



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 09:06 AM UTC

PDB ID : 7OE1 / pdb_00007oe1
EMDB ID : EMD-12857
Title : 30S ribosomal subunit from E. coli
Authors : Maksimova, E.; Korepanov, A.; Baymukhametov, T.; Kravchenko, O.; Stoboushkina, E.
Deposited on : 2021-04-30
Resolution : 3.05 Å(reported)
Based on initial model : 4V4Q

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:

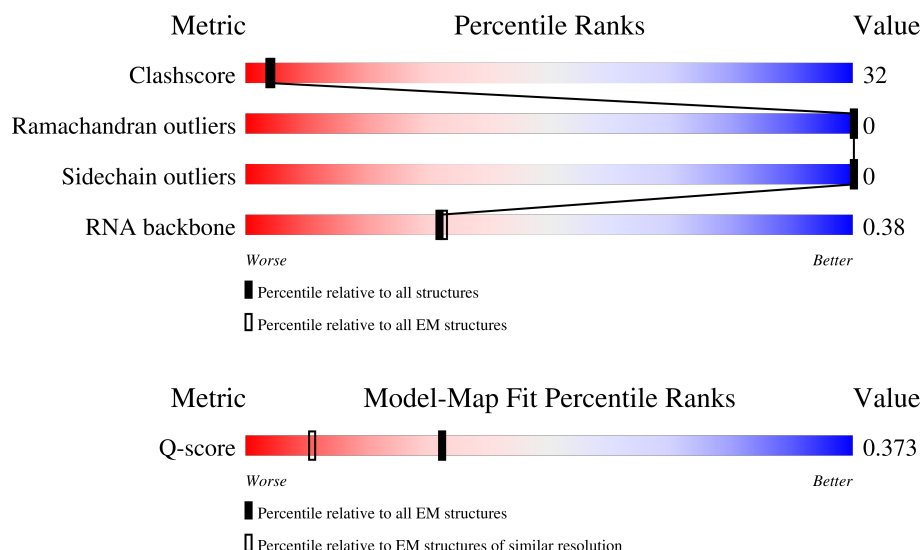
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.05 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	13971 (2.55 - 3.55)

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	1542	
2	D	205	
3	E	166	

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Mol	Chain	Length	Quality of chain
4	F	135	
5	H	129	
6	K	128	
7	L	123	
8	O	89	
9	P	82	
10	Q	83	
11	R	74	
12	T	86	
13	B	240	
14	U	71	
15	C	232	
16	G	178	
17	I	129	
18	J	103	
19	M	117	
20	N	100	
21	S	91	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 51092 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1530	Total	C	N	O	P	0	0
			32831	14642	6024	10635	1530		

- Molecule 2 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 4 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 6 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 7 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 8 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 9 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 10 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 11 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 12 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 13 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 14 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	18	Total	C	N	O	0	0
			148	94	28	26		

- Molecule 15 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 16 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 17 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 18 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 19 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 20 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

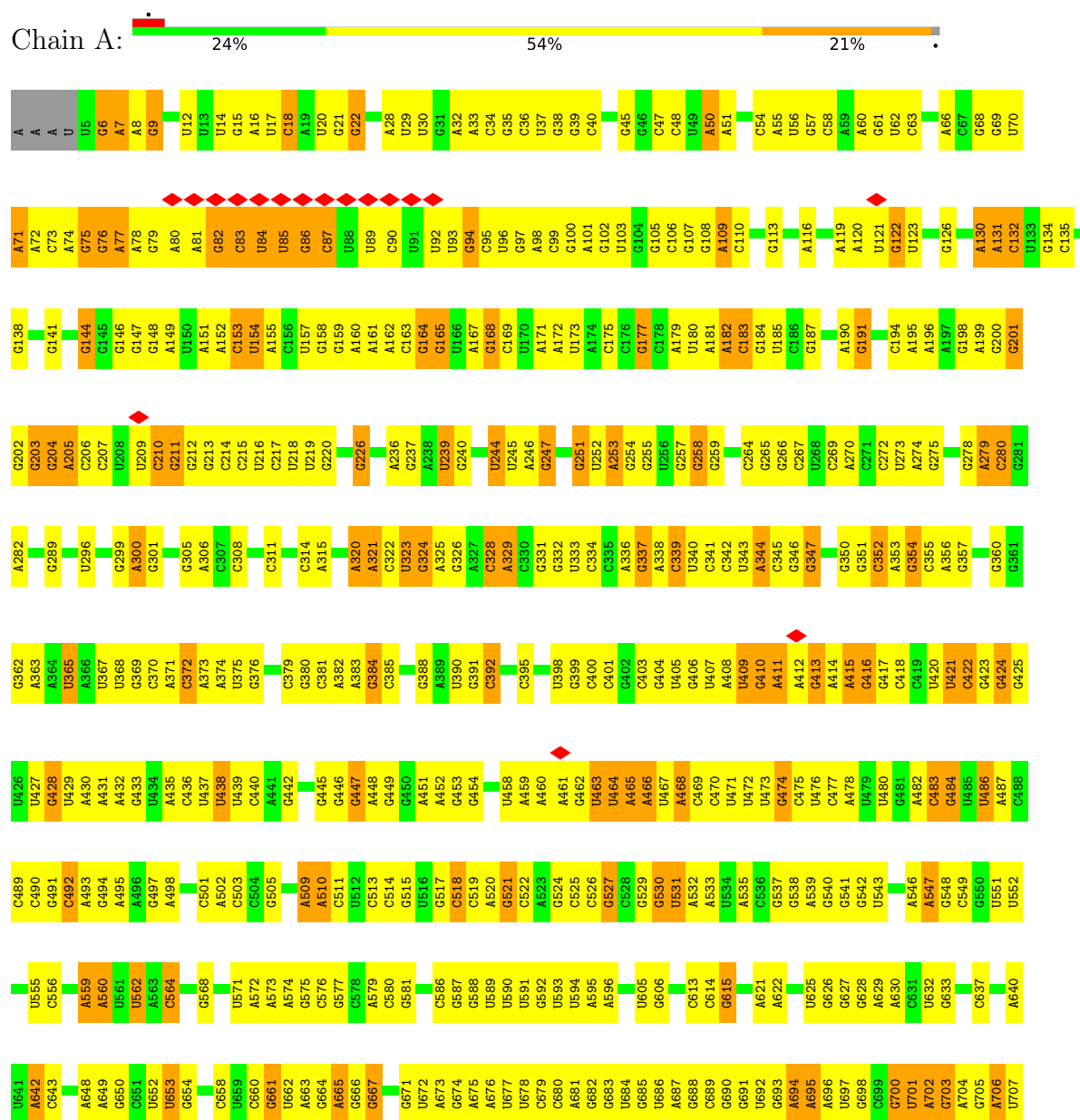
- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	S	79	637	408	120	107	2	0	0

3 Residue-property plots

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.

