



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 05:48 AM UTC

PDB ID : 7Y41 / pdb_00007y41
EMDB ID : EMD-33599
Title : Mycobacterium smegmatis 50S ribosomal subunit from Log Phase of growth
Authors : Sengupta, J.; Baid, P.
Deposited on : 2022-06-13
Resolution : 4.10 Å (reported)
Based on initial model : 5O60

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:

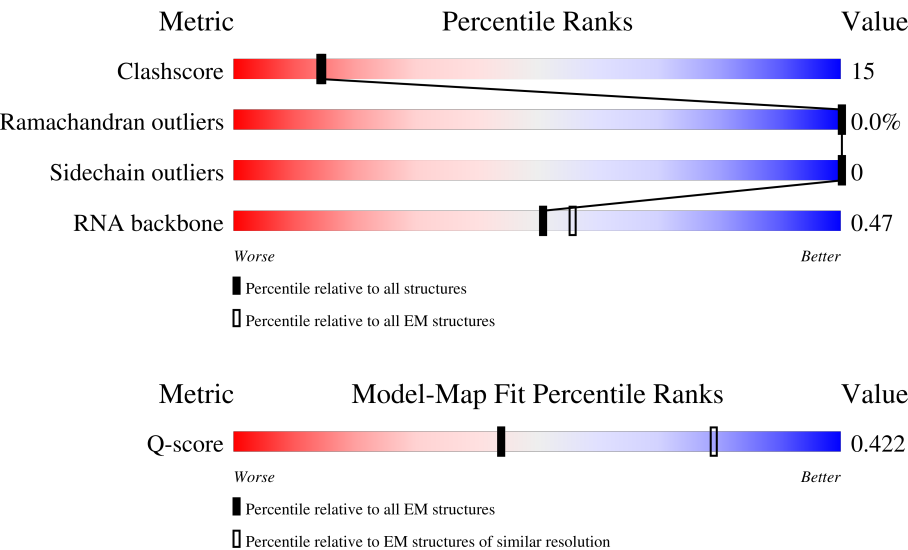
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.10 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.



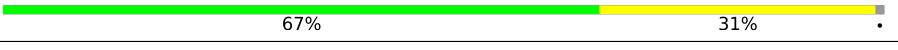
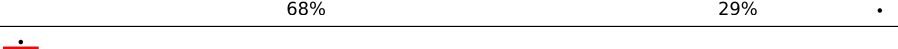
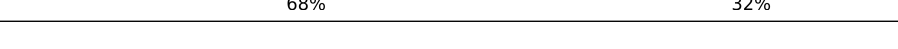
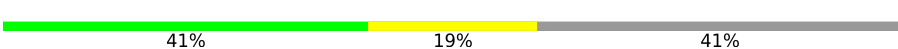
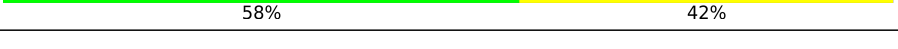
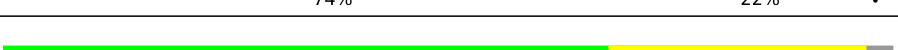
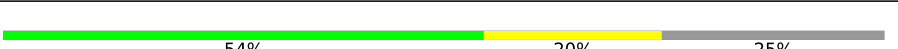
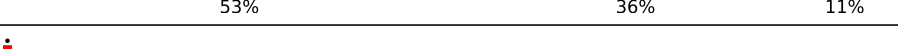
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	3	24	33% 71% 25% .
2	A	3120	40% 47% 13%
3	B	118	48% 42% 9%

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Mol	Chain	Length	Quality of chain
4	C	278	
5	D	217	
6	E	215	
7	F	187	
8	G	179	
9	I	175	
10	J	142	
11	K	147	
12	L	122	
13	M	147	
14	N	138	
15	O	199	
16	P	127	
17	Q	113	
18	R	129	
19	S	103	
20	T	153	
21	U	100	
22	V	105	
23	W	215	
24	X	88	
25	Y	64	
26	Z	77	
27	a	61	
28	b	57	

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Mol	Chain	Length	Quality of chain
29	c	55	
30	d	47	
31	e	64	
32	f	37	
33	g	75	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 97056 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 50S ribosomal subunit bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	274	Total	C	N	O	S	0	0
			2105	1295	437	369	4		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 29 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	63	Total	C	N	O		0	0
			502	302	115	85			

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
34	A	386	Total	Mg	0
			386	386	
34	B	9	Total	Mg	0
			9	9	

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Mol	Chain	Residues	Atoms		AltConf
34	C	5	Total 5	Mg 5	0
34	E	1	Total 1	Mg 1	0
34	F	1	Total 1	Mg 1	0
34	M	1	Total 1	Mg 1	0
34	N	2	Total 2	Mg 2	0
34	T	1	Total 1	Mg 1	0
34	e	1	Total 1	Mg 1	0

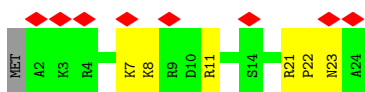
- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
35	Y	1	Total 1	Zn 1	0
35	c	1	Total 1	Zn 1	0
35	f	1	Total 1	Zn 1	0
35	g	1	Total 1	Zn 1	0

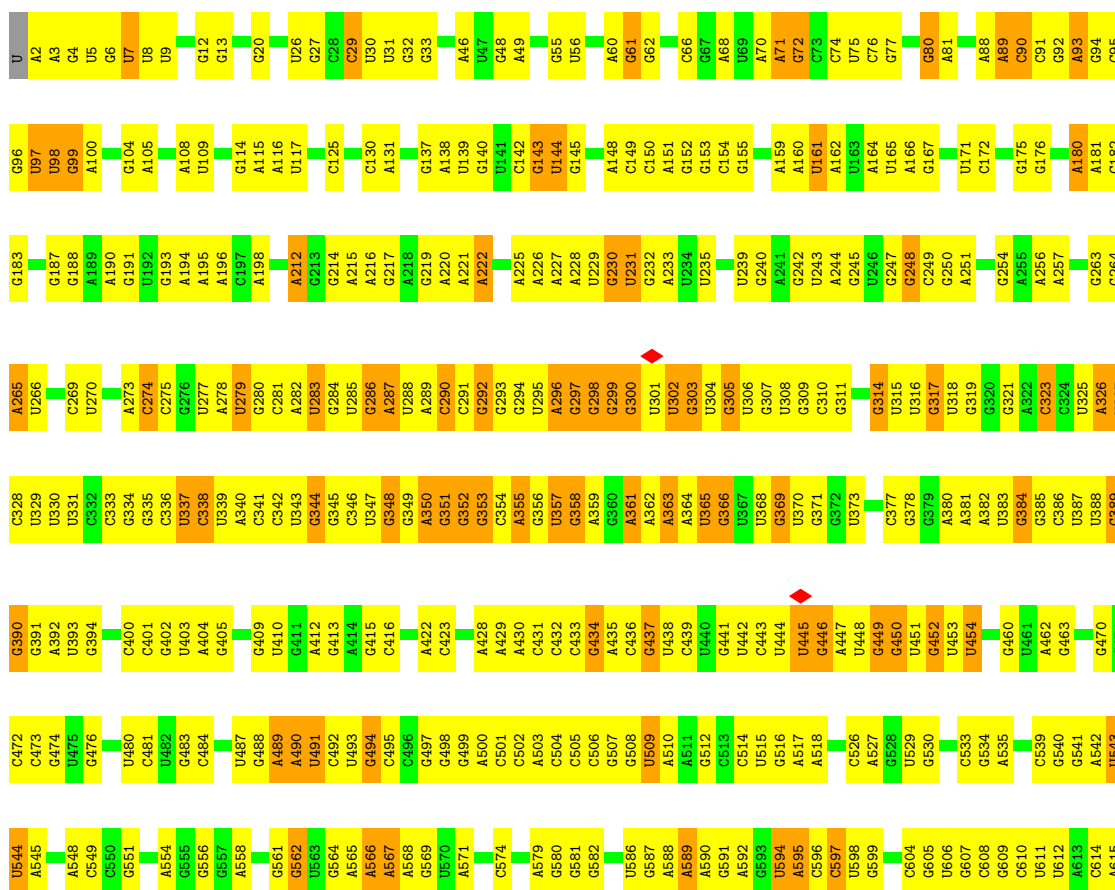
3 Residue-property plots

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: 50S ribosomal subunit bL37

