



wwPDB EM Validation Summary Report ⓘ

Jul 13, 2026 – 06:34 PM EDT

PDB ID : 11GG / pdb_000011gg
EMDB ID : EMD-75676
Title : Chimeric Escherichia coli 70S ribosome containing an evolved 16S rRNA from Pseudomonas aeruginosa (PA-ST)
Authors : Raskar, T.; Costello, A.; Fraser, J.; Badran, A.
Deposited on : 2026-02-22
Resolution : 3.02 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

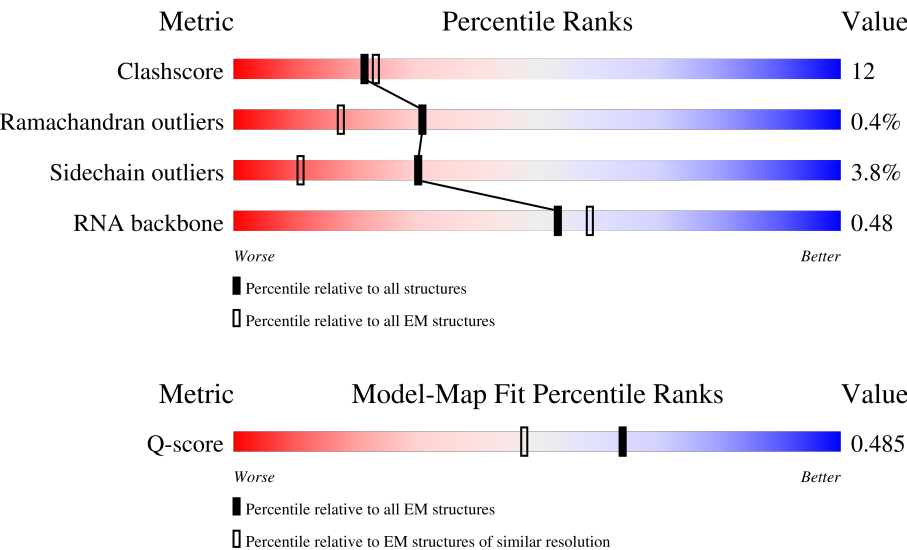
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.02 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	13913 (2.52 - 3.52)

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	C	1536	
2	1	92	
3	Z	103	

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Mol	Chain	Length	Quality of chain
4	2	87	
5	4	110	
6	3	71	
7	b	100	
8	c	104	
9	D	241	
10	d	94	
11	E	233	
12	e	85	
13	F	206	
14	f	78	
15	G	167	
16	g	63	
17	H	135	
18	h	59	
19	I	2904	
20	i	57	
21	J	120	
22	j	55	
23	K	273	
24	k	46	
25	L	209	
26	l	65	
27	M	201	
28	m	38	

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Mol	Chain	Length	Quality of chain
29	N	179	66% 66% 31% ..
30	n	179	14% 55% 28% 16%
31	O	177	67% 71% 28% ..
32	o	130	73% 24% ..
33	P	149	76% 79% 21% .
34	p	130	14% 58% 36% . .
35	Q	70	70% 59% 27% 14%
36	q	103	39% 61% 30% . 5%
37	R	142	78% 22%
38	r	129	70% 19% . 9%
39	S	123	74% 24% ..
40	t	124	61% 35% . .
41	T	144	28% 76% 22% .
42	u	118	5% 68% 27% . .
43	U	136	7% 65% 34% .
44	v	101	13% 57% 38% 5%
45	V	127	69% 25% . 6%
46	w	89	82% 16% ..
47	W	117	73% 26% ..
48	x	82	26% 55% 43% ..
49	X	115	74% 24% ..
50	y	84	14% 60% 33% . 5%
51	Y	118	10% 80% 19% ..
52	z	75	47% 25% . 27%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 142146 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	1526	Total	C	N	O	P	0	0
			32745	14606	6011	10603	1525		

- Molecule 2 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	81	Total	C	N	O	S	0	0
			651	416	124	109	2		

- Molecule 3 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 4 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	84	Total	C	N	O	S	0	0
			659	408	136	112	3		

- Molecule 5 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 6 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	3	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 7 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	b	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 8 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	c	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 9 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 10 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	d	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 11 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 12 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	e	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 14 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	f	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 15 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 16 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	g	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 17 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 18 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	h	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 19 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	I	2898	Total	C	N	O	P	2	0
			62271	27787	11455	20129	2900		

- Molecule 20 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	i	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 21 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	J	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	j	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 23 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	271	Total	C	N	O	S	1	0
			2093	1294	427	365	7		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	k	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	l	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 27 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	M	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	N	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 30 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	n	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 31 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 32 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 33 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 34 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 35 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Q	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 36 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 37 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 38 is a protein called 30S ribosomal protein S11.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 40 is a protein called 30S ribosomal protein S12.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 42 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	u	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 43 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 44 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 45 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 46 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	88	Total	C	N	O	S	0	0
			710	437	143	129	1		

- Molecule 47 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	116	Total	C	N	O	S	0	0
			892	552	178	162			

- Molecule 48 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 49 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 50 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 51 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	Y	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 52 is a protein called Small ribosomal subunit protein bS18.

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

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	C	90	Total	Mg	0
			90	90	
53	I	204	Total	Mg	0
			204	204	
53	i	1	Total	Mg	0
			1	1	
53	J	5	Total	Mg	0
			5	5	
53	K	1	Total	Mg	0
			1	1	
53	L	1	Total	Mg	0
			1	1	
53	l	1	Total	Mg	0
			1	1	
53	q	1	Total	Mg	0
			1	1	
53	V	2	Total	Mg	0
			2	2	

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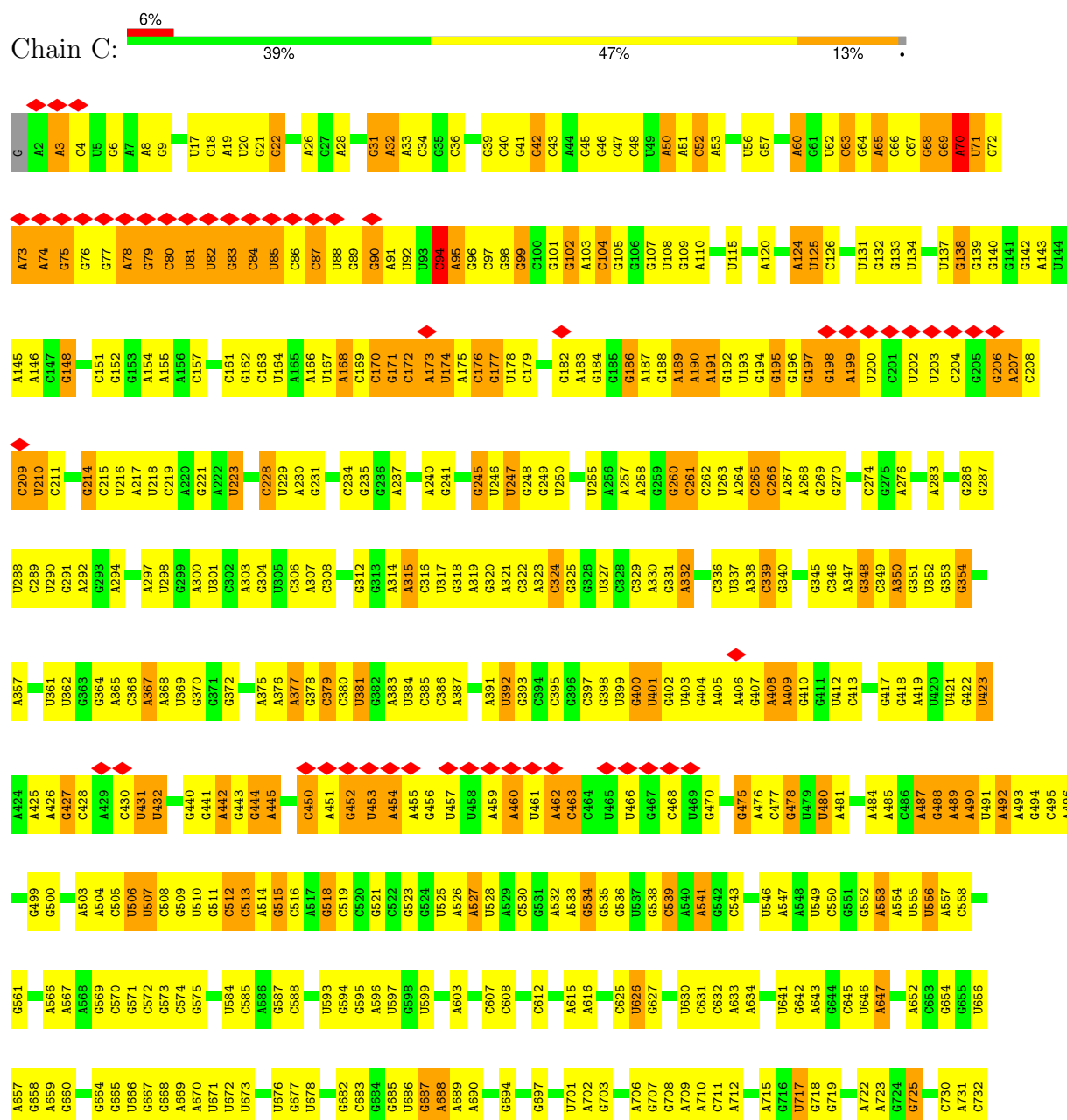
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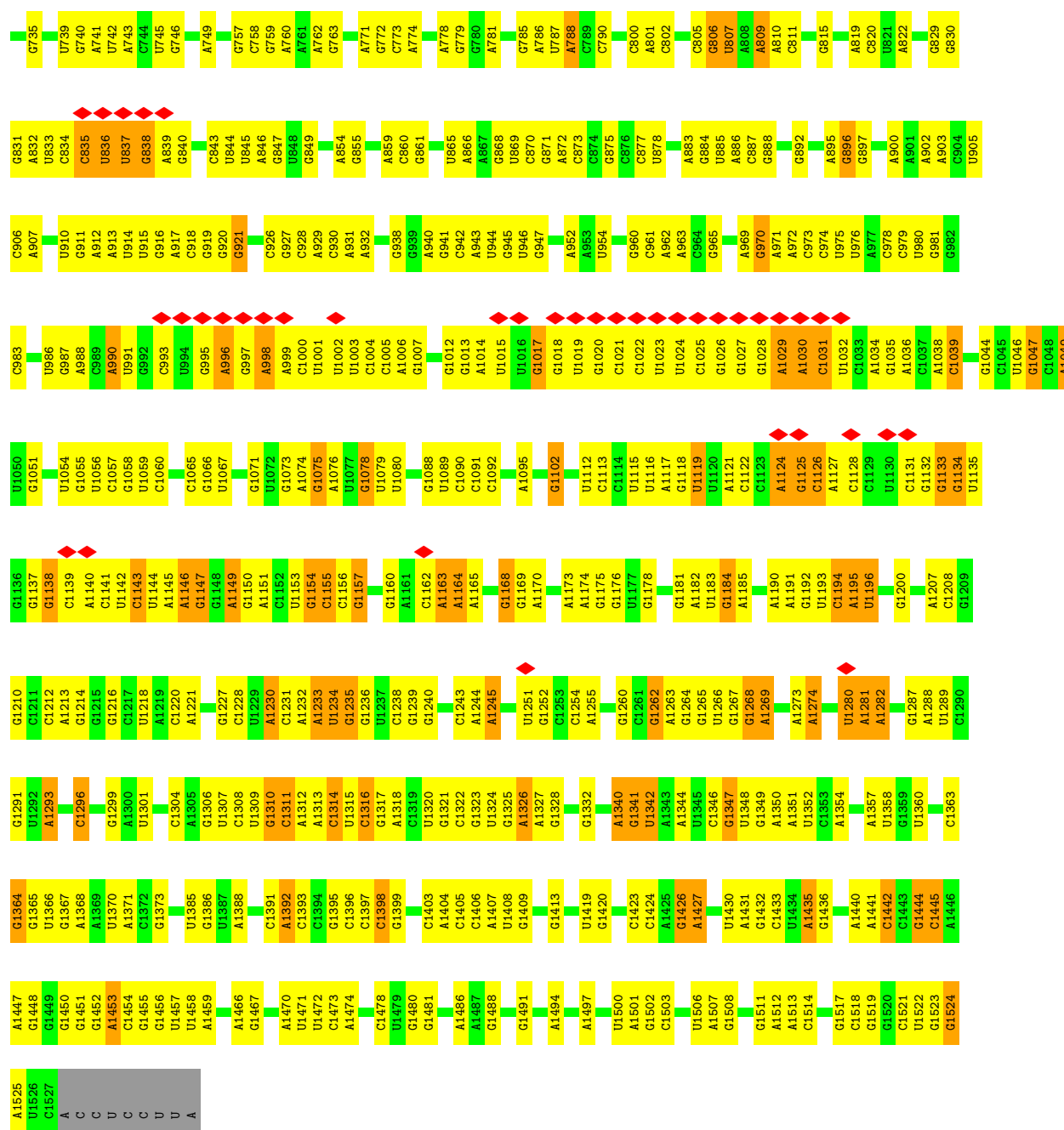
Mol	Chain	Residues	Atoms		AltConf
53	Y	1	Total	Mg	0
			1	1	

3 Residue-property plots

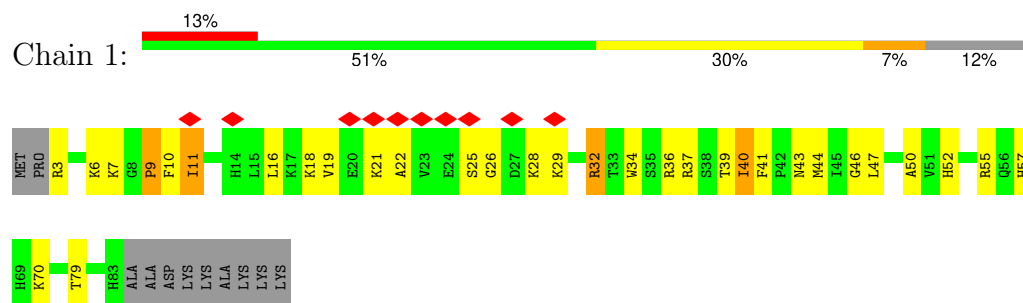
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S ribosomal RNA

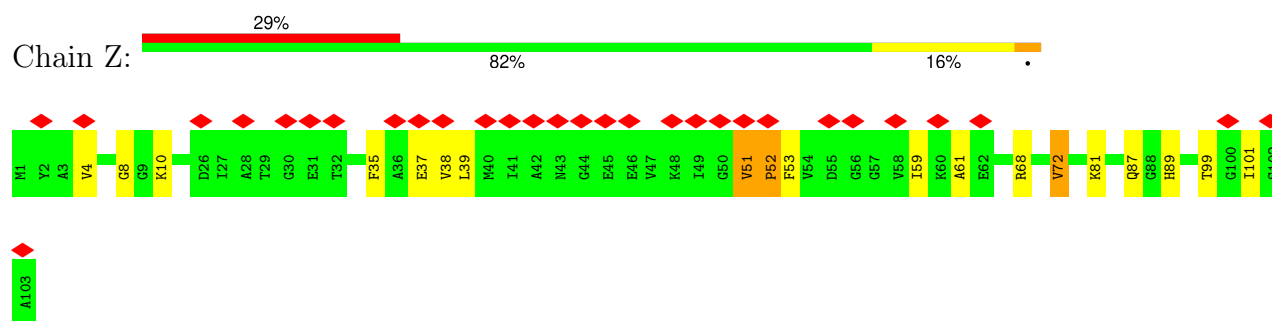




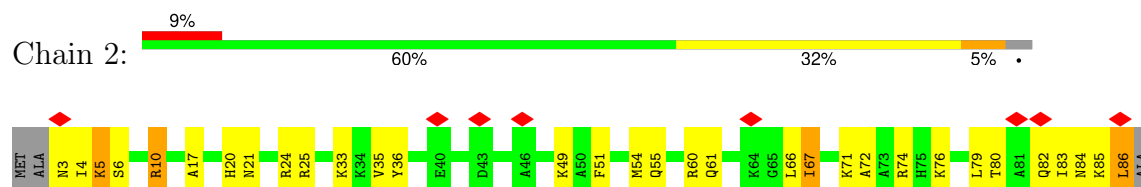
- Molecule 2: Small ribosomal subunit protein uS19



