



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 09:51 AM UTC

PDB ID : 1ML5 / pdb_00001ml5
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 : 1GIX, 1GIY, 1GQE

This is a Full wwPDB EM Validation 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

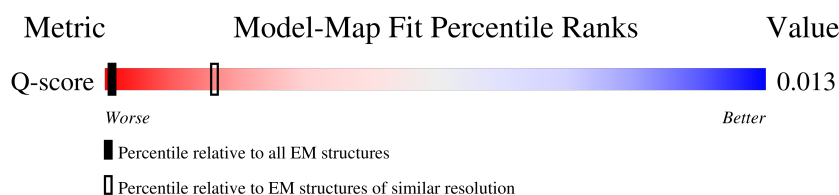
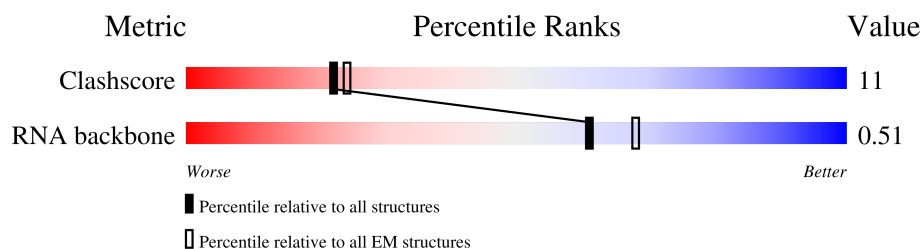
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

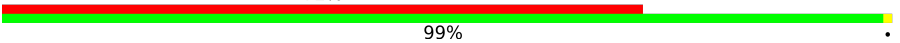
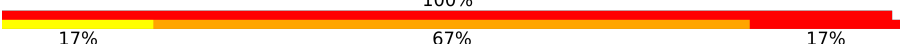
The reported resolution of this entry is 14.00 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
RNA backbone	8273	3508	-
Q-score	-	25397	61 (13.50 - 14.50)

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	A	1522	 72% 99% .
2	B	76	 62% 39% 38% 16% 7%
3	C	6	 100% 17% 67% 17%
4	a	2916	 71% 98% ..
5	b	123	 64% 98% .

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Mol	Chain	Length	Quality of chain
6	Z	365	87% 98%
7	E	256	73% 91% 9%
8	F	239	71% 85% 14%
9	G	209	79% 99%
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% 93% 5%
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% 96%
28	d	178	90% 92% 5%
29	e	338	48% 54% 43%
30	f	246	54% 72% 23%

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Mol	Chain	Length	Quality of chain
31	g	176	
32	h	177	
33	l	141	
34	m	145	
35	n	122	
36	o	164	
37	p	138	
38	q	186	
39	r	66	
40	s	113	
41	t	84	
42	u	119	
43	v	94	
44	w	70	
45	x	60	

2 Entry composition [i](#)

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		

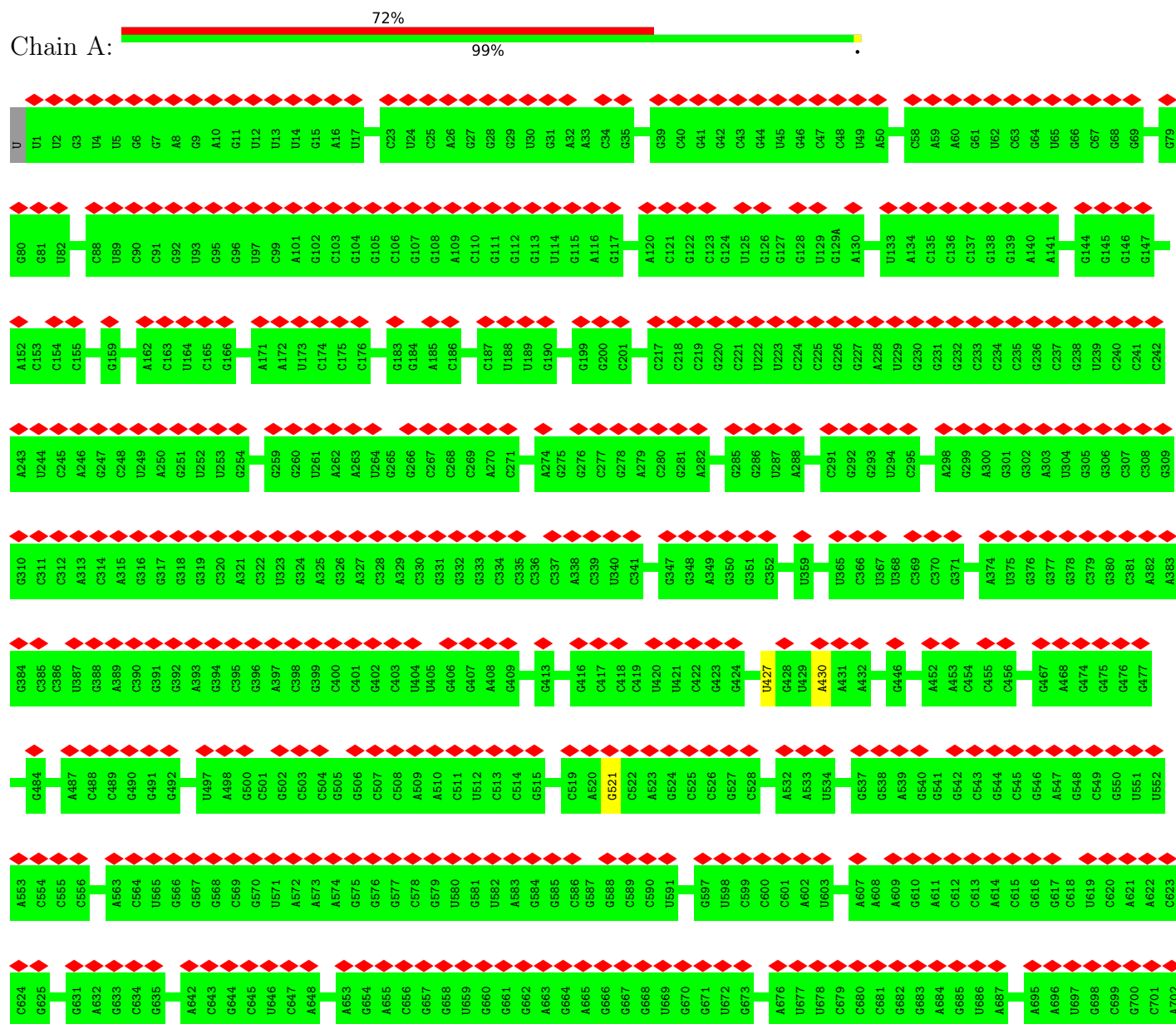
- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L30.

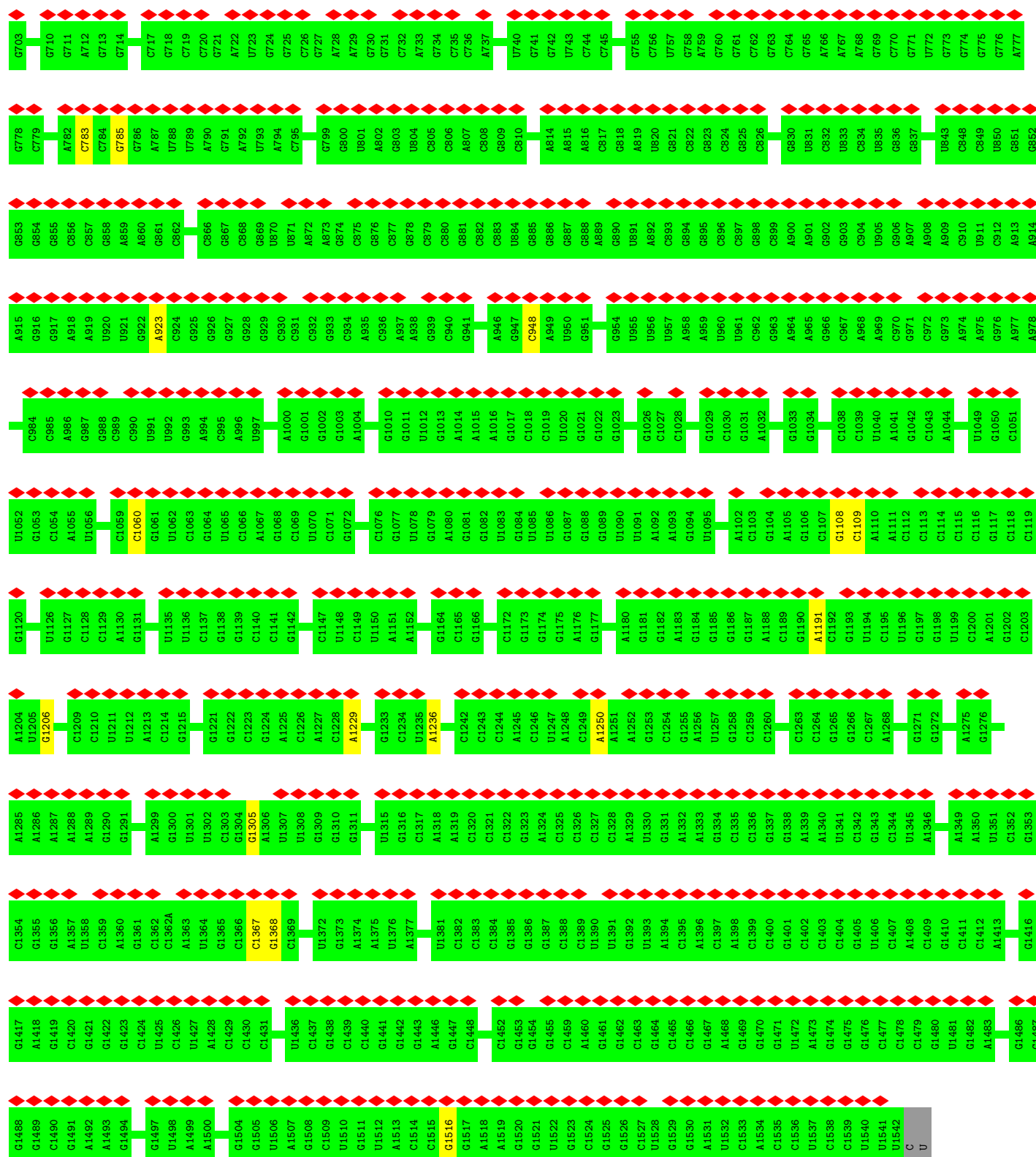
Mol	Chain	Residues	Atoms		AltConf	Trace
45	x	60	Total	C	0	60
			60	60		

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

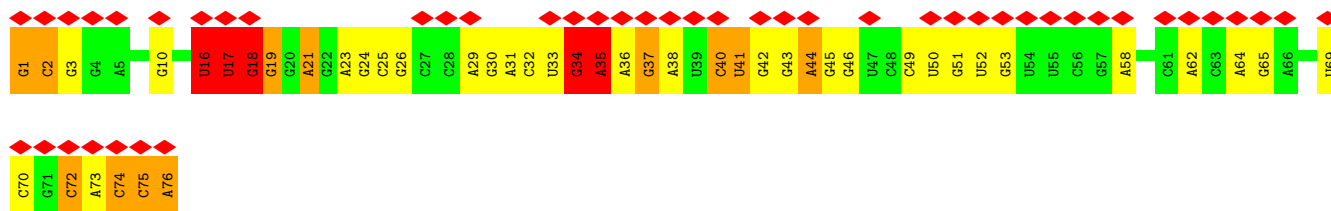




• Molecule 2: T-RNA(PHE)

Chain B:

