



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 01:57 pm BST

PDB ID : 9SKE / pdb_00009ske
EMDB ID : EMD-53627
Title : Model of M. pneumoniae 50S RRF EF-G
Authors : Dobbs, J.M.; Mahamid, J.
Deposited on : 2025-09-02
Resolution : 4.80 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:

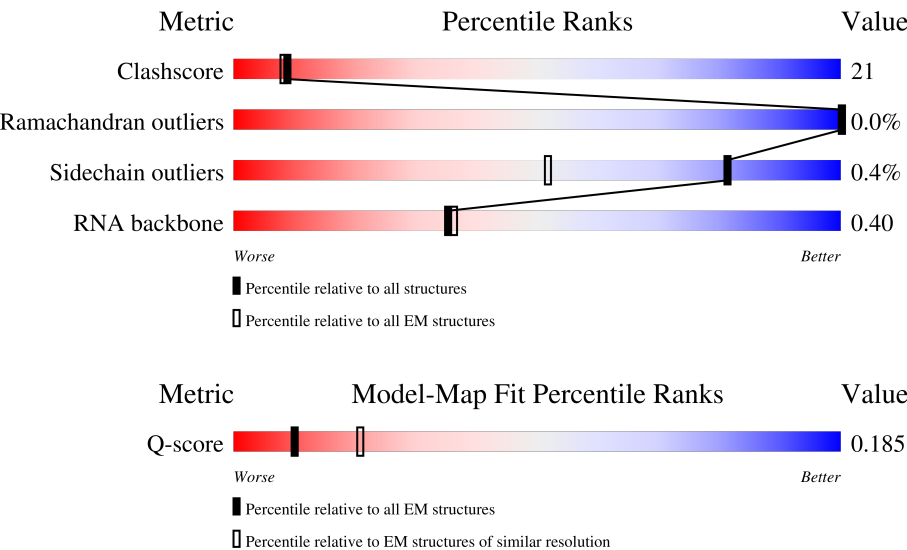
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 4.80 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.



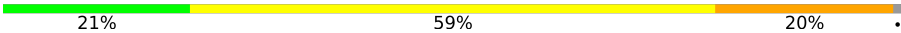
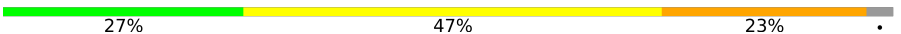
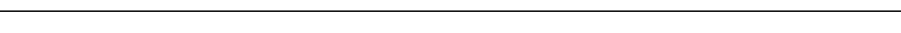
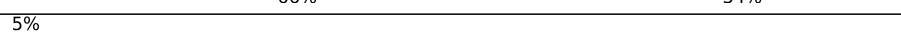
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1575 (4.30 - 5.30)

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	0	47	
2	1	59	
3	2	37	

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Mol	Chain	Length	Quality of chain
4	3	2893	
5	4	108	
6	7	184	
7	8	76	
8	A	675	
9	B	122	
9	C	122	
9	D	122	
9	E	122	
10	F	161	
11	a	285	
12	b	229	
13	c	210	
14	d	175	
15	e	176	
16	f	145	
17	h	128	
18	i	144	
19	j	122	
20	k	148	
21	l	136	
22	m	119	
23	n	116	
24	o	115	
25	p	114	

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Mol	Chain	Length	Quality of chain
26	q	99	 64%36%
27	r	139	 65%35%
28	s	92	 67%33%
29	t	111	 6%77%23%
30	u	86	 5%60%40%
31	v	63	 56%44%
32	w	108	 61%31%7%
33	x	44	 77%23%
34	y	56	 61%34%5%
35	z	50	 70%30%

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 100914 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 Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 5 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 6 is a protein called Ribosome-recycling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	184	Total	C	N	O	S	0	0
			1525	970	264	286	5		

- Molecule 7 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	51	Total	C	N	O	P	0	0
			1083	484	190	359	50		

- Molecule 8 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	675	Total	C	N	O	S	0	0
			5276	3335	905	1010	26		

- Molecule 9 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	29	Total	C	N	O	S	0	0
			231	146	34	49	2		
9	C	98	Total	C	N	O	S	0	0
			765	488	121	152	4		
9	D	29	Total	C	N	O	S	0	0
			231	146	34	49	2		
9	E	29	Total	C	N	O	S	0	0
			231	146	34	49	2		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	161	Total	C	N	O	S	0	0
			1239	796	213	225	5		

- Molecule 11 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 12 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 13 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 14 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 15 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 16 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 17 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 18 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	k	148	Total	C	N	O		
			1153	731	226	196	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	l	136	Total	C	N	O	S		
			1079	694	196	182	7	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	m	119	Total	C	N	O	S		
			958	609	175	171	3	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	n	112	Total	C	N	O	S		
			889	557	175	155	2	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	o	115	Total	C	N	O	S		
			938	592	180	165	1	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	p	114	Total	C	N	O	S		
			947	603	188	154	2	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	q	99	Total	C	N	O	S		
			811	525	148	134	4	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 29 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 30 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 31 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 32 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	w	100	Total	C	N	O		0	0
			818	517	153	148			

- Molecule 33 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 34 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 35 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

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: Large ribosomal subunit protein bL34

Chain 0: 



- Molecule 2: 50S ribosomal protein L35

Chain 1: 

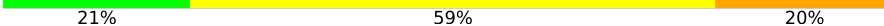


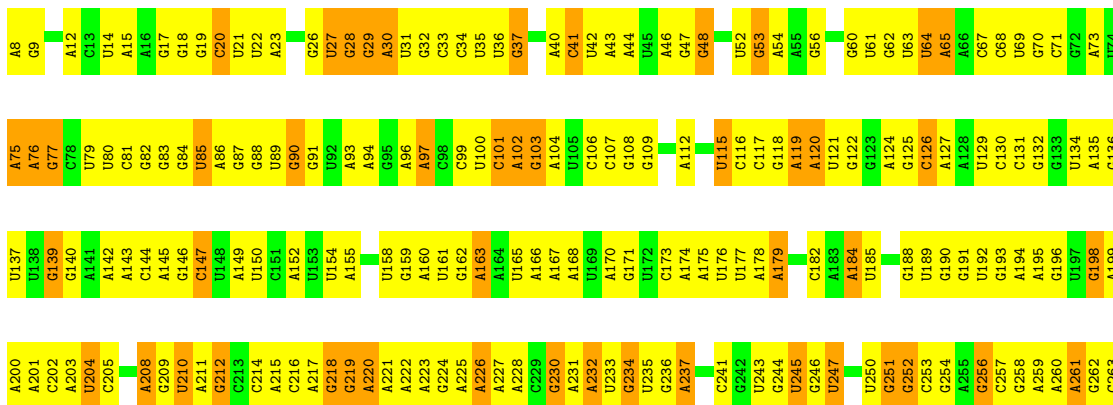
- Molecule 3: 50S ribosomal protein L36

Chain 2: 



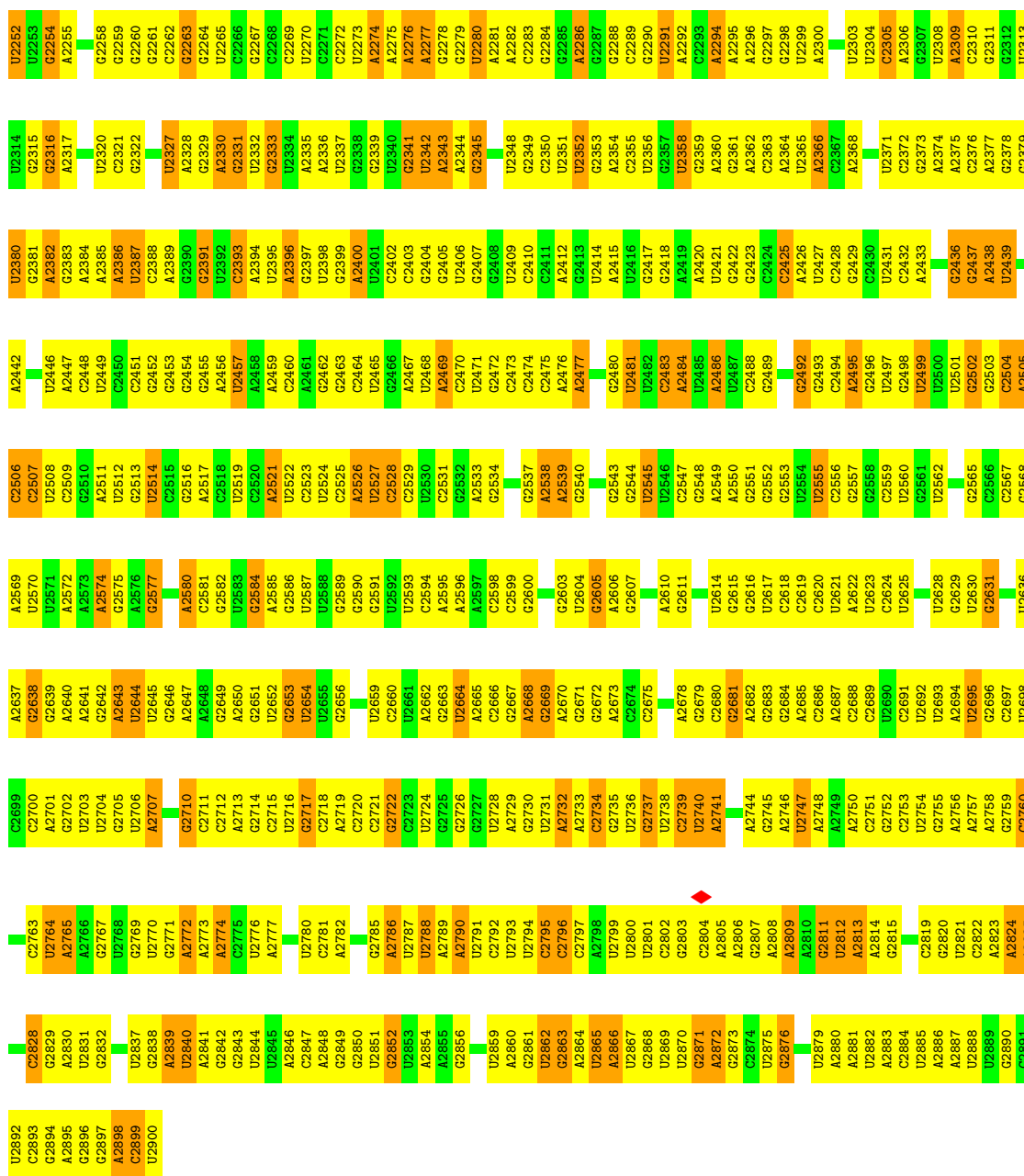
- Molecule 4: 23S ribosomal RNA

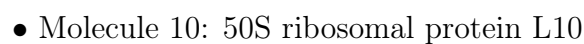
Chain 3: 

