



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 04:23 AM UTC

PDB ID : 7OOC / pdb_00007ooc
EMDB ID : EMD-11998
Title : Mycoplasma pneumoniae 30S subunit of ribosomes in chloramphenicol-treated cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-05-27
Resolution : 3.70 Å (reported)
Based on initial models : 3J9W, 4YBB, 5MMJ

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:

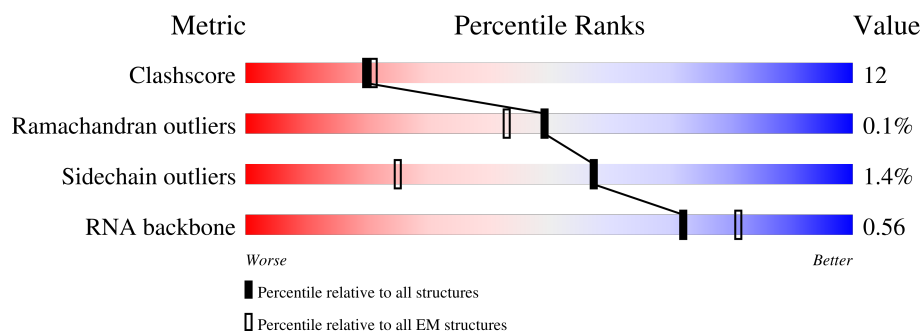
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	B	273	79% 58% 21% 21%
2	D	219	70% 49% 21% 30%
3	F	155	99% 69% 30% .
4	A	294	85% 57% 26% . 15%
5	H	132	97% 65% 32% .
6	J	121	94% 68% 26% 6%
7	C	205	99% 76% 23% .

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Mol	Chain	Length	Quality of chain
8	S	87	
9	O	94	
10	K	139	
11	M	61	
12	I	108	
13	L	124	
14	N	86	
15	R	87	
16	T	60	
17	G	142	
18	Q	104	
19	E	215	
20	P	85	
21	5	1520	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 51225 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 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	215	Total	C	N	O	S	0	0
			1682	1063	308	306	5		

- Molecule 2 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	153	Total	C	N	O	S	0	0
			1153	731	222	197	3		

- Molecule 3 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	154	Total	C	N	O	S	0	0
			1231	777	234	215	5		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	249	Total	C	N	O	S	0	0
			1917	1224	331	355	7		

- Molecule 5 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	128	Total	C	N	O	S	0	0
			993	634	184	174	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	114	Total	C	N	O	S	0	0
			828	514	153	155	6		

- Molecule 7 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	203	Total	C	N	O	S	0	0
			1605	1015	306	280	4		

- Molecule 8 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	77	Total	C	N	O		0	0
			629	383	135	111			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	87	Total	C	N	O	S	0	0
			690	445	128	115	2		

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	136	Total	C	N	O	S	0	0
			1055	667	209	177	2		

- Molecule 11 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	60	Total	C	N	O	S	0	0
			473	302	96	71	4		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	101	Total	C	N	O	S	0	0
			803	518	141	143	1		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	118	Total	C	N	O		0	0
			922	576	186	160			

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	83	Total	C	N	O	0	0
			673	428	125	120		

- Molecule 15 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	R	84	Total	C	N	O	S	0
			654	419	119	114	2	0

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	T	53	Total	C	N	O	S	0
			439	275	93	70	1	0

- Molecule 17 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	G	141	Total	C	N	O	S	0
			1103	720	192	189	2	0

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	65	Total	C	N	O	S	0
			535	342	103	86	4	0

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	E	167	Total	C	N	O	S	0
			1211	762	219	229	1	0

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	P	83	Total	C	N	O	0	0
			675	425	135	115		

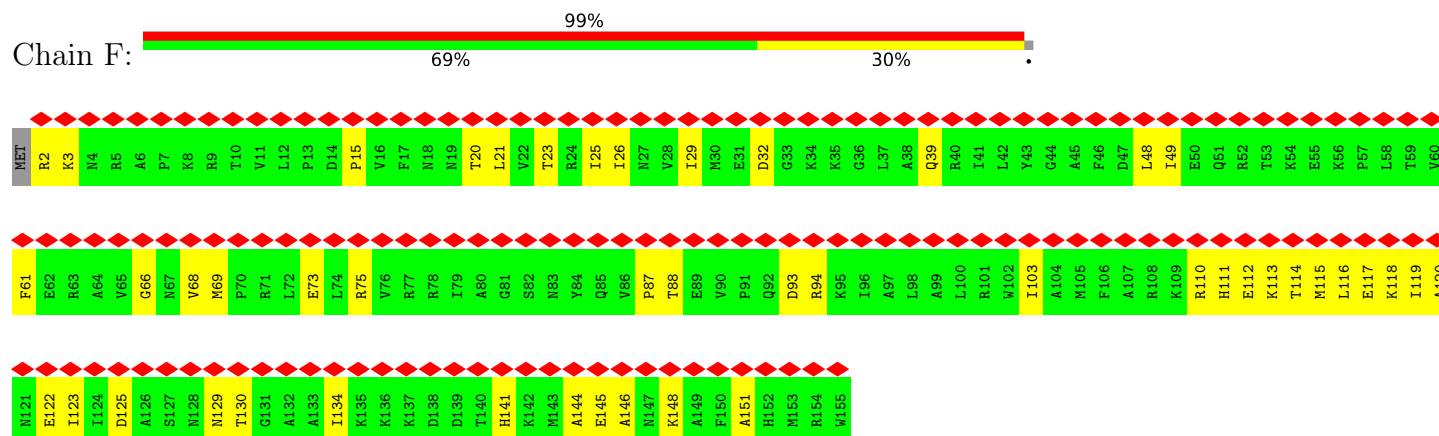
- Molecule 21 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	5	1493	Total	C	N	O	P	0	0
			31952	14279	5792	10388	1493		

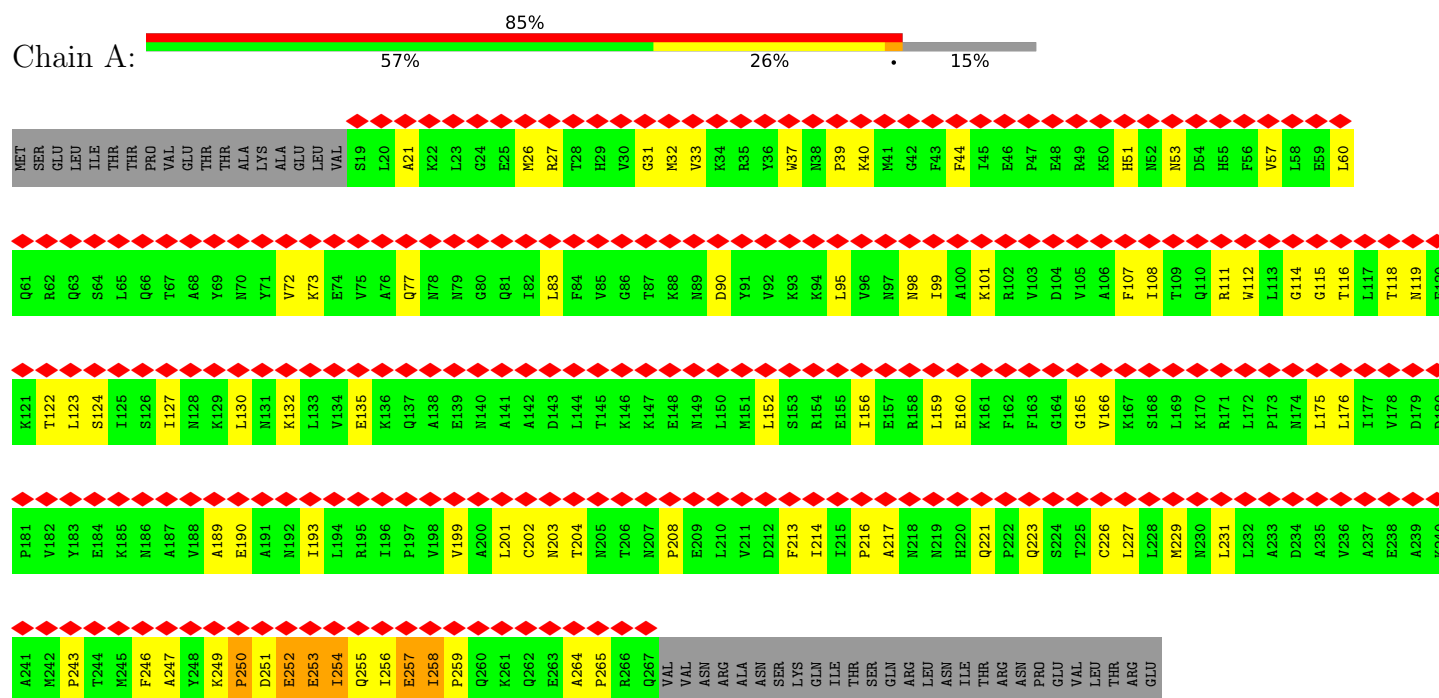
- Molecule 22 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
22	M	1	Total	Zn	0
			1	1	
22	Q	1	Total	Zn	0
			1	1	

