



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 01:00 AM UTC

PDB ID : 6H3J / pdb_00006h3j
EMDB ID : EMD-0134
Title : Structural snapshots of the Type 9 protein translocon Plug-complex
Authors : Deme, J.C.; Lea, S.M.
Deposited on : 2018-07-18
Resolution : 3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

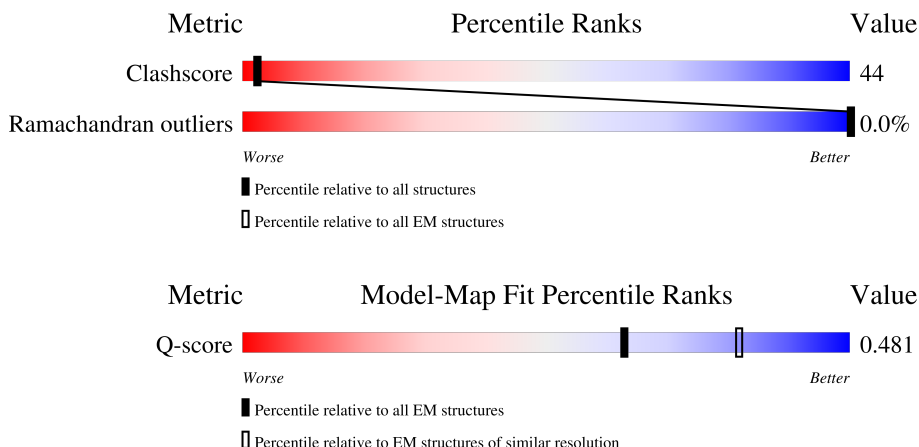
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	-
Q-score	-	25397	11569 (3.20 - 4.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2403	18% 30% 52% 17%
2	B	176	30% 34% 38% 28%
3	C	419	15% 40% 54% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20301 atoms, of which 212 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 Protein involved in gliding motility SprA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1988	Total	C	N	O	S	0	0
			15853	10006	2690	3116	41		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1114	THR	ALA	conflict	UNP A0A1M5G5I4

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	126	Total	C	H	N	O	0	0
			1185	624	212	158	191		

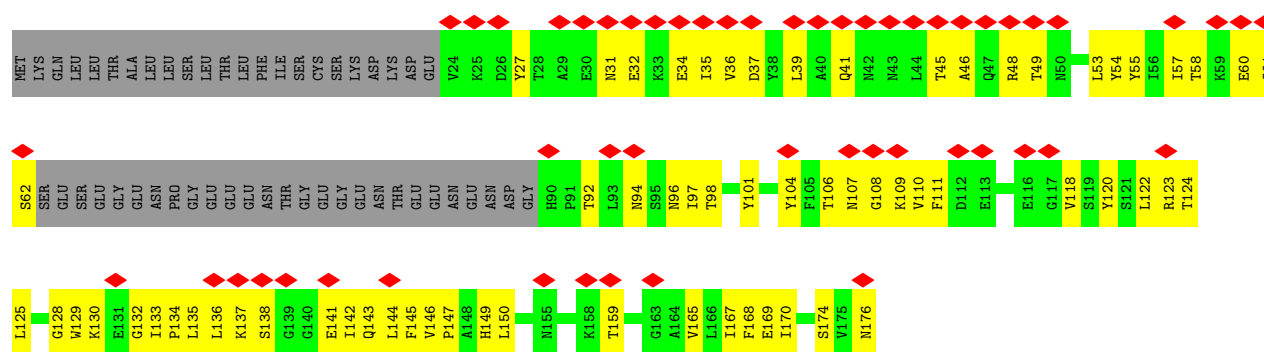
- Molecule 3 is a protein called Plug.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	397	Total	C	N	O	S	0	0
			3263	2085	541	631	6		