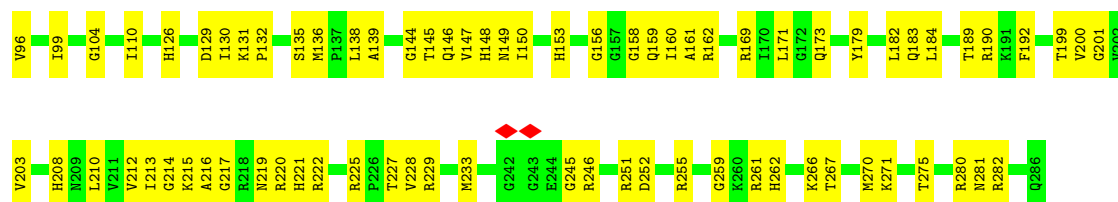


A1233	U1167	U1035	C974	A907	C841	C777	C708	G648	U585	C520	A458	A392	A331	G264
U1234	A1168	A1036	G975	A908	C842	U778	G709	A649	G586	C521	A459	C393	G332	G265
G1235	A1169	A1037	G976		U842	C779	A710	G650	U587	C522	G460	C394	A333	A266
U1236	C1170	G1038	C977	U911		G780	A711	A651	G588	A523	C461	U395	A334	A267
G1237	G1171		A977	A912	U846	U781	A712	G652	U589	G524	C462	A396	G335	C268
A1238	G1172	G1041	G978	U913	C847	U782	G713	G653	U590	A525	U463	G397	C336	A269
G1239	G1173	C1042		G914	U848	G783	G714	G654	G591	G526	A464	C398	U337	G270
U1240	G1174	C1043	A981	A915	C849	U784	G715	G655	G592	A527	A465	G399	G338	
U1241	C1175	C1044	G982	U916	G850	A785	G716	G656	C593	U528	A466	A400	U339	
G1242	A1176	A1045	A983	G917	U851	C787		A657	U594	G529	U467	G401	U340	A275
A1243	A1177	A1046	C984		C852	U786		G658	U595	G530	U468	A402	G341	A276
G1244	A1178	A1047	A985	G920	C853	G788	G719	G659	G596	G531		U403	G342	C277
G1245	G1179	A1048	G986	C921	A854	A789	G720	U660	G597	A532	A471	U404	A343	U278
		U1049	U857	C922		U790	C722	G661	G598	G533	A472	C405	A344	U279
				A	G859	U791	U723	U662	U599	U534	U473	U406		
C1247	A1182	C1053	G988	C	C860	G792	A724	A663	U600	G535	U474	U407	G345	C282
A1248	U1117	U1054	U861	U	U861	C793	G725	G664	U601	A536	U475	G408	G346	A283
A1249	U1118	A1055	U862	C	U862	G794		G665	U602	A537	G476	A409	G349	U284
G1250	A1119	A1056	U863	A	U863		U729	G666	G603	A538	U477	G410	C350	U285
C1251	A1186	G1057	A864	G928	A864	U797	G730	A687	A604	U539	U478	U411	G351	A286
G1252	C1187	U1058	A865	G929	A865	G798	A731	A688	A605	A540	G479	A412	C352	A287
U1253	A1188	C1001	G989	U935	C872	A806	G732	A689	G606	G541	C480	G413	G353	A288
G1254	G1189	A995	A996	C930	G866	A799	G733	G670	U607	A542	C481		C354	U289
U1255	A1190	A996	A996	G931	C867		G734	G671	A608	A482		G418	A355	A290
A1256	A1191	G997	G997	U932	C868	U802		G672	U609	U544	A483		A356	G291
G1257	U1192	A1061	C998	A933	U869	G803	G746	A679	G616	G551	A490	U426	U362	G297
U1258	U1193	A1062	G999	U934	A870	U804		A680	C617	C552	A491	U428	G363	U298
		A1063	U999	C934	A871	G805	U738	A681	G618	A553	G492	U430	U365	A299
A1259	U1194	U1000	U1000	U935	C871	G806	A739	A682		U554	A493	U431	G367	G300
U1260	A1195	C1001	C1001	G936	C872	A806	A740	A683	U622	A555	U494	U432	G368	G301
G1261	U1196	G1059	A995	A937	G873	U807	A741	G684	U623	U556	G495	G432	C369	G302
A1262	A1197	G1060	A996	G931	C867	U799	G742	G685	U624	G557	A496		U305	
G1263	C1132	A1067	A996	A938	U874	U808		G686		C588			C370	
U1264	U1136	U1068	U1004	U939	A875	G810	G746	G687	G625	C589	G499	A437	A309	A309
G1265	C1137	G1069	G1005	A940	A876	G811	A747	U688	U627	U560	U500	A438	G372	U310
U1266	U1200	U1070	U1006	C941	G877	G812	U749	U689	A628	A561	U373	U439	G373	G311
A1267	A1138		C1007	A942		G813		G683	U629	C562	A502	U440	U374	U312
U1268	U1140	G1075	U1008		A881	U814	C752	G684	C630	U563	G503	U441	U375	G313
G1269	U1141	U1076	A1009	U945	C882	A816	A753	G685	A631	A564	G504	G442	U376	G314
U1270	G1142	G1077	G1010	A946	A883	A817	C755	G686	A632	C565	G505	C443	U377	A315
A1271	U1143	C1078	A1011	A947	A884	U818	A756	U687	G633	U566	A506	C444	G378	C316
	U1209	U1079	U1012	A948	U885	A819		U688	U627	U567	A507	C445	A379	U317
A1272	A1210	A1080		C949	U886	U820	U759	U690	G630	G568	A508	A446	A380	U318
U1273	G1144	A1081	G1015	C951	A887	U821	G760	G691	C631	G569	G509	G447	A381	G319
A1274	G1145	A1082	A1016	U952	A888	C822		U692	A632	C570	G510	A448	U382	A320
G1275	U1213	A1083	U1017	U952	G889	C823	G761	U693	G632	C571	U511	C449	U383	A323
A1276	U1214	C1084	G1018	G953	U890	A823	A762	U694	A633	C572	G512	C450	G384	A324
U1277	G1215	A1085	A1019	A954	C891	A824		U695	G633	C573	A451	C451	U385	G325
G1278	U1216	G1086	G1020	A955	G892	U825	G763	U696	G634	U568	A514	U452	U386	G326
U1279	G1217	C1087	C1021	U956	A893	U826	A764	G697	G635	G568	A515	U453	U387	U327
G1280	G1218	A1088	G1022	G957	C894	C827	A765	U698	G636	U569	A516	G454	U388	U328
A1281	U1219	A1089	C1023	C958	G895	A828	C766	U697	U637	C570	G517	G455	C389	A329
U1282	A1220	G1090	A1024	C959	U896	U829		U698	U638	A571	G518	A456	A390	G329
G1283	G1221	G1091	G1025	A960	A897	A829	C767	A698	A638	U511	G519	A457	U391	A330
A1284	U1222	A1092	U1026	U961	A898	U830	G768	A699	G639	G512	C450	A451	G384	
U1285	A1159	U1093	U1027	U962	A899	U831	A769	U700	G639	G512	C450	A451	U385	C324
G1286	G1226	G1094	C1028		G900	C832	A770	A701	U640	G574	A451	U452	U386	G325
C1287	U1227	U1095	A1029	U965	C901	C833	C771	U702	U641	G574	A451	U452	U387	G326
U1288	G1228	U1096	U1030	U966	U902	C834	G772	U703	A642		A515	U453	U387	U327
G1289	U1229	U1097	U1031	U967	A903	U835	G773	A704	A643	U580	A516	G454	U388	U328
U1290	A1164	G1097	A1032	U968	C904	U836	A774	A705	C644	U583	G517	G455	C389	A329
G1291	U1230	C1098	A1033	U968	U905	A837	C775	C706	C645	U583	G517	G455	A390	G329
A1292	U1232	U1100	A1034	U971	G906	C707	U776	C707		G584	A519	U457	U391	A330

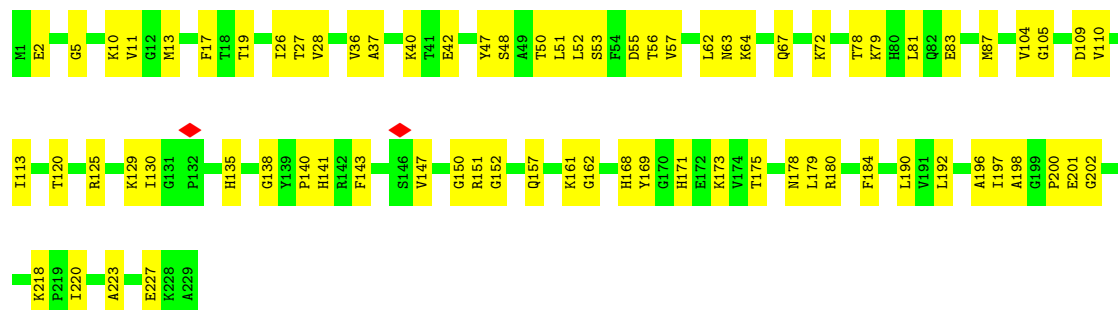
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G2190	A2124	G2063	U2002	A1935	A1861	A1799	A1734	U1670	U1609	U1546	G1484	A1421	G1356	G1294
G2191	U2125	G2064	C2003	A1936	A1862	C1800	A1735	C1672	U1610	A1547	U1485	A1422	U1357	A1295
U2192	A2126	A2065	G2004	G1937	G1863	C1801	G1738	G1676	C1611	U1548	U1486	U1610	C1358	A1423
U2193	G2127	G2066	G2005	U1938	A1864	C1802	G1739	U1677	U1612	U1549	U1487	U1424	U1359	U1297
G2194	G2128	A2067	C2006	A1939	A1865	U1803	G1740	G1678	C1613	U1550	U1488	U1425	U1360	A1298
U2195	U2129	G2068	U2007	G1940	G1866	A1804	U1743	U1678	A1613	U1551	G1489	C1426	U1361	A1299
G2196	A2130	A2069	A2008	C1941	G1867	U1805	U1744	U1679	G1614	U1552	G1490	U1427	C1362	C1300
U2197	G2132	C2070	U2009	A1943	A1868	C1807	A1745	U1679	G1615	G1553	G1491	U1428	C1363	C1301
G2198	A2133	C2071	A2010	A1944	G1870	C1808	U1746	U1680	U1618	A1554	G1492	U1431	C1302	C1302
C2199	U2136	C2072	C2012	A1945	U1871	A1809	G1747	G1681	A1619	U1555	A1493	A1432	U1303	U1303
U2200	A2137	G2073	A2013	U1946	U1872	U1748	U1748	G1682	A1620	U1556	U1494	A1433	U1304	U1304
G2202	U2138	U2075	U2014	U1947	A1873	A1749	A1749	G1683	U1621	A1558	A1496	U1434	G1306	G1306
U2205	U2139	A2077	G2015	C1948	C1881	A1750	A1750	G1684	U1622	U1559	U1497	U1437	U1307	G1307
A2206	G2140	G2077	G2016	C1949	G1882	A1751	A1751	G1685	U1623	U1557	U1494	A1438	U1308	G1305
A2207	A2141	A2078	U2017	U1950	G1883	A1752	A1752	G1686	A1624	U1558	U1495	U1439	G1371	G1308
U2208	U2142	G2080	G2019	G1952	A1884	U1754	U1754	G1687	G1625	U1559	U1497	U1440	C1373	U1310
U2209	G2143	U2081	A2020	U1953	G1885	G1818	A1755	A1689	U1627	U1560	U1500	U1441	G1374	G1311
U2210	C2144	U2082	A2021	C1954	G1886	G1819	A1756	C1690	U1628	U1561	U1501	A1442	U1375	G1312
G2211	A2145	U2083	A2022	G1955	U1887	U1820	G1757	U1691	G1635	U1572	U1503	U1443	C1378	G1313
U2212	A2146	A2084	U2023	G1956	U1888	G1821	G1758	A1692	U1630	U1573	U1505	A1444	C1379	A1314
U2213	G2147	C2085	C2024	G1957	U1889	U1822	G1759	U1693	A1631	C1574	U1506	U1445	C1379	A1315
A2214	U2148	U2086	C2025	U1958	A1891	A1823	G1760	U1694	G1632	U1575	G1507	U1446	U1380	C1316
G2215	U2149	G2087	A2026	A1959	A1892	G1824	C1761	G1695	C1633	U1576	U1509	A1447	U1381	U1317
U2216	G2150	U2088	G2027	A1960	C1895	U1825	A1762	C1696	A1634	U1577	U1510	U1448	U1382	U1318
G2217	C2151	A2089	G2028	U1961	G1895	G1826	G1763	C1697	U1635	U1578	G1511	U1449	G1383	C1319
U2218	U2152	G2090	U2029	U1962	A1896	U1827	G1764	A1698	U1636	U1579	U1512	G1450	U1384	G1320
U2219	C2153	C2091	A2030	U1963	G1897	U1828	G1765	A1699	A1637	G1574	U1513	G1451	U1385	C1321
A2220	A2154	U2092	G2031	C1969	A1903	U1829	A1766	G1700	U1638	C1575	U1514	G1452	U1387	A1322
U2221	G2155	U2093	G2032	C1970	G1904	G1830	A1767	G1701	C1639	U1576	A1515	U1455	U1388	A1323
C2222	C2156	A2094	G2033	U1970	U1905	G1831	G1768	U1702	G1640	U1577	U1516	A1456	U1389	A1324
C2223	A2157	G1971	G2034	G1972	G1906	G1832	A1769	C1703	A1641	A1578	C1518	C1456	C1325	C1325
A2224	U2160	U2096	U2035	U1973	A1907	U1835	A1770	U1705	G1642	G1580	A1519	A1457	G1327	G1327
G2225	G2161	A2097	G2036	U1974	A1908	U1836	C1771	U1706	A1644	U1581	A1520	A1458	A1393	A1328
C2229	U2162	U2098	A2037	G1975	G1910	C1837	G1772	U1707	C1645	G1582	A1521	A1459	U1329	U1330
A2230	U2163	G2100	G2039	A1976	G1911	A1838	G1776	G1708	G1646	U1583	U1522	A1461	A1394	U1331
G2232	A2165	A2101	A2040	C1977	C1912	C1839	G1777	C1709	A1647	U1584	C1523	A1462	C1398	U1334
A2233	U2166	U2104	C2041	U1978	G1913	C1840	G1778	U1710	A1648	A1585	C1524	G1463	G1399	A1335
C2234	G2167	G2105	C2043	G1979	G1914	U1841	G1779	U1711	C1649	U1586	C1525	G1464	G1399	A1336
A2235	C2168	G2106	C2044	U1981	C1915	G1842	A1780	U1713	U1650	U1587	U1526	U1465	U1400	A1337
G2236	G2169	A2107	C2045	G1982	G1916	C1854	C1781	U1714	A1651	A1588	U1527	U1466	A1401	G1337
U2237	A2170	C2108	G2046	C1987	U1917	C1844	U1782	A1715	A1652	A1589	G1528	U1467	G1402	G1338
U2238	U2175	U2110	A2049	A1988	A1920	G1845	U1783	U1716	C1653	U1590	U1529	U1468	G1403	U1339
U2239	G2176	G2111	G2050	U1989	A1921	U1848	U1785	C1717	G1654	A1592	G1530	C1470	C1404	U1340
A2241	A2177	U2112	C2051	C1990	U1922	G1849	A1786	U1718	U1655	U1593	A1532	A1471	A1406	C1342
G2242	G2178	U2113	G2052	U1991	A1923	C1850	A1787	G1721	A1656	G1594	A1533	C1472	U1407	C1343
G2243	A2179	A2115	C2053	C1992	C1921	U1851	A1788	U1722	C1659	U1597	A1535	C1473	G1408	U1344
U2244	G2180	U2116	G2054	U1993	A1926	C1852	C1789	A1723	A1660	U1598	C1536	C1474	G1409	G1345
G2245	A2181	G2117	A2055	U1994	C1927	G1853	U1790	G1724	A1661	U1599	A1537	C1475	U1410	G1346
G2246	G2182	U2118	C2056	A1996	G1928	U1854	A1792	U1726	G1662	A1600	U1538	C1476	A1413	C1347
A2249	U2183	A2119	G2057	C1997	G1929	A1855	A1793	U1727	A1664	A1601	U1539	U1477	C1349	C1348
G2250	A2184	G2120	G2058	U1998	U1930	G1856	A1794	A1728	G1665	G1602	G1540	A1478	A1415	C1349
G2251	C2185	A2121	G2059	U1999	C1931	G1857	C1795	G1731	A1666	A1603	G1541	A1479	G1416	G1350
	G2186	G2122	A2061	U2000	U1932	U1858	C1796	U1732	A1667	A1604	G1542	A1480	G1417	G1352
					U1933	U1859	C1797	A1732	G1668	A1605	G1544	U1482	U1418	U1354



