



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2025 – 07:49 am BST

PDB ID : 7ZP8 / pdb_00007zp8
EMDB ID : EMD-14850
Title : 70S E. coli ribosome with a stalled flamin domain 5 nascent chain
Authors : Mitropoulou, A.; Plessa, E.; Wlodarski, T.; Ahn, M.; Chan, S.H.S.; Becker, T.A.; Beckmann, R.; Cabrita, L.D.; Christodoulou, J.
Deposited on : 2022-04-26
Resolution : 2.20 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:

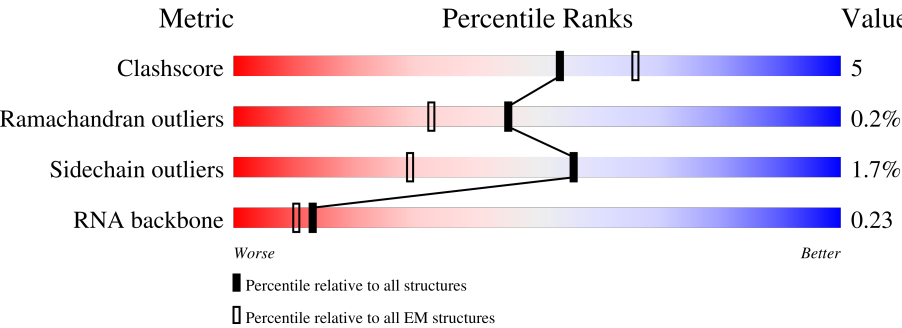
EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

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 2.20 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.









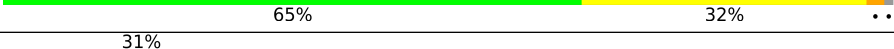
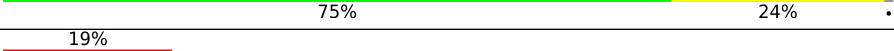
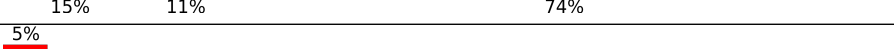
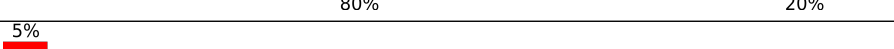
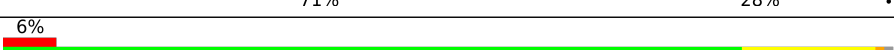

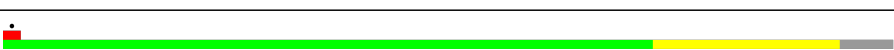

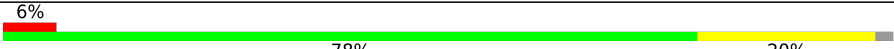





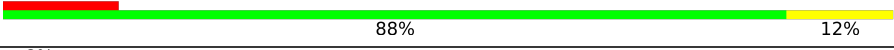
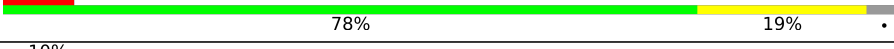
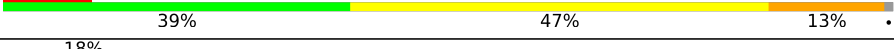


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	78	
2	1	63	
3	2	59	
4	3	57	
5	4	55	
6	6	46	
7	7	65	

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Mol	Chain	Length	Quality of chain
8	8	50	
9	a	120	
10	b	2904	
11	c	273	
12	d	209	
13	e	201	
14	f	179	
15	g	177	
16	h	149	
17	j	142	
18	k	123	
19	l	144	
20	m	136	
21	n	127	
22	o	117	
23	p	115	
24	q	118	
25	r	103	
26	s	110	
27	t	100	
28	u	104	
29	w	94	
30	y	85	
31	v	77	
32	z	148	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90951 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	2901	Total	C	N	O	P	0	0
			62281	27784	11464	20132	2901		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 15 is a protein called 50S ribosomal protein L6.

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

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	102	Total	C	N	O	S	0	0
			810	513	152	143	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	u	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	y	82	Total	C	N	O	S	0	0
			619	383	127	108	1		

- Molecule 31 is a RNA chain called Pro-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	76	Total	C	N	O	P	0	0
			1626	724	292	534	76		

- Molecule 32 is a protein called Gelation factor.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	z	33	Total	C	N	O	0	0
			277	186	44	47		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	20	MET	-	initiating methionine	UNP P13466
z	21	HIS	-	expression tag	UNP P13466
z	22	HIS	-	expression tag	UNP P13466
z	23	HIS	-	expression tag	UNP P13466
z	24	HIS	-	expression tag	UNP P13466
z	25	HIS	-	expression tag	UNP P13466
z	26	HIS	-	expression tag	UNP P13466
z	27	ALA	-	expression tag	UNP P13466
z	28	SER	-	expression tag	UNP P13466
z	149	GLU	-	expression tag	UNP P13466
z	150	LEU	-	expression tag	UNP P13466
z	151	PHE	-	expression tag	UNP P13466
z	152	SER	-	expression tag	UNP P13466

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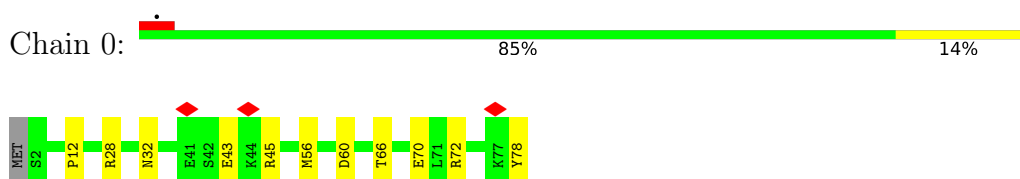
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Chain	Residue	Modelled	Actual	Comment	Reference
z	153	THR	-	expression tag	UNP P13466
z	154	PRO	-	expression tag	UNP P13466
z	155	VAL	-	expression tag	UNP P13466
z	156	TRP	-	expression tag	UNP P13466
z	157	ILE	-	expression tag	UNP P13466
z	158	TRP	-	expression tag	UNP P13466
z	159	TRP	-	expression tag	UNP P13466
z	160	TRP	-	expression tag	UNP P13466
z	161	PRO	-	expression tag	UNP P13466
z	162	ARG	-	expression tag	UNP P13466
z	163	ILE	-	expression tag	UNP P13466
z	164	ARG	-	expression tag	UNP P13466
z	165	GLY	-	expression tag	UNP P13466
z	166	PRO	-	expression tag	UNP P13466
z	167	PRO	-	expression tag	UNP P13466

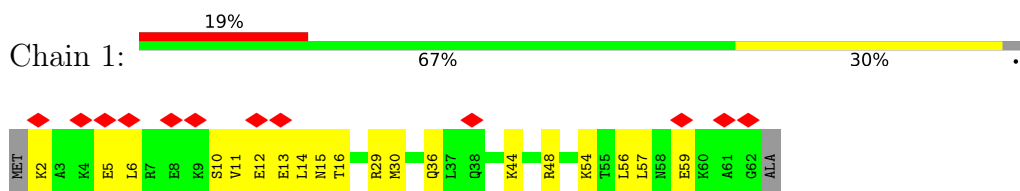
3 Residue-property plots [i](#)

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.