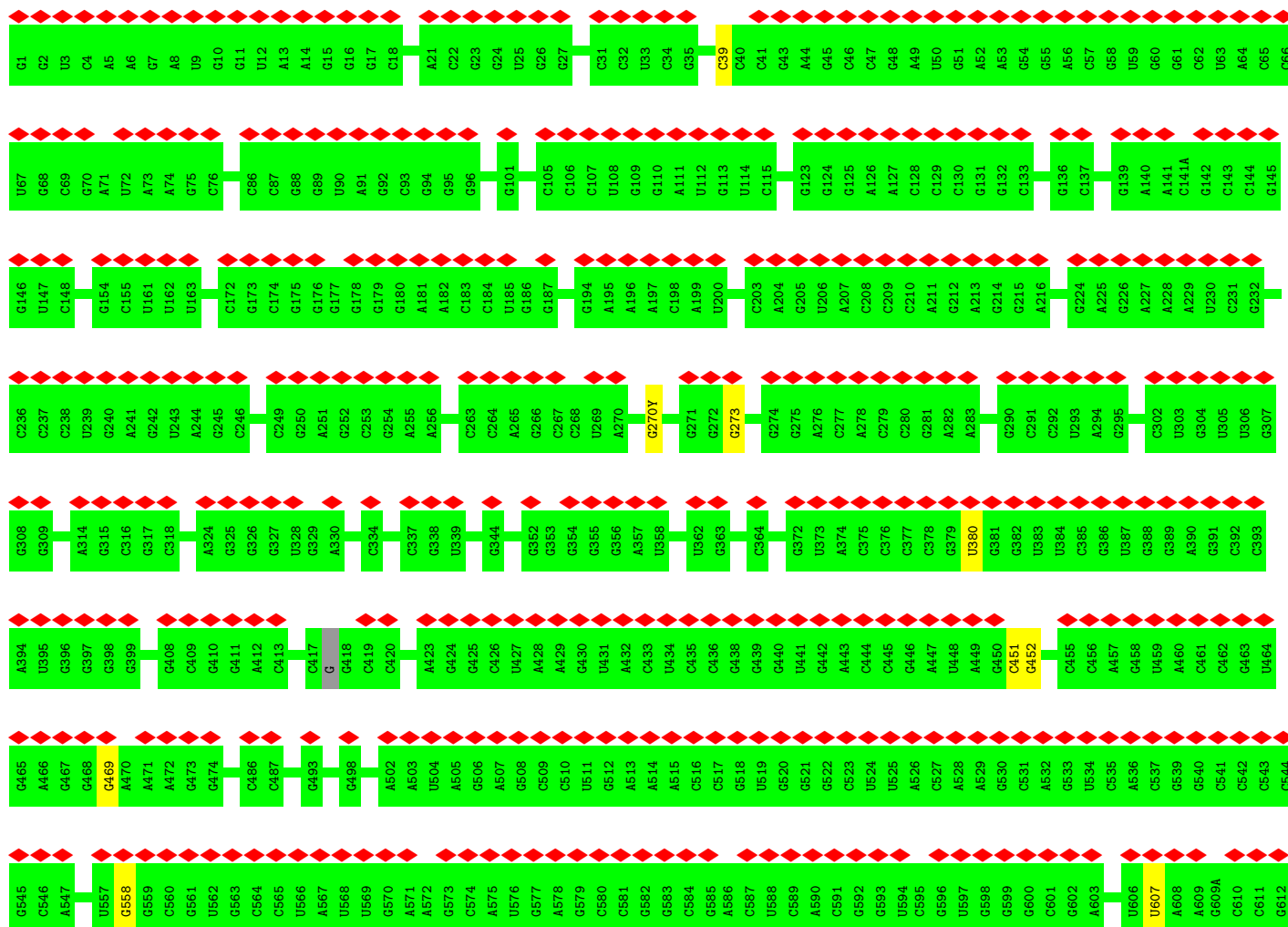


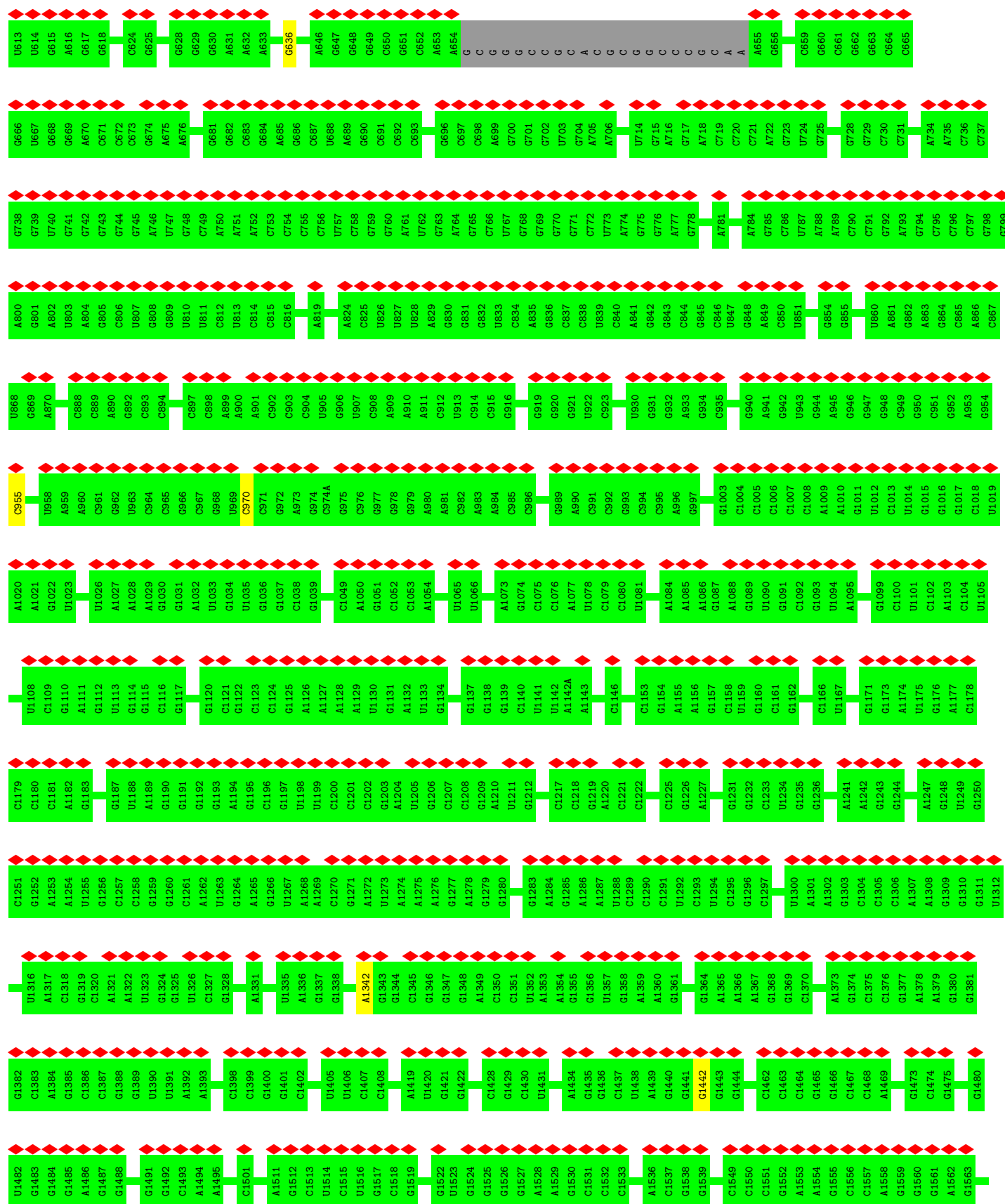


• Molecule 3: A- AND P-SITE MESSENGER RNA CODONS

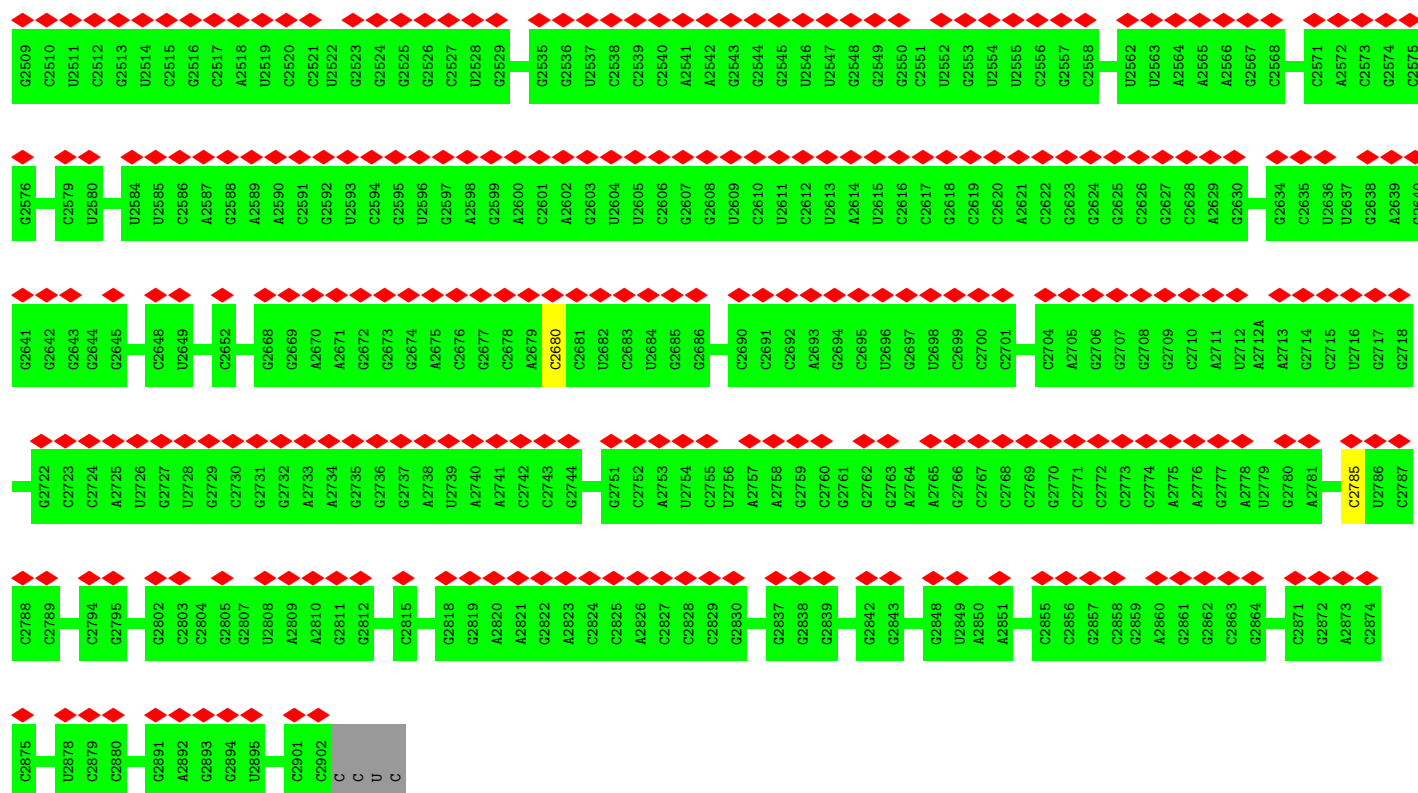


• Molecule 4: 50S 23S RIBOSOMAL RNA

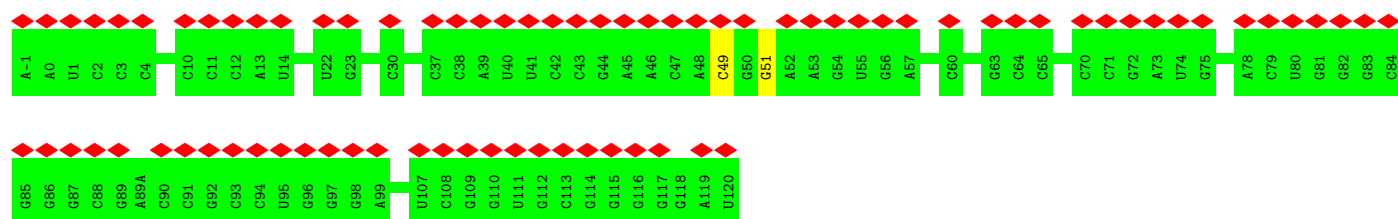




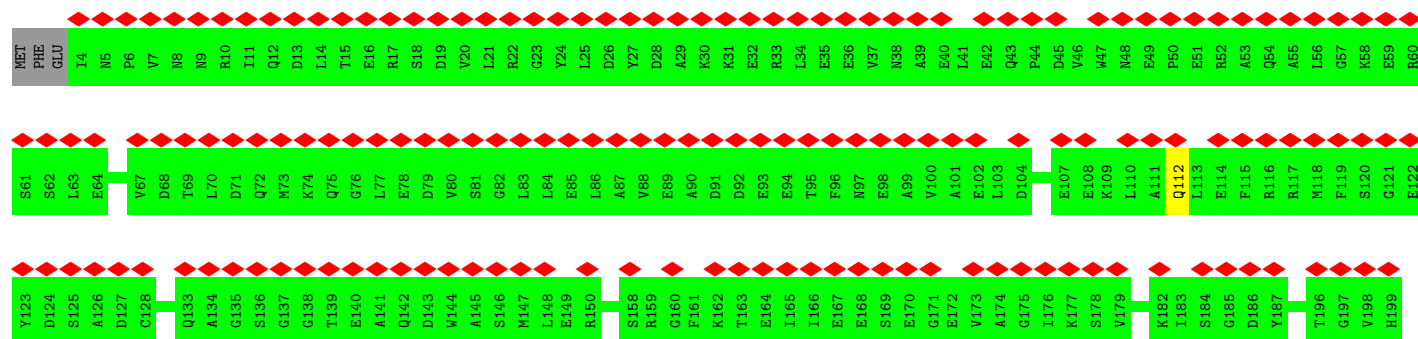
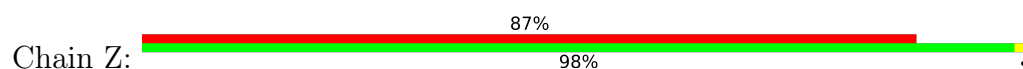
U2438	A2439	C2440	C2441	C2442	C2443	C2444	G2445	G2446	G2447	G2448	U2449	A2450	A2451	C2452	A2453	G2454	C2455	C2456	U2457	U2462	C2463	C2464	G2465	C2466	C2467	G2468	A2469	C2475	A2476	C2477	A2478	G2479	C2480	G2481	G2486	G2487	A2488	G2489	G2490	U2491	U2492	U2493	G2494	A2497	C2498	C2499	U2500	C2501	G2502	A2503	U2504	G2505	U2506	G2507	G2508		
C2368	A2369	G2370	G2371	A2378	G2379	C2380	C2381	G2382	C2383	G2384	C2385	C2386	U2387	A2388	C2389	U2390	C2391	A2392	A2393	C2394	C2395	G2396	G2397	U2398	G2399	C2400	U2401	C2402	C2403	C2404	U2405	U2406	G2407	U2408	G2409	G2410	G2413	G2414	G2415	C2416	U2417	A2418	U2419	C2424	A2425	A2426	C2427	G2428	A2429	A2430	U2431	A2432	A2433	G2436	U2437		
C2294	C2295	U2296	C2297	A2298	G2299	G2300	C2301	G2302	G2303	G2308	A2309	A2310	A2311	U2312	C2313	C2314	G2315	C2316	C2317	G2318	G2319	A2320	C2321	A2322	G2323	C2324	G2325	G2329	G2330	G2331	U2332	A2333	G2334	A2335	A2336	G2337	G2338	A2346	C2347	G2351	A2352	G2353	C2354	C2355	C2356	U2357	G2358	C2359	A2360	A2361	G2362	C2363	C2364	G2365			
A2227	C2228	C2229	G2230	C2231	U2232	U2233	G2234	C2235	C2236	G2237	C2238	G2239	C2240	A2241	C2242	U2243	U2244	U2245	G2246	A2247	C2248	U2249	C2250	G2251	G2252	G2253	C2254	G2255	G2256	U2257	C2258	G2259	C2260	G2261	U2262	C2263	C2264	U2265	A2266	A2267	A2268	A2269	G2270	G2271	U2272	C2273	A2274	C2275	U2276	G2277	A2278	A2288	G2289	G2290	U2291	C2292	C2293
C2139	C2140	U2144	C2145	G2148	G2149	U2150	G2151	G2155	G2156	G2157	A2158	G2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	G2250	G2251	G2252	G2253	C2254	G2255	G2256	U2257	C2258	G2259	C2260	C2261	U2262	C2263	C2264	U2265	A2266	A2267	A2268	A2269	G2270	G2271	U2272	C2273	A2274	C2275	U2276	G2277	A2278	A2288	G2289	G2290	U2291	C2292	C2293		
C2064	C2065	C2066	G2067	U2068	G2069	C2073	U2074	U2075	U2079	G2080	C2081	G2082	C2083	C2084	U2089	G2090	U2091	U2092	G2093	G2094	G2100	G2101	U2102	C2103	G2104	C2105	G2106	C2107	C2108	U2109	G2110	G2111	C2112	U2113	A2114	G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	C2128	C2129	U2130	G2131	C2136				
C1999	G2000	A2001	G2002	G2003	G2004	G2009	G2010	U2011	G2012	A2013	A2014	A2015	U2016	U2017	G2018	A2019	A2020	G2021	U2022	G2023	G2024	C2025	G2026	G2027	A2030	A2031	G2032	A2033	U2034	G2035	C2036	G2037	G2038	C2039	C2040	U2041	A2042	C2043	C2044	C2045	G2046	U2047	C2050	A2051	G2052	G2053	A2054	C2055	G2056	A2057	A2058	A2059	A2060	G2061	A2062	C2063	
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	C1902	G1903	G1904	G1905	G1906	G1907	C1908	G1909	G1910	U1911	U1915	A1916	U1917	A1918	G1921	G1922	C1925	U1926	A1927	U1931	A1932	G1933						
C1782	A1783	A1784	A1785	A1786	A1787	G1788	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	C1837	G1840	U1841	G1842	C1843
G1697	A1698	G1699	A1700	A1701	G1702	G1703	G1704	G1705	U1706	G1707	C1708	U1709	C1710	G1717	G1718	G1725	G1726	U1727	C1734	C1735	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		
G1633	A1634	G1635	U1639	C1640	A1641	G1642	G1643	G1644	G1645	G1646	G1647	G1648	G1649	G1650	G1651	A1652	G1653	A1654	A1655	C1656	C1657	C1658	U1659	C1660	G1661	C1662	A1663	A1664	G1665	G1666	G1667	C1670	U1671	C1672	U1673	G1674	C1675	A1676	A1677	G1678	U1679	U1680	G1681	G1682	C1683	C1684	C1685	C1686	G1687	A1690	C1691	U1692	U1693	C1694	G1695	G1696	
A1566	A1567	G1568	A1569	A1572	G1573	C1574	C1575	U1576	G1581	C1582	A1587	C1588	C1589	U1590	G1591	C1592	G1593	G1594	A1596	A1597	C1598	C1599	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			

