



wwPDB EM Validation Summary Report ⓘ

Apr 21, 2025 – 12:29 PM EDT

PDB ID : 8VPK / pdb_00008vpk
EMDB ID : EMD-43409
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX and erythromycin:50S-HflX-B-Ery
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-16
Resolution : 2.63 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.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

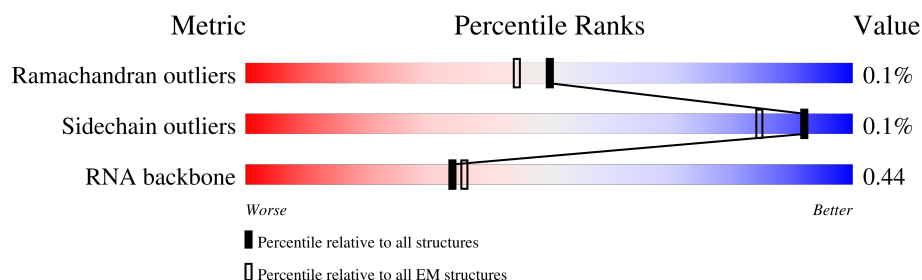
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.63 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.




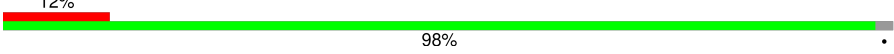
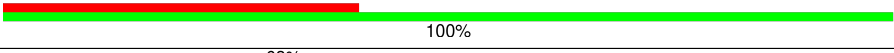

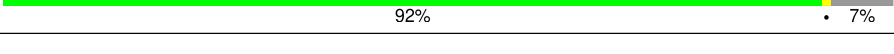
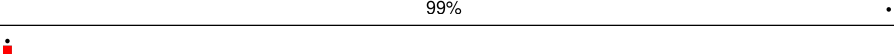
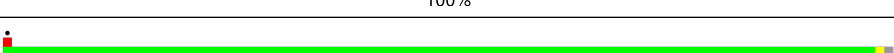
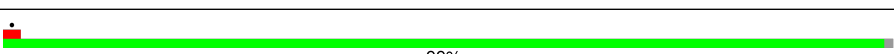
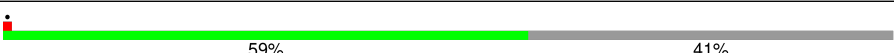
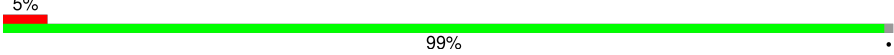
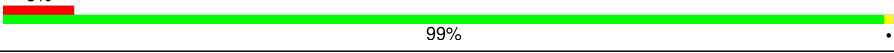
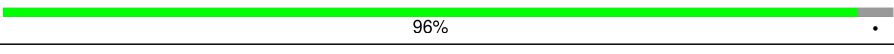
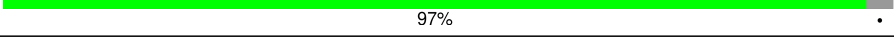
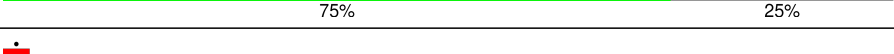
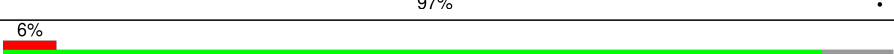
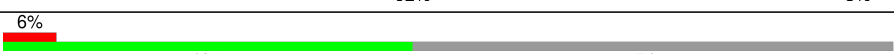
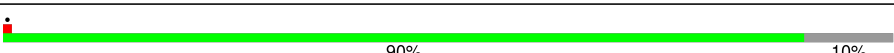
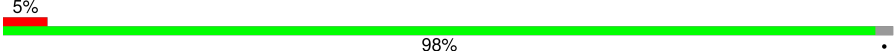

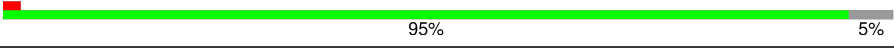

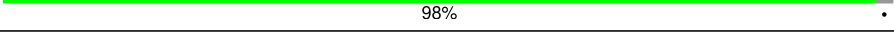
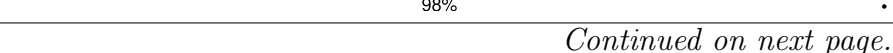


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	61	
2	3	24	
3	4	470	
4	A	3120	
5	B	118	
6	C	278	
7	D	217	
8	E	215	

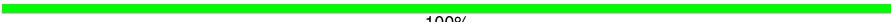

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Mol	Chain	Length	Quality of chain
9	F	187	
10	G	179	
11	H	151	
12	I	175	
13	J	142	
14	K	147	
15	L	122	
16	M	147	
17	N	138	
18	O	199	
19	P	127	
20	Q	113	
21	R	129	
22	S	103	
23	T	153	
24	U	100	
25	V	105	
26	W	215	
27	X	88	
28	Y	64	
29	Z	77	
30	b	57	
31	c	55	
32	d	47	
33	e	64	

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Mol	Chain	Length	Quality of chain
34	f	37	 100%
35	g	75	 41% 64%36%

2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 96925 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	466	Total	C	N	O	S	0	0
			3509	2165	649	688	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	2948	Total	C	N	O	P	0	0
			63320	28221	11648	20503	2948		

- 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	132	Total	C	N	O	S	0	0
			981	620	174	184	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	99	Total	C	N	O	0	0
			763	469	154	140		

- 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		

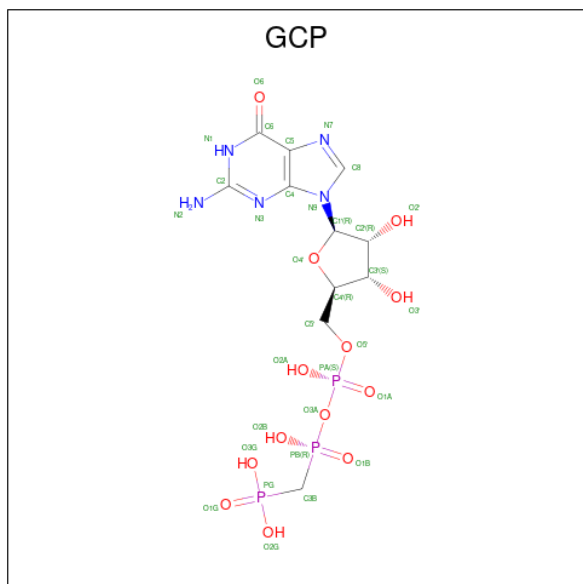
- Molecule 34 is a protein called 50S ribosomal protein L36.

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.

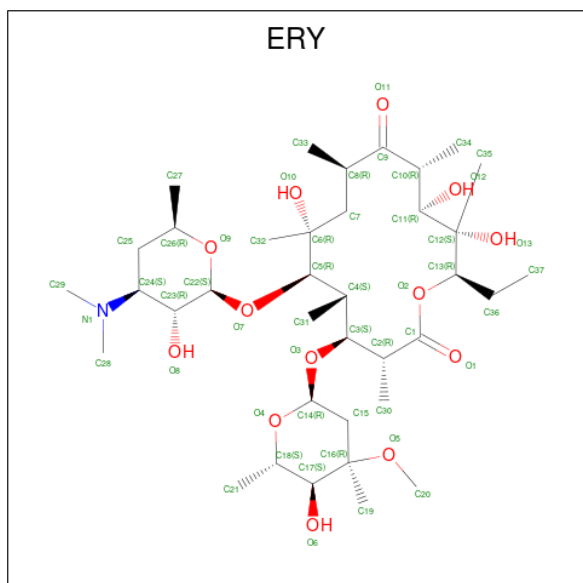
Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- 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).



Mol	Chain	Residues	Atoms					AltConf
36	4	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 37 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$).



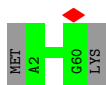
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
37	A	1	51	37	1	13	0

