



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:48 AM UTC

PDB ID : 8T5H / pdb_00008t5h
EMDB ID : EMD-41050
Title : Cryo-EM studies of the interplay between uS2 ribosomal protein and leaderless mRNA during bacterial translation initiation
Authors : Bhattacharjee, S.; Gottesman, M.E.; Frank, J.
Deposited on : 2023-06-13
Resolution : 3.30 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:

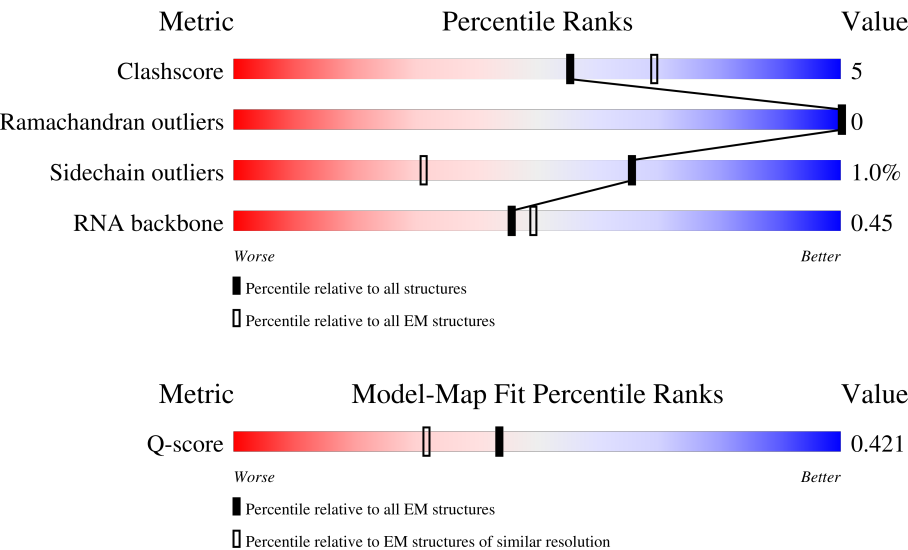
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	
2	1	51	
3	2	46	

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Mol	Chain	Length	Quality of chain
4	3	64	
5	4	38	
6	A	117	
7	B	2903	
8	C	272	
9	D	209	
10	E	201	
11	F	178	
12	G	176	
13	J	142	
14	K	122	
15	L	143	
16	M	136	
17	N	121	
18	O	116	
19	P	114	
20	Q	117	
21	R	103	
22	S	110	
23	T	94	
24	U	103	
25	V	94	
26	W	79	
27	X	77	
28	Y	63	

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Mol	Chain	Length	Quality of chain
29	Z	58	
30	b	206	
31	c	205	
32	d	150	
33	e	100	
34	f	151	
35	g	129	
36	h	127	
37	i	98	
38	j	117	
39	k	123	
40	l	114	
41	m	100	
42	n	88	
43	o	82	
44	p	80	
45	q	55	
46	r	79	
47	s	85	
48	u	59	
49	v	1539	
50	x	12	
51	5	77	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 140621 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	51	Total	C	N	O	0	1
			410	263	76	71		

- 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 RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 7 is a RNA chain called 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

- Molecule 9 is a protein called 50S ribosomal protein L3.

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

- Molecule 10 is a protein called 50S ribosomal protein L4.

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

- Molecule 11 is a protein called 50S ribosomal protein L5.

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

- Molecule 12 is a protein called 50S ribosomal protein L6.

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

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	122	Total	C	N	O	S	0	1
			931	582	180	164	5		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	121	Total	C	N	O	S	0	1
			961	593	197	166	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called Ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	1
			739	466	140	131	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O		0	1
			780	492	147	141			

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

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

- Molecule 29 is a protein called 50S ribosomal protein L30.

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

- Molecule 30 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 31 is a protein called 30S ribosomal protein S4.

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

- Molecule 32 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 33 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 34 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 35 is a protein called 30S ribosomal protein S8.

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

- Molecule 36 is a protein called 30S ribosomal protein S9.

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

- Molecule 37 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

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

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

- Molecule 39 is a protein called 30S ribosomal protein S12.

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

- Molecule 40 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 41 is a protein called 30S ribosomal protein S14.

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

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 43 is a protein called 30S ribosomal protein S16.

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

- Molecule 44 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 45 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	q	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 46 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 47 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 48 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	59	Total	C	N	O	S	0	0
			468	297	78	92	1		

- Molecule 49 is a RNA chain called 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 50 is a RNA chain called lmRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	12	Total	C	N	O	P	0	0
			257	117	53	76	11		

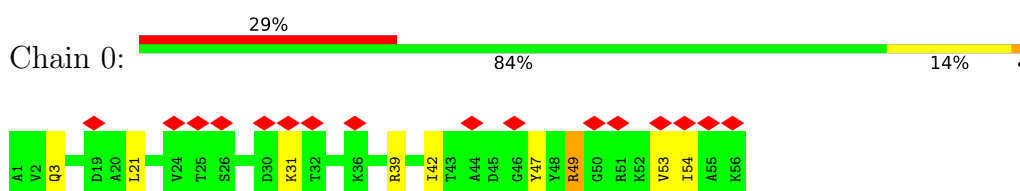
- Molecule 51 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

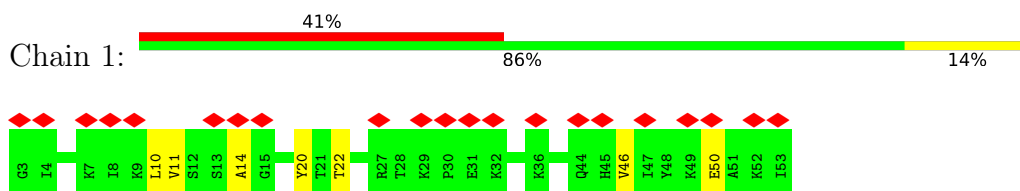
3 Residue-property plots [i](#)

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.

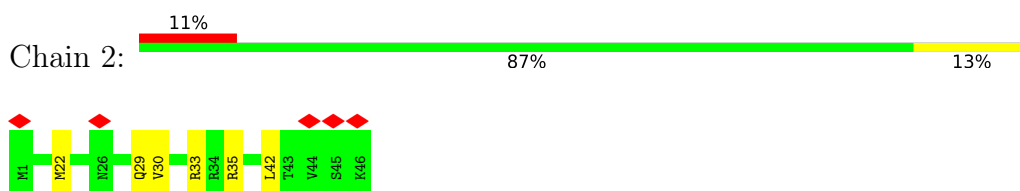
- Molecule 1: 50S ribosomal protein L32



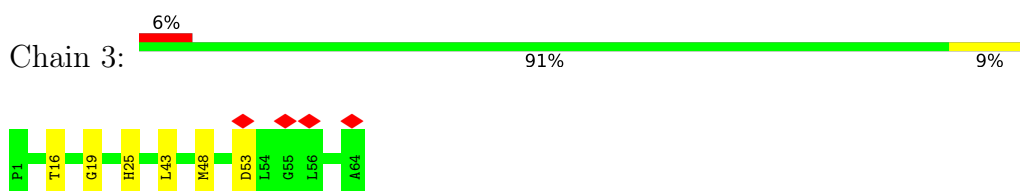
- Molecule 2: 50S ribosomal protein L33



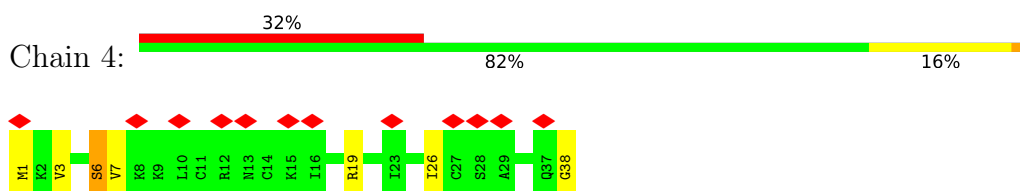
- Molecule 3: 50S ribosomal protein L34



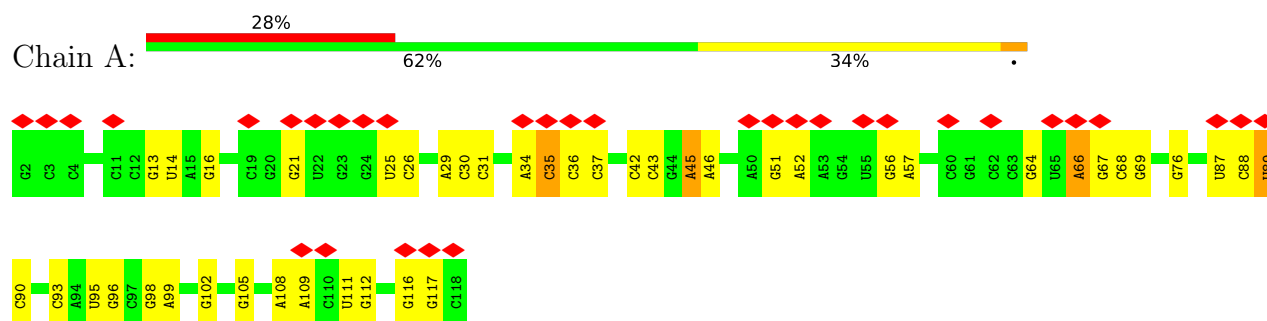
- Molecule 4: 50S ribosomal protein L35



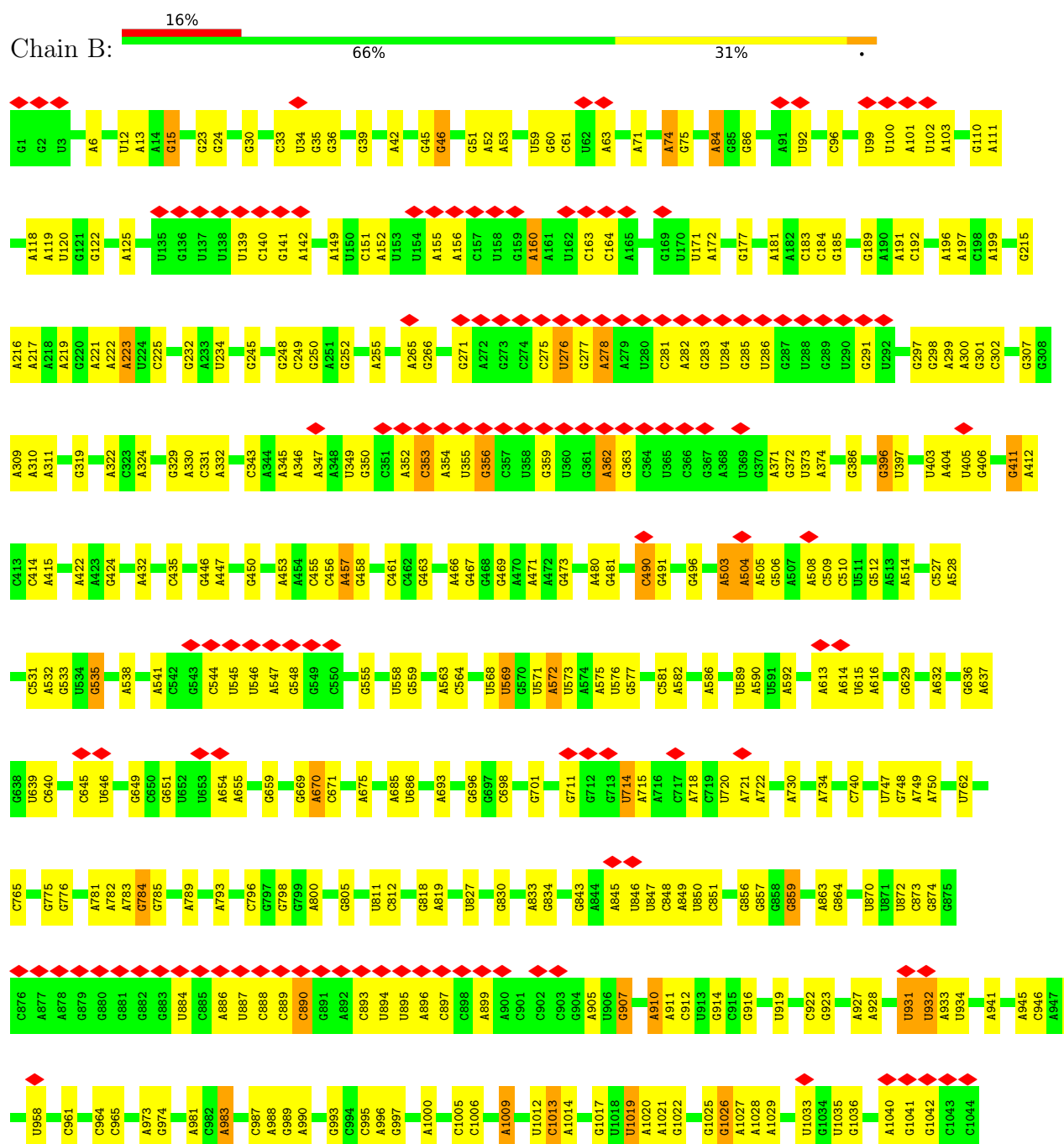
- Molecule 5: 50S ribosomal protein L36



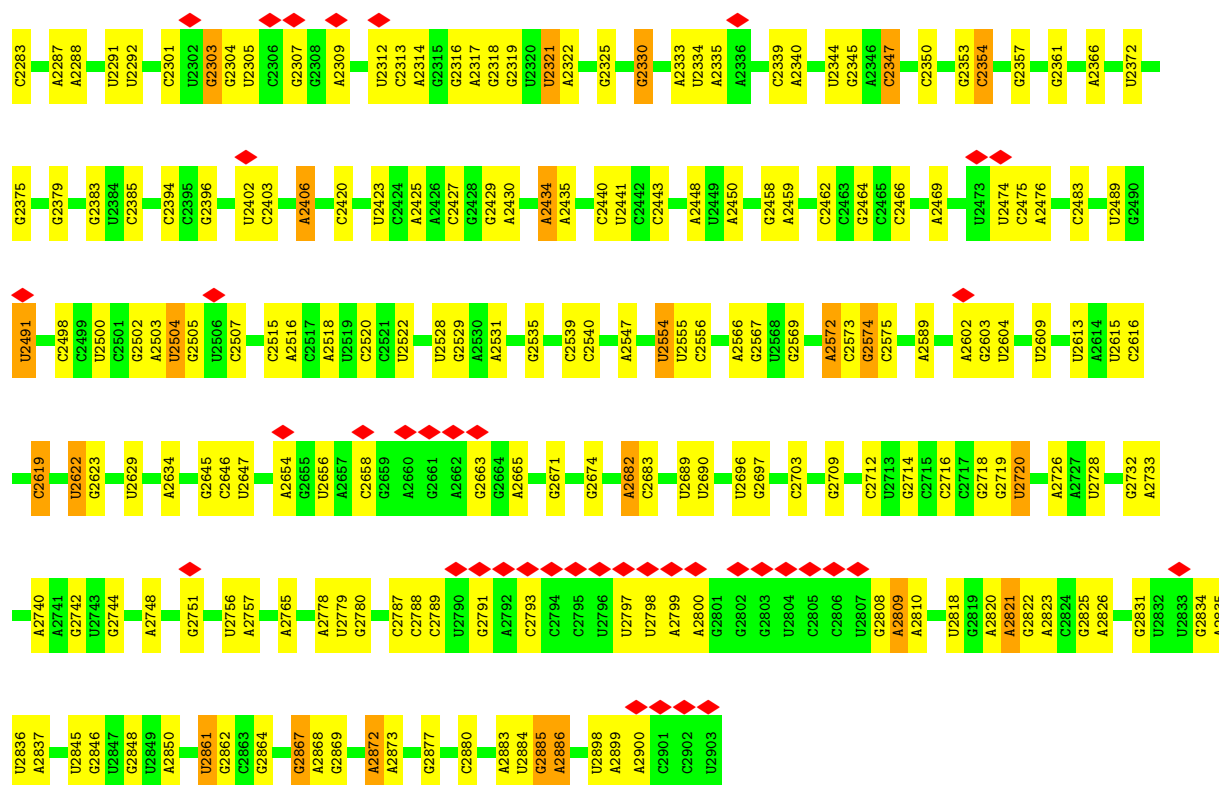
- Molecule 6: 5S



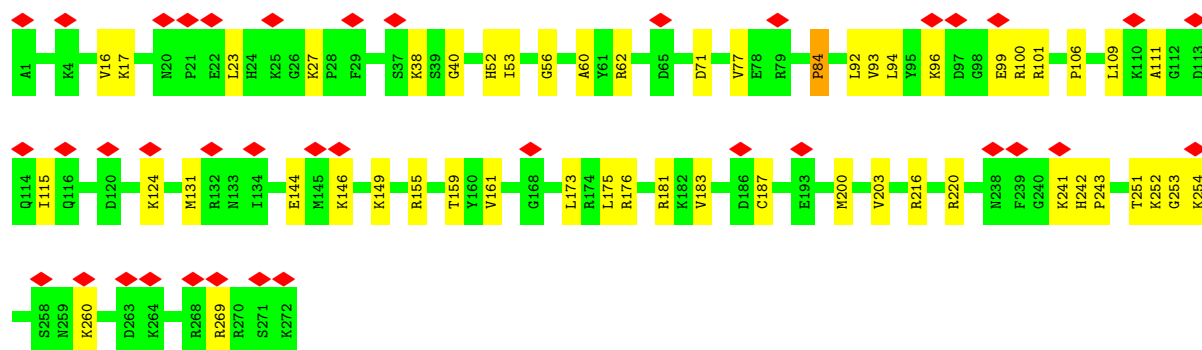
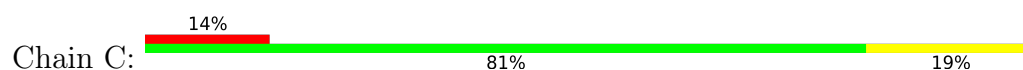
- Molecule 7: 23S