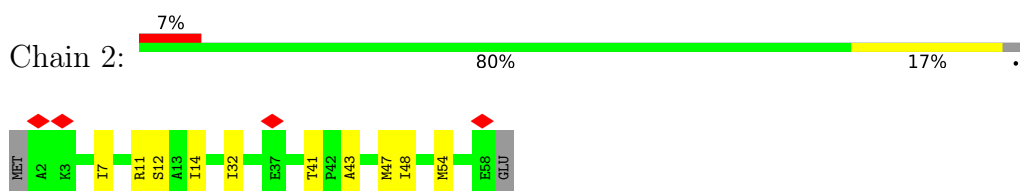
- Molecule 1: 50S ribosomal protein L28



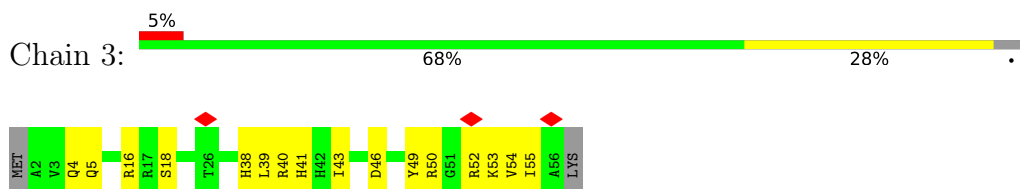
- Molecule 2: 50S ribosomal protein L29



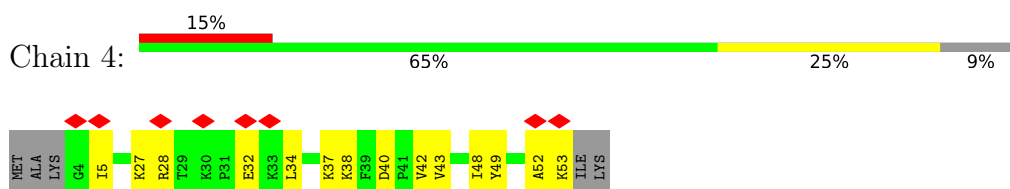
- Molecule 3: 50S ribosomal protein L30



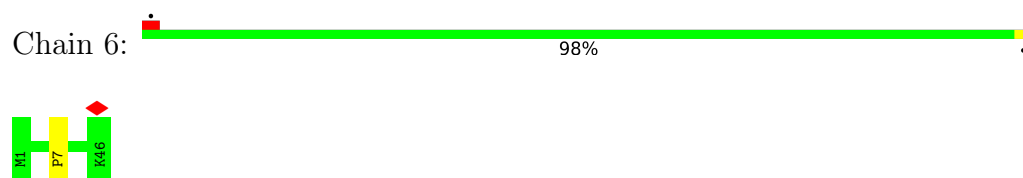
- Molecule 4: 50S ribosomal protein L32



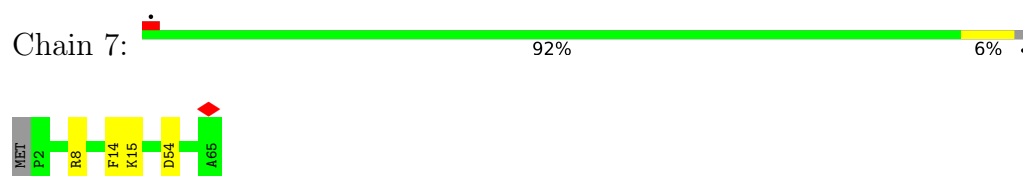
- Molecule 5: 50S ribosomal protein L33



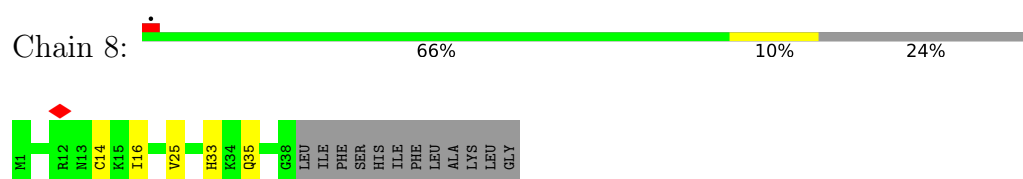
- Molecule 6: 50S ribosomal protein L34



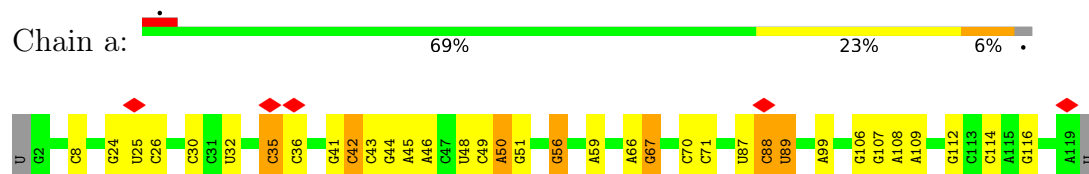
- Molecule 7: 50S ribosomal protein L35



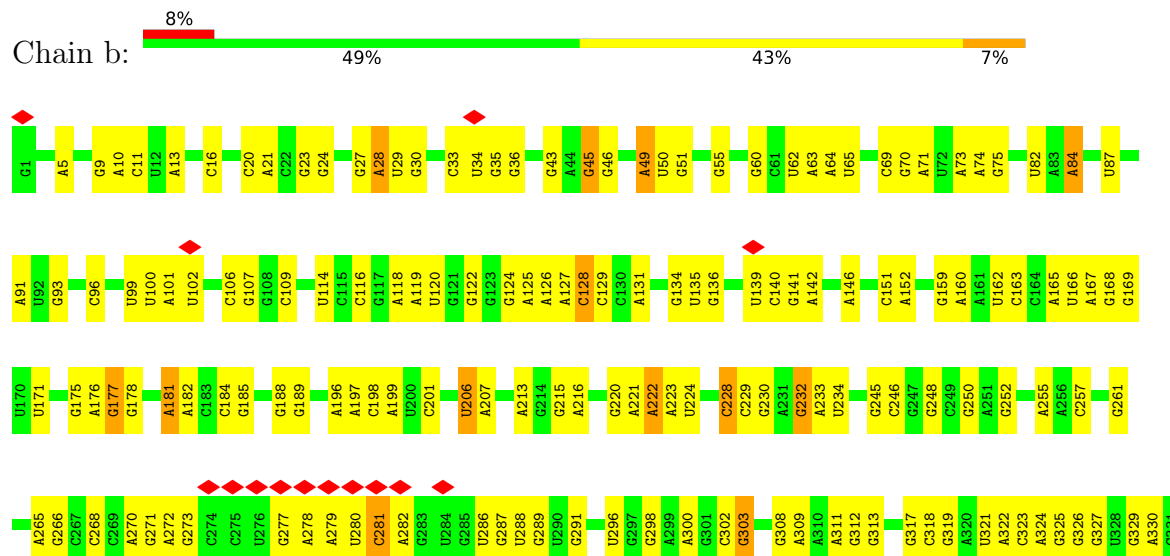
- Molecule 8: 50S ribosomal protein L36

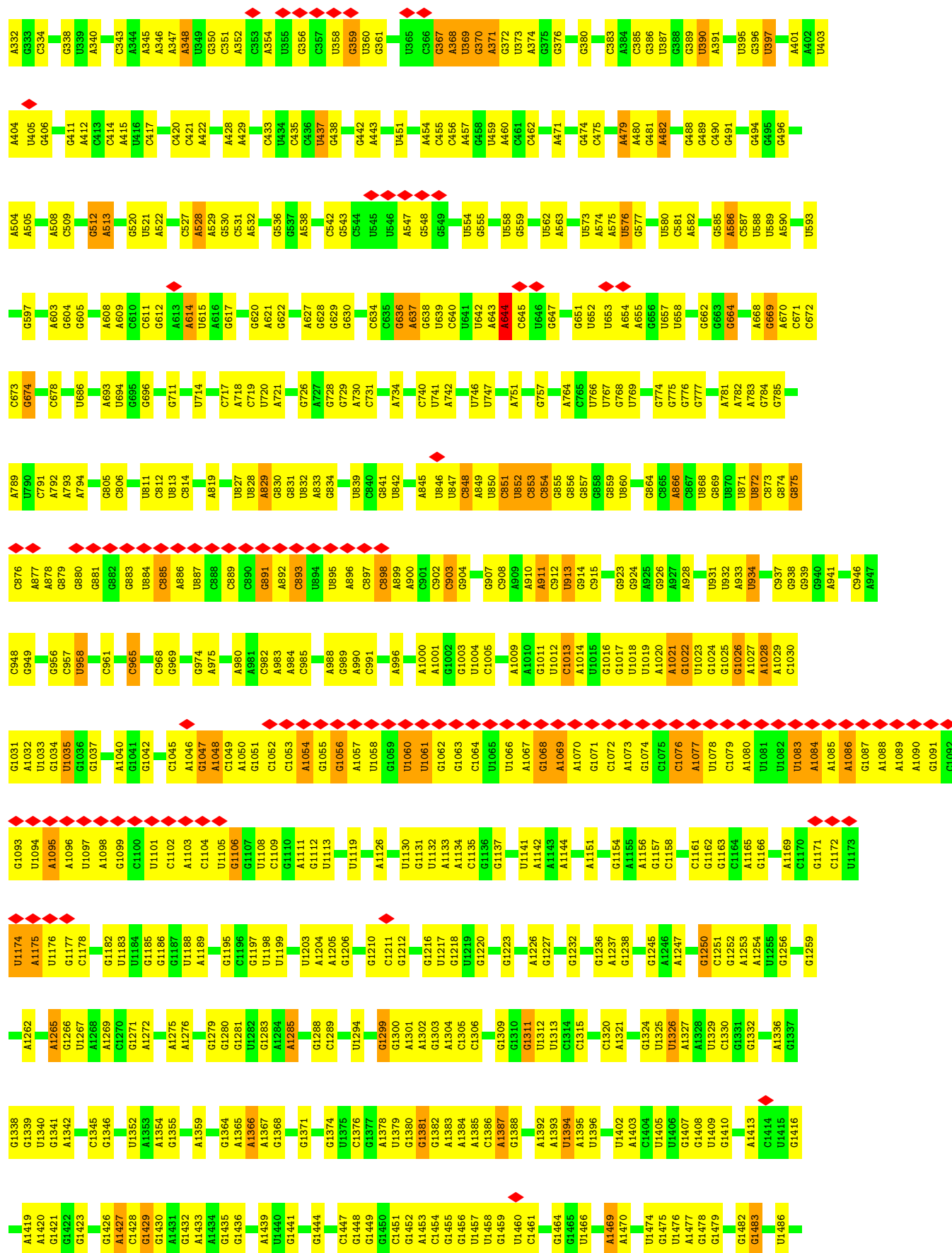


- Molecule 9: 5S rRNA

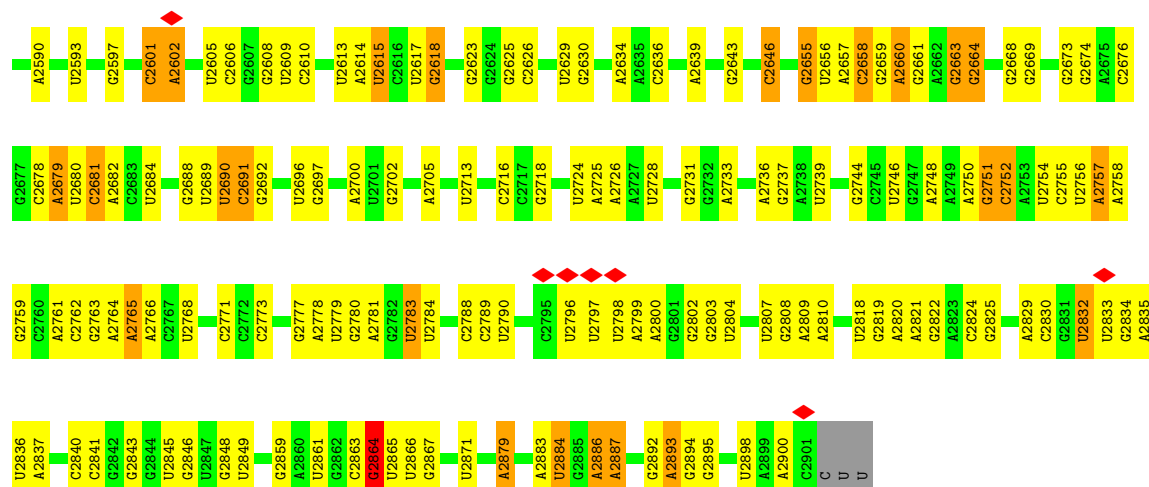


- Molecule 10: 23S rRNA

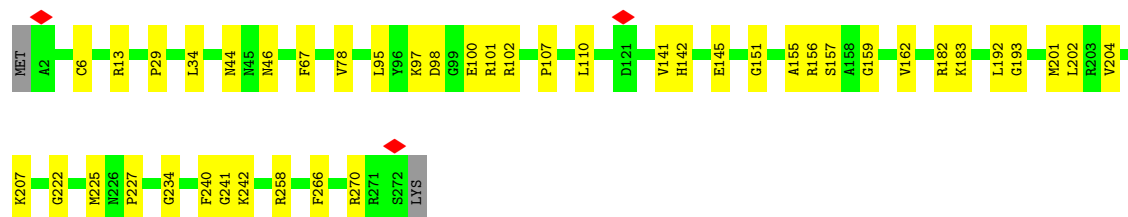
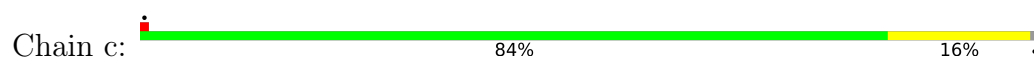




