L1211 P1212 G1213 L1214 Q1215 V1216 K1217 G1221 I1222 F1223 D1224 S1225 I1226 A1227 T1228 L1229 R1232 L1235 E1242 G1246 V1247 D1248 Q1249 A1250 L1251
D1252 L1253 L1254 E1258 F1259

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	82716	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.114	Depositor
Minimum map value	-0.108	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0496	Depositor
Map size (Å)	372.0, 372.93, 375.72	wwPDB
Map dimensions	400, 401, 404	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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	0.21	0/4536	0.47	3/6151 (0.0%)
2	B	0.20	1/4503 (0.0%)	0.54	3/6126 (0.0%)
All	All	0.21	1/9039 (0.0%)	0.51	6/12277 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1174	GLN	CA-C	-5.82	1.45	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1175	SER	N-CA-C	21.08	133.63	111.07
2	B	1174	GLN	N-CA-C	-14.69	87.83	108.54
1	A	529	ILE	N-CA-C	5.70	121.20	109.34
1	A	254	LEU	N-CA-C	5.57	122.11	109.81
1	A	356	ASP	N-CA-C	-5.15	100.51	108.90

There are no chirality outliers.

There are no planarity outliers.

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	4427	0	4343	116	0
2	B	4424	0	4394	70	0
All	All	8851	0	8737	183	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 10.

The worst 5 of 183 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:1211:LEU:HD23	2:B:1214:LEU:HD22	1.38	1.02
1:A:143:GLU:OE1	1:A:147:LYS:NZ	2.09	0.81
1:A:80:GLU:OE1	1:A:97:LYS:NZ	2.13	0.81
2:B:1209:TYR:OH	2:B:1214:LEU:O	2.01	0.79
1:A:60:ARG:NH2	1:A:63:ASP:OD2	2.19	0.74

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	554/577 (96%)	506 (91%)	44 (8%)	4 (1%)	18	56
2	B	579/1259 (46%)	532 (92%)	40 (7%)	7 (1%)	10	43
All	All	1133/1836 (62%)	1038 (92%)	84 (7%)	11 (1%)	15	48

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	PRO
1	A	529	ILE
1	A	133	ILE
2	B	1188	VAL
2	B	1139	SER

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	473/491 (96%)	468 (99%)	5 (1%)	65 76
2	B	480/1061 (45%)	477 (99%)	3 (1%)	78 82
All	All	953/1552 (61%)	945 (99%)	8 (1%)	70 80

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

Mol	Chain	Res	Type
2	B	1235	LEU
2	B	1175	SER
1	A	373	HIS
1	A	372	ASP
2	B	1174	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1190	ASN
2	B	1174	GLN
2	B	902	GLN
2	B	869	ASN
2	B	909	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)

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.

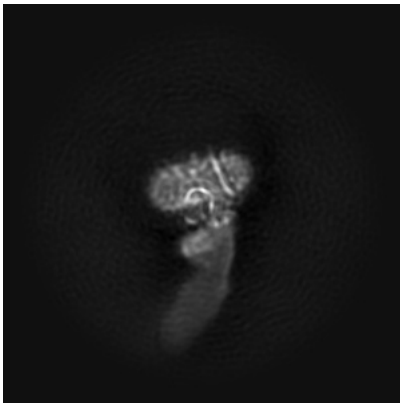
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55909. These allow visual inspection of the internal detail of the map and identification of artifacts.

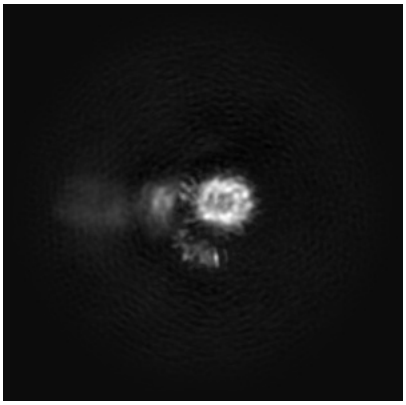
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