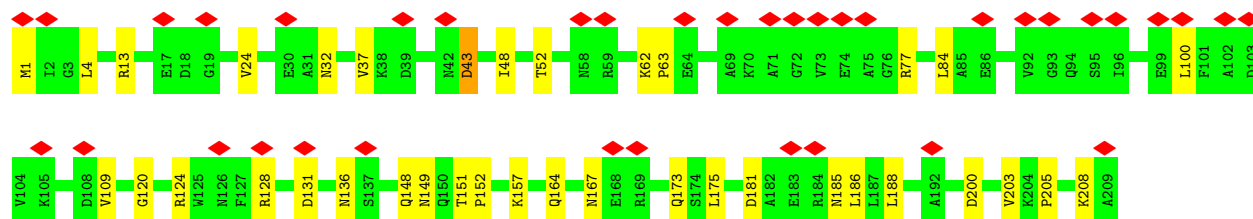
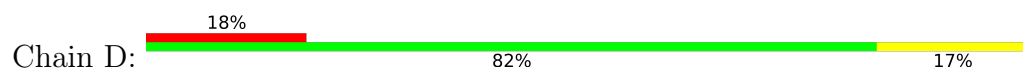
U185	G2125	U2034	C1914	G1799	G1721	U1594	U1506	G1419	G1317	A1213	U1105	C1045
G2186	A2126	C2043	U1915	C1800	A1722	A1603	C1507	A1420	A1321	A1214	G1106	A1046
U2187	G2127	A1801	A1916	A1801	G1723	C1604	A1508	G1421	A1322	U1219	G1107	G1047
U2188	G2128	G2049	U1917	A1802	G1724	C1607	A1509	A1427	C1324	G1220	U1108	A1048
U2189	U2129	A2082	A1918	G1807	U1725	A1608	G1510	C1428	U1325	G1225	C1109	U1049
A2191	U2130	C2085	A1919	A1808	C1726	A1609	U1513	G1432	A1328	U1231	G1110	A1050
U2192	U2132	G2056	U1923	A1810	C1727	A1610	A1514	A1432	U1329	G1227	A1111	G1051
G2193	A2133	A2060	A1927	G1811	U1728	G1613	A1515	G1437	G1332	U1231	U1113	C1053
U2194	G2134	A2061	A1928	A1812	C1729	A1614	A1522	U1438	G1333	G1232	C1114	A1054
G2198	A2135	A2062	G1929	G1813	U1730	A1615	U1523	A1439	U1336	G1236	G1115	G1055
A2199	G2136	C2069	G1930	G1814	C1731	A1616	U1524	U1440	A1337	G1237	G1116	G1056
U2202	U2137	A2070	A1936	C1816	C1732	G1627	G1527	G1441	G1338	G1238	C1117	U1057
U2203	A2138	A2071	A1937	A1819	G1733	A1635	A1528	C1447	G1341	A1241	U1118	U1058
G2204	U2139	U1939	A1938	U1820	G1734	U1635	G1529	G1452	G1342	U1242	A1126	G1059
C2208	G2140	U1940	U1939	U1827	A1735	C1639	G1530	A1453	U1346	U1244	A1127	U1060
G2209	U2141	G1945	G1945	A1828	U1736	G1645	G1531	C1454	C1350	A1247	A1129	U1061
U2210	A2142	U1955	U1955	A1829	G1737	U1646	A1532	U1458	G1351	G1248	U1132	G1062
A2211	C2143	C1958	C1958	C1837	U1741	U1647	C1533	G1459	U1352	U1249	A1133	G1063
U2212	G2144	A1965	A1965	A1847	U1742	A1651	U1534	U1460	A1353	G1250	A1134	C1064
U2213	C2145	C1966	C1966	A1848	G1743	A1652	A1535	C1461	A1359	G1251	C1135	U1065
G2216	G2146	C1967	C1967	A1853	A1744	G1653	G1537	U1467	A1365	U1252	U1139	U1066
U2220	A2147	A1970	A1970	A1857	C1748	A1665	G1538	U1468	U1368	A1253	G1140	A1067
A2225	U2148	G1980	G1980	A1858	G1753	G1666	U1539	A1469	G1368	A1254	U1141	G1068
C2226	C2150	A1981	A1981	A1859	U1756	U1667	G1540	A1470	U1374	U1255	U1142	A1069
A2227	U2151	U1982	U1982	G1860	U1757	A1676	U1541	G1477	G1374	G1257	A1143	A1070
U2233	G2152	G1982	G1982	G1861	U1758	A1677	C1542	G1475	A1378	A1262	C1153	G1071
G2234	C2153	U1991	U1991	G1867	A1762	U1680	A1552	U1481	A1382	A1265	C1167	C1072
U2238	U2155	C1992	C1992	C1868	G1763	U1681	A1553	U1476	U1379	G1266	G1168	A1073
G2239	G2156	U1993	U1993	G1869	C1764	U1683	U1554	G1482	G1386	U1271	A1169	G1074
U2243	U2157	C1996	C1996	A1870	A1773	G1684	U1559	G1483	A1387	U1272	C1170	C1075
G2246	G2158	C1997	C1997	A1871	G1776	U1688	G1568	U1484	U1392	G1288	U1174	A1077
A2247	C2160	A2009	A2009	A1872	U1779	C1694	A1569	U1486	U1396	U1294	A1175	A1080
U2249	U2161	G2012	G2012	U1882	A1780	A1700	U1576	U1487	G1407	G1295	G1177	U1081
G2250	G2162	A2013	A2013	U1883	U1781	G1710	C1577	C1488	G1408	G1296	C1178	U1082
G2251	A2163	U2016	U2016	G1884	U1782	A1711	U1578	C1489	U1409	G1300	G1179	U1084
U2258	C2164	G2027	G2027	U1888	A1783	U1712	A1579	A1490	G1410	A1301	U1180	A1085
G2262	U2165	U2022	U2022	G1888	U1784	U1713	A1580	C1493	U1411	C1306	U1181	A1086
A2266	G2167	C2023	C2023	A1889	A1785	U1714	A1581	A1494	U1412	G1311	G1187	G1087
A2270	U2168	G2027	G2027	A1890	U1786	G1715	C1582	A1495	A1413	G1311	U1188	A1088
U2273	A2169	A2031	A2031	A1901	A1787	U1716	U1583	A1496	C1414	C1315	A1189	A1089
G2279	C2170	G1903	G1903	C1902	G1790	A1717	U1584	U1497	U1415	U1316	G1190	A1090
U2282	U2171	G1906	G1906	U1901	A1791	G1718	C1585	G1501	G1416	A1205	A1206	G1091
A2286	A2172	A1912	A1912	U1892	C1795	U1718	A1586	A1502	G1417	G1207	C1207	C1092
U2287	C2173	A1913	A1913	U1893	U1796	U1718	G1587	A1503	G1418	C1211	G1212	U1093
A2290	G2174	U1913	U1913	G1894	U1797	U1718	U1588	A1504				U1094
U2293	C2175	U1913	U1913	U1895	U1798	U1718	U1589	A1505				A1095
G2298	A2176	U1913	U1913	U1896	U1799	U1718	A1590					A1096
U2299	C2177	U1913	U1913	U1897	U1799	U1718	A1591					U1097
A2300	U2178	U1913	U1913	U1898	U1799	U1718	A1592					A1098
U2301	G2179	U1913	U1913	U1899	U1799	U1718	A1593					G1099
A2302	U2180	U1913	U1913	U1900	U1799	U1718	A1594					C1100
U2303	U2181	U1913	U1913	U1901	U1799	U1718	A1595					U1101
A2304	C2182	U1913	U1913	U1902	U1799	U1718	A1596					G1102
U2305	G2183	U1913	U1913	U1903	U1799	U1718	A1597					A1103
A2306	U2184	U1913	U1913	U1904	U1799	U1718	A1598					C1104



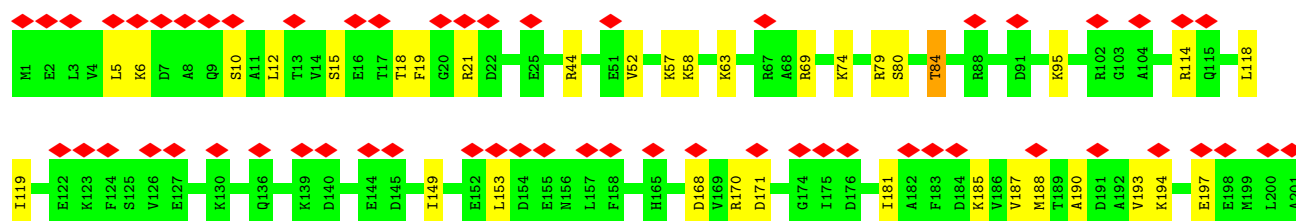
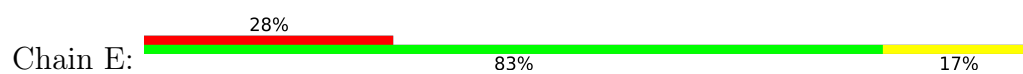
• Molecule 8: 50S ribosomal protein L2



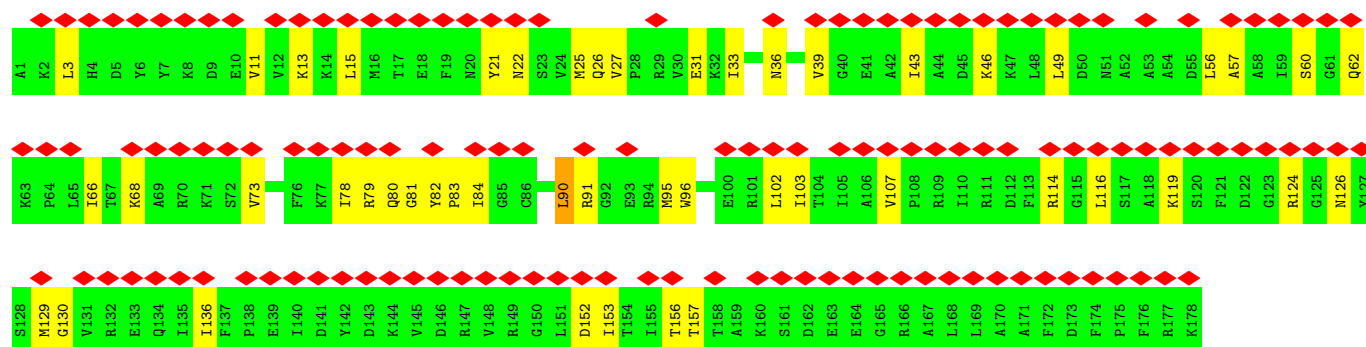
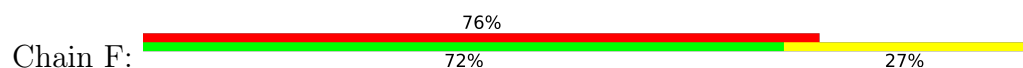
• Molecule 9: 50S ribosomal protein L3



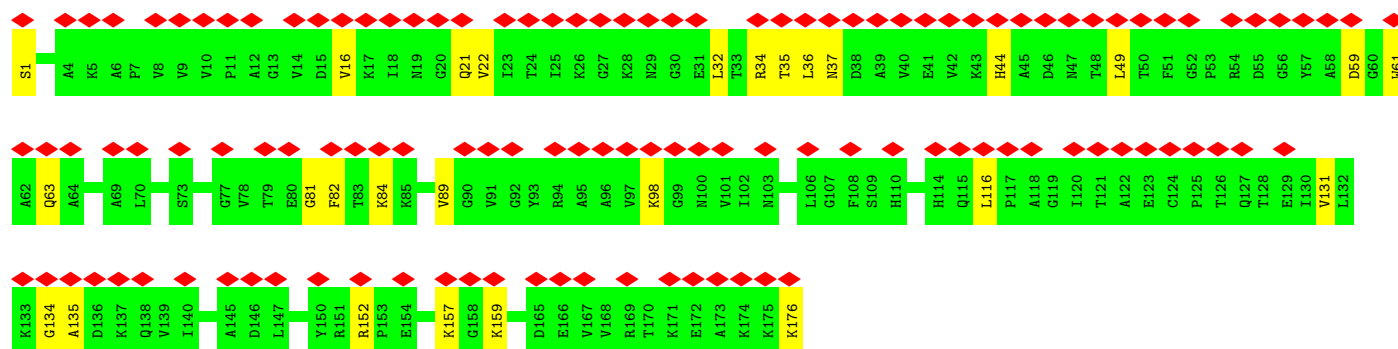
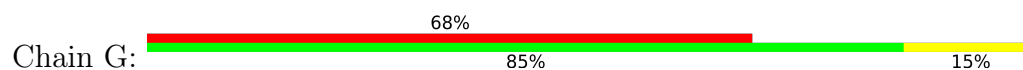
• Molecule 10: 50S ribosomal protein L4



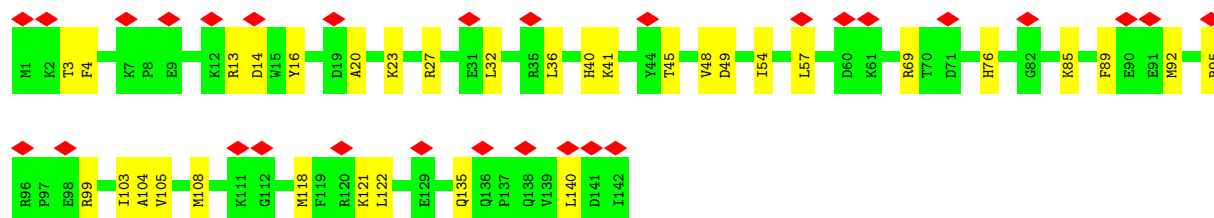
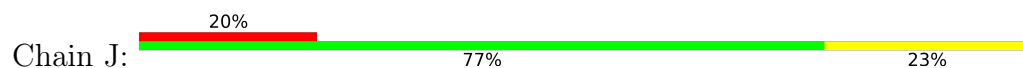
• Molecule 11: 50S ribosomal protein L5