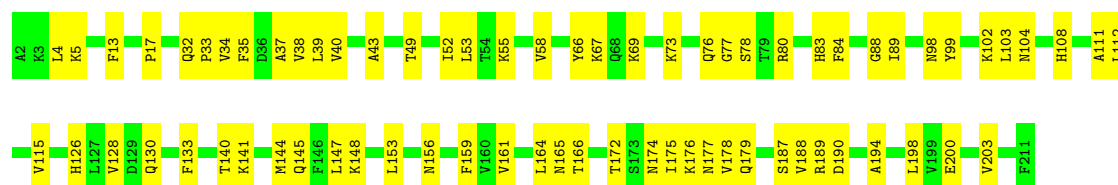




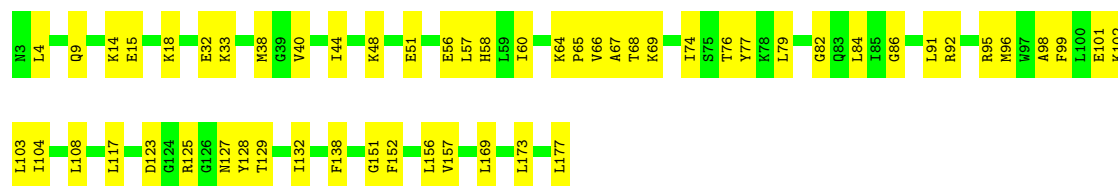
• Molecule 12: Large ribosomal subunit protein uL3



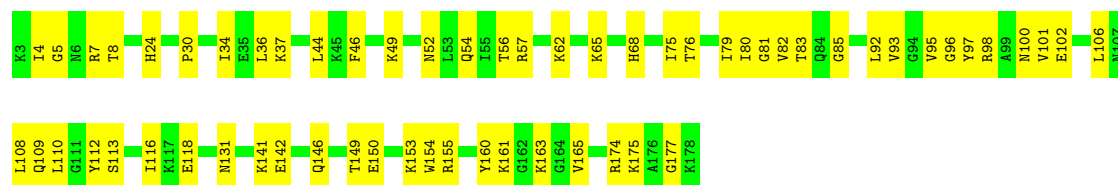
• Molecule 13: Large ribosomal subunit protein uL4



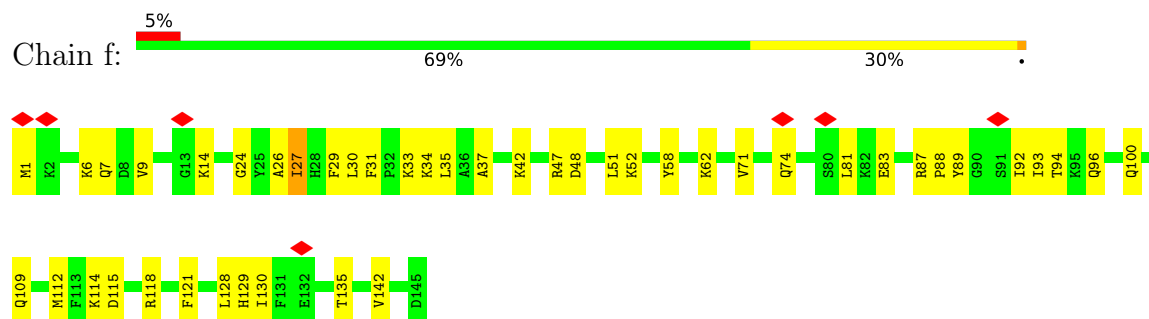
• Molecule 14: Large ribosomal subunit protein uL5



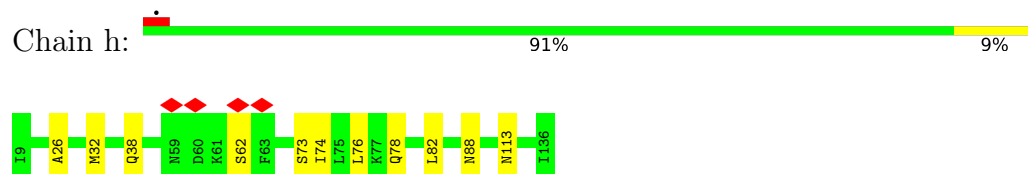
• Molecule 15: Large ribosomal subunit protein uL6



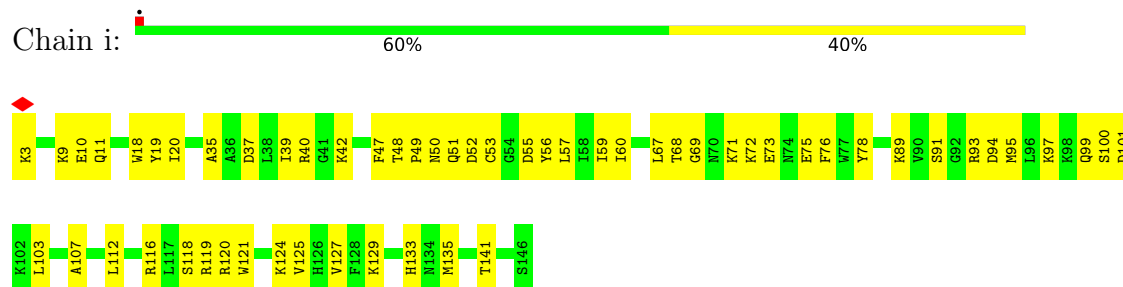
- Molecule 16: Large ribosomal subunit protein bL9



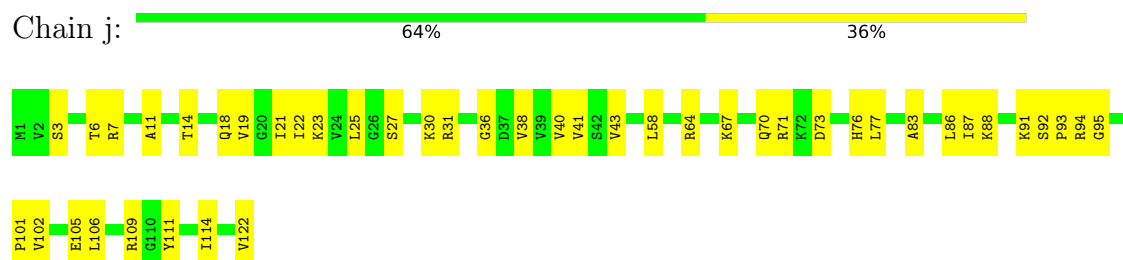
- Molecule 17: Large ribosomal subunit protein uL11



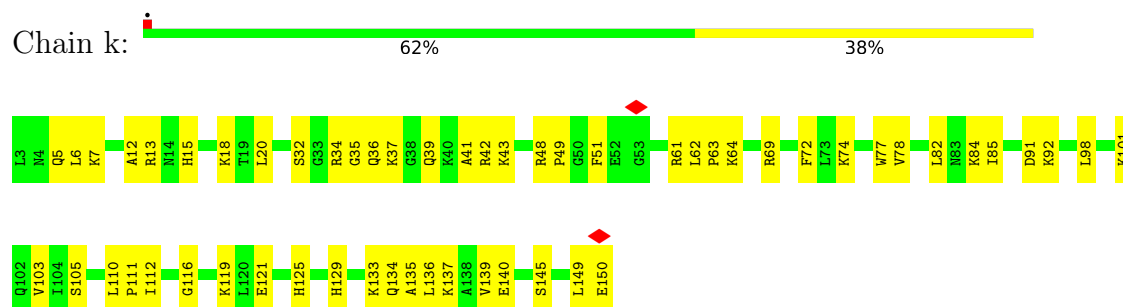
- Molecule 18: Large ribosomal subunit protein uL13