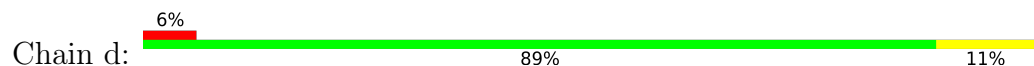
G2502	A2503	C2427	A2428	A2266	A2173	U2113	G2032	G1945	U1856	A1755	G1673	C1575	A1490
U2504	G2505	G2428	G2429	A2268	C2174	A2114	A2034	U1946	G1857	G1756	G1674	U1576	G1491
G2506	U2507	C2338	G2430	A2268	C2175	G2115	G2035	A1952	A1858	A1757	C1675	U1577	C1492
G2508	U2509	A2340	U2431	A2274	A2176	G2116	A2036	G1954	G1862	A1762	G1681	G1581	A1494
A2513	G2514	G2346	A2432	A2278	C2177	A2117	G2038	U1955	G1863	G1763	G1682	C1582	A1495
U2515	A2516	C2347	A2433	A2282	C2179	U2118	U2039	U1956	U1864	C1764	U1683	U1582	A1496
G2517	G2518	G2350	A2435	C2283	U2180	A2119	G2040	C1957	G1869	A1773	U1584	U1497	U1497
U2519	C2520	G2351	A2439	C2282	U2181	G2120	A2042	C1958	C1870	A1690	C1586	C1498	A1503
G2526	U2527	A2352	G2440	G2286	U2182	U2122	C2061	C1962	A1871	G1776	U1588	U1506	U1506
C2529	G2530	G2353	U2441	A2287	U2183	G2123	G2055	U1963	A1872	U1694	U1589	C1507	C1507
U2533	A2534	G2354	G2445	A2288	A2184	G2124	G2056	G1964	C1873	A1593	A1508	A1508	A1508
G2536	U2537	G2355	G2446	U2291	U2185	A2125	A2060	A1966	G1874	U1594	A1509	A1509	A1509
U2542	G2543	G2356	G2447	U2292	U2186	G2126	A2069	C1967	A1875	A1784	G1702	G1600	G1516
C2547	A2548	G2357	A2448	G2293	U2187	U2130	A2070	A1970	U1882	A1785	G1701	U1602	G1519
U2552	G2553	G2358	G2454	G2294	U2188	G2131	A2074	U1971	U1883	A1786	G1707	A1603	U1523
G2554	A2555	G2359	G2455	G2295	U2189	A2132	U2075	G1975	G1887	A1794	C1606	G1524	G1524
C2556	U2557	G2360	G2456	G2296	G2190	G2133	U2076	G1980	A1889	C1800	A1713	C1607	G1529
U2560	G2561	G2361	G2457	G2297	U2192	A2134	A2077	A1981	A1890	A1801	U1714	A1608	G1530
A2562	U2563	G2362	G2458	G2298	G2193	A2135	A2078	U1992	A1913	A1802	U1715	A1609	G1531
G2564	C2565	G2363	G2459	G2299	G2194	A2136	U2079	U1993	C1914	A1803	G1716	A1610	C1532
U2566	A2567	G2364	G2460	G2300	U2197	G2137	U2080	U1994	A1915	C1804	G1721	C1612	C1533
C2568	U2569	G2365	G2461	G2301	A2198	U2138	U2081	U1995	A1916	A1805	C1728	G1622	U1534
G2572	G2573	G2366	G2462	G2302	U2199	G2141	U2085	C1996	U1917	A1817	U1730	A1626	U1539
U2574	C2575	G2367	G2463	G2303	G2200	A2142	U2086	C1997	G1921	U1818	G1731	A1630	A1544
G2579	U2580	G2368	G2464	G2304	U2201	A2143	G2087	A1998	G1922	U1819	G1732	A1634	C1547
C2581	A2582	G2369	G2465	G2305	U2202	A2144	G2093	C1999	C1923	A1820	U1733	A1635	A1552
G2583	U2584	G2370	G2466	G2306	U2203	A2145	A2094	U2009	C1924	A1821	G1734	G1642	U1553
U2586	C2587	G2371	G2467	G2307	G2204	A2146	G2095	G2010	U1925	G1822	U1735	G1643	G1555
	G2588	G2372	G2468	G2308	U2205	A2147	A2096	U2011	A1926	U1827	G1737	U1647	C1558
	U2589	G2373	G2469	G2309	U2206	A2148	A2097	G2012	A1928	G1828	G1738	U1559	U1559
	G2590	G2374	G2470	G2310	U2207	A2149	G2098	A2013	G1929	A1829	U1740	G1649	G1560
	C2591	G2375	G2471	G2311	U2208	A2150	G2099	G2014	U1930	C1833	A1744	A1664	U1563
	U2592	G2376	G2472	G2312	U2209	A2151	G2100	A2015	U1931	C1836	A1745	A1665	C1564
	G2593	G2377	G2473	G2313	U2210	A2152	A2101	G2016	G1935	A1837	A1749	G1666	C1565
	C2594	G2378	G2474	G2314	U2211	A2153	G2102	G2017	A1937	A1838	G1750	A1667	A1566
	U2595	G2379	G2475	G2315	U2212	A2154	G2103	A2018	U1939	A1839	U1751	A1668	G1567
	G2596	G2380	G2476	G2316	U2213	A2155	C2104	A2019	U1940	A1840	G1752	G1568	U1569
	C2597	G2381	G2477	G2317	U2214	A2156	C2105	G2020	U1944	A1841	A1754	A1570	A1571
	U2598	G2382	G2478	G2318	U2215	A2157	C2106	G2021		A1842			
	G2599	G2383	G2479	G2319	U2216	A2158	G2022	U2022		A1843			
	C2600	G2384	G2480	G2320	U2217	A2159	G2023	G2023		A1844			
	U2601	G2385	G2481	G2321	U2218	A2160	G2024	G2024		A1845			
	G2602	G2386	G2482	G2322	U2219	A2161	G2025	G2025		A1846			
	C2603	G2387	G2483	G2323	U2220	A2162	G2026	G2026		A1847			
	U2604	G2388	G2484	G2324	U2221	A2163	G2027	G2027		A1848			
	G2605	G2389	G2485	G2325	U2222	A2164	G2028	G2028		A1849			
	C2606	G2390	G2486	G2326	U2223	A2165	G2029	G2029		A1850			
	U2607	G2391	G2487	G2327	U2224	A2166	G2030	G2030		A1851			
	G2608	G2392	G2488	G2328	U2225	A2167	G2031	G2031		A1852			
	C2609	G2393	G2489	G2329	U2226	A2168	G2032	G2032		A1853			
	U2610	G2394	G2490	G2330	U2227	A2169	G2033	G2033		A1854			
	G2611	G2395	G2491	G2331	U2228	A2170	G2034	G2034		A1855			
	C2612	G2396	G2492	G2332	U2229	A2171	G2035	G2035		A1856			
	U2613	G2397	G2493	G2333	U2230	A2172	G2036	G2036		A1857			
	G2614	G2398	G2494	G2334	U2231		G2037	G2037		A1858			
	C2615	G2399	G2495	G2335	U2232		G2038	G2038		A1859			
	U2616	G2400	G2496	G2336	U2233		G2039	G2039		A1860			
	G2617	G2401	G2497	G2337	U2234		G2040	G2040		A1861			
	C2618	G2402	G2498	G2338	U2235		G2041	G2041		A1862			
	U2619	G2403	G2499	G2339	U2236		G2042	G2042		A1863			
	G2620	G2404	G2500	G2340	U2237		G2043	G2043		A1864			
	C2621	G2405	G2501	G2341	U2238		G2044	G2044		A1865			
	U2622	G2406	G2502	G2342	U2239		G2045	G2045		A1866			
	G2623	G2407	G2503	G2343	U2240		G2046	G2046		A1867			
	C2624	G2408	G2504	G2344	U2241		G2047	G2047		A1868			
	U2625	G2409	G2505	G2345	U2242		G2048	G2048		A1869			
	G2626	G2410	G2506	G2346	U2243		G2049	G2049		A1870			
	C2627	G2411	G2507	G2347	U2244		G2050	G2050		A1871			
	U2628	G2412	G2508	G2348	U2245		G2051	G2051		A1872			
	G2629	G2413	G2509	G2349	U2246		G2052	G2052		A1873			
	C2630	G2414	G2510	G2350	U2247		G2053	G2053		A1874			
	U2631	G2415	G2511	G2351	U2248		G2054	G2054		A1875			
	G2632	G2416	G2512	G2352	U2249		G2055	G2055		A1876			
	C2633	G2417	G2513	G2353	U2250		G2056	G2056		A1877			
	U2634	G2418	G2514	G2354	U2251		G2057	G2057		A1878			
	G2635	G2419	G2515	G2355	U2252		G2058	G2058		A1879			
	C2636	G2420	G2516	G2356	U2253		G2059	G2059		A1880			
	U2637	G2421	G2517	G2357	U2254		G2060	G2060		A1881			
	G2638	G2422	G2518	G2358	U2255		G2061	G2061		A1882			
	C2639	G2423	G2519	G2359	U2256		G2062	G2062		A1883			
	U2640	G2424	G2520	G2360	U2257		G2063	G2063		A1884			
	G2641	G2425	G2521	G2361	U2258		G2064	G2064		A1885			
	C2642	G2426	G2522	G2362	U2259		G2065	G2065		A1886			
	U2643	G2427	G2523	G2363	U2260		G2066	G2066		A1887			
	G2644	G2428	G2524	G2364	U2261		G2067	G2067		A1888			
	C2645	G2429	G2525	G2365	U2262		G2068	G2068		A1889			
	U2646	G2430	G2526	G2366	U2263		G2069	G2069		A1890			
	G2647	G2431	G2527	G2367	U2264		G2070	G2070		A1891			
	C2648	G2432	G2528	G2368	U2265		G2071	G2071		A1892			
	U2649	G2433	G2529	G2369	U2266		G2072	G2072		A1893			
	G2650	G2434	G2530	G2370	U2267		G2073	G2073		A1894			
	C2651	G2435	G2531	G2371	U2268		G2074	G2074		A1895			
	U2652	G2436	G2532	G2372	U2269		G2075	G2075		A1896			
	G2653	G2437	G2533	G2373	U2270		G2076	G2076		A1897			
	C2654	G2438	G2534	G2374	U2271		G2077	G2077		A1898			
	U2655	G2439	G2535	G2375	U2272		G2078	G2078		A1899			
	G2656	G2440	G2536	G2376	U2273		G2079	G2079		A1900			
	C2657	G2441	G2537	G2377	U2274		G2080	G2080		A1901			
	U2658	G2442	G2538	G2378	U2275		G2081	G2081		A1902			
	G2659	G2443	G2539	G2379	U2276		G2082	G2082		A1903			
	C2660	G2444	G2540	G2380	U2277		G2083	G2083		A1904			
	U2661	G2445	G2541	G2381	U2278		G2084	G2084		A1905			
	G2662	G2446	G2542	G2382	U2279		G2085	G2085		A1906			
	C2663	G2447	G2543	G2383	U2280		G2086	G2086		A1907			
	U2664	G2448	G2544	G2384	U2281		G2087	G2087		A1908			
	G2665	G2449	G2545	G2385	U2282		G2088	G2088		A1909			
	C2666	G2450	G2546	G2386	U2283		G2089	G2089		A1910			
	U2667	G2451	G2547	G2387	U2284		G2090	G2090		A1911			
	G2668	G2452	G2548	G2388	U2285		G2091</						



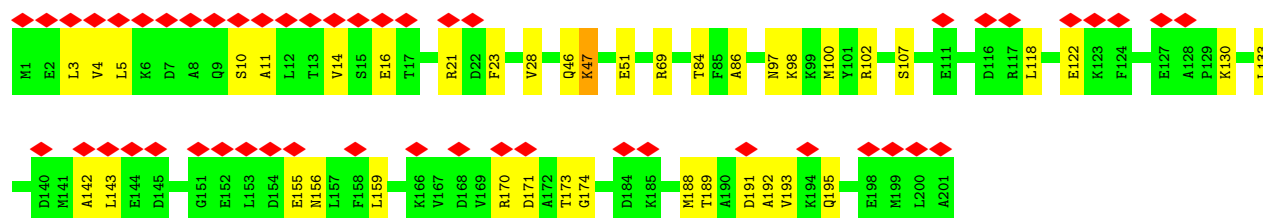
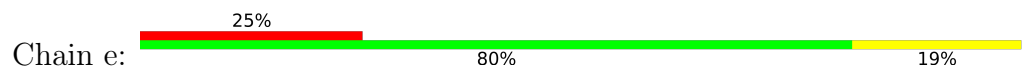
• Molecule 11: 50S ribosomal protein L2



• Molecule 12: 50S ribosomal protein L3

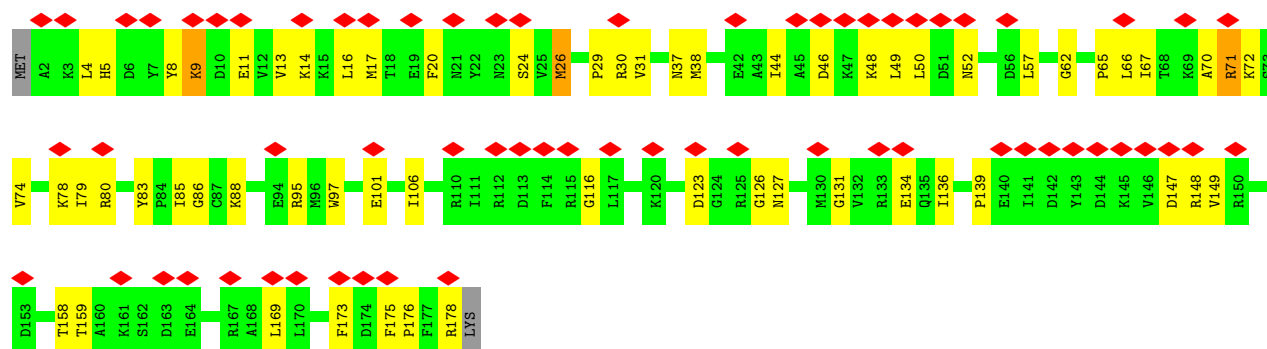


• Molecule 13: 50S ribosomal protein L4

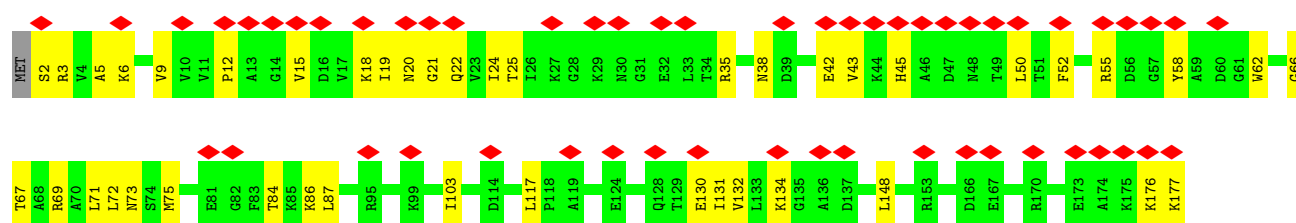
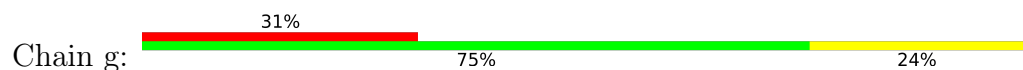


