



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 08:13 PM UTC

PDB ID : 8G34 / pdb_00008g34
EMDB ID : EMD-29688
Title : Time-resolved cryo-EM study of the 70S recycling by the HflX:1st intermediate
Authors : Bhattacharjee, S.; Brown, P.Z.; Frank, J.
Deposited on : 2023-02-06
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

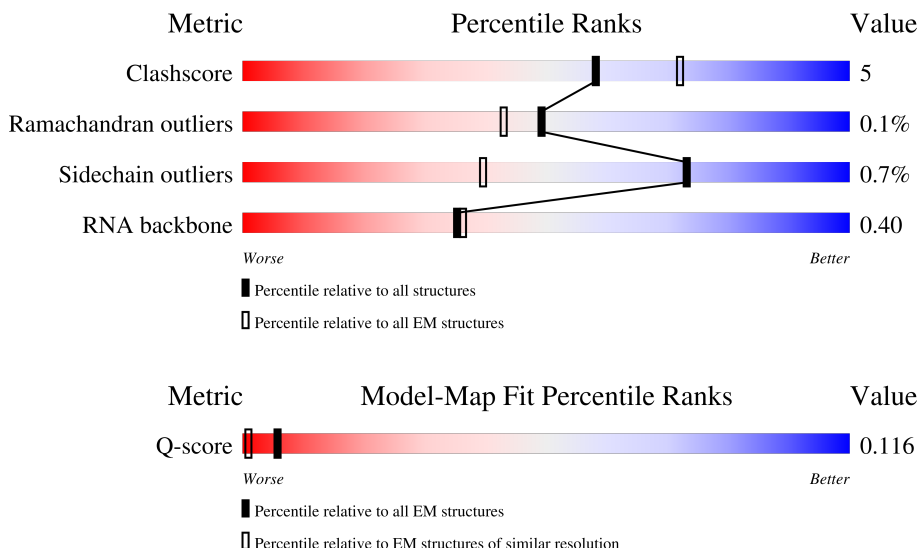
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	64	61% 77% 23%
5	4	38	74% 82% 18%
6	A	117	45% 57% 38% 5%
7	B	2903	54% 63% 32% .
8	C	272	83% 86% 14%
9	D	209	63% 82% 18%
10	E	201	78% 86% 14%
11	F	178	97% 81% 19%
12	G	176	85% 84% 16%
13	J	142	66% 87% 13%
14	K	122	76% 71% 28% .
15	L	143	62% 79% 21%
16	M	136	51% 85% 15%
17	N	121	64% 77% 21% .
18	O	116	73% 82% 18%
19	P	114	73% 74% 26%
20	Q	117	69% 83% 17%
21	R	103	64% 85% 14% .
22	S	110	70% 85% 15%
23	T	94	83% 71% 29%
24	U	103	81% 86% 14%
25	V	94	78% 82% 18%
26	W	79	56% 75% 25%
27	X	77	62% 83% 17%
28	Y	63	76% 86% 13% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Z	58	
30	6	426	
31	x	206	
32	f	151	
33	h	127	
34	i	98	
35	l	114	
36	m	100	
37	r	79	
38	u	59	
39	w	218	
40	c	205	
41	d	150	
42	e	100	
43	g	129	
44	j	117	
45	k	123	
46	n	88	
47	o	82	
48	p	80	
49	q	55	
50	s	85	
51	t	51	
52	v	1539	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 144256 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 GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	6	426	Total	C	N	O	S	0	0
			3403	2129	624	641	9		

- Molecule 31 is a protein called 30S ribosomal protein S3.

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

- Molecule 32 is a protein called 30S ribosomal protein S7.

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

- Molecule 33 is a protein called 30S ribosomal protein S9.

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

- Molecule 34 is a protein called 30S ribosomal protein S10.

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

- Molecule 35 is a protein called 30S ribosomal protein S13.

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

- Molecule 36 is a protein called 30S ribosomal protein S14.

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

- Molecule 37 is a protein called 30S ribosomal protein S19.

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

- Molecule 38 is a protein called Transcription termination/antitermination protein NusG.

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

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	w	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 40 is a protein called 30S ribosomal protein S4.

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

- Molecule 41 is a protein called 30S ribosomal protein S5.

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

- Molecule 42 is a protein called 30S ribosomal protein S6, non-modified isoform.

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

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S15.

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

- Molecule 47 is a protein called 30S ribosomal protein S16.

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

- Molecule 48 is a protein called 30S ribosomal protein S17.

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

- Molecule 49 is a protein called 30S ribosomal protein S18.

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

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21 (Fragment).

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 52 is a RNA chain called 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	1539	Total	C	N	O	P	0	0
			33010	14724	6050	10698	1538		

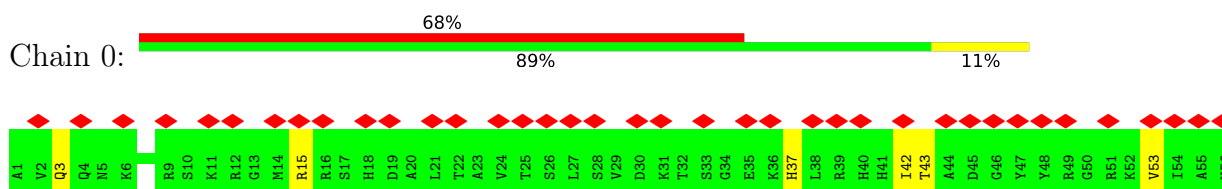
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	1408	C	A	conflict	GB 1758835854

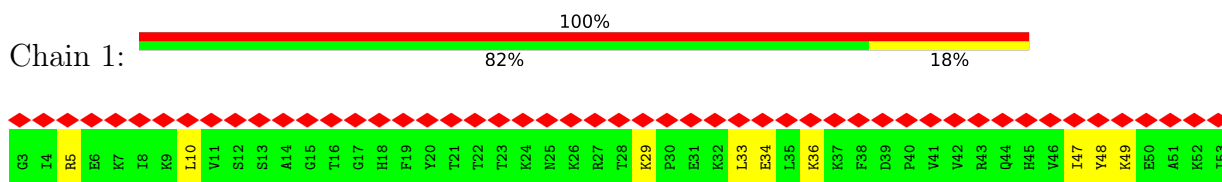
3 Residue-property plots [i](#)

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.