- Molecule 19: 50S ribosomal protein L14



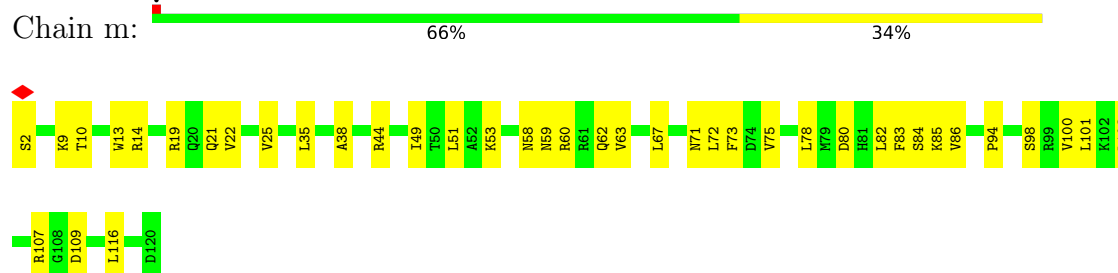
- Molecule 20: Large ribosomal subunit protein uL15



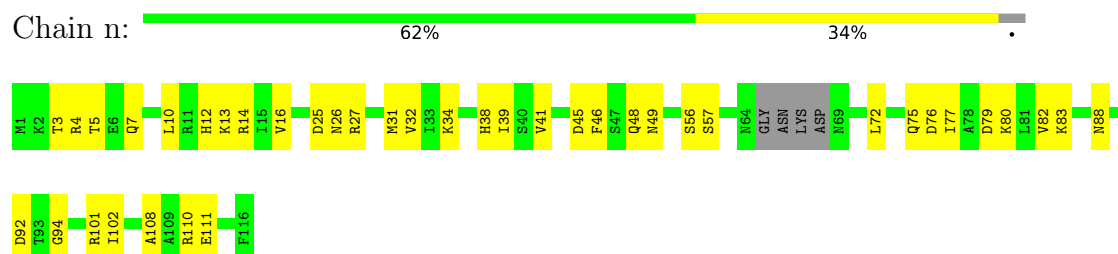
- Molecule 21: Large ribosomal subunit protein uL16



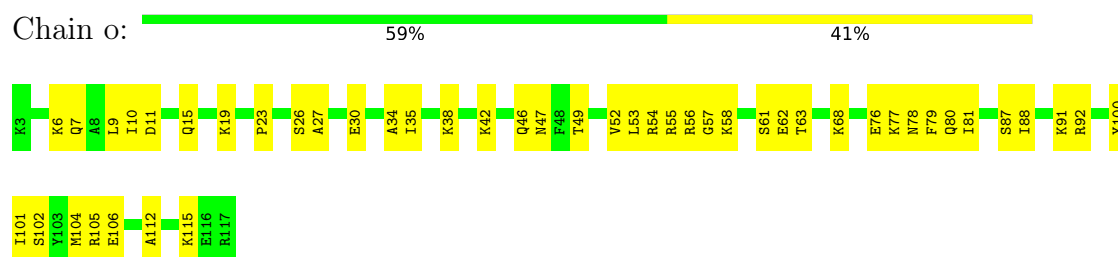
- Molecule 22: Large ribosomal subunit protein bL17



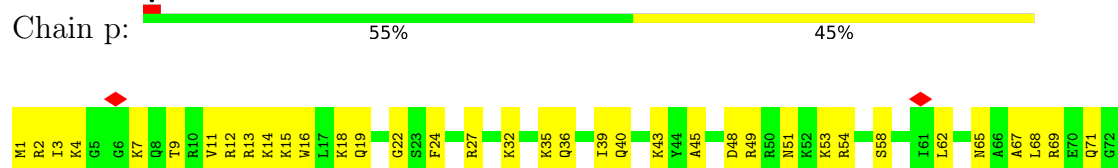
- Molecule 23: Large ribosomal subunit protein uL18



- Molecule 24: Large ribosomal subunit protein bL19



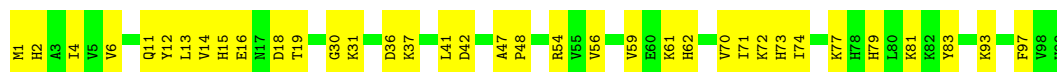
- Molecule 25: Large ribosomal subunit protein bL20





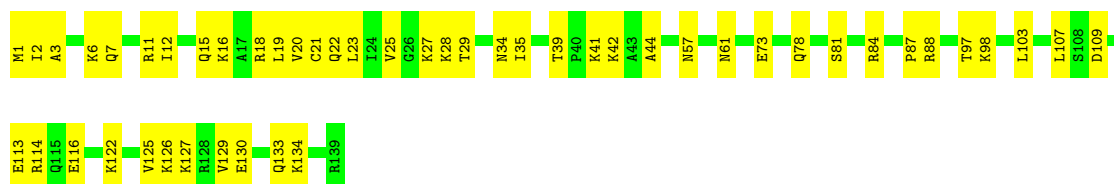
- Molecule 26: Large ribosomal subunit protein bL21

Chain q: 64% 36%



- Molecule 27: Large ribosomal subunit protein uL22

Chain r: 65% 35%



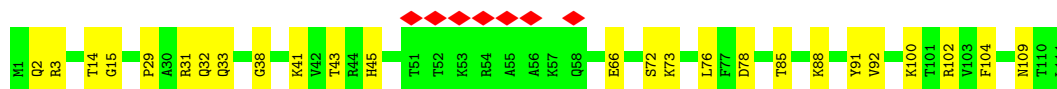
- Molecule 28: Large ribosomal subunit protein uL23

Chain s: 67% 33%



- Molecule 29: 50S ribosomal protein L24

Chain t: 6% 77% 23%



- Molecule 30: Large ribosomal subunit protein bL27

Chain u: 5% 60% 40%

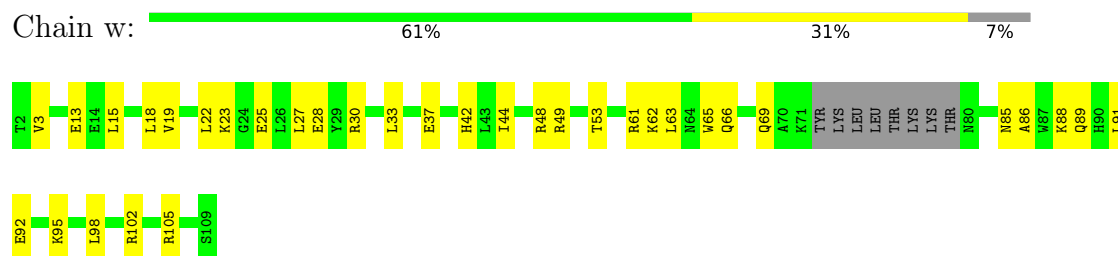


- Molecule 31: Large ribosomal subunit protein bL28

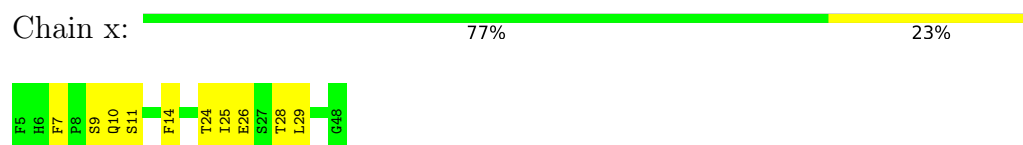
Chain v: 56% 44%



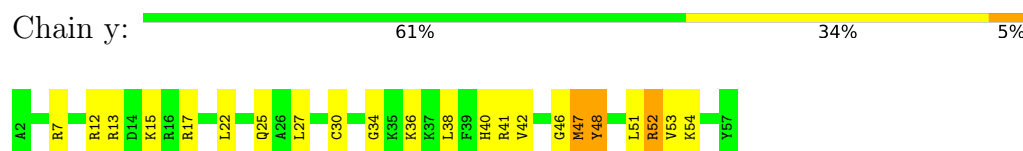
- Molecule 32: Large ribosomal subunit protein uL29



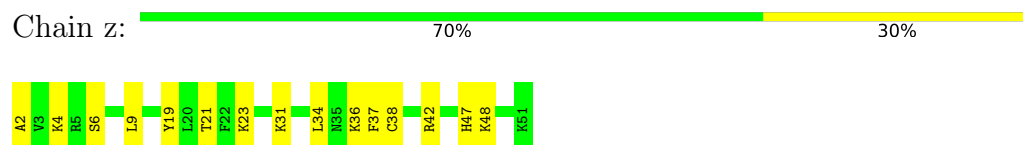
- Molecule 33: Large ribosomal subunit protein bL31



- Molecule 34: Large ribosomal subunit protein bL32



- Molecule 35: Large ribosomal subunit protein bL33A



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	7524	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.000517	Depositor
Map size (Å)	600.0, 600.0, 600.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.0, 2.0, 2.0	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	0	0.13	0/383	0.40	0/504
2	1	0.12	0/484	0.39	0/637
3	2	0.12	0/306	0.42	0/401
4	3	0.10	0/69073	0.25	0/107710
5	4	0.10	0/2505	0.27	0/3902
6	7	0.48	1/1550 (0.1%)	0.78	9/2081 (0.4%)
7	8	0.12	0/1208	0.31	0/1879
8	A	0.70	0/5368	1.14	3/7235 (0.0%)
9	B	0.63	0/231	1.16	2/307 (0.7%)
9	C	0.35	0/769	0.67	0/1029
9	D	0.63	0/231	1.04	0/307
9	E	0.63	0/231	1.07	0/307
10	F	0.68	0/1254	1.10	0/1677
11	a	0.15	0/2267	0.41	0/3044
12	b	0.14	0/1795	0.42	0/2412
13	c	0.13	0/1671	0.38	0/2246
14	d	0.15	0/1409	0.43	0/1894
15	e	0.15	0/1420	0.39	0/1912
16	f	0.15	0/1183	0.47	1/1587 (0.1%)
17	h	0.14	0/968	0.43	1/1298 (0.1%)
18	i	0.12	0/1186	0.40	0/1592
19	j	0.13	0/953	0.39	0/1275
20	k	0.15	0/1170	0.42	0/1559
21	l	0.15	0/1104	0.42	0/1481
22	m	0.13	0/973	0.40	0/1309
23	n	0.13	0/897	0.44	0/1198
24	o	0.15	0/948	0.42	0/1262
25	p	0.16	0/961	0.41	0/1278
26	q	0.15	0/828	0.42	0/1111
27	r	0.13	0/1077	0.37	0/1441
28	s	0.13	0/732	0.41	0/988
29	t	0.14	0/879	0.39	0/1165
30	u	0.15	0/665	0.47	0/884
31	v	0.14	0/519	0.41	0/695

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	w	0.14	0/826	0.40	0/1104
33	x	0.12	0/353	0.37	0/474
34	y	0.32	0/457	0.68	1/601 (0.2%)
35	z	0.14	0/412	0.38	0/547
All	All	0.22	1/109246 (0.0%)	0.41	17/162333 (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
8	A	0	2
21	l	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	7	107	MET	CA-C	-5.16	1.46	1.53

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	7	104	PHE	CA-CB-CG	-9.77	104.03	113.80
6	7	33	PRO	CA-C-N	7.39	134.14	121.35
6	7	33	PRO	C-N-CA	7.39	134.14	121.35
34	y	48	TYR	N-CA-C	-5.88	104.79	111.14
6	7	32	ARG	CA-C-N	5.86	125.56	119.82

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	A	211	ARG	Sidechain
8	A	94	ARG	Sidechain
21	l	14	ASN	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	0	380	0	429	23	0
2	1	477	0	530	25	0
3	2	304	0	350	21	0
4	3	61664	0	30948	2411	0
5	4	2239	0	1137	52	0
6	7	1525	0	1567	249	0
7	8	1083	0	550	57	0
8	A	5276	0	5284	187	0
9	B	231	0	237	10	0
9	C	765	0	809	35	0
9	D	231	0	237	9	0
9	E	231	0	237	7	0
10	F	1239	0	1309	101	0
11	a	2225	0	2301	106	0
12	b	1762	0	1808	65	0
13	c	1644	0	1731	57	0
14	d	1388	0	1469	41	0
15	e	1396	0	1481	45	0
16	f	1160	0	1172	32	0
17	h	959	0	1039	15	0
18	i	1164	0	1192	45	0
19	j	944	0	1019	37	0
20	k	1153	0	1256	54	0
21	l	1079	0	1134	52	0
22	m	958	0	1011	35	0
23	n	889	0	952	29	0
24	o	938	0	1008	47	0
25	p	947	0	1028	45	0
26	q	811	0	858	30	0
27	r	1068	0	1150	45	0
28	s	720	0	803	25	0
29	t	872	0	972	18	0
30	u	657	0	693	32	0
31	v	513	0	560	24	0
32	w	818	0	870	26	0
33	x	344	0	333	7	0
34	y	452	0	472	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	z	408	0	440	14	0
All	All	100914	0	70376	3369	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 21.