• Molecule 14: 50S ribosomal protein L5

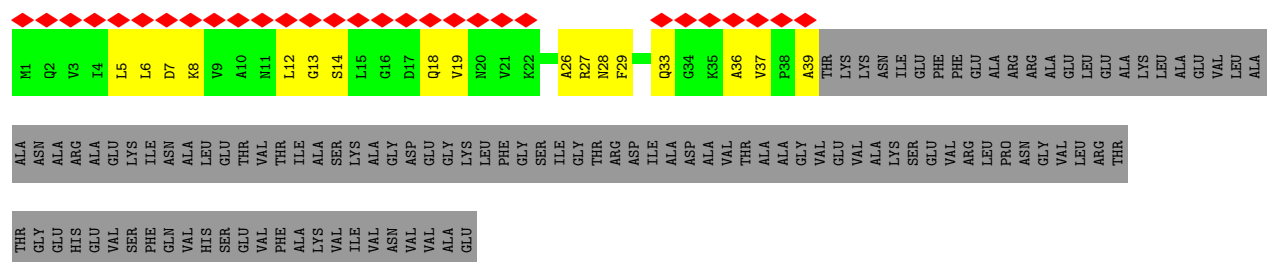




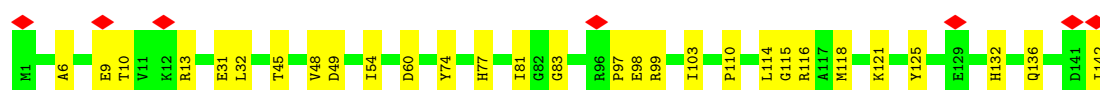
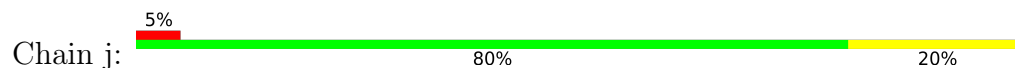
- Molecule 15: 50S ribosomal protein L6



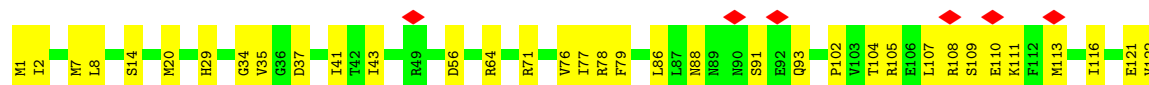
- Molecule 16: 50S ribosomal protein L9



- Molecule 17: 50S ribosomal protein L13




- Molecule 18: 50S ribosomal protein L14



LEU

- Molecule 19: 50S ribosomal protein L15

Chain l: 



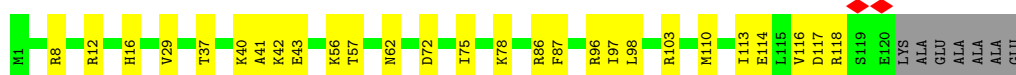
- Molecule 20: 50S ribosomal protein L16

Chain m: 




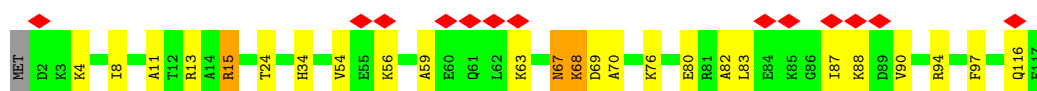
- Molecule 21: 50S ribosomal protein L17

Chain n: 




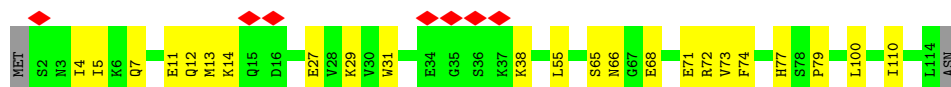
- Molecule 22: 50S ribosomal protein L18

Chain o: 




- Molecule 23: 50S ribosomal protein L19

Chain p: 

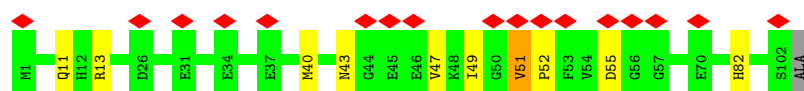
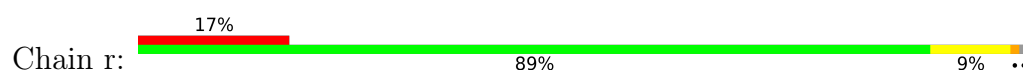


- Molecule 24: 50S ribosomal protein L20

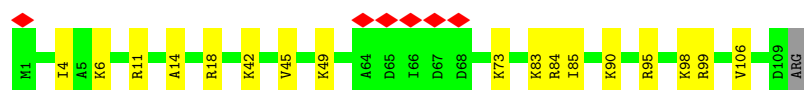
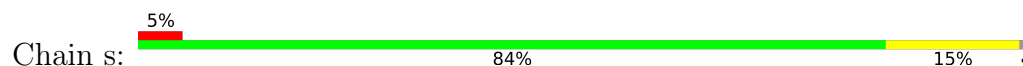
Chain q: 



- Molecule 25: 50S ribosomal protein L21



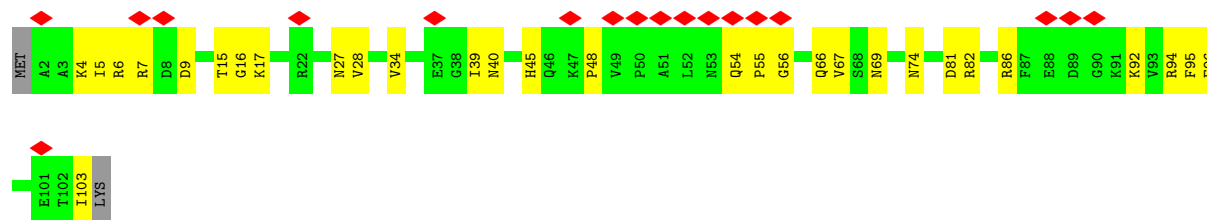
- Molecule 26: 50S ribosomal protein L22



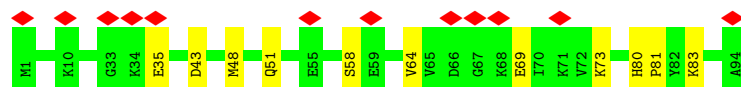
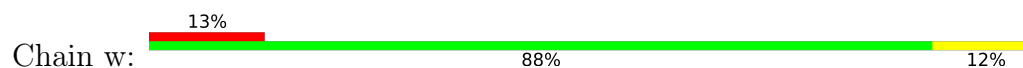
- Molecule 27: 50S ribosomal protein L23



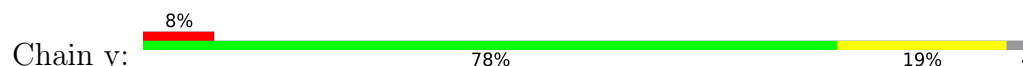
- Molecule 28: 50S ribosomal protein L24



- Molecule 29: 50S ribosomal protein L25

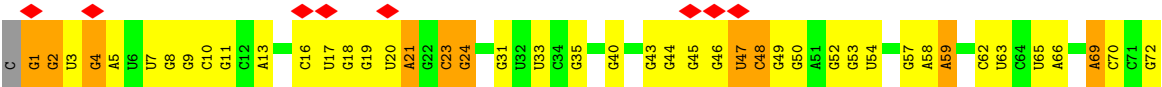


- Molecule 30: 50S ribosomal protein L27

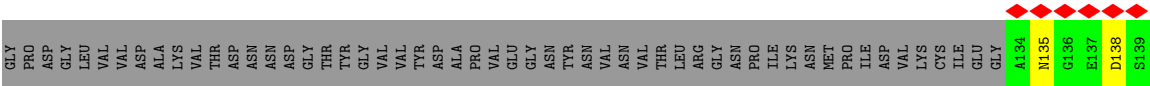
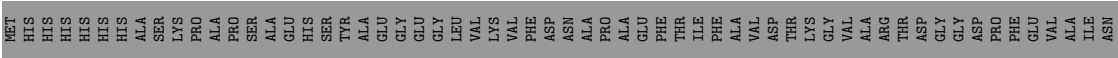


- Molecule 31: Pro-tRNA





● Molecule 32: Gelation factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	614463	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	14.45	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02965	Depositor
Map size (Å)	411.648, 411.648, 411.648	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	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	0.39	0/635	0.52	0/848
2	1	0.31	0/496	0.46	0/660
3	2	0.35	0/443	0.40	0/593
4	3	0.46	0/440	0.72	0/588
5	4	0.47	0/416	0.65	0/554
6	6	0.38	0/380	0.48	0/498
7	7	0.46	0/513	0.57	0/676
8	8	0.39	0/302	0.48	0/397
9	a	0.38	0/2828	0.36	0/4410
10	b	0.51	0/69757	0.72	19/108827 (0.0%)
11	c	0.37	0/2121	0.48	0/2852
12	d	0.40	0/1586	0.48	0/2134
13	e	0.33	0/1571	0.43	1/2113 (0.0%)
14	f	0.40	0/1434	0.62	0/1926
15	g	0.35	0/1343	0.51	0/1816
16	h	0.28	0/290	0.62	0/392
17	j	0.42	0/1152	0.47	1/1551 (0.1%)
18	k	0.40	0/947	0.47	0/1268
19	l	0.63	0/1052	0.82	1/1401 (0.1%)
20	m	0.36	0/1093	0.50	0/1460
21	n	0.40	0/973	0.52	0/1301
22	o	0.42	0/902	0.60	0/1209
23	p	0.38	0/920	0.43	0/1231
24	q	0.41	0/960	0.47	0/1278
25	r	0.53	0/823	0.65	0/1100
26	s	0.37	0/852	0.41	0/1142
27	t	0.39	0/744	0.53	0/994
28	u	0.39	0/787	0.57	0/1051
29	w	0.33	0/766	0.43	0/1025
30	y	0.39	0/627	0.55	0/829
31	v	0.52	0/1817	0.75	1/2832 (0.0%)
32	z	0.99	0/291	1.13	1/400 (0.2%)
All	All	0.48	0/99261	0.68	24/149356 (0.0%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2864	G	C2'-C3'-O3'	8.66	126.69	113.70
10	b	390	U	C2'-C3'-O3'	8.34	122.01	109.50
10	b	1595	C	C2'-C3'-O3'	7.92	125.58	113.70
10	b	2832	U	C4'-C3'-O3'	7.74	121.01	109.40
10	b	1626	A	C2'-C3'-O3'	7.08	124.33	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	625	0	652	7	0
2	1	495	0	526	15	0
3	2	439	0	482	6	0
4	3	434	0	445	12	0
5	4	409	0	440	8	0
6	6	377	0	418	1	0
7	7	504	0	572	3	0
8	8	301	0	341	3	0
9	a	2529	0	1281	15	0
10	b	62281	0	31323	387	0
11	c	2082	0	2154	27	0
12	d	1565	0	1616	21	0
13	e	1552	0	1619	24	0
14	f	1410	0	1444	44	0
15	g	1323	0	1371	26	0
16	h	287	0	307	12	0
17	j	1129	0	1162	21	0
18	k	938	0	1012	25	0
19	l	1043	0	1123	10	0
20	m	1074	0	1157	9	0
21	n	960	0	1000	19	0
22	o	892	0	923	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	p	908	0	956	21	0
24	q	947	0	1019	15	0
25	r	810	0	834	5	0
26	s	845	0	909	15	0
27	t	738	0	807	9	0
28	u	779	0	831	22	0
29	w	753	0	780	7	0
30	y	619	0	642	14	0
31	v	1626	0	821	11	0
32	z	277	0	250	3	0
All	All	90951	0	59217	755	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 755 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:892:A:C8	10:b:893:C:C6	1.96	1.54
10:b:892:A:H8	10:b:893:C:C6	1.26	1.52
10:b:892:A:C8	10:b:893:C:C5	2.13	1.34
10:b:370:G:OP2	10:b:370:G:C8	1.81	1.30
10:b:1871:A:H5"	10:b:1872:A:C2	1.74	1.22

