



## wwPDB EM Validation Summary Report ⓘ

Jul 9, 2025 – 02:43 PM EDT

PDB ID : 9E0N / pdb\_00009e0n  
EMDB ID : EMD-47363  
Title : M. smegmatis unmethylated 70S ribosome structure  
Authors : Nandi, S.; Conn, G.L.  
Deposited on : 2024-10-18  
Resolution : 3.24 Å(reported)  
Based on initial model : 5ZEB

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

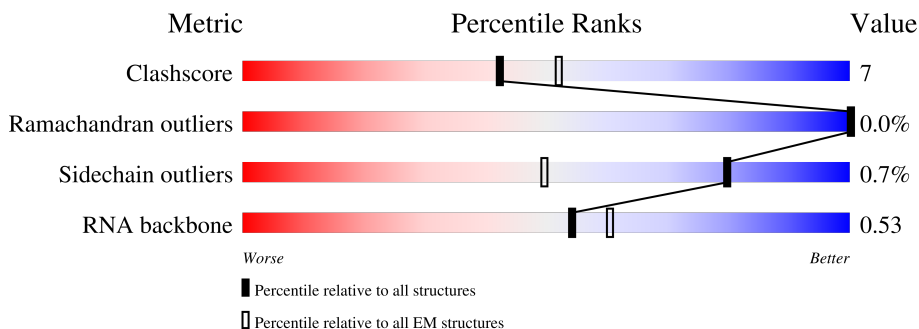
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.24 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	1	61	
2	2	75	
3	3	57	
4	4	55	
5	5	47	
6	6	64	
7	7	37	


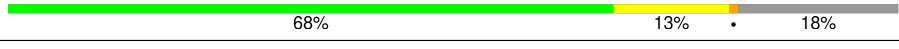

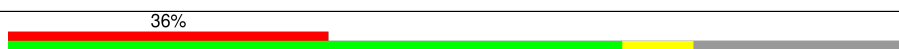



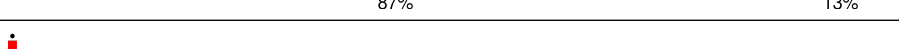



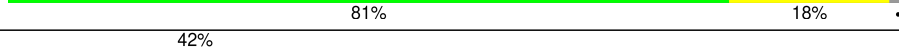

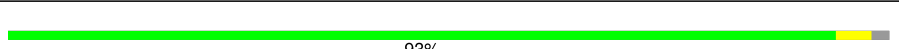


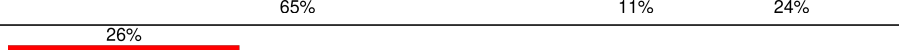

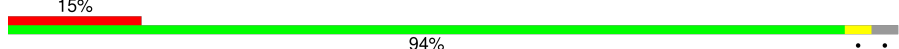




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Mol	Chain	Length	Quality of chain
8	8	24	
9	A	3120	
10	B	118	
11	C	278	
12	D	217	
13	E	215	
14	F	187	
15	G	179	
16	H	151	
17	I	174	
18	J	142	
19	K	147	
20	L	122	
21	M	147	
22	N	138	
23	O	174	
24	P	127	
25	Q	113	
26	R	129	
27	S	103	
28	T	153	
29	U	100	
30	V	105	
31	W	215	
32	X	88	

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Mol	Chain	Length	Quality of chain
33	Y	64	
34	Z	77	
35	a	1528	
36	b	277	
37	c	275	
38	d	201	
39	e	214	
40	f	96	
41	g	156	
42	h	132	
43	i	150	
44	j	101	
45	k	138	
46	l	124	
47	m	124	
48	n	61	
49	o	89	
50	p	156	
51	q	98	
52	r	84	
53	s	93	
54	t	86	
55	u	33	

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 148775 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 uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	60	Total	C	N	O	0	0
			483	298	97	88		

- Molecule 2 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

- Molecule 3 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 4 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

- Molecule 5 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 6 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	6	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 7 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

- Molecule 8 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	8	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 9 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

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

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

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 17 is a protein called Large ribosomal subunit protein uL10.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	147	Total	C	N	O	S	0	0
			1127	719	207	199	2		

- Molecule 20 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 21 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 22 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	134	Total	C	N	O	S	0	0
			1068	677	211	178	2		

- Molecule 23 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 25 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 26 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 27 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	102	Total	C	N	O		0	0
			768	487	140	141			

- Molecule 28 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 29 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	U	94	Total	C	N	O	0	0
			739	469	135	135		

- Molecule 30 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	97	Total	C	N	O	S	0	0
			731	456	137	136	2		

- Molecule 31 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	W	188	Total	C	N	O	0	0
			1407	869	251	287		

- Molecule 32 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	82	Total	C	N	O	0	0
			604	372	127	105		

- Molecule 33 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 34 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 35 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	1506	Total	C	N	O	P	0	0
			32341	14404	5921	10510	1506		

- Molecule 36 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 37 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	210	Total	C	N	O	S	0	0
			1672	1043	324	300	5		

- Molecule 38 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 39 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	198	Total	C	N	O	S	0	0
			1433	885	282	262	4		

- Molecule 40 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 41 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	156	Total	C	N	O	S	0	0
			1240	773	242	222	3		

- Molecule 42 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	130	Total	C	N	O	S	0	0
			1003	629	188	185	1		

- Molecule 43 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	126	Total	C	N	O	S	0	0
			994	630	194	170			

- Molecule 44 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 45 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	117	Total	C	N	O	S	0	0
			871	539	173	158	1		

- Molecule 46 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 47 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 48 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 49 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	o	87	Total	C	N	O	0	0
			709	443	143	123		

- Molecule 50 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	p	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	92	Total	C	N	O	S	0	0
			730	458	138	132	2		

- Molecule 52 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	64	Total	C	N	O	S	0	0
			512	319	102	88	3		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	78	Total	C	N	O	S	0	0
			630	405	117	107	1		

- Molecule 54 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	t	84	Total	C	N	O	0	0
			655	399	138	118		

- Molecule 55 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

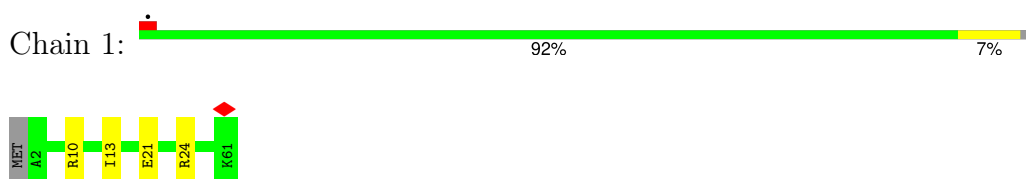
- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	2	1	Total 1	Mg 1	0
56	A	76	Total 76	Mg 76	0
56	C	1	Total 1	Mg 1	0
56	D	1	Total 1	Mg 1	0
56	a	28	Total 28	Mg 28	0

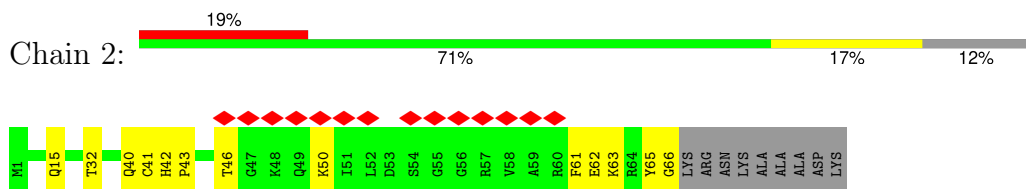
### 3 Residue-property plots [i](#)

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.

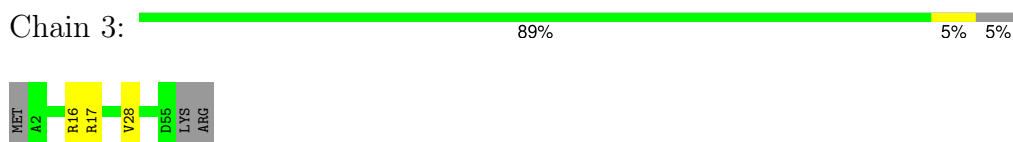
- Molecule 1: Large ribosomal subunit protein uL30



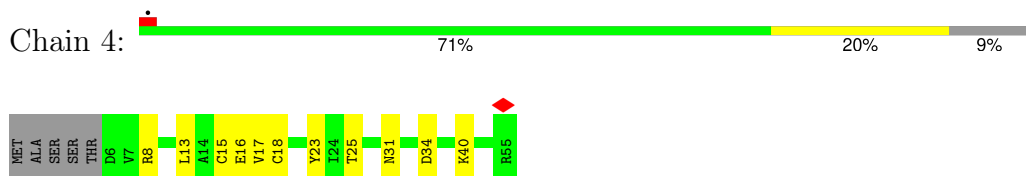
- Molecule 2: Large ribosomal subunit protein bL31



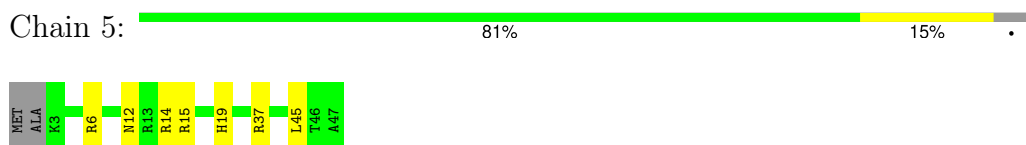
- Molecule 3: Large ribosomal subunit protein bL32




- Molecule 4: Large ribosomal subunit protein bL33A



- Molecule 5: Large ribosomal subunit protein bL34




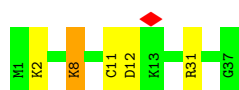
- Molecule 6: Large ribosomal subunit protein bL35

Chain 6:  83% 16%



- Molecule 7: 50S ribosomal protein L36

Chain 7:  86% 11%



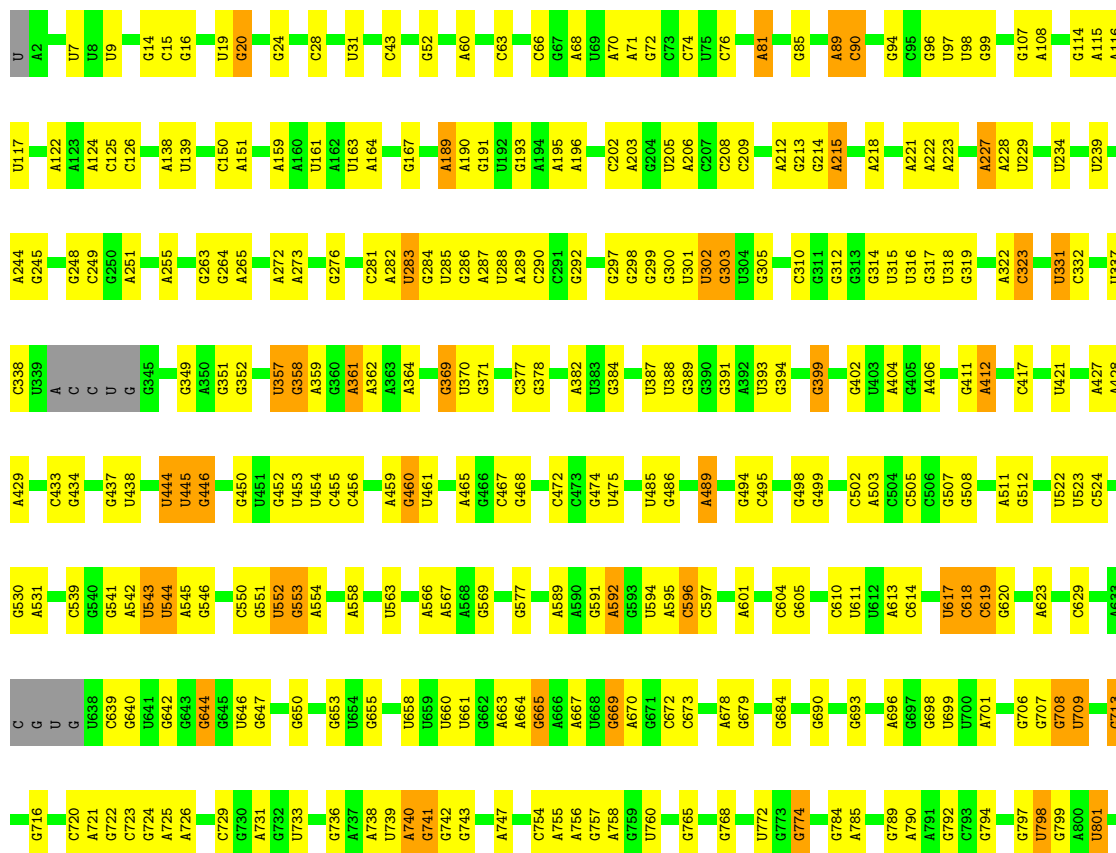
- Molecule 8: 50S ribosomal protein bL37