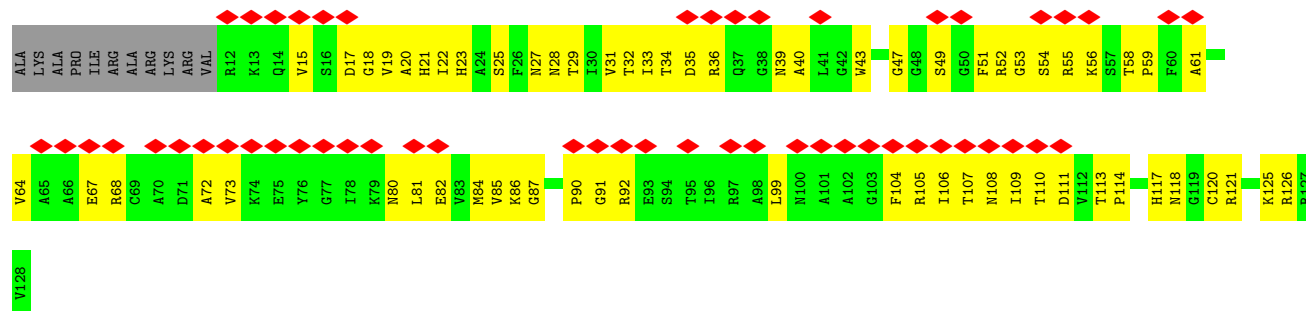
• Molecule 1: 16S rRNA



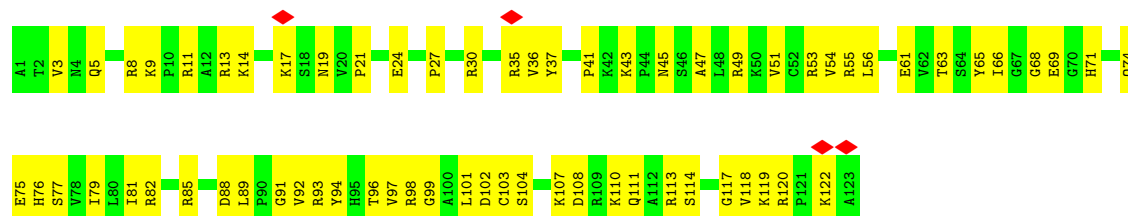
U	G1475	A1413	C1352	G1292	G1231	A1171	U1049	G988	G928	U850	G775	C708
A	A1476	U1414	G1363	C1293	U1232	C1112	U1052	U991	G929	G851	G776	U709
	U1477	G1415	U1354	G1294	G1233	C1113	U1053	U992	C930	G858	A777	G710
	U1478	G1416	U1295	G1295	C1234	C1114	C1054	G993	C931	G859	G778	G713
	C1479	G1417	G1356	U1296	U1235	U1115	A1055	A994	C932	A860	C779	G714
	A1480	G1418	G1357	G1297	U1236	U1116	U1056	A995	G933	A864	A781	A715
	U1481	U1358	U1358	C1237	G1237	A1117	G1057	A996	C934	A864	A782	A716
	G1482	U1298	C1369	A1238	G1178	U1118	G1058	U997	A935	A865	A787	U717
	U1420	A1299	A1360	A1239	A1179	C1119	G1059	U998	C935	A866	C786	C719
	G1421	U1301	U1301	U1240	G1180	U1120	U1060	U999	A937	C866	A787	C720
	G1422	G1302	C1302	G1241	G1181	U1121	U1061	C999	A938	C867	A788	G721
	U1423	C1303	G1242	U1182	U1183	U1122	G1062	A1000	G939	A873	A792	G722
	U1425	G1304	C1243	U1184	G1184	G1124	C1063	C1001	C940	G874	U793	U723
	G1426	G1305	G1244	G1185	G1185	U1125	G1064	G1002	G941	U876	A794	G724
	C1427	A1306	C1245	G1186	U1126	U1126	U1065	G1003	G942	C876	C795	G725
	A1428	U1307	U1246	G1187	G1127	G1127	A1004	A1004	G944	G877	C796	G726
	A1429	U1308	U1247	A1188	U1128	C1128	C1066	A1005	G945	A878	C797	C726
	A1430	G1309	A1248	U1189	C1129	U1129	U1067	A1006	A946	G881	G800	A729
	G1431	G1310	C1249	U1190	A1130	A1130	U1070	U1007	G947	G882	U801	A730
	G1432	A1311	G1190	A1191	U1131	G1131	C1071	U1008	C948	A802	A802	G731
	A1433	G1312	A1251	C1192	G1132	U1132	G1072	U1009	A949	C883	C732	C732
	A1434	U1313	G1252	G1193	G1133	G1133	U1073	U1010	U950	C805	C805	G733
	G1435	C1314	A1254	U1194	U1134	G1134	U1074	C1011	G951	C806	C806	G734
	A1436	U1315	G1255	C1195	U1135	U1135	U1075	A1012	U952	A807	A807	C735
	A1375	G1316	A1256	A1196	C1136	C1136	G1077	A1013	G953	G812	G812	C736
	U1376	C1317	A1257	A1197	G1137	G1137	U1078	A1014	G954	A813	A813	U740
	C1377	A1318	G1258	U1199	U1138	G1138	U1079	A1015	U955	U814	U814	G741
	G1379	C1320	C1259	C1200	G1139	G1139	A1080	U1016	U956	A815	A815	G742
	U1445	U1321	G1260	A1201	C1140	C1140	U1081	U1017	U957	A816	A816	A743
	A1446	C1322	A1261	U1202	C1141	C1141	A1082	A1019	A959	A817	A817	C744
	A1447	G1323	U1264	C1203	G1142	G1142	U1083	G1020	U960	G818	G818	C745
	C1448	A1324	C1265	A1204	G1143	G1143	G1084	A1021	U961	A901	A901	G746
	G1449	C1325	G1266	U1205	C1144	C1144	U1085	A1022	C962	G902	G902	A747
	U1450	U1326	C1267	G1206	U1145	U1145	U1086	U1023	G963	G903	G903	A748
	G1451	C1327	G1268	G1207	A1146	A1146	G1087	G1024	A964	U904	U904	C748
	C1452	C1328	A1269	C1208	C1147	C1147	G1088	U1025	U965	U905	U905	C749
	U1453	A1329	G1270	C1209	U1148	U1148	U1089	G1026	C966	C826	C826	U751
	G1454	U1330	A1271	C1210	C1149	C1149	U1090	C1027	C967	U827	U827	U752
	A1455	G1331	G1272	U1211	A1150	A1150	U1091	U1028	A968	U828	U828	A753
	A1456	A1333	C1273	U1212	C1151	C1151	A1092	U1029	A969	G829	G829	C754
	G1457	G1334	A1274	A1213	A1152	A1152	A1093	U1030	C970	G832	G832	C755
	A1394	U1335	C1275	C1214	G1153	G1153	G1094	C1031	G971	U835	U835	C756
	C1395	C1336	G1276	G1215	G1154	G1154	C1095	C1032	C972	U836	U836	U757
	G1459	G1337	C1277	A1216	A1155	A1155	C1096	G1033	G973	A913	A913	C758
	C1460	G1338	G1278	C1217	G1156	G1156	C1097	A874	A975	U837	U837	A759
	U1527	A1339	G1279	C1218	G1157	G1157	U1098	A976	A976	G838	G838	G760
	G1529	U1340	A1280	A1219	C1158	C1158	G1099	A1035	G976	C839	C839	C761
	U1463	U1341	C1281	G1220	U1159	U1159	C1100	C1036	A977	A918	A918	G763
	A1464	C1342	G1282	G1221	A1101	A1101	A1101	C1037	A978	A919	A919	C764
	A1465	G1343	U1283	G1222	C1160	C1160	A1102	C1038	C979	U840	U840	G765
	C1533	C1344	C1284	C1223	G1161	G1161	C1103	G1039	C980	U841	U841	C766
	A1466	U1345	A1285	U1224	C1162	C1162	G1104	U1040	U981	G844	G844	G769
	G1405	A1346	U1286	A1225	A1163	A1163	A1105	G1041	U982	A845	A845	C770
	U1406	G1347	U1287	C1226	G1164	G1164	G1106	A1042	U983	C924	C924	G771
	U1470	U1348	A1288	A1227	U1165	U1165	G1107	G1043	C984	G846	G846	U772
	A1408	A1349	A1289	C1228	G1166	G1166	G1108	A1044	C985	G847	G847	G773
	C1409	U1350	A1290	A1229	A1167	A1167	C1109	C1045	U986	C927	C927	G774
	A1410	U1351	U1291	C1230	A1168	A1168	A1110	A1046	G987	G849	G849	
					A1169	A1169		G1048				
					A1170	A1170						