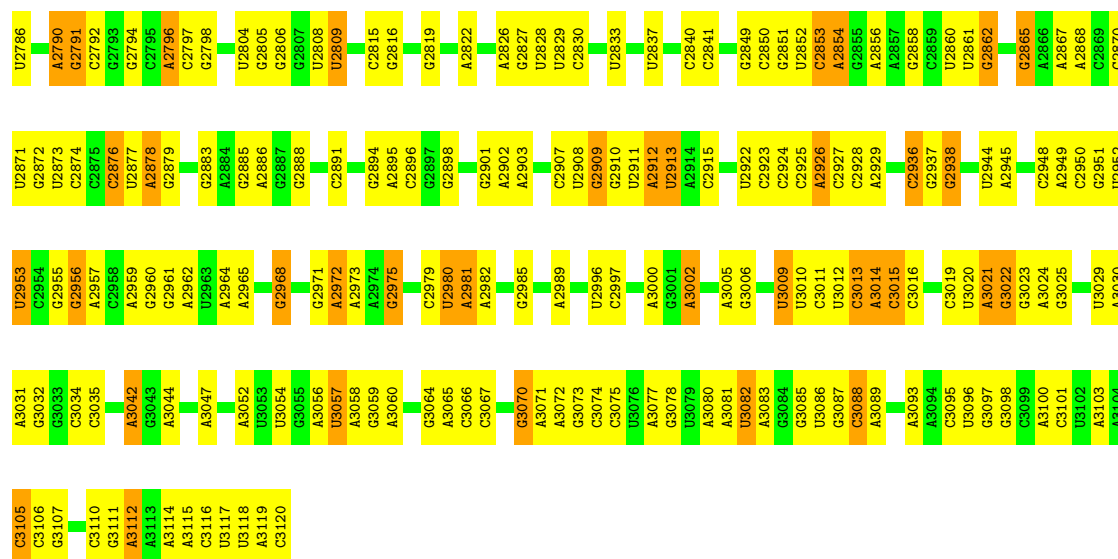


- Molecule 2: 23S ribosomal RNA



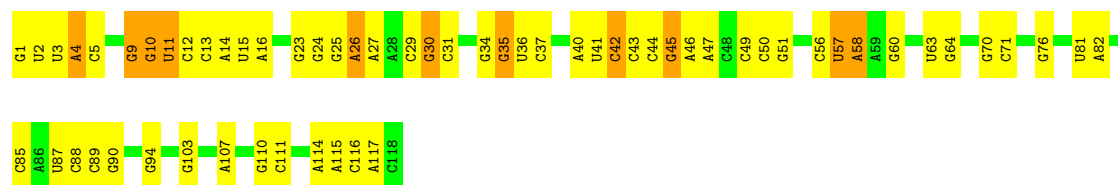
G1604	G1605	G1606	C1607	U1608	G1609	C1610	A1611	U1612	G1613	G1614	G1615	A1616	C1617	G1618	U1619	G1620	C1621	G1622	U1623	G1624	G1625	G1626	U1627	A1628	G1629	U1630	A1631	G1632	U1633	G1634	A1635	A1636	G1637	C1638	A1639	A1640	U1641	G1647	C1648	G1649	G1650	C1651	A1652	G1653	G1654	A1655	G1656	U1657	U1658	U1659	C1660	C1672	A1673					
U1544	C1545	A1546	G1547	C1548	G1549	G1550	U1551	A1552	C1553	U1554	A1555	A1556	C1557	C1558	U1559	U1560	C1561	C1562	A1563	U1564	A1565	A1566	C1567	C1568	A1569	C1570	C1571	U1572	U1573	G1574	A1575	C1576	C1577	G1578	C1579	A1580	C1581	C1582	U1583	U1584	U1585	C1586	C1587	G1588	U1589	G1590	U1591	U1592	U1593	G1594	G1595	C1596	U1597	U1598	U1599	G1600	G1601	U1602
C1472	G1473	G1476	C1477	G1478	G1479	A1480	A1481	C1482	C1485	G1486	U1487	A1488	A1489	A1493	U1494	A1499	A1500	U1624	C1501	G1502	A1566	C1567	G1504	U1505	U1506	G1507	A1508	U1509	A1510	U1511	U1512	G1516	U1517	A1518	G1522	U1523	G1524	U1525	A1526	U1527	C1528	U1529	G1530	C1531	G1532	U1533	C1534	C1535	U1536	U1537	U1538	G1539	U1540	G1541	A1542	A1543		
A1387	U1388	U1389	G1392	C1393	A1394	A1395	G1396	U1397	G1398	A1399	G1400	A1401	U1406	G1407	C1410	G1411	C1412	C1501	C1413	G1414	A1415	A1416	C1430	U1431	G1434	A1435	C1436	U1437	G1438	C1441	A1442	G1443	U1444	C1445	G1446	G1447	C1448	C1449	C1450	A1451	G1452	G1453	G1454	U1455	G1456	G1462	C1465	C1466	U1467	A1468	A1469							
C1298	G1302	U1303	C1311	G1312	U1313	U1314	C1315	U1316	U1317	C1318	U1325	U1326	U1327	U1328	U1329	A1328	G1329	G1332	C1333	C1334	G1335	C1336	U1338	G1339	G1343	A1344	G1345	U1346	G1347	G1348	U1349	G1350	G1351	A1352	G1353	G1354	G1355	U1356	G1359	A1369	U1370	G1371	C1372	A1373	G1374	A1377	U1378	C1379	A1380	G1384	C1385	G1386						
A1163	A1164	G1165	C1166	U1167	A1168	A1169	C1170	C1171	A1172	G1173	G1174	A1175	G1176	U1177	U1178	U1179	G1180	G1181	C1182	U1183	U1184	A1185	G1186	A1187	A1188	G1189	C1190	A1191	G1192	C1193	C1194	A1195	C1196	C1197	C1198	U1199	U1200	G1201	A1202	A1203	A1204	G1205	A1206	G1207	U1208	G1209	C1210	G1211	U1212	A1213	U1214	U1215	A1216	U1219	C1220	A1221	C1222	U1223
G1086	G1087	U1088	C1089	G1090	A1091	G1092	A1097	A1098	A1099	C1100	A1101	C1102	C1103	C1104	C1105	G1114	A1118	A1119	C1122	C1125	U1126	A1127	A1128	G1129	C1130	U1131	U1132	G1133	U1137	A1138	A1139	G1140	U1141	G1142	G1143	A1144	A1145	A1146	A1147	G1148	U1151	G1152	U1153	G1154	C1155	A1156	G1157	U1158	C1159	C1161	G1162							
C1004	A1005	G1006	G1007	G1008	U1009	U1010	A1011	C1012	U1013	G1014	A1015	C1016	G1017	U1018	C1019	A1020	A1025	C1027	U1028	C1029	A1033	U1040	A1041	A1042	G1043	U1044	C1045	C1046	A1047	A1048	G1049	U1052	G1053	U1060	G1063	A1064	C1065	G1066	G1070	G1071	A1074	U1075	A1076	C1077	G1078	C1081	U1084	G1085										
C929	C932	G933	A934	C939	U942	U943	A944	G945	G946	U947	G948	C949	A950	G951	U954	C955	G956	C957	A958	U959	G960	U961	C964	U965	U966	G967	C971	A972	G973	A974	U975	A976	G977	A978	G979	C980	U981	A982	G986	A987	G993	A994	U995	G996	C997	G998	C999	C1000	C1001	C1002	A1003							
G840	G841	G844	C845	C846	C847	G848	A854	C855	U856	U857	A858	U862	G863	C868	U869	G870	G871	G872	G875	A876	U877	G878	G885	G886	C887	U888	G889	G890	G891	A897	A898	G899	A908	A909	C910	U911	C912	A917	U918	G919	G920	C921	U922	G923	G924	C927	U928											
G757	A758	U759	G760	G761	U762	G763	U764	G765	U766	U767	G768	U772	G773	U774	U775	G776	U777	G778	G784	G789	G794	A800	U801	C802	U803	A804	C805	C806	C807	A808	C812	C813	G819	A820	G821	G822	C823	A828	U829	A830	A831	G832	C833	C836	C837	U838	U839											
U689	G690	U691	C692	G693	G694	G695	A696	A701	A702	G706	G707	G708	C639	G640	U641	G642	G643	G644	A671	G716	C717	G718	A721	G722	C723	U724	A725	U726	A727	G728	G729	G730	A731	G732	U733	C734	U735	G736	A737	U738	U739	A740	G743	G744	G745	U746	A747	U748	C749	A681	C682	U674						
A616	U617	C618	C619	G620	U621	C622	U630	C631	G635	U636	G637	U638	G639	G640	U641	G642	G643	G644	A671	G716	C717	G718	A721	G722	C723	U724	A725	U726	A727	G728	G729	G730	A731	G732	U733	C734	U735	G736	A737	U738	U739	A740	G743	G744	G745	U746	A747	U748	C749	A681	C682	U674						

A2700	A2609	C2537	C2450	G2382	G2322	C2245	U2164	U2091	G2014	G1845	G1746	G1674
U2701	G2613	A2538	G2458	U2363	G2323	U2246	C2165	U2092	U2015	A1848	A1750	U1675
A2702	G2614	G2539	G2459	G2384	A2324	A2247	C2166	G2093	C2016	G1677	G1676	G1676
G2705	U2615	G2540	G2460	G2385	U2325	C2248	U2167	G2094	C2017	A1850	C1752	U1678
A2616	G2616	U2541	G2461	U2386	A2326	A2249	U2168	G2095	G2018	G1851	C1753	U1679
G2710	U2543	G2542	G2462	U2387	G2327	A2250	G2169	G2096	A2019	A1852	G1754	A1680
G2621	U2544	G2388	G2463	G2388	G2328	G2251	U2170	G2097	A2020	A1853	A1755	U1681
C2622	U2464	U2389	A2465	U2390	U2330	U2252	C2171	U2098	G2024	A1854	G1756	
A2623	A2466	G2391	A2465	A2391	U2331	A2254	A2176	G2104	C2025	A1855	U1757	G1688
G2718	G2466	A2392	A2467	A2393	U2332	A2255	A2106	G2105	A2026	A1858	G1758	U1689
G2719	U2468	A2394	U2468	A2394	U2334	A2257	U2180	G2107	A2029	A1859	A1759	A1690
G2627	U2469	U2395	U2469	U2395	G2335	U2261	C2181	A2108	C2030	U1864	G1761	A1691
G2629	A2551	U2396	A2470	U2396	G2336	C2262	U2182	U2111	G2031	A1865	C1762	G1692
A2630	G2553	A2471	A2471	A2397	U2337	C2263	C2186	U2112	A2032	A1866	G1763	
G2631	U2554	C2472	C2472	C2397	G2338	G2267	U2187	U2113	U2033	A1868	A1764	U1697
A2635	G2555			C2398	A2337	G2268	U2188	A2114	G2034	A1869	A1765	A1698
A2727	U2481	A2400	U2481	A2399	G2338	C2267	C2188		U2035	U1869	G1768	G1701
U2728	U2482	C2400	U2482	C2400	G2339	G2268	G2189	C2118	G2040	U1871	A1702	A1702
G2729	G2483	U2401	G2483	U2401	A2340	C2269	A2190	C2119	G2041	A1872	G1703	G1703
G2737	C2484	C2402	C2484	C2402	A2341	C2270	C2191		A2042	A1873	U1704	U1704
G2738	G2485	U2403	G2485	U2403	A2342	G2271	G2192	A2124	C2043	C1874	C1782	C1782
C2739	U2486	G2404	U2486	G2404	G2343	G2272	A2193	A2125		U1875	G1783	G1706
C2644	C2487	A2405	C2487	A2405	G2344	G2276	A2194	C2126	A2046	A1876	C1784	A1708
A2742		U2406		U2406	U2345	G2277	U2195		G2047	A1877	G1785	U1709
U2743	A2490	C2407	A2490	C2407	G2346	A2278	G2196	C2129	C2048		G1786	U1710
C2744	A2491	G2408	A2491	G2408	G2347	C2279		G2130	G2049	A1883	A1787	A1710
A2649	A2492	U2409	A2492	U2409	G2348	C2280	C2206	G2131	C2050	U1884	U1788	G1711
G2749	G2493	U2410	G2493	U2410	A2349		U2207	U2132	U2051	A1885	A1789	U1713
G2750	A2497	U2411	A2497	U2411	G2350		C2211	G2133	G2052	A1886	A1790	A1714
G2753	G2503	G2413	G2503	G2413	C2352	A2284	A2212	U2135		A1887	A1791	U1715
G2754	G2504	G2414	G2504	G2414	U2353	G2285		A2136	U2058	U1888	A1792	A1716
A2755	C2507	G2415	C2507	G2415	G2354	A2286	G2216	A2137	C2060	C1971	U1889	U1717
G2756		G2416		G2416	U2355	C2287	U2217	U2139	U2061	A1891	G1795	C1718
C2757	A2510	C2417	A2510	C2417	G2356	C2288	G2218			G1892	U1796	G1719
A2758	A2511	U2418	A2511	U2418	A2357	C2289	U2219	U2141	A2064	C1893	U1798	G1720
G2759	A2512	G2419	A2512	G2419	G2358	C2291	C2220	A2142	A2065	A1896	G1800	C1722
G2760	G2513	U2420	G2513	U2420	C2359	A2294	A2221	A2143	G2066	A1897	U1799	C1723
U2761	G2514	A2421	G2514	A2421	C2360	C2295	A2222	C2144	G2067	U1906	G1801	U1724
A2672	U2515	A2422	U2515	A2422	G2361	C2296	C2223	C2145	U2068	G1905	G1802	G1725
C2763	G2516	C2423	G2516	C2423	U2362	U2297	C2224	U2147	U2069	A1803	A1803	C1726
C2764	C2517		C2517		A2363	U2298	A2225	A2146	A2070	G1804	G1804	A1727
A2765	U2518	G2427	U2518	G2427	C2364	C2304	A2227	U2148	G2072	G1906	A1806	U1728
U2771	A2523	A2434	A2523	A2434	A2365	C2305	A2227	C2149		U1907	C1807	U1730
G2772	C2524	U2435	C2524	U2435	C2366	A2305		U2150	G2075	A1908	A1808	U1731
C2775	G2525	U2436	G2525	U2436	G2367	U2308	U2231	A2151	C2079	A1919	U1809	U1732
U2776	U2526	U2437	U2526	U2437	G2367	U2309	C2232	G2152	C2080	G1920	C1822	C1733
U2777	G2527	C2438	G2527	C2438	C2368	G2310	G2233	A2153	G2081	G1921	C1823	U1735
U2778	G2528	G2439	G2528	G2439	C2369	G2311	G2234	G2154	A2084	G1922	A1828	A1737
U2779	A2529	G2440	A2529	G2440	G2370	G2316		U2155	C2085	G1923		G1738
C2780	G2530	U2441	G2530	U2441	G2371	G2317	A2237	G2157	C2086		A1832	A1739
G2781	G2531	U2442	G2531	U2442	U2372	G2318	A2238	A2160	C2087	C1927	A1844	U1745
G2694	G2532	U2443	G2694	U2443	U2373	U2318	A2239	A2161	C2088	C1928		
C2782	C2533	C2444	C2533	C2444	U2374	G2319	A2243	A2162	C2089	C2013		
C2783	A2534	A2445	A2534	A2445	U2375	G2320	C2243	A2163				
C2697	G2535	G2446	G2607	G2446	G2376	U2321	A2244					
A2785	G2608	A2449	U2536	A2449	G2377							
					U2378							
					G2379							
					G2380							
					A2381							



