wwPDB EM Validation Summary Report

Nov 18, 2025 – 10:31 AM JST

PDB ID	:	9LXH / pdb_00009lxh
EMDB ID	:	EMD-63477
Title	:	DOCK5/ELMO1 complex with RhoG and Rac1 on lipid membrane
Authors	:	Shinoda, T.; Katsura, K.; Kukimoto-Niino, M.; Shirouzu, M.
Deposited on	:	2025-02-18
Resolution	:	7.52 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:

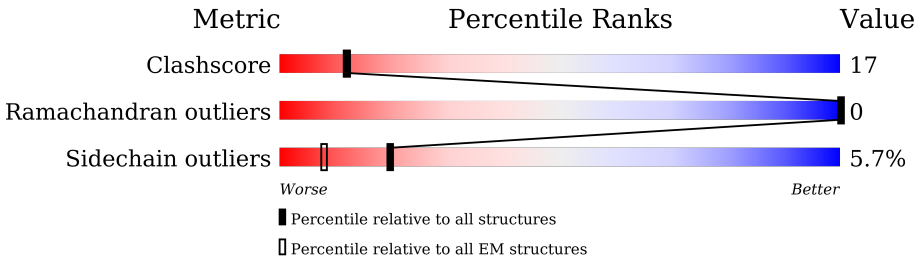
EMDB validation analysis	:	0.0.1.dev129
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

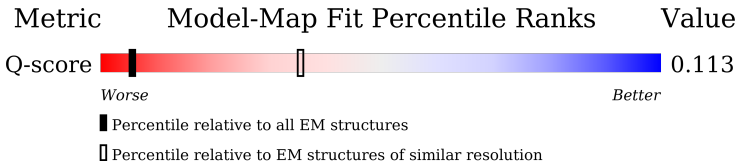
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.52 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	377 (7.02 - 8.01)

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	733	75% 72% 26%
2	B	1876	18% 35% 29% 33%
3	C	214	69% 63% 21% 15%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 17437 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 Engulfment and cell motility protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	727	5814	3686	995	1093	40	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q92556
A	-4	GLY	-	expression tag	UNP Q92556
A	-3	SER	-	expression tag	UNP Q92556
A	-2	VAL	-	expression tag	UNP Q92556
A	-1	GLY	-	expression tag	UNP Q92556
A	0	SER	-	expression tag	UNP Q92556

- Molecule 2 is a protein called Dedicator of cytokinesis protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1254	10207	6536	1733	1882	56	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	expression tag	UNP Q9H7D0
B	-4	GLY	-	expression tag	UNP Q9H7D0
B	-3	SER	-	expression tag	UNP Q9H7D0
B	-2	GLY	-	expression tag	UNP Q9H7D0
B	-1	GLY	-	expression tag	UNP Q9H7D0
B	0	SER	-	expression tag	UNP Q9H7D0
B	1285	ARG	LYS	variant	UNP Q9H7D0

- Molecule 3 is a protein called Rho-related GTP-binding protein RhoG.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	181	Total	C	N	O	S	0	0
			1416	897	248	263	8		

There are 24 discrepancies between the modelled and reference sequences:

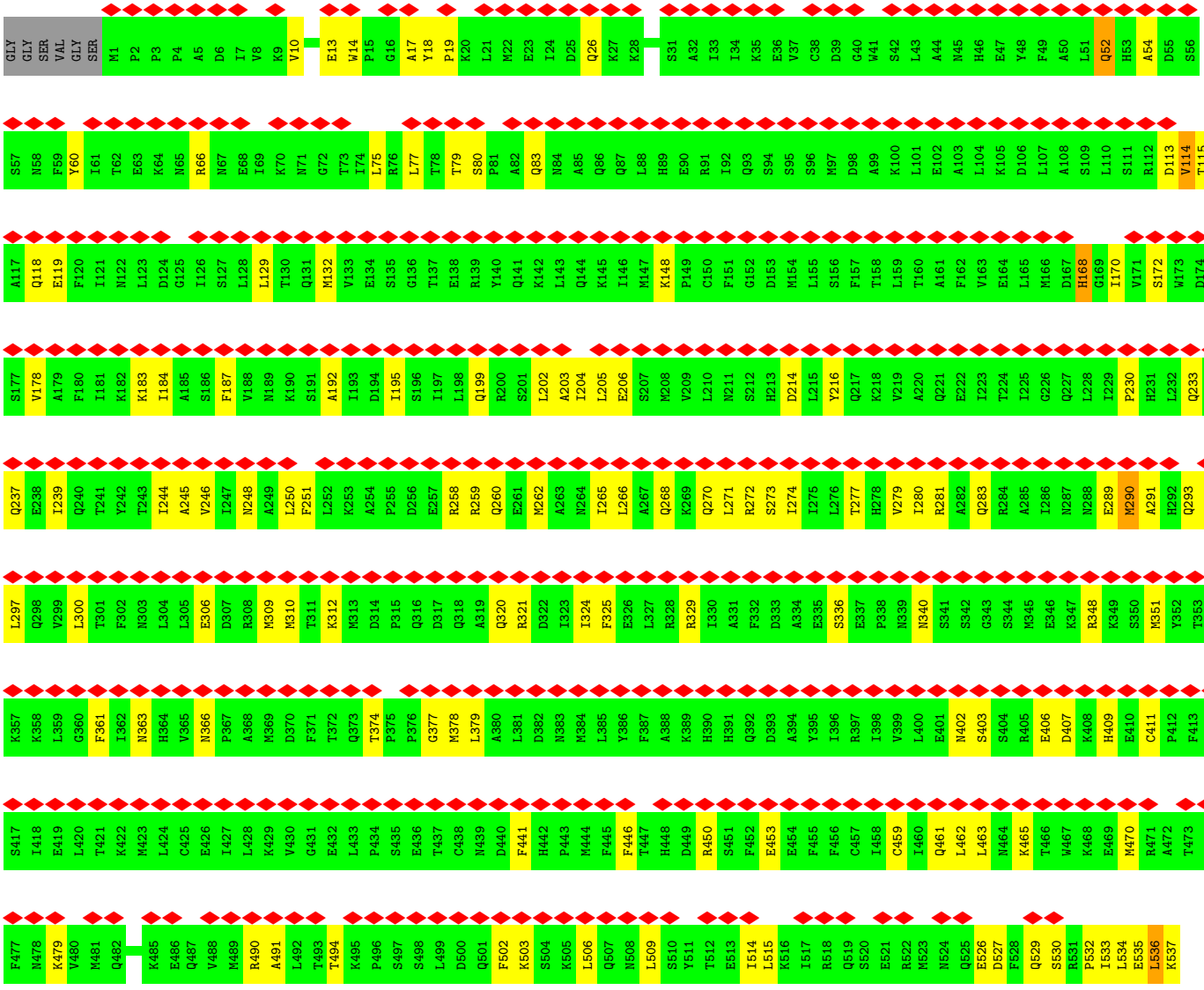
Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	GLY	-	expression tag	UNP P84095
C	-5	SER	-	expression tag	UNP P84095
C	-4	SER	-	expression tag	UNP P84095
C	-3	GLY	-	expression tag	UNP P84095
C	-2	SER	-	expression tag	UNP P84095
C	-1	SER	-	expression tag	UNP P84095
C	0	GLY	-	expression tag	UNP P84095
C	61	LEU	GLN	engineered mutation	UNP P84095
C	192	SER	-	expression tag	UNP P84095
C	193	GLY	-	expression tag	UNP P84095
C	194	PRO	-	expression tag	UNP P84095
C	195	SER	-	expression tag	UNP P84095
C	196	SER	-	expression tag	UNP P84095
C	197	GLY	-	expression tag	UNP P84095
C	198	HIS	-	expression tag	UNP P84095
C	199	HIS	-	expression tag	UNP P84095
C	200	HIS	-	expression tag	UNP P84095
C	201	HIS	-	expression tag	UNP P84095
C	202	HIS	-	expression tag	UNP P84095
C	203	HIS	-	expression tag	UNP P84095
C	204	HIS	-	expression tag	UNP P84095
C	205	HIS	-	expression tag	UNP P84095
C	206	HIS	-	expression tag	UNP P84095
C	207	HIS	-	expression tag	UNP P84095