• Molecule 6: 30S ribosomal protein S11



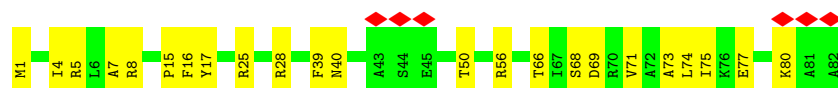
• Molecule 7: 30S ribosomal protein S12



• Molecule 8: 30S ribosomal protein S15

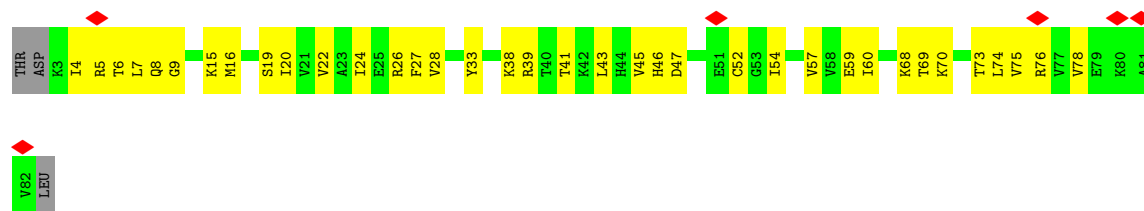


• Molecule 9: 30S ribosomal protein S16

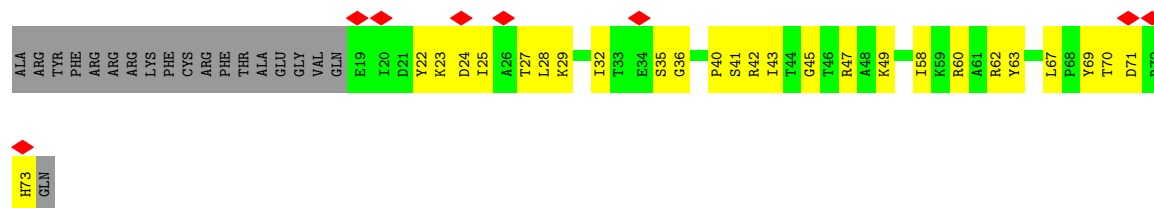


• Molecule 10: 30S ribosomal protein S17

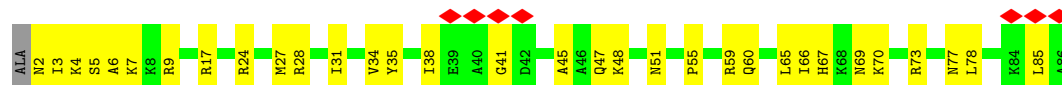




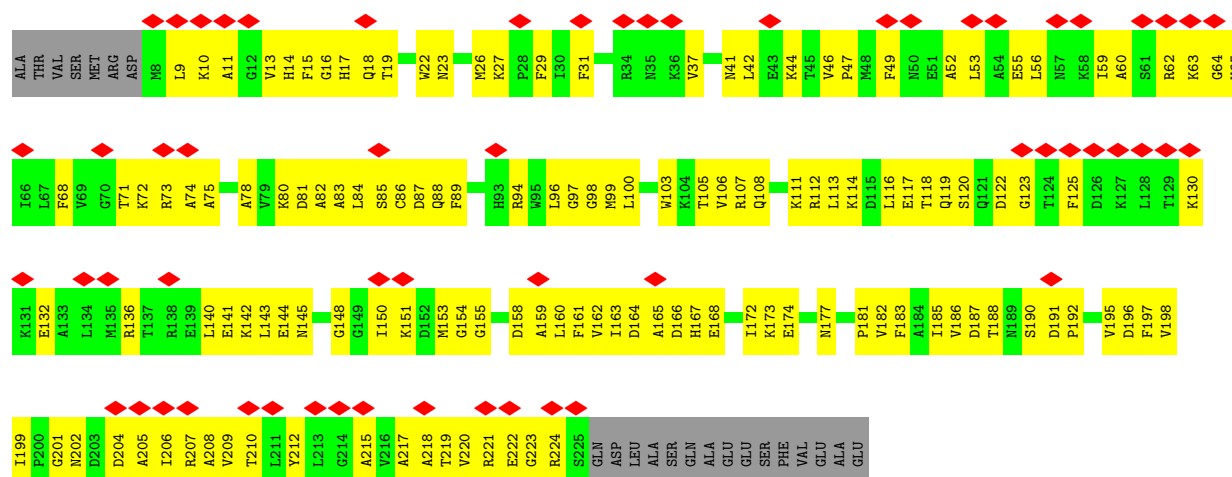
• Molecule 11: 30S ribosomal protein S18



• Molecule 12: 30S ribosomal protein S20

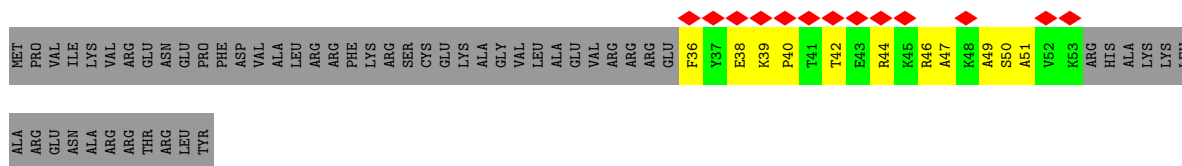


• Molecule 13: 30S ribosomal protein S2

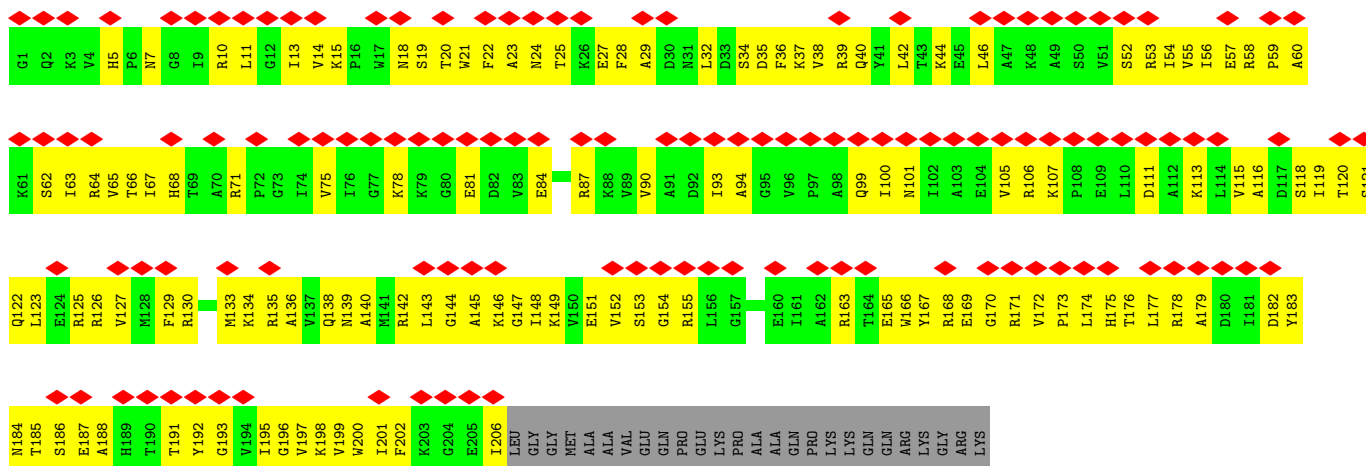


• Molecule 14: 30S ribosomal protein S21

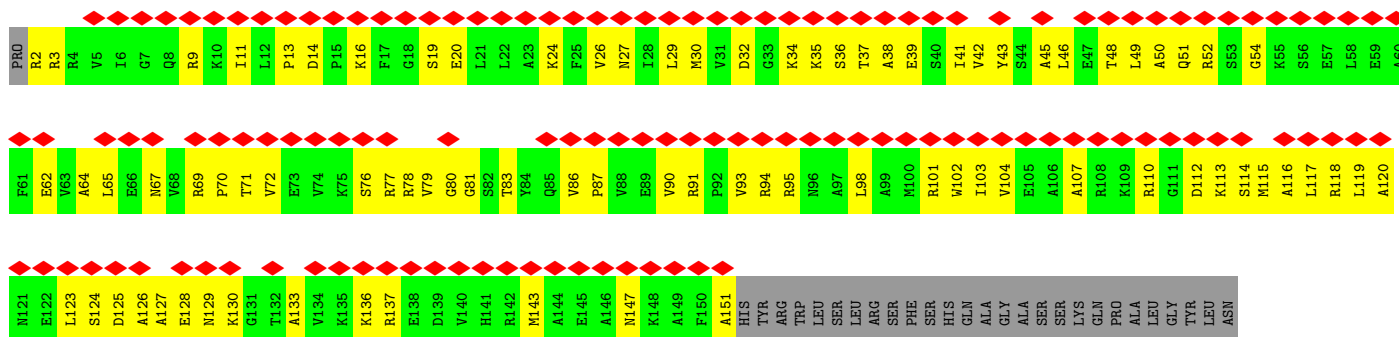
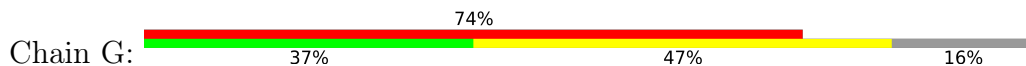




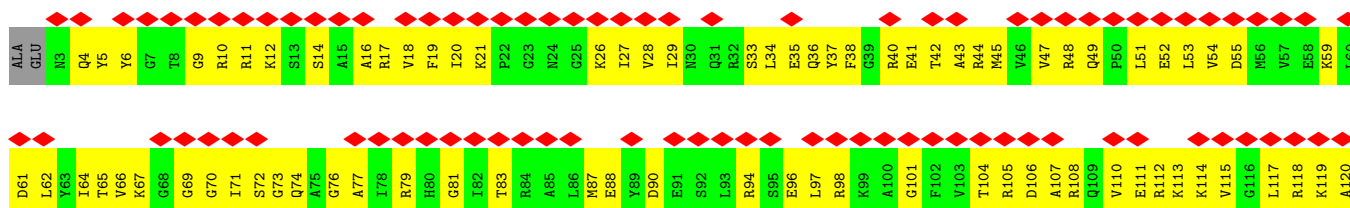
• Molecule 15: 30S ribosomal protein S3

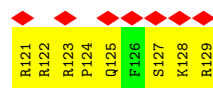


• Molecule 16: 30S ribosomal protein S7

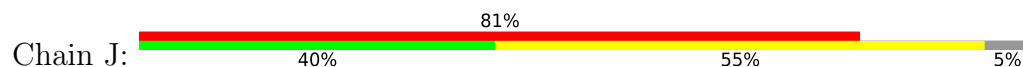


• Molecule 17: 30S ribosomal protein S9

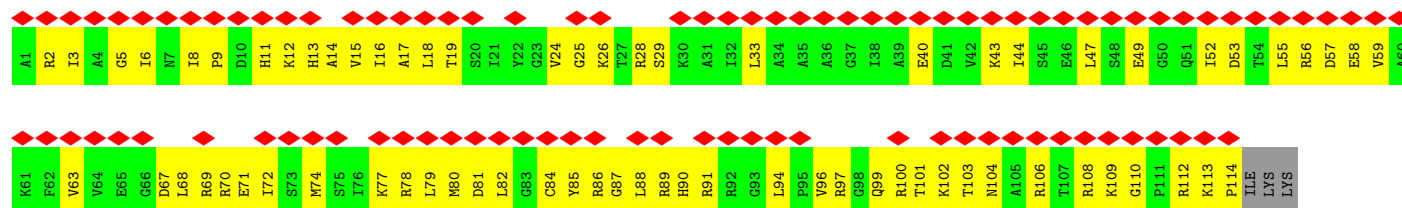
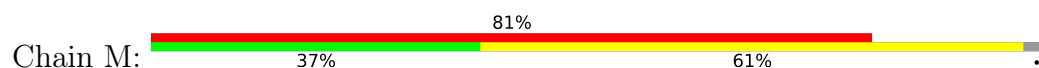