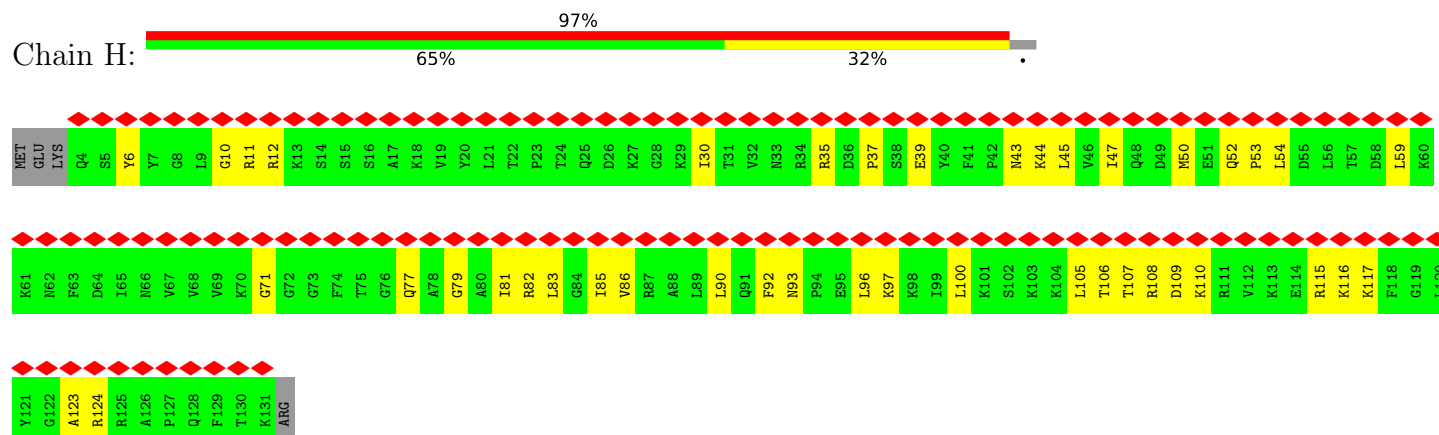
- Molecule 3: 30S ribosomal protein S7

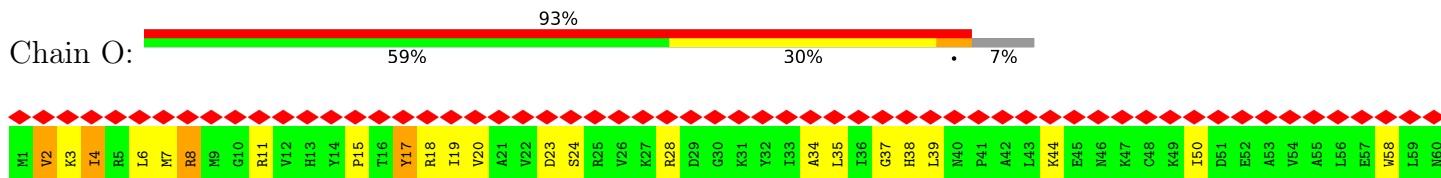


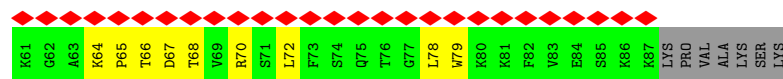
- Molecule 4: 30S ribosomal protein S2



- Molecule 5: 30S ribosomal protein S9



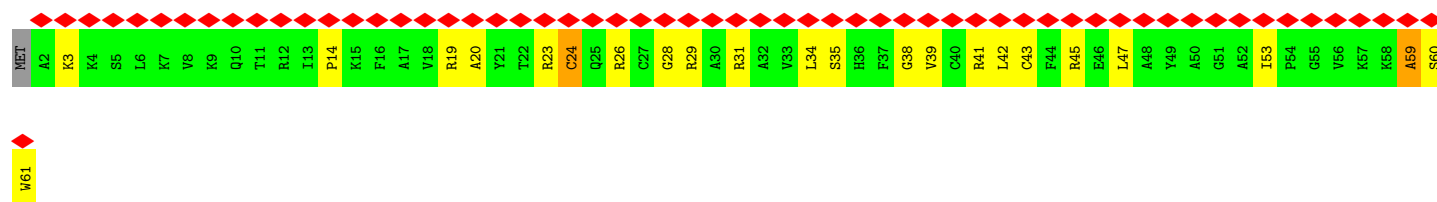




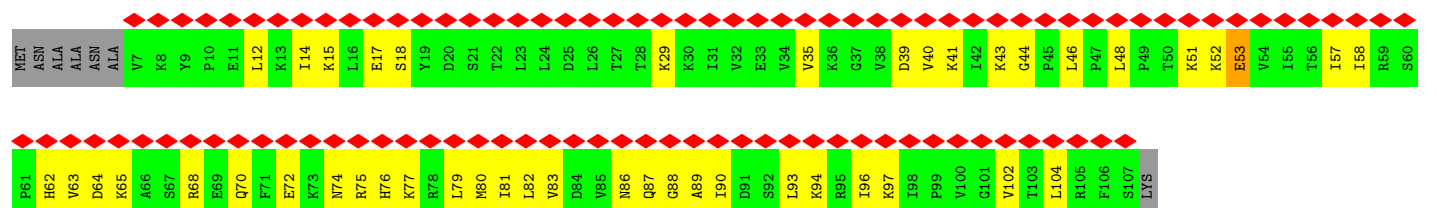
• Molecule 10: 30S ribosomal protein S12



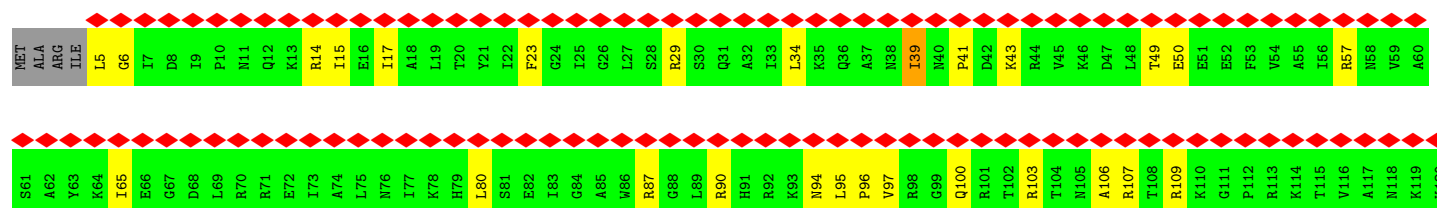
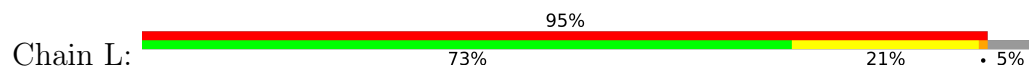
• Molecule 11: 30S ribosomal protein S14 type Z



• Molecule 12: 30S ribosomal protein S10

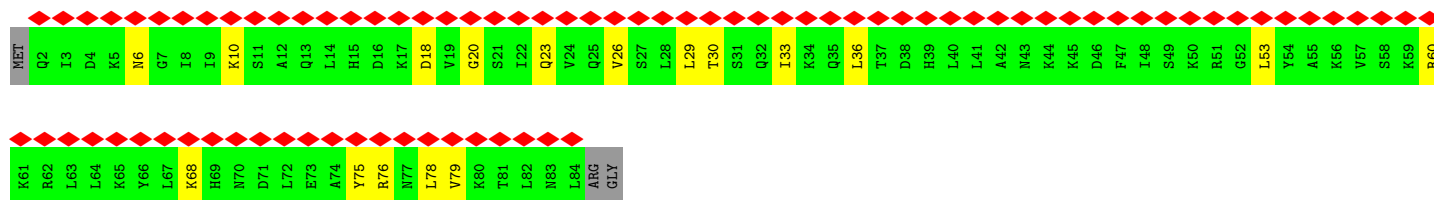
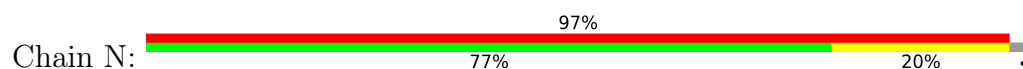


• Molecule 13: 30S ribosomal protein S13

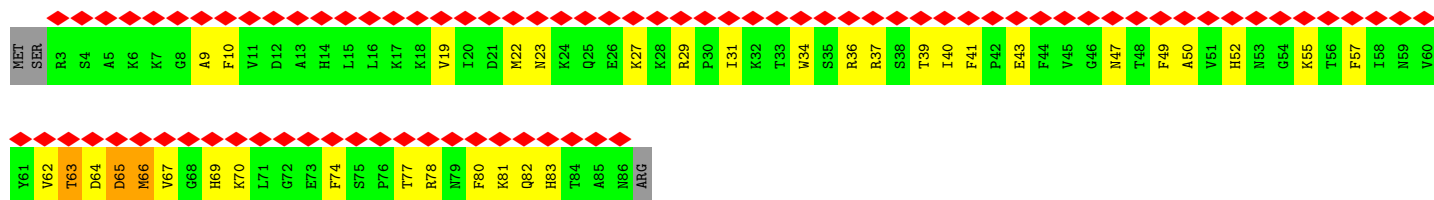




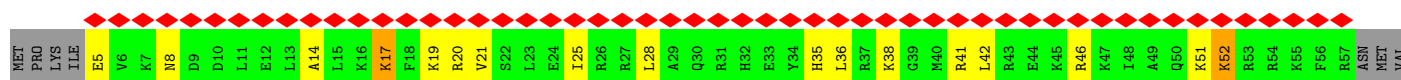
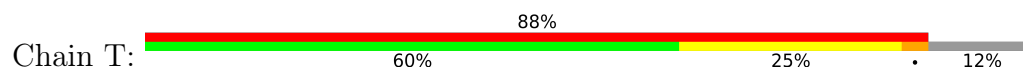
• Molecule 14: 30S ribosomal protein S15