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L30

Chain 2:  97%



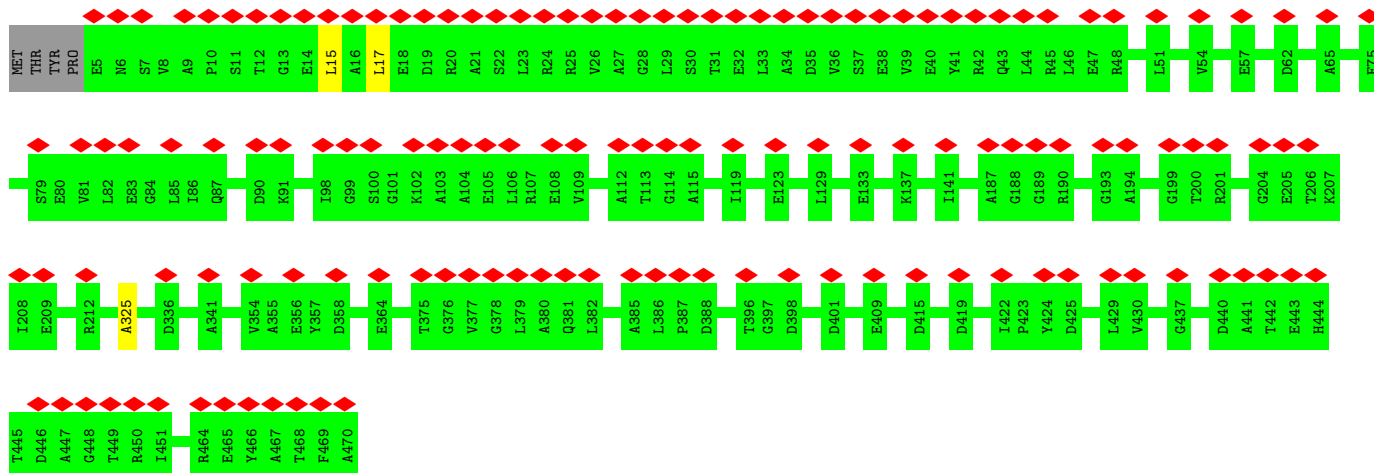
- Molecule 2: 50S Ribosomal Protein L37

Chain 3:  96%



- Molecule 3: GTPase HflX

Chain 4:  99%

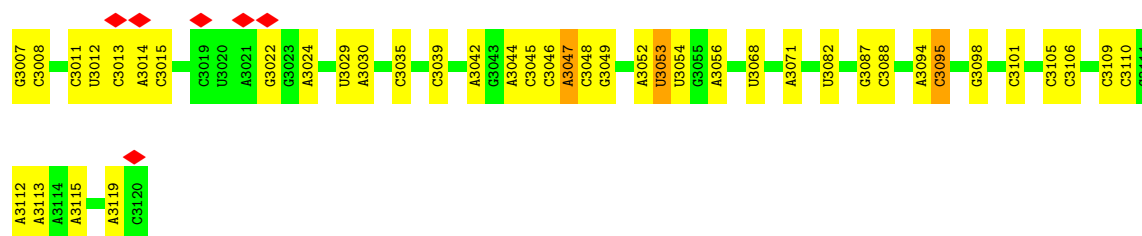


- Molecule 4: 23S ribosomal RNA

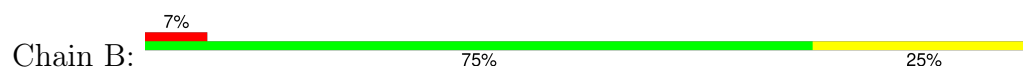
Chain A:  64% 30% 6%



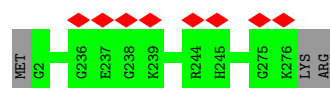
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C2859	U2716	G2608	A2535	A2399	G2339	G2216	U	G	U1946	A1791	G1642	C
U2860	U2717	A2609	U2536	C2400	A2340	G2217	G	A	U1947	A1792	G1643	U
G2861	G2718	U2610	C2537	U2401	U2341	U2218	U	G	U1948	U1798	G1644	U
G2862	G2719	A2611	G2538	C2402	A2342	C2220	A	C	G1950	U1799	G1645	U
C2870	G2726	G2612	G2539	U2403	G2343	A2221	A	C	U1951	U1800	U1646	C
U2873	U2727	U2613	G2540	U2404	G2344	A2222	C	C	A1952	G1801	G1647	G
U2880	G2729	G2614	U2541	G2405	U2345	U2223	U	C	U1953	G1802	C1648	G
A2881	U2730	C2621	U2542	A2406	G2346	U2224	A	C	A1954	G1803	A1649	G
C2882	U2742	G2622	U2543	U2407	G2347	U2225	U	C	U1955	G1804	U1675	U
G2883	G2743	U2623	G2544	C2408	G2348	U2226	A	C	U1956	G1805	A1679	G
A2884	C2744	A2624	U2545	U2409	G2349	A2227	A	C	A1957	A1806	U1681	G
U2889	U2746	G2625	A2546	A2410	A2350	A2228	C	C	U1958	C1813	G1703	C
U2906	U2752	U2626	U2547	U2411	G2351	G2259	A	C	U1959	G1814	A1706	U
U2913	G2753	A2630	G2548	A2412	A2352	G2260	U	C	U1960	G1815	A1727	C
A2914	C2754	U2631	U2549	G2427	U2353	C2267	U	C	U1961	G1816	U1728	A
C2936	U2756	G2632	G2550	A2434	G2354	C2279	A	C	A2000	A1821	G1710	G
G2937	U2757	U2633	U2551	U2435	G2355	G2280	U	C	A2001	G1822	G1711	U
U2938	G2758	A2634	G2552	C2451	U2356	A2284	G	C	A2002	C1825	U1712	G
C2950	U2768	G2635	U2553	U2452	G2357	G2285	G	C	A2003	A1826	G1713	G
U2957	G2777	U2636	G2554	U2453	A2358	A2286	G	C	A2004	A1827	A1714	G
A2964	U2778	A2637	U2555	C2454	G2359	A2306	G	C	G2016	C1828	U1717	U
C2966	U2779	G2638	G2556	U2455	C2360	C2307	G	C	C2017	C1829	A1737	C
U2967	A2788	U2639	U2557	C2456	U2361	U2308	A	C	C2018	A1832	U1729	C
G2968	U2789	A2640	C2558	A2457	A2362	G2310	U	C	A2019	G1837	U1730	A
C2969	G2791	G2641	U2559	U2458	C2363	G2311	C	C	U2033	U1864	A1731	G
U2970	U2792	U2642	G2560	C2459	U2364	U2312	G	C	G2034	C1865	G1738	G
G2971	G2806	A2643	U2561	C2460	G2365	A2313	A	C	A2038	G1869	A1744	C
A2972	U2809	U2644	G2562	U2461	U2366	U2314	U	C	C2039	U1870	G1761	C
U2973	A2826	G2645	U2563	U2462	C2367	G2315	U	C	A2046	A1871	A1755	U
C2974	G2827	A2646	G2564	A2463	G2368	U2316	C	C	U2051	G1872	G1756	G
U2975	U2833	U2647	U2565	C2464	C2369	U2317	C	C	C2052	G1885	U1757	C
G2976	U2837	G2648	G2566	U2465	U2370	U2318	U	C	C2053	G1886	G1758	C
U2977	A2838	A2649	U2567	U2466	A2371	G2319	U	C	C2054	C1903	A1759	C
C2978	U2839	C2650	C2568	A2511	G2372	U2320	C	C	C2055	C1904	G1760	U
U2979	U2845	U2651	U2569	A2512	U2373	A2321	A	C	G	U1911	C1768	G
A2980	G2846	G2652	G2570	U2520	U2374	G2322	U	C	U	G1938	G1769	U
A2981	U2847	A2653	U2571	A2521	G2375	U2323	A	C	C	U1912	U1774	C
U2982	U2848	U2654	U2572	A2522	U2376	A2324	A	C	A	G1939	G1780	C
G2986	G2851	G2655	G2573	A2523	G2377	U2325	C	C	G	U1913	A1788	C
C2987	U2852	A2656	U2574	A2524	U2378	A2326	A	C	U	U1914	G1789	C
A2988	U2853	U2657	U2575	A2525	U2379	G2327	U	C	C	G1939	A1789	C
A3002	A2854	G2658	G2576	U2526	G2380	U2328	C	C	A	U1915	U1790	C
C3003	U2855	A2659	U2577	A2527	A2381	G2329	A	C	G	U1916	G1791	C
U3004	U2856	U2660	U2578	U2528	U2382	U2330	C	C	A	G1939	G1792	C
A3005	U2857	G2661	G2579	G2529	G2383	U2331	C	C	G	U1917	A1791	C
G3006	U2858	U2662	U2580	U2530	U2384	U2332	C	C	U	C1943	G1792	C
		U2663	U2581	U2531	G2385	U2333	C	C	U	C1944	A1792	C
		G2664	U2582	U2532	U2386	U2334	C	C	A			C
		A2665	U2583	U2533	U2387	U2335	C	C	U			C
		U2666	U2584	U2534	G2388	A2336	C	C	A			C
		G2667	G2585	U2535	U2389	U2337	C	C	U			C
		A2668	U2586	U2536	U2390	G2338	C	C	U			C
		U2669	U2587	U2537	G2391	A2339	C	C	U			C
		G2670	U2588	U2538	A2392	U2392	C	C	A			C
		U2671	U2589	U2539	U2393	U2393	C	C	U			C
		A2672	U2590	U2540	U2394	U2394	C	C	U			C
		G2673	U2591	U2541	U2395	U2395	C	C	U			C
		U2674	U2592	U2542	U2396	U2396	C	C	U			C
		A2675	U2593	U2543	U2397	U2397	C	C	U			C
		G2676	U2594	U2544	U2398	U2398	C	C	U			C
		U2677	U2595	U2545	U2399	U2399	C	C	U			C
		A2678	U2596	U2546	U2400	U2400	C	C	U			C
		G2679	U2597	U2547	U2401	U2401	C	C	U			C
		U2680	U2598	U2548	U2402	U2402	C	C	U			C
		A2681	U2599	U2549	U2403	U2403	C	C	U			C
		G2682	U2600	U2550	U2404	U2404	C	C	U			C
		U2683	A2601	U2551	U2405	U2405	C	C	U			C
		A2684	U2602	U2552	U2406	U2406	C	C	U			C
		G2685	G2603	U2553	U2407	U2407	C	C	U			C
		U2686	U2604	U2554	U2408	U2408	C	C	U			C
		A2687	G2605	U2555	U2409	U2409	C	C	U			C
		G2688	U2606	U2556	U2410	U2410	C	C	U			C
		U2689	U2607	U2557	U2411	U2411	C	C	U			C
		A2690	G2608	U2558	U2412	U2412	C	C	U			C
		G2691	U2609	U2559	U2413	U2413	C	C	U			C
		U2692	U2610	U2560	U2414	U2414	C	C	U			C
		A2693	U2611	U2561	U2415	U2415	C	C	U			C
		G2694	U2612	U2562	U2416	U2416	C	C	U			C
		U2695	U2613	U2563	U2417	U2417	C	C	U			C
		A2696	U2614	U2564	U2418	U2418	C	C	U			C
		G2697	U2615	U2565	U2419	U2419	C	C	U			C
		U2698	U2616	U2566	U2420	U2420	C	C	U			C
		A2699	U2617	U2567	U2421	U2421	C	C	U			C
		G2700	U2618	U2568	U2422	U2422	C	C	U			C
		U2701	U2619	U2569	U2423	U2423	C	C	U			C
		A2702	U2620	U2570	U2424	U2424	C	C	U			C
		G2703	U2621	U2571	U2425	U2425	C	C	U			C
		U2704	U2622	U2572	U2426	U2426	C	C	U			C
		A2705	U2623	U2573	U2427	U2427	C	C	U			C
		G2706	U2624	U2574	U2428	U2428	C	C	U			C
		U2707	U2625	U2575	U2429	U2429	C	C	U			C
		A2708	U2626	U2576	U2430	U2430	C	C	U			C
		G2709	U2627	U2577	U2431	U2431	C	C	U			C
		U2710	U2628	U2578	U2432	U2432	C	C	U			C
		A2711	U2629	U2579	U2433	U2433	C	C	U			C
		G2712	U2630	U2580	U2434	U2434	C	C	U			C
		U2713	U2631	U2581	U2435	U2435	C	C	U			C
		A2714	U2632	U2582	U2436	U2436	C	C	U			C
		G2715	U2633	U2583	U2437	U2437	C	C	U			C
		U2716	U2634	U2584	U2438	U2438	C	C	U			C
		A2717	U2635	U2585	U2439	U2439	C	C	U			C
		G2718	U2636	U2586	U2440	U2440	C	C	U			C
		U2719	U2637	U2587	U2441	U2441	C	C	U			C
		A2720	U2638	U2588	U2442	U2442	C	C	U			C
		G2721	U2639	U2589	U2443	U2443	C	C	U			C
		U2722	U2640	U2590	U2444	U2444	C	C	U			C
		A2723	U2641	U2591	U2445	U2445	C	C	U			C
		G2724	U2642	U2592	U2446	U2446	C	C	U			C
		U2725	U2643	U2593	U2447	U2447	C	C	U			C
		A2726	U2644	U2594	U2448	U2448	C	C	U			C
		G2727	U2645	U2595	U2449	U2449	C	C	U			C
		U2728	U2646	U2596	U2450	U2450	C	C	U			C
		A2729	U2647	U2597	U2451	U2451	C	C	U			C
		G2730	U2648	U2598	U2452	U2452	C	C	U			C
		U2731	U2649	U2599	U2453	U2453	C	C	U			C
		A2732	U2650	U2600	U2454	U2454	C	C	U			C
		G2733	U2651	U2601	U2455	U2455	C	C	U			C
		U2734	U2652	U2602	U2456	U2456	C	C	U			C
		A2735	U2653	U2603	U2457	U2457	C	C	U			C
		G2736	U2654	U2604	U2458	U2458	C	C	U			C
		U2737	U2655	U2605	U2459	U2459	C	C	U			C
		A2738	U2656	U2606	U2460	U2460	C	C	U			C
		G2739	U2657	U2607	U2461	U2461	C	C	U			C
		U2740										