Chain 8:  8% 71% 25%

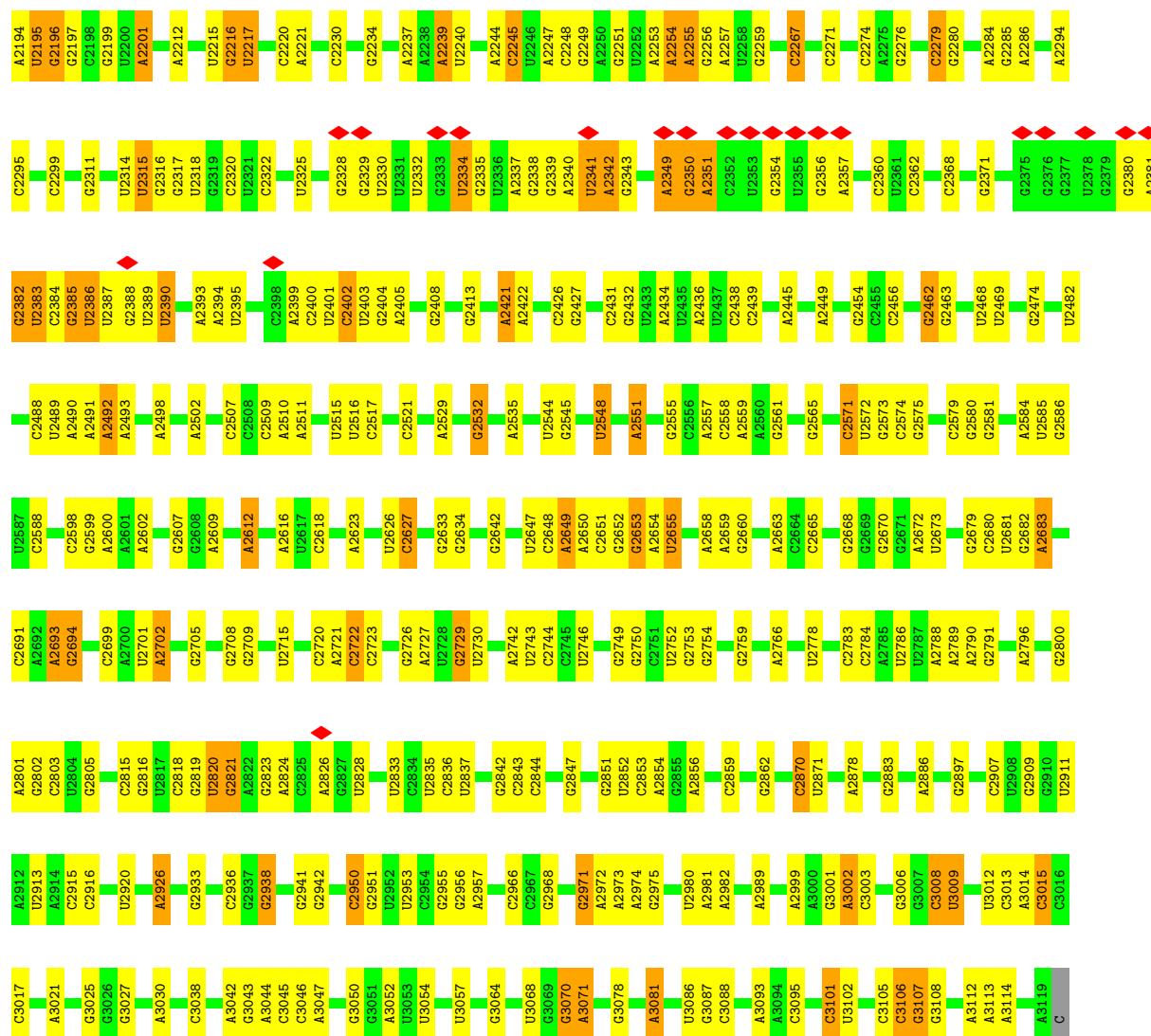


- Molecule 9: 23S rRNA

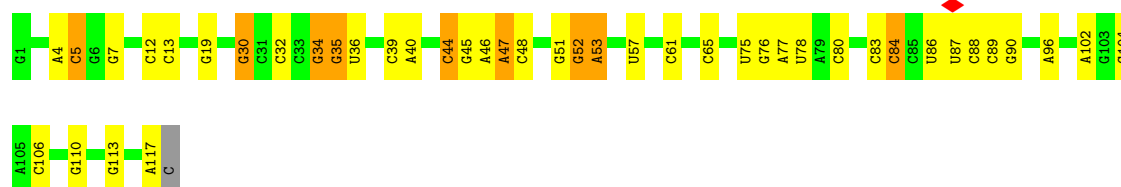
Chain A:  61% 32% 6%



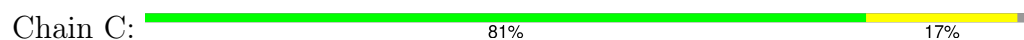
C2126	C2043	G1950	G1845	G1724	A1616	G1550	U1444	U1338	A1214	C1125	G1031	C805
G2127	U2044	G1951	G1846	A1727	C1617	U1551	U1444	G1339	G1217	U1126	A1032	A808
C2128	G2045	C1952	U1847	U1728	C1618	A1552	C1448	A1340	G1217	A1127	A1033	U809
G2130	C2046	C1953	A1848	A1729	G1625	U1553	U1554	A1344	U1223	C1129	G1035	C813
U2132	C2047	A1956	G1851	U1730	G1626	A1555	A1451	U1349	G1224	G1130	U1040	A814
G2133	G2048	G1957	A1852	A1731	U1629	A1556	U1455	G1350	G1225	G1131	C1045	G824
G2134	G2052	G1970	G1853	G1736	U1630	C1557	U1455	G1351	C1227	C1136	C1046	G824
U2135	C2053	C1971	A1858	A1737	G1631	C1558	G1458	G1352	A1228	U1137	A1047	A934
A2137	C2054	A1972	G1633	A1737	U1632	A1559	G1458	G1353	A1229	U1138	A1048	A830
C2138	C2055	C1973	U1634	G1743	G1634	U1560	G1461	G1361	G1230	A1144	G1049	A936
U2139	G2056	A1974	A1865	A1744	A1640	A1564	U1464	G1365	G1238	U1151	A1050	C837
A2140	U2061	A1976	G1866	C1753	A1640	A1565	A1464	G1365	G1239	U1151	A1050	G838
A2141	A2064	A1977	G1867	G1754	G1642	A1566	C1466	U1369	G1240	G1162	G1053	U839
A2142	G2065	G1979	U1870	A1755	G1643	C1568	U1467	U1370	G1243	G1163	A1058	G840
A2143	A2065	A1980	G1871	G	G1644	A1569	A1468	G1371	A1244	A1164	G1063	G841
C2144	U2069	U1981	A1872	U	G1647	C1570	G1473	G1372	U1248	G1165	U1060	A842
C2145	G2072	A1982	A1873	G1758	A1648	C1571	G1474	A1377	G1252	G1170	G1070	C845
A2146	A2073	A1983	U1874	A1764	G1649	G1572	A1475	G1374	G1250	U1171	A1062	A849
U2147	G2074	G1984	U1875	G1770	A1652	U1573	G1476	G1377	A1251	C1172	G1063	C855
A2150	G2075	U1985	A1876	G1777	C1668	G1574	G1479	U1378	G1252	A1172	G1071	A858
A2151	C2079	U1986	U1880	U1777	G1669	A1575	A1480	G1379	C1253	G1173	A1076	G859
A2152	G2080	A1987	A1881	A1778	G1670	C1576	G1492	A1380	G1254	A1175	G1077	G860
G2153	U2081	G1988	A1882	A1778	U1671	C1577	A1493	G1381	G1255	G1174	A1077	U861
U2154	U2082	U1989	G1883	A1787	G1672	G1578	U1494	G1384	G1256	A1175	G1078	U862
A2155	A2083	C1998	A1888	A1788	A1673	C1579	G1495	G1385	C1268	U1178	G1083	G863
C2156	C2084	U2001	U1889	A1789	G1674	A1580	A1499	G1386	U1259	U1179	U1084	A864
U2157	A2085	C2005	G1892	A1790	U1675	C1581	U1499	A1387	G1260	G1180	A1085	A865
C2158	U2086	C2006	A1895	A1791	G1676	C1582	A1510	U1388	A1261	C1182	G1089	U869
G2159	C2087	U2007	A1691	G1793	A1679	U1583	G1516	U1389	A1262	U1183	C1089	G870
A2160	C2088	C2008	A1696	C1794	A1680	U1584	U1517	A1402	G1272	U1184	G1090	A871
U2161	U2089	A2009	U1697	C1795	U1681	U1585	A1518	C1403	A1275	U1185	A1091	G872
C2162	U2090	U2091	A1698	G1796	A1682	U1586	U1522	C1404	C1287	G1186	G1092	G885
U2163	C2091	G2014	G1703	C1813	C1683	C1587	G1528	U1405	U1290	A1187	A1093	G890
C2165	G2092	U2015	A1710	C1818	A1691	G1588	G1528	G1411	G1291	G1188	G1096	G891
U2166	U2093	U2016	G1711	C1822	A1696	U1589	C1531	A1415	U1292	G1189	A1099	C
C2167	C2094	C2017	G1712	C1823	U1697	G1590	U1532	A1416	U1293	A1191	C1100	U894
U2167	G2096	G2018	U1713	C1828	A1698	U1591	U1533	U1424	U1294	C1192	A1101	A
A2176	U2097	U2021	A1716	A1828	G1703	U1592	C1534	G1425	U1295	C1193	G1102	G895
A2177	G2098	C2023	U1717	A1831	A1710	G1594	A1536	G1426	G1300	U1200	G1105	A896
C2178	U2099	G2024	G1718	A1832	G1711	U1595	U1537	U1427	G1301	G1201	A1106	A897
U2179	C2103	C2025	C1719	C1833	G1712	G1596	A1536	U1428	U1302	A1202	G1111	U1009
U2180	G2104	A2026	G1720	A1834	U1713	C1597	U1537	C1429	A1304	A1203	G1112	U1010
C2181	U2105	G2028	G1721	A1835	U1714	G1598	A1541	U1436	G1326	A1206	G1113	A903
C2182	A2106	U2031	U1717	A1836	A1716	U1599	A1542	G1437	A1327	G1207	G1114	A904
U2187	G2107	U2032	U1718	A1837	A1717	U1599	A1543	G1438	A1336	G1211	G1115	U905
A2190	A2114	U2033	U1719	A1838	G1718	G1600	A1543	G1439	A1337	U1212	C1022	A908
C2191	A2123	G2034	G1720	A1839	G1719	G1601	A1548	C1440	A1338	A1025	A1015	A917
U2192	A2124	U2035	G1721	A1840	G1720	U1602	G1549	G1441	G1337	A1213	G1014	
A2193	A2125	G2040	G1722	A1841	G1721	G1603					G1015	
			G1723	A1842	G1722	G1604					A1016	
			G1724	A1843	G1723	G1605					A1017	
			G1725	A1844	G1724	G1606					A1018	
			G1726	A1845	G1725	G1607					A1019	
			G1727	A1846	G1726	G1608					A1020	
			G1728	A1847	G1727	G1609					A1021	
			G1729	A1848	G1728	G1610					A1022	
			G1730	A1849	G1729	G1611					A1023	
			G1731	A1850	G1730	G1612					A1024	
			G1732	A1851	G1731	G1613					A1025	
			G1733	A1852	G1732	G1614					A1026	
			G1734	A1853	G1733	G1615					A1027	
			G1735	A1854	G1734	G1616					A1028	
			G1736	A1855	G1735	G1617					A1029	
			G1737	A1856	G1736	G1618					A1030	
			G1738	A1857	G1737	G1619					A1031	
			G1739	A1858	G1738	G1620					A1032	
			G1740	A1859	G1739	G1621					A1033	
			G1741	A1860	G1740	G1622					A1034	
			G1742	A1861	G1741	G1623					A1035	
			G1743	A1862	G1742	G1624					A1036	
			G1744	A1863	G1743	G1625					A1037	
			G1745	A1864	G1744	G1626					A1038	
			G1746	A1865	G1745	G1627					A1039	
			G1747	A1866	G1746	G1628					A1040	
			G1748	A1867	G1747	G1629					A1041	
			G1749	A1868	G1748	G1630					A1042	
			G1750	A1869	G1749	G1631					A1043	
			G1751	A1870	G1750	G1632					A1044	
			G1752	A1871	G1751	G1633					A1045	
			G1753	A1872	G1752	G1634					A1046	
			G1754	A1873	G1753	G1635					A1047	
			G1755	A1874	G1754	G1636					A1048	
			G1756	A1875	G1755	G1637					A1049	
			G1757	A1876	G1756	G1638					A1050	
			G1758	A1877	G1757	G1639					A1051	
			G1759	A1878	G1758	G1640					A1052	
			G1760	A1879	G1759	G1641					A1053	
			G1761	A1880	G1760	G1642					A1054	
			G1762	A1881	G1761	G1643					A1055	
			G1763	A1882	G1762	G1644					A1056	
			G1764	A1883	G1763	G1645					A1057	
			G1765	A1884	G1764	G1646					A1058	
			G1766	A1885	G1765	G1647					A1059	
			G1767	A1886	G1766	G1648					A1060	
			G1768	A1887	G1767	G1649					A1061	
			G1769	A1888	G1768	G1650					A1062	
			G1770	A1889	G1769	G1651					A1063	
			G1771	A1890	G1770	G1652					A1064	
			G1772	A1891	G1771	G1653					A1065	
			G1773	A1892	G1772	G1654					A1066	
			G1774	A1893	G1773	G1655					A1067	
			G1775	A1894	G1774	G1656					A1068	
			G1776	A1895	G1775	G1657					A1069	
			G1777	A1896	G1776	G1658					A1070	
			G1778	A1897	G1777	G1659					A1071	
			G1779	A1898	G1778	G1660					A1072	
			G1780	A1899	G1779	G1661					A1073	
			G1781	A1900	G1780	G1662					A1074	
			G1782	A1901	G1781	G1663					A1075	
			G1783	A1902	G1782	G1664					A1076	
			G1784	A1903	G1783	G1665					A1077	
			G1785	A1904	G1784	G1666					A1078	
			G1786	A1905	G1785	G1667					A1079	
			G1787	A1906	G1786	G1668					A1080	
			G1788	A1907	G1787	G1669					A1081	
			G1789	A1908	G1788	G1670					A1082	
			G1790	A1909	G1789	G1671					A1083	
			G1791	A1910	G1790	G1672					A1084	
			G1792	A1911	G1791	G1673					A1085	
			G1793	A1912	G1792	G1674					A1086	
			G1794	A1913	G1793	G1675					A1087	
			G1795	A1914	G1794	G1676					A1088	
			G1796	A1915	G1795	G1677					A1089	
			G1797	A1916	G1796	G1678					A1090	
			G1798	A1917	G1797	G1679					A1091	
			G1799	A1918	G1798	G1680					A1092	
			G1800	A191								



### • Molecule 10: 5S rRNA



### • Molecule 11: Large ribosomal subunit protein uL2





- Molecule 12: Large ribosomal subunit protein uL3

Chain D: 86% 12% ..



