



# wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 06:07 PM EST

PDB ID : 1ML5  
EMDB ID : EMD-1005  
Title : Structure of the E. coli ribosomal termination complex with release factor 2  
Authors : Klaholz, B.P.; Pape, T.; Zavialov, A.V.; Myasnikov, A.G.; Orlova, E.V.; Vestergaard, B.; Ehrenberg, M.; van Heel, M.  
Deposited on : 2002-08-30  
Resolution : 14.00 Å (reported)  
Based on initial models : 1GIY, 1GQE, 1GIX

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

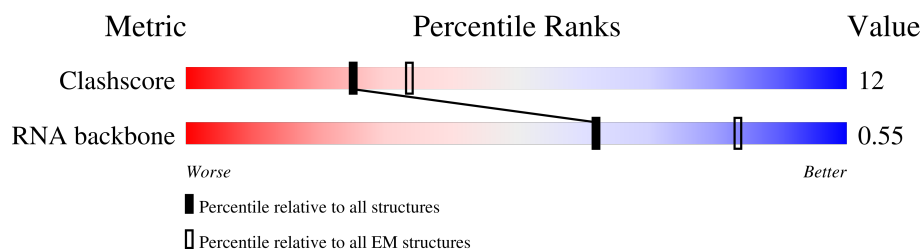
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 14.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	1522	
2	B	76	
3	C	6	
4	a	2916	
5	b	123	
6	Z	365	
7	E	256	
8	F	239	
9	G	209	

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Mol	Chain	Length	Quality of chain
10	H	162	81% 92% 7%
11	I	101	72% 100%
12	J	156	64% 99%
13	K	138	85% 100%
14	L	128	84% 97% ..
15	M	105	66% 90% 7%
16	N	129	60% 92% 8%
17	O	135	59% 91% 8%
18	P	126	77% 98% ..
19	Q	61	93% 92% 7%
20	R	89	73% 99%
21	S	91	89% 91% 9%
22	T	105	90% 99%
23	U	88	74% 83% 17%
24	V	93	80% 86% 14%
25	W	106	79% 93% 7%
26	X	26	92% 92% 8%
27	c	228	96% 98%
28	d	178	90% 97%
29	e	338	48% 57% 43%
30	f	246	54% 77% 23%
31	g	176	59% 69% 31%
32	h	177	64% 93% 7%
33	l	141	68% 94% 6%
34	m	145	72% 81% 19%

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Mol	Chain	Length	Quality of chain
35	n	122	<div> <div>97%</div> <div>100%</div> </div>
36	o	164	<div> <div>33%</div> <div>51%</div> <div>49%</div> </div>
37	p	138	<div> <div>94%</div> <div>100%</div> </div>
38	q	186	<div> <div>44%</div> <div>61%</div> <div>39%</div> </div>
39	r	66	<div> <div>79%</div> <div>79%</div> <div>21%</div> </div>
40	s	113	<div> <div>88%</div> <div>97%</div> <div>.</div> </div>
41	t	84	<div> <div>80%</div> <div>90%</div> <div>10%</div> </div>
42	u	119	<div> <div>80%</div> <div>92%</div> <div>8%</div> </div>
43	v	94	<div> <div>47%</div> <div>95%</div> <div>5%</div> </div>
44	w	70	<div> <div>60%</div> <div>91%</div> <div>9%</div> </div>
45	x	60	<div> <div>87%</div> <div>100%</div> </div>

## 2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 11392 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 30S 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	1519	Total	P	0	1519
			1519	1519		

- Molecule 2 is a RNA chain called T-RNA(PHE).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	76	Total	C	N	O	P	0	0
			1652	746	294	536	76		

- Molecule 3 is a RNA chain called A- AND P-SITE MESSENGER RNA CODONS.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	6	Total	C	N	O	P	0	0
			120	54	12	48	6		

- Molecule 4 is a RNA chain called 50S 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	a	2889	Total	P	0	2889
			2889	2889		

- Molecule 5 is a RNA chain called 50S 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	b	123	Total	P	0	123
			123	123		

- Molecule 6 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	Z	362	Total	C	0	362
			362	362		

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	E	234	Total	C	0	234
			234	234		

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	F	206	Total	C	0	206
			206	206		

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	G	208	Total	C	0	208
			208	208		

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms		AltConf	Trace
10	H	150	Total	C	0	150
			150	150		

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	I	101	Total	C	0	101
			101	101		

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	J	155	Total	C	0	155
			155	155		

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	K	138	Total	C	0	138
			138	138		

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	L	127	Total	C	0	127
			127	127		

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	M	98	Total	C	0	98
			98	98		

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms		AltConf	Trace
16	N	119	Total	C	0	119
			119	119		

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms		AltConf	Trace
17	O	124	Total	C	0	124
			124	124		

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms		AltConf	Trace
18	P	125	Total	C	0	125
			125	125		

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms		AltConf	Trace
19	Q	60	Total	C	0	60
			60	60		

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms		AltConf	Trace
20	R	88	Total	C	0	88
			88	88		

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms		AltConf	Trace
21	S	83	Total	C	0	83
			83	83		

- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms		AltConf	Trace
22	T	104	Total	C	0	104
			104	104		

- Molecule 23 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms		AltConf	Trace
23	U	73	Total	C	0	73
			73	73		

- Molecule 24 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms		AltConf	Trace
24	V	80	Total	C	0	80
			80	80		

- Molecule 25 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms		AltConf	Trace
25	W	99	Total	C	0	99
			99	99		

- Molecule 26 is a protein called 30S RIBOSOMAL PROTEIN THX.

Mol	Chain	Residues	Atoms		AltConf	Trace
26	X	24	Total	C	0	24
			24	24		

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms		AltConf	Trace
27	c	224	Total	C	0	224
			224	224		

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L2.



Mol	Chain	Residues	Atoms		AltConf	Trace
28	d	173	Total	C	0	173
			173	173		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms		AltConf	Trace
29	e	191	Total	C	0	191
			191	191		

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms		AltConf	Trace
30	f	189	Total	C	0	189
			189	189		

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms		AltConf	Trace
31	g	122	Total	C	0	122
			122	122		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms		AltConf	Trace
32	h	164	Total	C	0	164
			164	164		

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms		AltConf	Trace
33	l	133	Total	C	0	133
			133	133		

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms		AltConf	Trace
34	m	117	Total	C	0	117
			117	117		

- Molecule 35 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms		AltConf	Trace
35	n	122	Total	C	0	122
			122	122		

- Molecule 36 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms		AltConf	Trace
36	o	84	Total	C	0	84
			84	84		

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms		AltConf	Trace
37	p	138	Total	C	0	138
			138	138		

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms		AltConf	Trace
38	q	113	Total	C	0	113
			113	113		

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms		AltConf	Trace
39	r	52	Total	C	0	52
			52	52		

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms		AltConf	Trace
40	s	110	Total	C	0	110
			110	110		

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms		AltConf	Trace
41	t	76	Total	C	0	76
			76	76		

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms		AltConf	Trace
42	u	110	Total	C	0	110
			110	110		

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms		AltConf	Trace
43	v	89	Total	C	0	89
			89	89		

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms		AltConf	Trace
44	w	64	Total	C	0	64
			64	64		

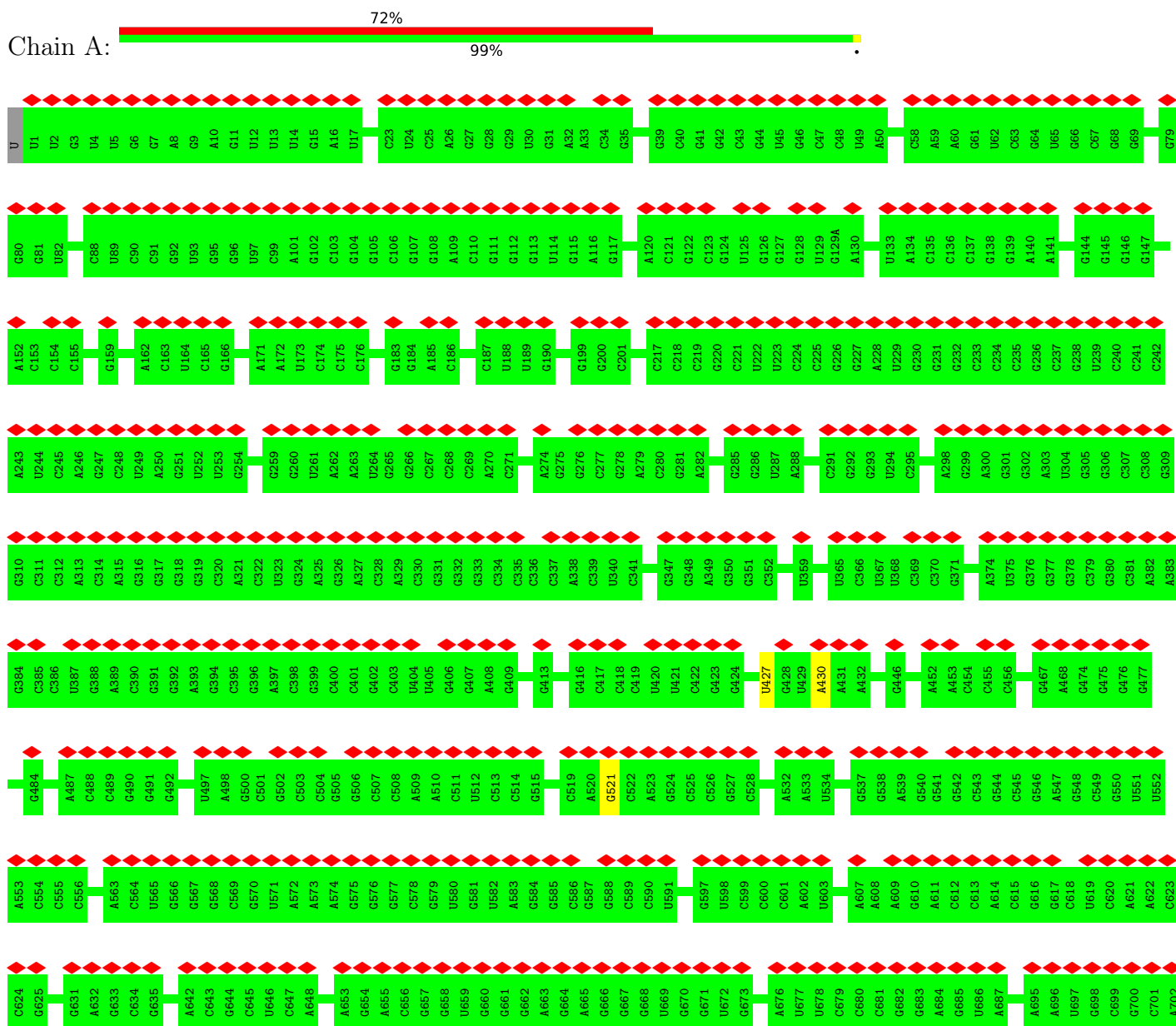
- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms		AltConf	Trace
45	x	60	Total	C	0	60
			60	60		

