



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:01 AM UTC

PDB ID : 5AKA / pdb_00005aka
EMDB ID : EMD-2917
Title : EM structure of ribosome-SRP-FtsY complex in closed state
Authors : von Loeffelholz, O.; Jiang, Q.; Ariosa, A.; Karuppasamy, M.; Huard, K.;
Berger, I.; Shan, S.; Schaffitzel, C.
Deposited on : 2015-03-03
Resolution : 5.70 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

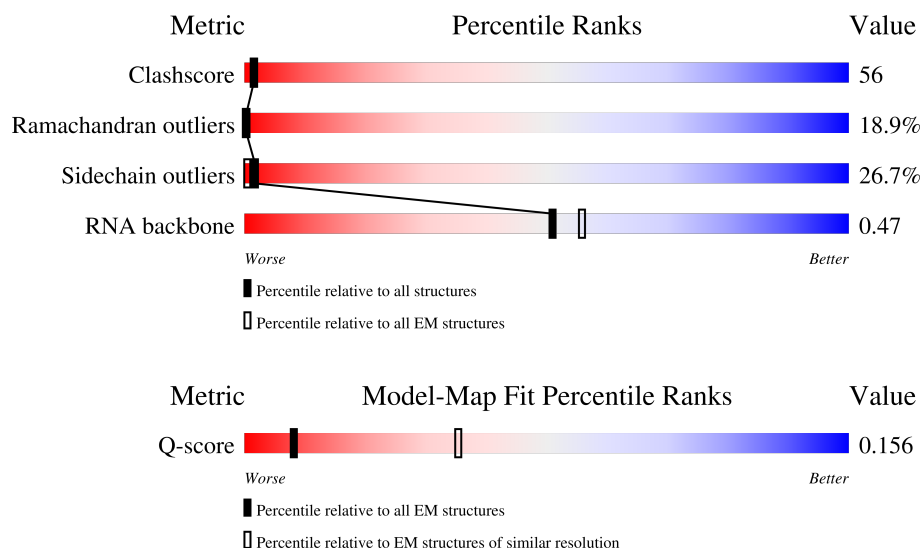
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	503 (5.20 - 6.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	56	39% 14% 46% 23% 16%
2	1	54	35% 15% 46% 33% 6%
3	2	46	46% 22% 50% 28%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	64	
5	4	38	
6	5	109	
7	6	8	
8	7	74	
9	A	120	
10	B	2904	
11	C	273	
12	D	209	
13	E	201	
14	F	178	
15	G	176	
16	H	149	
17	I	141	
18	J	142	
19	K	123	
20	L	144	
21	M	136	
22	N	127	
23	O	117	
24	P	114	
25	Q	117	
26	R	103	
27	S	110	
28	T	100	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	U	103	
30	V	94	
31	W	84	
32	X	63	
33	Y	58	
34	Z	70	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 92737 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S RIBOSOMAL PROTEIN L32.

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

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called SIGNAL RECOGNITION PARTICLE PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	109	Total	C	N	O	S	0	0
			850	523	159	153	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	406	SER	CYS	conflict	UNP P0AGD7

- Molecule 7 is a protein called ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	6	8	Total	C	N	O	0	0
			41	24	8	9		

- Molecule 8 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	74	Total	C	N	O	P	0	0
			1591	709	298	511	73		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	117	Total	C	N	O	P	0	0
			2507	1116	459	815	117		

- Molecule 10 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	2841	Total	C	N	O	P	0	0
			60995	27210	11229	19715	2841		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	2798	U	UNK	conflict	GB 731469900
B	2800	A	UNK	conflict	GB 731469900

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 12 is a protein called 50S RIBOSOMAL PROTEIN L3.

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

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L4.

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

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L6.

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

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L9.

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

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	138	Total	C	N	O	S	0	0
			1002	623	197	181	1		

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L19.

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

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L20.

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

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L21.

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

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L22.

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

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L25.

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

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L30.

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

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	B	110	Total	Mg	0
			110	110	

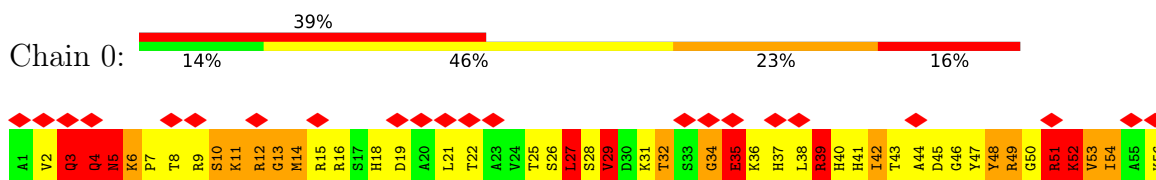
- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	B	497	Total	O	0
			497	497	
36	C	1	Total	O	0
			1	1	
36	E	5	Total	O	0
			5	5	
36	L	2	Total	O	0
			2	2	
36	N	1	Total	O	0
			1	1	

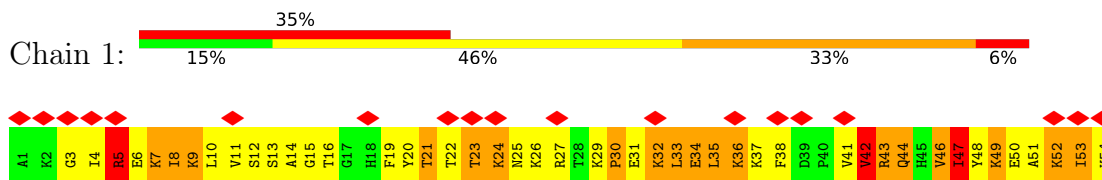
3 Residue-property plots [i](#)

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.

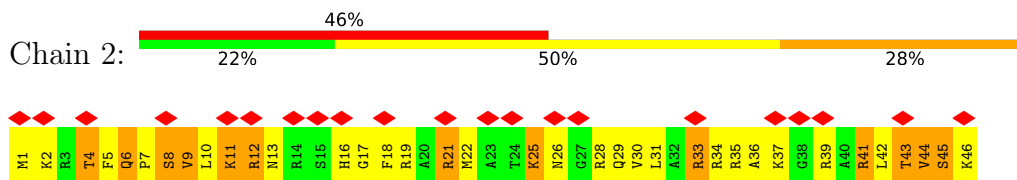
- Molecule 1: 50S RIBOSOMAL PROTEIN L32



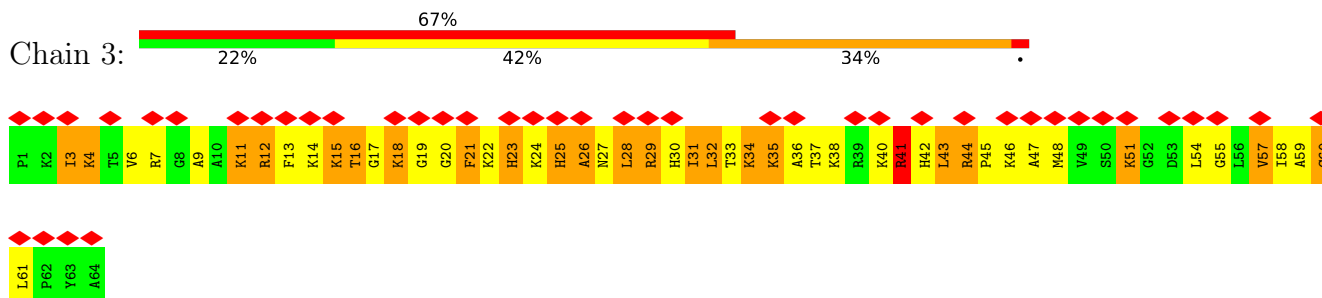
- Molecule 2: 50S RIBOSOMAL PROTEIN L33



- Molecule 3: 50S RIBOSOMAL PROTEIN L34



- Molecule 4: 50S RIBOSOMAL PROTEIN L35

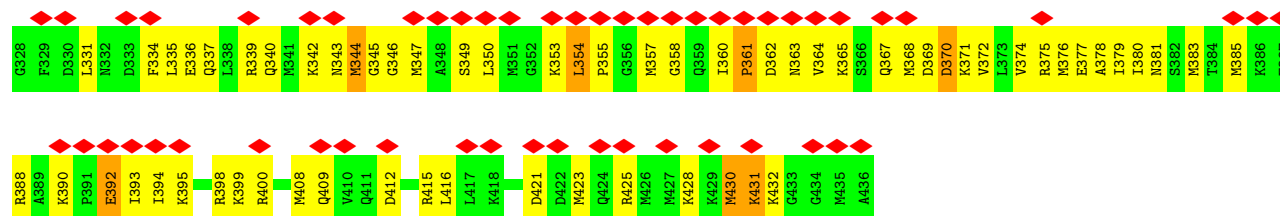


- Molecule 5: 50S RIBOSOMAL PROTEIN L36

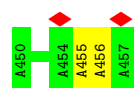
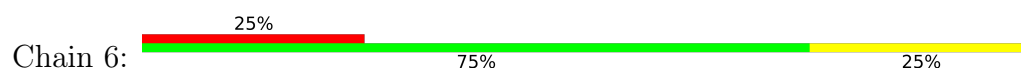




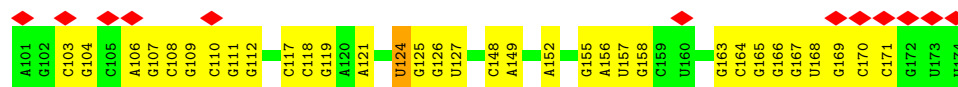
• Molecule 6: SIGNAL RECOGNITION PARTICLE PROTEIN



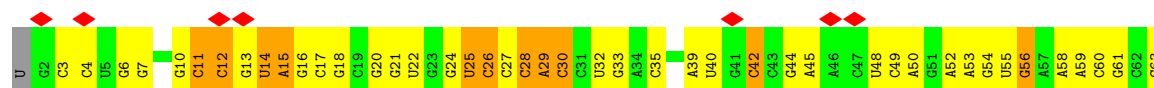
• Molecule 7: ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA



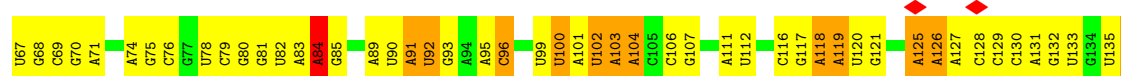
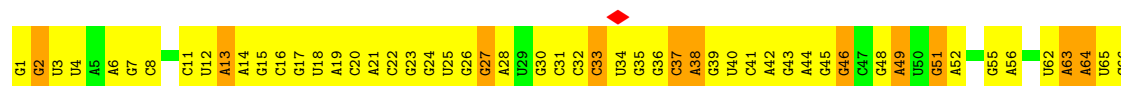
• Molecule 8: 4.5S ribosomal RNA