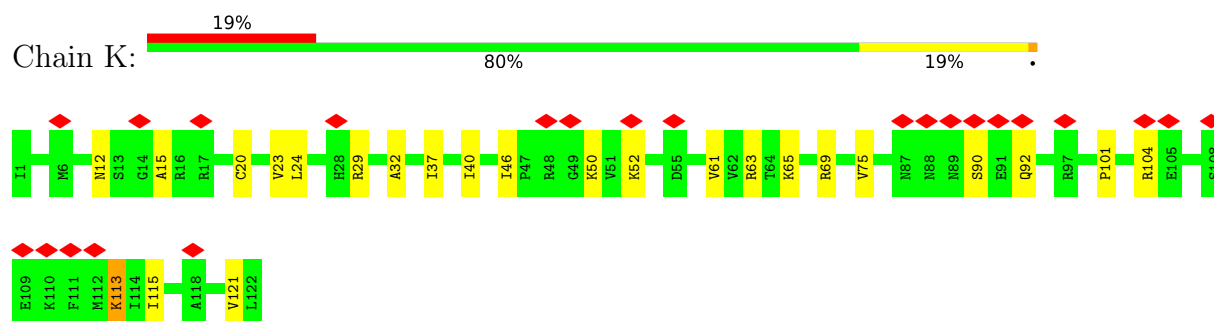
• Molecule 12: 50S ribosomal protein L6



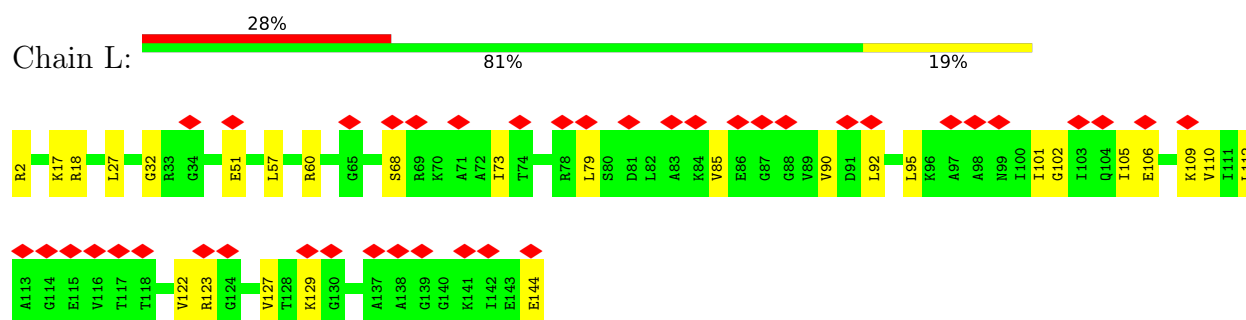
• Molecule 13: 50S ribosomal protein L13



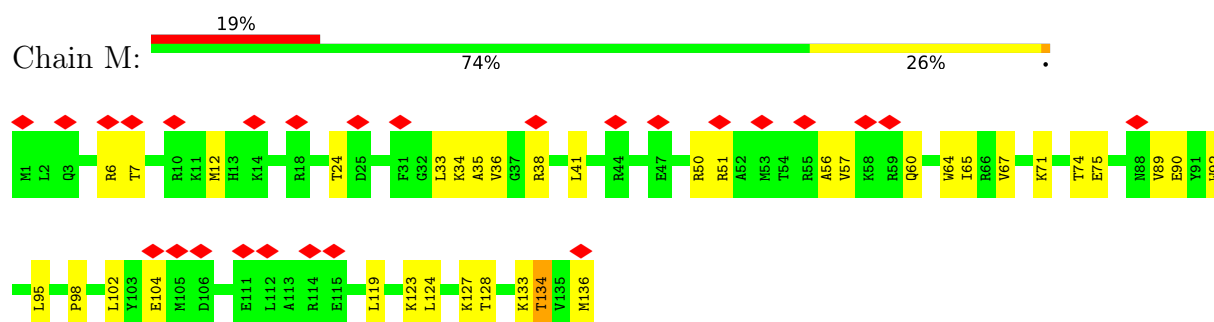
- Molecule 14: 50S ribosomal protein L14



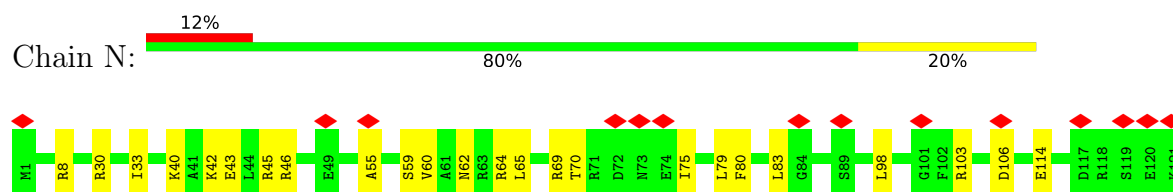
- Molecule 15: 50S ribosomal protein L15



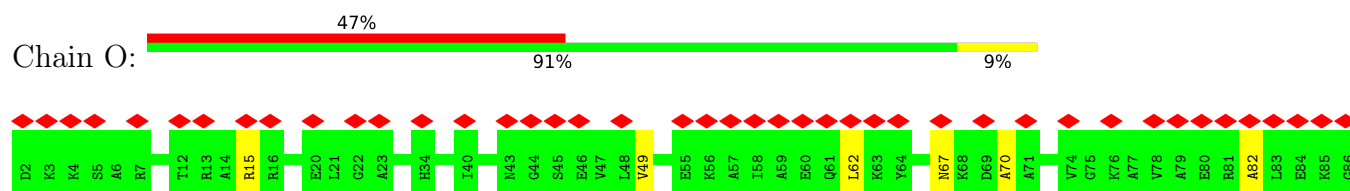
- Molecule 16: 50S ribosomal protein L16



- Molecule 17: 50S ribosomal protein L17

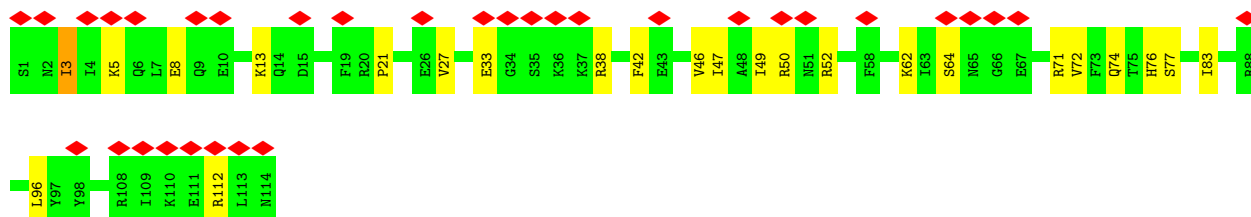
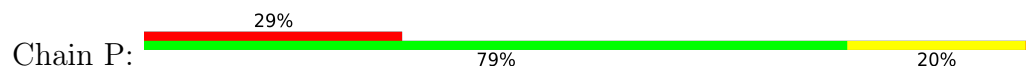


- Molecule 18: 50S ribosomal protein L18

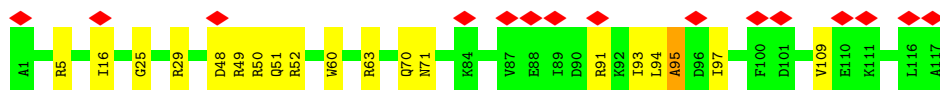
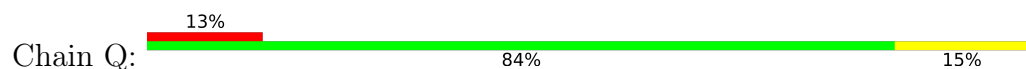




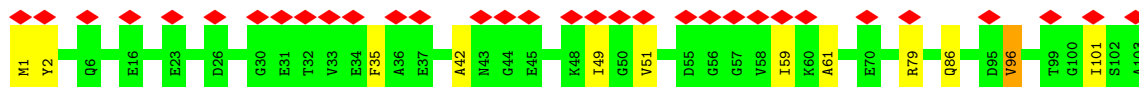
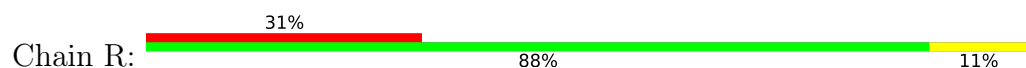
- Molecule 19: 50S ribosomal protein L19



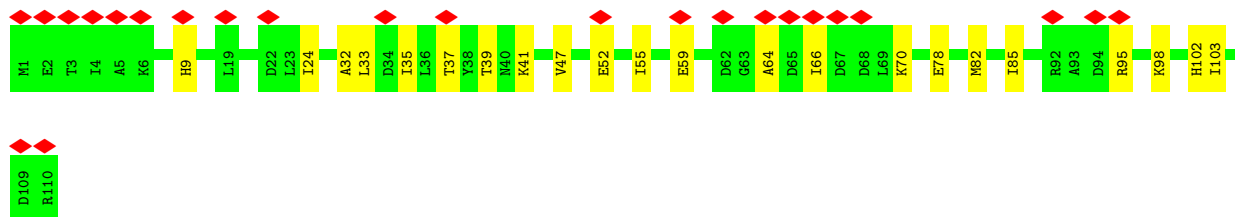
- Molecule 20: 50S ribosomal protein L20



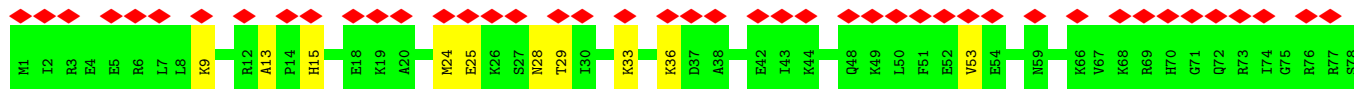
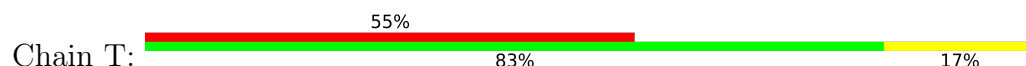
- Molecule 21: Ribosomal protein L21

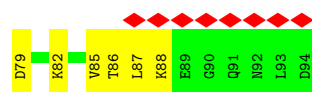


- Molecule 22: 50S ribosomal protein L22

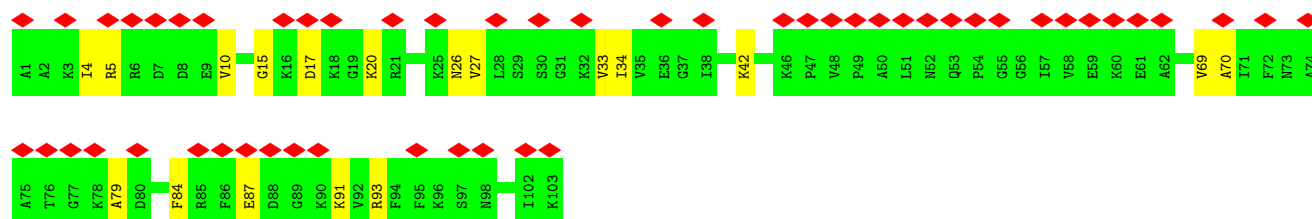
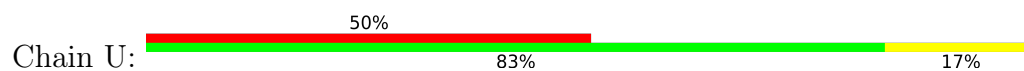


- Molecule 23: 50S ribosomal protein L23

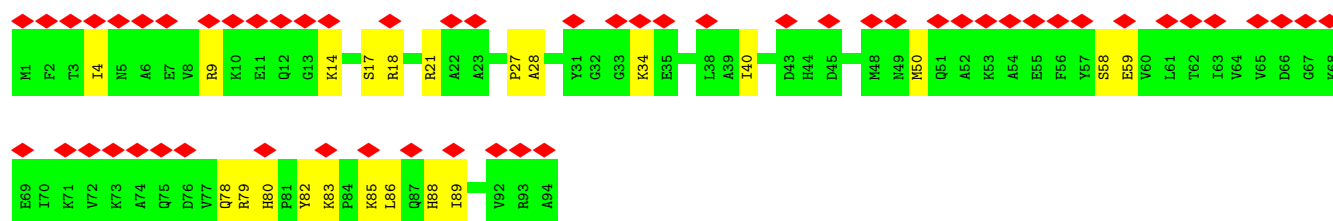
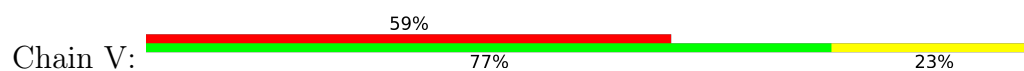




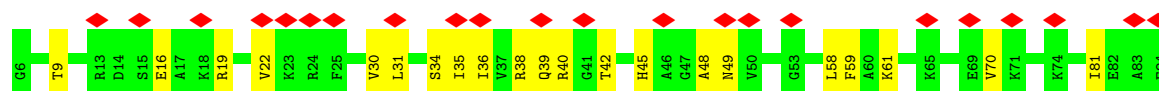
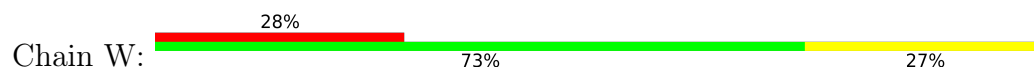
- Molecule 24: 50S ribosomal protein L24



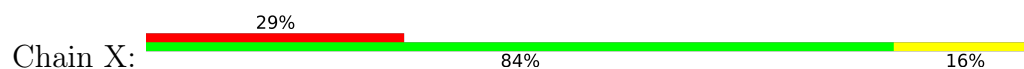
- Molecule 25: 50S ribosomal protein L25



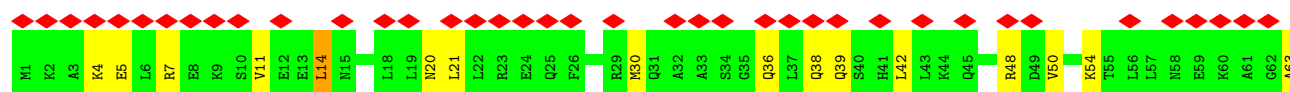
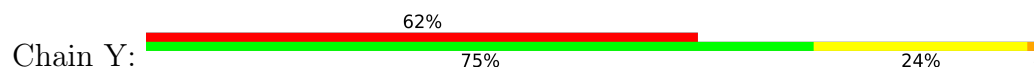
- Molecule 26: 50S ribosomal protein L27



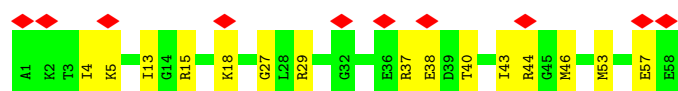
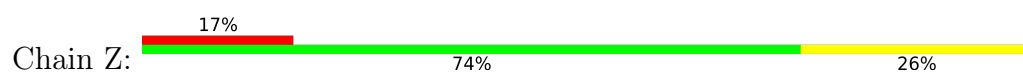
- Molecule 27: 50S ribosomal protein L28



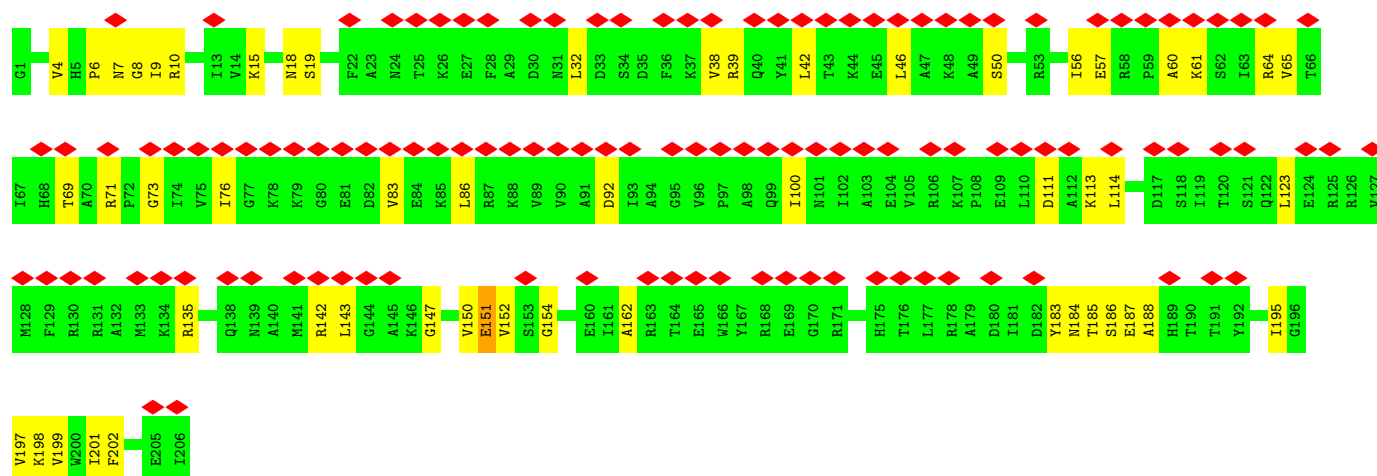
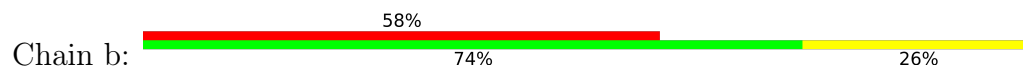
- Molecule 28: 50S ribosomal protein L29