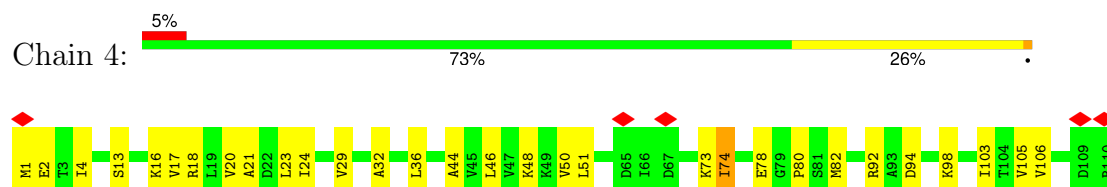
- Molecule 3: Ribosomal protein L21



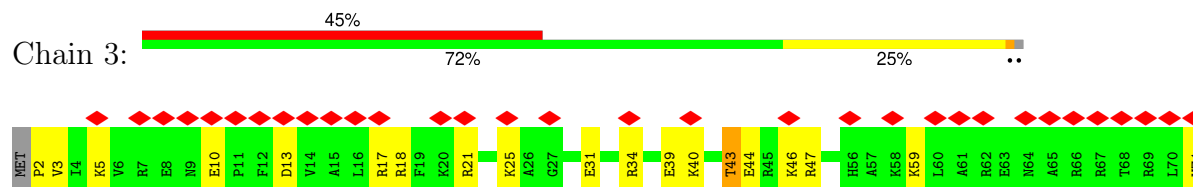
- Molecule 4: Small ribosomal subunit protein bS20



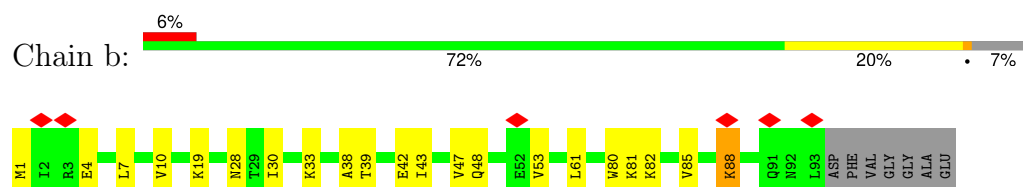
- Molecule 5: Large ribosomal subunit protein uL22



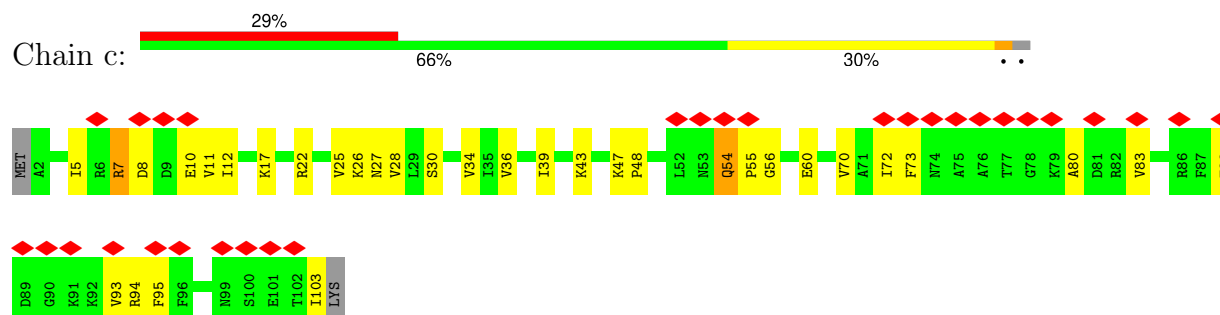
- Molecule 6: Small ribosomal subunit protein bS21



- Molecule 7: 50S ribosomal protein L23

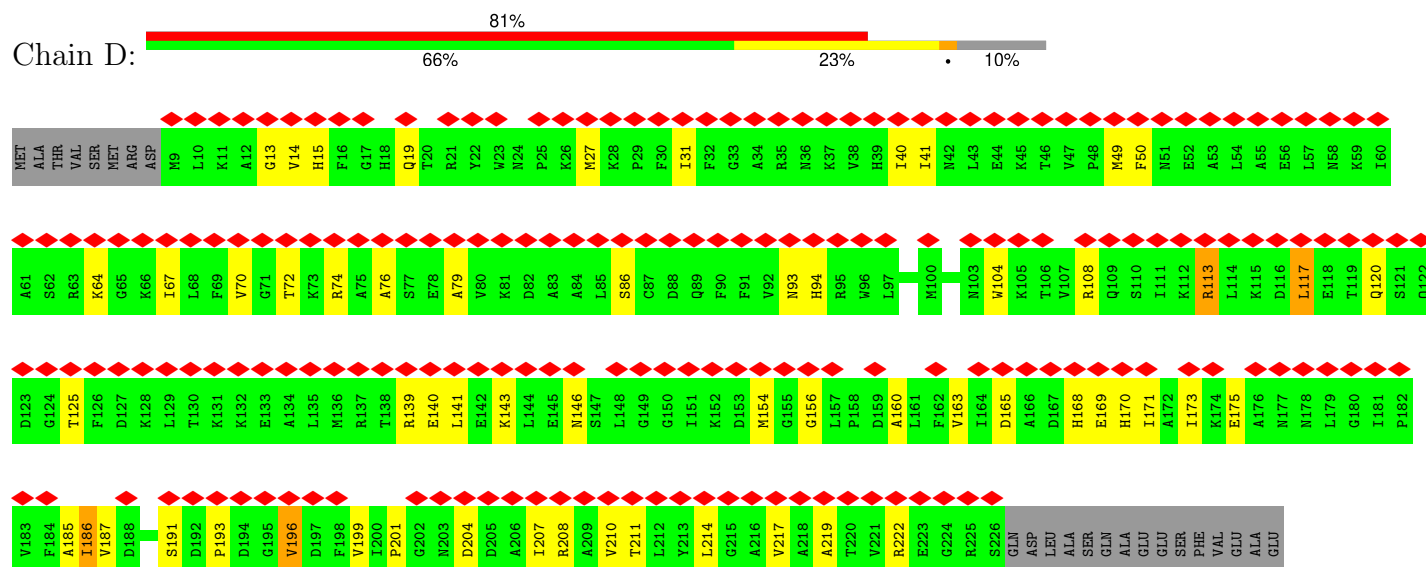


- Molecule 8: 50S ribosomal protein L24



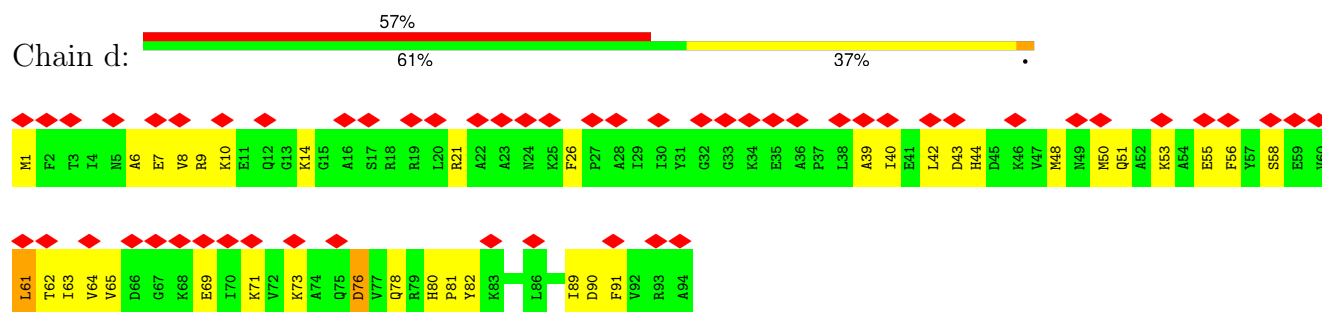
- Molecule 9: Small ribosomal subunit protein uS2

Chain D:



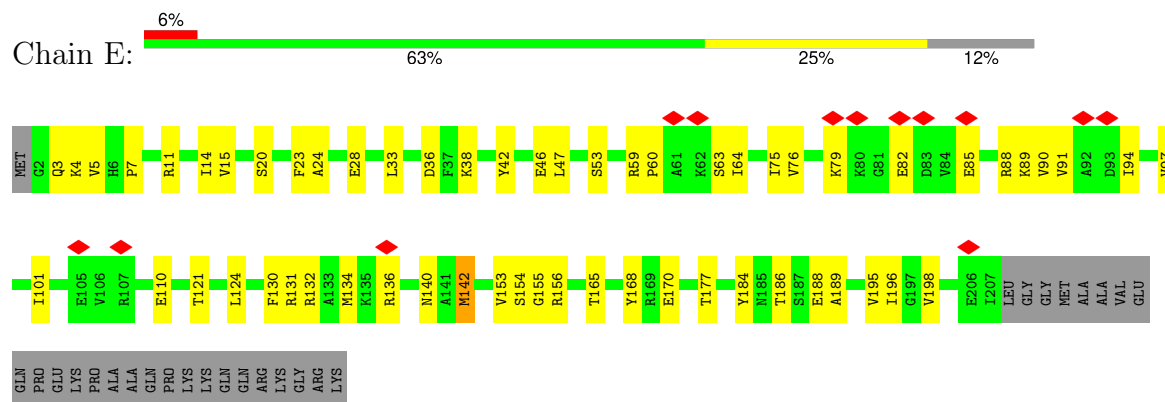
- Molecule 10: Large ribosomal subunit protein bL25

Chain d:



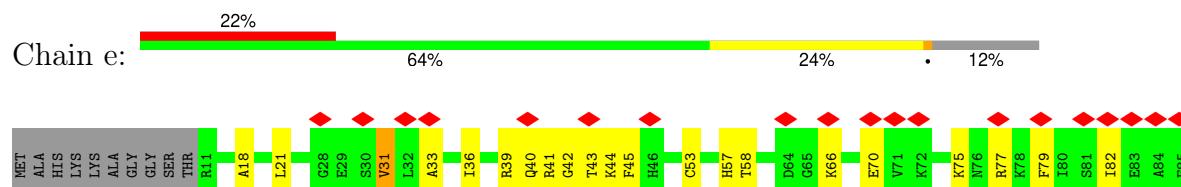
- Molecule 11: Small ribosomal subunit protein uS3

Chain E:

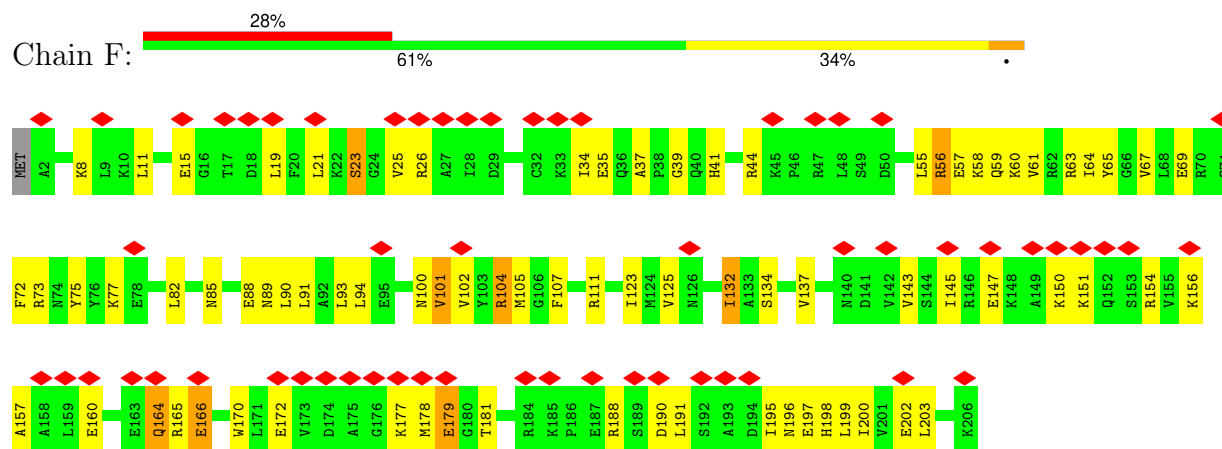


- Molecule 12: 50S ribosomal protein L27

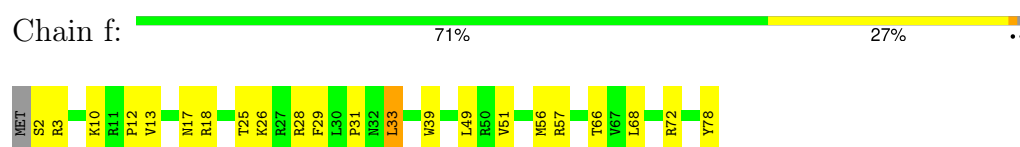
Chain e:



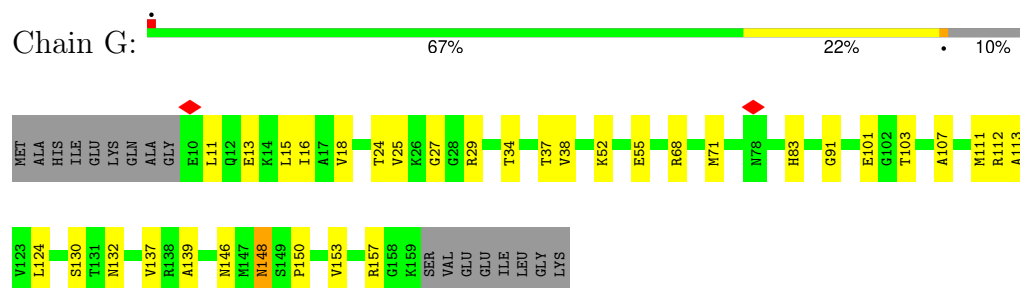
- Molecule 13: Small ribosomal subunit protein uS4



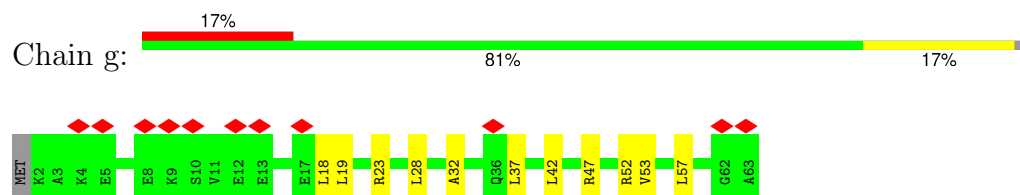
- Molecule 14: 50S ribosomal protein L28



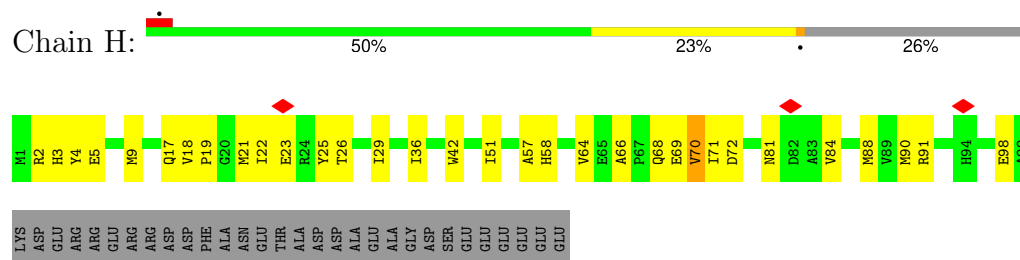
- Molecule 15: Small ribosomal subunit protein uS5

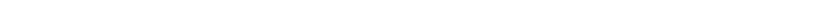


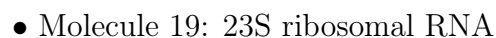
- Molecule 16: Large ribosomal subunit protein uL29