- Molecule 13: Large ribosomal subunit protein uL4

Chain E: 77% 19% . .



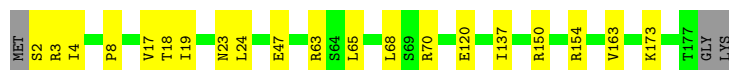
- Molecule 14: Large ribosomal subunit protein uL5

Chain F: 75% 21% .



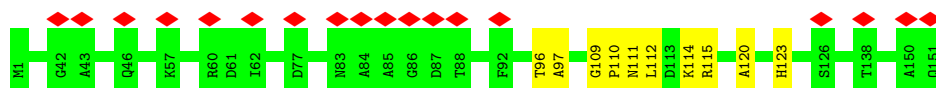
- Molecule 15: Large ribosomal subunit protein uL6

Chain G: 87% 11% .



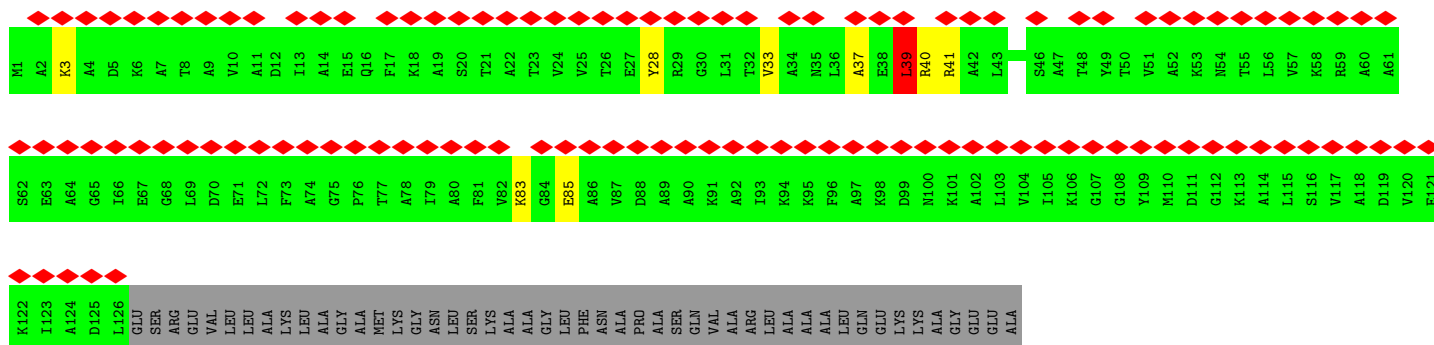
- Molecule 16: 50S ribosomal protein L9

Chain H: 12% 93% 7%

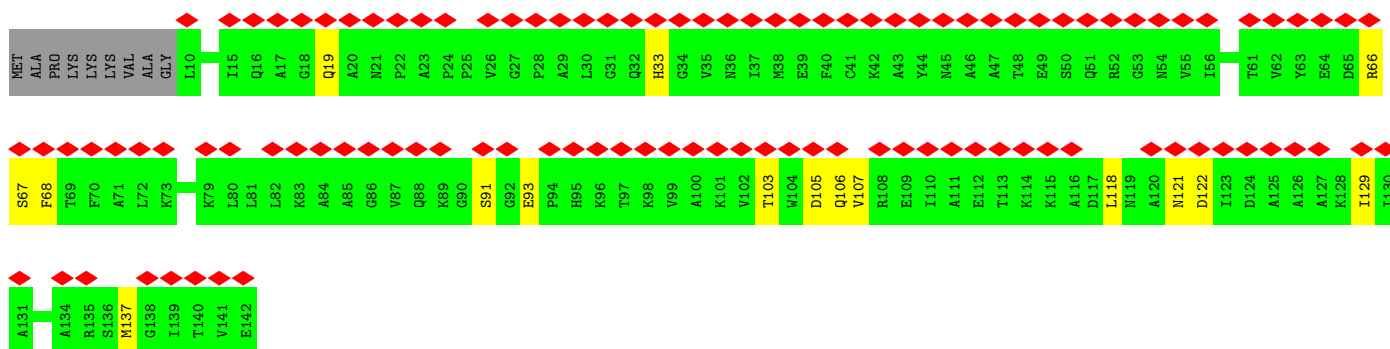
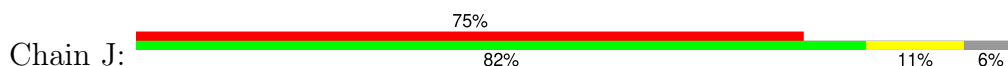


- Molecule 17: Large ribosomal subunit protein uL10

Chain I: 66% 67% 5% 28%



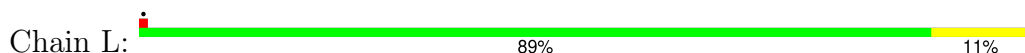
- Molecule 18: Large ribosomal subunit protein uL11



- Molecule 19: Large ribosomal subunit protein uL13




- Molecule 20: Large ribosomal subunit protein uL14



- Molecule 21: Large ribosomal subunit protein uL15



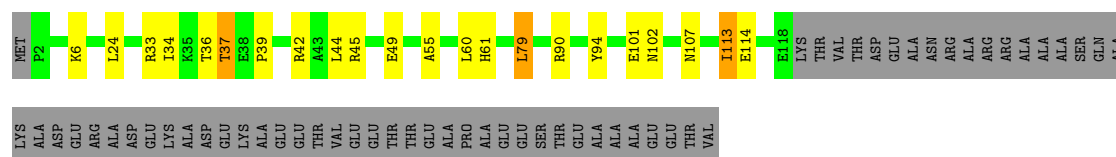
- Molecule 22: Large ribosomal subunit protein uL16

Chain N:  83% 14%




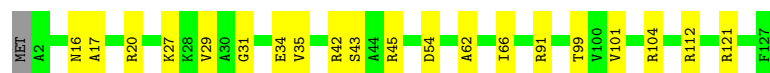
- Molecule 23: Large ribosomal subunit protein bL17

Chain O:  55% 11% 33%




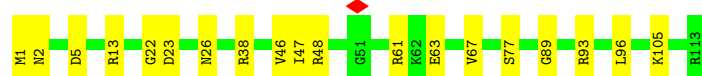
- Molecule 24: Large ribosomal subunit protein uL18

Chain P:  83% 16%




- Molecule 25: Large ribosomal subunit protein bL19

Chain Q:  83% 17%




- Molecule 26: Large ribosomal subunit protein bL20

Chain R:  86% 10%



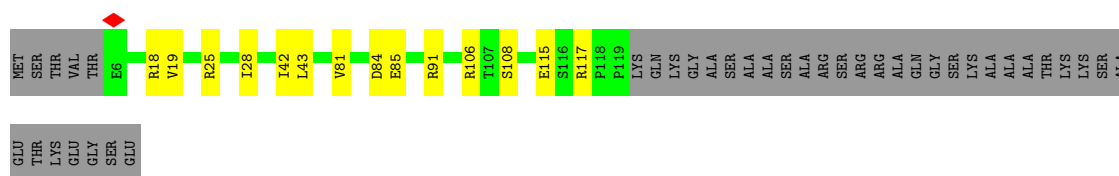
- Molecule 27: Large ribosomal subunit protein bL21

Chain S:  81% 18%



- Molecule 28: Large ribosomal subunit protein uL22

Chain T:  65% 9% 25%



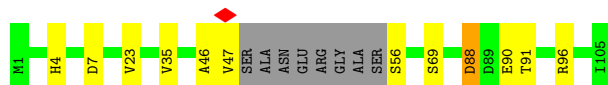
- Molecule 29: Large ribosomal subunit protein uL23

Chain U: 86% 8% 6%



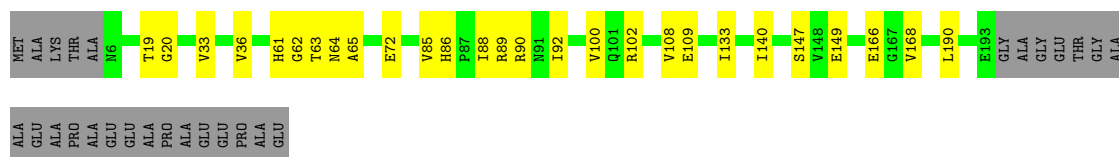
- Molecule 30: Large ribosomal subunit protein uL24

Chain V: 81% 10% 8%



- Molecule 31: Large ribosomal subunit protein bL25

Chain W: 75% 13% 13%



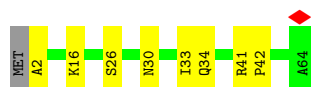
- Molecule 32: Large ribosomal subunit protein bL27

Chain X: 6% 78% 15% 7%



- Molecule 33: Large ribosomal subunit protein bL28

Chain Y: 86% 12% 2%



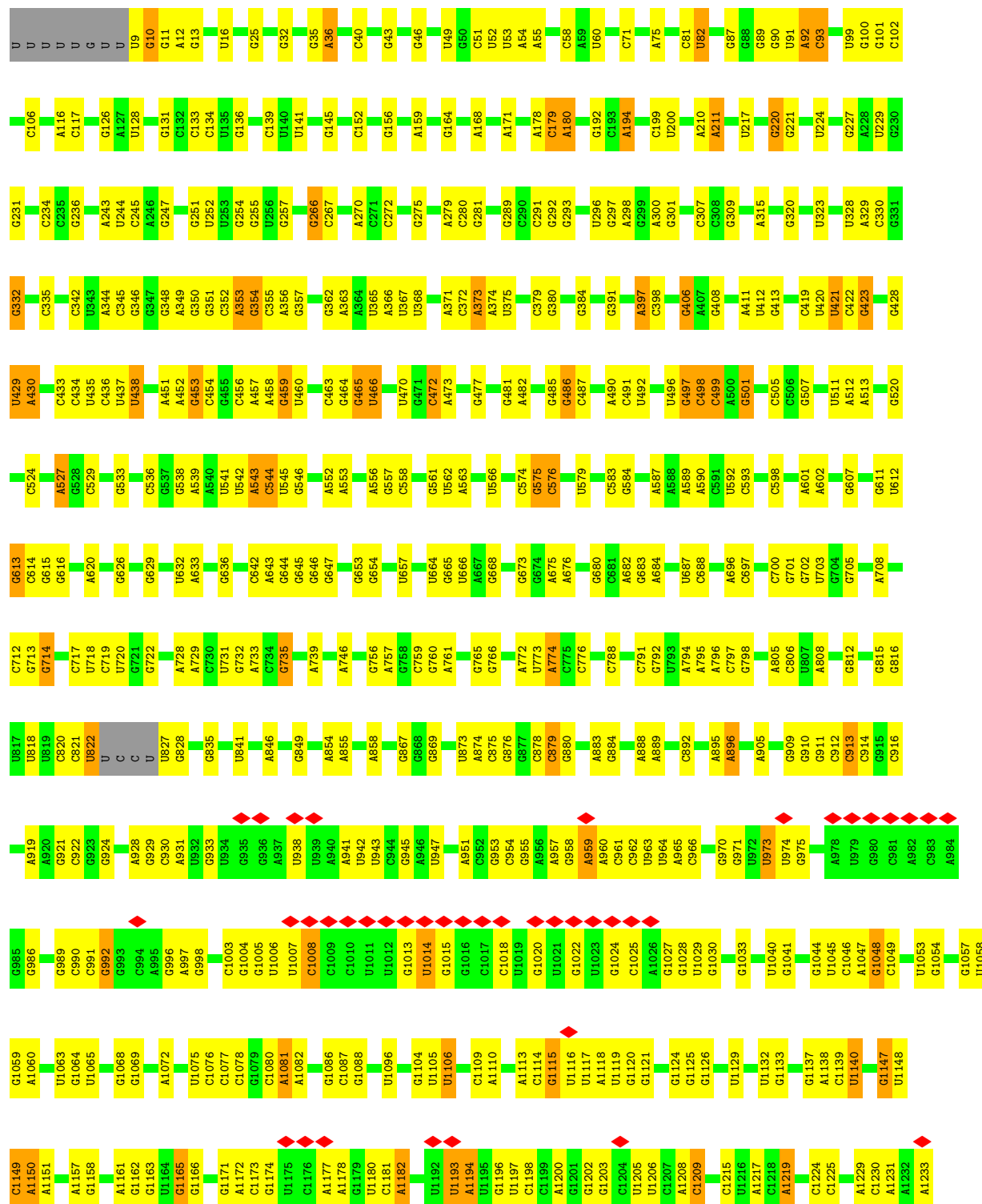
- Molecule 34: Large ribosomal subunit protein uL29