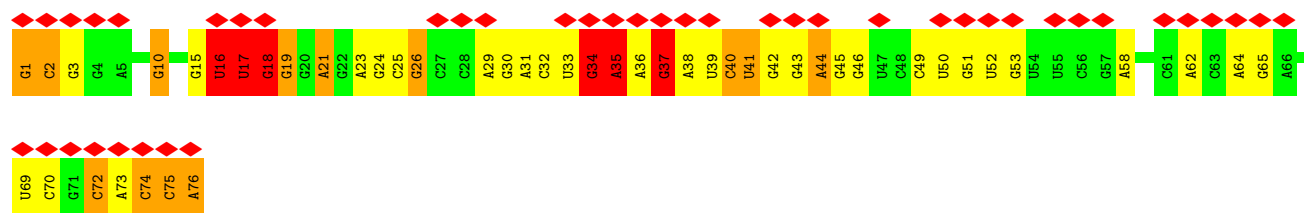
### 3 Residue-property plots

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: 30S 16S RIBOSOMAL RNA



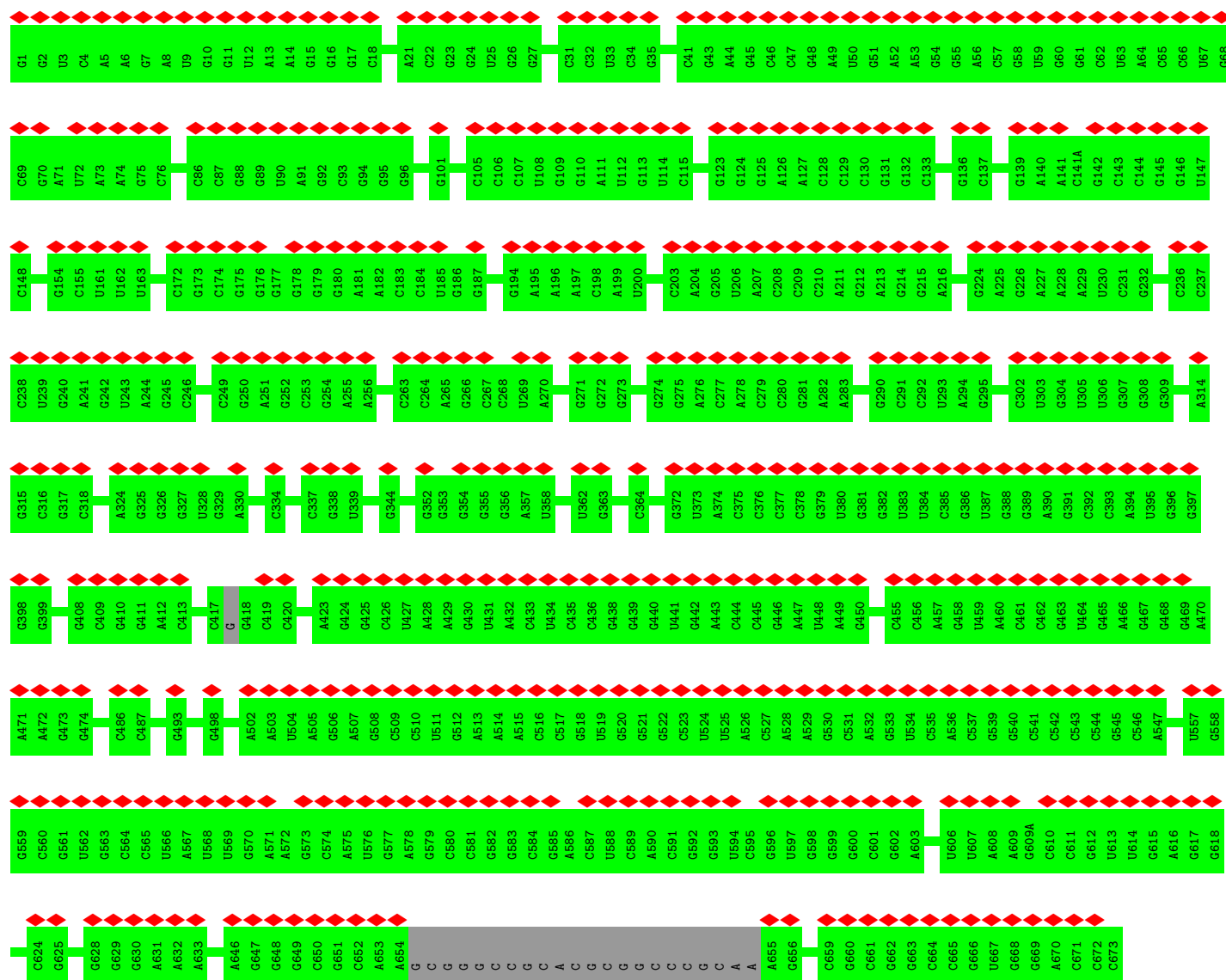




• Molecule 3: A- AND P-SITE MESSENGER RNA CODONS



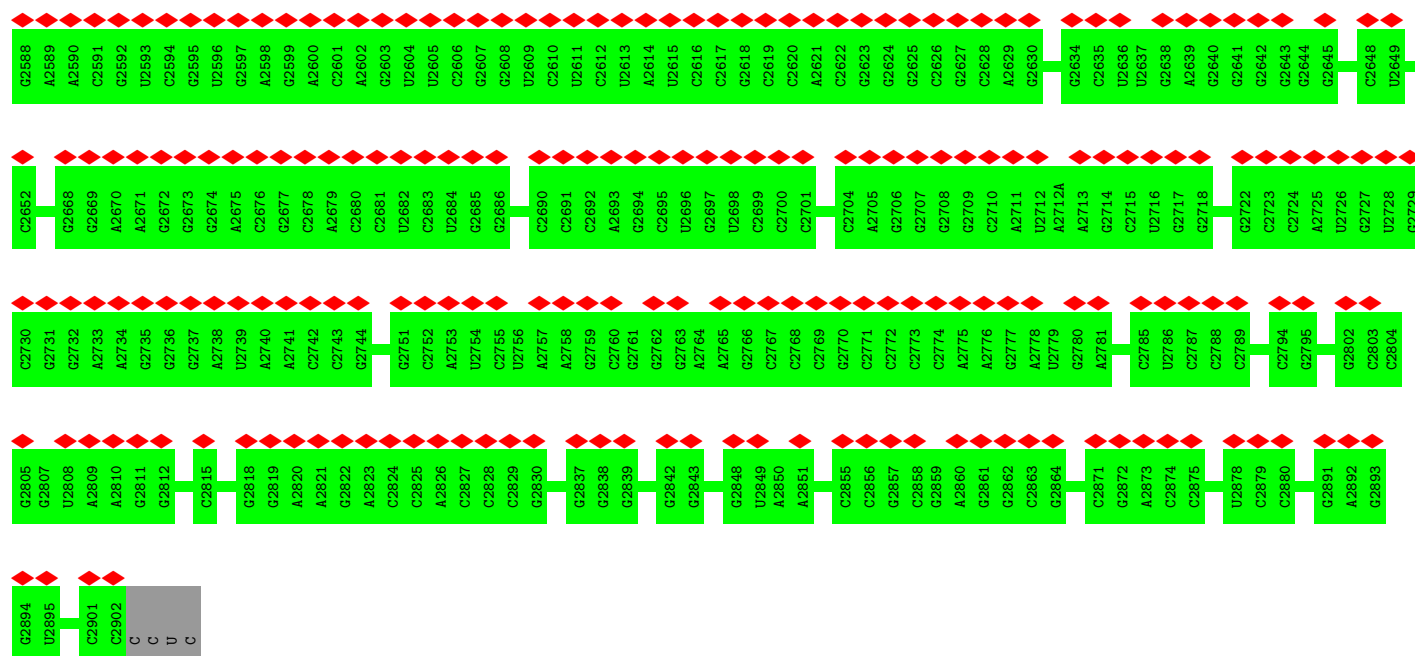
• Molecule 4: 50S 23S RIBOSOMAL RNA



C1575	U1576	G1581	C1582	A1587	C1588	C1589	U1590	G1591	C1592	G1593	G1594	G1595	A1596	A1597	C1598	C1600	G1601	C1604	C1605	G1606	C1607	A1608	A1609	A1610	C1611	C1612	G1613	A1614	C1615	A1616	C1617	A1618	G1619	G1620	U1621	G1622	G1623	G1624	C1625	G1626	G1627	G1628	U1629	G1630	C1630A	A1631	A1632	C1633	A1634	G1635	U1639	C1640	A1641	G1642			
G1491	G1492	C1493	A1494	A1495	C1501	A1511	G1512	C1513	U1514	C1515	U1516	G1517	C1518	G1519	G1522	U1523	G1524	G1525	G1526	G1527	A1528	A1529	A1530	C1531	C1532	C1533	A1536	C1537	G1538	G1539	C1549	C1550	C1551	G1552	A1553	A1554	G1555	C1556	C1557	A1558	G1559	G1560	U1561	A1562	G1563	A1566	A1567	G1568	A1569	A1572	G1573	G1574					
U1390	U1391	A1392	A1393	C1398	C1399	G1400	G1401	C1402	U1405	U1406	C1407	C1408	A1419	U1420	G1421	G1422	C1428	G1429	C1430	U1431	A1434	G1435	G1436	C1437	U1438	A1439	G1440	G1441	G1442	G1443	G1444	C1462	C1463	C1464	G1465	G1466	C1467	C1468	A1469	G1473	C1474	G1475	G1480	U1482	G1483	G1484	G1485	A1486	G1487	G1488							
U1323	G1324	U1325	U1326	C1327	G1328	A1331	U1335	A1336	G1337	G1338	A1342	G1343	G1344	C1345	G1346	G1347	G1348	A1349	C1350	C1351	U1352	A1353	A1354	G1355	G1356	U1357	G1358	A1359	A1360	G1361	G1364	A1365	A1366	A1367	G1368	G1369	C1370	A1373	G1374	C1375	C1376	G1377	A1378	A1379	G1380	G1381	G1382	C1383	A1384	G1385	C1386	C1387	G1388	G1389			
G1259	G1260	C1261	A1262	G1264	A1265	G1266	U1267	A1268	A1269	C1270	G1271	A1272	U1273	A1274	A1275	A1276	G1277	A1278	G1279	G1280	G1283	A1284	G1285	A1286	A1287	U1288	C1289	C1290	C1291	U1292	C1293	U1294	C1295	G1296	C1297	U1300	A1301	A1302	G1303	C1304	C1305	C1306	G1307	A1308	G1309	G1310	G1311	U1312	U1316	A1317	C1318	G1319	A1321	A1322			
A1189	G1190	G1191	G1192	G1193	A1194	G1195	G1196	G1197	U1198	U1199	C1200	C1201	C1202	G1203	A1204	U1205	G1206	C1207	C1208	G1209	A1210	U1211	G1212	C1217	G1218	A1286	A1287	U1288	C1289	C1290	C1291	U1292	C1293	U1294	G1296	C1297	U1300	A1301	A1302	G1303	C1304	C1305	C1306	G1307	A1308	G1309	G1310	G1311	U1312	U1316	A1317	C1318	G1319	A1321	A1322		
G1115	C1116	G1117	G1120	C1121	G1122	C1123	C1124	G1125	A1126	A1127	A1128	A1129	U1130	G1131	A1132	U1133	G1134	G1137	G1138	C1140	U1141	U1142	A1142A	A1143	G1146	G1153	G1154	A1155	A1156	G1157	U1158	U1159	G1160	C1161	G1162	C1166	U1167	G1171	G1173	A1174	U1175	G1176	A1177	C1178	C1179	C1180	G1181	A1182	G1183	G1187	U1188						
A1029	G1030	G1031	A1032	U1033	G1034	U1035	G1036	G1037	C1038	G1039	C1049	A1050	G1051	C1052	C1053	A1054	U1065	U1066	A1073	G1074	C1075	C1076	A1077	U1078	C1079	C1080	U1081	A1084	A1085	A1086	G1087	A1088	G1089	U1090	G1091	C1092	G1093	U1094	A1095	G1099	C1100	U1101	C1102	A1103	C1104	U1105	U1108	C1109	G1110	A1111	G1112	U1113	G1114				
C893	C894	C897	C898	A899	A900	A901	C902	C903	C904	U905	G906	U907	C908	A909	A910	A911	C912	U913	C914	C915	G916	G919	G920	G921	U922	C923	U930	G931	G932	A933	G934	C935	G940	A941	G942	U943	G944	A945	G946	U947	A961	G962	A963	G964	C965	A966	C967	U968	G969	A970	C988	C989	C990	G992			
G808	G809	U810	U811	C812	U813	C814	C815	C816	A819	A824	C825	U826	U827	U828	A829	G830	G831	G832	U833	C834	A835	G836	C837	C838	U839	C840	A841	G842	G843	C844	G845	C846	U847	G848	A849	C850	U851	G854	G855	U860	A861	G862	A863	G864	C865	A866	C867	U868	G869	A870	C988	C989	A990	G992			
A746	U747	G748	C749	A750	A751	A752	C753	C754	C755	C756	U757	C758	G759	G760	A761	U762	G763	A764	G765	C766	U767	G768	G769	G770	G771	C772	U773	A774	G775	G776	A777	G778	A781	A784	G785	C786	G787	U788	A789	C790	G791	G792	A793	G794	C795	C796	C797	G798	G799	A800	G801	A802	U803	A804	G805	C806	U807
G674	A675	A676	G681	G682	C683	G684	A685	G686	C687	U688	A689	G690	C691	C692	C693	G696	C697	C698	A699	G700	G701	G702	U703	G704	A705	A706	U714	G715	A716	G717	A718	C719	C720	G721	A722	G723	U724	G725	G728	G729	C730	C731	A734	A735	G736	C737	G738	G739	U740	G741	G742	G743	G744	G745			