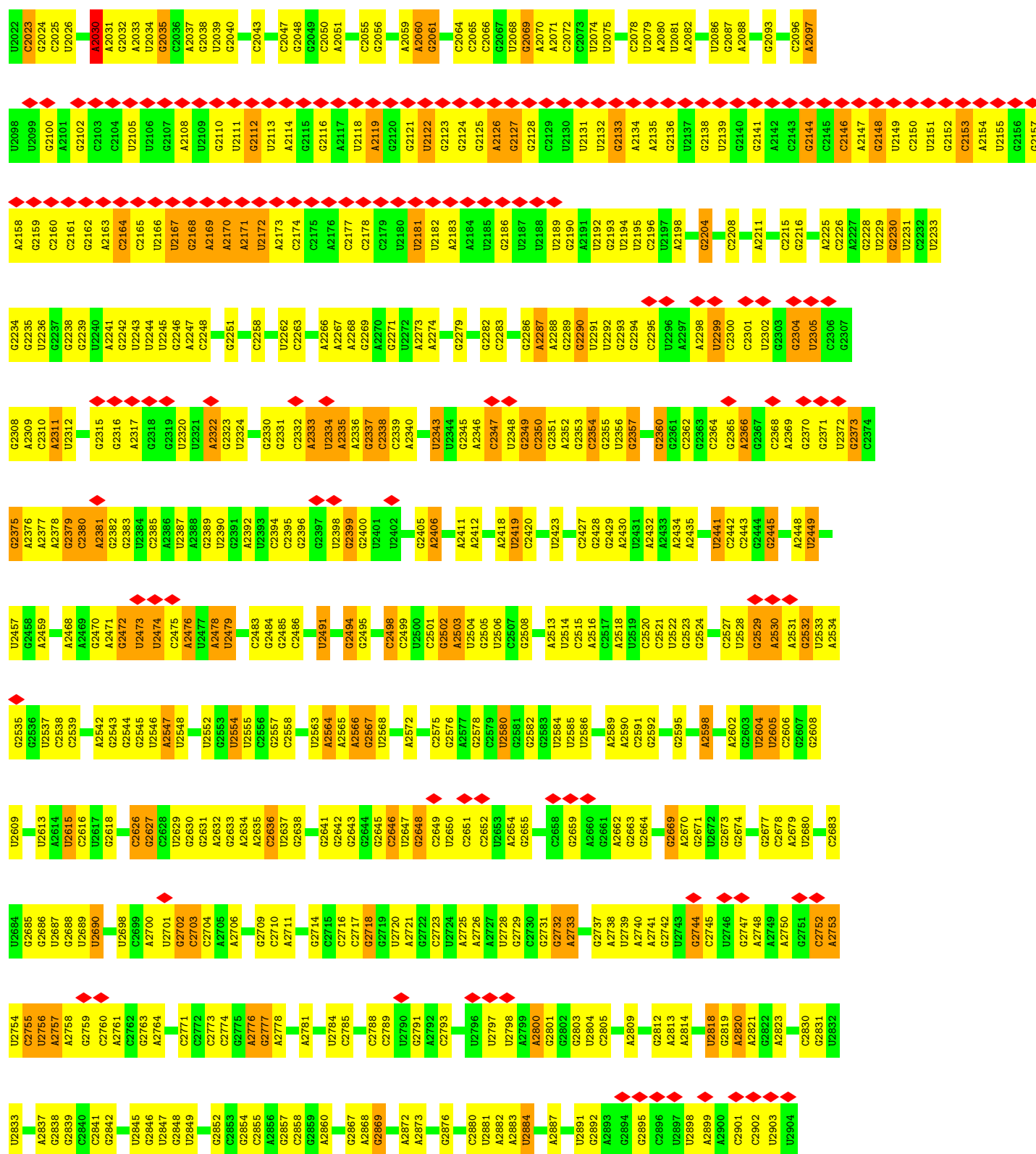
- Molecule 17: Small ribosomal subunit protein bS6



- Chain h:  19% 73% 24%



A1927	A1928	G1929	G1930	A1936	A1937	A1938	A1939	C1942	C1943	C1944	C1945	G1954	G1955	C1960	C1961	C1962	G1963	G1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	G1980	G1981	G1982	A1987	G1988	G1989	C1990	G1991	A1991	G1992	G1993	C1997	C1998	C1999	C2006	C2007	C2008	A2009	G2010	C2011	C2012	G2013	A2014	A2015	C2021						
A1829	C1830	G1831	C1832	G1835	G1839	G1840	A1847	A1853	A1854	U1855	U1856	U1857	A1858	G1862	G1863	U1864	U1865	A1866	G1867	G1868	G1869	C1870	C1871	A1872	G1873	C1874	G1875	A1876	C1879	C1880	A1881	A1882	U1883	G1884	A1889	A1890	C1902	G1903	G1906	G1906	U1911	A1912	A1913	C1914	C1822	3TD1915	A1916	U1917	U1923	C1924							
A1749	G1750	U1751	C1752	G1753	A1754	C1760	C1761	G1762	G1763	C1764	C1771	A1772	A1773	G1776	U1779	U1782	A1783	A1784	A1785	A1786	A1789	C1790	A1791	A1794	C1795	U1796	U1797	U1798	C1799	C1800	A1801	A1802	A1803	A1808	A1809	U1812	G1813	C1816	G1817	U1818	A1819	U1820	A1821	C1822	U1825	G1826	U1827	G1828									
A1672	G1673	G1674	U1680	G1681	G1682	U1683	G1684	C1685	G1686	G1687	A1689	A1690	G1696	G1699	G1703	C1704	U1709	G1710	A1711	U1712	A1713	U1714	G1715	U1716	A1717	U1720	G1721	A1722	G1723	G1724	U1725	C1726	C1727	C1728	U1729	C1730	G1731	C1732	C1733	A1650	G1651	A1652	G1653	A1654	A1655	G1659	G1666	A1667	A1668								
A1572	U1576	C1577	U1578	G1581	A1583	U1584	C1585	A1586	G1588	A1589	A1590	A1591	C1592	A1593	A1597	A1598	C1604	C1607	A1608	A1609	A1610	A1618	G1622	G1628	U1629	A1630	U1636	A1637	C1638	G1645	C1646	U1647	U1648	G1649	A1650	G1651	A1652	G1653	A1654	A1655	G1659	G1666	A1667	A1668													
C1493	A1494	A1495	A1496	U1497	C1498	C1499	G1500	A1504	A1505	U1506	C1507	G1510	G1511	A1515	C1526	A1528	G1529	G1530	C1531	A1532	A1533	U1534	A1535	C1536	G1537	G1538	U1539	G1540	C1541	U1542	G1543	A1544	A1548	A1549	C1550	A1551	U1554	C1558	C1561	U1562	U1563	C1564	C1565	A1566	G1567	G1568	A1569	A1570	A1571								
G1418	A1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	A1427	C1428	G1429	G1430	A1431	G1432	A1433	A1434	G1435	A1436	C1437	U1440	G1441	U1442	U1443	G1444	G1445	C1446	C1447	G1448	G1449	G1450	C1451	G1452	A1453	C1454	G1455	A1456	U1457	U1458	G1459	U1460	C1461	C1462	A1469	A1470	G1473	U1474	G1482	U1483	U1484	U1485	U1486	U1487	C1488	C1489	A1490		
G1311	C1315	G1316	G1317	A1327	A1328	U1329	G1332	U1340	G1341	U1352	A1353	A1354	C1357	G1358	A1359	G1360	G1361	C1362	G1363	A1365	A1366	A1367	G1368	U1379	A1383	A1384	A1385	C1386	A1387	A1392	A1395	U1396	U1397	U1400	G1401	G1407	G1410	U1411	U1412	A1413	C1414	U1415	G1416	C1417													
U1219	G1220	G1223	U1224	G1225	A1226	G1227	U1231	A1232	G1232	U1233	U1234	G1235	G1236	A1237	G1238	G1239	U1240	G1248	U1249	G1250	C1251	A1253	A1254	U1255	G1256	G1266	U1267	A1271	A1272	C1278	G1279	G1280	U1281	U1282	G1283	A1286	A1287	G1288	G1292	C1293	U1294	C1295	G1296	C1297	C1298	U1299	G1300	A1301	C1306	A1307							
A1133	A1134	C1135	G1138	G1139	C1140	U1141	A1142	C1145	C1146	C1150	A1151	C1152	G1153	A1155	A1156	G1157	C1164	A1165	C1170	G1171	C1172	U1173	U1174	A1175	U1176	G1177	C1178	G1179	U1180	U1181	U1182	U1183	U1184	G1185	G1186	G1187	U1188	A1189	G1190	G1191	C1196	G1197	U1198	U1199	C1200	G1212	A1213	G1215	G1216								
A1069	A1070	G1071	C1072	G1073	A1074	C1075	C1076	A1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	A1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	C1104	U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112	C1117	A1118	U1119	G1120	C1121	G1122	C1123	G1124	G1125	A1126	A1129	U1130	G1131	U1132
U1004	C1005	C1006	C1007	A1008	A1009	A1010	G1011	U1012	C1013	A1014	A1020	A1021	G1022	U1023	G1026	A1027	A1028	A1029	C1030	G1031	A1032	U1033	G1034	U1035	G1036	G1037	G1038	A1039	A1040	G1041	C1042	C1043	C1044	A1046	G1047	A1048	G1049	A1050	G1051	C1052	C1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	G1068	
G923	G924	A925	G926	A927	G930	U931	U932	A933	U934	C935	A936	C937	G938	G939	G940	C946	A947	C948	G949	G953	G954	U955	G956	A959	A960	C961	U963	C964	G965	G966	U967	G971	A972	A973	G974	A975	G976	A983	C987	G993	C994	C995	A996	U999	A1000	A1001	G1002	G1003									

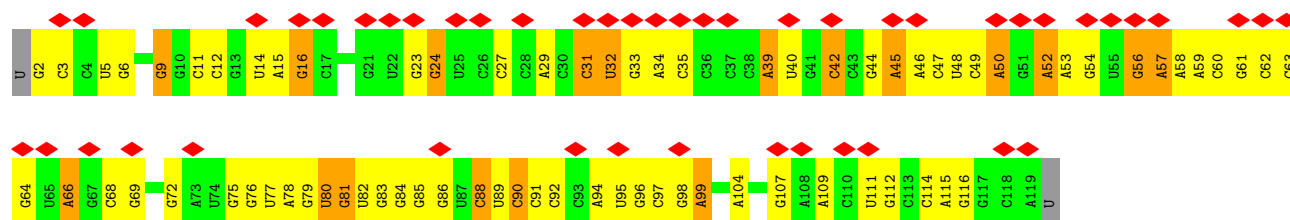


- Molecule 20: 50S ribosomal protein L32

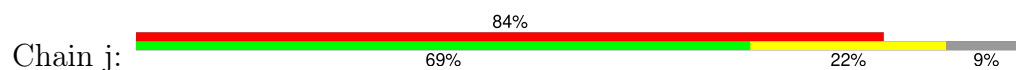
Chain i: 72% 25%



• Molecule 21: 5S ribosomal RNA



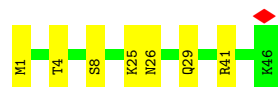
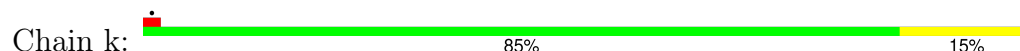
• Molecule 22: 50S ribosomal protein L33



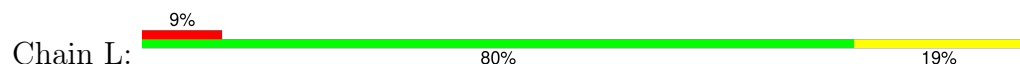
• Molecule 23: 50S ribosomal protein L2

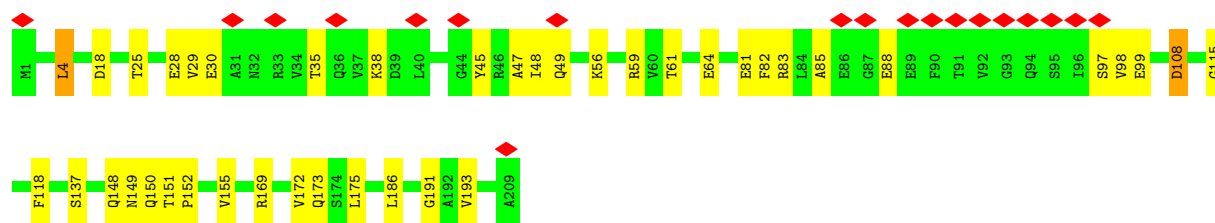


• Molecule 24: 50S ribosomal protein L34

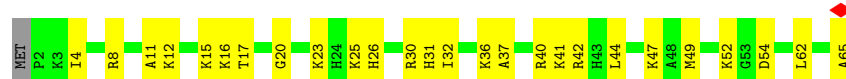


• Molecule 25: Large ribosomal subunit protein uL3

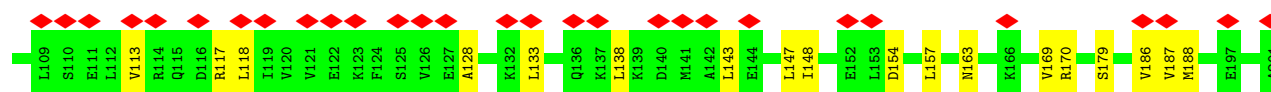
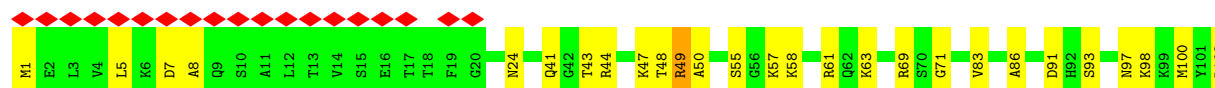
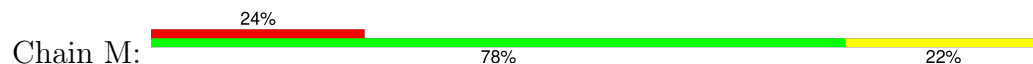




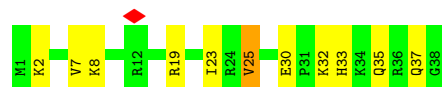
- Molecule 26: 50S ribosomal protein L35



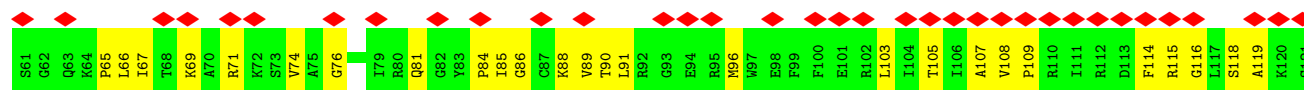
- Molecule 27: Large ribosomal subunit protein uL4



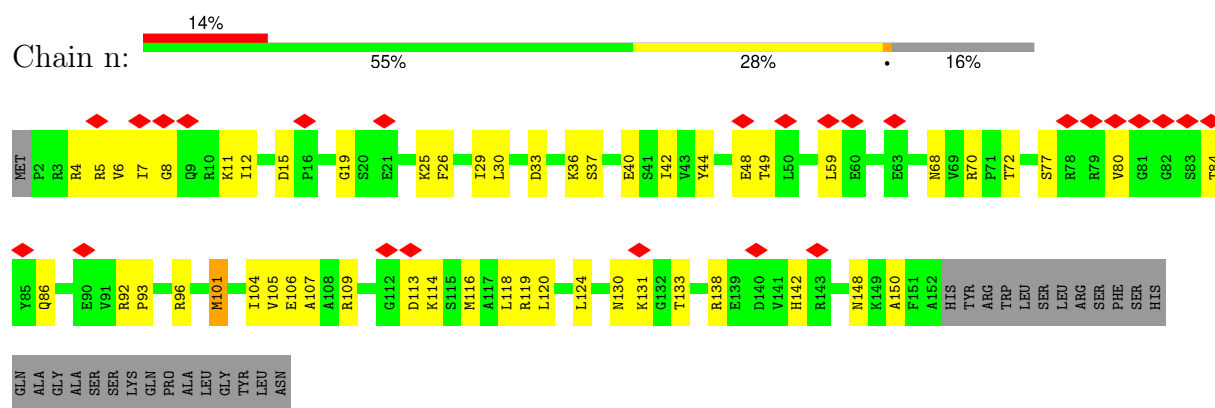
- Molecule 28: 50S ribosomal protein L36