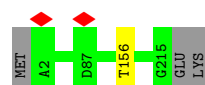
- Molecule 5: 5S ribosomal RNA



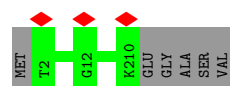
- Molecule 6: 50S ribosomal protein L2



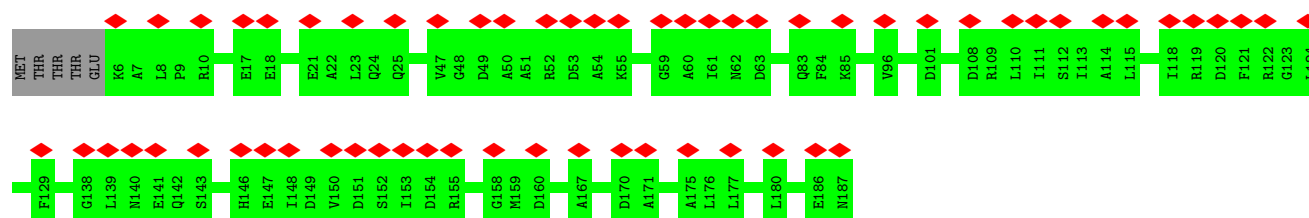
- Molecule 7: 50S ribosomal protein L3



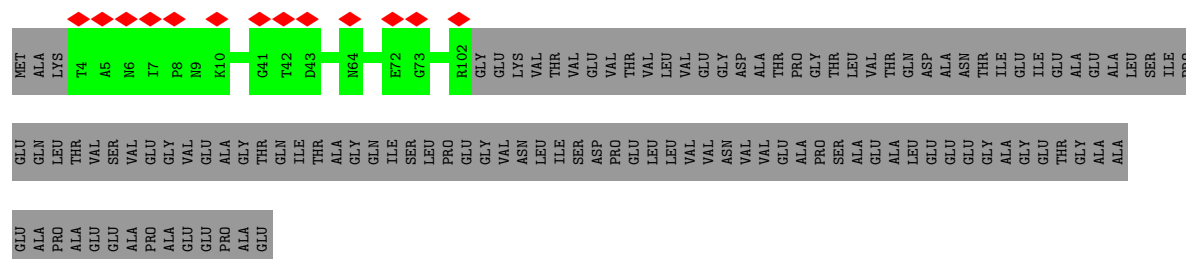
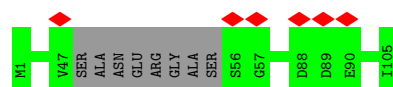
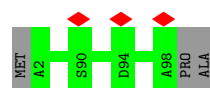
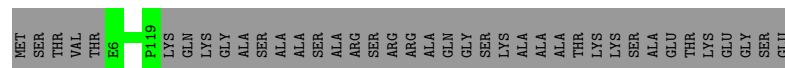
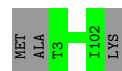
- Molecule 8: 50S Ribosomal Protein L4



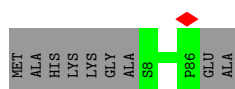
- Molecule 9: 50S Ribosomal Protein L5



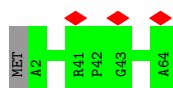
- Molecule 10: 50S ribosomal protein L6



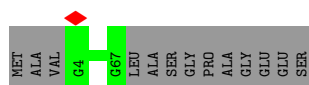
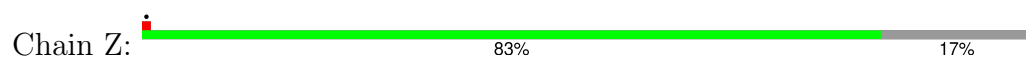
- Molecule 27: 50S ribosomal protein L27



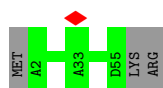
- Molecule 28: 50S Ribosomal Protein L28



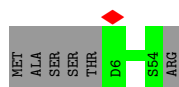
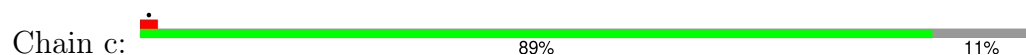
- Molecule 29: 50S ribosomal protein L29



- Molecule 30: 50S ribosomal protein L32



- Molecule 31: 50S Ribosomal Protein L33



- Molecule 32: 50S ribosomal protein L34



- Molecule 33: 50S ribosomal protein L35



● Molecule 34: 50S ribosomal protein L36

Chain f:

100%

There are no outlier residues recorded for this chain.

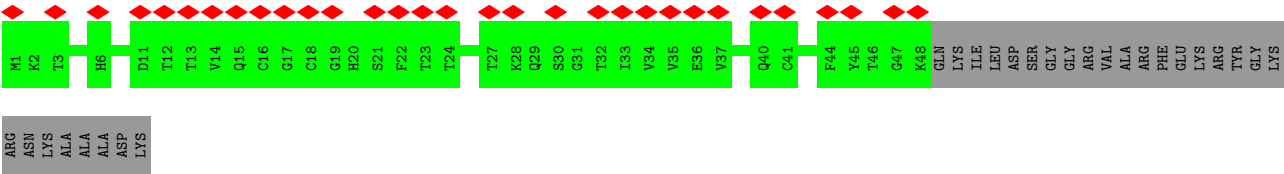
● Molecule 35: 50S Ribosomal Protein L31

Chain g:

41%

64%

36%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	113394	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 ($e^-/\text{\AA}^2$)	62.87	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.749	Depositor
Minimum map value	-0.854	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	433.152, 433.152, 433.152	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.846, 0.846, 0.846	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ERY, 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	0.25	0/477	0.57	0/640
2	3	0.27	0/191	0.68	0/247
3	4	0.25	0/3550	0.55	0/4811
4	A	0.41	0/70902	0.81	47/110629 (0.0%)
5	B	0.33	0/2821	0.84	2/4396 (0.0%)
6	C	0.28	0/2153	0.59	0/2895
7	D	0.40	0/1609	0.60	0/2165
8	E	0.28	0/1592	0.51	0/2153
9	F	0.25	0/1467	0.56	0/1973
10	G	0.27	0/1369	0.55	0/1848
11	H	0.25	0/1027	0.48	0/1398
12	I	0.27	0/925	0.49	0/1246
13	J	0.25	0/997	0.45	0/1352
14	K	0.29	0/1157	0.50	0/1567
15	L	0.29	0/946	0.56	0/1268
16	M	0.29	0/1091	0.55	0/1457
17	N	0.28	0/1118	0.55	0/1506
18	O	0.29	0/945	0.55	0/1267
19	P	0.27	0/966	0.59	0/1298
20	Q	0.29	0/921	0.55	0/1236
21	R	0.28	0/1000	0.55	0/1341
22	S	0.31	0/764	0.49	0/1030
23	T	0.27	0/887	0.57	0/1204
24	U	0.27	0/766	0.52	0/1030
25	V	0.27	0/738	0.50	0/987
26	W	0.25	0/773	0.55	0/1048
27	X	0.30	0/595	0.59	0/798
28	Y	0.31	0/478	0.60	0/641
29	Z	0.27	0/534	0.59	0/713
30	b	0.27	0/427	0.62	0/572
31	c	0.27	0/413	0.54	0/553
32	d	0.26	0/380	0.71	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	e	0.24	0/507	0.62	0/672
34	f	0.29	0/303	0.59	0/401
35	g	0.27	0/372	0.47	0/503
All	All	0.38	0/105161	0.75	49/157345 (0.0%)

There are no bond length outliers.

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2553	G	N3-C4-N9	-6.83	121.90	126.00
4	A	2553	G	C5-C6-O6	6.82	132.69	128.60
4	A	2245	C	C2-N1-C1'	6.76	126.24	118.80
4	A	3053	U	C2-N1-C1'	6.67	125.71	117.70
4	A	2566	C	N3-C2-O2	-6.61	117.27	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	21 (100%)	0	0	100	100
3	4	464/470 (99%)	395 (85%)	66 (14%)	3 (1%)	22	32
6	C	273/278 (98%)	254 (93%)	19 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D	212/217 (98%)	203 (96%)	9 (4%)	0	100	100
8	E	207/215 (96%)	200 (97%)	7 (3%)	0	100	100
9	F	180/187 (96%)	163 (91%)	17 (9%)	0	100	100
10	G	174/179 (97%)	152 (87%)	22 (13%)	0	100	100
11	H	149/151 (99%)	133 (89%)	16 (11%)	0	100	100
12	I	124/175 (71%)	102 (82%)	22 (18%)	0	100	100
13	J	130/142 (92%)	105 (81%)	25 (19%)	0	100	100
14	K	144/147 (98%)	141 (98%)	3 (2%)	0	100	100
15	L	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
16	M	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
17	N	134/138 (97%)	132 (98%)	2 (2%)	0	100	100
18	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
19	P	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
20	Q	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
21	R	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
22	S	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
23	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
24	U	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
25	V	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
26	W	97/215 (45%)	91 (94%)	6 (6%)	0	100	100
27	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100
28	Y	61/64 (95%)	57 (93%)	4 (7%)	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%)	44 (94%)	3 (6%)	0	100	100
32	d	44/47 (94%)	44 (100%)	0	0	100	100
33	e	61/64 (95%)	61 (100%)	0	0	100	100
34	f	35/37 (95%)	35 (100%)	0	0	100	100
35	g	46/75 (61%)	44 (96%)	2 (4%)	0	100	100
All	All	3985/4461 (89%)	3711 (93%)	271 (7%)	3 (0%)	50	65

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	4	325	ALA
3	4	15	LEU
3	4	17	LEU