G1643	C1644	G1645	C1646	G1647	C1648	G1649	G1650	G1651	C1652	G1653	A1654	A1655	C1656	C1657	C1658	C1659	C1660	G1661	C1662	C1663	A1664	A1665	G1666	G1667	C1670	U1671	C1672	U1673	G1674	C1675	A1676	A1677	G1678	U1679	U1680	G1681	C1682	C1683	C1684	C1685	C1686	C1687	A1690	C1691	U1692	U1693	C1694	G1695	G1696	G1697	A1698	G1699	A1700	A1701	G1702	G1703	G1704
G1705	U1706	G1707	C1708	U1709	C1710	G1717	G1718	G1725	G1726	U1727	G1734	C1735	C1736	C1737	C1741	C1742	G1743	G1746	G1747	G1748	A1749	G1750	C1751	C1752	G1753	C1754	A1755	G1756	U1757	G1758	C1761	A1762	C1765	U1766	C1767	U1768	G1769	G1770	C1771	G1772	A1773	C1774	U1775	G1776	U1777	U1778	U1779	A1780	C1781	C1782	A1783	A1784	A1785	A1786	A1787	C1788	A1789
C1790	A1791	G1792	C1793	U1794	C1795	U1796	C1797	U1798	G1799	C1800	G1801	A1802	A1803	C1804	U1805	C1806	G1807	U1808	A1809	A1810	G1811	A1812	G1813	G1814	A1815	G1816	G1817	U1818	A1819	U1820	A1821	G1822	G1823	G1824	A1825	G1826	C1827	G1828	G1831	C1832	U1833	U1834	G1835	C1836	G1840	U1841	G1842	C1843	C1844	G1845	G1846	A1847	A1848	G1849	G1850	U1851	C1852
A1853	A1854	G1855	G1856	G1857	G1858	A1859	G1860	C1870	C1879	C1880	C1881	C1882	G1883	A1884	A1885	G1891	C1892	C1893	A1900	A1901	G1902	G1903	G1904	C1905	G1906	G1907	C1908	C1909	G1910	U1911	U1915	A1916	U1917	A1918	G1921	G1922	C1925	U1926	A1927	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1939	U1940	C1941	C1942						
U1943	U1944	G1945	U1946	C1947	U1951	A1952	U1956	C1957	C1958	G1959	A1960	C1961	C1962	U1963	G1964	C1965	A1966	C1967	G1968	A1969	A1970	A1971	A1972	G1973	C1974	G1975	U1976	A1977	C1978	C1979	G1980	A1981	C1982	C1983	G1984	G1985	A1986	G1987	C1988	G1989	C1990	U1991	C1994	U1995	C1996	G1997	G1998	C1999	G2000	A2001	G2002	G2003	G2004	G2009	G2010		
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A2518	U2519	C2520	C2521	U2522	C2523	G2524	G2525	C2526	C2527	U2528	G2529	G2535	G2536	U2537	C2538	C2539	C2540	A2541	G2543	G2544	G2545	U2546	U2547	G2548	G2549	G2550	C2551	U2552	A2553	U2554	U2555	C2556	U2557	C2558	U2562	U2563	A2564	C2565	A2566	G2567	C2568	C2571	A2572	C2573	G2574	C2575	G2576	C2579	U2580	U2584	U2585	C2586	A2587				

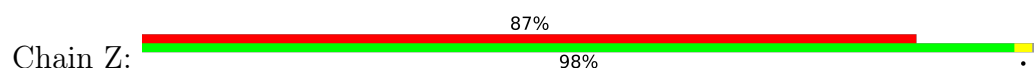


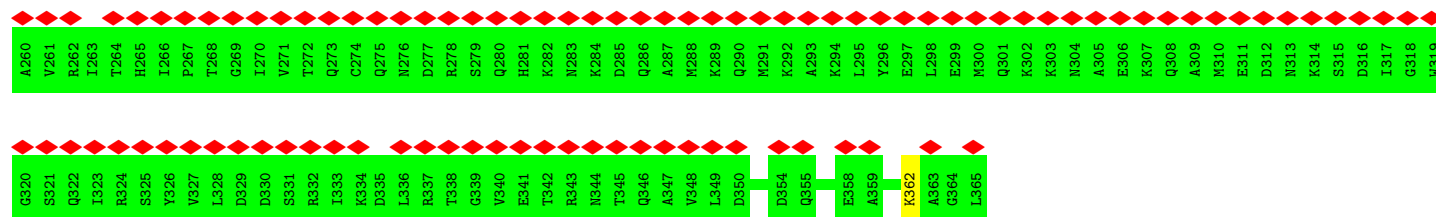


• Molecule 5: 50S 5S RIBOSOMAL RNA

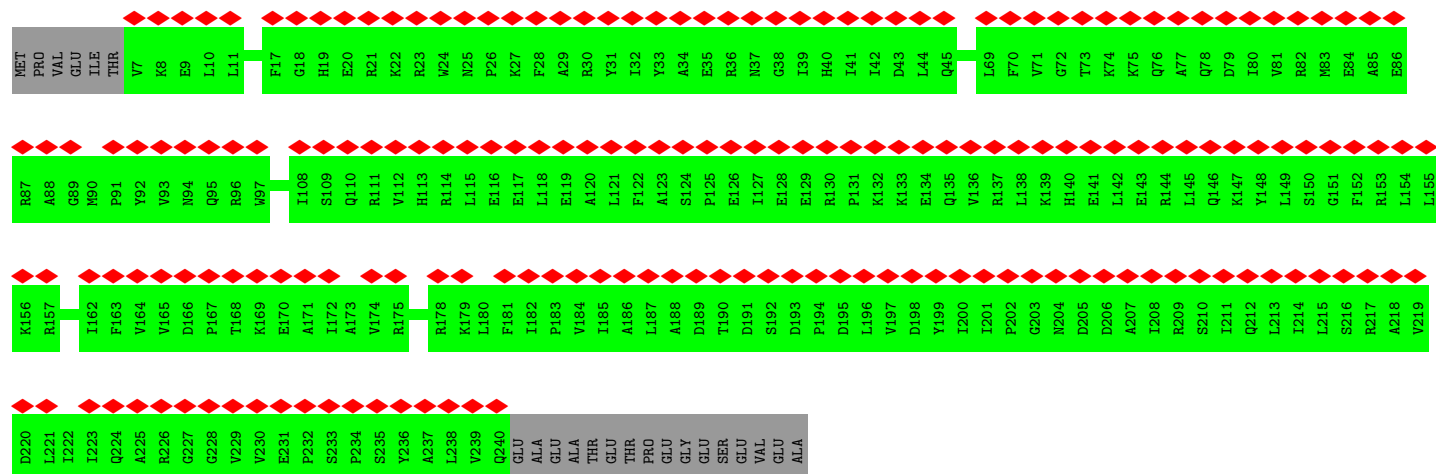
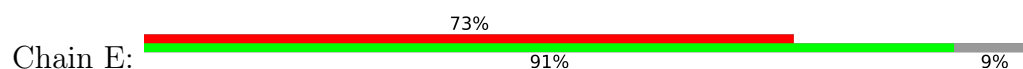


• Molecule 6: Peptide chain release factor 2

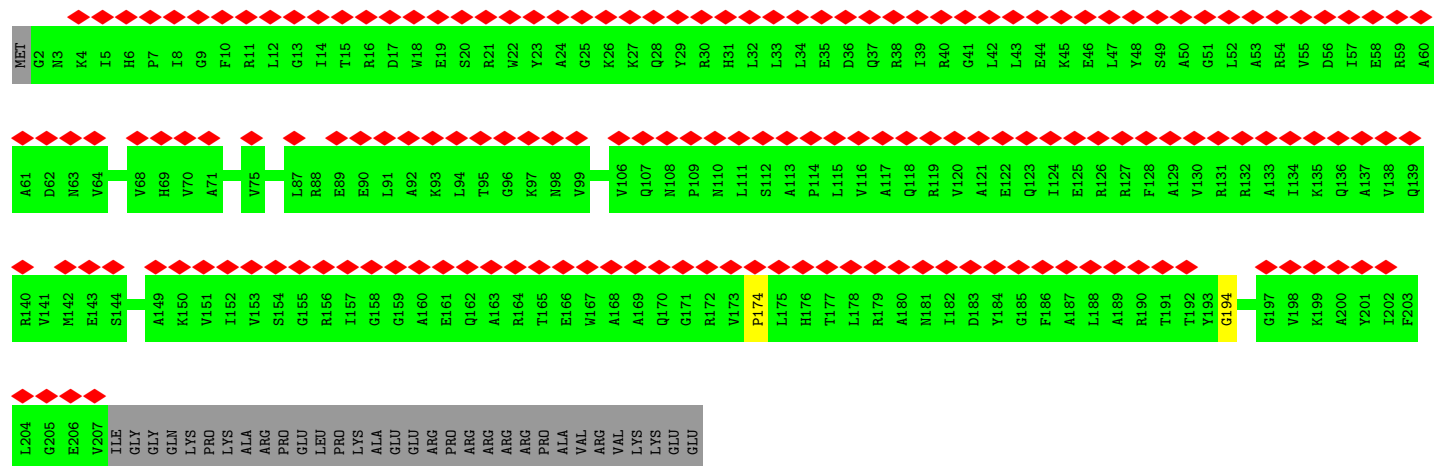
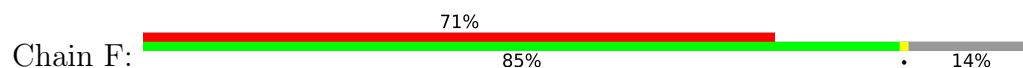




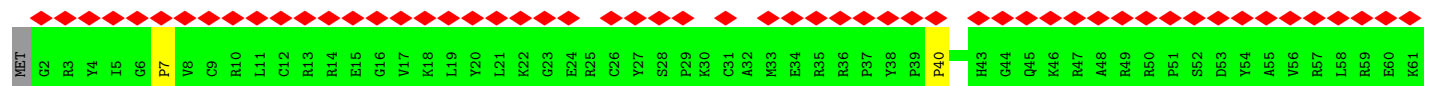
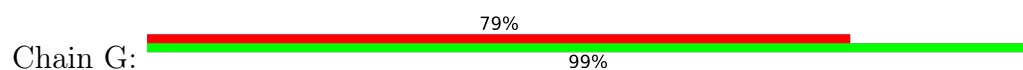
• Molecule 7: 30S RIBOSOMAL PROTEIN S2



• Molecule 8: 30S RIBOSOMAL PROTEIN S3

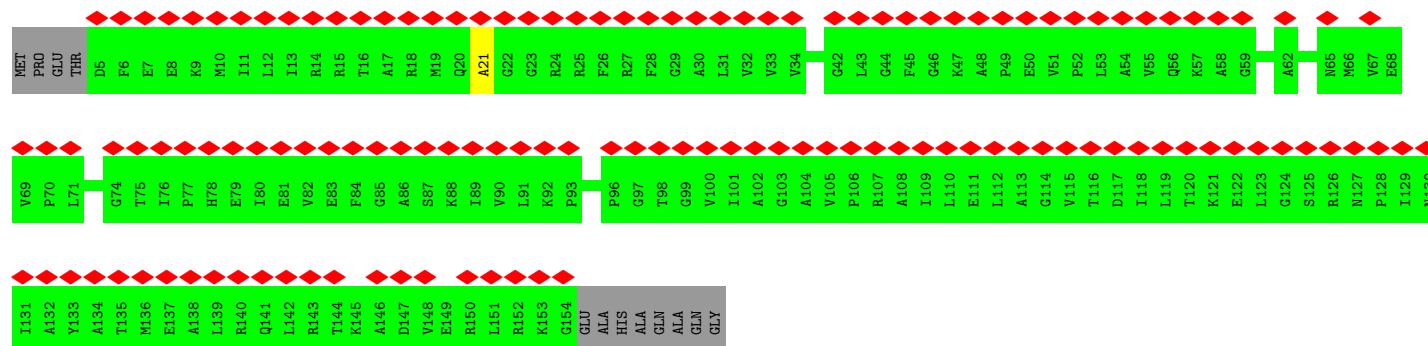
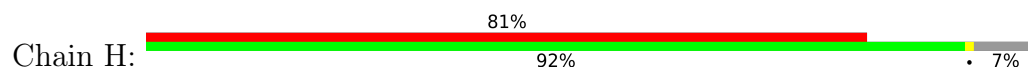