The worst 5 of 3369 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)
6:7:63:PRO:CG	8:A:444:GLY:HA2	1.47	1.44
4:3:1970:C:N4	6:7:129:GLU:HG3	1.15	1.42
4:3:1081:A:C8	10:F:7:LYS:CD	2.00	1.42
4:3:1081:A:N7	10:F:7:LYS:HD2	1.19	1.42
4:3:1081:A:C8	10:F:7:LYS:HD2	1.58	1.37

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	0	45/47 (96%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
6	7	182/184 (99%)	172 (94%)	10 (6%)	0	100	100
8	A	673/675 (100%)	662 (98%)	10 (2%)	1 (0%)	48	83
9	B	27/122 (22%)	27 (100%)	0	0	100	100
9	C	94/122 (77%)	90 (96%)	4 (4%)	0	100	100
9	D	27/122 (22%)	27 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	E	27/122 (22%)	27 (100%)	0	0	100	100
10	F	159/161 (99%)	154 (97%)	4 (2%)	1 (1%)	21	58
11	a	283/285 (99%)	260 (92%)	23 (8%)	0	100	100
12	b	227/229 (99%)	213 (94%)	14 (6%)	0	100	100
13	c	208/210 (99%)	199 (96%)	9 (4%)	0	100	100
14	d	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
15	e	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
16	f	143/145 (99%)	130 (91%)	13 (9%)	0	100	100
17	h	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
18	i	142/144 (99%)	130 (92%)	12 (8%)	0	100	100
19	j	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
20	k	146/148 (99%)	137 (94%)	9 (6%)	0	100	100
21	l	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
22	m	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
23	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
24	o	113/115 (98%)	104 (92%)	9 (8%)	0	100	100
25	p	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
26	q	97/99 (98%)	83 (86%)	14 (14%)	0	100	100
27	r	137/139 (99%)	128 (93%)	9 (7%)	0	100	100
28	s	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
29	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
30	u	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
31	v	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
32	w	96/108 (89%)	88 (92%)	8 (8%)	0	100	100
33	x	42/44 (96%)	38 (90%)	4 (10%)	0	100	100
34	y	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
35	z	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
All	All	4470/4861 (92%)	4227 (95%)	241 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	A	499	GLY

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Mol	Chain	Res	Type
10	F	106	MET

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	
1	0	40/40 (100%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
6	7	172/172 (100%)	166 (96%)	6 (4%)	32	53
8	A	572/572 (100%)	567 (99%)	5 (1%)	70	77
9	B	26/98 (26%)	26 (100%)	0	100	100
9	C	84/98 (86%)	84 (100%)	0	100	100
9	D	26/98 (26%)	26 (100%)	0	100	100
9	E	26/98 (26%)	26 (100%)	0	100	100
10	F	129/129 (100%)	129 (100%)	0	100	100
11	a	241/241 (100%)	241 (100%)	0	100	100
12	b	186/186 (100%)	186 (100%)	0	100	100
13	c	182/182 (100%)	182 (100%)	0	100	100
14	d	150/150 (100%)	150 (100%)	0	100	100
15	e	153/153 (100%)	153 (100%)	0	100	100
16	f	123/131 (94%)	123 (100%)	0	100	100
17	h	102/102 (100%)	102 (100%)	0	100	100
18	i	126/126 (100%)	126 (100%)	0	100	100
19	j	103/103 (100%)	103 (100%)	0	100	100
20	k	123/123 (100%)	123 (100%)	0	100	100
21	l	113/113 (100%)	113 (100%)	0	100	100
22	m	105/105 (100%)	105 (100%)	0	100	100
23	n	96/99 (97%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	o	101/101 (100%)	101 (100%)	0	100	100
25	p	100/100 (100%)	100 (100%)	0	100	100
26	q	90/90 (100%)	90 (100%)	0	100	100
27	r	116/116 (100%)	116 (100%)	0	100	100
28	s	82/82 (100%)	82 (100%)	0	100	100
29	t	96/96 (100%)	96 (100%)	0	100	100
30	u	69/69 (100%)	69 (100%)	0	100	100
31	v	58/58 (100%)	58 (100%)	0	100	100
32	w	87/95 (92%)	87 (100%)	0	100	100
33	x	41/41 (100%)	41 (100%)	0	100	100
34	y	48/48 (100%)	45 (94%)	3 (6%)	16	38
35	z	47/47 (100%)	47 (100%)	0	100	100
All	All	3899/4148 (94%)	3885 (100%)	14 (0%)	81	83

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	A	23	LYS
8	A	89	THR
34	y	52	ARG
34	y	47	MET
34	y	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
19	j	76	HIS
27	r	112	ASN
23	n	38	HIS
24	o	80	GLN
27	r	132	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	3	2875/2893 (99%)	844 (29%)	34 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	4	103/108 (95%)	42 (40%)	3 (2%)
7	8	49/76 (64%)	22 (44%)	1 (2%)
All	All	3027/3077 (98%)	908 (29%)	38 (1%)

5 of 908 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	3	12	A
4	3	14	U
4	3	15	A
4	3	20	C
4	3	27	U

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	3	2506	C
5	4	54	U
4	3	2668	A
4	3	2862	U
7	8	57	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 ⓘ

There are no chain breaks in this entry.

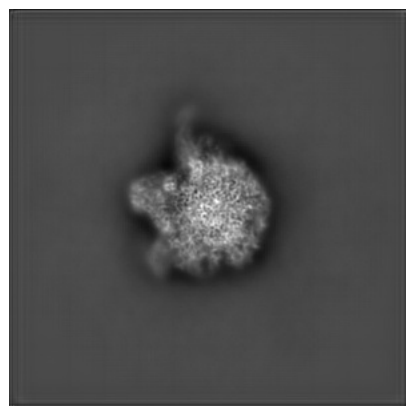
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53627. These allow visual inspection of the internal detail of the map and identification of artifacts.

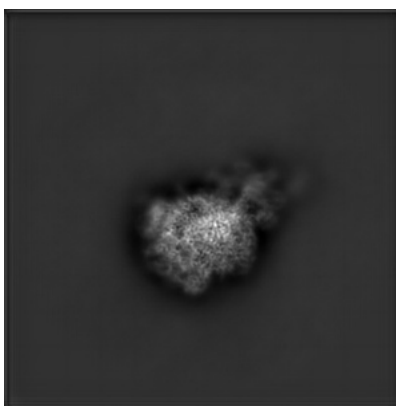
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

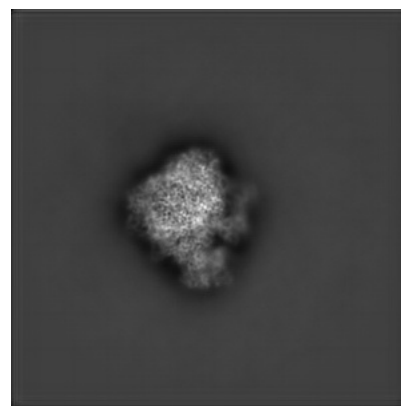
6.1.1 Primary map



X

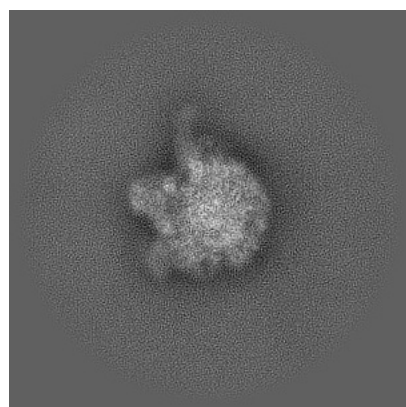


Y

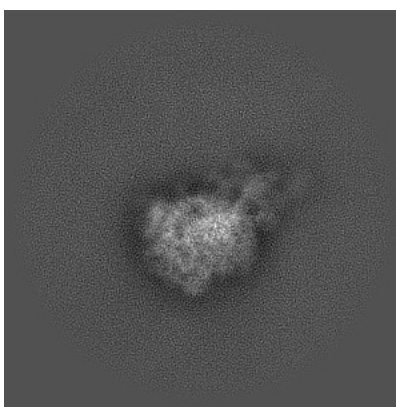


Z

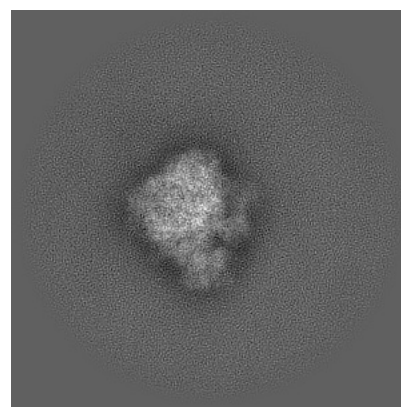
6.1.2 Raw map



X



Y

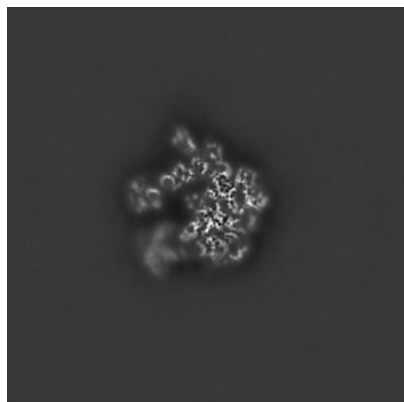


Z

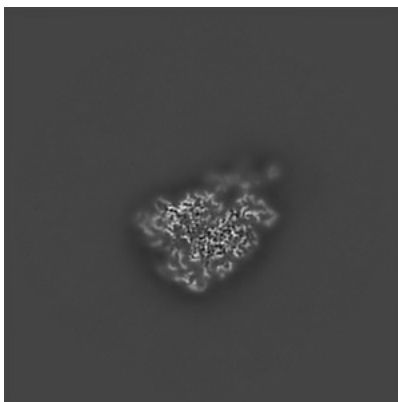
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