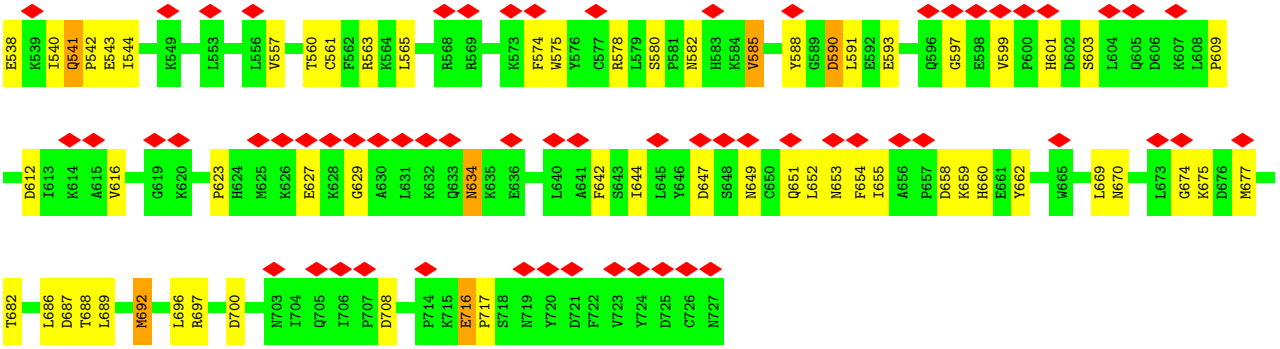
3 Residue-property plots (i)

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: Engulfment and cell motility protein 1

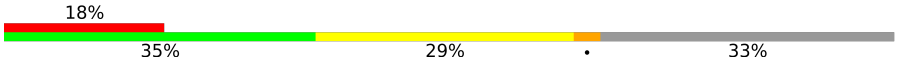
Chain A:

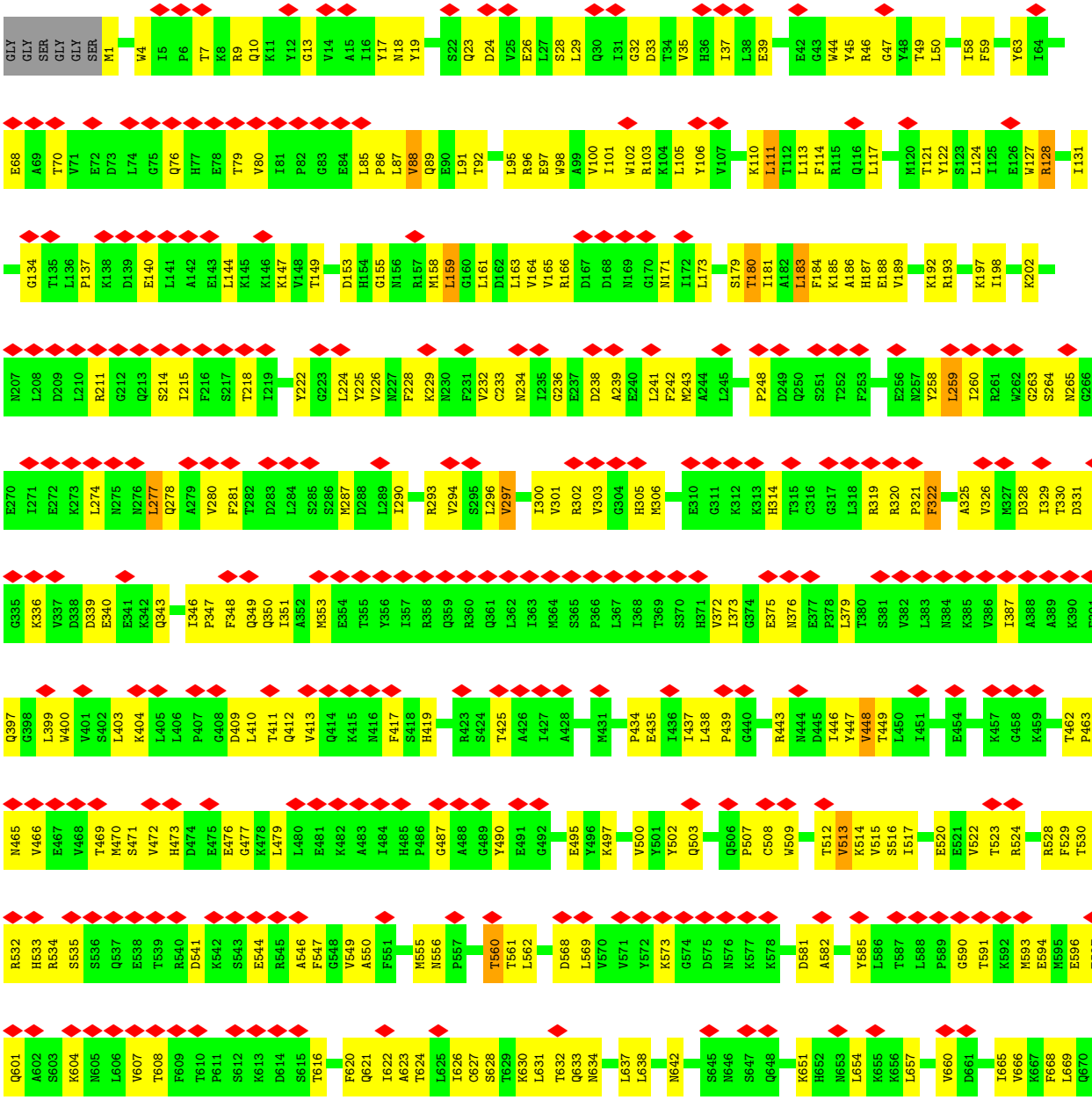


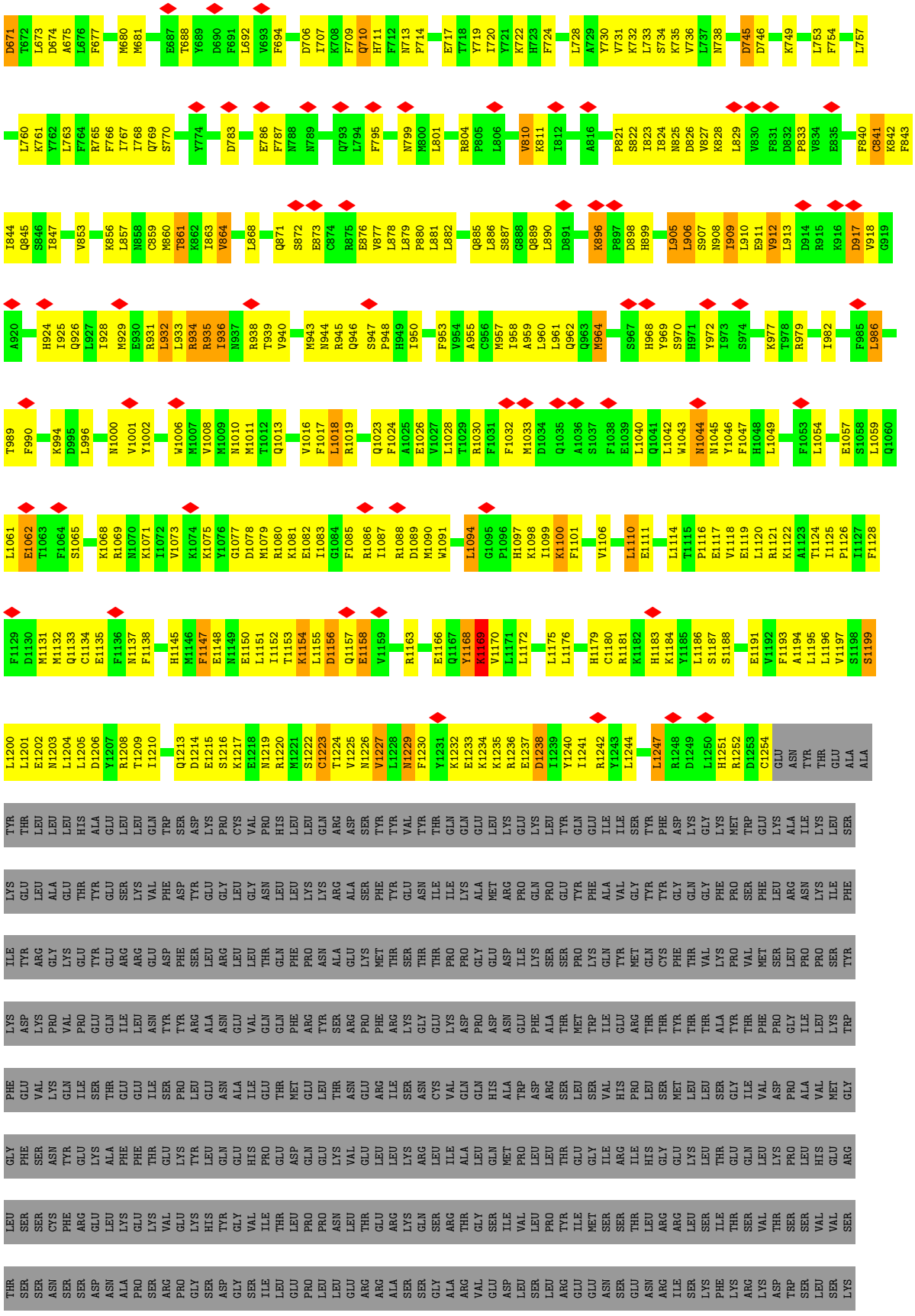


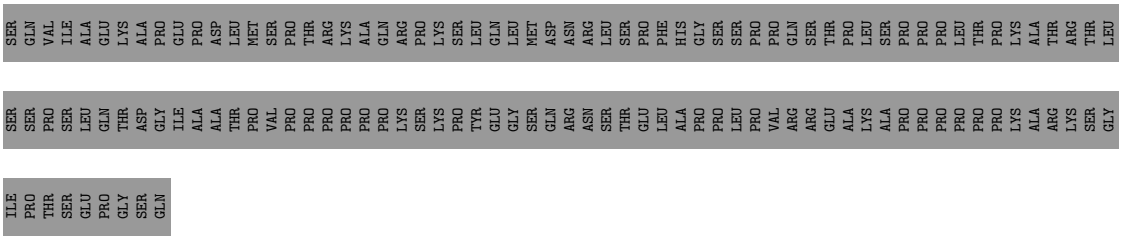
• Molecule 2: Dedicator of cytokinesis protein 5

Chain B:



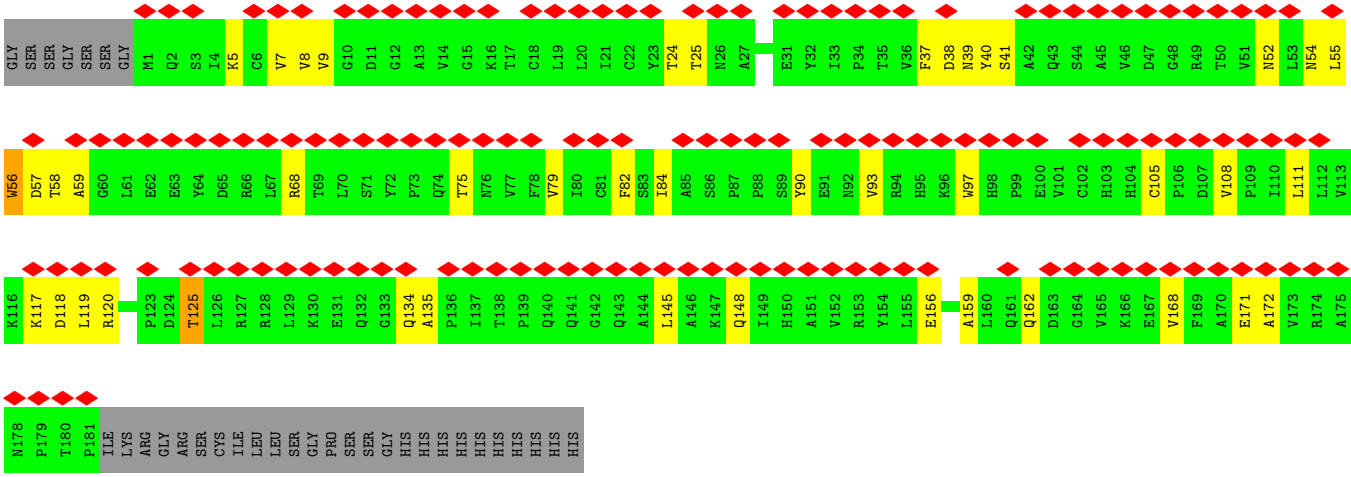



D671 T672 L673 D674 A675 L676 F677 M680 M681 E687 T688 Y689 D690 F691 L692 V693 F694 D706 I707 K708 F709 Q710 H711 F712 N713 P714 E717 T718 Y719 I720 Y721 K722 H723 F724 L728 A729 Y730 V731 K732 L733 S734 K735 V736 L737 N738 D745 D746 K749 L753 F754 L757
L760 K761 Y762 L763 F764 R765 F766 I767 I768 Q769 S770 Y774 D783 E786 F787 N788 N789 Q793 L794 F795 N799 M800 L801 R804 F805 L806 V810 K811 I812 A816 P821 S822 I823 I824 N825 D826 V827 K828 L829 V830 F831 D832 P833 V834 E835 F840 C841 K842 F843
I844 Q845 S846 I847 V853 K856 L857 N858 C859 M860 T861 K862 I863 V864 L868 Q871 S872 E873 C874 R875 E876 V877 L878 L879 P880 L881 L882 Q885 L886 S887 G888 Q889 L890 D891 K896 P897 D898 H899 L905 L906 S907 N908 I909 L910 E911 V912 L913 D914 R915 K916 D917 V918 G919
A920 H924 I925 Q926 L927 I928 M929 E930 R931 L932 L933 R934 R935 I936 N937 R938 T939 V940 M943 N944 R945 Q946 S947 P948 H949 I950 F953 V954 A955 C956 M957 I958 A959 L960 L961 Q962 Q963 M964 S967 H968 Y969 S970 H971 Y972 I973 S974 K977 T978 R979 I982 F985 L986
T989 F990 K994 D995 L996 N1000 V1001 Y1002 W1006 M1007 V1008 M1009 N1010 M1011 T1012 Q1013 V1016 F1017 L1018 R1019 Q1023 F1024 A1025 E1026 V1027 L1028 T1029 R1030 F1031 F1032 M1033 D1034 Q1035 A1036 S1037 F1038 E1039 L1040 Q1041 L1042 W1043 N1044 N1045 Y1046 F1047 H1048 L1049 F1053 L1054 E1057 S1058 L1059 Q1060
L1061 E1062 T1063 F1064 S1065 K1068 R1069 N1070 K1071 I1072 V1073 K1074 K1075 Y1076 G1077 D1078 M1079 R1080 K1081 E1082 I1083 G1084 F1085 R1086 I1087 R1088 D1089 M1090 W1091 L1094 G1095 P1096 H1097 K1098 I1099 K1100 F1101 V1106 L1110 E1111 L1114 T1115 P1116 E1117 V1118 E1119 L1120 R1121 K1122 A1123 T1124 I1125 P1126 I1127 F1128
F1129 D1130 M1131 M1132 Q1133 C1134 E1135 F1136 N1137 F1138 H1145 M1146 F1147 E1148 N1149 E1150 L1151 I1152 T1153 K1154 L1155 D1156 Q1157 E1158 V1159 R1163 E1166 Q1167 Y1168 K1169 V1170 L1171 L1172 L1175 L1176 H1179 C1180 R1181 K1182 H1183 K1184 Y1185 L1186 S1187 S1188 E1191 V1192 F1193 A1194 L1195 L1196 V1197 S1198 S1199
L1200 L1201 E1202 N1203 L1204 L1205 D1206 Y1207 R1208 T1209 I1210 Q1213 D1214 E1215 S1216 K1217 E1218 N1219 R1220 M1221 S1222 C1223 T1224 V1225 N1226 V1227 L1228 N1229 F1230 Y1231 K1232 E1233 K1234 K1235 R1236 E1237 D1238 I1239 Y1240 I1241 R1242 Y1243 L1244 L1247 R1248 D1249 L1250 H1251 R1252 D1253 C1254 GLU ASN TYR THR GLU ALA ALA
TYR THR LEU LEU LEU HIS ALA GLU GLU LEU LEU GLN TRP SER ASP LYS PRO CYS VAL PRO HIS LEU LEU LEU GLN ARG ASP SER TYR TYR VAL TYR THR GLN GLN GLU LEU LYS GLU LYS LEU TYR GLN GLU ILE ILE SER TYR PHE ASP LYS GLY LYS MET TRP GLU LYS ALA ILE LYS LEU SER
LYS GLU LEU ALA GLU THR TYR GLU SER LYS VAL PHE ASP TYR GLU GLY LEU GLY ASN LEU LEU LYS LYS ARG ALA SER PHE TYR GLU ASN ILE ILE LYS ALA MET ARG PRO GLN PRO GLU TYR PHE ALA VAL GLY TYR PRO PHE LEU ARG ASN ILE PHE
ILE TYR ARG GLY LYS GLU TYR GLU ARG ARG GLU ASP PHE SER LEU ARG LEU LEU THR GLN PHE PRO ASN ALA GLU LYS MET THR SER THR THR PRO LYS GLN TYR MET GLN CYS PHE THR VAL LYS PRO VAL MET SER LEU PRO PRO TYR
LYS ASP LYS PRO VAL PRO GLU GLN ILE LEU ASN TYR ARG ALA ASN GLU VAL GLN LEU PHE ARG LYS GLY GLU LYS ASP PRO ASP ASN GLU PHE ALA THR MET TRP ILE GLU ARG THR THR TYR THR THR THR ALA TYR THR PHE PRO GLY ILE LEU LYS PHE
PHE GLU VAL LYS GLN ILE SER PRO LEU GLU ASN ALA ILE GLU THR MET GLU LEU THR ASN GLU ARG ILE SER SER ASN CYS VAL GLN GLN HIS ALA TRP ASP ARG SER LEU SER VAL HIS PRO LEU SER MET LEU LEU SER GLY ILE VAL ASP PRO ALA VAL MET GLY
GLY PHE SER ASN TYR GLU LYS ALA PHE PHE THR GLU LYS TYR LEU GLN GLU HIS PRO GLU ASP GLN GLU LYS VAL GLU LEU LEU LYS ARG LEU GLN MET PRO LEU LEU THR GLU GLY ILE ARG ILE HIS GLY GLU LYS LEU SER ILE THR GLU GLN LEU LYS PRO LEU HIS GLU ARG
LEU SER SER CYS PHE ARG GLU LEU LYS GLU VAL GLU LYS HIS TYR GLY VAL ILE THR LEU PRO PRO ASN LEU THR GLU GLY ARG LYS GLN SER ARG THR GLY SER ILE VAL LEU LEU PRO TYR ILE MET SER SER THR LEU ARG ARG LEU SER LYS PHE LYS ARG LYS ASP TRP SER LEU SER
THR SER SER ASN SER ASP ASN ALA PRO SER ARG PRO GLY SER ILE LEU GLU PRO LEU LEU GLU ARG ARG ALA SER SER GLY ALA ARG VAL GLU ASP LEU SER LEU ARG GLU GLU ASN SER GLU ASN ARG ILE SER LYS PHE LYS ARG LYS ASP TRP SER LEU SER LYS