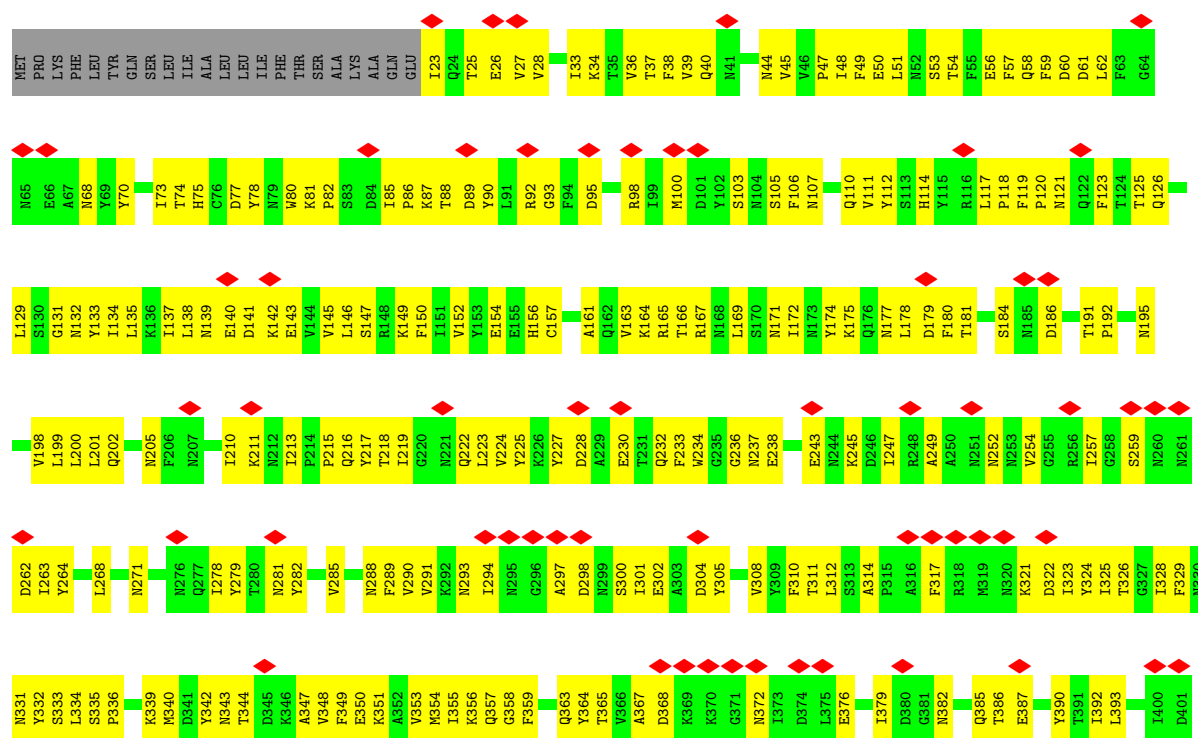
GLY	E839	E840	Y641	N642	T845	N848	A849	N850	Q851	Y854	V855	F856	N857	N858	N859	Y860	R861	N862	T863	Q864	A865	G866	A867	L868	Q869	D870	S871	D872	K873	N874	L877	L878	R879	G880	K881	Y882	K883	SER	ASN	ASN	GLY	SER	ASN	GLY	ILE	PRO	PRO	ILE	GLY	ALA	PHE	ASN	VAL	PRO	GLN	GLY	SER			
VAL	VAL	VAL	THR	THR	ALA	GLY	ARG	VAL	VAL	LEU	VAL	SER	SER	VAL	VAL	ASP	GLN	PHE	LYS	THR	GLN	VAL	GLN	ILE	LEU	ASP	PRO	SER	LEU	ALA	SER	ASN	THR	PRO	ILE	GLU	SER	LEU	ASN	ASN	SER	ILE	PHE	ASN	GLY	GLN	GLN	T754	R755	R756	F760	N819	L820	P882	I762	E763				
H764	K765	I766	S767	D768	K769	F770	I771	I772	G773	G774	T775	Y776	L777	K778	M779	T780	E781	R782	PRO	THR	GLN	LYS	THR	GLN	THR	GLY	GLU	GLN	GLU	GLN	ASN	Y795	I799	F800	G801	F802	N803	G804	N805	Y806	S807	T808	E809	V810	P811	F812	S872	L813	T814	R815	L816	N817	N818	K819	L820	P821	I822	N823	D824	T825
D826	V827	P828	S829	N830	L831	S832	I833	R834	G835	E836	V837	A838	F839	L840	R841	P842	ASP	ALA	PRO	LYS	THR	SER	ASP	PHE	GLN	GLY	GLU	ALA	THR	P815	I856	Y857	V858	D859	D860	F861	E862	G863	S864	Q865	S866	T867	I868	D869	M870	R871	S872	A873	Y874	A875	W876	A879	S880	T881	P882	F883	I884	T885	S886	
I887	N888	D889	N890	T891	F892	N893	A894	N895	S896	N897	T898	L899	E900	Y901	G902	F903	K904	A905	K907	L908	S909	W910	Y911	T912	I913	D914	P915	V916	F917	Y918	S919	S920	K921	P922	S923	G924	I925	S926	N927	D928	D929	L930	S931	L932	R937	I938	Y939	S940	N941	E942	L943	N946	THR	ASP	ILE	ALA				
GLN	GLY	GLN	ILE	Q955	T959	L960	D961	T962	Y964	P965	G967	E968	R969	G970	P971	Y972	N973	N974	S977	F978	G979	A980	S981	N982	P983	N986	G988	I990	N991	R992	A993	L994	N995	F999	E1000	Q1001	G1002	M1003	V1004	E1005	Y1006	I1007	Q1008	F1009	W1010	L1011	L1012	D1013	P1014	Y1015	V1016									
GLI017	M1018	G1019	E1020	A1023	T1024	M1025	A1026	G1027	K1028	I1029	Y1030	F1031	M1032	L1033	G1034	E1035	I1036	S1037	E1038	D1039	V1040	L1041	K1042	D1043	G1044	R1045	Q1046	Y1048	E1049	M1050	G1051	L1052	G1053	P1054	D1055	Q1056	V1057	M1058	V1059	M1060	Q1061	Q1062	P1063	L1064	V1065	G1066	D1067	V1068	P1069	S1073	L1074	I1075	Y1076	A1077	F1078	D1079				
T1080	N1081	P1082	D1083	K1085	K1086	N1087	V1090	G1091	L1092	D1093	G1094	P1096	S1097	E1100	I1103	N1106	Y1107	A1108	G1109	E1110	A1111	ASP	R1114	G1115	D1116	D1117	Y1119	Y1120	Y1121	L1122	N1123	A1124	D1125	V1128	L1129	R1131	N1134	Y1135	N1136	G1137	T1138	E1139	G1140	N1141	V1144	S1145	I1146													
M1147	D1148	P1149	M1150	R1151	G1152	S1153	L1156	P1157	D1158	V1159	E1160	D1161	I1162	M1163	R1164	D1165	T1166	M1168	S1169	T1170	I1171	M1172	A1173	Y1174	Y1175	E1176	Y1177	S1178	I1179	D1180	V1181	K1182	P1183	G1184	M1185	Q1186	V1187	G1188	E1189	N1190	Y1191	I1192	T1193	D1194	I1195	R1196	E1197	V1198	T1199	N1200	V1201	D1202	L1203	P1204	M1205	G1206	G1207			
T1208	T1209	N1210	A1211	W1213	I1214	Q1215	F1216	K1217	I1218	P1219	S1221	Q1222	P1223	Q1224	N1225	T1226	I1227	G1228	N1229	I1230	T1231	D1232	F1233	R1234	S1235	T1236	R1237	M1238	R1240	M1241	F1242	M1243	T1244	G1245	F1246	Q1249	M1250	T1251	V1252	R1253	F1254	G1255	A1256	D1258	L1259	V1260	R1261	W1264	Y1267	THR	GLY	THR								
LEU	ASP	ALA	ASN	ASP	GLN	ASN	PRO	ASP	ASP	GLY	V1283	E1284	F1285	D1286	V1287	A1288	A1289	V1290	I1291	I1292	Q1293	E1294	M1295	K1298	C1299	P1300	Y1303	P1306	P1307	G1308	V1309	Q1310	ARG	GLU	GLN	TYR	ASN	ASN	ASN	THR	VAL	ILE	ASN	GLN	ASN	E1325	Q1326	A1327	L1328	A1329	Q1331	V1330	R1331	I1332	G1333					
G1334	A1335	G1336	L1337	Q1338	Y1339	Q1340	D1341	S1342	R1343	A1344	V1345	F1346	K1347	N1348	V1349	S1350	V1351	D1352	M1353	Y1356	K1357	K1358	L1359	K1360	M1361	F1362	L1363	H1364	A1365	E1366	S1367	L1368	P1369	Q1370	N1371	P1372	L1373	L1374	E1375	D1376	D1377	E1378	M1379	V1380	I1383	R1384	F1385	F1389	N1390	Q1391	I1392	F1393	Y1394	Q1395	I1398					
P1399	L1400	K1401	V1402	T1403	K1404	T1405	G1406	G1407	S1408	C1409	S1410	I1411	S1412	P1413	D1414	L1415	L1416	W1417	M1418	D1419	D1420	N1421	D1424	L1425	A1426	L1427	D1428	L1429	L1430	T1431	R1432	M1433	K1434	I1435	K1436	A1437	M1438	S1439	I1440	D1441	I1442	N1443	S1444	S1445	K1446	R1447	I1448	V1449	N1450	G1451	I1452	Y1453	N1457	D1458	P1459	ASP				