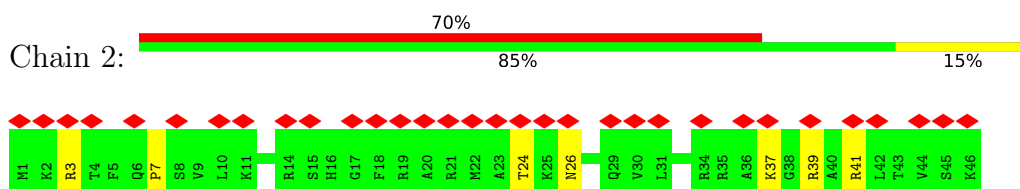
- Molecule 1: 50S ribosomal protein L32



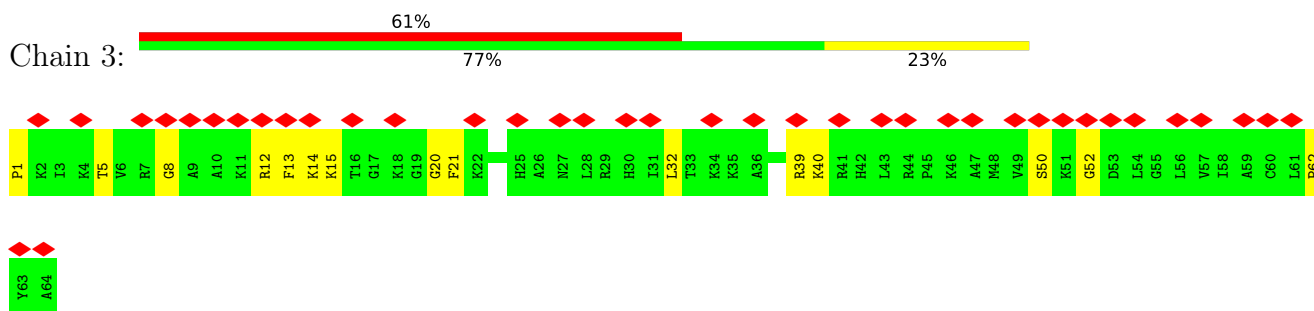
- Molecule 2: 50S ribosomal protein L33



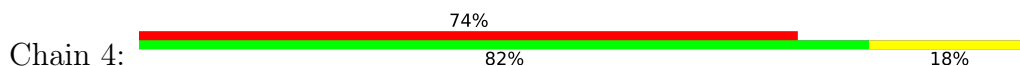
- Molecule 3: 50S ribosomal protein L34

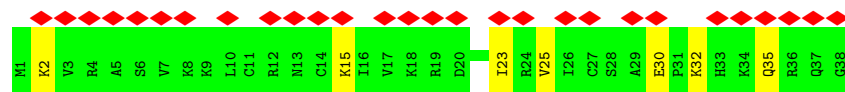


- Molecule 4: 50S ribosomal protein L35

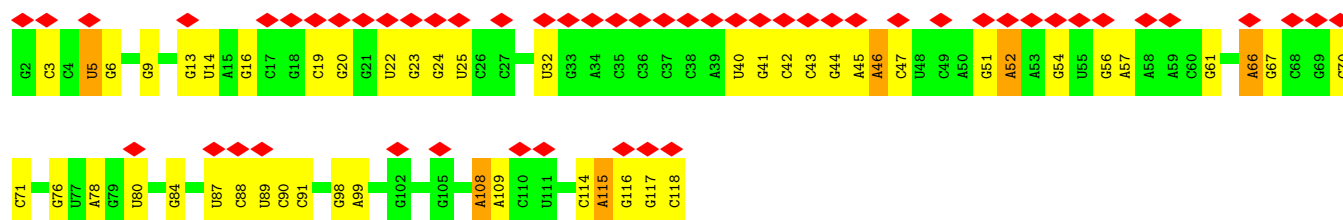


- Molecule 5: 50S ribosomal protein L36

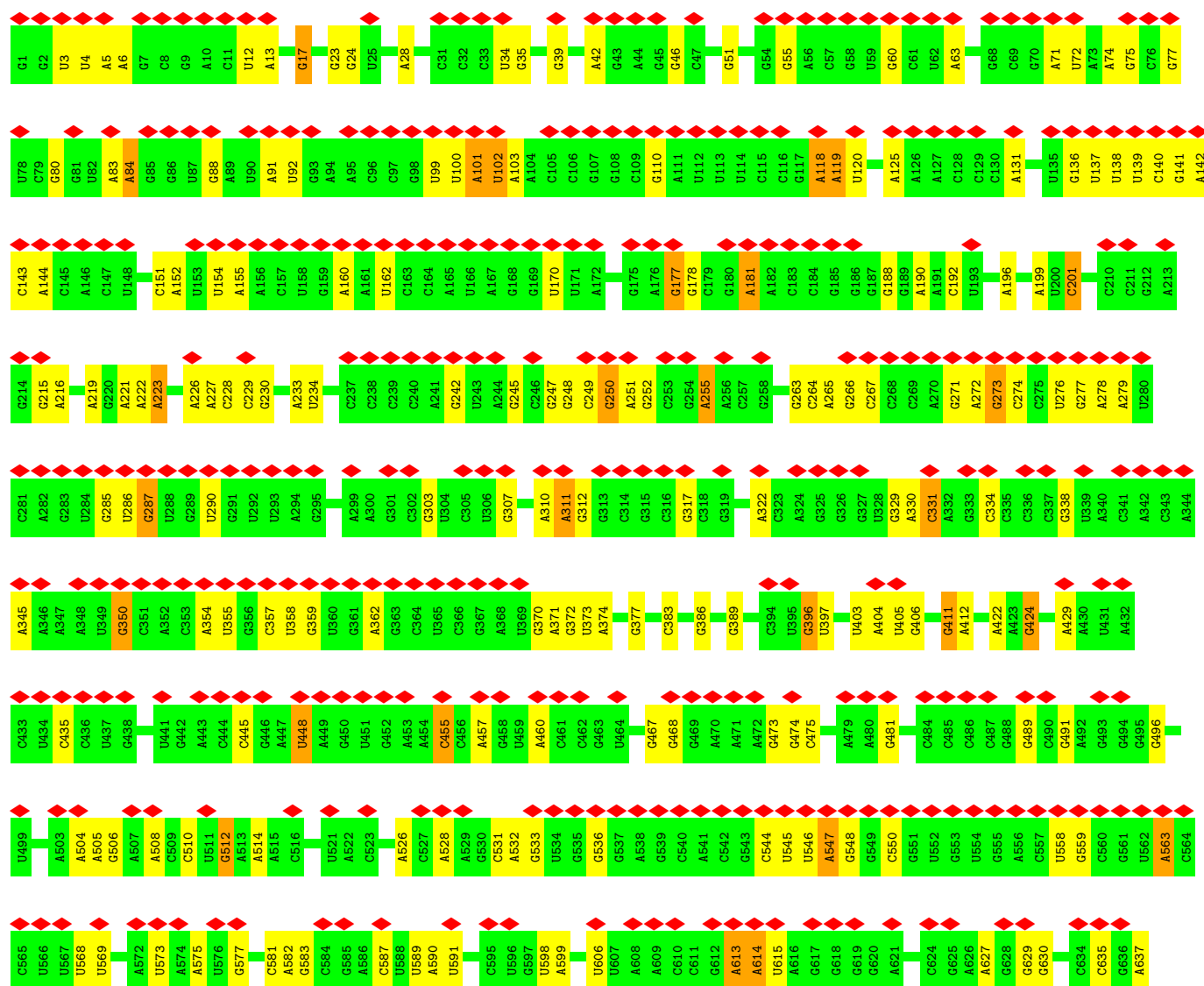


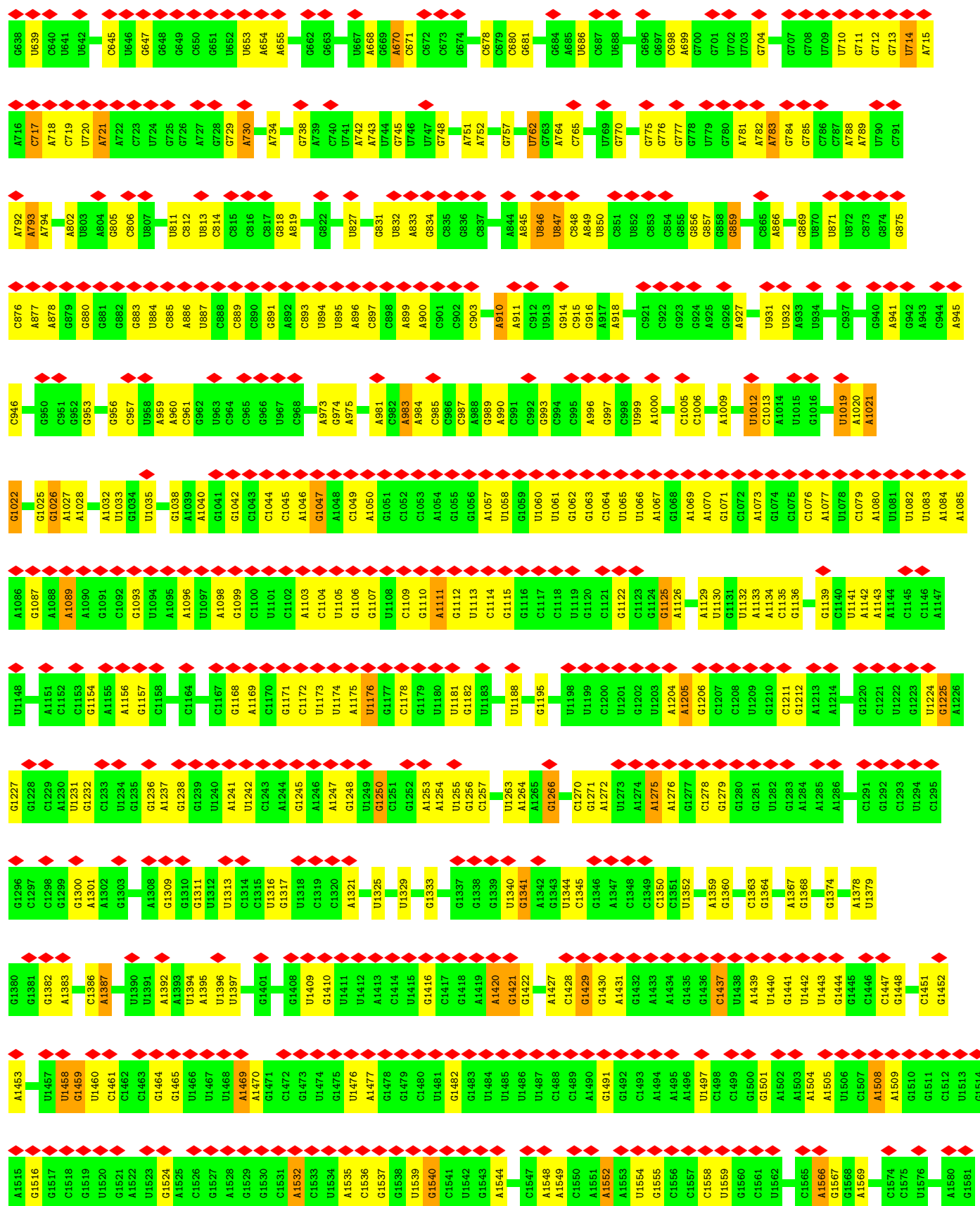


• Molecule 6: 5S

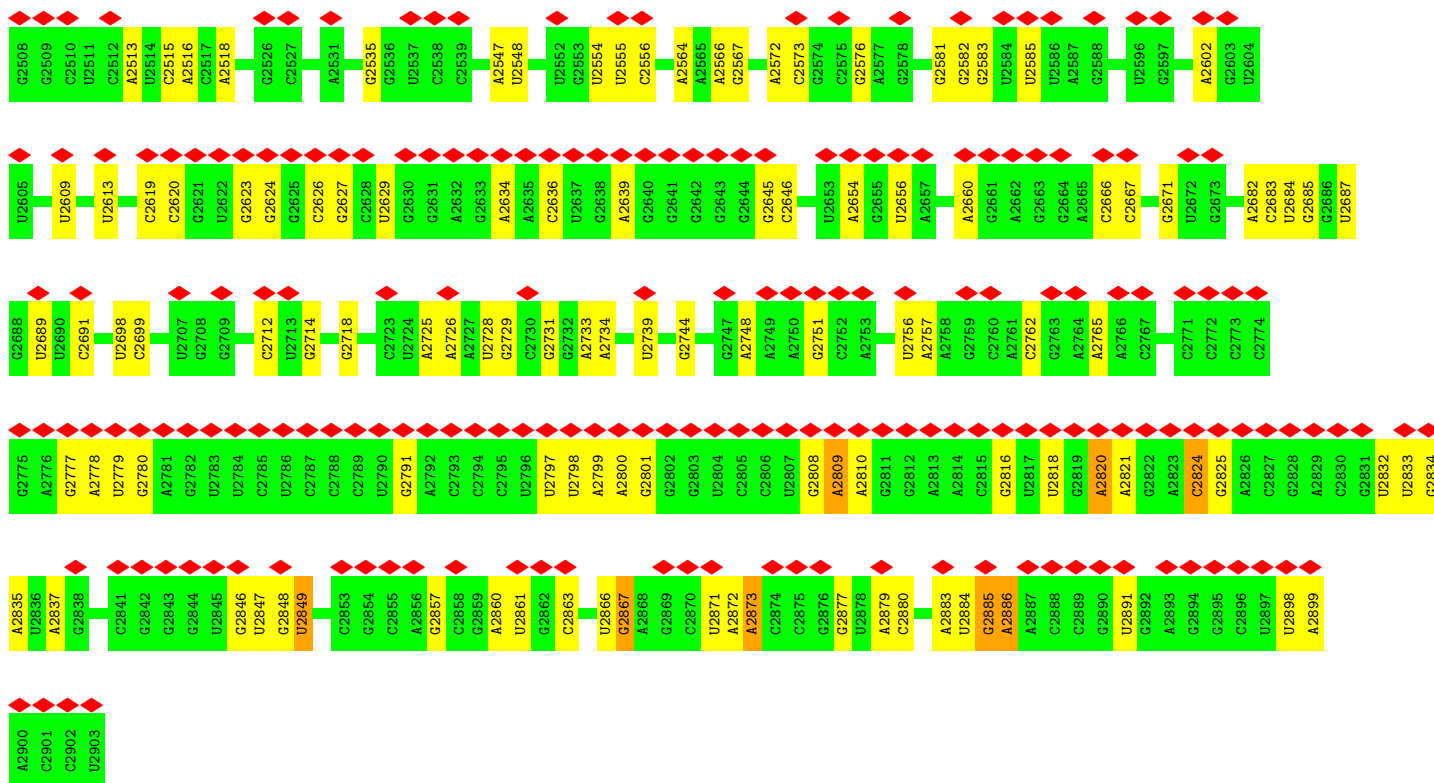


• Molecule 7: 23S

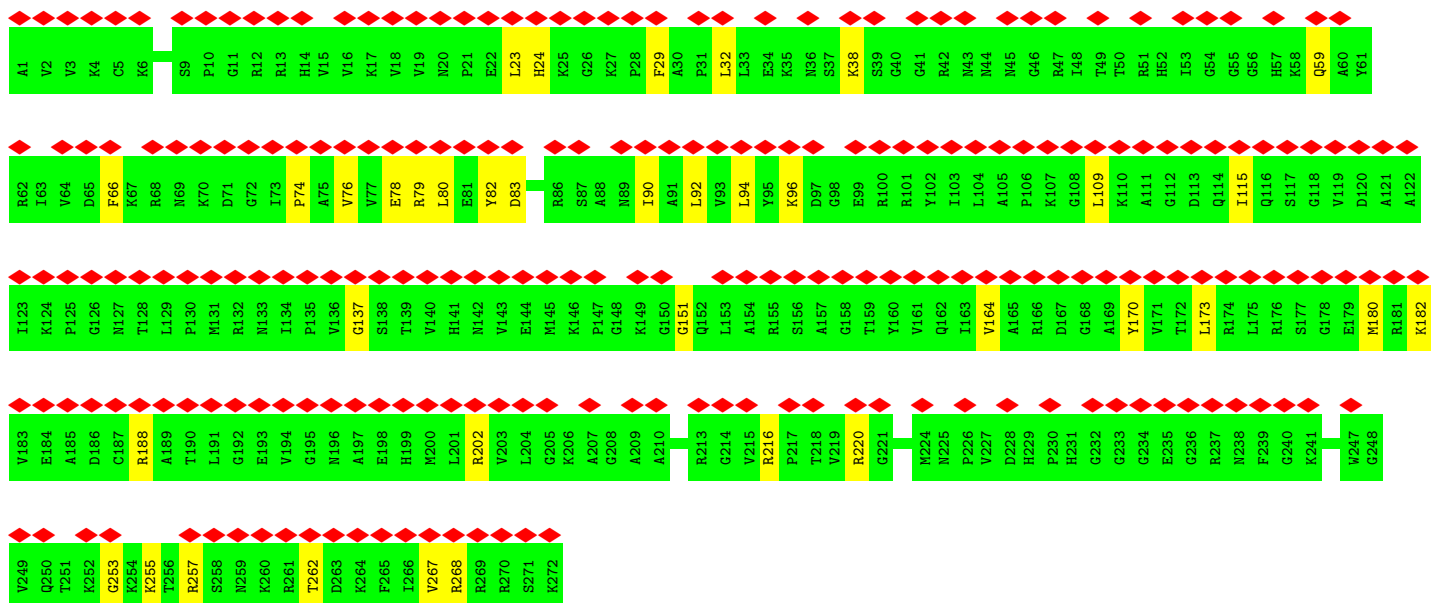
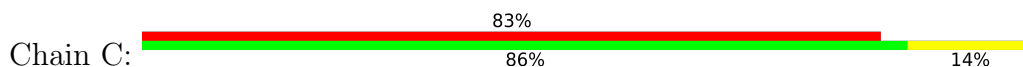




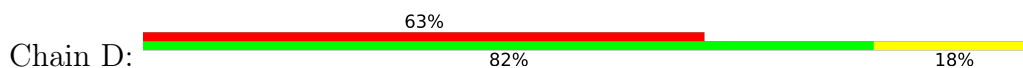
U2423	C2424	A2425	A2426	C2427	C2428	G2429	A2430	U2431	A2432	A2433	A2434	A2435	G2436	C2437	U2438	U2441	G2444	G2447	A2448	U2449	A2450	A2451	G2452	G2458	C2466	C2467	A2468	A2469	C2472	U2473	U2474	C2475	A2476	U2477	A2478	G2481	G2485	U2491	U2492	U2493	G2494	U2500	C2501	G2502	A2503	U2504	G2505	U2506	G2507										
G2325	G2330	G2331	A2332	A2333	C2334	A2335	A2336	G2341	G2345	A2346	C2347	U2348	G2349	C2350	G2354	G2355	U2356	G2357	G2360	G2361	G2362	G2371	C2374	A2377	A2378	G2379	C2380	A2381	G2382	C2383	U2384	C2385	G2389	U2390	G2391	U2392	G2395	G2396	U2402	C2403	U2404	G2405	A2406	A2412	G2413	C2422													
C2258	U2259	U2262	C2263	C2264	U2265	A2266	A2267	A2268	C2269	A2270	G2271	U2272	A2273	A2274	C2275	G2276	G2277	A2278	G2279	G2280	C2283	A2284	G2285	G2286	A2287	A2288	U2291	U2292	U2295	U2296	A2297	A2298	U2299	C2300	C2301	U2302	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310	A2311	U2312	C2313	A2314	G2319	U2320	U2321	A2322	G2323	U2324					
U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	A2198	A2199	U2202	U2203	G2204	A2205	C2206	G2207	C2208	G2209	U2210	A2211	A2212	U2213	C2214	G2215	G2216	G2217	U2218	U2219	U2220	G2221	C2222	G2223	G2224	A2225	C2226	U2231	G2232	U2233	G2234	G2235	U2236	G2237	G2238	G2239	U2243	U2244	U2245	G2246	A2247	C2248	U2249	U2250	G2251	G2254						
G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	C2146	A2147	U2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	G2159	C2160	G2161	G2162	A2163	C2164	G2165	C2166	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	U2187
G2057	A2058	A2059	A2060	G2061	A2062	G2066	G2067	U2068	G2069	A2070	A2071	G2072	U2076	A2077	U2081	A2082	U2086	C2091	U2092	G2093	A2094	A2095	C2096	A2097	U2098	U2099	G2100	A2101	G2102	A2103	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127					
A1987	G1988	G1989	G1990	U1991	G1992	U1993	C1994	U1995	C1996	C1997	A1998	C1999	G2002	A2003	G2004	A2005	C2008	G2012	U2016	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	A2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041	A2042	C2043	C2044	G2045	G2046	C2047	G2048	G2049	C2050	A2051	A2052	C2055	G2056						
A1919	C1920	G1921	G1922	U1923	C1924	C1925	U1926	U1927	A1928	G1929	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1939	G1945	U1946	C1947	U1948	G1949	G1950	U1951	A1952	A1953	G1954	U1955	U1956	U1957	C1958	G1959	A1960	C1961	C1962	U1963	G1964	C1965	A1966	G1968	A1969	U1970	U1971	G1972	G1973	C1974	U1975	U1976	A1977	A1978	U1979	C1985	C1986			
A1848	G1849	G1850	U1851	U1852	G1857	A1858	G1861	G1862	G1867	C1868	G1869	C1870	A1871	A1872	G1873	A1874	G1875	A1876	U1880	C1881	U1882	U1883	G1884	A1885	U1886	G1887	G1888	A1889	C1893	C1894	G1895	G1896	U1897	U1898	A1899	A1900	A1901	C1902	G1903	G1904	C1905	G1906	G1907	C1908	C1909	G1910	U1911	A1912	A1913	C1914	U1915	A1916	U1917	A1918					
U1781	U1782	A1783	U1784	A1785	A1786	A1789	C1790	A1791	G1792	C1793	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803	G1804	A1808	A1809	A1810	G1811	U1812	U1886	G1813	G1814	A1815	C1816	A1819	U1820	G1823	G1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834	G1835	C1836	C1837	C1838	G1839	G1842	C1843	C1844	G1845	G1846	A1847					
A1649	A1650	G1651	A1652	G1653	A1654	A1655	U1657	G1660	G1661	U1662	G1663	A1664	A1665	G1666	G1667	A1668	A1669	G1674	C1675	U1680	G1681	G1682	U1683	G1684	C1685	C1686	G1687	U1688	A1689	A1690	C1691	U1692	U1693	C1694	G1695	G1696	G1697	A1698	G1699	A1700	A1701	G1702	G1703	C1704	A1705	C1706	U1709	G1710	A1711	U1712	A1713	U1714	G1715	U1716					
A1582	A1583	U1584	C1585	A1586	G1587	G1588	U1589	A1590	A1591	C1592	A1593	U1594	C1595	A1596	A1597	A1598	U1599	C1600	G1601	U1602	A1603	C1604	C1605	C1606	C1607	A1610	C1611	C1612	G1613	A1614	C1617	A1618	G1619	C1625	A1626	G1627	G1628	U1629	A1630	G1631	A1632	G1633	A1634	A1635	U1636	A1637	A1640	A1641	G1642	G1643	G1644	G1645	C1646	U1647	U1648				

