



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 08:02 AM UTC

PDB ID : 9H3R / pdb_00009h3r
EMDB ID : EMD-51835
Title : 50S subunit precursor C-CP_YjgA_(L22)-
Authors : Lauer, S.; Nikolay, R.; Spahn, C.M.T.
Deposited on : 2024-10-17
Resolution : 4.12 Å(reported)
Based on initial model : 8RPY

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

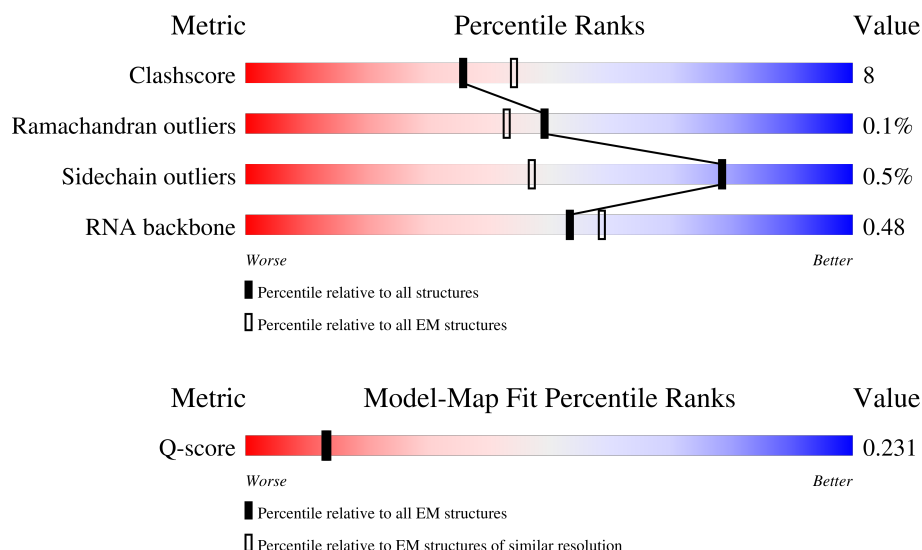
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.12 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.










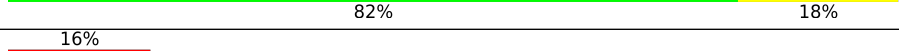
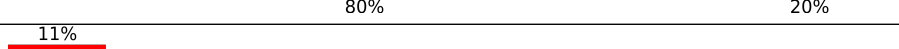
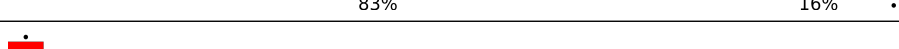
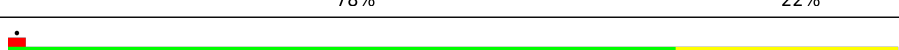

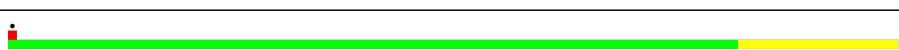

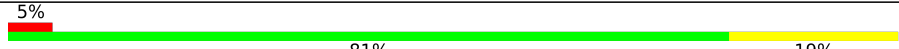





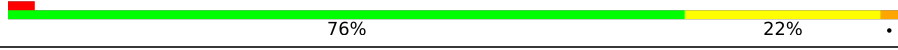

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5662 (3.62 - 4.62)

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	C	183	
2	2	46	
3	4	38	

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Mol	Chain	Length	Quality of chain
4	A	2903	
5	B	120	
6	D	209	
7	E	201	
8	F	177	
9	G	176	
10	H	149	
11	J	142	
12	K	122	
13	L	143	
14	N	120	
15	O	116	
16	P	114	
17	Q	117	
18	R	103	
19	T	93	
20	U	102	
21	V	94	
22	W	75	
23	X	77	
24	Y	63	
25	Z	58	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 77649 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 UPF0307 protein YjgA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	158	Total	C	N	O	S	0	0
			1298	805	253	238	2		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	38	Total	C	N	O	S	0	0
			309	185	77	46	1		

- Molecule 3 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	2576	Total	C	N	O	P	0	0
			55316	24673	10186	17881	2576		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	173	Total	C	N	O	S	0	0
			1284	805	231	244	4		

- Molecule 7 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	176	Total	C	N	O	S	0	0
			1368	862	243	258	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 10 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	51	Total	C	N	O	S	0	0
			395	253	72	69	1		

- Molecule 11 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 16 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 17 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 18 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 20 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 21 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 22 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL29.

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

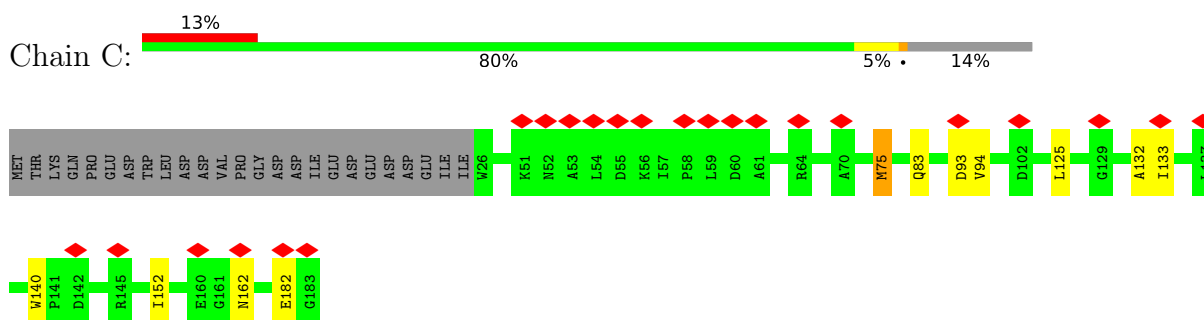
- Molecule 25 is a protein called Large ribosomal subunit protein uL30.

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

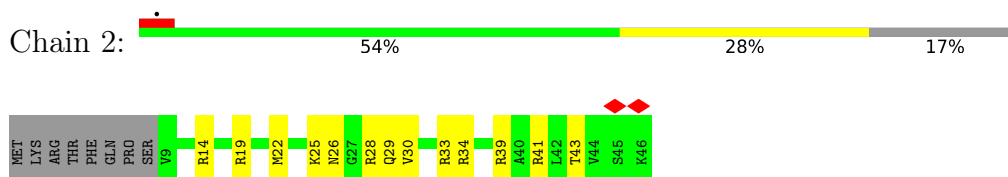
3 Residue-property plots [i](#)

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.

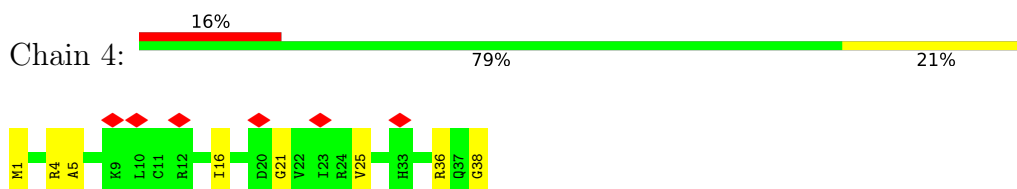
- Molecule 1: UPF0307 protein YjgA



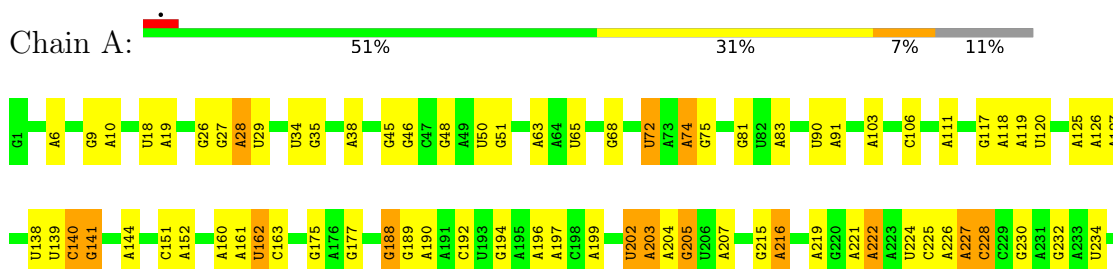
- Molecule 2: Large ribosomal subunit protein bL34