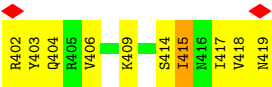


- Molecule 2: Peptidyl-prolyl cis-trans isomerase



- Molecule 3: Plug





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	150000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.251	Depositor
Minimum map value	-0.101	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.0874	Depositor
Map size (Å)	246.0, 246.0, 246.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	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	0.32	0/16188	0.54	2/21960 (0.0%)
2	B	0.26	0/992	0.43	0/1347
3	C	0.33	0/3341	0.48	1/4542 (0.0%)
All	All	0.32	0/20521	0.53	3/27849 (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	A	0	6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	415	ILE	N-CA-C	-5.84	106.80	112.29
1	A	216	ILE	N-CA-C	-5.76	108.23	113.71
1	A	2250	SER	N-CA-C	-5.28	101.33	109.41

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1675	GLU	Peptide
1	A	394	GLY	Peptide
1	A	563	SER	Peptide
1	A	564	PHE	Peptide
1	A	821	PRO	Peptide

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	15853	0	15281	1437	0
2	B	973	212	966	65	0
3	C	3263	0	3109	264	0
All	All	20089	212	19356	1726	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 44.

The worst 5 of 1726 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:A:251:ARG:HB3	1:A:765:LYS:HB3	1.33	1.06
1:A:2033:MET:HE3	1:A:2176:PRO:HG2	1.39	1.03
1:A:527:VAL:HG22	1:A:618:ILE:HG12	1.43	0.99
1:A:225:VAL:HG11	1:A:257:VAL:HG13	1.45	0.98
1:A:216:ILE:HG23	1:A:217:ILE:HD12	1.44	0.97

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	1952/2403 (81%)	1453 (74%)	498 (26%)	1 (0%)	48	78
2	B	122/176 (69%)	102 (84%)	20 (16%)	0	100	100
3	C	395/419 (94%)	326 (82%)	69 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2469/2998 (82%)	1881 (76%)	587 (24%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	ASN

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

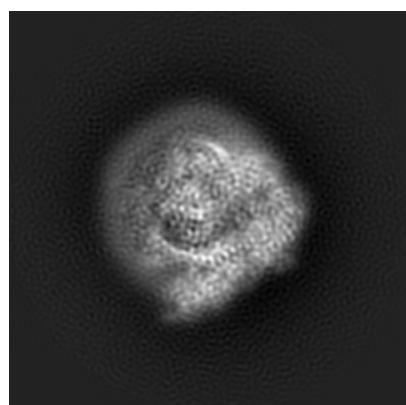
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0134. These allow visual inspection of the internal detail of the map and identification of artifacts.

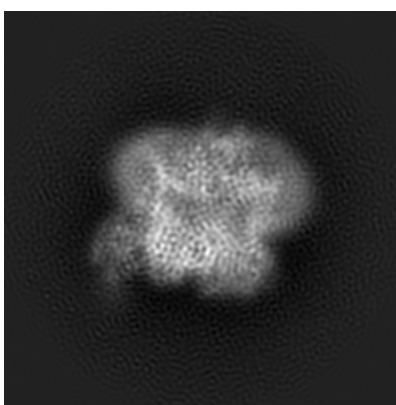
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

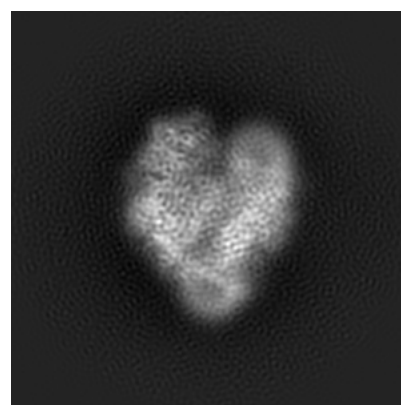
6.1.1 Primary map



X



Y

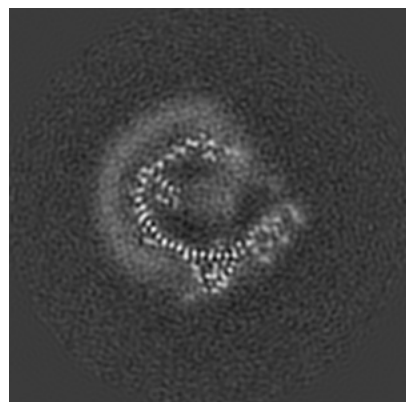


Z

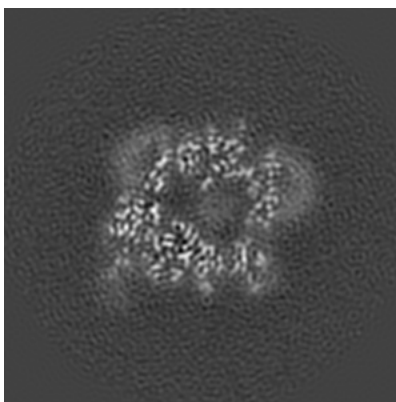
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