• Molecule 15: 30S ribosomal protein S19



• Molecule 16: 30S ribosomal protein S21

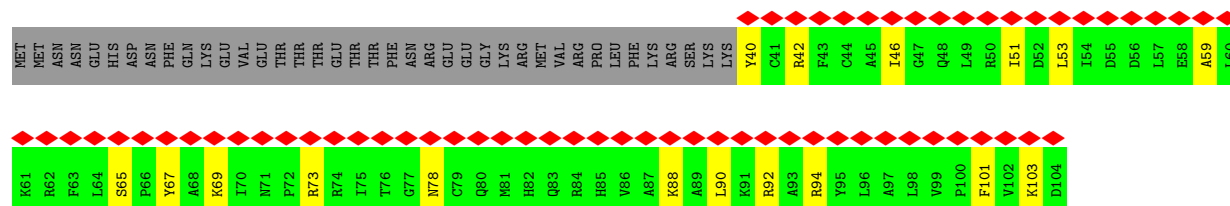


• Molecule 17: 30S ribosomal protein S8

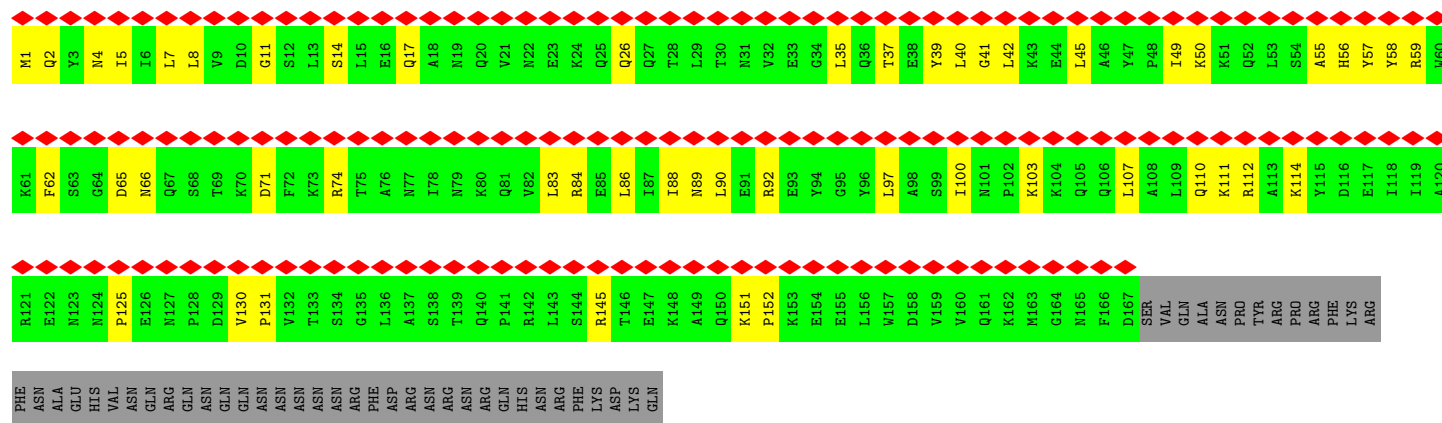
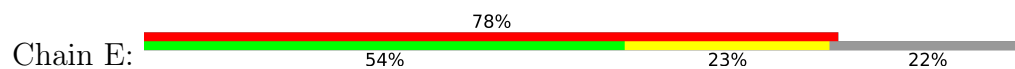


• Molecule 18: 30S ribosomal protein S18





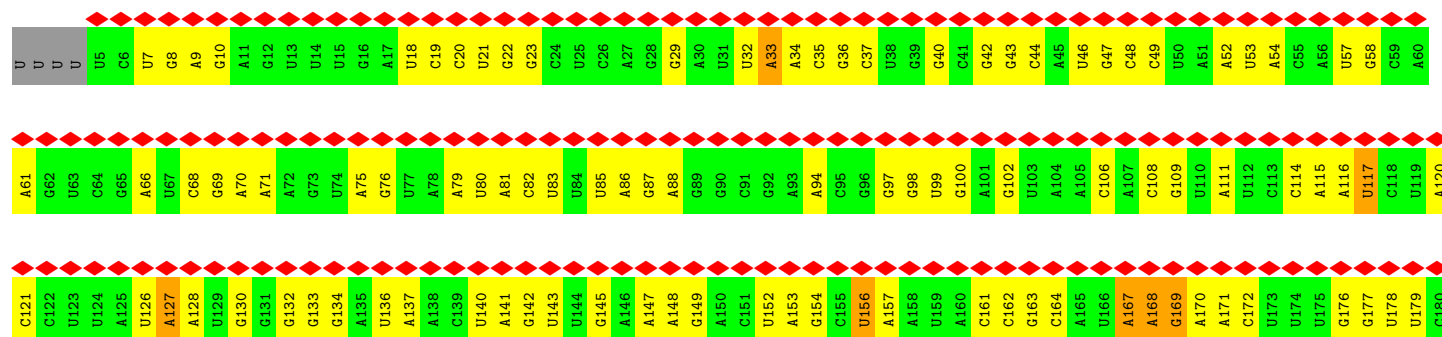
• Molecule 19: 30S ribosomal protein S6



• Molecule 20: 30S ribosomal protein S17



• Molecule 21: 16S rRNA



G961	A901	C941	A781	G721	G661	U601	C541	U481	G421	U361	G301	G
G962	A902	C942	G782	G722	G662	G602	G542	G482	A422	U362	A302	C241
U963	A903	C943	G783	C723	G663	U603	C543	U483	A423	U363	A303	A242
C964	C904	U844	A784	G724	A664	U604	A544	A484	U424	U364	U304	C244
C965	U905	C945	U785	A725	G665	A605	A545	A485	G425	U365	A305	C245
A966	C906	G946	U786	A726	U666	A606	G546	C486	U426	C366	G306	U246
A967	A907	C947	U787	G727	U667	A607	G547	C487	U427	C367	C307	A247
G968	A908	U948	G788	G728	U668	G608	G548	U488	A428	C368	C308	U248
A969	A909	A949	U789	C729	U669	G609	U549	U489	A429	A369	A309	U249
A970	C910	G950	U790	G730	G670	C610	U550	U490	G430	A370	C310	G250
U971	U951	U851	A791	A731	A671	A611	A551	U491	U431	U371	A311	G251
A972	G912	G852	C792	A732	A672	G612	U552	G492	U432	C372	A312	U252
A973	A913	C853	C793	A733	A673	C613	C553	C493	A433	G373	U313	U253
C974	A914	A854	C794	A734	U674	U614	C554	A494	U434	G374	G314	G254
C975	U915	G855	U795	C735	U675	G615	G555	U495	U435	C375	G315	G255
U976	U916	U856	A796	U736	U676	C616	G556	A496	U436	G376	G316	G256
U977	U917	U857	G797	U737	C677	U617	A557	A497	U437	A377	A317	U257
A978	A918	A858	U798	A738	A678	U618	U558	G498	A438	A378	C318	A258
C979	C919	A859	A799	G739	U679	A619	U559	U499	U439	A379	U319	A259
C980	G920	C860	G800	G740	G680	A620	U560	G500	U440	G380	G320	C260
U981	U921	A861	U801	C741	U681	C621	A561	A501	U441	C381	A321	G261
A982	G922	C862	C802	C742	G682	A622	U562	C502	G442	U382	G322	G262
G983	G923	A863	C803	A743	G683	G623	U563	G503	G443	U383	A323	C263
A984	A924	U864	A804	U744	A684	U624	G564	A504	G444	G384	C324	C264
C985	C925	U865	C805	U745	G685	U625	G565	C505	A445	A385	A325	U265
U986	C926	A866	A806	A746	C686	G626	G566	U506	A446	U386	C326	A266
U987	C927	U867	C807	C747	G687	U627	G567	A507	G447	G387	G327	C267
G988	G928	G868	G808	U748	G688	A628	C568	A508	A448	G388	G328	C268
C989	C929	U869	G809	G749	U689	U629	U569	C509	A449	A389	C329	A269
C990	A930	A870	U810	A750	G690	G630	A570	U510	U450	G390	C330	A270
A991	C931	U871	A811	C751	A691	C631	A571	A511	G451	C391	C331	G271
U992	A932	C872	A812	G752	A692	A632	A572	U512	A452	A392	A332	G272
C993	C933	U873	A813	C753	A693	U633	G573	G513	C453	C393	U333	C273
C994	G934	C874	C814	U754	U694	U634	C574	U514	U454	U394	A334	A274
U995	U935	G875	G815	U755	G695	G635	A575	G515	U455	G395	C335	A275
U996	G936	C876	A816	A756	C696	G636	A576	C516	U456	C396	U336	U276
G997	C937	C877	U817	G757	G697	A637	C577	C517	A457	C397	U337	U277
G998	U938	U878	A818	G758	U698	A638	C578	A518	G458	G398	C338	A278
C999	C939	G879	G819	C759	U699	A639	G579	G519	C459	C399	U339	C279
A1000	G940	G880	A820	U760	G700	C640	C580	C520	A460	G400	A340	G280
A1001	A941	C881	U821	U761	A701	U641	A581	A521	G461	U401	C341	U281
A1002	G942	U882	A822	G762	U702	A642	G582	G522	G462	G402	G342	G282
G1003	C943	G883	C823	A763	A703	U643	G583	U523	U463	A403	G283	G283
U1004	A944	U884	U824	A764	U704	U644	C584	C524	A464	A404	G344	A284
U1005	U945	U885	A825	A765	A705	A645	G585	G525	A465	C405	A345	G285
A1006	G946	A886	G826	G766	U706	A646	G586	C526	U466	G406	G346	C286
U1007	U947	C887	C827	U767	G707	U647	A587	G527	U467	A407	G287	U287
G1008	U948	U888	U828	G768	A708	C648	U588	G528	G468	U408	C348	A288
G1009	C949	U889	G829	U769	A709	U649	U589	U529	C469	G409	A349	U289
A1010	C950	U890	U830	G770	G710	A650	G590	A530	U470	A410	G350	G290
A1011	U951	C891	C831	G771	G711	G651	A591	A531	G471	A411	C351	C291
U952	U952	G892	G832	G772	A712	A652	A592	U532	G472	G412	A352	U292
C1013	C953	C893	A833	G773	A713	G653	A593	A533	A473	G413	G353	G293
A1014	A954	A894	G834	A774	C714	U654	A594	C534	G474	U414	U354	A294
U1015	U955	A895	G835	G775	A715	G655	G595	A535	U475	C415	A355	G295
A1016	U956	G896	C836	C776	C716	U656	U596	U536	U476	U416	G356	A296
A1017	U957	A897	G837	A777	C717	G657	C597	A537	U477	U417	G357	A297
U1018	G958	U898	A838	A778	A718	G658	U598	G538	G478	U418	G358	G298
G1019	C959	U899	U839	A779	G719	U659	G599	A539	A479	A419	A359	U299
	A960	G900	C840	U780	U720	G660	G600	U540	C480	A370	A310	A240