• Molecule 18: 30S ribosomal protein S10



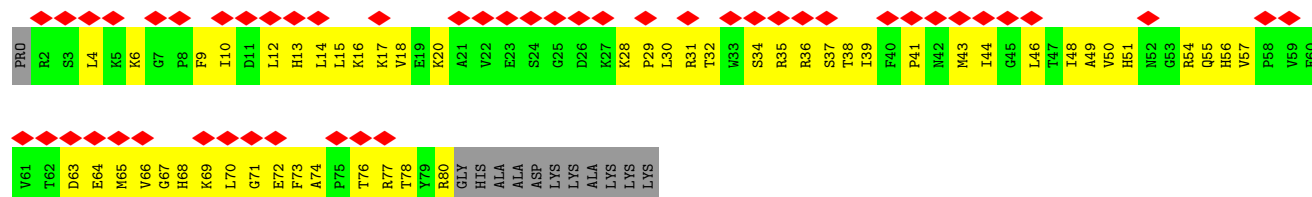
• Molecule 19: 30S ribosomal protein S13



• Molecule 20: 30S ribosomal protein S14



• Molecule 21: 30S ribosomal protein S19



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	169371	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	8.320	Depositor
Minimum map value	-4.514	Depositor
Average map value	0.012	Depositor
Map value standard deviation	0.094	Depositor
Recommended contour level	0.428	Depositor
Map size ($\text{\AA}$)	344.0, 344.0, 344.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.47	1/36762 (0.0%)	0.43	2/57350 (0.0%)
2	D	0.41	0/1665	0.65	0/2227
3	E	0.56	0/1118	0.70	0/1504
4	F	0.31	0/835	0.56	0/1128
5	H	0.52	0/989	0.65	0/1326
6	K	0.28	0/893	0.57	0/1205
7	L	0.51	0/969	0.75	0/1300
8	O	0.44	0/724	0.61	0/966
9	P	0.51	0/659	0.68	0/884
10	Q	0.50	0/657	0.63	0/881
11	R	0.42	0/462	0.66	0/621
12	T	0.38	0/671	0.65	0/888
13	B	0.32	0/1735	0.60	0/2338
14	U	0.24	0/150	0.67	0/198
15	C	0.19	0/1651	0.47	0/2225
16	G	0.17	0/1187	0.46	0/1591
17	I	0.20	0/1034	0.54	0/1375
18	J	0.16	0/796	0.45	0/1077
19	M	0.16	0/892	0.51	0/1193
20	N	0.25	0/785	0.61	0/1043
21	S	0.21	0/652	0.56	0/877
All	All	0.44	1/55286 (0.0%)	0.49	2/82197 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	918	A	C6-N1	-5.15	1.25	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	860	A	O5'-P-OP1	-5.58	91.27	108.00
1	A	1392	G	O4'-C1'-N9	5.45	116.37	108.20

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	32831	0	16519	1548	0
2	D	1643	0	1710	129	0
3	E	1105	0	1148	67	0
4	F	817	0	808	68	0
5	H	979	0	1034	52	0
6	K	877	0	887	89	0
7	L	955	0	1019	75	0
8	O	716	0	742	35	0
9	P	649	0	666	20	0
10	Q	648	0	691	39	0
11	R	455	0	478	45	0
12	T	665	0	714	30	0
13	B	1704	0	1732	140	0
14	U	148	0	157	13	0
15	C	1624	0	1699	146	0
16	G	1174	0	1230	109	0
17	I	1022	0	1070	107	0
18	J	786	0	828	90	0
19	M	883	0	944	94	0
20	N	774	0	827	93	0
21	S	637	0	665	96	0
All	All	51092	0	35568	2735	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 32.

The worst 5 of 2735 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:1117:A:C2	1:A:1156:G:N1	2.10	1.19
1:A:945:G:H1	1:A:1236:A:N6	1.37	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1156:G:N2	1:A:1179:A:C2	2.11	1.18
2:D:104:MET:HG2	2:D:106:PHE:CE2	1.91	1.06
21:S:39:ILE:CG2	21:S:43:MET:HE3	1.85	1.06

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	
2	D	203/205 (99%)	174 (86%)	29 (14%)	0	100	100
3	E	148/166 (89%)	119 (80%)	29 (20%)	0	100	100
4	F	98/135 (73%)	80 (82%)	18 (18%)	0	100	100
5	H	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
6	K	115/128 (90%)	94 (82%)	21 (18%)	0	100	100
7	L	121/123 (98%)	96 (79%)	25 (21%)	0	100	100
8	O	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
9	P	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
10	Q	78/83 (94%)	66 (85%)	12 (15%)	0	100	100
11	R	53/74 (72%)	45 (85%)	8 (15%)	0	100	100
12	T	83/86 (96%)	77 (93%)	6 (7%)	0	100	100
13	B	216/240 (90%)	172 (80%)	44 (20%)	0	100	100
14	U	16/71 (22%)	10 (62%)	6 (38%)	0	100	100
15	C	204/232 (88%)	176 (86%)	28 (14%)	0	100	100
16	G	148/178 (83%)	129 (87%)	19 (13%)	0	100	100
17	I	125/129 (97%)	107 (86%)	18 (14%)	0	100	100
18	J	96/103 (93%)	78 (81%)	18 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	M	112/117 (96%)	98 (88%)	14 (12%)	0	100	100
20	N	92/100 (92%)	86 (94%)	6 (6%)	0	100	100
21	S	77/91 (85%)	64 (83%)	13 (17%)	0	100	100
All	All	2278/2561 (89%)	1935 (85%)	343 (15%)	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	
2	D	172/172 (100%)	172 (100%)	0	100	100
3	E	113/125 (90%)	113 (100%)	0	100	100
4	F	87/116 (75%)	87 (100%)	0	100	100
5	H	104/104 (100%)	104 (100%)	0	100	100
6	K	90/98 (92%)	90 (100%)	0	100	100
7	L	103/103 (100%)	103 (100%)	0	100	100
8	O	76/77 (99%)	76 (100%)	0	100	100
9	P	65/65 (100%)	65 (100%)	0	100	100
10	Q	74/77 (96%)	74 (100%)	0	100	100
11	R	48/64 (75%)	48 (100%)	0	100	100
12	T	65/65 (100%)	65 (100%)	0	100	100
13	B	180/198 (91%)	180 (100%)	0	100	100
14	U	15/61 (25%)	15 (100%)	0	100	100
15	C	170/189 (90%)	170 (100%)	0	100	100
16	G	123/146 (84%)	123 (100%)	0	100	100
17	I	105/106 (99%)	105 (100%)	0	100	100
18	J	86/90 (96%)	86 (100%)	0	100	100
19	M	92/95 (97%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	N	79/83 (95%)	79 (100%)	0	100	100
21	S	70/78 (90%)	70 (100%)	0	100	100
All	All	1917/2112 (91%)	1917 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
11	R	73	HIS
20	N	3	GLN
12	T	77	ASN
15	C	138	GLN
12	T	60	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1529/1542 (99%)	468 (30%)	15 (0%)

5 of 468 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	A
1	A	9	G
1	A	18	C
1	A	20	U

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	923	A
1	A	1388	C
1	A	931	C
1	A	1390	U
1	A	1210	C

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.

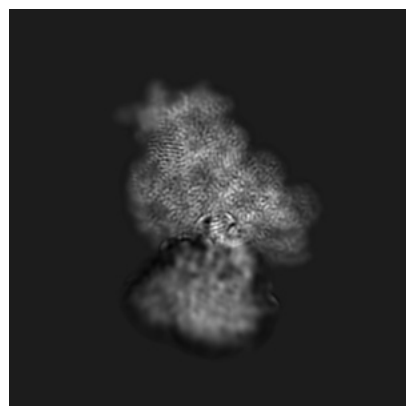
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12857. These allow visual inspection of the internal detail of the map and identification of artifacts.