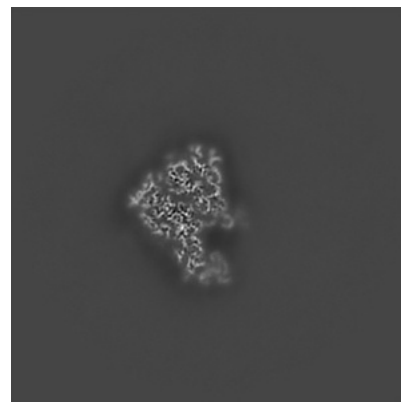
6.2.1 Primary map



X Index: 150

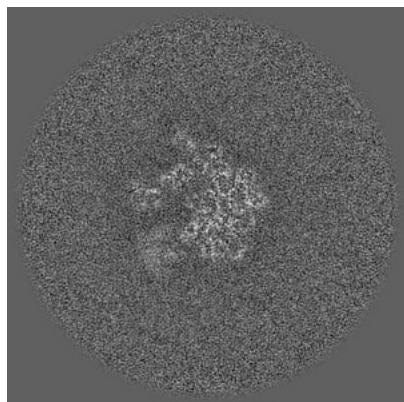


Y Index: 150

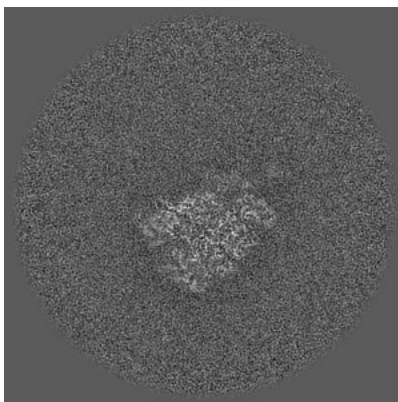


Z Index: 150

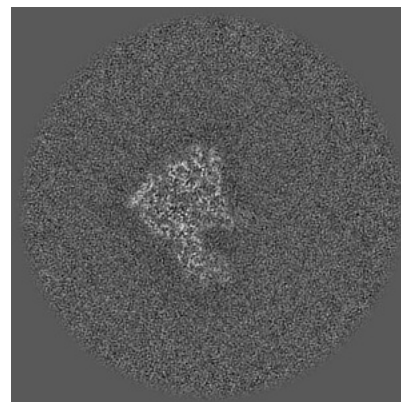
6.2.2 Raw map



X Index: 150



Y Index: 150

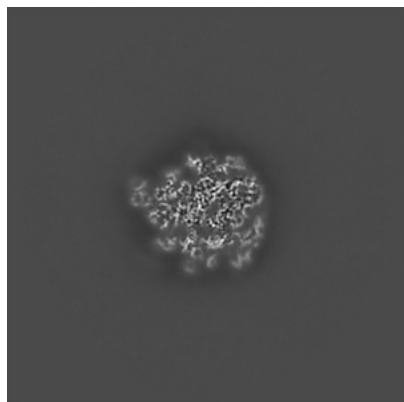


Z Index: 150

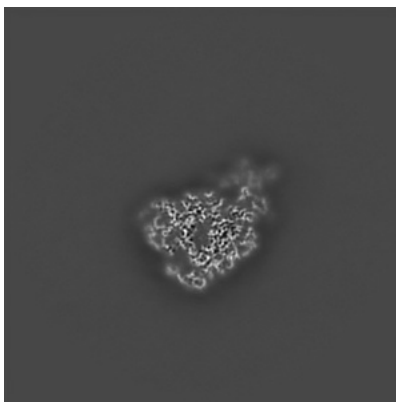
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

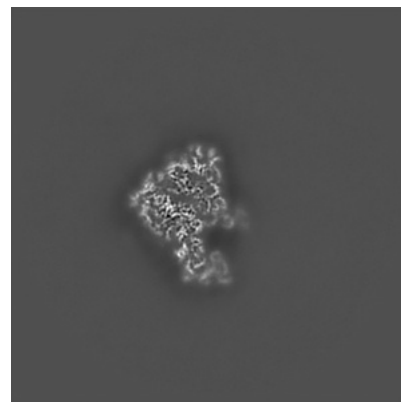
6.3.1 Primary map



X Index: 131

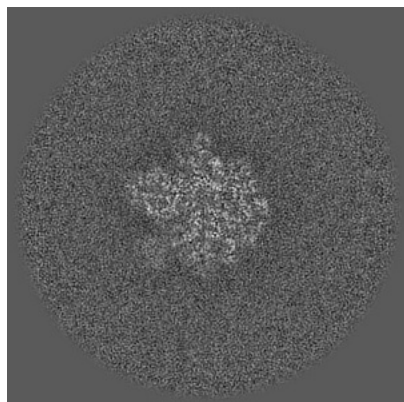


Y Index: 154

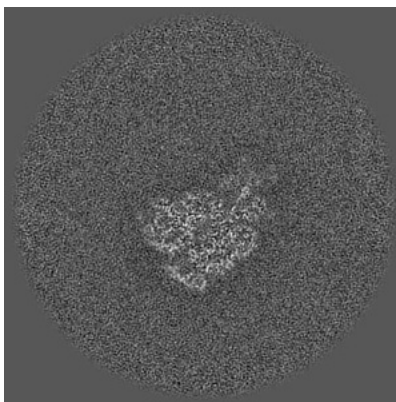


Z Index: 151

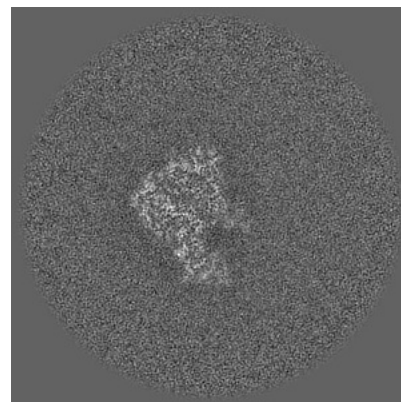
6.3.2 Raw map



X Index: 140



Y Index: 153

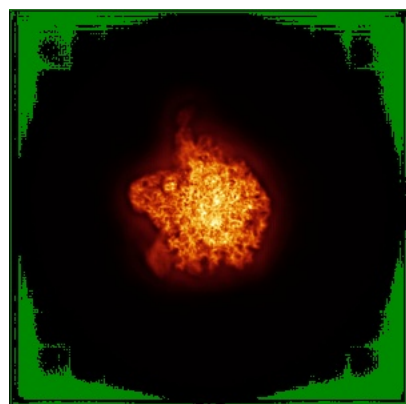


Z Index: 151

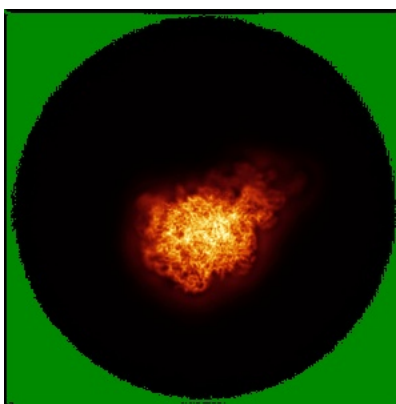
The images above show the largest variance slices of the map in three orthogonal directions.

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

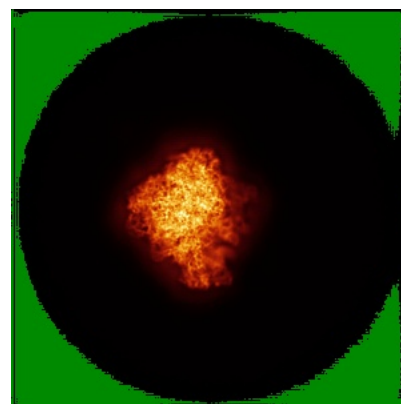
6.4.1 Primary map



X

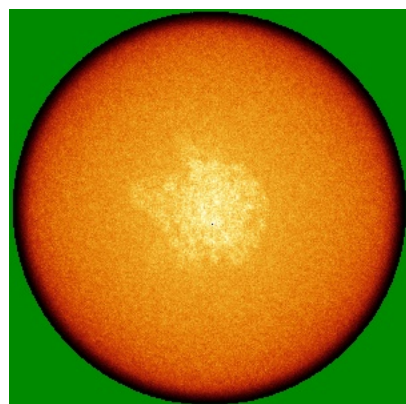


Y

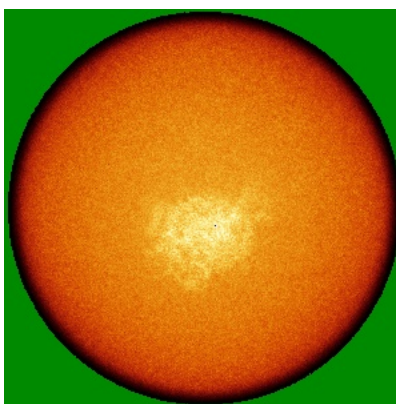


Z

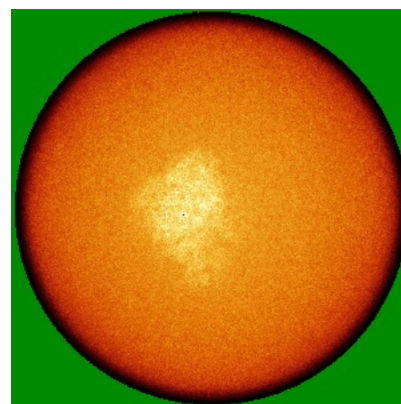
6.4.2 Raw map



X



Y

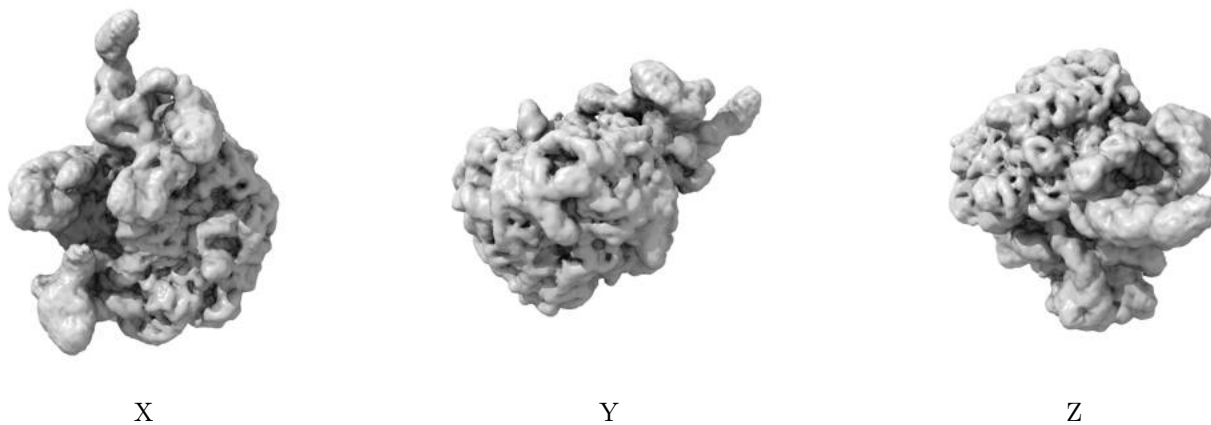


Z

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.

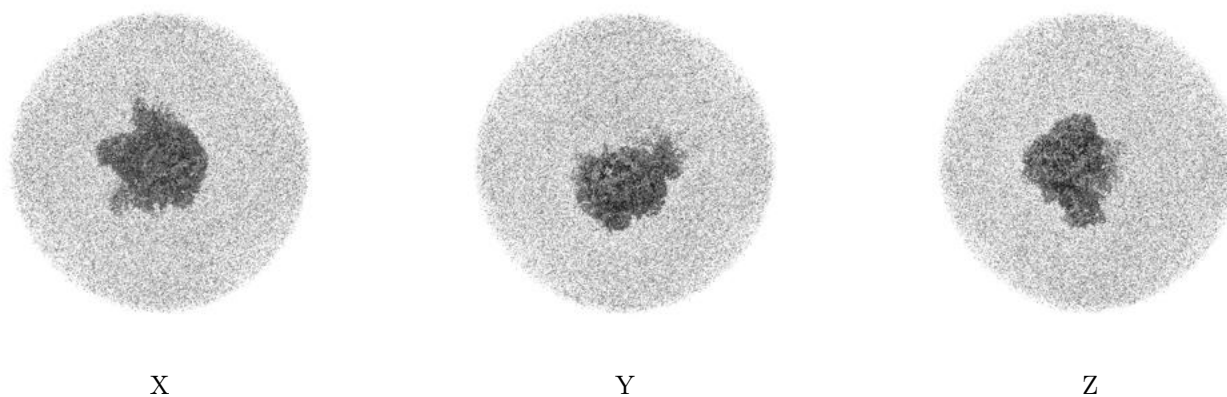
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.000517. 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.