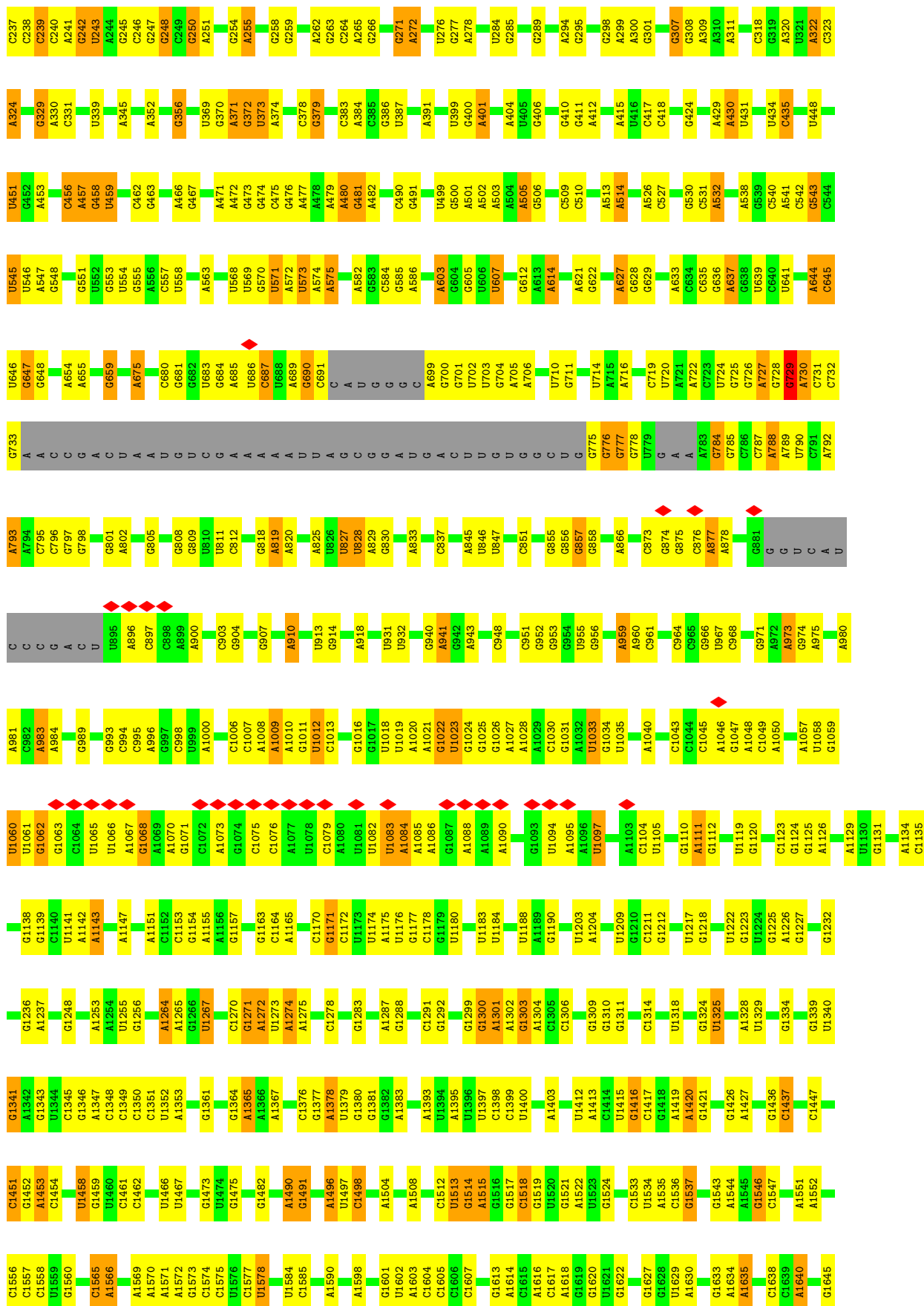


- Molecule 3: Large ribosomal subunit protein bL36A



- Molecule 4: 23S ribosomal RNA

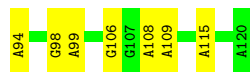




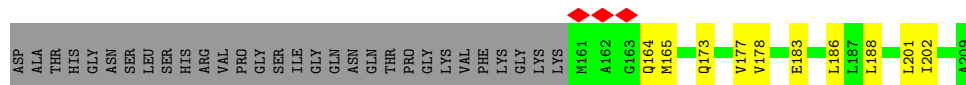
U2728	A2639	G2545	G2454	A2369	G2264	A2170	A2108	A2030	C	U	C	U	G	U	U	G1710	C1646
G2729	G2643	U2546	U2457	C2374	U2265	A2171	U2109	A2031	G	A	G	U	A	A	U	A1711	U1647
G2730	G2644	A2547	U2457	C2375	A2266	U2172	G2110	G2032	C	A	U	U	A	A	U	A1712	U1648
G2731	G2645	U2554	U2457	A2376	A2267	A2173	U2111	U2034	U	C	U	U	C	C	U	A1713	G1649
A2732	G2646	G2554	G2472	A2377	A2270	C2175	G2112	G2035	C	C	A	A	C	C	A	G1715	A1650
A2733	U2647	G2566	U2473	A2378	G2271	A2176	A2113	C2036	G	C	C	C	C	C	A	U1716	G1651
U2743	A2654	G2567	U2474	A2379	U2272	C2177	A2114	U2039	C	C	C	C	C	C	A	A1652	G1653
G2744	U2655	G2570	C2475	G2380	A2273	C2178	G2115	C2043	C	G	G	G	G	G	A	U1720	A1654
A2748	U2656	C2573	U2477	G2381	A2279	C2179	G2116	C2044	C	C	A	C	C	C	A	G1721	A1655
A2749	A2657	G2576	U2478	G2382	G2279	U2180	A2117	U2047	A	C	C	C	C	C	A	C1726	G1656
A2750	G2658	A2577	U2479	G2383	G2282	U2181	U2118	C2047	U	U	A	C	C	C	A	C1727	U1657
G2751	G2659	A2578	U2480	G2384	G2283	U2182	U2119	U2048	U	A	U	U	U	U	A	G1728	G1663
A2752	A2662	G2578	U2481	U2385	U2284	U2183	G2120	C2050	G	A	A	C	C	C	A	U1729	A1664
A2753	G2663	U2579	U2482	U2386	A2287	U2184	A2121	A2051	G	A	A	C	C	C	A	G1730	A1665
U2754	G2664	G2580	U2483	A2387	U2288	U2185	G2122	A2052	C	C	A	A	C	C	A	G1731	G1666
G2755	A2665	G2581	U2484	U2388	U2289	U2186	U2123	G2053	U	U	A	U	U	U	C	C1732	G1667
U2756	A2666	G2582	U2485	U2389	U2290	U2187	U2124	A2054	C	A	U	G	C	C	A	G1733	A1668
A2757	C2676	U2583	U2486	G2390	A2291	U2188	G2125	U2055	A	U	U	U	U	U	G	G1734	A1669
U2764	G2677	U2584	U2487	U2391	A2292	U2189	G2126	C2056	A	A	A	A	A	A	U	U1735	C1670
A2765	C2678	U2585	U2488	U2392	U2202	U2190	G2127	G2057	U	U	U	U	U	U	U	U1736	U
A2766	A2679	G2586	U2489	U2393	G2203	U2191	A2128	A2058	G	C	C	C	C	C	A	G1737	A
U2767	U2680	A2587	G2494	U2402	G2204	U2192	G2129	A2059	U	U	G	G	G	G	A	A1738	G
G2768	C2681	A2588	C2496	C2403	U2205	U2193	U2130	U2060	C	C	U	U	U	U	A	A1739	C
A2769	A2682	A2589	A2497	U2404	C2207	U2194	U2131	A2061	C	C	C	C	C	C	A	A1744	A
U2770	G2683	U2590	U2498	G2405	C2208	U2195	G2132	A2062	C	C	U	U	U	U	A	A1745	A
U2771	C2684	G2591	U2499	A2406	U2213	U2196	U2133	C2063	C	C	U	U	U	U	A	A1746	A
G2772	U2685	U2592	U2500	U2407	C2215	U2197	U2134	U2064	C	C	A	C	C	C	A	U1747	A
U2773	G2686	G2502	G2501	U2408	C2216	U2198	G2135	C2066	C	C	A	C	C	C	A	G1748	U
A2774	U2687	U2503	G2502	G2409	G2217	U2199	A2136	U2067	U	U	U	U	U	U	A	A1749	U
G2775	U2688	A2504	U2504	A2418	G2221	U2200	G2137	U2068	C	A	A	A	A	A	U	G1750	G
U2776	U2689	U2505	U2505	C2422	U2222	U2201	U2138	C2069	U	A	A	A	A	A	U	U1751	C
G2777	U2690	G2506	U2506	U2423	A2225	U2202	C2136	C2072	G	C	C	C	C	C	A	C	G
A2778	C2691	G2507	C2507	C2424	A2226	U2203	U2137	C2073	C	C	C	C	C	C	A	C	A
U2779	G2692	U2508	U2508	A2425	A2227	G2204	G2138	U2076	C	C	C	C	C	C	A	G	A
G2780	U2693	U2509	G2509	U2426	U2228	U2205	U2139	A2077	C	A	A	A	A	A	A	A	U1688
A2781	G2694	A2600	U2510	C2427	U2229	U2206	G2140	C2078	U	U	U	U	U	U	A	A	A
U2782	U2695	A2601	U2511	G2428	G2230	U2207	A2141	A2079	C	A	C	C	C	C	A	C	C
G2783	U2696	U2602	U2512	U2429	G2231	U2208	A2142	A2080	G	U	U	U	U	U	A	C	C
U2784	U2697	U2603	C2513	A2430	A2232	U2209	G2143	U2081	C	C	C	C	C	C	A	C	C
G2785	U2698	U2604	A2514	U2431	A2233	U2210	G2144	A2082	C	U	U	U	U	U	A	C	C
U2786	C2699	U2605	U2515	A2432	G2234	U2211	C2145	U2086	C	U	U	U	U	U	A	C	C
G2787	U2699	U2606	U2516	A2433	A2235	U2212	C2146	A2090	C	C	C	C	C	C	A	C	C
U2788	U2700	U2607	U2517	A2434	A2236	U2213	A2147	C2091	G	C	C	C	C	C	A	C	C
G2789	U2701	U2608	C2517	A2435	A2237	U2214	G2148	U2092	C	A	A	A	A	A	U	C	C
U2790	U2702	U2609	U2518	A2436	U2238	U2215	U2152	A2093	C	C	C	C	C	C	A	C	C
G2791	U2703	U2610	U2519	A2437	G2239	U2216	C2153	A2094	C	C	C	C	C	C	A	C	C
U2792	U2704	U2611	C2520	G2438	G2240	U2217	A2154	A2095	C	C	C	C	C	C	A	C	C
A2813	U2705	U2612	U2521	A2439	A2241	U2218	G2155	A2096	C	C	C	C	C	C	A	C	C
U2814	U2706	U2613	U2522	U2440	A2242	U2219	U2156	C2097	C	C	C	C	C	C	A	C	C
G2815	U2707	U2614	U2523	U2441	A2243	U2220	G2157	A2098	C	C	C	C	C	C	A	C	C
U2816	U2708	U2615	U2524	G2442	A2244	U2221	A2158	A2099	C	C	C	C	C	C	A	C	C
G2817	U2709	U2616	U2525	U2443	A2245	U2222	C2160	A2100	C	C	C	C	C	C	A	C	C
U2818	U2710	U2617	U2526	U2444	A2246	U2223	G2161	A2101	C	C	C	C	C	C	A	C	C
G2819	U2711	U2618	U2527	U2445	A2247	U2224	A2162	A2102	C	C	C	C	C	C	A	C	C
U2820	U2712	U2619	U2528	U2446	A2248	U2225	G2163	A2103	C	C	C	C	C	C	A	C	C
G2821	U2713	U2620	U2529	U2447	A2249	U2226	A2164	A2104	C	C	C	C	C	C	A	C	C
U2822	U2714	U2621	U2530	U2448	A2250	U2227	C2165	A2105	C	C	C	C	C	C	A	C	C
G2823	U2715	U2622	U2531	U2449	A2251	U2228	U2166	A2106	C	C	C	C	C	C	A	C	C
U2824	U2716	U2623	U2532	U2450	A2252	U2229	G2167	U2107	C	C	C	C	C	C	A	C	C
G2825	U2717	U2624	U2533	U2451	A2253	U2230	A2168	G2029	C	C	C	C	C	C	A	C	C
U2826	U2718	U2625	U2534	U2452	A2254	U2231	G2169	U2108	C	C	C	C	C	C	A	C	C
G2827	U2719	U2626	U2535	U2453	A2255	U2232	C2170	U2109	C	C	C	C	C	C	A	C	C
U2828	U2720	U2627	U2536	U2454	A2256	U2233	A2171	U2110	C	C	C	C	C	C	A	C	C
G2829	U2721	U2628	U2537	U2455	A2257	U2234	G2172	U2111	C	C	C	C	C	C	A	C	C
U2830	U2722	U2629	U2538	U2456	A2258	U2235	A2173	U2112	C	C	C	C	C	C	A	C	C
G2831	U2723	U2630	U2539	U2457	A2259	U2236	G2174	U2113	C	C	C	C	C	C	A	C	C
U2832	U2724	U2631	U2540	U2458	A2260	U2237	A2175	U2114	C	C	C	C	C	C	A	C	C
G2833	U2725	U2632	U2541	U2459	A2261	U2238	G2176	U2115	C	C	C	C	C	C	A	C	C
U2834	U2726	U2633	U2542	U2460	A2262	U2239	A2177	U2116	C	C	C	C	C	C	A	C	C
G2835	U2727	U2634	U2543	U2461	A2263	U2240	G2178	U2117	C	C	C	C	C	C	A	C	C
U2836	U2728	U2635	U2544	U2462	A2264	U2241	A2179	U2118	C	C	C	C	C	C	A	C	C
G2837	U2729	U2636	U2545	U2463	A2265	U2242	G2180	U2119	C	C	C	C	C	C	A	C	C
U2838	U2730	U2637	U2546	U2464	A2266	U2243	A2181	U2120	C	C	C	C	C	C	A	C	C
G2839	U2731	U2638	U2547	U2465	A2267	U2244	G2182	U2121	C	C	C	C	C	C	A	C	C
U2840	U2732	U2639	U2548	U2466	A2268	U2245	A2183	U2122	C	C	C	C	C	C	A	C	C
G2841	U2733	U2640	U2549	U2467	A2269	U2246	G2184	U2123	C	C	C	C	C	C	A	C	C
U2842	U2734	U2641	U2550	U2468	A2270	U2247	A2185	U2124	C	C	C	C	C	C	A	C	C
G2843	U2735	U2642	U2551	U2469	A2271	U2248	G2186	U2125	C	C	C	C	C	C	A	C	C
U2844	U2736	U2643	U2552	U2470	A2272	U2249	A2187	U2126	C	C	C	C	C	C	A	C	C
G2845	U2737	U2644	U2553	U2471	A2273	U2250	G2188	U2127	C	C	C	C	C	C	A	C	C
U2846	U2738	U2645	U2554	U2472	A2274	U2251	A2189	U2128	C	C	C	C	C	C	A	C	C
G2847	U2739	U2646	U2555	U2473	A2275	U2252	G2190	U2129	C	C	C	C	C	C	A	C	C
U2848	U2740	U2647	U2556	U2474	A2276	U2253	A2191	U2130	C	C	C	C	C	C	A	C	C
G2849	U2741	U2648	U2557	U2475	A2277	U2254	G2192	U2131	C	C	C	C	C	C	A	C	C
U2850	U2742	U2649	U2558	U2476	A2278	U2255	A2193	U2132	C	C	C	C	C	C	A	C	C
G2851	U2743	U2650	U2559	U2477	A2279	U2256	G2194	U2133	C	C	C	C	C	C	A	C	C
U2852	U2744	U2651	U2560	U2478	A2280	U2257	A2195	U2134	C	C	C	C	C	C	A	C	C
G2853	U2745	U2652	U2561	U2479	A2281	U2258	G2196	U2135	C	C	C	C	C	C	A	C	C
U2854	U2746	U2653	U2562	U2480	A2282	U22											