• Molecule 9: 30S RIBOSOMAL PROTEIN S4

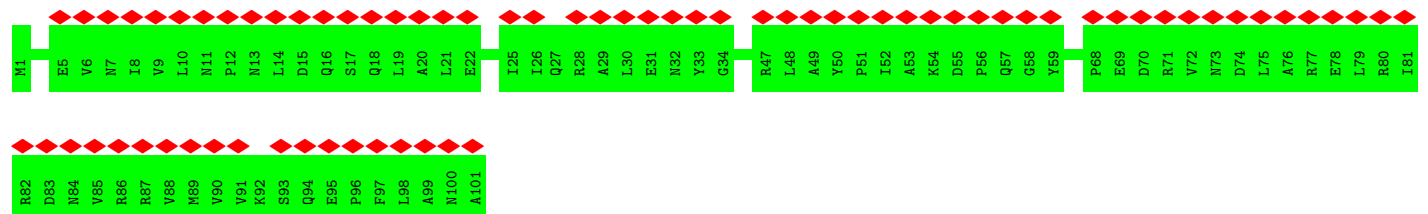




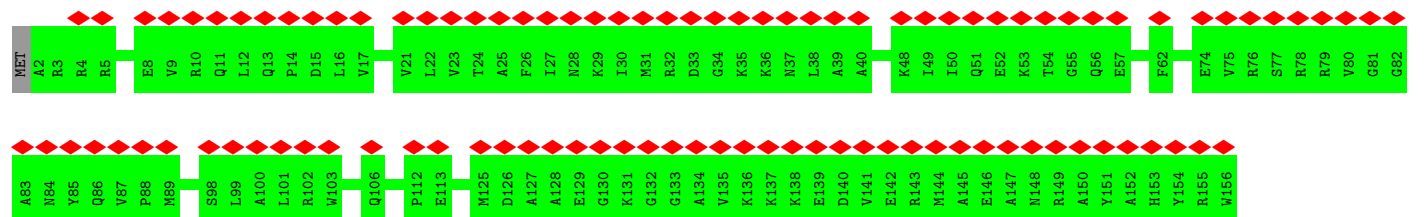
• Molecule 10: 30S RIBOSOMAL PROTEIN S5



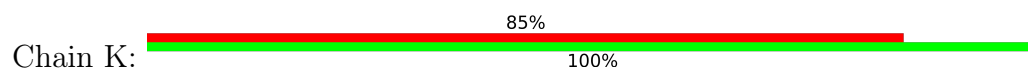
• Molecule 11: 30S RIBOSOMAL PROTEIN S6

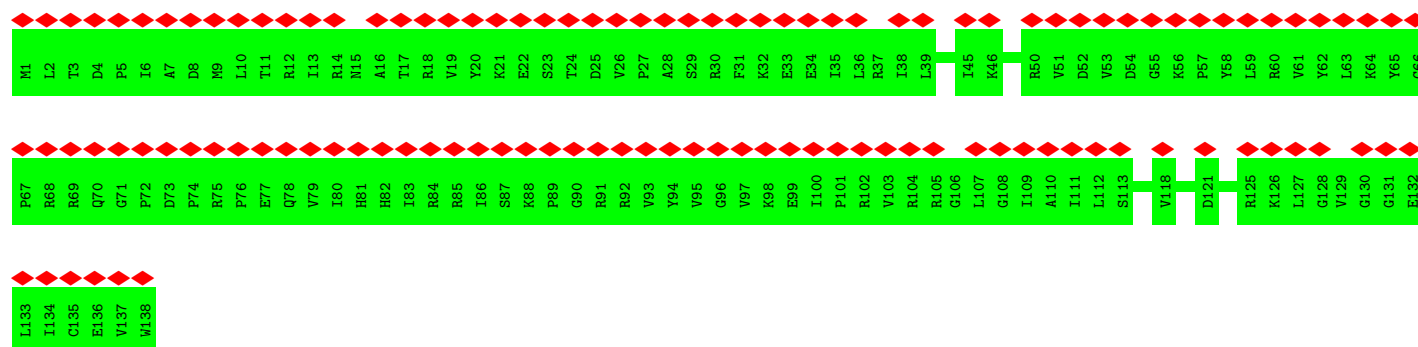


• Molecule 12: 30S RIBOSOMAL PROTEIN S7



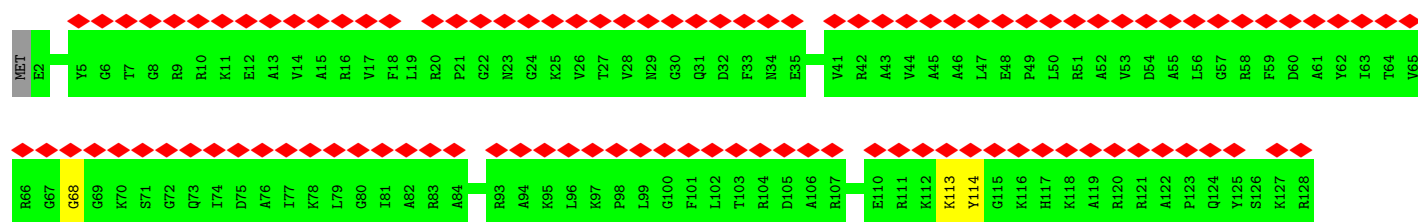
• Molecule 13: 30S RIBOSOMAL PROTEIN S8





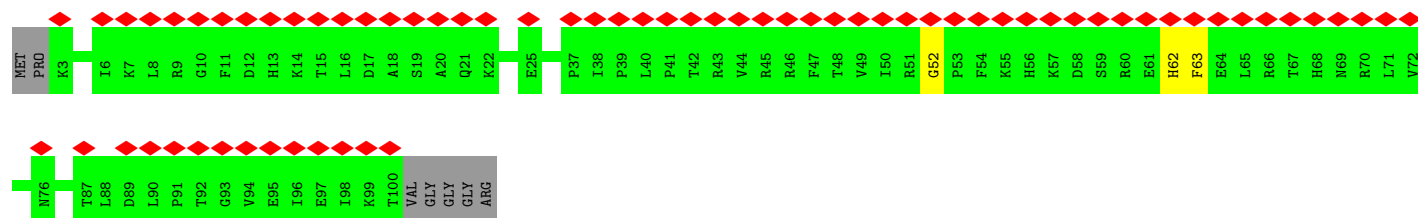
• Molecule 14: 30S RIBOSOMAL PROTEIN S9

Chain L: 84% 97% ..



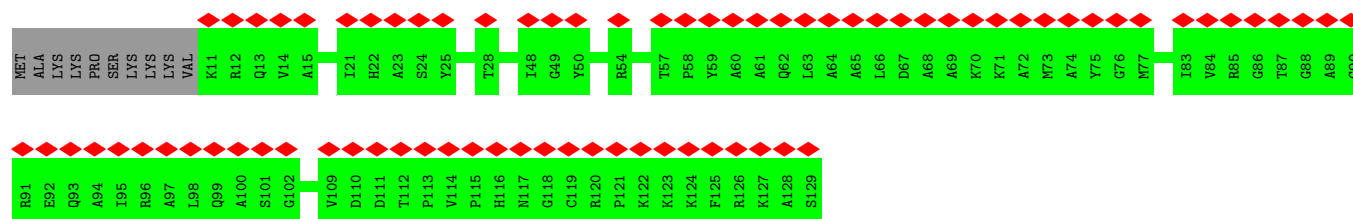
• Molecule 15: 30S RIBOSOMAL PROTEIN S10

Chain M: 66% 90% 7%



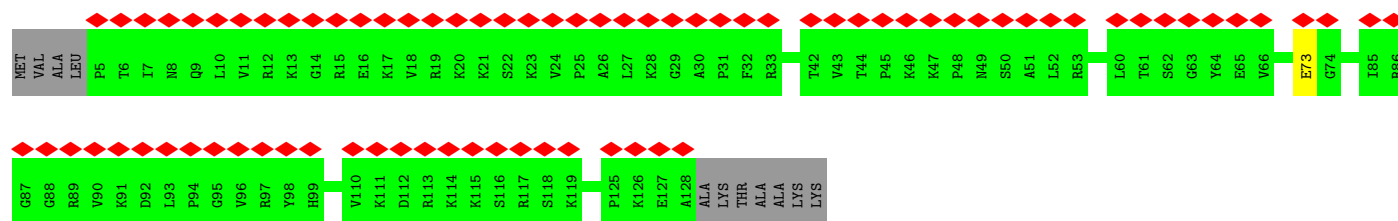
• Molecule 16: 30S RIBOSOMAL PROTEIN S11

Chain N: 60% 92% 8%

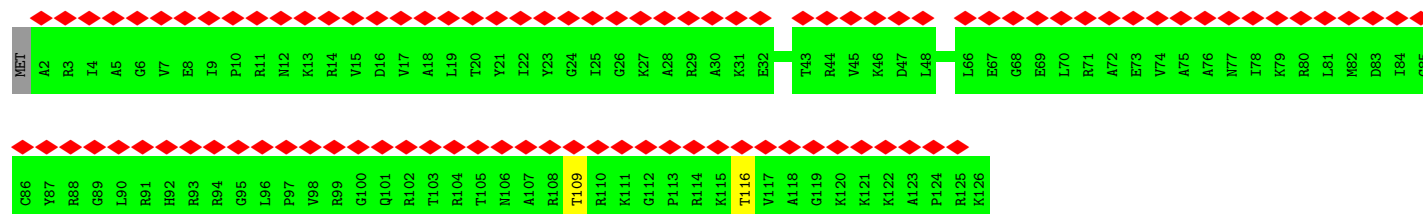
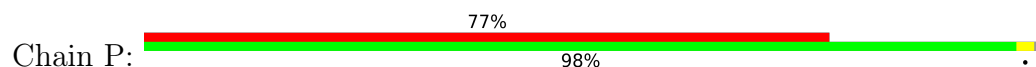


• Molecule 17: 30S RIBOSOMAL PROTEIN S12

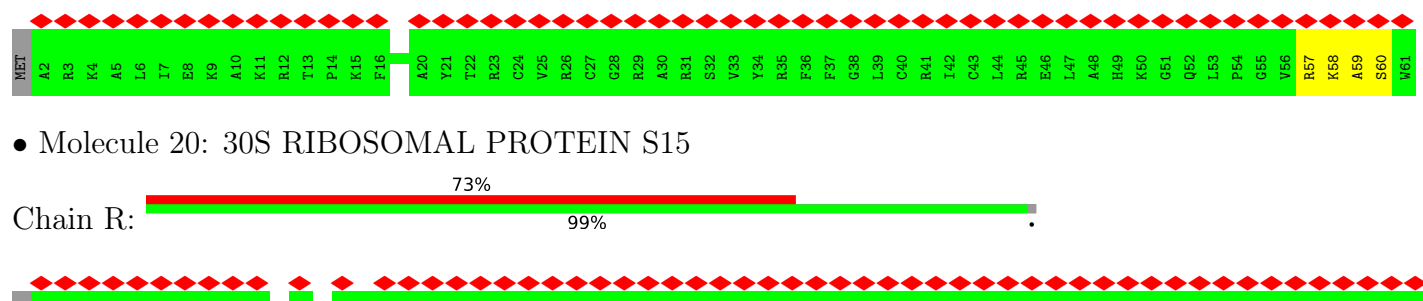
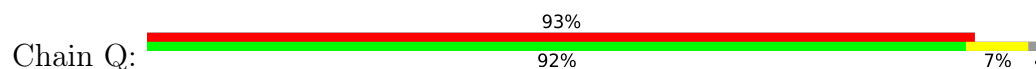
Chain O: 59% 91% 8%



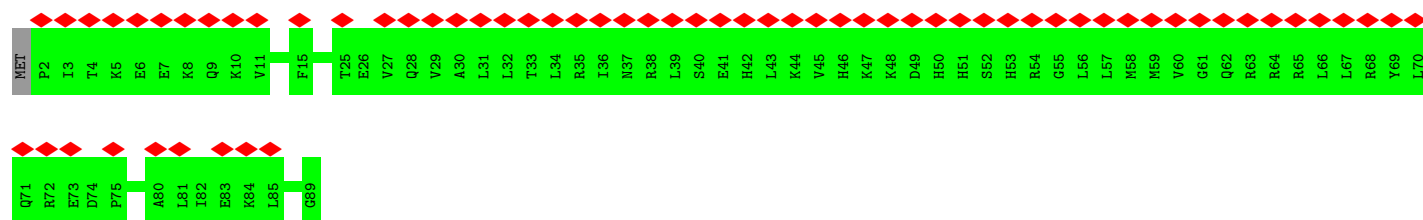
• Molecule 18: 30S RIBOSOMAL PROTEIN S13



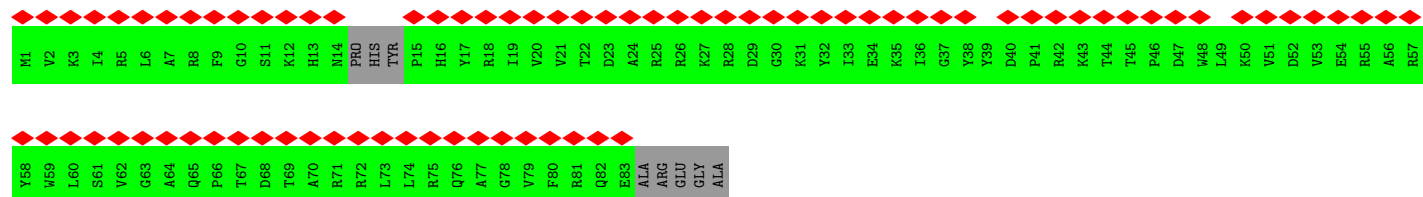
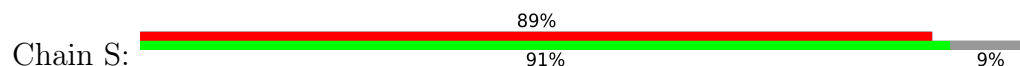
• Molecule 19: 30S RIBOSOMAL PROTEIN S14