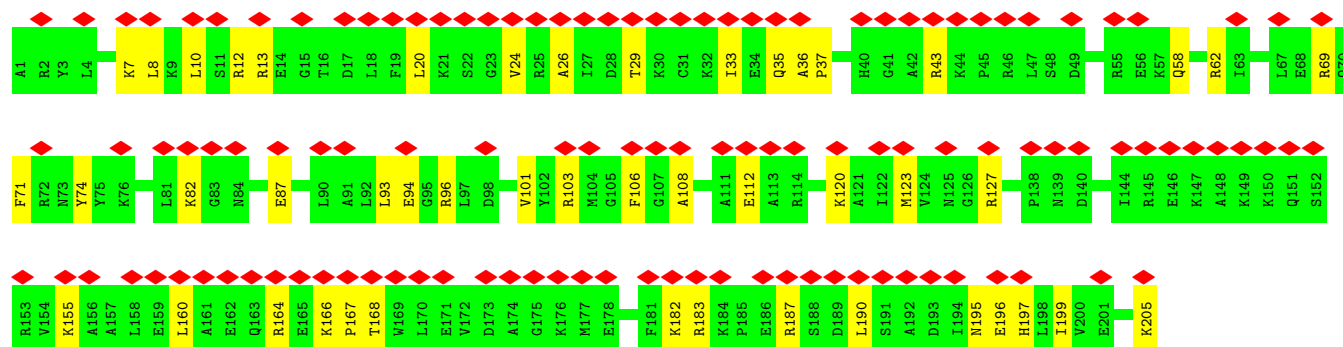
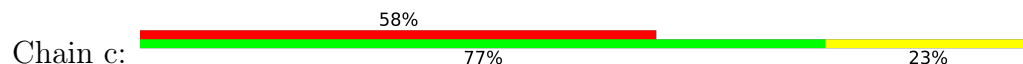
- Molecule 29: 50S ribosomal protein L30



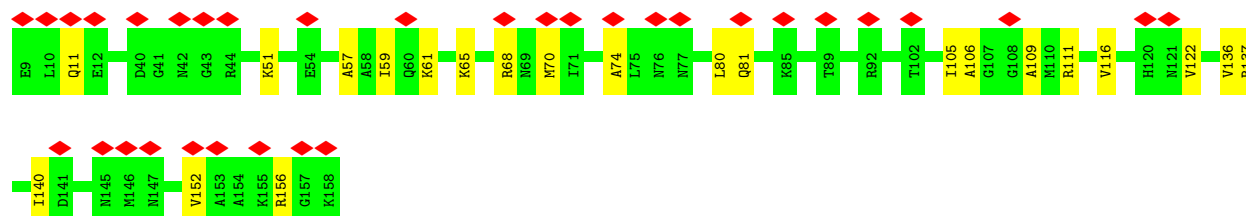
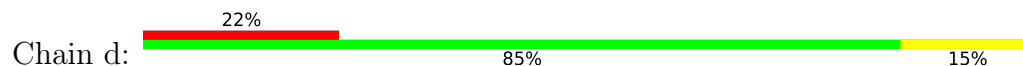
• Molecule 30: 30S ribosomal protein S3



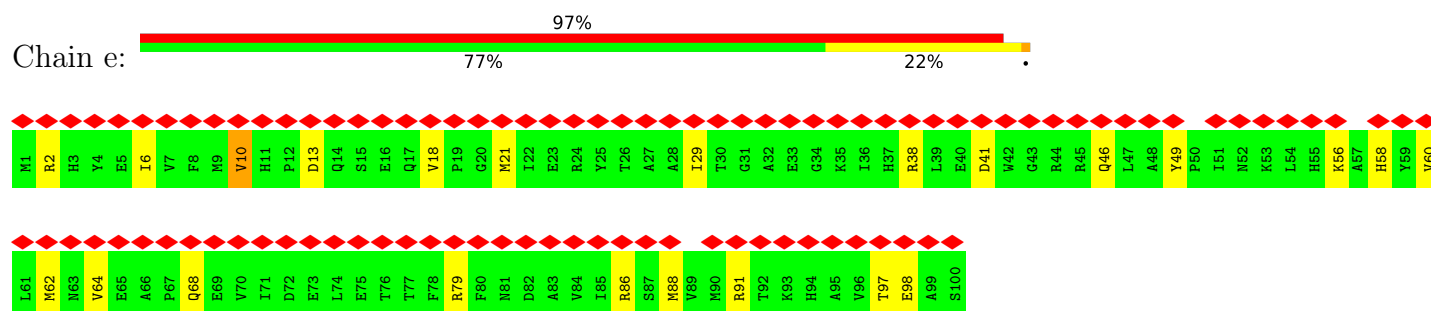
• Molecule 31: 30S ribosomal protein S4



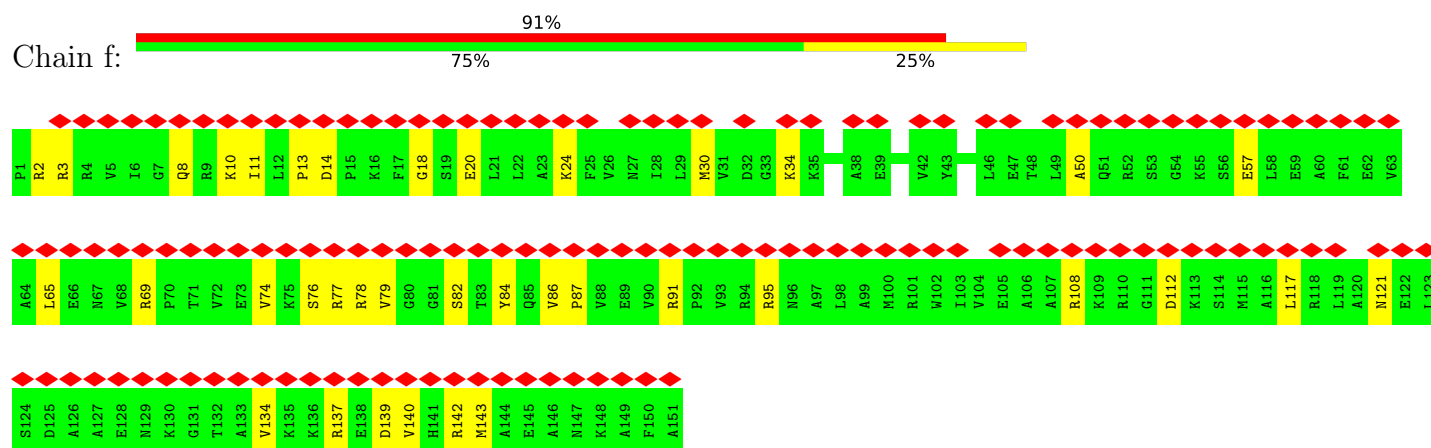
• Molecule 32: 30S ribosomal protein S5



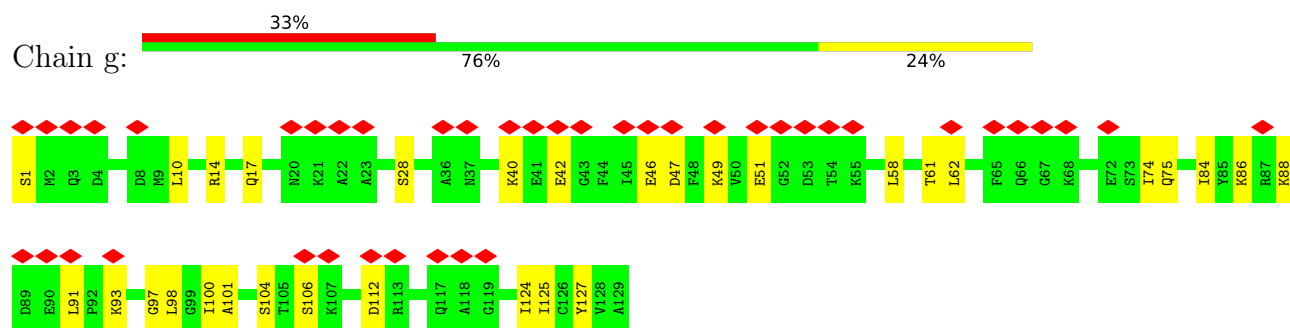
- Molecule 33: 30S ribosomal protein S6, non-modified isoform



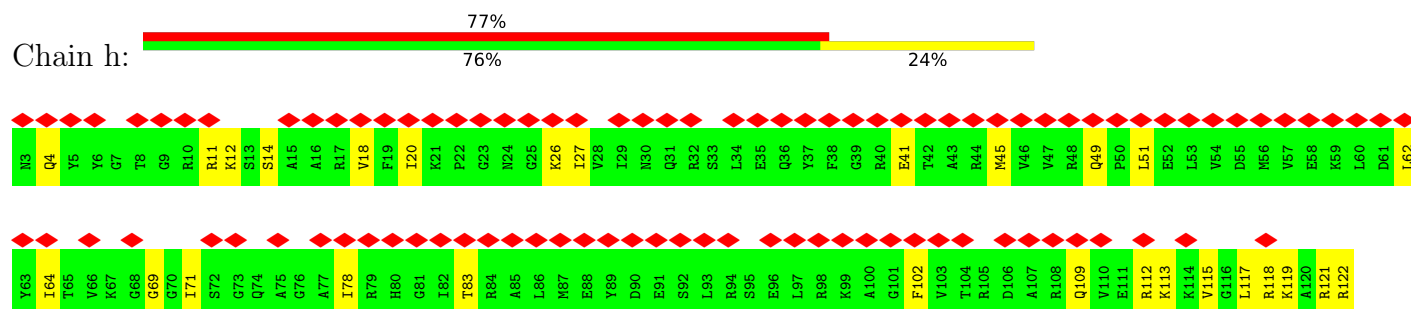
- Molecule 34: 30S ribosomal protein S7

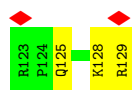


- Molecule 35: 30S ribosomal protein S8

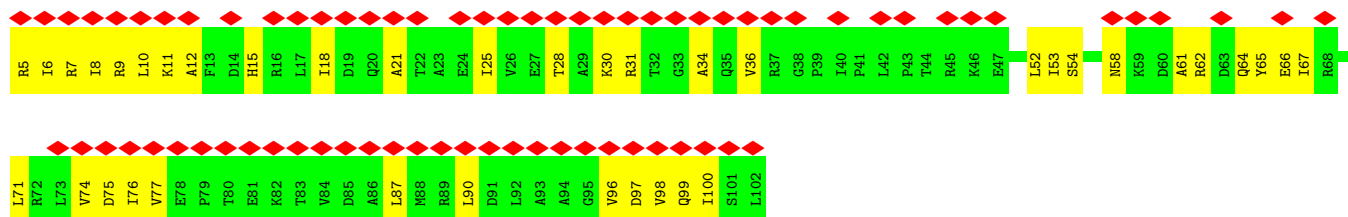
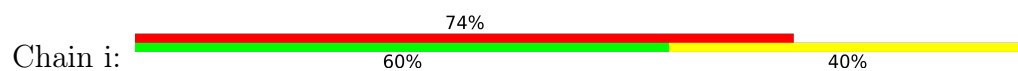


- Molecule 36: 30S ribosomal protein S9

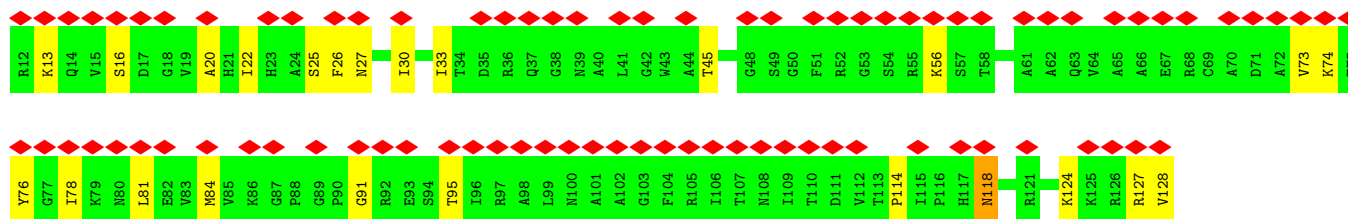
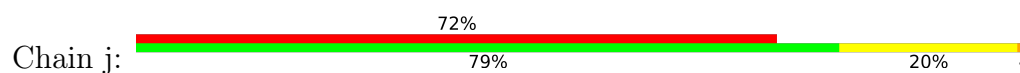




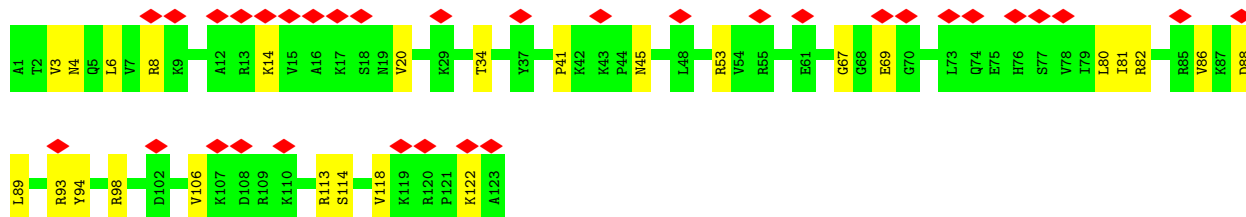
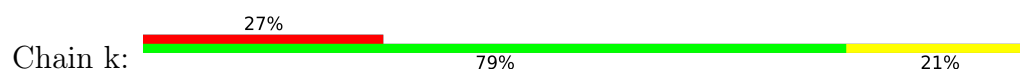
- Molecule 37: 30S ribosomal protein S10



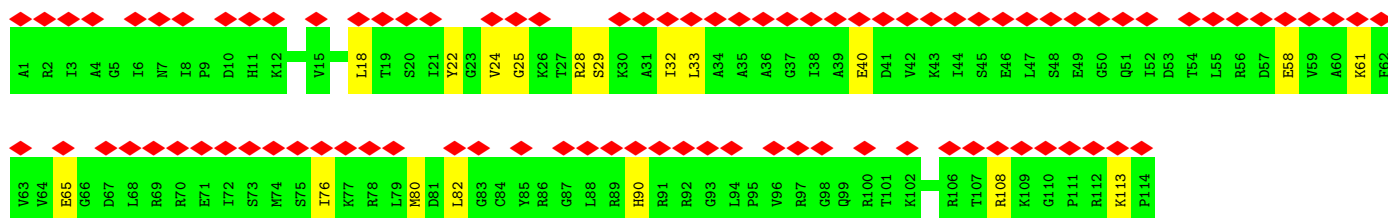
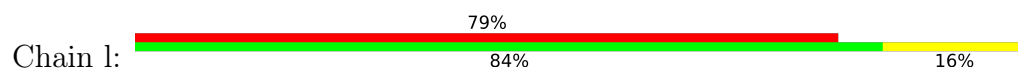
- Molecule 38: 30S ribosomal protein S11



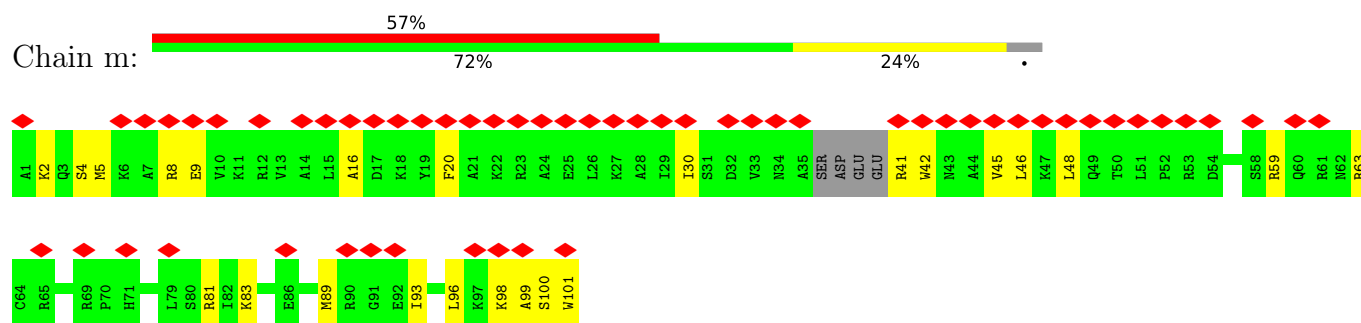
- Molecule 39: 30S ribosomal protein S12