• Molecule 3: Rho-related GTP-binding protein RhoG

Chain C:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55365	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)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	5.181	Depositor
Minimum map value	-3.568	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.064	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	478.80002, 478.80002, 478.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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	0.11	0/5926	0.27	0/8005
2	B	0.14	0/10408	0.40	6/14037 (0.0%)
3	C	0.11	0/1449	0.27	0/1977
All	All	0.13	0/17783	0.35	6/24019 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1168	TYR	CA-C-N	-8.02	110.06	120.65
2	B	1168	TYR	C-N-CA	-8.02	110.06	120.65
2	B	673	LEU	CA-C-N	-7.45	110.82	120.65
2	B	673	LEU	C-N-CA	-7.45	110.82	120.65
2	B	1155	LEU	O-C-N	6.49	129.82	122.22

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	5814	0	5799	135	0
2	B	10207	0	10318	448	0
3	C	1416	0	1414	36	0
All	All	17437	0	17531	598	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 598 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:871:GLN:HG3	2:B:918:VAL:HG13	1.62	0.81
2:B:868:LEU:HD13	2:B:878:LEU:HD23	1.64	0.80
2:B:1110:LEU:HD21	2:B:1158:GLU:HB2	1.65	0.77
2:B:1081:LYS:HA	2:B:1120:LEU:HD22	1.66	0.77
3:C:119:LEU:HB3	3:C:125:THR:HG21	1.67	0.77

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	725/733 (99%)	697 (96%)	28 (4%)	0	100	100
2	B	1252/1876 (67%)	1172 (94%)	80 (6%)	0	100	100
3	C	179/214 (84%)	173 (97%)	6 (3%)	0	100	100
All	All	2156/2823 (76%)	2042 (95%)	114 (5%)	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	645/665 (97%)	621 (96%)	24 (4%)	29 49
2	B	1140/1703 (67%)	1057 (93%)	83 (7%)	11 31
3	C	157/184 (85%)	154 (98%)	3 (2%)	52 69
All	All	1942/2552 (76%)	1832 (94%)	110 (6%)	20 38

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	745	ASP
2	B	932	LEU
3	C	125	THR
2	B	1158	GLU
2	B	810	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	710	GLN
2	B	1023	GLN
3	C	104	HIS
2	B	889	GLN
2	B	1066	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.

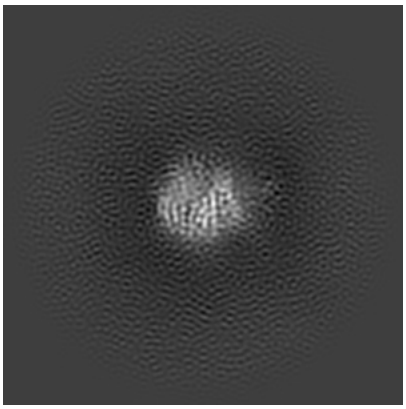
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-63477. These allow visual inspection of the internal detail of the map and identification of artifacts.

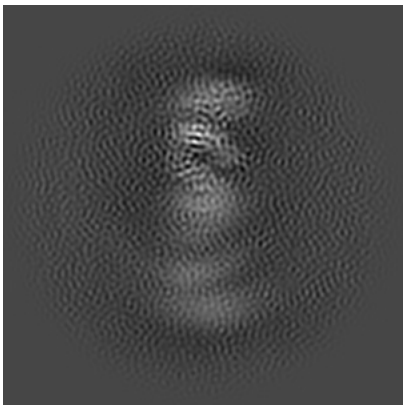
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

6.1.1 Primary map



X



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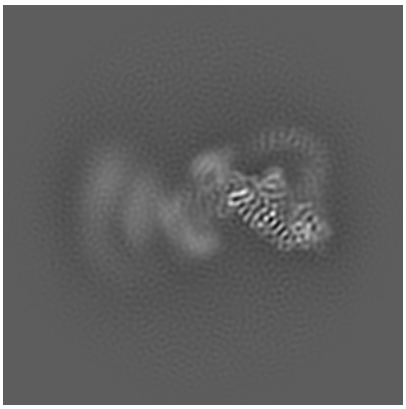
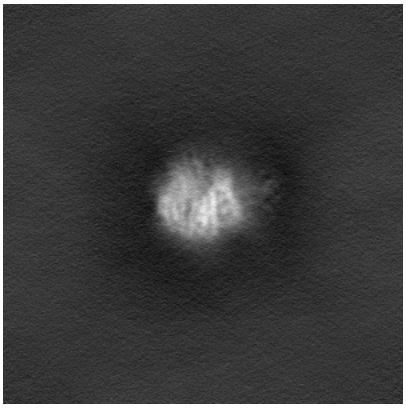
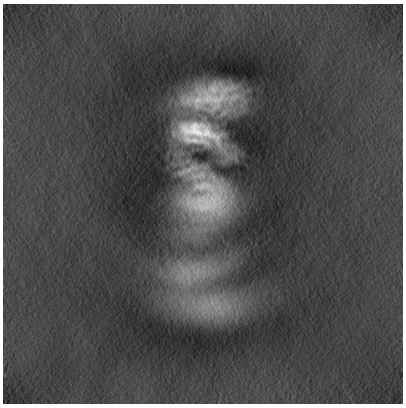


Z

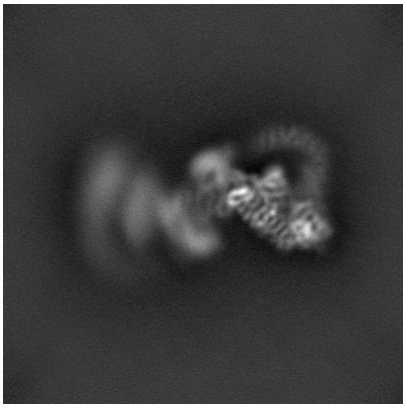
6.1.2 Raw map



X



Y

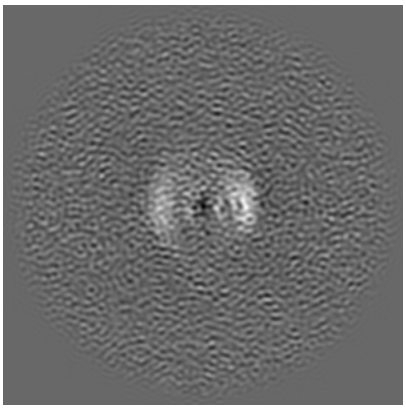


Z

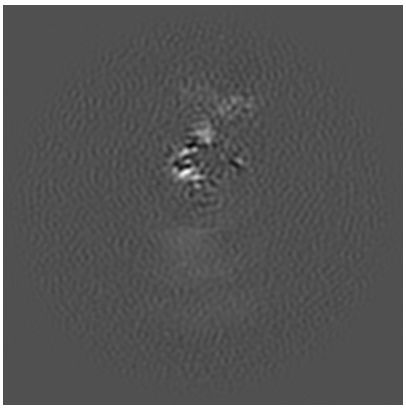
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