A	U1081	C1201	A1261	G1321	U1381	C1441	G1501
G	U1082	A1202	A1262	U1322	C1382	A1442	G1502
G	A1083	A1203	A1263	A1323	A1383	A1443	U1503
U	A1084	A1204	G1264	A1324	A1384	G1444	G1504
U	A1085	G1205	U1265	U1325	A1385	G1445	G1505
A	U1086	C1206	U1266	C1326	C1386	A1446	A1506
A	C1028	U1207	G1267	G1327	U1387	U1447	U1507
C1029	C1087	G1208	U1268	C1328	A1388	A1448	C1508
G1030	C1088	C1209	U1269	G1329	U1389	G1449	A1509
A1031	C1089	U1210	C1270	A1330	G1390	C1450	C
G1032	C1090	A1211	U1271	A1331	A1391	A1451	C
U1033	C1091	C1212	C1272	U1332	A1392	C1452	U
U1033	A1092	A1213	A1273	C1333	A1393	C1453	C
G1034	A1093	A1214	G1274	A1334	G1394	G1454	C
A1035	C1094	U1215	U1275	G1335	C1395	G1455	U
C1036	G1095	G1216	U1276	C1336	U1396	U1456	U
A1037	A1096	G1217	C1277	U1337	G1397	G1457	U
G1038	C1097	C1218	G1278	A1338	G1398	A1458	C
U1039	G1098	C1219	G1279	U1339	U1399	U1459	U
G1040	G1099	A1220	A1280	G1340	A1400	U1460	A
U1041	C1100	G1161	U1281	U1341	A1401	G1461	
G1042	A1101	G1162	U1282	C1342	U1402	G1462	
U1043	A1102	A1163	G1283	G1343	A1403	A1463	
G1044	C1103	U1164	A1284	C1344	U1404	G1464	
C1045	C1104	G1165	G1285	G1345	U1405	U1465	
A1046	C1105	A1166	U1286	G1346	U1406	U1466	
U1047	C1106	G1167	G1287	U1347	A1407	A1467	
G1048	U1107	C1168	C1288	G1348	A1408	A1468	
U1049	A1108	U1169	U1289	A1349	A1409	G1469	
U1050	A1109	G1170	G1290	A1350	A1410	U1470	
U1051	C1110	A1171	C1291	U1351	A1411	C1471	
G1052	G1111	A1172	A1292	A1352	G1412	G1472	
U1053	U1112	U1173	A1293	C1353	G1413	U1473	
C1054	A1113	U1174	G1294	G1354	U1414	A1474	
G1055	U1114	C1175	U1295	U1355	G1415	A1475	
U1056	G1115	A1176	C1296	U1356	U1416	C1476	
C1057	U1116	U1177	G1297	C1357	U1417	A1477	
A1058	U1117	C1178	U1298	U1358	G1418	A1478	
G1059	A1118	U1179	C1299	C1359	C1419	G1479	
U1060	C1119	U1180	U1300	G1360	U1420	G1480	
U1061	A1120	G1181	G1301	G1361	A1421	U1481	
C1062	U1121	C1182	U1242	G1362	A1422	A1482	
G1063	U1122	C1183	A1243	U1363	C1423	C1483	
U1064	G1123	C1184	A1244	C1364	G1424	C1484	
G1065	U1124	C1185	A1245	U1365	A1425	C1485	
U1066	C1125	U1186	A1246	U1366	U1426	C1486	
C1067	U1126	U1187	G1247	G1367	U1427	U1487	
G1068	A1127	A1188	U1248	U1368	A1428	A1488	
U1069	G1128	U1189	G1249	A1369	G1429	C1489	
G1070	C1129	G1190	A1250	C1370	G1430	U1490	
A1071	U1130	U1191	G1251	A1371	A1431	A1491	
G1072	A1131	C1192	C1252	C1372	A1432	G1492	
A1073	G1132	U1193	A1253	A1373	G1433	A1493	
U1074	A1133	U1194	A1254	C1374	C1434	A1494	
G1075	C1134	G1195	A1255	C1375	G1435	C1495	
U1076	U1135	G1196	U1256	G1376	G1436	C1496	
U1077	G1136	G1197	C1257	C1377	A1437	U1497	
G1078	C1137	C1198	U1258	C1378	U1438	G1498	
G1079	U1138	U1199	U1259	C1379	G1439	G1499	
G1080	A1140	G1200	U1260	A1380	U1440	G1500	

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	17890	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0023	Depositor
Map size (Å)	323.095, 323.095, 323.095	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85025, 0.85025, 0.85025	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.14	0/1705	0.40	0/2304
2	D	0.15	0/1168	0.43	0/1568
3	F	0.15	0/1250	0.46	0/1682
4	A	0.33	0/1951	0.67	5/2652 (0.2%)
5	H	0.17	0/1009	0.51	0/1354
6	J	0.13	0/843	0.36	0/1136
7	C	0.14	0/1635	0.40	0/2202
8	S	0.14	0/631	0.42	0/838
9	O	0.39	0/703	0.80	1/945 (0.1%)
10	K	0.23	0/1073	0.59	0/1445
11	M	0.51	1/482 (0.2%)	0.84	1/643 (0.2%)
12	I	0.24	0/814	0.56	0/1096
13	L	0.32	0/933	0.63	0/1254
14	N	0.13	0/679	0.37	0/907
15	R	0.41	0/670	0.87	1/904 (0.1%)
16	T	0.45	0/442	0.86	0/582
17	G	0.16	0/1119	0.47	0/1508
18	Q	0.17	0/545	0.46	0/730
19	E	0.16	0/1229	0.45	0/1670
20	P	0.13	0/684	0.40	0/913
21	5	0.11	0/35777	0.23	0/55776
All	All	0.17	1/55342 (0.0%)	0.36	8/82109 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	M	60	SER	CA-CB	-6.59	1.47	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	259	PRO	N-CA-C	-13.90	83.84	112.47
11	M	59	ALA	N-CA-C	5.91	119.72	110.32
9	O	2	VAL	N-CA-C	-5.82	101.07	108.93
4	A	250	PRO	N-CA-C	5.76	124.33	112.47
4	A	253	GLU	N-CA-C	-5.52	100.93	108.38

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	B	1682	0	1733	40	0
2	D	1153	0	1231	34	0
3	F	1231	0	1285	37	0
4	A	1917	0	1894	71	0
5	H	993	0	1023	33	0
6	J	828	0	855	24	0
7	C	1605	0	1603	44	0
8	S	629	0	681	19	0
9	O	690	0	726	39	0
10	K	1055	0	1124	29	0
11	M	473	0	505	16	0
12	I	803	0	876	33	0
13	L	922	0	957	20	0
14	N	673	0	730	12	0
15	R	654	0	629	31	0
16	T	439	0	467	11	0
17	G	1103	0	1218	33	0
18	Q	535	0	559	15	0
19	E	1211	0	1108	42	0
20	P	675	0	728	20	0
21	5	31952	0	16055	598	0
22	M	1	0	0	0	0
22	Q	1	0	0	0	0
All	All	51225	0	35987	1072	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 1072 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)
21:5:1013:C:N4	21:5:1014:A:N6	2.06	1.03
21:5:1331:A:H61	21:5:1340:G:H1	1.02	0.96
21:5:242:A:H62	21:5:277:G:H21	1.13	0.94
21:5:1013:C:N4	21:5:1014:A:H62	1.65	0.94
21:5:242:A:H62	21:5:277:G:N2	1.64	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	213/273 (78%)	202 (95%)	11 (5%)	0	100	100
2	D	151/219 (69%)	141 (93%)	10 (7%)	0	100	100
3	F	152/155 (98%)	135 (89%)	17 (11%)	0	100	100
4	A	247/294 (84%)	227 (92%)	18 (7%)	2 (1%)	16	48
5	H	126/132 (96%)	109 (86%)	17 (14%)	0	100	100
6	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
7	C	201/205 (98%)	186 (92%)	15 (8%)	0	100	100
8	S	75/87 (86%)	72 (96%)	3 (4%)	0	100	100
9	O	85/94 (90%)	75 (88%)	10 (12%)	0	100	100
10	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
11	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
12	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	L	116/124 (94%)	107 (92%)	9 (8%)	0	100	100
14	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
15	R	82/87 (94%)	75 (92%)	7 (8%)	0	100	100
16	T	51/60 (85%)	45 (88%)	6 (12%)	0	100	100
17	G	139/142 (98%)	126 (91%)	13 (9%)	0	100	100
18	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
19	E	165/215 (77%)	146 (88%)	19 (12%)	0	100	100
20	P	81/85 (95%)	72 (89%)	9 (11%)	0	100	100
All	All	2431/2791 (87%)	2218 (91%)	211 (9%)	2 (0%)	49	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	250	PRO
4	A	254	ILE

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	B	176/232 (76%)	175 (99%)	1 (1%)	78	79
2	D	117/178 (66%)	117 (100%)	0	100	100
3	F	128/132 (97%)	128 (100%)	0	100	100
4	A	200/262 (76%)	197 (98%)	3 (2%)	57	68
5	H	101/115 (88%)	100 (99%)	1 (1%)	68	74
6	J	91/97 (94%)	91 (100%)	0	100	100
7	C	164/183 (90%)	164 (100%)	0	100	100
8	S	70/77 (91%)	70 (100%)	0	100	100
9	O	71/82 (87%)	66 (93%)	5 (7%)	14	41
10	K	111/120 (92%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	M	47/48 (98%)	45 (96%)	2 (4%)	26	50
12	I	93/99 (94%)	91 (98%)	2 (2%)	45	63
13	L	92/105 (88%)	89 (97%)	3 (3%)	33	55
14	N	76/78 (97%)	76 (100%)	0	100	100
15	R	66/77 (86%)	59 (89%)	7 (11%)	6	27
16	T	43/56 (77%)	38 (88%)	5 (12%)	5	24
17	G	121/124 (98%)	121 (100%)	0	100	100
18	Q	56/94 (60%)	56 (100%)	0	100	100
19	E	107/196 (55%)	107 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
All	All	2003/2430 (82%)	1974 (99%)	29 (1%)	57	70

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	39	ILE
16	T	51	LYS
15	R	63	THR
16	T	17	LYS
13	L	50	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
9	O	75	GLN
17	G	23	ASN
14	N	13	GLN
17	G	56	ASN
4	A	137	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	5	1490/1520 (98%)	231 (15%)	5 (0%)

5 of 231 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	5	7	U
21	5	10	G
21	5	32	U
21	5	33	A
21	5	40	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	5	168	A
21	5	419	A
21	5	481	U
21	5	838	A
21	5	1338	A

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

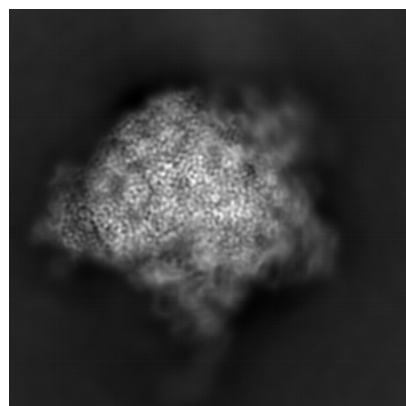
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11998. These allow visual inspection of the internal detail of the map and identification of artifacts.