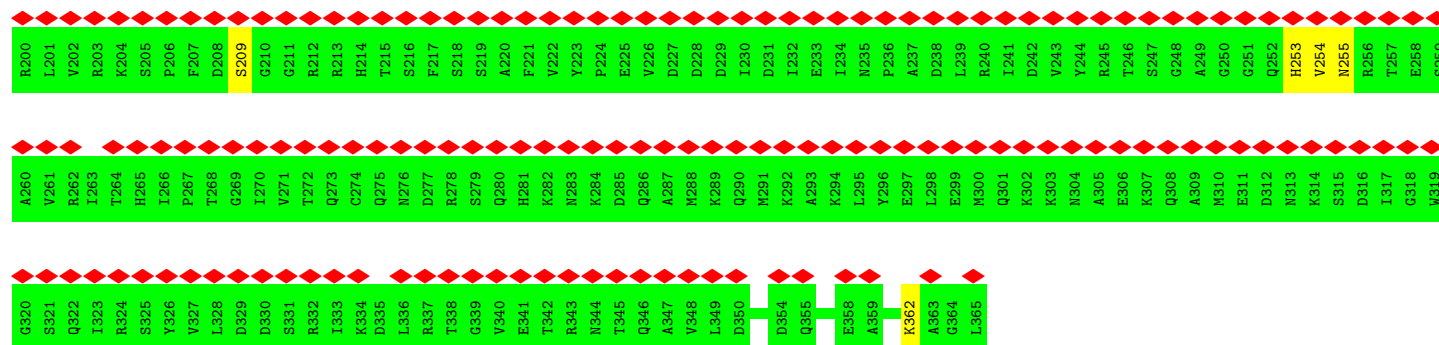


• Molecule 5: 50S 5S RIBOSOMAL RNA

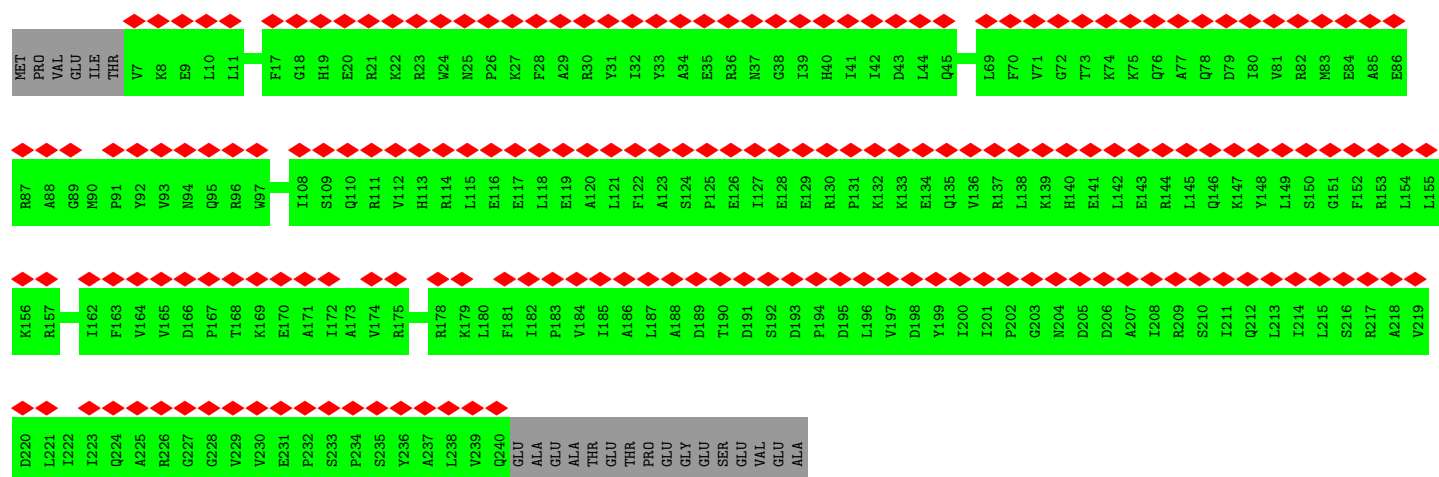
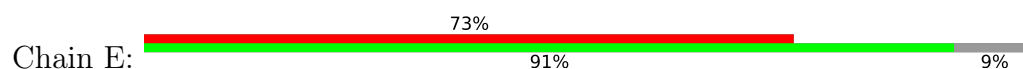


• Molecule 6: Peptide chain release factor 2

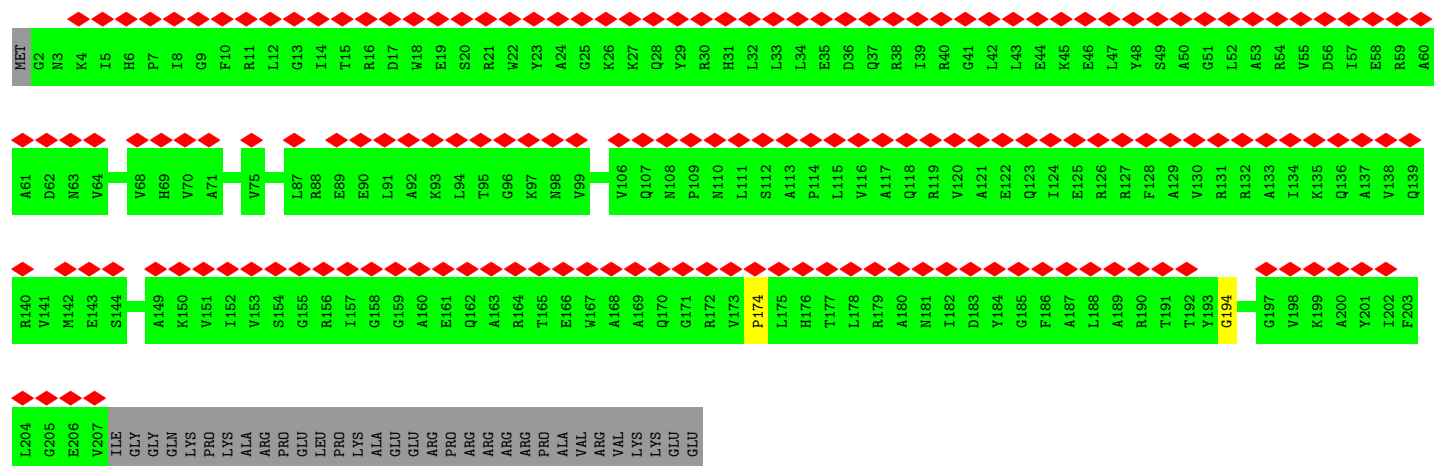
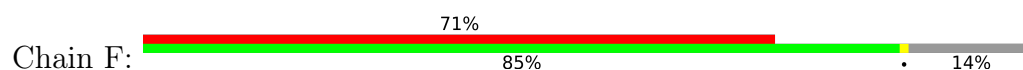




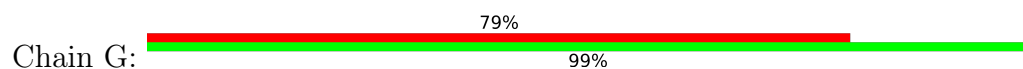
• Molecule 7: 30S RIBOSOMAL PROTEIN S2

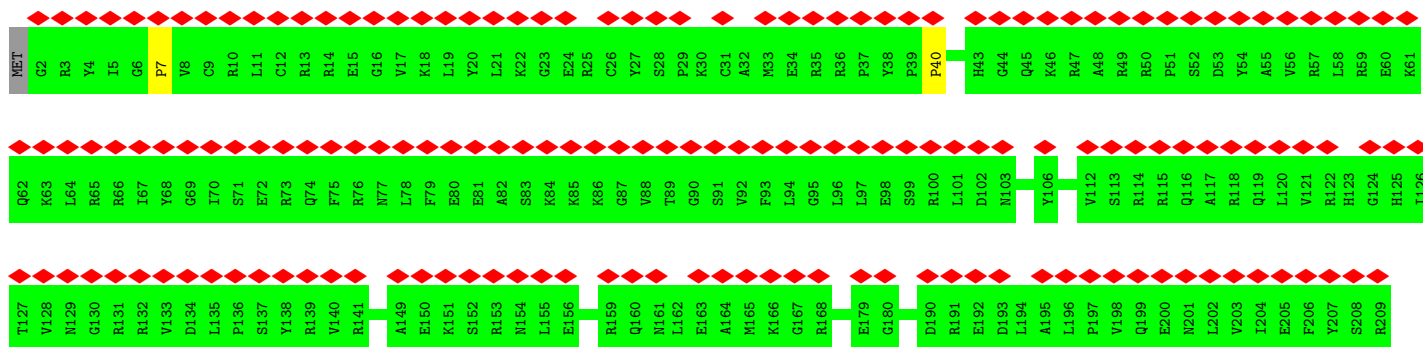


• Molecule 8: 30S RIBOSOMAL PROTEIN S3



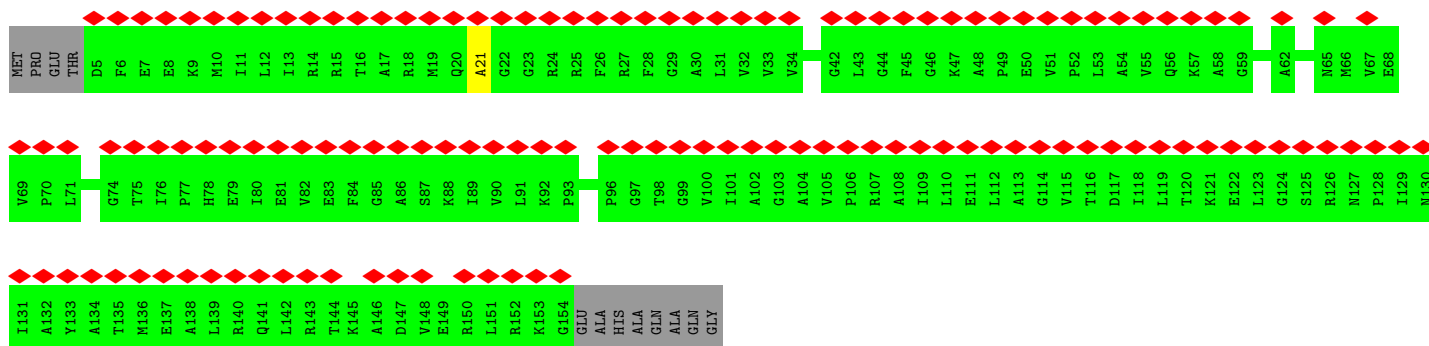
• Molecule 9: 30S RIBOSOMAL PROTEIN S4





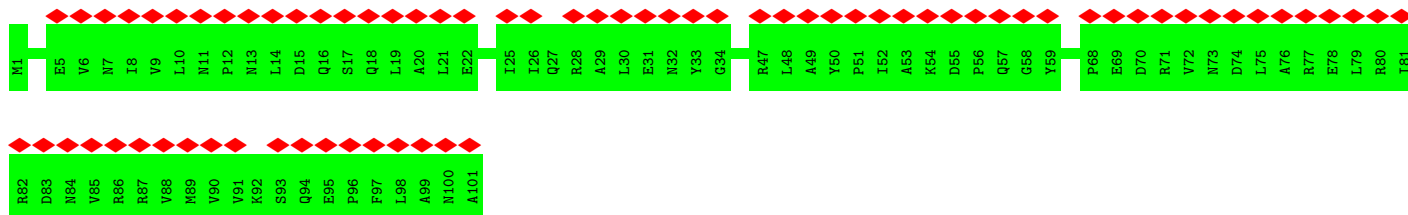
• Molecule 10: 30S RIBOSOMAL PROTEIN S5

Chain H: 81% 92% 7%



• Molecule 11: 30S RIBOSOMAL PROTEIN S6

Chain I: 72% 100%

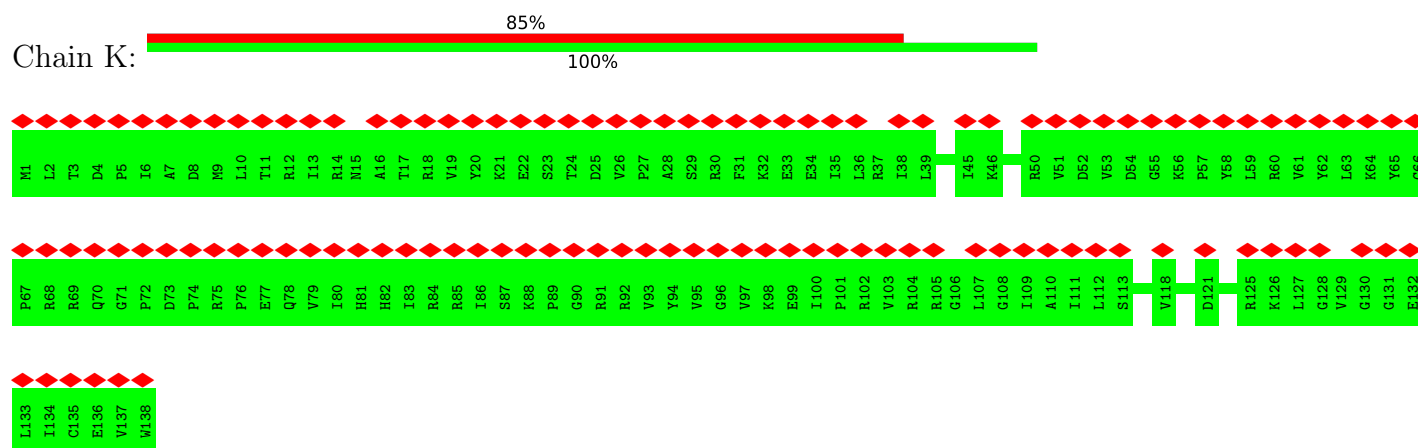


• Molecule 12: 30S RIBOSOMAL PROTEIN S7

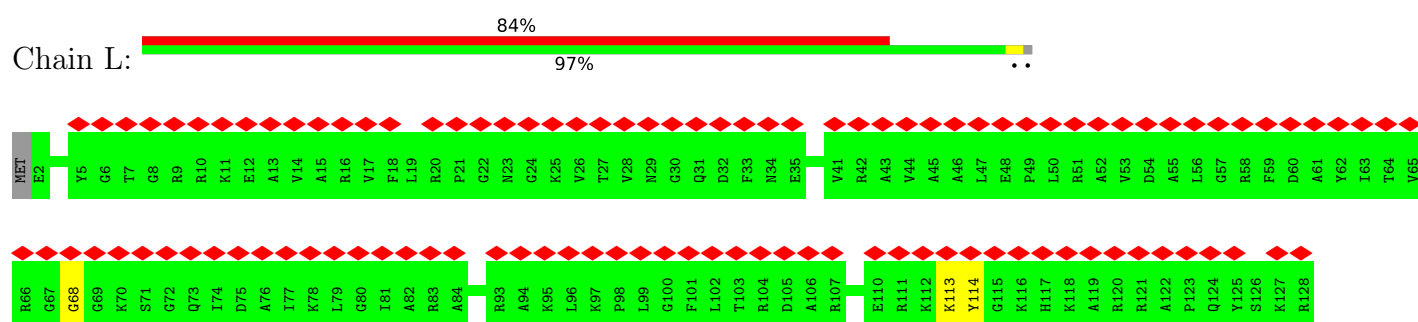
Chain J: 64% 99%



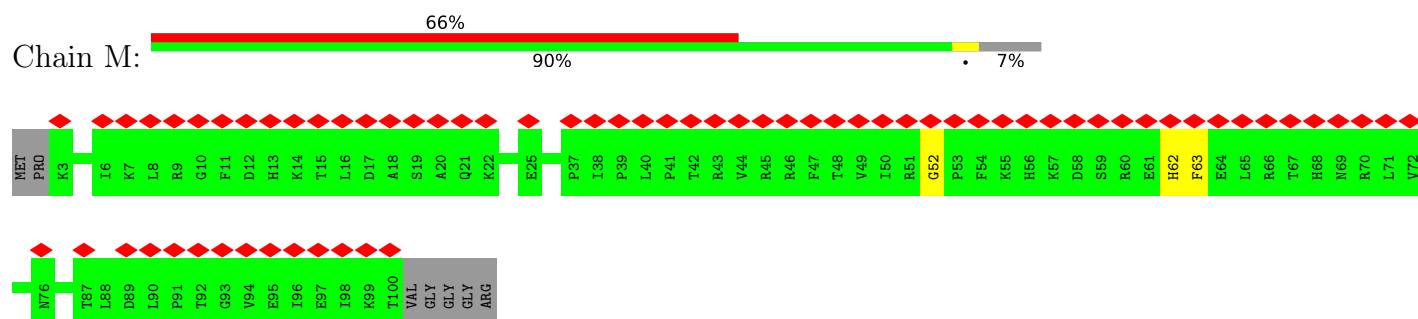
• Molecule 13: 30S RIBOSOMAL PROTEIN S8



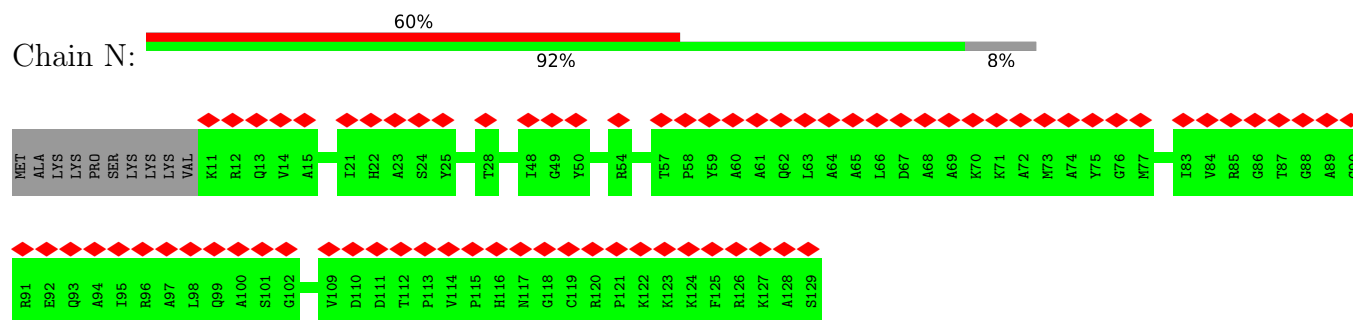
• Molecule 14: 30S RIBOSOMAL PROTEIN S9



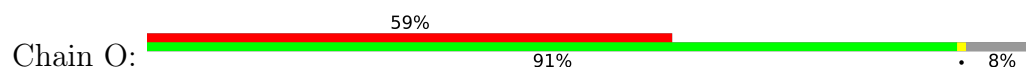
• Molecule 15: 30S RIBOSOMAL PROTEIN S10