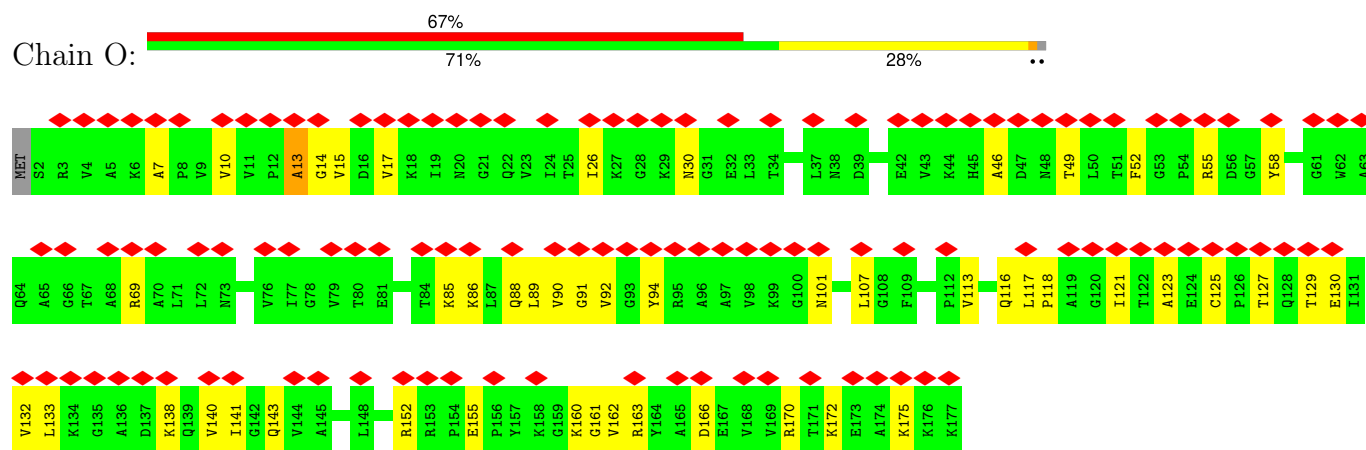
- Molecule 29: Large ribosomal subunit protein uL5



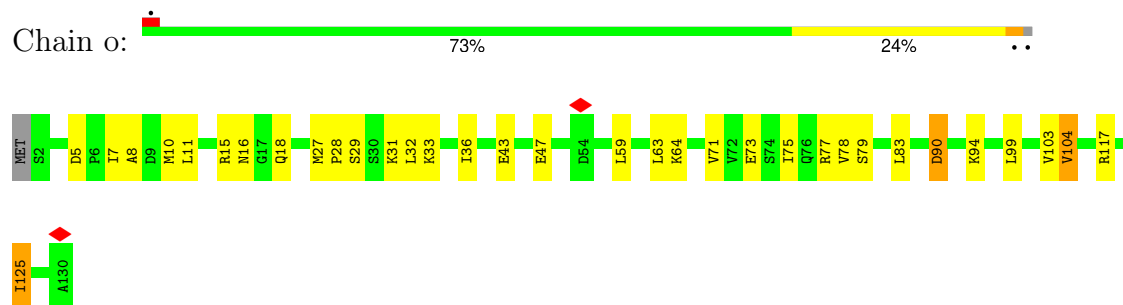
- Molecule 30: Small ribosomal subunit protein uS7



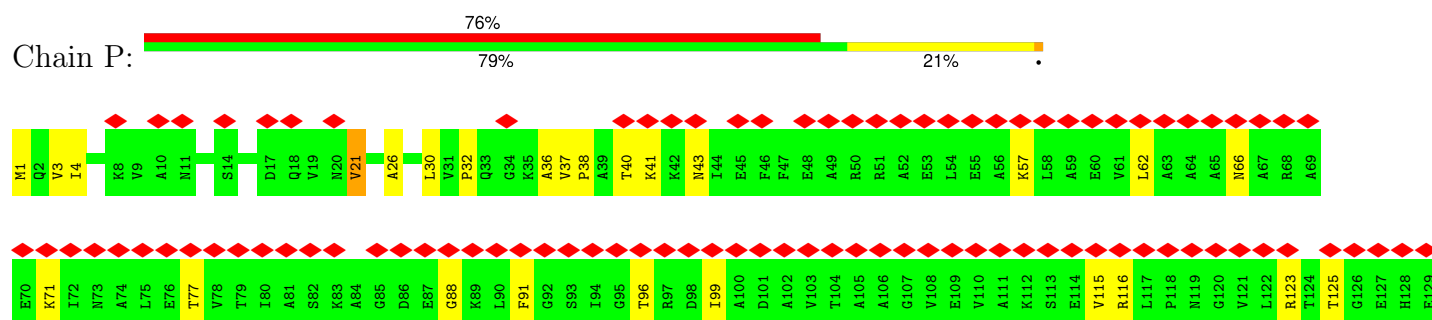
- Molecule 31: Large ribosomal subunit protein uL6

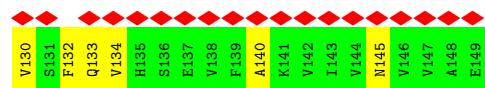


- Molecule 32: Small ribosomal subunit protein uS8

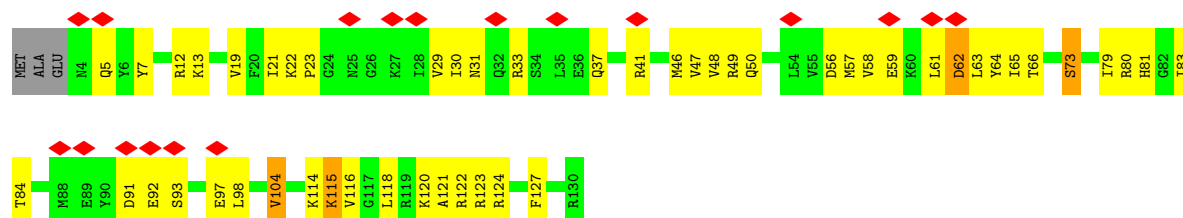


- Molecule 33: Large ribosomal subunit protein bL9

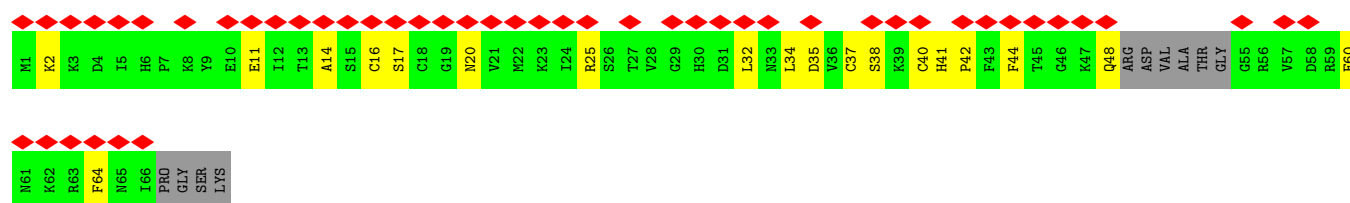




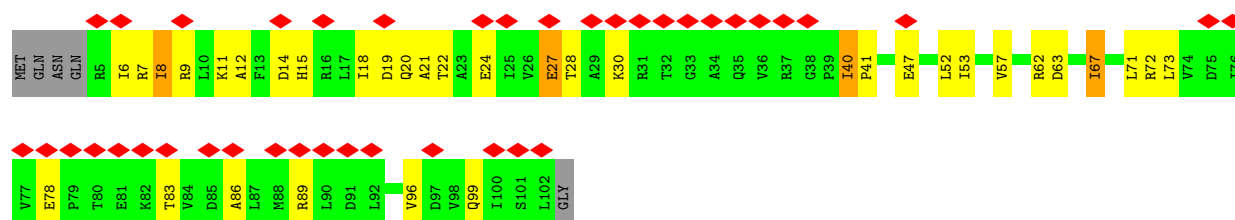
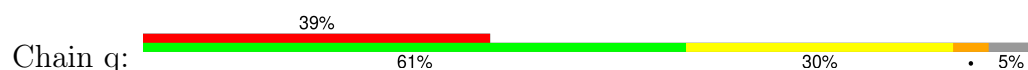
- Molecule 34: Small ribosomal subunit protein uS9



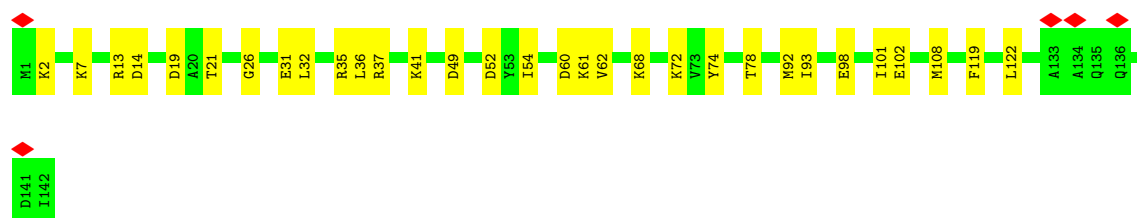
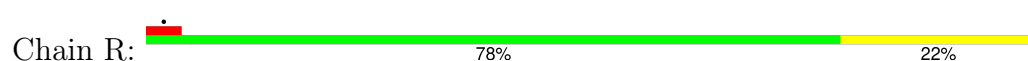
- Molecule 35: 50S ribosomal protein L31



- Molecule 36: Small ribosomal subunit protein uS10

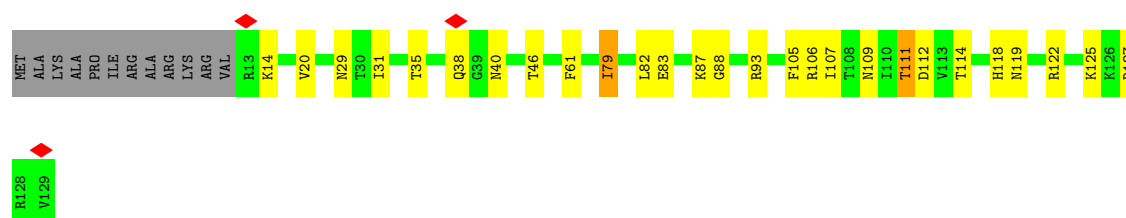


- Molecule 37: Large ribosomal subunit protein uL13



- Molecule 38: 30S ribosomal protein S11

Chain r: 



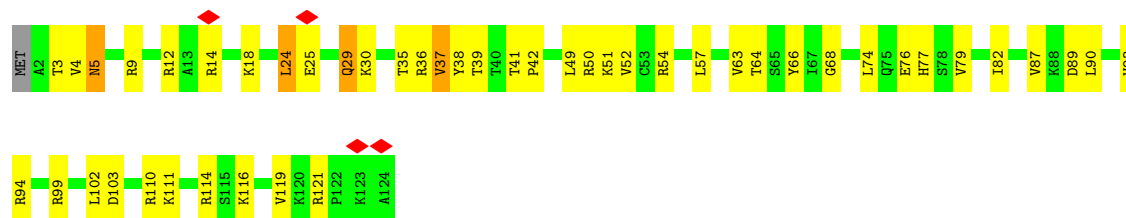
- Molecule 39: Large ribosomal subunit protein uL14

Chain S: 



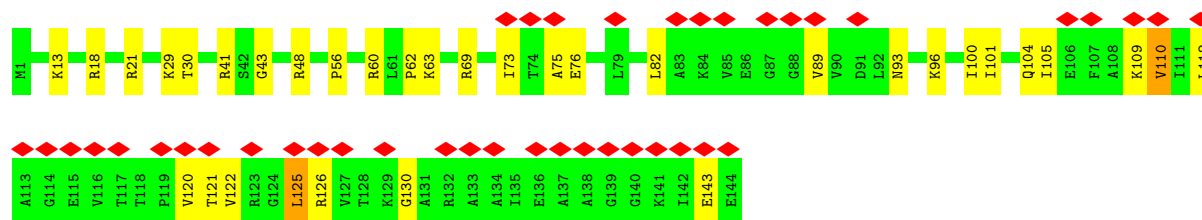
- Molecule 40: 30S ribosomal protein S12

Chain t: 



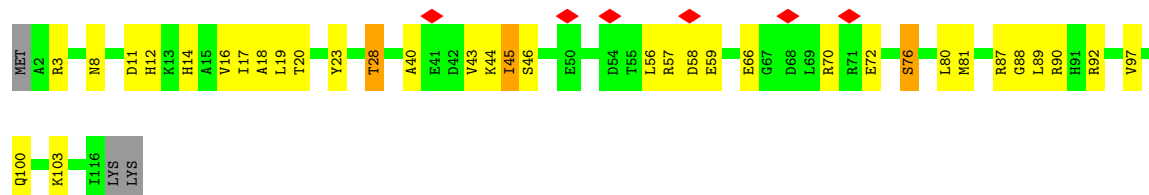
- Molecule 41: Large ribosomal subunit protein uL15

Chain T: 

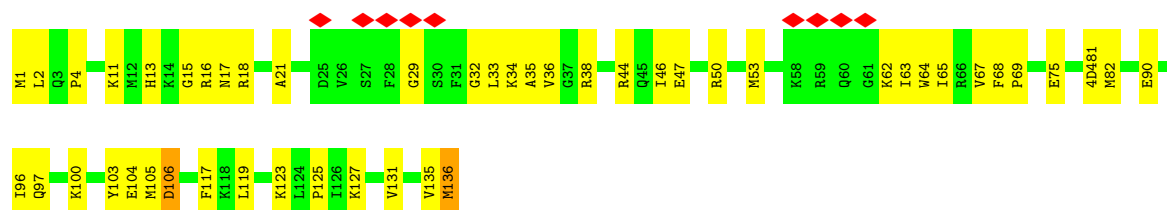


- Molecule 42: Small ribosomal subunit protein uS13

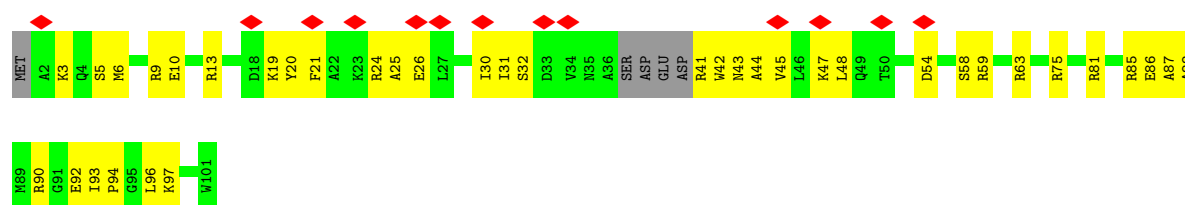
Chain u: 



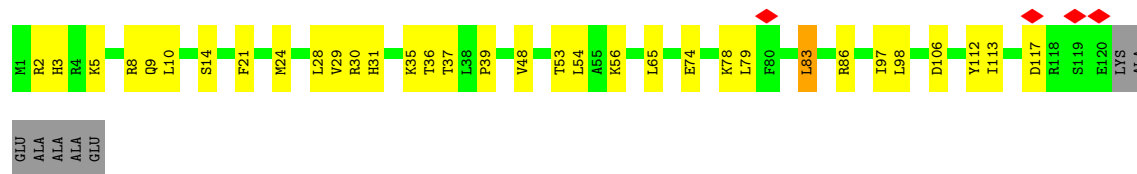
- Molecule 43: Large ribosomal subunit protein uL16