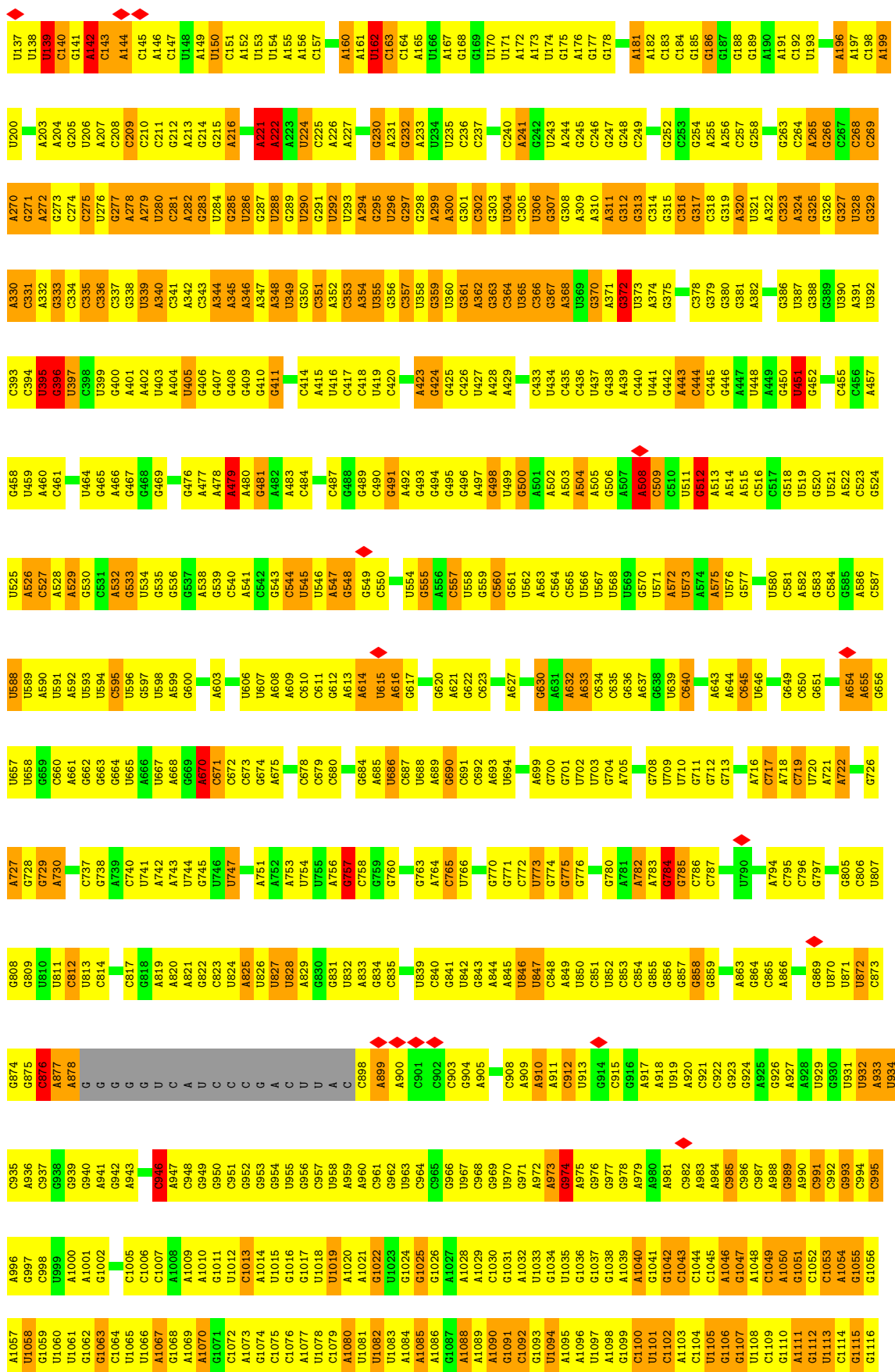


• Molecule 9: 5S ribosomal RNA



• Molecule 10: 23S ribosomal RNA



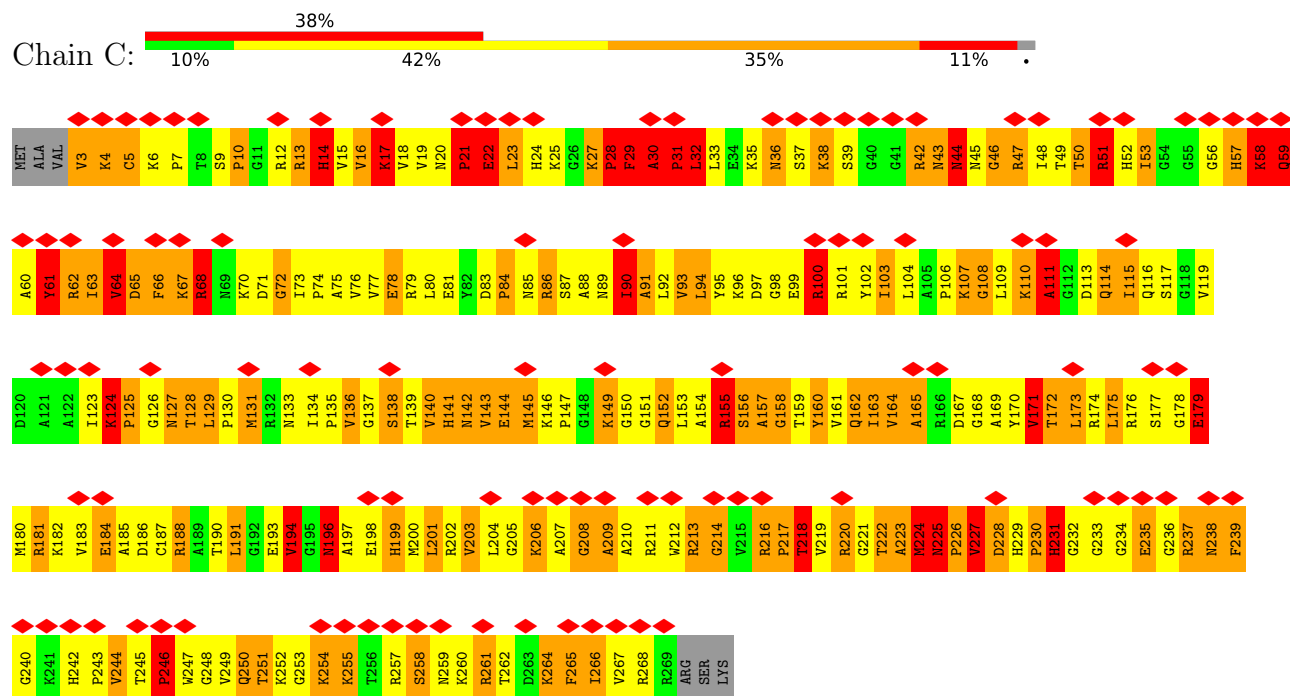


A1918	G1842	U1775	A1711	G1645	G1573	U1513	C1447	G1381	G1311	A1245	U1181	G1117
A1919	C1843	G1776	U1712	C1646	C1574	G1514	G1448	G1382	U1312	A1247	U1182	C1118
C1920	C1844		U1713	U1647	U1578	A1516	G1449	A1383	U1313	U1248	U1183	U1119
G1921	G1845	U1779	U1714	U1648	U1579	G1515	G1450	A1384	C1314	U1249	U1184	G1249
G1922	G1846	A1780	G1715	G1649	A1580	G1517	C1451	A1385	U1315	G1250	G1185	C1121
U1923	A1847	U1781	U1716			G1518	G1452	C1386	U1316	C1251	G1186	G1122
C1924	A1848	U1782	U1717	A1652	A1581	G1519	A1453	A1387	U1317	G1252	G1187	G1123
		A1783	G1718	G1653	U1584	U1520	C1454		U1318	G1253	U1188	G1124
	U1851	A1784	G1719	U1654	U1585	G1521	G1455	A1392	C1319	A1254	U1189	G1125
A1928	U1852	A1785	U1720	A1655	C1586	A1522	U1456	U1393	U1320	U1255	G1190	A1126
G1929	A1853	A1786	G1721	C1656	A1586	U1523	U1457	U1394	A1321	G1256	G1191	
G1930	A1854	A1787	A1722	U1657	G1587	G1524	U1458	U1395	A1322	C1257	G1192	U1130
U1931	U1855	C1788	G1723	U1658	U1588	A1525	U1459	U1396	C1323	U1258	G1193	G1131
A1932	U1856	A1789	G1724	G1661	U1589	C1526	U1460	U1397	G1324	G1259	U1194	U1132
G1933	G1857	G1790	G1725	U1662	A1590	G1527	C1461	U1398	U1325	C1261	G1195	A1134
	A1858	A1791	U1726	G1663	A1591	A1528	G1462	C1399	U1326		C1196	A1133
G1935	U1864	C1792	C1727	A1664	C1592	G1529	G1463	U1400	A1327	G1266	G1197	G1135
A1936	C1793	C1728	U1729	A1665	A1593	U1530	G1464	U1401	U1328	U1267	U1198	G1136
U1937	U1865	U1729	G1730	G1666	C1595	A1531	G1465	U1402	U1329	U1268	U1199	G1137
A1938	U1866	C1795	G1731	G1667	A1596	A1532		U1403	C1330	A1269	U1200	G1138
U1939	G1867	U1796	C1732	U1668	A1597	U1533	A1469	A1404	G1331	U1270	U1201	G1139
U1940	G1868	G1797	G1733	A1669	A1598	A1534	G1470	U1405	G1332	G1271	G1202	C1140
	G1869	U1798	G1734	A1670	U1599	G1535	G1471	U1406	G1333	G1272	U1203	U1141
U1943	C1870	G1799	G1735	C1670	U1600	G1536	G1472	G1407	G1334	A1272	A1204	A1143
A1944	A1871	C1800	A1736	U1671	G1601	G1537	U1474	G1408	A1335	U1273	A1205	A1144
G1945	A1872	A1801	U1737	A1672	U1602	U1538	G1475	U1409	A1336	A1274	G1206	G1145
U1946	G1873	A1802	G1738	G1673	A1603	U1539	U1476	G1410	G1337	A1275	C1207	
C1947	C1874	A1803	A1739	G1675	A1604	G1540	G1477	U1411	U1341	G1276	G1210	G1149
G1948	G1875	C1804	G1740	A1676	A1605	C1541	G1478	U1412	C1345	G1278	C1211	C1150
U1949	A1876	A1805	C1741	A1677	C1606	G1543	G1479	A1413	A1346	G1279	G1212	A1151
U1950	A1877		U1742		C1607	A1544	C1480	C1414	G1347	G1280	C1152	C1153
G1951	G1878	A1808	G1743	G1681	A1608	U1545	U1481	U1415	C1348	G1281	G1215	G1154
U1952	C1879	A1809	A1744	U1682	A1609	A1546	G1482	G1416	C1349	G1282	G1216	A1155
A1953	U1880	A1810	U1745	G1683	C1611	C1547	U1483		C1350	U1283	U1217	A1156
G1954	G1881	G1811	A1746	G1684	G1612	A1548	U1484	A1419	C1351	A1284	G1218	G1157
U1955	U1882	U1812	U1747	C1685	G1613	C1549	U1485	A1420	U1352	A1285	G1219	G1158
U1956	G1883	G1813	C1748	C1686	U1616	C1550	U1486		A1353	A1286	U1219	U1159
C1957	G1884	A1814			A1617	A1551	U1487	G1424	G1354	G1287	G1220	G1160
A1958	A1885	A1815	A1749	U1687	A1618	U1552	U1488	G1425	U1355	G1288	C1221	C1161
		C1816	G1750	U1688	A1619	U1553	C1489	G1426		C1289	U1224	G1162
G1959	G1888	G1817	C1752	A1690	G1622	U1554	A1490	A1427	A1359	C1290	G1225	G1163
U1963	A1889	U1818	G1753	C1691	G1623	C1555			G1360	G1291	A1226	C1164
G1964	A1890	A1819	U1754	U1692	U1624	U1556	C1493	G1429	G1361	G1292	G1227	A1165
C1965		U1820	A1755	U1693	U1625	C1557	A1494	G1430	C1362	C1293	G1228	G1166
A1966	U1898	A1821	G1756	C1694	U1626	C1558	A1495	A1431	C1363	U1294	C1229	C1167
C1967		C1822	A1757	G1695	U1629	U1559	A1496	A1432	G1364	C1295	A1230	G1168
	A1901	G1823	U1758	G1696		G1560		A1433	A1365	G1296	U1231	G1169
U1970	C1902		U1759		G1633	C1561	G1501	A1434		C1297	G1232	
G1971	G1824	U1825		A1700	U1634	U1562	A1502		G1368	C1298	G1236	G1171
G1972	C1903	G1826	G1762	A1701	A1634	U1563	A1503	C1437	U1369	G1299	A1237	C1172
C1973	G1904	U1827	U1763	G1702	A1635	C1564	A1504	U1438	A1373	G1300	A1238	U1173
G1974	G1905	G1828	C1764	G1703	U1636	C1565	A1505	A1439	U1374	A1301	G1239	U1174
		A1829	U1765	G1704	A1637	U1566	U1506	U1440	U1375	A1302	U1240	A1175
U1979	C1909	C1830	G1766	A1705	C1638	G1567	C1507	G1441	G1376	G1303	U1241	U1176
G1980	G1910	G1831		A1706	C1639	U1568	A1508	U1442	G1377	C1304	G1177	G1177
A1981		C1832	C1771	G1707	A1640	A1569	A1509	U1443	A1378	C1305	U1242	C1178
	A1913	C1833	U1772	G1708	A1641	U1570	A1510	G1444	U1379	G1309	A1243	G1179
G1986	C1914	A1773	A1773	U1709	G1642	A1571	G1511	G1445	G1380		A1244	G1245
A1987			C1774	G1710		A1572	C1512					U1180