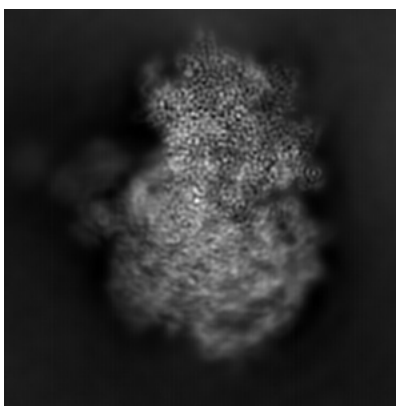
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

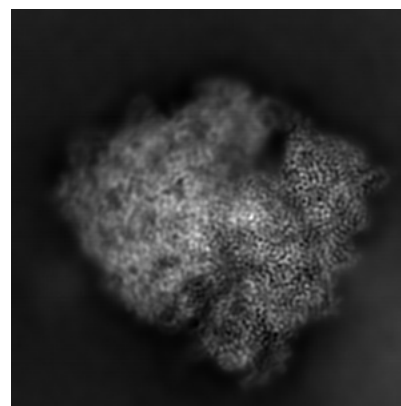
6.1.1 Primary map



X

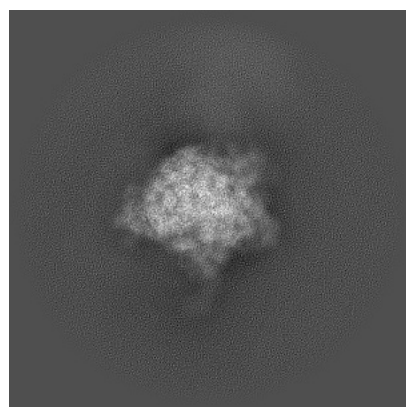


Y

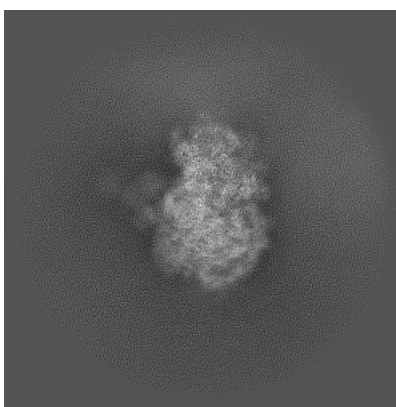


Z

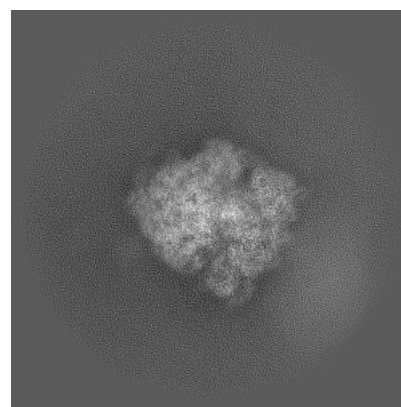
6.1.2 Raw map



X



Y

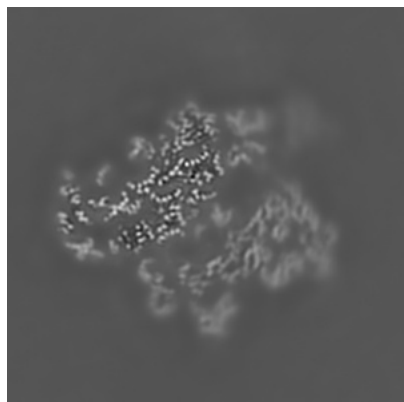


Z

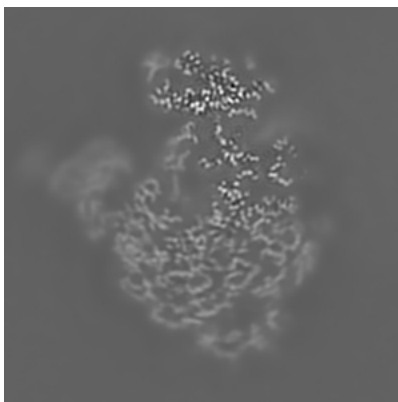
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

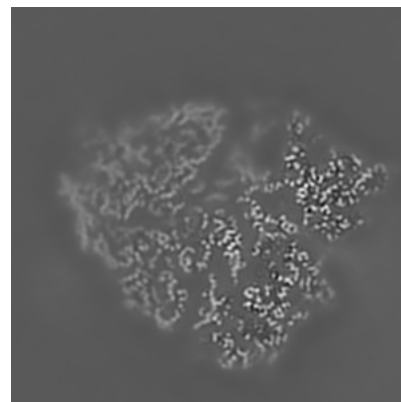
6.2.1 Primary map



X Index: 190

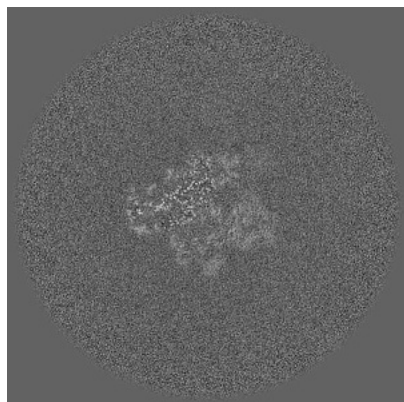


Y Index: 190

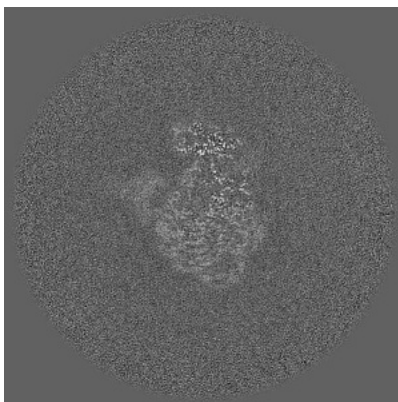


Z Index: 190

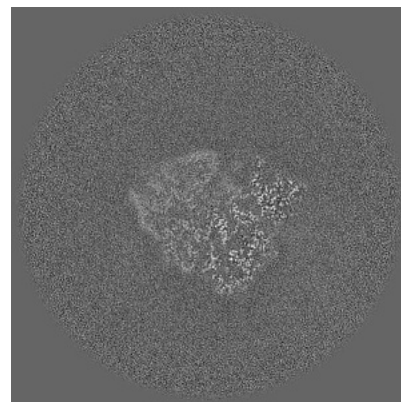
6.2.2 Raw map



X Index: 176



Y Index: 176

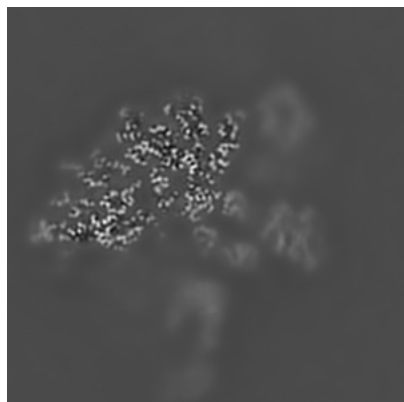


Z Index: 176

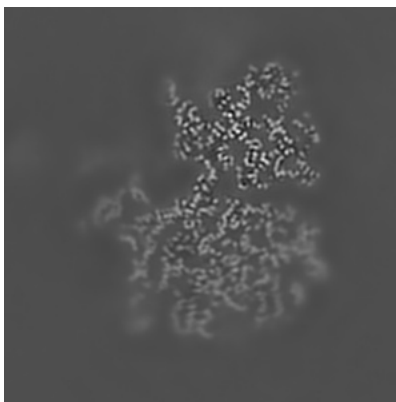
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

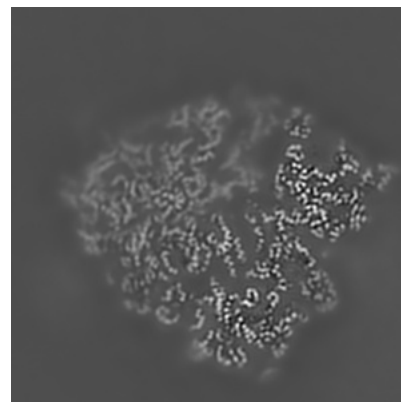
6.3.1 Primary map



X Index: 231

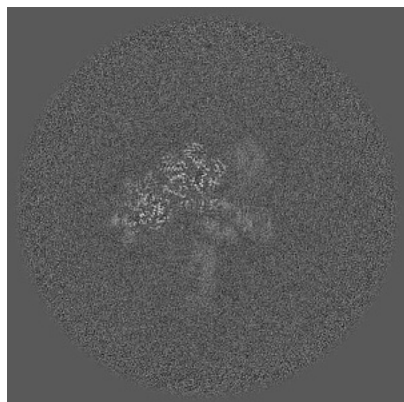


Y Index: 152

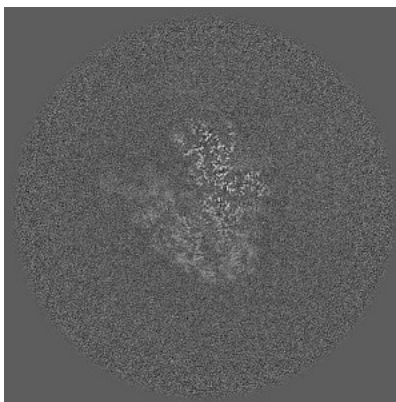


Z Index: 184

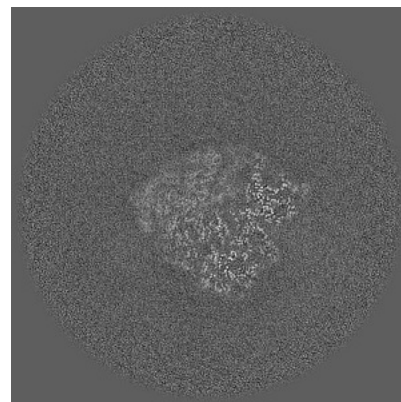
6.3.2 Raw map



X Index: 194



Y Index: 169

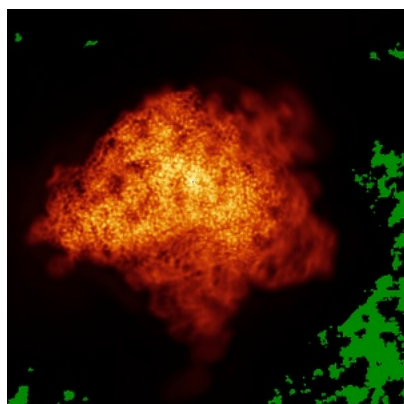


Z Index: 173

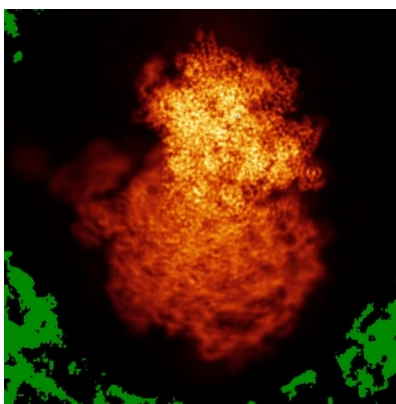
The images above show the largest variance slices of the map in three orthogonal directions.