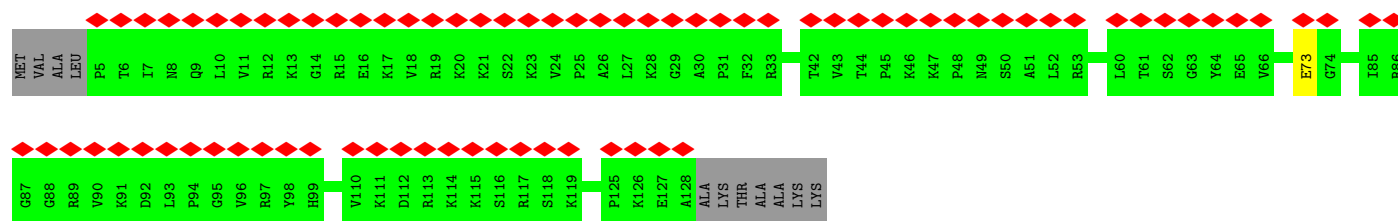


• Molecule 16: 30S RIBOSOMAL PROTEIN S11

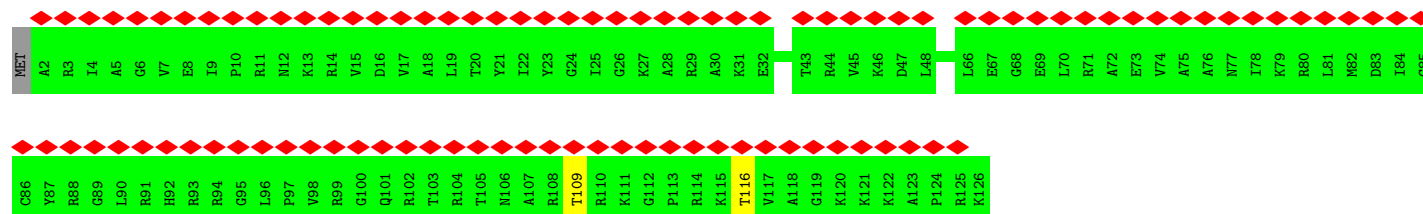
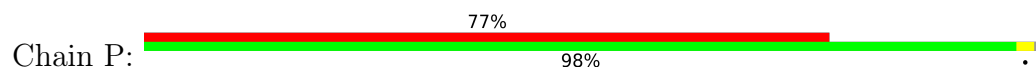


• Molecule 17: 30S RIBOSOMAL PROTEIN S12

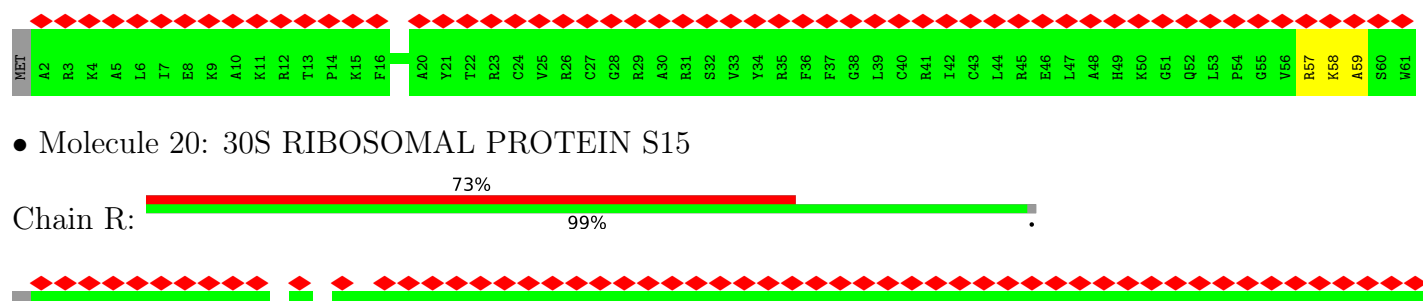
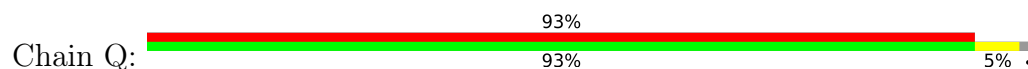




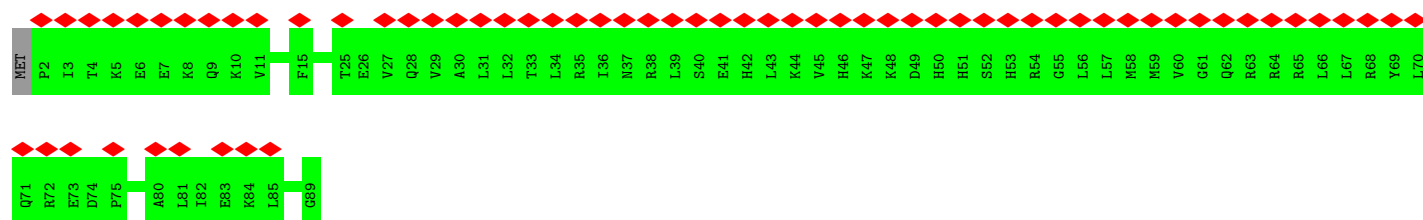
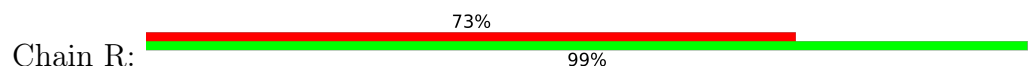
• Molecule 18: 30S RIBOSOMAL PROTEIN S13



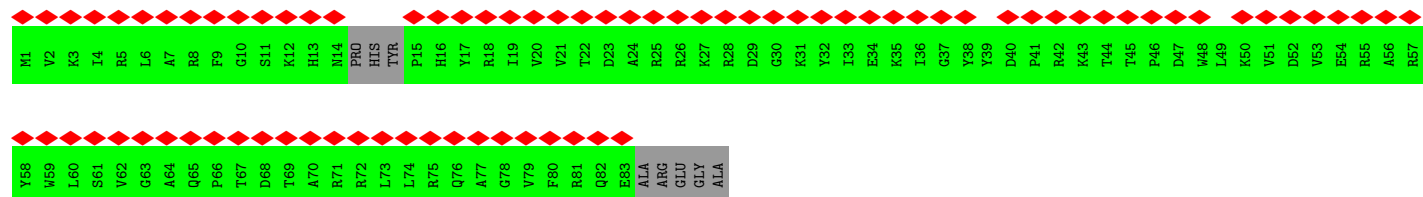
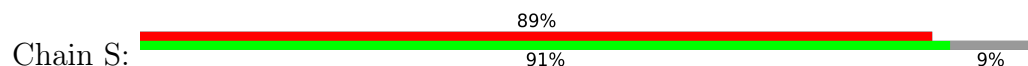
• Molecule 19: 30S RIBOSOMAL PROTEIN S14



• Molecule 20: 30S RIBOSOMAL PROTEIN S15



• Molecule 21: 30S RIBOSOMAL PROTEIN S16

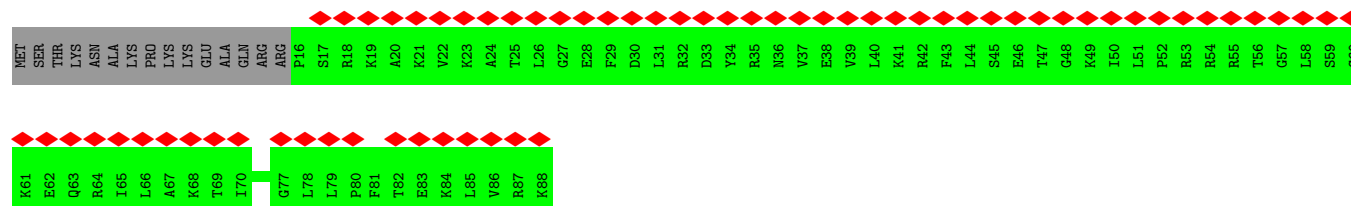
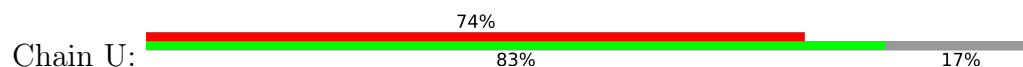


• Molecule 22: 30S RIBOSOMAL PROTEIN S17

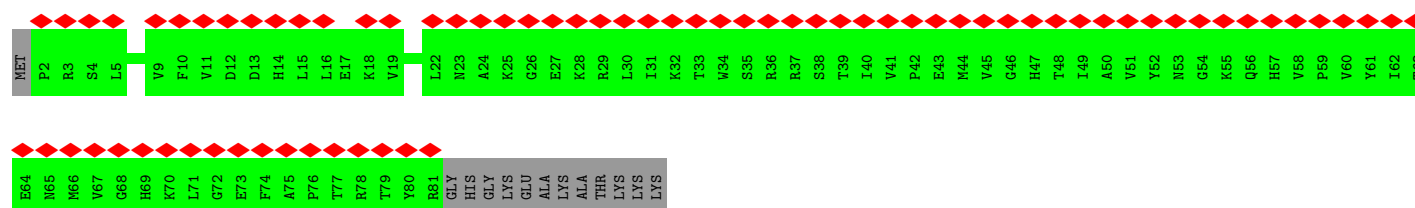
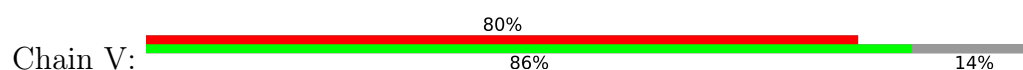




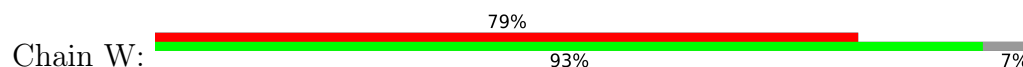
• Molecule 23: 30S RIBOSOMAL PROTEIN S18



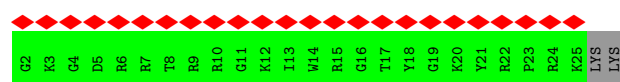
• Molecule 24: 30S RIBOSOMAL PROTEIN S19



• Molecule 25: 30S RIBOSOMAL PROTEIN S20

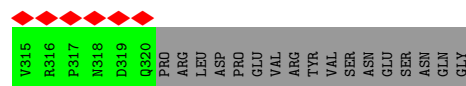


• Molecule 26: 30S RIBOSOMAL PROTEIN THX

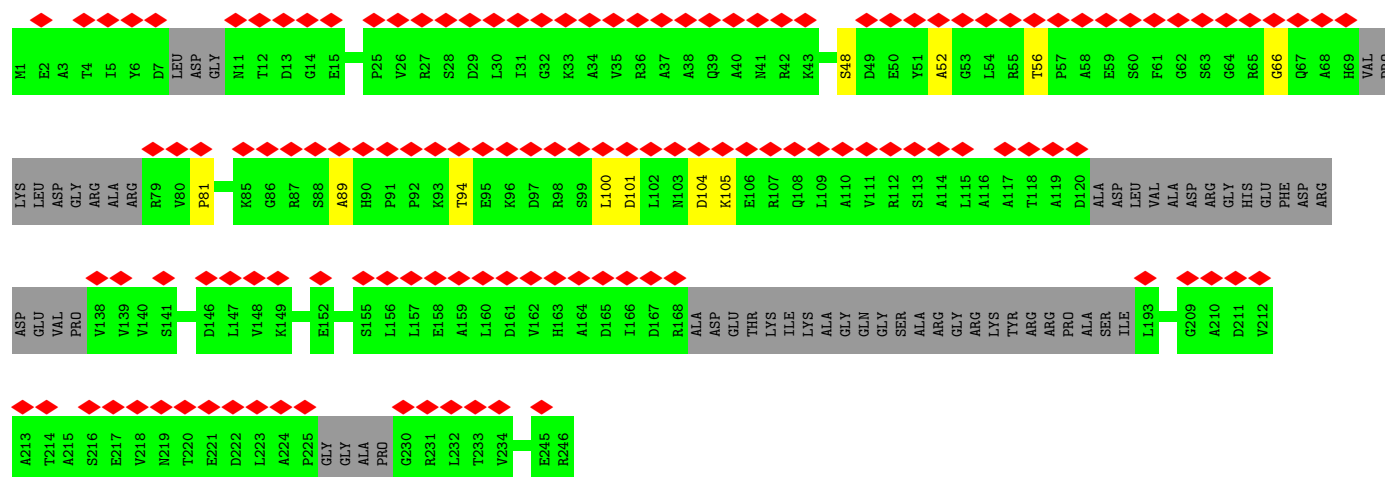
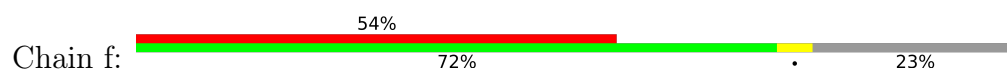