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	56 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	55/59 (93%)	53 (96%)	2 (4%)	0	100	100
4	3	53/57 (93%)	49 (92%)	4 (8%)	0	100	100
5	4	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
6	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
7	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
8	8	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
11	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
12	d	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
13	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
14	f	175/179 (98%)	164 (94%)	10 (6%)	1 (1%)	22	23
15	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
16	h	37/149 (25%)	32 (86%)	5 (14%)	0	100	100
17	j	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
18	k	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
19	l	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
20	m	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
21	n	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
22	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
23	p	111/115 (96%)	110 (99%)	1 (1%)	0	100	100
24	q	115/118 (98%)	115 (100%)	0	0	100	100
25	r	100/103 (97%)	93 (93%)	5 (5%)	2 (2%)	6	4
26	s	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
27	t	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
28	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
29	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
30	y	80/85 (94%)	76 (95%)	3 (4%)	1 (1%)	10	8
32	z	31/148 (21%)	23 (74%)	6 (19%)	2 (6%)	1	0
All	All	3087/3427 (90%)	2937 (95%)	144 (5%)	6 (0%)	45	52

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	r	52	PRO

Continued on next page...

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Mol	Chain	Res	Type
32	z	148	VAL
25	r	51	VAL
30	y	44	LYS
14	f	71	ARG

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	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	47/49 (96%)	47 (100%)	0	100	100
4	3	46/48 (96%)	44 (96%)	2 (4%)	25	32
5	4	45/49 (92%)	44 (98%)	1 (2%)	47	61
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/44 (77%)	34 (100%)	0	100	100
11	c	216/218 (99%)	216 (100%)	0	100	100
12	d	164/164 (100%)	164 (100%)	0	100	100
13	e	165/165 (100%)	165 (100%)	0	100	100
14	f	148/150 (99%)	144 (97%)	4 (3%)	40	53
15	g	137/138 (99%)	136 (99%)	1 (1%)	81	90
16	h	30/114 (26%)	30 (100%)	0	100	100
17	j	116/116 (100%)	116 (100%)	0	100	100
18	k	103/104 (99%)	103 (100%)	0	100	100
19	l	102/103 (99%)	94 (92%)	8 (8%)	10	11
20	m	109/109 (100%)	109 (100%)	0	100	100
21	n	100/103 (97%)	100 (100%)	0	100	100
22	o	86/87 (99%)	82 (95%)	4 (5%)	22	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	p	98/100 (98%)	98 (100%)	0	100	100
24	q	89/90 (99%)	89 (100%)	0	100	100
25	r	84/84 (100%)	79 (94%)	5 (6%)	16	19
26	s	92/93 (99%)	92 (100%)	0	100	100
27	t	80/84 (95%)	78 (98%)	2 (2%)	42	56
28	u	83/85 (98%)	82 (99%)	1 (1%)	67	80
29	w	78/78 (100%)	78 (100%)	0	100	100
30	y	61/63 (97%)	61 (100%)	0	100	100
32	z	29/121 (24%)	14 (48%)	15 (52%)	0	0
All	All	2552/2772 (92%)	2509 (98%)	43 (2%)	56	71

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	z	135	ASN
32	z	149	GLU
32	z	138	ASP
32	z	145	THR
32	z	152	SER

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

Mol	Chain	Res	Type
22	o	98	GLN
24	q	81	ASN
22	o	116	GLN
23	p	66	ASN
26	s	7	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	2900/2904 (99%)	1200 (41%)	0
31	v	75/77 (97%)	41 (54%)	0
9	a	117/120 (97%)	21 (17%)	0
All	All	3092/3101 (99%)	1262 (40%)	0

5 of 1262 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	25	U
9	a	26	C
9	a	30	C
9	a	32	U
9	a	35	C

There are no RNA pucker outliers to report.

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.

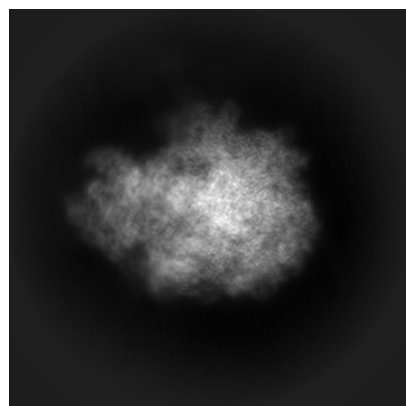
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14850. These allow visual inspection of the internal detail of the map and identification of artifacts.

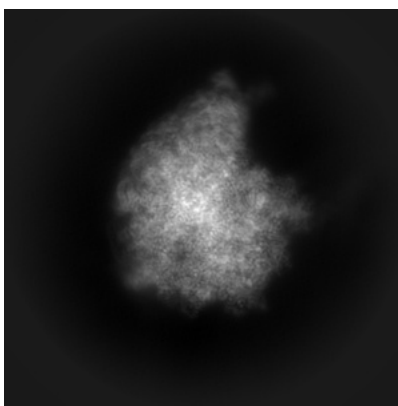
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

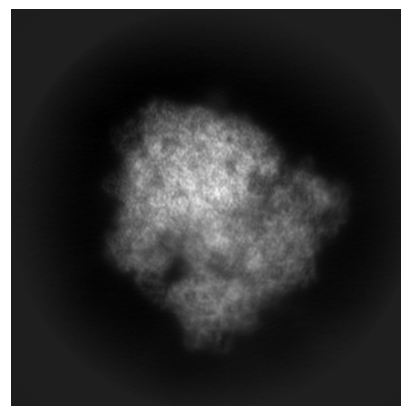
6.1.1 Primary map



X

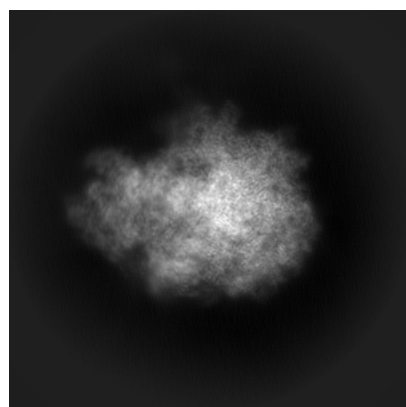


Y

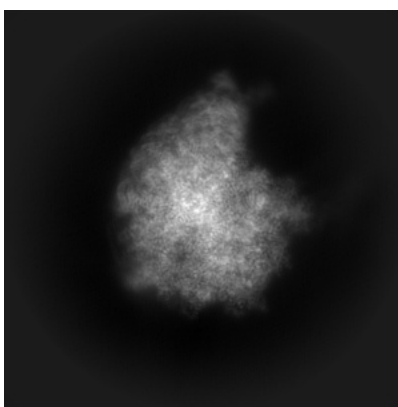


Z

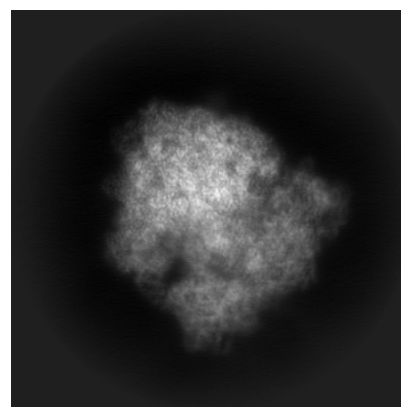
6.1.2 Raw map



X



Y

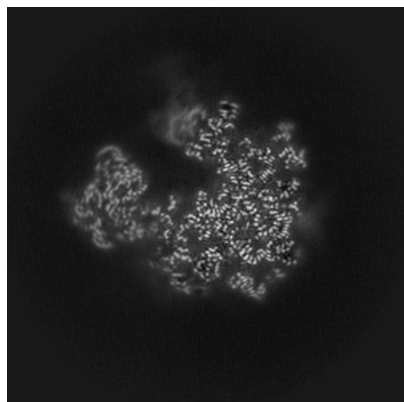


Z

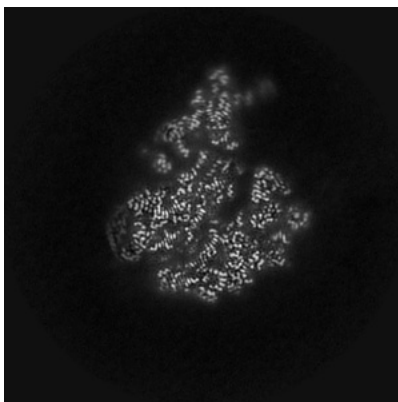
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

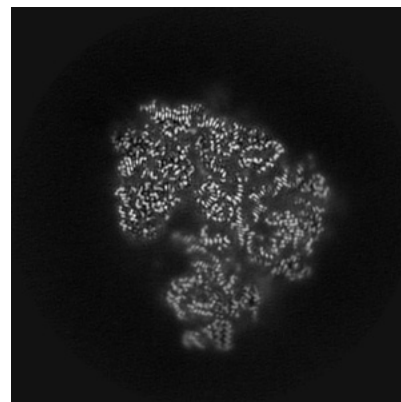
6.2.1 Primary map



X Index: 192

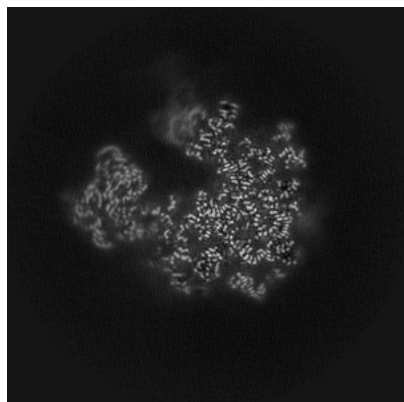


Y Index: 192

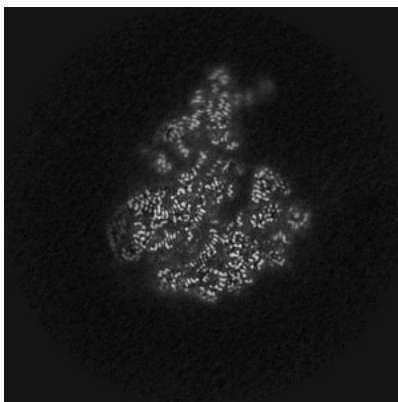


Z Index: 192

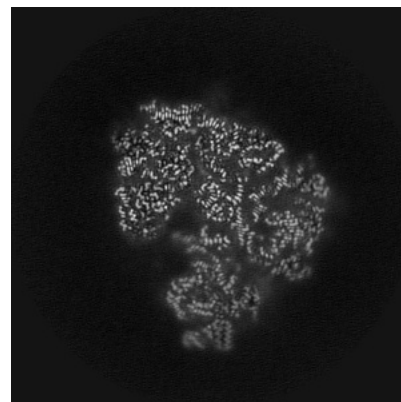
6.2.2 Raw map



X Index: 192



Y Index: 192

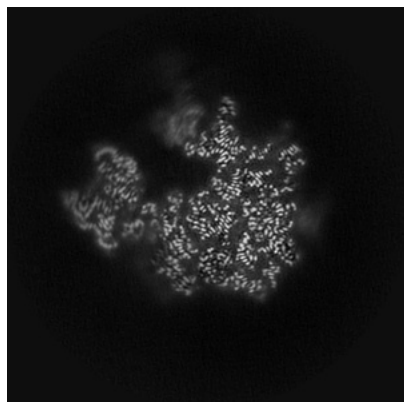


Z Index: 192

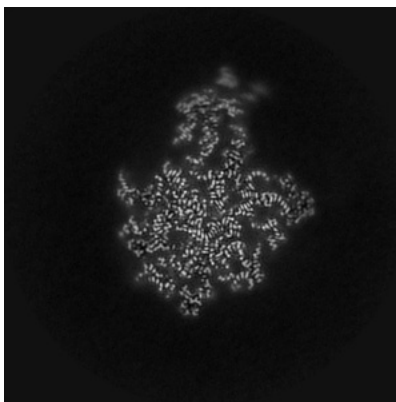
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