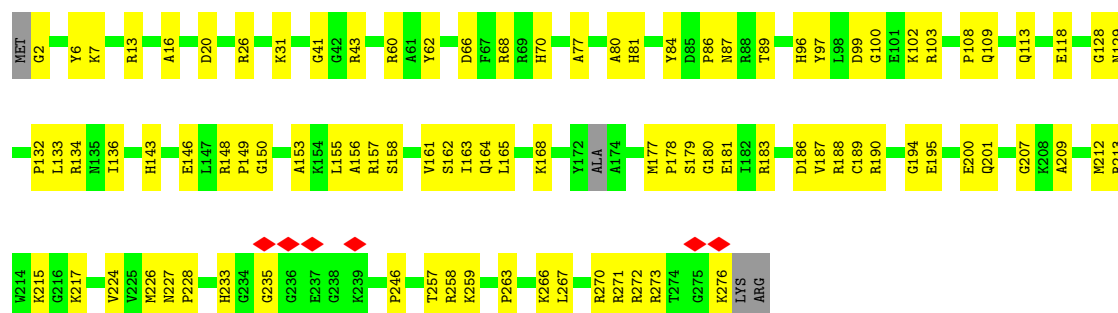
• Molecule 3: 5S ribosomal RNA

Chain B: 48% 42% 9%



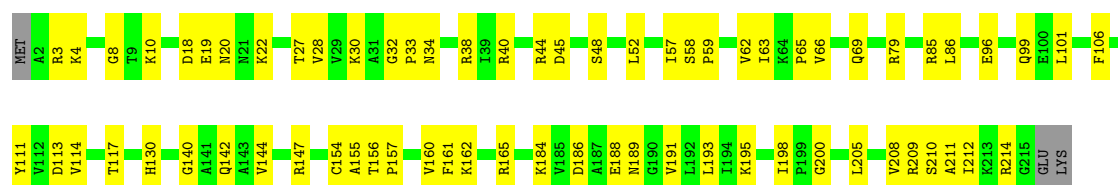
• Molecule 4: 50S ribosomal protein L2

Chain C: 65% 33% 2%



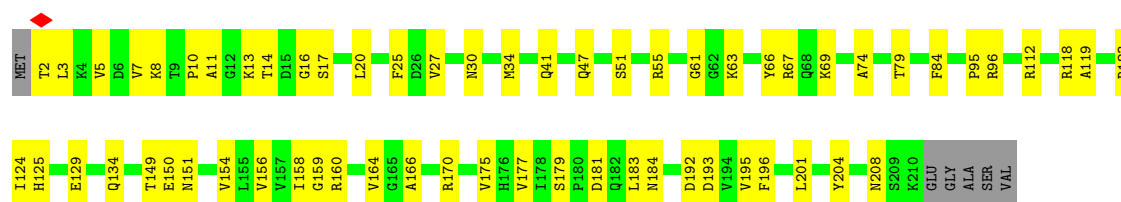
• Molecule 5: 50S ribosomal protein L3

Chain D: 67% 31% 2%



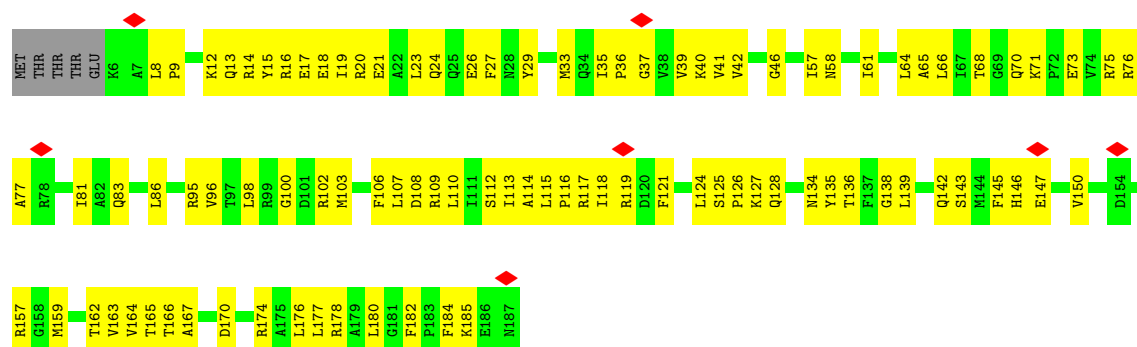
- Molecule 6: 50S ribosomal protein L4

Chain E: 



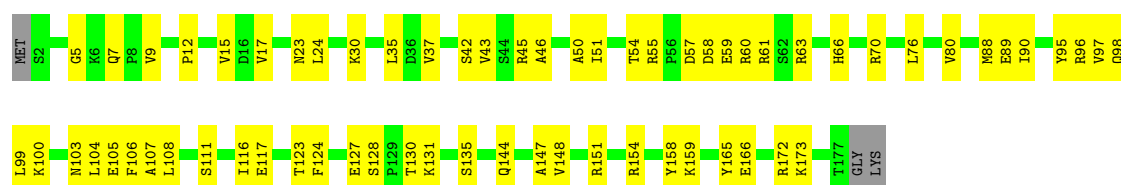
- Molecule 7: 50S ribosomal protein L5

Chain F: 



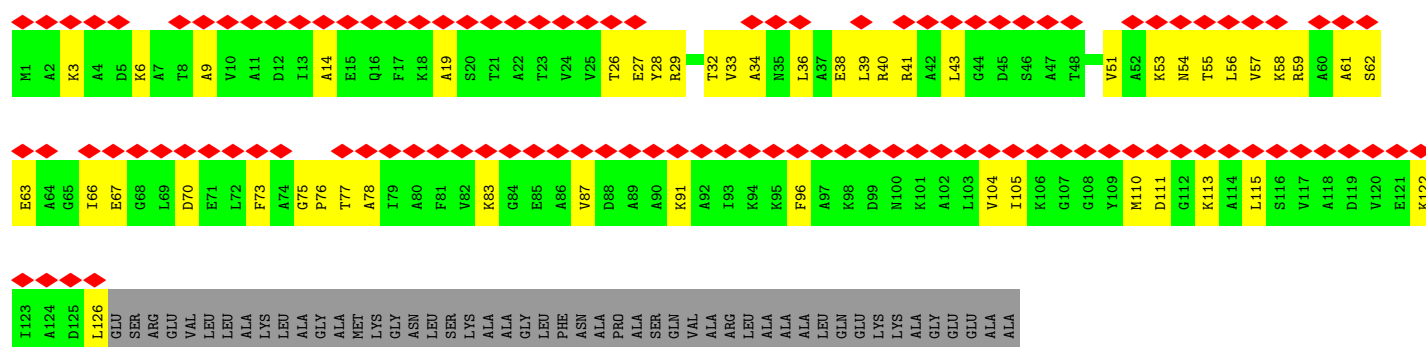
- Molecule 8: 50S ribosomal protein L6

Chain G: 

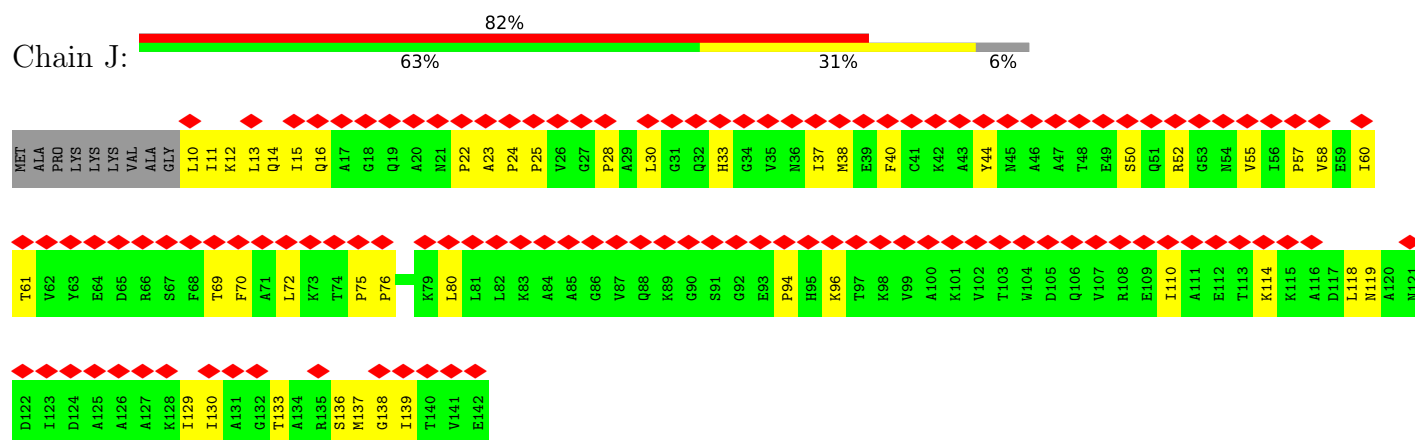


- Molecule 9: 50S ribosomal protein L10

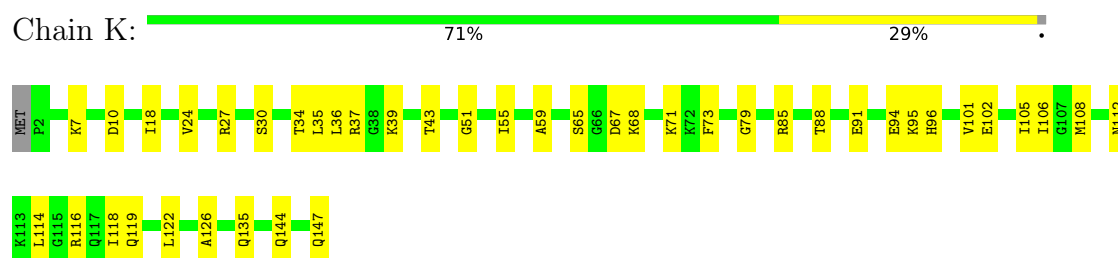
Chain I: 



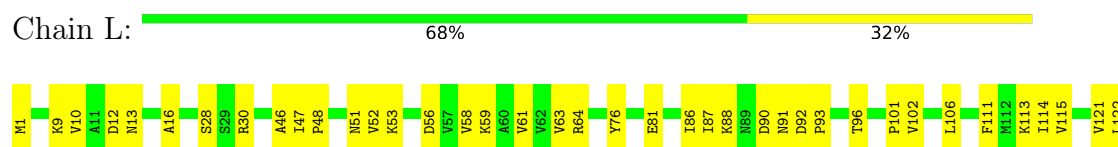
- Molecule 10: 50S ribosomal protein L11



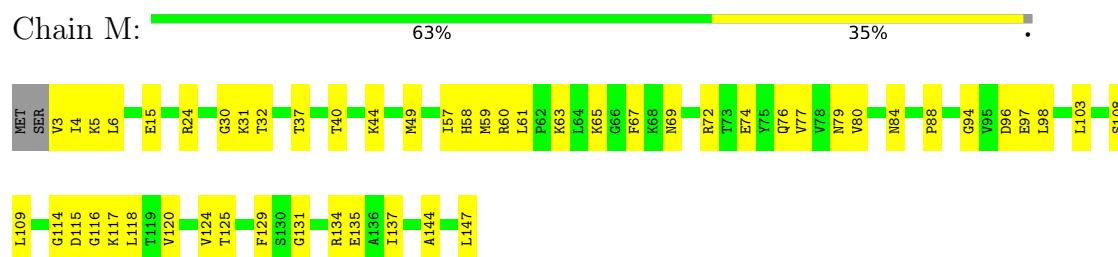
- Molecule 11: 50S ribosomal protein L13



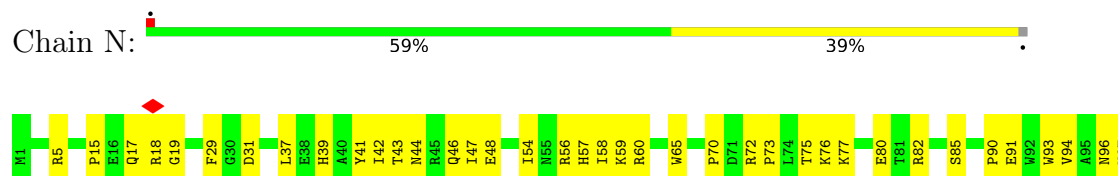
- Molecule 12: 50S ribosomal protein L14