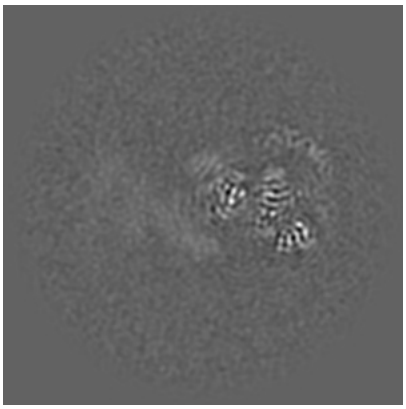
6.2.1 Primary map



X Index: 180

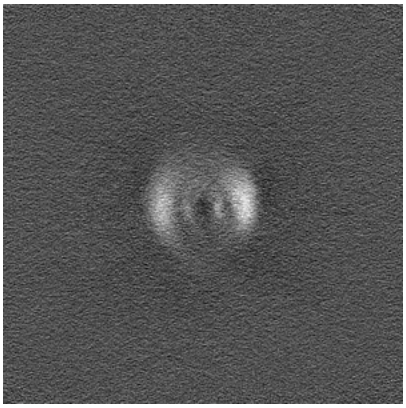


Y Index: 180

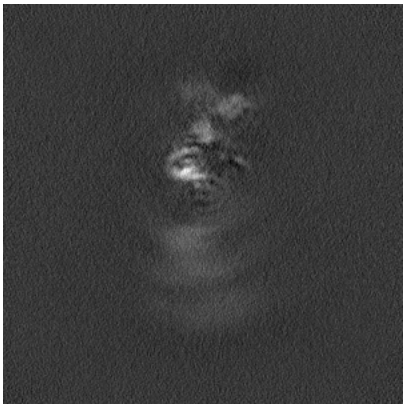


Z Index: 180

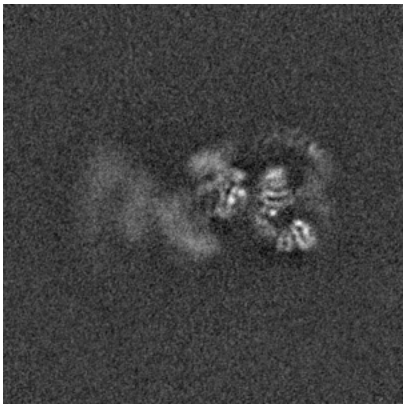
6.2.2 Raw map



X Index: 180



Y Index: 180

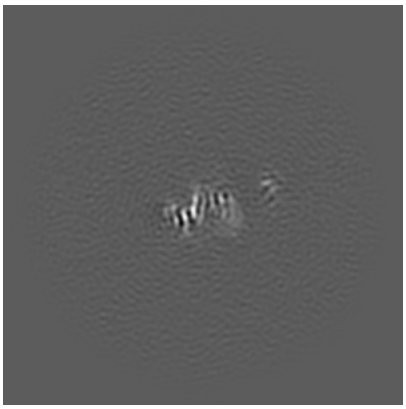


Z Index: 180

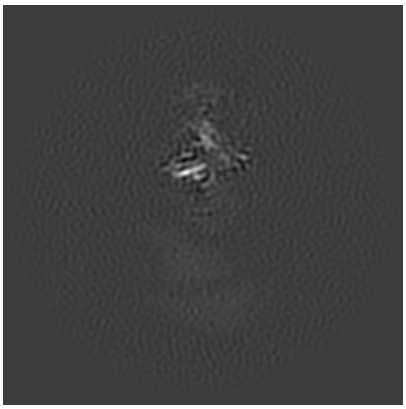
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



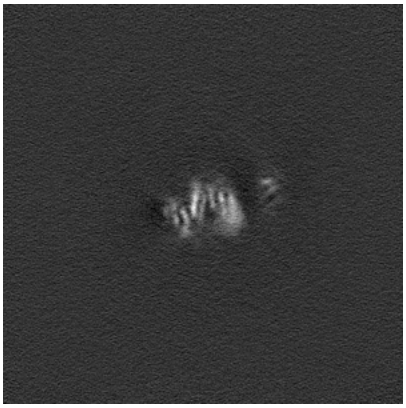
X Index: 243



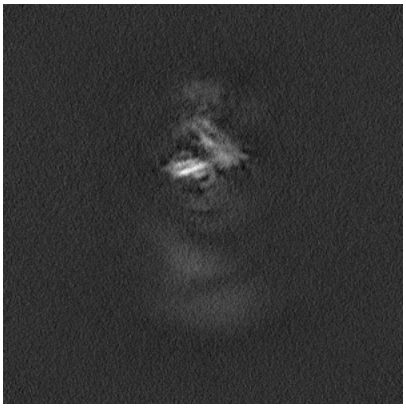
Y Index: 189

Z Index: 168

6.3.2 Raw map



X Index: 243



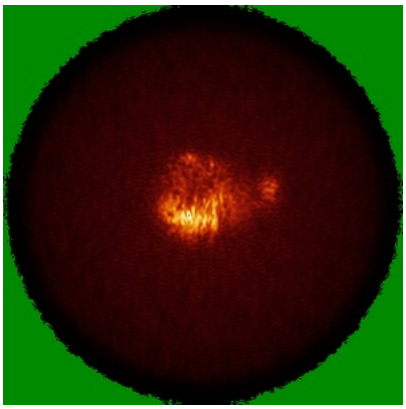
Y Index: 190

Z Index: 172

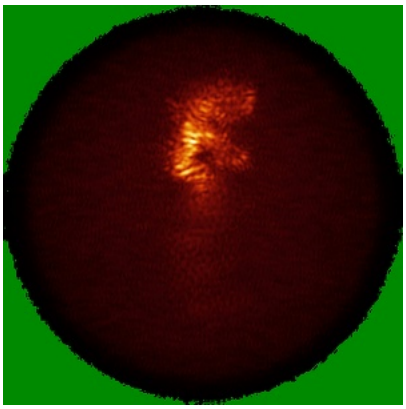
The images above show the largest variance slices of the map in three orthogonal directions.

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

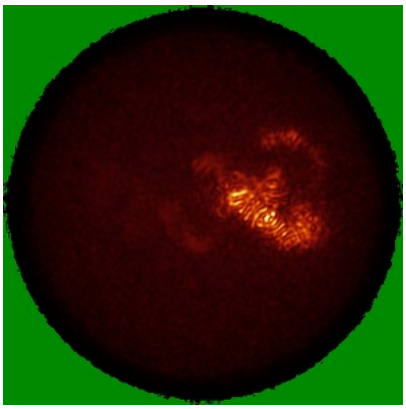
6.4.1 Primary map



X

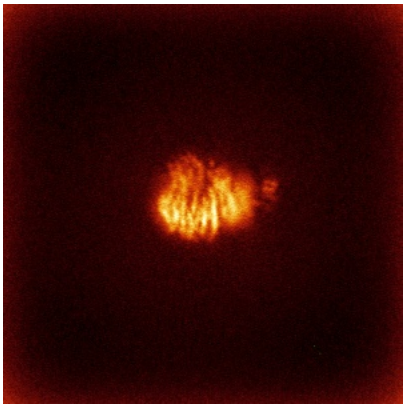


Y

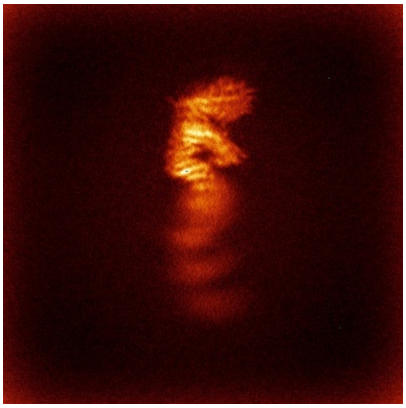


Z

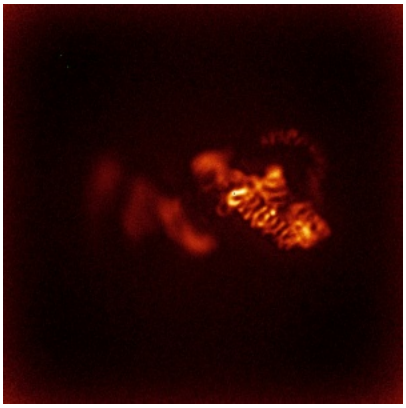
6.4.2 Raw map



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.