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	366/372 (98%)	366 (100%)	0	100	100
6	C	215/218 (99%)	215 (100%)	0	100	100
7	D	160/163 (98%)	159 (99%)	1 (1%)	84	92
8	E	169/173 (98%)	169 (100%)	0	100	100
9	F	151/156 (97%)	151 (100%)	0	100	100
10	G	148/150 (99%)	148 (100%)	0	100	100
11	H	90/116 (78%)	90 (100%)	0	100	100
12	I	89/120 (74%)	89 (100%)	0	100	100
13	J	101/108 (94%)	100 (99%)	1 (1%)	73	85
14	K	119/120 (99%)	119 (100%)	0	100	100
15	L	100/100 (100%)	100 (100%)	0	100	100
16	M	112/114 (98%)	111 (99%)	1 (1%)	75	87
17	N	114/116 (98%)	114 (100%)	0	100	100
18	O	97/158 (61%)	97 (100%)	0	100	100
19	P	93/94 (99%)	93 (100%)	0	100	100
20	Q	100/100 (100%)	99 (99%)	1 (1%)	73	85
21	R	97/99 (98%)	97 (100%)	0	100	100
22	S	81/83 (98%)	81 (100%)	0	100	100
23	T	90/117 (77%)	90 (100%)	0	100	100
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%)	81 (100%)	0	100	100
26	W	80/168 (48%)	80 (100%)	0	100	100
27	X	58/63 (92%)	58 (100%)	0	100	100
28	Y	50/51 (98%)	50 (100%)	0	100	100
29	Z	58/66 (88%)	58 (100%)	0	100	100
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%)	35 (100%)	0	100	100
35	g	43/63 (68%)	43 (100%)	0	100	100
All	All	3228/3555 (91%)	3224 (100%)	4 (0%)	92	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	D	156	THR
13	J	83	LYS
16	M	49	MET
20	Q	79	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
3	4	330	HIS
3	4	342	GLN
13	J	16	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	2945/3120 (94%)	911 (30%)	54 (1%)
5	B	117/118 (99%)	27 (23%)	1 (0%)
All	All	3062/3238 (94%)	938 (30%)	55 (1%)

5 of 938 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	3	A
4	A	7	U
4	A	33	G
4	A	52	G
4	A	60	A

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	1208	U
4	A	2168	U
5	B	10	G
4	A	2975	G
4	A	1285	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](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
37	ERY	A	3201	-	53,53,53	1.42	9 (16%)	82,82,82	2.22	30 (36%)
36	GCP	4	501	-	27,34,34	1.30	3 (11%)	35,54,54	1.86	8 (22%)

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
37	ERY	A	3201	-	-	12/72/107/107	0/3/3/3
36	GCP	4	501	-	-	2/15/38/38	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	A	3201	ERY	O10-C6	-4.05	1.38	1.44
36	4	501	GCP	C5-C6	3.89	1.48	1.41
37	A	3201	ERY	O2-C13	-3.32	1.40	1.46
37	A	3201	ERY	O2-C1	3.19	1.41	1.34
37	A	3201	ERY	C10-C9	-2.84	1.48	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	A	3201	ERY	O5-C16-C17	9.04	116.97	103.86
37	A	3201	ERY	O5-C16-C15	-5.49	104.50	112.95
37	A	3201	ERY	O3-C3-C4	5.14	114.30	108.23
36	4	501	GCP	C2-N3-C4	4.90	120.77	115.48
36	4	501	GCP	C2-N1-C6	4.28	121.91	115.96

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

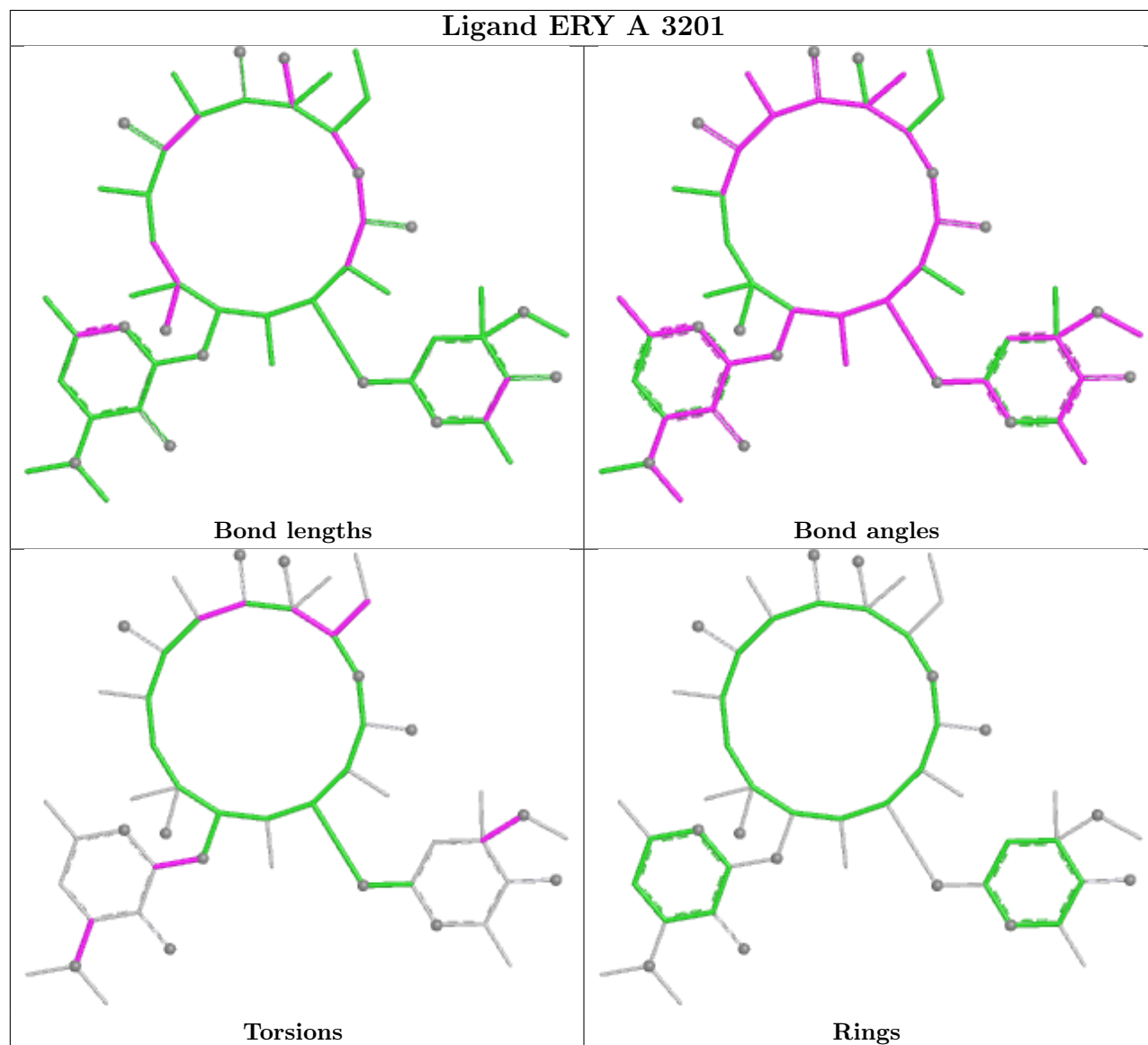
Mol	Chain	Res	Type	Atoms
37	A	3201	ERY	O13-C12-C13-O2
37	A	3201	ERY	O13-C12-C13-C36
37	A	3201	ERY	C17-C16-O5-C20
36	4	501	GCP	O4'-C4'-C5'-O5'
37	A	3201	ERY	C35-C12-C13-O2

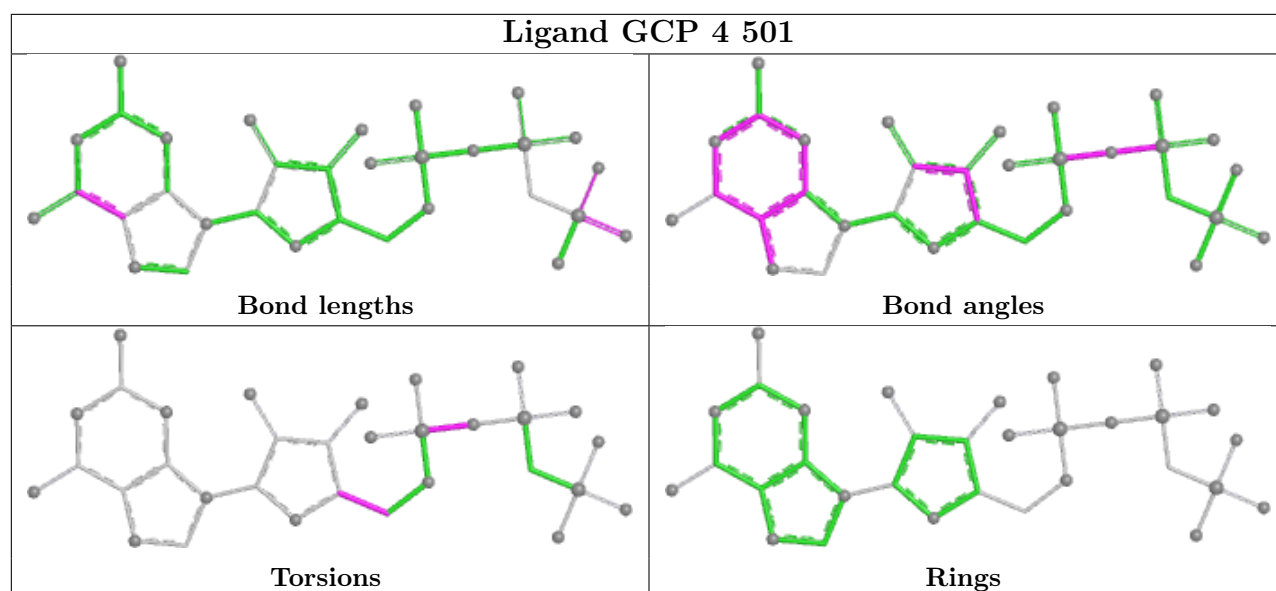
There are no ring outliers.

No monomer is involved in short contacts.

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.

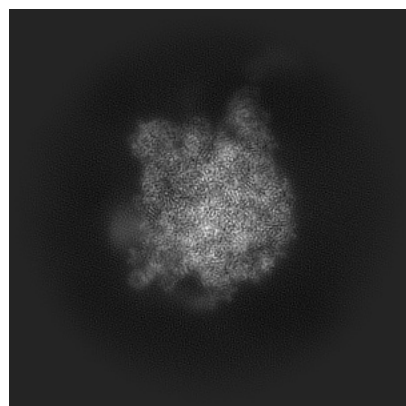
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43409. These allow visual inspection of the internal detail of the map and identification of artifacts.