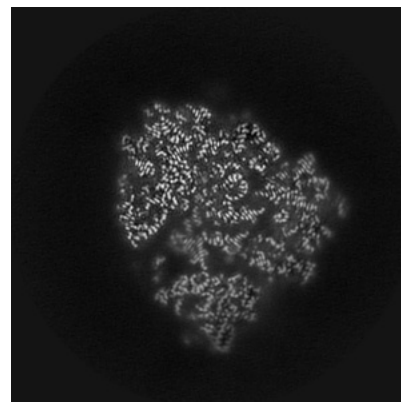
6.3.1 Primary map



X Index: 197

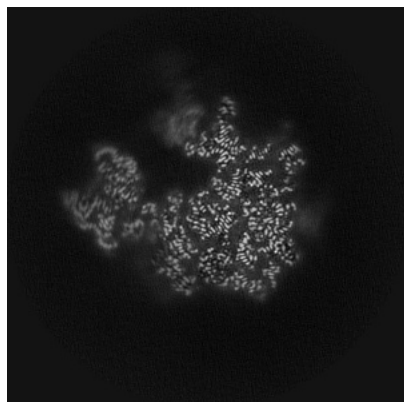


Y Index: 211

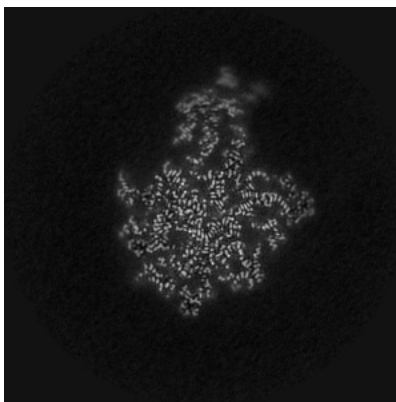


Z Index: 198

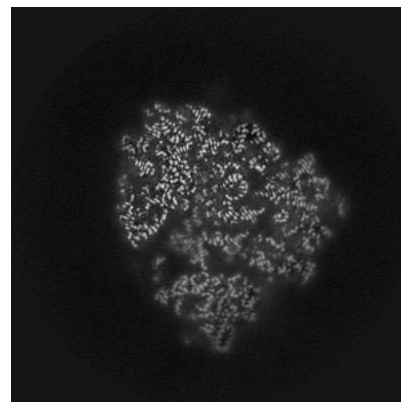
6.3.2 Raw map



X Index: 197



Y Index: 211

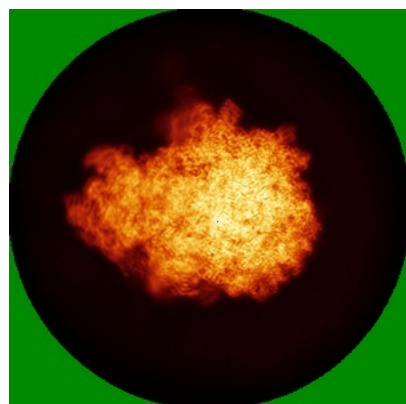


Z Index: 198

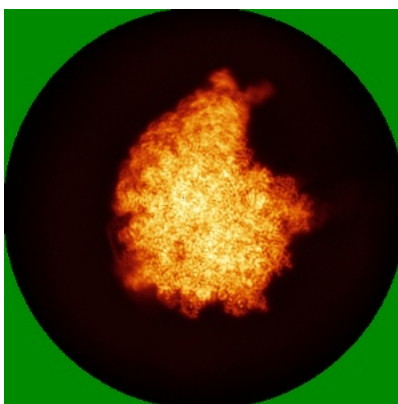
The images above show the largest variance slices of the map in three orthogonal directions.

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

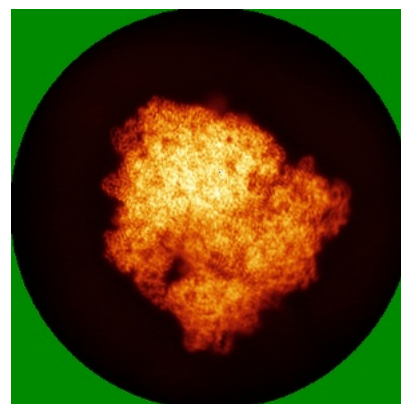
6.4.1 Primary map



X



Y

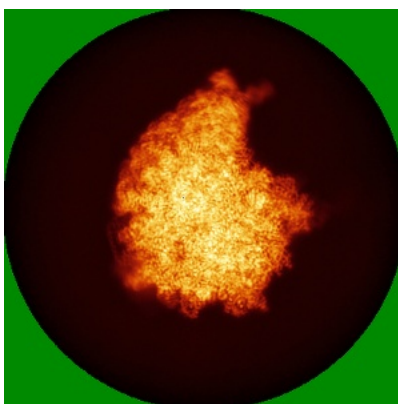


Z

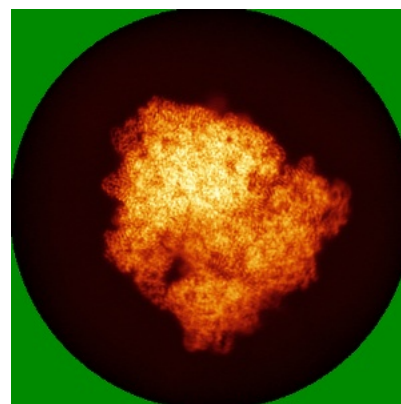
6.4.2 Raw map



X



Y

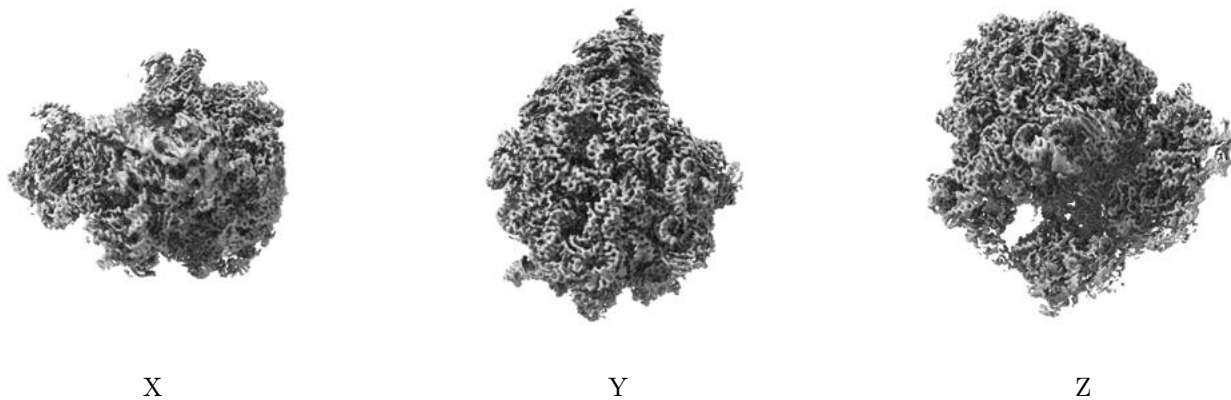


Z

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

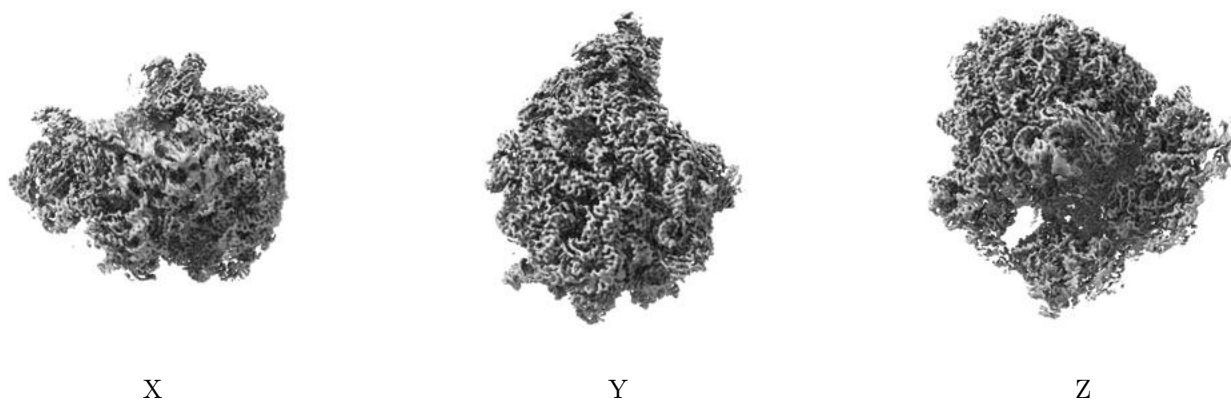
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02965. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

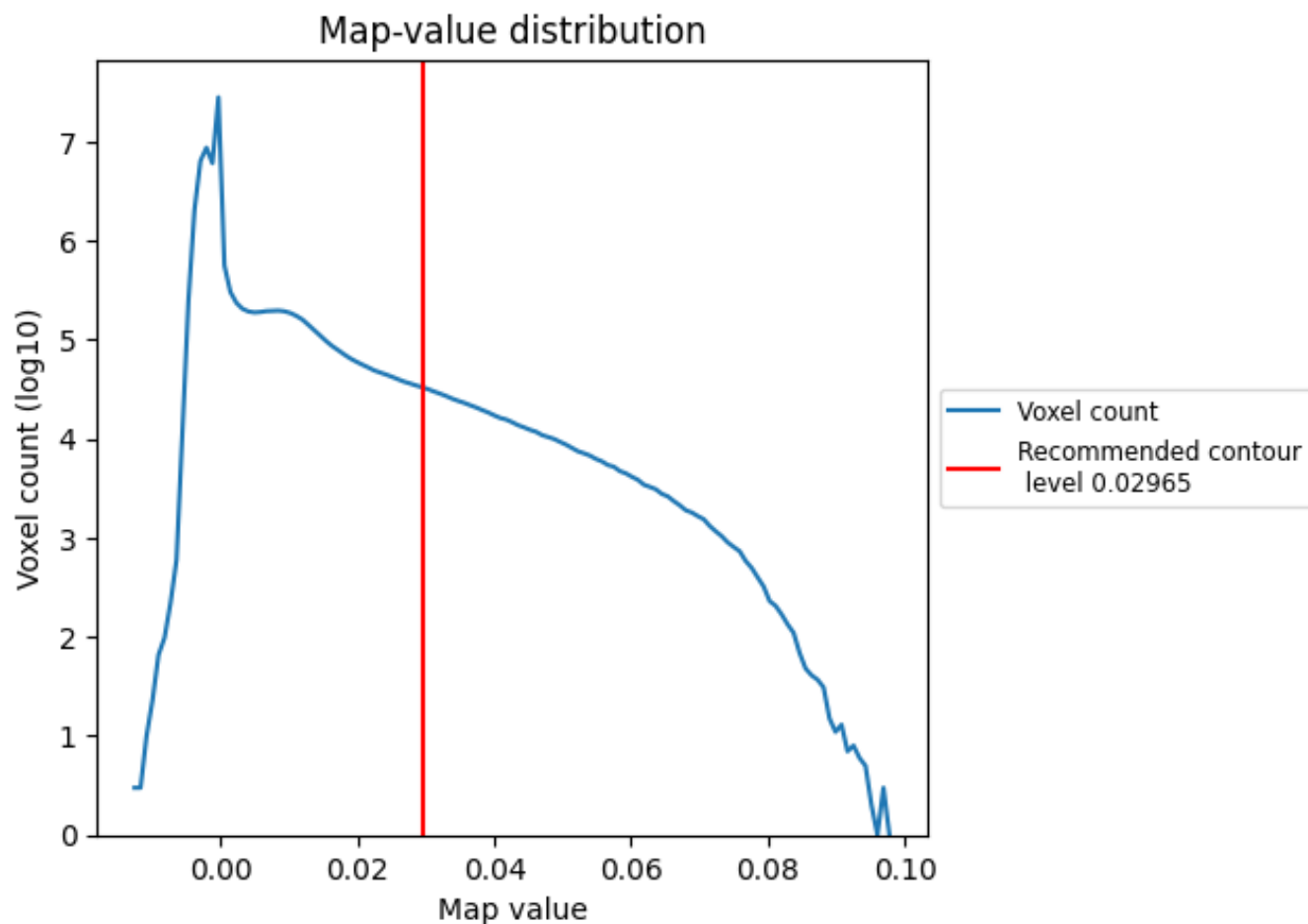
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