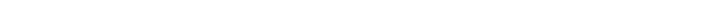
- Molecule 13: 50S ribosomal protein L15

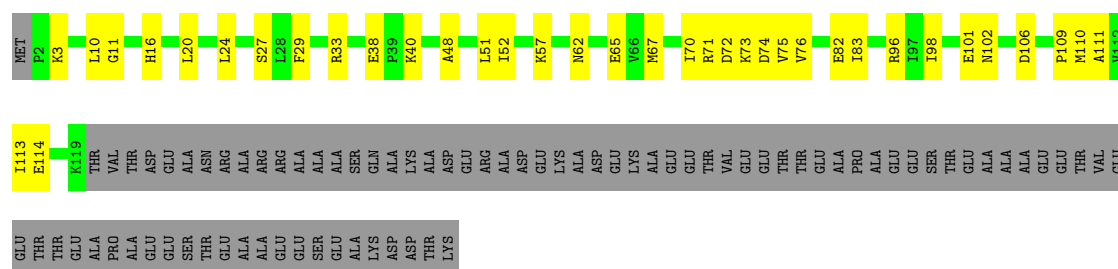


- Molecule 14: 50S ribosomal protein L16



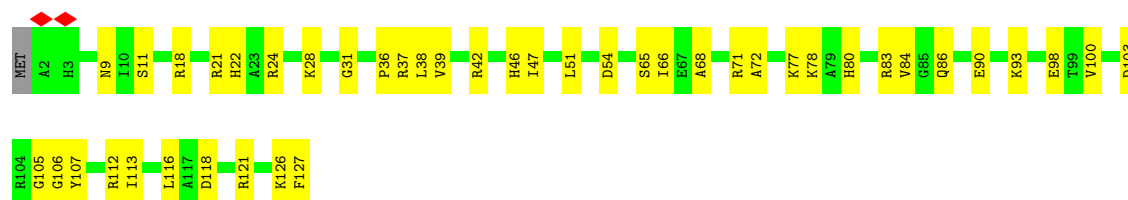
- Molecule 15: 50S ribosomal protein L17

Chain 0:  41% 19% 41%



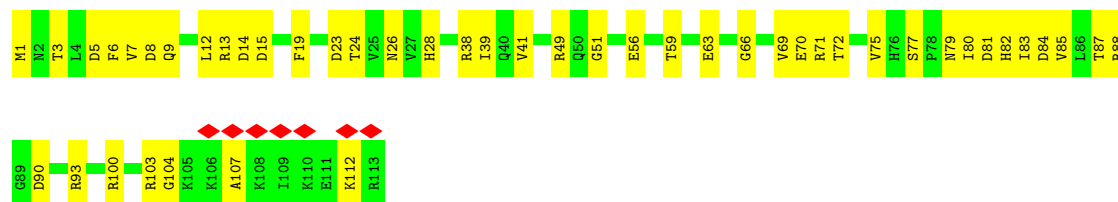
- Molecule 16: 50S ribosomal protein L18

Chain P: 65% 34%



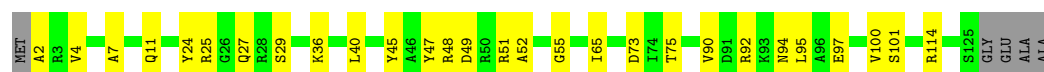
- Molecule 17: 50S ribosomal protein L19

Chain Q:



- Molecule 18: 50S ribosomal protein L20

Chain R:  74% 22% .

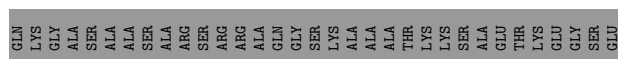


- Molecule 19: 50S ribosomal protein L21

Chain S: 68% 29% .



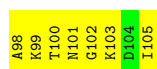
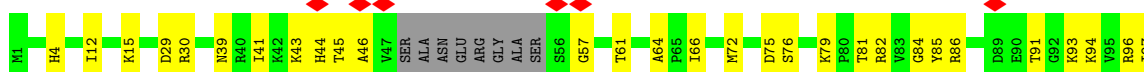
- Molecule 20: 50S ribosomal protein L22



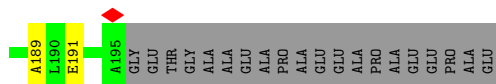
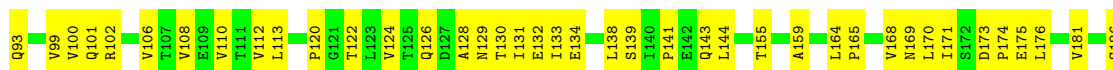
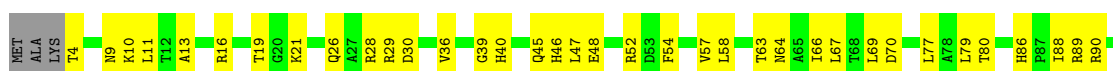
- Molecule 21: 50S ribosomal protein L23



- Molecule 22: 50S ribosomal protein L24



- Molecule 23: 50S ribosomal protein L25

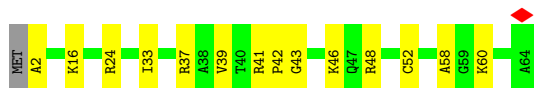
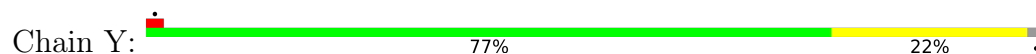


- Molecule 24: 50S ribosomal protein L27

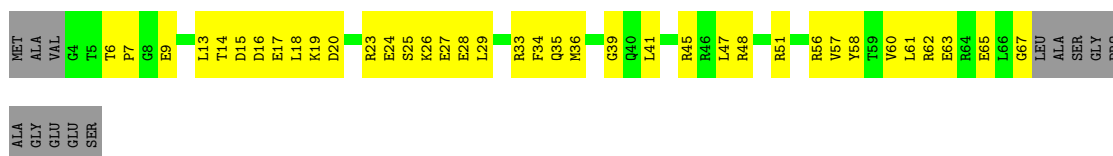




- Molecule 25: 50S ribosomal protein L28



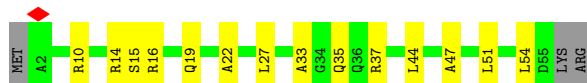
- Molecule 26: 50S ribosomal protein L29



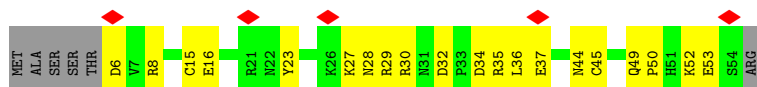
- Molecule 27: 50S ribosomal protein L30



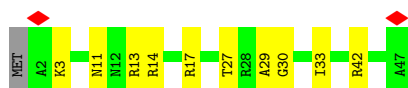
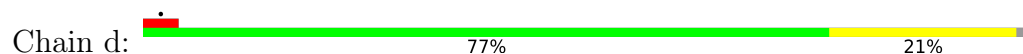
- Molecule 28: 50S ribosomal protein L32



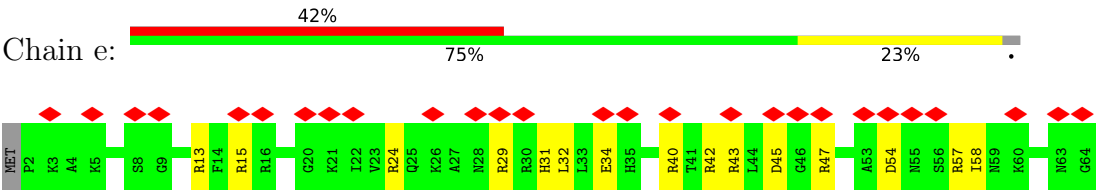
- Molecule 29: 50S ribosomal protein L33 1



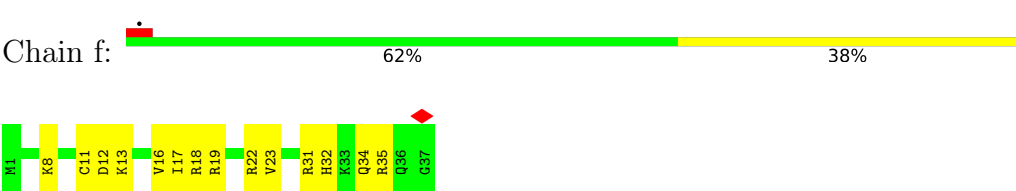
- Molecule 30: 50S ribosomal protein L34



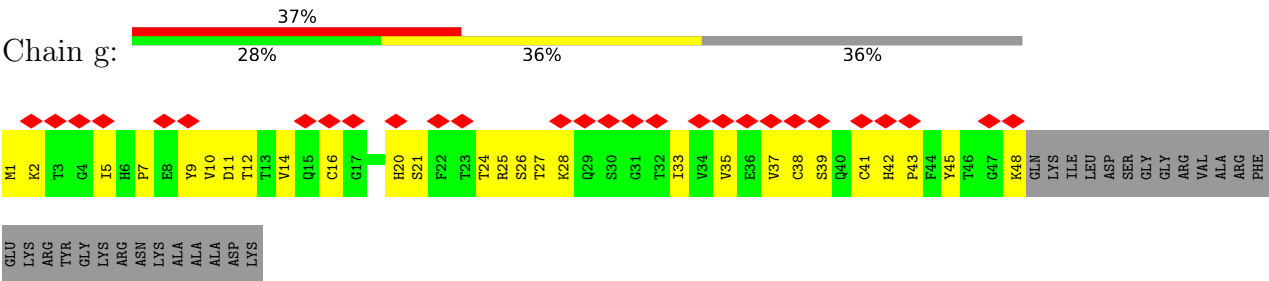
• Molecule 31: 50S ribosomal protein L35



• Molecule 32: 50S ribosomal protein L36



• Molecule 33: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29350	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 ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.212	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	483.0, 483.0, 483.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	3	0.17	0/191	0.37	0/247
2	A	0.24	0/75001	0.29	0/117027
3	B	0.21	0/2821	0.27	0/4396
4	C	0.24	0/2147	0.44	0/2885
5	D	0.26	0/1609	0.46	0/2165
6	E	0.23	0/1592	0.39	0/2153
7	F	0.21	0/1467	0.50	0/1973
8	G	0.23	0/1369	0.43	0/1848
9	I	0.16	0/925	0.47	0/1246
10	J	0.20	0/1006	0.56	0/1364
11	K	0.28	0/1157	0.47	0/1567
12	L	0.23	0/946	0.47	0/1268
13	M	0.25	0/1091	0.52	0/1457
14	N	0.26	0/1118	0.51	0/1506
15	O	0.26	0/945	0.48	0/1267
16	P	0.21	0/966	0.40	0/1298
17	Q	0.24	0/921	0.49	0/1236
18	R	0.24	0/1000	0.39	0/1341
19	S	0.23	0/764	0.42	0/1030
20	T	0.25	0/887	0.42	0/1204
21	U	0.24	0/766	0.45	0/1030
22	V	0.23	0/738	0.49	0/987
23	W	0.24	0/1443	0.47	1/1970 (0.1%)
24	X	0.24	0/595	0.42	0/798
25	Y	0.27	0/478	0.47	0/641
26	Z	0.27	0/534	0.63	0/713
27	a	0.26	0/477	0.48	0/640
28	b	0.22	0/427	0.38	0/572
29	c	0.21	0/413	0.55	0/553
30	d	0.22	0/380	0.35	0/500
31	e	0.17	0/507	0.39	0/672
32	f	0.21	0/303	0.39	0/401

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.19	0/372	0.49	0/503
All	All	0.24	0/105356	0.34	1/158458 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	141	PRO	CA-N-CD	-6.08	103.48	112.00

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	3	189	0	205	7	0
2	A	66981	0	33693	1562	0
3	B	2522	0	1285	55	0
4	C	2105	0	2159	73	0
5	D	1587	0	1629	54	0
6	E	1569	0	1607	45	0
7	F	1445	0	1476	93	0
8	G	1348	0	1399	45	0
9	I	918	0	959	58	0
10	J	990	0	1021	44	0
11	K	1130	0	1167	41	0
12	L	938	0	1000	32	0
13	M	1078	0	1151	48	0
14	N	1092	0	1127	37	0
15	O	928	0	972	31	0
16	P	956	0	991	32	0
17	Q	907	0	938	39	0
18	R	988	0	1038	20	0
19	S	754	0	802	19	0
20	T	873	0	909	27	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	U	756	0	802	22	0
22	V	732	0	781	34	0
23	W	1428	0	1443	57	0
24	X	586	0	601	14	0
25	Y	470	0	480	13	0
26	Z	531	0	541	37	0
27	a	474	0	500	13	0
28	b	423	0	463	13	0
29	c	405	0	407	17	0
30	d	377	0	411	8	0
31	e	502	0	541	19	0
32	f	299	0	321	10	0
33	g	364	0	348	34	0
34	A	386	0	0	0	0
34	B	9	0	0	0	0
34	C	5	0	0	0	0
34	E	1	0	0	0	0
34	F	1	0	0	0	0
34	M	1	0	0	0	0
34	N	2	0	0	0	0
34	T	1	0	0	0	0
34	e	1	0	0	0	0
35	Y	1	0	0	0	0
35	c	1	0	0	0	0
35	f	1	0	0	0	0
35	g	1	0	0	0	0
All	All	97056	0	63167	2392	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 15.