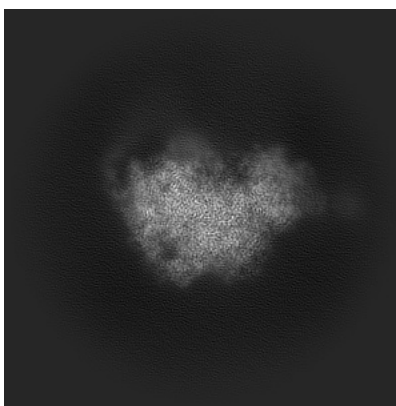
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

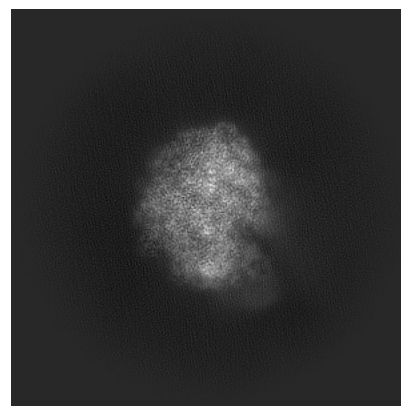
6.1.1 Primary map



X

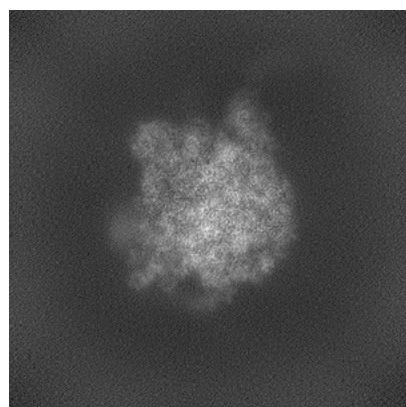


Y

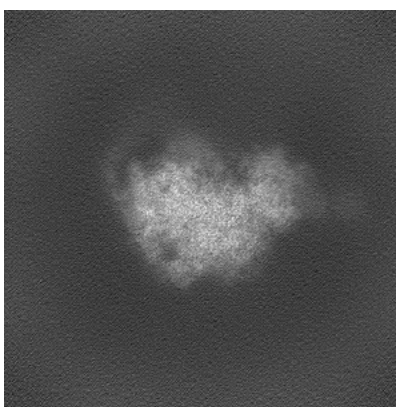


Z

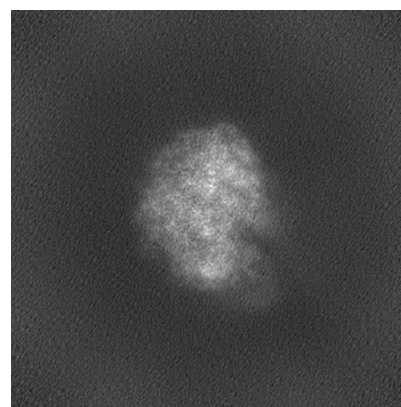
6.1.2 Raw map



X



Y

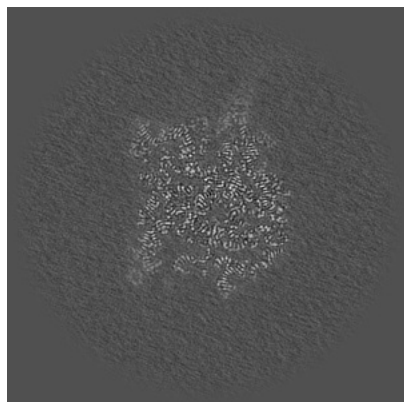


Z

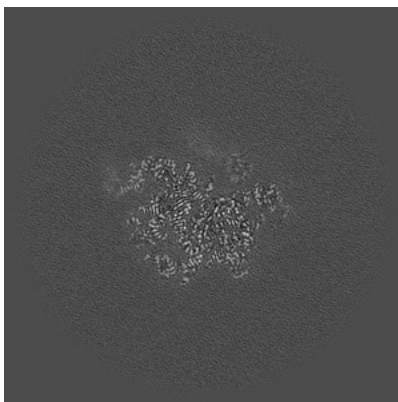
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

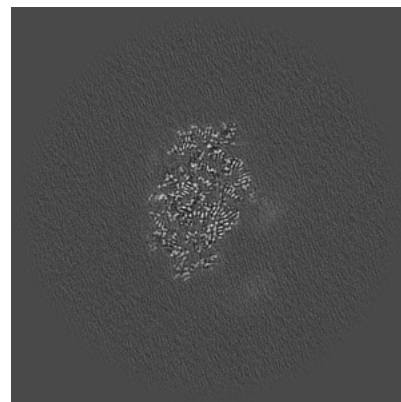
6.2.1 Primary map



X Index: 256

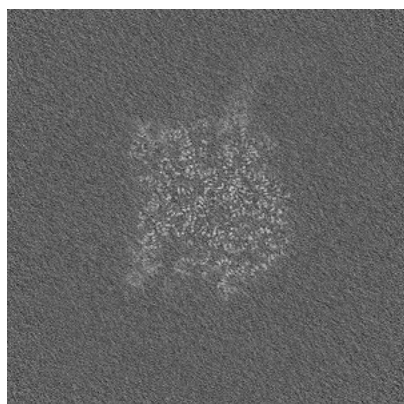


Y Index: 256

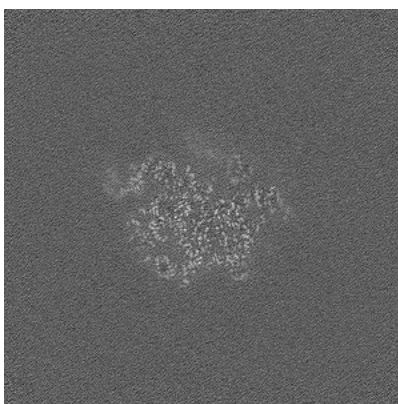


Z Index: 256

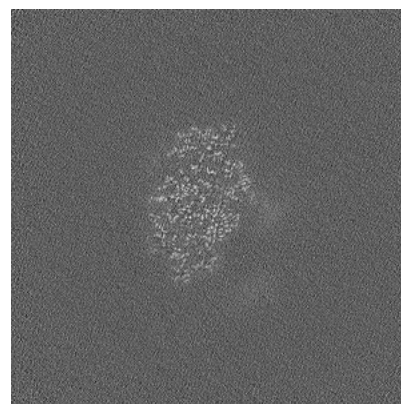
6.2.2 Raw map



X Index: 256



Y Index: 256

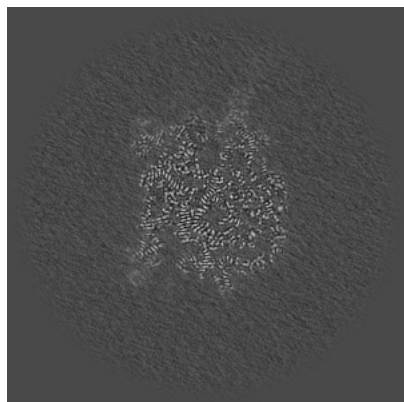


Z Index: 256

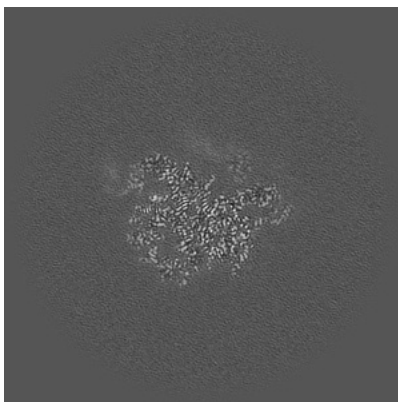
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

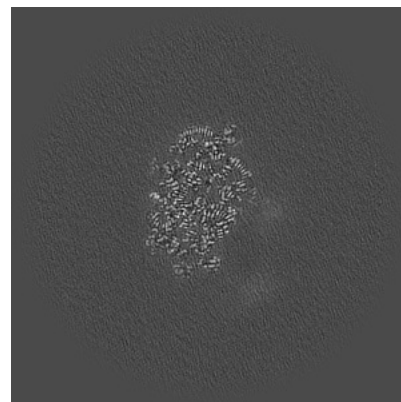
6.3.1 Primary map



X Index: 252

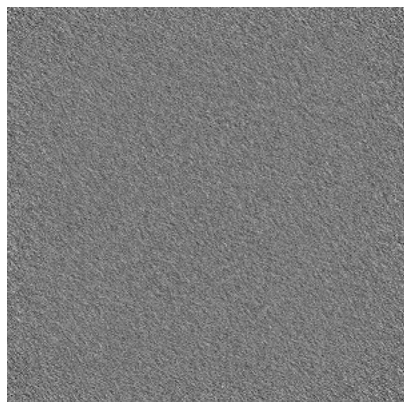


Y Index: 253

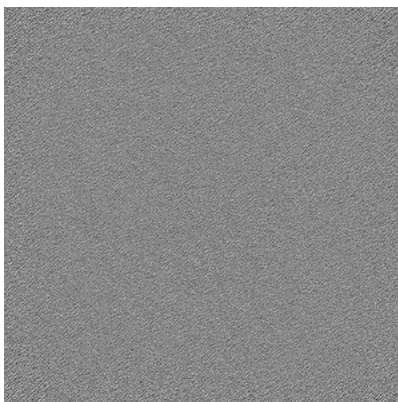


Z Index: 253

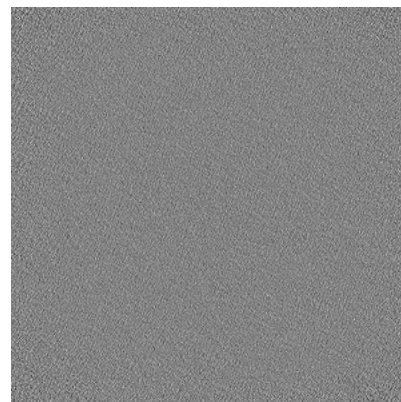
6.3.2 Raw map



X Index: 0



Y Index: 0

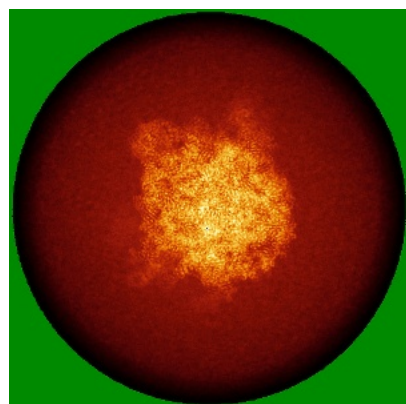


Z Index: 0

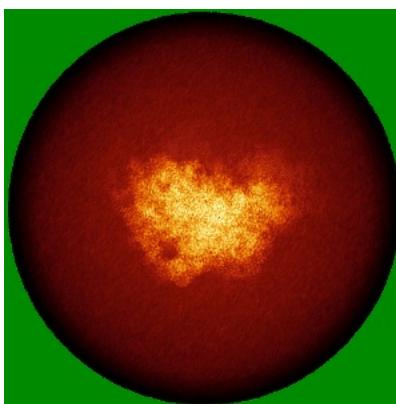
The images above show the largest variance slices of the map in three orthogonal directions.