• Molecule 27: 50S RIBOSOMAL PROTEIN L1

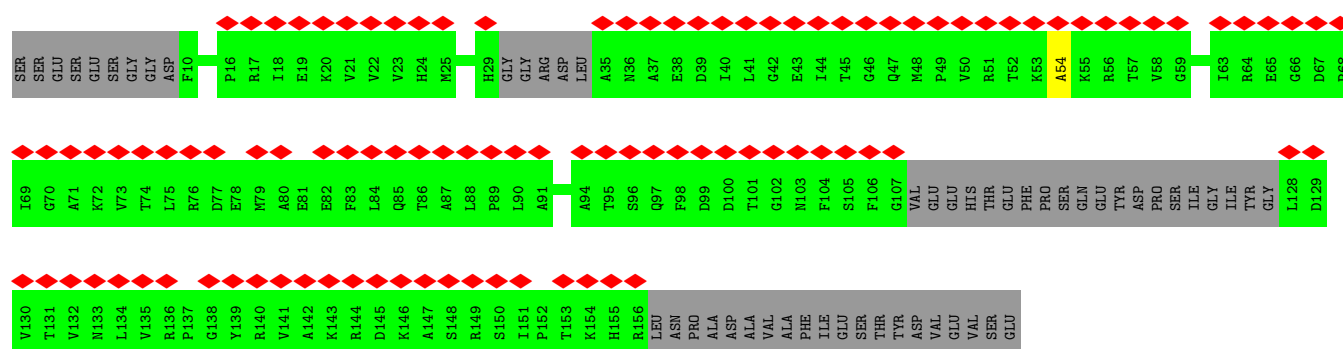




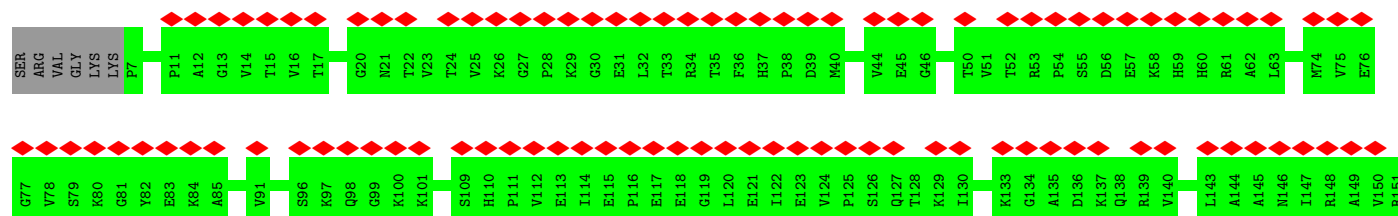
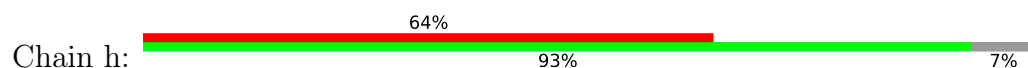
• Molecule 30: 50S RIBOSOMAL PROTEIN L4

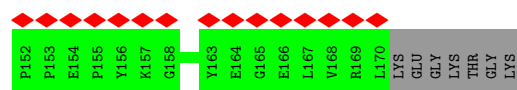


• Molecule 31: 50S RIBOSOMAL PROTEIN L5



• Molecule 32: 50S RIBOSOMAL PROTEIN L6

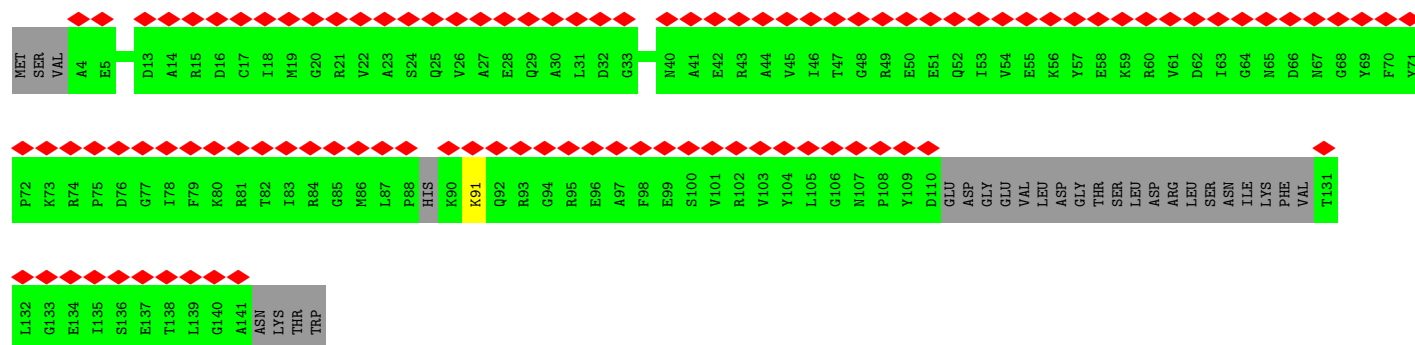
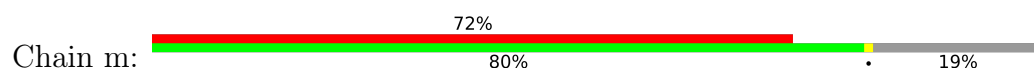




• Molecule 33: 50S RIBOSOMAL PROTEIN L11



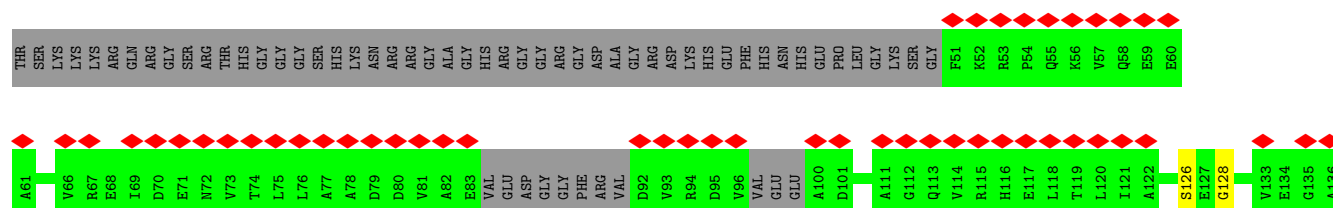
• Molecule 34: 50S RIBOSOMAL PROTEIN L13

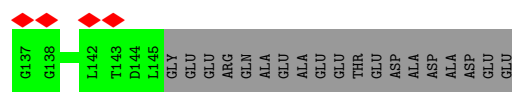


• Molecule 35: 50S RIBOSOMAL PROTEIN L14

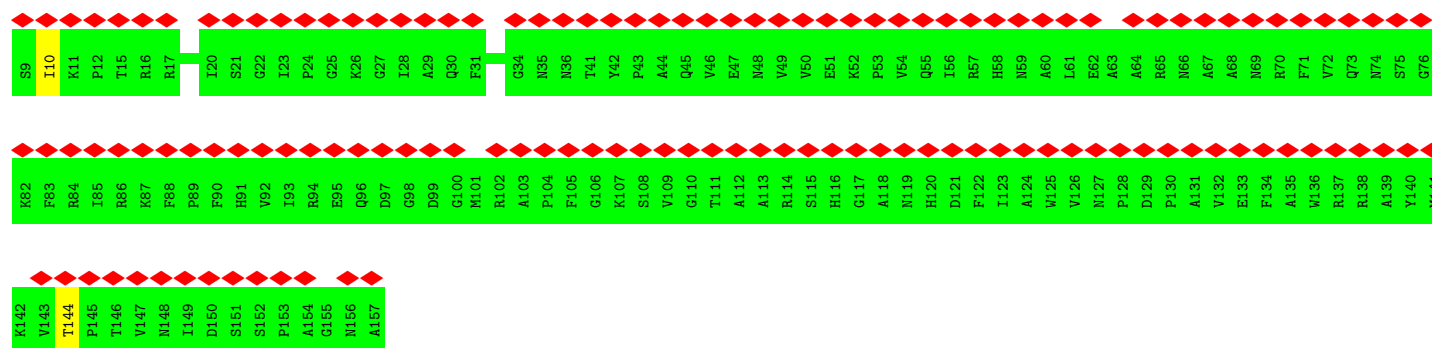


• Molecule 36: 50S RIBOSOMAL PROTEIN L15

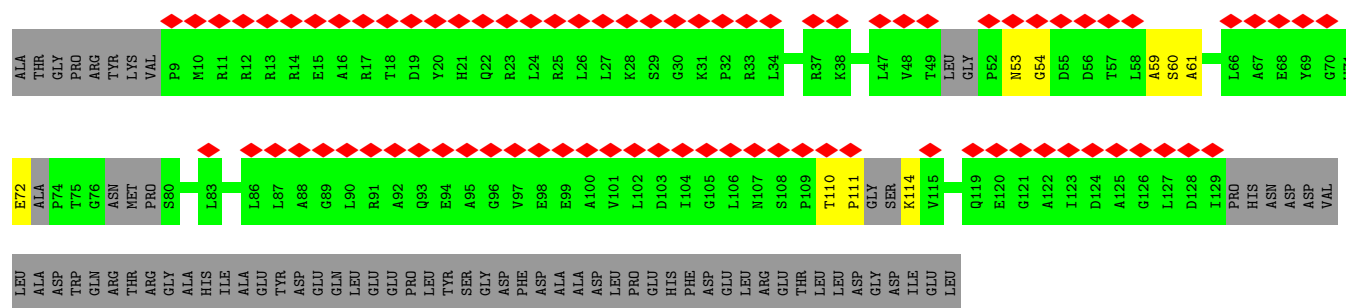
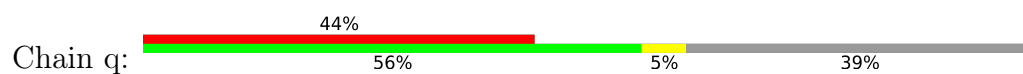




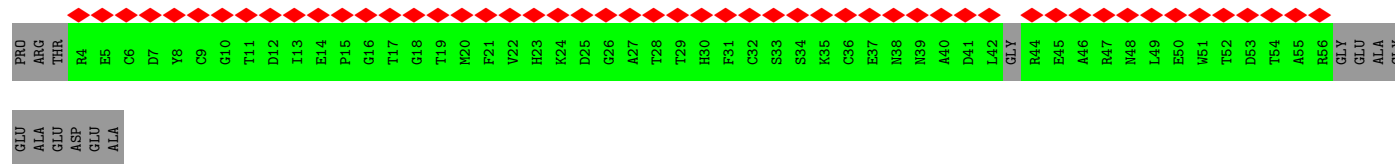
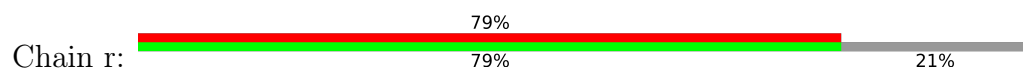
• Molecule 37: 50S RIBOSOMAL PROTEIN L16



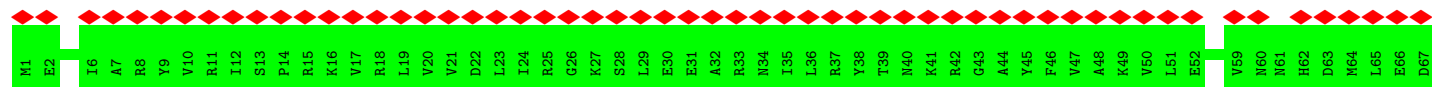
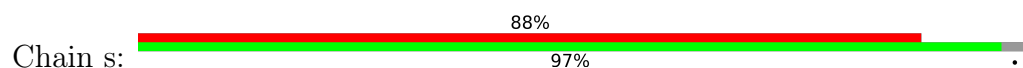
• Molecule 38: 50S RIBOSOMAL PROTEIN L18

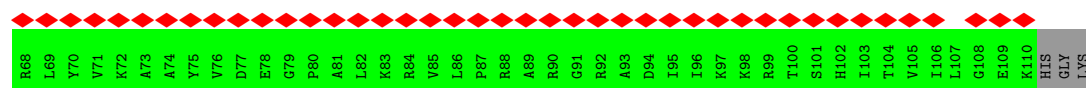


• Molecule 39: 50S RIBOSOMAL PROTEIN L19

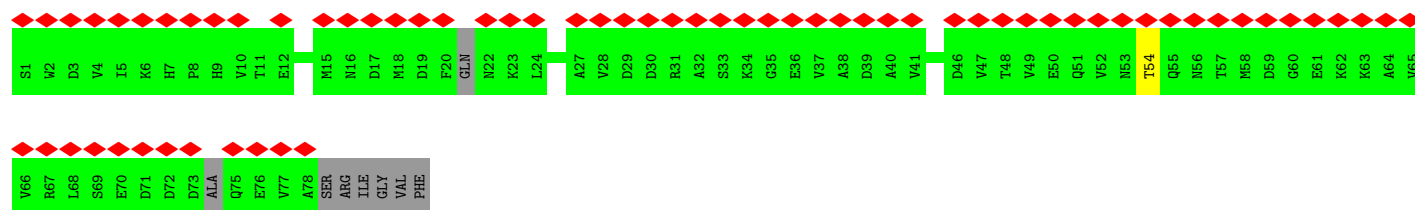
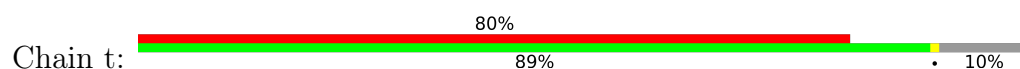


• Molecule 40: 50S RIBOSOMAL PROTEIN L22

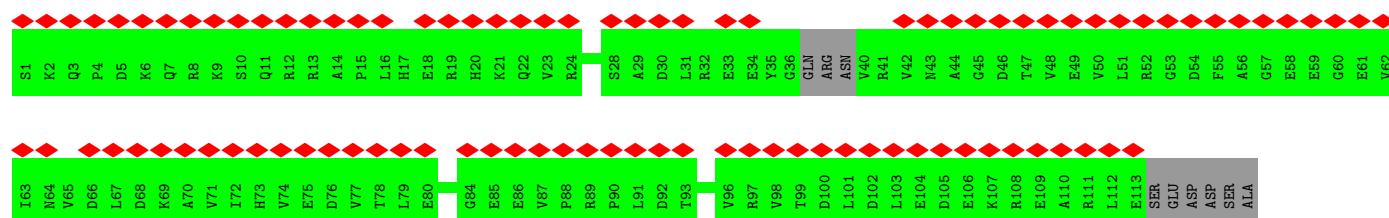
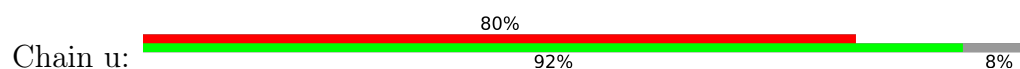




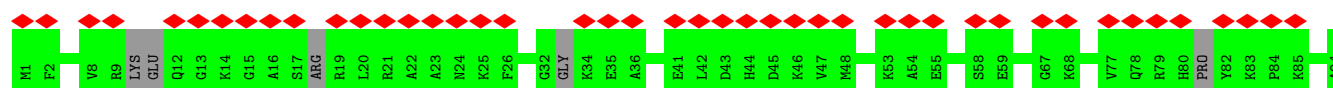
• Molecule 41: 50S RIBOSOMAL PROTEIN L23



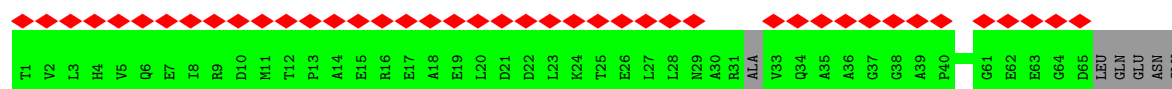
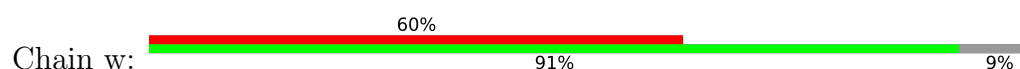
• Molecule 42: 50S RIBOSOMAL PROTEIN L24