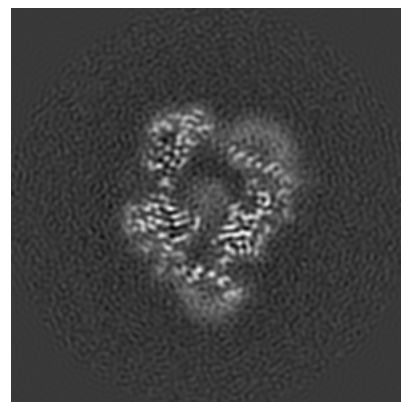
6.2.1 Primary map



X Index: 150



Y Index: 150

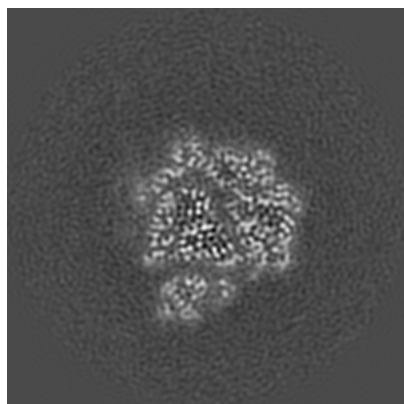


Z Index: 150

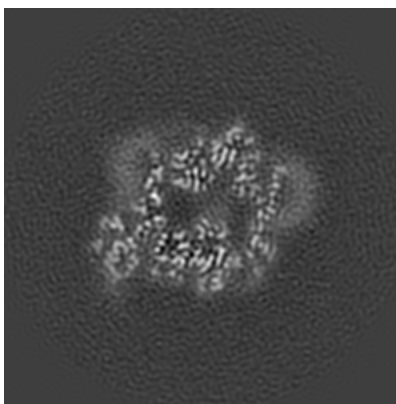
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

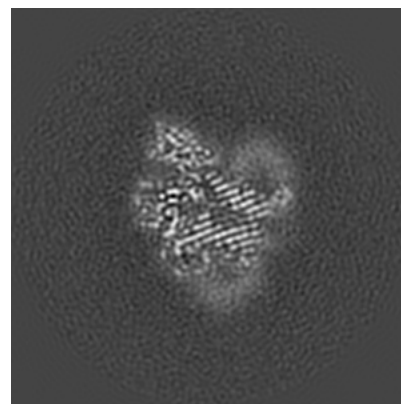
6.3.1 Primary map



X Index: 120



Y Index: 141

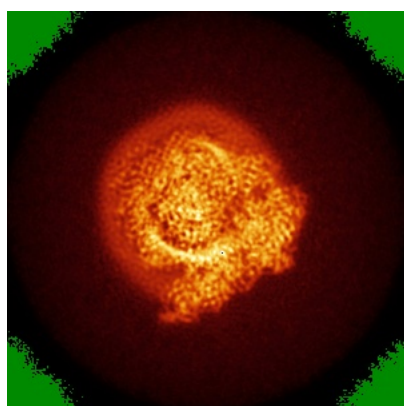


Z Index: 118

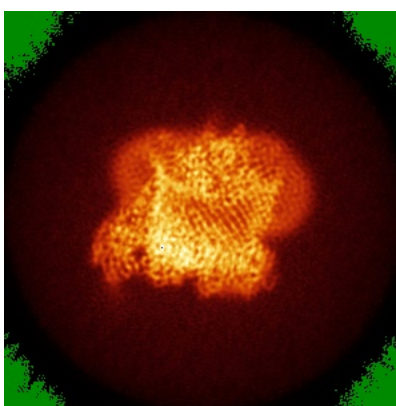
The images above show the largest variance slices of the map in three orthogonal directions.

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

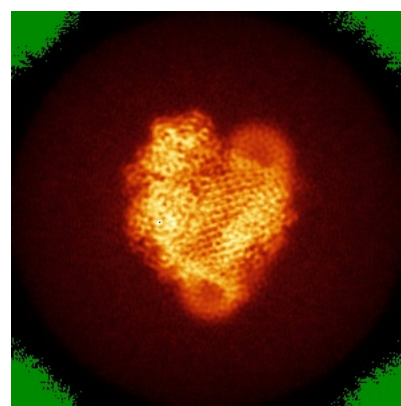
6.4.1 Primary map



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

This section was not generated.