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

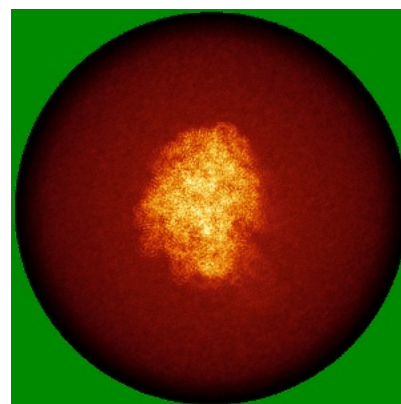
6.4.1 Primary map



X

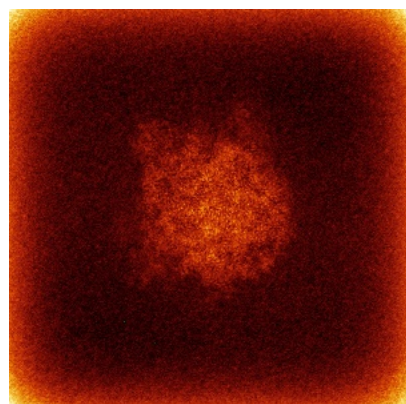


Y

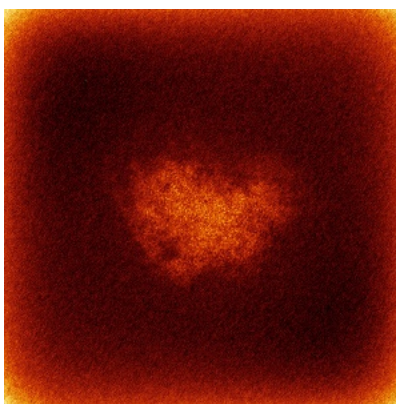


Z

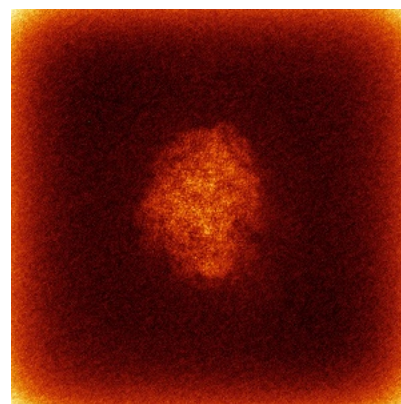
6.4.2 Raw map



X



Y

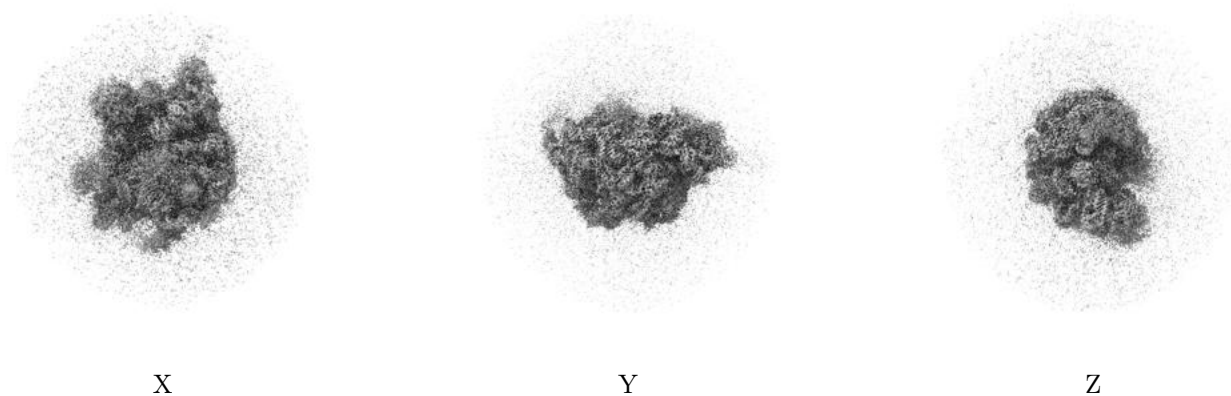


Z

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.

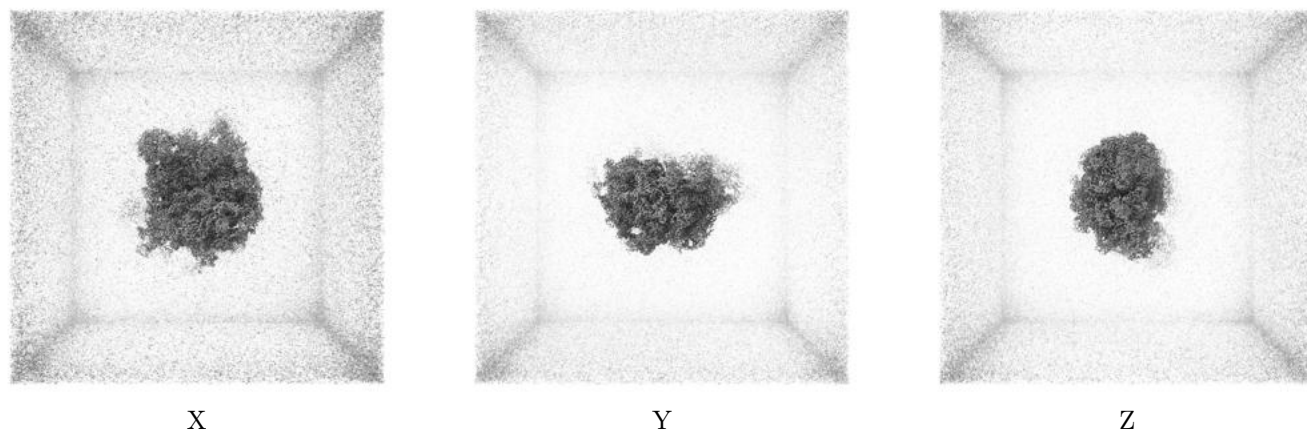
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

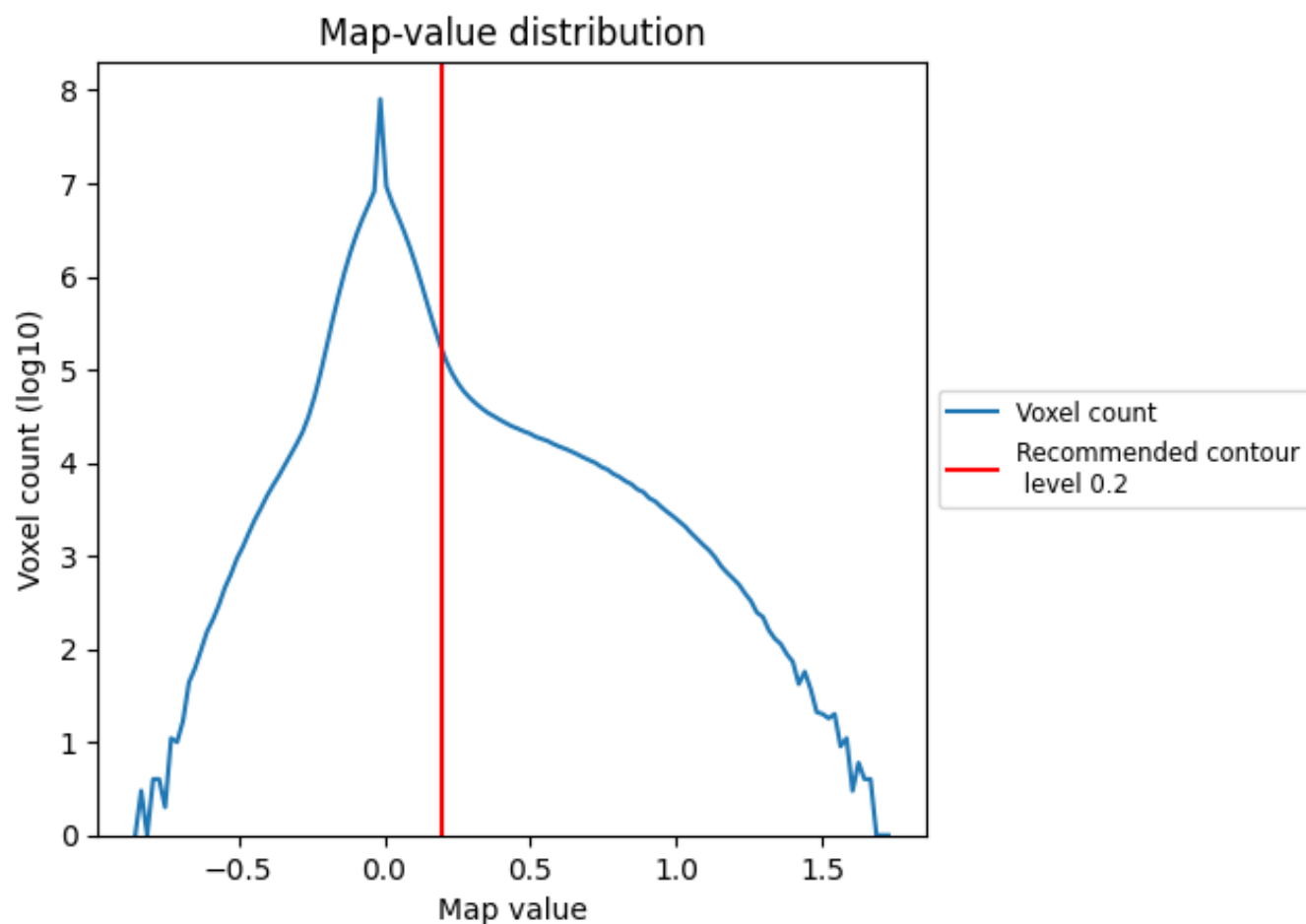
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

