



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 09:27 PM UTC

PDB ID : 8VK0 / pdb_00008vk0
EMDB ID : EMD-43294
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX:50S-HflX-A
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-08
Resolution : 3.14 Å (reported)
Based on initial models : 5O61, 6DZI

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:

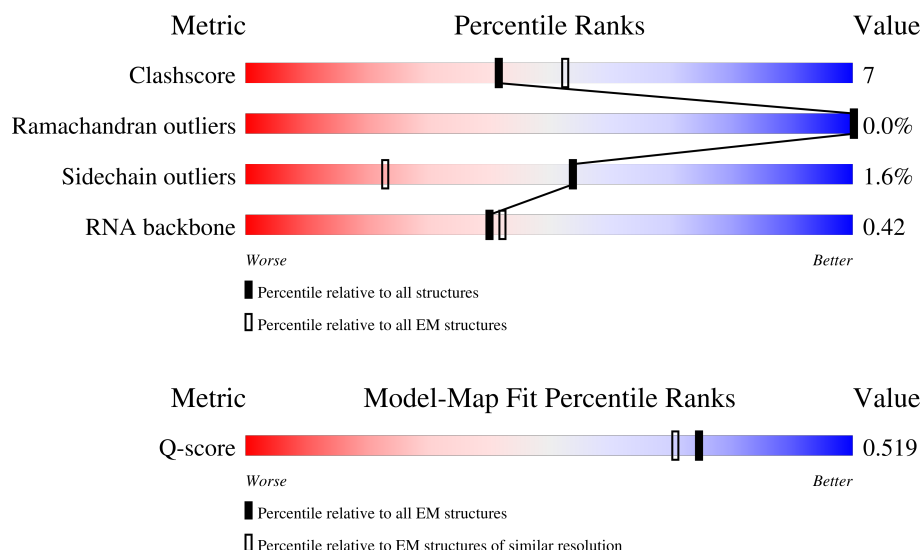
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.14 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	14483 (2.64 - 3.64)

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	2	61	92% 5% .
2	3	24	83% 12% .

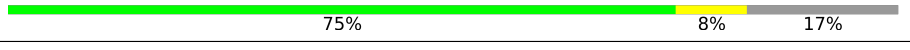
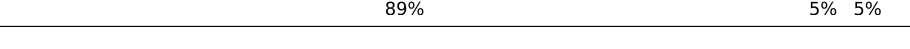
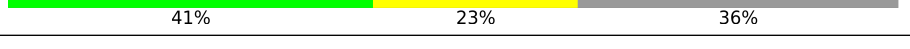
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Mol	Chain	Length	Quality of chain
3	4	470	
4	A	3120	
5	B	118	
6	C	278	
7	D	217	
8	E	215	
9	F	187	
10	G	179	
11	H	151	
12	I	175	
13	J	142	
14	K	147	
15	L	122	
16	M	147	
17	N	138	
18	O	199	
19	P	127	
20	Q	113	
21	R	129	
22	S	103	
23	T	153	
24	U	100	
25	V	105	
26	W	215	
27	X	88	

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Mol	Chain	Length	Quality of chain
28	Y	64	
29	Z	77	
30	b	57	
31	c	55	
32	d	47	
33	e	64	
34	f	37	
35	g	75	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
36	GCP	4	501	-	-	X	-

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 100928 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 L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	426	Total	C	N	O	S	0	0
			3228	1997	599	625	7		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 5 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 8 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 9 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 13 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 14 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 17 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 19 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 20 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 21 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 22 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 23 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 24 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 28 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 31 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	e	63	Total	C	N	O	0	0
			502	302	115	85		

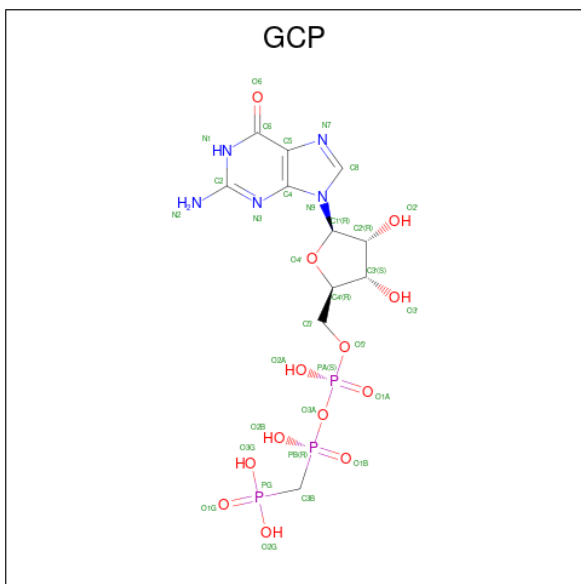
- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 35 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

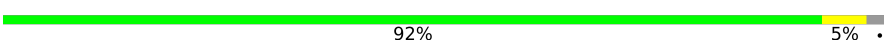
- Molecule 36 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 50S ribosomal protein L30

Chain 2: 

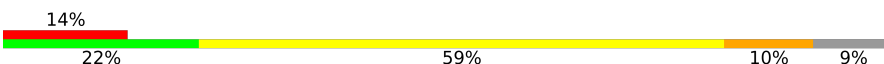


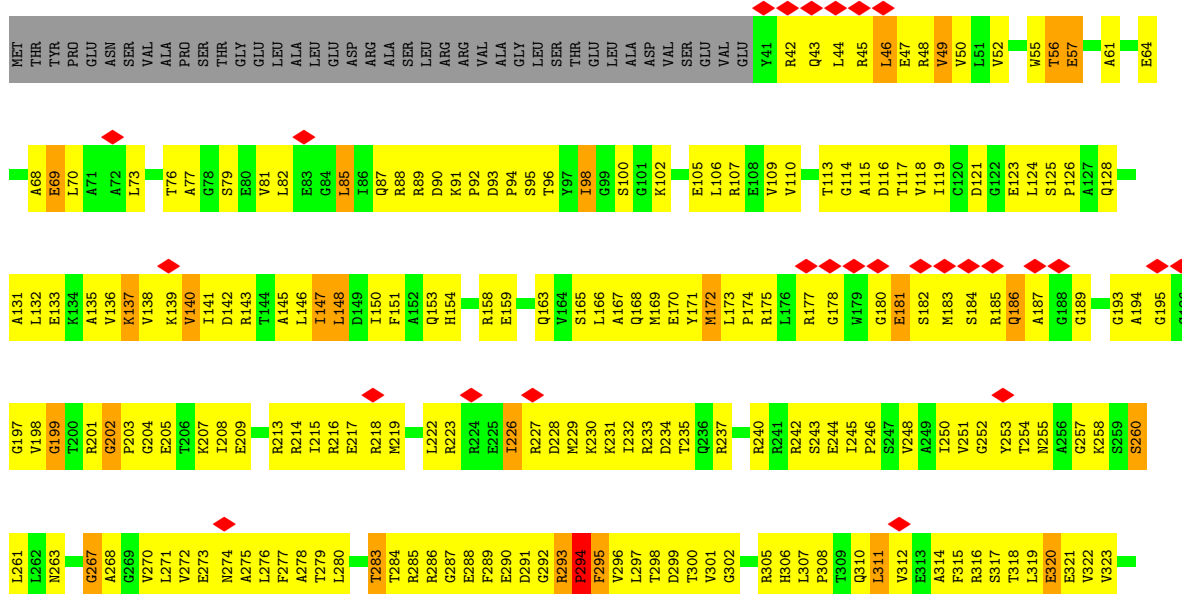
- Molecule 2: 50S Ribosomal Protein L37

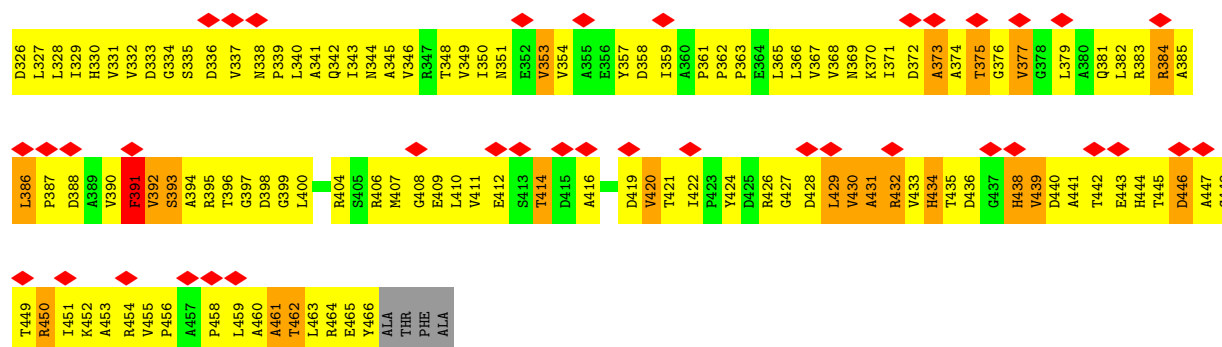
Chain 3: 



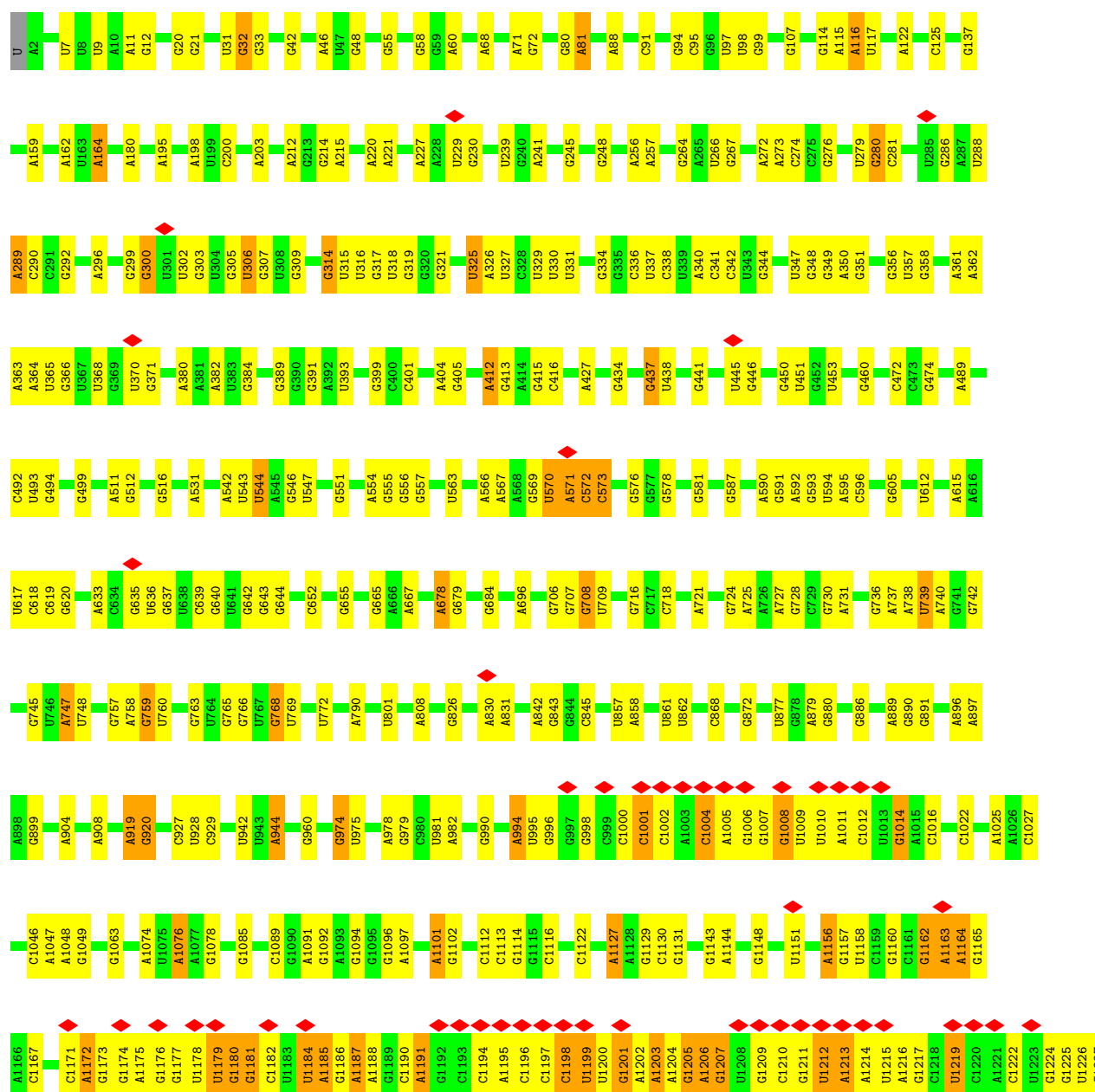
- Molecule 3: GTPase HflX

Chain 4: 