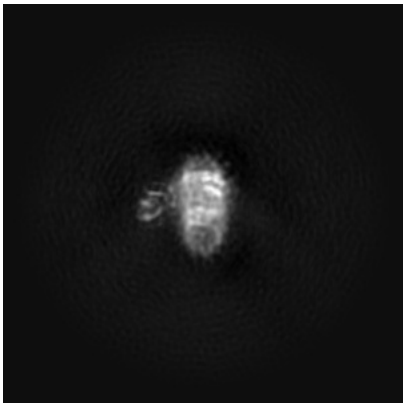
6.1.1 Primary map



X



Y

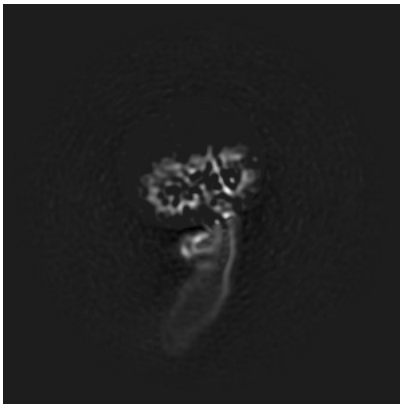


Z

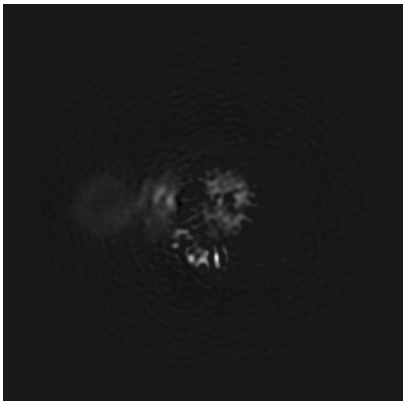
The images above show the map projected in three orthogonal directions.

6.2 Central slices

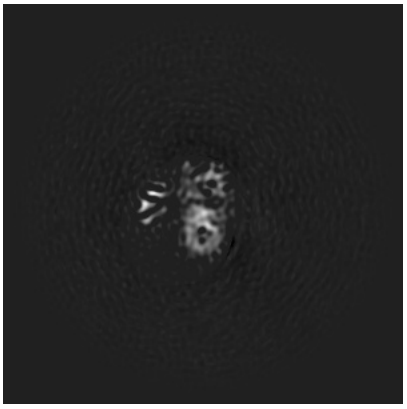
6.2.1 Primary map



X Index: 200



Y Index: 200

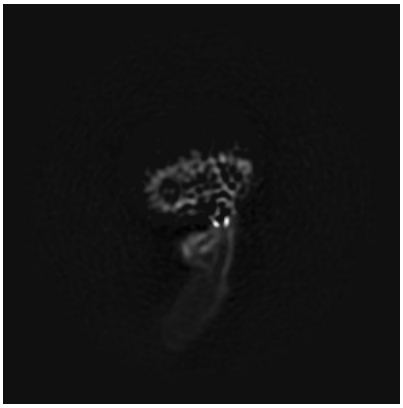


Z Index: 202

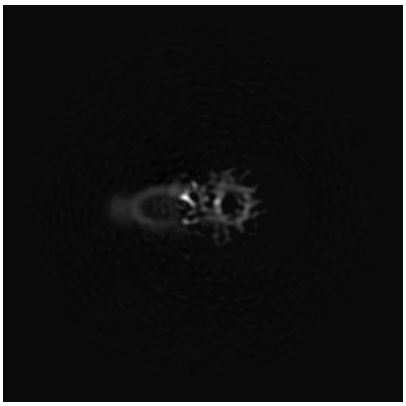
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

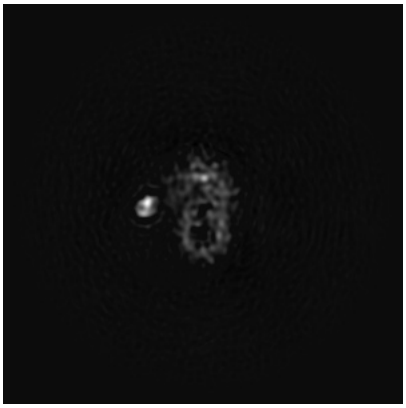
6.3.1 Primary map



X Index: 205



Y Index: 225

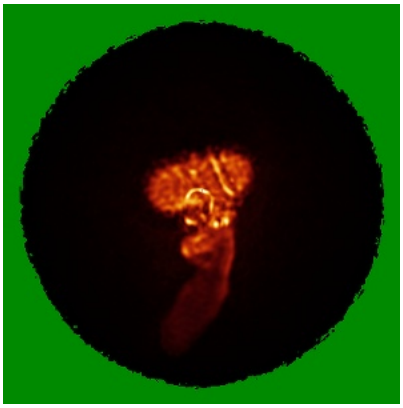


Z Index: 215

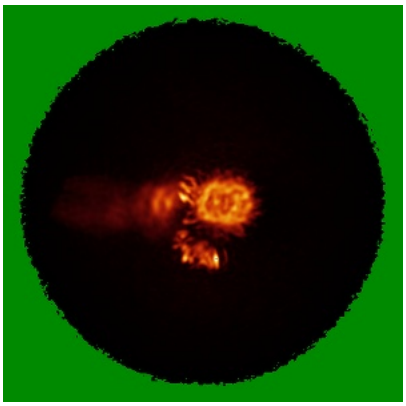
The images above show the largest variance slices of the map in three orthogonal directions.