The worst 5 of 2392 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1541:G:H1	2:A:1631:A:N6	1.34	1.20
2:A:2131:G:C2	2:A:2148:C:C2	2.49	1.00
2:A:1540:U:H3	2:A:1632:G:H1	1.04	0.98
2:A:280:G:H1	2:A:306:U:H3	1.09	0.97
2:A:2131:G:C2	2:A:2148:C:O2	2.18	0.96

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
4	C	270/278 (97%)	258 (96%)	12 (4%)	0	100	100
5	D	212/217 (98%)	199 (94%)	13 (6%)	0	100	100
6	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
7	F	180/187 (96%)	169 (94%)	11 (6%)	0	100	100
8	G	174/179 (97%)	168 (97%)	6 (3%)	0	100	100
9	I	124/175 (71%)	115 (93%)	9 (7%)	0	100	100
10	J	131/142 (92%)	121 (92%)	10 (8%)	0	100	100
11	K	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
12	L	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
13	M	143/147 (97%)	130 (91%)	13 (9%)	0	100	100
14	N	134/138 (97%)	129 (96%)	4 (3%)	1 (1%)	18	55
15	O	116/199 (58%)	110 (95%)	6 (5%)	0	100	100
16	P	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
17	Q	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
18	R	122/129 (95%)	117 (96%)	5 (4%)	0	100	100
19	S	98/103 (95%)	92 (94%)	6 (6%)	0	100	100
20	T	112/153 (73%)	111 (99%)	1 (1%)	0	100	100
21	U	95/100 (95%)	92 (97%)	3 (3%)	0	100	100
22	V	93/105 (89%)	92 (99%)	1 (1%)	0	100	100
23	W	190/215 (88%)	183 (96%)	7 (4%)	0	100	100
24	X	77/88 (88%)	72 (94%)	5 (6%)	0	100	100
25	Y	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
26	Z	62/77 (80%)	59 (95%)	3 (5%)	0	100	100
27	a	57/61 (93%)	55 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	b	52/57 (91%)	52 (100%)	0	0	100	100
29	c	47/55 (86%)	44 (94%)	3 (6%)	0	100	100
30	d	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
31	e	61/64 (95%)	61 (100%)	0	0	100	100
32	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
33	g	46/75 (61%)	43 (94%)	3 (6%)	0	100	100
All	All	3463/3840 (90%)	3310 (96%)	152 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	N	59	LYS

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	3	18/19 (95%)	18 (100%)	0	100	100
4	C	215/218 (99%)	215 (100%)	0	100	100
5	D	160/163 (98%)	160 (100%)	0	100	100
6	E	169/173 (98%)	169 (100%)	0	100	100
7	F	151/156 (97%)	151 (100%)	0	100	100
8	G	148/150 (99%)	148 (100%)	0	100	100
9	I	89/120 (74%)	89 (100%)	0	100	100
10	J	102/108 (94%)	102 (100%)	0	100	100
11	K	119/120 (99%)	119 (100%)	0	100	100
12	L	100/100 (100%)	100 (100%)	0	100	100
13	M	112/114 (98%)	112 (100%)	0	100	100
14	N	114/116 (98%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	O	97/158 (61%)	97 (100%)	0	100	100
16	P	93/94 (99%)	93 (100%)	0	100	100
17	Q	100/100 (100%)	100 (100%)	0	100	100
18	R	97/99 (98%)	97 (100%)	0	100	100
19	S	81/83 (98%)	81 (100%)	0	100	100
20	T	90/117 (77%)	90 (100%)	0	100	100
21	U	83/85 (98%)	83 (100%)	0	100	100
22	V	81/86 (94%)	81 (100%)	0	100	100
23	W	155/168 (92%)	155 (100%)	0	100	100
24	X	58/63 (92%)	58 (100%)	0	100	100
25	Y	50/51 (98%)	50 (100%)	0	100	100
26	Z	58/66 (88%)	58 (100%)	0	100	100
27	a	52/54 (96%)	52 (100%)	0	100	100
28	b	43/46 (94%)	43 (100%)	0	100	100
29	c	47/52 (90%)	47 (100%)	0	100	100
30	d	35/36 (97%)	35 (100%)	0	100	100
31	e	53/54 (98%)	53 (100%)	0	100	100
32	f	35/35 (100%)	35 (100%)	0	100	100
33	g	43/63 (68%)	43 (100%)	0	100	100
All	All	2848/3067 (93%)	2848 (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 31 such sidechains are listed below:

Mol	Chain	Res	Type
16	P	8	GLN
28	b	12	ASN
17	Q	79	ASN
31	e	59	ASN
23	W	93	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	3118/3120 (99%)	721 (23%)	28 (0%)
3	B	117/118 (99%)	22 (18%)	1 (0%)
All	All	3235/3238 (99%)	743 (22%)	29 (0%)

5 of 743 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	7	U
2	A	9	U
2	A	12	G
2	A	20	G
2	A	29	C

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	1084	U
2	A	2980	U
2	A	1603	G
2	A	2350	G
2	A	1253	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](#)

Of 411 ligands modelled in this entry, 411 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 [i](#)

There are no chain breaks in this entry.

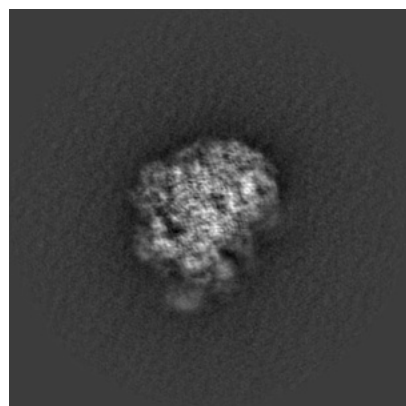
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33599. These allow visual inspection of the internal detail of the map and identification of artifacts.

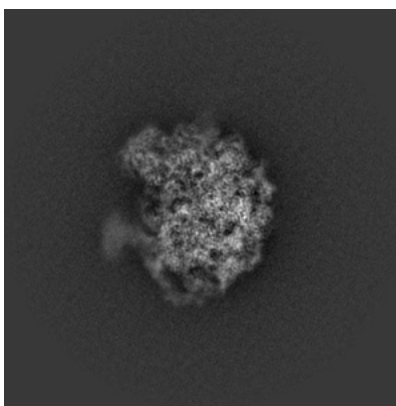
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

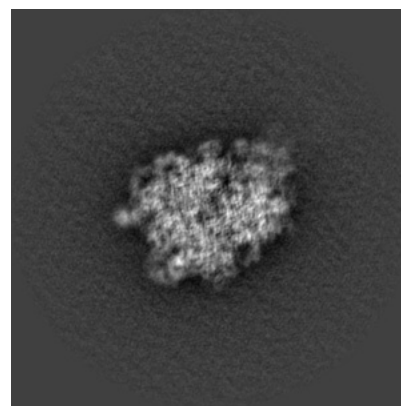
6.1.1 Primary map



X

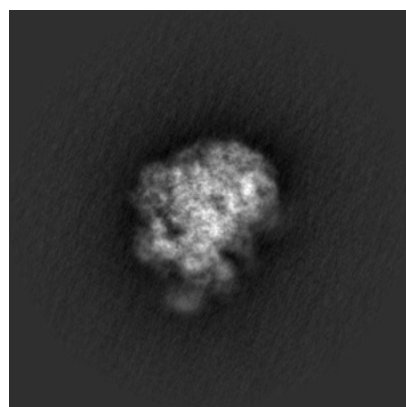


Y

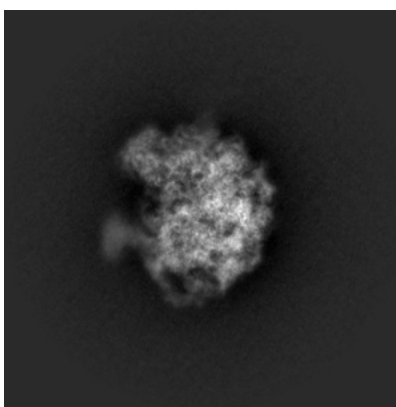


Z

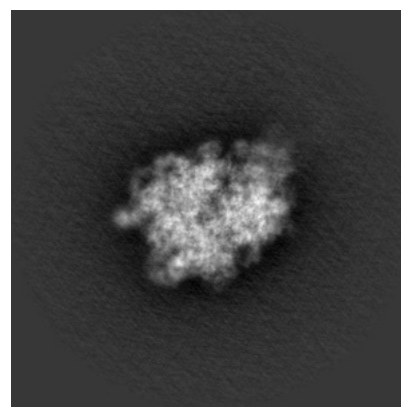
6.1.2 Raw map



X



Y

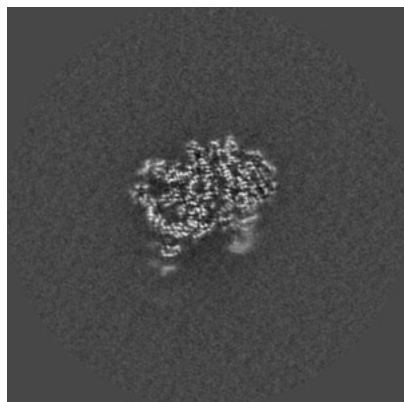


Z

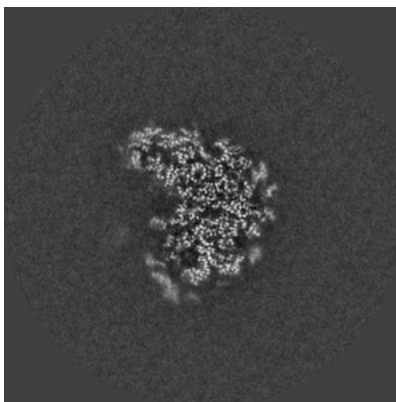
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