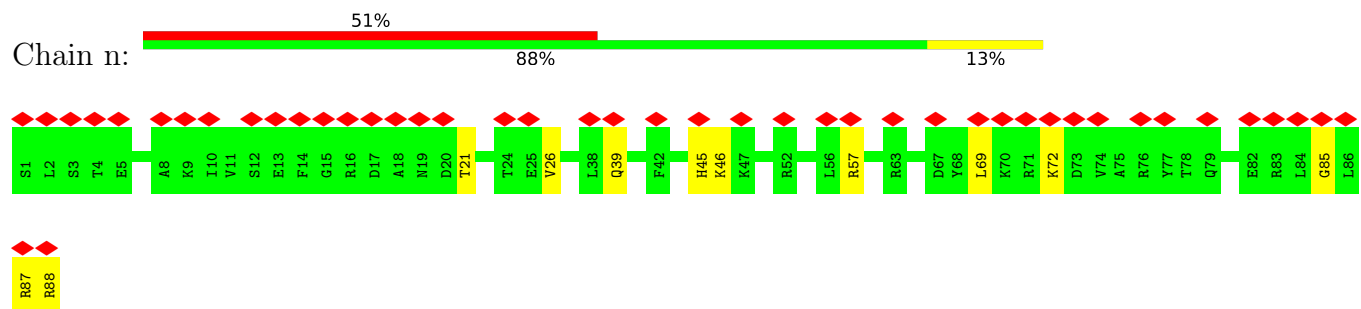
- Molecule 40: 30S ribosomal protein S13



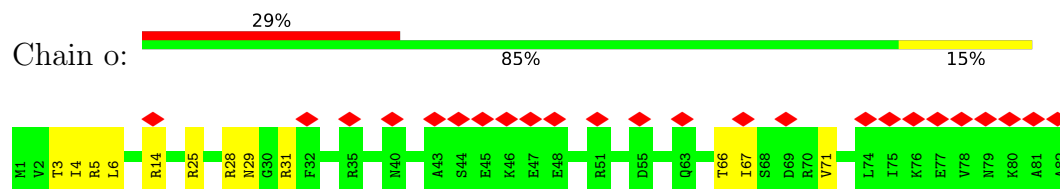
- Molecule 41: 30S ribosomal protein S14



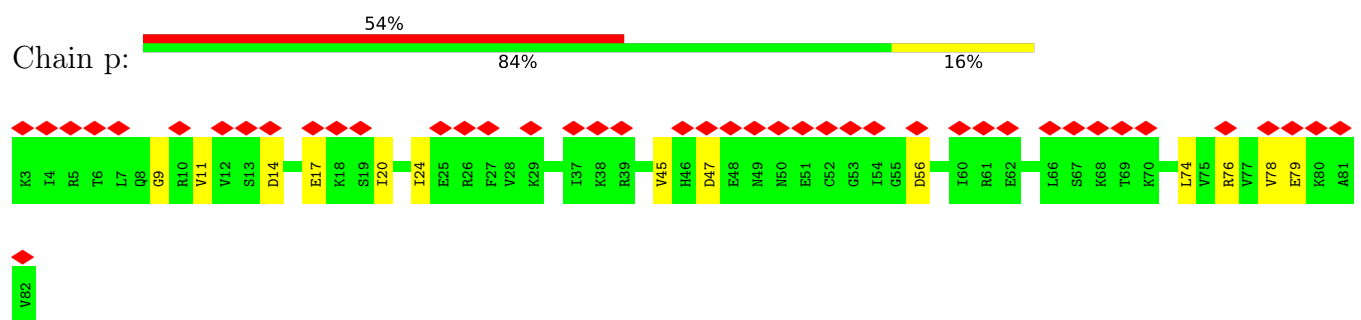
- Molecule 42: 30S ribosomal protein S15



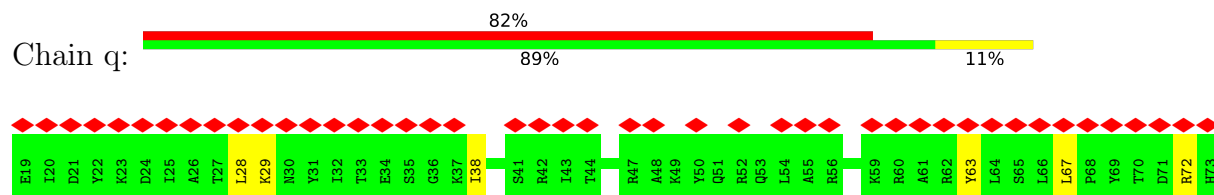
- Molecule 43: 30S ribosomal protein S16



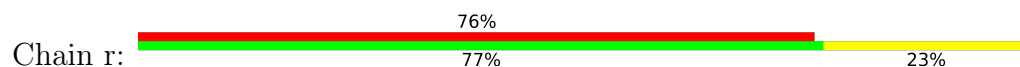
- Molecule 44: 30S ribosomal protein S17

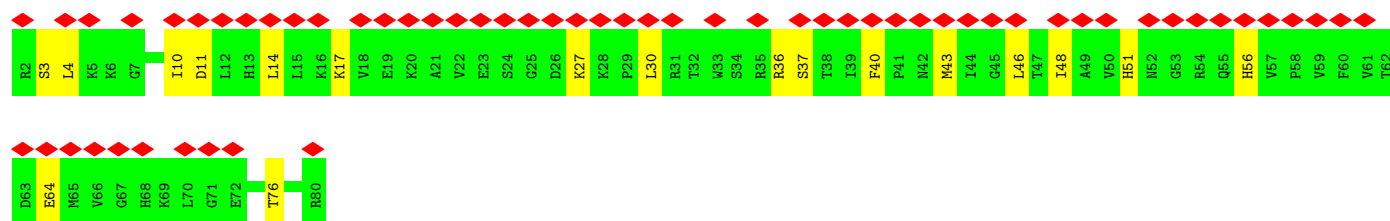


- Molecule 45: 30S ribosomal protein S18

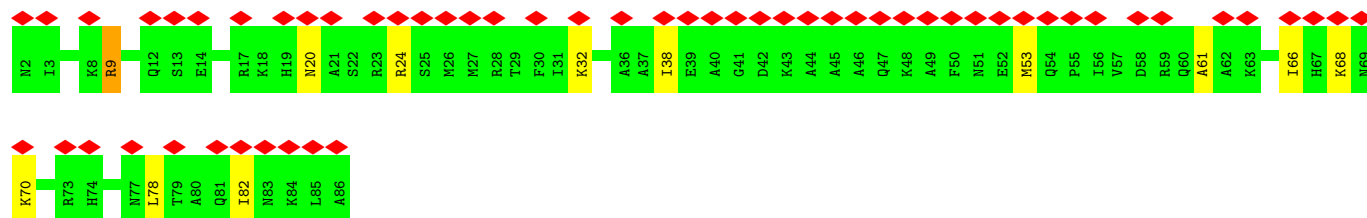
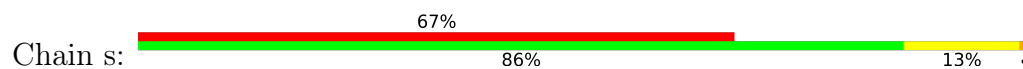


- Molecule 46: 30S ribosomal protein S19

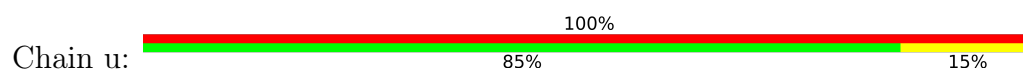




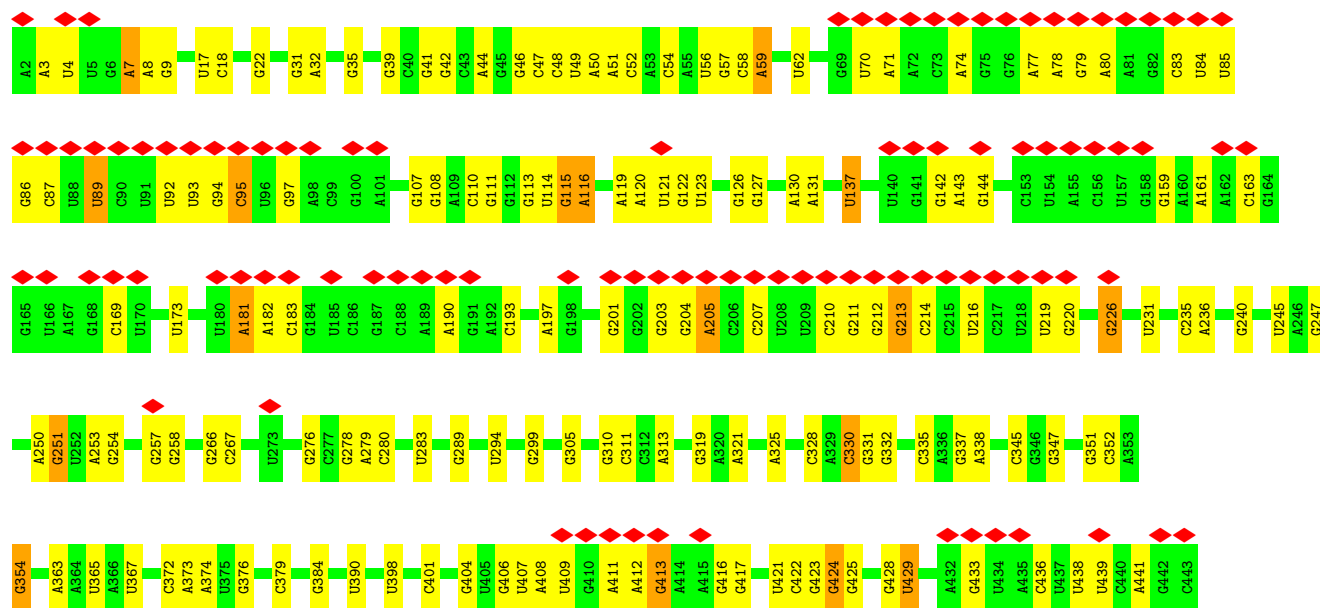
• Molecule 47: 30S ribosomal protein S20

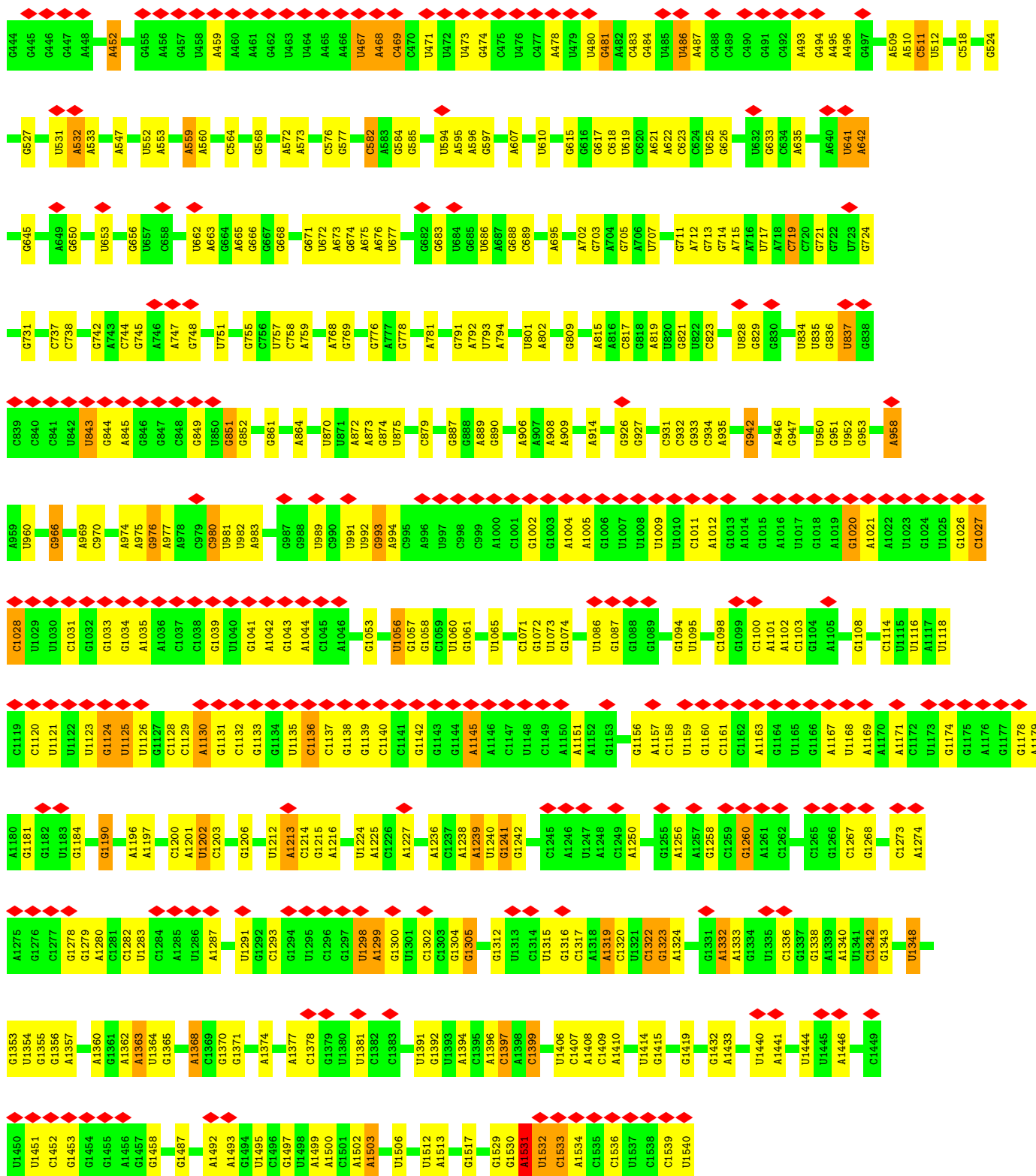


• Molecule 48: Transcription termination/antitermination protein NusG



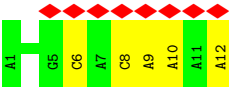
• Molecule 49: 16S



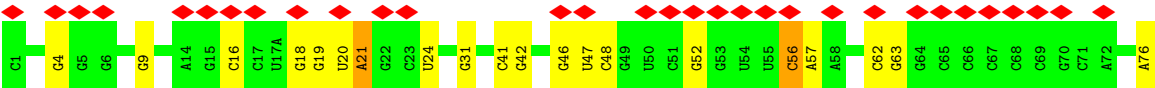


• Molecule 50: lmrRNA





• Molecule 51: tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	96000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.327	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.255	Depositor
Map size ($\text{\AA}$)	332.0, 332.0, 332.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.40	0/450	0.66	0/599
2	1	0.33	0/417	0.55	0/556
3	2	0.46	0/380	0.50	0/498
4	3	0.44	0/513	0.73	0/676
5	4	0.36	0/303	0.66	0/397
6	A	0.36	0/2800	0.41	0/4367
7	B	0.49	0/69796	0.44	3/108888 (0.0%)
8	C	0.71	4/2122 (0.2%)	1.05	5/2854 (0.2%)
9	D	0.45	0/1586	0.72	0/2134
10	E	0.38	0/1571	0.63	0/2113
11	F	0.31	0/1444	0.68	0/1937
12	G	0.27	0/1343	0.58	0/1816
13	J	0.40	0/1152	0.65	0/1551
14	K	0.43	0/940	0.70	0/1260
15	L	0.40	0/1054	0.62	0/1403
16	M	0.36	0/1093	0.58	0/1460
17	N	0.42	0/974	0.62	0/1303
18	O	0.30	0/902	0.54	0/1209
19	P	0.36	0/929	0.64	0/1242
20	Q	0.43	0/960	0.55	0/1278
21	R	0.37	0/829	0.60	0/1107
22	S	0.43	0/864	0.63	0/1156
23	T	0.29	0/745	0.64	0/996
24	U	0.32	0/788	0.68	0/1053
25	V	0.26	0/766	0.53	0/1025
26	W	0.40	0/603	0.80	0/797
27	X	0.33	0/635	0.55	0/848
28	Y	0.29	0/510	0.74	3/677 (0.4%)
29	Z	0.36	0/453	0.52	0/605
30	b	0.32	0/1652	0.63	0/2225
31	c	0.31	0/1665	0.64	0/2227
32	d	0.39	0/1119	0.71	1/1504 (0.1%)
33	e	0.21	0/836	0.56	0/1128
34	f	0.21	0/1196	0.55	0/1602