Chain Z: 68% 13% 18%



• Molecule 35: 16S rRNA


Chain a: 55% 37% 6%






SER  
ALA  
GLY  
THR  
THR  
THR  
SER  
THR  
GLU  
GLU  
ALA  
GLY  
ARG  
ALA  
ALA  
THR  
SER  
ASP  
ALA  
PRO  
ALA  
GLY  
THR  
ALA  
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ALA  
GLU  
ALA  
PRO  
ALA  
GLU  
SER  
THR  
GLU  
SER

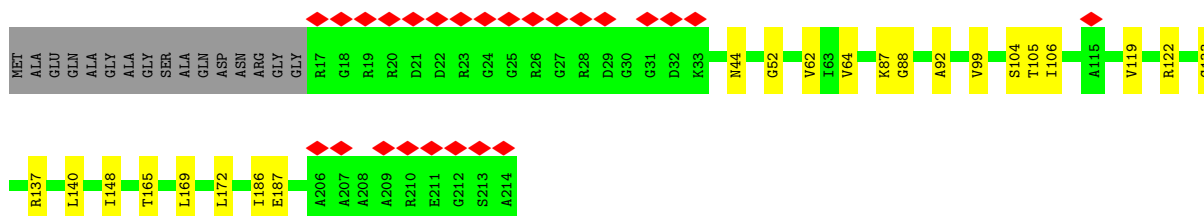
- Molecule 38: Small ribosomal subunit protein uS4

Chain d:  85% 14%




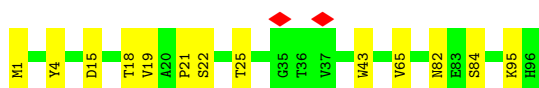
- Molecule 39: Small ribosomal subunit protein uS5

Chain e:  12% 82% 10% 7%




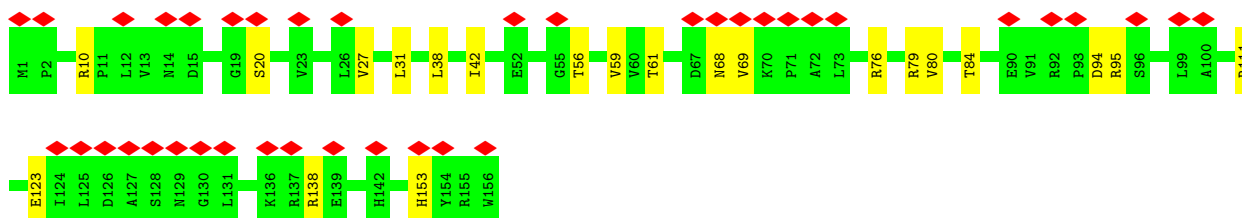
- Molecule 40: Small ribosomal subunit protein bS6

Chain f:  86% 14%




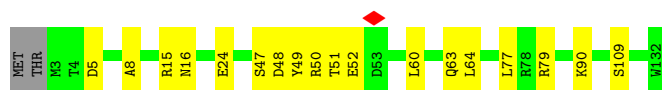
- Molecule 41: Small ribosomal subunit protein uS7

Chain g:  25% 87% 13%



- Molecule 42: Small ribosomal subunit protein uS8

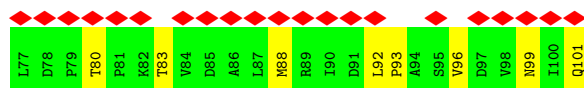
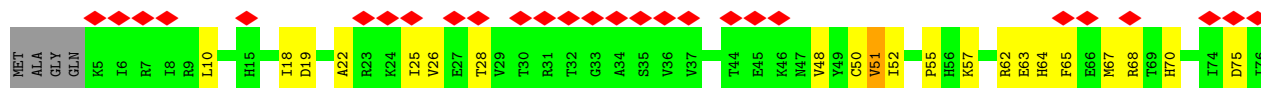
Chain h:  85% 14%



- Molecule 43: Small ribosomal subunit protein uS9



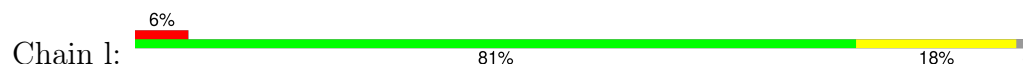
- Molecule 44: Small ribosomal subunit protein uS10



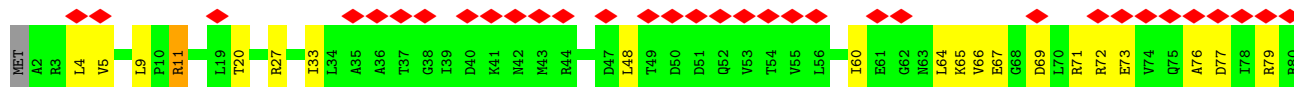
- Molecule 45: Small ribosomal subunit protein uS11



- Molecule 46: Small ribosomal subunit protein uS12

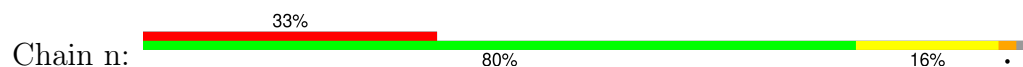


- Molecule 47: Small ribosomal subunit protein uS13

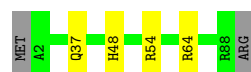




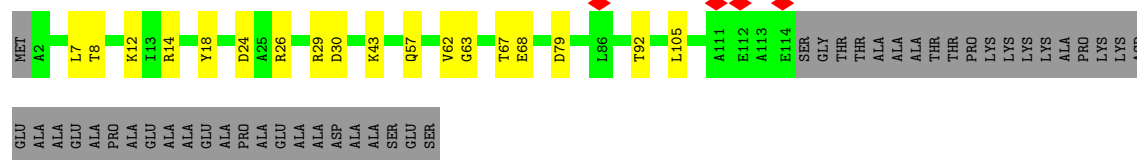
- Molecule 48: Small ribosomal subunit protein uS14B



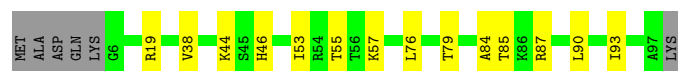
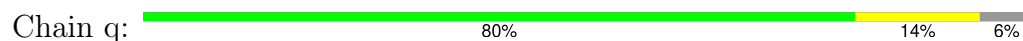
- Molecule 49: Small ribosomal subunit protein uS15



- Molecule 50: Small ribosomal subunit protein bS16



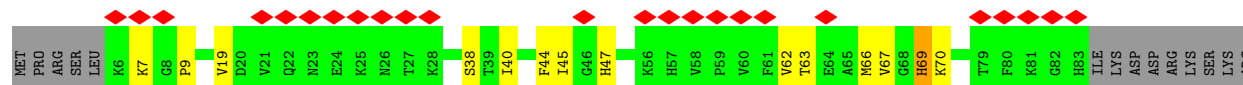
- Molecule 51: Small ribosomal subunit protein uS17



- Molecule 52: Small ribosomal subunit protein bS18B

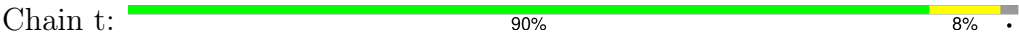


- Molecule 53: Small ribosomal subunit protein uS19



ARG

- Molecule 54: Small ribosomal subunit protein bS20



- Molecule 55: Conserved domain protein



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	227969	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 ( $e^-/\text{\AA}^2$ )	52.51	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.026	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	427.6, 427.6, 427.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.069, 1.069, 1.069	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

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	1	0.12	0/486	0.28	0/651
2	2	0.16	0/520	0.31	0/698
3	3	0.10	0/427	0.24	0/572
4	4	0.11	0/424	0.29	0/567
5	5	0.13	0/375	0.33	0/493
6	6	0.10	0/507	0.31	0/672
7	7	0.16	0/302	0.38	0/401
8	8	0.11	0/191	0.27	0/247
9	A	0.10	3/74597 (0.0%)	0.27	22/116386 (0.0%)
10	B	0.06	0/2797	0.17	0/4357
11	C	0.10	0/2140	0.27	0/2879
12	D	0.09	0/1609	0.23	0/2165
13	E	0.10	0/1576	0.27	0/2132
14	F	0.12	0/1459	0.34	0/1962
15	G	0.10	0/1369	0.22	0/1848
16	H	0.11	0/1027	0.24	0/1398
17	I	0.12	0/925	0.27	0/1246
18	J	0.10	0/1006	0.23	0/1364
19	K	0.10	0/1154	0.22	0/1565
20	L	0.11	0/938	0.27	0/1257
21	M	0.08	0/1091	0.20	0/1457
22	N	0.12	0/1094	0.27	0/1474
23	O	0.09	0/936	0.26	0/1256
24	P	0.10	0/966	0.22	0/1298
25	Q	0.11	0/921	0.24	0/1236
26	R	0.11	0/1000	0.23	0/1341
27	S	0.07	0/778	0.19	0/1048
28	T	0.10	0/887	0.28	0/1204
29	U	0.09	0/749	0.24	0/1006
30	V	0.12	0/737	0.26	0/987
31	W	0.10	0/1422	0.24	0/1941
32	X	0.12	0/613	0.32	0/821

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Y	0.10	0/478	0.27	0/641
34	Z	0.10	0/530	0.26	0/708
35	a	0.13	3/36201 (0.0%)	0.31	11/56488 (0.0%)
36	b	0.09	0/1822	0.21	0/2457
37	c	0.11	0/1696	0.30	0/2276
38	d	0.10	0/1672	0.24	0/2251
39	e	0.09	0/1449	0.27	0/1949
40	f	0.11	0/782	0.23	0/1059
41	g	0.11	0/1260	0.28	0/1701
42	h	0.09	0/1018	0.24	0/1375
43	i	0.11	0/1012	0.32	0/1362
44	j	0.14	0/789	0.38	0/1069
45	k	0.08	0/889	0.24	0/1201
46	l	0.11	0/969	0.33	0/1294
47	m	0.15	0/942	0.34	0/1260
48	n	0.09	0/488	0.24	0/650
49	o	0.09	0/718	0.27	0/963
50	p	0.10	0/908	0.24	0/1226
51	q	0.09	0/741	0.25	0/993
52	r	0.10	0/517	0.28	0/691
53	s	0.13	0/647	0.34	0/871
54	t	0.10	0/658	0.26	0/875
55	u	0.12	0/280	0.29	0/359
All	All	0.11	6/161489 (0.0%)	0.28	33/241648 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2137	A	O3'-P	-10.55	1.45	1.61
35	a	1171	G	C6-O6	-8.58	1.06	1.24
35	a	1236	G	N9-C4	8.06	1.54	1.38
9	A	1224	G	N9-C4	7.85	1.53	1.38
35	a	1236	G	N9-C8	-7.67	1.22	1.37

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1224	G	N7-C8-N9	-26.15	34.66	113.10
35	a	1236	G	N7-C8-N9	-26.00	35.10	113.10
9	A	1224	G	C4-C5-N7	-22.59	43.02	110.80
35	a	1236	G	C4-C5-N7	-22.58	43.05	110.80
35	a	1171	G	N1-C6-O6	-22.45	52.53	119.90

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	1	483	0	513	4	0
2	2	510	0	501	18	0
3	3	423	0	463	3	0
4	4	416	0	422	8	0
5	5	372	0	406	7	0
6	6	502	0	541	8	0
7	7	298	0	321	4	0
8	8	189	0	205	7	0
9	A	66623	0	33523	700	0
10	B	2501	0	1273	29	0
11	C	2097	0	2149	38	0
12	D	1587	0	1630	23	0
13	E	1553	0	1587	34	0
14	F	1437	0	1470	40	0
15	G	1348	0	1399	19	0
16	H	1018	0	988	7	0
17	I	918	0	959	8	0
18	J	990	0	1021	10	0
19	K	1127	0	1154	8	0
20	L	930	0	989	11	0
21	M	1078	0	1151	11	0
22	N	1068	0	1107	16	0
23	O	919	0	959	16	0
24	P	956	0	991	15	0
25	Q	907	0	938	13	0
26	R	988	0	1038	11	0
27	S	768	0	820	15	0
28	T	873	0	909	11	0
29	U	739	0	785	6	0
30	V	731	0	782	8	0
31	W	1407	0	1423	20	0
32	X	604	0	622	9	0
33	Y	470	0	484	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	Z	527	0	538	6	0
35	a	32341	0	16271	418	0
36	b	1793	0	1839	9	0
37	c	1672	0	1722	15	0
38	d	1641	0	1668	25	0
39	e	1433	0	1490	12	0
40	f	771	0	797	8	0
41	g	1240	0	1293	14	0
42	h	1003	0	1039	12	0
43	i	994	0	1050	12	0
44	j	775	0	808	31	0
45	k	871	0	885	10	0
46	l	958	0	1045	19	0
47	m	935	0	986	35	0
48	n	477	0	503	9	0
49	o	709	0	747	3	0
50	p	891	0	935	13	0
51	q	730	0	774	9	0
52	r	512	0	543	5	0
53	s	630	0	640	21	0
54	t	655	0	707	7	0
55	u	280	0	342	1	0
56	2	1	0	0	0	0
56	A	76	0	0	0	0
56	C	1	0	0	0	0
56	D	1	0	0	0	0
56	a	28	0	0	0	0
All	All	148775	0	100145	1525	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 7.