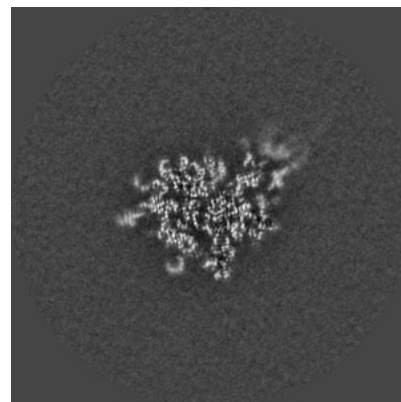
6.2.1 Primary map



X Index: 175

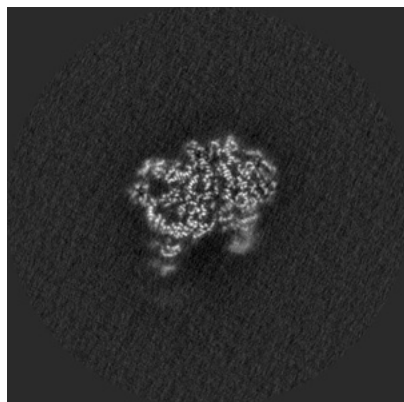


Y Index: 175

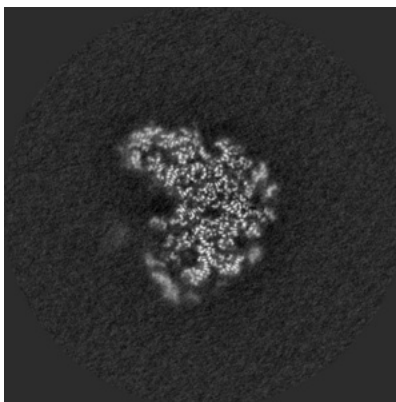


Z Index: 175

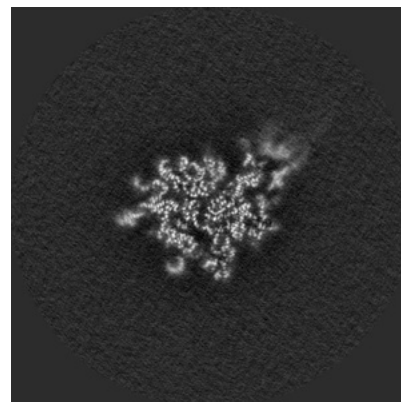
6.2.2 Raw map



X Index: 175



Y Index: 175

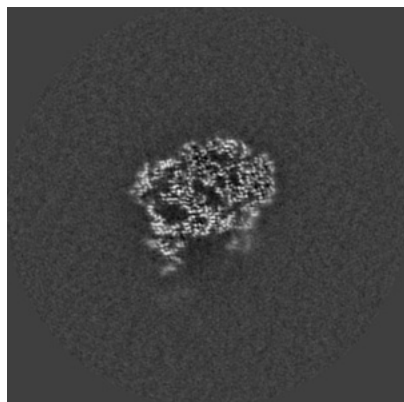


Z Index: 175

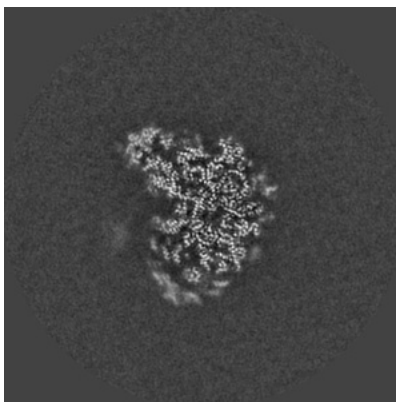
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

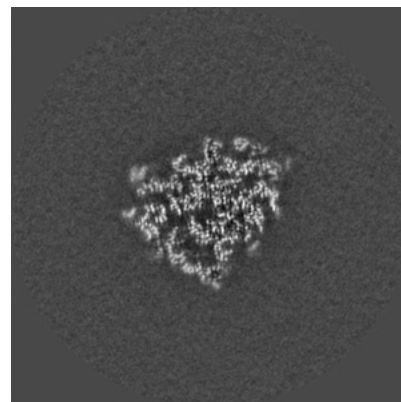
6.3.1 Primary map



X Index: 172

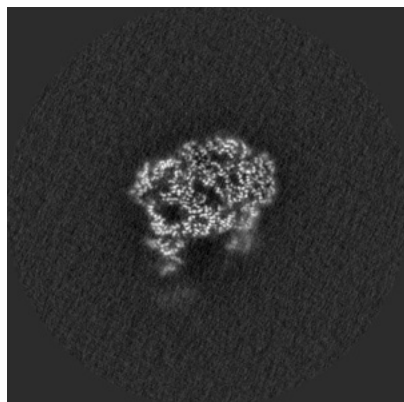


Y Index: 172

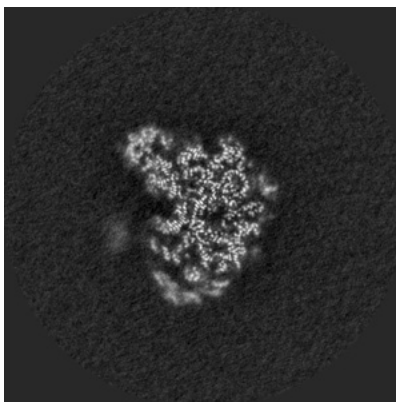


Z Index: 189

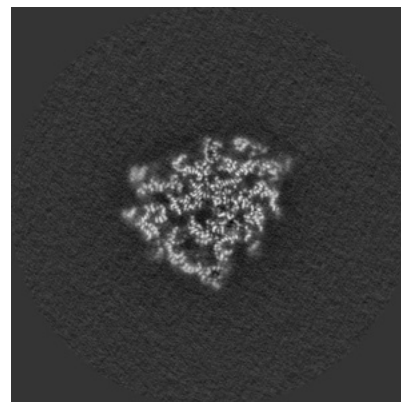
6.3.2 Raw map



X Index: 172



Y Index: 171

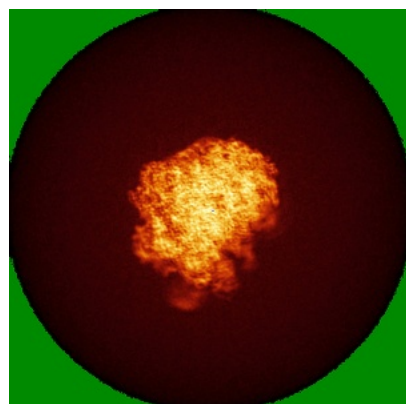


Z Index: 189

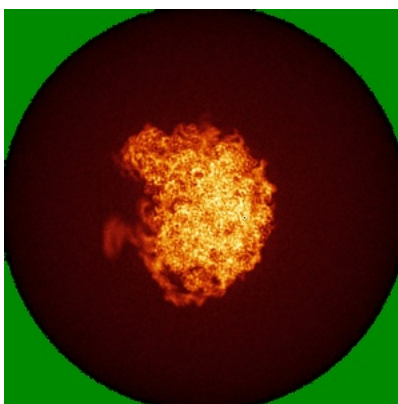
The images above show the largest variance slices of the map in three orthogonal directions.

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

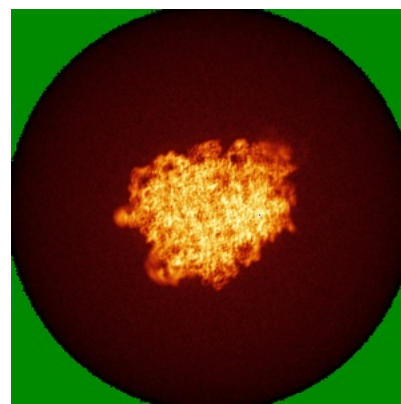
6.4.1 Primary map



X

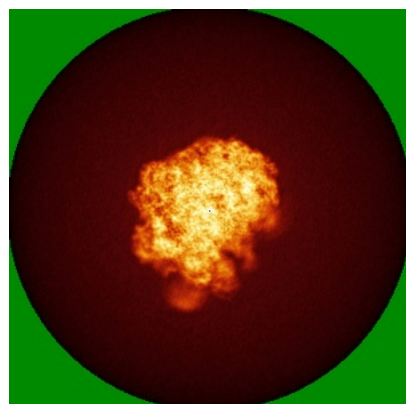


Y

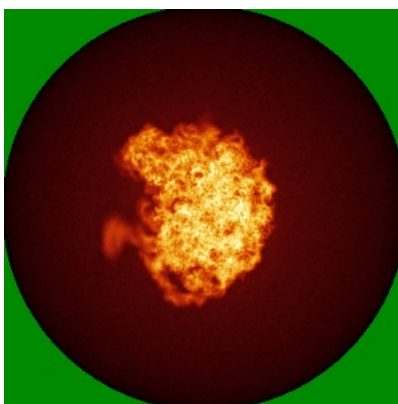


Z

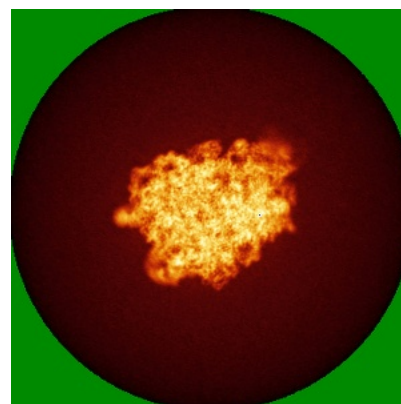
6.4.2 Raw map



X



Y

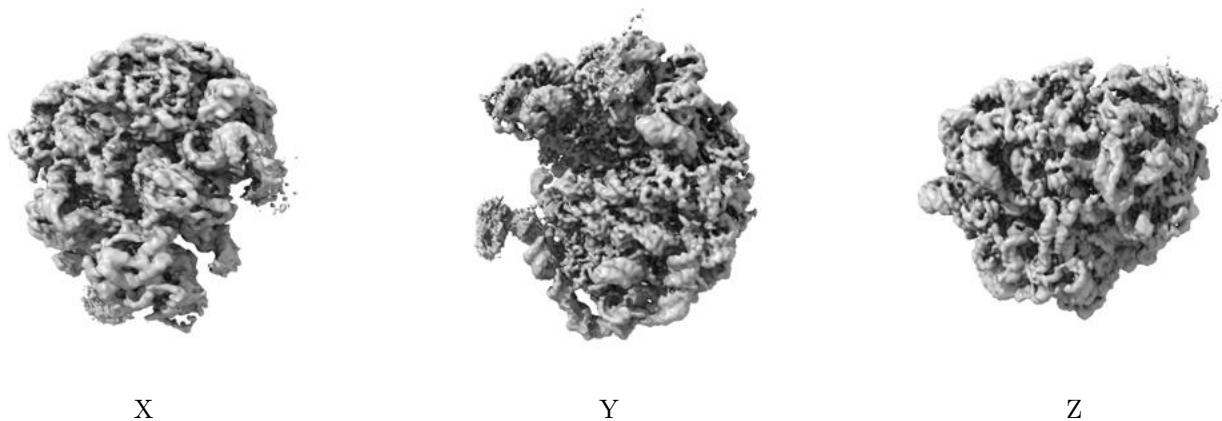


Z

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 0.03. 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.