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.32	0/989	0.60	0/1326
36	h	0.27	0/1034	0.61	0/1375
37	i	0.29	0/797	0.61	0/1077
38	j	0.26	0/893	0.53	0/1205
39	k	0.39	0/969	0.65	0/1300
40	l	0.24	0/893	0.52	0/1193
41	m	0.32	0/785	0.56	0/1043
42	n	0.27	0/722	0.52	0/964
43	o	0.33	0/659	0.58	0/884
44	p	0.29	0/658	0.67	0/881
45	q	0.20	0/463	0.48	0/621
46	r	0.26	0/653	0.59	0/877
47	s	0.28	0/671	0.58	0/888
48	u	0.26	0/477	0.60	0/642
49	v	0.42	1/36963 (0.0%)	0.43	4/57662 (0.0%)
50	x	0.26	0/289	0.32	0/449
51	5	0.31	0/1832	0.36	0/2855
All	All	0.44	5/153137 (0.0%)	0.50	16/229733 (0.0%)

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
1	0	0	2
8	C	0	1
11	F	0	2
17	N	0	1
20	Q	0	1
30	b	0	1
38	j	0	1
All	All	0	9

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	84	PRO	CG-CD	-21.37	0.78	1.50
49	v	1531	A	O3'-P	14.57	1.83	1.61
8	C	84	PRO	CA-CB	-8.08	1.42	1.53
8	C	84	PRO	CB-CG	7.77	1.88	1.49
8	C	84	PRO	N-CA	5.33	1.54	1.47

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	84	PRO	N-CD-CG	-30.08	58.09	103.20
8	C	84	PRO	CA-CB-CG	-21.38	63.88	104.50
8	C	84	PRO	N-CA-CB	-17.03	85.37	103.25
49	v	1531	A	O3'-P-O5'	-16.68	78.97	104.00
8	C	84	PRO	CA-N-CD	-10.96	96.65	112.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	47	TYR	Peptide
1	0	49	ARG	Sidechain
8	C	155	ARG	Sidechain
11	F	80	GLN	Peptide
11	F	90	LEU	Peptide

5.2 Too-close contacts [i](#)

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	7	0
2	1	410	0	440	4	0
3	2	377	0	418	4	0
4	3	504	0	574	3	0
5	4	302	0	343	6	0
6	A	2504	0	1271	15	0
7	B	62317	0	31345	323	0
8	C	2083	0	2157	37	0
9	D	1565	0	1616	28	0
10	E	1552	0	1619	24	0
11	F	1420	0	1460	33	0
12	G	1323	0	1374	17	0
13	J	1129	0	1162	26	0
14	K	931	0	1003	15	0
15	L	1045	0	1117	19	0
16	M	1074	0	1157	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	N	961	0	1000	14	0
18	O	892	0	923	6	0
19	P	917	0	965	15	0
20	Q	947	0	1022	15	0
21	R	816	0	839	9	0
22	S	857	0	922	14	0
23	T	739	0	807	11	0
24	U	780	0	834	12	0
25	V	753	0	780	15	0
26	W	596	0	610	16	0
27	X	625	0	655	11	0
28	Y	509	0	543	11	0
29	Z	449	0	491	10	0
30	b	1625	0	1699	35	0
31	c	1643	0	1710	33	0
32	d	1106	0	1148	13	0
33	e	818	0	808	18	0
34	f	1182	0	1240	27	0
35	g	979	0	1034	23	0
36	h	1022	0	1070	22	0
37	i	787	0	828	33	0
38	j	877	0	887	15	0
39	k	955	0	1019	15	0
40	l	884	0	944	12	0
41	m	774	0	827	22	0
42	n	714	0	737	9	0
43	o	649	0	666	10	0
44	p	649	0	691	7	0
45	q	456	0	478	6	0
46	r	638	0	665	13	0
47	s	665	0	714	11	0
48	u	468	0	458	9	0
49	v	33012	0	16618	204	0
50	x	257	0	133	0	0
51	5	1640	0	837	7	0
All	All	140621	0	93119	1097	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 5.

The worst 5 of 1097 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)
7:B:1724:G:H1	7:B:1736:U:H3	1.10	0.96
7:B:2114:A:N7	7:B:2167:U:O2	2.03	0.90
7:B:1311:G:H21	7:B:1603:A:H62	1.19	0.86
7:B:1311:G:N2	7:B:1603:A:H62	1.76	0.84
49:v:137:U:H3	49:v:226:G:H1	1.26	0.82

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%)	51 (94%)	3 (6%)	0	100	100
2	1	49/51 (96%)	49 (100%)	0	0	100	100
3	2	44/46 (96%)	44 (100%)	0	0	100	100
4	3	62/64 (97%)	57 (92%)	5 (8%)	0	100	100
5	4	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
8	C	270/272 (99%)	261 (97%)	9 (3%)	0	100	100
9	D	207/209 (99%)	193 (93%)	14 (7%)	0	100	100
10	E	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
11	F	176/178 (99%)	160 (91%)	16 (9%)	0	100	100
12	G	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
13	J	140/142 (99%)	127 (91%)	13 (9%)	0	100	100
14	K	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
15	L	141/143 (99%)	135 (96%)	6 (4%)	0	100	100
16	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
17	N	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
18	O	114/116 (98%)	113 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	P	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
20	Q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
21	R	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
22	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
23	T	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
24	U	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
25	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
26	W	77/79 (98%)	66 (86%)	11 (14%)	0	100	100
27	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
28	Y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
29	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	b	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
31	c	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
32	d	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
33	e	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
34	f	149/151 (99%)	148 (99%)	1 (1%)	0	100	100
35	g	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
36	h	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
37	i	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
38	j	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
39	k	121/123 (98%)	112 (93%)	9 (7%)	0	100	100
40	l	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
41	m	92/100 (92%)	91 (99%)	1 (1%)	0	100	100
42	n	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
43	o	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
44	p	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
45	q	53/55 (96%)	53 (100%)	0	0	100	100
46	r	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
47	s	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
48	u	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
All	All	5133/5231 (98%)	4916 (96%)	217 (4%)	0	100	100

There are no Ramachandran outliers to report.

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%)	47 (100%)	0	100	100
2	1	45/46 (98%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/51 (100%)	50 (98%)	1 (2%)	48	68
5	4	34/34 (100%)	33 (97%)	1 (3%)	37	62
8	C	216/217 (100%)	212 (98%)	4 (2%)	50	68
9	D	164/164 (100%)	162 (99%)	2 (1%)	63	75
10	E	165/165 (100%)	163 (99%)	2 (1%)	63	75
11	F	149/149 (100%)	146 (98%)	3 (2%)	48	68
12	G	137/137 (100%)	136 (99%)	1 (1%)	76	80
13	J	116/116 (100%)	116 (100%)	0	100	100
14	K	102/103 (99%)	98 (96%)	4 (4%)	28	56
15	L	102/102 (100%)	102 (100%)	0	100	100
16	M	109/109 (100%)	107 (98%)	2 (2%)	51	70
17	N	100/101 (99%)	100 (100%)	0	100	100
18	O	86/86 (100%)	86 (100%)	0	100	100
19	P	99/99 (100%)	98 (99%)	1 (1%)	68	76
20	Q	89/89 (100%)	89 (100%)	0	100	100
21	R	84/84 (100%)	82 (98%)	2 (2%)	43	65
22	S	93/93 (100%)	93 (100%)	0	100	100
23	T	80/81 (99%)	78 (98%)	2 (2%)	42	64
24	U	83/84 (99%)	83 (100%)	0	100	100
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	59/59 (100%)	57 (97%)	2 (3%)	32	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	X	67/67 (100%)	67 (100%)	0	100	100
28	Y	55/55 (100%)	54 (98%)	1 (2%)	51	70
29	Z	48/48 (100%)	48 (100%)	0	100	100
30	b	170/170 (100%)	166 (98%)	4 (2%)	43	65
31	c	172/172 (100%)	171 (99%)	1 (1%)	78	81
32	d	113/113 (100%)	113 (100%)	0	100	100
33	e	87/87 (100%)	86 (99%)	1 (1%)	65	76
34	f	124/124 (100%)	124 (100%)	0	100	100
35	g	104/104 (100%)	104 (100%)	0	100	100
36	h	105/105 (100%)	104 (99%)	1 (1%)	68	76
37	i	86/86 (100%)	86 (100%)	0	100	100
38	j	90/90 (100%)	89 (99%)	1 (1%)	65	76
39	k	103/103 (100%)	101 (98%)	2 (2%)	50	68
40	l	92/92 (100%)	92 (100%)	0	100	100
41	m	79/83 (95%)	79 (100%)	0	100	100
42	n	76/76 (100%)	76 (100%)	0	100	100
43	o	65/65 (100%)	65 (100%)	0	100	100
44	p	74/74 (100%)	73 (99%)	1 (1%)	59	73
45	q	48/48 (100%)	48 (100%)	0	100	100
46	r	70/70 (100%)	69 (99%)	1 (1%)	59	73
47	s	65/65 (100%)	64 (98%)	1 (2%)	57	72
48	u	52/52 (100%)	52 (100%)	0	100	100
All	All	4271/4281 (100%)	4230 (99%)	41 (1%)	65	76

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	b	92	ASP
38	j	76	TYR
30	b	151	GLU
31	c	123	MET
39	k	81	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
33	e	14	GLN
41	m	3	GLN
33	e	63	ASN
35	g	75	GLN
43	o	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	v	1538/1539 (99%)	356 (23%)	0
50	x	11/12 (91%)	5 (45%)	0
51	5	76/77 (98%)	14 (18%)	0
6	A	116/117 (99%)	26 (22%)	1 (0%)
7	B	2902/2903 (99%)	637 (21%)	8 (0%)
All	All	4643/4648 (99%)	1038 (22%)	9 (0%)

5 of 1038 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	13	G
6	A	14	U
6	A	16	G
6	A	21	G
6	A	25	U

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	B	2756	U
7	B	2808	G
7	B	669	G
7	B	670	A
7	B	827	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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
49	v	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	1531:A	O3'	1532:U	P	1.83

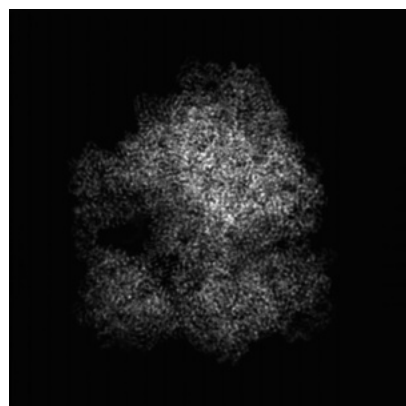
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41050. These allow visual inspection of the internal detail of the map and identification of artifacts.

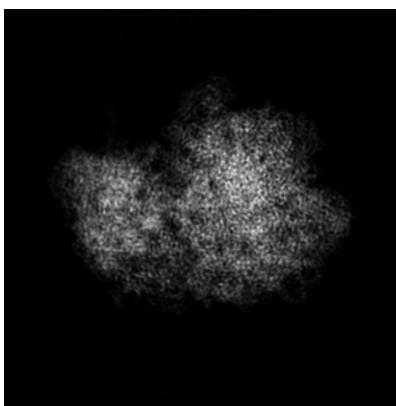
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

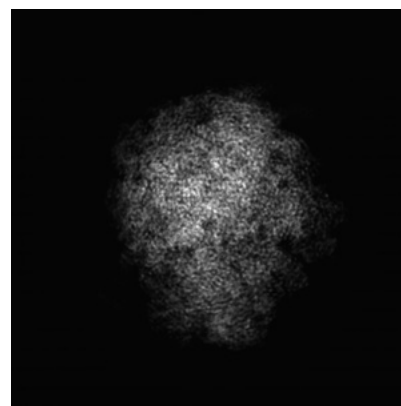
6.1.1 Primary map



X

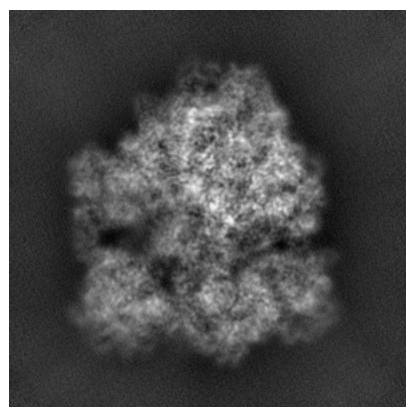


Y

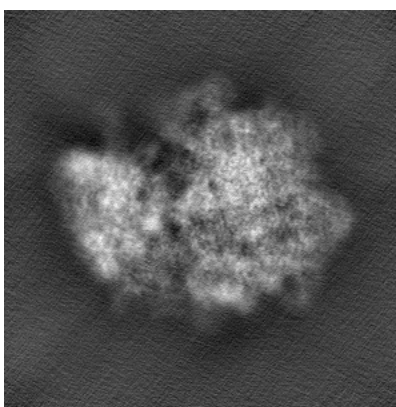


Z

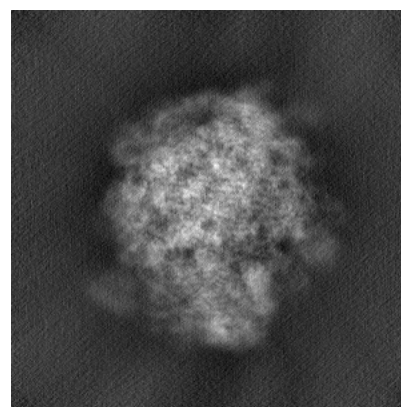
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 200

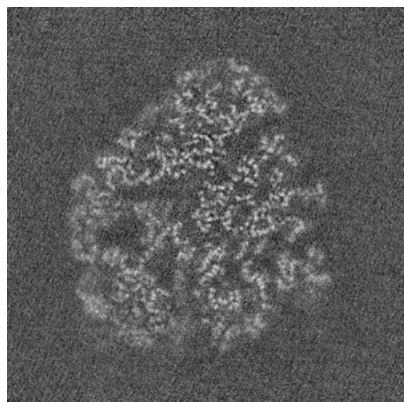


Y Index: 200

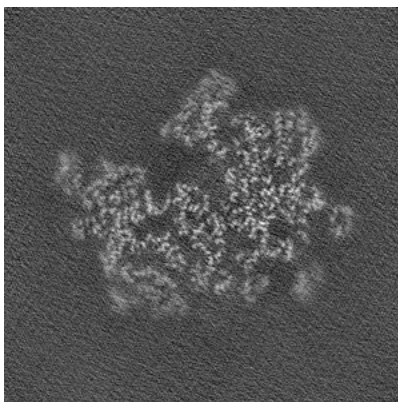


Z Index: 200

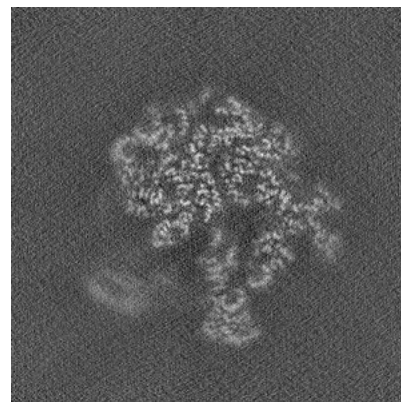
6.2.2 Raw map



X Index: 200



Y Index: 200



Z Index: 200

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

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 204

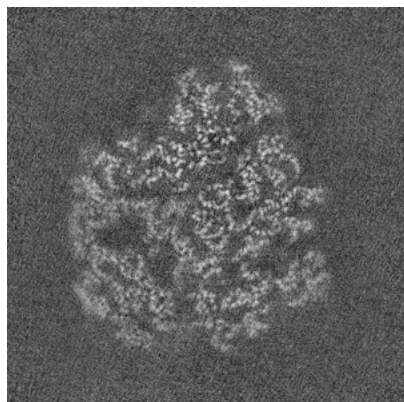


Y Index: 204

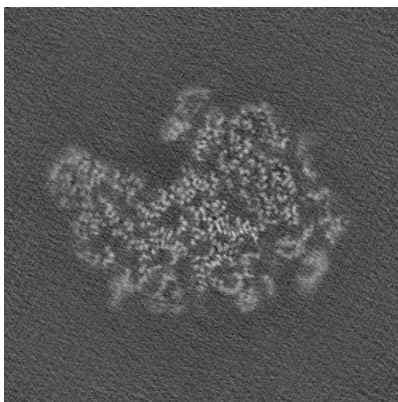


Z Index: 230

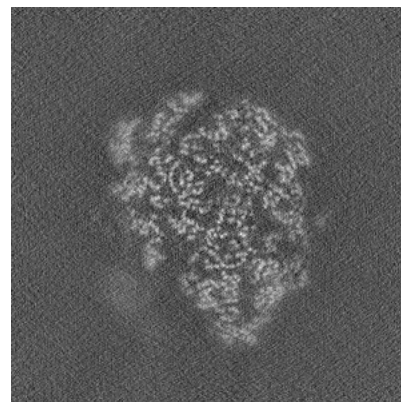
6.3.2 Raw map



X Index: 204



Y Index: 214

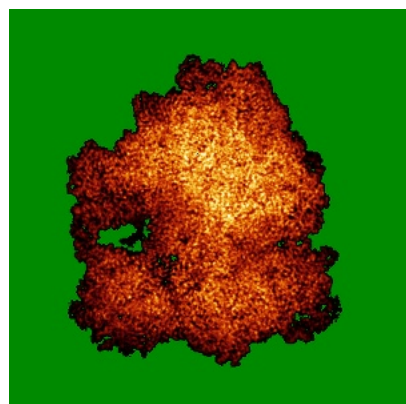


Z Index: 234

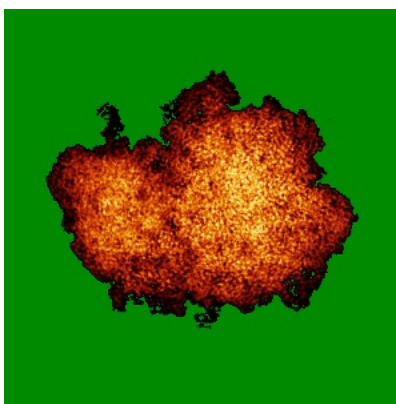
The images above show the largest variance slices of the map in three orthogonal directions.