The worst 5 of 1525 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)
9:A:1171:C:O2	9:A:1224:G:N2	1.85	1.10
9:A:592:A:HO2'	9:A:596:C:HO2'	1.14	0.95
35:a:1139:C:O2	35:a:1162:G:N2	2.00	0.94
35:a:1335:G:N2	44:j:63:GLU:O	2.01	0.94
9:A:1558:C:O2	9:A:1613:G:N2	2.02	0.93

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	1	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
2	2	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
3	3	52/57 (91%)	52 (100%)	0	0	100	100
4	4	48/55 (87%)	40 (83%)	8 (17%)	0	100	100
5	5	43/47 (92%)	42 (98%)	1 (2%)	0	100	100
6	6	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
7	7	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
8	8	21/24 (88%)	21 (100%)	0	0	100	100
11	C	271/278 (98%)	259 (96%)	12 (4%)	0	100	100
12	D	212/217 (98%)	201 (95%)	11 (5%)	0	100	100
13	E	205/215 (95%)	185 (90%)	20 (10%)	0	100	100
14	F	179/187 (96%)	161 (90%)	18 (10%)	0	100	100
15	G	174/179 (97%)	171 (98%)	3 (2%)	0	100	100
16	H	149/151 (99%)	140 (94%)	9 (6%)	0	100	100
17	I	124/174 (71%)	119 (96%)	4 (3%)	1 (1%)	16	48
18	J	131/142 (92%)	128 (98%)	3 (2%)	0	100	100
19	K	145/147 (99%)	140 (97%)	5 (3%)	0	100	100
20	L	119/122 (98%)	108 (91%)	11 (9%)	0	100	100
21	M	143/147 (97%)	138 (96%)	5 (4%)	0	100	100
22	N	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
23	O	115/174 (66%)	110 (96%)	5 (4%)	0	100	100
24	P	124/127 (98%)	121 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Q	111/113 (98%)	107 (96%)	4 (4%)	0	100	100
26	R	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
27	S	100/103 (97%)	99 (99%)	1 (1%)	0	100	100
28	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
29	U	92/100 (92%)	84 (91%)	8 (9%)	0	100	100
30	V	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
31	W	186/215 (86%)	178 (96%)	8 (4%)	0	100	100
32	X	80/88 (91%)	68 (85%)	12 (15%)	0	100	100
33	Y	61/64 (95%)	61 (100%)	0	0	100	100
34	Z	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
36	b	226/277 (82%)	222 (98%)	4 (2%)	0	100	100
37	c	208/275 (76%)	190 (91%)	18 (9%)	0	100	100
38	d	198/201 (98%)	192 (97%)	6 (3%)	0	100	100
39	e	196/214 (92%)	190 (97%)	6 (3%)	0	100	100
40	f	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
41	g	154/156 (99%)	149 (97%)	5 (3%)	0	100	100
42	h	128/132 (97%)	124 (97%)	4 (3%)	0	100	100
43	i	124/150 (83%)	116 (94%)	8 (6%)	0	100	100
44	j	95/101 (94%)	82 (86%)	13 (14%)	0	100	100
45	k	115/138 (83%)	110 (96%)	5 (4%)	0	100	100
46	l	120/124 (97%)	108 (90%)	12 (10%)	0	100	100
47	m	114/124 (92%)	102 (90%)	12 (10%)	0	100	100
48	n	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
49	o	85/89 (96%)	84 (99%)	1 (1%)	0	100	100
50	p	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
51	q	90/98 (92%)	87 (97%)	3 (3%)	0	100	100
52	r	62/84 (74%)	55 (89%)	7 (11%)	0	100	100
53	s	76/93 (82%)	69 (91%)	7 (9%)	0	100	100
54	t	82/86 (95%)	82 (100%)	0	0	100	100
55	u	30/33 (91%)	29 (97%)	1 (3%)	0	100	100
All	All	5989/6653 (90%)	5688 (95%)	300 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	I	39	LEU

### 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	1	53/54 (98%)	53 (100%)	0	100	100
2	2	57/63 (90%)	56 (98%)	1 (2%)	54	75
3	3	43/46 (94%)	43 (100%)	0	100	100
4	4	48/52 (92%)	48 (100%)	0	100	100
5	5	35/36 (97%)	35 (100%)	0	100	100
6	6	53/54 (98%)	53 (100%)	0	100	100
7	7	35/35 (100%)	34 (97%)	1 (3%)	37	64
8	8	18/19 (95%)	18 (100%)	0	100	100
11	C	214/218 (98%)	214 (100%)	0	100	100
12	D	160/163 (98%)	158 (99%)	2 (1%)	65	81
13	E	167/173 (96%)	163 (98%)	4 (2%)	44	68
14	F	150/156 (96%)	150 (100%)	0	100	100
15	G	148/150 (99%)	147 (99%)	1 (1%)	81	90
16	H	90/116 (78%)	90 (100%)	0	100	100
17	I	89/120 (74%)	88 (99%)	1 (1%)	70	84
18	J	102/108 (94%)	102 (100%)	0	100	100
19	K	117/120 (98%)	117 (100%)	0	100	100
20	L	99/100 (99%)	99 (100%)	0	100	100
21	M	112/114 (98%)	112 (100%)	0	100	100
22	N	110/116 (95%)	109 (99%)	1 (1%)	75	87
23	O	96/138 (70%)	93 (97%)	3 (3%)	35	63
24	P	93/94 (99%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Q	100/100 (100%)	100 (100%)	0	100	100
26	R	97/99 (98%)	97 (100%)	0	100	100
27	S	82/83 (99%)	81 (99%)	1 (1%)	67	83
28	T	90/117 (77%)	90 (100%)	0	100	100
29	U	82/85 (96%)	82 (100%)	0	100	100
30	V	81/86 (94%)	79 (98%)	2 (2%)	42	68
31	W	154/168 (92%)	154 (100%)	0	100	100
32	X	59/63 (94%)	59 (100%)	0	100	100
33	Y	50/51 (98%)	50 (100%)	0	100	100
34	Z	58/66 (88%)	57 (98%)	1 (2%)	56	76
36	b	191/218 (88%)	189 (99%)	2 (1%)	73	85
37	c	171/212 (81%)	171 (100%)	0	100	100
38	d	175/176 (99%)	174 (99%)	1 (1%)	84	91
39	e	139/147 (95%)	138 (99%)	1 (1%)	81	90
40	f	85/85 (100%)	83 (98%)	2 (2%)	44	68
41	g	132/132 (100%)	132 (100%)	0	100	100
42	h	106/108 (98%)	105 (99%)	1 (1%)	75	87
43	i	102/125 (82%)	101 (99%)	1 (1%)	73	85
44	j	88/90 (98%)	86 (98%)	2 (2%)	45	69
45	k	91/105 (87%)	90 (99%)	1 (1%)	70	84
46	l	103/105 (98%)	103 (100%)	0	100	100
47	m	99/104 (95%)	98 (99%)	1 (1%)	73	85
48	n	49/50 (98%)	46 (94%)	3 (6%)	15	45
49	o	75/77 (97%)	74 (99%)	1 (1%)	65	81
50	p	92/118 (78%)	91 (99%)	1 (1%)	70	84
51	q	78/83 (94%)	78 (100%)	0	100	100
52	r	55/72 (76%)	54 (98%)	1 (2%)	54	75
53	s	69/84 (82%)	68 (99%)	1 (1%)	62	80
54	t	69/70 (99%)	69 (100%)	0	100	100
55	u	30/31 (97%)	30 (100%)	0	100	100
All	All	4941/5355 (92%)	4904 (99%)	37 (1%)	80	90

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	k	78	ASN
52	r	70	ASN
47	m	11	ARG
48	n	24	CYS
23	O	79	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
29	U	58	ASN
45	k	110	GLN
36	b	94	GLN
52	r	61	GLN
42	h	35	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	116/118 (98%)	19 (16%)	2 (1%)
35	a	1504/1528 (98%)	275 (18%)	0
9	A	3096/3120 (99%)	534 (17%)	32 (1%)
All	All	4716/4766 (98%)	828 (17%)	34 (0%)

5 of 828 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	7	U
9	A	19	U
9	A	20	G
9	A	24	G
9	A	31	U

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	2626	U
9	A	2693	A
10	B	34	G
9	A	1040	U

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Mol	Chain	Res	Type
9	A	1010	U

## 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 107 ligands modelled in this entry, 107 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.

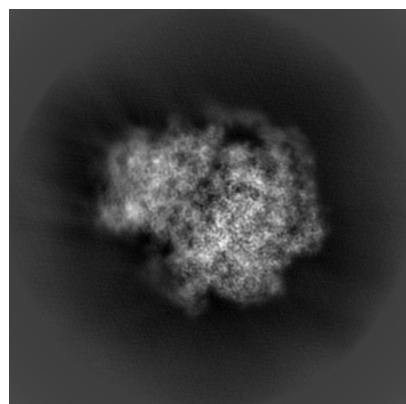
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47363. These allow visual inspection of the internal detail of the map and identification of artifacts.

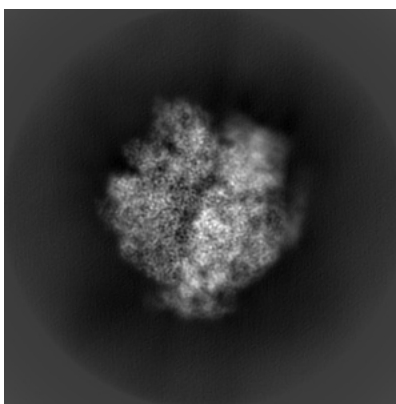
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

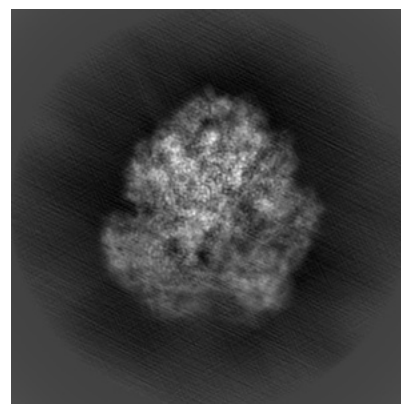
#### 6.1.1 Primary map



X

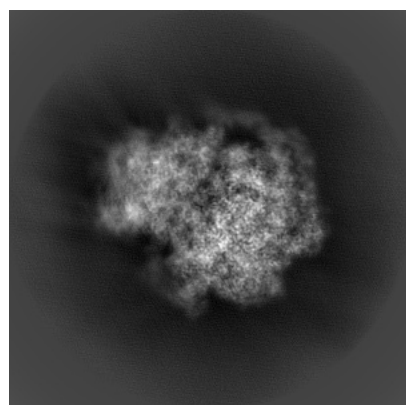


Y

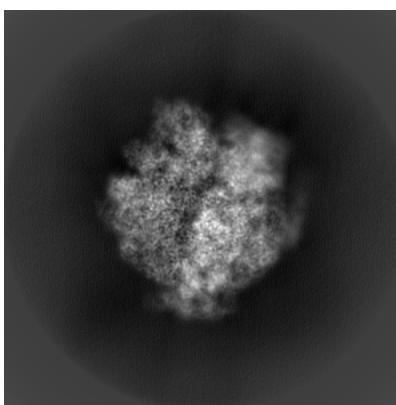


Z

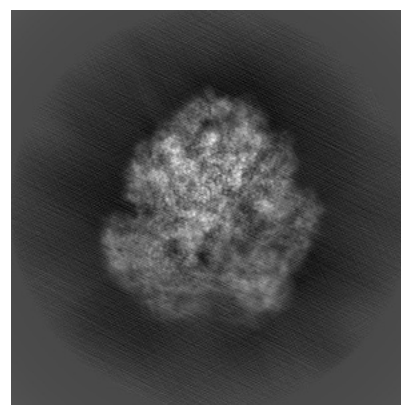
#### 6.1.2 Raw map



X



Y

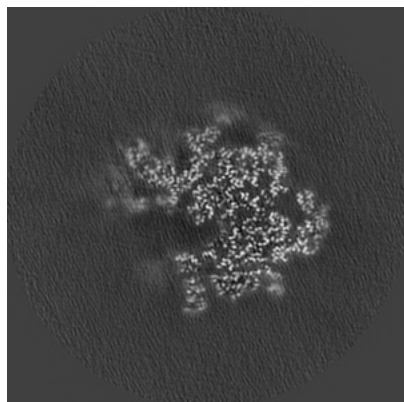


Z

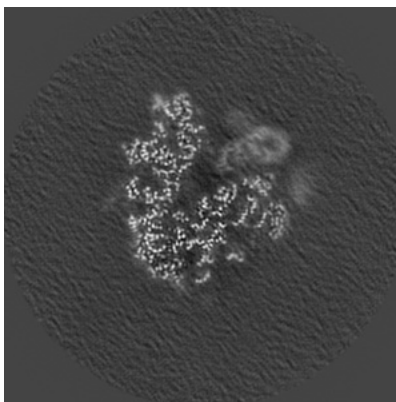
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

