



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 04:30 AM UTC

PDB ID : 5ZET / pdb_00005zet
EMDB ID : EMD-6922
Title : M. smegmatis P/P state 50S ribosomal subunit
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on : 2018-02-28
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

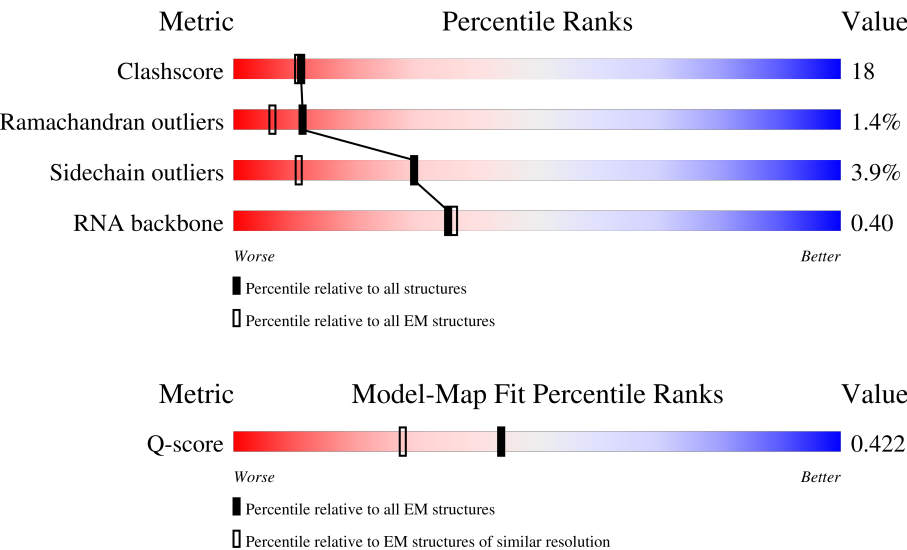
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



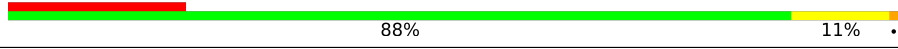
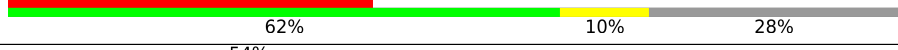
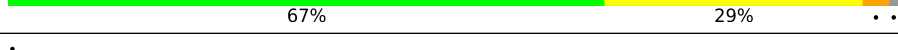
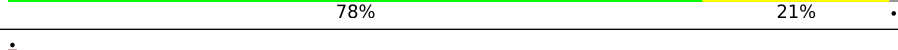
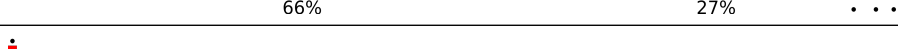
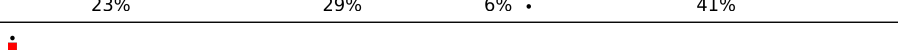
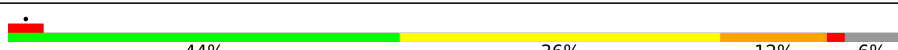
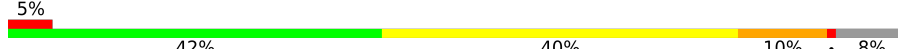
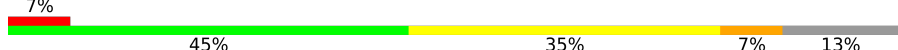
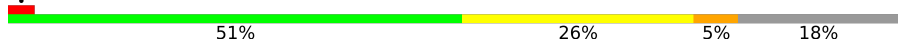
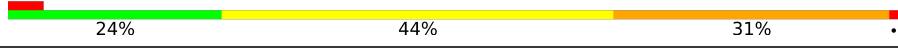
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	C	278	56%36%...
2	D	217	81%16%..
3	E	215	53%39%...

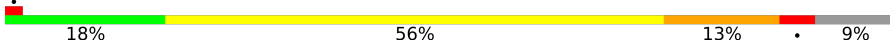
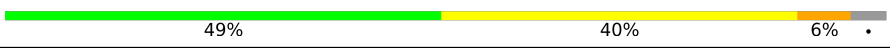
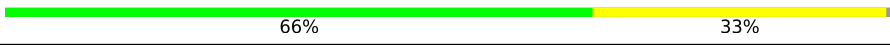
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Mol	Chain	Length	Quality of chain
4	F	187	
5	G	179	
6	H	151	
7	I	175	
8	J	142	
9	K	147	
10	L	122	
11	M	147	
12	N	138	
13	O	199	
14	P	127	
15	Q	113	
16	R	129	
17	S	103	
18	T	153	
19	U	100	
20	V	105	
21	W	215	
22	X	88	
23	Y	64	
24	Z	77	
25	B	118	
26	A	3120	
27	1	61	
28	2	75	

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Mol	Chain	Length	Quality of chain
29	3	57	
30	4	55	
31	5	47	
32	6	64	
33	7	37	
34	8	24	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 97374 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

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

- Molecule 8 is a protein called 50S ribosomal protein L11.

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

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	147	Total	C	N	O	S	0	0
			1138	727	208	201	2		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	134	Total	C	N	O	S	0	0
			1074	680	211	181	2		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	S	102	Total	C	N	O	0	0
			768	487	140	141		

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	U	94	Total	C	N	O	0	0
			739	469	135	135		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	V	97	Total	C	N	O	S	0
			731	456	137	136	2	0

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	W	188	Total	C	N	O	0	0
			1407	869	251	287		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	X	82	Total	C	N	O	0	0
			604	372	127	105		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 25 is a RNA chain called P-tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	1	60	Total	C	N	O	0	0
			483	298	97	88		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	6	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

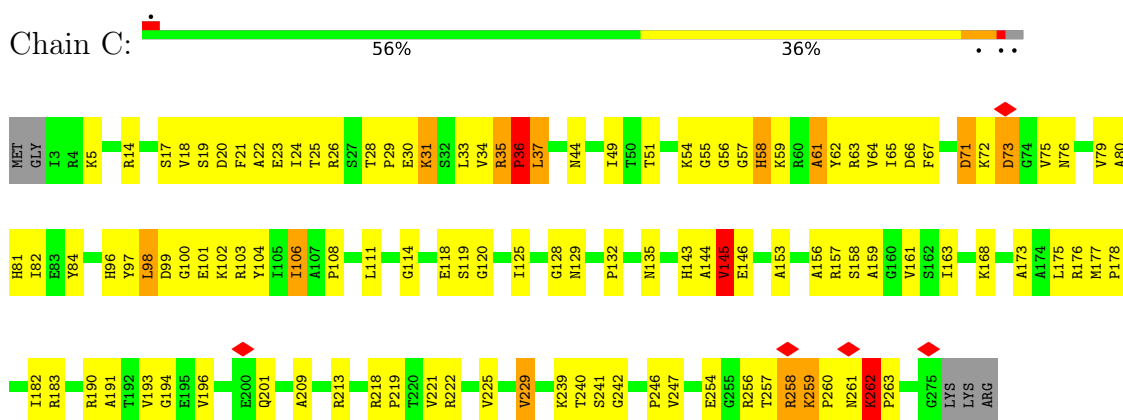
- Molecule 34 is a protein called Uncharacterized protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	8	23	Total	C	N	O	0	0
			189	111	50	28		