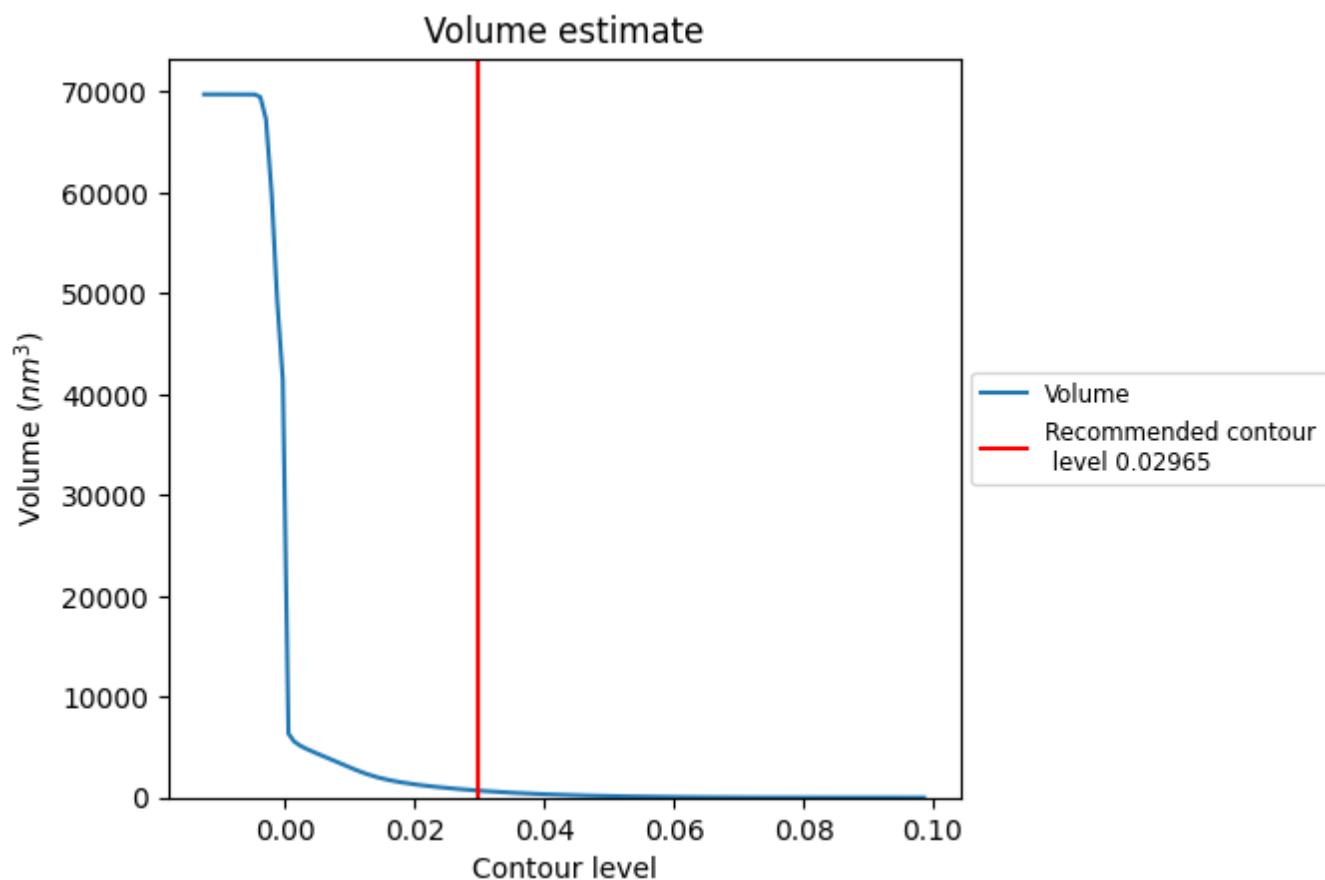
This section contains the results of statistical analysis of the map.

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.

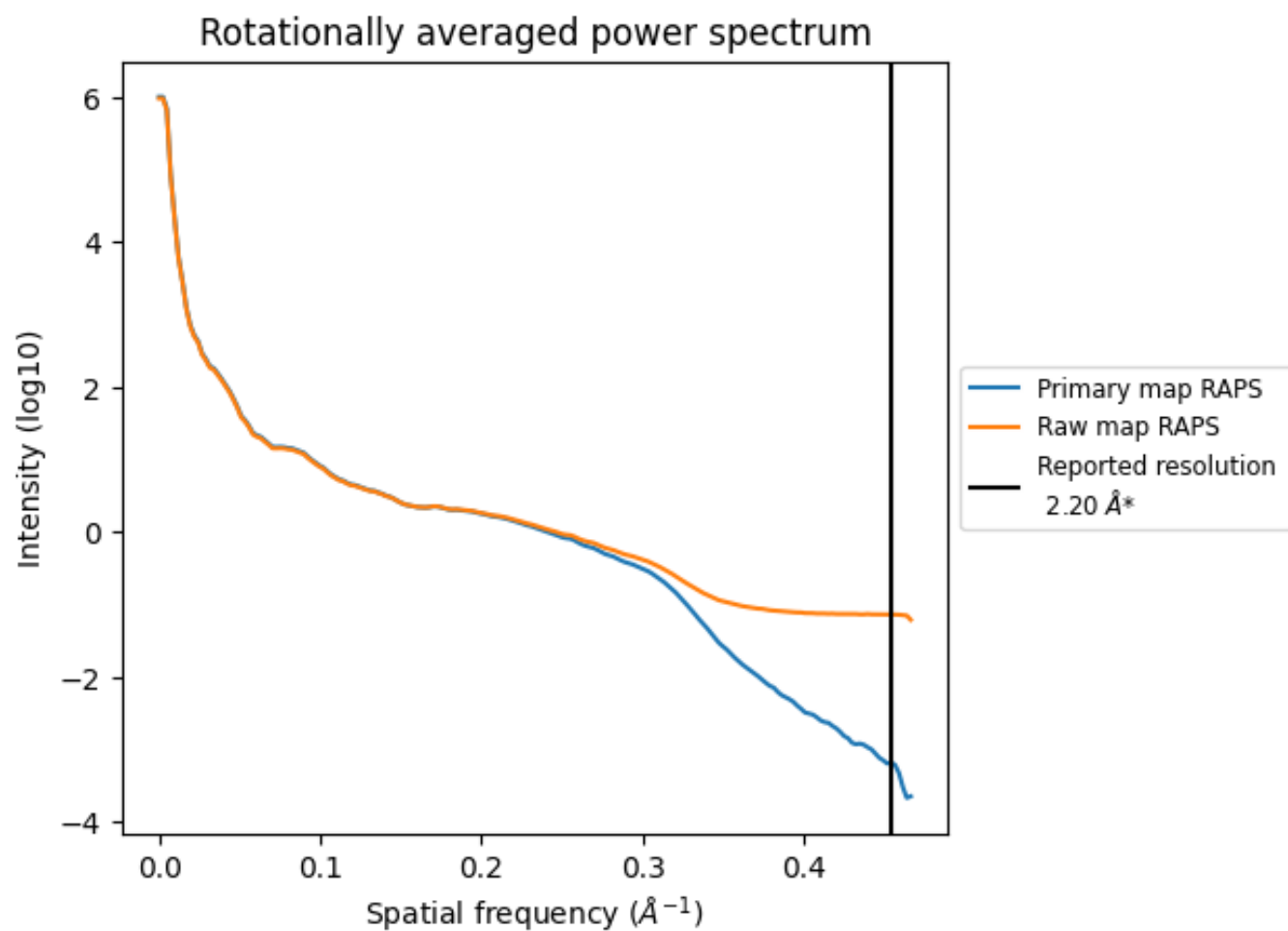
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 698 nm³; this corresponds to an approximate mass of 631 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 ⓘ