• Molecule 20: 30S RIBOSOMAL PROTEIN S15



• Molecule 21: 30S RIBOSOMAL PROTEIN S16

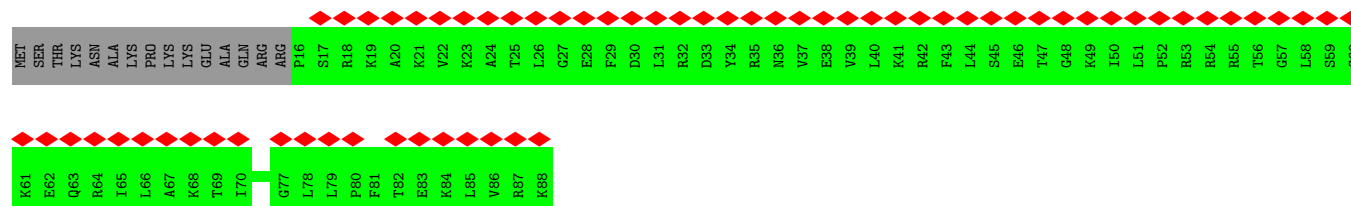
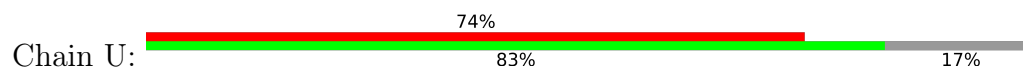


• Molecule 22: 30S RIBOSOMAL PROTEIN S17

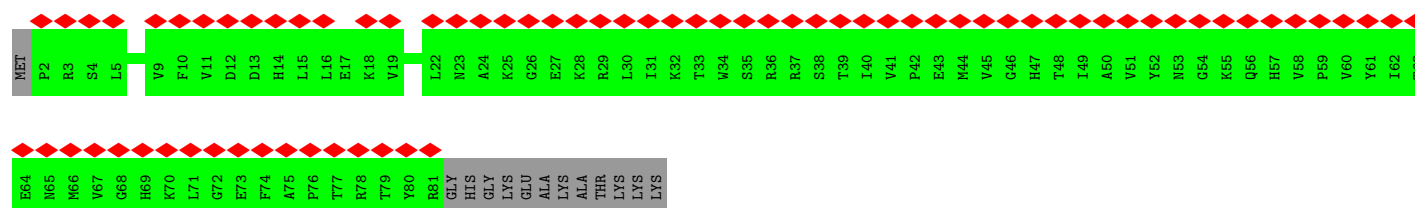
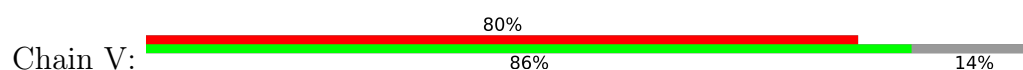




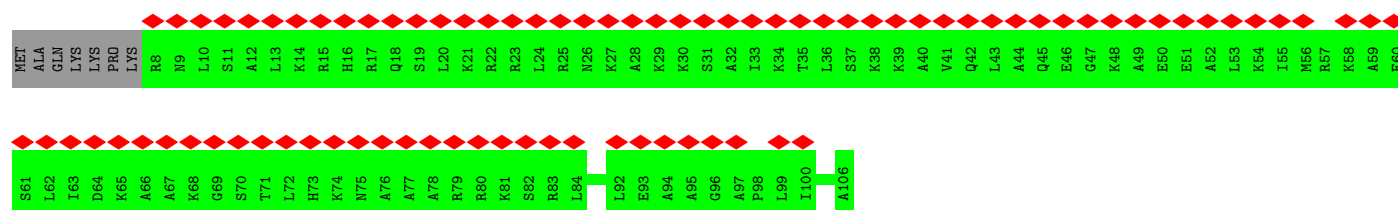
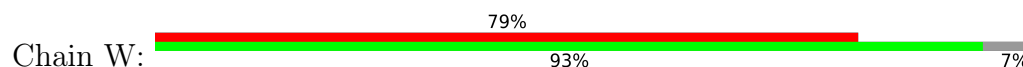
• Molecule 23: 30S RIBOSOMAL PROTEIN S18



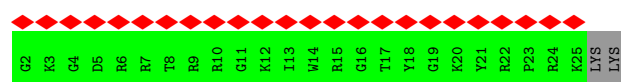
• Molecule 24: 30S RIBOSOMAL PROTEIN S19



• Molecule 25: 30S RIBOSOMAL PROTEIN S20

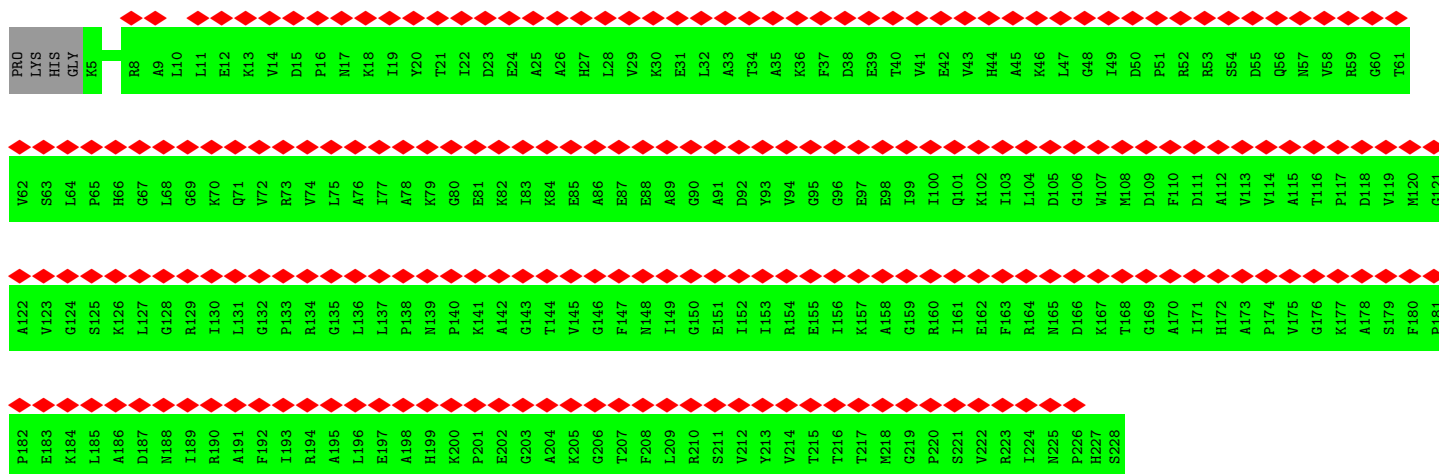


• Molecule 26: 30S RIBOSOMAL PROTEIN THX



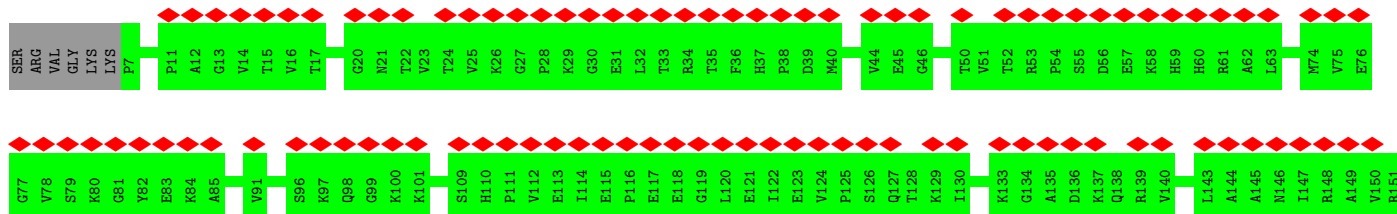
• Molecule 27: 50S RIBOSOMAL PROTEIN L1



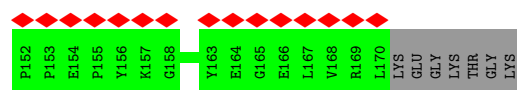


• Molecule 28: 50S RIBOSOMAL PROTEIN L2





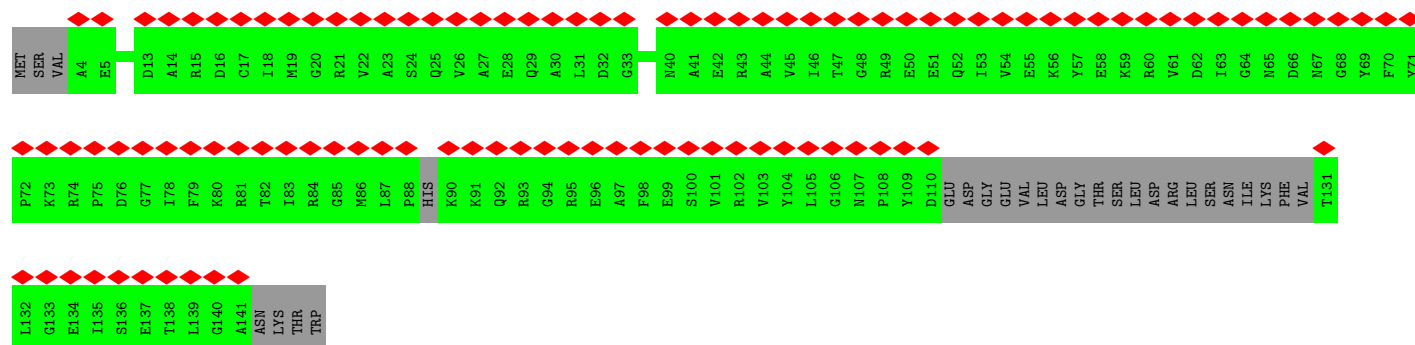
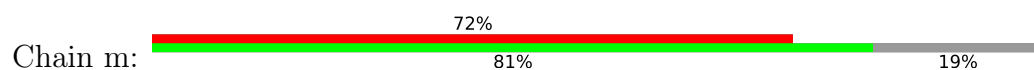




• Molecule 33: 50S RIBOSOMAL PROTEIN L11



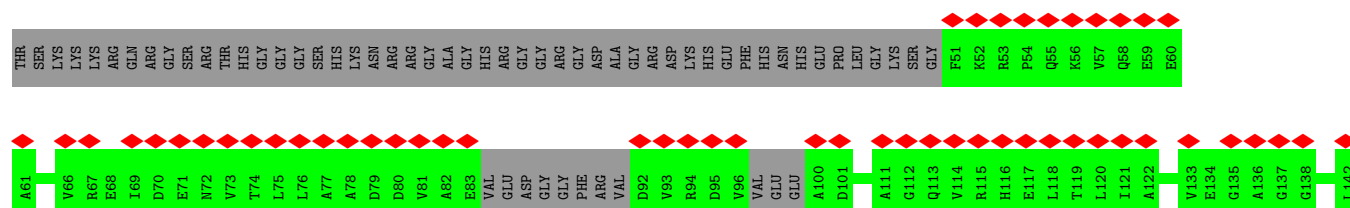
• Molecule 34: 50S RIBOSOMAL PROTEIN L13