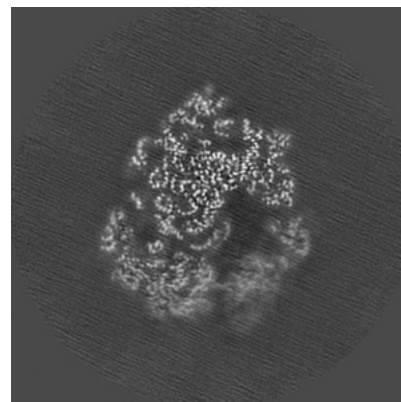
### 6.2.1 Primary map



X Index: 200

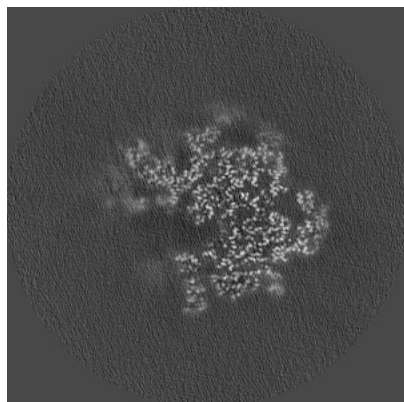


Y Index: 200

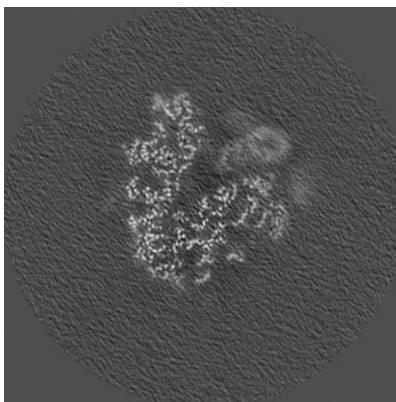


Z Index: 200

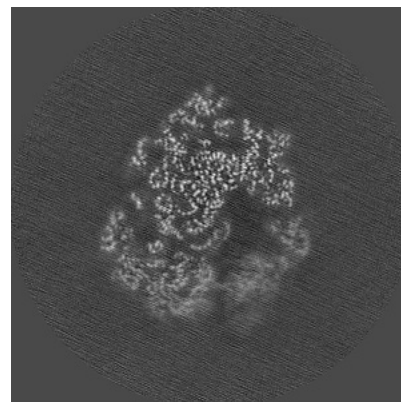
### 6.2.2 Raw map



X Index: 200



Y Index: 200

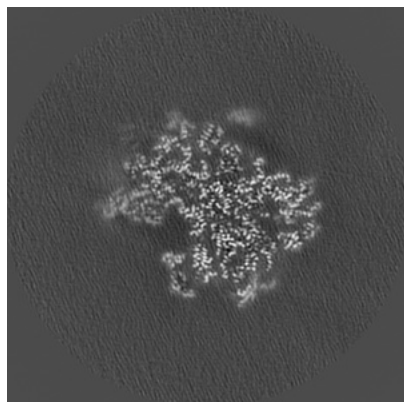


Z Index: 200

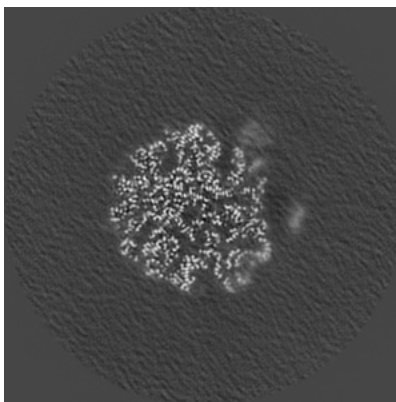
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

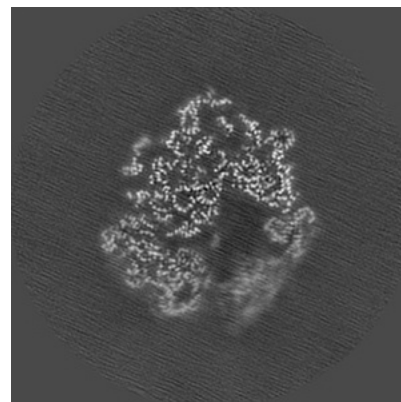
### 6.3.1 Primary map



X Index: 183

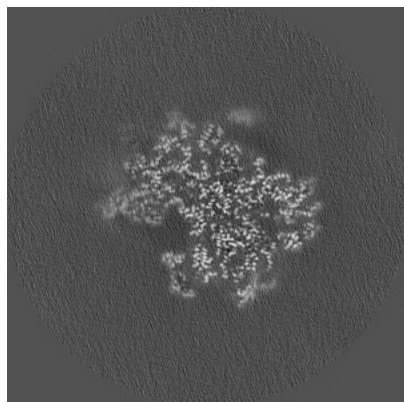


Y Index: 229

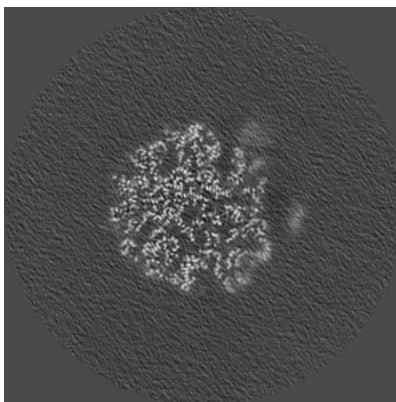


Z Index: 194

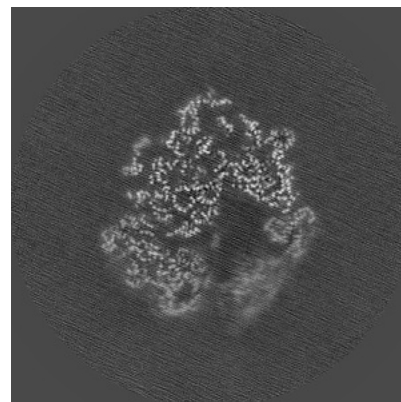
### 6.3.2 Raw map



X Index: 183



Y Index: 229

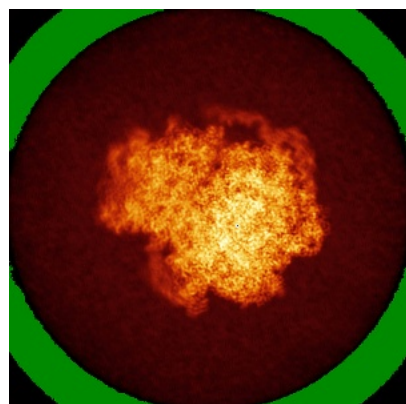


Z Index: 194

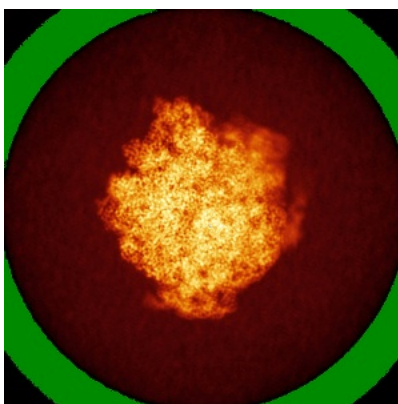
The images above show the largest variance slices of the map in three orthogonal directions.

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

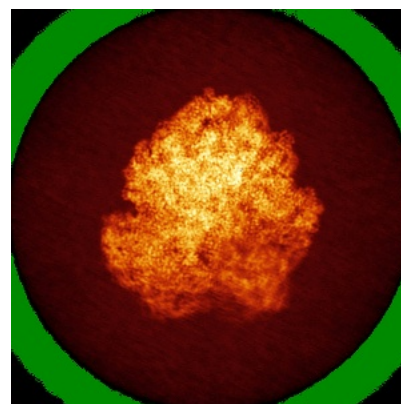
### 6.4.1 Primary map



X

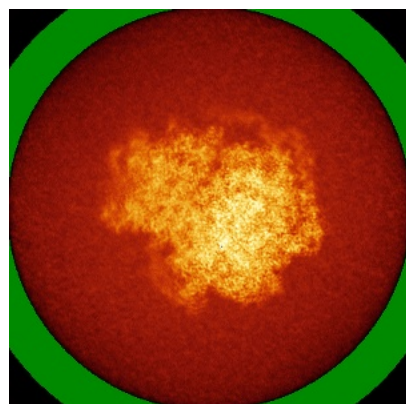


Y

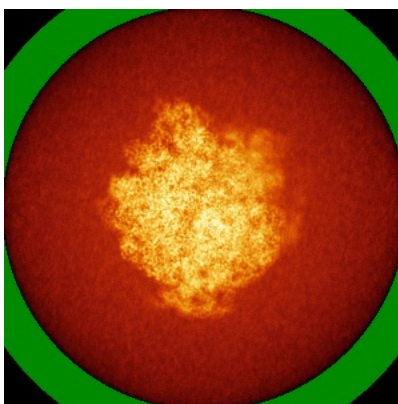


Z

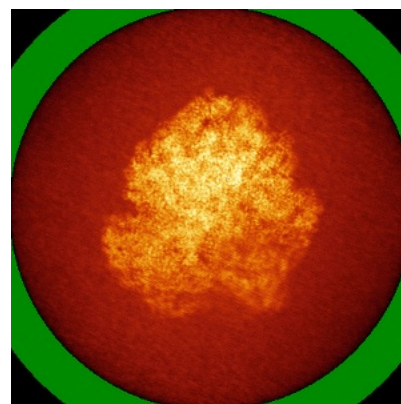
### 6.4.2 Raw map



X



Y

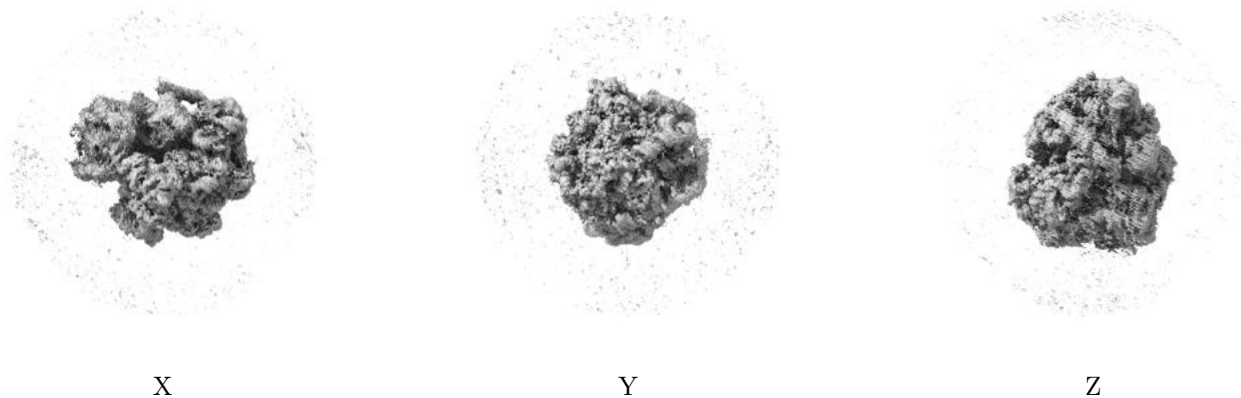


Z

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.