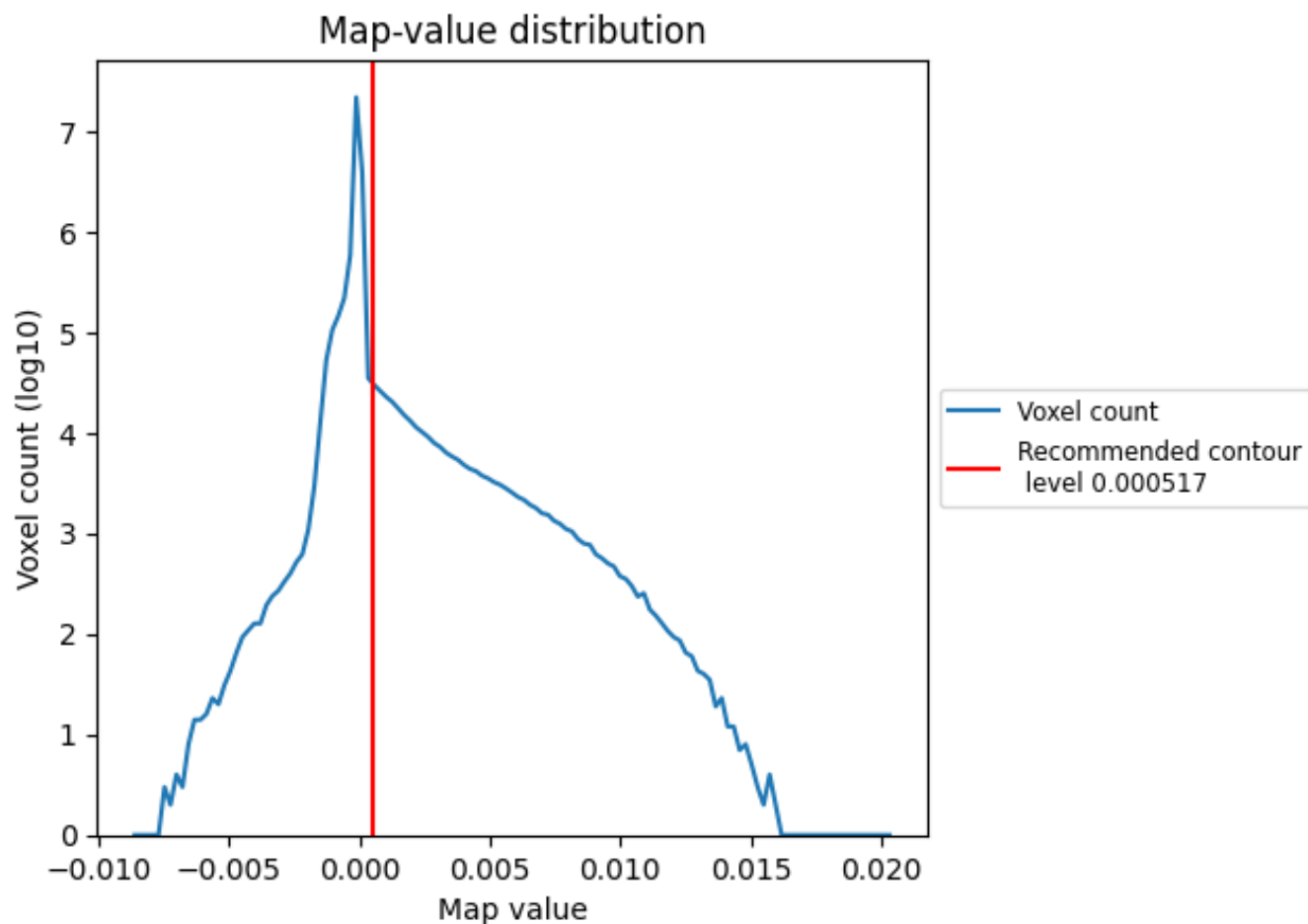
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

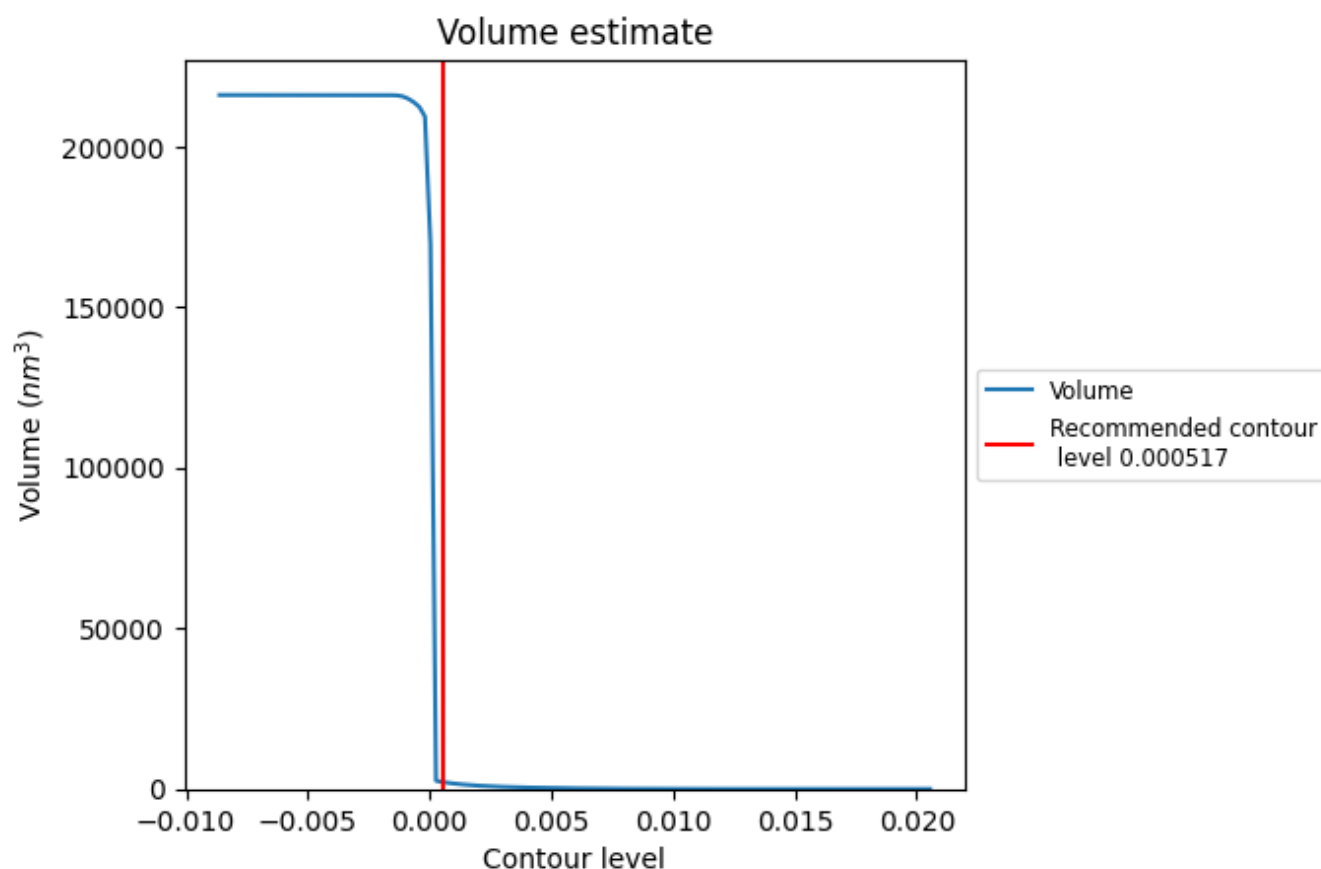
This section contains the results of statistical analysis of the map.

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.

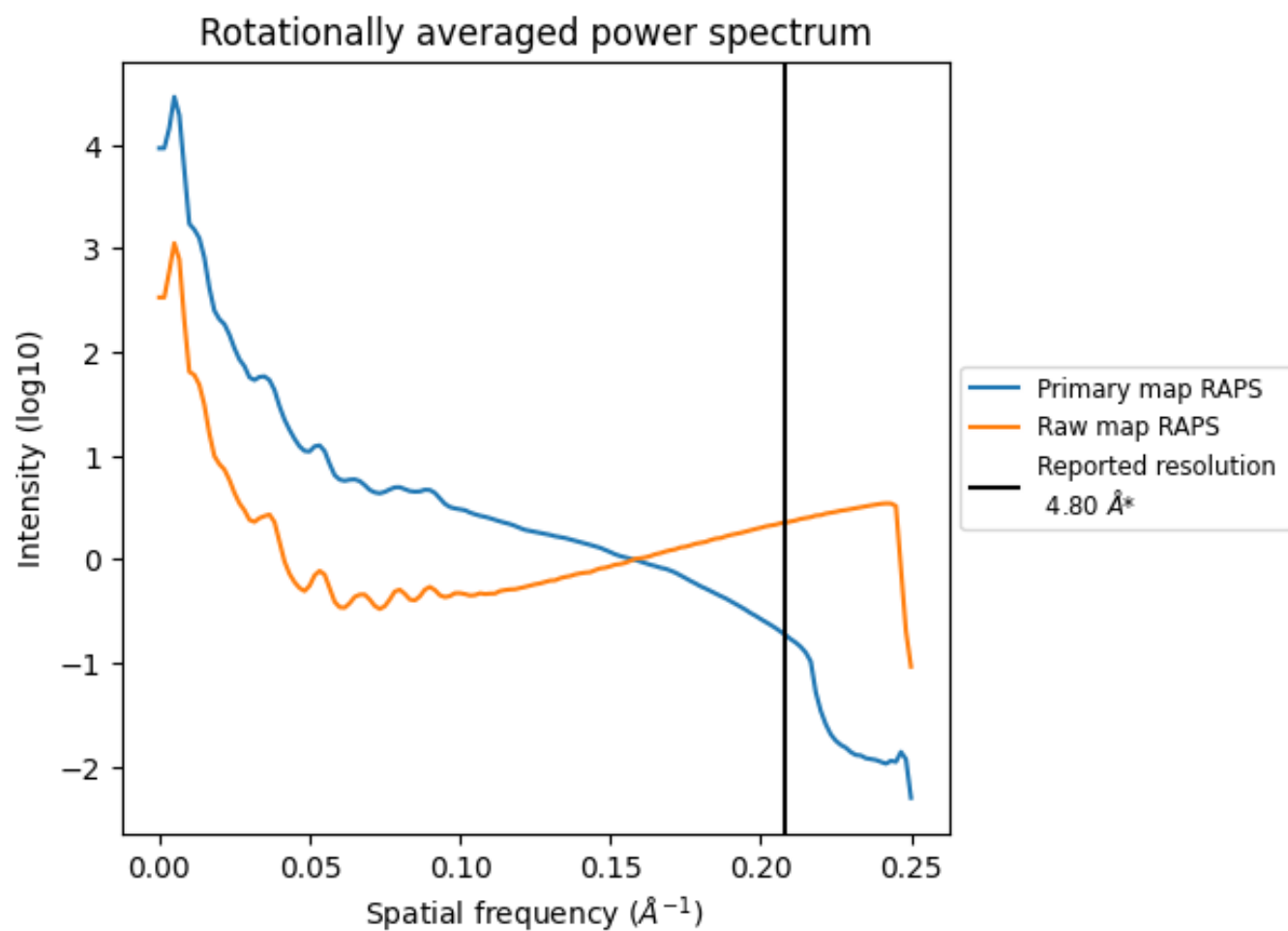
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2161 nm^3 ; this corresponds to an approximate mass of 1952 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 ⓘ