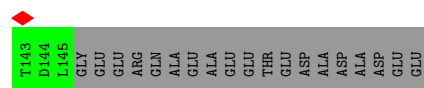


• Molecule 35: 50S RIBOSOMAL PROTEIN L14

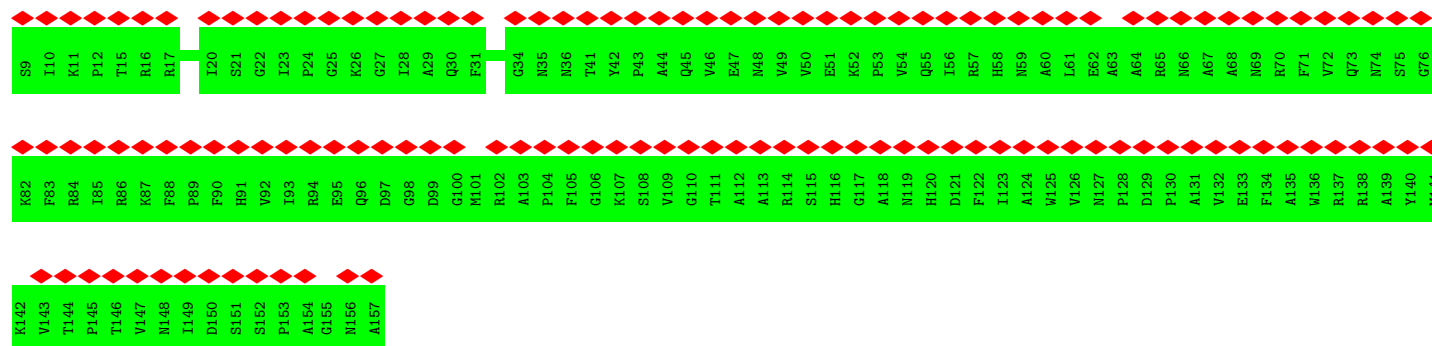


• Molecule 36: 50S RIBOSOMAL PROTEIN L15

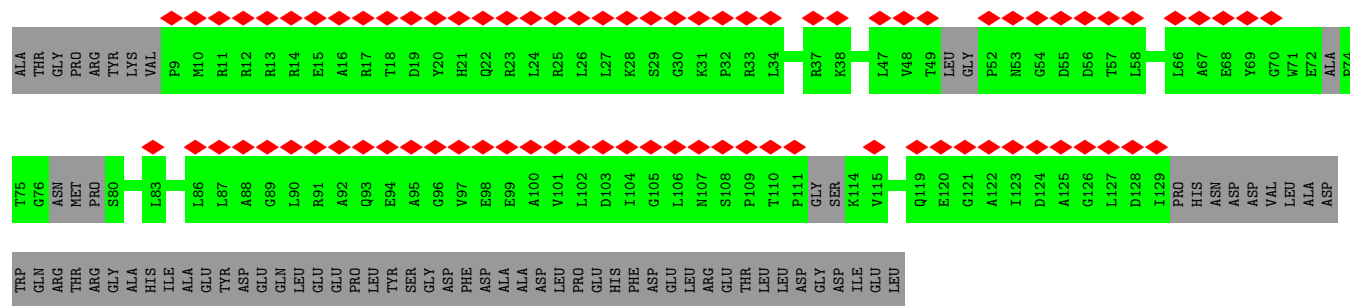




• Molecule 37: 50S RIBOSOMAL PROTEIN L16



• Molecule 38: 50S RIBOSOMAL PROTEIN L18



M1	P2	R3	L4	K5	V6	K7	L8	P12	Y15	P16	K17	D18	Q19	K20	A21	A21	A22	L23	K24	A25	L26	G27	L28	R29	R30	L31	Q32	Q33	E34	R35	V36	L37	E38	D39	I43	R44	G45	N46	V47	E48	K49	V50	A51	H52	L53	V54	R55	V56	E57	V58	V59
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	15800	Depositor
Resolution determination method	Not provided	
CTF correction method	phase flipping CTF correction of each particle as function of position in the micrograph	Depositor
Microscope	FEI/PHILIPS CM200FEG/ST	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	10	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	48000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.214	Depositor
Minimum map value	-0.160	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.0401	Depositor
Map size ( $\text{\AA}$ )	290.28, 290.28, 290.28	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.419, 2.419, 2.419	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, 5MU, OMG, PSU, 7MG, 5MC, 1MA, M2G, H2U, YG, OMC

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	$\# Z  > 5$
2	B	1.44	7/1487 (0.5%)	1.47	22/2315 (1.0%)
3	C	2.34	5/131 (3.8%)	2.47	3/200 (1.5%)
All	All	1.53	12/1618 (0.7%)	1.57	25/2515 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	74	C	O3'-P	-26.96	1.28	1.61
2	B	75	C	O3'-P	-25.74	1.30	1.61
2	B	44	A	O3'-P	-16.95	1.40	1.61
2	B	72	C	O3'-P	-15.83	1.42	1.61
3	C	14	U	O3'-P	-12.23	1.46	1.61

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	13	U	P-O3'-C3'	27.70	152.94	119.70
2	B	35	A	P-O3'-C3'	27.03	152.14	119.70
2	B	74	C	O3'-P-O5'	24.45	150.46	104.00
2	B	35	A	OP1-P-O3'	14.59	137.30	105.20
2	B	72	C	O3'-P-O5'	13.95	130.50	104.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	18	G	Sidechain
2	B	19	G	Sidechain
2	B	62	A	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	A	1519	0	0	15	0
2	B	1652	0	862	67	0
3	C	120	0	61	11	0
4	a	2889	0	0	0	0
5	b	123	0	0	0	0
6	Z	362	0	0	23	0
7	E	234	0	0	0	0
8	F	206	0	0	2	0
9	G	208	0	0	2	0
10	H	150	0	0	1	0
11	I	101	0	0	0	0
12	J	155	0	0	0	0
13	K	138	0	0	0	0
14	L	127	0	0	3	0
15	M	98	0	0	5	0
16	N	119	0	0	0	0
17	O	124	0	0	1	0
18	P	125	0	0	2	0
19	Q	60	0	0	5	0
20	R	88	0	0	0	0
21	S	83	0	0	0	0
22	T	104	0	0	0	0
23	U	73	0	0	0	0
24	V	80	0	0	0	0
25	W	99	0	0	0	0
26	X	24	0	0	0	0
27	c	224	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	d	173	0	0	0	0
29	e	191	0	0	0	0
30	f	189	0	0	0	0
31	g	122	0	0	0	0
32	h	164	0	0	0	0
33	l	133	0	0	0	0
34	m	117	0	0	0	0
35	n	122	0	0	0	0
36	o	84	0	0	0	0
37	p	138	0	0	0	0
38	q	113	0	0	0	0
39	r	52	0	0	0	0
40	s	110	0	0	0	0
41	t	76	0	0	0	0
42	u	110	0	0	0	0
43	v	89	0	0	0	0
44	w	64	0	0	0	0
45	x	60	0	0	0	0
All	All	11392	0	923	98	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 98 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:A:H3'	6:Z:255:ASN:CA	1.33	1.51
1:A:430:A:P	9:G:7:PRO:CA	2.16	1.34
2:B:73:A:C3'	6:Z:255:ASN:CA	2.05	1.33
2:B:1:G:N2	2:B:2:C:H41	1.22	1.32
2:B:1:G:N2	2:B:2:C:N4	1.77	1.30

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	0/1522	-	-
2	B	75/76 (98%)	13 (17%)	3 (4%)
3	C	5/6 (83%)	1 (20%)	0
4	a	0/2916	-	-
5	b	0/123	-	-
All	All	80/4643 (1%)	14 (17%)	3 (3%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	C
2	B	3	G
2	B	17	H2U
2	B	18	G
2	B	19	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	16	H2U
2	B	18	G
2	B	35	A

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

14 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
2	1MA	B	58	2	16,25,26	2.84	4 (25%)	18,37,40	2.21	5 (27%)
2	7MG	B	46	2	22,26,27	1.09	2 (9%)	29,39,42	1.20	3 (10%)
2	OMC	B	32	2	19,22,23	0.47	0	26,31,34	0.57	0
2	H2U	B	17	2	18,21,22	0.68	1 (5%)	21,30,33	1.02	2 (9%)
2	2MG	B	10	2	18,26,27	1.10	1 (5%)	16,38,41	0.75	0
2	5MU	B	54	2	19,22,23	0.52	0	28,32,35	0.65	0
2	YG	B	37	2	31,42,43	0.92	1 (3%)	33,62,65	2.59	10 (30%)
2	5MC	B	49	2	18,22,23	0.75	0	26,32,35	0.73	1 (3%)
2	PSU	B	55	2	18,21,22	0.74	0	22,30,33	0.85	0
2	OMG	B	34	3,2	18,26,27	1.04	1 (5%)	19,38,41	0.87	1 (5%)
2	PSU	B	39	2	18,21,22	0.70	0	22,30,33	0.69	0
2	M2G	B	26	2	20,27,28	1.20	2 (10%)	22,40,43	0.79	0
2	H2U	B	16	2	18,21,22	0.74	1 (5%)	21,30,33	1.14	2 (9%)
2	5MC	B	40	2	18,22,23	0.47	0	26,32,35	0.70	1 (3%)

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
2	1MA	B	58	2	-	0/3/25/26	0/3/3/3
2	7MG	B	46	2	-	2/7/37/38	0/3/3/3
2	OMC	B	32	2	-	0/9/27/28	0/2/2/2
2	H2U	B	17	2	-	1/7/38/39	0/2/2/2
2	2MG	B	10	2	-	0/5/27/28	0/3/3/3
2	5MU	B	54	2	-	0/7/25/26	0/2/2/2
2	YG	B	37	2	-	7/20/42/43	0/3/4/4
2	5MC	B	49	2	-	0/7/25/26	0/2/2/2
2	PSU	B	55	2	-	0/7/25/26	0/2/2/2
2	OMG	B	34	3,2	-	1/5/27/28	0/3/3/3
2	PSU	B	39	2	-	0/7/25/26	0/2/2/2
2	M2G	B	26	2	-	0/7/29/30	0/3/3/3
2	H2U	B	16	2	-	4/7/38/39	0/2/2/2
2	5MC	B	40	2	-	1/7/25/26	0/2/2/2

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	58	1MA	C6-N6	8.05	1.48	1.27
2	B	58	1MA	C2-N3	6.96	1.37	1.29
2	B	26	M2G	C5-C6	-3.16	1.41	1.47
2	B	10	2MG	C5-C6	-3.10	1.41	1.47
2	B	46	7MG	C4-N9	3.03	1.41	1.37

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	37	YG	C11-C12-N1	8.56	111.36	106.53
2	B	37	YG	C24-O23-C21	6.24	123.03	115.66
2	B	58	1MA	CM1-N1-C6	-5.19	112.41	120.27
2	B	37	YG	C3-N3-C4	4.94	125.48	116.71
2	B	58	1MA	CM1-N1-C2	4.58	130.18	120.55

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	16	H2U	O4'-C1'-N1-C2
2	B	16	H2U	O4'-C1'-N1-C6
2	B	16	H2U	C2'-C1'-N1-C6
2	B	37	YG	C12-C13-C14-C15
2	B	37	YG	C15-C16-O18-C19

There are no ring outliers.

9 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	32	OMC	1	0
2	B	17	H2U	3	0
2	B	10	2MG	3	0
2	B	37	YG	7	0
2	B	34	OMG	4	0
2	B	39	PSU	1	0
2	B	26	M2G	6	0
2	B	16	H2U	3	0
2	B	40	5MC	3	0

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	25:C	O3'	26:M2G	P	2.12
1	B	75:C	O3'	76:A	P	1.30
1	B	74:C	O3'	75:C	P	1.28
1	B	36:A	O3'	37:YG	P	1.18

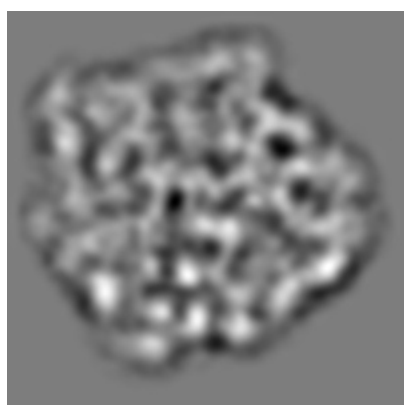
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1005. These allow visual inspection of the internal detail of the map and identification of artifacts.

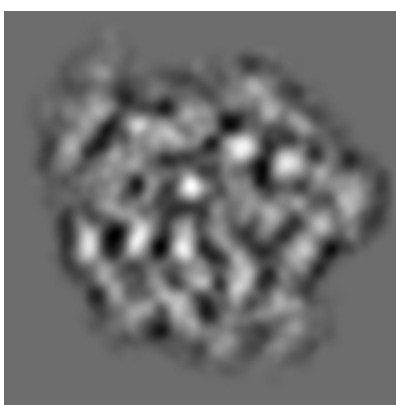
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

#### 6.1.1 Primary map



X



Y

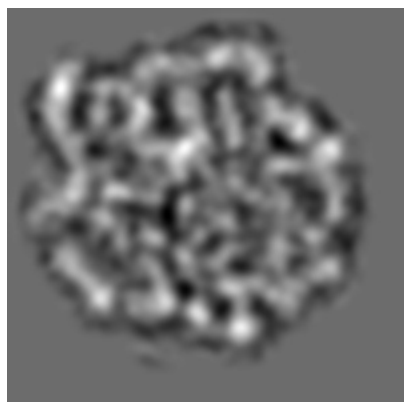


Z

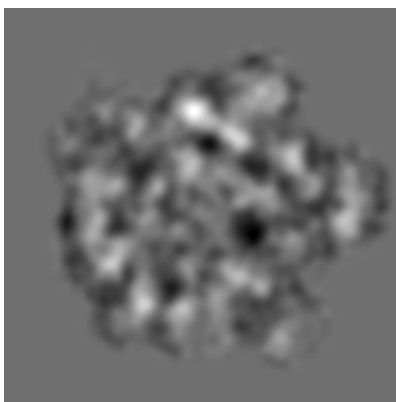
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

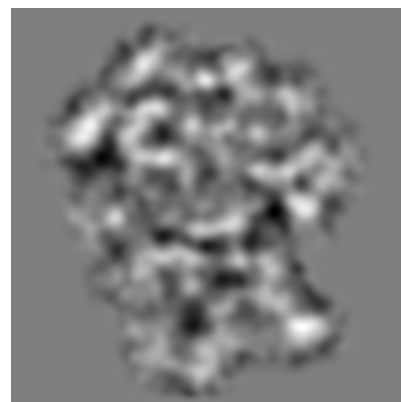
#### 6.2.1 Primary map



X Index: 60



Y Index: 60

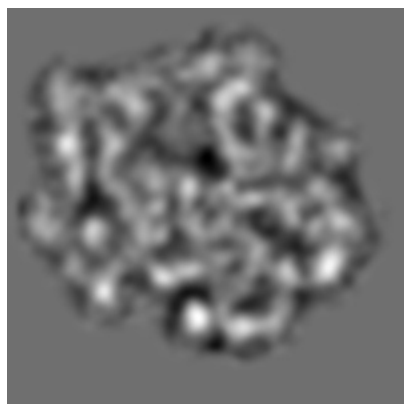


Z Index: 60

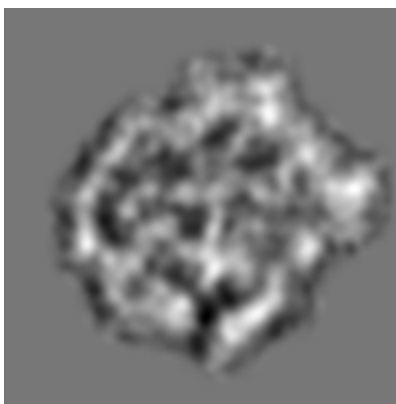
The images above show central slices of the map in three orthogonal directions.