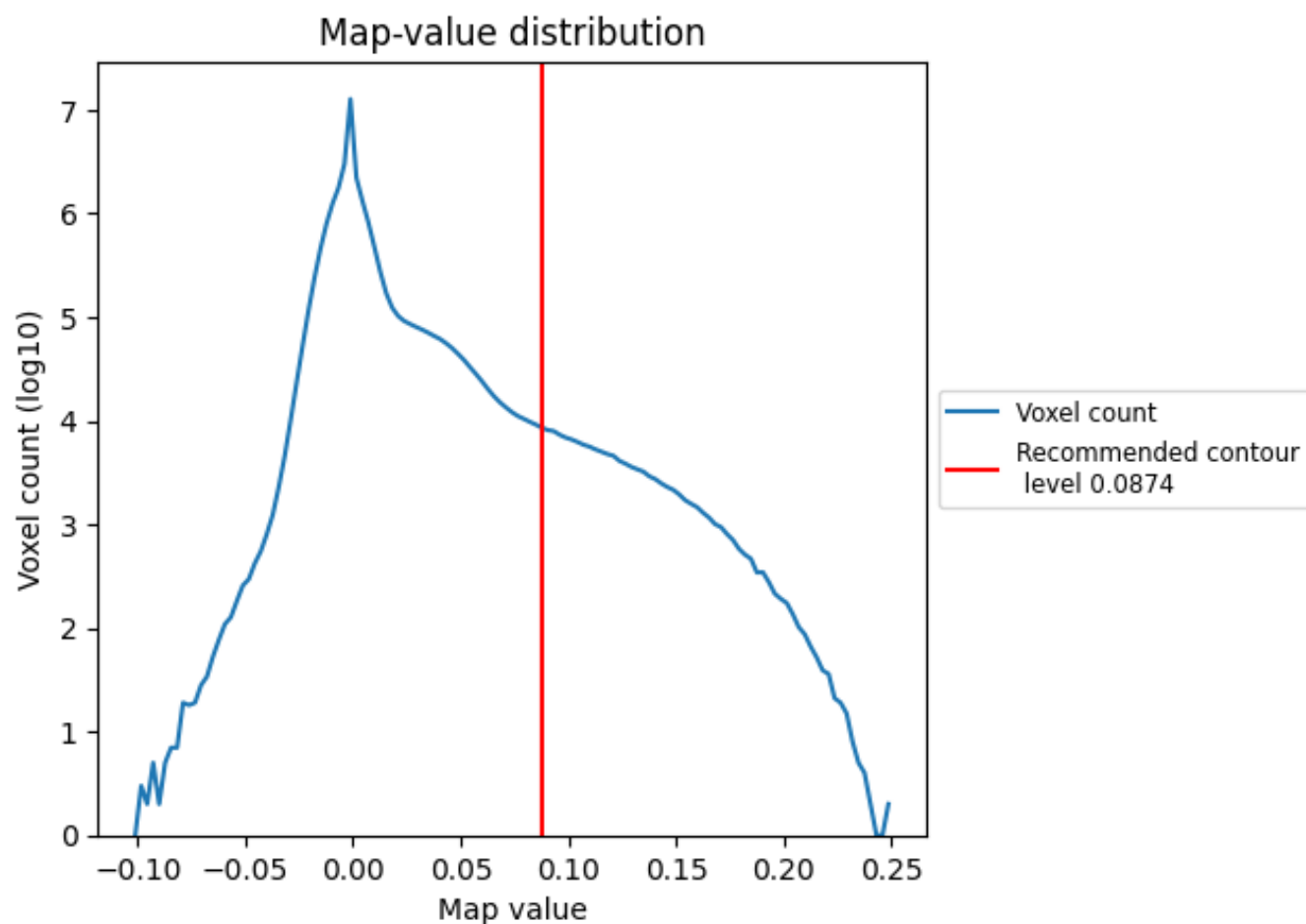
6.6 Mask visualisation

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

7 Map analysis [i](#)

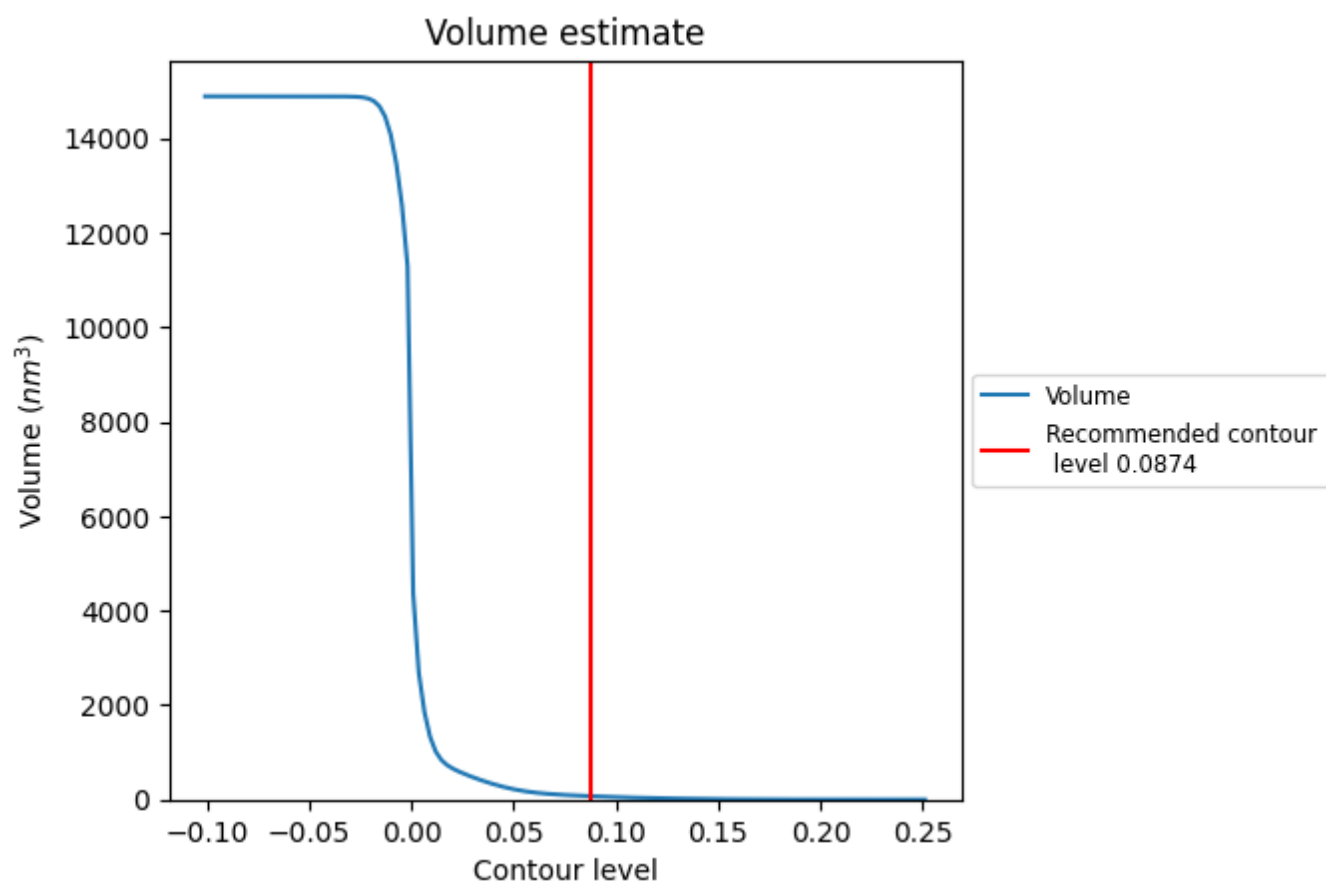
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