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

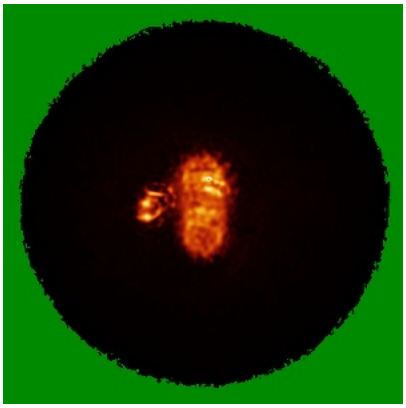
6.4.1 Primary map



X



Y



Z

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 0.0496. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

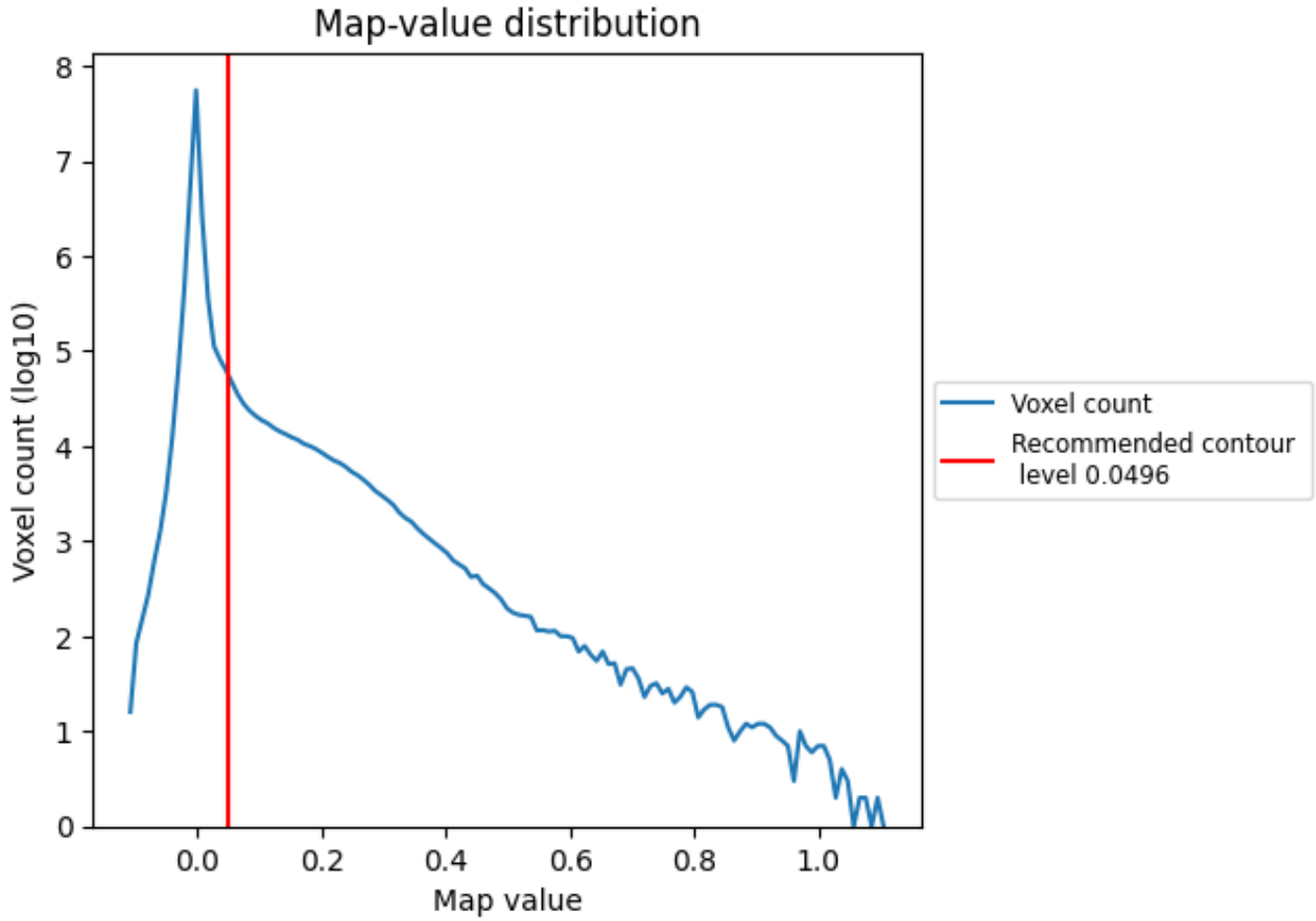
6.6 Mask visualisation (i)