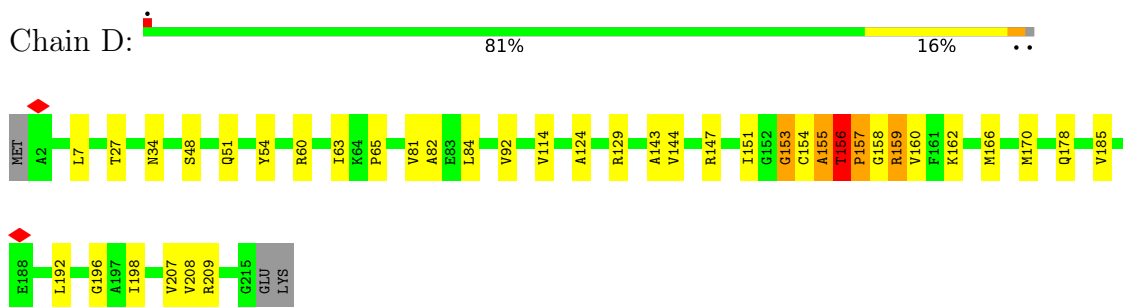
3 Residue-property plots

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

- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

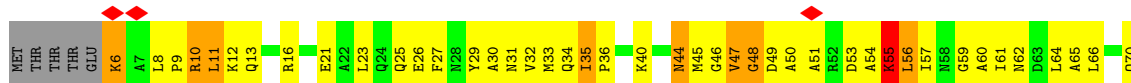


- Molecule 3: 50S ribosomal protein L4

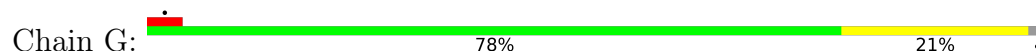




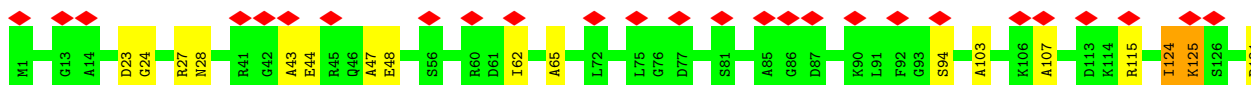
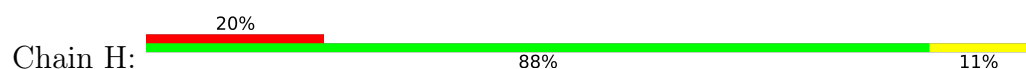
• Molecule 4: 50S ribosomal protein L5



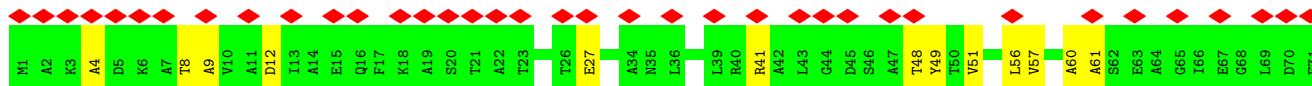
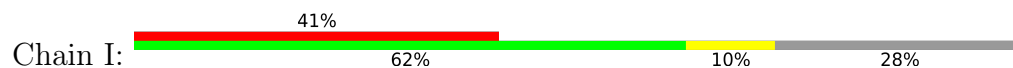
• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9