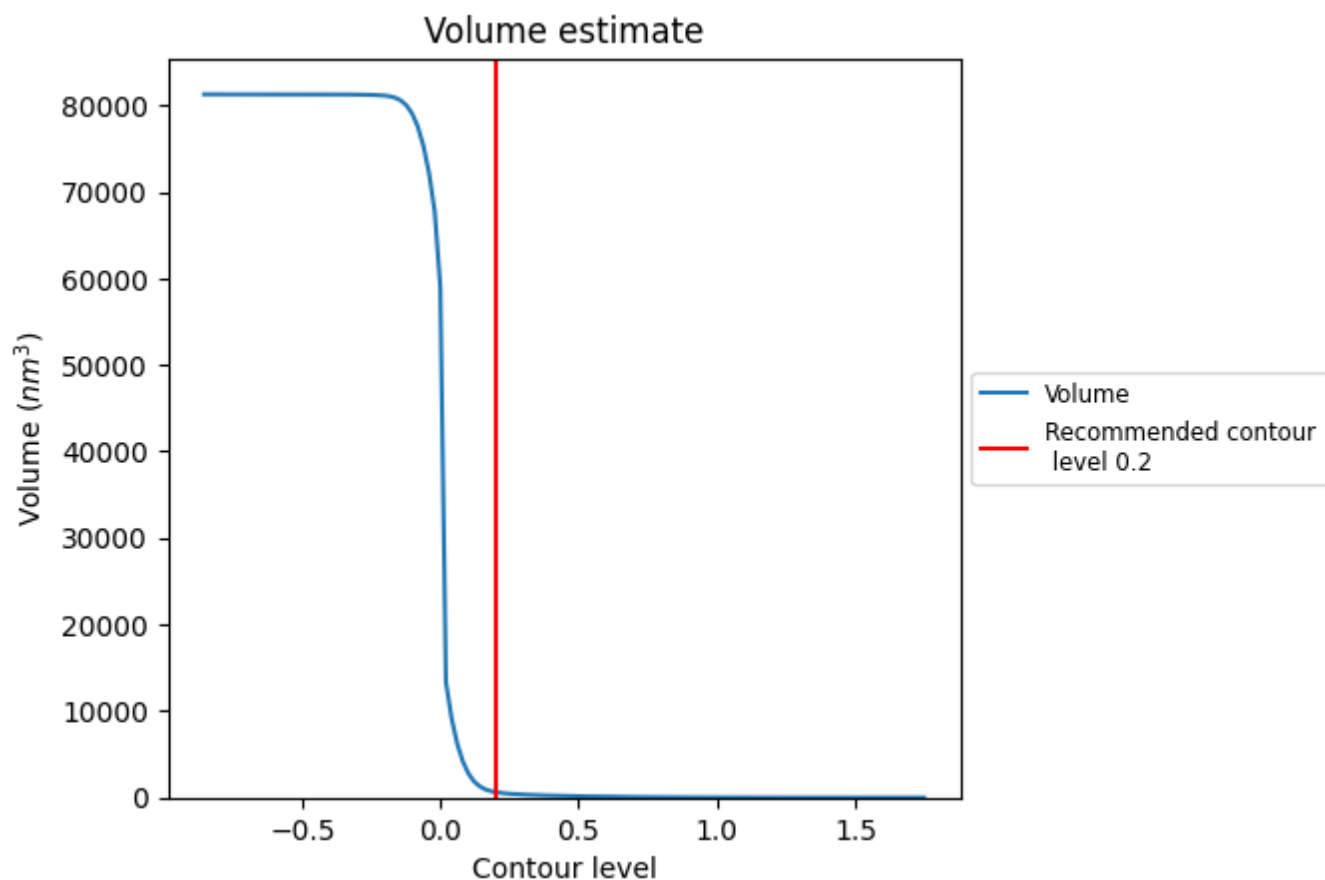
This section contains the results of statistical analysis of the map.

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.

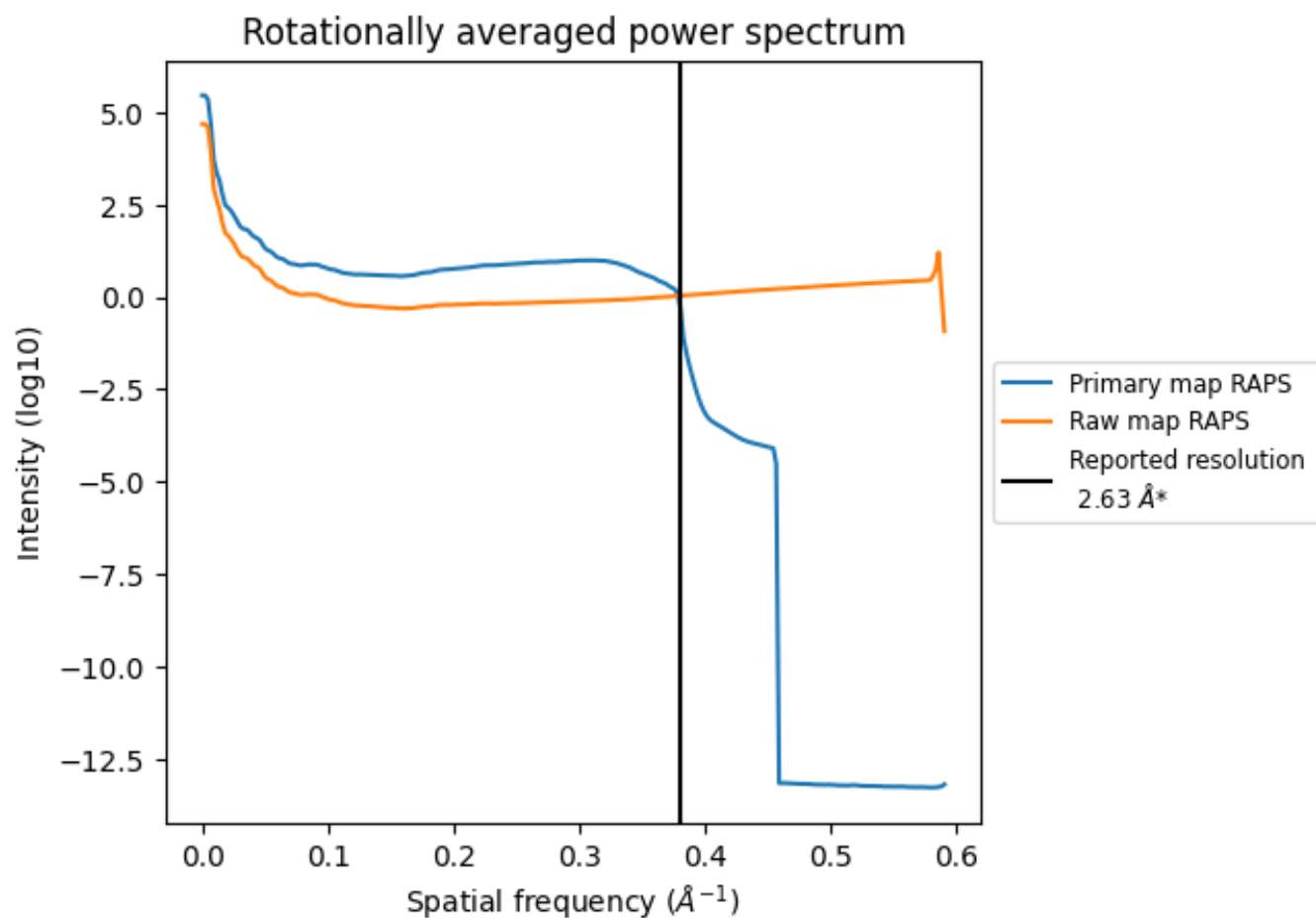
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 624 nm³; this corresponds to an approximate mass of 564 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 ⓘ