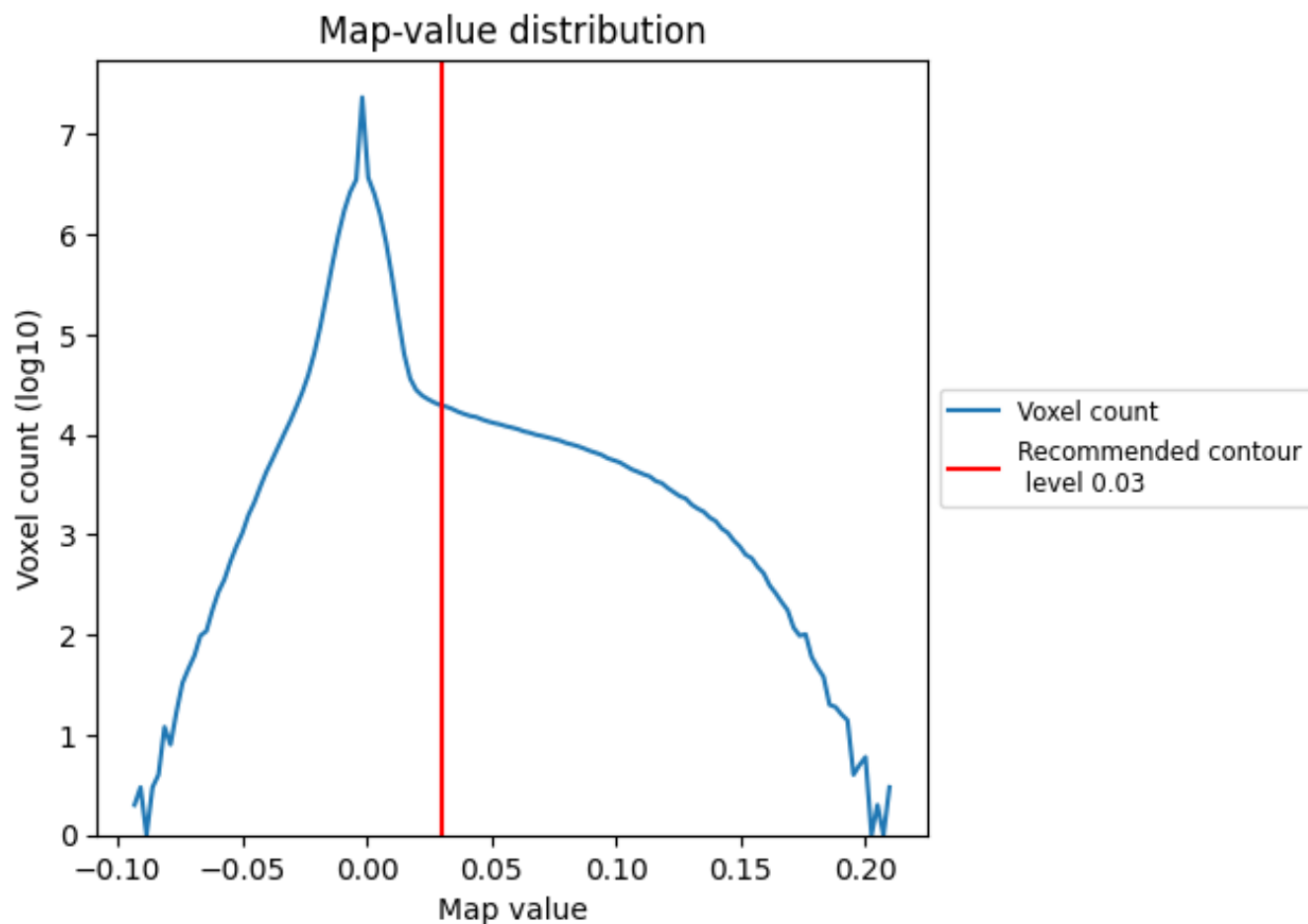
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

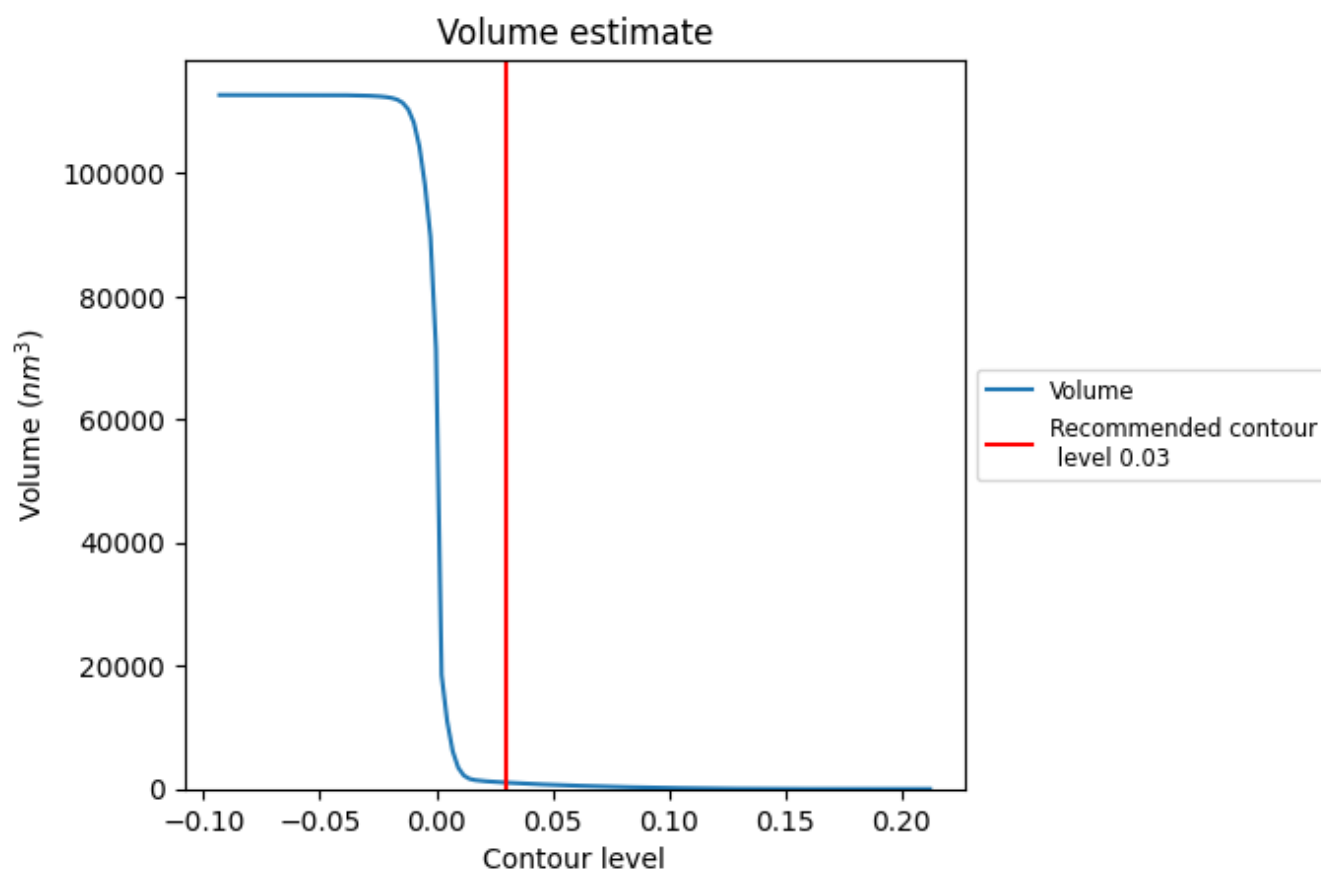
This section contains the results of statistical analysis of the map.

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.

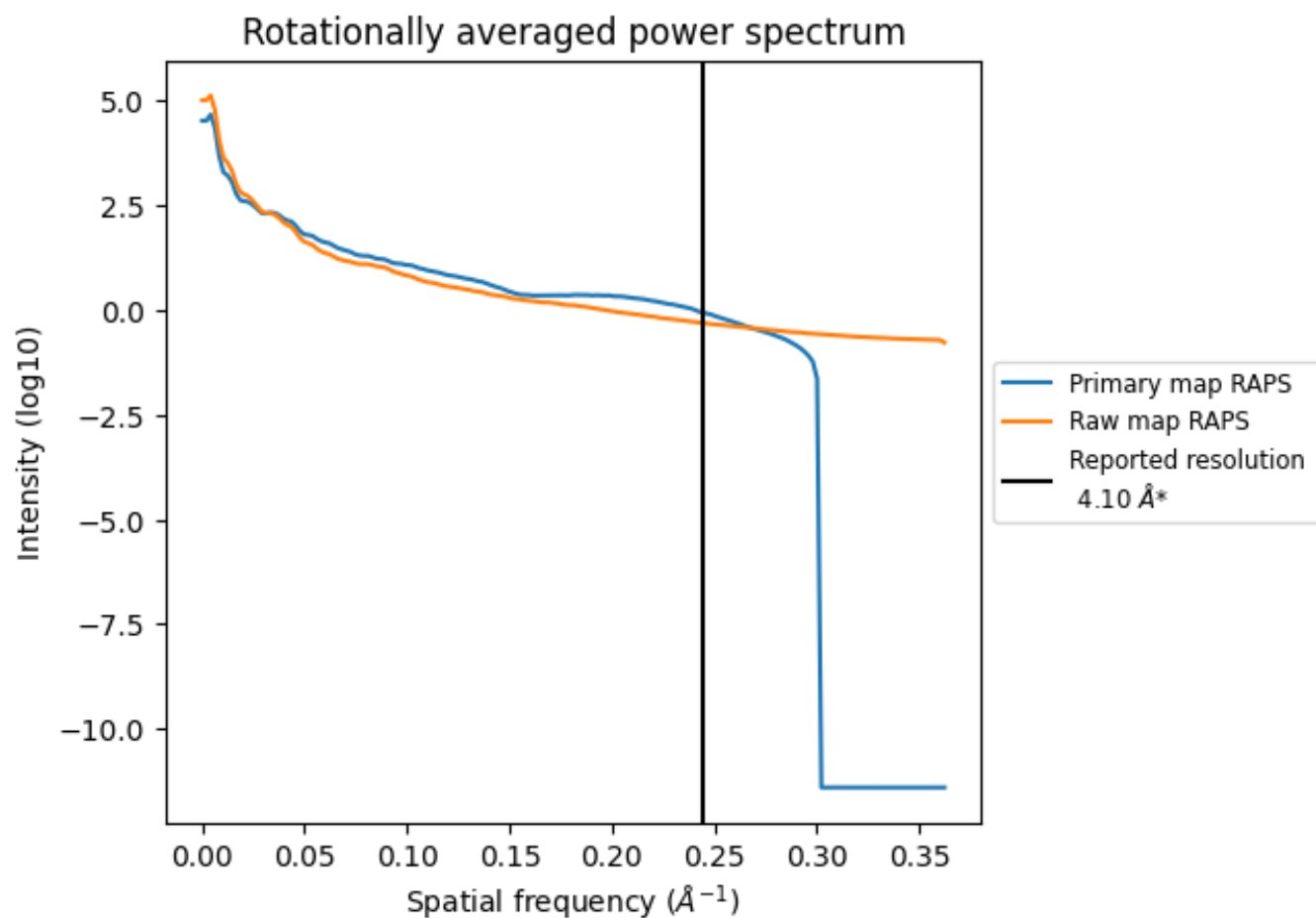
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1034 nm^3 ; this corresponds to an approximate mass of 934 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 ⓘ