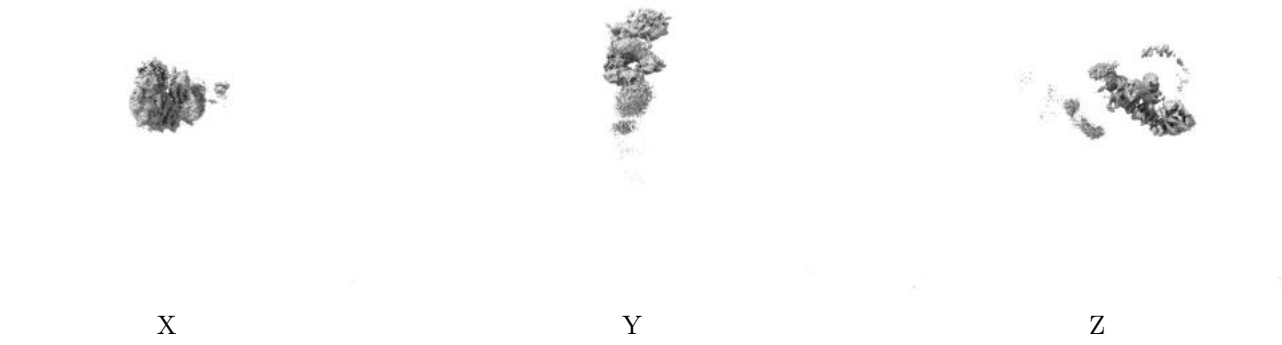
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

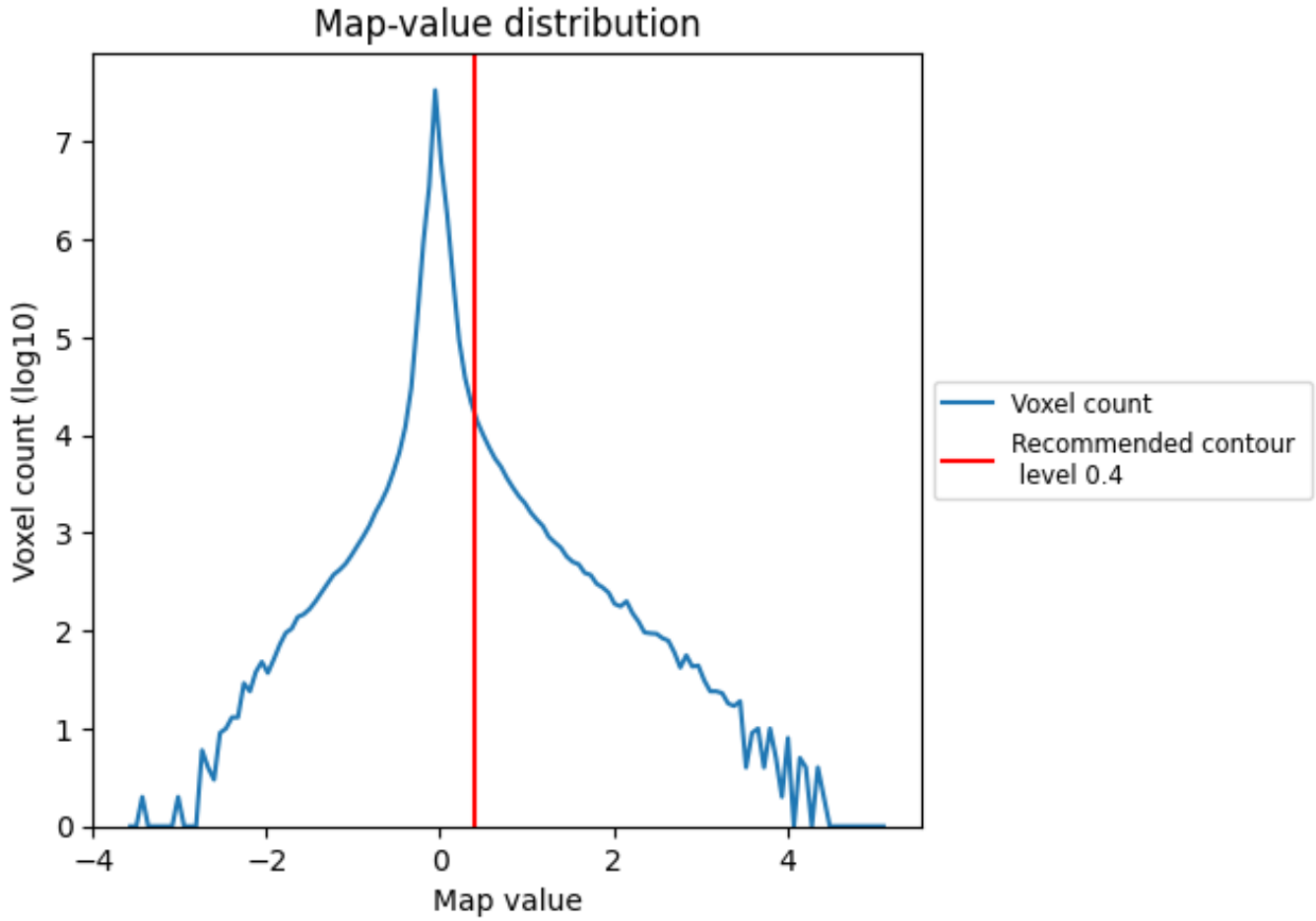
6.6 Mask visualisation (i)

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

7 Map analysis

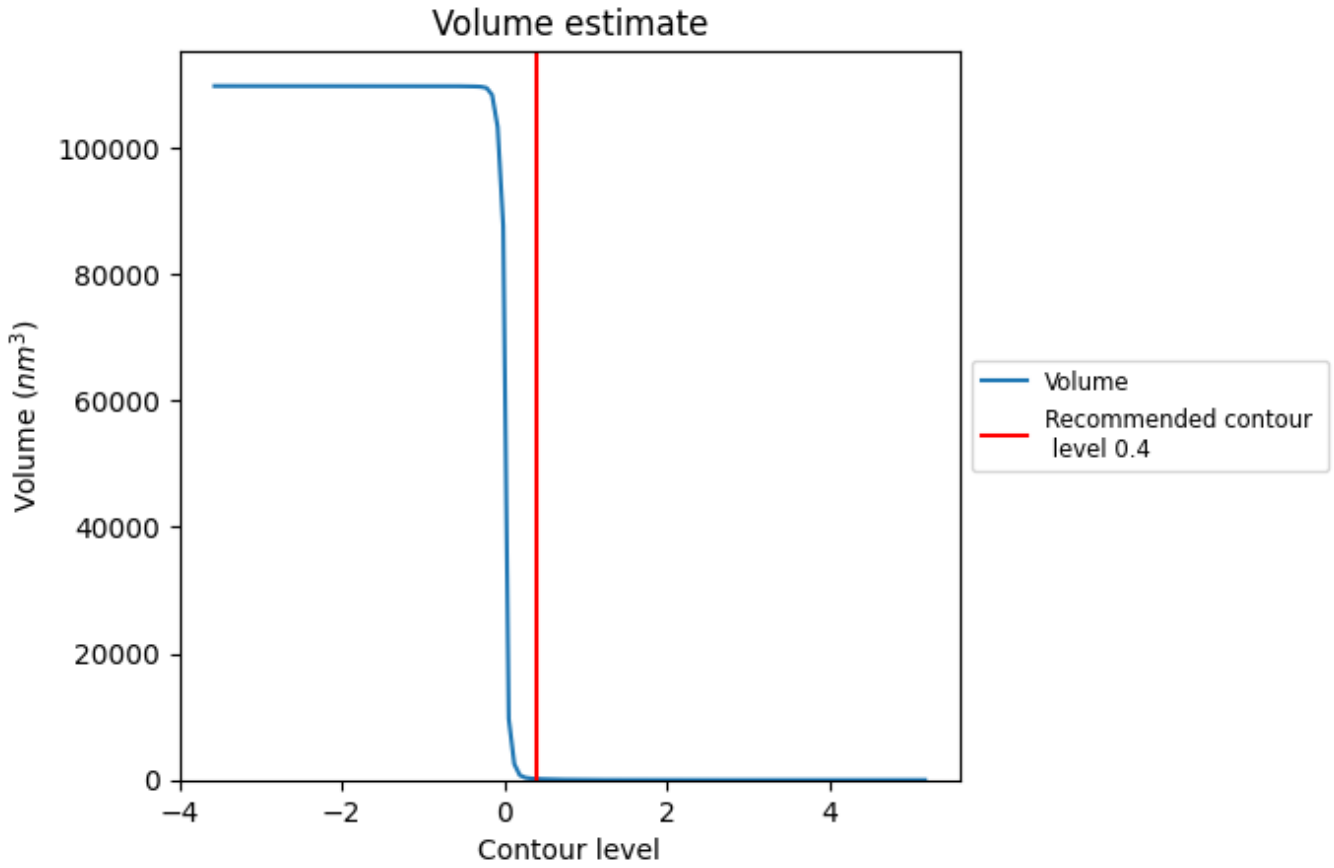
This section contains the results of statistical analysis of the map.