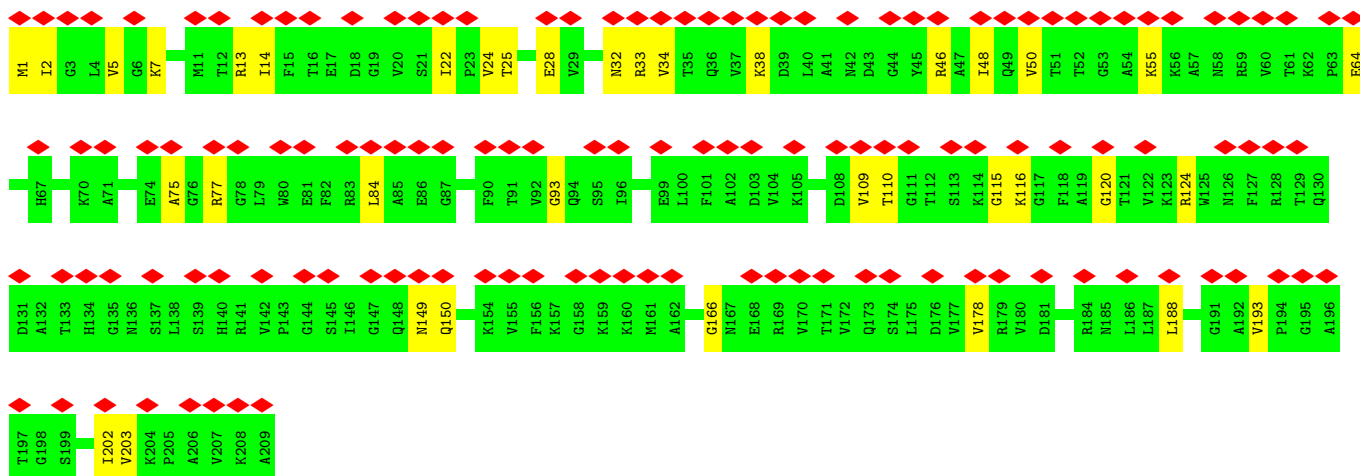


• Molecule 8: 50S ribosomal protein L2

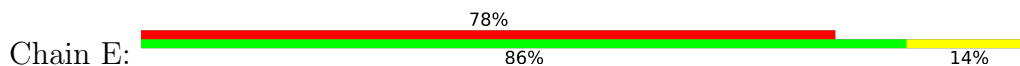


• Molecule 9: 50S ribosomal protein L3

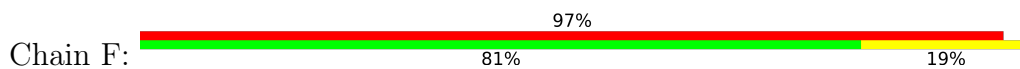




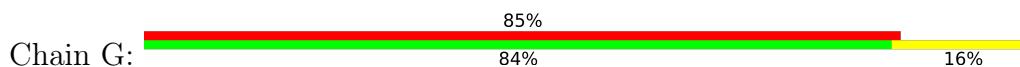
• Molecule 10: 50S ribosomal protein L4

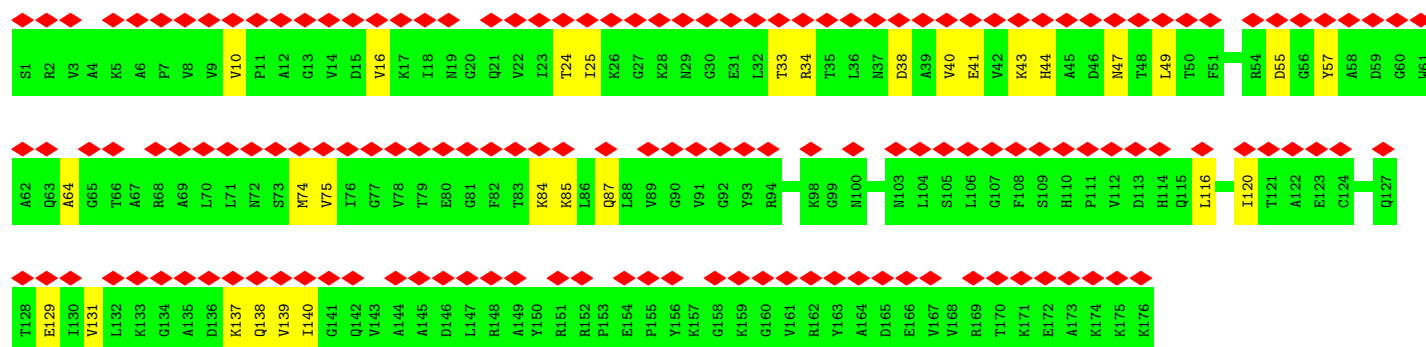


• Molecule 11: 50S ribosomal protein L5

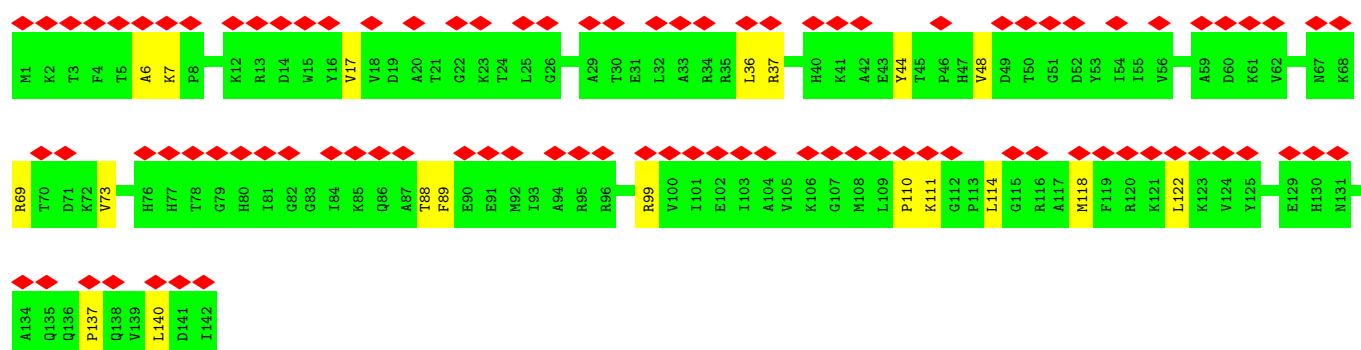
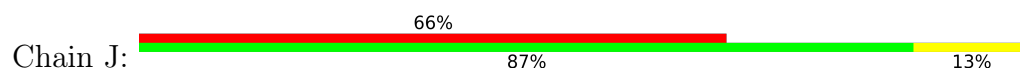


• Molecule 12: 50S ribosomal protein L6

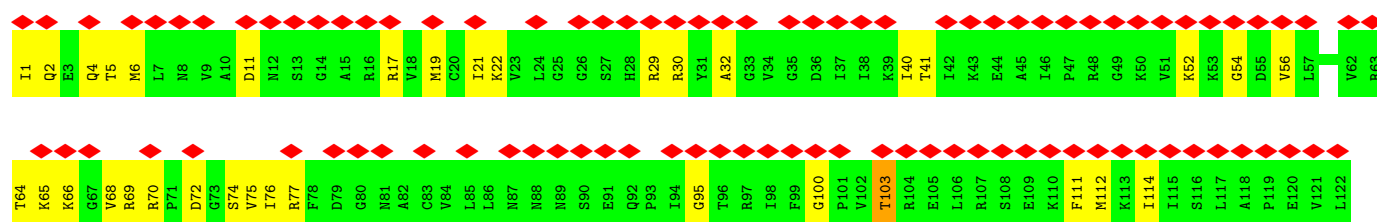
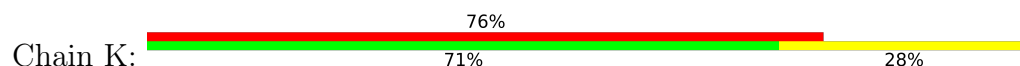




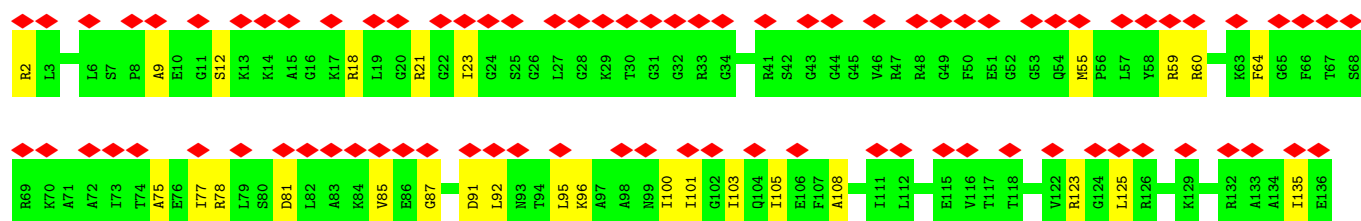
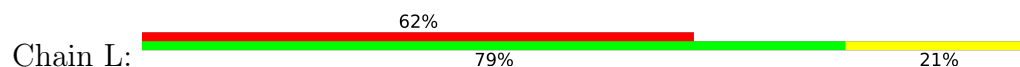
• Molecule 13: 50S ribosomal protein L13

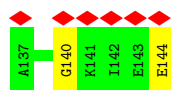


• Molecule 14: 50S ribosomal protein L14

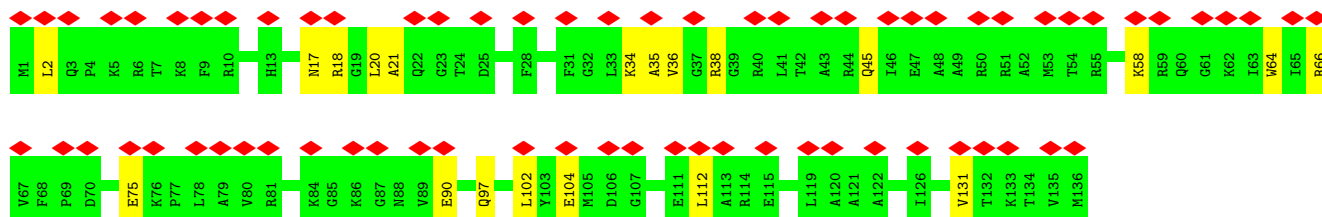
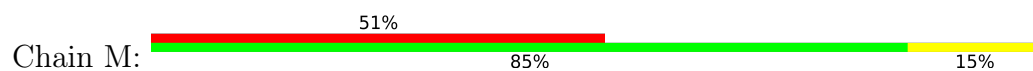


• Molecule 15: 50S ribosomal protein L15

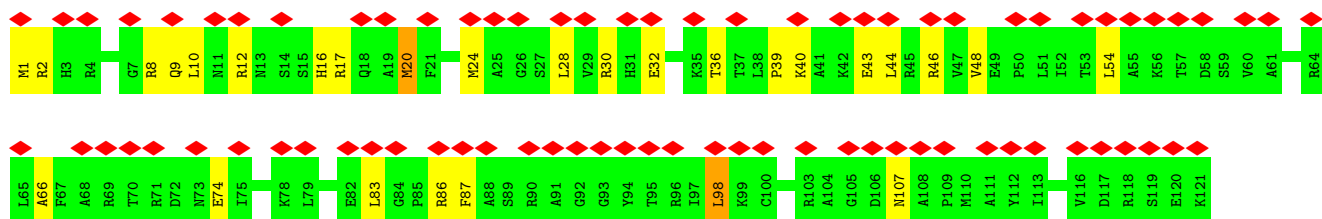
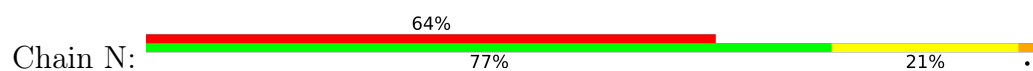




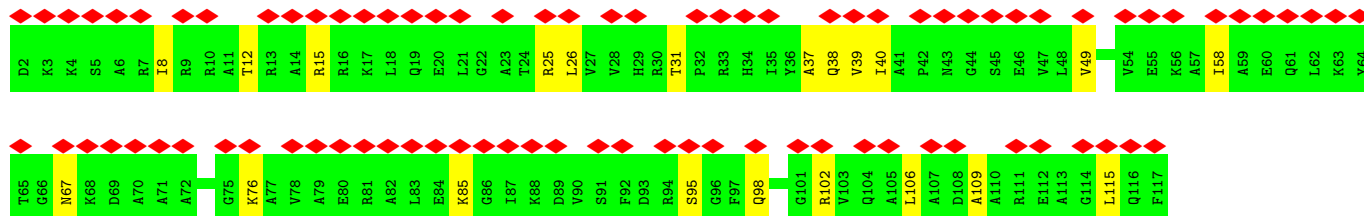
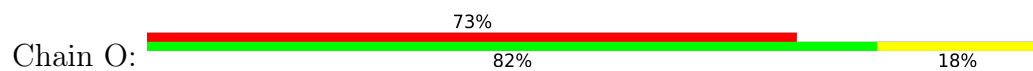
- Molecule 16: 50S ribosomal protein L16



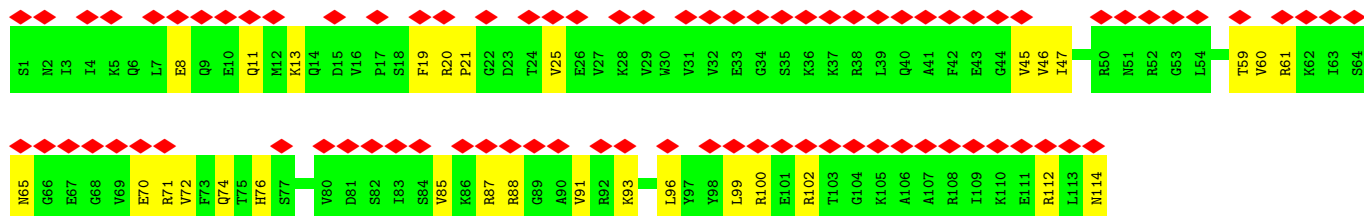
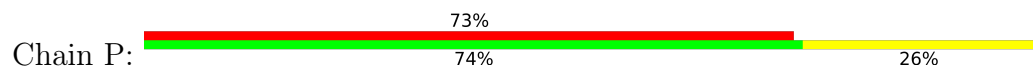
- Molecule 17: 50S ribosomal protein L17



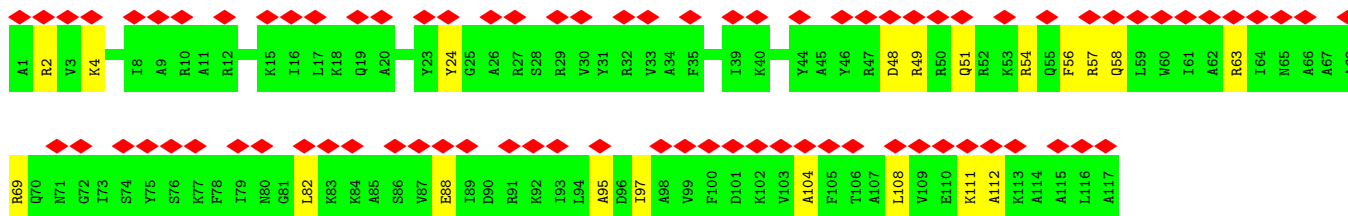
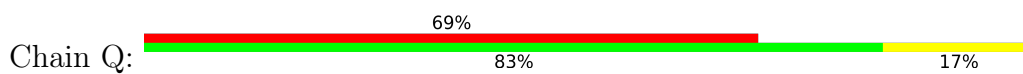
- Molecule 18: 50S ribosomal protein L18



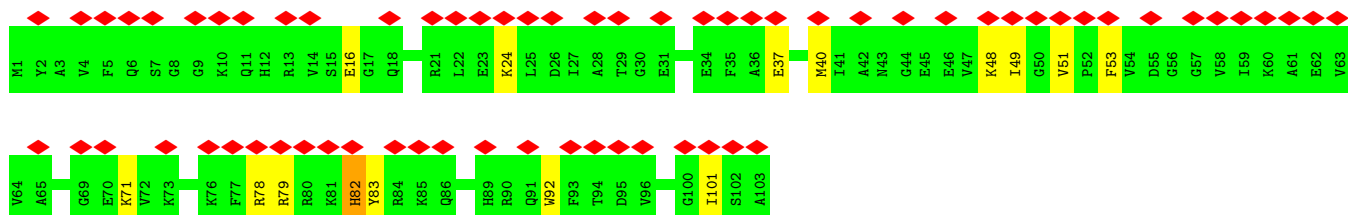
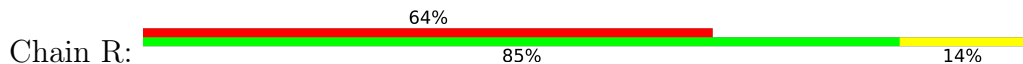
- Molecule 19: 50S ribosomal protein L19



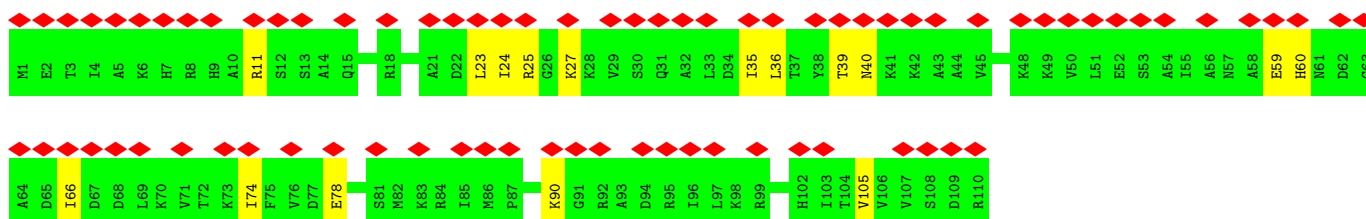
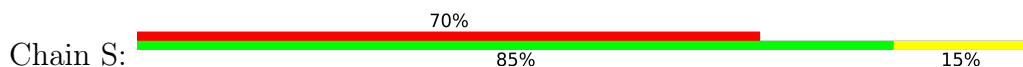
- Molecule 20: 50S ribosomal protein L20