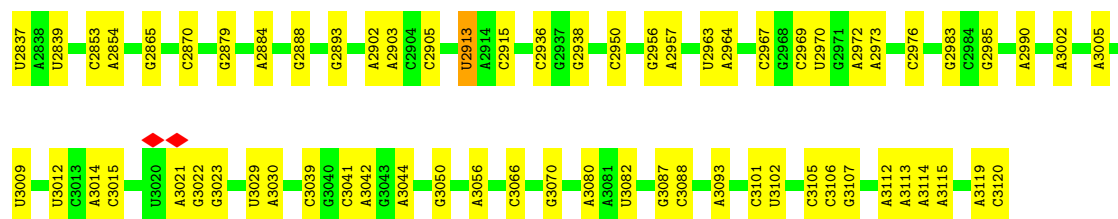




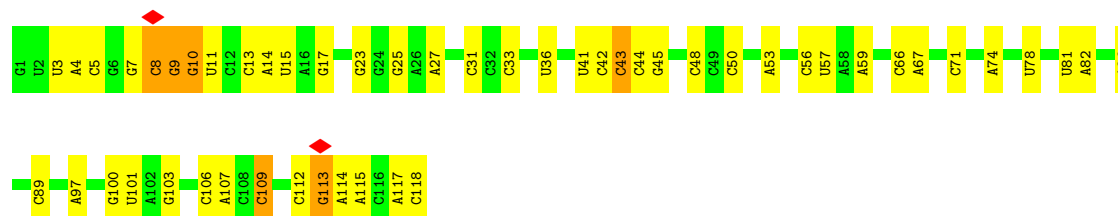
• Molecule 4: 23S ribosomal RNA



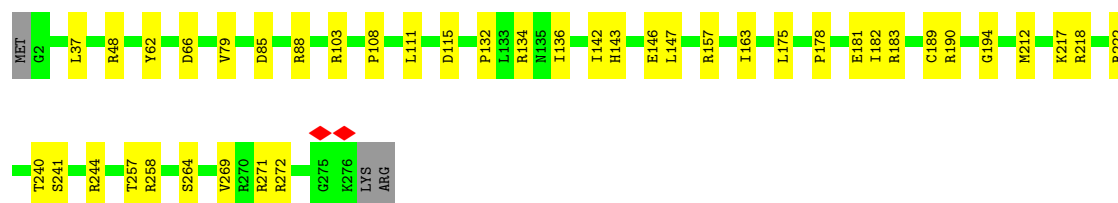
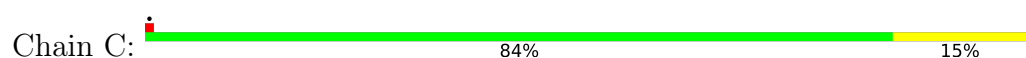
U2697	C2698	A2553	C2431	G2359	G2263	U2141	G2014	A1844	A1706	G1606	A1539	U1378	A1228
A2699	A2700	A2559	A2434	C2360	C2267	A2143	U2015	U1847	G1707	G1607	U1540	G1379	A1229
U2701	U2702	U2567	G2446	U2361	C2145	C2144	G2016	A1848	U1709	U1608	G1386	U1380	G1230
A2703	U2704	U2568	A2449	C2362	G2270	A2146	C2017	G1851	A1710	G1609	A1387	U1231	U1231
U2705	U2706	U2569	A2450	A2363	G2271	U2147	G2018	A1852	U1713	C1610	U1388	U1232	A1233
U2707	U2708	A2570	G2462	C2364	G2272	C2148	C2025	G1863	A1716	A1611	U1389	U1234	U1235
U2709	U2710	U2571	G2463	A2365	C2273	A2151	A2026	U1864	U1717	G1615	G1398	G1236	G1236
U2711	U2712	U2572	U2467	C2366	G2274	A2152	U2033	U1865	C1718	C1616	U1399	U1237	U1237
U2713	U2714	U2573	U2468	G2367	G2275	G2153	G2034	A1866	U1723	C1617	A1400	G1238	G1238
U2715	U2716	C2574	A2470	C2368	A2284	G2154	U2035	G1867	U1729	U1619	A1401	C1239	C1239
U2717	U2718	A2582	G2474	C2369	G2285	A2160	C2043	A1871	U1728	U1620	A1402	G1240	G1240
U2719	U2720	C2583	G2475	A2370	A2286	A2161	U2044	A1872	A1729	C1621	A1246	A1246	A1246
U2721	U2722	U2584	G2476	G2371	G2287	A2162	G2045	A1873	U1730	G1622	A1247	U1247	U1247
U2723	U2724	U2585	G2477	U2372	G2288	U2163	A2046	U1877	A1731	U1623	A1415	G1248	G1248
U2725	U2726	U2586	G2478	G2373	U2314	A2176	A2070	G1885	G1736	G1625	A1416	U1250	U1250
U2727	U2728	U2587	G2479	U2374	U2315	U2179	A2071	G1892	A1737	A1628	C1436	A1251	A1251
U2729	U2730	G2588	G2480	U2375	G2316	U2187	G2075	C1893	A1744	G1629	U1444	G1252	G1252
U2731	U2732	U2589	G2481	G2376	C2320	U2188	A2083	C1904	U1745	A1630	U1455	C1253	C1253
U2733	U2734	A2600	A2491	U2377	G2321	U2189	U2086	U1911	G1746	A1631	U1456	G1254	G1254
U2735	U2736	A2601	A2492	U2378	G2322	A2180	A2087	C1912	U1754	G1632	U1466	C1260	C1260
U2737	U2738	A2602	G2503	G2379	G2323	C2191	U2088	U1916	A1755	A1636	C1465	A1261	A1261
U2739	U2740	G2607	G2504	U2380	A2326	A2194	U2089	A1917	G1756	G1637	C1466	C1269	C1269
U2741	U2742	A2608	G2505	A2327	G2327	U2195	C2089	A1918	U1757	G1638	U1467	G1270	G1270
U2743	U2744	A2609	G2506	U2328	G2328	G2196	U2090	A1919	U1758	G1639	A1468	C1271	C1271
U2745	U2746	G2609	C2507	U2329	G2329	U2197	U2091	A1920	A1759	G1640	A1469	C1272	C1272
U2747	U2748	G2610	C2508	U2330	G2330	G2204	U2092	A1921	A1764	A1648	U1470	A1274	A1274
U2749	U2750	G2611	C2509	U2331	G2331	A2205	U2093	A1922	U1767	C1649	C1478	A1275	A1275
U2751	U2752	G2612	A2510	U2332	G2332	A2206	U2094	A1923	C1768	C1668	U1479	U1292	U1292
U2753	U2754	G2613	A2511	U2333	G2333	U2215	U2095	A1924	U1769	G1669	A1480	G1293	G1293
U2755	U2756	G2614	U2512	U2334	G2334	U2216	U2096	A1925	U1777	G1670	A1493	G1302	G1302
U2757	U2758	G2615	U2513	U2335	G2335	U2217	U2097	A1926	U1778	C1671	U1494	U1303	U1303
U2759	U2760	G2616	U2514	U2336	G2336	U2218	U2098	A1927	A1779	C1672	A1499	C1314	C1314
U2761	U2762	G2617	U2515	U2337	G2337	U2219	U2099	A1928	U1780	C1673	A1508	G1332	G1332
U2763	U2764	G2618	U2516	U2338	G2338	U2220	U2100	A1929	U1781	G1674	U1509	G1337	G1337
U2765	U2766	G2619	U2517	U2339	G2339	U2221	U2101	A1930	U1782	G1675	A1518	G1343	G1343
U2767	U2768	G2620	U2518	U2340	G2340	U2222	U2102	A1931	U1783	G1676	A1519	A1344	A1344
U2769	U2770	G2621	U2519	U2341	G2341	U2223	U2103	A1932	U1784	G1677	G1522	G1353	G1353
U2771	U2772	G2622	U2520	U2342	G2342	U2224	U2104	A1933	U1785	G1678	G1530	A1362	A1362
U2773	U2774	G2623	U2521	U2343	G2343	U2225	U2105	A1934	U1786	G1679	G1531	G1363	G1363
U2775	U2776	G2624	U2522	U2344	G2344	U2226	U2106	A1935	U1787	U1680	G1532	U1364	U1364
U2777	U2778	G2625	U2523	U2345	G2345	U2227	U2107	A1936	U1788	U1681	G1533	G1365	G1365
U2779	U2780	G2626	U2524	U2346	G2346	U2228	U2108	A1937	U1789	U1682	G1534	C1366	C1366
U2781	U2782	G2627	U2525	U2347	G2347	U2229	U2109	A1938	U1790	G1683	G1535	G1371	G1371
U2783	U2784	G2628	U2526	U2348	G2348	U2230	U2110	A1939	U1791	U1684	G1536	U1537	U1537
U2785	U2786	G2629	U2527	U2349	G2349	U2231	U2111	A1940	U1792	U1685	G1538	G1538	G1538
U2787	U2788	G2630	U2528	U2350	G2350	U2232	U2112	A1941	U1793	U1686	G1539	G1539	G1539
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U2793	U2794	G2633	U2531	U2353	G2353	U2235	U2115	A1944	U1796	U1689	G1542	G1542	G1542
U2795	U2796	G2634	U2532	U2354	G2354	U2236	U2116	A1945	U1797	U1690	G1543	G1543	G1543
U2797	U2798	G2635	U2533	U2355	G2355	U2237	U2117	A1946	U1798	U1691	G1544	G1544	G1544
U2799	U2800	G2636	U2534	U2356	G2356	U2238	U2118	A1947	U1799	U1692	G1545	G1545	G1545
U2801	U2802	G2637	U2535	U2357	G2357	U2239	U2119	A1948	U1800	U1693	G1546	G1546	G1546
U2803	U2804	G2638	U2536	U2358	G2358	U2240	U2120	A1949	U1801	U1694	G1547	G1547	G1547
U2805	U2806	G2639	U2537	U2359	G2359	U2241	U2121	A1950	U1802	U1695	G1548	G1548	G1548
U2807	U2808	G2640	U2538	U2360	G2360	U2242	U2122	A1951	U1803	U1696	G1549	G1549	G1549
U2809	U2810	G2641	U2539	U2361	G2361	U2243	U2123	A1952	U1804	U1697	G1550	G1550	G1550
U2811	U2812	G2642	U2540	U2362	G2362	U2244	U2124	A1953	U1805	U1698	G1551	G1551	G1551
U2813	U2814	G2643	U2541	U2363	G2363	U2245	U2125	A1954	U1806	U1699	G1552	G1552	G1552
U2815	U2816	G2644	U2542	U2364	G2364	U2246	U2126	A1955	U1807	U1700	G1553	G1553	G1553
U2817	U2818	G2645	U2543	U2365	G2365	U2247	U2127	A1956	U1808	U1701	G1554	G1554	G1554
U2819	U2820	G2646	U2544	U2366	G2366	U2248	U2128	A1957	U1809	U1702	G1555	G1555	G1555
U2821	U2822	G2647	U2545	U2367	G2367	U2249	U2129	A1958	U1810	U1703	G1556	G1556	G1556
U2823	U2824	G2648	U2546	U2368	G2368	U2250	U2130	A1959	U1811	U1704	G1557	G1557	G1557
U2825	U2826	G2649	U2547	U2369	G2369	U2251	U2131	A1960	U1812	U1705	G1558	G1558	G1558
U2827	U2828	G2650	U2548	U2370	G2370	U2252	U2132	A1961	U1813	U1706	G1559	G1559	G1559
U2829	U2830	G2651	U2549	U2371	G2371	U2253	U2133	A1962	U1814	U1707	G1560	G1560	G1560
U2831	U2832	G2652	U2550	U2372	G2372	U2254	U2134	A1963	U1815	U1708	G1561	G1561	G1561
U2833	U2834	G2653	U2551	U2373	G2373	U2255	U2135	A1964	U1816	U1709	G1562	G1562	G1562
U2835	U2836	G2654	U2552	U2374	G2374	U2256	U2136	A1965	U1817	U1710	G1563	G1563	G1563
U2837	U2838	G2655	U2553	U2375	G2375	U2257	U2137	A1966	U1818	U1711	G1564	G1564	G1564
U2839	U2840	G2656	U2554	U2376	G2376	U2258	U2138	A1967	U1819	U1712	G1565	G1565	G1565
U2841	U2842	G2657	U2555	U2377	G2377	U2259	U2139	A1968	U1820	U1713	G1566	G1566	G1566
U2843	U2844	G2658	U2556	U2378	G2378	U2260	U2140	A1969	U1821	U1714	G1567	G1567	G1567
U2845	U2846	G2659	U2557	U2379	G2379	U2261	U2141	A1970	U1822	U1715	G1568	G1568	G1568
U2847	U2848	G2660	U2558	U2380	G2380	U2262	U2142	A1971	U1823	U1716	G1569	G1569	G1569
U2849	U2850	G2661	U2559	U2381	G2381	U2263	U2143	A1972	U1824	U1717	G1570	G1570	G1570
U2851	U2852	G2662	U2560	U2382	G2382	U2264	U2144	A1973	U1825	U1718	G1571	G1571	G1571
U2853	U2854	G2663	U2561	U2383	G2383	U2265	U2145	A1974	U1826	U1719	G1572	G1572	G1572
U2855	U2856	G2664	U2562	U2384	G2384	U2266	U2146	A1975	U1827	U1720	G1573	G1573	G1573
U2857	U2858	G2665	U2563	U2385	G2385	U2267	U2147	A1976	U1828	U1721	G1574	G1574	G1574
U2859	U2860	G2666	U2564	U2386	G2386	U2268	U2148	A1977	U1829	U1722	G1575	G1575	G1575
U2861	U2862	G2667	U2565	U2387	G2387	U2269	U2149	A1978	U1830	U1723	G1576	G1576	G1576
U2863	U2864	G2668	U2566	U2388	G2388	U2270	U2150	A1979	U1831	U1724	G1577	G1577	G1577
U2865	U2866	G2669	U2567	U2389	G2389	U2271	U2151	A1980	U1832	U1725	G1578	G1578	G1578
U2867	U2868	G2670	U2568	U2390	G2390	U2272	U2152	A1981	U1833	U1726	G1579	G1579	G1579
U2869	U2870	G2671	U2569	U2391	G2391	U2273	U2153	A1982	U1834	U1727	G1580	G1580	G1580
U2871	U2872	G2672	U2570	U2392	G2392	U2274	U2154	A1983	U1835	U1728	G1581	G1581	G1581
U2873	U2874	G2673	U2571	U2393	G2393	U2275	U2155	A1984	U1836	U1729	G1582	G1582	G1582
U2875	U2876	G2674	U2572	U2394									