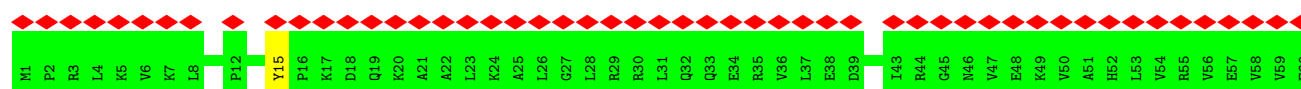
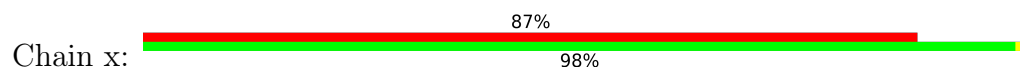
• Molecule 43: 50S RIBOSOMAL PROTEIN L25



• Molecule 44: 50S RIBOSOMAL PROTEIN L29



• Molecule 45: 50S RIBOSOMAL PROTEIN L30



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 (Å)	290.28, 290.28, 290.28	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	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: 5MC, M2G, OMC, 5MU, YG, 2MG, OMG, PSU, 1MA, H2U, 7MG

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	1.10	6/1487 (0.4%)	1.44	23/2315 (1.0%)
3	C	1.89	5/131 (3.8%)	2.09	3/200 (1.5%)
All	All	1.18	11/1618 (0.7%)	1.50	26/2515 (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

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	74	C	O3'-P	-21.57	1.28	1.61
2	B	75	C	O3'-P	-20.59	1.30	1.61
2	B	44	A	O3'-P	-13.56	1.40	1.61
2	B	72	C	O3'-P	-12.66	1.42	1.61
3	C	14	U	O3'-P	-9.78	1.46	1.61
3	C	15	U	O3'-P	-9.78	1.46	1.61
3	C	11	U	O3'-P	-9.72	1.46	1.61
3	C	12	U	O3'-P	-9.71	1.46	1.61
3	C	13	U	O3'-P	-7.16	1.50	1.61
2	B	35	A	O3'-P	6.48	1.70	1.61
2	B	76	A	C2'-O2'	5.05	1.50	1.42

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	74	C	O3'-P-O5'	30.97	150.46	104.00
3	C	13	U	P-O3'-C3'	21.83	152.94	120.20
2	B	35	A	P-O3'-C3'	21.29	152.14	120.20
2	B	72	C	O3'-P-O5'	17.66	130.50	104.00
3	C	13	U	O3'-P-O5'	17.05	129.58	104.00
2	B	34	OMG	O3'-P-O5'	12.19	122.28	104.00
2	B	44	A	O3'-P-O5'	-9.90	89.14	104.00
2	B	75	C	P-O3'-C3'	9.87	135.01	120.20
2	B	35	A	OP1-P-O3'	9.77	137.30	108.00
2	B	75	C	O3'-P-O5'	9.60	118.40	104.00
2	B	1	G	P-O3'-C3'	8.57	133.06	120.20
2	B	74	C	OP2-P-O3'	-8.40	82.79	108.00
2	B	35	A	OP2-P-O3'	-8.00	84.00	108.00
2	B	34	OMG	OP2-P-O3'	-7.75	84.76	108.00
2	B	72	C	OP1-P-O3'	-7.54	85.38	108.00
2	B	76	A	C4'-C3'-O3'	-7.20	102.20	113.00
2	B	74	C	P-O3'-C3'	-6.83	109.95	120.20
2	B	18	G	C5'-C4'-O4'	-6.71	99.04	109.10
2	B	72	C	P-O3'-C3'	-6.63	110.25	120.20
2	B	74	C	N1-C1'-C2'	6.22	121.33	112.00
2	B	44	A	OP2-P-O3'	6.08	126.23	108.00
2	B	35	A	O3'-P-O5'	-6.06	94.90	104.00
2	B	76	A	C3'-C2'-O2'	-5.65	102.22	110.70
2	B	21	A	C5'-C4'-C3'	5.36	124.05	116.00
3	C	13	U	OP2-P-O3'	-5.28	92.15	108.00
2	B	76	A	N9-C1'-C2'	5.21	119.82	112.00

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	16	0
2	B	1652	0	862	65	0
3	C	120	0	61	11	0
4	a	2889	0	0	29	0
5	b	123	0	0	2	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	4	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	4	0
28	d	173	0	0	6	0
29	e	191	0	0	7	0
30	f	189	0	0	9	0
31	g	122	0	0	1	0
32	h	164	0	0	0	0
33	l	133	0	0	0	0
34	m	117	0	0	1	0
35	n	122	0	0	0	0
36	o	84	0	0	2	0
37	p	138	0	0	2	0
38	q	113	0	0	6	0
39	r	52	0	0	0	0
40	s	110	0	0	0	0
41	t	76	0	0	1	0
42	u	110	0	0	0	0
43	v	89	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	w	64	0	0	0	0
45	x	60	0	0	1	0
All	All	11392	0	923	140	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 11.

All (140) 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)
30:f:100:LEU:CA	30:f:101:ASP:CA	1.80	1.58
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
28:d:196:ASN:CA	28:d:197:GLY:CA	2.06	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
38:q:59:ALA:CA	38:q:60:SER:CA	2.12	1.26
4:a:955:C:P	37:p:10:ILE:CA	2.26	1.24
1:A:923:A:P	10:H:21:ALA:CA	2.26	1.23
2:B:73:A:P	6:Z:254:VAL:CA	2.32	1.18
4:a:636:G:P	36:o:126:SER:CA	2.32	1.17
15:M:63:PHE:CA	19:Q:58:LYS:CA	2.24	1.16
2:B:73:A:OP2	6:Z:254:VAL:CA	1.93	1.16
2:B:25:C:O3'	2:B:26:M2G:P	2.12	1.05
3:C:15:U:O4	6:Z:209:SER:CA	2.02	1.05
4:a:451:C:P	30:f:48:SER:CA	2.45	1.05
4:a:2060:A:P	30:f:66:GLY:CA	2.45	1.04
28:d:113:MET:CA	28:d:114:GLU:CA	2.35	1.03
15:M:62:HIS:CA	19:Q:59:ALA:CA	2.40	0.99
5:b:51:G:P	38:q:72:GLU:CA	2.53	0.97
2:B:73:A:C2'	6:Z:255:ASN:CA	2.41	0.97
3:C:15:U:C4	6:Z:209:SER:CA	2.50	0.94
1:A:948:C:P	18:P:109:THR:CA	2.55	0.94
2:B:73:A:O5'	6:Z:254:VAL:CA	2.16	0.94
4:a:452:G:P	30:f:52:ALA:CA	0.84	0.94
2:B:73:A:OP2	6:Z:253:HIS:CA	2.16	0.93
2:B:73:A:H8	6:Z:254:VAL:CA	1.81	0.93
29:e:184:GLY:CA	29:e:185:GLY:CA	2.46	0.93
4:a:380:U:P	4:a:2233:U:P	2.66	0.93
2:B:1:G:H22	2:B:2:C:N4	1.65	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:a:607:U:P	30:f:105:LYS:CA	2.58	0.92
2:B:41:U:H6	2:B:41:U:H5'	1.35	0.92
2:B:33:U:C2	2:B:35:A:H5'	2.06	0.90
2:B:74:C:OP1	6:Z:255:ASN:CA	2.22	0.88
4:a:1820:U:P	28:d:158:GLY:CA	2.61	0.88
4:a:1997:G:P	29:e:221:LYS:CA	2.62	0.87
4:a:1994:C:P	29:e:224:GLY:CA	2.63	0.87
4:a:2785:C:P	29:e:99:VAL:CA	2.63	0.86
4:a:469:G:P	30:f:56:THR:CA	2.64	0.86
2:B:10:2MG:C5	2:B:26:M2G:HM12	2.12	0.84
2:B:73:A:C8	6:Z:254:VAL:CA	2.62	0.83
3:C:15:U:H3	6:Z:209:SER:CA	1.93	0.82
2:B:33:U:O2	2:B:35:A:H3'	1.80	0.81
2:B:25:C:H2'	2:B:26:M2G:O4'	1.80	0.81
3:C:15:U:N3	6:Z:209:SER:CA	2.43	0.81
4:a:1826:G:P	28:d:227:VAL:CA	2.70	0.80
1:A:521:G:P	17:O:73:GLU:CA	2.69	0.80
4:a:2123:G:P	27:c:129:ARG:CA	2.70	0.79
2:B:1:G:H21	2:B:2:C:N4	1.80	0.78
6:Z:112:GLN:CA	6:Z:362:LYS:CA	2.62	0.77
2:B:1:G:H22	2:B:2:C:H41	1.25	0.76
2:B:73:A:H2'	6:Z:255:ASN:CA	2.17	0.74
2:B:34:OMG:H8	2:B:34:OMG:OP1	1.71	0.73
2:B:10:2MG:C4	2:B:26:M2G:HM12	2.22	0.73
1:A:1060:C:P	15:M:52:GLY:CA	2.77	0.72
2:B:10:2MG:C5	2:B:26:M2G:CM1	2.71	0.72
4:a:558:G:P	34:m:91:LYS:CA	2.78	0.72
5:b:49:C:P	38:q:110:THR:CA	2.78	0.71
4:a:1995:U:P	29:e:223:LYS:CA	2.79	0.71
2:B:34:OMG:HN1	3:C:13:U:H3	1.40	0.69
2:B:37:YG:H1'	2:B:37:YG:H31	1.74	0.68
2:B:1:G:N2	2:B:2:C:C4	2.61	0.66
29:e:97:THR:CA	29:e:98:GLU:CA	2.74	0.66
3:C:16:U:O4	6:Z:209:SER:CA	2.44	0.66
2:B:44:A:C2'	2:B:45:G:H5'	2.25	0.66
38:q:53:ASN:CA	38:q:54:GLY:CA	2.74	0.65
38:q:60:SER:CA	38:q:61:ALA:CA	2.75	0.65
2:B:26:M2G:HM22	2:B:44:A:C2	2.32	0.65
2:B:72:C:H3'	6:Z:254:VAL:CA	2.27	0.64
2:B:74:C:P	6:Z:255:ASN:CA	2.88	0.62
30:f:81:PRO:CA	30:f:89:ALA:CA	2.76	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:62:HIS:CA	19:Q:58:LYS:CA	2.78	0.62
3:C:16:U:C4	6:Z:209:SER:CA	2.83	0.61
2:B:40:5MC:H2'	2:B:41:U:H5'	1.82	0.61
4:a:636:G:P	36:o:128:GLY:CA	2.88	0.61
2:B:44:A:O2'	2:B:45:G:H5'	2.00	0.61
4:a:2680:C:P	29:e:205:THR:CA	2.89	0.61
2:B:41:U:H5'	2:B:41:U:C6	2.27	0.59
4:a:270(Y):G:P	4:a:273:G:P	3.01	0.59
4:a:2125:G:P	27:c:104:LEU:CA	2.91	0.59
2:B:41:U:H2'	2:B:42:G:O4'	2.03	0.59
2:B:64:A:H2'	2:B:65:G:O4'	2.04	0.58
2:B:73:A:C8	6:Z:255:ASN:CA	2.87	0.58
2:B:41:U:H6	2:B:41:U:C5'	2.13	0.57
1:A:1109:C:P	1:A:1191:A:P	3.03	0.57
2:B:44:A:H2'	2:B:45:G:O4'	2.04	0.57
4:a:970:C:P	45:x:15:TYR:CA	2.93	0.56
1:A:427:U:P	9:G:40:PRO:CA	2.93	0.56
2:B:37:YG:H31	2:B:37:YG:C1'	2.36	0.56
1:A:1236:A:P	1:A:1305:G:P	3.04	0.56
27:c:156:ILE:CA	27:c:157:LYS:CA	2.85	0.55
2:B:16:H2U:H1'	2:B:17:H2U:OP2	2.07	0.55
1:A:1367:C:P	14:L:114:TYR:CA	2.95	0.55
4:a:607:U:P	30:f:104:ASP:CA	2.95	0.54
4:a:2312:U:P	31:g:54:ALA:CA	2.96	0.54
2:B:29:A:O2'	2:B:30:G:H5'	2.06	0.54
2:B:72:C:C3'	6:Z:254:VAL:CA	2.88	0.52
2:B:40:5MC:H2'	2:B:41:U:C5'	2.40	0.51
2:B:37:YG:H32	2:B:38:A:O4'	2.10	0.51
2:B:69:U:H2'	2:B:70:C:C6	2.46	0.50
4:a:1342:A:P	41:t:54:THR:CA	3.00	0.50
28:d:116:MET:CA	28:d:117:SER:CA	2.91	0.49
2:B:16:H2U:O2'	2:B:17:H2U:OP2	2.21	0.49
1:A:785:G:P	4:a:1837:C:P	3.10	0.49
28:d:76:ARG:CA	28:d:113:MET:CA	2.91	0.49
2:B:23:A:O2'	2:B:24:G:H5'	2.12	0.49
2:B:30:G:O2'	2:B:31:A:H5'	2.12	0.48
15:M:63:PHE:CA	19:Q:57:ARG:CA	2.91	0.48
1:A:1250:A:P	14:L:68:GLY:CA	3.02	0.48
2:B:33:U:O2	2:B:35:A:H5'	2.13	0.48
1:A:1229:A:P	18:P:116:THR:CA	3.02	0.48
1:A:1108:G:P	8:F:174:PRO:CA	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:A:N9	6:Z:255:ASN:CA	2.78	0.46
1:A:1206:G:P	8:F:194:GLY:CA	3.04	0.46
38:q:111:PRO:CA	38:q:114:LYS:CA	2.95	0.45
4:a:2486:G:P	37:p:144:THR:CA	3.05	0.45
2:B:43:G:H2'	2:B:44:A:C8	2.53	0.44
2:B:50:U:O2'	2:B:51:G:H5'	2.17	0.44
3:C:14:U:H2'	3:C:15:U:C6	2.52	0.44
2:B:34:OMG:OP1	2:B:34:OMG:C8	2.64	0.44
2:B:16:H2U:C2'	2:B:17:H2U:OP2	2.65	0.44
2:B:23:A:H2'	2:B:24:G:C8	2.52	0.44
3:C:12:U:H2'	3:C:13:U:C6	2.52	0.44
2:B:50:U:C2'	2:B:51:G:H5'	2.48	0.44
3:C:11:U:H2'	3:C:12:U:C6	2.52	0.44
3:C:15:U:H2'	3:C:16:U:C6	2.52	0.43
1:A:783:C:P	1:A:1516:G:P	3.16	0.43
2:B:32:OMC:H6	2:B:32:OMC:O5'	2.01	0.43
2:B:37:YG:C21	2:B:37:YG:H101	2.48	0.43
2:B:34:OMG:H3'	2:B:35:A:H5''	2.00	0.42
4:a:1442:G:P	4:a:1630:G:P	3.18	0.42
27:c:159:GLY:CA	27:c:160:ARG:CA	2.97	0.42
4:a:39:C:P	30:f:94:THR:CA	3.08	0.42
2:B:37:YG:C3	2:B:37:YG:C2'	2.97	0.42
2:B:44:A:C2'	2:B:45:G:C5'	2.96	0.42
2:B:37:YG:C1'	2:B:37:YG:C3	2.98	0.42
1:A:1368:G:P	14:L:113:LYS:CA	3.08	0.41
4:a:2393:A:P	4:a:2429:G:P	3.18	0.41
2:B:52:U:O2'	2:B:53:G:H5'	2.20	0.41

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 ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	0/1522	-	-
2	B	73/76 (96%)	12 (16%)	3 (4%)
3	C	5/6 (83%)	1 (20%)	0
4	a	0/2916	-	-
5	b	0/123	-	-
All	All	78/4643 (1%)	13 (16%)	3 (3%)

All (13) 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
2	B	21	A
2	B	34	OMG
2	B	35	A
2	B	36	A
2	B	41	U
2	B	75	C
2	B	76	A
3	C	14	U