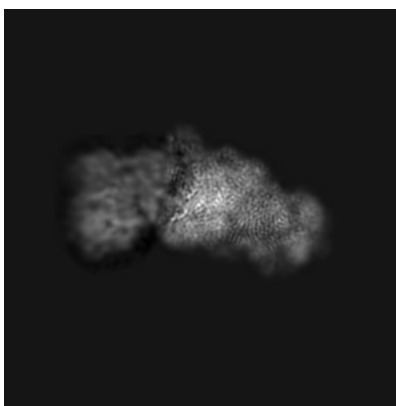
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

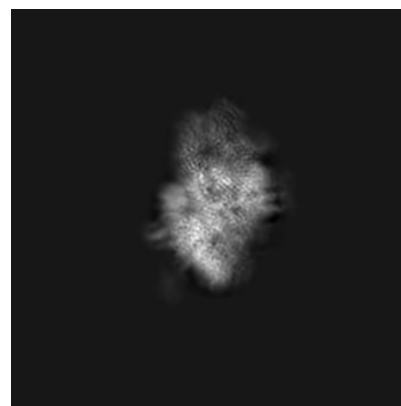
6.1.1 Primary map



X

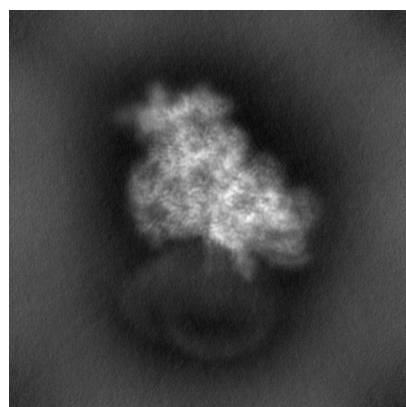


Y

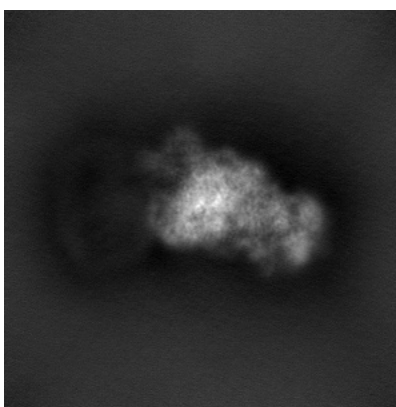


Z

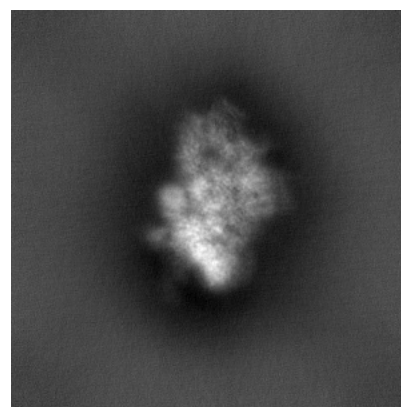
6.1.2 Raw map



X



Y

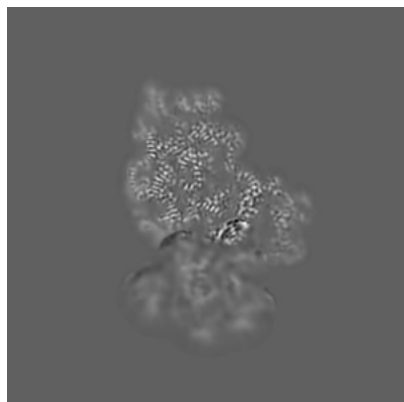


Z

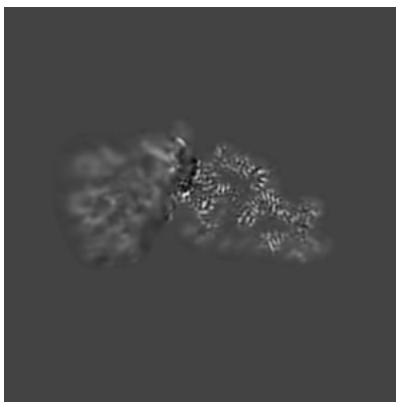
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

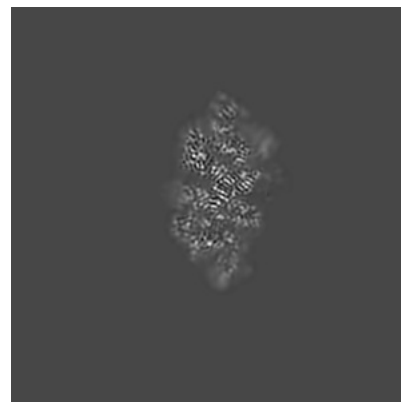
6.2.1 Primary map



X Index: 200

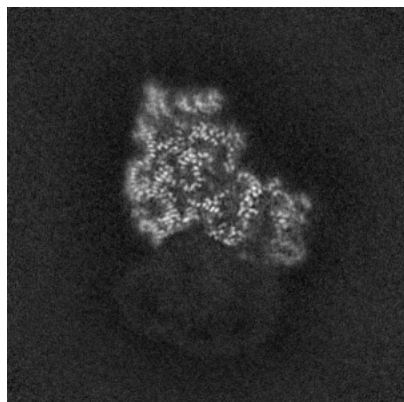


Y Index: 200

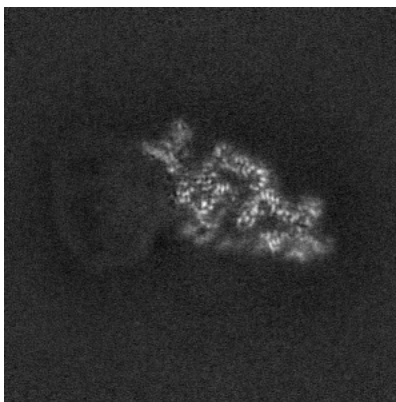


Z Index: 200

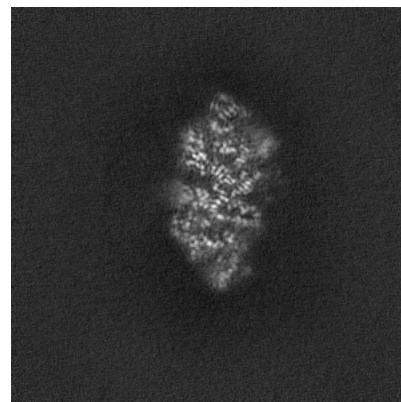
6.2.2 Raw map



X Index: 200



Y Index: 200

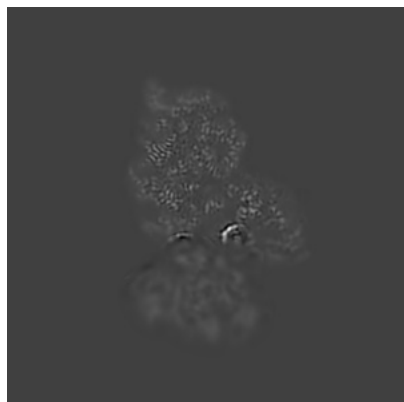


Z Index: 200

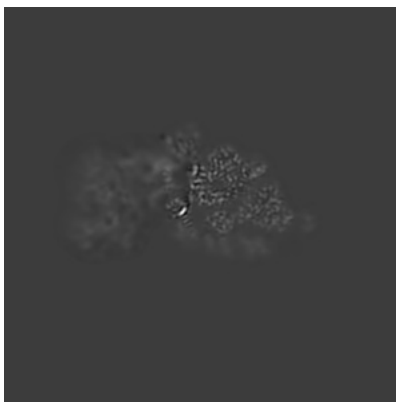
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

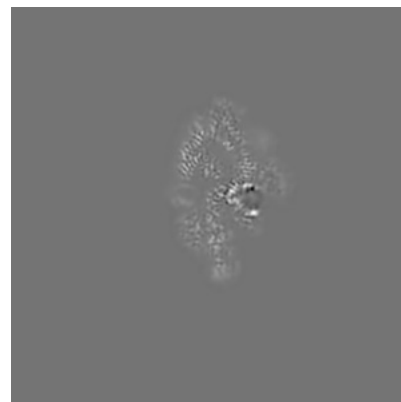
6.3.1 Primary map



X Index: 194

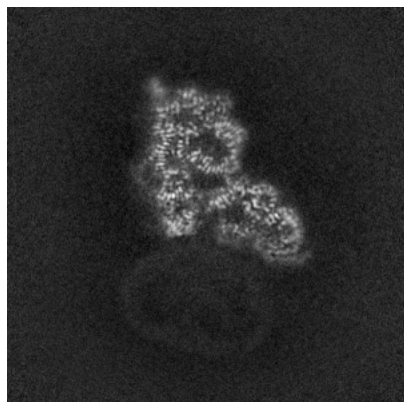


Y Index: 222

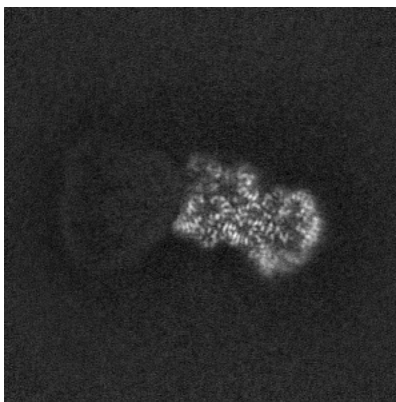


Z Index: 191

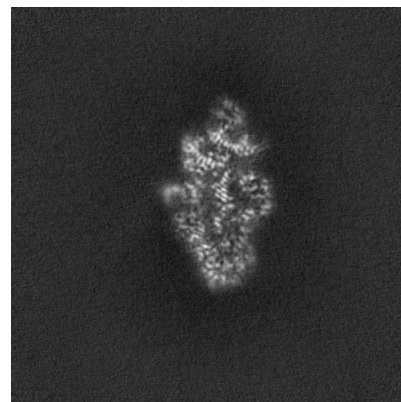
6.3.2 Raw map



X Index: 187



Y Index: 177

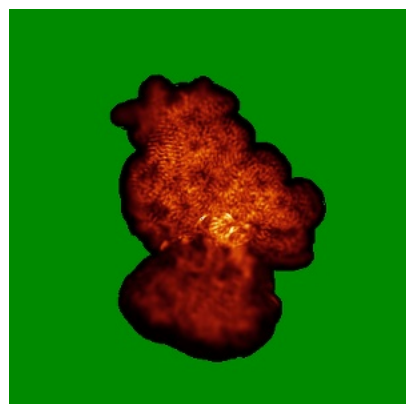


Z Index: 214

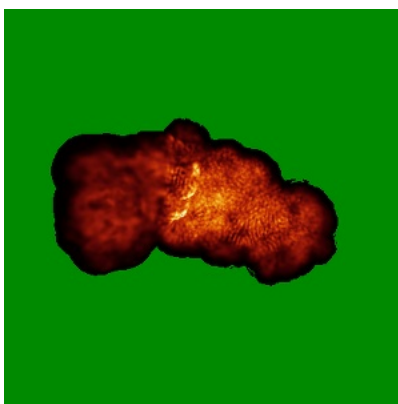
The images above show the largest variance slices of the map in three orthogonal directions.