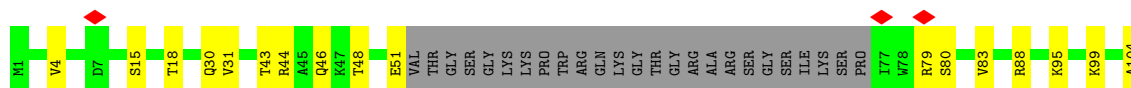
• Molecule 5: 5S ribosomal RNA



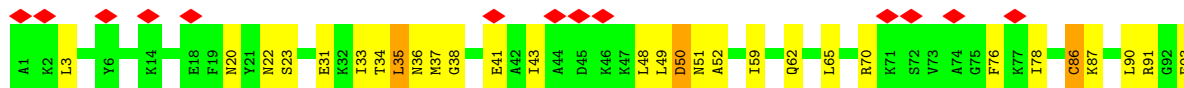
• Molecule 6: 50S ribosomal protein L3



• Molecule 7: Large ribosomal subunit protein uL4




• Molecule 8: Large ribosomal subunit protein uL5




• Molecule 9: Large ribosomal subunit protein uL6

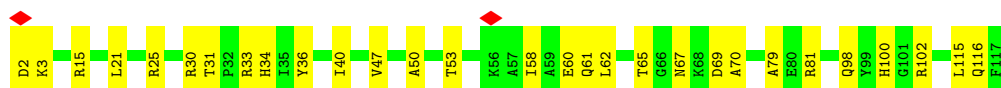


Chain N:  78% 22%




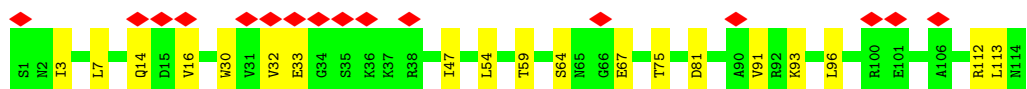
- Molecule 15: Large ribosomal subunit protein uL18

Chain O:  75% 25%




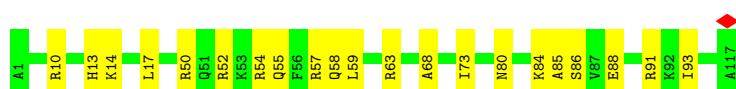
- Molecule 16: Large ribosomal subunit protein bL19

Chain P:  14% 83% 17%




- Molecule 17: Large ribosomal subunit protein bL20

Chain Q:  82% 18%




- Molecule 18: Large ribosomal subunit protein bL21

Chain R:  83% 16%




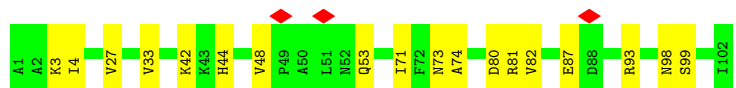
- Molecule 19: Large ribosomal subunit protein uL23

Chain T:  5% 81% 19%

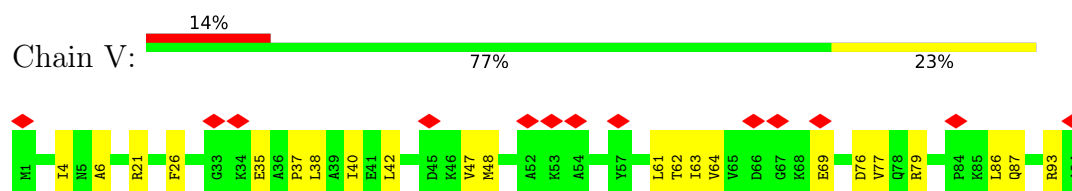


- Molecule 20: Large ribosomal subunit protein uL24

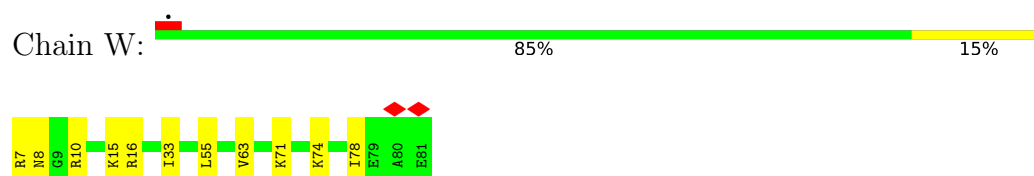
Chain U:  82% 18%



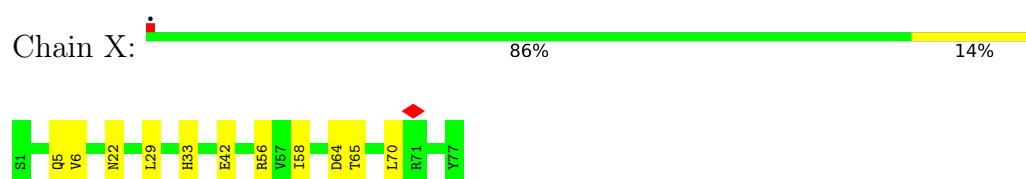
- Molecule 21: Large ribosomal subunit protein bL25



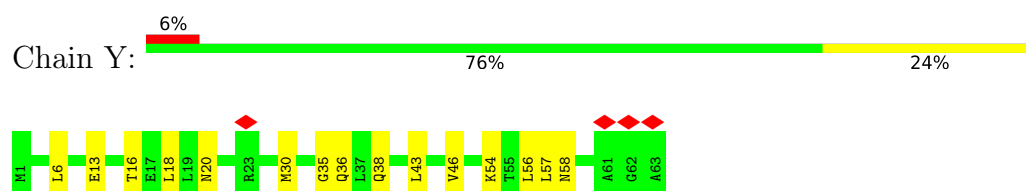
- Molecule 22: Large ribosomal subunit protein bL27