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 ⓘ

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	YG	B	37	2	38,42,43	0.90	2 (5%)	45,62,65	2.32	10 (22%)
2	7MG	B	46	2	23,26,27	0.98	2 (8%)	27,39,42	1.26	2 (7%)
2	1MA	B	58	2	21,25,26	2.09	2 (9%)	30,37,40	1.86	7 (23%)
2	OMC	B	32	2	19,22,23	0.45	0	25,31,34	0.59	0
2	PSU	B	55	2	18,21,22	0.74	0	21,30,33	0.89	0
2	OMG	B	34	2,3	23,26,27	0.54	0	32,38,41	0.51	0
2	M2G	B	26	2	24,27,28	0.47	0	33,40,43	0.42	0
2	H2U	B	17	2	18,21,22	0.70	1 (5%)	19,30,33	0.93	1 (5%)
2	PSU	B	39	2	18,21,22	0.70	0	21,30,33	0.73	0
2	5MU	B	54	2	19,22,23	0.46	0	27,32,35	0.67	0
2	2MG	B	10	2	23,26,27	0.49	0	33,38,41	0.43	0
2	5MC	B	49	2	19,22,23	0.73	0	26,32,35	0.76	1 (3%)
2	H2U	B	16	2	18,21,22	0.76	1 (5%)	19,30,33	1.02	1 (5%)
2	5MC	B	40	2	19,22,23	0.71	1 (5%)	26,32,35	0.71	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	YG	B	37	2	-	7/24/42/43	0/4/4/4
2	7MG	B	46	2	-	2/7/37/38	0/3/3/3
2	1MA	B	58	2	-	0/7/25/26	0/3/3/3
2	OMC	B	32	2	-	0/9/27/28	0/2/2/2
2	PSU	B	55	2	-	0/7/25/26	0/2/2/2
2	OMG	B	34	2,3	-	1/9/27/28	0/3/3/3
2	M2G	B	26	2	-	0/11/29/30	0/3/3/3
2	H2U	B	17	2	-	0/7/38/39	0/2/2/2
2	PSU	B	39	2	-	0/7/25/26	0/2/2/2
2	5MU	B	54	2	-	0/7/25/26	0/2/2/2
2	2MG	B	10	2	-	0/9/27/28	0/3/3/3
2	5MC	B	49	2	-	0/7/25/26	0/2/2/2
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

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	58	1MA	C6-N6	8.47	1.48	1.28
2	B	58	1MA	C2-N3	3.74	1.37	1.30
2	B	37	YG	C2-N2	3.11	1.38	1.33
2	B	46	7MG	C4-N9	2.75	1.41	1.37
2	B	16	H2U	C2-N1	2.62	1.39	1.35
2	B	40	5MC	C5-C4	-2.54	1.42	1.44
2	B	46	7MG	C5-N7	2.49	1.38	1.35
2	B	37	YG	C3-N3	2.25	1.51	1.47
2	B	17	H2U	C2-N1	2.15	1.38	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	37	YG	C11-C12-N1	8.59	111.36	105.31
2	B	37	YG	C24-O23-C21	6.39	123.03	115.63
2	B	58	1MA	CM1-N1-C6	-4.99	112.41	120.15
2	B	46	7MG	C4-C5-N7	4.85	111.11	105.38
2	B	37	YG	C5-C4-N3	4.76	127.86	123.99
2	B	58	1MA	CM1-N1-C2	4.73	130.18	120.50
2	B	37	YG	O23-C21-N20	4.60	118.51	110.77
2	B	58	1MA	N1-C2-N3	4.26	131.05	126.00
2	B	37	YG	C10-C11-N2	3.61	126.55	119.32
2	B	37	YG	C2-N1-C12	-3.59	103.48	109.94
2	B	37	YG	O23-C21-O22	-3.40	119.66	124.62
2	B	37	YG	N3-C2-N2	-3.17	122.25	126.62
2	B	58	1MA	C6-C5-N7	-3.01	126.83	132.16
2	B	37	YG	C19-O18-C16	2.92	122.53	115.92
2	B	46	7MG	N9-C8-N7	2.79	107.32	103.37
2	B	58	1MA	N1-C6-N6	2.72	126.53	119.71
2	B	49	5MC	C5-C6-N1	-2.41	120.70	123.31
2	B	37	YG	O18-C16-C15	2.40	117.60	111.49
2	B	16	H2U	O3'-C3'-C2'	2.39	119.47	111.82
2	B	40	5MC	C5-C6-N1	-2.38	120.73	123.31
2	B	17	H2U	C5-C4-N3	-2.27	114.27	116.69
2	B	58	1MA	C6-C5-C4	2.27	123.14	118.32
2	B	58	1MA	C5-C4-N3	-2.06	124.24	127.27

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	16	H2U	O4'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
2	B	16	H2U	O4'-C1'-N1-C6
2	B	16	H2U	C2'-C1'-N1-C6
2	B	37	YG	C15-C16-O18-C19
2	B	46	7MG	C2'-C1'-N9-C8
2	B	37	YG	O17-C16-O18-C19
2	B	37	YG	C12-C13-C14-C15
2	B	16	H2U	C2'-C1'-N1-C2
2	B	37	YG	C13-C14-C15-C16
2	B	40	5MC	O4'-C4'-C5'-O5'
2	B	46	7MG	C2'-C1'-N9-C4
2	B	34	OMG	C4'-C5'-O5'-P
2	B	37	YG	C13-C14-C15-N20
2	B	37	YG	C14-C15-C16-O18
2	B	37	YG	C14-C15-C16-O17

There are no ring outliers.

8 monomers are involved in 22 short contacts:

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

5.5 Carbohydrates [i](#)

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

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

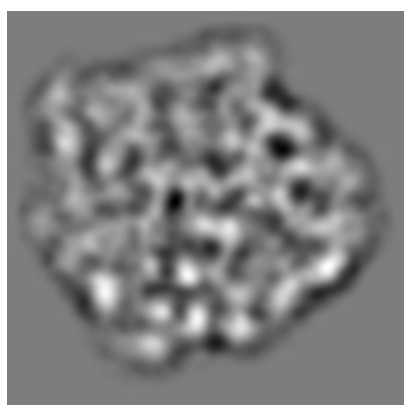
6 Map visualisation [i](#)

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.

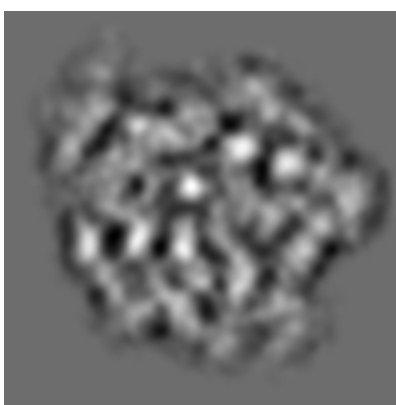
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

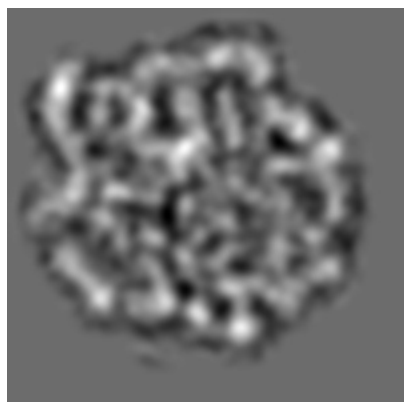


Z

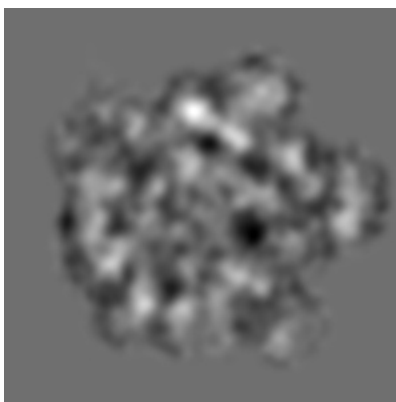
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

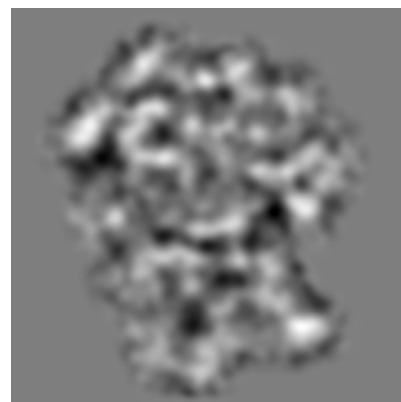
6.2.1 Primary map



X Index: 60



Y Index: 60

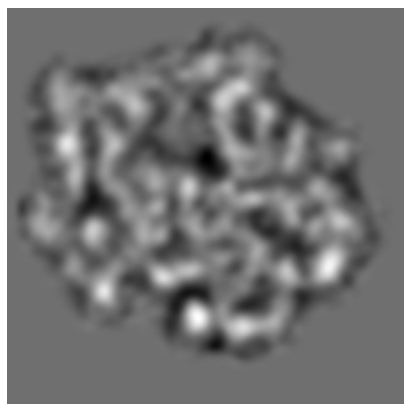


Z Index: 60

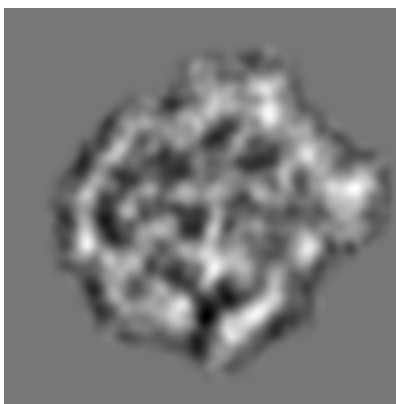
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

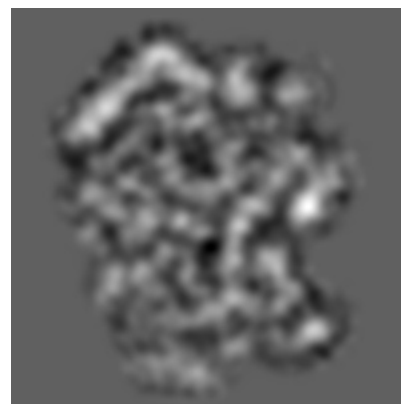
6.3.1 Primary map



X Index: 53



Y Index: 74

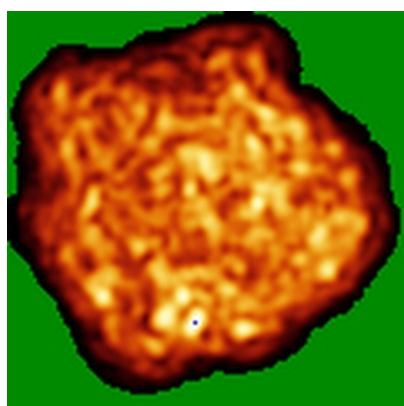


Z Index: 56

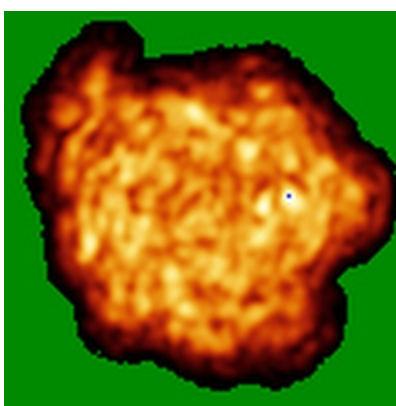
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