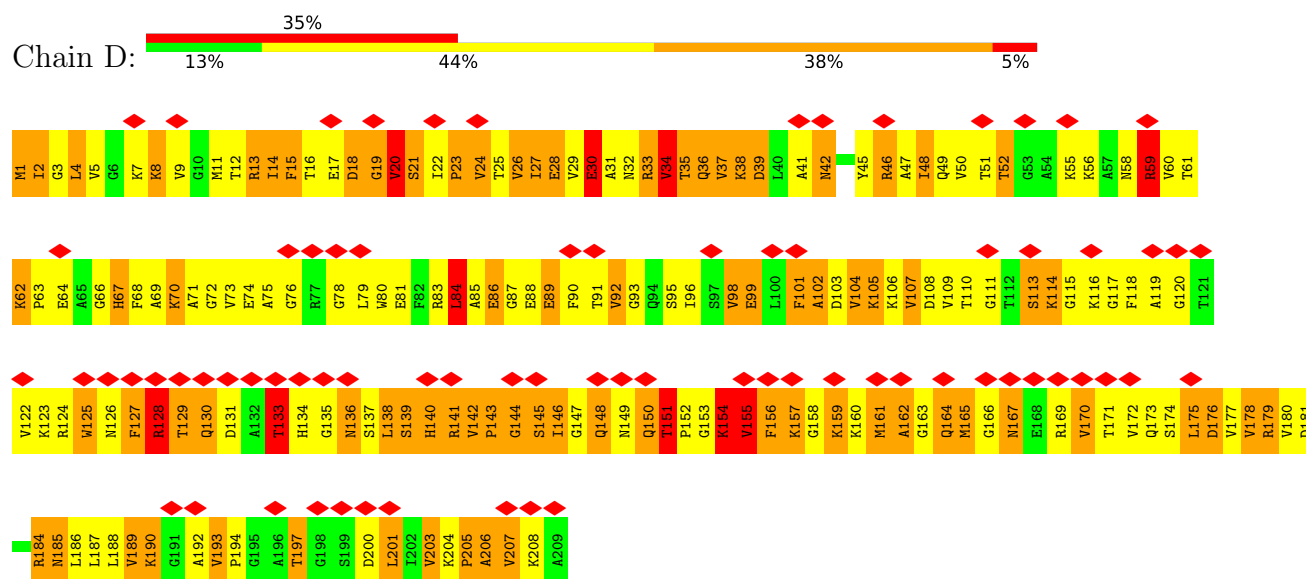
G1989	C1990	U1991	G1992	U1993	G1994	U1995	C1996	C1997	A1998	C1999	C2000	C2001	U2007	C2008	A2009	G2010	U2011	A2014	A2015	U2016	U2017	G2018	U2019	A2020	C2021	U2022	C2023	G2024	C2025	U2026	C2027	U2028	G2029	A2030	A2031	C2032	A2033	U2034	G2035	C2036	A2037	G2038	U2039	U2040	U2041	A2042	C2043	C2044	C2045	U2046	G2047	G2048	G2049	C2050	A2051	A2052	G2053	
A2054	C2055	G2056	U2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	U2075	U2076	C2077	U2078	U2079	A2080	U2081	A2082	G2083	C2084	U2085	U2086	G2087	A2088	C2089	A2090	C2091	U2092	G2093	A2094	A2095	C2096	A2097	U2098	U2099	G2100	A2101	G2102	C2103	C2104	U2105	U2106	G2110	U	G	U	A	A	G	G	A
U	A	G	G	U	C	G	G	A	C	G	U	U	U	G2133	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A	G	C	C	U	U	U	C	A	A	A	U	U	A	C	C	C	C2179					
U2180	U2181	U2182	A2183	U2184	U2185	U2186	U2187	U2188	U2189	G2190	A2191	U2192	U2193	U2194	U2195	C2196	U2197	A2198	A2199	C2200	U2203	G2204	A2205	C2206	G2207	G2208	G2209	U2210	A2211	G2212	U2213	C2214	C2215	G2216	G2217	G2218	U2219	U2220	G2221	G2222	G2223	G2224	A2225	C2226	A2227	G2228	U2229	G2230	U2231	C2232	U2236	G2237	G2238	G2239	U2240	A2241	G2242	
U2243	G2246	G2247	G2248	U2249	G2250	G2251	C2258	U2259	C2260	C2261	U2262	C2263	C2264	U2265	A2266	A2267	A2268	G2269	A2270	G2271	U2272	A2273	A2274	C2275	G2276	G2277	A2278	G2282	C2283	A2284	C2285	G2286	A2287	G2288	G2289	C2290	U2291	U2292	G2293	G2294	C2295	U2296	A2297	U2298	U2299	C2300	C2301	U2302	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310		
A2311	U2312	C2313	A2314	G2315	G2316	A2317	G2318	U2319	U2320	U2321	A2322	G2323	U2324	G2325	A2328	U2329	C2330	G2331	C2332	A2333	U2334	A2335	A2336	G2337	C2338	C2339	A2340	G2341	U2344	A2345	G2346	C2347	U2348	G2349	C2350	G2351	A2352	G2353	C2354	G2355	C2364	G2365	A2369	G2370	G2371	U2372	G2373	C2374	U2379	C2380	G2383	U2384	C2385					
A2386	U2387	A2388	U2390	G2391	A2392	U2393	C2394	C2395	G2396	G2397	U2398	C2399	G2400	U2401	U2402	G2405	A2406	A2412	G2413	G2414	G2415	C2416	U2419	C2420	U2423	C2424	A2425	U2426	C2427	G2428	G2429	A2430	A2433	A2434	U2438	A2439	C2440	U2441	C2442	G2443	G2444	G2445	G2446	G2447	U2448	U2449	A2450	G2454	G2455	G2456	U2457							
G2458	A2459	U2460	C2461	C2462	C2465	C2466	C2467	A2468	A2469	G2470	A2471	G2472	C2475	A2476	U2477	A2478	U2479	C2483	G2484	G2485	U2489	G2490	U2491	U2492	U2493	C2498	C2499	U2500	C2501	G2502	A2503	U2504	G2505	U2506	C2507	G2508	U2511	C2512	A2513	U2514	C2515	A2516	C2517	A2518	U2519	C2520	C2521	U2522	G2523	G2524	G2525	C2527						
U2528	G2529	A2530	A2531	G2532	U2533	A2534	G2535	U2537	C2538	C2539	C2540	G2543	G2544	G2545	U2546	U2547	U2548	G2553	U2554	U2555	C2556	G2557	C2558	U2563	A2566	G2567	U2568	C2569	G2570	U2571	U2572	C2573	G2574	C2575	U2576	G2577	G2578	C2579	U2580	G2581	U2585	U2586	A2587	A2590	C2591	G2592	G2597	A2598	U2599	A2600	C2601							
A2602	G2603	U2604	U2605	C2606	G2607	G2608	C2609	C2610	U2613	U2614	U2615	G2616	U2617	G2618	C2619	C2620	G2621	U2622	G2623	G2624	G2625	G2626	G2627	G2628	U2629	G2630	G2631	A2632	G2633	A2634	A2635	C2636	U2637	G2638	G2639	G2640	G2641	G2642	G2643	G2644	G2645	C2646	U2647	G2648	C2649	U2650	C2651	C2652	U2653	A2654	A2657	C2658	G2659	A2660	G2661	A2662	G2663	
G2664	A2665	C2666	G2669	A2670	G2671	U2672	G2673	G2674	A2675	G2676	G2677	C2678	A2679	U2680	A2681	C2682	G2683	U2684	G2685	G2686	U2687	G2688	U2689	U2690	C2691	G2692	G2693	G2694	U2698	C2699	U2700	U2701	G2704	A2705	U2706	U2707	G2708	G2709	C2712	U2713	G2714	C2715	G2716	G2717	G2718	U2719	U2720	A2721	G2722	G2723	U2724	A2725	A2726	A2727	U2728			
G2729	C2730	G2731	G2732	A2733	A2734	G2735	A2736	G2737	A2738	U2739	A2740	A2741	G2742	U2743	U2744	U2745	G2746	G2747	A2748	A2749	A2750	G2751	C2752	A2753	U2754	C2755	U2756	A2757	U2758	G2759	C2760	C2761	A2765	U2768	U2769	G2770	C2771	C2772	C2773	C2774	G2775	A2776	G2777	U2778	U2779	A2780	A2781	G2782	U2783	U2784	G2785	U2786	C2787	C2788	U2789	U2790	G2791	
C2794	C2795	U2796	U2797	U2798	A2799	A2800	G2801	G2802	G2803	U2804	C2805	C2806	U2807	U2808	A2809	A2810	G2811	A2812	A2813	A2814	C2815	G2819	A2820	A2821	G2822	A2823	G2828	A2829	G2834	U2835	U2836	A2837	G2838	C2839	C2840	C2841	U2845	G2846	U2847	G2848	U2849	A2850	A2851	G2852	C2853	G2857	C2858	G2859	A2860	U2861	G2862	C2863	G2864					



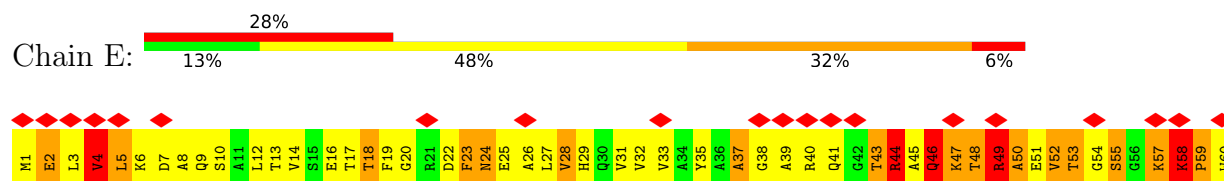
• Molecule 11: 50S RIBOSOMAL PROTEIN L2

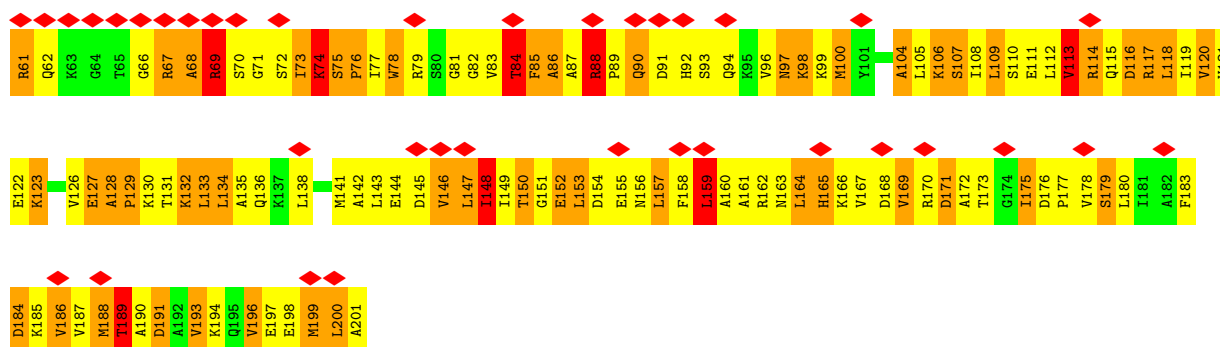


• Molecule 12: 50S RIBOSOMAL PROTEIN L3

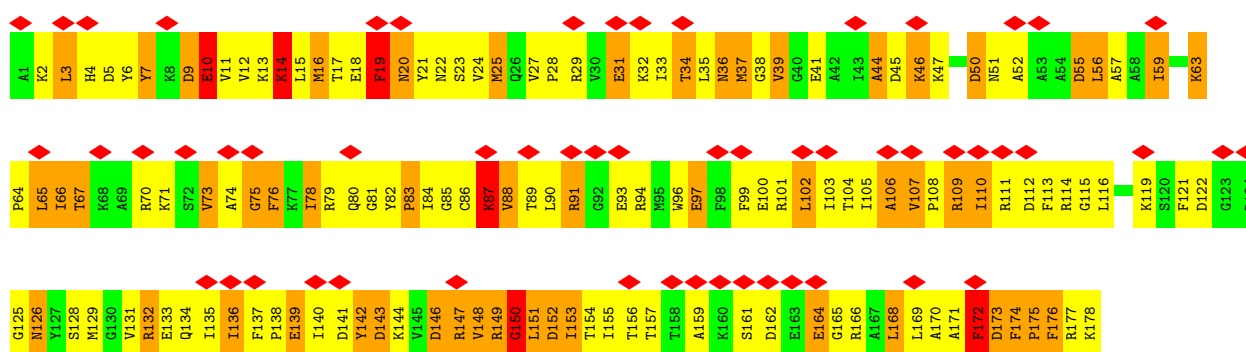
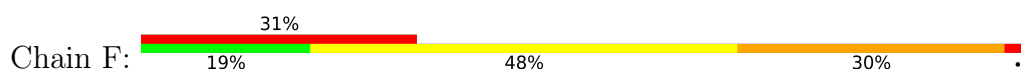