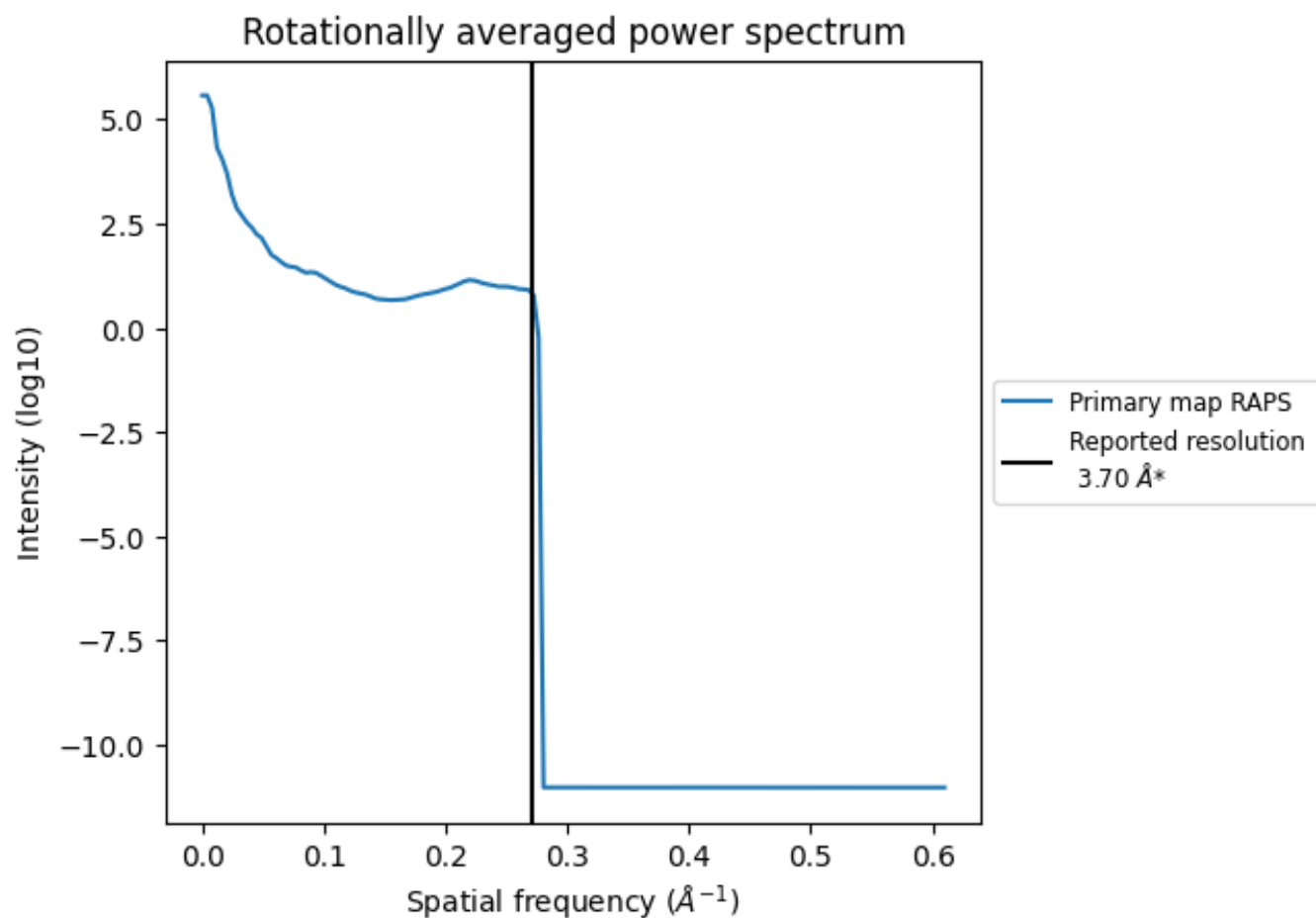
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 72 nm³; this corresponds to an approximate mass of 65 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