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

7 Map analysis

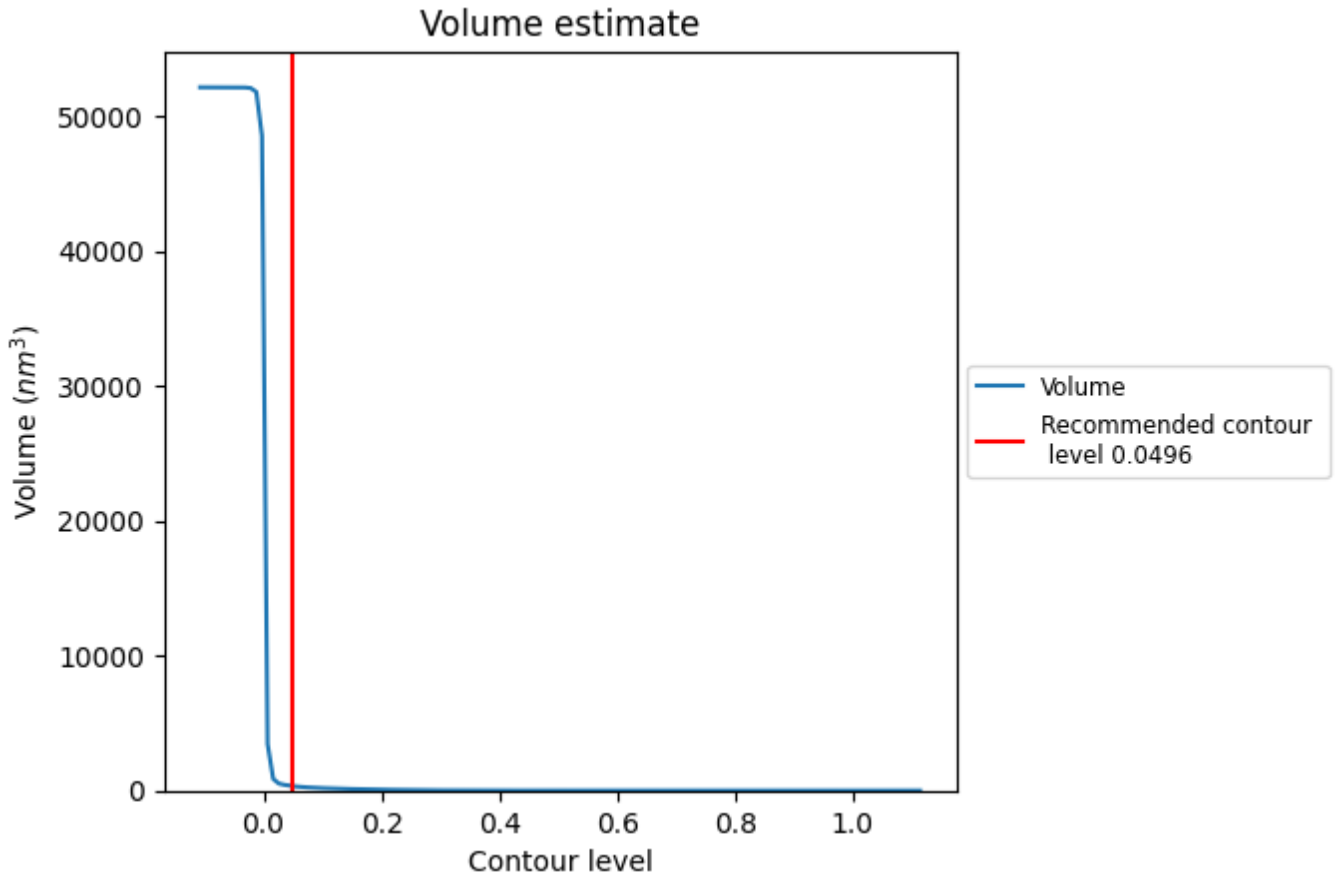
This section contains the results of statistical analysis of the map.