• Molecule 13: 50S RIBOSOMAL PROTEIN L4

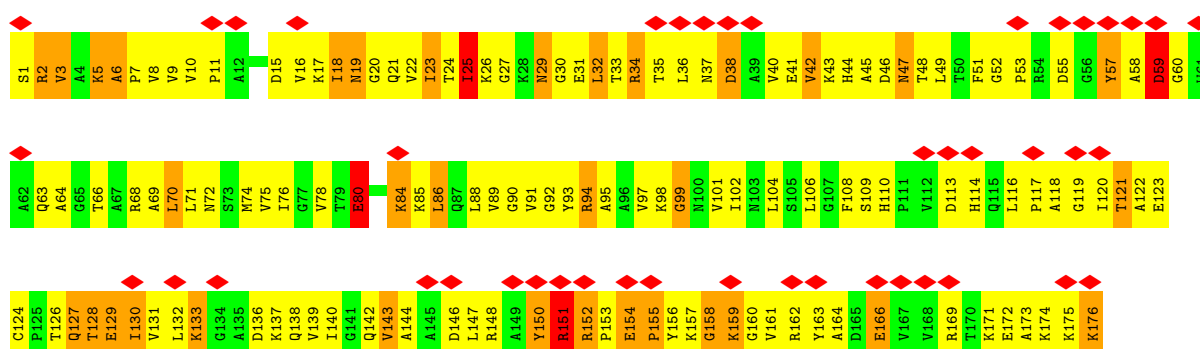




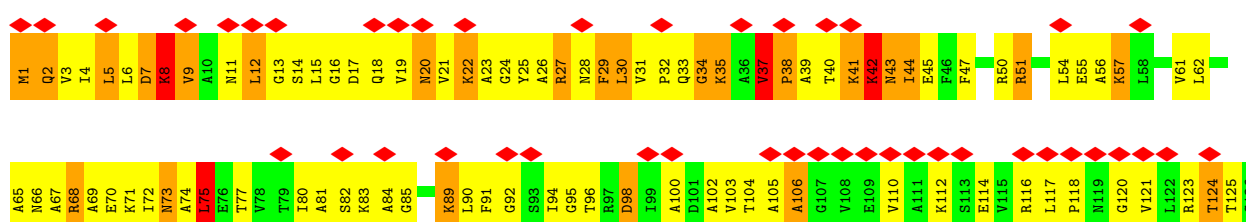
• Molecule 14: 50S RIBOSOMAL PROTEIN L5

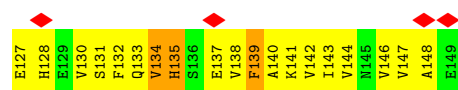


• Molecule 15: 50S RIBOSOMAL PROTEIN L6

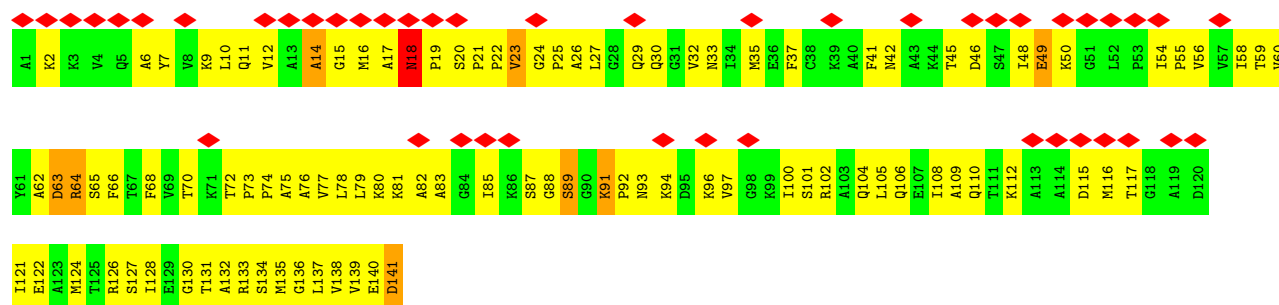


• Molecule 16: 50S RIBOSOMAL PROTEIN L9

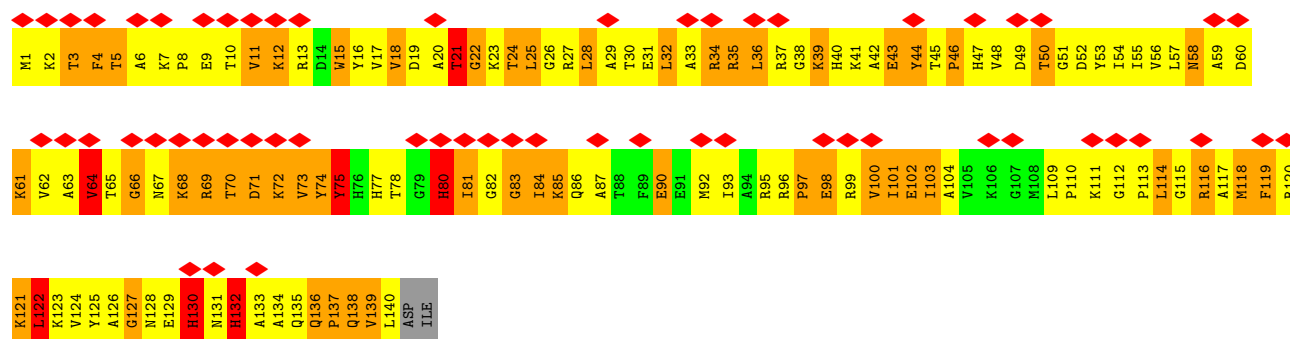




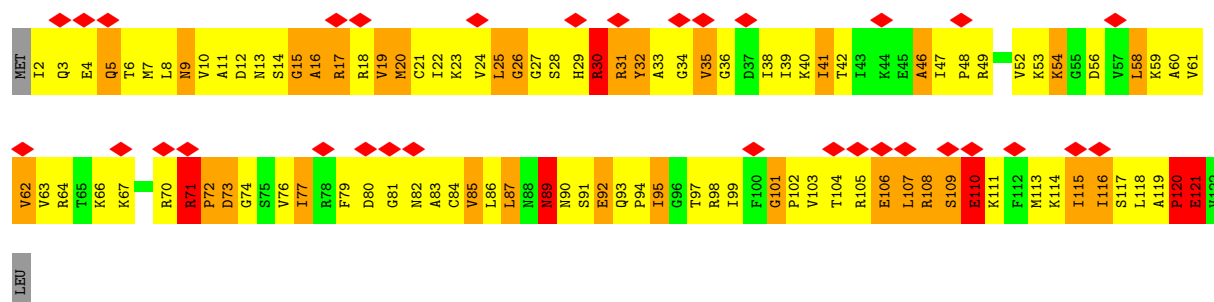
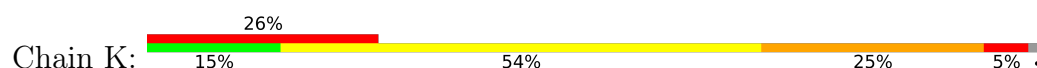
• Molecule 17: 50S RIBOSOMAL PROTEIN L11



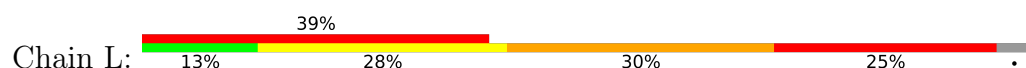
• Molecule 18: 50S RIBOSOMAL PROTEIN L13

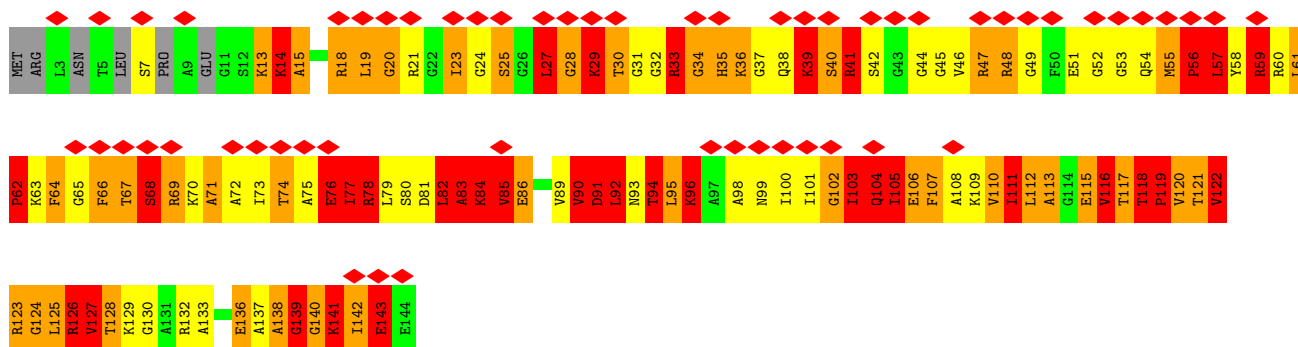


• Molecule 19: 50S RIBOSOMAL PROTEIN L14

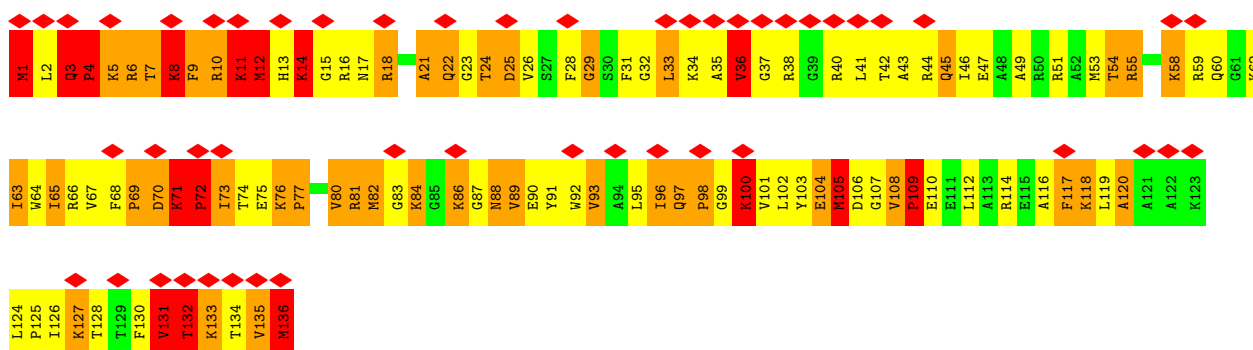
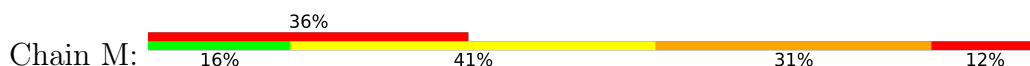


• Molecule 20: 50S RIBOSOMAL PROTEIN L15

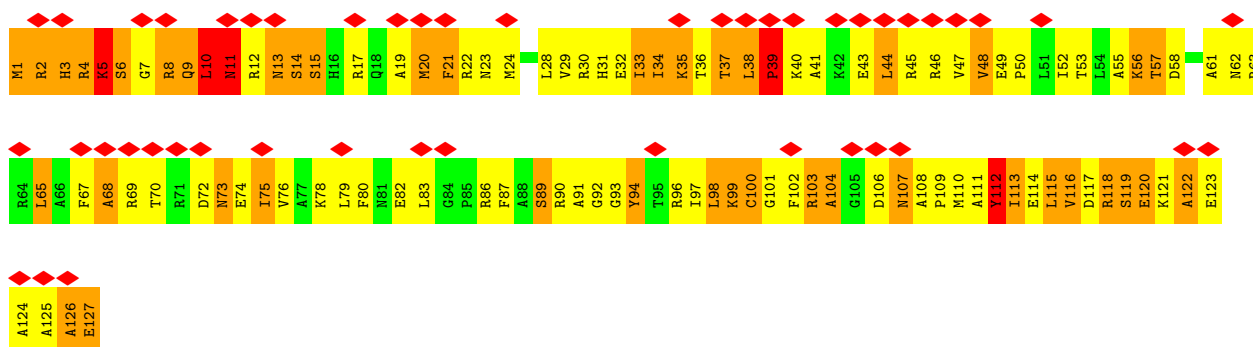
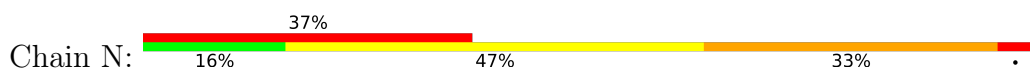




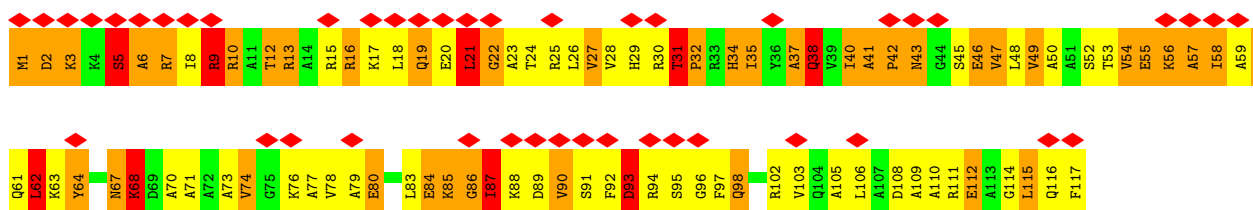
• Molecule 21: 50S RIBOSOMAL PROTEIN L16



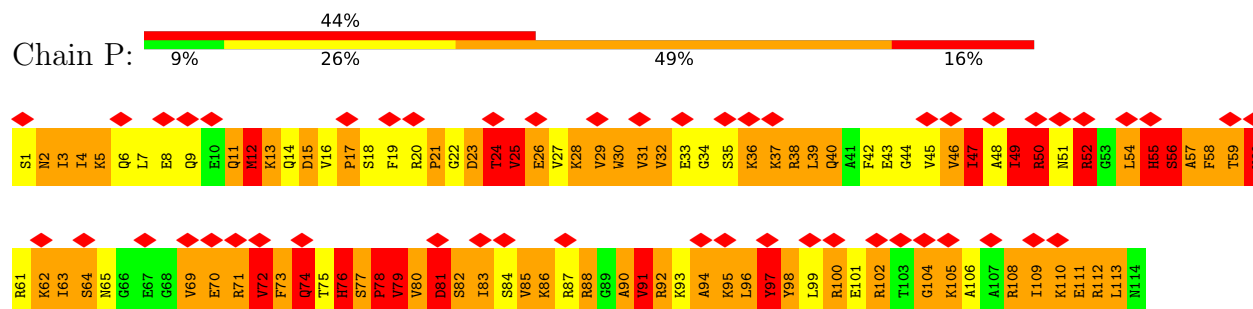
• Molecule 22: 50S RIBOSOMAL PROTEIN L17