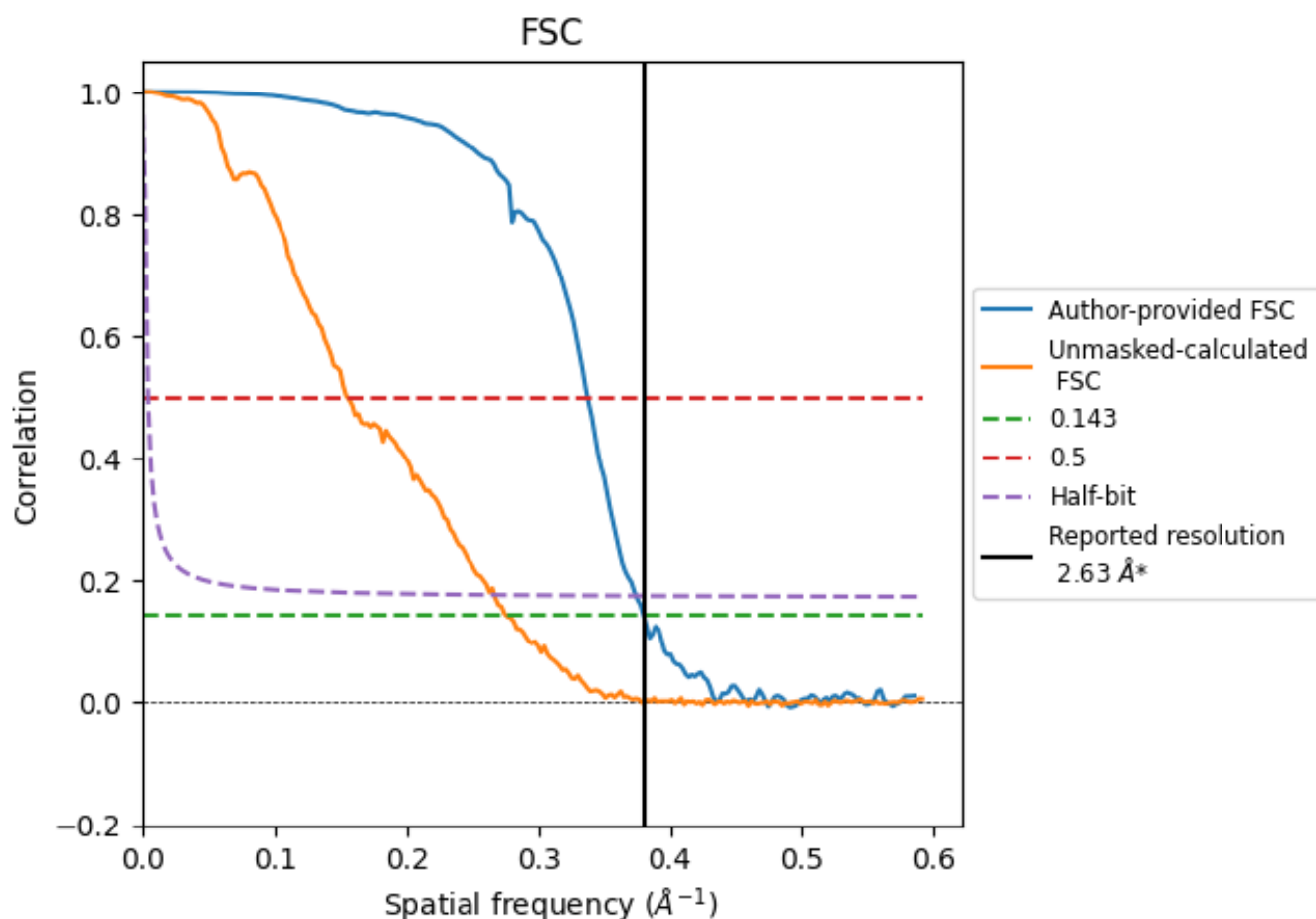


*Reported resolution corresponds to spatial frequency of 0.380 Å⁻¹

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 0.380 \AA^{-1}

8.2 Resolution estimates [i](#)

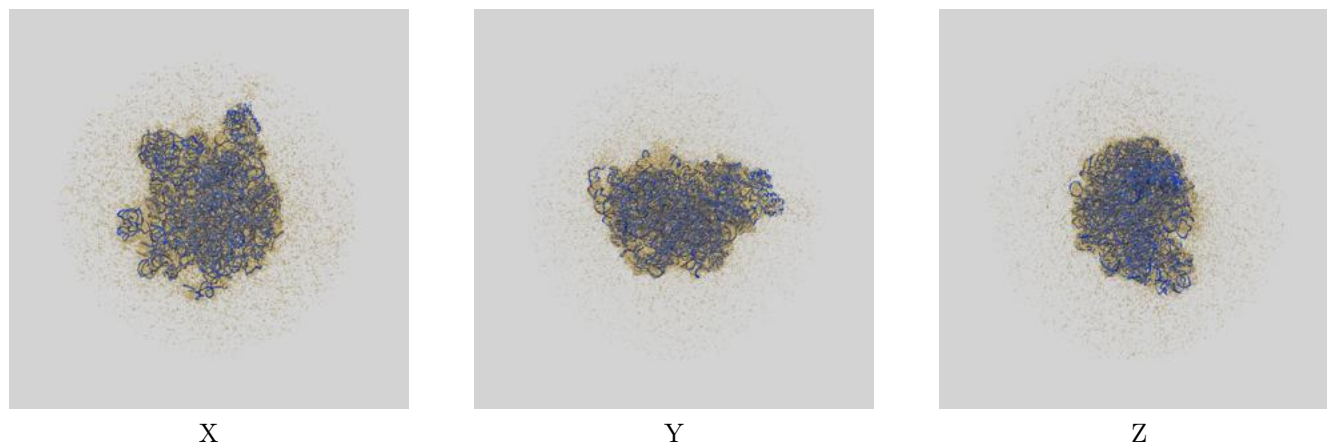
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.63	-	-
Author-provided FSC curve	2.63	2.96	2.67
Unmasked-calculated*	3.62	6.43	3.75

*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 3.62 differs from the reported value 2.63 by more than 10 %

9 Map-model fit [i](#)

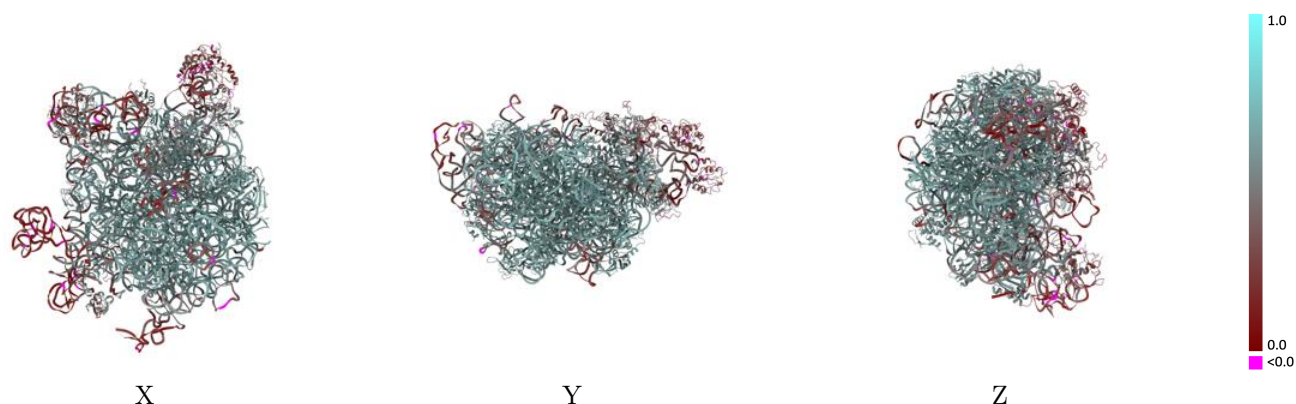
This section contains information regarding the fit between EMDB map EMD-43409 and PDB model 8VPK. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



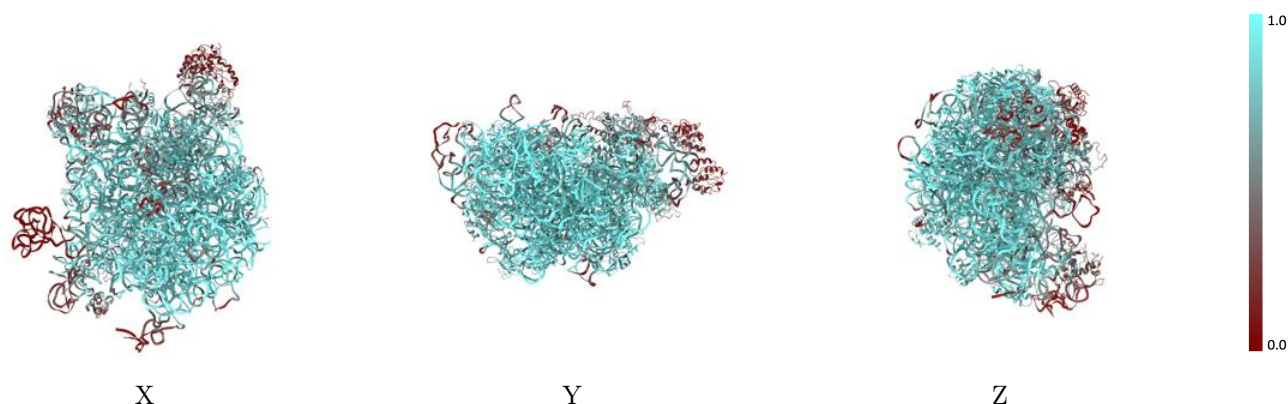
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



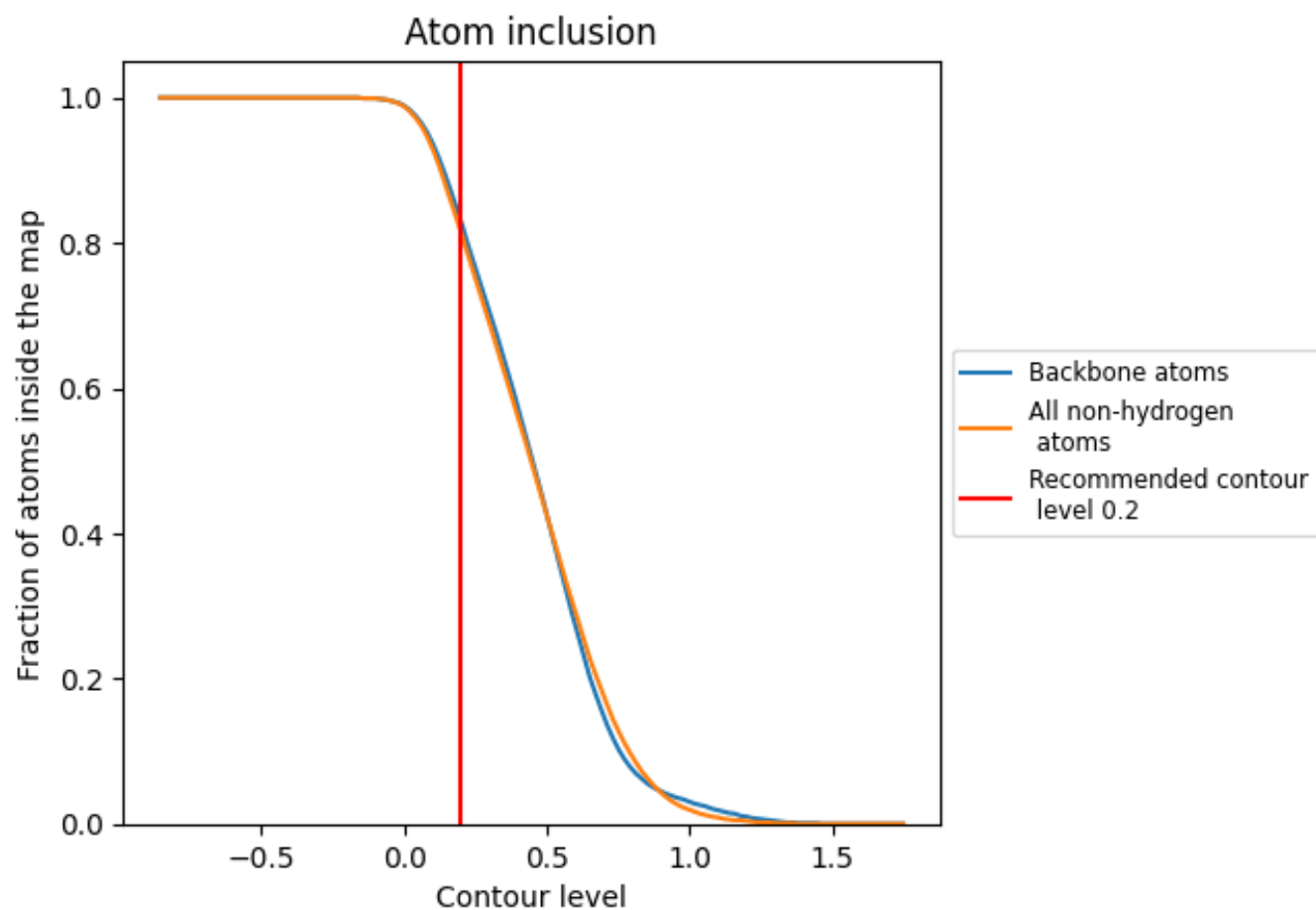
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).









































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8140	 0.5300
2	 0.9300	 0.6410
3	 0.9390	 0.6360
4	 0.5770	 0.4460
A	 0.8370	 0.5260
B	 0.7490	 0.4250
C	 0.9000	 0.6130
D	 0.9200	 0.6250
E	 0.8890	 0.6120
F	 0.5250	 0.4180
G	 0.7030	 0.4970
H	 0.5310	 0.4640
I	 0.1820	 0.2760
J	 0.1650	 0.2540
K	 0.9390	 0.6320
L	 0.9040	 0.6170
M	 0.8830	 0.6010
N	 0.9180	 0.6220
O	 0.9360	 0.6260
P	 0.8010	 0.5330
Q	 0.8300	 0.5890
R	 0.9480	 0.6360
S	 0.9440	 0.6390
T	 0.9300	 0.6300
U	 0.8650	 0.5960
V	 0.8070	 0.5690
W	 0.7450	 0.5410
X	 0.9310	 0.6370
Y	 0.9140	 0.6090
Z	 0.8390	 0.5970
b	 0.9030	 0.6170
c	 0.8730	 0.6020
d	 0.9570	 0.6370
e	 0.9690	 0.6370
f	 0.9440	 0.6310
g	 0.3530	 0.3220