• Molecule 5: 5S ribosomal RNA



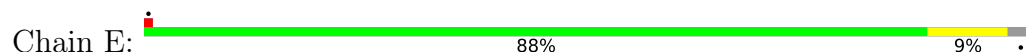
• Molecule 6: 50S ribosomal protein L2



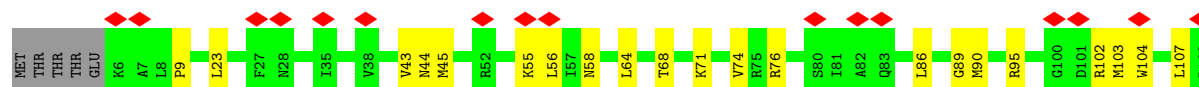
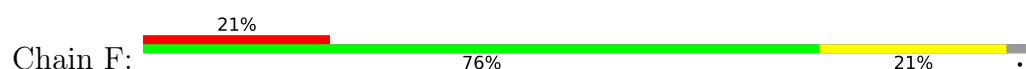
• Molecule 7: 50S ribosomal protein L3

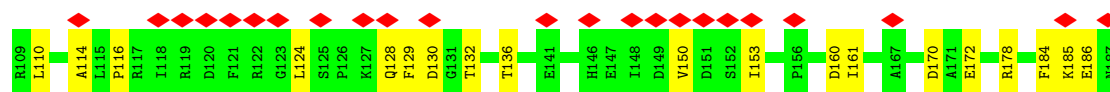


• Molecule 8: 50S Ribosomal Protein L4

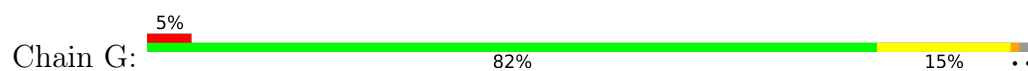


• Molecule 9: 50S Ribosomal Protein L5

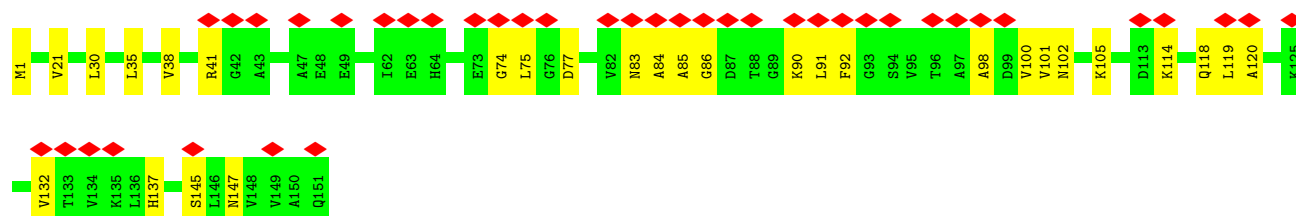
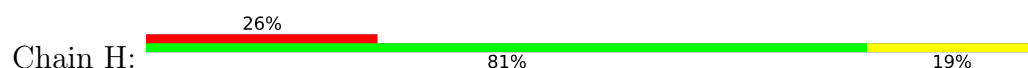




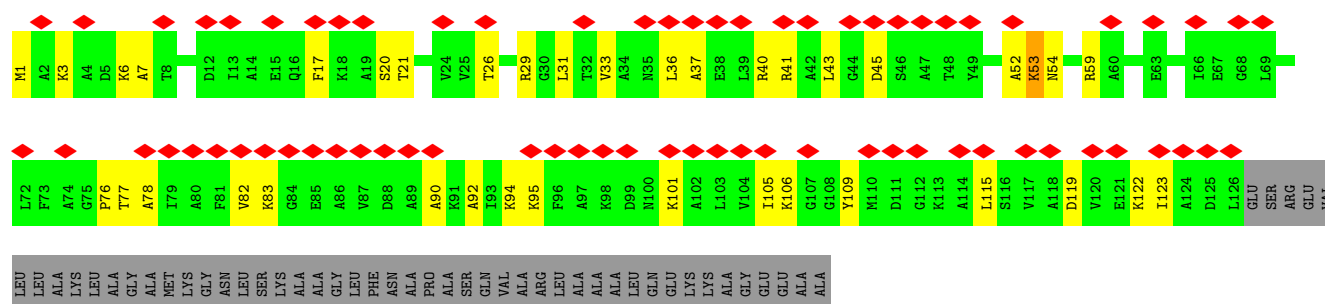
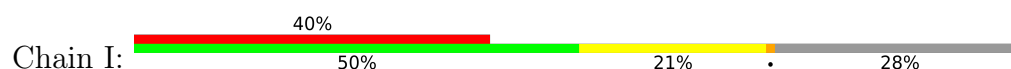
- Molecule 10: 50S ribosomal protein L6



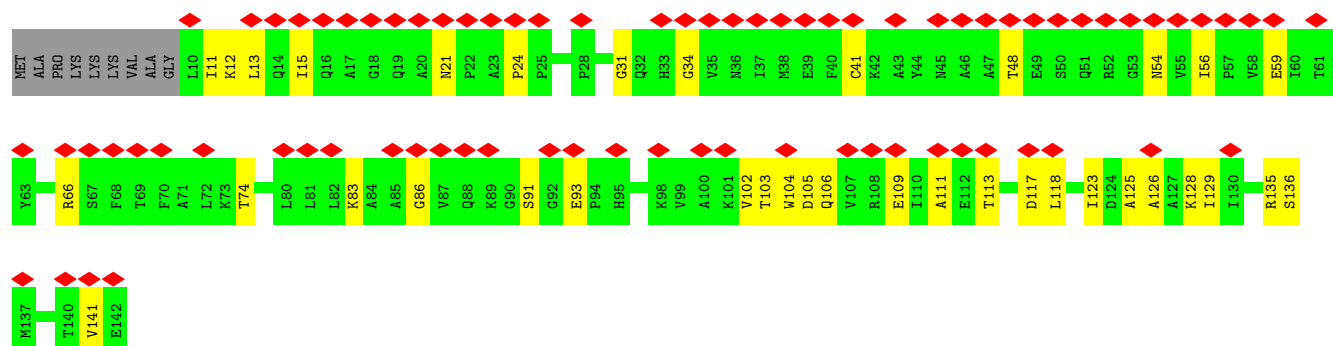
- Molecule 11: 50S ribosomal protein L9

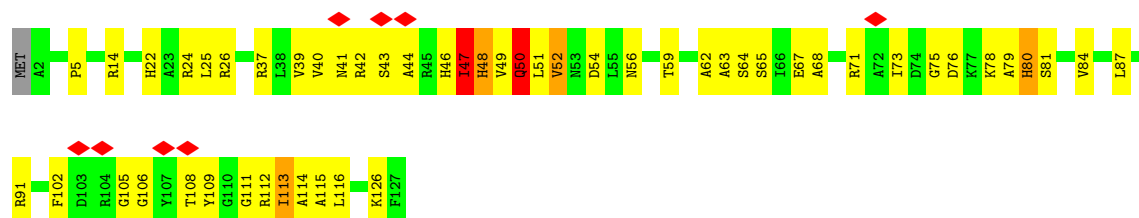
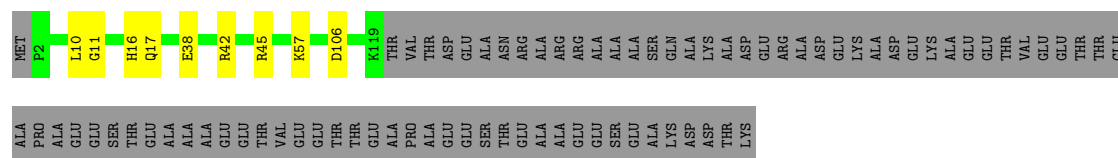
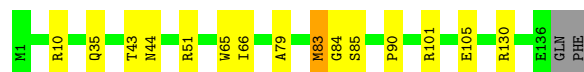
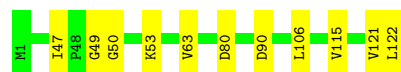
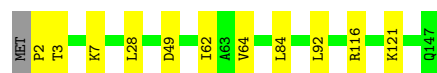


- Molecule 12: 50S ribosomal protein L10



- Molecule 13: 50S ribosomal protein L11





- Molecule 20: 50S ribosomal protein L19

Chain Q:  89% 11%



- Molecule 21: 50S Ribosomal Protein L20

Chain R:  87% 9% . .



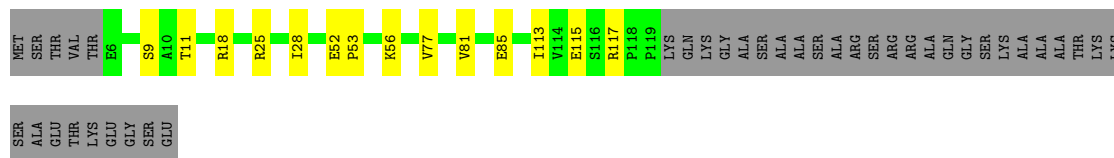
- Molecule 22: 50S Ribosomal Protein L21

Chain S:  84% 13% .