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

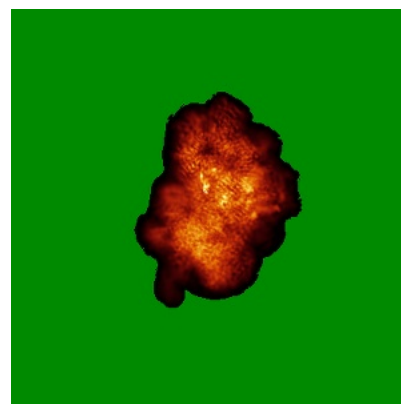
6.4.1 Primary map



X

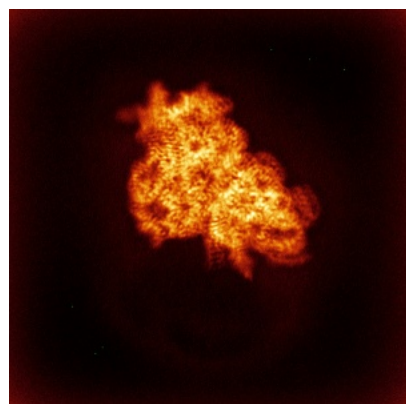


Y

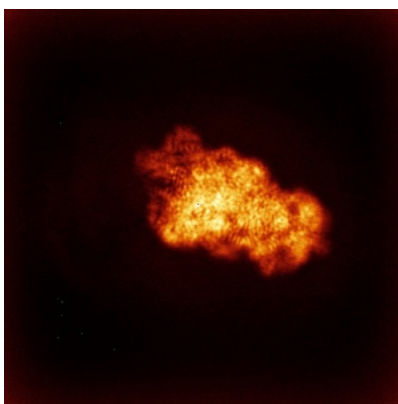


Z

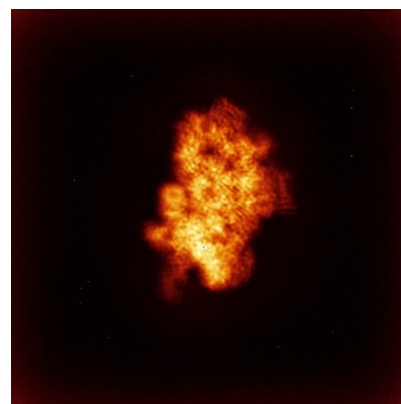
6.4.2 Raw map



X



Y

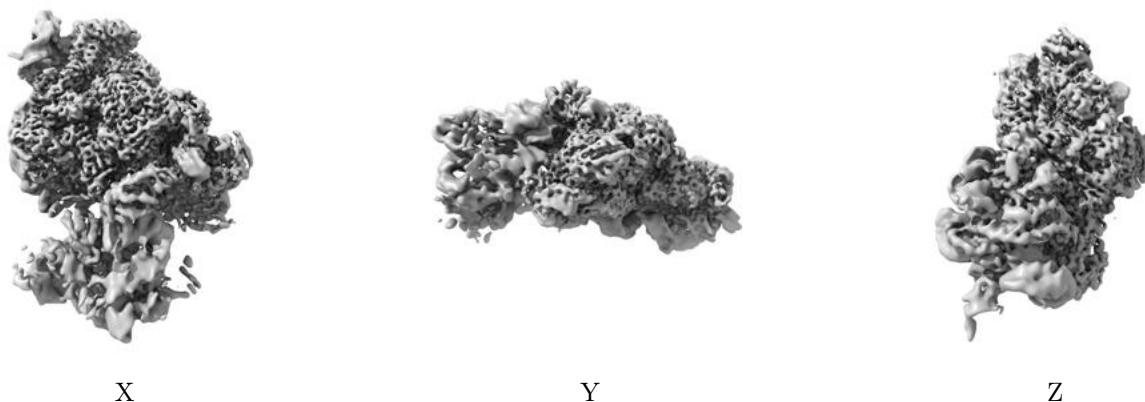


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.428. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

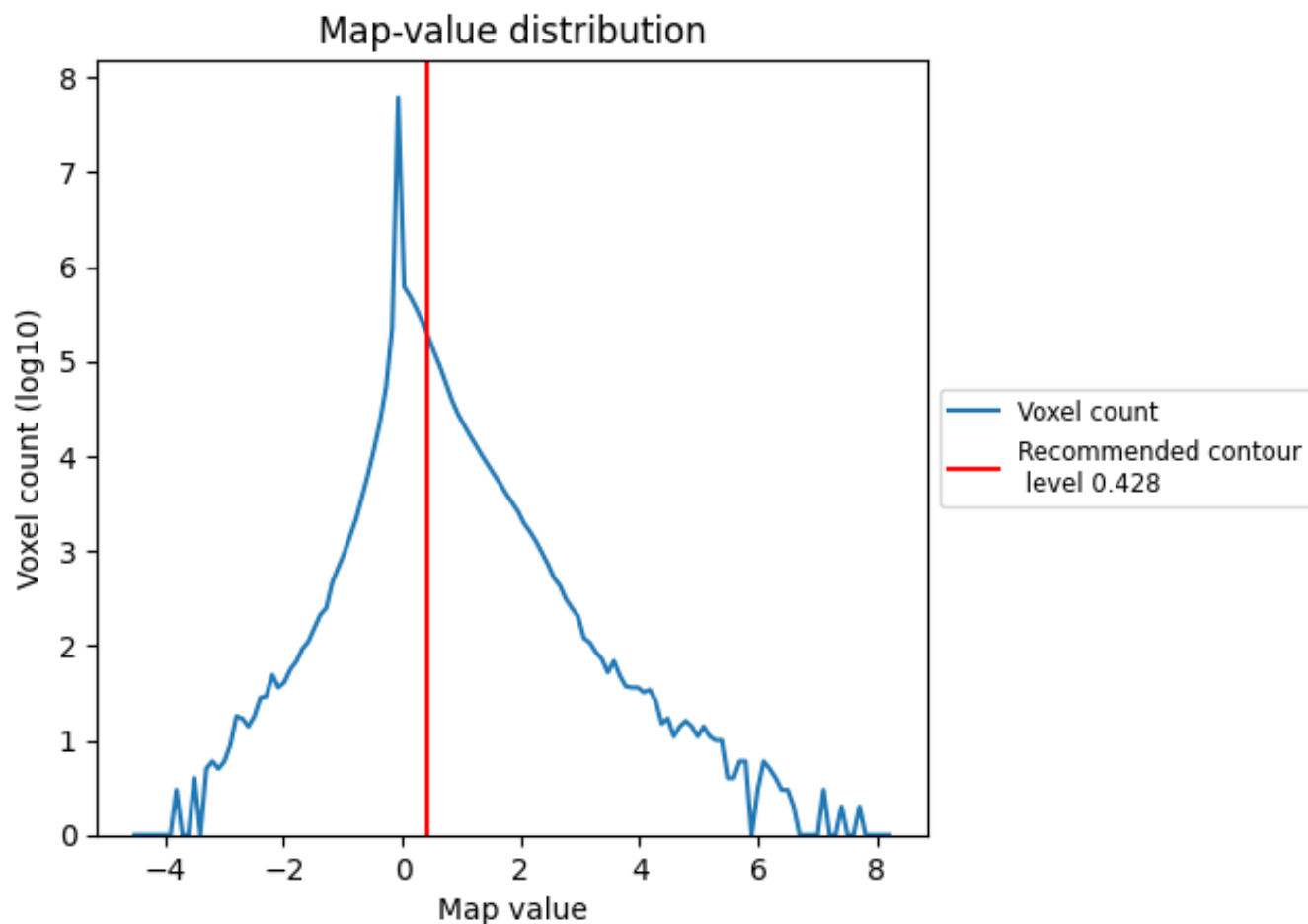
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