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.

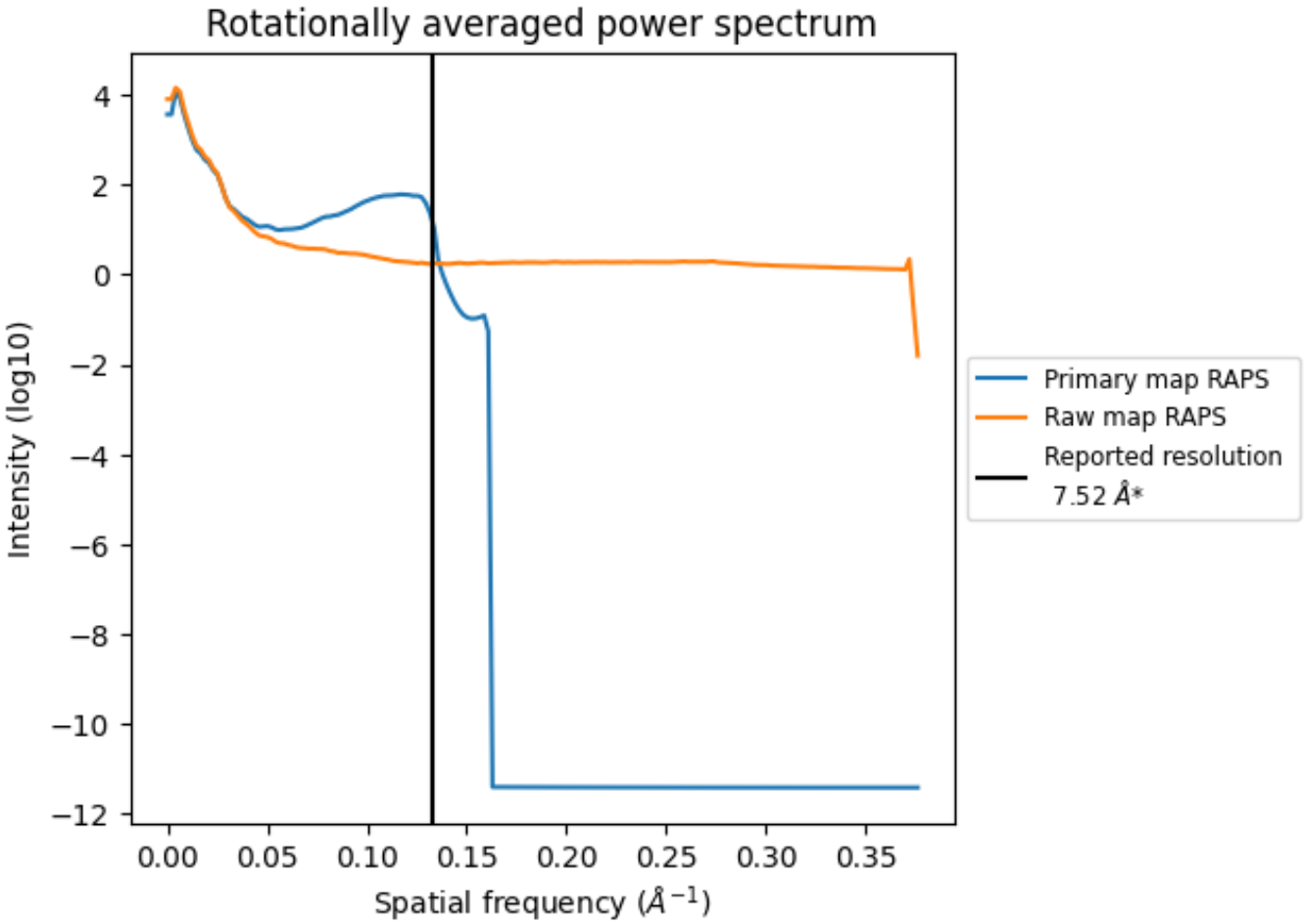
7.2 Volume estimate (i)



The volume at the recommended contour level is 170 nm^3; this corresponds to an approximate mass of 153 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)

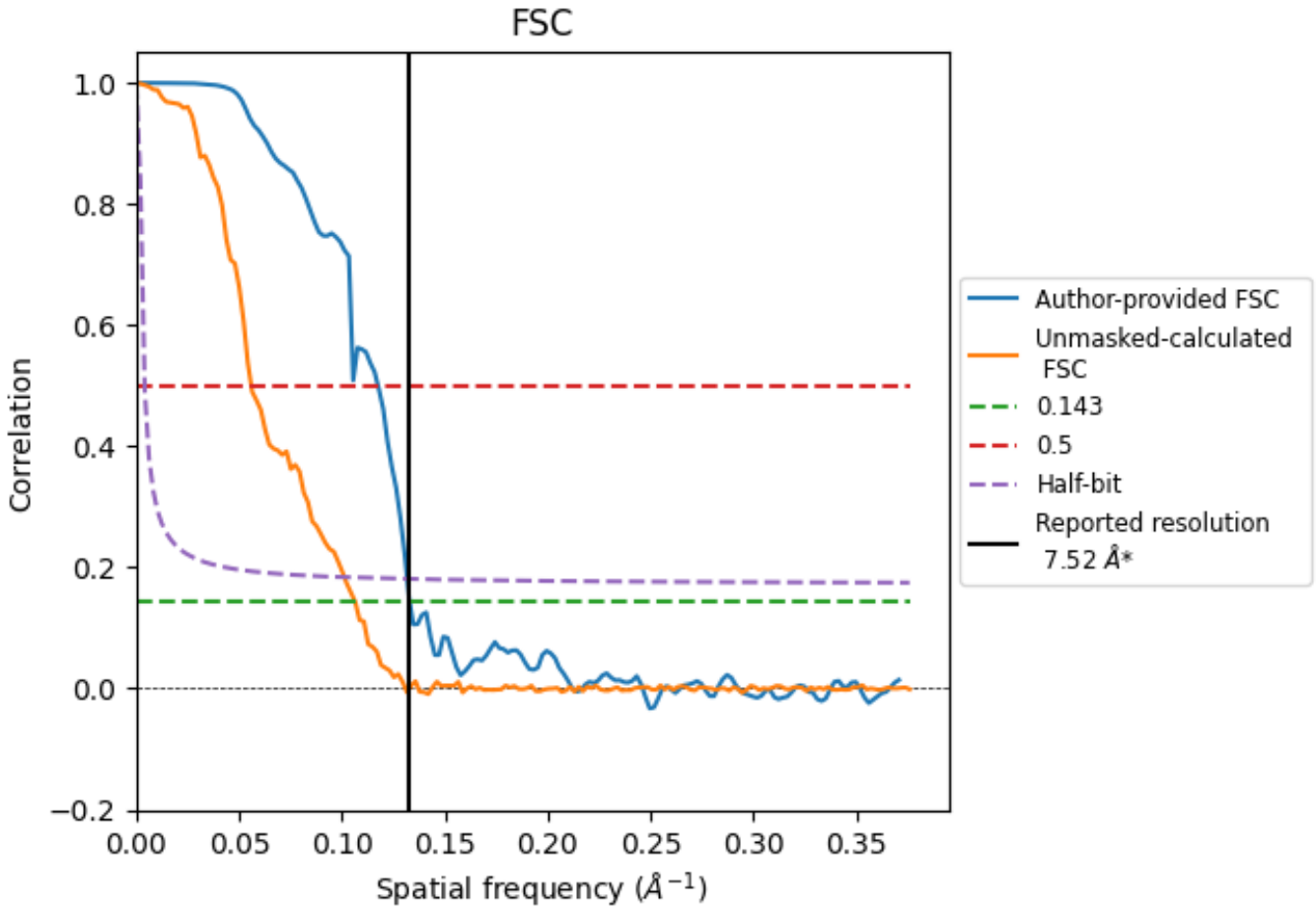


*Reported resolution corresponds to spatial frequency of 0.133 Å^{-1}

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 0.133 Å^{-1}

8.2 Resolution estimates (i)

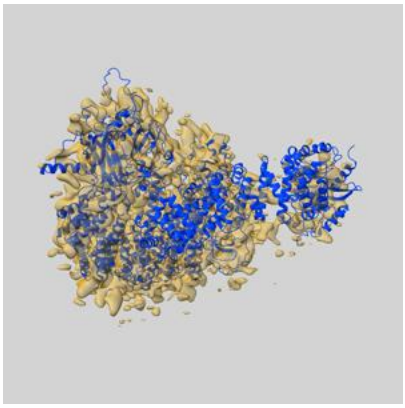
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.52	-	-
Author-provided FSC curve	7.52	8.50	7.59
Unmasked-calculated*	9.39	17.86	9.88

*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 9.39 differs from the reported value 7.52 by more than 10 %

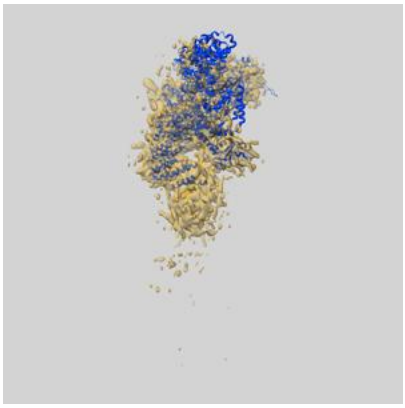
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-63477 and PDB model 9LXH. Per-residue inclusion information can be found in section 3 on page 5.