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

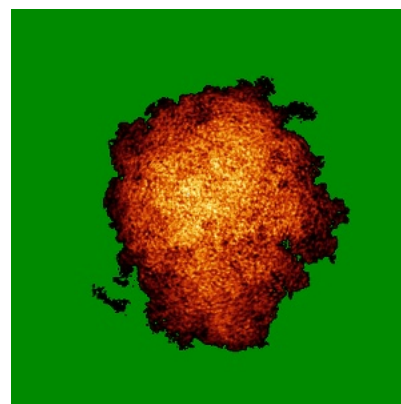
6.4.1 Primary map



X

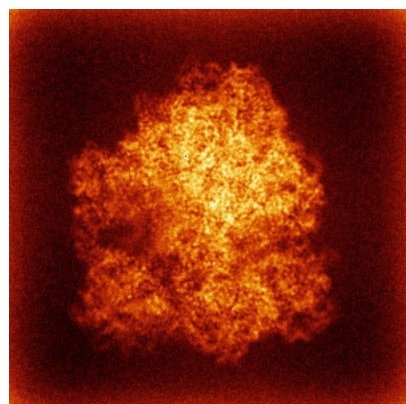


Y

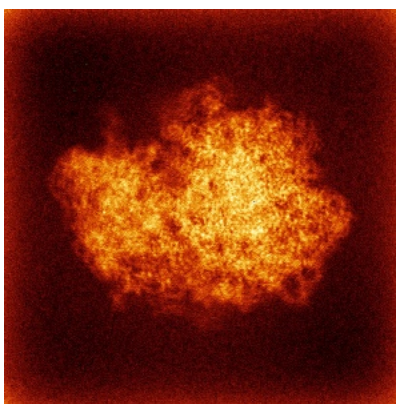


Z

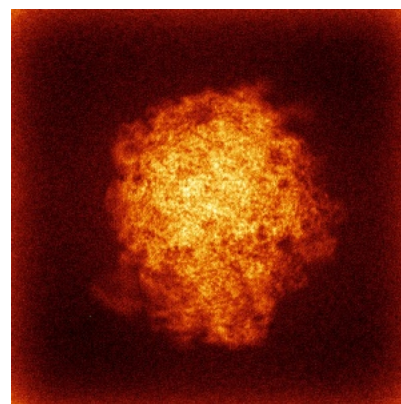
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

This section was not generated.

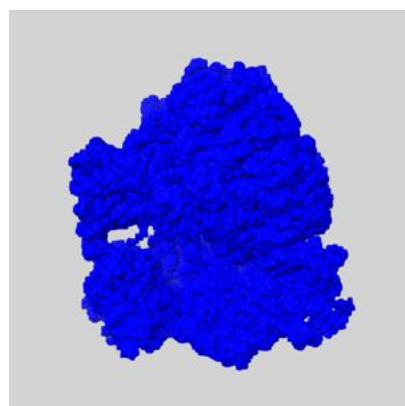
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

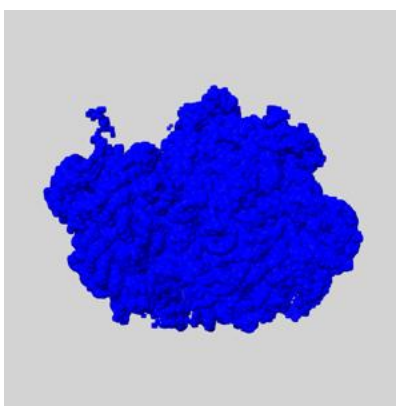
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

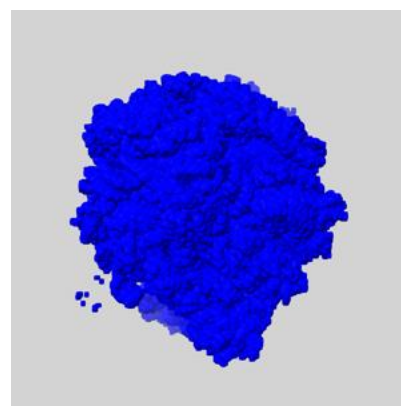
6.6.1 emd_41050_msk_1.map [i](#)



X



Y

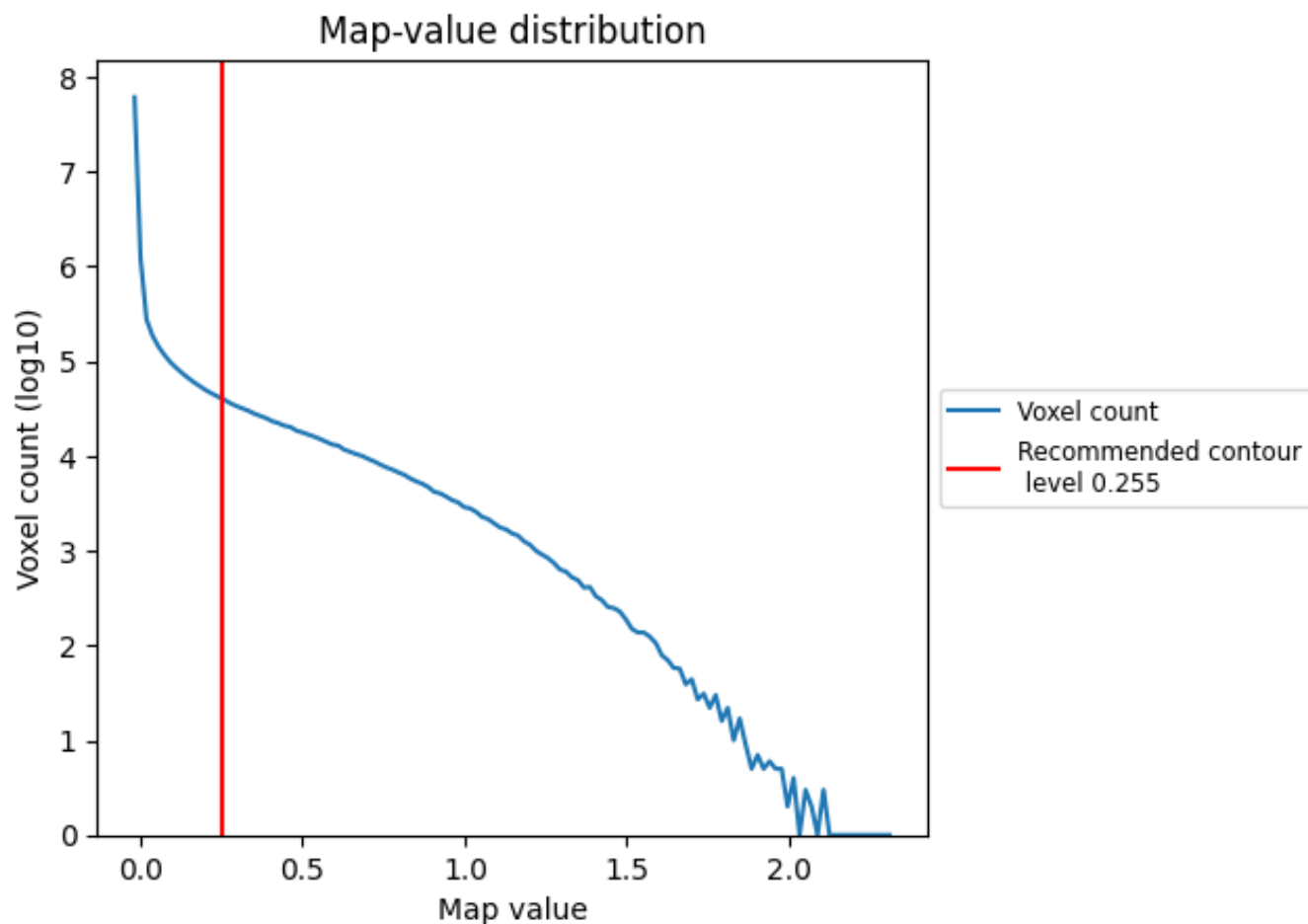


Z

7 Map analysis [i](#)

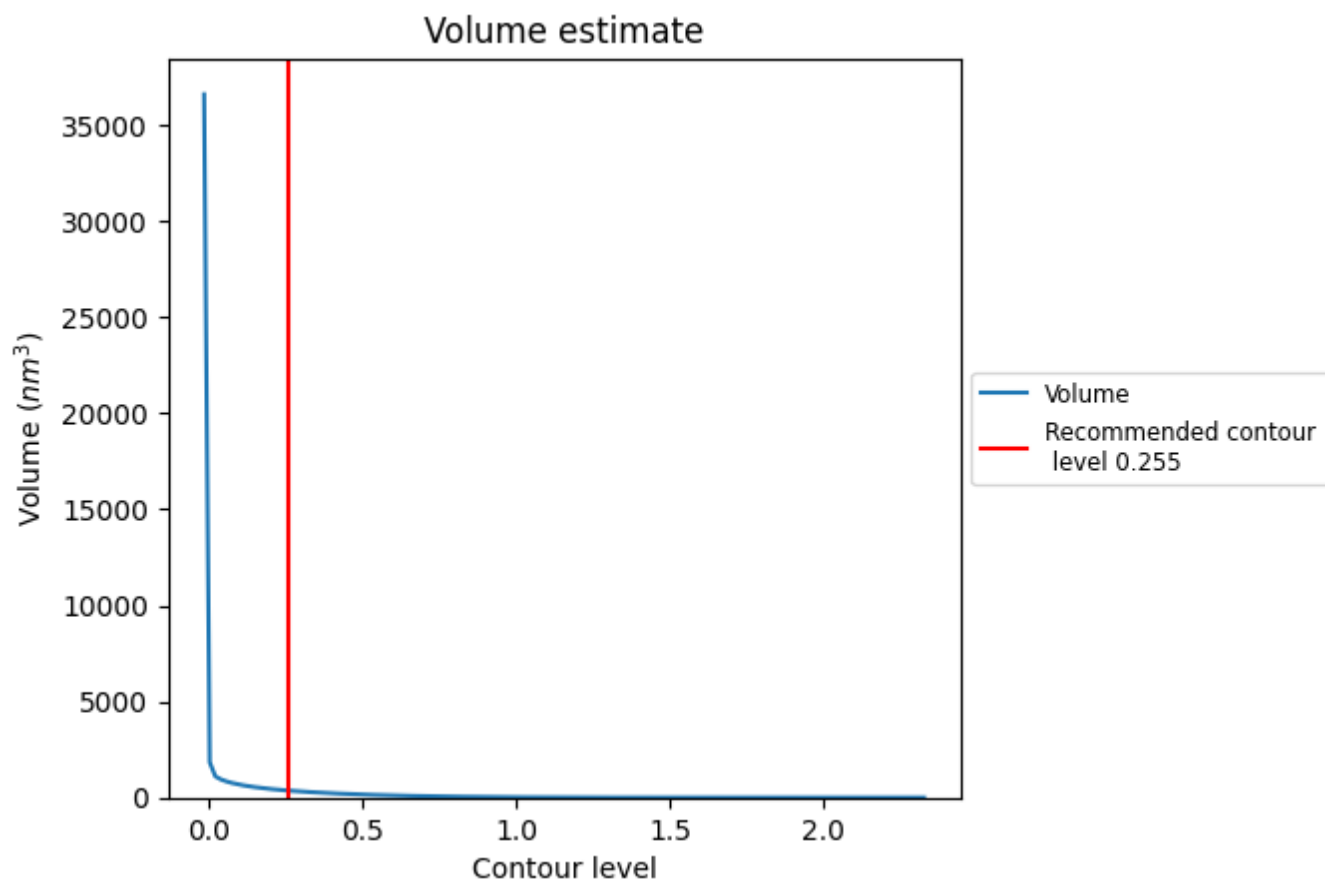
This section contains the results of statistical analysis of the map.

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.