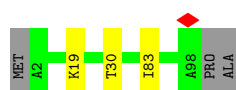
- Molecule 23: 50S Ribosomal Protein L22

Chain T:  65% 9% 25%



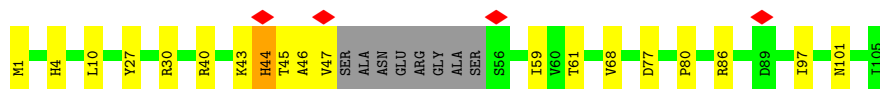
- Molecule 24: 50S Ribosomal Protein L23

Chain U:  94% . .



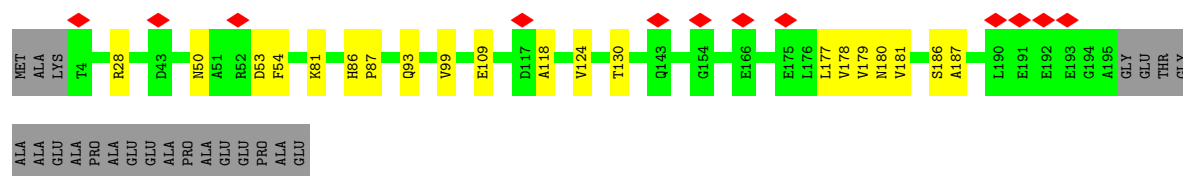
- Molecule 25: 50S ribosomal protein L24

Chain V:  74% 17% . 8%

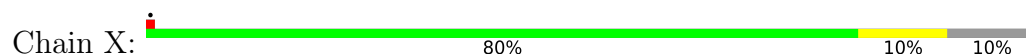


- Molecule 26: 50S ribosomal protein L25

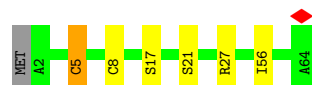
Chain W:  6% 80% 9% 11%



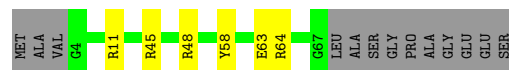
- Molecule 27: 50S ribosomal protein L27



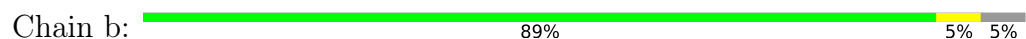
- Molecule 28: 50S Ribosomal Protein L28



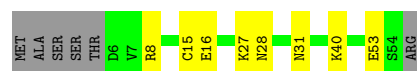
- Molecule 29: 50S ribosomal protein L29



- Molecule 30: 50S ribosomal protein L32



- Molecule 31: 50S Ribosomal Protein L33



- Molecule 32: 50S ribosomal protein L34



- Molecule 33: 50S ribosomal protein L35

Chain e:

91%

8%

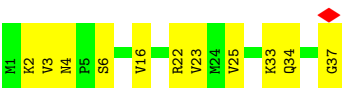


• Molecule 34: 50S ribosomal protein L36

Chain f:

70%

30%



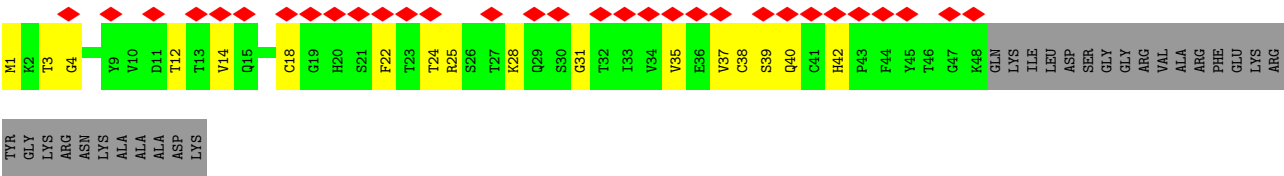
• Molecule 35: 50S Ribosomal Protein L31

Chain g:

41%

23%

36%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	57434	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 ($e^-/\text{\AA}^2$)	51.22	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.771	Depositor
Minimum map value	-0.951	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.19	Depositor
Map size (Å)	433.19998, 433.19998, 433.19998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP

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	2	0.45	0/477	0.52	0/640
2	3	0.38	0/191	0.56	0/247
3	4	0.83	0/3268	1.09	27/4428 (0.6%)
4	A	0.44	0/75001	0.47	2/117027 (0.0%)
5	B	0.36	0/2821	0.51	0/4396
6	C	0.45	0/2153	0.57	0/2895
7	D	0.46	0/1609	0.61	0/2165
8	E	0.42	0/1592	0.60	2/2153 (0.1%)
9	F	0.27	0/1467	0.66	0/1973
10	G	0.30	0/1369	0.62	0/1848
11	H	0.28	0/1027	0.71	0/1398
12	I	0.24	0/925	0.63	0/1246
13	J	0.29	0/1006	0.75	2/1364 (0.1%)
14	K	0.43	0/1157	0.50	0/1567
15	L	0.42	0/946	0.55	0/1268
16	M	0.40	0/1091	0.53	0/1457
17	N	0.42	0/1118	0.59	1/1506 (0.1%)
18	O	0.48	0/945	0.58	0/1267
19	P	0.45	1/966 (0.1%)	0.94	3/1298 (0.2%)
20	Q	0.43	0/921	0.60	0/1236
21	R	0.50	0/1000	0.56	0/1341
22	S	0.40	0/764	0.47	0/1030
23	T	0.45	0/887	0.56	0/1204
24	U	0.43	0/766	0.52	0/1030
25	V	0.38	0/738	0.64	0/987
26	W	0.27	0/1443	0.55	0/1970
27	X	0.41	0/595	0.61	0/798
28	Y	0.42	0/478	0.53	0/641
29	Z	0.39	0/534	0.52	0/713
30	b	0.45	0/427	0.61	0/572
31	c	0.36	0/413	0.49	0/553
32	d	0.47	0/380	0.56	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.42	0/507	0.52	0/672
34	f	0.39	0/303	0.53	0/401
35	g	0.23	0/372	0.58	0/503
All	All	0.44	1/109657 (0.0%)	0.53	37/164294 (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
9	F	0	1
10	G	0	2
11	H	0	1
12	I	0	2
13	J	0	1
18	O	0	1
19	P	0	4
26	W	0	1
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	P	50	GLN	N-CA	5.72	1.53	1.46

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4	373	ALA	N-CA-C	-11.96	98.92	113.15
3	4	375	THR	N-CA-C	-9.38	100.44	113.20
3	4	260	SER	N-CA-C	-8.79	102.47	113.55
3	4	393	SER	N-CA-C	-8.47	103.53	114.04
3	4	432	ARG	N-CA-C	-7.50	102.05	113.89

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	F	68	THR	Peptide
10	G	46	ALA	Peptide

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Mol	Chain	Res	Type	Group
10	G	52	VAL	Peptide
11	H	137	HIS	Peptide
12	I	52	ALA	Peptide

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	2	474	0	500	2	0
2	3	189	0	205	3	0
3	4	3228	0	3284	534	0
4	A	66981	0	33700	316	0
5	B	2522	0	1285	21	0
6	C	2110	0	2165	28	0
7	D	1587	0	1630	12	0
8	E	1569	0	1607	14	0
9	F	1445	0	1476	25	0
10	G	1348	0	1399	20	0
11	H	1018	0	988	18	0
12	I	918	0	959	29	0
13	J	990	0	1021	26	0
14	K	1130	0	1167	8	0
15	L	938	0	1000	7	0
16	M	1078	0	1151	9	0
17	N	1092	0	1128	8	0
18	O	928	0	972	5	0
19	P	956	0	991	43	0
20	Q	907	0	938	8	0
21	R	988	0	1038	10	0
22	S	754	0	802	7	0
23	T	873	0	909	8	0
24	U	756	0	802	2	0
25	V	732	0	782	15	0
26	W	1428	0	1443	11	0
27	X	586	0	601	7	0
28	Y	470	0	482	4	0
29	Z	531	0	541	3	0
30	b	423	0	463	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	c	405	0	411	6	0
32	d	377	0	411	3	0
33	e	502	0	541	5	0
34	f	299	0	324	6	0
35	g	364	0	352	11	0
36	4	32	0	14	15	0
All	All	100928	0	67482	1104	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 7.

The worst 5 of 1104 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)
3:4:445:THR:CG2	3:4:450:ARG:HB2	1.86	1.06
3:4:202:GLY:HA3	4:A:2676:C:C4'	1.86	1.05
3:4:354:VAL:HG11	3:4:361:PRO:HG3	1.38	1.04
3:4:426:ARG:HG3	3:4:429:LEU:HB2	1.38	1.04
3:4:85:LEU:HD11	3:4:106:LEU:HD21	1.40	1.02

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	2	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
2	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
3	4	424/470 (90%)	343 (81%)	79 (19%)	2 (0%)	24	54
6	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
7	D	212/217 (98%)	196 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	E	207/215 (96%)	192 (93%)	15 (7%)	0	100	100
9	F	180/187 (96%)	146 (81%)	34 (19%)	0	100	100
10	G	174/179 (97%)	151 (87%)	23 (13%)	0	100	100
11	H	149/151 (99%)	110 (74%)	39 (26%)	0	100	100
12	I	124/175 (71%)	108 (87%)	16 (13%)	0	100	100
13	J	131/142 (92%)	100 (76%)	31 (24%)	0	100	100
14	K	144/147 (98%)	137 (95%)	7 (5%)	0	100	100
15	L	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
16	M	143/147 (97%)	130 (91%)	13 (9%)	0	100	100
17	N	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
18	O	116/199 (58%)	107 (92%)	9 (8%)	0	100	100
19	P	124/127 (98%)	88 (71%)	36 (29%)	0	100	100
20	Q	111/113 (98%)	95 (86%)	16 (14%)	0	100	100
21	R	122/129 (95%)	118 (97%)	4 (3%)	0	100	100
22	S	98/103 (95%)	92 (94%)	6 (6%)	0	100	100
23	T	112/153 (73%)	110 (98%)	2 (2%)	0	100	100
24	U	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
25	V	93/105 (89%)	82 (88%)	11 (12%)	0	100	100
26	W	190/215 (88%)	170 (90%)	20 (10%)	0	100	100
27	X	77/88 (88%)	71 (92%)	6 (8%)	0	100	100
28	Y	61/64 (95%)	55 (90%)	6 (10%)	0	100	100
29	Z	62/77 (80%)	62 (100%)	0	0	100	100
30	b	52/57 (91%)	52 (100%)	0	0	100	100
31	c	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
32	d	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
33	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
34	f	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
35	g	46/75 (61%)	41 (89%)	5 (11%)	0	100	100
All	All	4039/4461 (90%)	3594 (89%)	443 (11%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	4	294	PRO
3	4	431	ALA

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	2	52/54 (96%)	52 (100%)	0	100	100
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	337/372 (91%)	309 (92%)	28 (8%)	10	32
6	C	215/218 (99%)	215 (100%)	0	100	100
7	D	160/163 (98%)	158 (99%)	2 (1%)	61	73
8	E	169/173 (98%)	169 (100%)	0	100	100
9	F	151/156 (97%)	150 (99%)	1 (1%)	76	79
10	G	148/150 (99%)	147 (99%)	1 (1%)	76	79
11	H	90/116 (78%)	89 (99%)	1 (1%)	65	75
12	I	89/120 (74%)	89 (100%)	0	100	100
13	J	102/108 (94%)	102 (100%)	0	100	100
14	K	119/120 (99%)	118 (99%)	1 (1%)	73	78
15	L	100/100 (100%)	100 (100%)	0	100	100
16	M	112/114 (98%)	112 (100%)	0	100	100
17	N	114/116 (98%)	113 (99%)	1 (1%)	70	77
18	O	97/158 (61%)	97 (100%)	0	100	100
19	P	93/94 (99%)	87 (94%)	6 (6%)	15	40
20	Q	100/100 (100%)	100 (100%)	0	100	100
21	R	97/99 (98%)	96 (99%)	1 (1%)	68	76
22	S	81/83 (98%)	78 (96%)	3 (4%)	30	57
23	T	90/117 (77%)	89 (99%)	1 (1%)	65	75
24	U	83/85 (98%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	V	81/86 (94%)	80 (99%)	1 (1%)	63	74
26	W	155/168 (92%)	154 (99%)	1 (1%)	78	80
27	X	58/63 (92%)	57 (98%)	1 (2%)	53	70
28	Y	50/51 (98%)	49 (98%)	1 (2%)	48	68
29	Z	58/66 (88%)	57 (98%)	1 (2%)	53	70
30	b	43/46 (94%)	43 (100%)	0	100	100
31	c	47/52 (90%)	47 (100%)	0	100	100
32	d	35/36 (97%)	35 (100%)	0	100	100
33	e	53/54 (98%)	53 (100%)	0	100	100
34	f	35/35 (100%)	33 (94%)	2 (6%)	18	45
35	g	43/63 (68%)	43 (100%)	0	100	100
All	All	3275/3555 (92%)	3222 (98%)	53 (2%)	54	71