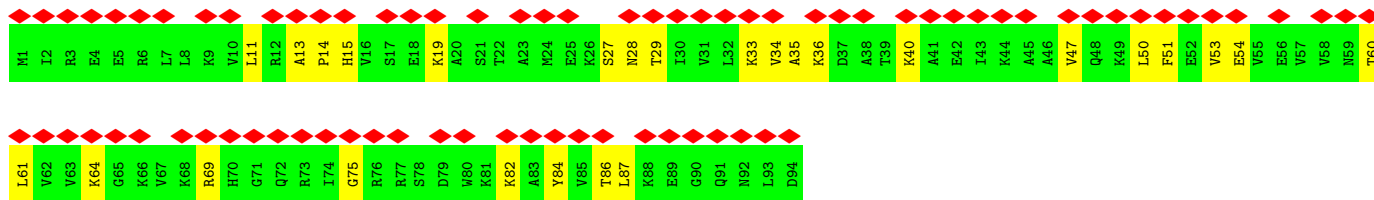
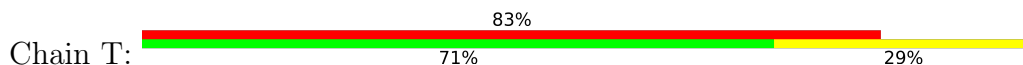
• Molecule 21: Ribosomal protein L21



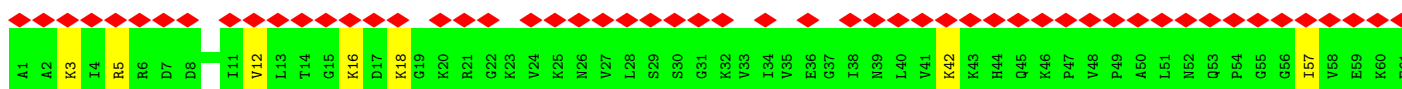
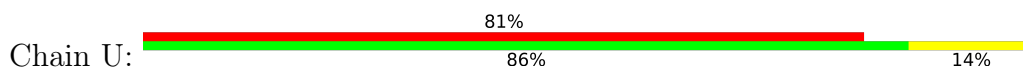
• Molecule 22: 50S ribosomal protein L22



• Molecule 23: 50S ribosomal protein L23



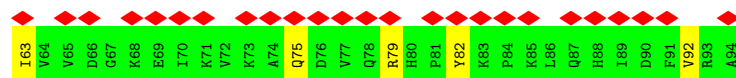
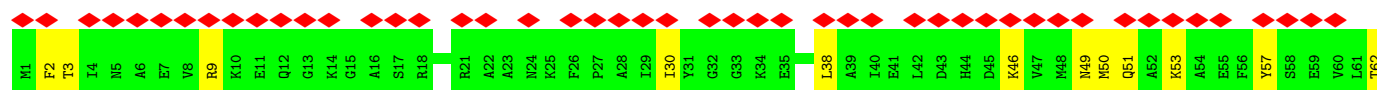
• Molecule 24: 50S ribosomal protein L24





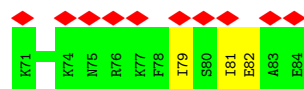
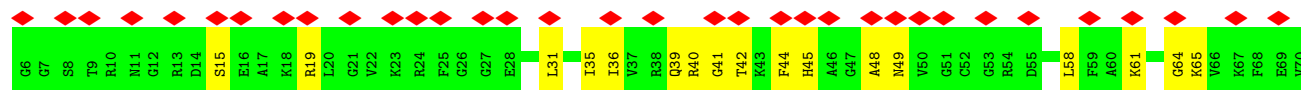
• Molecule 25: 50S ribosomal protein L25

Chain V: 78% 82% 18%



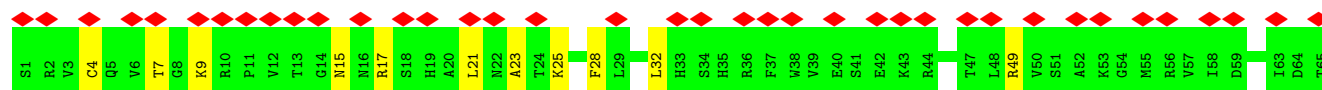
• Molecule 26: 50S ribosomal protein L27

Chain W: 56% 75% 25%



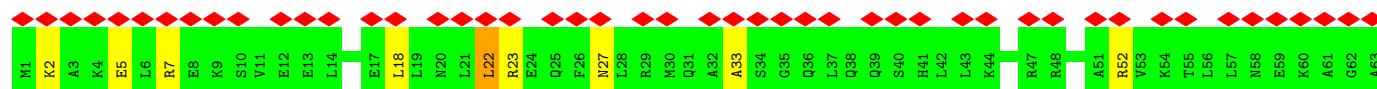
• Molecule 27: 50S ribosomal protein L28

Chain X: 62% 83% 17%



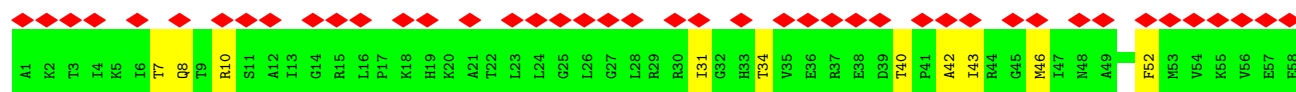
• Molecule 28: 50S ribosomal protein L29

Chain Y: 76% 86% 13%

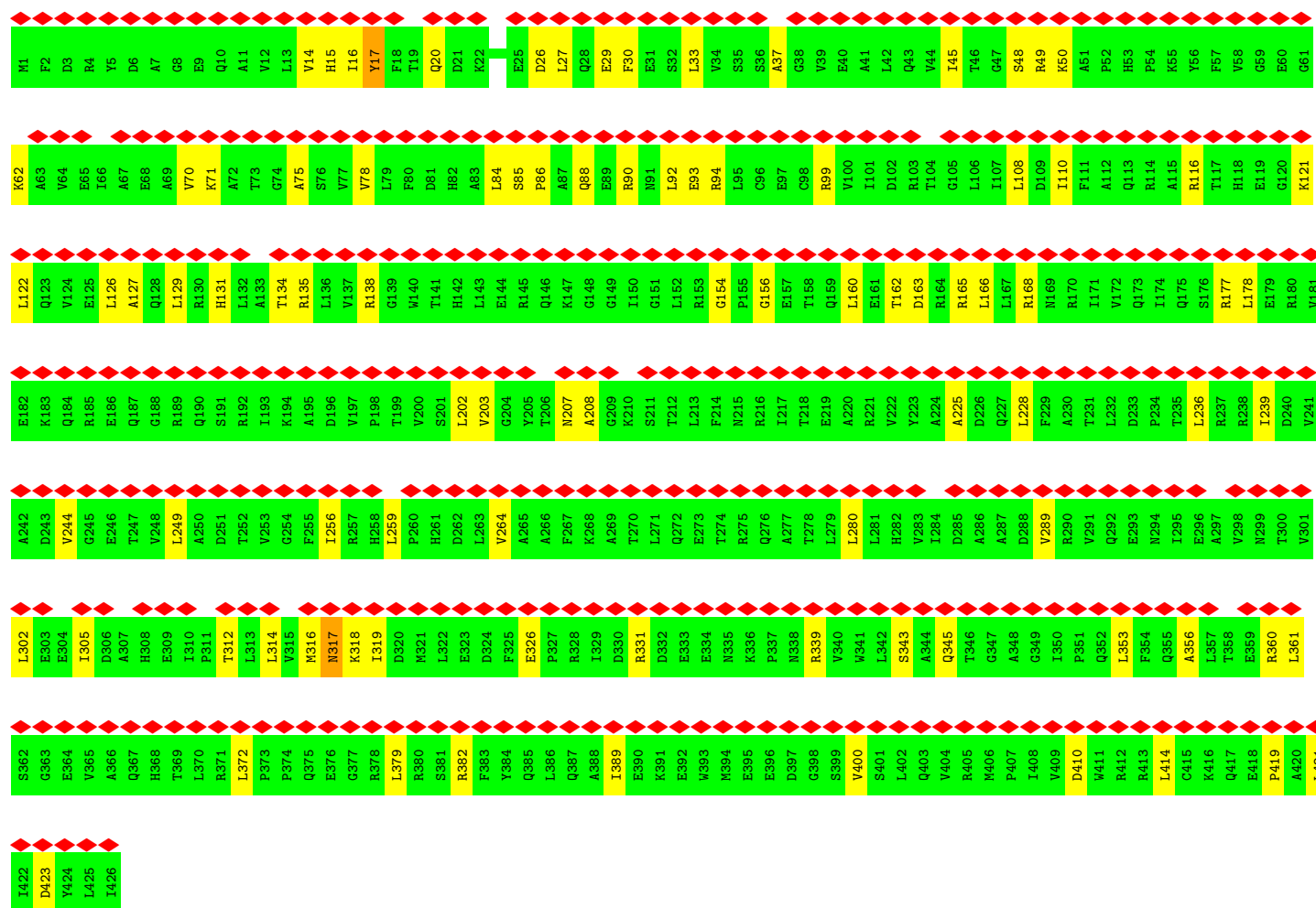
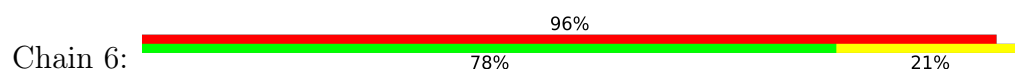


• Molecule 29: 50S ribosomal protein L30

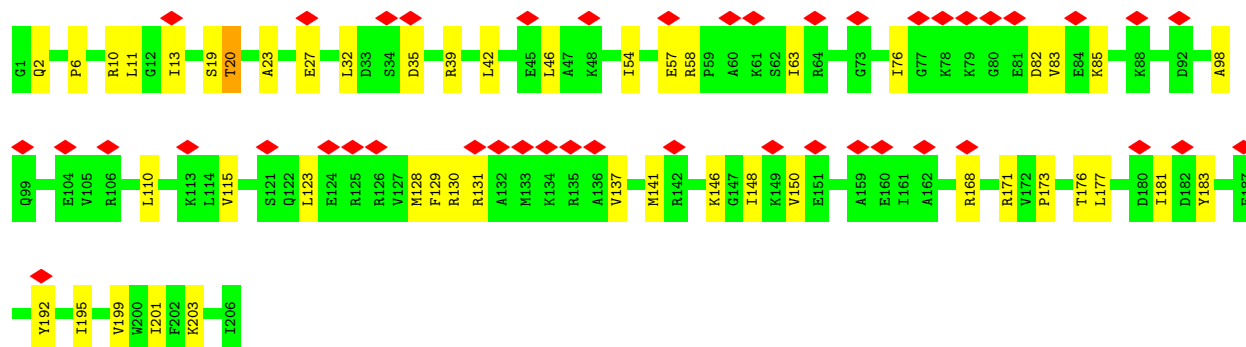
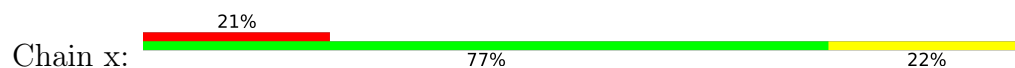
Chain Z: 74% 83% 17%



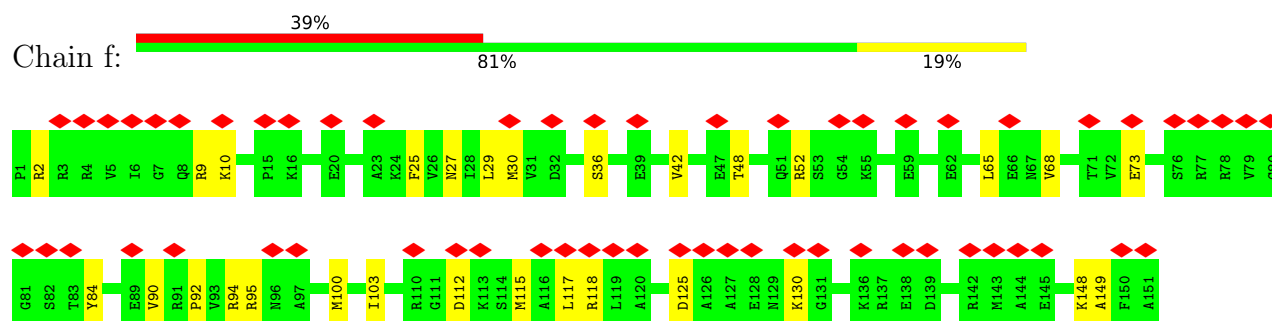
• Molecule 30: GTPase HflX



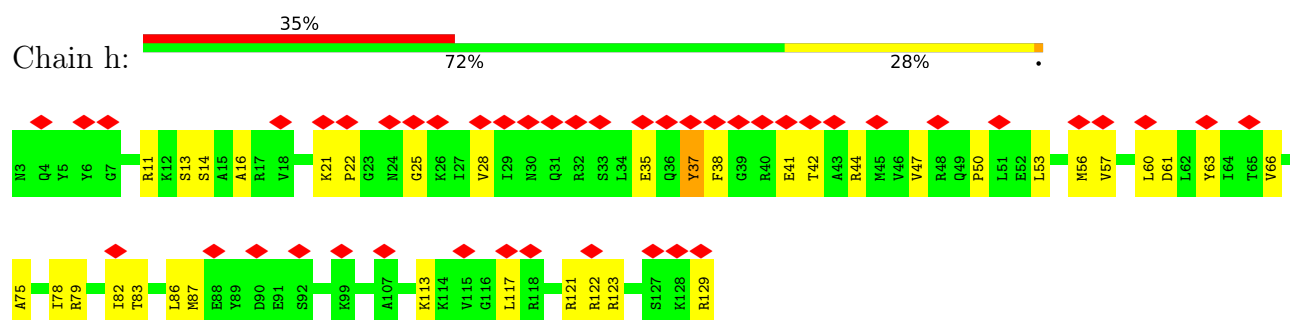
• Molecule 31: 30S ribosomal protein S3



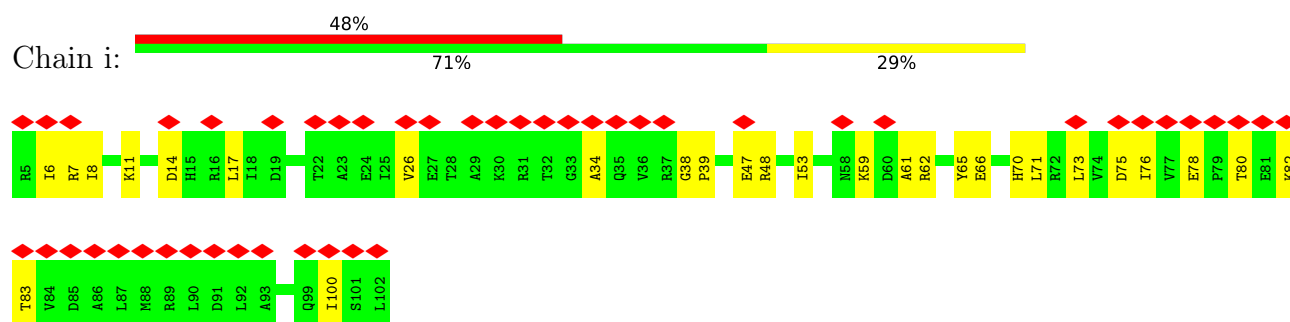
- Molecule 32: 30S ribosomal protein S7



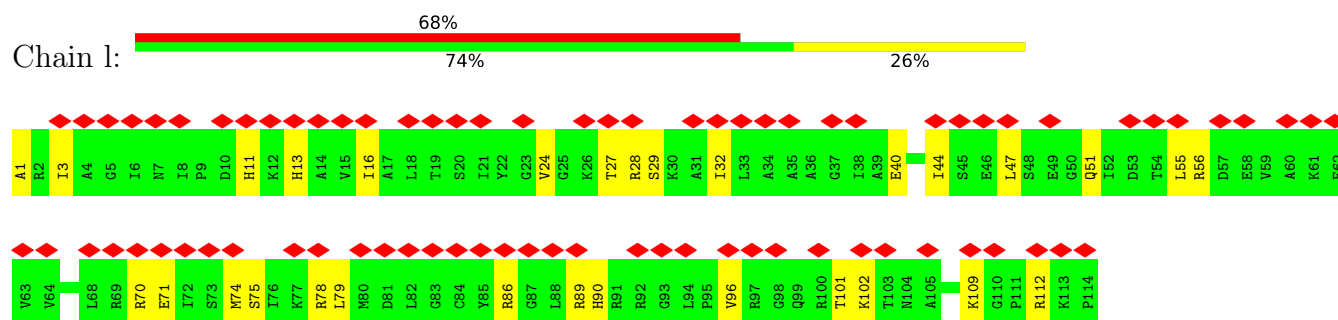
- Molecule 33: 30S ribosomal protein S9



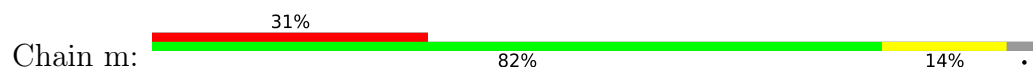
- Molecule 34: 30S ribosomal protein S10