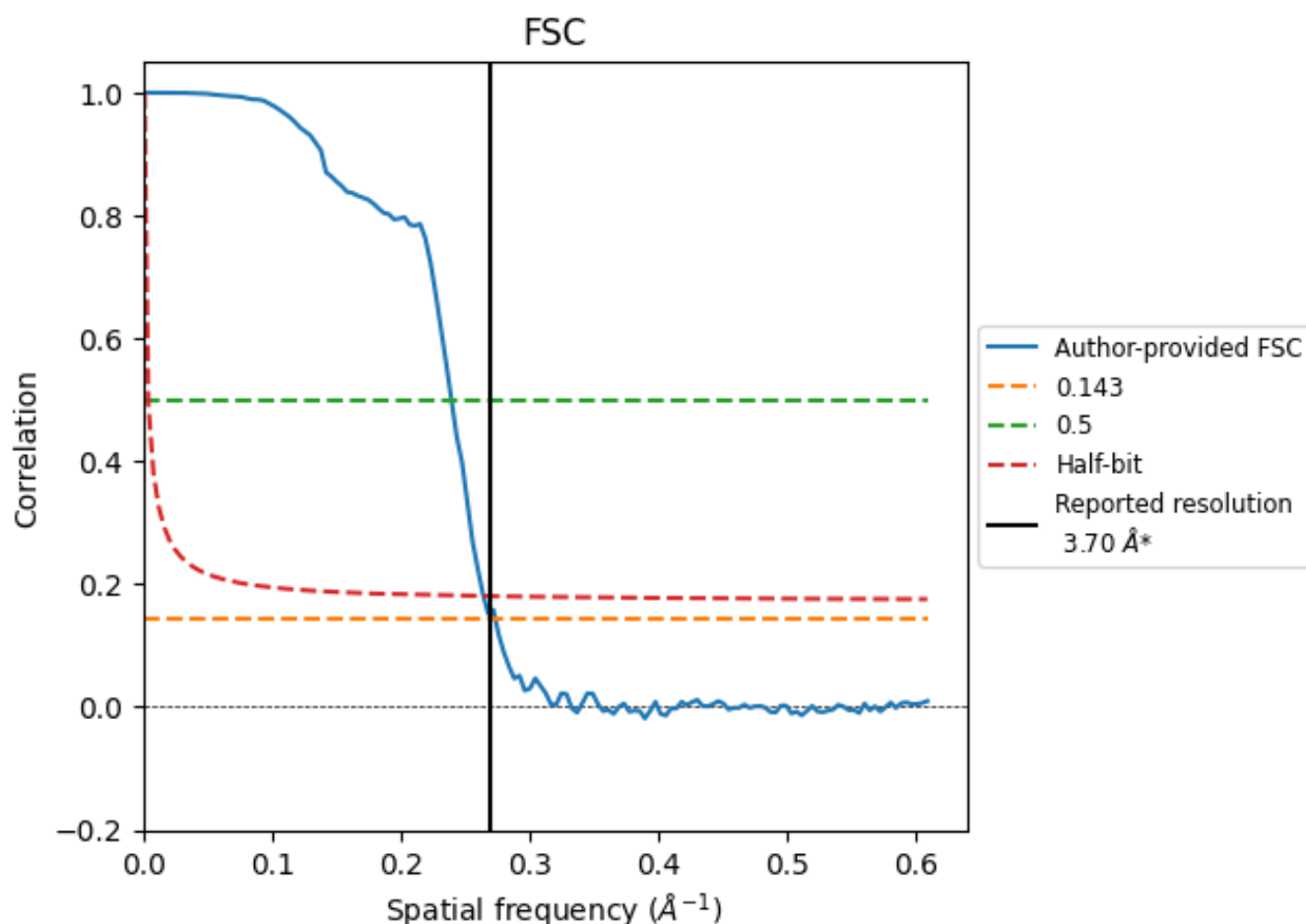


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

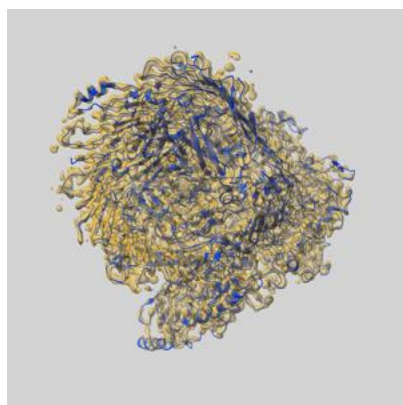
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.65	4.17	3.78
Unmasked-calculated*	-	-	-

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

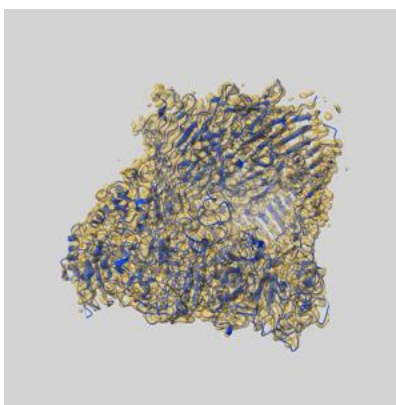
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0134 and PDB model 6H3J. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

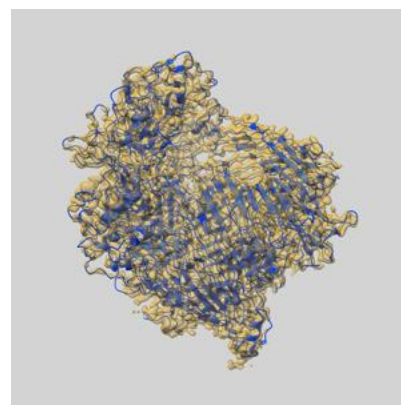
9.1 Map-model overlay [i](#)