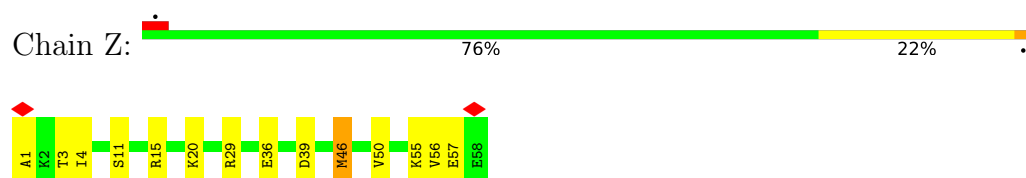
- Molecule 23: Large ribosomal subunit protein bL28



- Molecule 24: Large ribosomal subunit protein uL29



- Molecule 25: Large ribosomal subunit protein uL30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6435	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.582	Depositor
Minimum map value	-0.376	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.337	Depositor
Map size (Å)	424.0, 424.0, 424.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4133333, 1.4133333, 1.4133333	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	C	0.08	0/1311	0.19	0/1753
2	2	0.06	0/310	0.17	0/405
3	4	0.12	0/303	0.18	0/397
4	A	0.13	0/61949	0.23	1/96631 (0.0%)
5	B	0.07	0/2876	0.19	0/4483
6	D	0.08	0/1296	0.21	0/1742
7	E	0.09	0/1382	0.20	0/1860
8	F	0.11	0/1434	0.26	0/1926
9	G	0.09	0/1343	0.21	0/1816
10	H	0.11	0/400	0.24	0/537
11	J	0.09	0/1152	0.19	0/1551
12	K	0.10	0/947	0.25	0/1268
13	L	0.08	0/1054	0.26	0/1403
14	N	0.11	0/973	0.25	0/1301
15	O	0.08	0/902	0.23	0/1209
16	P	0.09	0/929	0.21	0/1242
17	Q	0.09	0/960	0.18	0/1278
18	R	0.11	0/829	0.27	0/1107
19	T	0.10	0/744	0.21	0/994
20	U	0.11	0/787	0.26	0/1051
21	V	0.11	0/766	0.24	0/1025
22	W	0.06	0/582	0.19	0/769
23	X	0.10	0/635	0.20	0/848
24	Y	0.12	0/510	0.30	0/677
25	Z	0.12	0/453	0.23	0/605
All	All	0.12	0/84827	0.23	1/127878 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	729	G	C2'-C3'-O3'	5.67	118.01	109.50

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	C	1298	0	1352	8	0
2	2	309	0	344	9	0
3	4	302	0	343	8	0
4	A	55316	0	27824	604	0
5	B	2572	0	1302	32	0
6	D	1284	0	1339	30	0
7	E	1368	0	1421	31	0
8	F	1410	0	1447	47	0
9	G	1323	0	1374	21	0
10	H	395	0	418	6	0
11	J	1129	0	1162	24	0
12	K	938	0	1012	18	0
13	L	1045	0	1117	22	0
14	N	960	0	1000	22	0
15	O	892	0	923	26	0
16	P	917	0	965	15	0
17	Q	947	0	1022	17	0
18	R	816	0	839	18	0
19	T	738	0	807	17	0
20	U	779	0	834	13	0
21	V	753	0	780	19	0
22	W	575	0	592	11	0
23	X	625	0	655	8	0
24	Y	509	0	543	8	0
25	Z	449	0	491	13	0
All	All	77649	0	49906	941	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 8.

The worst 5 of 941 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)
4:A:775:G:OP2	4:A:778:G:O4'	1.54	1.25
4:A:775:G:O5'	4:A:777:G:N3	1.96	0.98
4:A:775:G:OP2	4:A:777:G:O2'	1.82	0.97
4:A:2123:G:C2	4:A:2176:A:N6	2.34	0.95
4:A:2676:C:O2	4:A:2732:G:N2	2.00	0.95

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	C	156/183 (85%)	152 (97%)	4 (3%)	0	100	100
2	2	36/46 (78%)	36 (100%)	0	0	100	100
3	4	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
6	D	169/209 (81%)	165 (98%)	4 (2%)	0	100	100
7	E	172/201 (86%)	167 (97%)	4 (2%)	1 (1%)	21	58
8	F	175/177 (99%)	168 (96%)	7 (4%)	0	100	100
9	G	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
10	H	49/149 (33%)	46 (94%)	3 (6%)	0	100	100
11	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
12	K	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
13	L	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
14	N	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
15	O	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
16	P	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	101/103 (98%)	95 (94%)	5 (5%)	1 (1%)	12	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	T	91/93 (98%)	85 (93%)	6 (7%)	0	100	100
20	U	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
21	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
22	W	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
23	X	75/77 (97%)	75 (100%)	0	0	100	100
24	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
25	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
All	All	2476/2718 (91%)	2385 (96%)	89 (4%)	2 (0%)	49	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	R	54	VAL
7	E	83	VAL

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	C	137/161 (85%)	136 (99%)	1 (1%)	76	79
2	2	30/38 (79%)	30 (100%)	0	100	100
3	4	34/34 (100%)	34 (100%)	0	100	100
6	D	134/164 (82%)	134 (100%)	0	100	100
7	E	146/165 (88%)	146 (100%)	0	100	100
8	F	148/148 (100%)	145 (98%)	3 (2%)	48	66
9	G	137/137 (100%)	137 (100%)	0	100	100
10	H	41/114 (36%)	41 (100%)	0	100	100
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	103/103 (100%)	103 (100%)	0	100	100
13	L	102/102 (100%)	99 (97%)	3 (3%)	37	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	100/100 (100%)	100 (100%)	0	100	100
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	99 (100%)	0	100	100
17	Q	89/89 (100%)	89 (100%)	0	100	100
18	R	84/84 (100%)	83 (99%)	1 (1%)	63	73
19	T	80/80 (100%)	80 (100%)	0	100	100
20	U	83/83 (100%)	83 (100%)	0	100	100
21	V	78/78 (100%)	78 (100%)	0	100	100
22	W	57/57 (100%)	57 (100%)	0	100	100
23	X	67/67 (100%)	67 (100%)	0	100	100
24	Y	55/55 (100%)	53 (96%)	2 (4%)	31	53
25	Z	48/48 (100%)	47 (98%)	1 (2%)	47	65
All	All	2054/2208 (93%)	2043 (100%)	11 (0%)	78	82

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	R	25	LEU
24	Y	30	MET
25	Z	46	MET
24	Y	36	GLN
13	L	6	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
15	O	29	HIS
15	O	38	GLN
25	Z	19	HIS
18	R	82	HIS
22	W	53	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	2568/2903 (88%)	541 (21%)	17 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	B	119/120 (99%)	17 (14%)	2 (1%)
All	All	2687/3023 (88%)	558 (20%)	19 (0%)

5 of 558 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	10	A
4	A	26	G
4	A	27	G
4	A	28	A
4	A	34	U

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	2599	G
5	B	52	A
5	B	66	A
4	A	2655	G
4	A	732	C

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 ⓘ

There are no chain breaks in this entry.

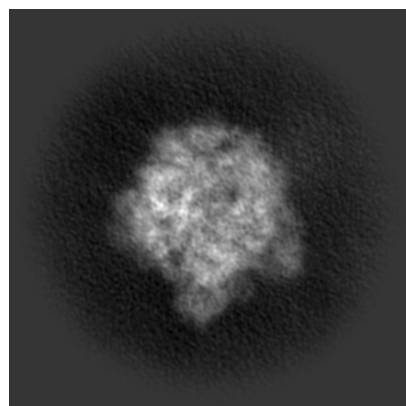
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51835. These allow visual inspection of the internal detail of the map and identification of artifacts.

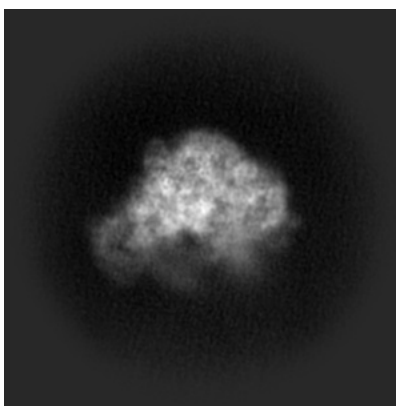
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

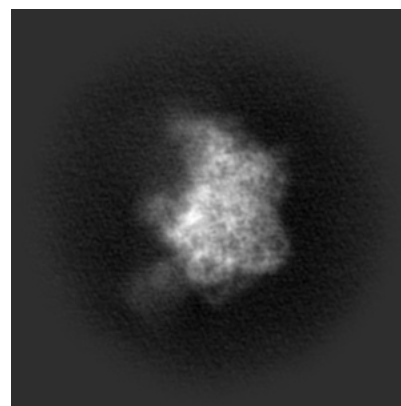
6.1.1 Primary map



X

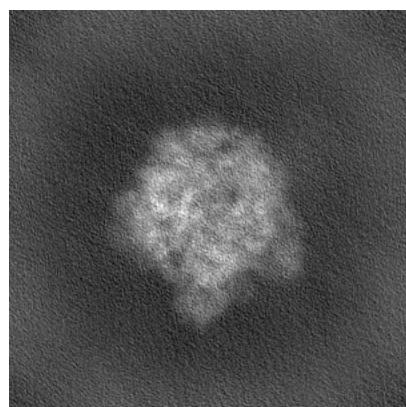


Y

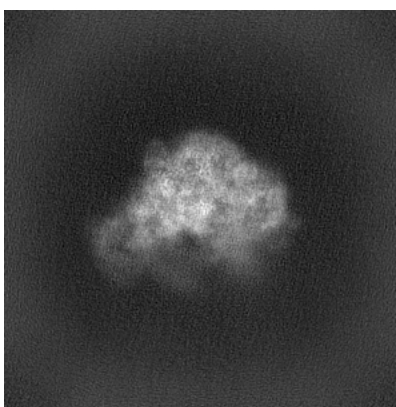


Z

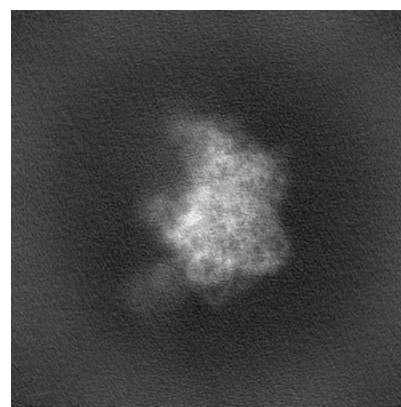
6.1.2 Raw map



X



Y

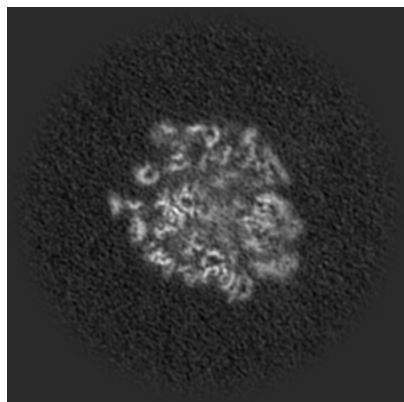


Z

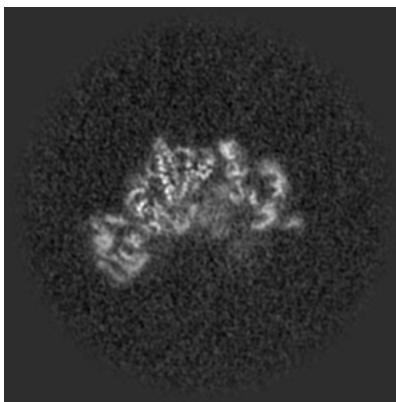
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