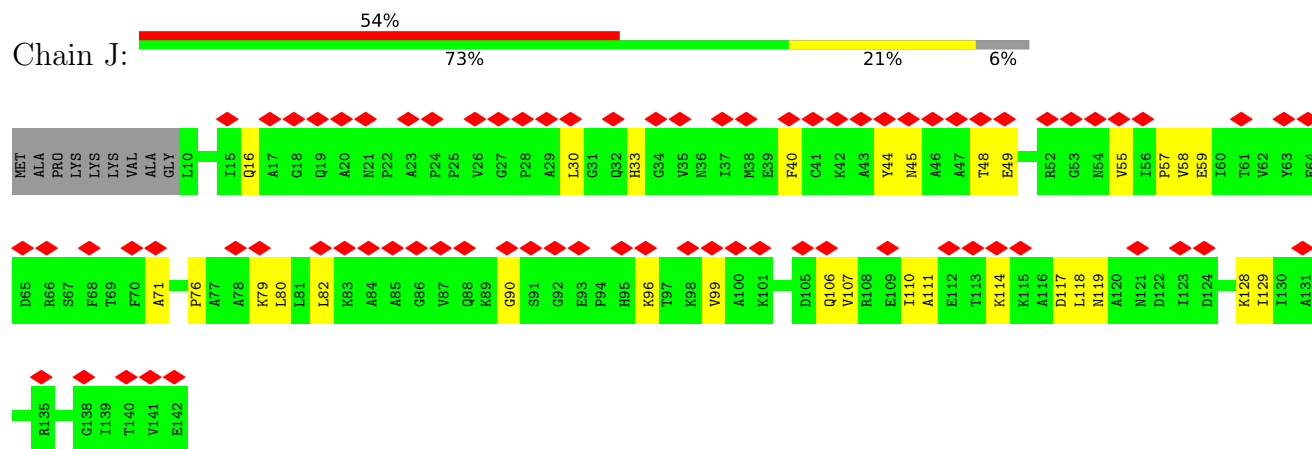


• Molecule 7: 50S ribosomal protein L10

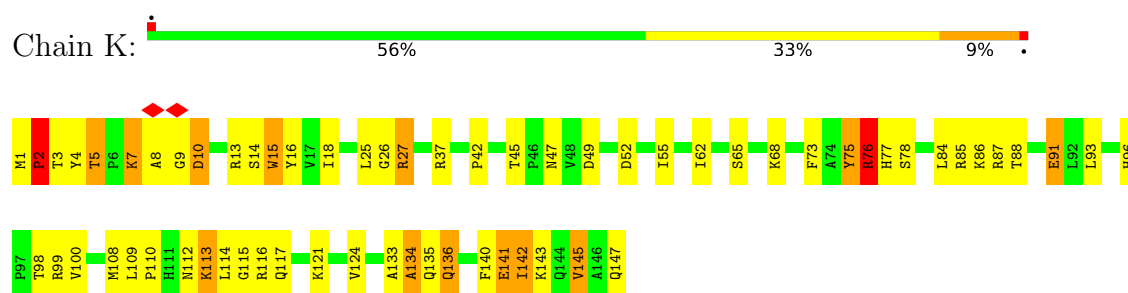


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GLY
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GLY
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SER
GLN
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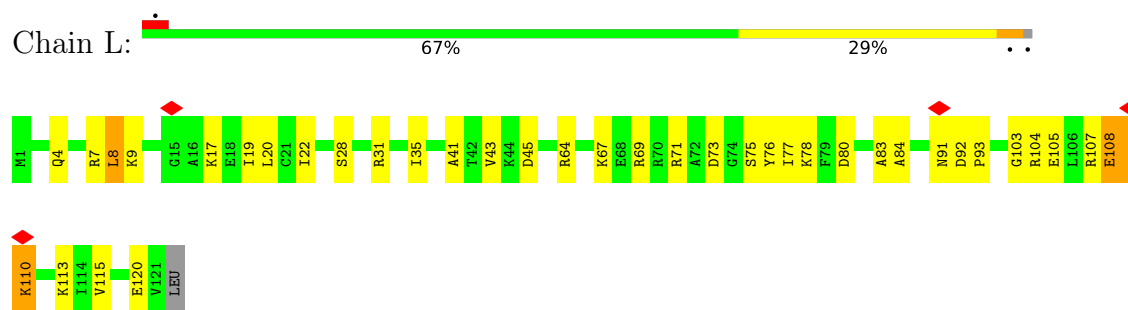
• Molecule 8: 50S ribosomal protein L11



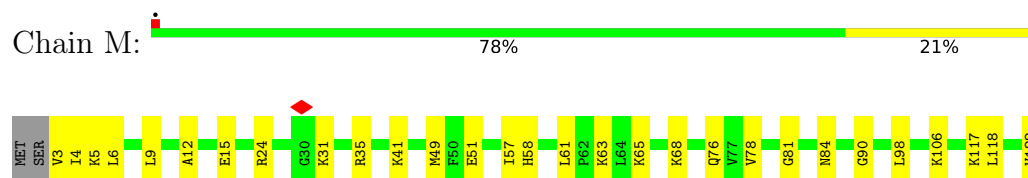
• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

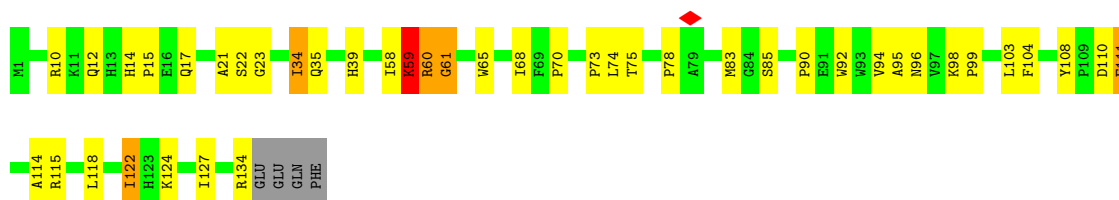


• Molecule 11: 50S ribosomal protein L15

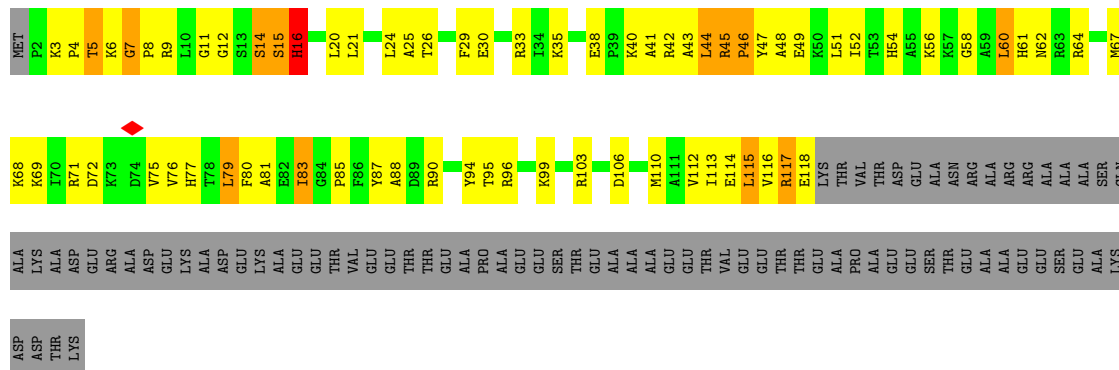
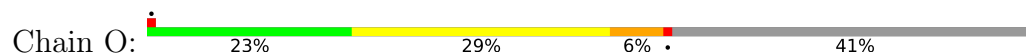


• Molecule 12: 50S ribosomal protein L16

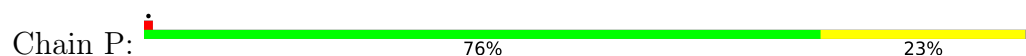




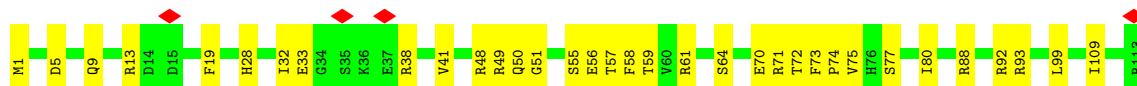
• Molecule 13: 50S ribosomal protein L17



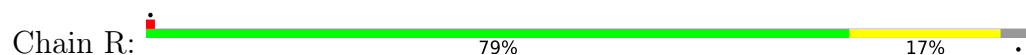
• Molecule 14: 50S ribosomal protein L18



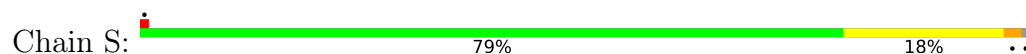
• Molecule 15: 50S ribosomal protein L19