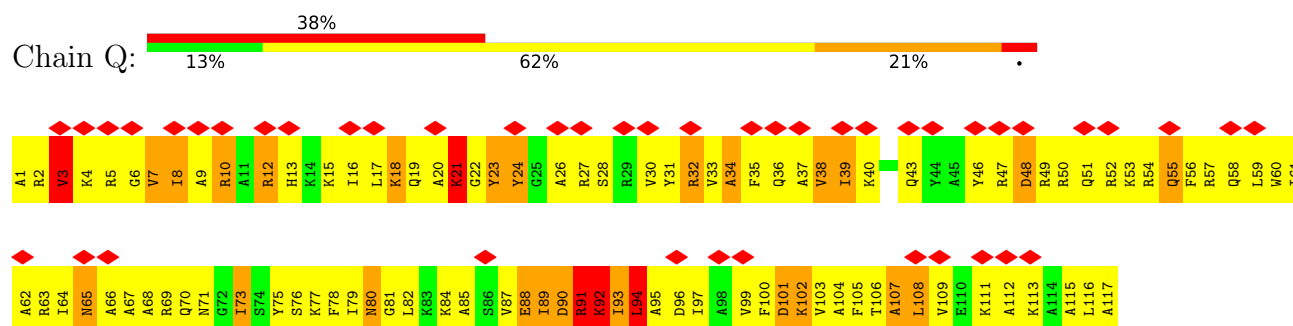
• Molecule 23: 50S RIBOSOMAL PROTEIN L18



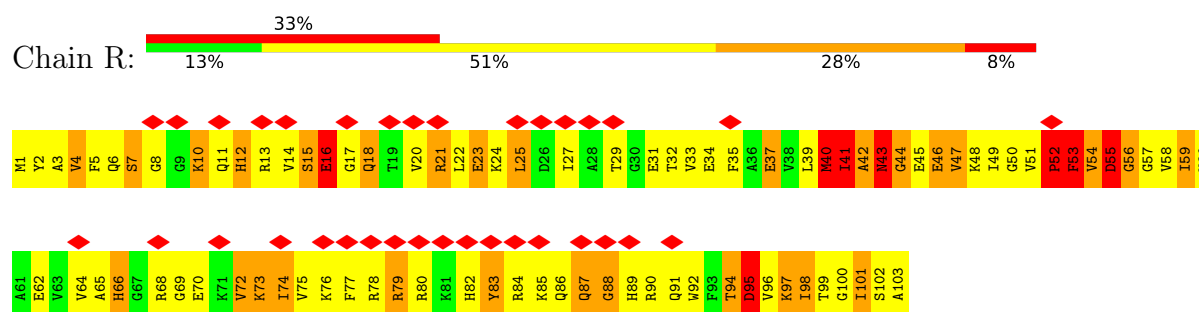
• Molecule 24: 50S RIBOSOMAL PROTEIN L19



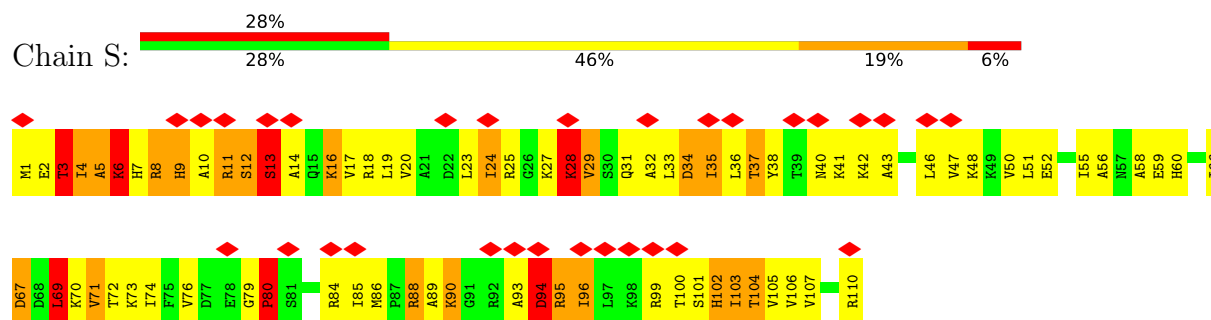
• Molecule 25: 50S RIBOSOMAL PROTEIN L20



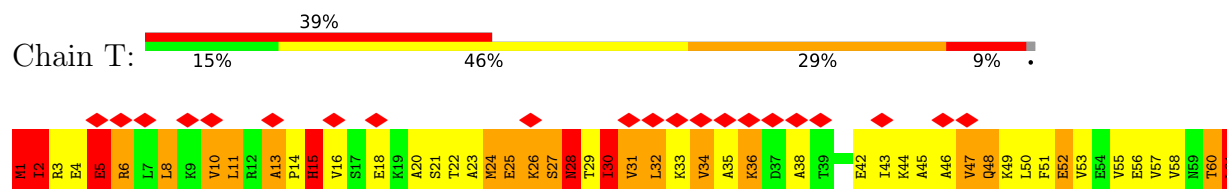
• Molecule 26: 50S RIBOSOMAL PROTEIN L21



• Molecule 27: 50S RIBOSOMAL PROTEIN L22

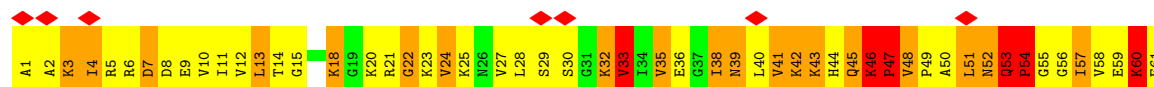
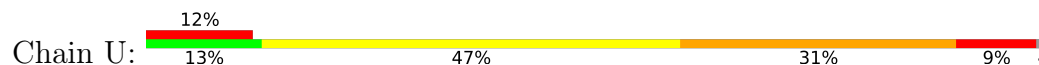


• Molecule 28: 50S RIBOSOMAL PROTEIN L23

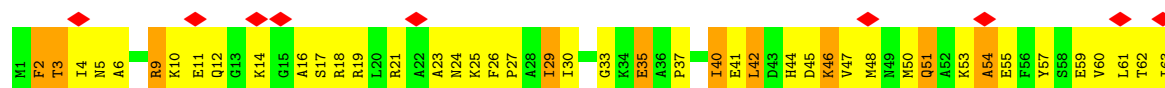




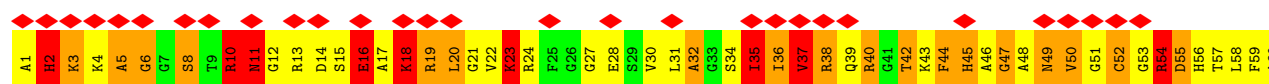
• Molecule 29: 50S RIBOSOMAL PROTEIN L24



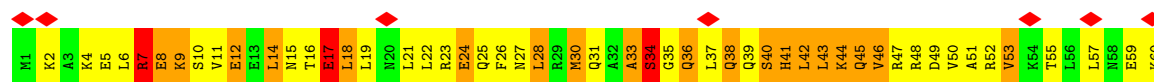
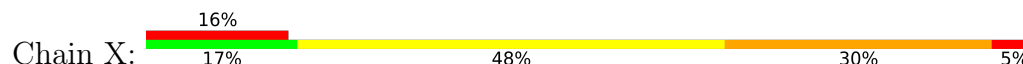
• Molecule 30: 50S RIBOSOMAL PROTEIN L25



• Molecule 31: 50S RIBOSOMAL PROTEIN L27



• Molecule 32: 50S RIBOSOMAL PROTEIN L29

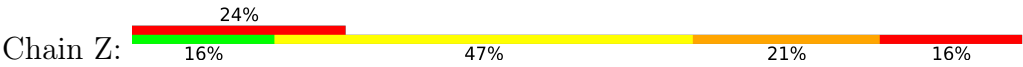


• Molecule 33: 50S RIBOSOMAL PROTEIN L30





• Molecule 34: 50S RIBOSOMAL PROTEIN L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32170	Depositor
Resolution determination method	Not provided	
CTF correction method	PER MICROGRAPH	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	77769	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.158	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	360.0, 360.0, 360.0	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.0, 2.0, 2.0	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	0	0.79	1/450 (0.2%)	1.63	17/599 (2.8%)
2	1	0.42	0/448	0.92	2/594 (0.3%)
3	2	0.41	0/380	0.97	2/498 (0.4%)
4	3	0.57	0/513	1.15	4/676 (0.6%)
5	4	0.54	1/303 (0.3%)	1.10	3/397 (0.8%)
6	5	0.27	0/855	0.67	0/1124
7	6	0.43	0/40	0.78	0/53
8	7	0.25	0/1781	0.48	0/2779
9	A	0.28	0/2803	0.62	0/4371
10	B	0.30	4/68314 (0.0%)	0.67	93/106569 (0.1%)
11	C	0.51	0/2092	1.23	25/2813 (0.9%)
12	D	0.52	0/1586	1.17	16/2134 (0.7%)
13	E	0.55	2/1571 (0.1%)	1.40	24/2113 (1.1%)
14	F	0.41	0/1444	1.36	31/1937 (1.6%)
15	G	0.39	0/1343	1.00	7/1816 (0.4%)
16	H	0.33	0/1122	0.90	4/1515 (0.3%)
17	I	0.34	0/1046	1.00	8/1410 (0.6%)
18	J	0.43	0/1135	1.06	11/1529 (0.7%)
19	K	0.44	0/939	1.46	20/1258 (1.6%)
20	L	0.97	5/1006 (0.5%)	2.33	62/1331 (4.7%)
21	M	0.68	2/1093 (0.2%)	1.43	24/1460 (1.6%)
22	N	0.42	0/1021	1.11	13/1364 (1.0%)
23	O	0.36	0/910	1.08	11/1219 (0.9%)
24	P	0.79	1/929 (0.1%)	2.00	43/1242 (3.5%)
25	Q	0.53	1/960 (0.1%)	1.25	8/1278 (0.6%)
26	R	1.37	7/829 (0.8%)	1.74	24/1107 (2.2%)
27	S	0.35	0/864	0.93	4/1156 (0.3%)
28	T	0.53	1/784 (0.1%)	1.04	9/1048 (0.9%)
29	U	0.50	3/787 (0.4%)	1.08	12/1051 (1.1%)
30	V	0.39	0/766	0.82	1/1025 (0.1%)
31	W	0.44	0/642	1.34	15/848 (1.8%)
32	X	0.36	0/509	1.10	4/674 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.41	0/453	0.84	1/605 (0.2%)
34	Z	0.57	0/559	1.51	10/745 (1.3%)
All	All	0.39	28/100277 (0.0%)	0.86	508/150338 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	55
11	C	0	3
18	J	0	2
20	L	0	1
24	P	0	1
25	Q	0	1
26	R	0	1
All	All	0	64

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	R	54	VAL	N-CA	-18.62	1.23	1.46
26	R	54	VAL	CA-CB	17.38	1.78	1.54
26	R	54	VAL	CA-C	14.98	1.71	1.52
26	R	53	PHE	CB-CG	13.47	1.81	1.50
26	R	53	PHE	CA-CB	11.06	1.70	1.53

The worst 5 of 508 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	E	73	ILE	N-CA-C	20.84	131.61	112.43
13	E	74	LYS	N-CA-C	-19.19	90.85	112.72
26	R	54	VAL	CB-CA-C	17.58	140.12	111.29
24	P	40	GLN	N-CA-C	-16.77	89.15	112.13
26	R	54	VAL	N-CA-C	-16.53	74.96	109.34

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	B	136	G	Sidechain
10	B	139	U	Sidechain
10	B	142	A	Sidechain
10	B	143	C	Sidechain
10	B	51	G	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	108	0
2	1	441	0	485	68	0
3	2	377	0	418	54	0
4	3	504	0	574	111	0
5	4	302	0	343	44	0
6	5	850	0	897	99	0
7	6	41	0	39	2	0
8	7	1591	0	806	24	0
9	A	2507	0	1270	86	0
10	B	60995	0	30659	4158	0
11	C	2053	0	2122	453	0
12	D	1565	0	1616	391	0
13	E	1552	0	1617	301	0
14	F	1420	0	1460	177	0
15	G	1323	0	1374	173	0
16	H	1111	0	1148	198	0
17	I	1032	0	1088	207	0
18	J	1112	0	1147	230	0
19	K	930	0	1000	125	0
20	L	1002	0	1070	298	0
21	M	1074	0	1157	257	0
22	N	1008	0	1036	236	0
23	O	900	0	935	141	0
24	P	917	0	965	213	0
25	Q	947	0	1022	181	0
26	R	816	0	839	172	0
27	S	857	0	922	123	0
28	T	777	0	840	138	0
29	U	779	0	831	264	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	V	753	0	780	109	0
31	W	634	0	656	163	0
32	X	509	0	541	71	0
33	Y	449	0	491	64	0
34	Z	549	0	552	120	0
35	B	110	0	0	0	0
36	B	497	0	0	17	0
36	C	1	0	0	0	0
36	E	5	0	0	0	0
36	L	2	0	0	0	0
36	N	1	0	0	0	0
All	All	92737	0	61161	8592	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 56.