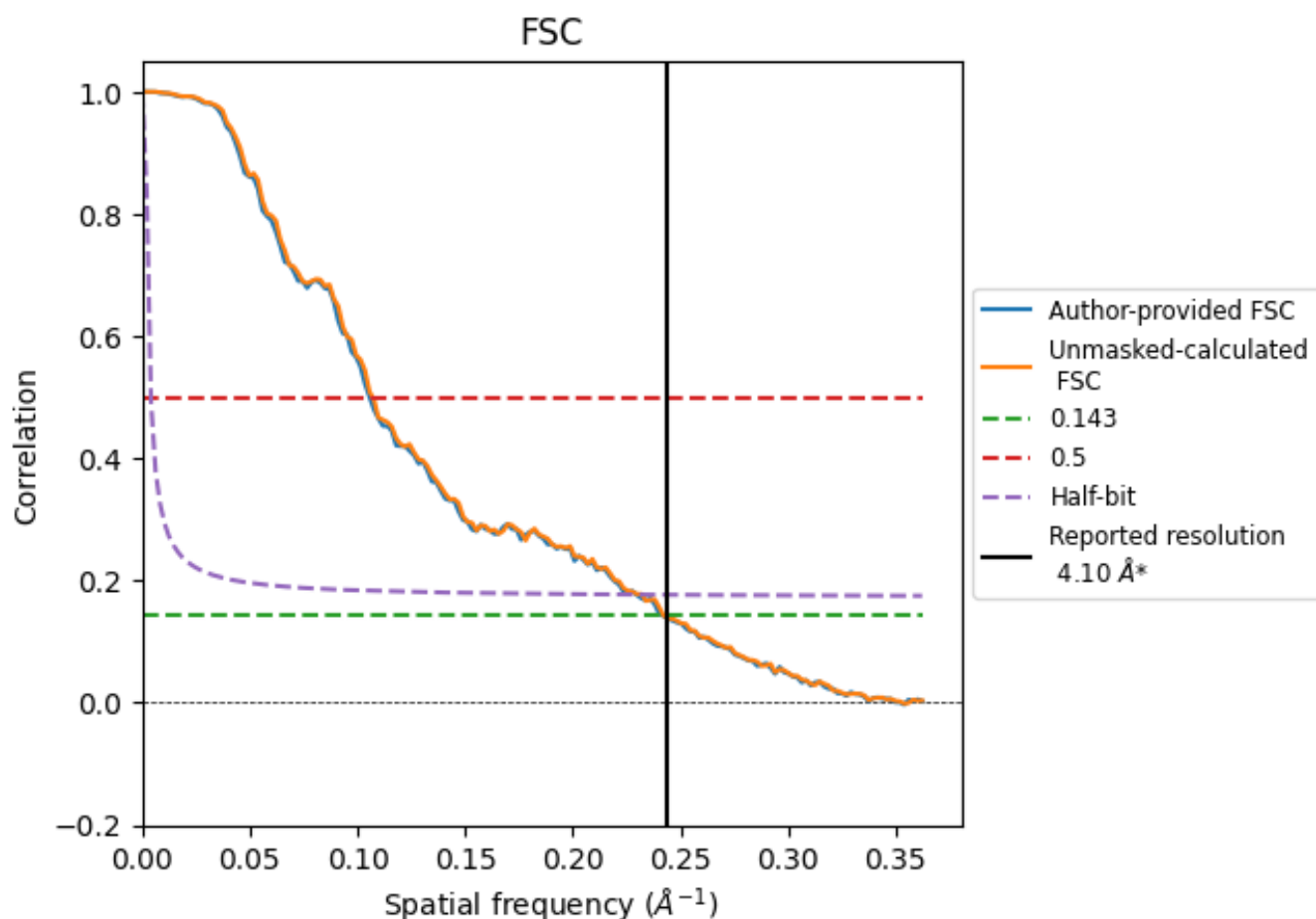


*Reported resolution corresponds to spatial frequency of 0.244 $\text{\AA}^{-1}$

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

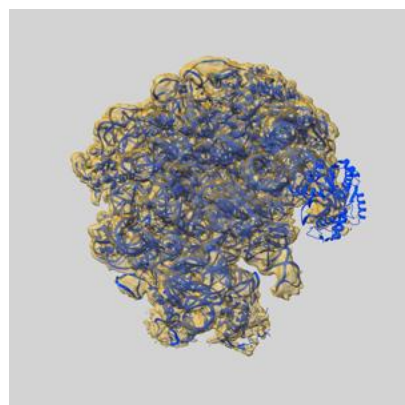
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.14	9.47	4.36
Unmasked-calculated*	4.13	9.35	4.31

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

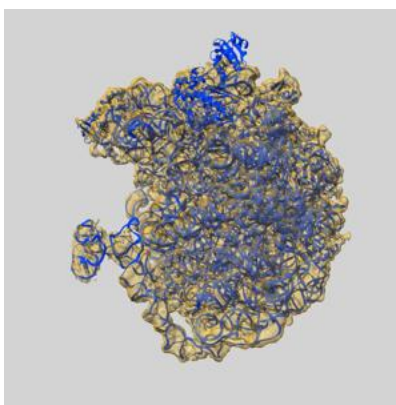
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33599 and PDB model 7Y41. Per-residue inclusion information can be found in section [3](#) on page [11](#).

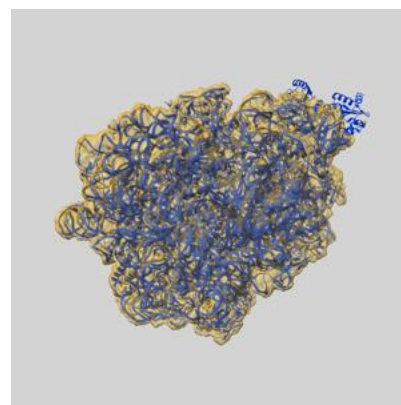
9.1 Map-model overlay [i](#)



X



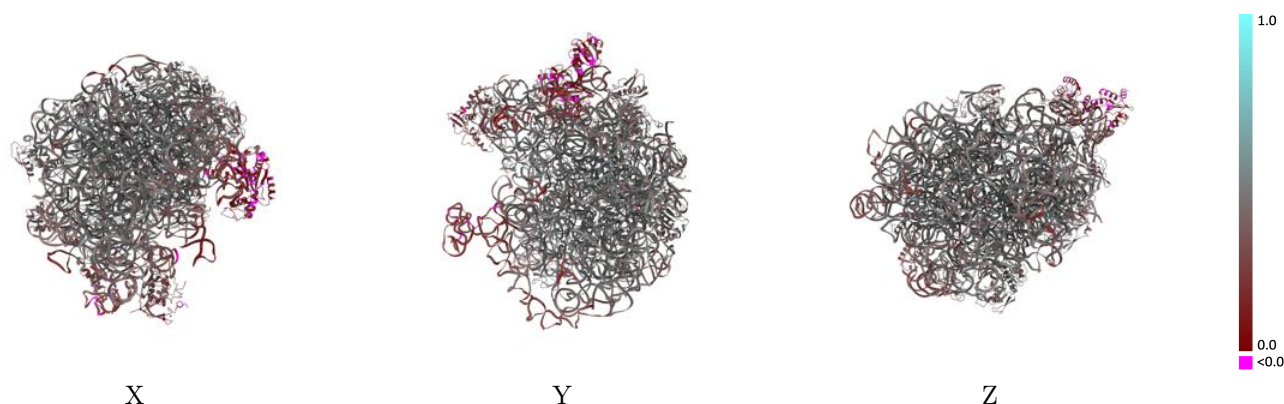
Y



Z

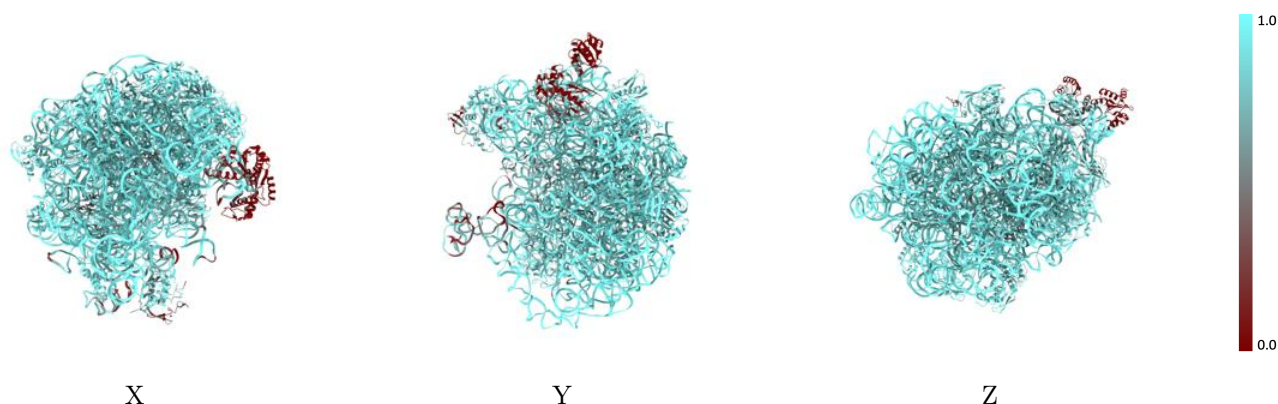
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



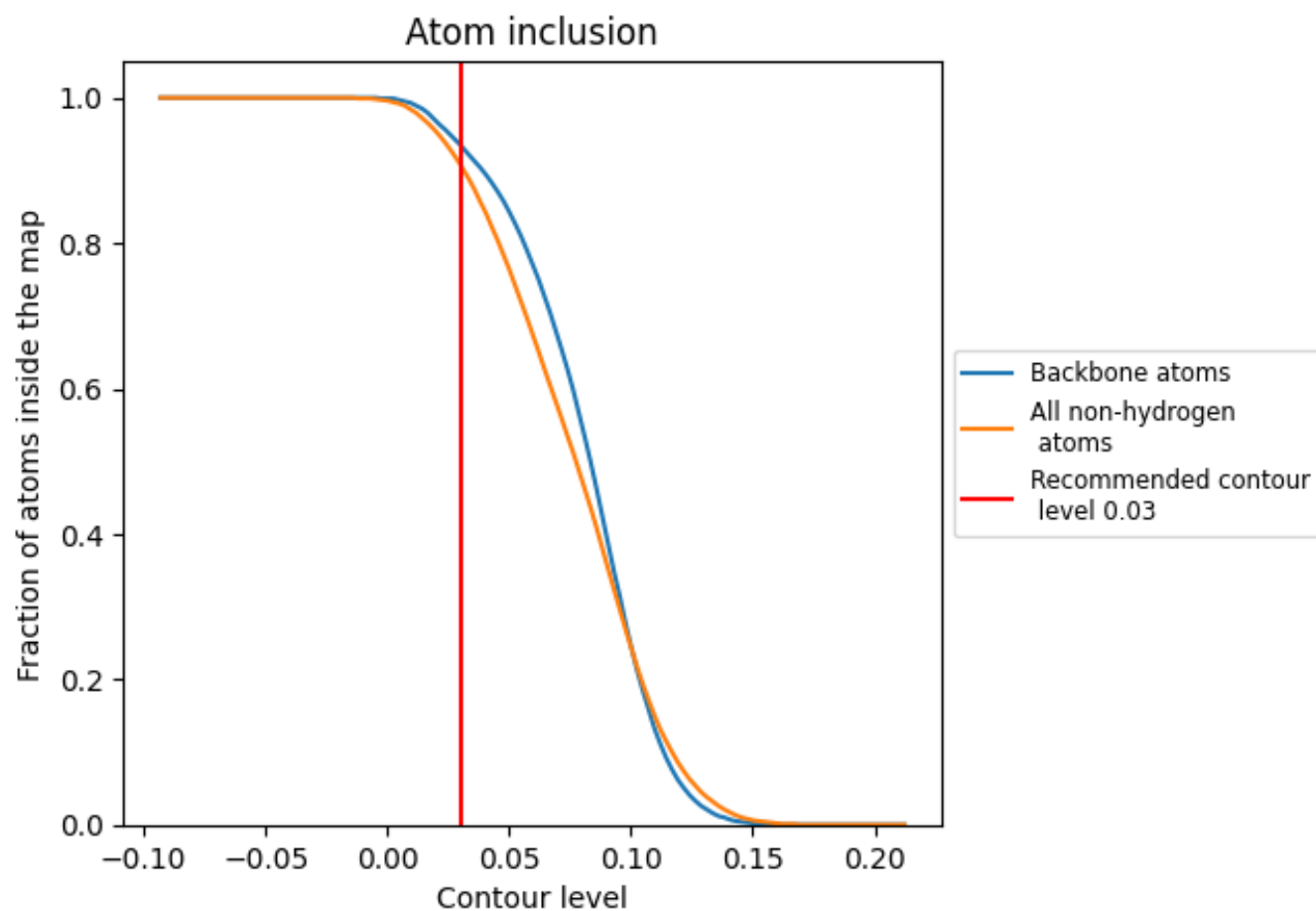
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 91% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9080	 0.4220
3	 0.5870	 0.4360
A	 0.9550	 0.4270
B	 0.9820	 0.4200
C	 0.8560	 0.4650
D	 0.8800	 0.4600
E	 0.8760	 0.4470
F	 0.7710	 0.3090
G	 0.8940	 0.3970
I	 0.1230	 0.1180
J	 0.1240	 0.1420
K	 0.8820	 0.4650
L	 0.8360	 0.4370
M	 0.8460	 0.4490
N	 0.8430	 0.4520
O	 0.8630	 0.4590
P	 0.8750	 0.4080
Q	 0.8280	 0.4130
R	 0.8670	 0.4600
S	 0.8990	 0.4750
T	 0.8600	 0.4610
U	 0.8150	 0.4410
V	 0.8360	 0.4020
W	 0.8000	 0.4020
X	 0.8730	 0.4700
Y	 0.8790	 0.4670
Z	 0.8800	 0.3930
a	 0.8630	 0.4460
b	 0.8660	 0.4700
c	 0.6810	 0.4250
d	 0.8200	 0.4770
e	 0.4370	 0.4400
f	 0.8120	 0.4700
g	 0.3300	 0.1850