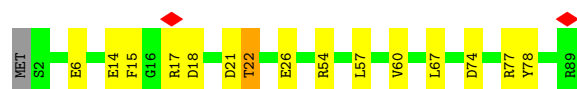
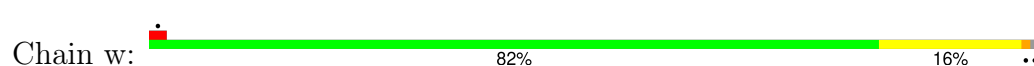
- Molecule 44: Small ribosomal subunit protein uS14



- Molecule 45: Large ribosomal subunit protein bL17



- Molecule 46: Small ribosomal subunit protein uS15

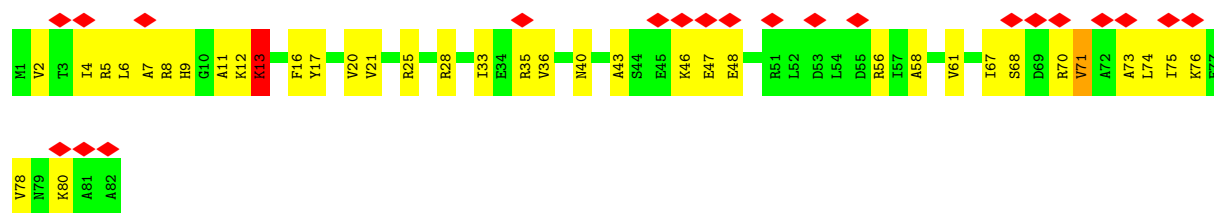


- Molecule 47: Large ribosomal subunit protein uL18



- Molecule 48: Small ribosomal subunit protein bS16





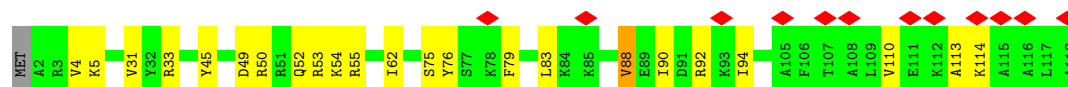
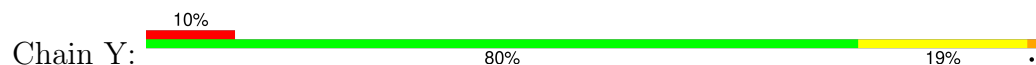
- Molecule 49: Large ribosomal subunit protein bL19



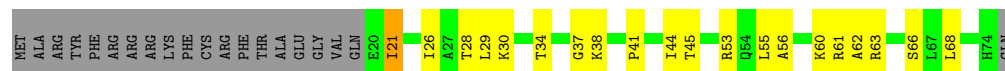
- Molecule 50: Small ribosomal subunit protein uS17



- Molecule 51: 50S ribosomal protein L20



- Molecule 52: Small ribosomal subunit protein bS18



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	560442	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	30.211	Depositor
Minimum map value	-15.495	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Map size (Å)	425.984, 425.984, 425.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, MG, 5MU, 3TD, OMC, PSU, 1MG, 6MZ, 4D4, 2MA, 5MC, H2U, 2MG, OMU, OMG

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	C	0.14	0/36668	0.33	9/57204 (0.0%)
2	1	0.24	0/667	0.58	0/897
3	Z	0.15	0/829	0.39	0/1107
4	2	0.19	0/665	0.40	0/881
5	4	0.12	0/864	0.29	0/1156
6	3	0.12	0/598	0.32	0/792
7	b	0.12	0/744	0.33	0/994
8	c	0.15	0/787	0.37	0/1051
9	D	0.14	0/1735	0.36	0/2338
10	d	0.16	0/766	0.42	0/1025
11	E	0.12	0/1651	0.32	0/2225
12	e	0.12	0/582	0.38	0/769
13	F	0.16	0/1665	0.44	0/2227
14	f	0.11	0/635	0.29	0/848
15	G	0.15	0/1118	0.41	0/1504
16	g	0.13	0/502	0.29	0/667
17	H	0.17	0/835	0.45	0/1128
18	h	0.12	0/453	0.30	0/605
19	I	0.12	0/69168	0.30	20/107901 (0.0%)
20	i	0.09	0/450	0.23	0/599
21	J	0.12	0/2828	0.29	0/4410
22	j	0.08	0/416	0.25	0/554
23	K	0.14	0/2132	0.32	0/2866
24	k	0.11	0/380	0.29	0/498
25	L	0.13	0/1586	0.32	0/2134
26	l	0.10	0/513	0.25	0/676
27	M	0.12	0/1571	0.29	0/2113
28	m	0.16	0/303	0.37	0/397
29	N	0.16	0/1434	0.39	0/1926
30	n	0.15	0/1195	0.41	0/1602
31	O	0.13	0/1343	0.36	0/1816
32	o	0.12	0/989	0.27	0/1326

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	P	0.12	0/1122	0.36	0/1515
34	p	0.22	0/1034	0.59	0/1375
35	Q	0.10	0/488	0.31	0/649
36	q	0.13	0/796	0.36	0/1077
37	R	0.11	0/1152	0.31	0/1551
38	r	0.14	0/893	0.35	0/1205
39	S	0.14	0/947	0.34	0/1268
40	t	0.16	0/969	0.44	2/1300 (0.2%)
41	T	0.10	0/1062	0.33	0/1413
42	u	0.16	0/900	0.49	0/1204
43	U	0.13	0/1081	0.34	0/1443
44	v	0.19	0/785	0.36	0/1043
45	V	0.10	0/973	0.27	0/1301
46	w	0.13	0/718	0.28	0/959
47	W	0.11	0/902	0.28	0/1209
48	x	0.21	0/659	0.68	0/884
49	X	0.13	0/929	0.29	0/1242
50	y	0.18	0/657	0.54	0/881
51	Y	0.11	0/960	0.24	0/1278
52	z	0.13	0/462	0.28	0/621
All	All	0.13	0/153561	0.33	31/229654 (0.0%)

There are no bond length outliers.

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	69	G	OP2-P-O3'	-11.99	72.03	108.00
1	C	70	A	O5'-P-OP2	-11.55	73.35	108.00
1	C	94	C	OP1-P-O3'	-9.34	79.98	108.00
19	I	673	C	OP1-P-O3'	-9.03	80.92	108.00
19	I	2723	C	OP1-P-O3'	-9.02	80.94	108.00

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	C	32745	0	16474	700	0
2	1	651	0	675	27	0
3	Z	816	0	839	14	0
4	2	659	0	709	26	0
5	4	857	0	922	20	0
6	3	590	0	629	13	0
7	b	738	0	807	12	0
8	c	779	0	831	25	0
9	D	1704	0	1732	38	0
10	d	753	0	780	23	0
11	E	1624	0	1696	38	0
12	e	575	0	592	19	0
13	F	1643	0	1707	54	0
14	f	625	0	652	19	0
15	G	1105	0	1148	28	0
16	g	501	0	531	7	0
17	H	817	0	808	24	0
18	h	449	0	488	9	0
19	I	62271	0	31340	1060	0
20	i	444	0	458	12	0
21	J	2529	0	1281	80	0
22	j	409	0	440	8	0
23	K	2093	0	2166	56	0
24	k	377	0	418	6	0
25	L	1565	0	1616	29	0
26	l	504	0	572	22	0
27	M	1552	0	1619	34	0
28	m	302	0	343	8	0
29	N	1410	0	1444	44	0
30	n	1181	0	1238	34	0
31	O	1323	0	1371	37	0
32	o	979	0	1031	27	0
33	P	1111	0	1148	21	0
34	p	1022	0	1070	36	0
35	Q	480	0	482	14	0
36	q	786	0	828	23	0
37	R	1129	0	1162	23	0
38	r	877	0	887	29	0
39	S	938	0	1012	23	0
40	t	955	0	1016	31	0
41	T	1053	0	1129	29	0
42	u	891	0	952	24	0
43	U	1075	0	1154	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	v	774	0	824	30	0
45	V	960	0	1000	23	0
46	w	710	0	728	12	0
47	W	892	0	923	27	0
48	x	649	0	666	33	0
49	X	917	0	962	19	0
50	y	648	0	691	26	0
51	Y	947	0	1019	18	0
52	z	455	0	478	13	0
53	C	90	0	0	0	0
53	I	204	0	0	0	0
53	J	5	0	0	0	0
53	K	1	0	0	0	0
53	L	1	0	0	0	0
53	V	2	0	0	0	0
53	Y	1	0	0	0	0
53	i	1	0	0	0	0
53	l	1	0	0	0	0
53	q	1	0	0	0	0
All	All	142146	0	95488	2724	0

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

The worst 5 of 2724 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)
19:I:2747:G:H21	19:I:2757:A:N6	1.38	1.20
19:I:2747:G:N2	19:I:2757:A:H62	1.41	1.18
19:I:2741:A:H62	19:I:2763:G:N2	1.44	1.13
19:I:2741:A:N6	19:I:2763:G:H21	1.47	1.12
21:J:72:G:N2	21:J:104:A:H62	1.56	1.03

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	
2	1	79/92 (86%)	72 (91%)	5 (6%)	2 (2%)	4	21
3	Z	101/103 (98%)	99 (98%)	1 (1%)	1 (1%)	12	43
4	2	82/87 (94%)	79 (96%)	2 (2%)	1 (1%)	10	38
5	4	108/110 (98%)	108 (100%)	0	0	100	100
6	3	68/71 (96%)	68 (100%)	0	0	100	100
7	b	91/100 (91%)	90 (99%)	1 (1%)	0	100	100
8	c	100/104 (96%)	91 (91%)	8 (8%)	1 (1%)	12	43
9	D	216/241 (90%)	207 (96%)	8 (4%)	1 (0%)	24	59
10	d	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
11	E	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
12	e	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
13	F	203/206 (98%)	184 (91%)	18 (9%)	1 (0%)	24	59
14	f	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
15	G	148/167 (89%)	142 (96%)	6 (4%)	0	100	100
16	g	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
17	H	98/135 (73%)	95 (97%)	3 (3%)	0	100	100
18	h	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
20	i	54/57 (95%)	54 (100%)	0	0	100	100
22	j	48/55 (87%)	44 (92%)	4 (8%)	0	100	100
23	K	270/273 (99%)	259 (96%)	11 (4%)	0	100	100
24	k	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
25	L	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
26	l	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
27	M	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
28	m	36/38 (95%)	36 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	N	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
30	n	149/179 (83%)	137 (92%)	10 (7%)	2 (1%)	9	36
31	O	174/177 (98%)	157 (90%)	15 (9%)	2 (1%)	11	41
32	o	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
33	P	147/149 (99%)	141 (96%)	6 (4%)	0	100	100
34	p	125/130 (96%)	99 (79%)	20 (16%)	6 (5%)	2	10
35	Q	56/70 (80%)	53 (95%)	3 (5%)	0	100	100
36	q	96/103 (93%)	93 (97%)	2 (2%)	1 (1%)	12	43
37	R	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
38	r	115/129 (89%)	111 (96%)	4 (4%)	0	100	100
39	S	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
40	t	121/124 (98%)	111 (92%)	10 (8%)	0	100	100
41	T	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
42	u	113/118 (96%)	95 (84%)	15 (13%)	3 (3%)	4	20
43	U	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
44	v	92/101 (91%)	89 (97%)	3 (3%)	0	100	100
45	V	118/127 (93%)	115 (98%)	3 (2%)	0	100	100
46	w	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
47	W	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
48	x	80/82 (98%)	63 (79%)	16 (20%)	1 (1%)	9	36
49	X	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
50	y	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
51	Y	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
52	z	53/75 (71%)	52 (98%)	1 (2%)	0	100	100
All	All	5555/5913 (94%)	5262 (95%)	271 (5%)	22 (0%)	31	63

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	9	PRO
4	2	5	LYS
8	c	54	GLN
30	n	59	LEU
34	p	73	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	71/79 (90%)	64 (90%)	7 (10%)	7	28
3	Z	84/84 (100%)	81 (96%)	3 (4%)	31	64
4	2	65/66 (98%)	61 (94%)	4 (6%)	16	47
5	4	93/93 (100%)	92 (99%)	1 (1%)	65	82
6	3	60/61 (98%)	57 (95%)	3 (5%)	22	54
7	b	80/84 (95%)	78 (98%)	2 (2%)	42	71
8	c	83/85 (98%)	80 (96%)	3 (4%)	31	64
9	D	180/199 (90%)	174 (97%)	6 (3%)	33	65
10	d	78/78 (100%)	72 (92%)	6 (8%)	12	38
11	E	170/190 (90%)	163 (96%)	7 (4%)	27	60
12	e	57/63 (90%)	55 (96%)	2 (4%)	32	64
13	F	172/173 (99%)	159 (92%)	13 (8%)	12	39
14	f	67/68 (98%)	65 (97%)	2 (3%)	36	68
15	G	113/126 (90%)	109 (96%)	4 (4%)	32	64
16	g	54/55 (98%)	52 (96%)	2 (4%)	30	63
17	H	87/116 (75%)	86 (99%)	1 (1%)	65	82
18	h	48/49 (98%)	47 (98%)	1 (2%)	47	74
20	i	47/48 (98%)	45 (96%)	2 (4%)	26	59
22	j	45/49 (92%)	44 (98%)	1 (2%)	45	73
23	K	217/218 (100%)	213 (98%)	4 (2%)	51	76
24	k	38/38 (100%)	35 (92%)	3 (8%)	11	37
25	L	164/164 (100%)	159 (97%)	5 (3%)	36	68
26	l	51/52 (98%)	50 (98%)	1 (2%)	48	75
27	M	165/165 (100%)	163 (99%)	2 (1%)	63	81
28	m	34/34 (100%)	32 (94%)	2 (6%)	18	49
29	N	148/150 (99%)	143 (97%)	5 (3%)	32	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	n	124/147 (84%)	116 (94%)	8 (6%)	15	45
31	O	137/138 (99%)	136 (99%)	1 (1%)	76	85
32	o	104/105 (99%)	100 (96%)	4 (4%)	29	62
33	P	114/114 (100%)	109 (96%)	5 (4%)	25	58
34	p	105/107 (98%)	101 (96%)	4 (4%)	29	62
35	Q	55/62 (89%)	54 (98%)	1 (2%)	51	76
36	q	86/90 (96%)	79 (92%)	7 (8%)	11	36
37	R	116/116 (100%)	113 (97%)	3 (3%)	40	71
38	r	90/99 (91%)	88 (98%)	2 (2%)	45	73
39	S	103/104 (99%)	100 (97%)	3 (3%)	37	68
40	t	103/104 (99%)	92 (89%)	11 (11%)	6	25
41	T	103/103 (100%)	101 (98%)	2 (2%)	50	75
42	u	93/96 (97%)	88 (95%)	5 (5%)	20	52
43	U	108/108 (100%)	103 (95%)	5 (5%)	24	57
44	v	79/84 (94%)	77 (98%)	2 (2%)	42	71
45	V	100/103 (97%)	99 (99%)	1 (1%)	68	83
46	w	75/77 (97%)	74 (99%)	1 (1%)	61	80
47	W	86/87 (99%)	84 (98%)	2 (2%)	44	72
48	x	65/65 (100%)	62 (95%)	3 (5%)	24	57
49	X	99/100 (99%)	95 (96%)	4 (4%)	28	60
50	y	74/78 (95%)	71 (96%)	3 (4%)	27	60
51	Y	89/90 (99%)	85 (96%)	4 (4%)	24	57
52	z	48/65 (74%)	44 (92%)	4 (8%)	10	35
All	All	4627/4829 (96%)	4450 (96%)	177 (4%)	30	62

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	q	6	ILE
42	u	14	HIS
36	q	67	ILE
40	t	5	ASN
43	U	119	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
26	l	28	ASN
33	P	2	GLN
48	x	59	HIS
30	n	148	ASN
36	q	56	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	1525/1536 (99%)	398 (26%)	20 (1%)
19	I	2894/2904 (99%)	564 (19%)	11 (0%)
21	J	117/120 (97%)	24 (20%)	0
All	All	4536/4560 (99%)	986 (21%)	31 (0%)