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

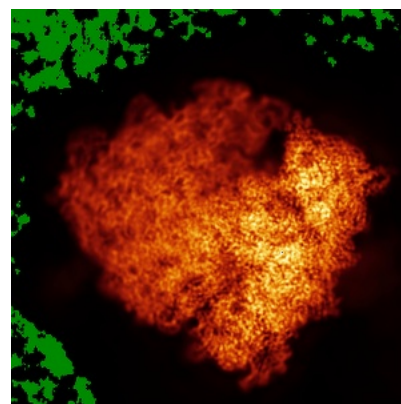
6.4.1 Primary map



X

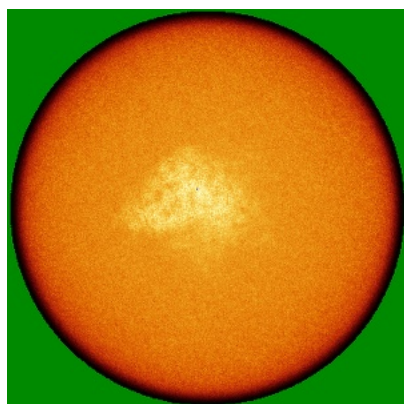


Y

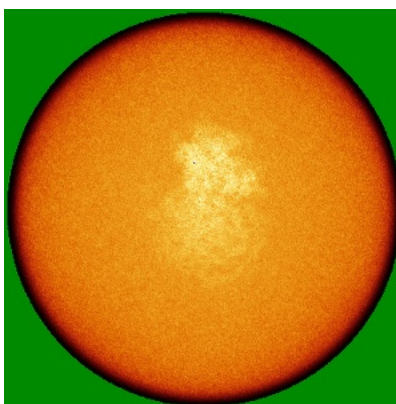


Z

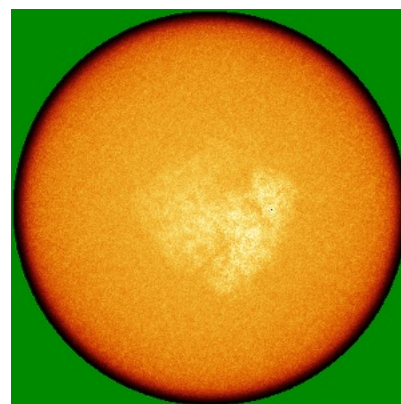
6.4.2 Raw map



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.

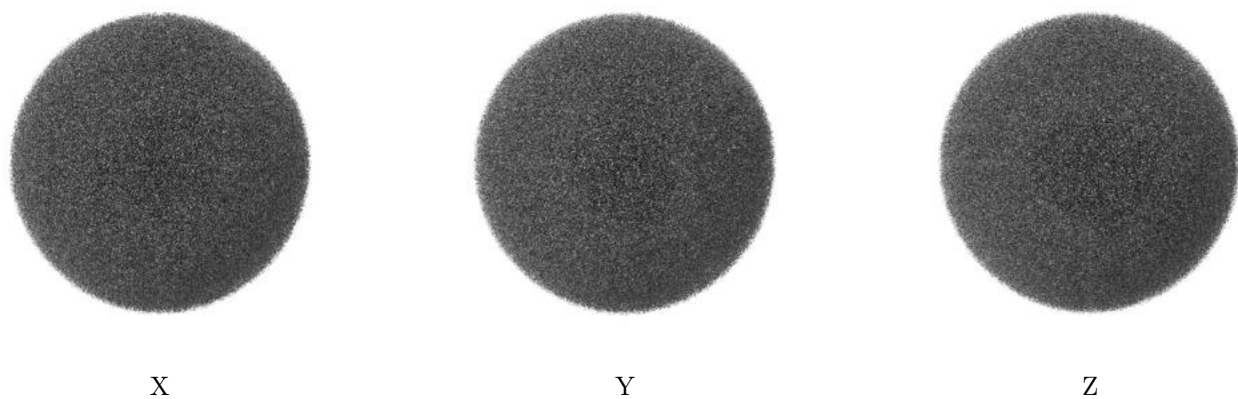
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0023. 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



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.

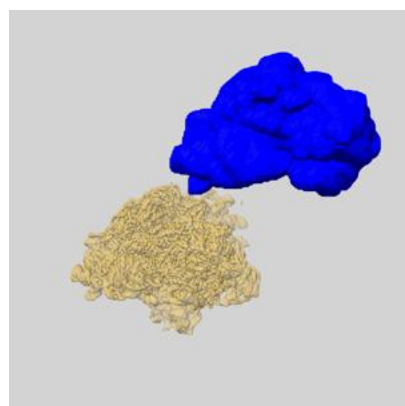
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

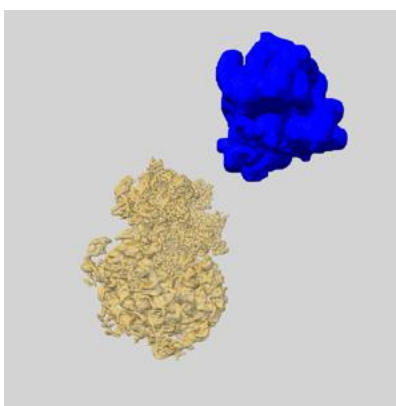
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

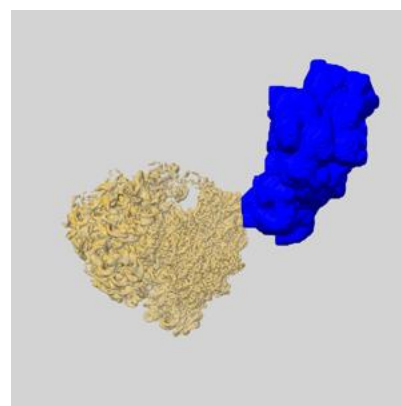
6.6.1 emd_11998_msk_1.map [i](#)