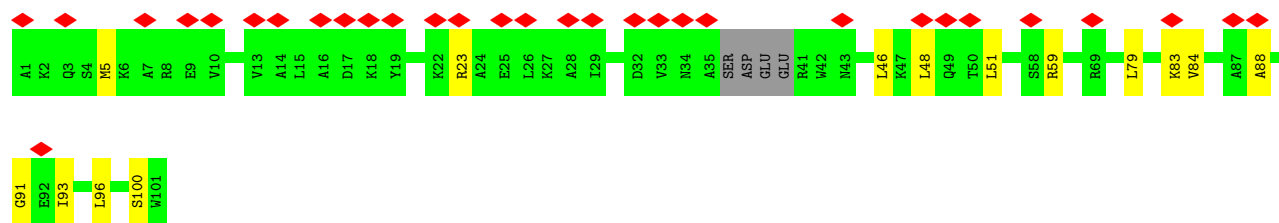


- Molecule 35: 30S ribosomal protein S13

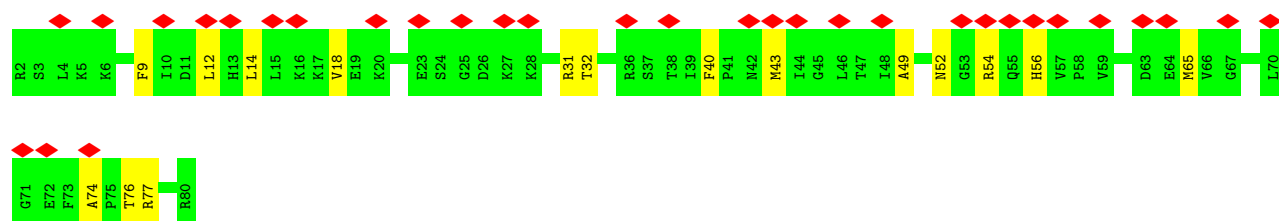
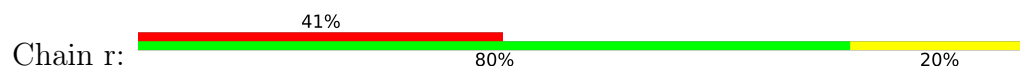


- Molecule 36: 30S ribosomal protein S14

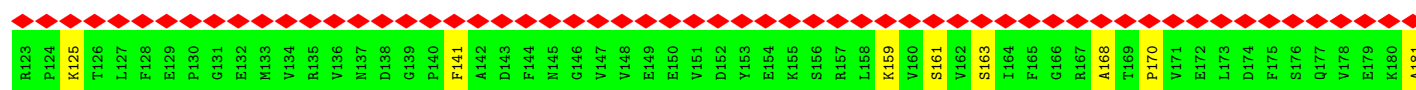
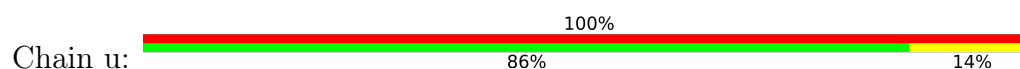




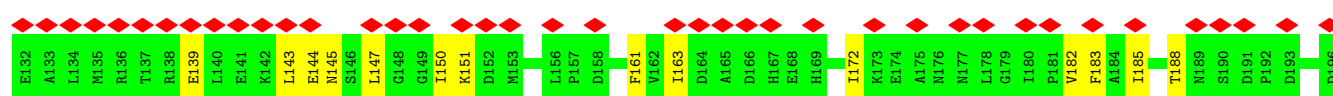
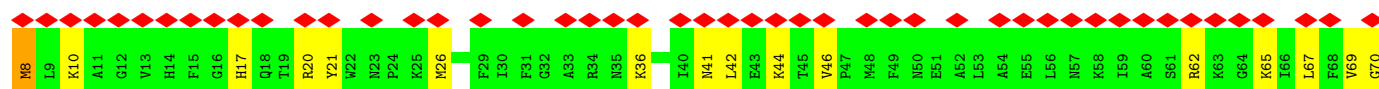
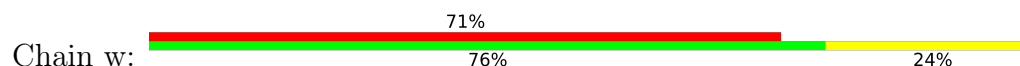
- Molecule 37: 30S ribosomal protein S19



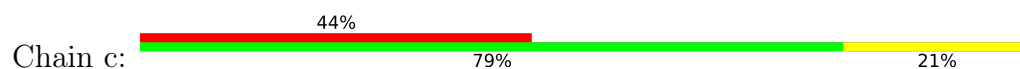
- Molecule 38: Transcription termination/antitermination protein NusG

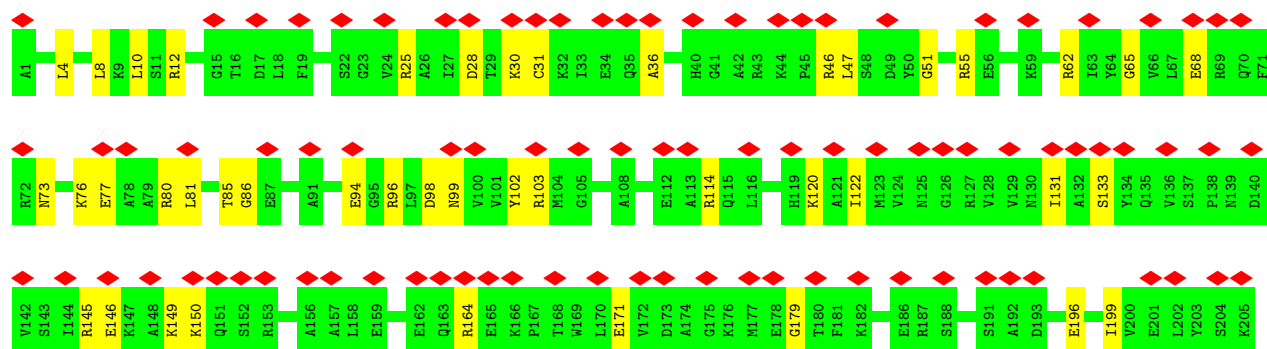


- Molecule 39: 30S ribosomal protein S2

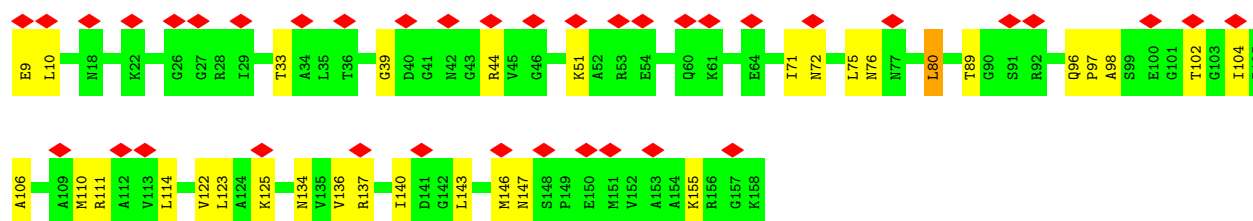


- Molecule 40: 30S ribosomal protein S4

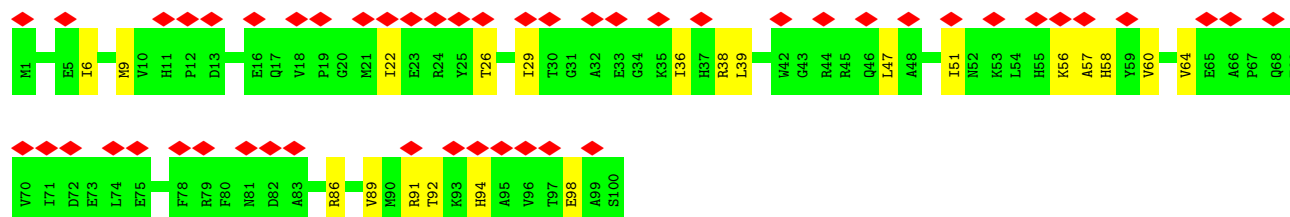
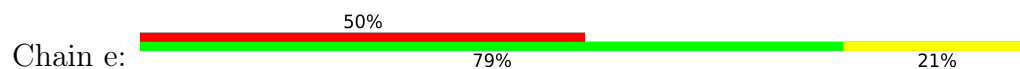




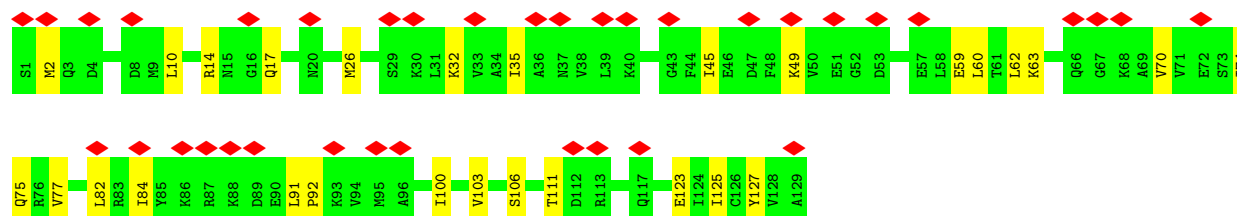
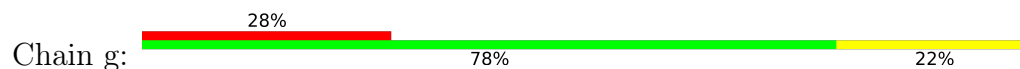
- Molecule 41: 30S ribosomal protein S5



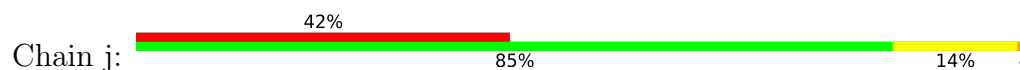
- Molecule 42: 30S ribosomal protein S6, non-modified isoform

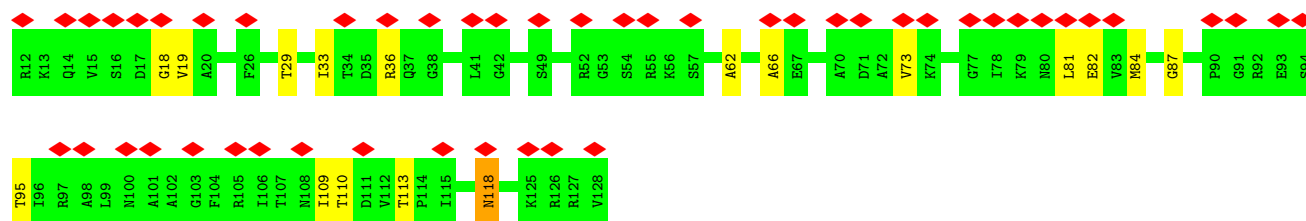


- Molecule 43: 30S ribosomal protein S8

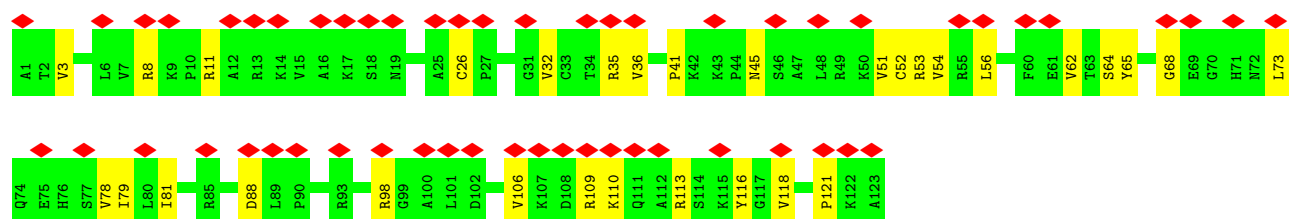
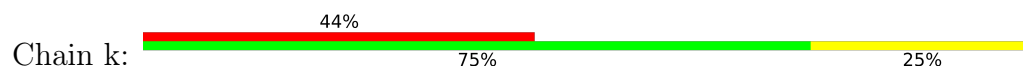


- Molecule 44: 30S ribosomal protein S11

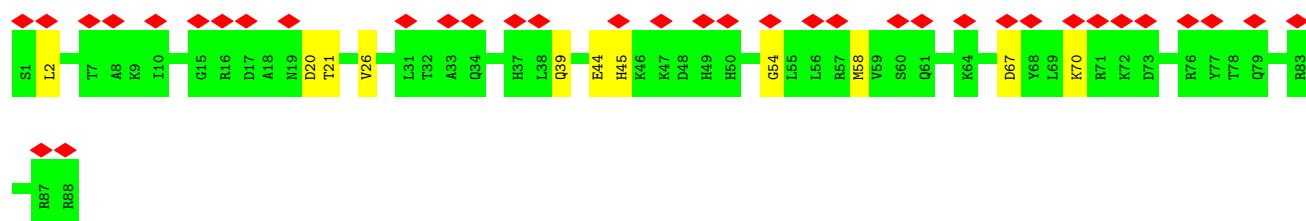
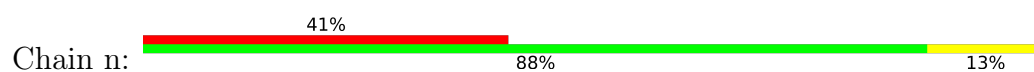




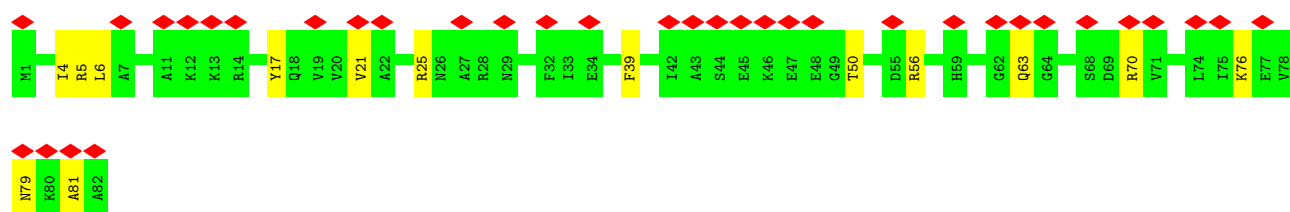
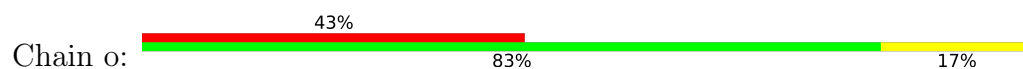
• Molecule 45: 30S ribosomal protein S12



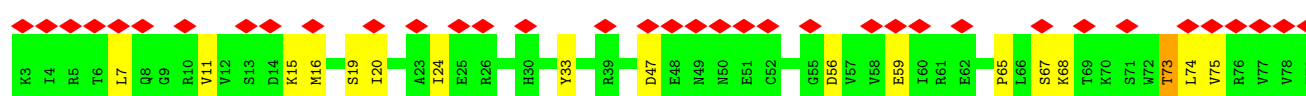
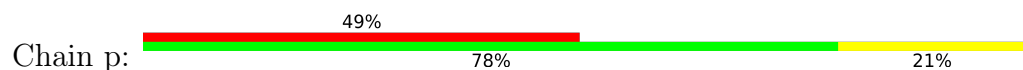
• Molecule 46: 30S ribosomal protein S15



• Molecule 47: 30S ribosomal protein S16

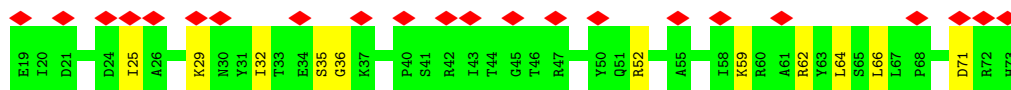
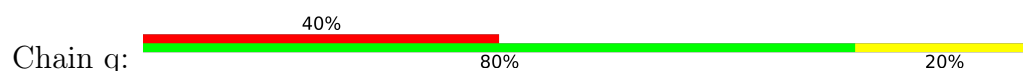