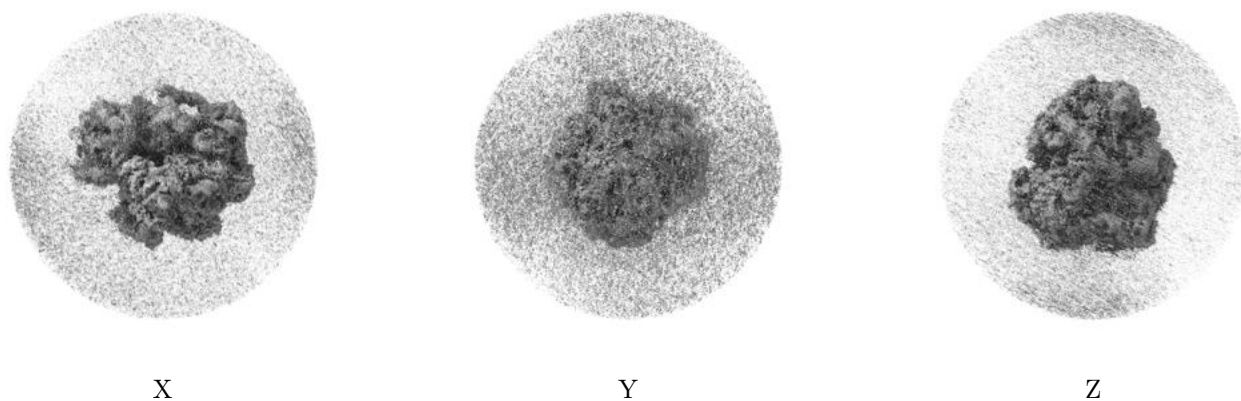
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

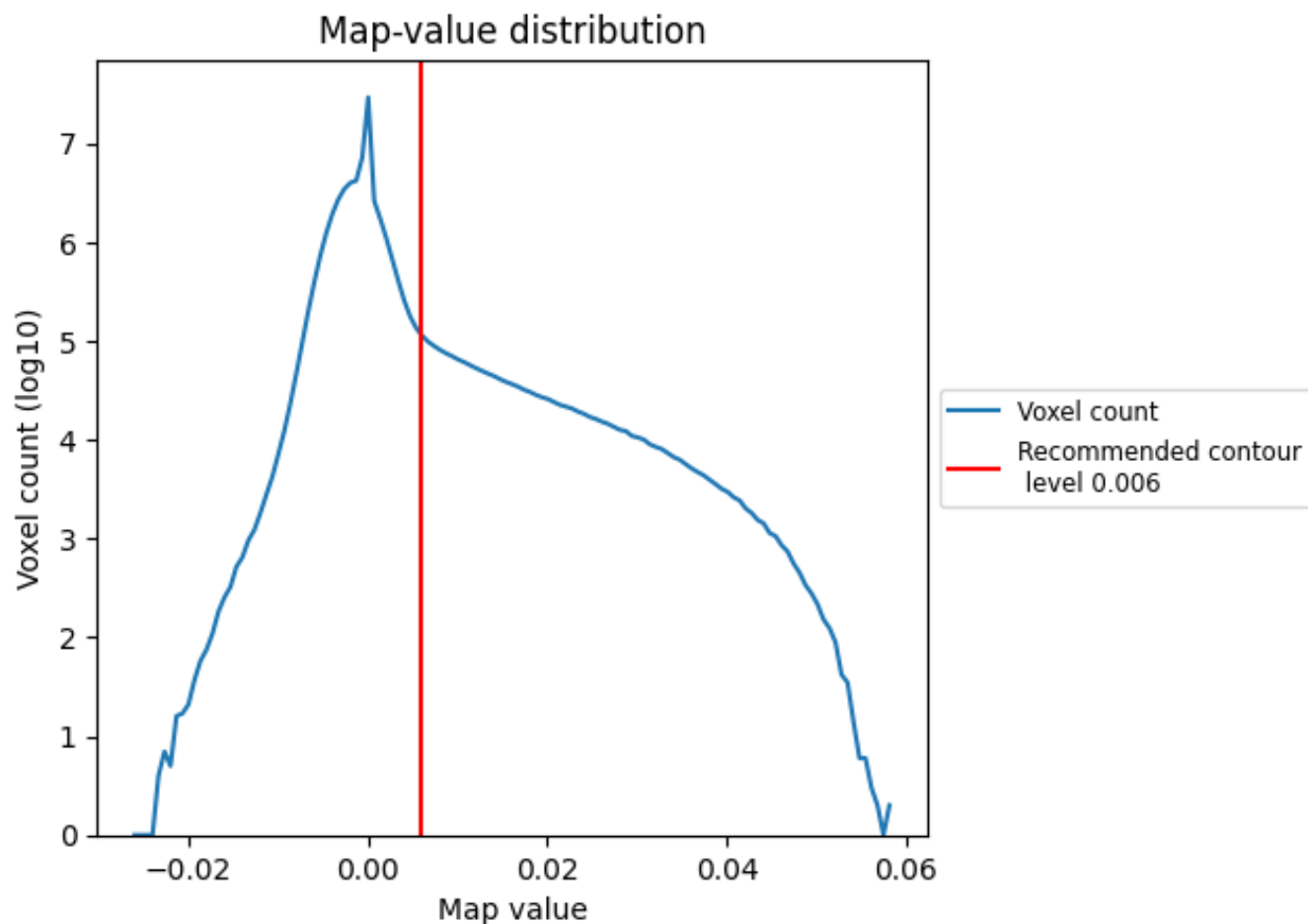
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

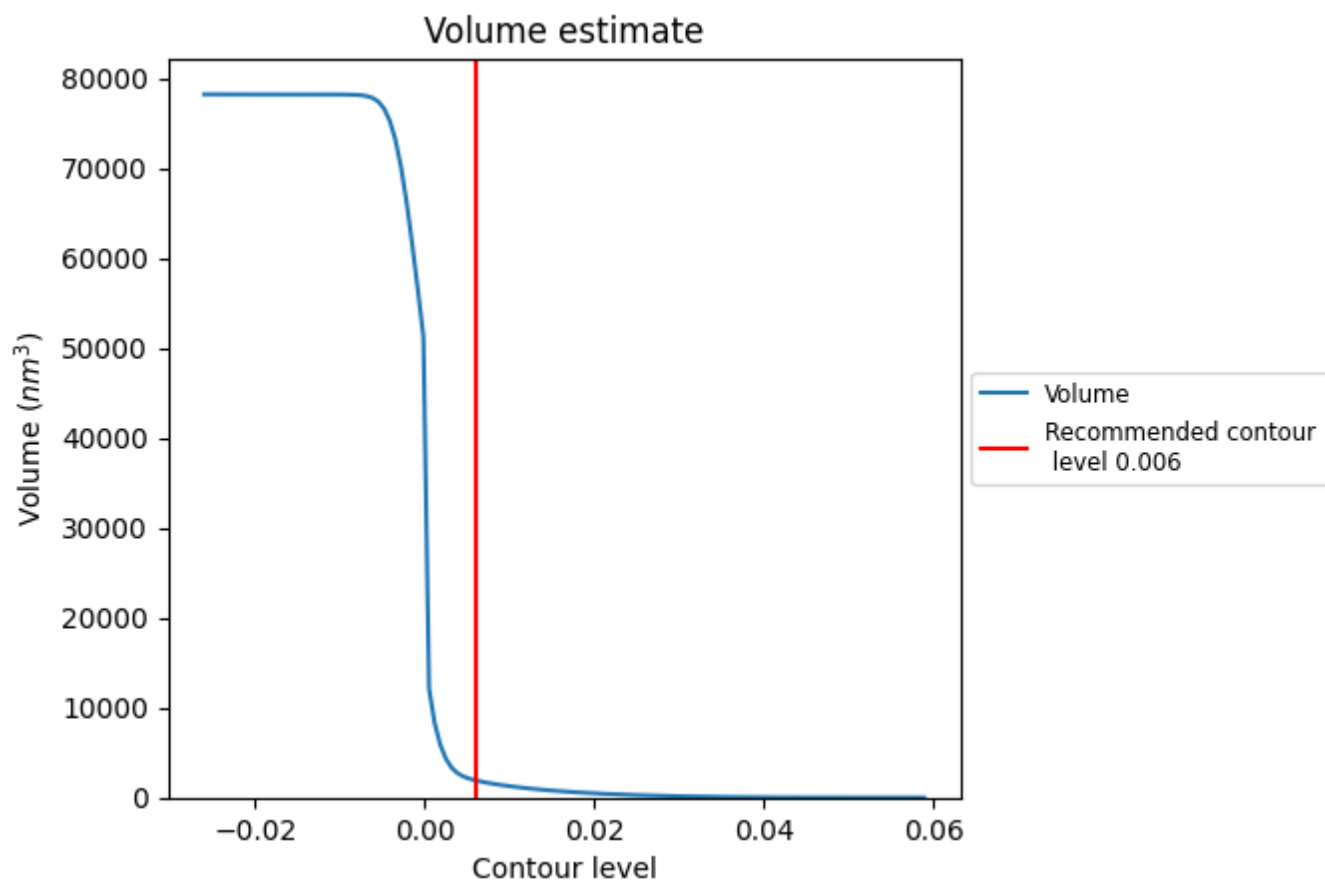
This section contains the results of statistical analysis of the map.

### 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.

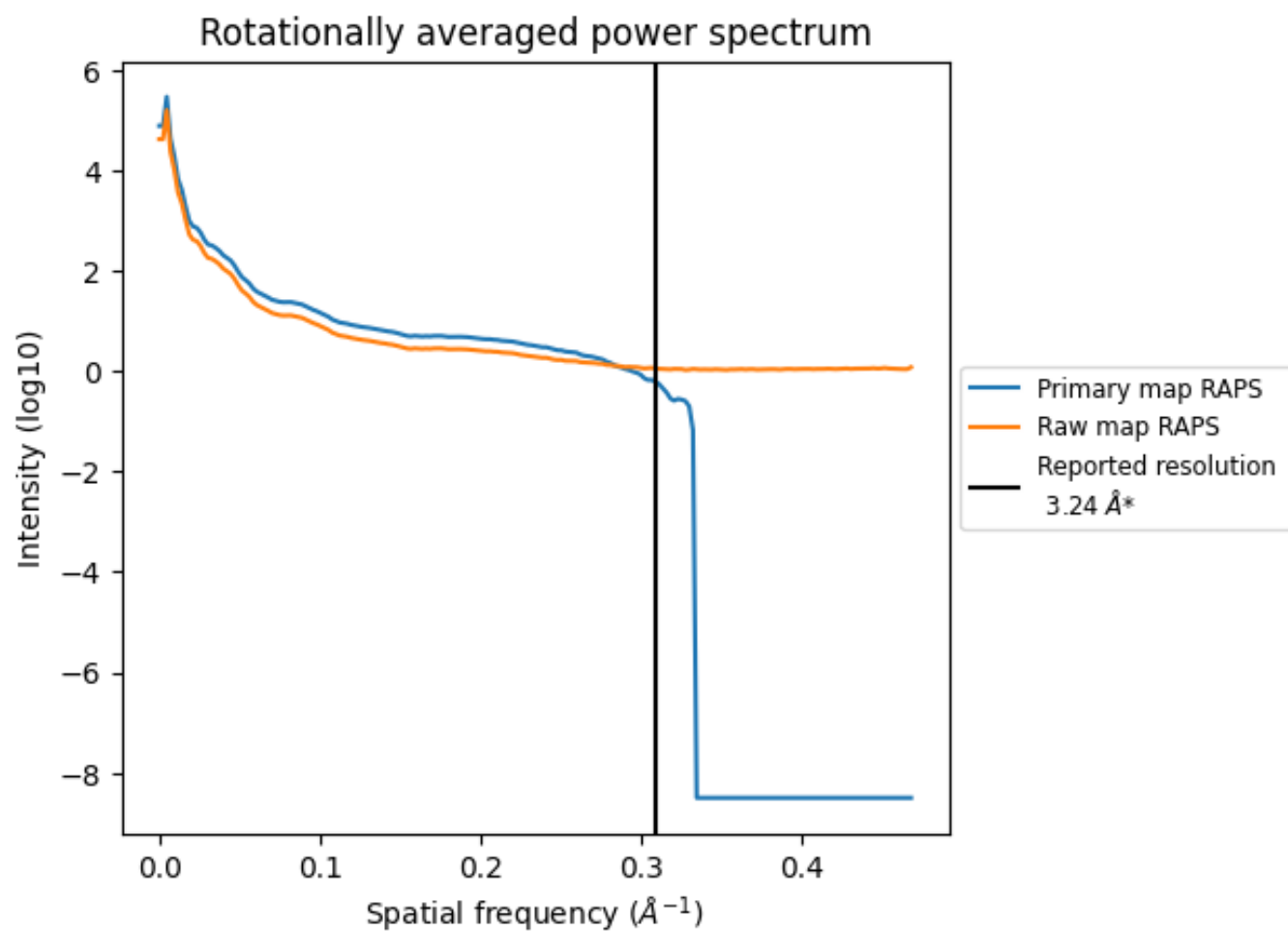
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is  $1913 \text{ nm}^3$ ; this corresponds to an approximate mass of 1728 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 ⓘ

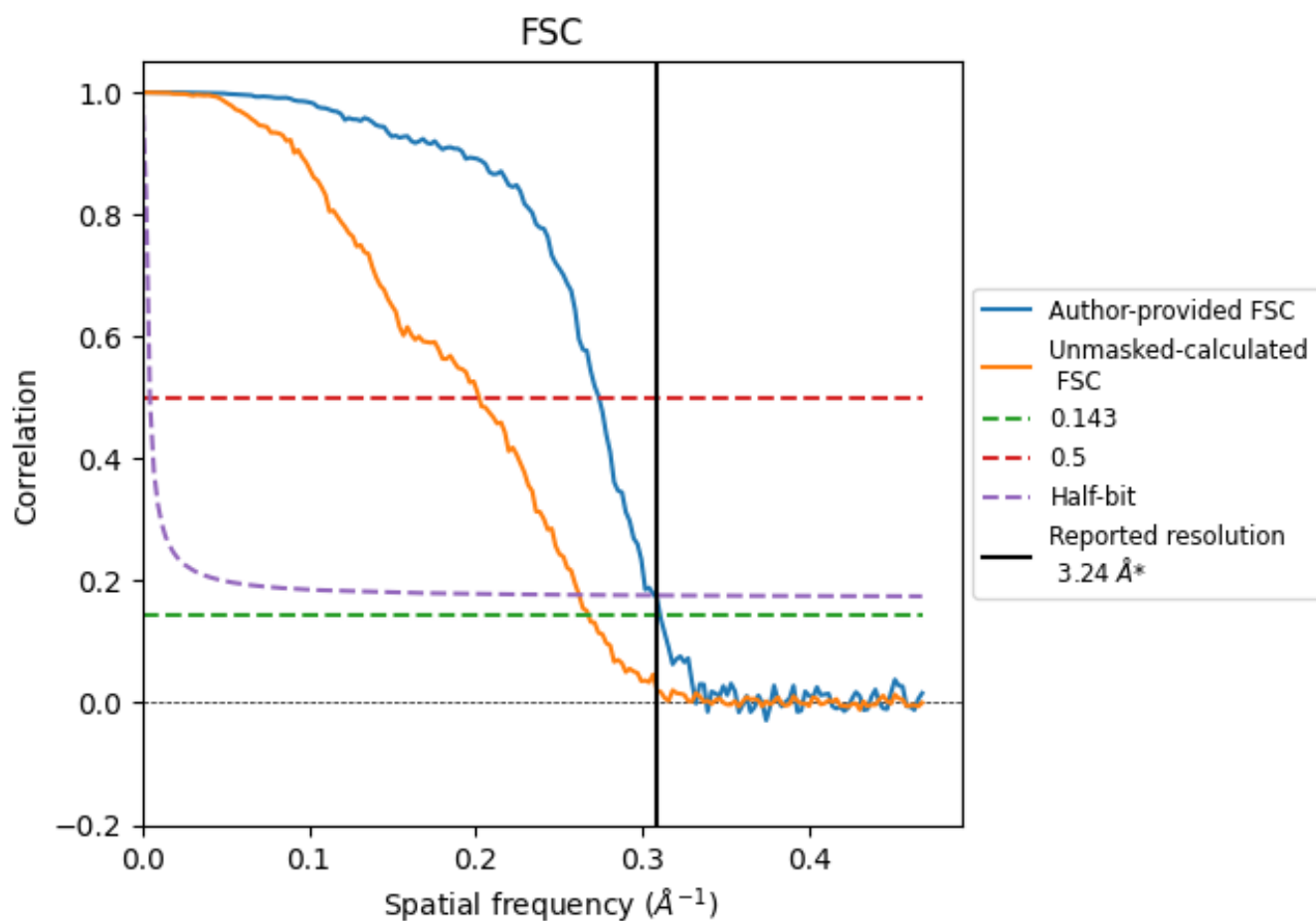


\*Reported resolution corresponds to spatial frequency of 0.309  $\text{\AA}^{-1}$