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	D	26	VAL
19	P	47	ILE
28	Y	5	CYS
7	D	156	THR
11	H	38	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
15	L	91	ASN
19	P	16	ASN
35	g	40	GLN
16	M	69	ASN
16	M	127	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	3118/3120 (99%)	760 (24%)	22 (0%)
5	B	117/118 (99%)	37 (31%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3235/3238 (99%)	797 (24%)	24 (0%)

5 of 797 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	7	U
4	A	9	U
4	A	11	A
4	A	12	G
4	A	20	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	2135	U
4	A	2328	G
4	A	2320	C
4	A	2345	U
4	A	974	G

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	GCP	4	501	-	32,34,34	1.38	6 (18%)	49,54,54	1.87	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GCP	4	501	-	-	5/19/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	4	501	GCP	PG-O2G	2.85	1.61	1.55
36	4	501	GCP	C5-C4	2.76	1.46	1.38
36	4	501	GCP	PG-O3G	2.61	1.60	1.55
36	4	501	GCP	C6-N1	-2.58	1.34	1.38
36	4	501	GCP	C5-N7	-2.15	1.34	1.39

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	4	501	GCP	C5-C4-N3	-5.78	119.19	128.39
36	4	501	GCP	C2-N3-C4	4.88	120.70	112.30
36	4	501	GCP	PB-O3A-PA	-4.58	117.42	132.37
36	4	501	GCP	N9-C4-N3	4.18	134.31	125.95
36	4	501	GCP	C6-C5-N7	3.58	136.80	130.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

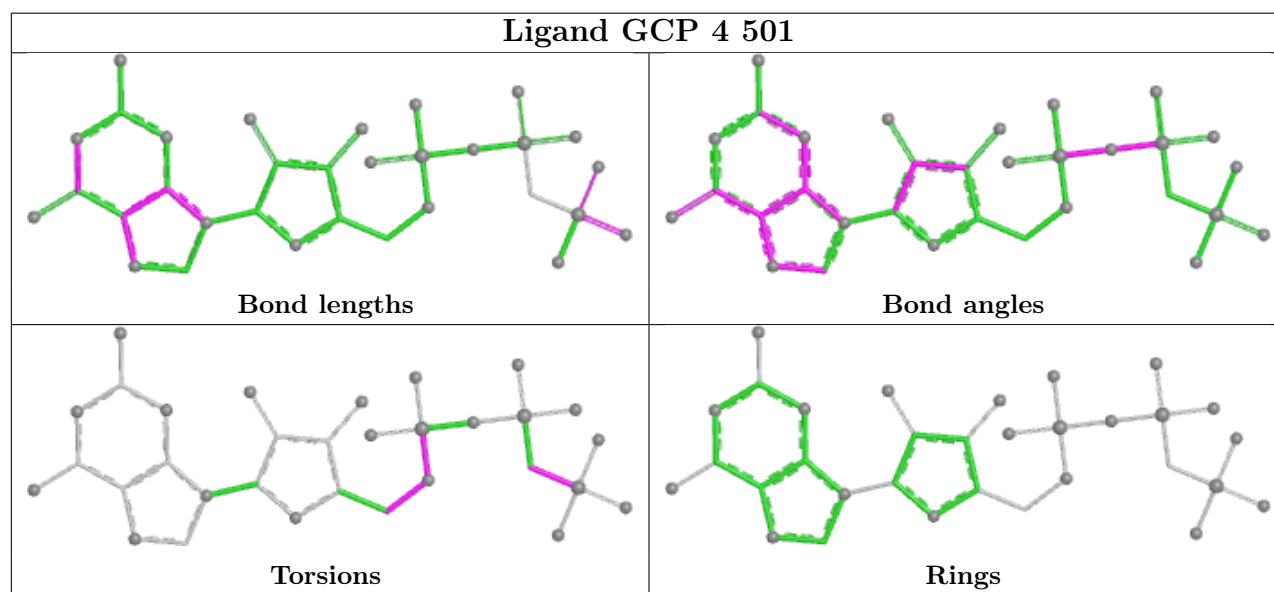
Mol	Chain	Res	Type	Atoms
36	4	501	GCP	PB-C3B-PG-O1G
36	4	501	GCP	PB-C3B-PG-O2G
36	4	501	GCP	PB-C3B-PG-O3G
36	4	501	GCP	C5'-O5'-PA-O1A
36	4	501	GCP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	4	501	GCP	15	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

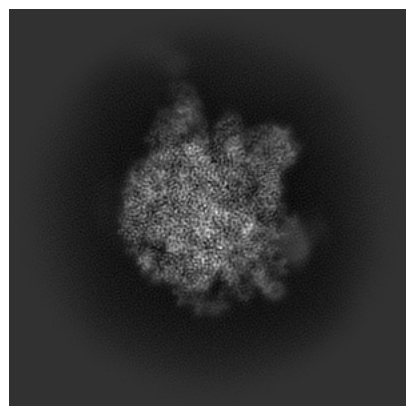
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43294. These allow visual inspection of the internal detail of the map and identification of artifacts.

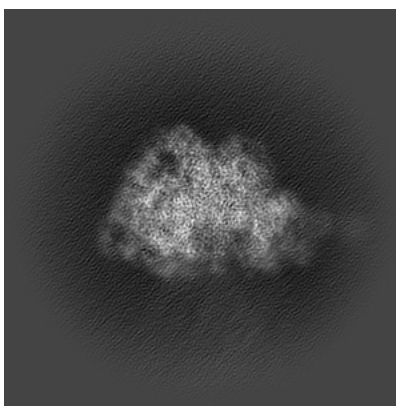
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

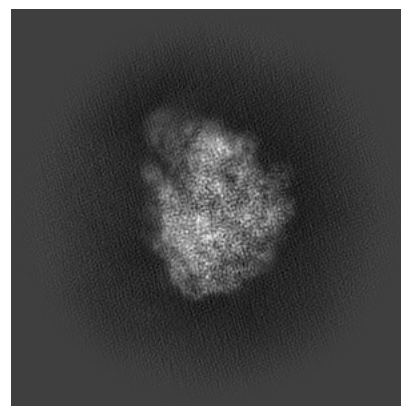
6.1.1 Primary map



X

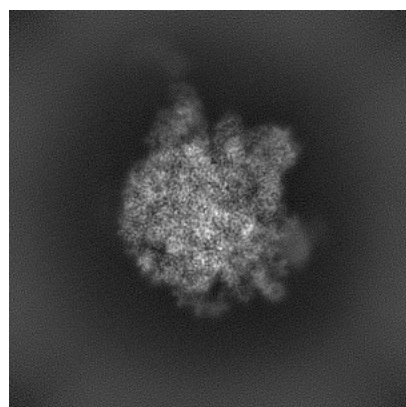


Y

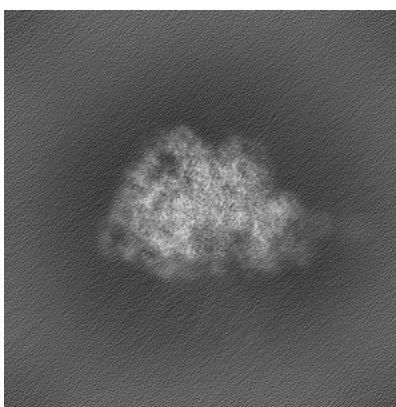


Z

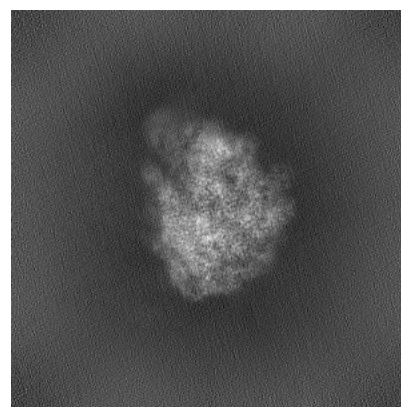
6.1.2 Raw map



X



Y

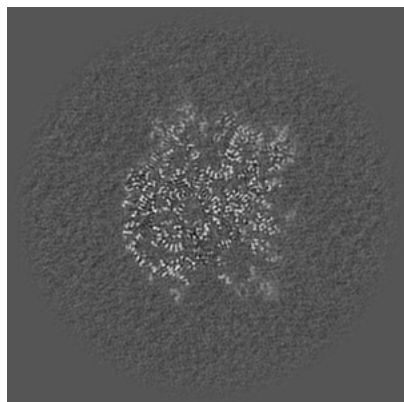


Z

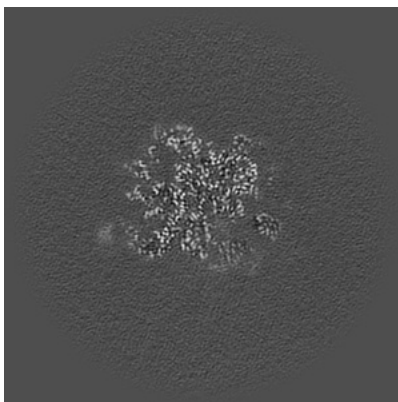
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

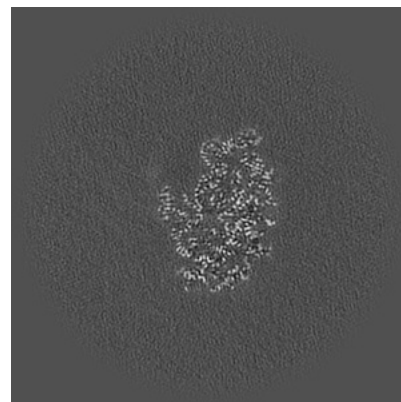
6.2.1 Primary map



X Index: 200

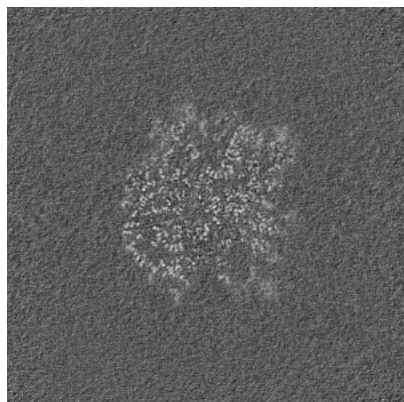


Y Index: 200

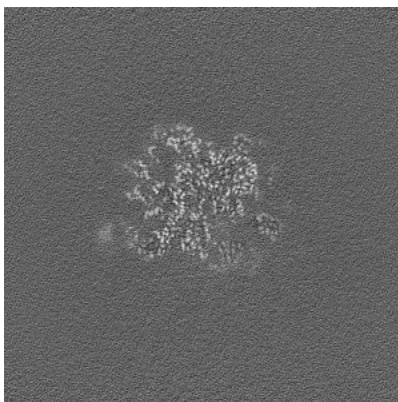


Z Index: 200

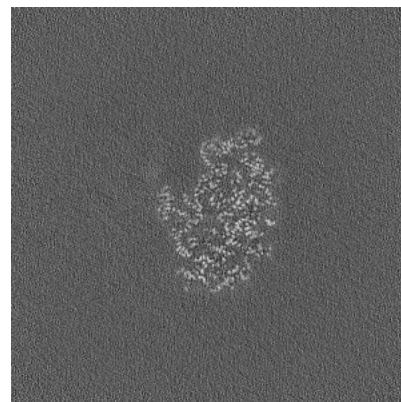
6.2.2 Raw map



X Index: 200



Y Index: 200

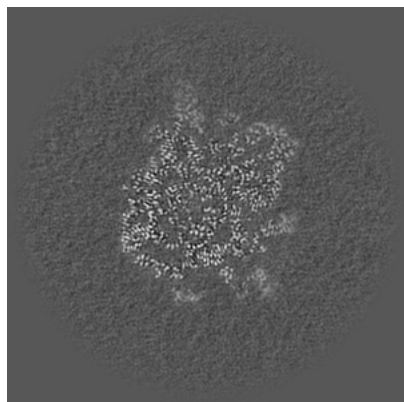


Z Index: 200

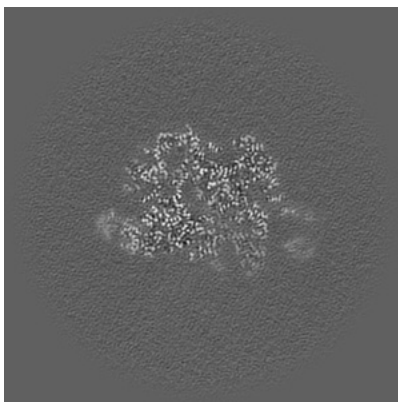
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