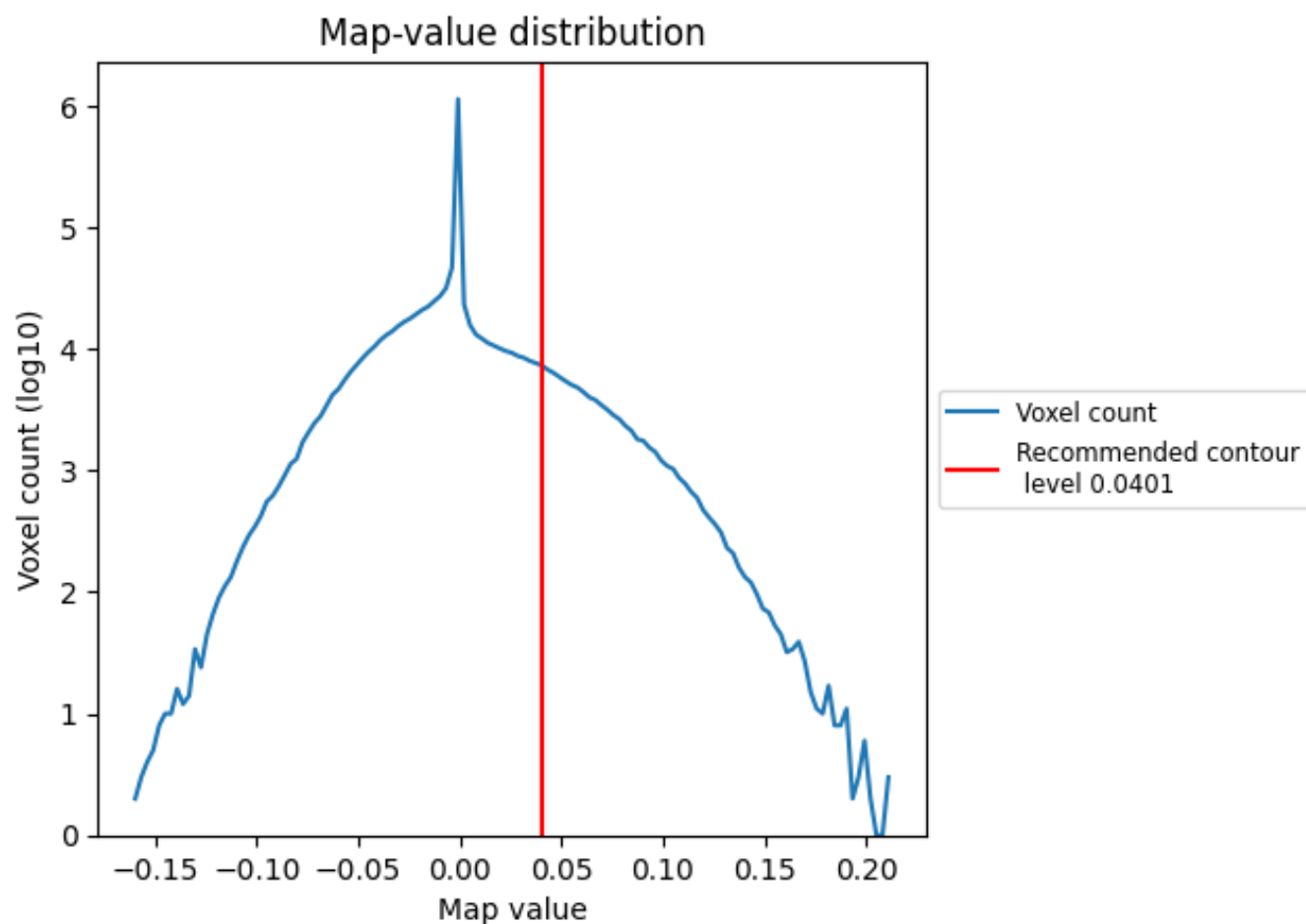
6.6 Mask visualisation

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

7 Map analysis [i](#)

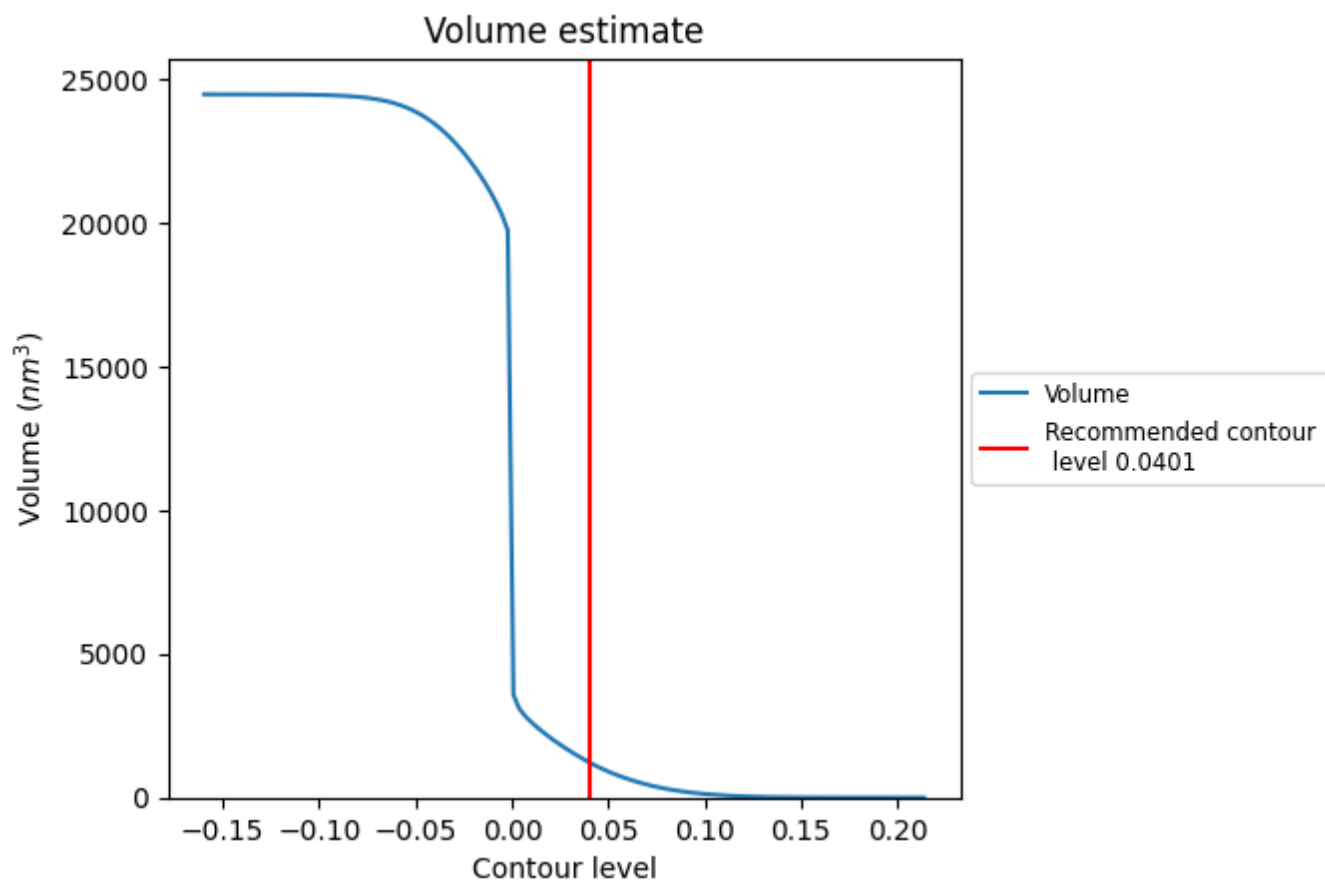
This section contains the results of statistical analysis of the map.

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.

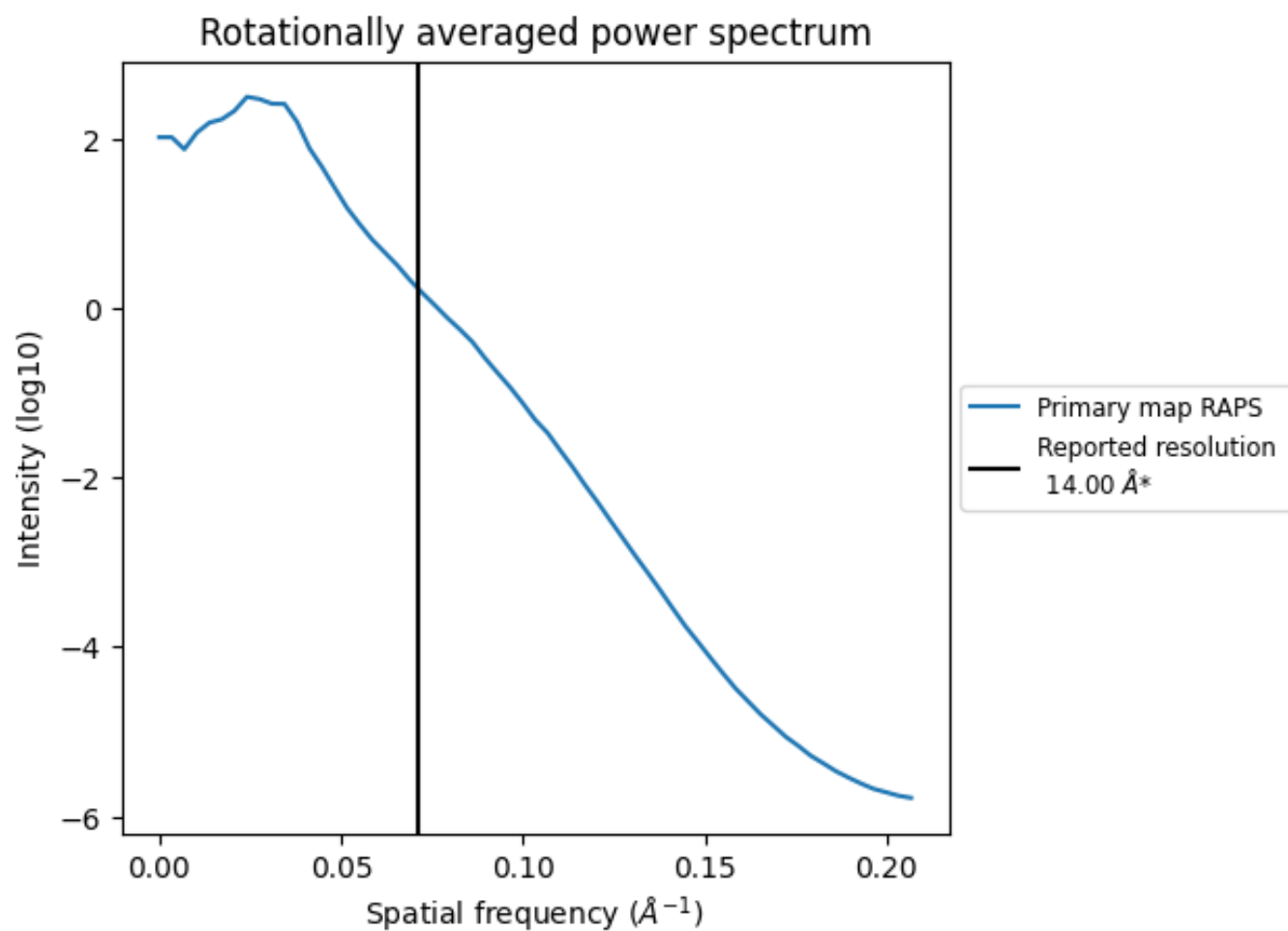
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1226 nm³; 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 Å⁻¹

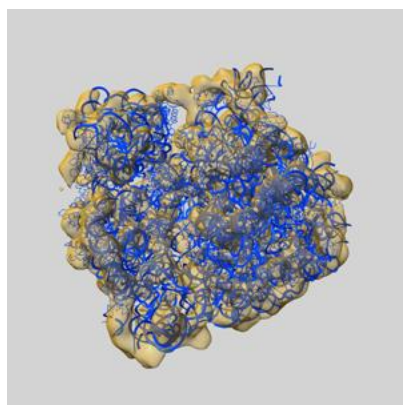
8 Fourier-Shell correlation

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

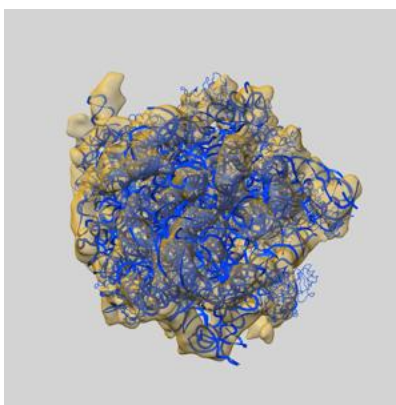
9 Map-model fit [i](#)

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.

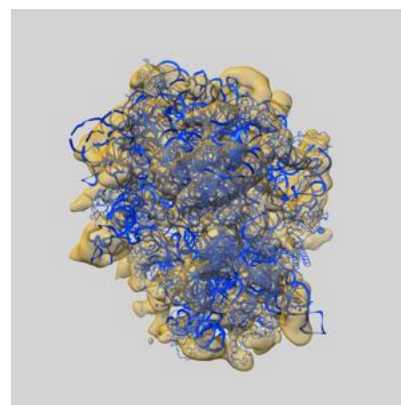
9.1 Map-model overlay [i](#)



X



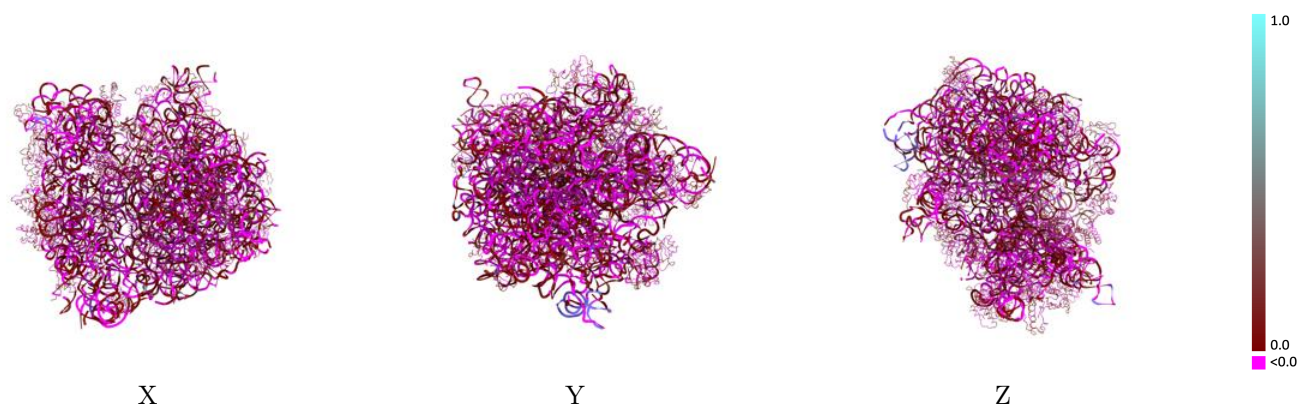
Y



Z

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](#)

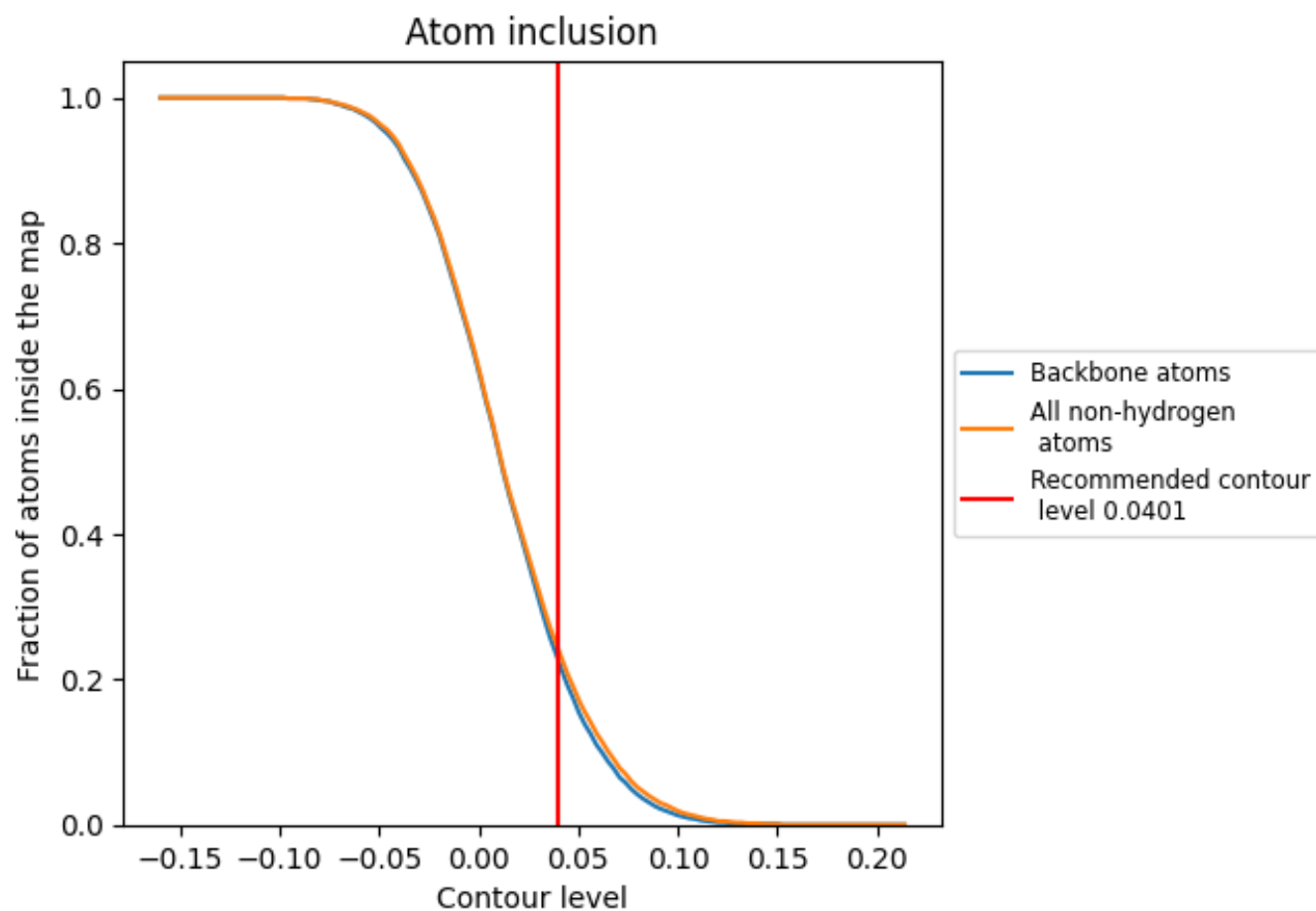


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

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	0.2410	0.0130
A	0.2630	0.0080
B	0.3490	0.0370
C	0.0000	-0.0190
E	0.2050	0.0140
F	0.1750	0.0200
G	0.2070	0.0190
H	0.1270	0.0090
I	0.2770	0.0010
J	0.3550	0.0190
K	0.1520	-0.0160
L	0.1580	0.0120
M	0.2960	0.0050
N	0.3530	0.0310
O	0.3630	0.0280
P	0.2240	0.0190
Q	0.0500	-0.0220
R	0.2610	0.0430
S	0.0240	0.0070
T	0.0960	0.0070
U	0.1100	-0.0070
V	0.0750	0.0320
W	0.1510	-0.0240
X	0.0000	-0.0200
Z	0.1270	0.0250
a	0.2740	0.0090
b	0.3500	0.0050
c	0.0270	-0.0150
d	0.0690	0.0200
e	0.1570	0.0030
f	0.2960	0.0060
g	0.1470	-0.0100
h	0.3110	0.0200
l	0.2780	0.0250
m	0.1110	-0.0110



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Chain	Atom inclusion	Q-score
n	 0.0330	 0.0130
o	 0.3570	 0.0110
p	 0.0580	 -0.0190
q	 0.2740	 0.0160
r	 0.0000	 -0.0410
s	 0.1000	 -0.0170
t	 0.1180	 0.0430
u	 0.1360	 -0.0120
v	 0.5060	 0.0340
w	 0.3440	 0.0800
x	 0.1330	 0.0170