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

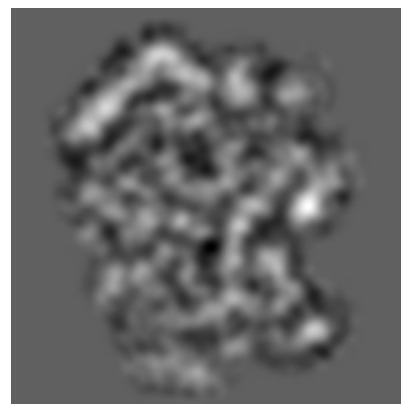
### 6.3.1 Primary map



X Index: 53



Y Index: 74



Z Index: 56

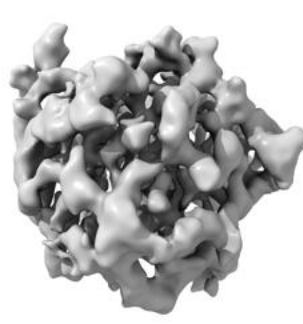
The images above show the largest variance slices of the map in three orthogonal directions.

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

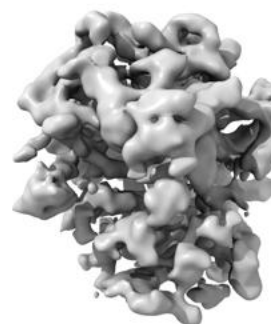
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0401. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

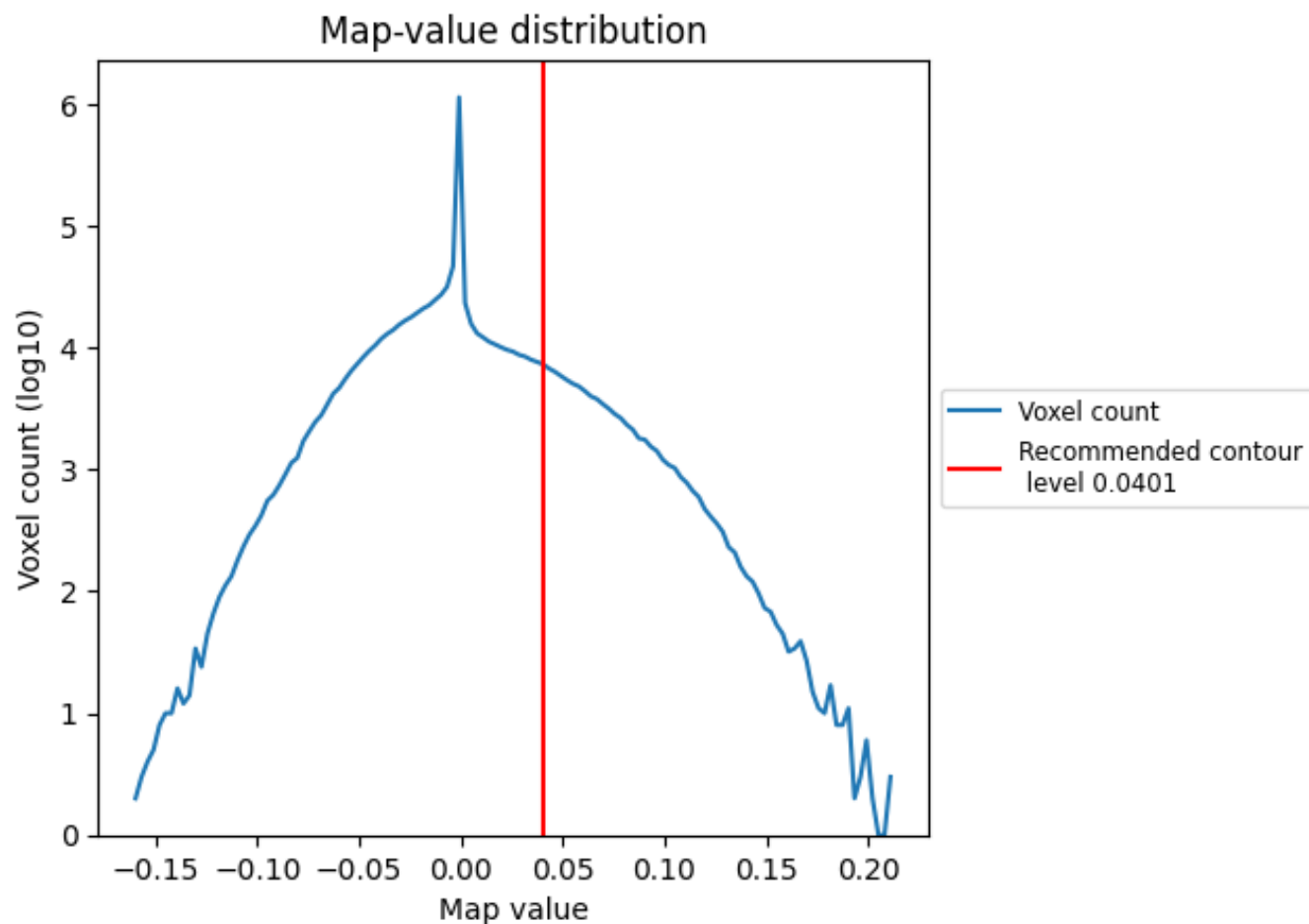
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

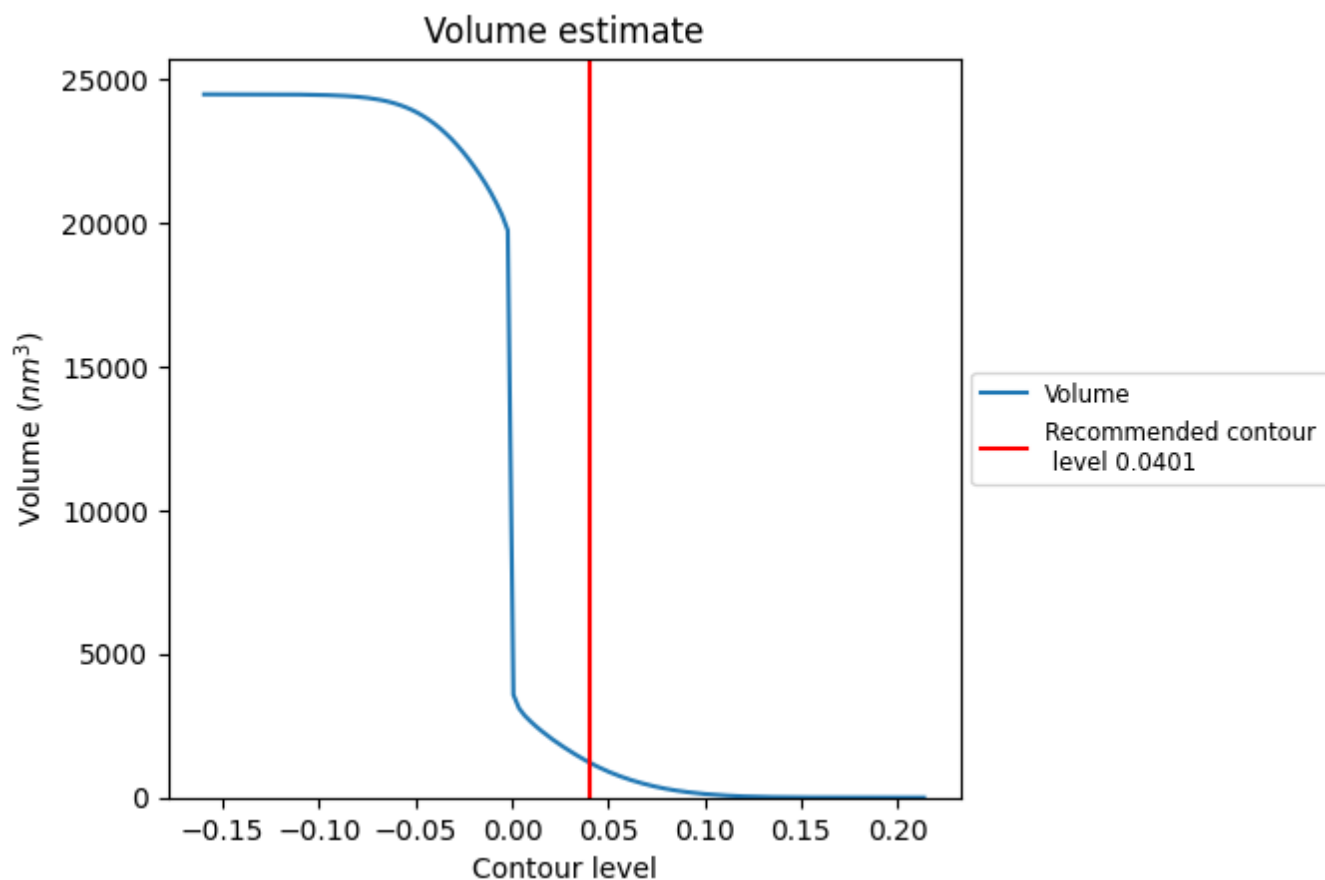
This section contains the results of statistical analysis of the map.

### 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](#)

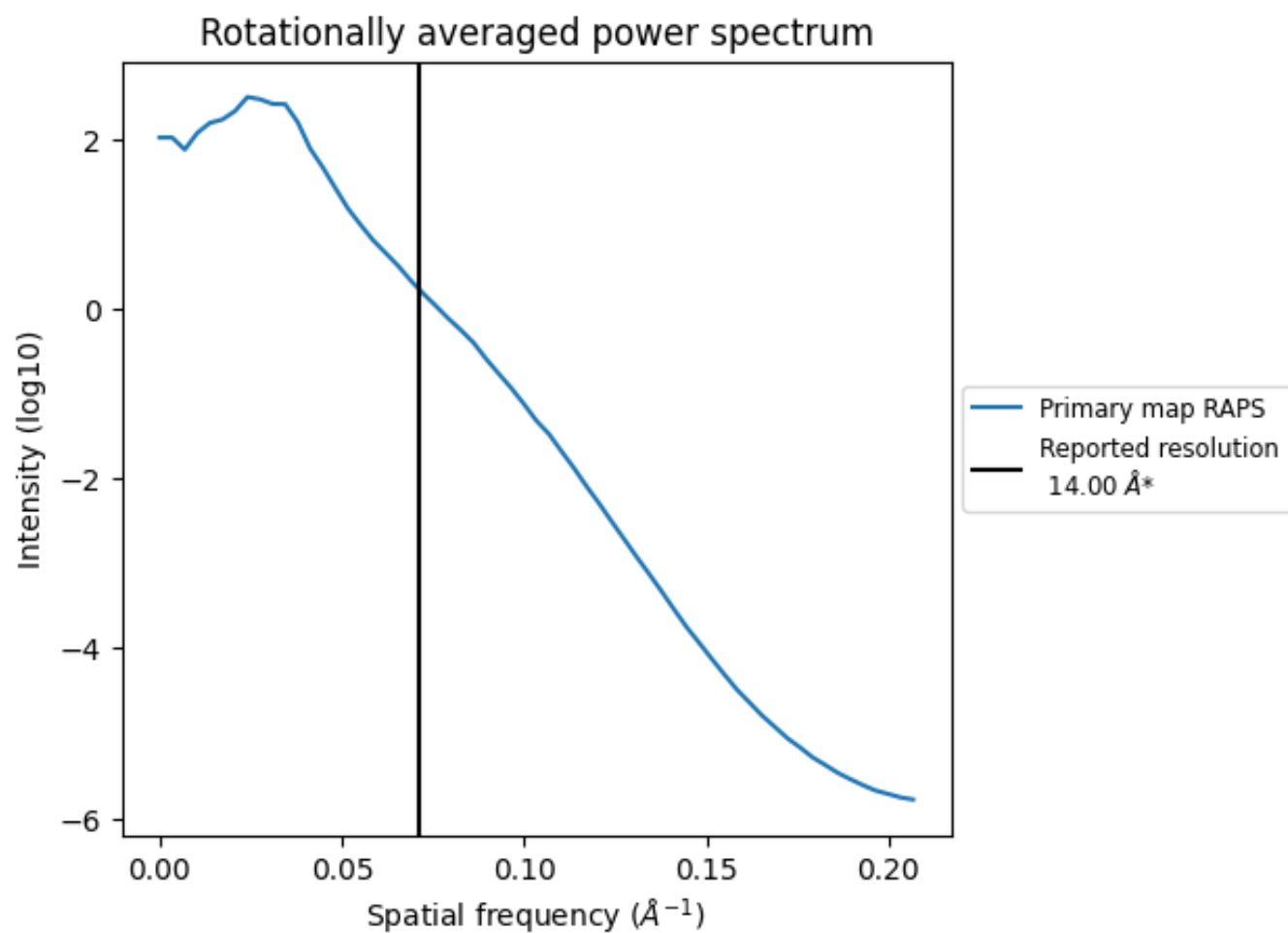


The volume at the recommended contour level is 1226 nm<sup>3</sup>; this corresponds to an approximate mass of 1107 kDa.