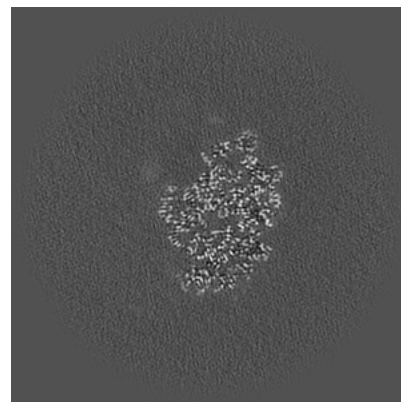
6.3.1 Primary map



X Index: 194

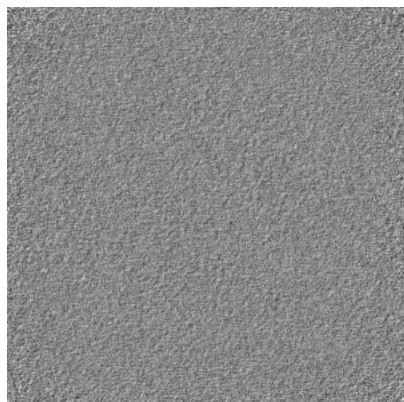


Y Index: 190

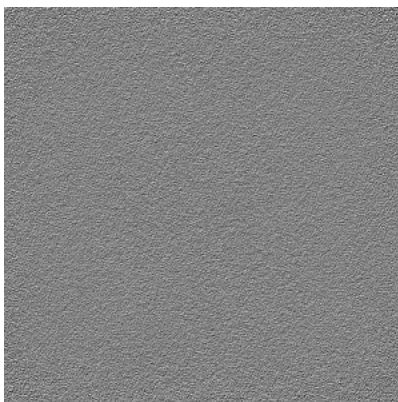


Z Index: 196

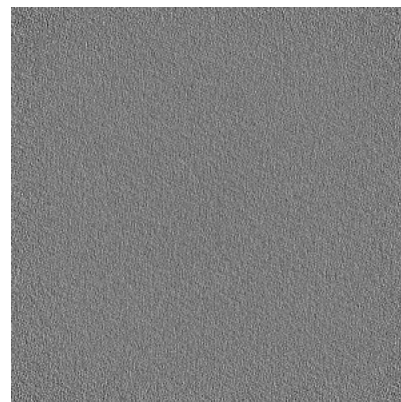
6.3.2 Raw map



X Index: 0



Y Index: 0

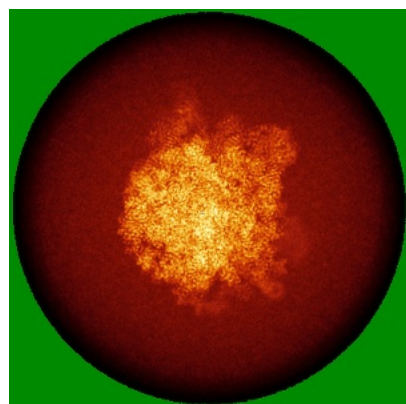


Z Index: 0

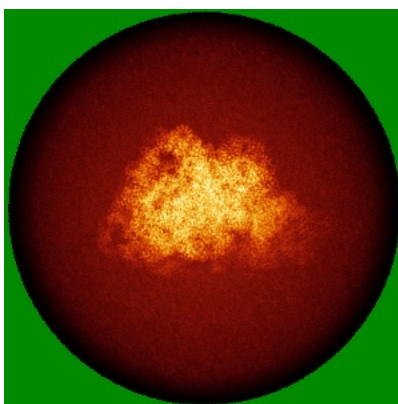
The images above show the largest variance slices of the map in three orthogonal directions.

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

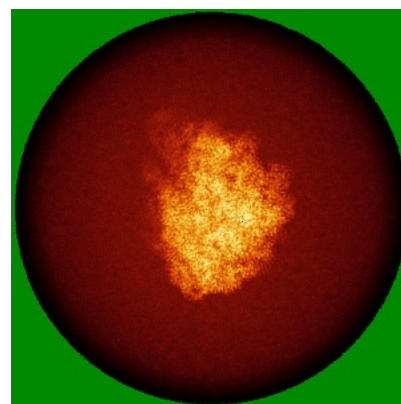
6.4.1 Primary map



X

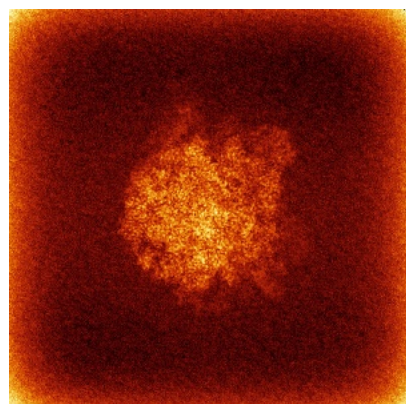


Y

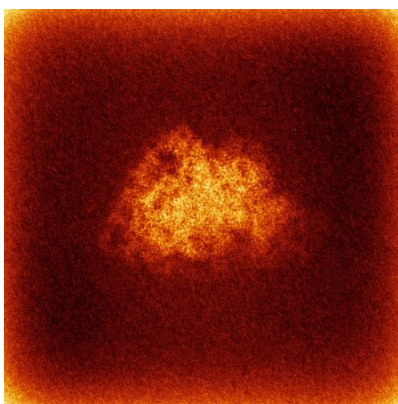


Z

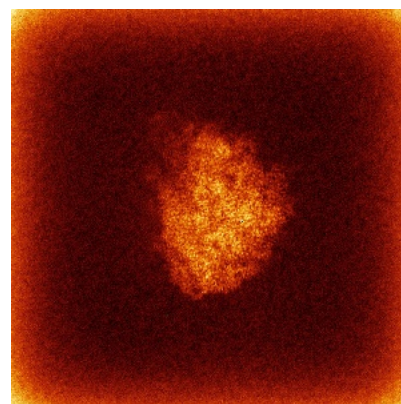
6.4.2 Raw map



X



Y

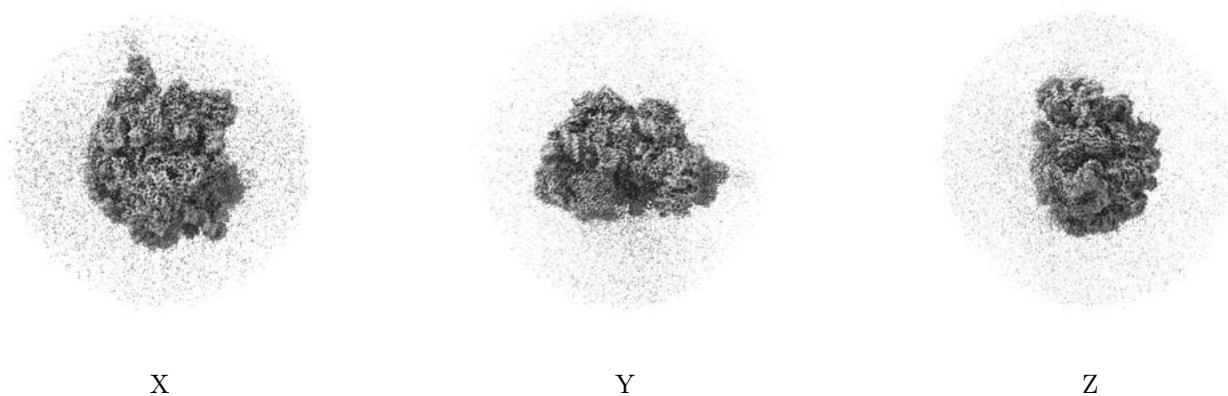


Z

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.

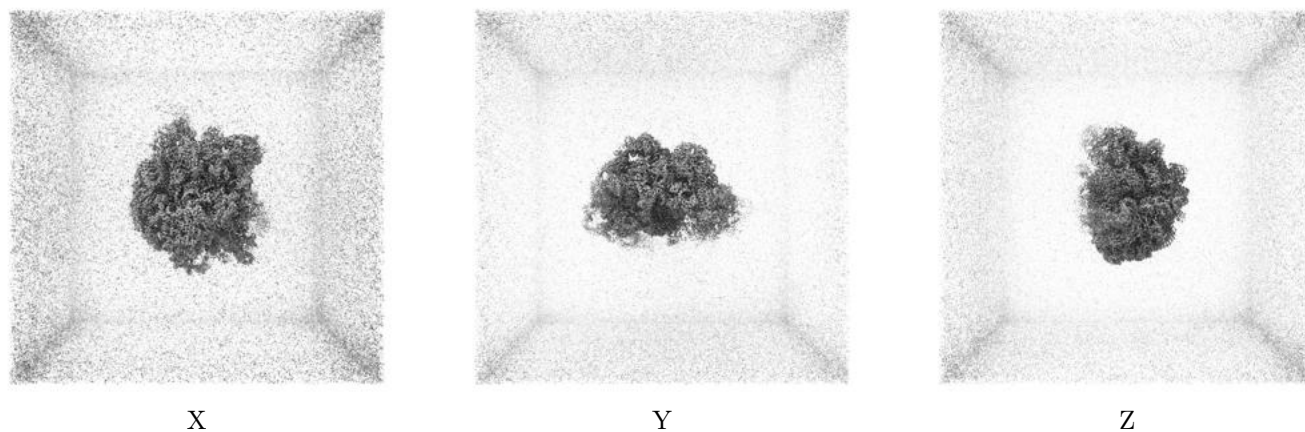
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.19. 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.