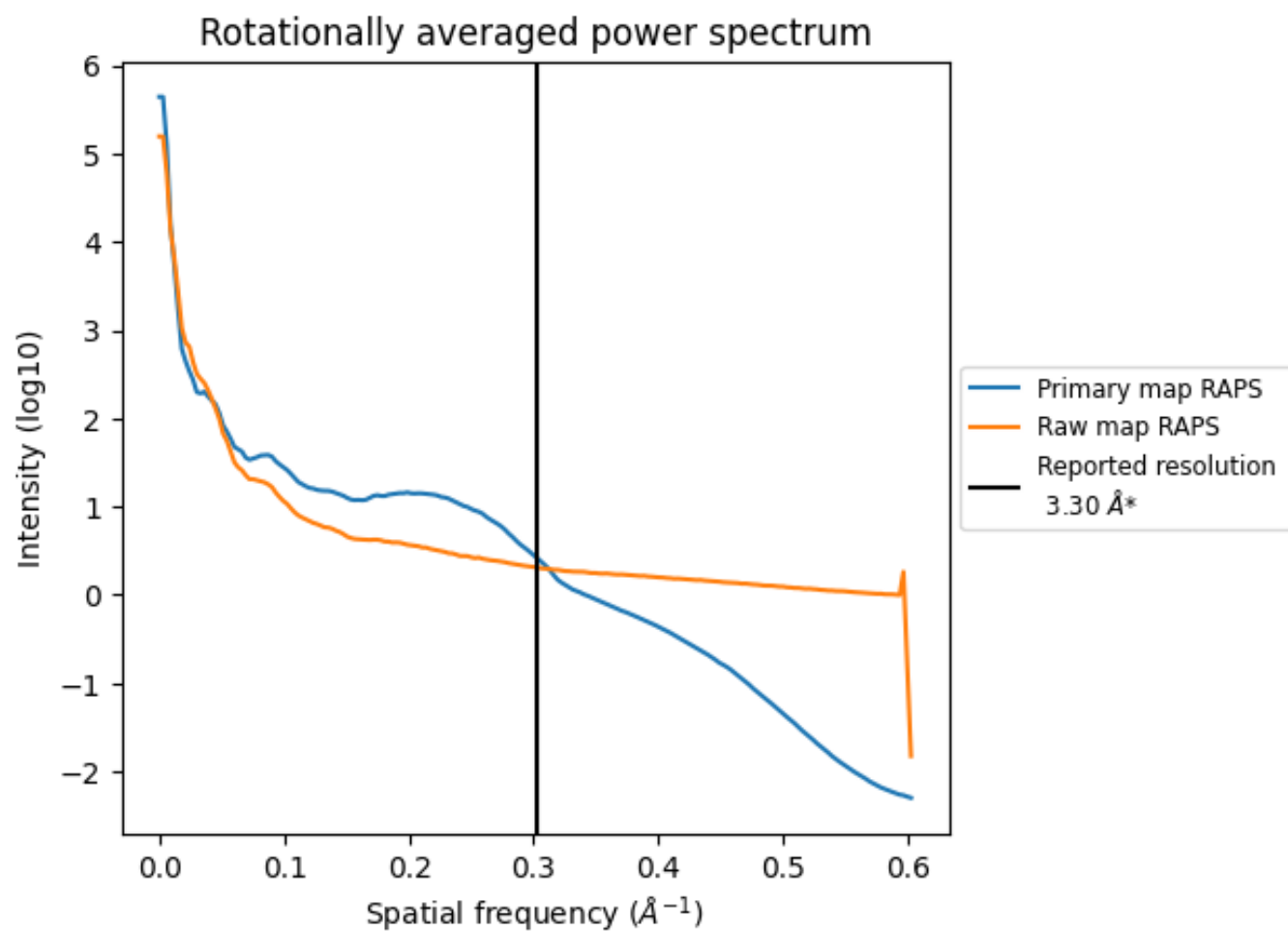
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 366 nm^3 ; this corresponds to an approximate mass of 330 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 ⓘ

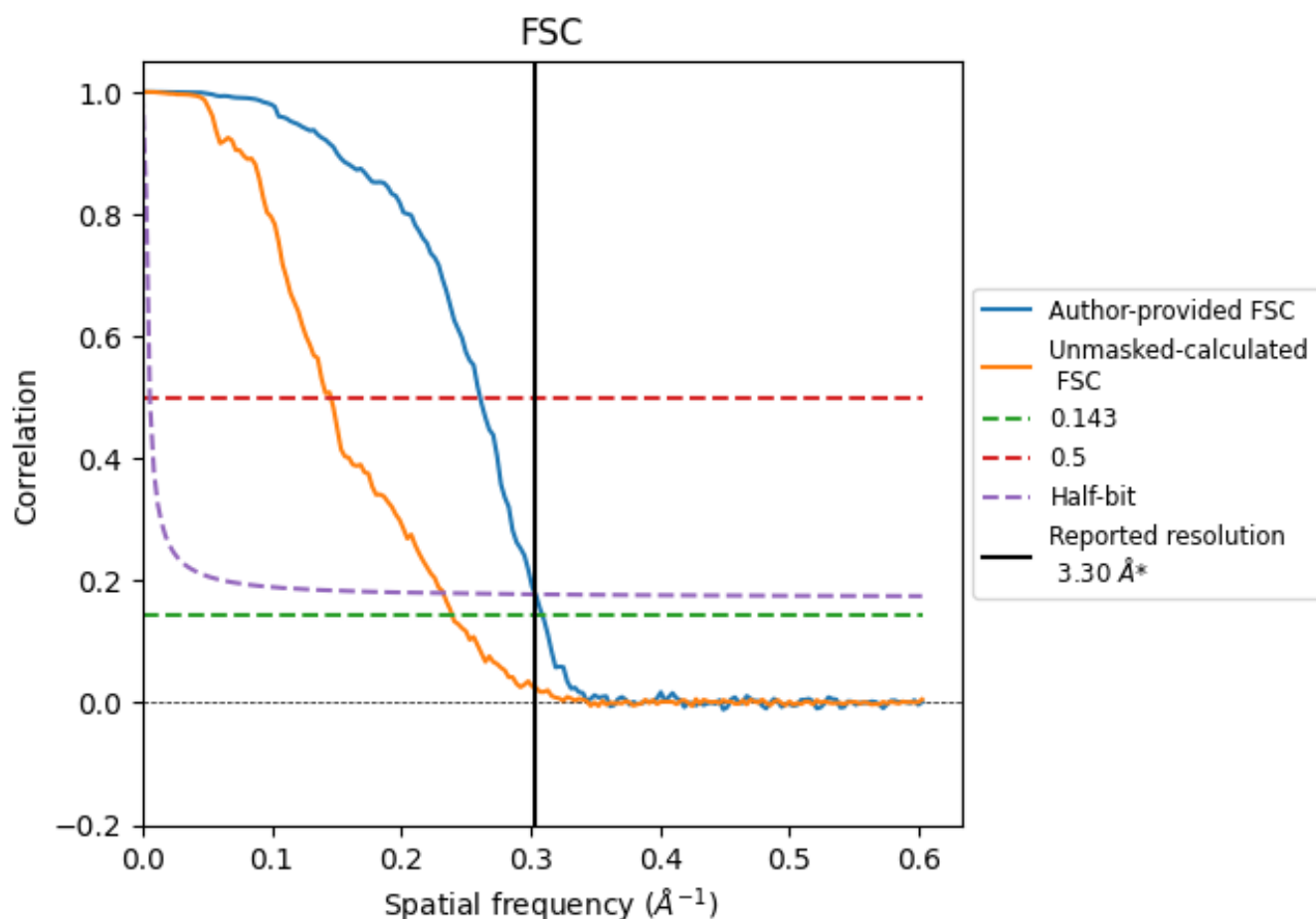


*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

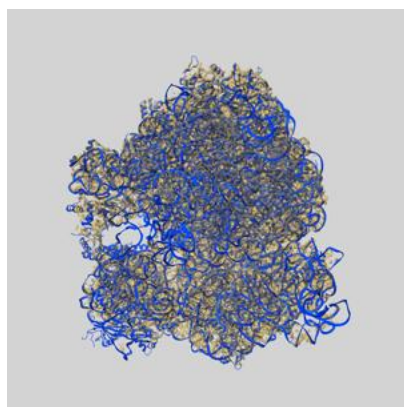
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.23	3.83	3.29
Unmasked-calculated*	4.18	6.87	4.30

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.18 differs from the reported value 3.3 by more than 10 %

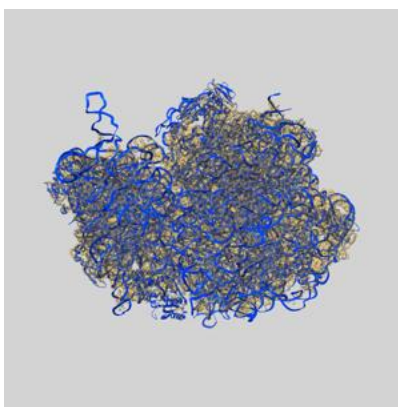
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41050 and PDB model 8T5H. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

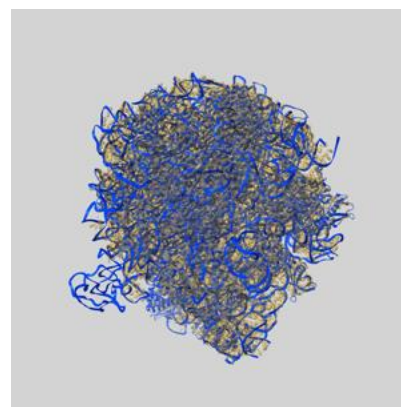
9.1 Map-model overlay [i](#)



X



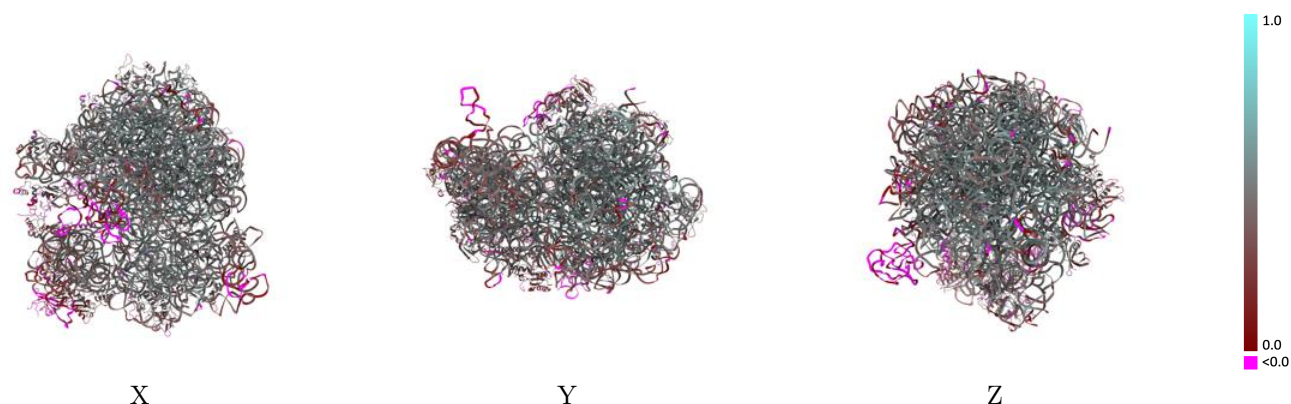
Y



Z

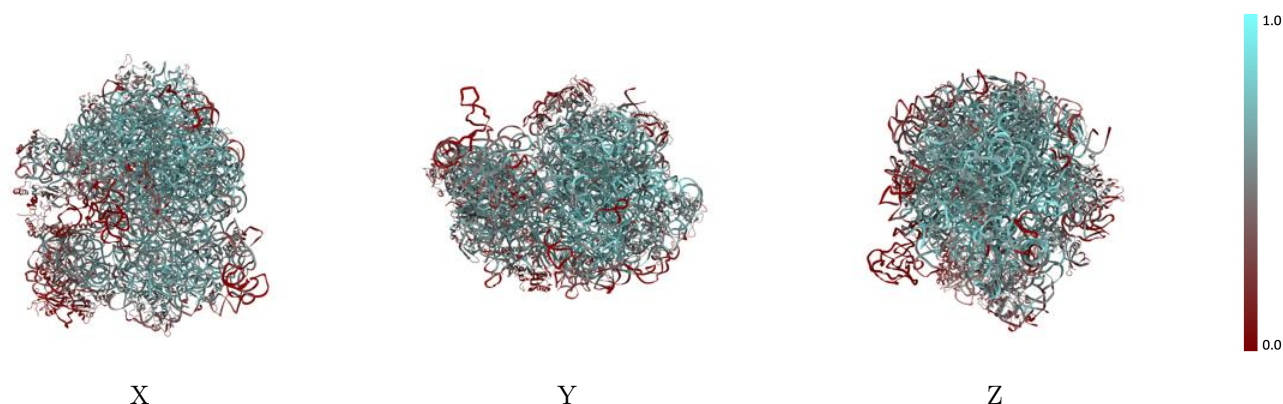
The images above show the 3D surface view of the map at the recommended contour level 0.255 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



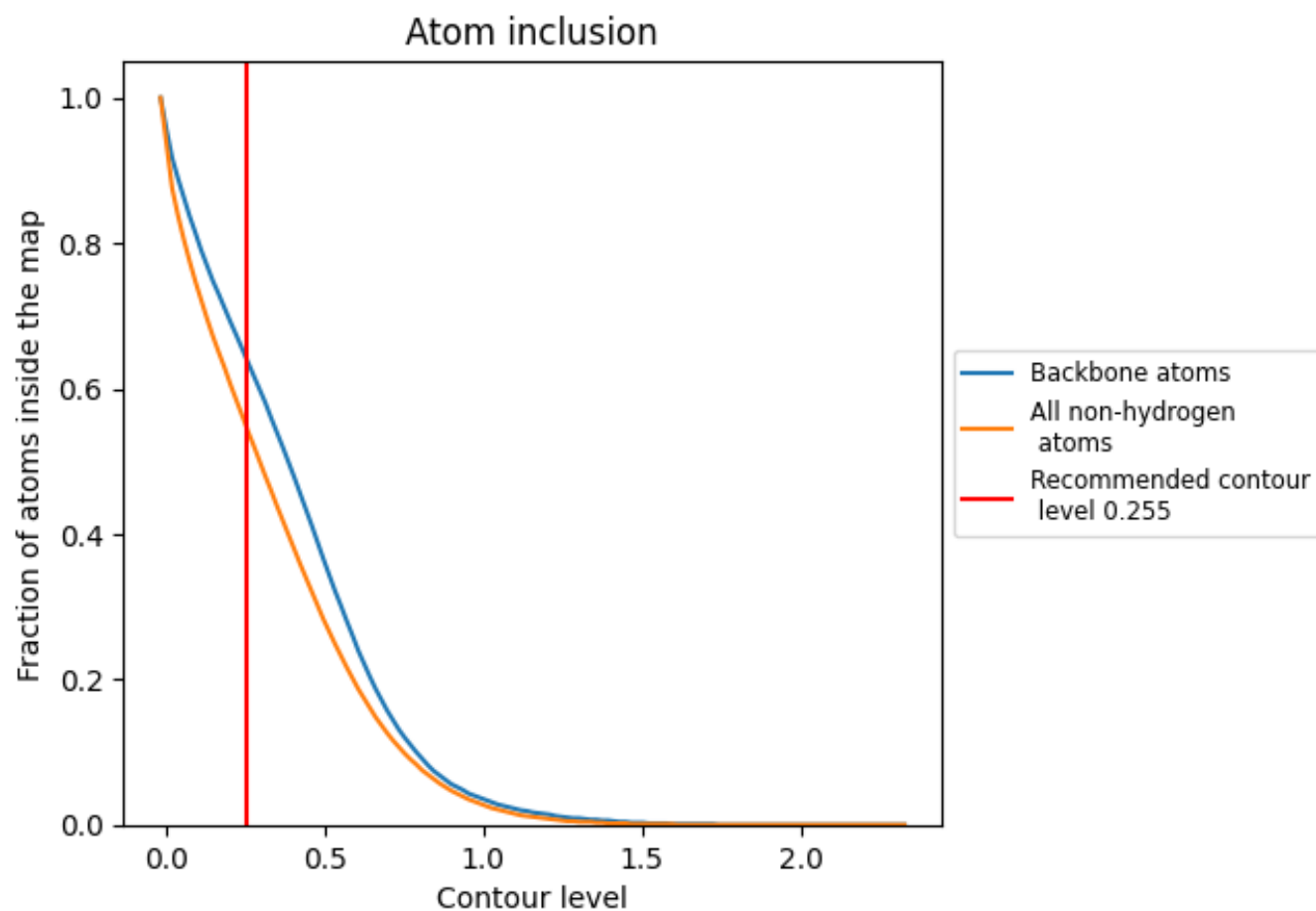
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.255).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 55% 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 (0.255) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5450	 0.4210
0	 0.5490	 0.4460
1	 0.4530	 0.4160
2	 0.6680	 0.5230
3	 0.6760	 0.5420
4	 0.5100	 0.4750
5	 0.4330	 0.3960
A	 0.5090	 0.4060
B	 0.6250	 0.4520
C	 0.6160	 0.5100
D	 0.5770	 0.4730
E	 0.5140	 0.4590
F	 0.2420	 0.1860
G	 0.2910	 0.3170
J	 0.5610	 0.4630
K	 0.5730	 0.4670
L	 0.5410	 0.4730
M	 0.5560	 0.4820
N	 0.6230	 0.4930
O	 0.4240	 0.3970
P	 0.5270	 0.4340
Q	 0.6310	 0.4970
R	 0.5160	 0.4500
S	 0.5530	 0.4550
T	 0.3760	 0.3350
U	 0.4080	 0.3820
V	 0.3820	 0.3880
W	 0.5400	 0.3920
X	 0.4890	 0.4470
Y	 0.3400	 0.3110
Z	 0.5450	 0.4800
b	 0.3630	 0.3530
c	 0.3670	 0.3350
d	 0.5320	 0.4420
e	 0.0820	 0.1820



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Chain	Atom inclusion	Q-score
f	 0.1140	 0.1470
g	 0.4880	 0.4370
h	 0.2400	 0.2790
i	 0.2650	 0.2590
j	 0.2640	 0.3040
k	 0.5250	 0.4570
l	 0.2490	 0.3060
m	 0.3510	 0.3400
n	 0.4160	 0.3680
o	 0.4780	 0.4090
p	 0.3820	 0.3570
q	 0.2060	 0.2930
r	 0.2700	 0.3290
s	 0.3480	 0.3680
u	 0.0000	 -0.0060
v	 0.5410	 0.4110
x	 0.2610	 0.2120