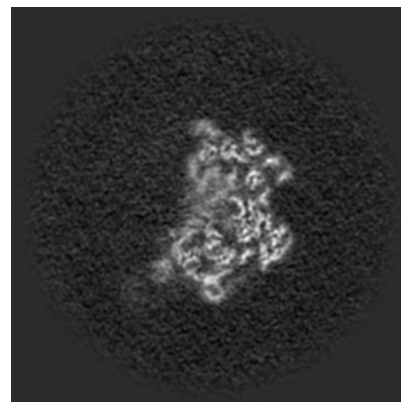
6.2.1 Primary map



X Index: 150

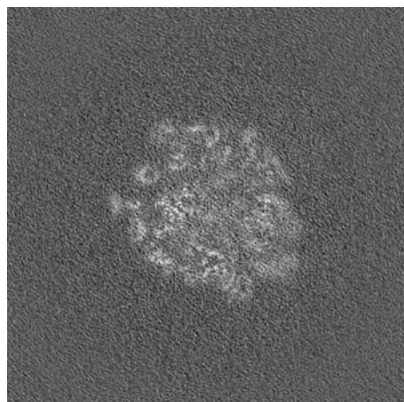


Y Index: 150

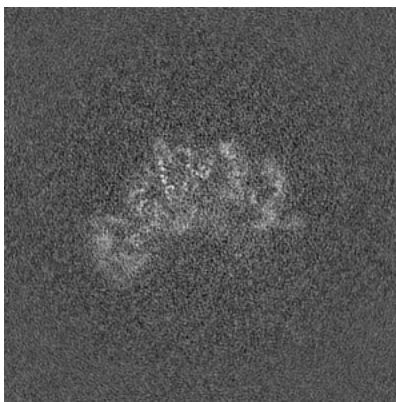


Z Index: 150

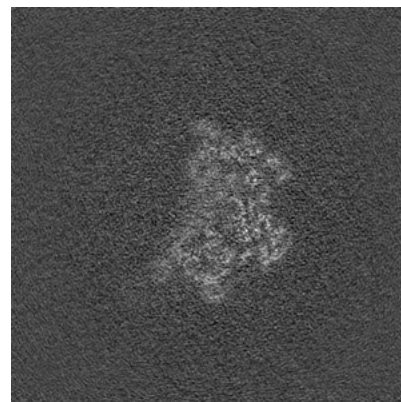
6.2.2 Raw map



X Index: 150



Y Index: 150

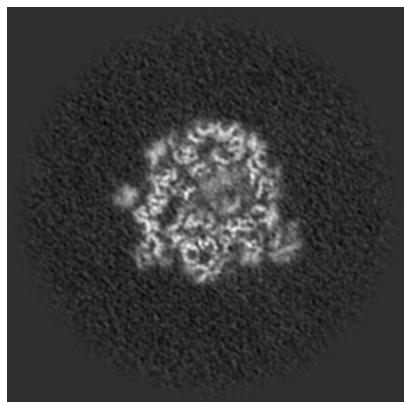


Z Index: 150

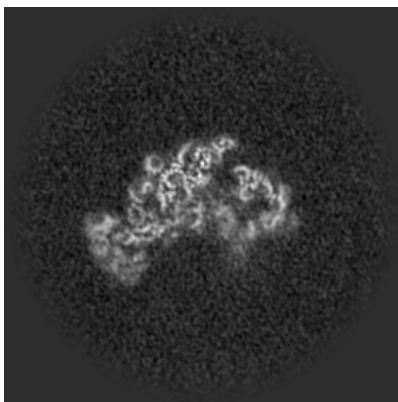
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

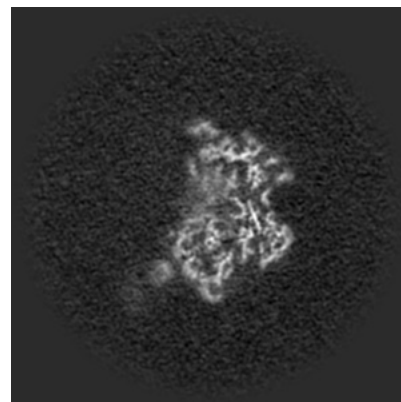
6.3.1 Primary map



X Index: 163

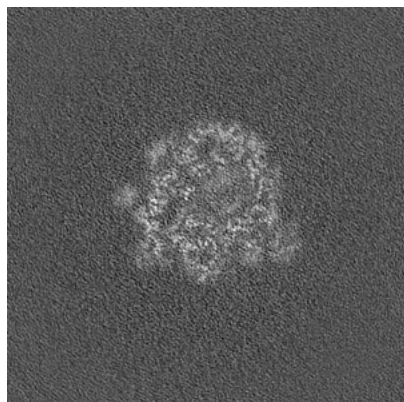


Y Index: 142

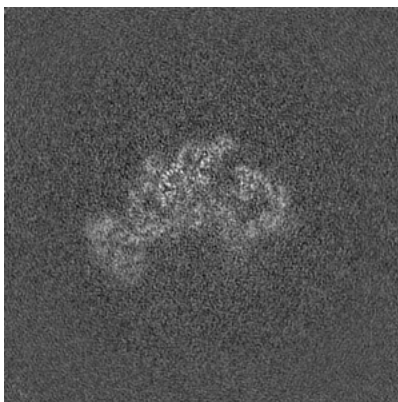


Z Index: 148

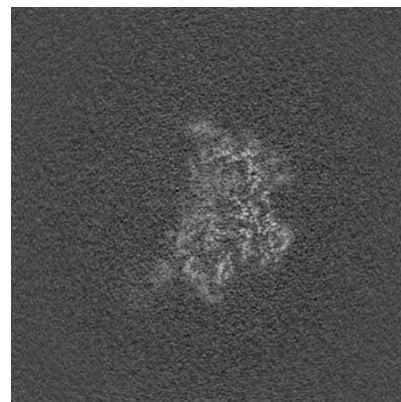
6.3.2 Raw map



X Index: 163



Y Index: 142

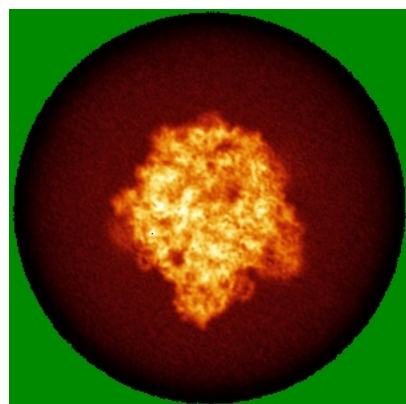


Z Index: 147

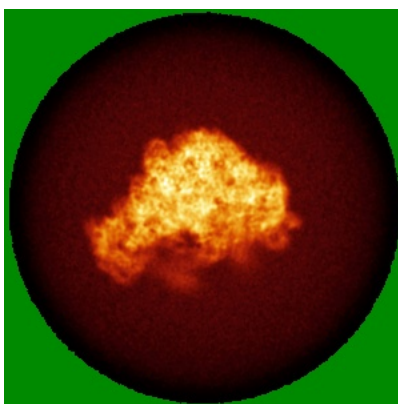
The images above show the largest variance slices of the map in three orthogonal directions.

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

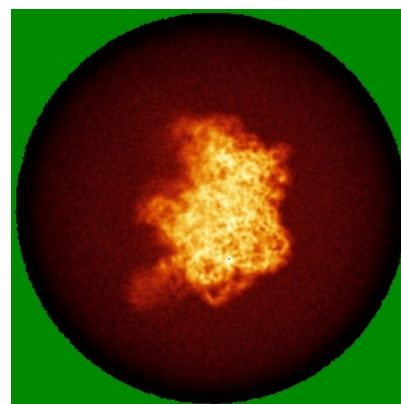
6.4.1 Primary map



X

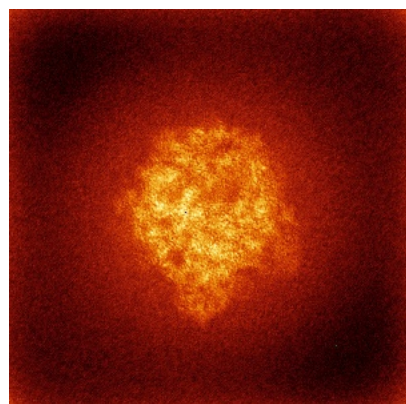


Y

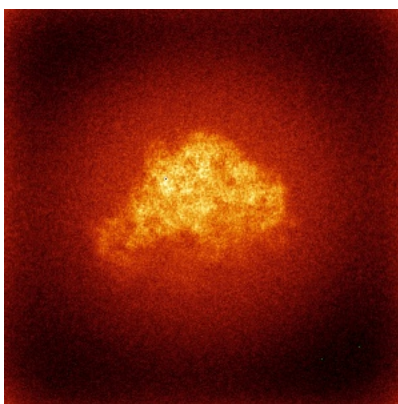


Z

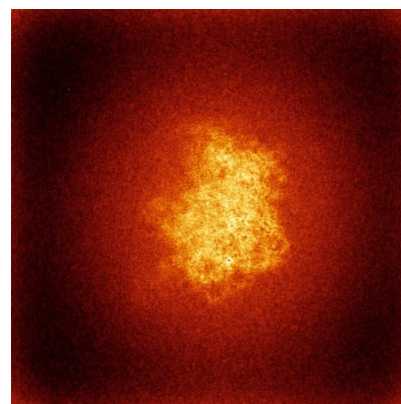
6.4.2 Raw map



X



Y



Z

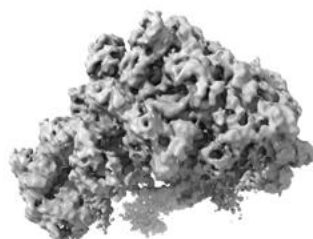
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