The worst 5 of 8592 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)
10:B:1062:G:H21	17:I:134:SER:CB	1.09	1.62
10:B:1059:G:C5'	17:I:117:THR:HG23	1.22	1.60
26:R:54:VAL:CA	26:R:54:VAL:CB	1.78	1.59
26:R:53:PHE:CB	26:R:53:PHE:CG	1.81	1.58
10:B:2881:U:C6	22:N:120:GLU:CD	1.80	1.55

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	0	54/56 (96%)	30 (56%)	15 (28%)	9 (17%)	0 2

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	52/54 (96%)	19 (36%)	23 (44%)	10 (19%)	0	2
3	2	44/46 (96%)	23 (52%)	14 (32%)	7 (16%)	0	2
4	3	62/64 (97%)	30 (48%)	25 (40%)	7 (11%)	0	5
5	4	36/38 (95%)	18 (50%)	9 (25%)	9 (25%)	0	1
6	5	107/109 (98%)	83 (78%)	19 (18%)	5 (5%)	2	16
7	6	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
11	C	265/273 (97%)	103 (39%)	82 (31%)	80 (30%)	0	0
12	D	207/209 (99%)	90 (44%)	69 (33%)	48 (23%)	0	1
13	E	199/201 (99%)	98 (49%)	60 (30%)	41 (21%)	0	2
14	F	176/178 (99%)	95 (54%)	48 (27%)	33 (19%)	0	2
15	G	174/176 (99%)	118 (68%)	39 (22%)	17 (10%)	0	7
16	H	147/149 (99%)	85 (58%)	47 (32%)	15 (10%)	0	6
17	I	139/141 (99%)	124 (89%)	11 (8%)	4 (3%)	3	23
18	J	138/142 (97%)	67 (49%)	42 (30%)	29 (21%)	0	2
19	K	119/123 (97%)	71 (60%)	32 (27%)	16 (13%)	0	3
20	L	132/144 (92%)	55 (42%)	36 (27%)	41 (31%)	0	0
21	M	134/136 (98%)	69 (52%)	37 (28%)	28 (21%)	0	2
22	N	125/127 (98%)	71 (57%)	34 (27%)	20 (16%)	0	2
23	O	115/117 (98%)	64 (56%)	26 (23%)	25 (22%)	0	2
24	P	112/114 (98%)	39 (35%)	36 (32%)	37 (33%)	0	0
25	Q	115/117 (98%)	81 (70%)	22 (19%)	12 (10%)	0	6
26	R	101/103 (98%)	44 (44%)	31 (31%)	26 (26%)	0	1
27	S	108/110 (98%)	63 (58%)	27 (25%)	18 (17%)	0	2
28	T	97/100 (97%)	41 (42%)	39 (40%)	17 (18%)	0	2
29	U	100/103 (97%)	30 (30%)	47 (47%)	23 (23%)	0	1
30	V	92/94 (98%)	62 (67%)	22 (24%)	8 (9%)	0	8
31	W	82/84 (98%)	29 (35%)	26 (32%)	27 (33%)	0	0
32	X	60/63 (95%)	28 (47%)	20 (33%)	12 (20%)	0	2
33	Y	56/58 (97%)	29 (52%)	17 (30%)	10 (18%)	0	2
34	Z	68/70 (97%)	29 (43%)	26 (38%)	13 (19%)	0	2
All	All	3422/3507 (98%)	1793 (52%)	982 (29%)	647 (19%)	0	2

5 of 647 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	10	SER
1	0	29	VAL
1	0	35	GLU
2	1	46	VAL
3	2	4	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	31 (66%)	16 (34%)	0	1
2	1	48/48 (100%)	30 (62%)	18 (38%)	0	1
3	2	38/38 (100%)	28 (74%)	10 (26%)	0	3
4	3	51/51 (100%)	34 (67%)	17 (33%)	0	2
5	4	34/34 (100%)	21 (62%)	13 (38%)	0	1
6	5	92/92 (100%)	89 (97%)	3 (3%)	33	54
11	C	213/218 (98%)	137 (64%)	76 (36%)	0	1
12	D	164/164 (100%)	108 (66%)	56 (34%)	0	1
13	E	165/165 (100%)	116 (70%)	49 (30%)	0	2
14	F	149/149 (100%)	123 (83%)	26 (17%)	2	10
15	G	137/137 (100%)	106 (77%)	31 (23%)	1	6
16	H	114/114 (100%)	86 (75%)	28 (25%)	1	4
17	I	109/109 (100%)	106 (97%)	3 (3%)	38	59
18	J	114/116 (98%)	83 (73%)	31 (27%)	0	3
19	K	102/104 (98%)	78 (76%)	24 (24%)	1	5
20	L	97/103 (94%)	53 (55%)	44 (45%)	0	0
21	M	109/109 (100%)	78 (72%)	31 (28%)	0	3
22	N	103/103 (100%)	80 (78%)	23 (22%)	1	6
23	O	87/87 (100%)	56 (64%)	31 (36%)	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	P	99/99 (100%)	76 (77%)	23 (23%)	1	5
25	Q	89/89 (100%)	67 (75%)	22 (25%)	1	4
26	R	84/84 (100%)	68 (81%)	16 (19%)	1	8
27	S	93/93 (100%)	72 (77%)	21 (23%)	1	6
28	T	83/84 (99%)	54 (65%)	29 (35%)	0	1
29	U	83/84 (99%)	57 (69%)	26 (31%)	0	2
30	V	78/78 (100%)	63 (81%)	15 (19%)	1	8
31	W	62/62 (100%)	44 (71%)	18 (29%)	0	2
32	X	55/55 (100%)	36 (66%)	19 (34%)	0	1
33	Y	48/48 (100%)	37 (77%)	11 (23%)	1	6
34	Z	62/62 (100%)	43 (69%)	19 (31%)	0	2
All	All	2809/2826 (99%)	2060 (73%)	749 (27%)	2	3

5 of 749 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	M	76	LYS
25	Q	108	LEU
22	N	1	MET
21	M	73	ILE
23	O	68	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
18	J	80	HIS
34	Z	30	HIS
22	N	9	GLN
33	Y	19	HIS
30	V	51	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	2837/2904 (97%)	552 (19%)	19 (0%)
8	7	73/74 (98%)	3 (4%)	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	A	116/120 (96%)	23 (19%)	0
All	All	3026/3098 (97%)	578 (19%)	19 (0%)

5 of 578 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	121	A
8	7	124	U
8	7	168	U
9	A	11	C
9	A	12	C

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	2258	C
10	B	2425	A
10	B	2756	U
10	B	2336	A
10	B	1236	G

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 110 ligands modelled in this entry, 110 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	X	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	1:MET	C	2:LYS	N	3.26

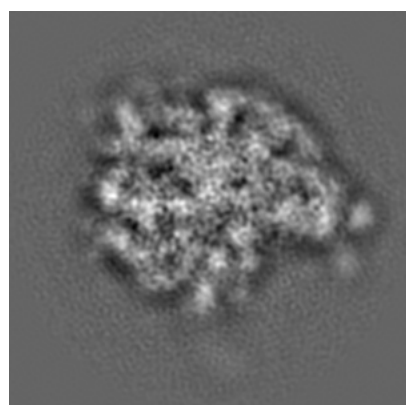
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2917. These allow visual inspection of the internal detail of the map and identification of artifacts.

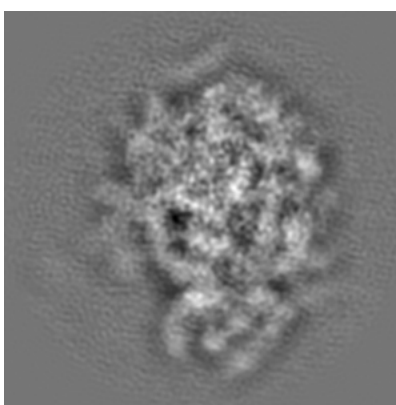
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

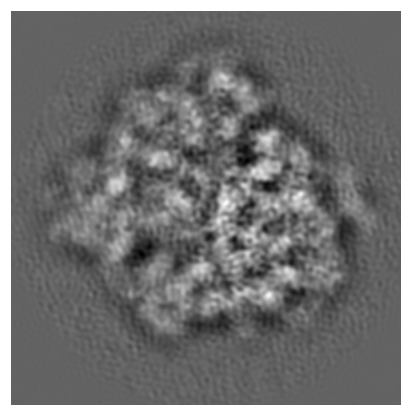
6.1.1 Primary map



X



Y

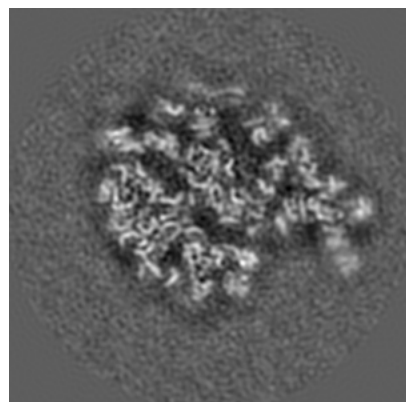


Z

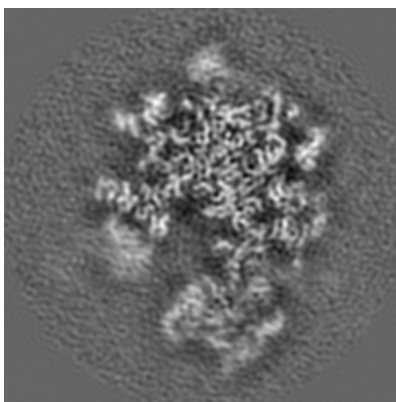
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

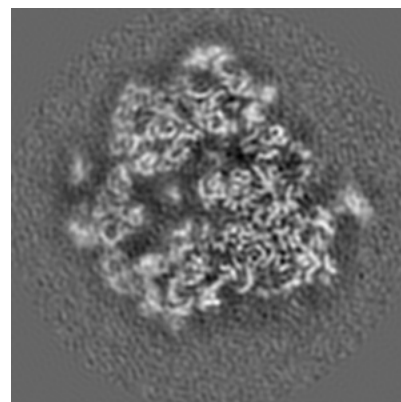
6.2.1 Primary map



X Index: 90



Y Index: 90

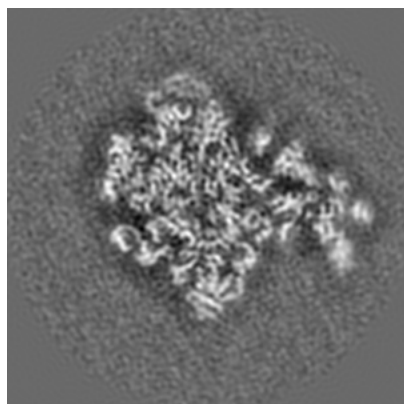


Z Index: 90

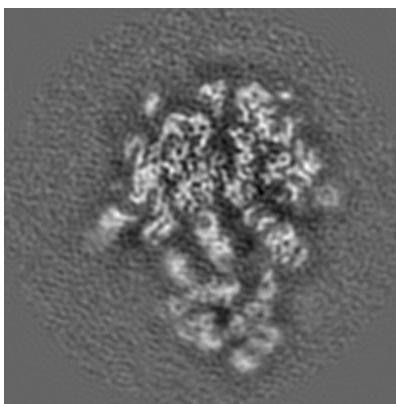
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

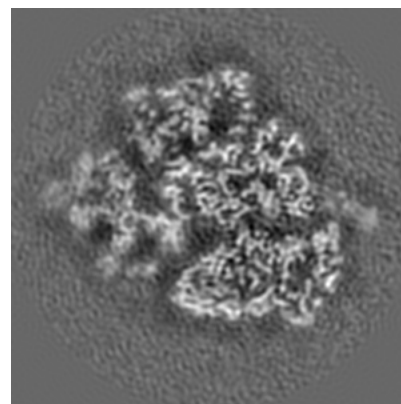
6.3.1 Primary map



X Index: 95



Y Index: 79

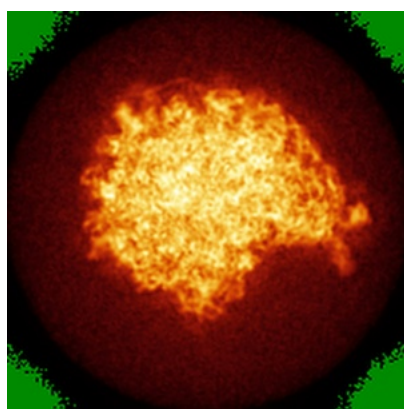


Z Index: 98

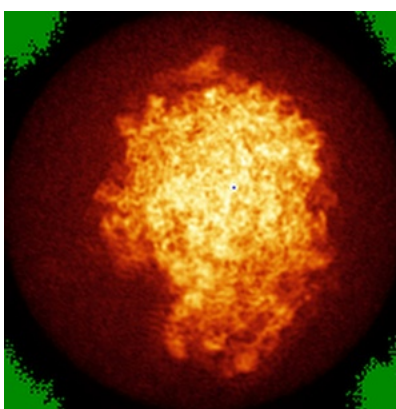
The images above show the largest variance slices of the map in three orthogonal directions.