• Molecule 48: 30S ribosomal protein S17

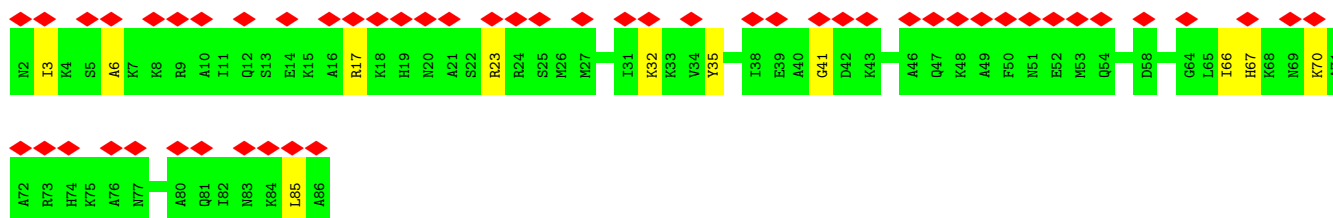
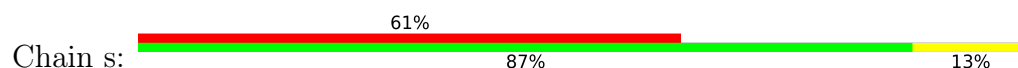




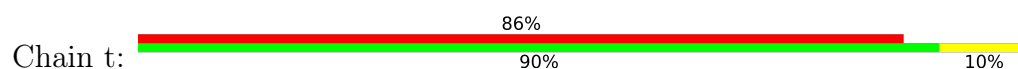
- Molecule 49: 30S ribosomal protein S18



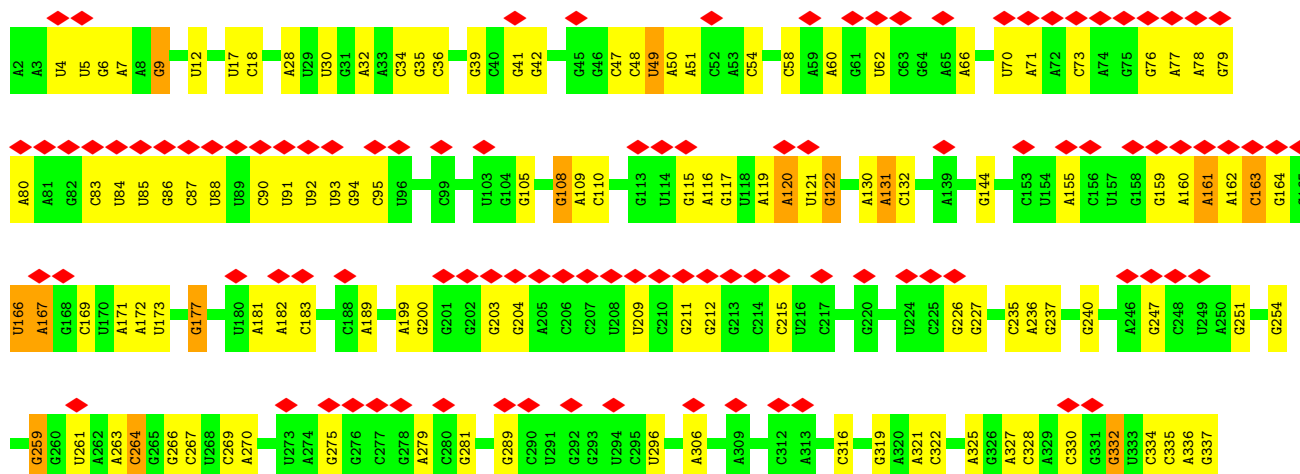
- Molecule 50: 30S ribosomal protein S20

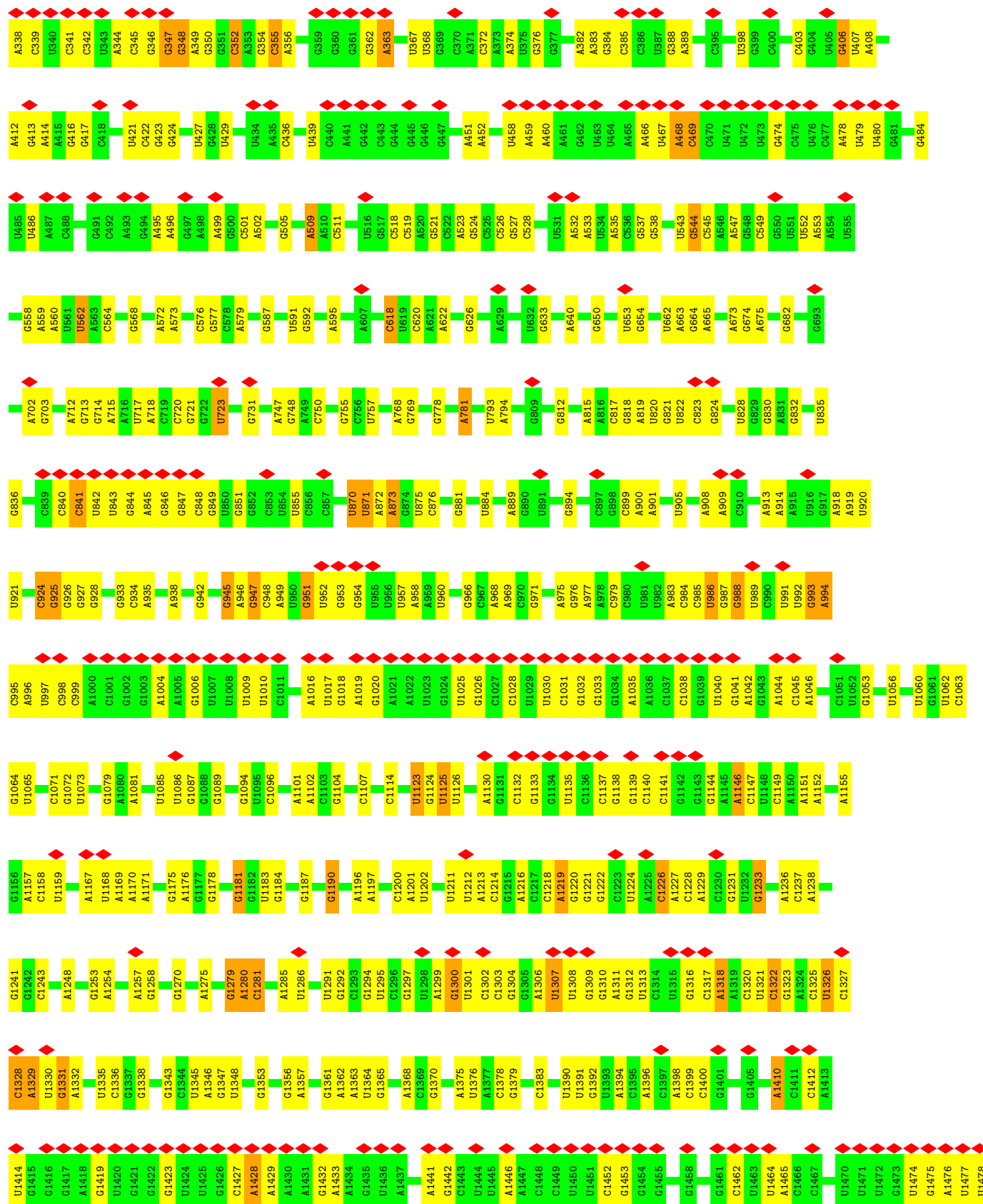


- Molecule 51: 30S ribosomal protein S21 (Fragment)



- Molecule 52: 16S







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	140682	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	2.490	Depositor
Minimum map value	-0.066	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.176	Depositor
Map size ($\text{\AA}$)	350.19998, 350.19998, 350.19998	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.03, 1.03, 1.03	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	0.38	0/450	0.68	0/599
2	1	0.23	0/417	0.54	0/556
3	2	0.40	0/380	0.47	0/498
4	3	0.40	0/513	0.64	0/676
5	4	0.28	0/303	0.57	0/397
6	A	0.32	0/2800	0.41	0/4367
7	B	0.42	5/69796 (0.0%)	0.45	7/108888 (0.0%)
8	C	0.29	0/2122	0.51	0/2854
9	D	0.41	0/1586	0.65	1/2134 (0.0%)
10	E	0.35	0/1571	0.56	0/2113
11	F	0.25	0/1444	0.61	2/1937 (0.1%)
12	G	0.26	0/1343	0.64	0/1816
13	J	0.37	0/1152	0.59	0/1551
14	K	0.41	0/940	0.69	1/1260 (0.1%)
15	L	0.37	0/1054	0.71	0/1403
16	M	0.35	0/1093	0.56	0/1460
17	N	0.44	0/974	0.68	1/1303 (0.1%)
18	O	0.30	0/902	0.64	0/1209
19	P	0.34	0/929	0.62	0/1242
20	Q	0.39	0/960	0.62	0/1278
21	R	0.35	0/829	0.61	0/1107
22	S	0.38	0/864	0.65	2/1156 (0.2%)
23	T	0.36	0/745	0.72	3/996 (0.3%)
24	U	0.33	0/788	0.61	0/1053
25	V	0.31	0/766	0.65	0/1025
26	W	0.36	0/603	0.82	0/797
27	X	0.39	0/635	0.60	0/848
28	Y	0.30	0/510	0.63	2/677 (0.3%)
29	Z	0.35	0/453	0.56	0/605
30	6	0.29	0/3456	0.65	6/4675 (0.1%)
31	x	0.39	0/1652	0.64	1/2225 (0.0%)
32	f	0.34	0/1196	0.58	0/1602
33	h	0.42	0/1034	0.85	5/1375 (0.4%)
34	i	0.39	0/797	0.64	0/1077

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.36	0/893	0.73	0/1193
36	m	0.39	0/785	0.65	0/1043
37	r	0.37	0/653	0.73	2/877 (0.2%)
38	u	0.17	0/477	0.46	0/642
39	w	0.35	0/1736	0.69	0/2338
40	c	0.39	0/1665	0.63	0/2227
41	d	0.46	0/1119	0.76	4/1504 (0.3%)
42	e	0.34	0/836	0.73	0/1128
43	g	0.44	0/989	0.62	0/1326
44	j	0.35	0/893	0.60	0/1205
45	k	0.40	0/969	0.68	0/1300
46	n	0.37	0/722	0.61	0/964
47	o	0.41	0/659	0.56	0/884
48	p	0.36	0/658	0.69	1/881 (0.1%)
49	q	0.38	0/463	0.60	0/621
50	s	0.36	0/671	0.57	0/888
51	t	0.33	0/431	0.65	0/570
52	v	0.43	0/36960	0.46	1/57657 (0.0%)
All	All	0.40	5/156636 (0.0%)	0.51	39/234007 (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
39	w	0	2
40	c	0	1
44	j	0	1
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1916	A	N9-C4	11.71	1.61	1.37
7	B	1916	A	C5-C4	-9.68	1.19	1.38
7	B	1916	A	N9-C8	-8.03	1.21	1.37
7	B	1916	A	N7-C5	7.85	1.54	1.39
7	B	1916	A	N3-C4	5.22	1.45	1.34

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	1916	A	C4-C5-N7	-26.17	32.19	110.70
7	B	1916	A	N7-C8-N9	-22.48	46.37	113.80
7	B	1916	A	N9-C4-C5	-12.78	67.47	105.80
7	B	1916	A	C5-N7-C8	10.92	136.67	103.90
7	B	1916	A	N3-C4-N9	10.37	158.50	127.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	c	46	ARG	Peptide
44	j	118	ASN	Peptide
39	w	70	GLY	Peptide
39	w	8	MET	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	5	0
2	1	410	0	440	7	0
3	2	377	0	418	6	0
4	3	504	0	574	10	0
5	4	302	0	343	5	0
6	A	2504	0	1271	17	0
7	B	62317	0	31345	313	0
8	C	2083	0	2157	26	0
9	D	1565	0	1616	22	0
10	E	1552	0	1619	18	0
11	F	1420	0	1460	20	0
12	G	1323	0	1374	17	0
13	J	1129	0	1162	13	0
14	K	931	0	1003	45	0
15	L	1045	0	1117	22	0
16	M	1074	0	1157	14	0
17	N	961	0	1000	23	0
18	O	892	0	923	14	0
19	P	917	0	965	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	Q	947	0	1022	17	0
21	R	816	0	839	12	0
22	S	857	0	922	9	0
23	T	739	0	807	14	0
24	U	780	0	834	9	0
25	V	753	0	780	11	0
26	W	596	0	610	15	0
27	X	625	0	655	12	0
28	Y	509	0	543	8	0
29	Z	449	0	491	5	0
30	6	3403	0	3434	57	0
31	x	1625	0	1699	29	0
32	f	1182	0	1240	21	0
33	h	1022	0	1070	24	0
34	i	787	0	828	17	0
35	l	884	0	944	20	0
36	m	774	0	827	14	0
37	r	638	0	665	13	0
38	u	468	0	458	4	0
39	w	1705	0	1732	32	0
40	c	1643	0	1710	27	0
41	d	1106	0	1148	19	0
42	e	818	0	808	13	0
43	g	979	0	1034	19	0
44	j	877	0	887	10	0
45	k	955	0	1019	23	0
46	n	714	0	737	6	0
47	o	649	0	666	11	0
48	p	649	0	691	12	0
49	q	456	0	478	8	0
50	s	665	0	714	12	0
51	t	426	0	449	3	0
52	v	33010	0	16618	184	0
All	All	144256	0	97764	1116	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 1116 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:1952:A:C6	14:K:21:ILE:HB	2.08	0.88
48:p:59:GLU:O	48:p:75:VAL:HA	1.75	0.85
7:B:1667:G:H5'	14:K:4:GLN:O	1.77	0.85
7:B:1311:G:H21	7:B:1603:A:H62	1.27	0.81
7:B:1664:A:N3	14:K:66:LYS:HE2	2.03	0.73

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%)	50 (93%)	4 (7%)	0	100	100
2	1	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
3	2	44/46 (96%)	44 (100%)	0	0	100	100
4	3	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
8	C	270/272 (99%)	264 (98%)	6 (2%)	0	100	100
9	D	207/209 (99%)	193 (93%)	14 (7%)	0	100	100
10	E	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
11	F	176/178 (99%)	163 (93%)	13 (7%)	0	100	100
12	G	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
13	J	140/142 (99%)	130 (93%)	10 (7%)	0	100	100
14	K	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
15	L	141/143 (99%)	133 (94%)	8 (6%)	0	100	100
16	M	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
17	N	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
18	O	114/116 (98%)	112 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	P	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
20	Q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
21	R	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
22	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
23	T	92/94 (98%)	83 (90%)	7 (8%)	2 (2%)	5	29
24	U	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
25	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
26	W	77/79 (98%)	72 (94%)	5 (6%)	0	100	100
27	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
28	Y	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
29	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
30	6	424/426 (100%)	403 (95%)	20 (5%)	1 (0%)	43	73
31	x	204/206 (99%)	200 (98%)	4 (2%)	0	100	100
32	f	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
33	h	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
34	i	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
35	l	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
36	m	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
37	r	77/79 (98%)	74 (96%)	3 (4%)	0	100	100
38	u	57/59 (97%)	57 (100%)	0	0	100	100
39	w	216/218 (99%)	198 (92%)	18 (8%)	0	100	100
40	c	203/205 (99%)	191 (94%)	12 (6%)	0	100	100
41	d	148/150 (99%)	139 (94%)	9 (6%)	0	100	100
42	e	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
43	g	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
44	j	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
45	k	121/123 (98%)	112 (93%)	9 (7%)	0	100	100
46	n	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
47	o	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
48	p	78/80 (98%)	73 (94%)	5 (6%)	0	100	100
49	q	53/55 (96%)	53 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	s	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
51	t	49/51 (96%)	44 (90%)	5 (10%)	0	100	100
All	All	5822/5926 (98%)	5549 (95%)	270 (5%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	T	35	ALA
23	T	27	SER
30	6	17	TYR