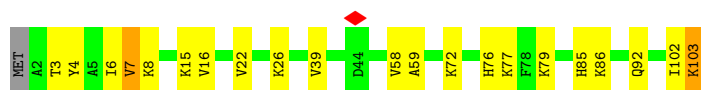


• Molecule 16: 50S ribosomal protein L20

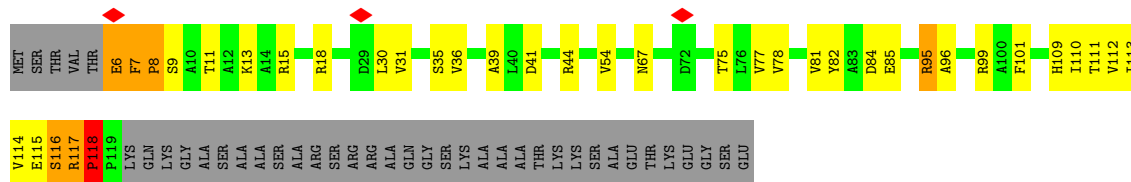


• Molecule 17: 50S ribosomal protein L21

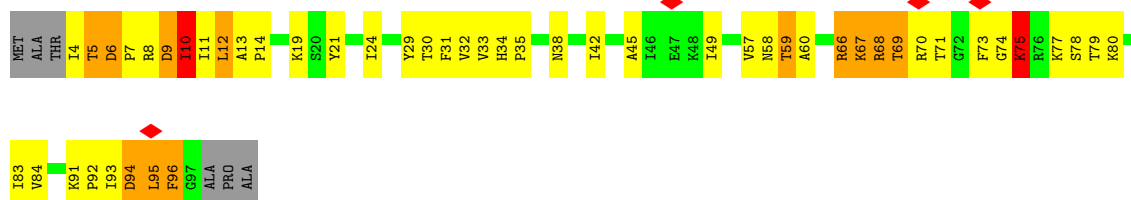




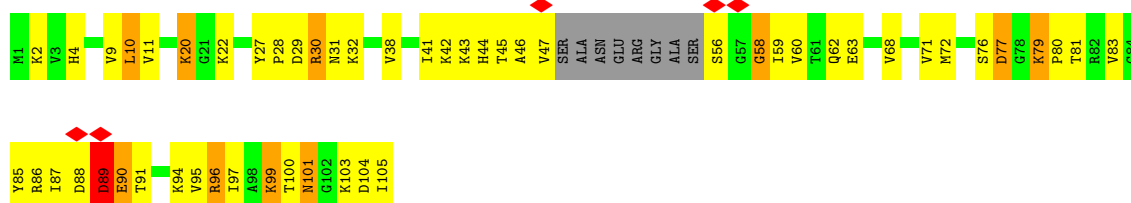
- Molecule 18: 50S ribosomal protein L22



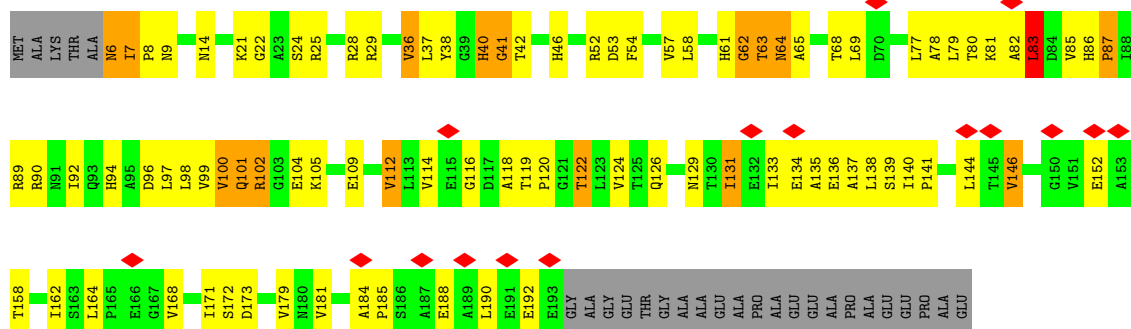
- Molecule 19: 50S ribosomal protein L23



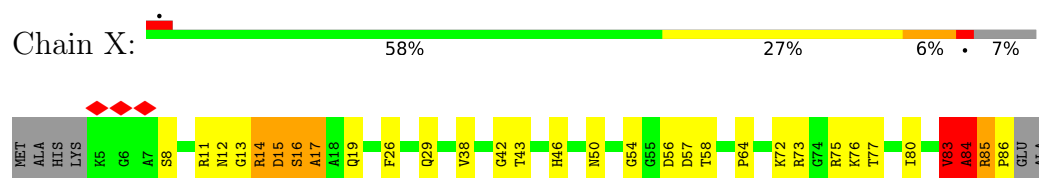
- Molecule 20: 50S ribosomal protein L24



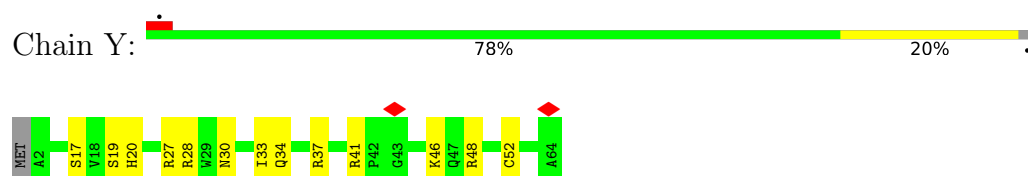
- Molecule 21: 50S ribosomal protein L25



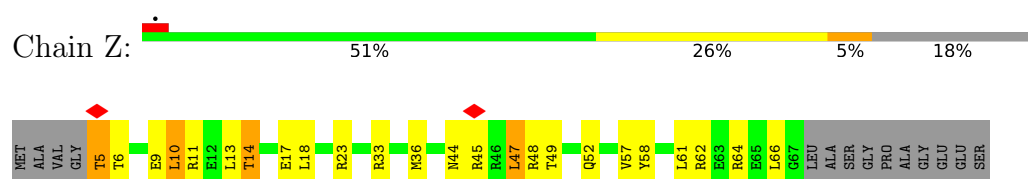
- Molecule 22: 50S ribosomal protein L27



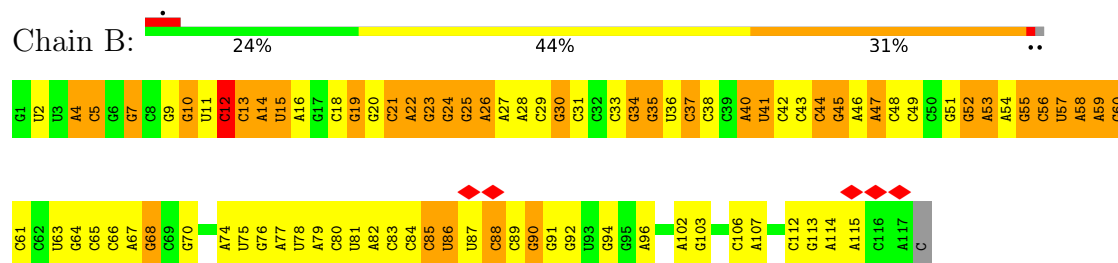
- Molecule 23: 50S ribosomal protein L28