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

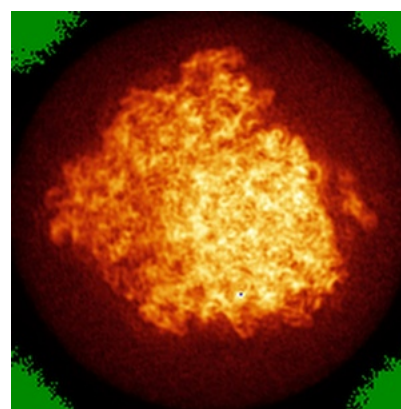
6.4.1 Primary map



X



Y



Z

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

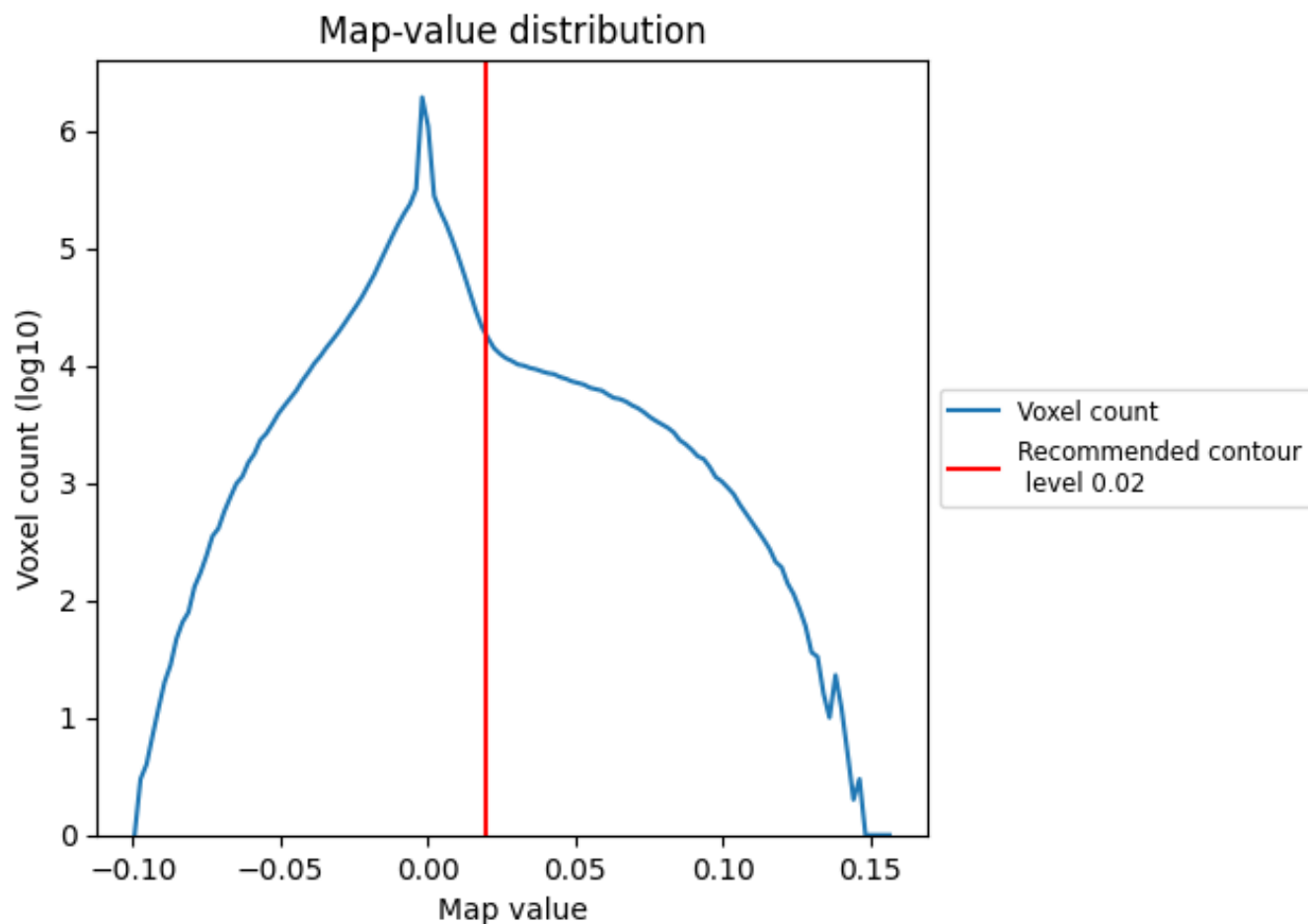
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

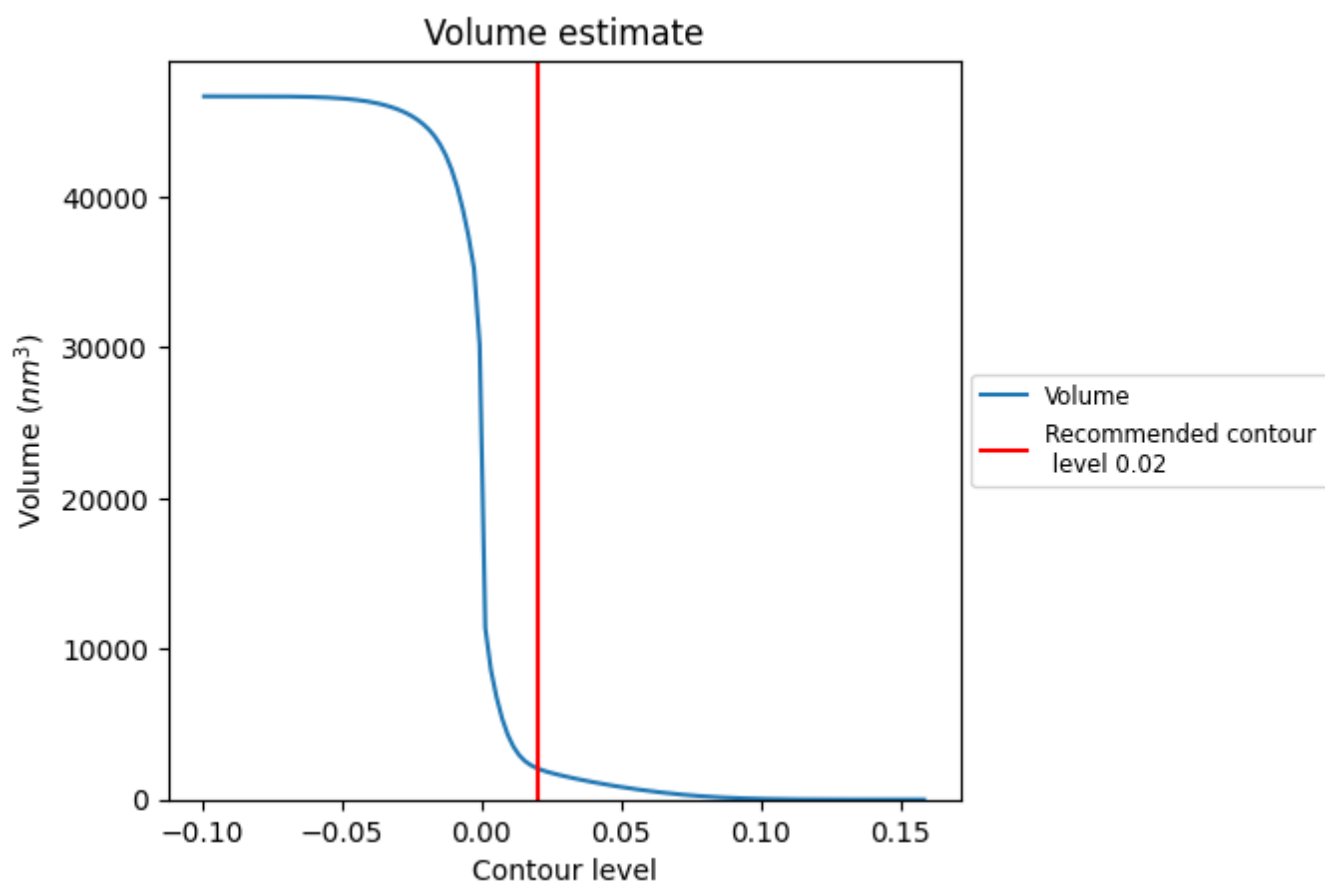
This section contains the results of statistical analysis of the map.

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.

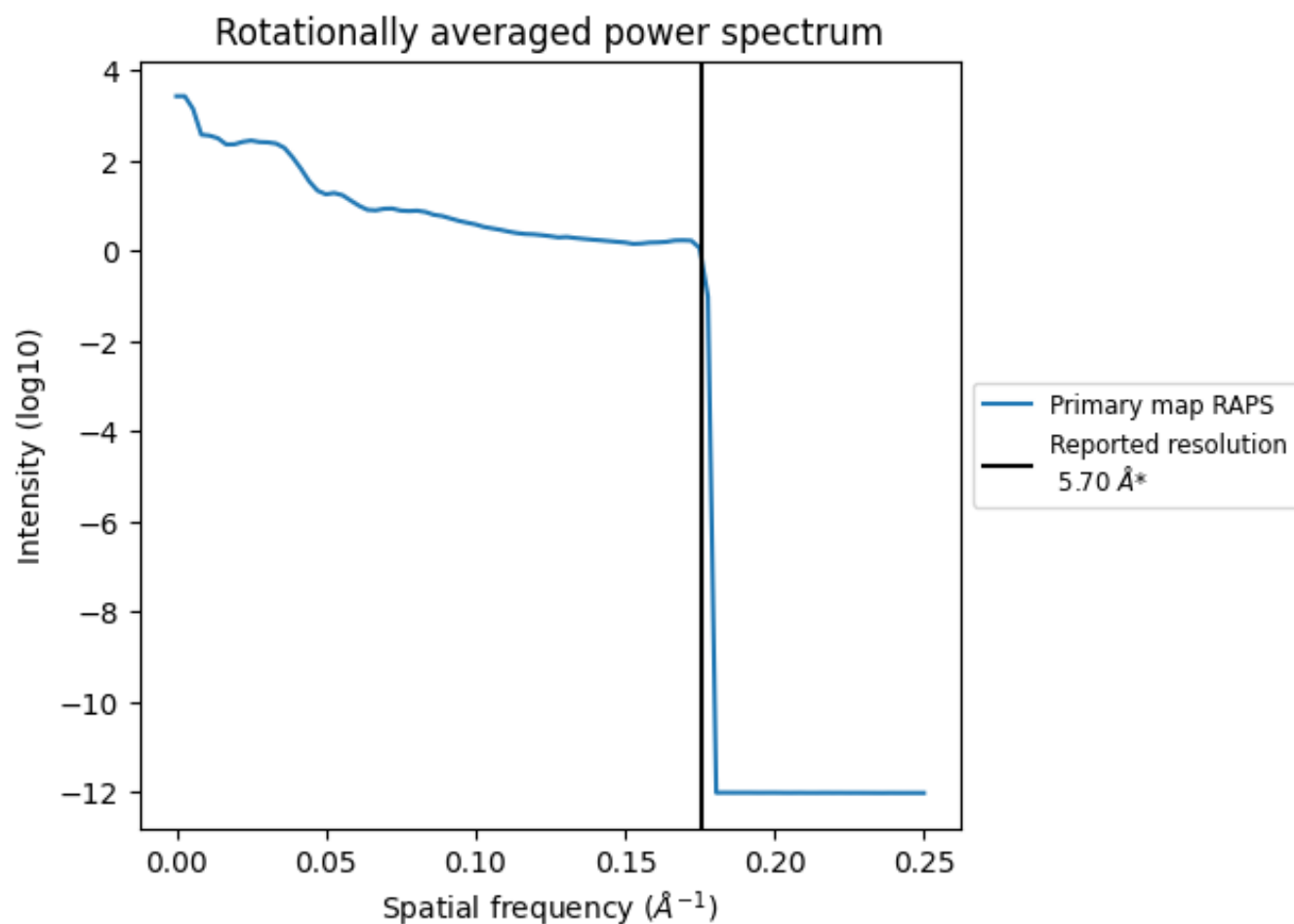
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2076 nm³; this corresponds to an approximate mass of 1875 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 ⓘ