## 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 0.309  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

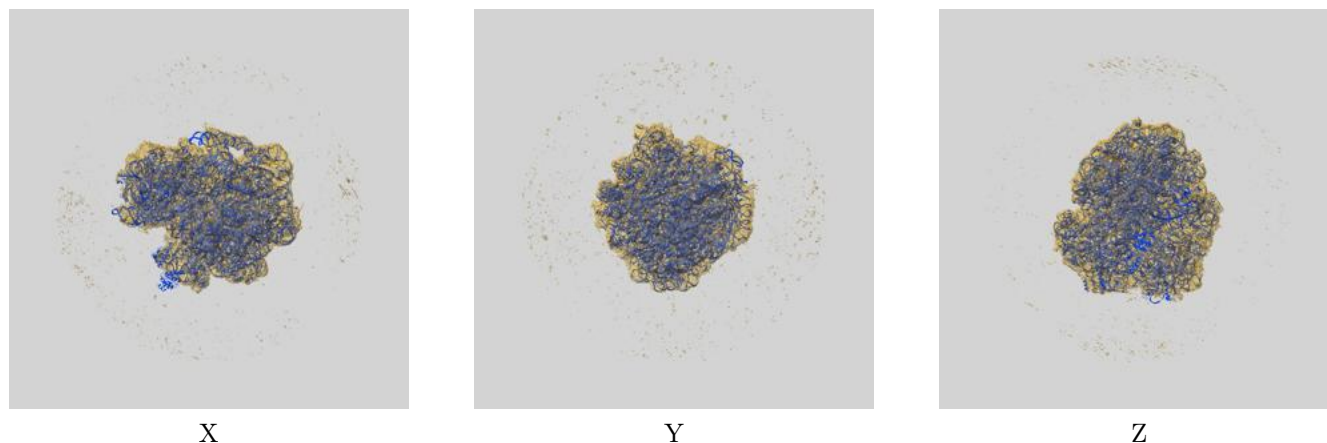
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	3.22	3.65	3.26
Unmasked-calculated*	3.74	4.95	3.82

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 3.24 by more than 10 %

## 9 Map-model fit [i](#)

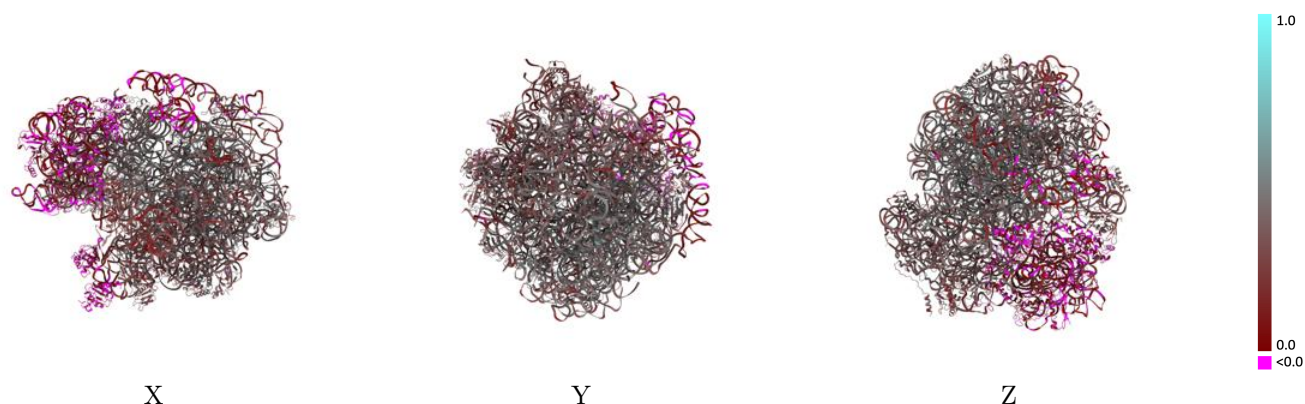
This section contains information regarding the fit between EMDB map EMD-47363 and PDB model 9E0N. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

### 9.1 Map-model overlay [i](#)



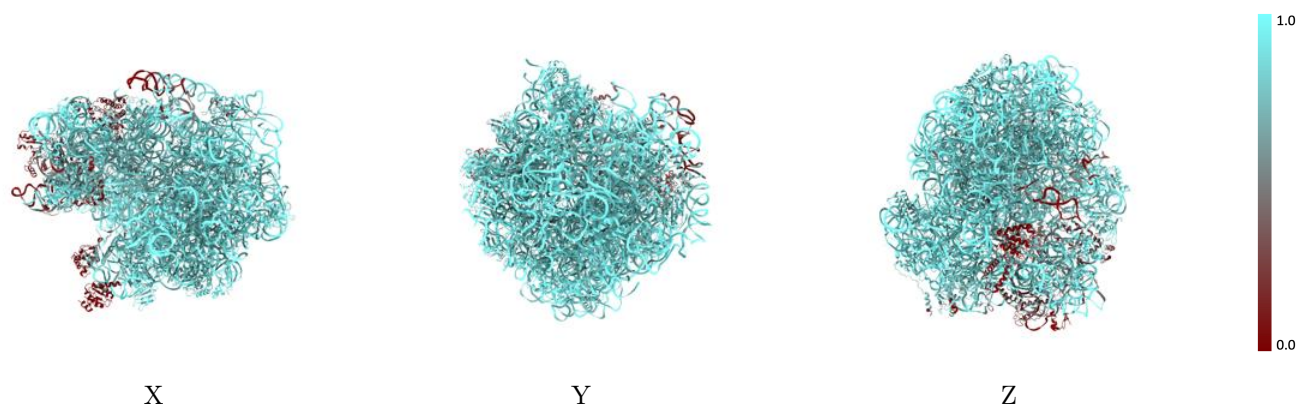
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



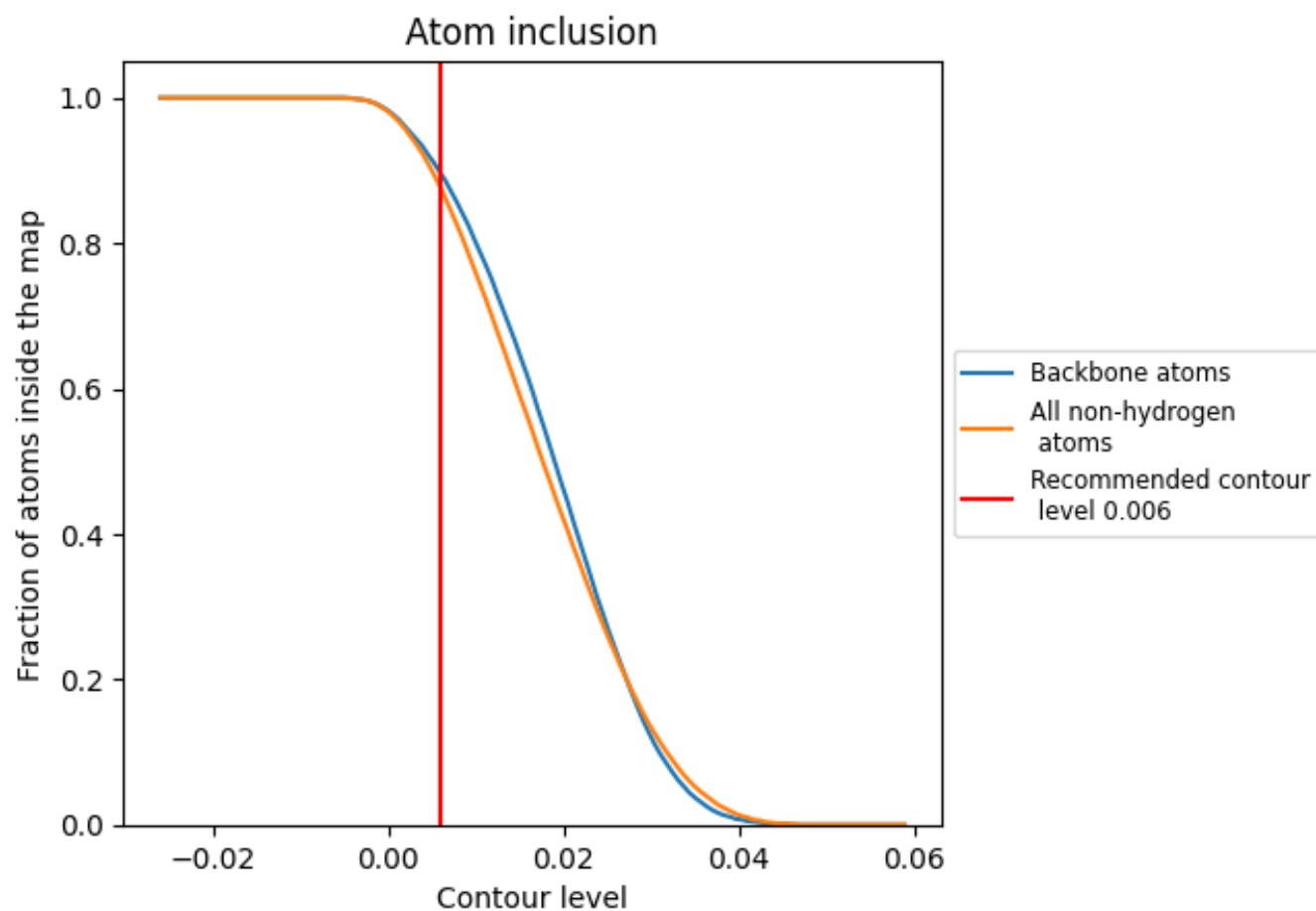
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.3250
1	 0.8180	 0.3150
2	 0.7440	 0.1580
3	 0.9180	 0.4070
4	 0.9060	 0.3460
5	 0.9100	 0.4610
6	 0.8460	 0.3800
7	 0.8710	 0.3280
8	 0.8100	 0.3610
A	 0.9310	 0.3580
B	 0.9340	 0.2580
C	 0.9070	 0.4570
D	 0.9130	 0.4070
E	 0.8730	 0.3620
F	 0.8540	 0.2670
G	 0.8930	 0.3280
H	 0.6840	 0.3380
I	 0.0860	 0.0190
J	 0.1820	 0.0250
K	 0.8730	 0.3540
L	 0.8480	 0.4080
M	 0.8800	 0.3600
N	 0.8420	 0.3600
O	 0.9190	 0.4200
P	 0.9100	 0.2970
Q	 0.9040	 0.4100
R	 0.8950	 0.3830
S	 0.8880	 0.3810
T	 0.8780	 0.4110
U	 0.8930	 0.4090
V	 0.9110	 0.3920
W	 0.8330	 0.2960
X	 0.8060	 0.3020
Y	 0.8940	 0.4430
Z	 0.9110	 0.4200



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Chain	Atom inclusion	Q-score
a	 0.9090	 0.3050
b	 0.1170	 0.0360
c	 0.4340	 0.1290
d	 0.8270	 0.3310
e	 0.7520	 0.2990
f	 0.9000	 0.3860
g	 0.6870	 0.0560
h	 0.9120	 0.3860
i	 0.8480	 0.1070
j	 0.4510	 0.0110
k	 0.8480	 0.3660
l	 0.7800	 0.3300
m	 0.5020	 0.0330
n	 0.5410	 0.1160
o	 0.9150	 0.4020
p	 0.8620	 0.3690
q	 0.8800	 0.3710
r	 0.9290	 0.3740
s	 0.6220	 0.0540
t	 0.9040	 0.3510
u	 0.6410	 0.3470