X



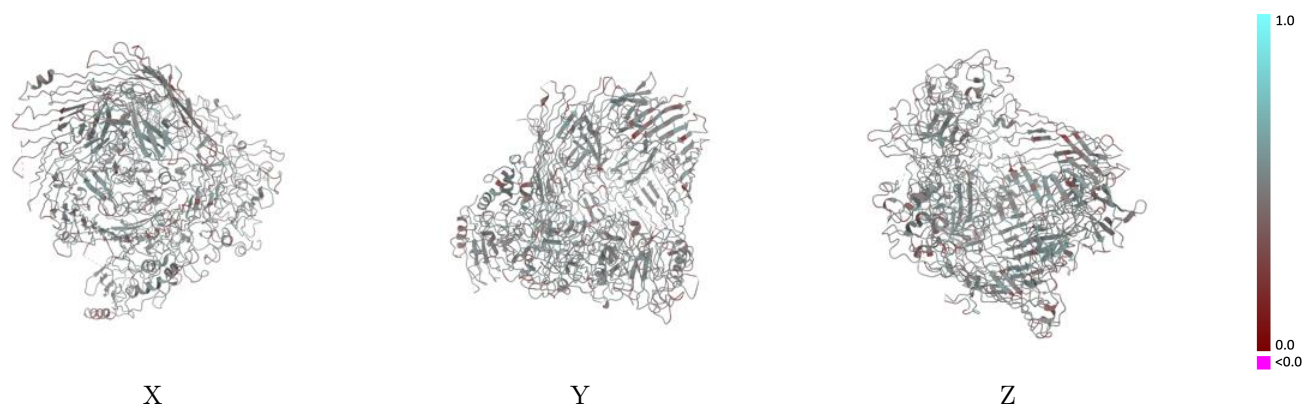
Y



Z

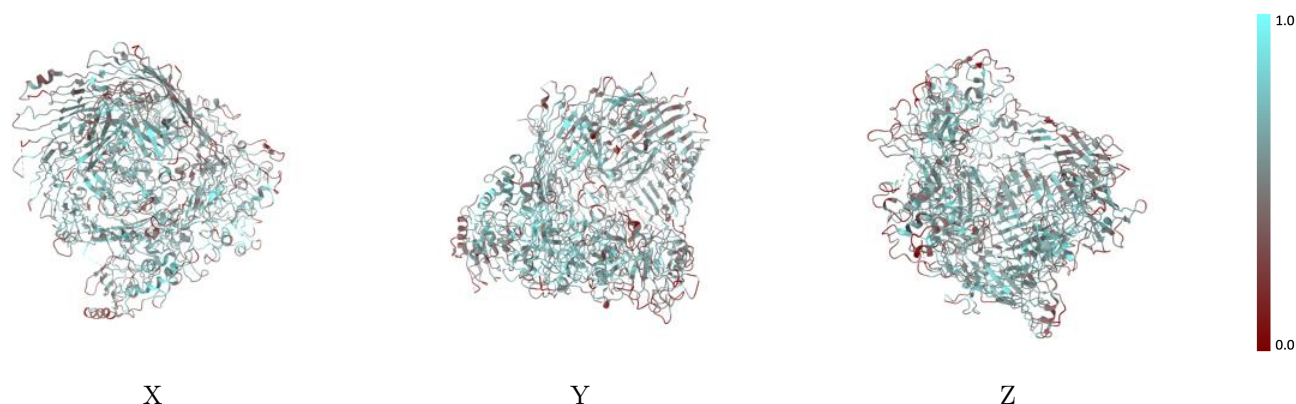
The images above show the 3D surface view of the map at the recommended contour level 0.0874 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



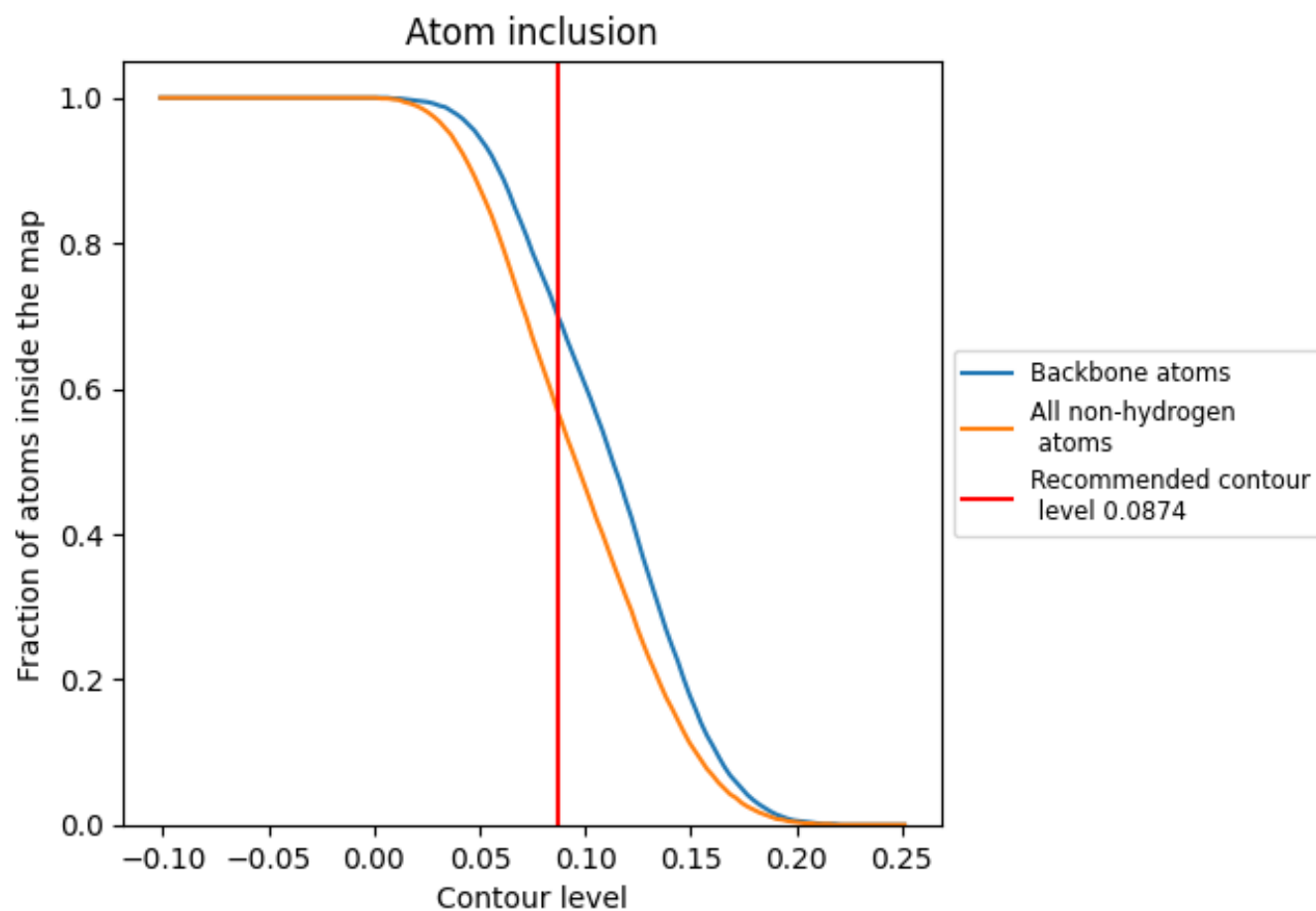
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0874).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 56% 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 (0.0874) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5650	0.4810
A	0.5660	0.4790
B	0.4260	0.4630
C	0.6020	0.4970