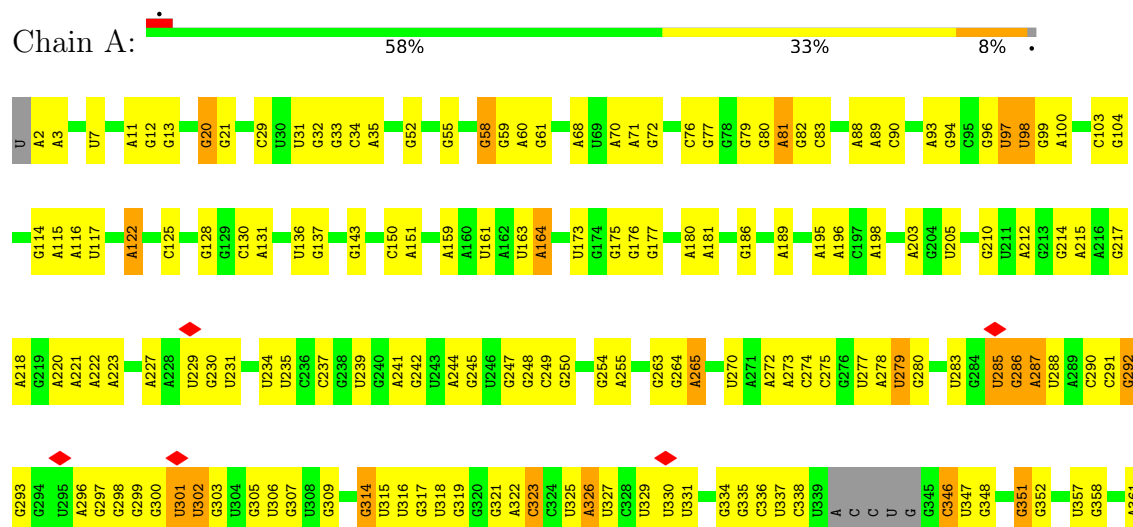
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: P-tRNA^{fMet}



- Molecule 26: 23S rRNA





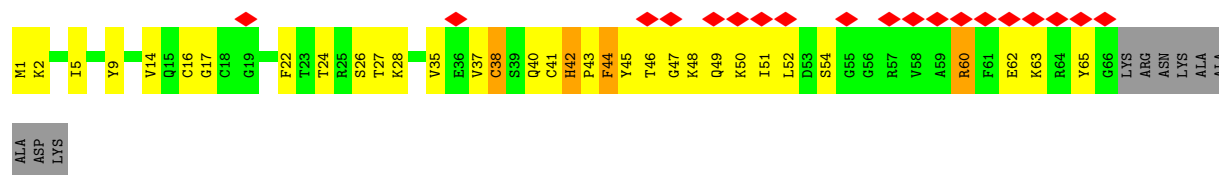
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U2906	C2907	C2908	U2908	C2909	U2913	A2914	C2915	A2926	G2932	C2933	C2936	C2937	C2938	G2942	C2950	C2956	U2963	U2964	C2965	C2966	A2967	U2968	A2969	C2976	A2977	U2980	A2981	A2982	C2985	U2986	A2987	C2988	C2989	A2990	U2993	U2994	U2995	G3001	A3002	C3003	C3004	A3005	U3009	U3010									
G2798	C2799	G2800	A2801	C2802	C2803	U2810	A2814	C2815	G2708	G2713	G2714	U2715	G2718	U2833	U2837	A2838	U2839	C2843	U2851	U2852	C2853	U2860	U2861	G2862	G2865	A2866	C2870	U2873	C2876	U2877	A2878	C2879	U2880	A2881	C2885	A2886	G2887	G2888	C2891	G2892	C2893	A2894	C2895	C2896	G2897	C2900							
G2694	C2698	C2699	A2700	U2701	A2702	G2705	G2708	G2713	G2714	U2715	G2718	G2726	G2729	G2737	A2742	U2743	C2744	C2745	U2746	C2747	G2750	G2753	A2754	A2755	G2756	C2757	A2758	C2759	C2764	G2781	C2782	G2783	C2784	A2785	U2786	U2787	A2788	C2789	A2790	C2791	C2792	G2793	G2794	C2795	A2796	C2797							
C2610	U2611	A2612	G2613	U2614	G2615	A2616	U2617	C2618	U2626	U2627	C2628	U2629	A2630	G2631	G2634	A2635	G2640	U2643	C2644	U2647	C2648	A2649	C2650	C2651	G2652	C2653	U2655	A2658	C2659	C2665	C2666	C2667	G2668	C2669	G2670	G2671	A2672	U2673	C2676	A2677	G2678	G2682	U2686	U2687	C2689	A2693							
A2511	A2512	U2515	U2516	C2517	A2522	C2527	C2528	A2529	C2530	U2531	C2532	U2536	C2537	A2538	C2539	U2540	C2545	A2546	C2547	U2548	C2549	U2550	A2551	C2557	C2558	A2559	C2560	U2567	C2571	C2574	C2575	U2578	A2582	U2585	C2586	A2593	C2594	U2595	C2596	A2601	C2507	C2508	C2509	A2609									
U2418	A2421	A2422	C2423	C2424	G2427	C2431	G2432	U2433	A2434	U2435	A2436	G2446	C2449	C2450	A2451	U2453	U2457	G2458	U2468	A2471	C2472	U2473	G2476	U2482	C2485	U2486	C2487	A2490	A2497	A2498	C2499	G2500	A2501	A2502	G2503	G2506	C2507	C2508	C2509	A2510	U2411	U2412	G2413	G2414									
G2348	A2349	C2350	A2351	U2353	C2354	U2355	G2356	A2357	A2358	U2361	C2362	A2363	C2364	A2365	C2366	G2367	C2368	G2371	U2374	G2375	C2376	G2377	U2378	C2379	G2380	A2381	C2382	U2383	C2384	C2385	U2386	U2387	G2388	U2389	U2390	G2391	A2392	A2393	A2394	U2395	A2396	U2403	G2404	A2405	U2406	C2407	G2408	U2409	A2410	U2411	U2412	G2413	G2414
A2244	C2245	U2246	A2247	G2251	A2255	G2256	A2257	G2263	C2267	G2276	C2279	G2280	A2284	G2285	A2286	C2287	C2288	C2289	C2299	U2309	U2315	G2316	G2317	U2318	C2319	G2320	U2321	C2322	G2323	A2324	U2325	A2326	C2327	G2328	G2329	U2334	G2335	A2337	G2338	G2339	A2340	U2341	A2342	G2343	G2346	G2347							
G2127	G2130	G2131	A2137	C2138	U2139	U2141	A2142	A2143	C2144	A2151	A2152	G2153	G2154	A2160	A2161	U2163	U2167	A2176	U2179	A2190	C2191	G2192	A2193	A2194	U2195	G2196	C2206	C2211	A2212	U2215	G2216	U2217	C2220	A2221	C2224	C2230	C2236	A2237	A2238	A2239													
A2019	A2020	C2025	C2026	A2027	G2028	G2031	A2032	U2033	C2043	A2046	G2052	G2059	G2062	G2063	A2064	A2070	A2071	A2072	A2073	G2074	G2075	U2081	U2082	A2083	A2084	C2085	U2086	C2087	C2088	C2089	U2090	U2091	U2092	G2093	G2094	G2095	G2096	A2106	G2107	U2111	U2112	C2118	C2119	G2120	G2121	U2122							
A1790	A1791	A1792	U1798	A1803	G1804	G1805	A1806	C1813	A1826	C1830	A1836	G1837	G1845	A1850	G1851	A1852	A1853	U1854	A1855	C1856	U1857	A1858	G1863	A1864	A1865	C1866	G1869	U1870	A1871	A1872	U1875	A1876	U1877	G1878	A1882	A1885	A1886	A1887	G1892	C1893	U1898	U2015	G2016	C2017	G2018								
G1703	U1704	C1705	A1710	G1711	G1712	U1713	A1714	A1715	U1717	C1718	G1719	G1720	U1721	G1724	G1725	C1726	A1727	U1728	U1730	A1731	A1737	A1744	A1748	C1753	G1754	A1755	G	U	G1758	A1759	G1760	G1761	C1762	G1763	A1764	U1767	C1768	G1769	U1774	A1778	U1779	G1780	C1785	G1786	A1787	G1788	A1789						