5 of 986 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	3	A
1	C	9	G
1	C	22	G
1	C	31	G
1	C	32	A

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	836	U
19	I	1962	5MC
1	C	1268	G
19	I	2349	G
19	I	1542	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

25 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	PSU	I	746	19,53	18,21,22	1.00	2 (11%)	21,30,33	1.88	4 (19%)
19	PSU	I	2457	19	18,21,22	0.96	0	21,30,33	1.98	5 (23%)
19	6MZ	I	2030	19	22,25,26	1.06	1 (4%)	29,36,39	2.31	9 (31%)
19	PSU	I	1917	19	18,21,22	0.91	0	21,30,33	1.91	5 (23%)
19	2MG	I	2445	19	23,26,27	0.77	1 (4%)	33,38,41	2.18	10 (30%)
19	H2U	I	2449	19	18,21,22	0.45	0	19,30,33	1.10	1 (5%)
19	6MZ	I	1618	19	22,25,26	1.11	1 (4%)	29,36,39	2.16	8 (27%)
19	2MA	I	2503	19,53	22,25,26	1.34	3 (13%)	32,37,40	2.04	7 (21%)
43	4D4	U	81	43	9,11,12	0.88	0	7,13,15	1.75	2 (28%)
19	PSU	I	955	19	18,21,22	0.95	0	21,30,33	1.95	4 (19%)
19	5MU	I	1939	19	19,22,23	1.05	3 (15%)	27,32,35	2.14	6 (22%)
19	5MC	I	1962	19	19,22,23	1.25	2 (10%)	26,32,35	1.13	2 (7%)
19	PSU	I	2580	19	18,21,22	1.07	1 (5%)	21,30,33	1.99	4 (19%)
19	1MG	I	745	19	23,26,27	0.93	1 (4%)	33,39,42	1.76	5 (15%)
19	PSU	I	2605	19	18,21,22	0.95	0	21,30,33	1.90	4 (19%)
19	5MU	I	747	19	19,22,23	1.02	2 (10%)	27,32,35	2.10	5 (18%)
19	G7M	I	2069	19	23,26,27	0.54	0	34,39,42	0.91	1 (2%)
19	2MG	I	1835	19	23,26,27	0.77	0	33,38,41	2.19	9 (27%)
19	OMC	I	2498	19,53	19,22,23	0.89	1 (5%)	25,31,34	1.07	2 (8%)
19	PSU	I	2604	19	18,21,22	0.93	0	21,30,33	1.87	4 (19%)
19	PSU	I	2504	19	18,21,22	0.92	1 (5%)	21,30,33	2.02	4 (19%)
19	PSU	I	1911	19	18,21,22	0.91	1 (5%)	21,30,33	1.96	4 (19%)
19	3TD	I	1915	19	19,22,23	1.06	2 (10%)	23,32,35	1.95	3 (13%)
19	OMG	I	2251	19	23,26,27	0.72	0	32,38,41	1.99	10 (31%)
19	OMU	I	2552	19	19,22,23	0.97	2 (10%)	25,31,34	1.93	6 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	PSU	I	746	19,53	-	1/7/25/26	0/2/2/2
19	PSU	I	2457	19	-	0/7/25/26	0/2/2/2
19	6MZ	I	2030	19	-	2/9/27/28	0/3/3/3
19	PSU	I	1917	19	-	2/7/25/26	0/2/2/2
19	2MG	I	2445	19	-	1/9/27/28	0/3/3/3
19	H2U	I	2449	19	-	0/7/38/39	0/2/2/2
19	6MZ	I	1618	19	-	2/9/27/28	0/3/3/3
19	2MA	I	2503	19,53	-	3/7/25/26	0/3/3/3
43	4D4	U	81	43	-	1/11/12/14	-
19	PSU	I	955	19	-	0/7/25/26	0/2/2/2
19	5MU	I	1939	19	-	0/7/25/26	0/2/2/2
19	5MC	I	1962	19	-	0/7/25/26	0/2/2/2
19	PSU	I	2580	19	-	1/7/25/26	0/2/2/2
19	1MG	I	745	19	-	0/7/25/26	0/3/3/3
19	PSU	I	2605	19	-	0/7/25/26	0/2/2/2
19	5MU	I	747	19	-	0/7/25/26	0/2/2/2
19	G7M	I	2069	19	-	0/7/25/26	0/3/3/3
19	2MG	I	1835	19	-	1/9/27/28	0/3/3/3
19	OMC	I	2498	19,53	-	0/9/27/28	0/2/2/2
19	PSU	I	2604	19	-	0/7/25/26	0/2/2/2
19	PSU	I	2504	19	-	1/7/25/26	0/2/2/2
19	PSU	I	1911	19	-	0/7/25/26	0/2/2/2
19	3TD	I	1915	19	-	5/7/25/26	0/2/2/2
19	OMG	I	2251	19	-	0/9/27/28	0/3/3/3
19	OMU	I	2552	19	-	0/9/27/28	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	I	1962	5MC	C5-C4	-4.02	1.41	1.44
19	I	2503	2MA	C6-N1	4.01	1.40	1.35
19	I	1618	6MZ	C6-N6	3.99	1.38	1.34
19	I	2030	6MZ	C6-N6	3.59	1.38	1.34
19	I	2503	2MA	C5-N7	-2.88	1.33	1.39

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	I	1835	2MG	C2-N3-C4	7.29	121.11	112.00
19	I	2445	2MG	C2-N3-C4	7.16	120.95	112.00
19	I	1915	3TD	N1-C2-N3	6.47	120.84	116.13
19	I	2503	2MA	C5-C4-N3	-6.13	120.72	127.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	I	745	1MG	C5-C4-N3	-5.70	119.31	128.39

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	I	746	PSU	O4'-C1'-C5-C6
19	I	1618	6MZ	O4'-C4'-C5'-O5'
19	I	1618	6MZ	C3'-C4'-C5'-O5'
19	I	1915	3TD	O4'-C1'-C5-C4
19	I	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	I	2030	6MZ	3	0
19	I	2445	2MG	2	0
19	I	2449	H2U	1	0
19	I	2503	2MA	1	0
19	I	1939	5MU	1	0
19	I	1962	5MC	2	0
19	I	2580	PSU	1	0
19	I	745	1MG	1	0
19	I	2605	PSU	1	0
19	I	2604	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 307 ligands modelled in this entry, 307 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

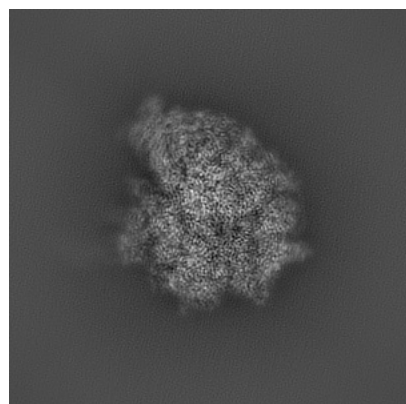
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75676. These allow visual inspection of the internal detail of the map and identification of artifacts.

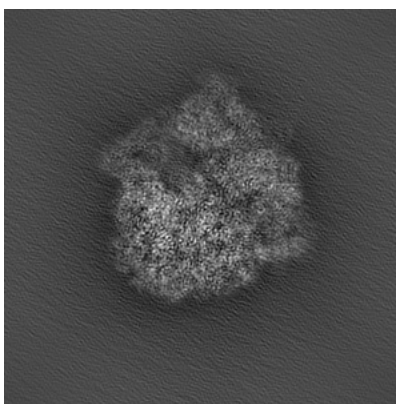
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

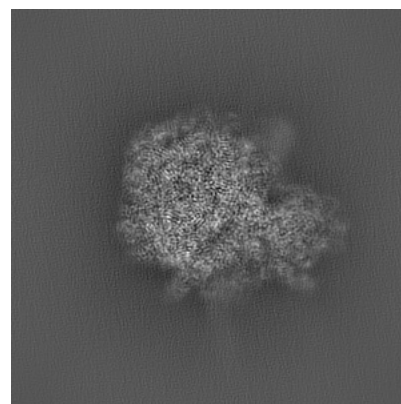
6.1.1 Primary map



X

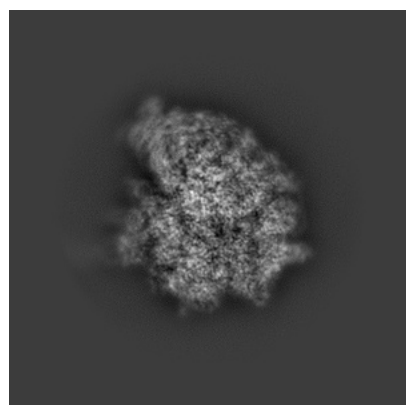


Y

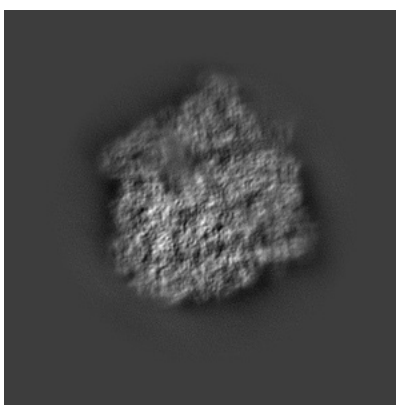


Z

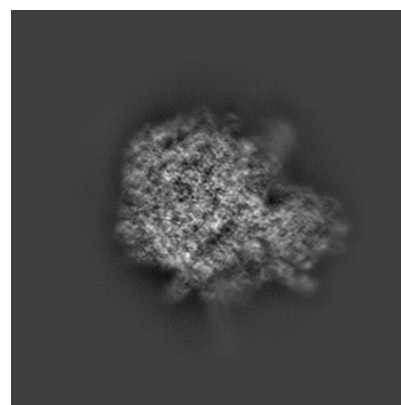
6.1.2 Raw map



X



Y

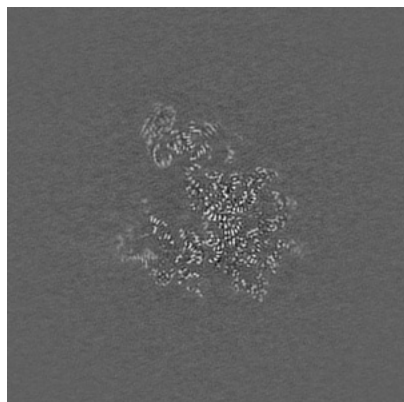


Z

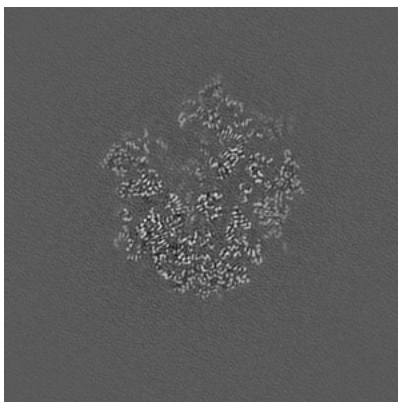
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

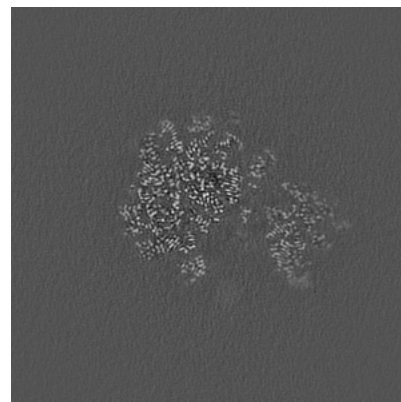
6.2.1 Primary map



X Index: 256

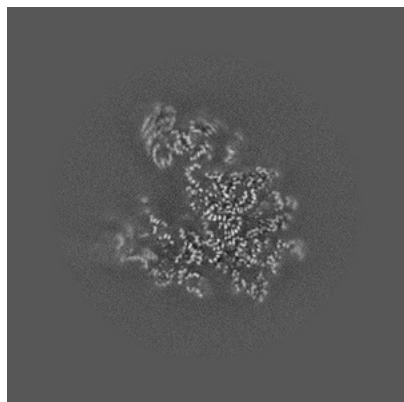


Y Index: 256

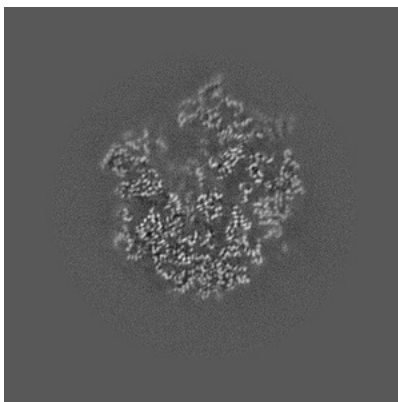


Z Index: 256

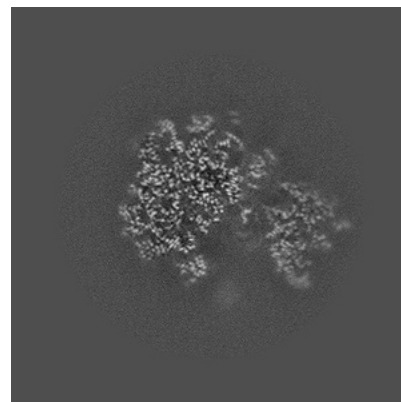
6.2.2 Raw map



X Index: 256



Y Index: 256

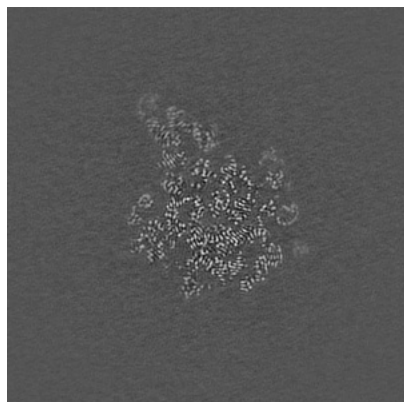


Z Index: 256

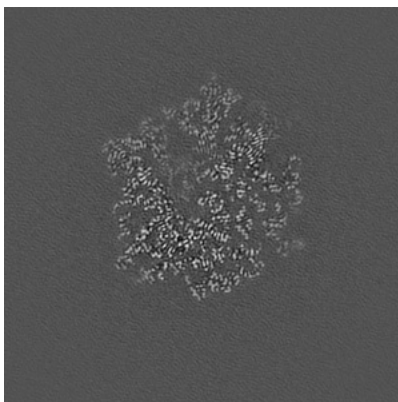
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

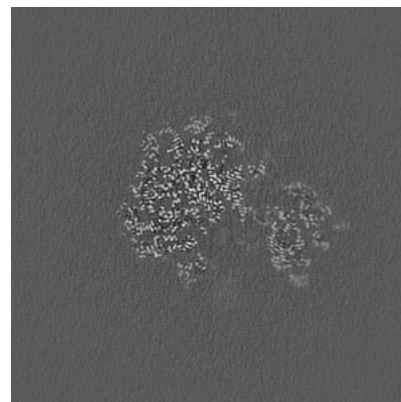
6.3.1 Primary map



X Index: 234

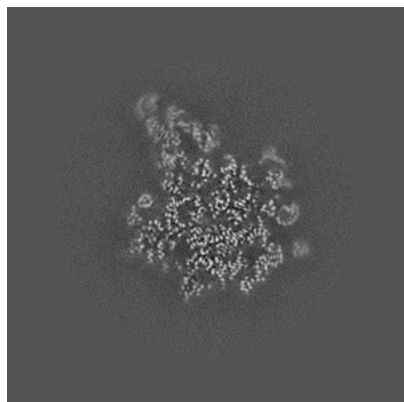


Y Index: 247

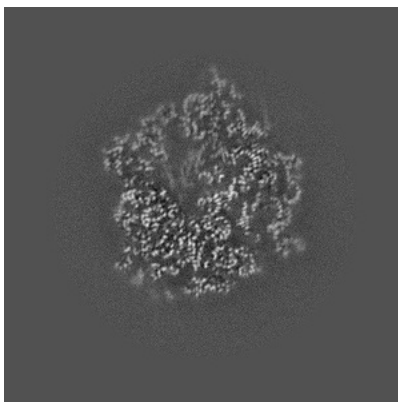


Z Index: 253

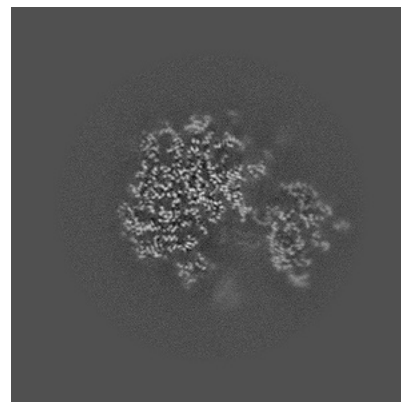
6.3.2 Raw map



X Index: 234



Y Index: 241

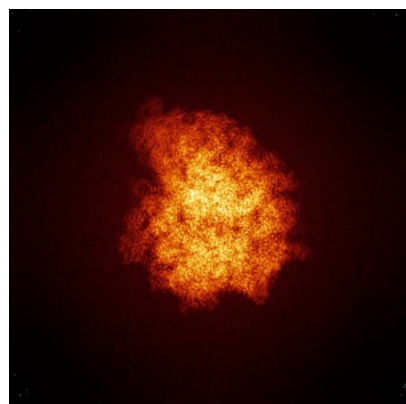


Z Index: 253

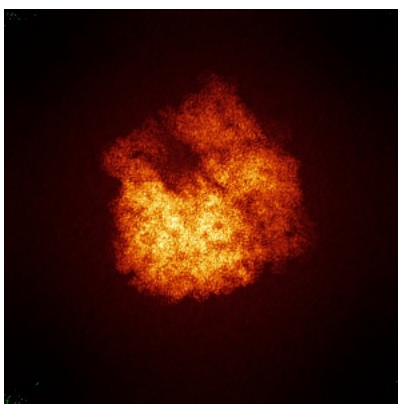
The images above show the largest variance slices of the map in three orthogonal directions.