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



The volume at the recommended contour level is 332 nm^3; this corresponds to an approximate mass of 299 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

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

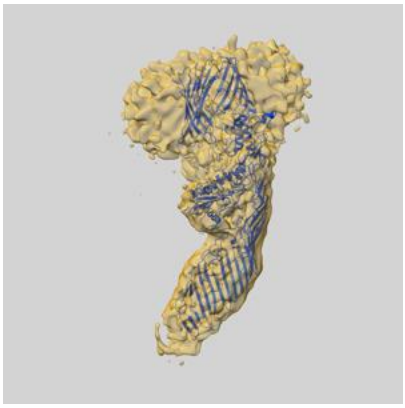
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55909 and PDB model 9TGR. Per-residue inclusion information can be found in section 3 on page 4.

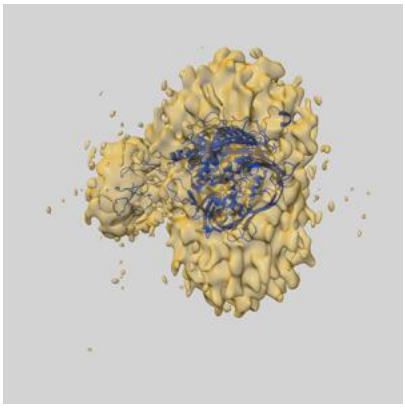
9.1 Map-model overlay



X



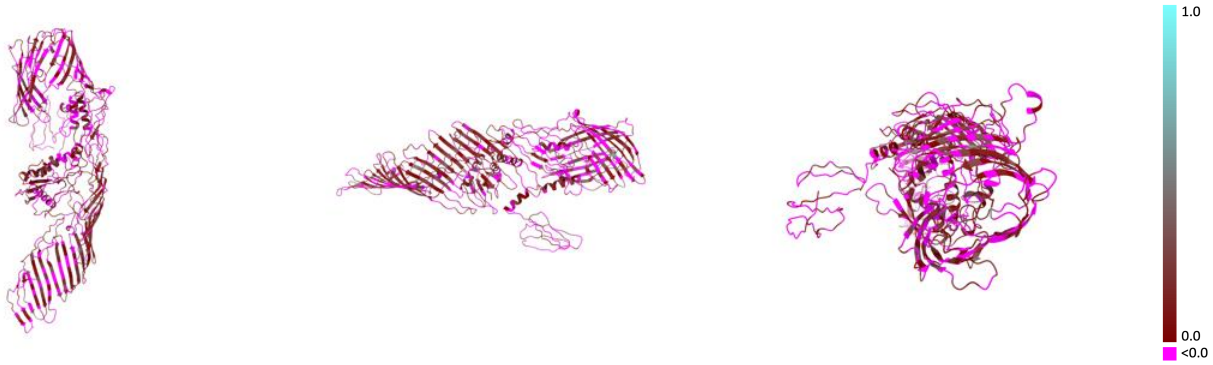
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0496 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.

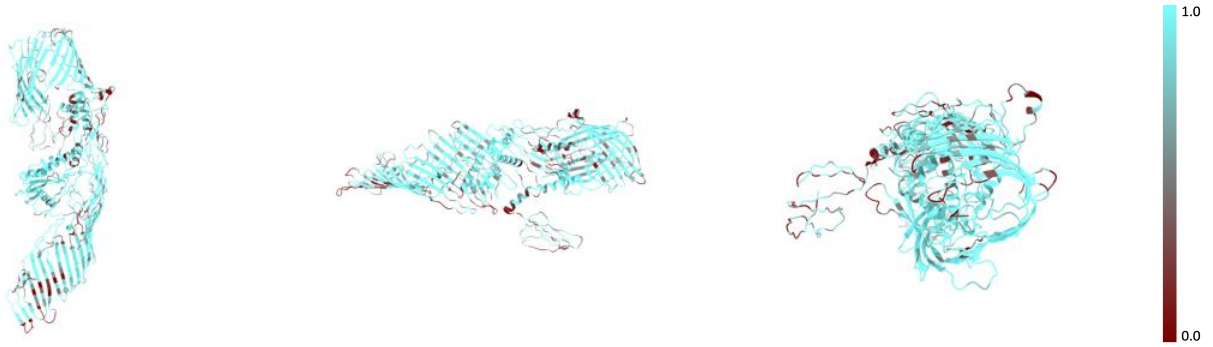
9.2 Q-score mapped to coordinate model



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.