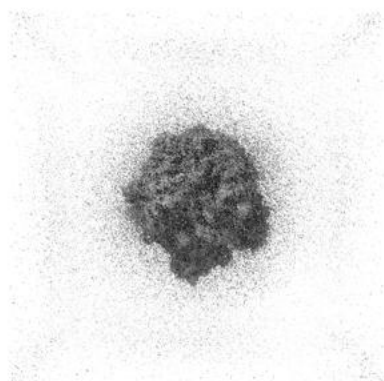
Y



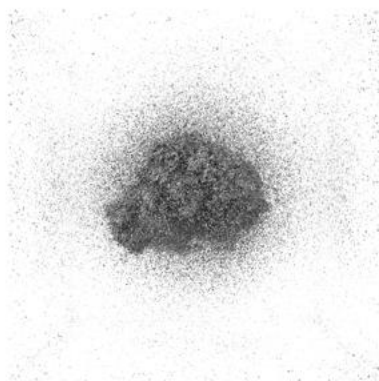
Z

The images above show the 3D surface view of the map at the recommended contour level 0.337. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

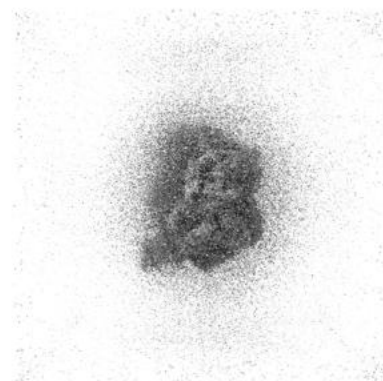
6.5.2 Raw map



X



Y



Z

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.

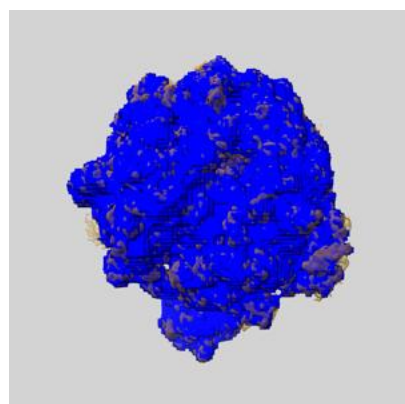
6.6 Mask visualisation [i](#)

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

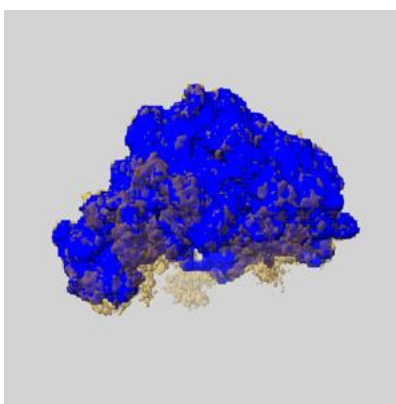
A mask typically either:

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

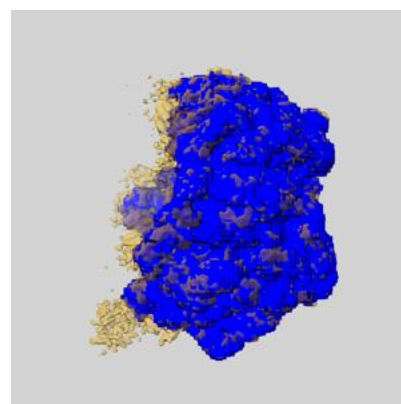
6.6.1 emd_51835_msk_1.map [i](#)