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

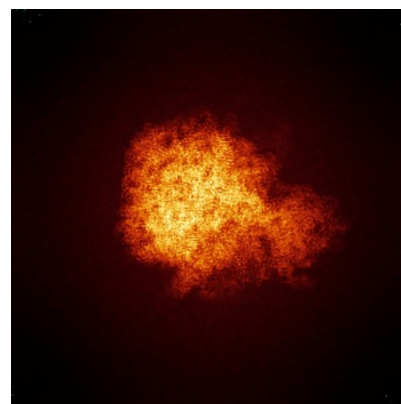
6.4.1 Primary map



X

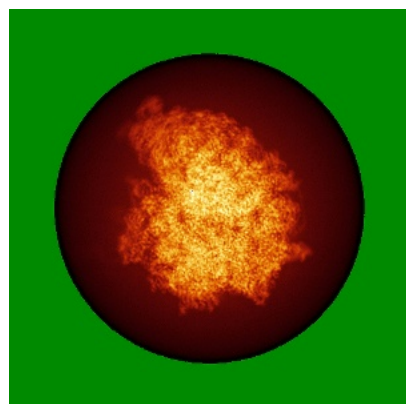


Y

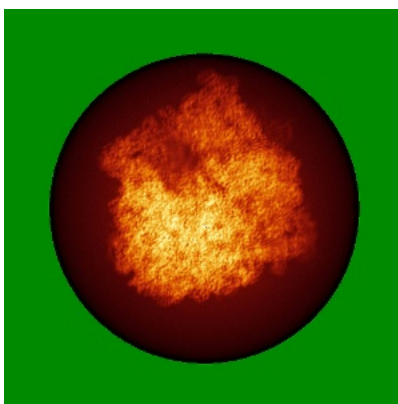


Z

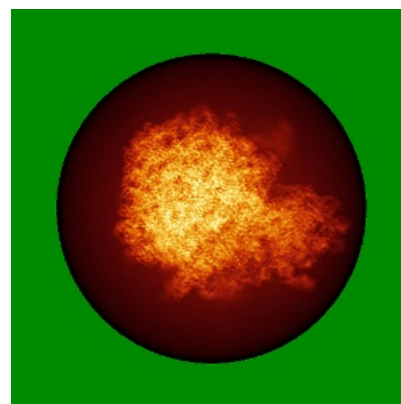
6.4.2 Raw map



X



Y

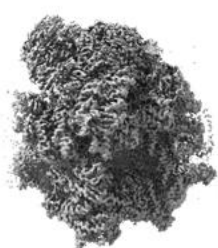


Z

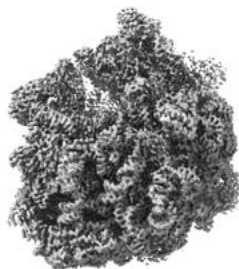
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

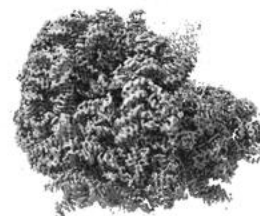
6.5.1 Primary map



X



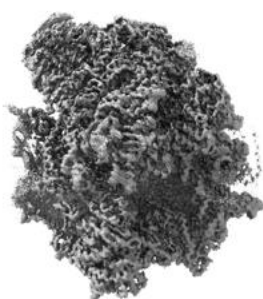
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

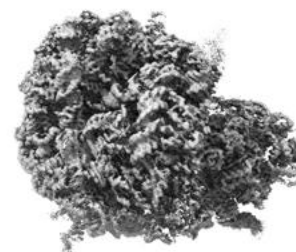
6.5.2 Raw map



X



Y



Z

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.

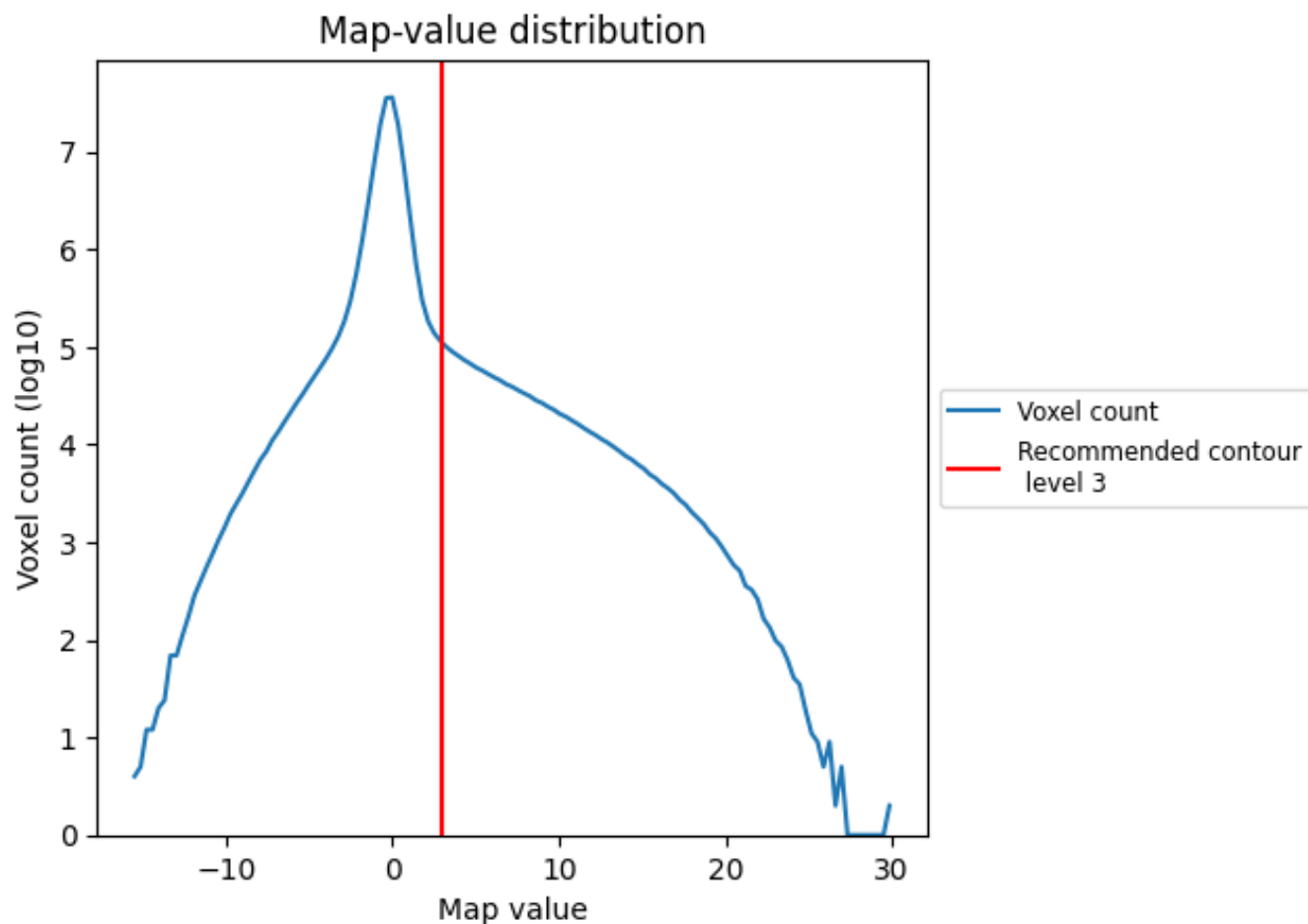
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

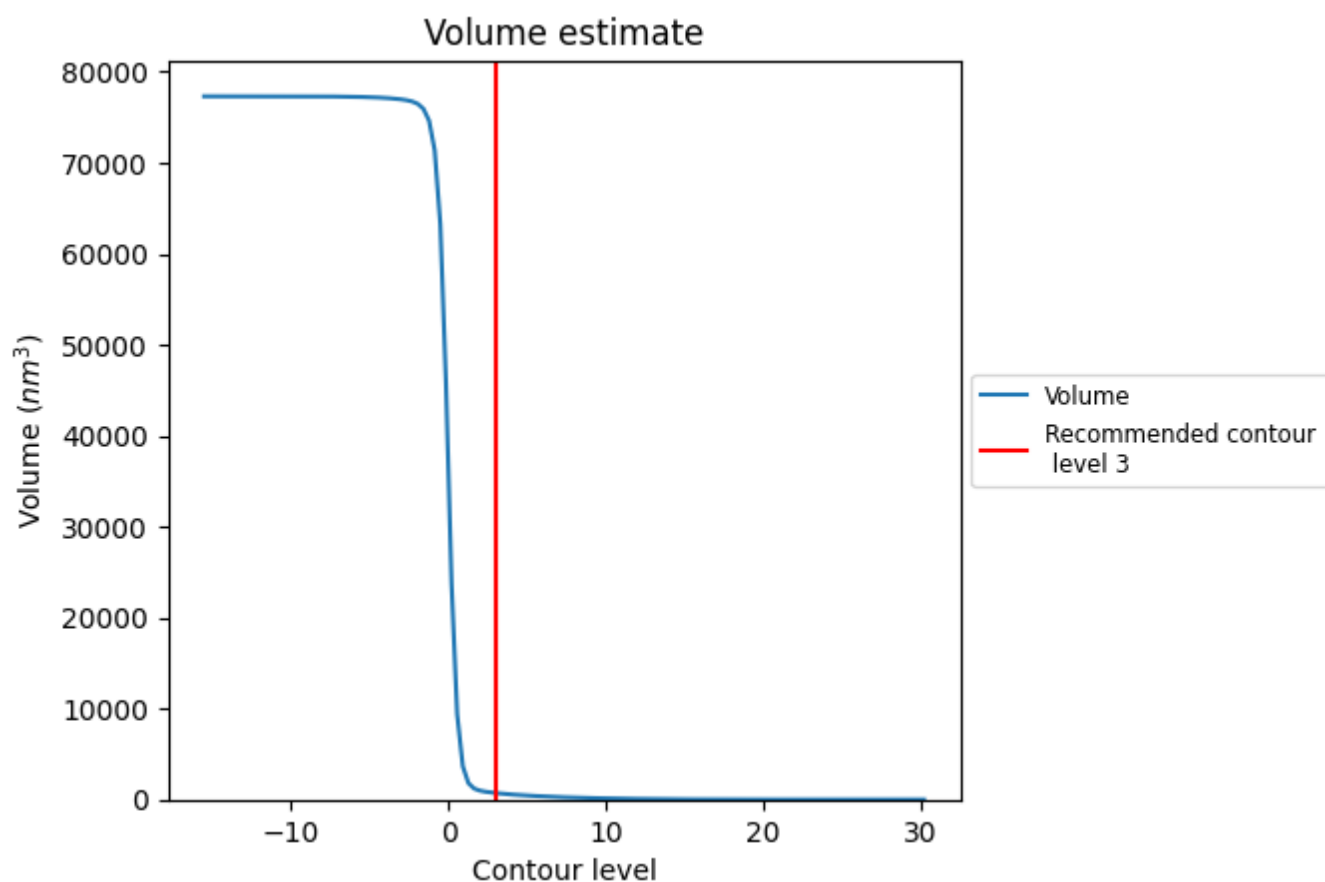
This section contains the results of statistical analysis of the map.

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.

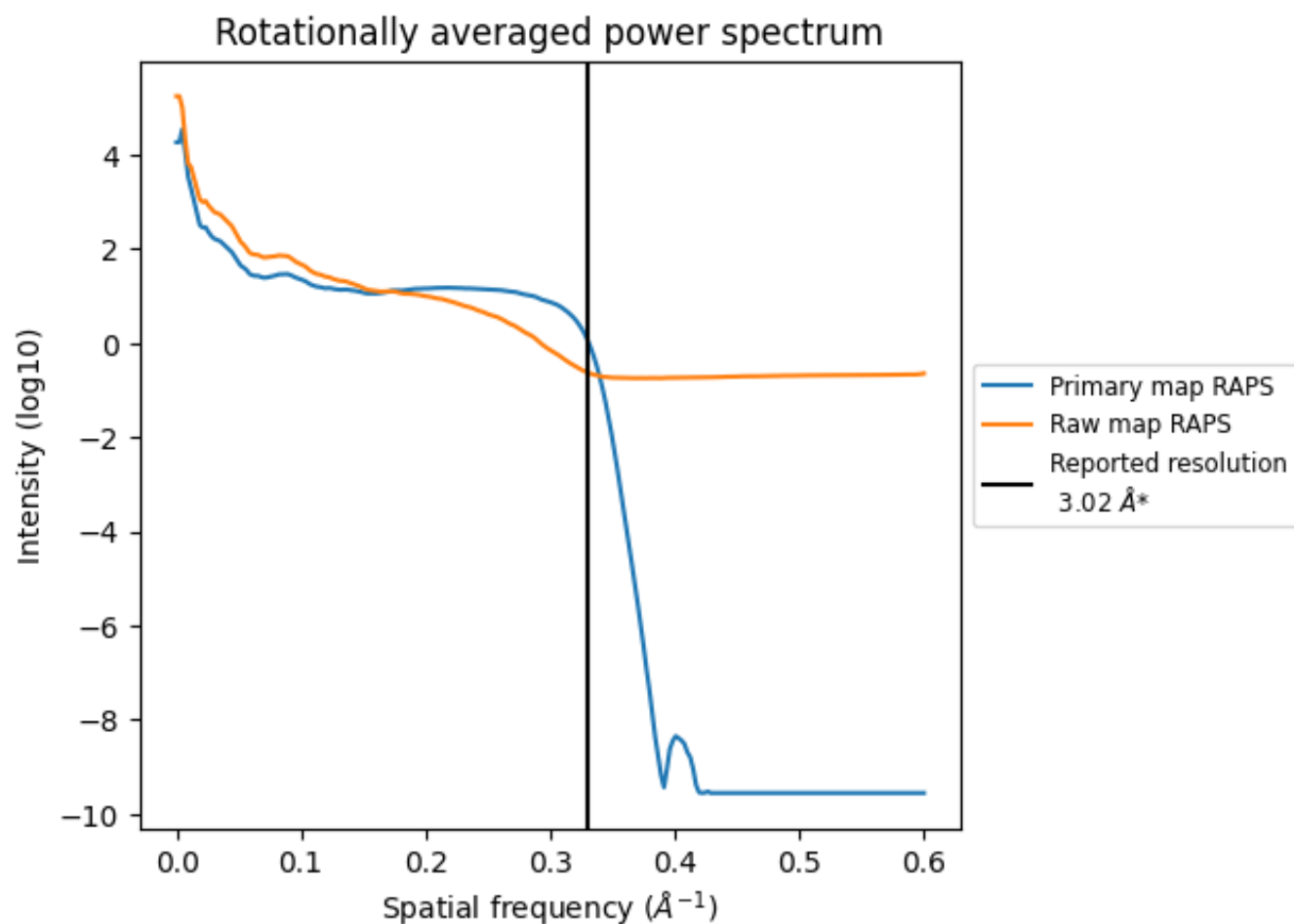
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 720 nm³; this corresponds to an approximate mass of 651 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 ⓘ