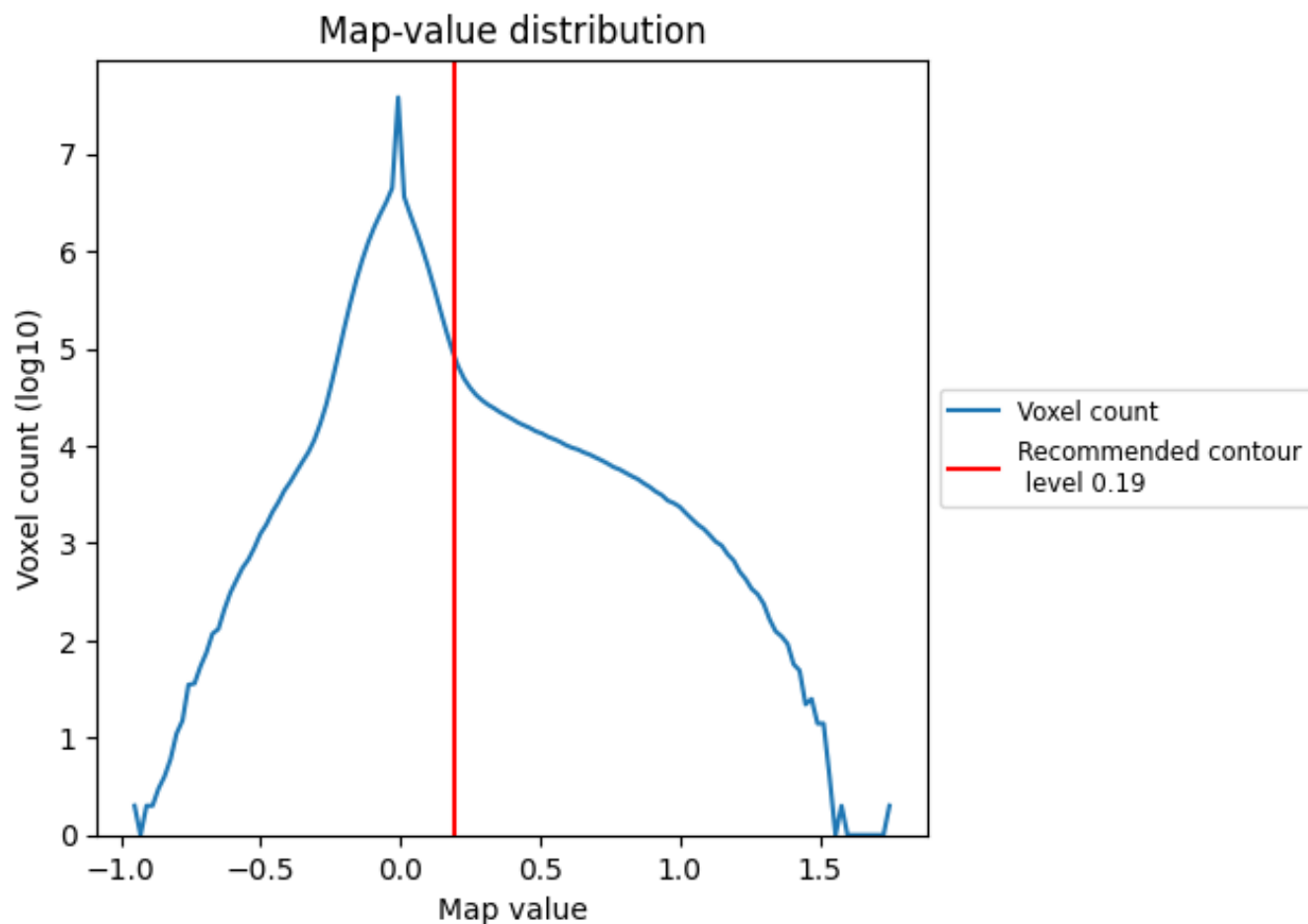
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

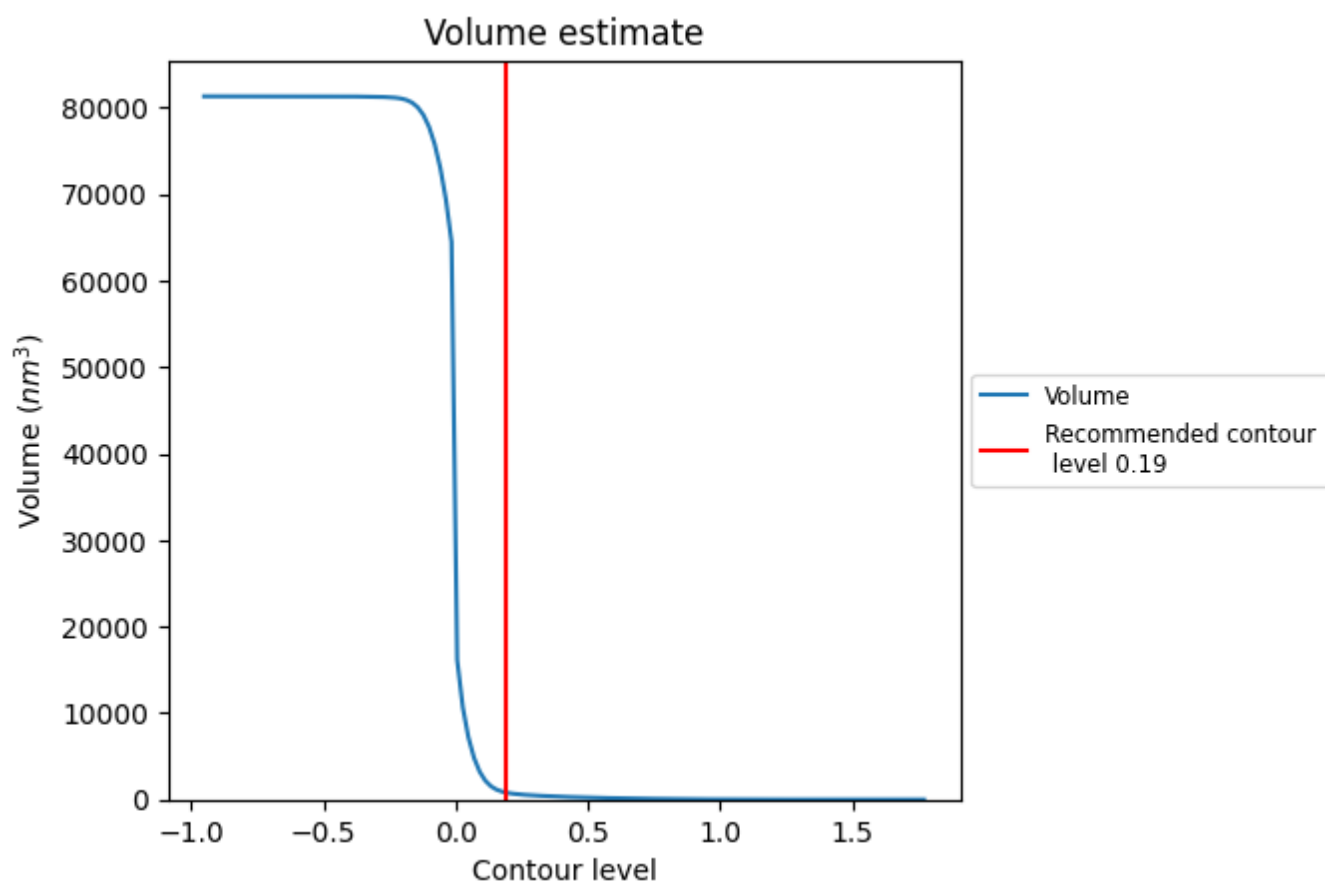
This section contains the results of statistical analysis of the map.

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.

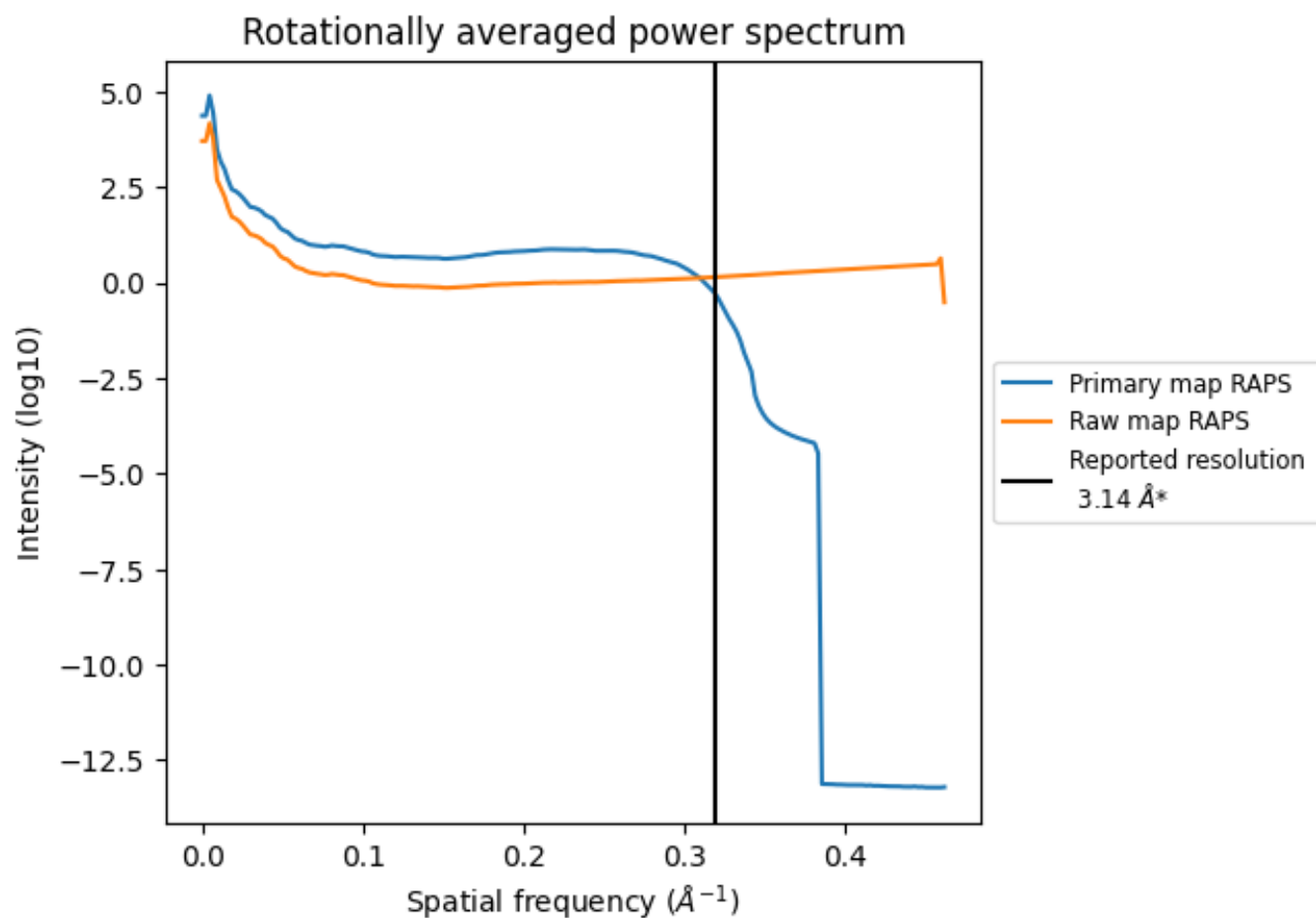
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 817 nm³; this corresponds to an approximate mass of 738 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 ⓘ

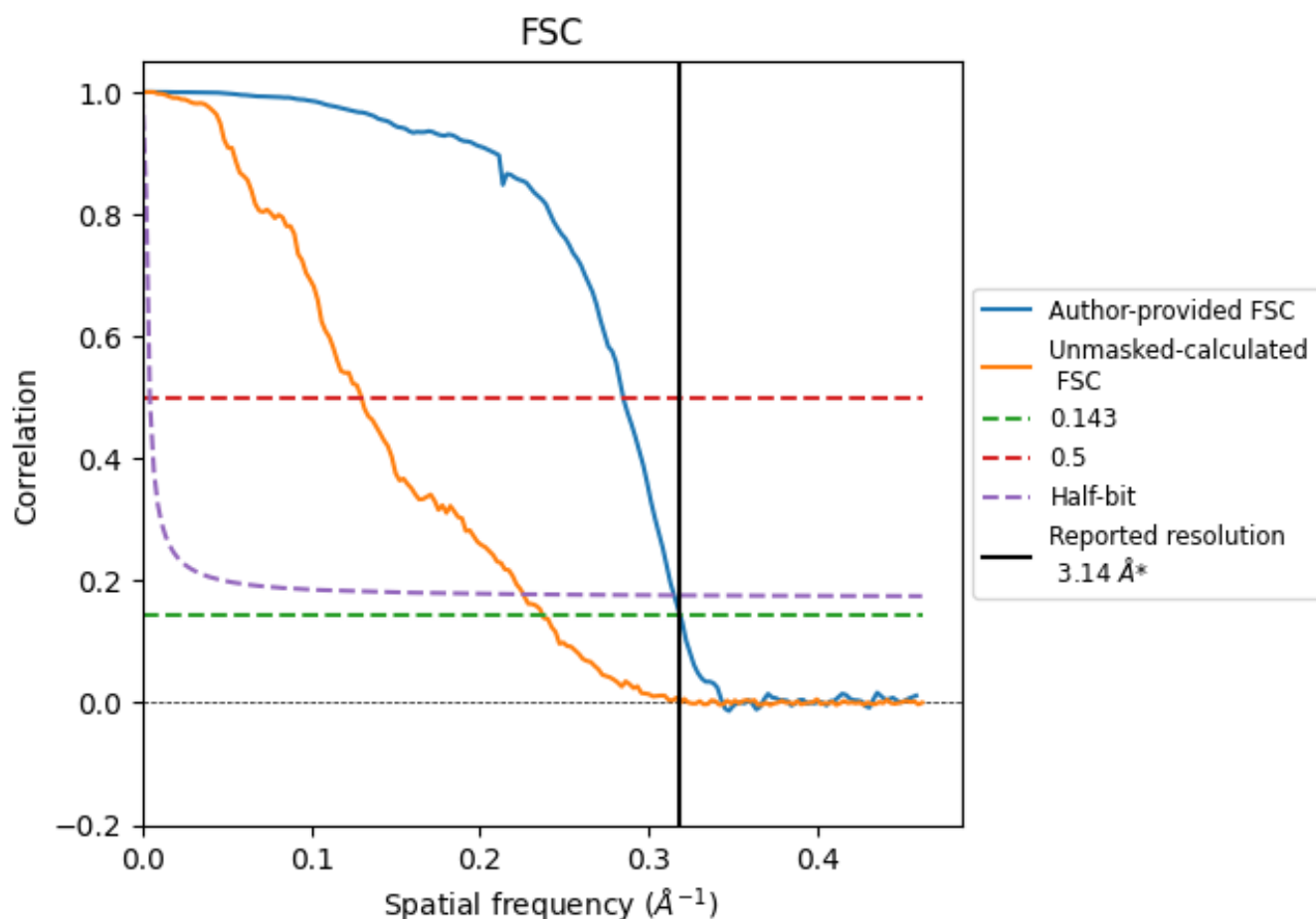


*Reported resolution corresponds to spatial frequency of 0.318 Å⁻¹

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 0.318 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