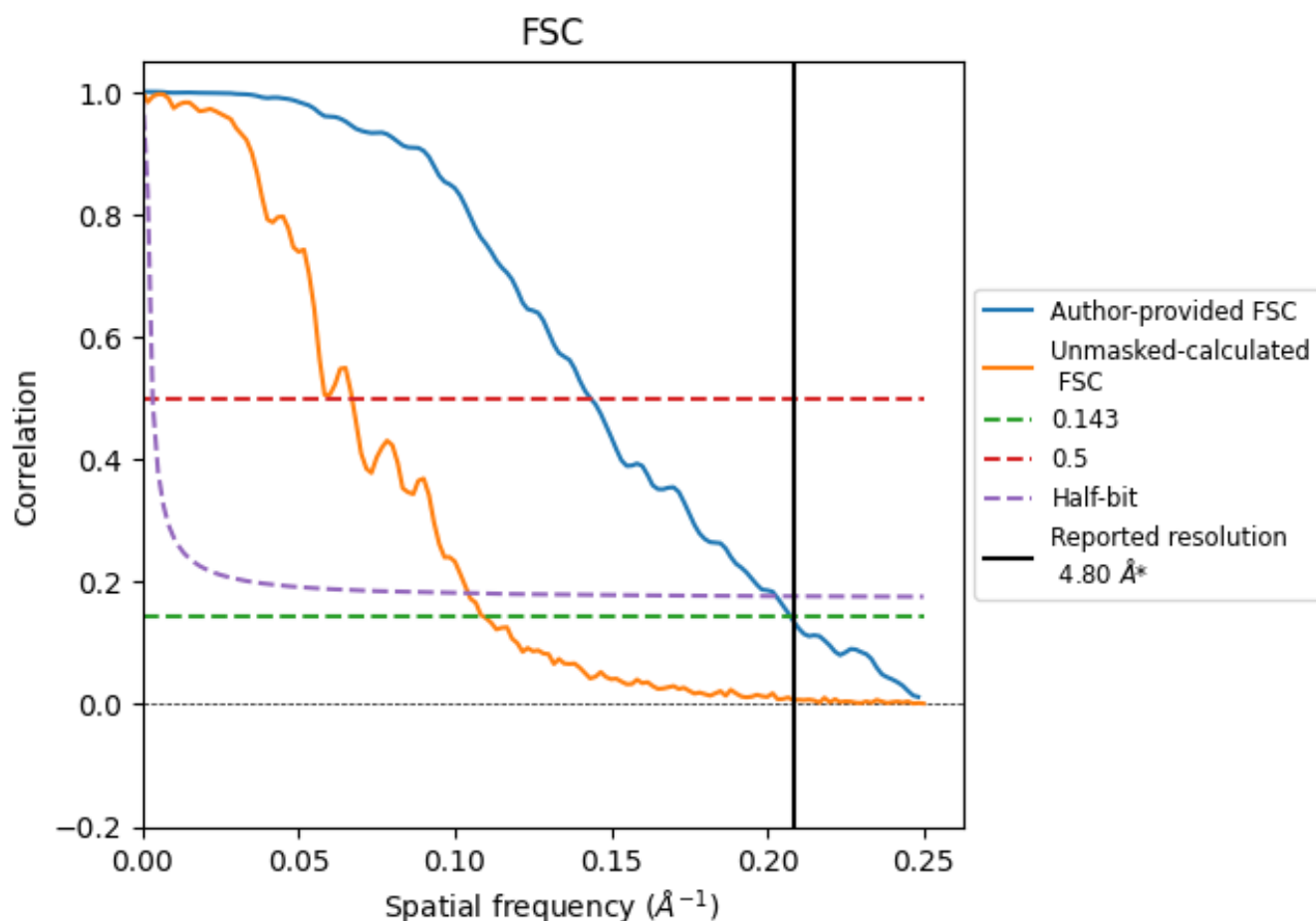


*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

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 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

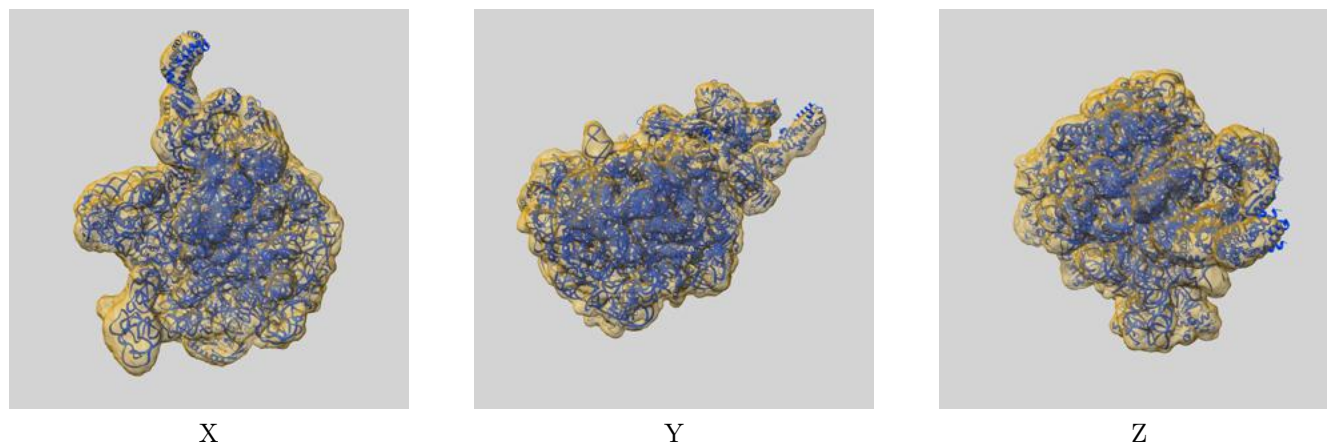
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	4.82	6.98	4.93
Unmasked-calculated*	9.16	14.93	9.59

*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 9.16 differs from the reported value 4.8 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53627 and PDB model 9SKE. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



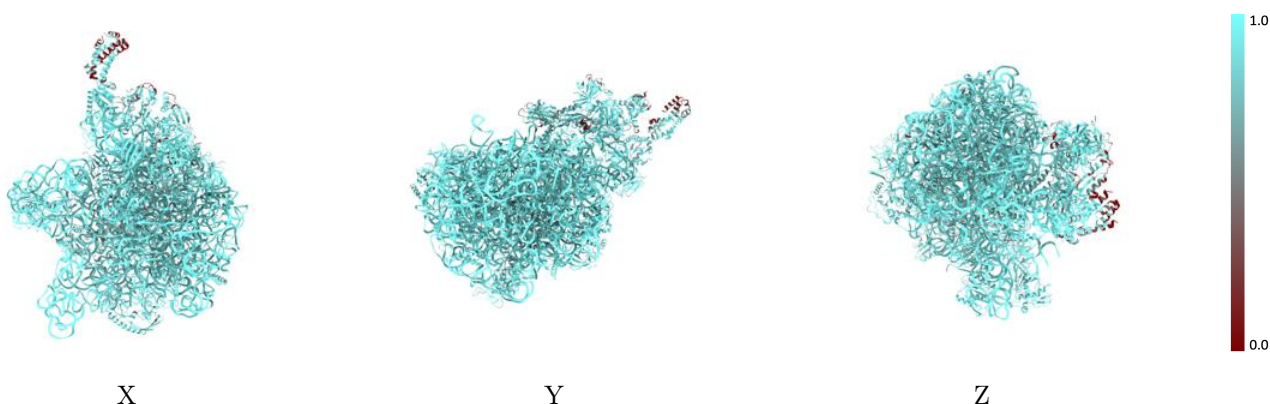
The images above show the 3D surface view of the map at the recommended contour level 0.000517 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



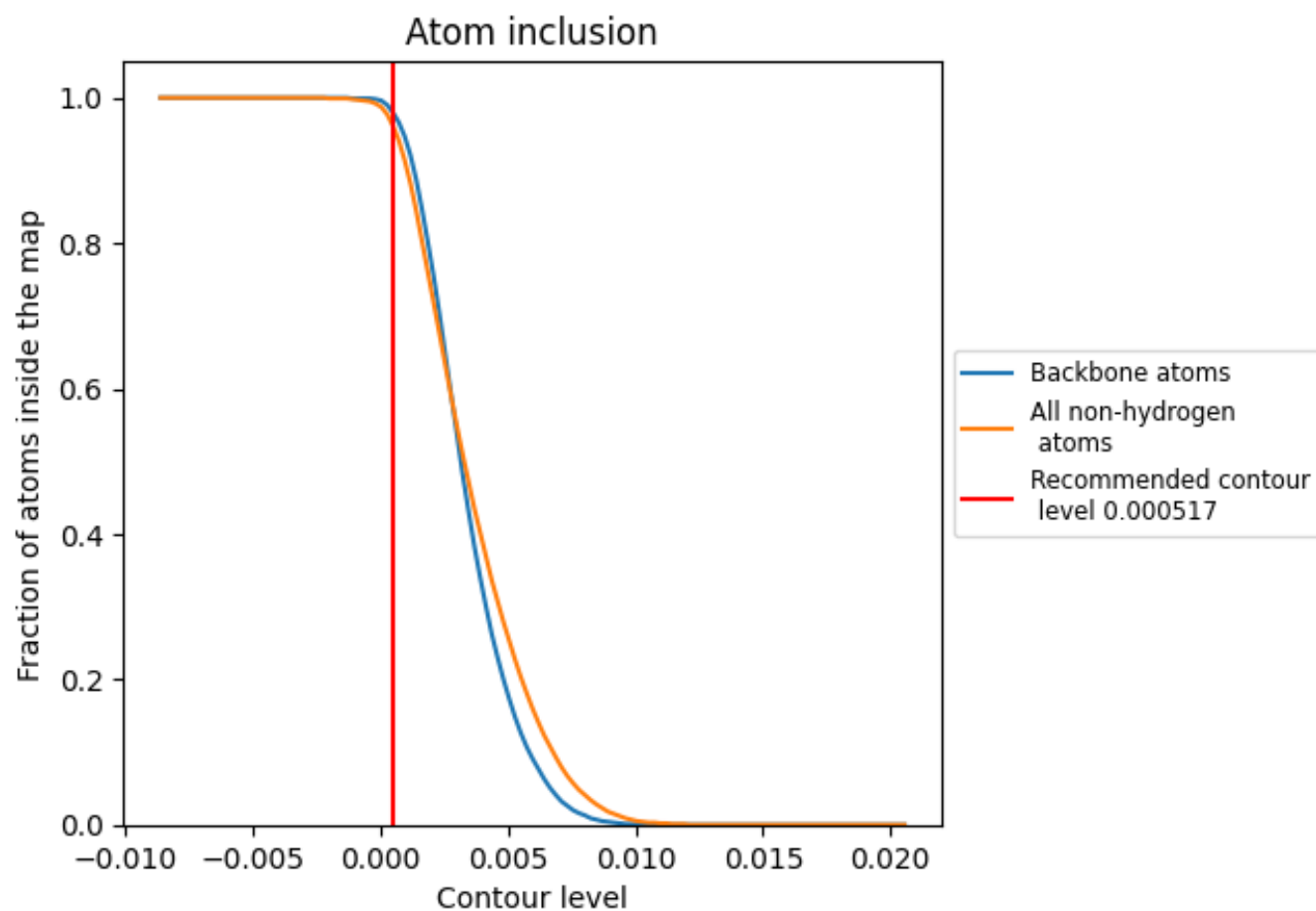
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.000517).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.000517) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9590	 0.1850
0	 0.8790	 0.1540
1	 0.9140	 0.1470
2	 0.9360	 0.1010
3	 0.9880	 0.2220
4	 0.9990	 0.2050
7	 0.8560	 0.1150
8	 0.9710	 0.0980
A	 0.8680	 0.0970
B	 0.8310	 0.0690
C	 0.7230	 0.0730
D	 0.6280	 0.0920
E	 0.3550	 0.0680
F	 0.8720	 0.1040
a	 0.9360	 0.1380
b	 0.9230	 0.1420
c	 0.9100	 0.1360
d	 0.9700	 0.1260
e	 0.9570	 0.1280
f	 0.8990	 0.0970
h	 0.9220	 0.0920
i	 0.9220	 0.1470
j	 0.9180	 0.1560
k	 0.9420	 0.1480
l	 0.9170	 0.1280
m	 0.8970	 0.1670
n	 0.9760	 0.1560
o	 0.9520	 0.1160
p	 0.8810	 0.1140
q	 0.9440	 0.1580
r	 0.9300	 0.1530
s	 0.9420	 0.1620
t	 0.9020	 0.1040
u	 0.9020	 0.1270
v	 0.9600	 0.1450



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Chain	Atom inclusion	Q-score
w	 0.9550	 0.1440
x	 0.9850	 0.1280
y	 0.9350	 0.1320
z	 0.9550	 0.1030