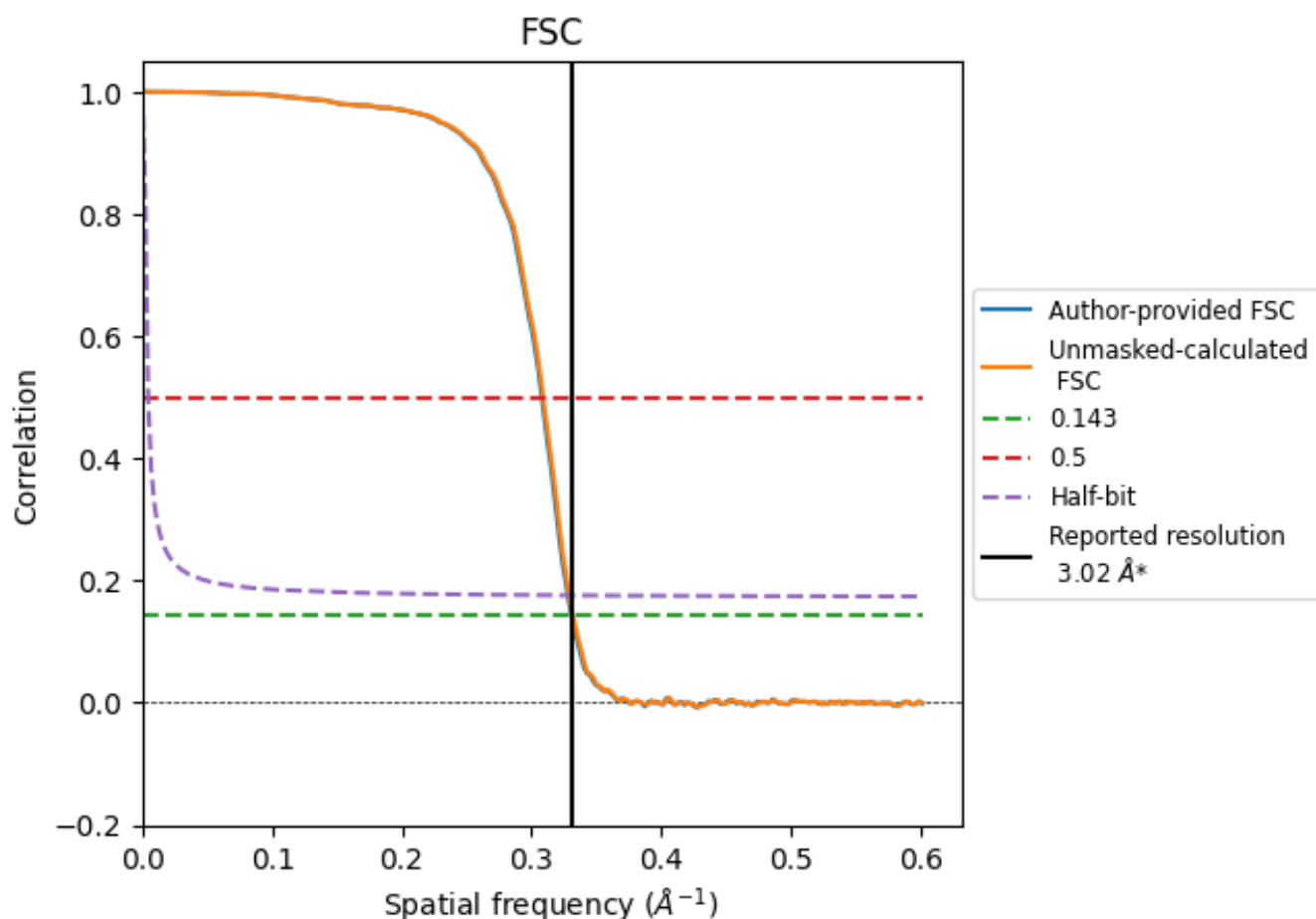


*Reported resolution corresponds to spatial frequency of 0.331 $\text{\AA}^{-1}$

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 0.331 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

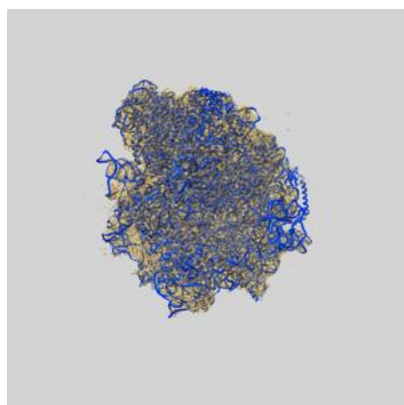
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	3.02	3.25	3.05
Unmasked-calculated*	3.01	3.24	3.04

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

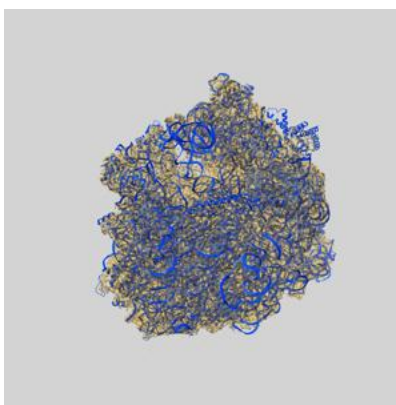
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75676 and PDB model 11GG. Per-residue inclusion information can be found in section [3](#) on page [14](#).

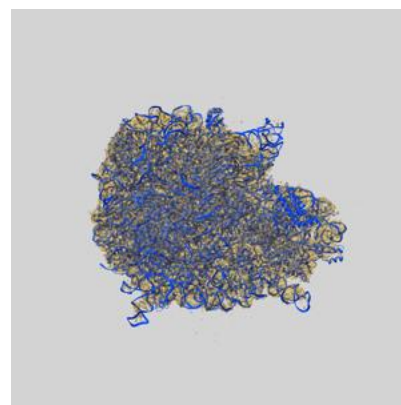
9.1 Map-model overlay [i](#)



X



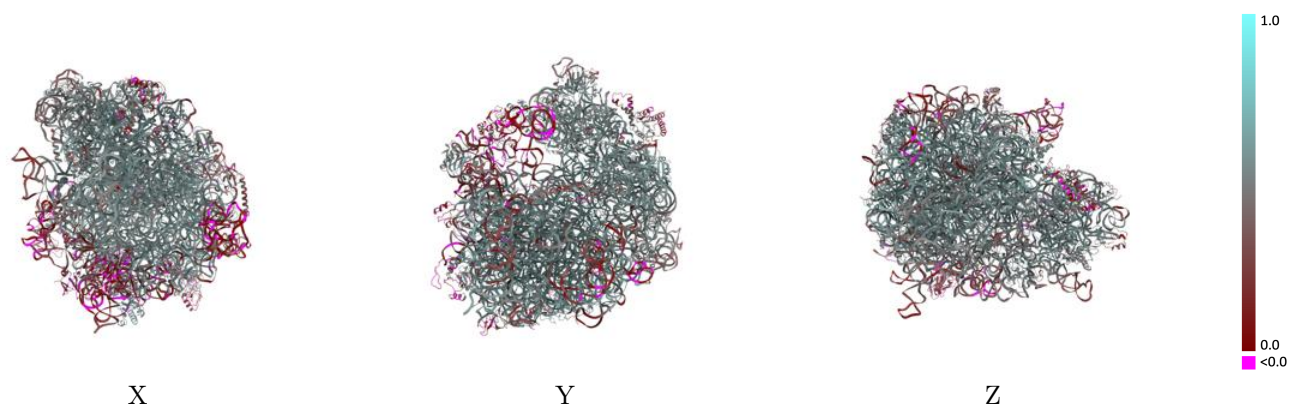
Y



Z

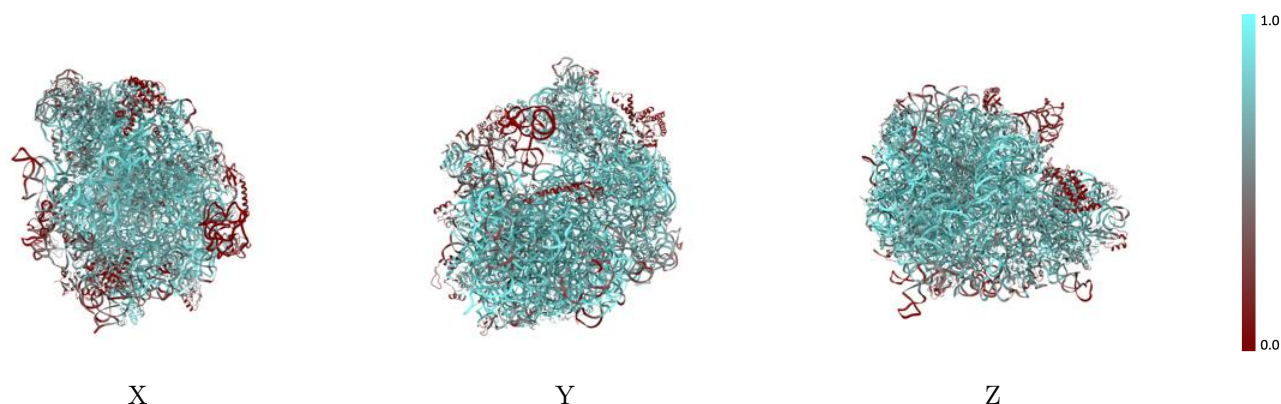
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



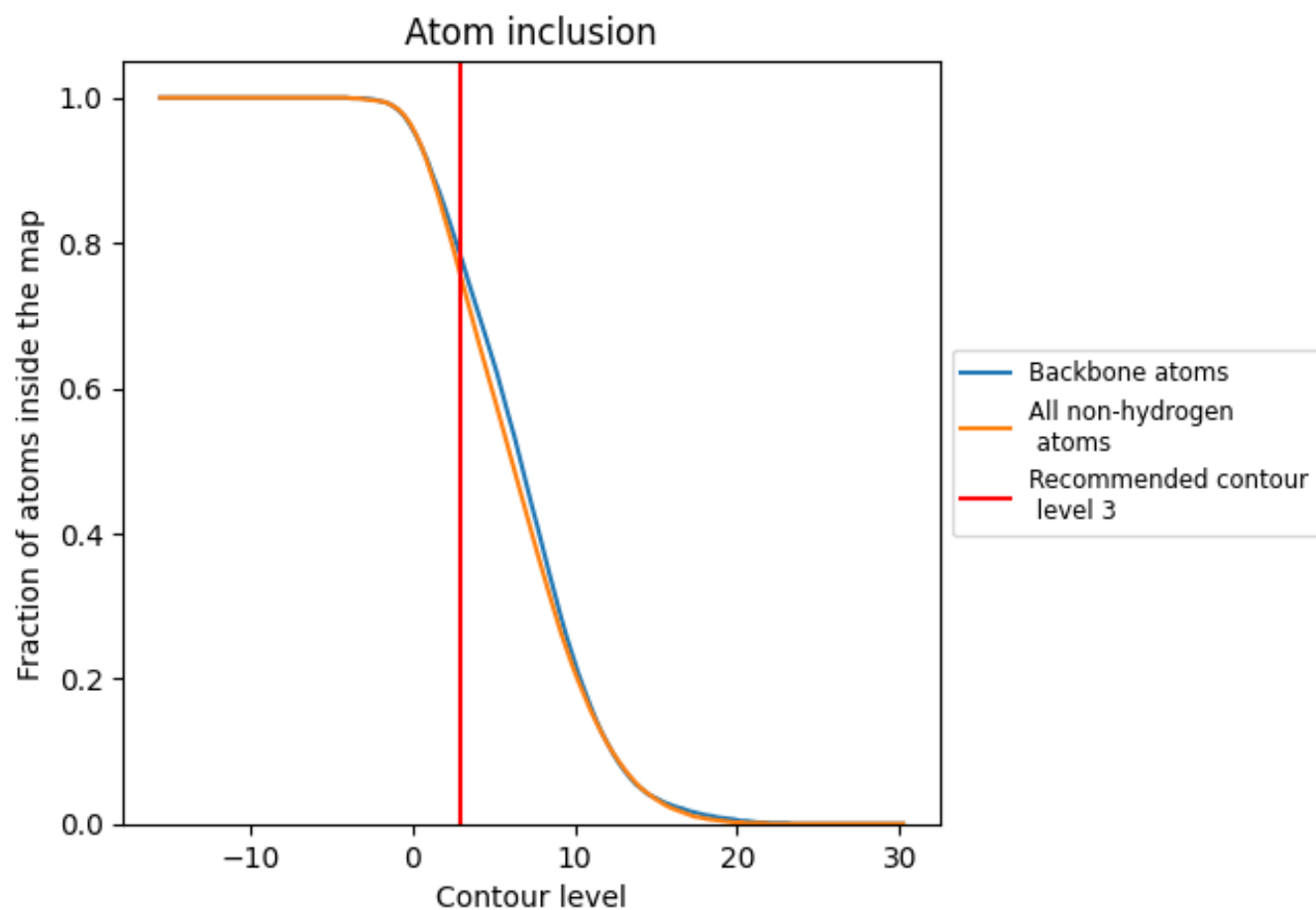
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 75% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7530	 0.4850
1	 0.6690	 0.5010
2	 0.6910	 0.5140
3	 0.4230	 0.4620
4	 0.8230	 0.5830
C	 0.8220	 0.5230
D	 0.1490	 0.3410
E	 0.7160	 0.5490
F	 0.5380	 0.5120
G	 0.7670	 0.5590
H	 0.7060	 0.5180
I	 0.8030	 0.4840
J	 0.4450	 0.2020
K	 0.8770	 0.5860
L	 0.7940	 0.5350
M	 0.6480	 0.4210
N	 0.2910	 0.1390
O	 0.2880	 0.1360
P	 0.2610	 0.3880
Q	 0.1800	 0.1440
R	 0.8380	 0.5640
S	 0.8470	 0.5840
T	 0.6480	 0.3860
U	 0.7970	 0.5350
V	 0.8700	 0.5860
W	 0.7580	 0.5360
X	 0.8450	 0.6030
Y	 0.7870	 0.5110
Z	 0.6150	 0.3710
b	 0.7510	 0.5480
c	 0.5500	 0.3680
d	 0.3560	 0.1850
e	 0.6310	 0.3790
f	 0.8590	 0.5850
g	 0.6360	 0.4360



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Chain	Atom inclusion	Q-score
h	 0.6960	 0.4400
i	 0.8460	 0.5970
j	 0.1200	 0.1290
k	 0.9070	 0.6160
l	 0.8920	 0.6110
m	 0.8360	 0.5460
n	 0.5870	 0.5160
o	 0.7790	 0.5690
p	 0.6460	 0.5170
q	 0.4950	 0.4560
r	 0.7540	 0.5450
t	 0.7360	 0.5170
u	 0.6990	 0.5330
v	 0.7030	 0.5180
w	 0.7940	 0.5510
x	 0.6120	 0.4740
y	 0.6770	 0.5250
z	 0.8190	 0.5510