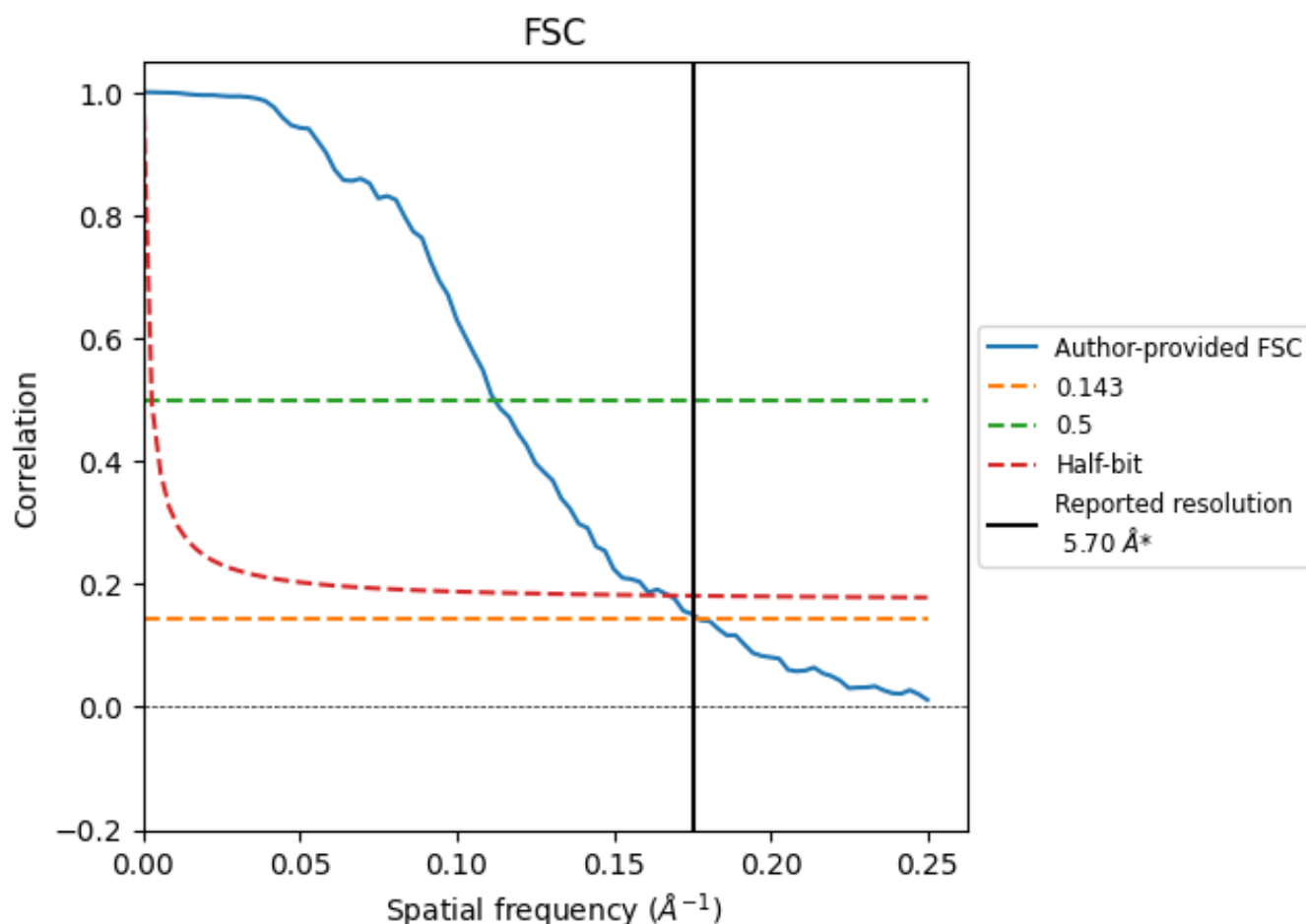


*Reported resolution corresponds to spatial frequency of 0.175 $\text{\AA}^{-1}$

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 0.175 Å⁻¹

8.2 Resolution estimates [i](#)

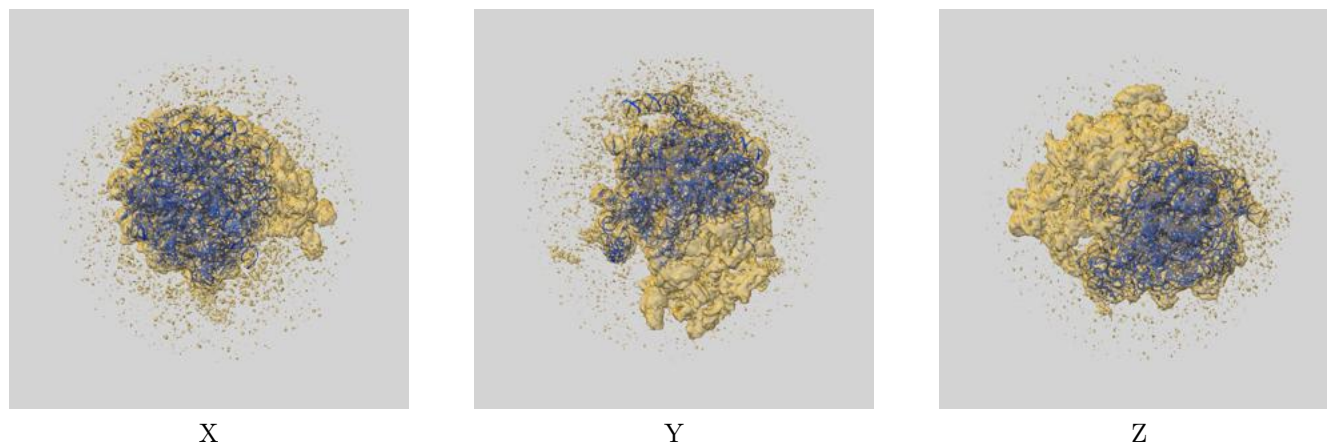
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	5.64	8.93	5.97
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

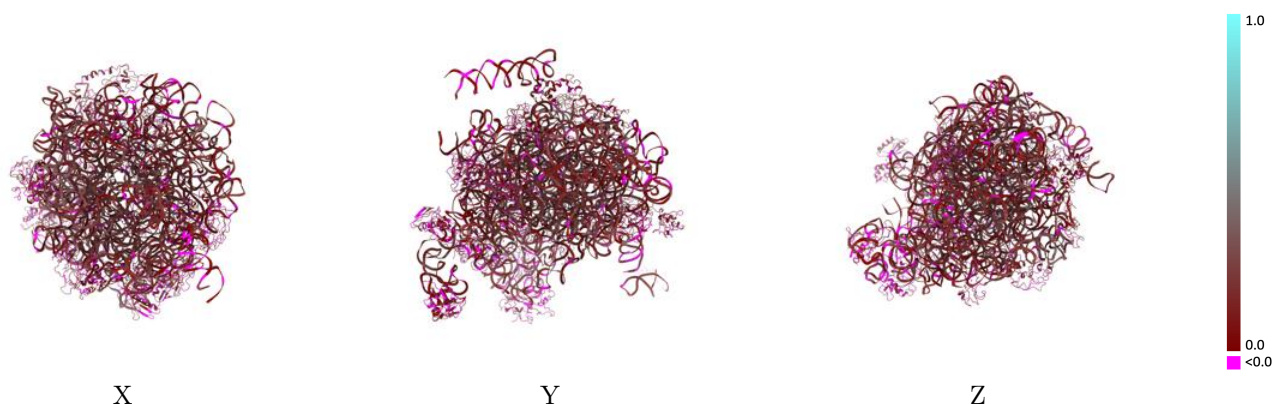
This section contains information regarding the fit between EMDB map EMD-2917 and PDB model 5AKA. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



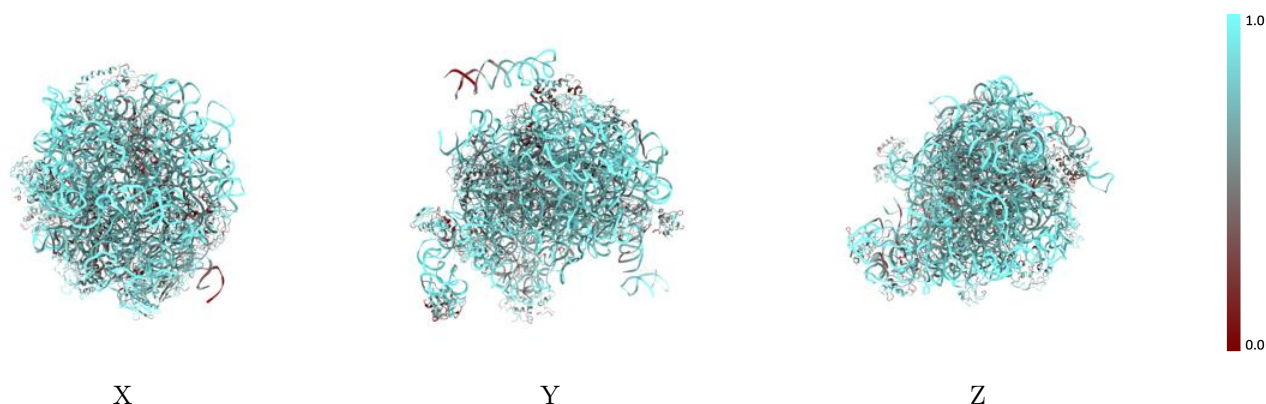
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



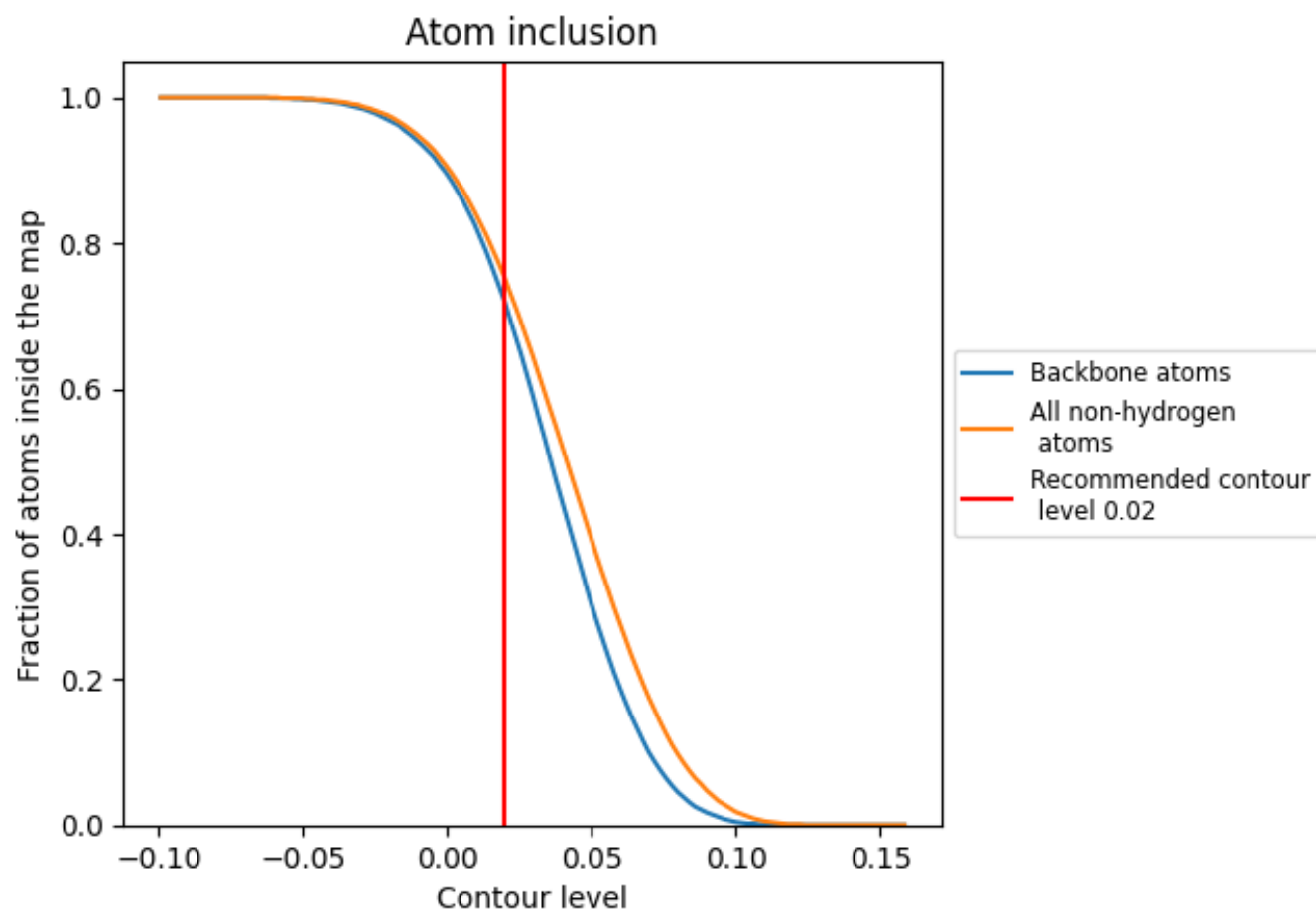
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7520	 0.1560
0	 0.5400	 0.1450
1	 0.5500	 0.0750
2	 0.4200	 0.1470
3	 0.3120	 0.1210
4	 0.4380	 0.0500
5	 0.4330	 0.1280
6	 0.6580	 0.3100
7	 0.7370	 0.0860
A	 0.7890	 0.1070
B	 0.8420	 0.1890
C	 0.5050	 0.0930
D	 0.5270	 0.0790
E	 0.5940	 0.1120
F	 0.6180	 0.0300
G	 0.6460	 0.0390
H	 0.5770	 0.1080
I	 0.5860	 0.0720
J	 0.5010	 0.0970
K	 0.5710	 0.1020
L	 0.4920	 0.0690
M	 0.5100	 0.0930
N	 0.5260	 0.1220
O	 0.5300	 0.0150
P	 0.4710	 0.0770
Q	 0.5370	 0.0980
R	 0.5850	 0.0930
S	 0.5290	 0.1330
T	 0.4910	 0.1170
U	 0.7500	 0.1510
V	 0.6980	 0.0690
W	 0.4470	 0.0640
X	 0.6740	 0.1360
Y	 0.6130	 0.1120
Z	 0.5450	 0.0960