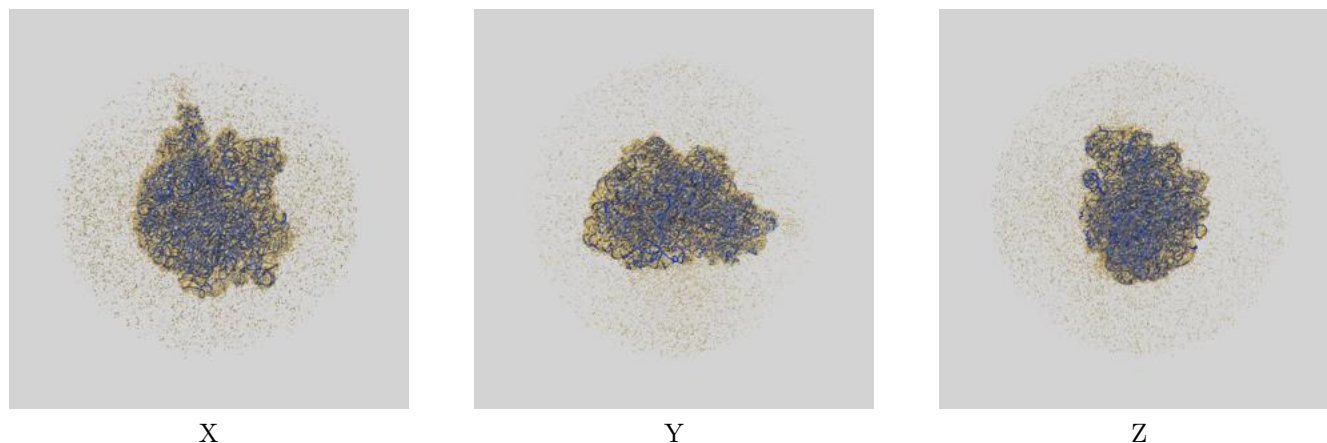
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.14	3.51	3.18
Unmasked-calculated*	4.22	7.72	4.43

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.22 differs from the reported value 3.14 by more than 10 %

9 Map-model fit [i](#)

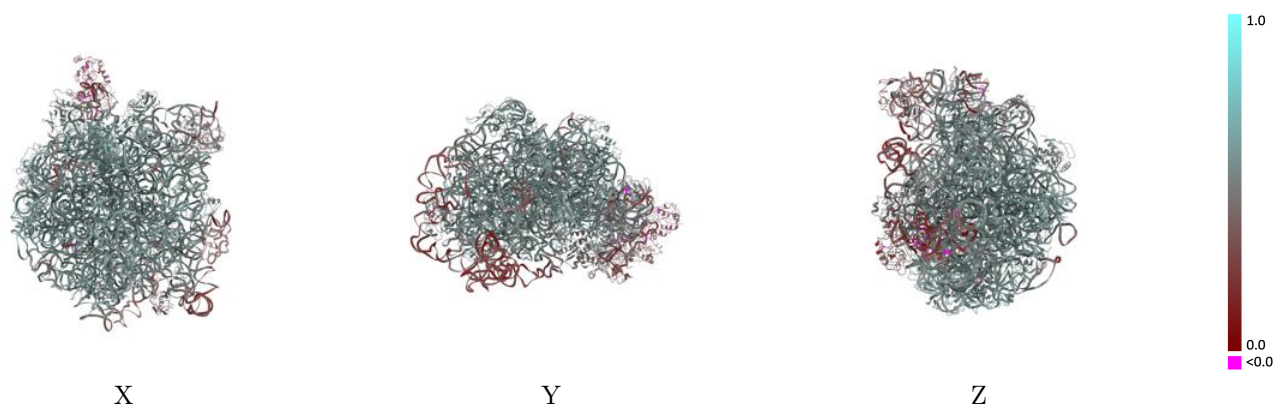
This section contains information regarding the fit between EMDB map EMD-43294 and PDB model 8VK0. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



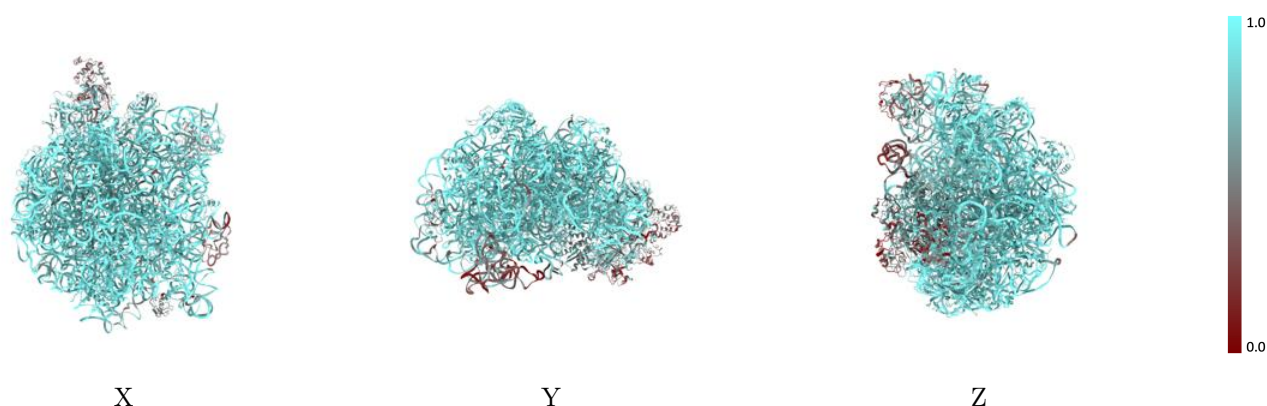
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



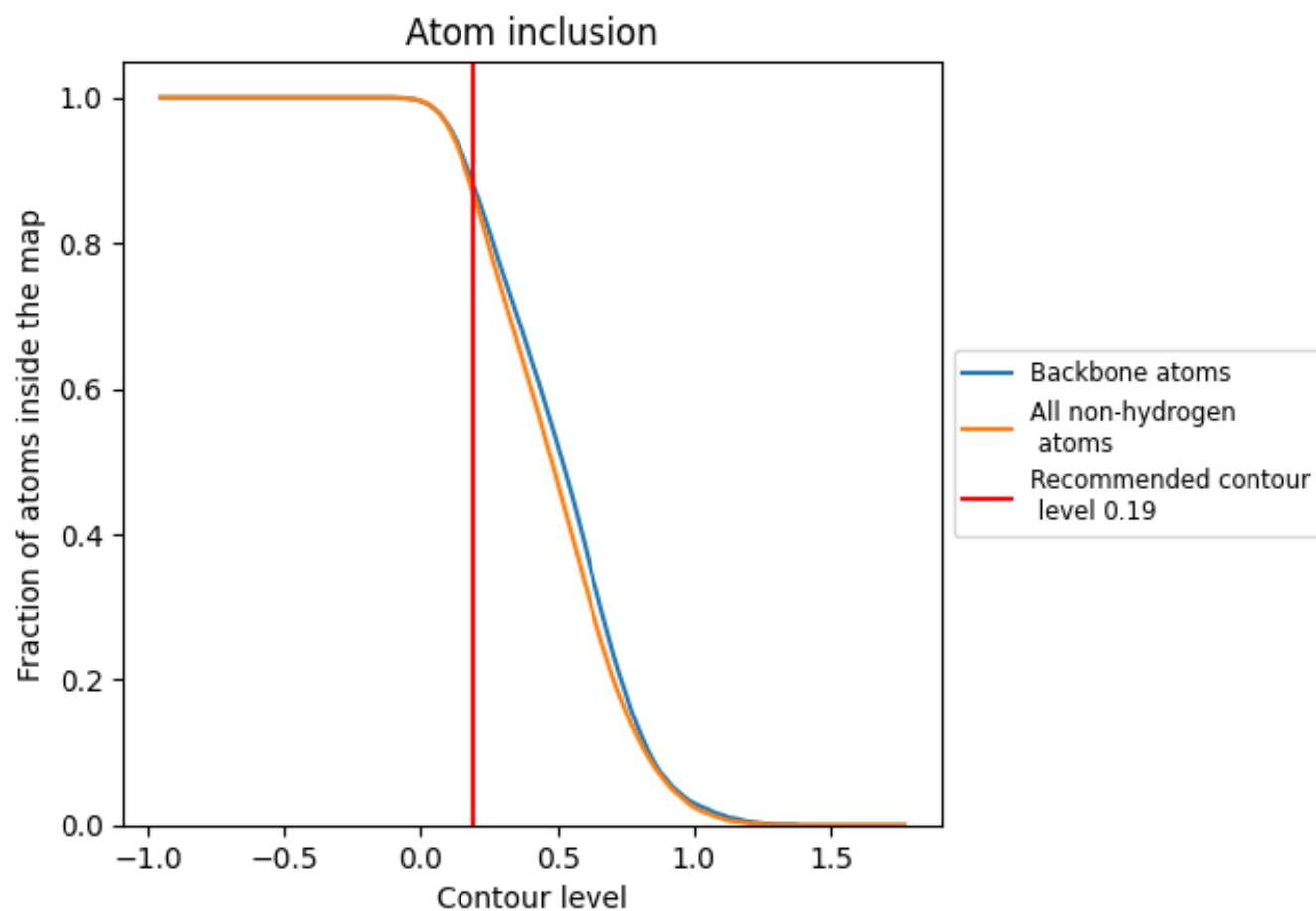
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.19).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 87% 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 (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.5190
2	 0.9410	 0.5870
3	 0.8660	 0.5910
4	 0.6210	 0.4740
A	 0.9060	 0.5190
B	 0.9180	 0.4820
C	 0.9240	 0.5820
D	 0.9270	 0.5810
E	 0.9000	 0.5690
F	 0.6140	 0.3960
G	 0.7870	 0.4960
H	 0.5930	 0.4280
I	 0.3830	 0.2960
J	 0.3570	 0.2730
K	 0.9350	 0.5860
L	 0.8990	 0.5700
M	 0.9170	 0.5720
N	 0.8540	 0.5740
O	 0.9300	 0.5840
P	 0.7640	 0.4290
Q	 0.8660	 0.5520
R	 0.9370	 0.5890
S	 0.9310	 0.5870
T	 0.9240	 0.5810
U	 0.9120	 0.5700
V	 0.8560	 0.5250
W	 0.7330	 0.5330
X	 0.9190	 0.5790
Y	 0.9230	 0.5720
Z	 0.8900	 0.5520
b	 0.9030	 0.5800
c	 0.9090	 0.5780
d	 0.9230	 0.5910
e	 0.9190	 0.5970
f	 0.8570	 0.5790
g	 0.3360	 0.3560