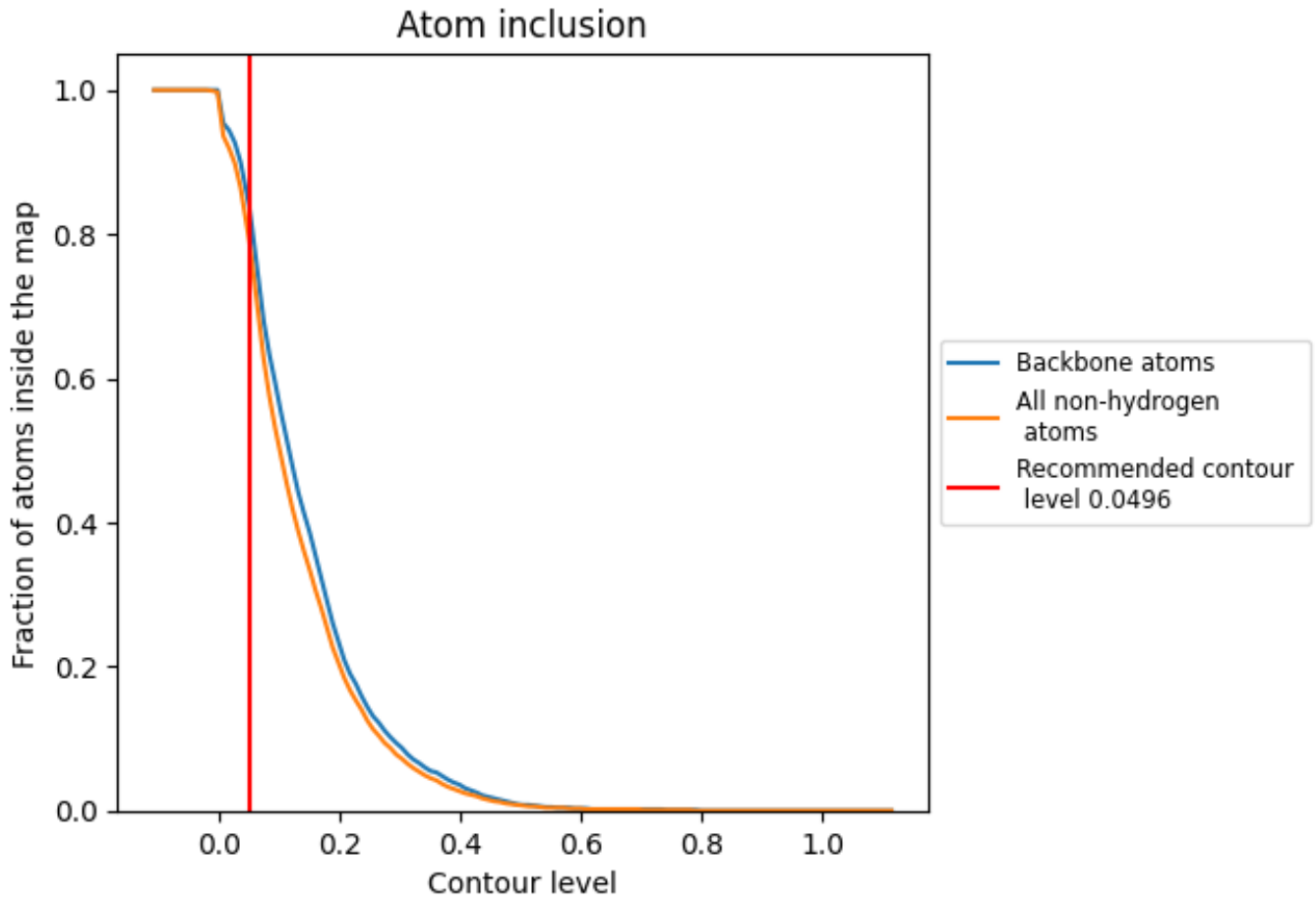
9.3 Atom inclusion mapped to coordinate model



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 (0.0496).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0496) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.7920	0.0410
A	0.8400	0.0310
B	0.7450	0.0520