X



Y

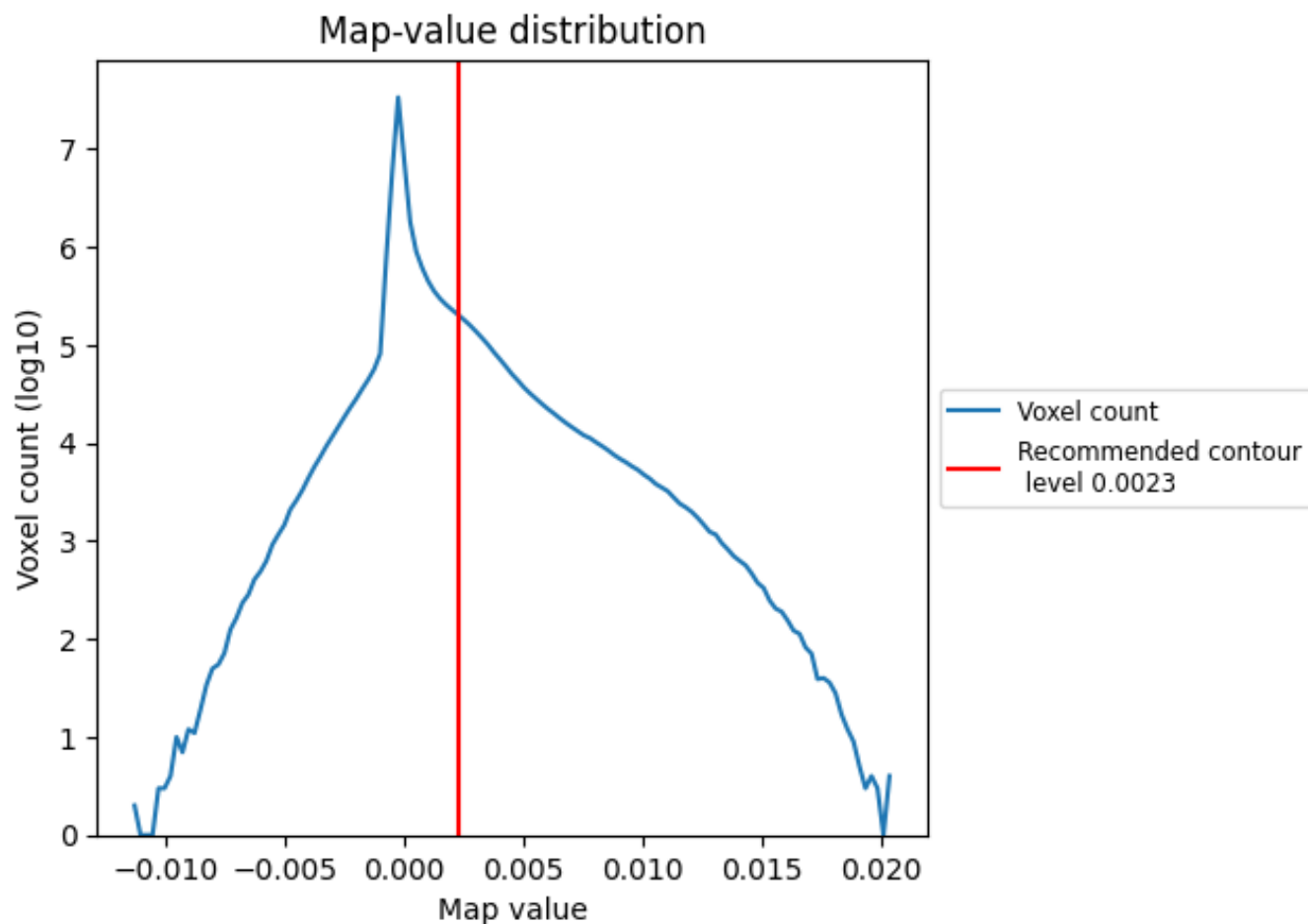


Z

7 Map analysis [i](#)

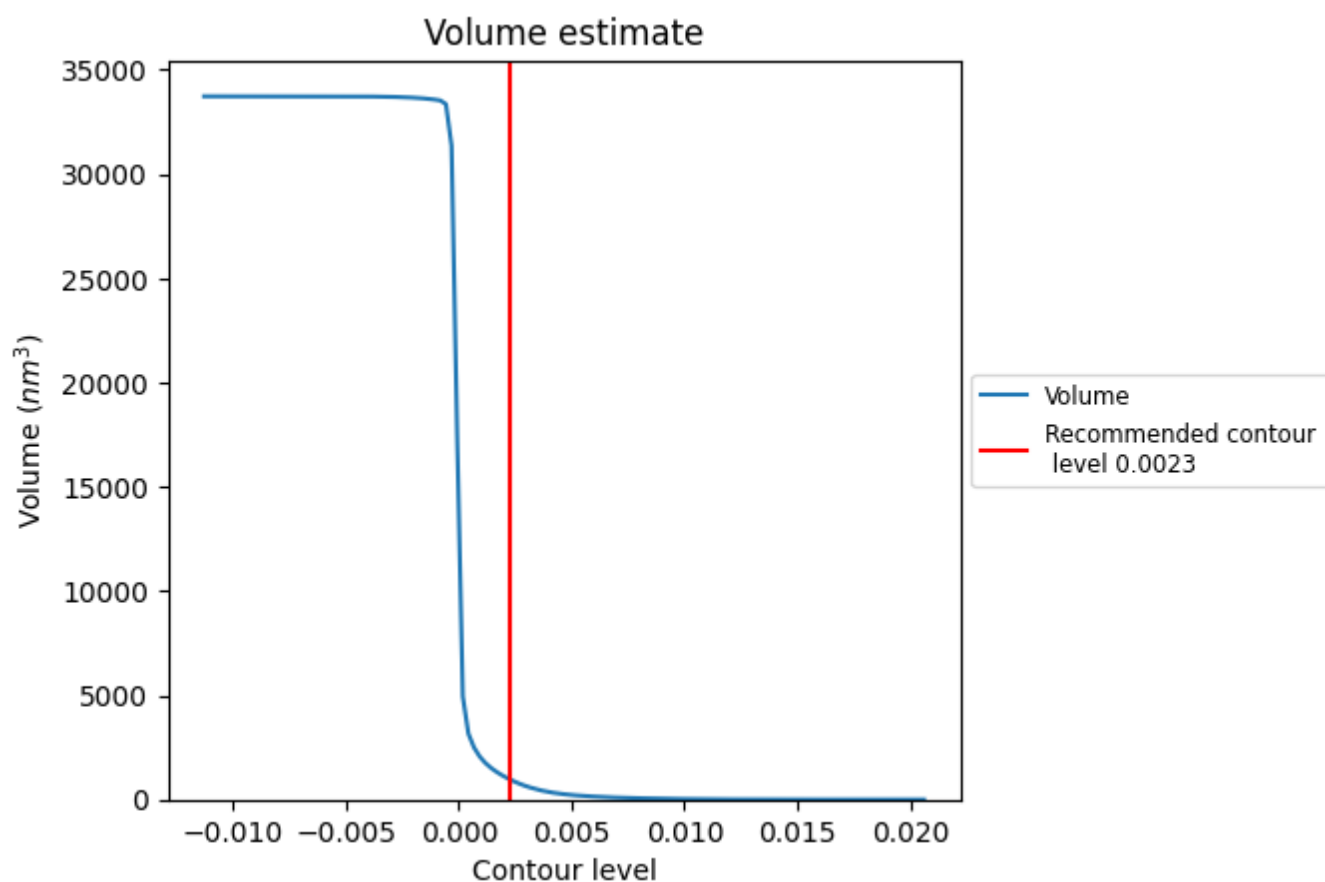
This section contains the results of statistical analysis of the map.

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.

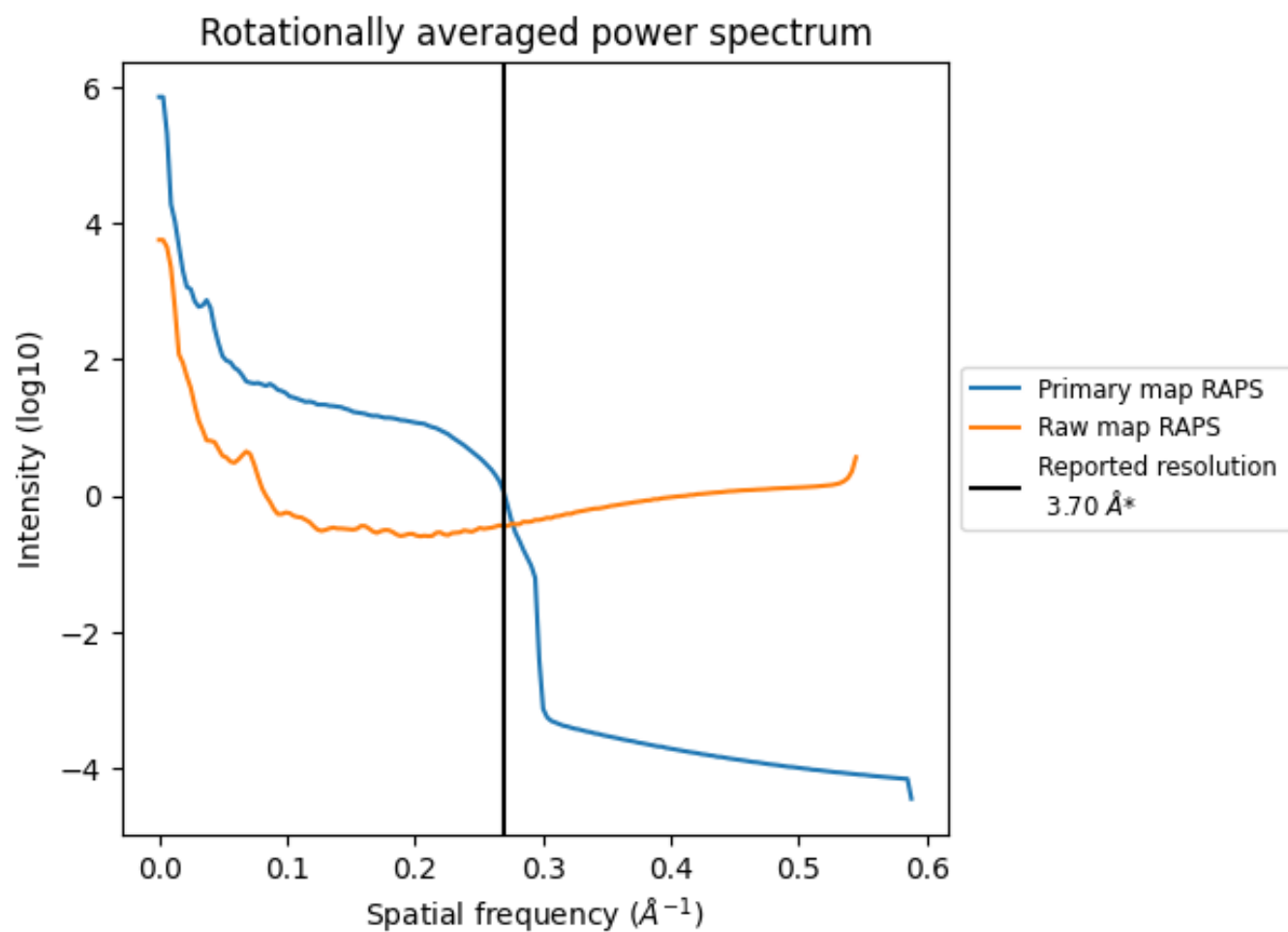
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 952 nm³; this corresponds to an approximate mass of 860 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 ⓘ