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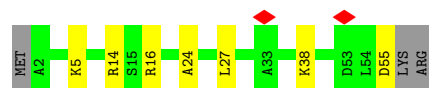
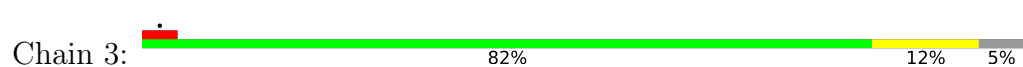
- Molecule 27: 50S ribosomal protein L30



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



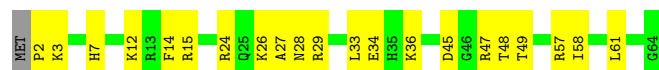
- Molecule 30: 50S ribosomal protein L33 1



- Molecule 31: 50S ribosomal protein L34



- Molecule 32: 50S ribosomal protein L35



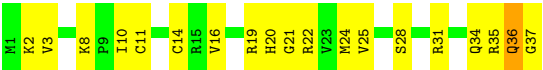
- Molecule 33: 50S ribosomal protein L36

Chain 7:

49%

49%

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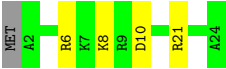
● Molecule 34: Uncharacterized protein bL37

Chain 8:

79%

17%

.



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.781	Depositor
Minimum map value	-0.495	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	361.19998, 361.19998, 361.19998	wwPDB
Map dimensions	344, 344, 344	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	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	1.01	0/2140	1.16	14/2879 (0.5%)
2	D	0.53	0/1609	0.77	2/2165 (0.1%)
3	E	0.86	0/1576	1.06	3/2132 (0.1%)
4	F	0.63	0/1459	1.13	14/1962 (0.7%)
5	G	0.31	0/1369	0.60	0/1848
6	H	0.30	0/1027	0.69	2/1398 (0.1%)
7	I	0.22	0/925	0.56	0/1246
8	J	0.27	0/1006	0.71	0/1364
9	K	0.80	0/1165	1.21	16/1578 (1.0%)
10	L	0.89	0/938	1.12	6/1257 (0.5%)
11	M	0.49	0/1091	0.72	0/1457
12	N	0.92	0/1100	1.19	7/1482 (0.5%)
13	O	0.84	1/936 (0.1%)	1.33	16/1256 (1.3%)
14	P	0.38	0/966	0.62	0/1298
15	Q	0.46	0/921	0.70	0/1236
16	R	0.51	0/1000	0.64	0/1341
17	S	0.44	0/778	0.63	0/1048
18	T	0.95	1/887 (0.1%)	1.16	7/1204 (0.6%)
19	U	0.75	0/749	1.04	4/1006 (0.4%)
20	V	0.66	0/737	1.05	4/987 (0.4%)
21	W	0.65	1/1422 (0.1%)	1.18	9/1941 (0.5%)
22	X	0.92	0/613	1.04	1/821 (0.1%)
23	Y	0.52	0/478	0.77	0/641
24	Z	0.69	0/530	0.92	0/708
25	B	0.32	0/2797	0.55	1/4357 (0.0%)
26	A	0.48	0/74597	0.51	4/116386 (0.0%)
27	1	0.84	0/486	1.00	1/651 (0.2%)
28	2	0.40	0/520	0.84	1/698 (0.1%)
29	3	0.54	0/427	0.70	0/572
30	4	0.71	0/424	1.05	2/567 (0.4%)
31	5	0.95	0/375	1.34	4/493 (0.8%)
32	6	1.00	0/507	1.03	1/672 (0.1%)
33	7	0.85	0/302	1.02	0/401
34	8	0.46	0/191	0.75	0/247

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.54	3/106048 (0.0%)	0.65	119/159299 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	4
2	D	0	2
3	E	0	5
4	F	0	1
9	K	0	1
12	N	0	1
13	O	0	1
18	T	0	1
22	X	0	2
All	All	0	18

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	W	7	ILE	C-N	6.25	1.39	1.33
18	T	117	ARG	C-N	5.74	1.40	1.33
13	O	45	ARG	C-N	5.50	1.40	1.34

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	W	62	GLY	N-CA-C	19.02	133.80	111.93
12	N	61	GLY	N-CA-C	14.65	128.50	111.36
21	W	61	HIS	CA-C-N	11.66	131.18	120.10
21	W	61	HIS	C-N-CA	11.66	131.18	120.10
4	F	117	ARG	N-CA-C	10.63	122.86	111.28

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	ALA	Peptide
1	C	229	VAL	Peptide

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Mol	Chain	Res	Type	Group
1	C	246	PRO	Peptide
1	C	61	ALA	Peptide
2	D	153	GLY	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2097	0	2147	212	0
2	D	1587	0	1629	70	0
3	E	1553	0	1587	149	0
4	F	1437	0	1463	212	0
5	G	1348	0	1399	26	0
6	H	1018	0	988	12	0
7	I	918	0	959	13	0
8	J	990	0	1021	28	0
9	K	1138	0	1174	119	0
10	L	930	0	989	58	0
11	M	1078	0	1151	46	0
12	N	1074	0	1116	67	0
13	O	919	0	959	158	0
14	P	956	0	989	41	0
15	Q	907	0	938	31	0
16	R	988	0	1038	20	0
17	S	768	0	820	48	0
18	T	873	0	909	54	0
19	U	739	0	777	123	0
20	V	731	0	782	114	0
21	W	1407	0	1423	159	0
22	X	604	0	622	56	0
23	Y	470	0	484	9	0
24	Z	527	0	537	56	0
25	B	2501	0	1269	294	0
26	A	66623	0	33514	1038	0
27	1	483	0	513	22	0
28	2	510	0	497	60	0
29	3	423	0	463	12	0
30	4	416	0	421	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	5	372	0	406	41	0
32	6	502	0	541	31	0
33	7	298	0	320	26	0
34	8	189	0	205	4	0
All	All	97374	0	64050	2879	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 18.