X



Y

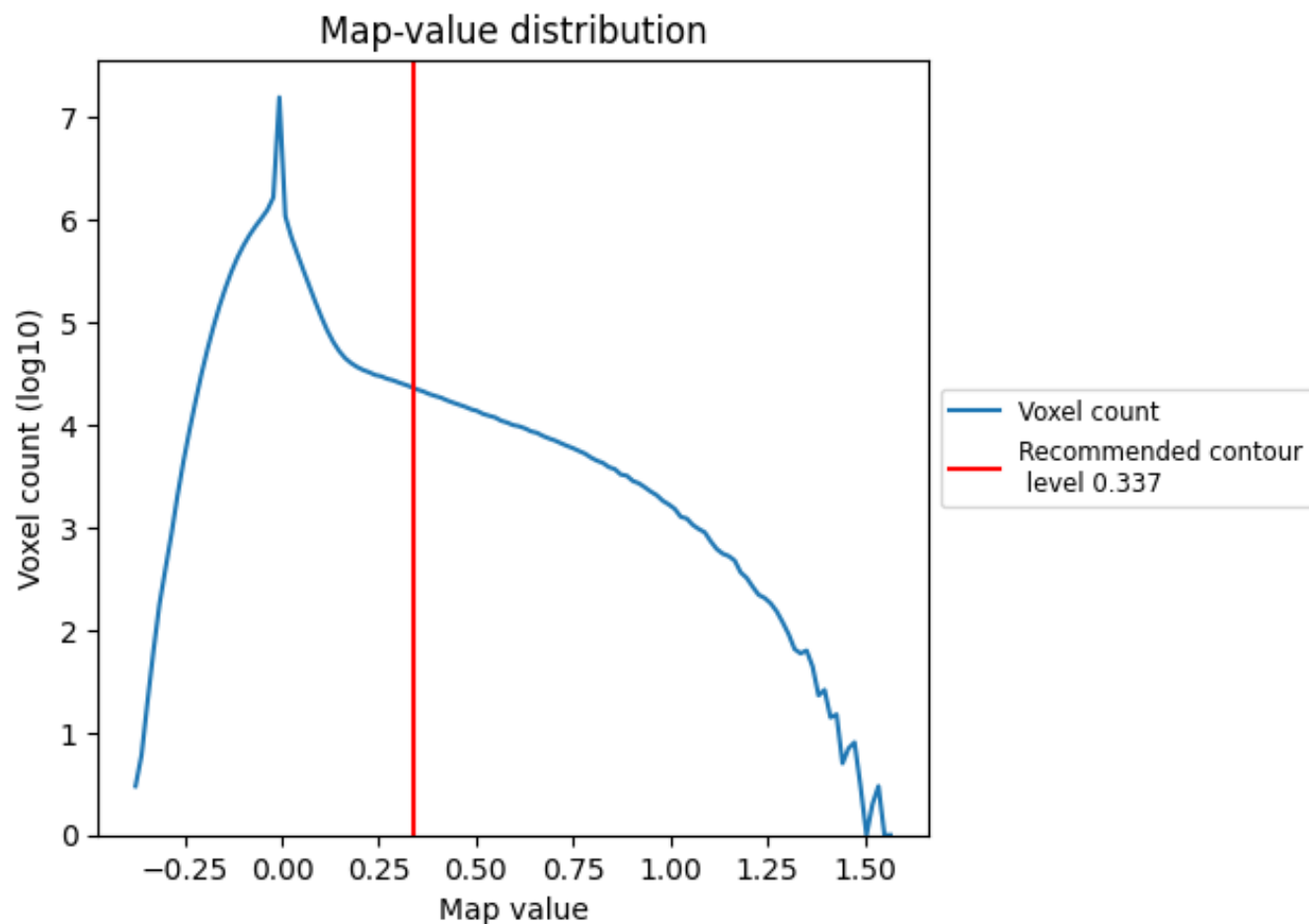


Z

7 Map analysis [i](#)

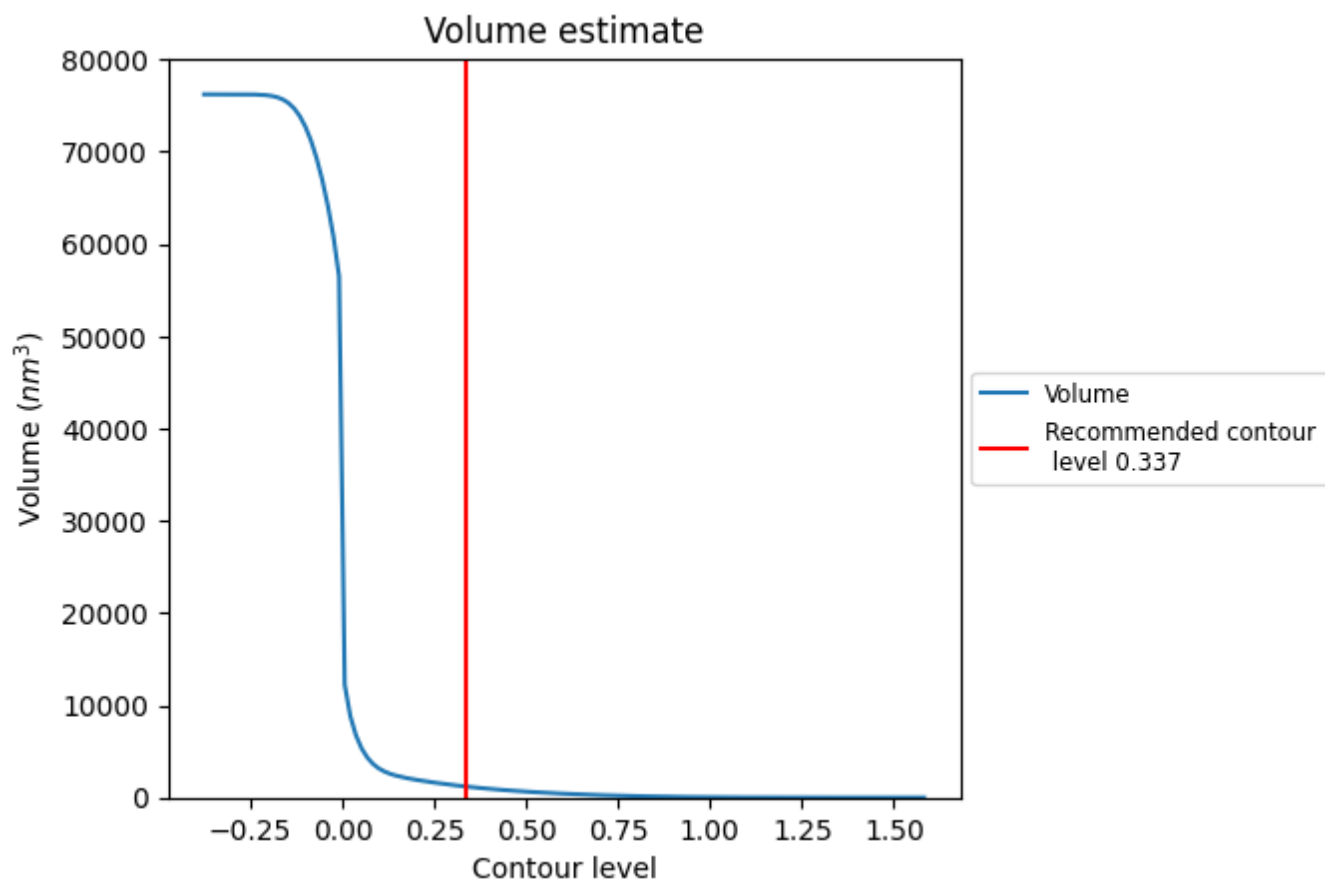
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

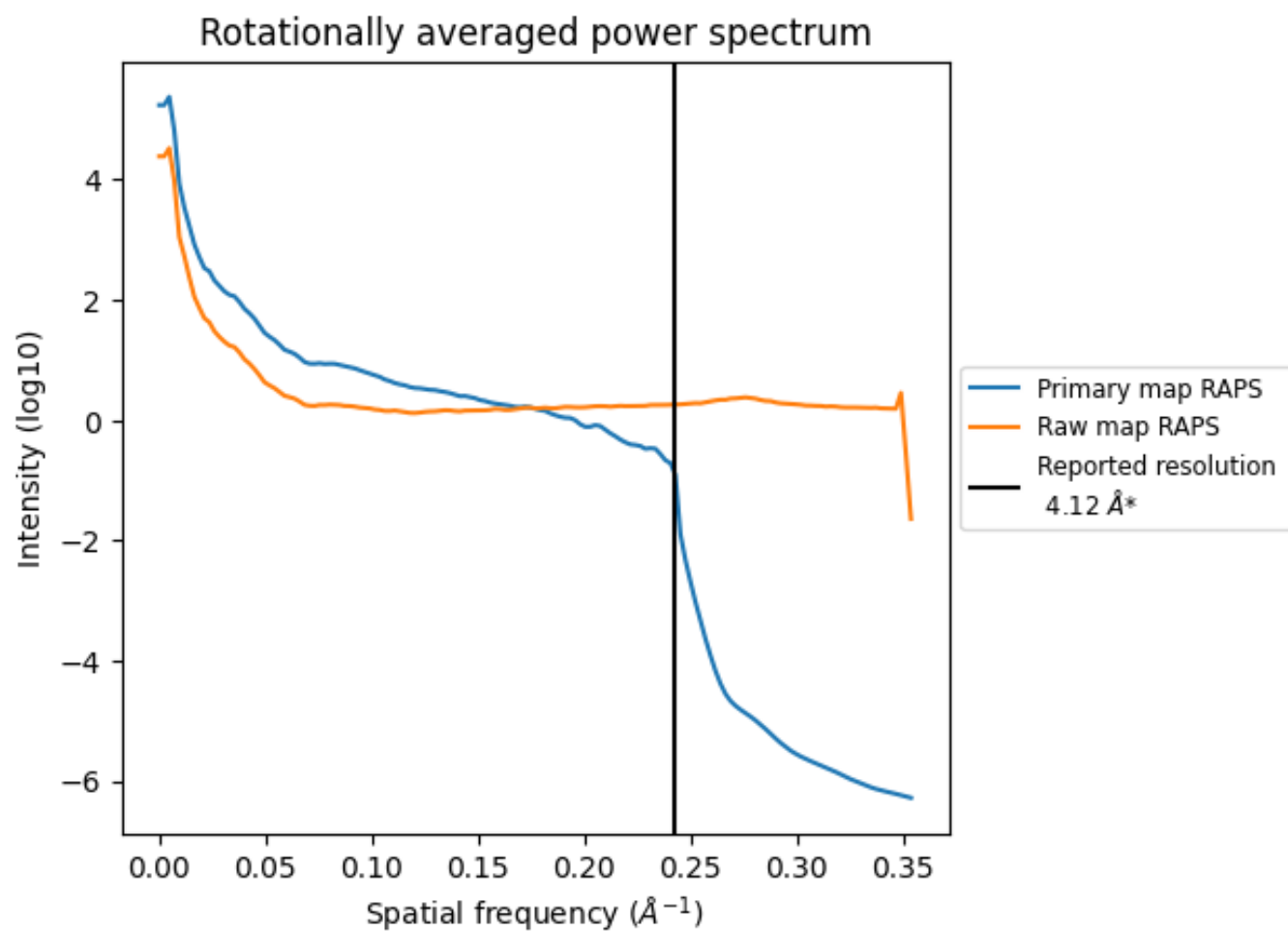
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1192 nm³; this corresponds to an approximate mass of 1077 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 ⓘ

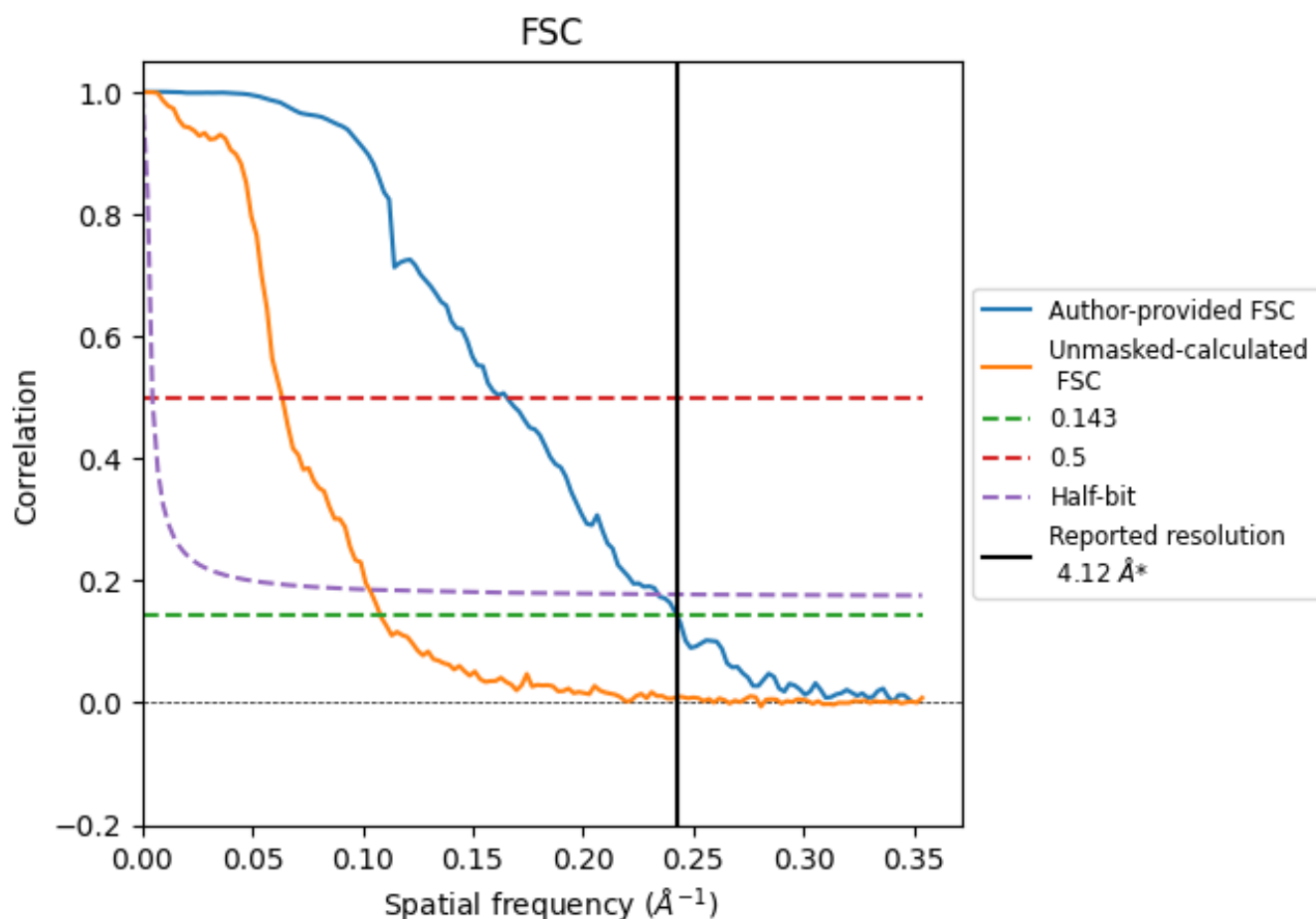


*Reported resolution corresponds to spatial frequency of 0.243 Å⁻¹

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 0.243 \AA^{-1}

8.2 Resolution estimates [i](#)

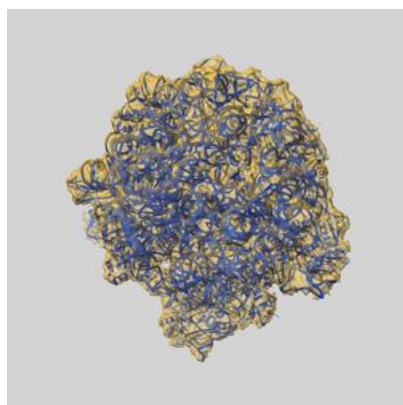
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.12	-	-
Author-provided FSC curve	4.12	6.05	4.27
Unmasked-calculated*	9.25	15.77	9.70

*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 9.25 differs from the reported value 4.12 by more than 10 %

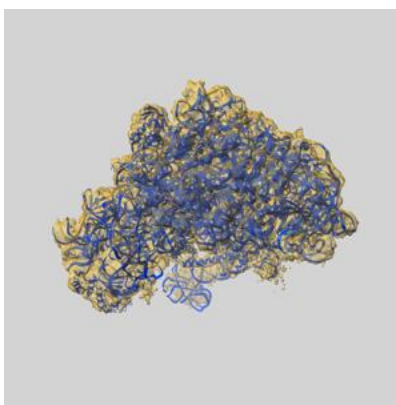
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51835 and PDB model 9H3R. Per-residue inclusion information can be found in section [3](#) on page [8](#).