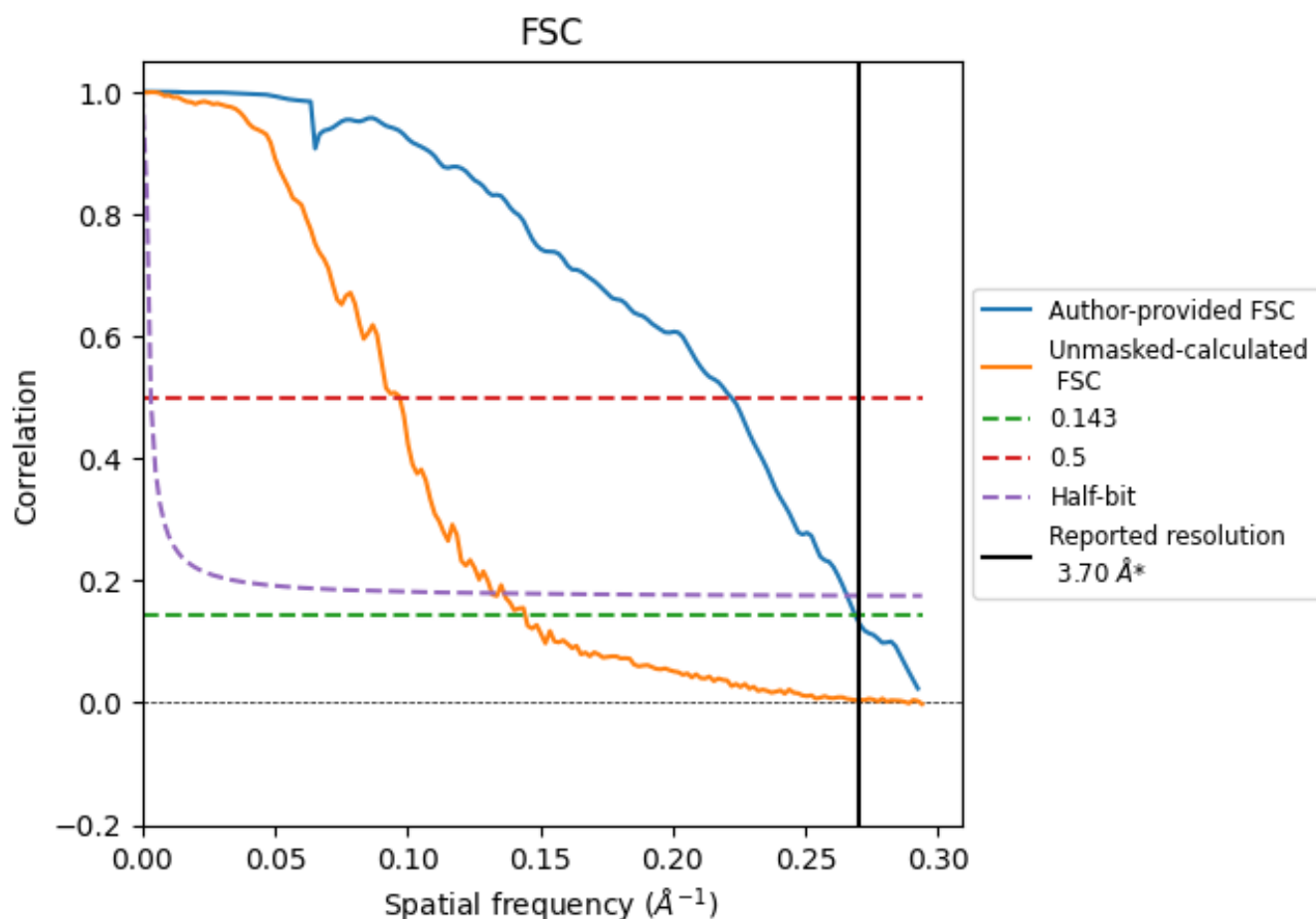


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

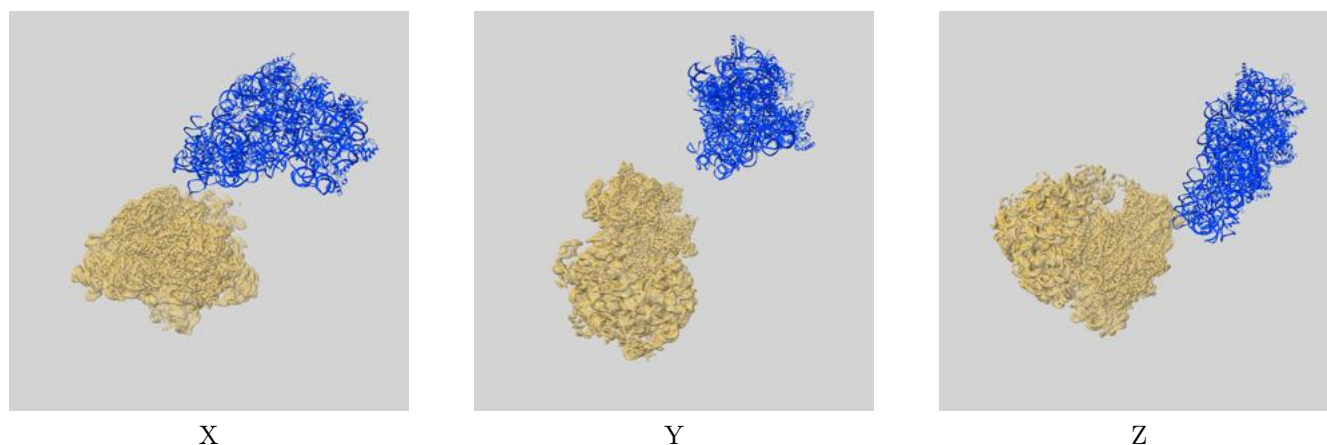
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.72	4.51	3.76
Unmasked-calculated*	6.93	10.31	7.59

*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 6.93 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11998 and PDB model 7OOC. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



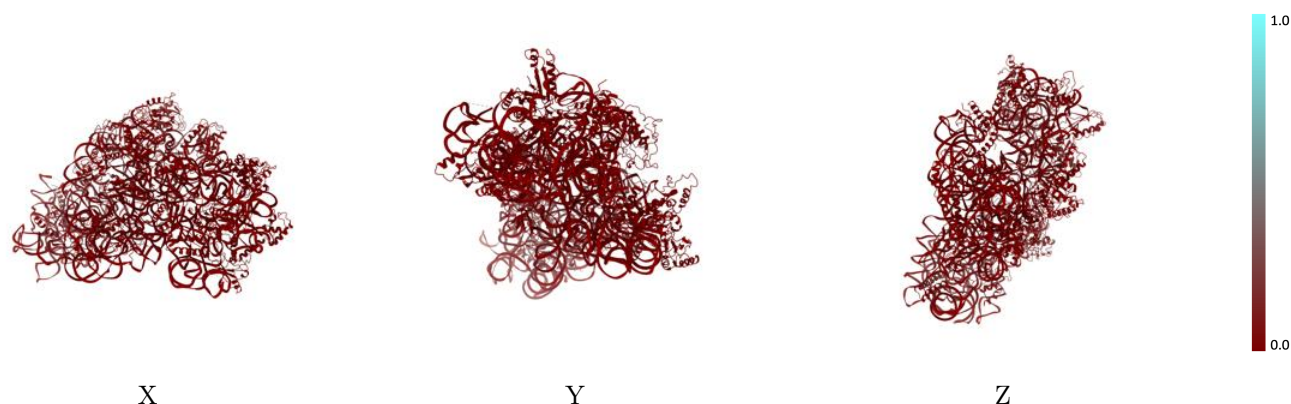
The images above show the 3D surface view of the map at the recommended contour level 0.0023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



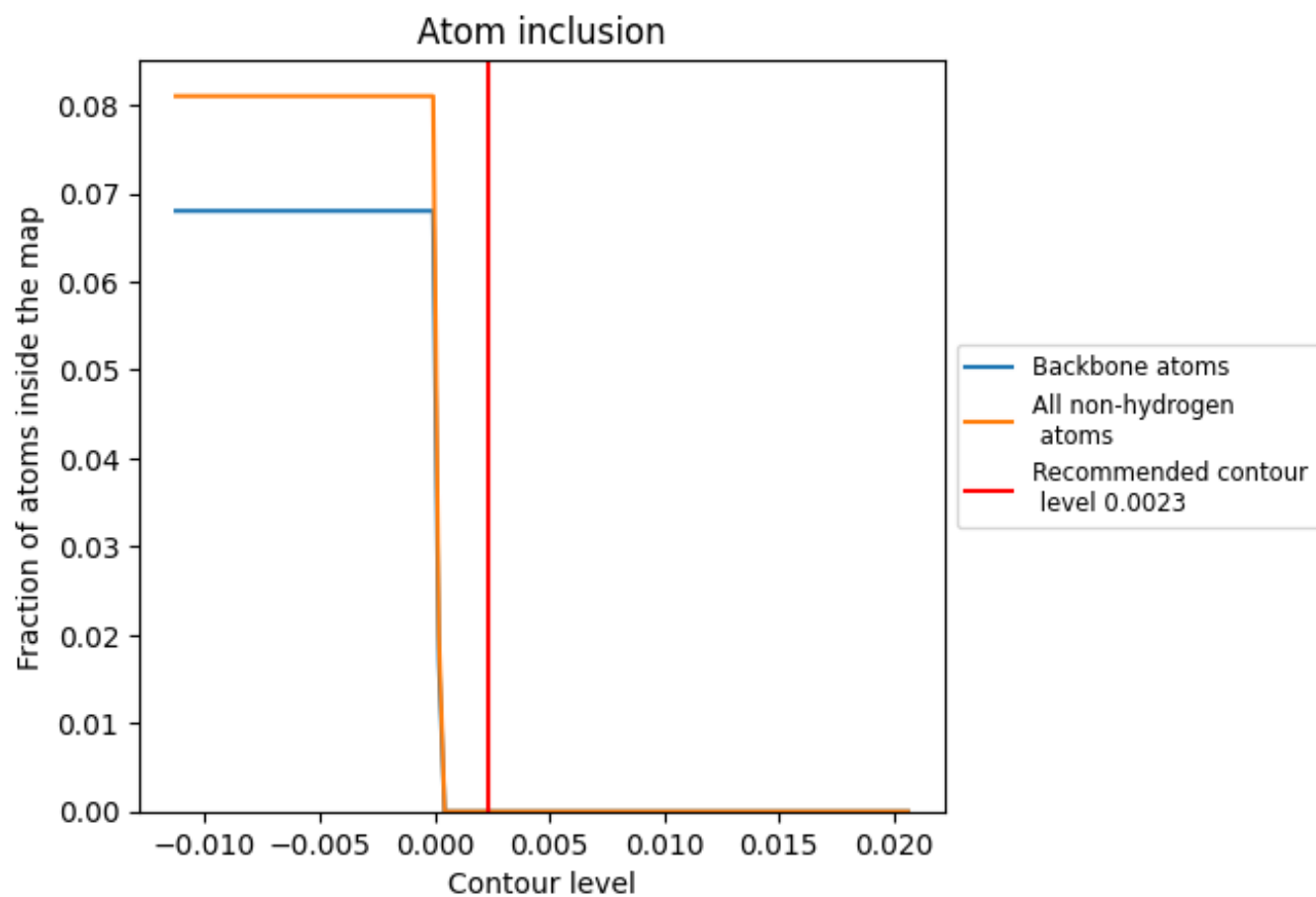
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% 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 (0.0023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	-0.0000
5	0.0000	-0.0010
A	0.0000	0.0000
B	0.0000	0.0000
C	0.0000	0.0000
D	0.0000	0.0000
E	0.0000	0.0000
F	0.0000	0.0000
G	0.0000	0.0000
H	0.0000	0.0000
I	0.0000	0.0000
J	0.0000	0.0000
K	0.0000	0.0000
L	0.0000	0.0000
M	0.0000	0.0000
N	0.0000	0.0000
O	0.0000	0.0000
P	0.0000	-0.0030
Q	0.0000	0.0000
R	0.0000	0.0000
S	0.0000	0.0250
T	0.0000	0.0000

1.0

0.0

<0.0