The worst 5 of 2879 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)
17:S:3:THR:CG2	17:S:102:ILE:HD13	1.26	1.66
19:U:83:ILE:HD11	26:A:1456:G:C2	1.14	1.64
26:A:1561:C:C4	26:A:1562:C:C5	1.86	1.62
26:A:1565:A:N3	26:A:1606:G:C5	1.69	1.60
17:S:58:VAL:HG23	17:S:103:LYS:CG	1.24	1.60

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	271/278 (98%)	233 (86%)	33 (12%)	5 (2%)	6	34
2	D	212/217 (98%)	199 (94%)	11 (5%)	2 (1%)	14	47
3	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	24
4	F	179/187 (96%)	162 (90%)	15 (8%)	2 (1%)	11	43
5	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
6	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	18	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
8	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
9	K	145/147 (99%)	133 (92%)	9 (6%)	3 (2%)	5	31
10	L	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
11	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
12	N	132/138 (96%)	113 (86%)	19 (14%)	0	100	100
13	O	115/199 (58%)	102 (89%)	10 (9%)	3 (3%)	4	26
14	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
15	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
16	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
17	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	12	45
18	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	25
19	U	92/100 (92%)	70 (76%)	16 (17%)	6 (6%)	1	8
20	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	5	29
21	W	186/215 (86%)	171 (92%)	10 (5%)	5 (3%)	4	25
22	X	80/88 (91%)	61 (76%)	13 (16%)	6 (8%)	1	5
23	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
24	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	7	36
27	1	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
28	2	64/75 (85%)	61 (95%)	2 (3%)	1 (2%)	7	36
29	3	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
30	4	48/55 (87%)	37 (77%)	7 (15%)	4 (8%)	0	4
31	5	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
32	6	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
33	7	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	8	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	3623/3991 (91%)	3287 (91%)	285 (8%)	51 (1%)	11	39

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	58	HIS
1	C	145	VAL

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Mol	Chain	Res	Type
1	C	262	LYS
3	E	94	LYS
3	E	152	LYS

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	214/218 (98%)	204 (95%)	10 (5%)	23	57
2	D	160/163 (98%)	157 (98%)	3 (2%)	50	73
3	E	167/173 (96%)	158 (95%)	9 (5%)	20	53
4	F	150/156 (96%)	138 (92%)	12 (8%)	11	40
5	G	148/150 (99%)	147 (99%)	1 (1%)	76	83
6	H	90/116 (78%)	90 (100%)	0	100	100
7	I	89/120 (74%)	89 (100%)	0	100	100
8	J	102/108 (94%)	102 (100%)	0	100	100
9	K	120/120 (100%)	116 (97%)	4 (3%)	33	65
10	L	99/100 (99%)	98 (99%)	1 (1%)	68	80
11	M	112/114 (98%)	111 (99%)	1 (1%)	70	81
12	N	112/116 (97%)	107 (96%)	5 (4%)	24	58
13	O	96/158 (61%)	90 (94%)	6 (6%)	16	48
14	P	93/94 (99%)	93 (100%)	0	100	100
15	Q	100/100 (100%)	99 (99%)	1 (1%)	68	80
16	R	97/99 (98%)	97 (100%)	0	100	100
17	S	82/83 (99%)	81 (99%)	1 (1%)	63	79
18	T	90/117 (77%)	88 (98%)	2 (2%)	45	71
19	U	82/85 (96%)	71 (87%)	11 (13%)	4	19
20	V	81/86 (94%)	71 (88%)	10 (12%)	4	22
21	W	154/168 (92%)	137 (89%)	17 (11%)	6	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	X	59/63 (94%)	56 (95%)	3 (5%)	21	54
23	Y	50/51 (98%)	50 (100%)	0	100	100
24	Z	58/66 (88%)	55 (95%)	3 (5%)	21	54
27	1	53/54 (98%)	52 (98%)	1 (2%)	50	73
28	2	57/63 (90%)	54 (95%)	3 (5%)	20	53
29	3	43/46 (94%)	43 (100%)	0	100	100
30	4	48/52 (92%)	40 (83%)	8 (17%)	2	11
31	5	35/36 (97%)	34 (97%)	1 (3%)	37	67
32	6	53/54 (98%)	53 (100%)	0	100	100
33	7	35/35 (100%)	33 (94%)	2 (6%)	18	51
34	8	18/19 (95%)	18 (100%)	0	100	100
All	All	2947/3183 (93%)	2832 (96%)	115 (4%)	30	62

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	U	10	ILE
30	4	37	GLU
20	V	41	ILE
30	4	36	LEU
24	Z	47	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
19	U	58	ASN
27	1	42	GLN
21	W	46	HIS
22	X	79	ASN
28	2	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	B	116/118 (98%)	42 (36%)	3 (2%)
26	A	3096/3120 (99%)	788 (25%)	44 (1%)

Continued on next page...

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3212/3238 (99%)	830 (25%)	47 (1%)

5 of 830 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	B	4	A
25	B	5	C
25	B	7	G
25	B	10	G
25	B	12	C

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	A	1575	A
26	A	1590	G
26	A	1576	C
26	A	1579	C
26	A	1596	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 [i](#)

There are no chain breaks in this entry.

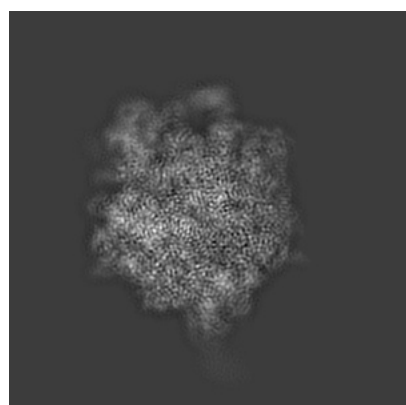
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6922. These allow visual inspection of the internal detail of the map and identification of artifacts.