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%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
8	C	216/217 (100%)	216 (100%)	0	100	100
9	D	164/164 (100%)	162 (99%)	2 (1%)	63	79
10	E	165/165 (100%)	165 (100%)	0	100	100
11	F	149/149 (100%)	147 (99%)	2 (1%)	61	78
12	G	137/137 (100%)	136 (99%)	1 (1%)	76	83
13	J	116/116 (100%)	114 (98%)	2 (2%)	53	75
14	K	102/103 (99%)	101 (99%)	1 (1%)	68	80
15	L	102/102 (100%)	102 (100%)	0	100	100
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	100/101 (99%)	99 (99%)	1 (1%)	68	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	O	86/86 (100%)	86 (100%)	0	100	100
19	P	99/99 (100%)	98 (99%)	1 (1%)	68	80
20	Q	89/89 (100%)	89 (100%)	0	100	100
21	R	84/84 (100%)	83 (99%)	1 (1%)	63	79
22	S	93/93 (100%)	92 (99%)	1 (1%)	65	79
23	T	80/81 (99%)	79 (99%)	1 (1%)	61	78
24	U	83/84 (99%)	82 (99%)	1 (1%)	63	79
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	59/59 (100%)	59 (100%)	0	100	100
27	X	67/67 (100%)	67 (100%)	0	100	100
28	Y	55/55 (100%)	55 (100%)	0	100	100
29	Z	48/48 (100%)	48 (100%)	0	100	100
30	6	364/364 (100%)	359 (99%)	5 (1%)	59	77
31	x	170/170 (100%)	167 (98%)	3 (2%)	51	74
32	f	124/124 (100%)	124 (100%)	0	100	100
33	h	105/105 (100%)	104 (99%)	1 (1%)	68	80
34	i	86/86 (100%)	86 (100%)	0	100	100
35	l	92/92 (100%)	90 (98%)	2 (2%)	45	71
36	m	79/83 (95%)	79 (100%)	0	100	100
37	r	70/70 (100%)	70 (100%)	0	100	100
38	u	52/52 (100%)	51 (98%)	1 (2%)	50	73
39	w	180/180 (100%)	179 (99%)	1 (1%)	78	84
40	c	172/172 (100%)	170 (99%)	2 (1%)	63	79
41	d	113/113 (100%)	111 (98%)	2 (2%)	51	74
42	e	87/87 (100%)	85 (98%)	2 (2%)	44	70
43	g	104/104 (100%)	104 (100%)	0	100	100
44	j	90/90 (100%)	90 (100%)	0	100	100
45	k	103/103 (100%)	102 (99%)	1 (1%)	68	80
46	n	76/76 (100%)	75 (99%)	1 (1%)	61	78
47	o	65/65 (100%)	65 (100%)	0	100	100
48	p	74/74 (100%)	74 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	q	48/48 (100%)	48 (100%)	0	100	100
50	s	65/65 (100%)	65 (100%)	0	100	100
51	t	44/44 (100%)	44 (100%)	0	100	100
All	All	4859/4869 (100%)	4824 (99%)	35 (1%)	73	83

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	c	122	ILE
41	d	80	LEU
42	e	94	HIS
23	T	15	HIS
22	S	11	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
24	U	45	GLN
50	s	47	GLN
31	x	101	ASN
50	s	19	HIS
46	n	61	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	v	1538/1539 (99%)	425 (27%)	0
6	A	116/117 (99%)	30 (25%)	2 (1%)
7	B	2902/2903 (99%)	775 (26%)	9 (0%)
All	All	4556/4559 (99%)	1230 (26%)	11 (0%)

5 of 1230 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	3	C
6	A	5	U
6	A	9	G
6	A	13	G
6	A	14	U

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	B	1906	G
7	B	2458	G
7	B	2808	G
7	B	2756	U
7	B	984	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

There are no chain breaks in this entry.

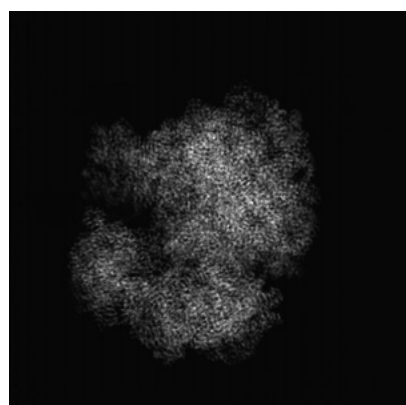
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29688. These allow visual inspection of the internal detail of the map and identification of artifacts.

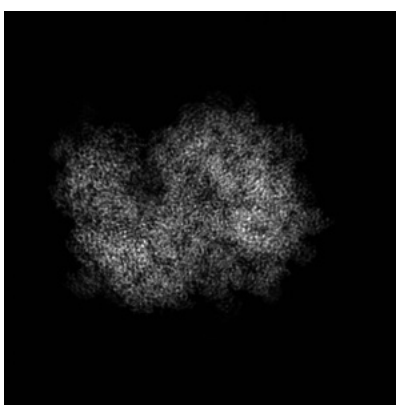
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

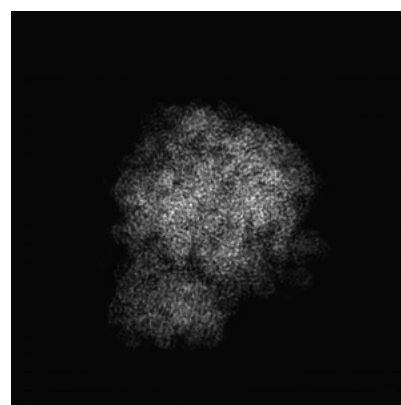
6.1.1 Primary map



X



Y

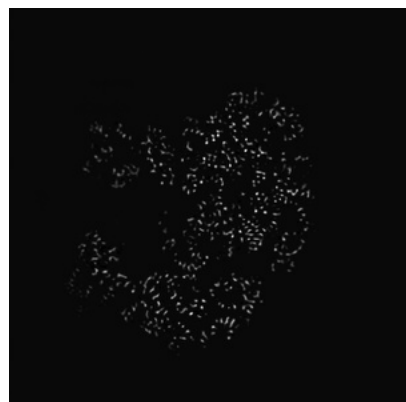


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 170



Y Index: 170



Z Index: 170

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: 143



Y Index: 177

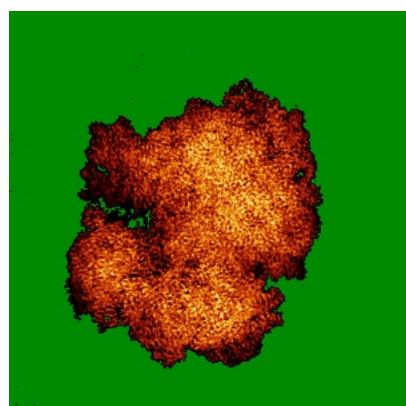


Z Index: 215

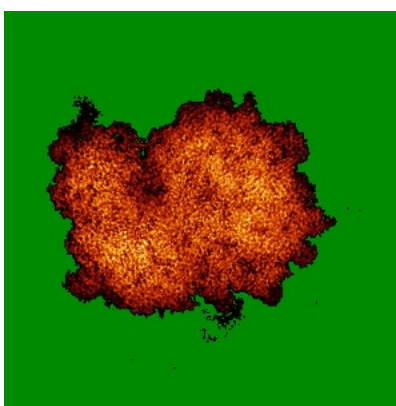
The images above show the largest variance slices of the map in three orthogonal directions.

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

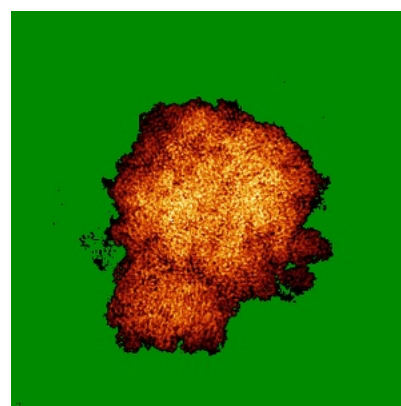
6.4.1 Primary map



X



Y

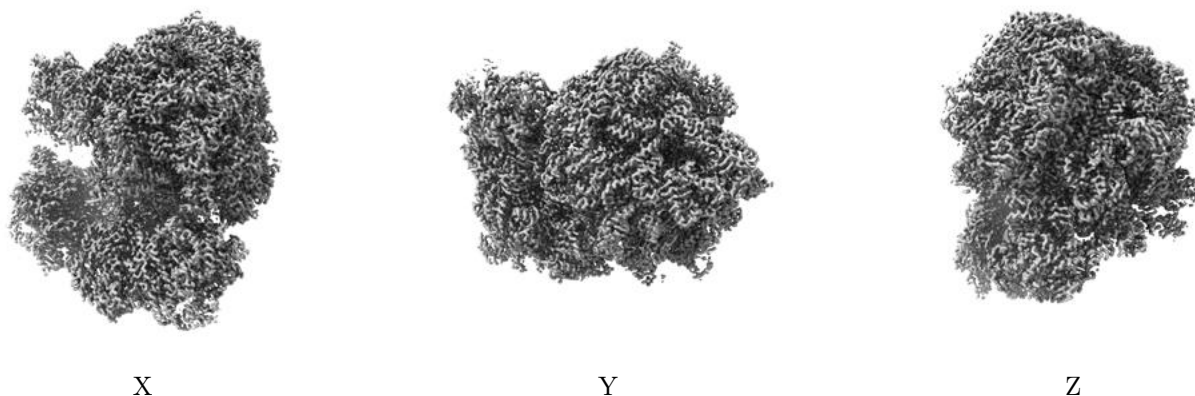


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.176. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

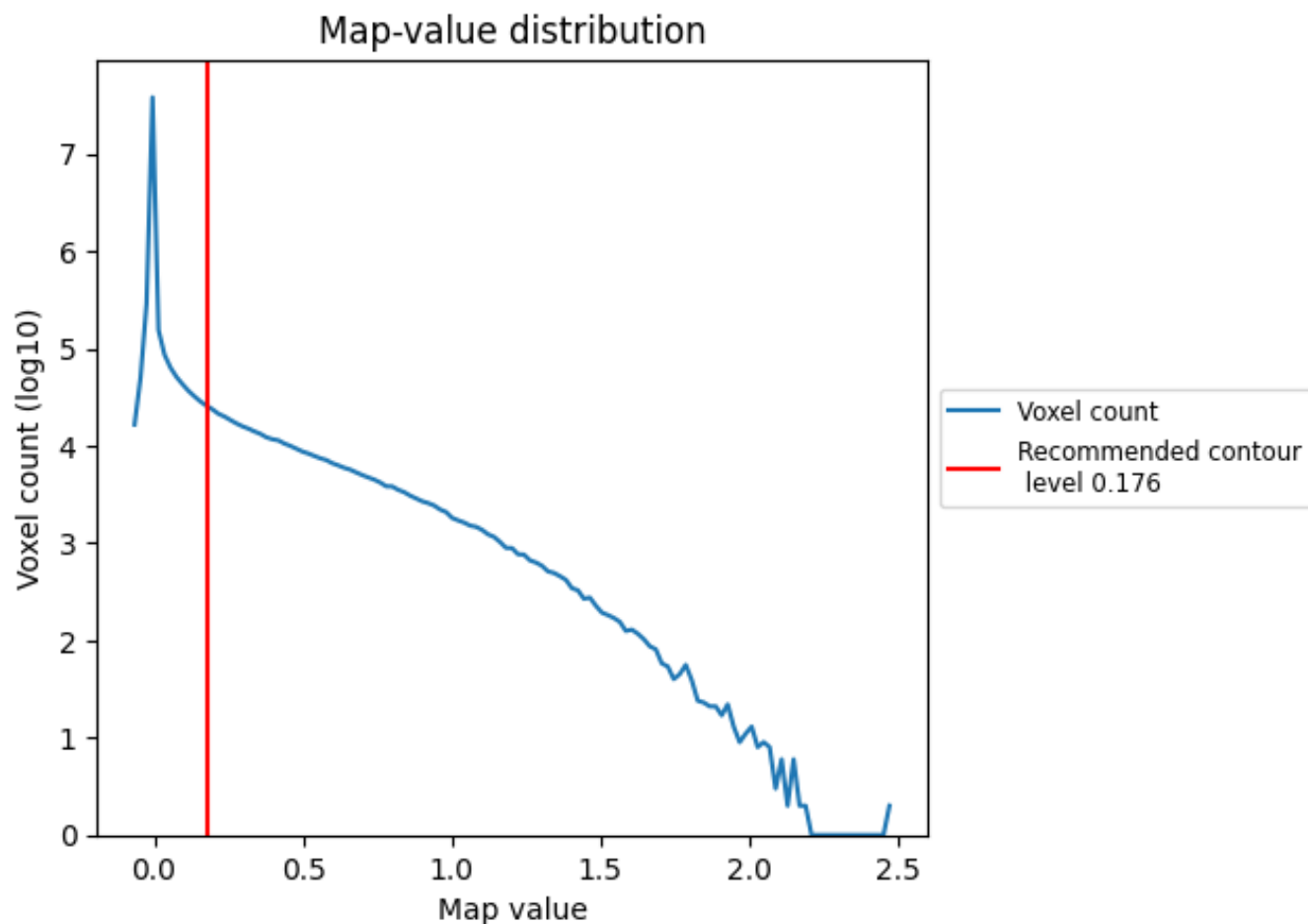
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

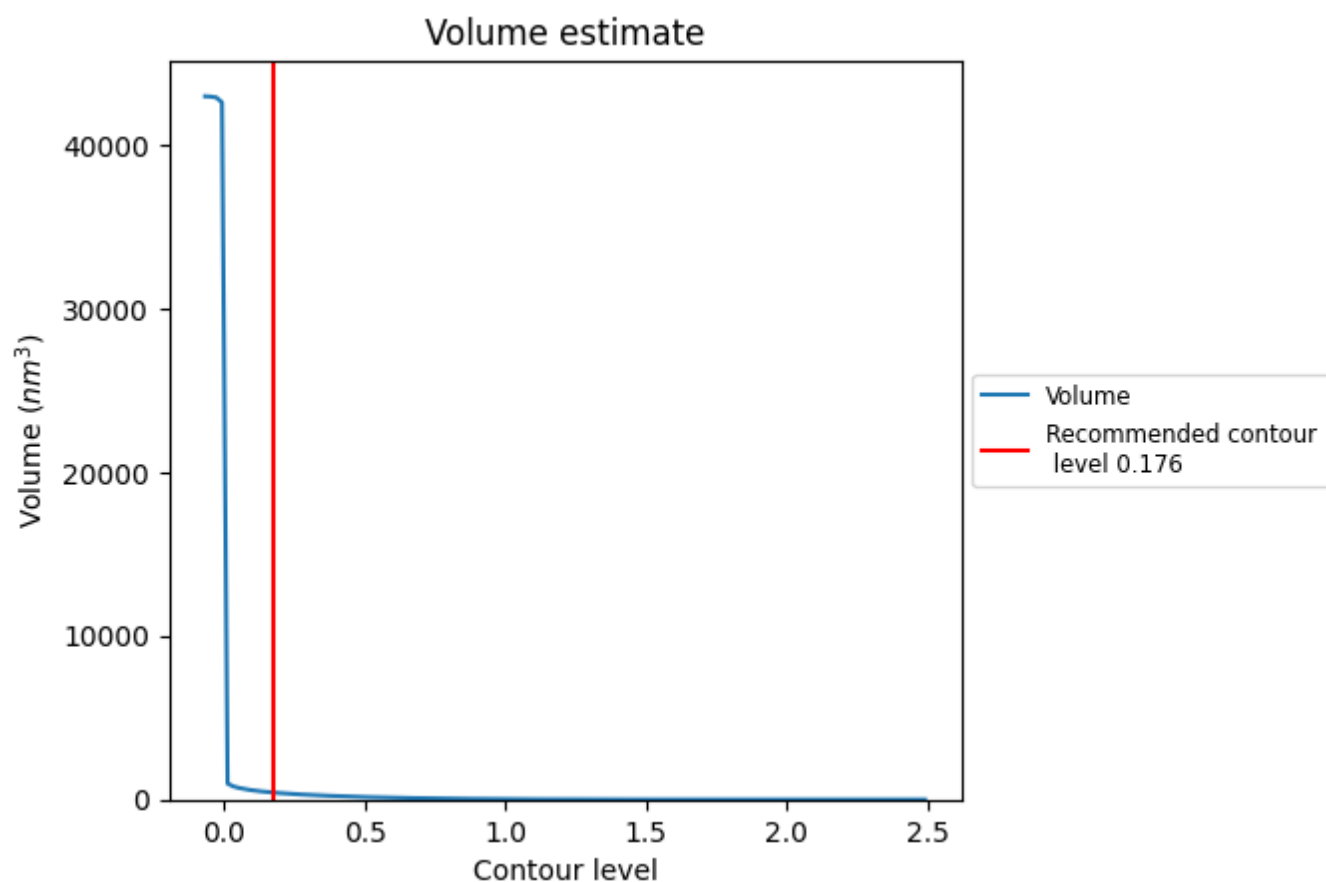
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