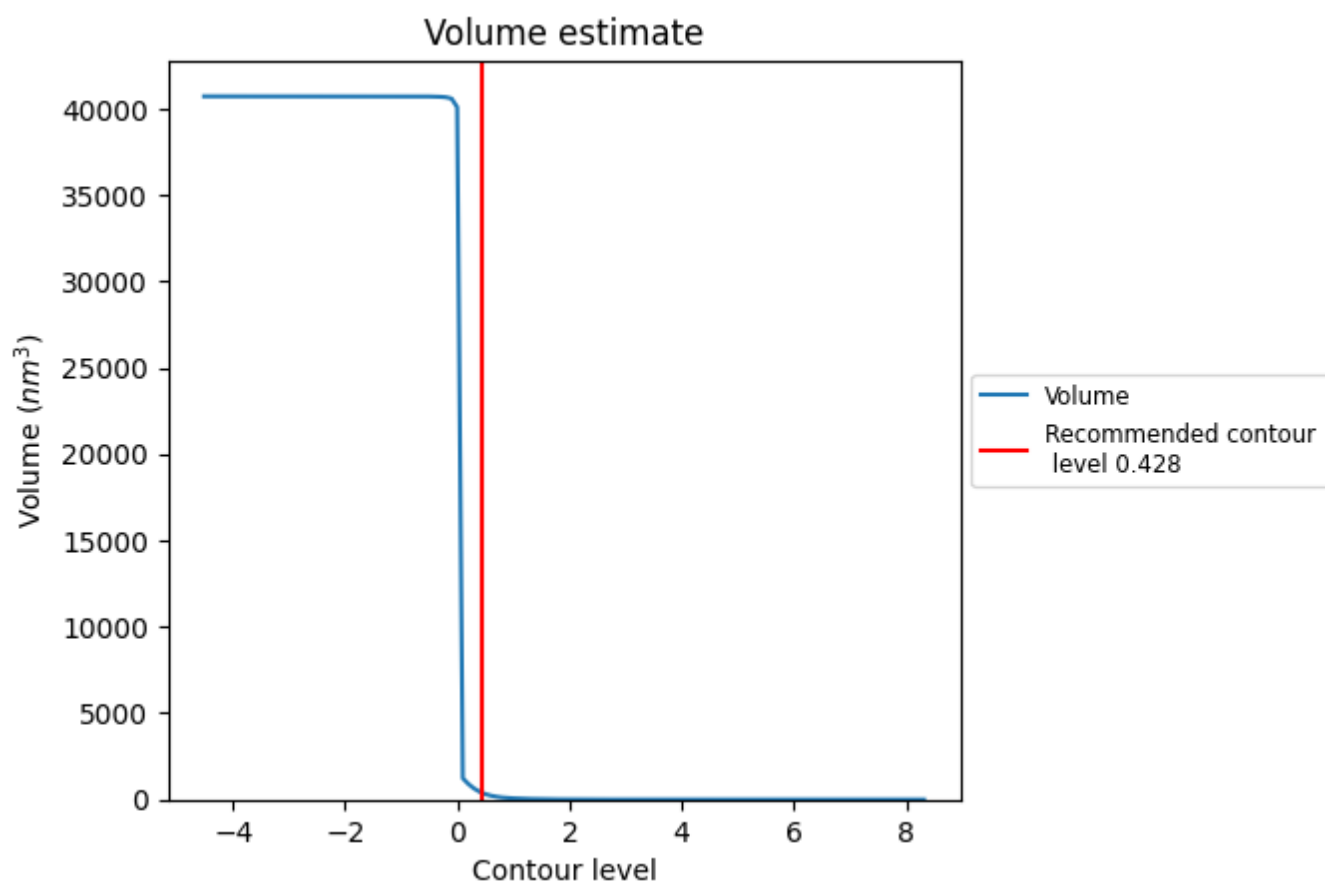
This section contains the results of statistical analysis of the map.

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.

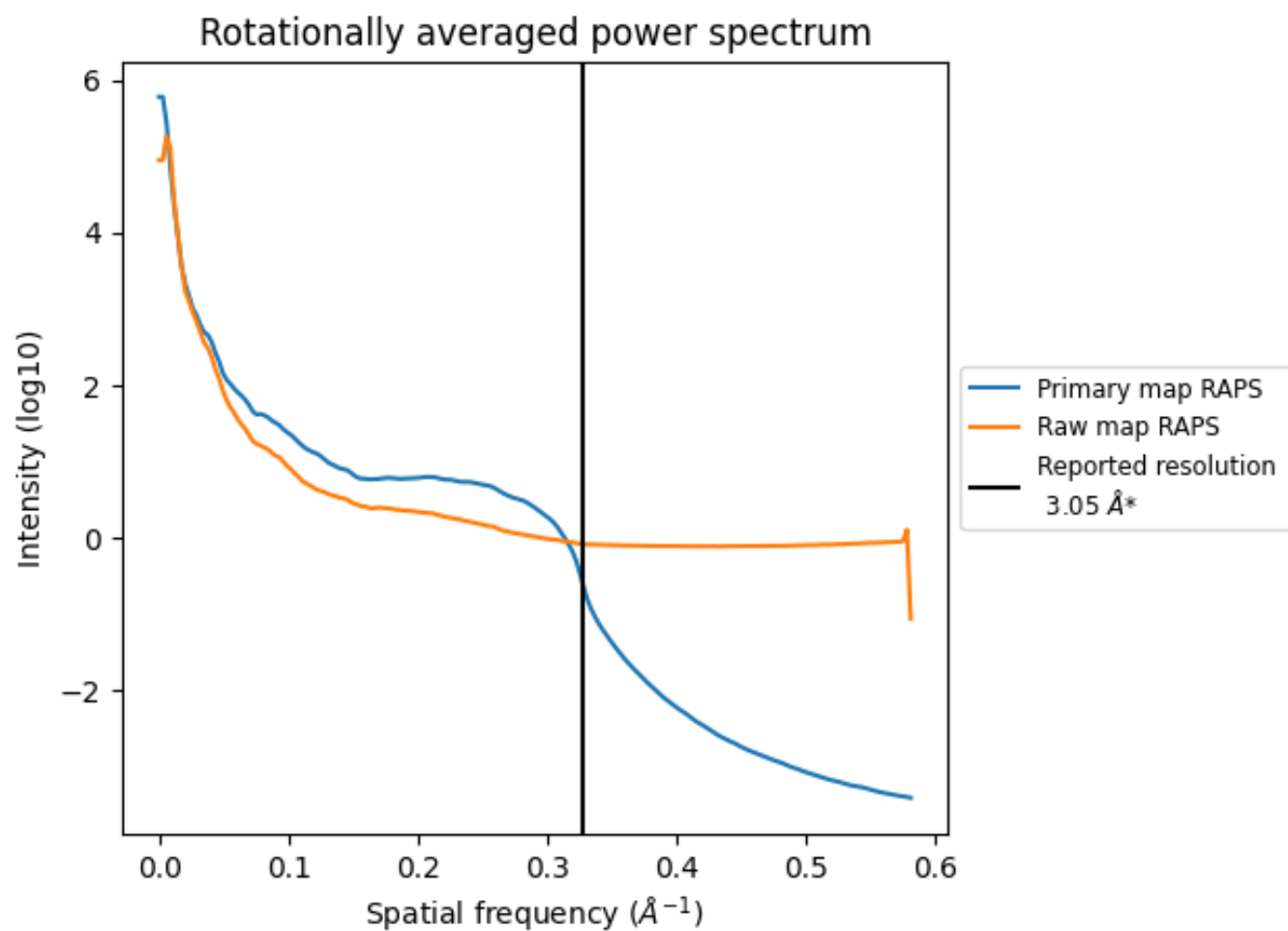
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 412 nm^3 ; this corresponds to an approximate mass of 373 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 ⓘ