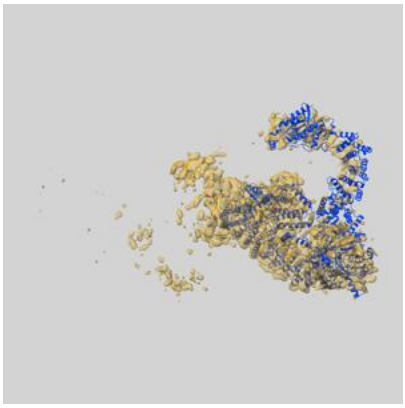
9.1 Map-model overlay



X



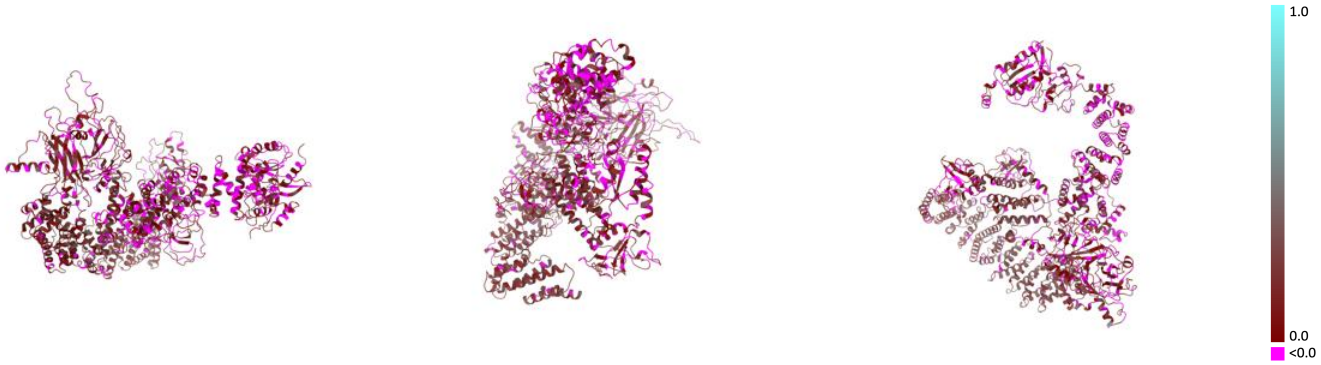
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.4 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.

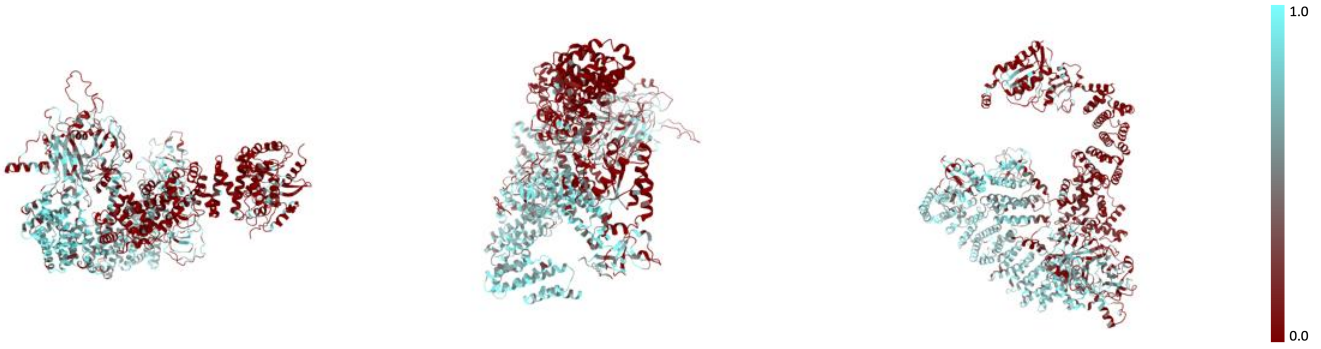
9.2 Q-score mapped to coordinate model



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.

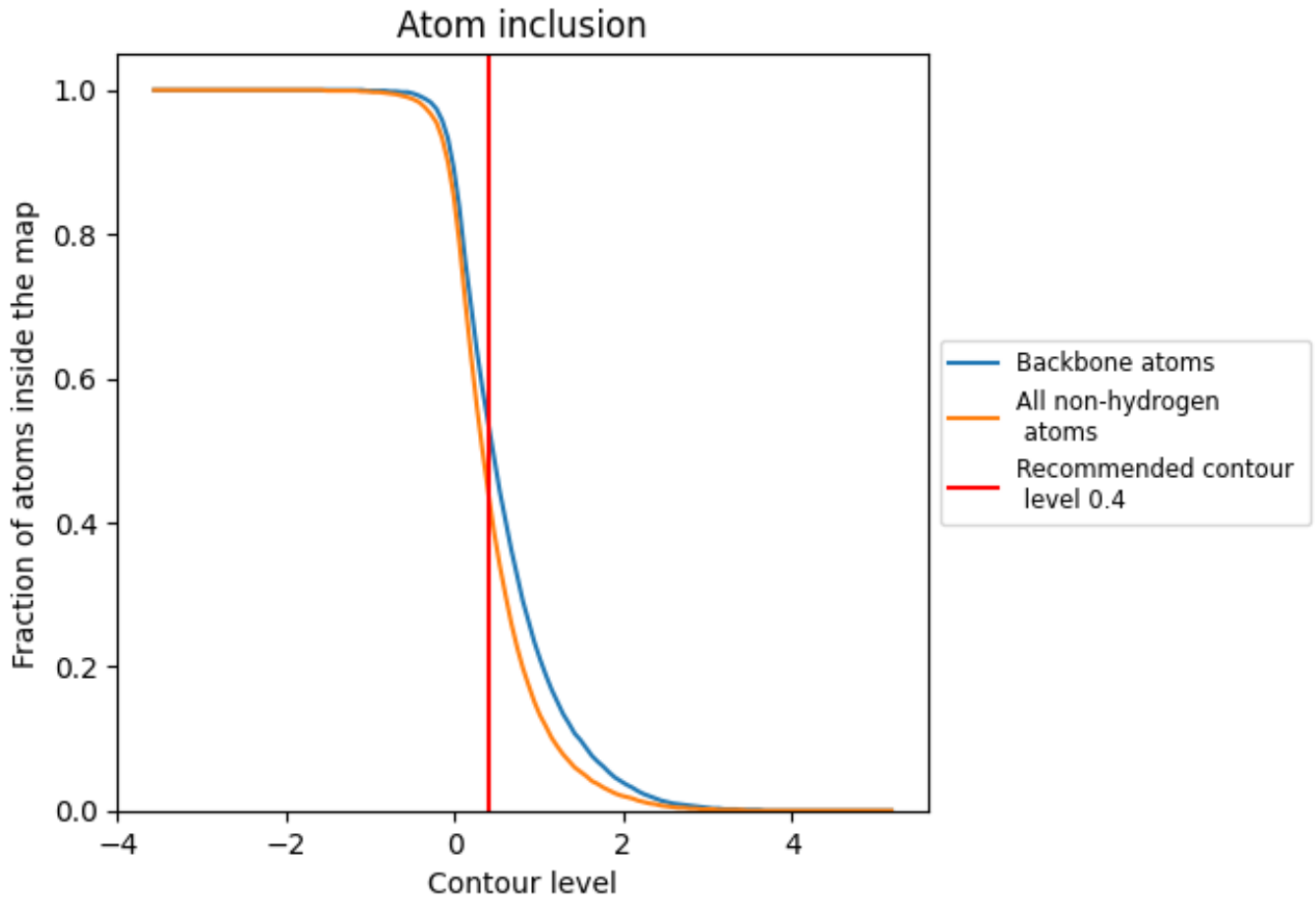
9.3 Atom inclusion mapped to coordinate model



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 (0.4).

9.4 Atom inclusion (i)



At the recommended contour level, 54% of all backbone atoms, 44% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4390	0.1130
A	0.2180	0.0730
B	0.6000	0.1450
C	0.1840	0.0560