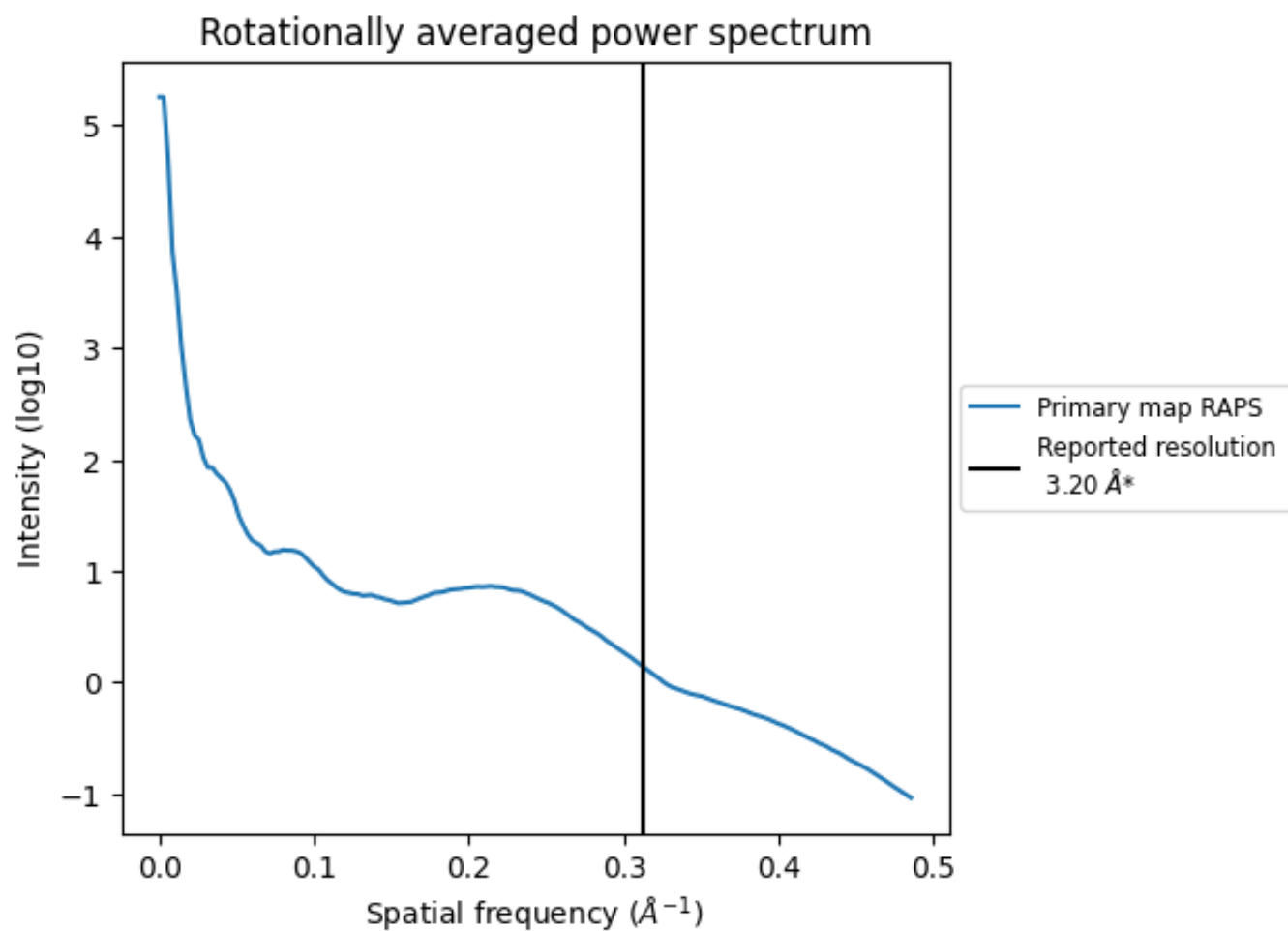
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 429 nm³; this corresponds to an approximate mass of 388 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 0.312 Å⁻¹

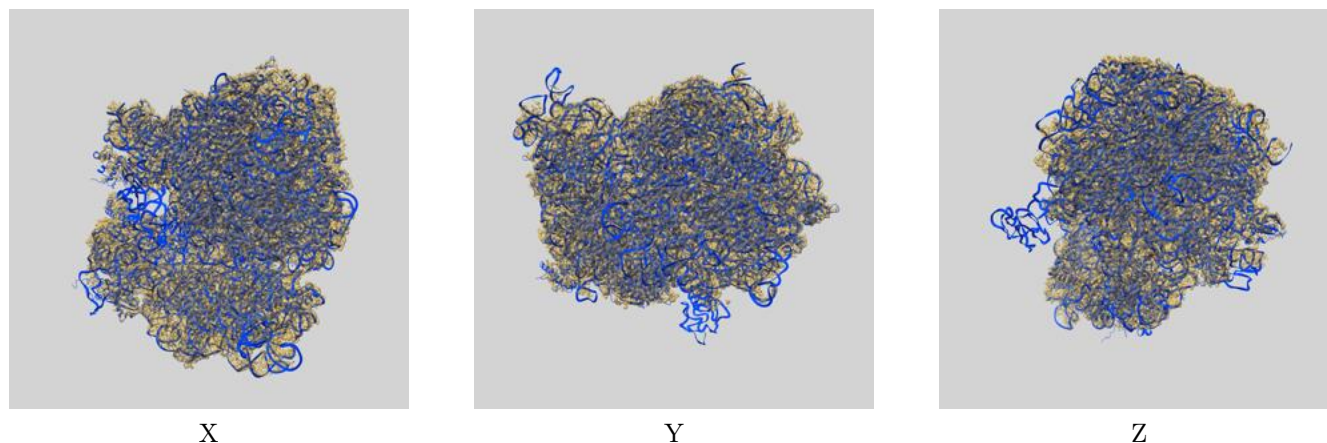
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

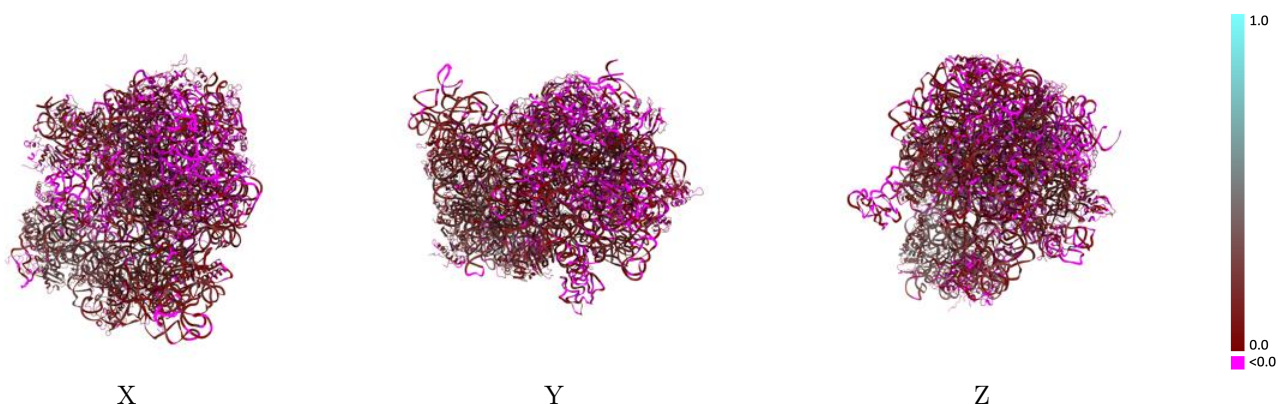
This section contains information regarding the fit between EMDB map EMD-29688 and PDB model 8G34. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



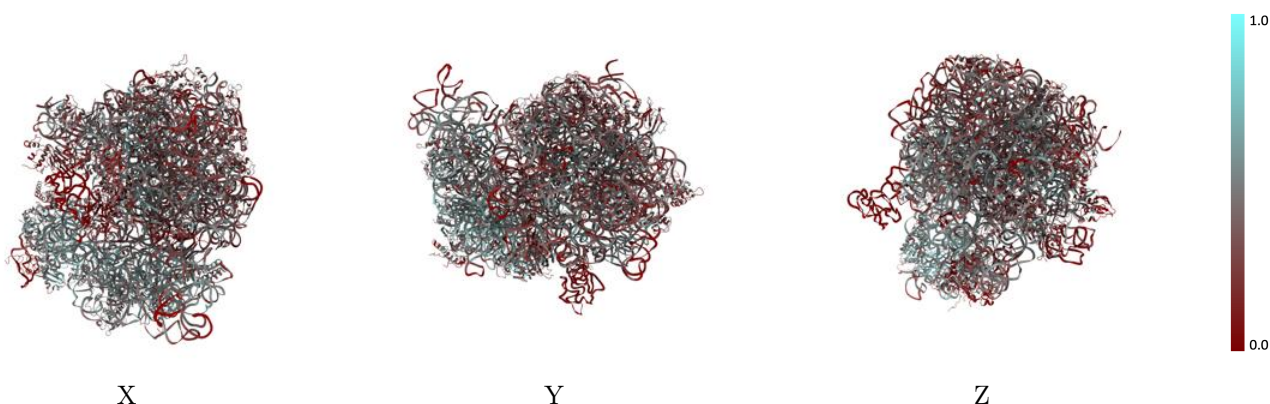
The images above show the 3D surface view of the map at the recommended contour level 0.176 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



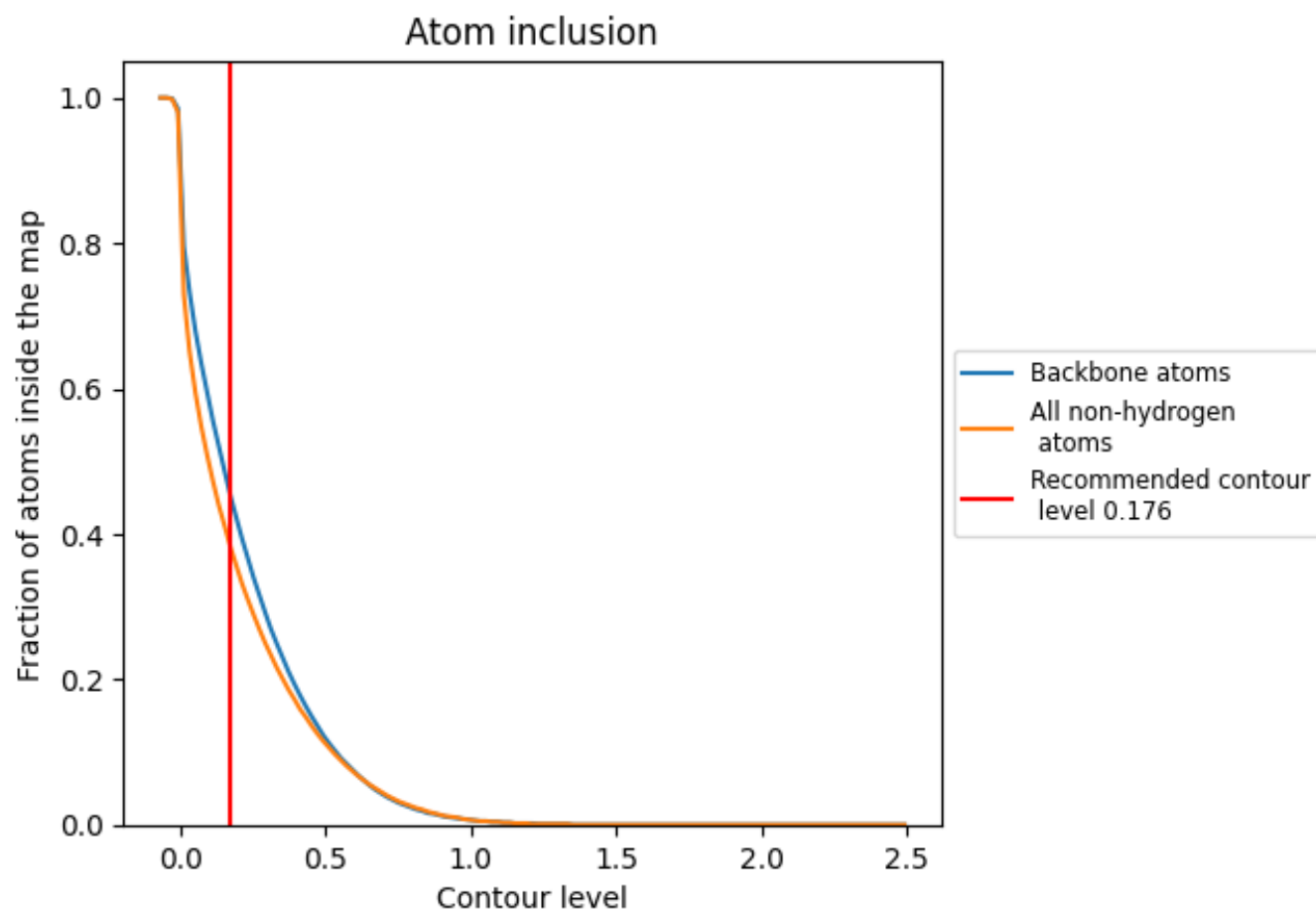
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.176).

9.4 Atom inclusion [i](#)



At the recommended contour level, 45% of all backbone atoms, 38% 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 (0.176) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3800	 0.1160
0	 0.3080	 0.0550
1	 0.0070	 0.0490
2	 0.3380	 0.0790
3	 0.3440	 0.1210
4	 0.3080	 0.1070
6	 0.0580	 -0.0280
A	 0.4040	 0.1580
B	 0.3660	 0.0850
C	 0.1890	 0.0770
D	 0.3410	 0.0680
E	 0.2640	 0.0320
F	 0.0870	 0.0270
G	 0.1990	 0.0560
J	 0.3260	 0.0520
K	 0.2610	 0.0880
L	 0.3430	 0.0710
M	 0.3840	 0.1190
N	 0.3380	 0.0480
O	 0.3200	 0.1210
P	 0.2730	 0.0670
Q	 0.3130	 0.0210
R	 0.3150	 0.0530
S	 0.3100	 0.0520
T	 0.2520	 -0.0090
U	 0.2200	 0.0270
V	 0.2970	 0.0800
W	 0.3310	 0.0740
X	 0.3710	 0.1120
Y	 0.2620	 0.0460
Z	 0.2910	 0.0330
c	 0.4520	 0.1880
d	 0.5320	 0.2230
e	 0.4050	 0.1630
f	 0.4590	 0.2300



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.5190	 0.2240
h	 0.4630	 0.2170
i	 0.3860	 0.2190
j	 0.4460	 0.1810
k	 0.4360	 0.1840
l	 0.3190	 0.0650
m	 0.5060	 0.2610
n	 0.4750	 0.1780
o	 0.4450	 0.1320
p	 0.3840	 0.1620
q	 0.4710	 0.2040
r	 0.4450	 0.1890
s	 0.3830	 0.1030
t	 0.1670	 0.0880
u	 0.0000	 -0.0080
v	 0.4870	 0.1870
w	 0.2800	 0.1310
x	 0.5540	 0.2920