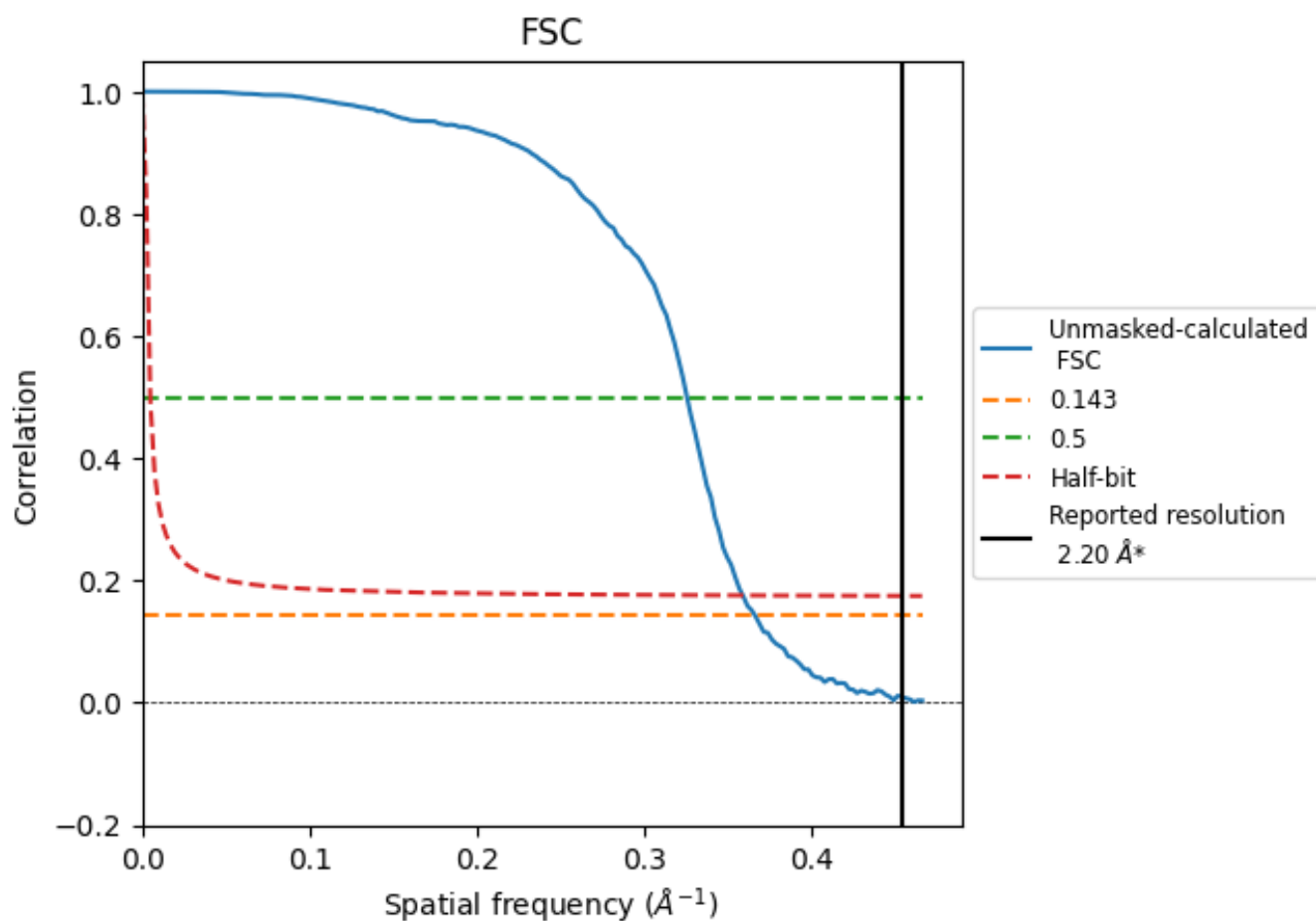


*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

8.2 Resolution estimates [i](#)

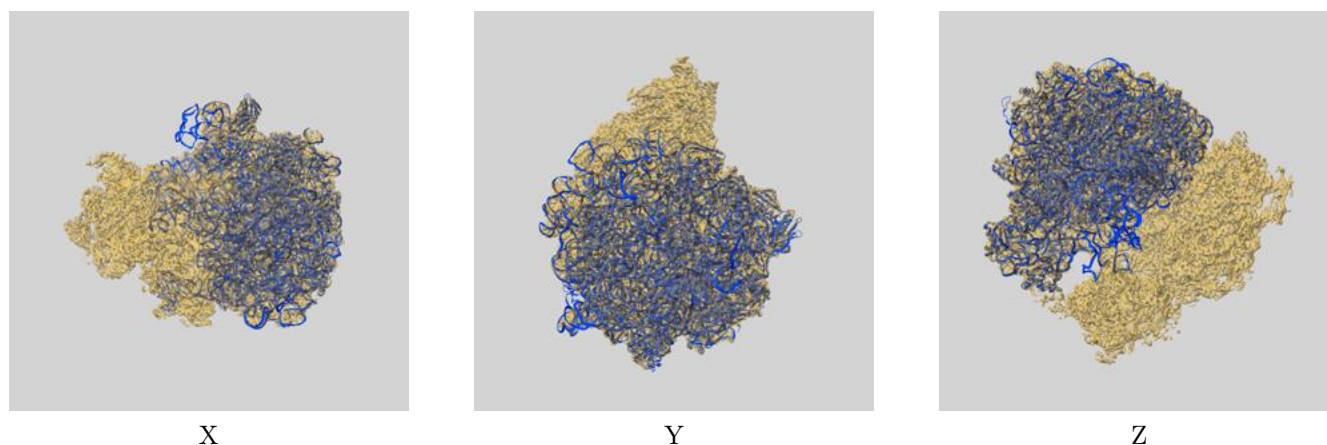
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.73	3.07	2.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.73 differs from the reported value 2.2 by more than 10 %

9 Map-model fit [i](#)

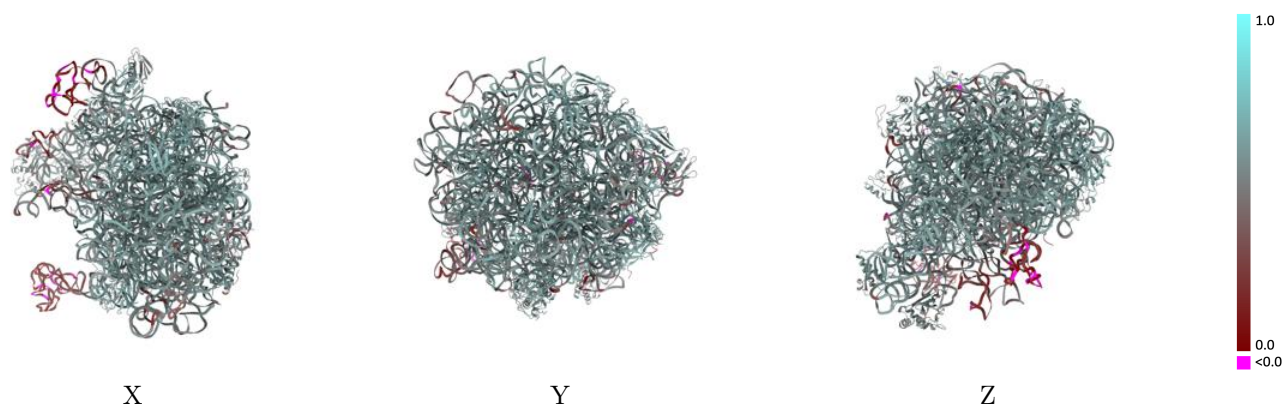
This section contains information regarding the fit between EMDB map EMD-14850 and PDB model 7ZP8. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



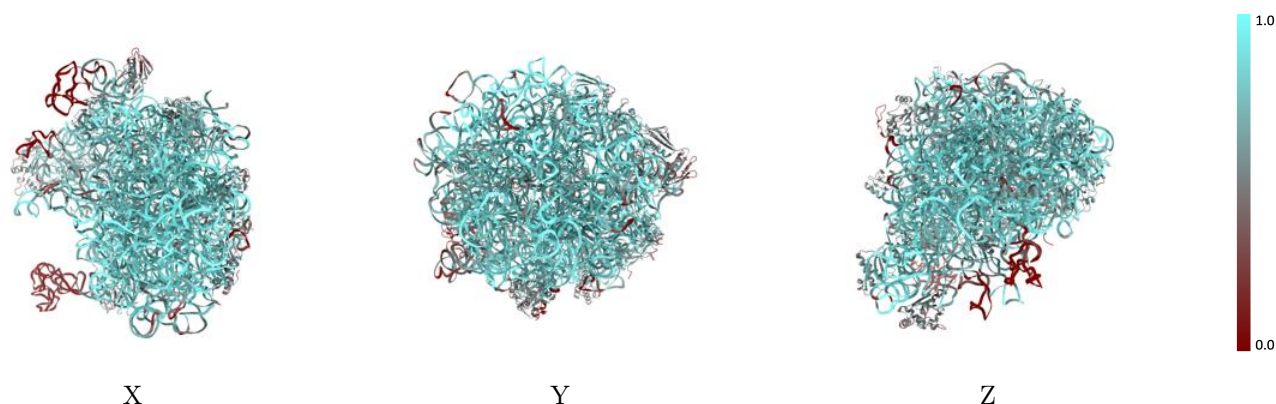
The images above show the 3D surface view of the map at the recommended contour level 0.02965 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



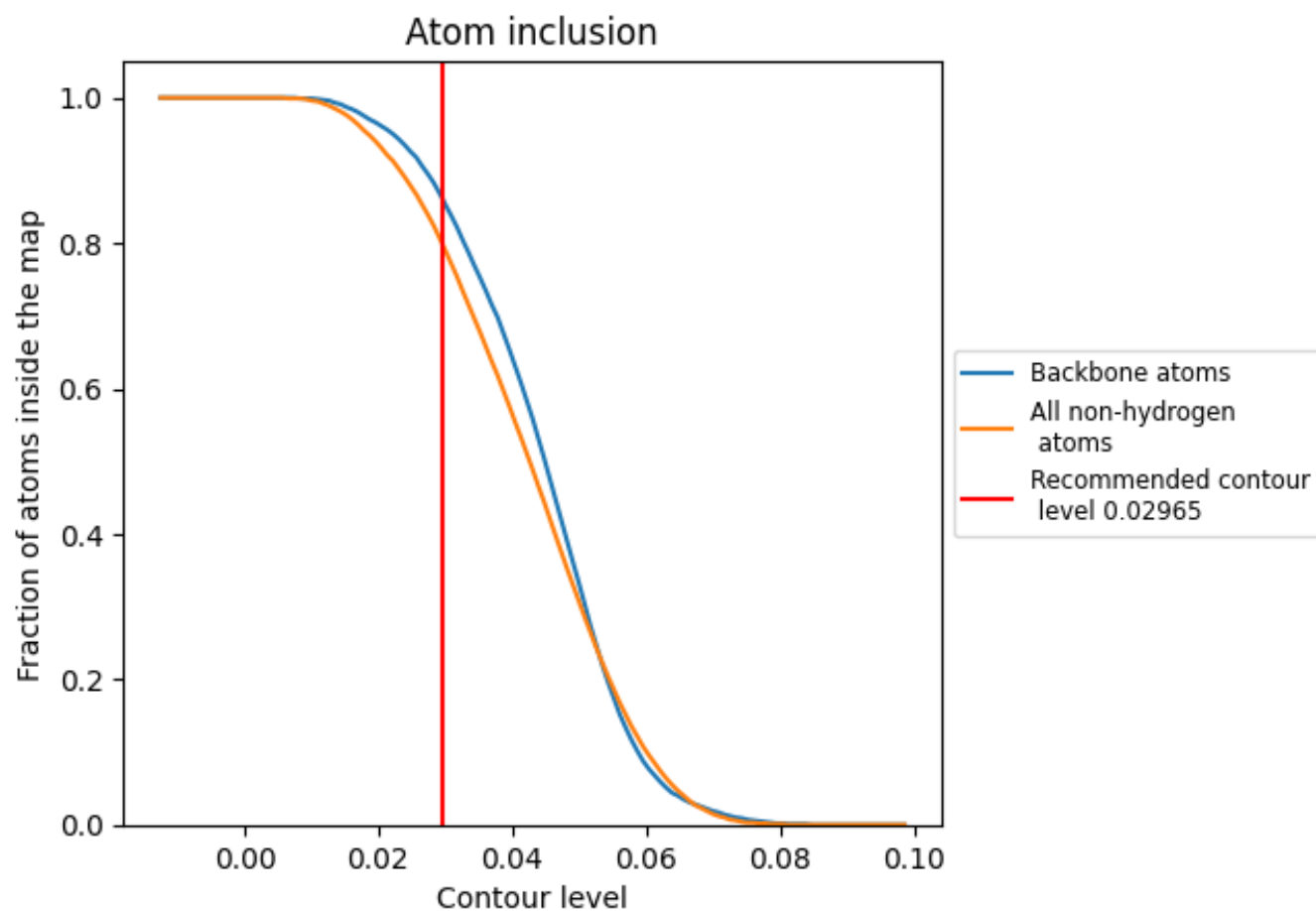
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02965).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.02965) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.5450
0	 0.8050	 0.6060
1	 0.5900	 0.5440
2	 0.7490	 0.5970
3	 0.7490	 0.5780
4	 0.6230	 0.5630
6	 0.9150	 0.6310
7	 0.8660	 0.6240
8	 0.7770	 0.6060
a	 0.8650	 0.5650
b	 0.8380	 0.5330
c	 0.8400	 0.6180
d	 0.7650	 0.6110
e	 0.6060	 0.5800
f	 0.4740	 0.5080
g	 0.4990	 0.5400
h	 0.1970	 0.4970
j	 0.7710	 0.5980
k	 0.7360	 0.6060
l	 0.7310	 0.5870
m	 0.7730	 0.6040
n	 0.8080	 0.6130
o	 0.6360	 0.5540
p	 0.7530	 0.6060
q	 0.8090	 0.6100
r	 0.6570	 0.5740
s	 0.7590	 0.6060
t	 0.6510	 0.5780
u	 0.5500	 0.5500
v	 0.6440	 0.4040
w	 0.6580	 0.5880
y	 0.7550	 0.5950
z	 0.1780	 0.3270