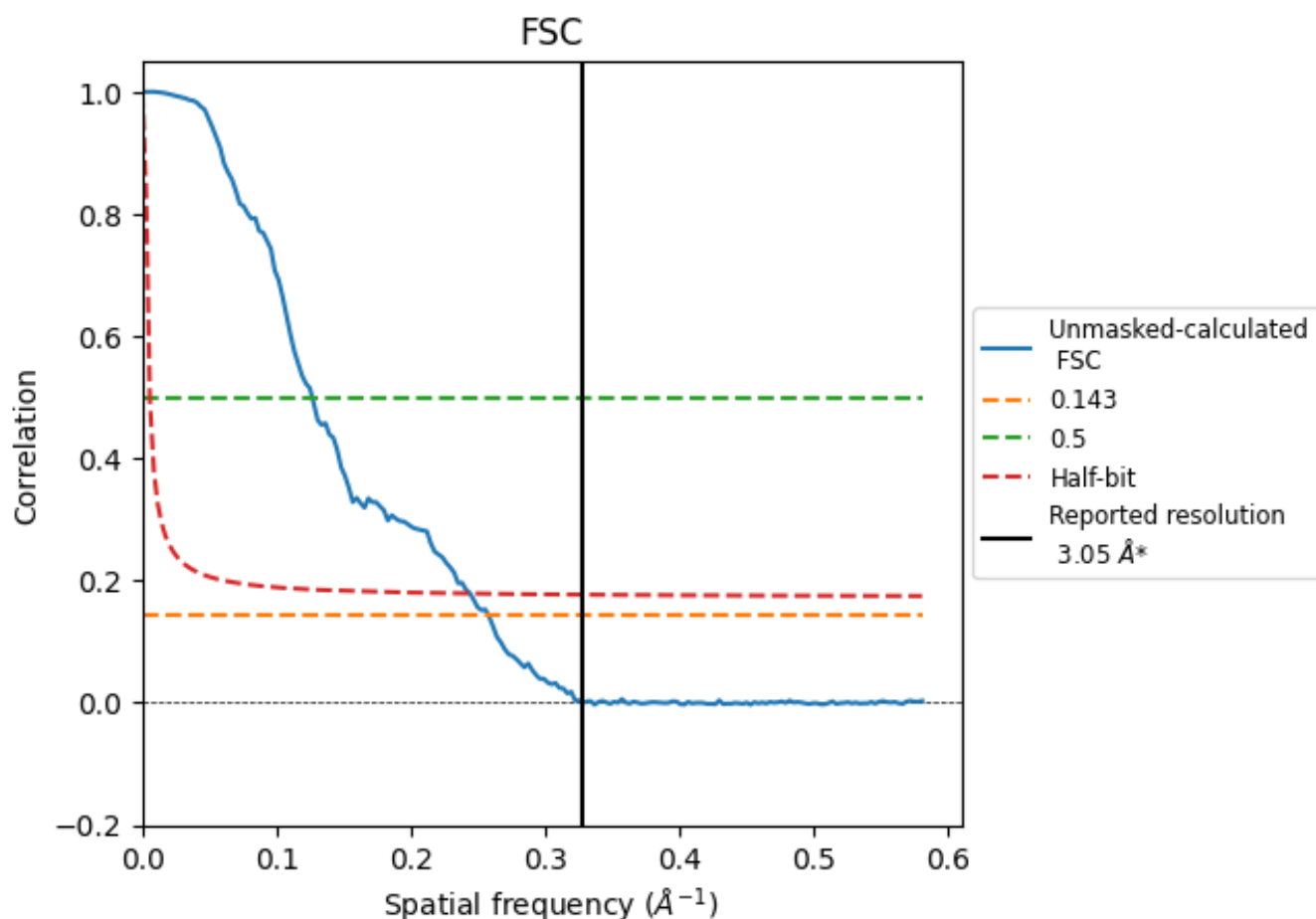


*Reported resolution corresponds to spatial frequency of 0.328 $\text{\AA}^{-1}$

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 0.328 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.87	7.89	4.09

*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 3.87 differs from the reported value 3.05 by more than 10 %

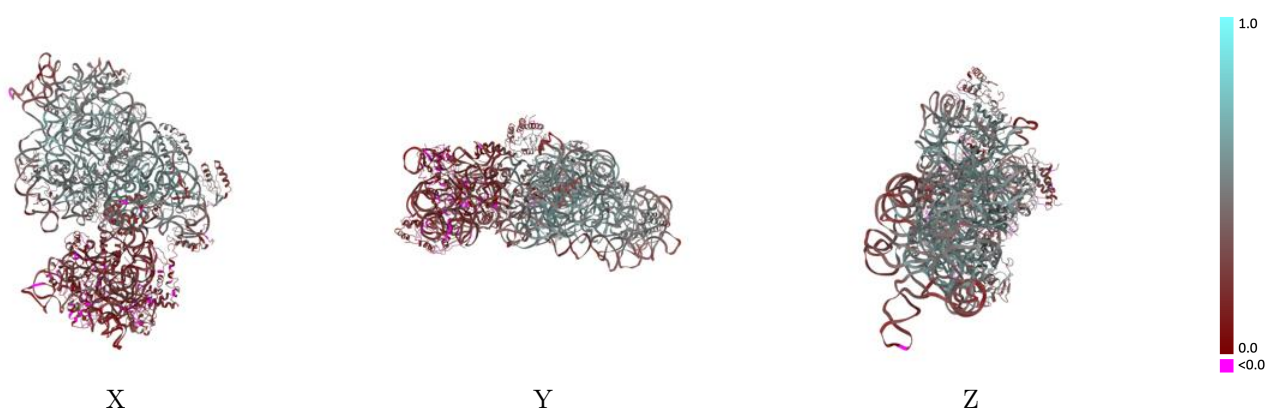
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-12857 and PDB model 7OE1. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay ⓘ

This section was not generated.

9.2 Q-score mapped to coordinate model ⓘ

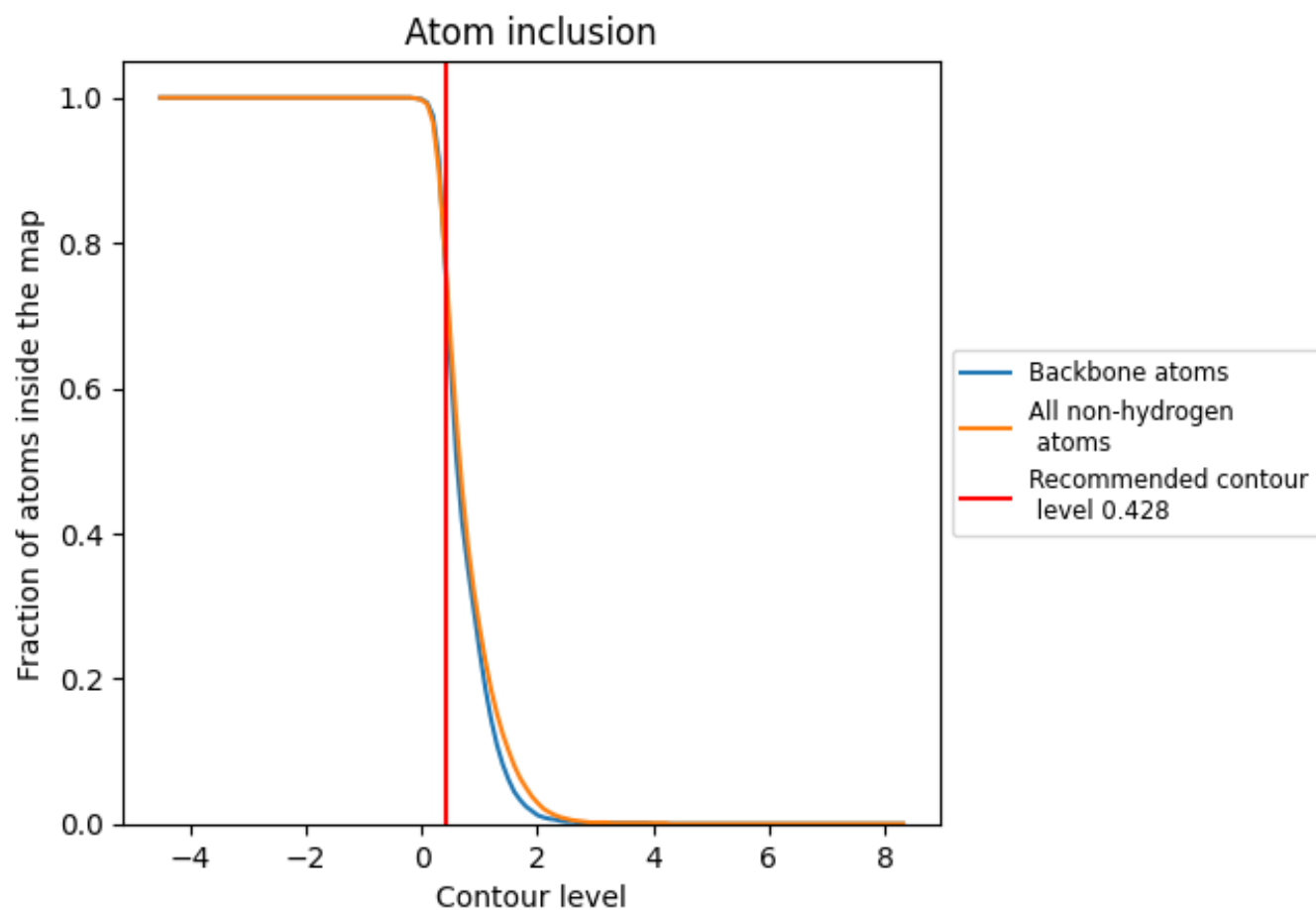


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 ⓘ

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 75% of all backbone atoms, 76% 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 (0.428) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7560	 0.3730
A	 0.8750	 0.4040
B	 0.6050	 0.2910
C	 0.3320	 0.1720
D	 0.6910	 0.4170
E	 0.8230	 0.4900
F	 0.5510	 0.3490
G	 0.1390	 0.1240
H	 0.8530	 0.5140
I	 0.2340	 0.1370
J	 0.1580	 0.1120
K	 0.4530	 0.3110
L	 0.8180	 0.4880
M	 0.1610	 0.1170
N	 0.3660	 0.1580
O	 0.7940	 0.4790
P	 0.8610	 0.5250
Q	 0.8100	 0.4950
R	 0.7500	 0.4740
S	 0.3240	 0.1270
T	 0.7940	 0.4650
U	 0.1820	 0.2380