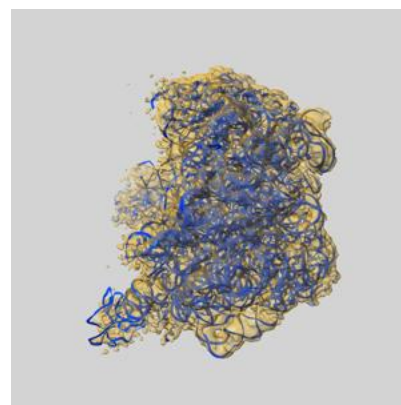
9.1 Map-model overlay [i](#)



X



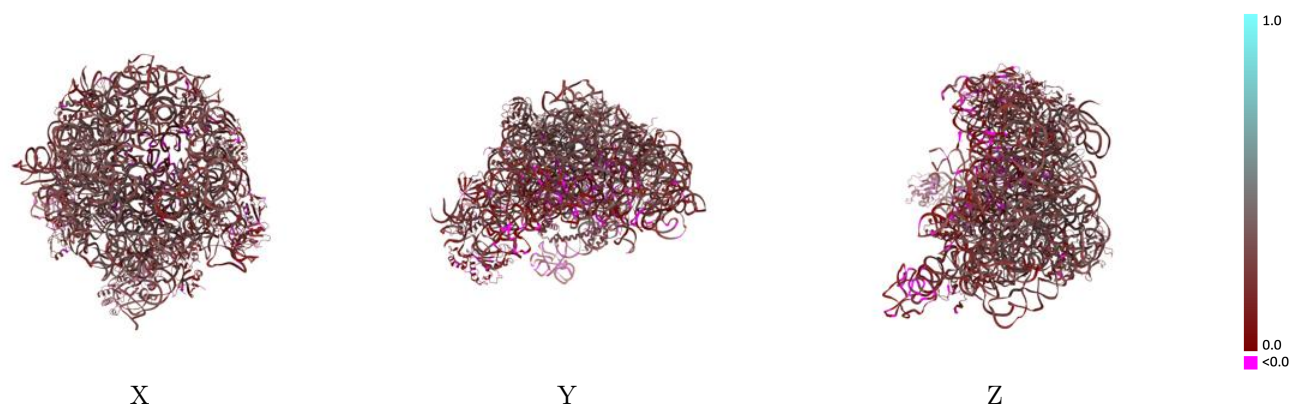
Y



Z

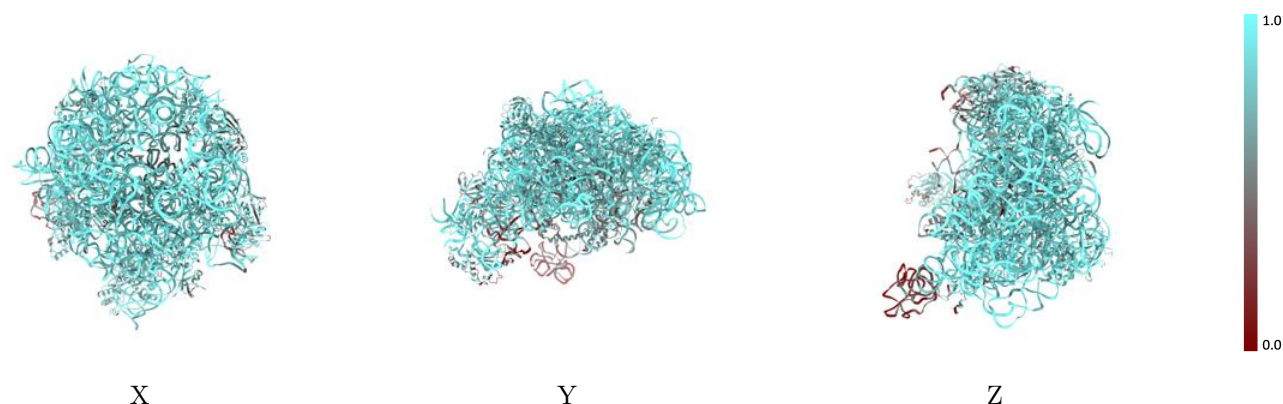
The images above show the 3D surface view of the map at the recommended contour level 0.337 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



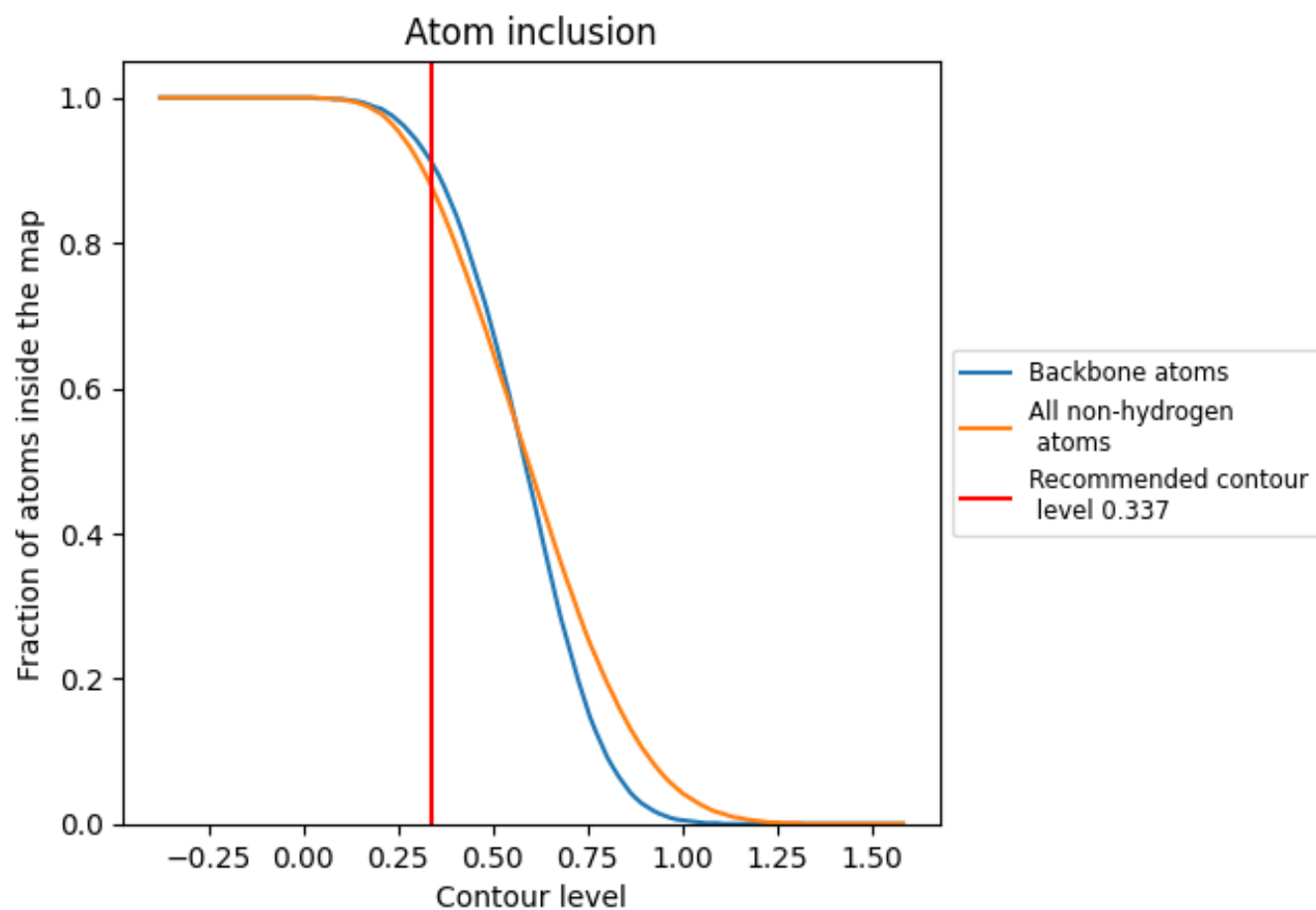
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.337).





















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.337) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.2310
2	 0.8580	 0.2480
4	 0.7190	 0.1200
A	 0.9120	 0.2370
B	 0.9570	 0.2280
C	 0.6580	 0.2010
D	 0.8100	 0.2350
E	 0.8150	 0.2510
F	 0.6760	 0.1020
G	 0.7030	 0.1600
H	 0.6160	 0.1150
J	 0.8720	 0.2850
K	 0.6540	 0.1930
L	 0.7220	 0.1950
N	 0.8410	 0.2180
O	 0.8600	 0.1800
P	 0.6980	 0.1950
Q	 0.8890	 0.2820
R	 0.8460	 0.2800
T	 0.8310	 0.2720
U	 0.8310	 0.2760
V	 0.7100	 0.1720
W	 0.8410	 0.2680
X	 0.8420	 0.2380
Y	 0.8050	 0.2330
Z	 0.8560	 0.2580