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

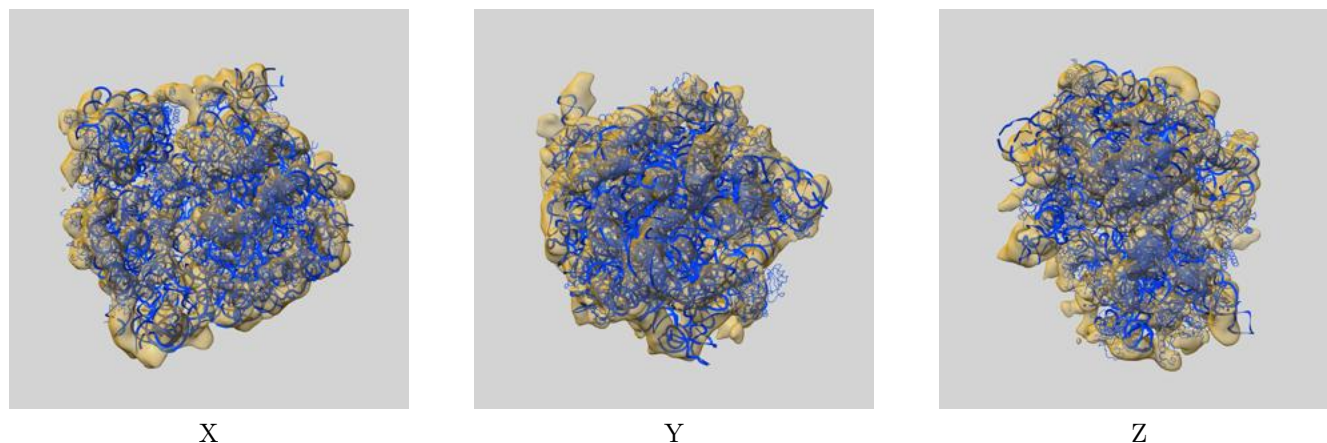
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

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

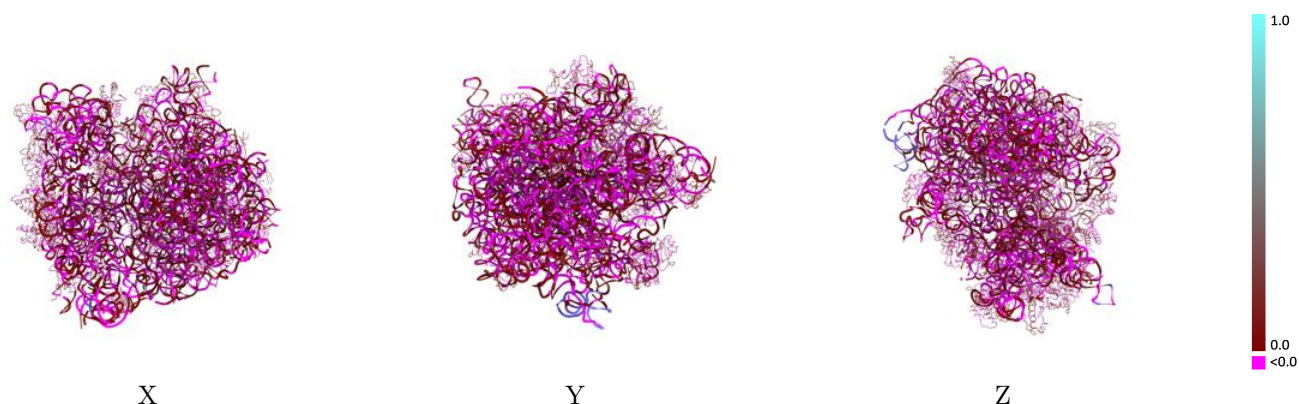
This section contains information regarding the fit between EMDB map EMD-1005 and PDB model 1ML5. Per-residue inclusion information can be found in section 3 on page 12.

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



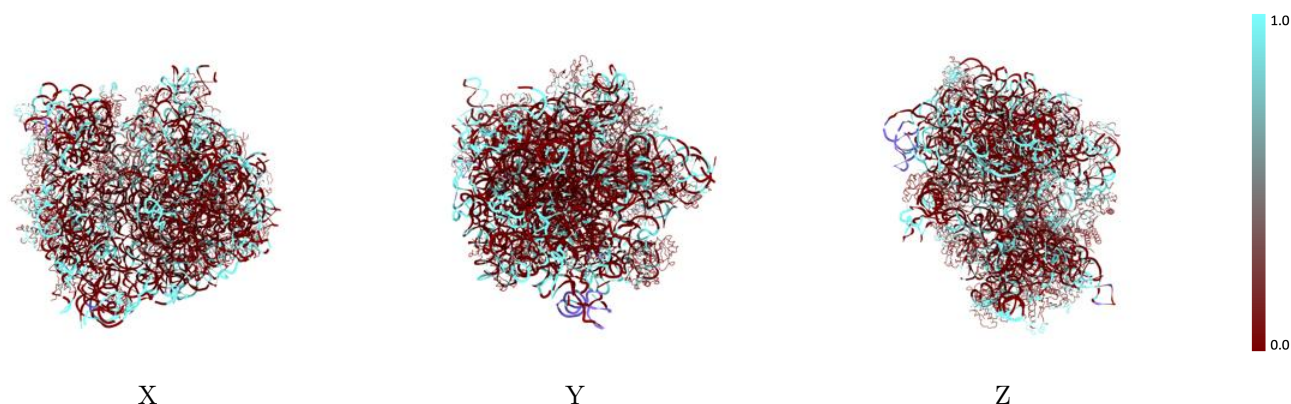
The images above show the 3D surface view of the map at the recommended contour level 0.0401 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



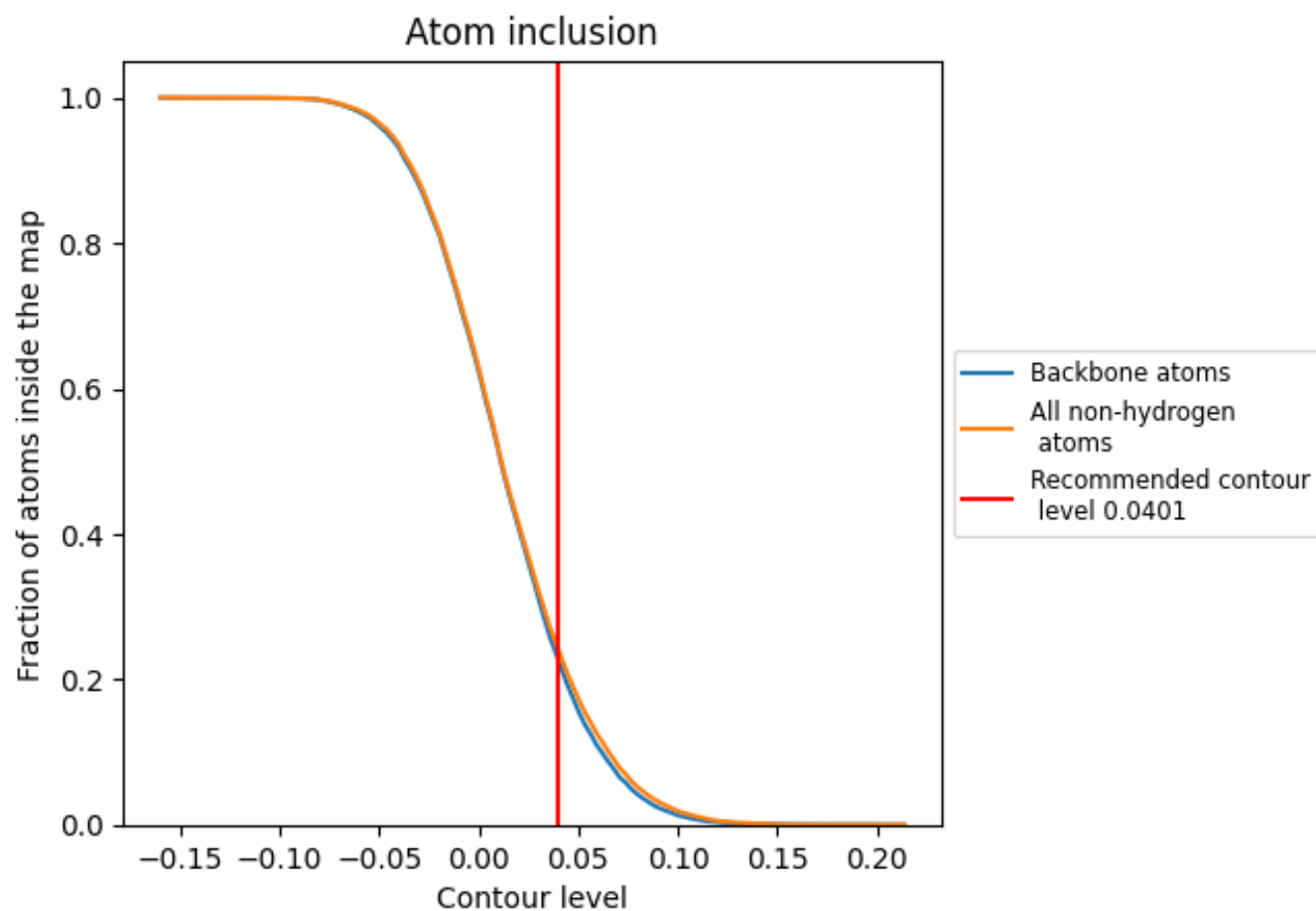
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0401).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 23% of all backbone atoms, 24% 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 (0.0401) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2408	 0.0130
A	 0.2633	 0.0080
B	 0.3487	 0.0370
C	 0.0000	 -0.0190
E	 0.2051	 0.0140
F	 0.1748	 0.0200
G	 0.2067	 0.0190
H	 0.1267	 0.0090
I	 0.2772	 0.0010
J	 0.3548	 0.0190
K	 0.1522	 -0.0160
L	 0.1575	 0.0120
M	 0.2959	 0.0050
N	 0.3529	 0.0310
O	 0.3629	 0.0280
P	 0.2240	 0.0190
Q	 0.0500	 -0.0220
R	 0.2614	 0.0430
S	 0.0241	 0.0070
T	 0.0962	 0.0070
U	 0.1096	 -0.0070
V	 0.0750	 0.0320
W	 0.1515	 -0.0240
X	 0.0000	 -0.0200
Z	 0.1271	 0.0250
a	 0.2738	 0.0090
b	 0.3496	 0.0050
c	 0.0268	 -0.0150
d	 0.0694	 0.0200
e	 0.1571	 0.0030
f	 0.2963	 0.0060
g	 0.1475	 -0.0100
h	 0.3110	 0.0200
l	 0.2782	 0.0250
m	 0.1111	 -0.0110



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Chain	Atom inclusion	Q-score
n	 0.0328	 0.0130
o	 0.3571	 0.0110
p	 0.0580	 -0.0190
q	 0.2743	 0.0160
r	 0.0000	 -0.0410
s	 0.1000	 -0.0170
t	 0.1184	 0.0430
u	 0.1364	 -0.0120
v	 0.5056	 0.0340
w	 0.3438	 0.0800
x	 0.1333	 0.0170