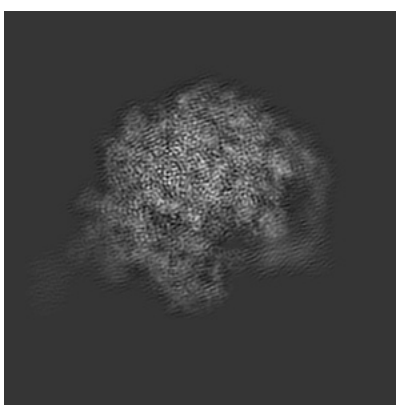
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

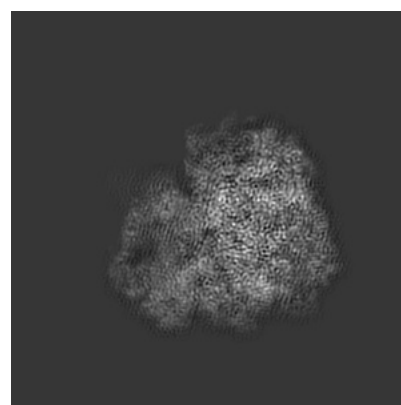
6.1.1 Primary map



X



Y

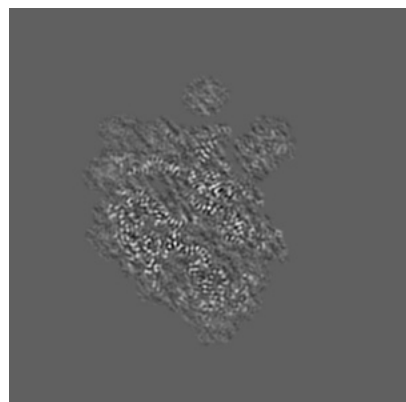


Z

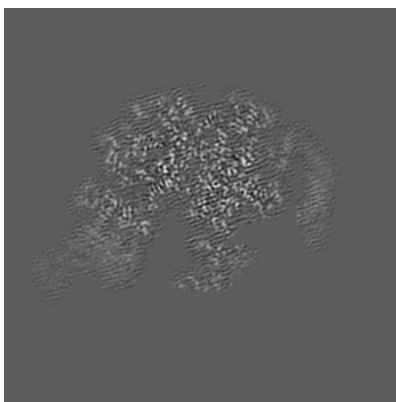
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

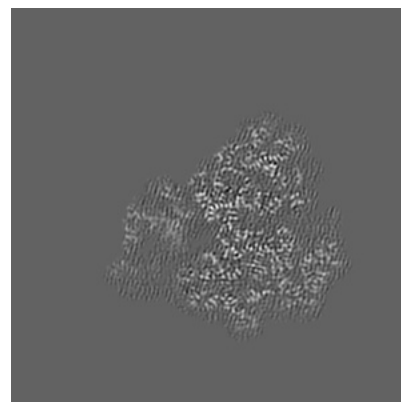
6.2.1 Primary map



X Index: 172



Y Index: 172

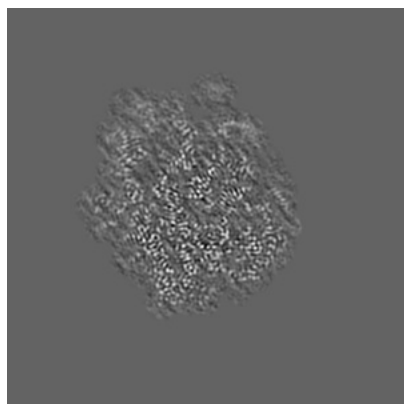


Z Index: 172

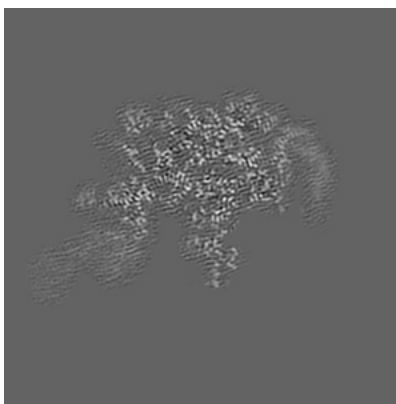
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

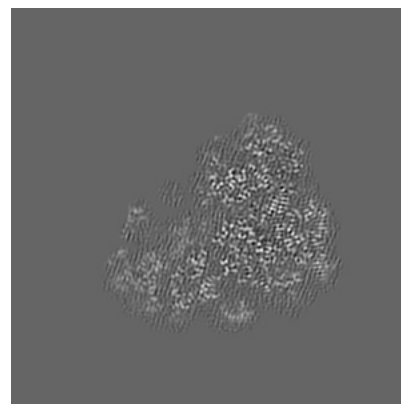
6.3.1 Primary map



X Index: 205



Y Index: 181

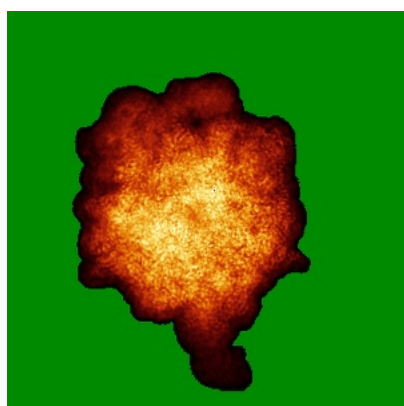


Z Index: 154

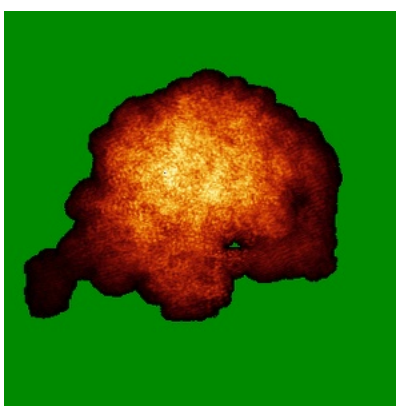
The images above show the largest variance slices of the map in three orthogonal directions.

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

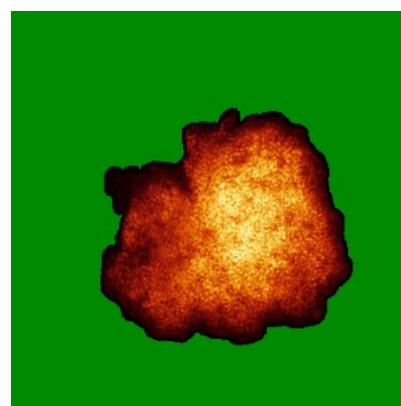
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

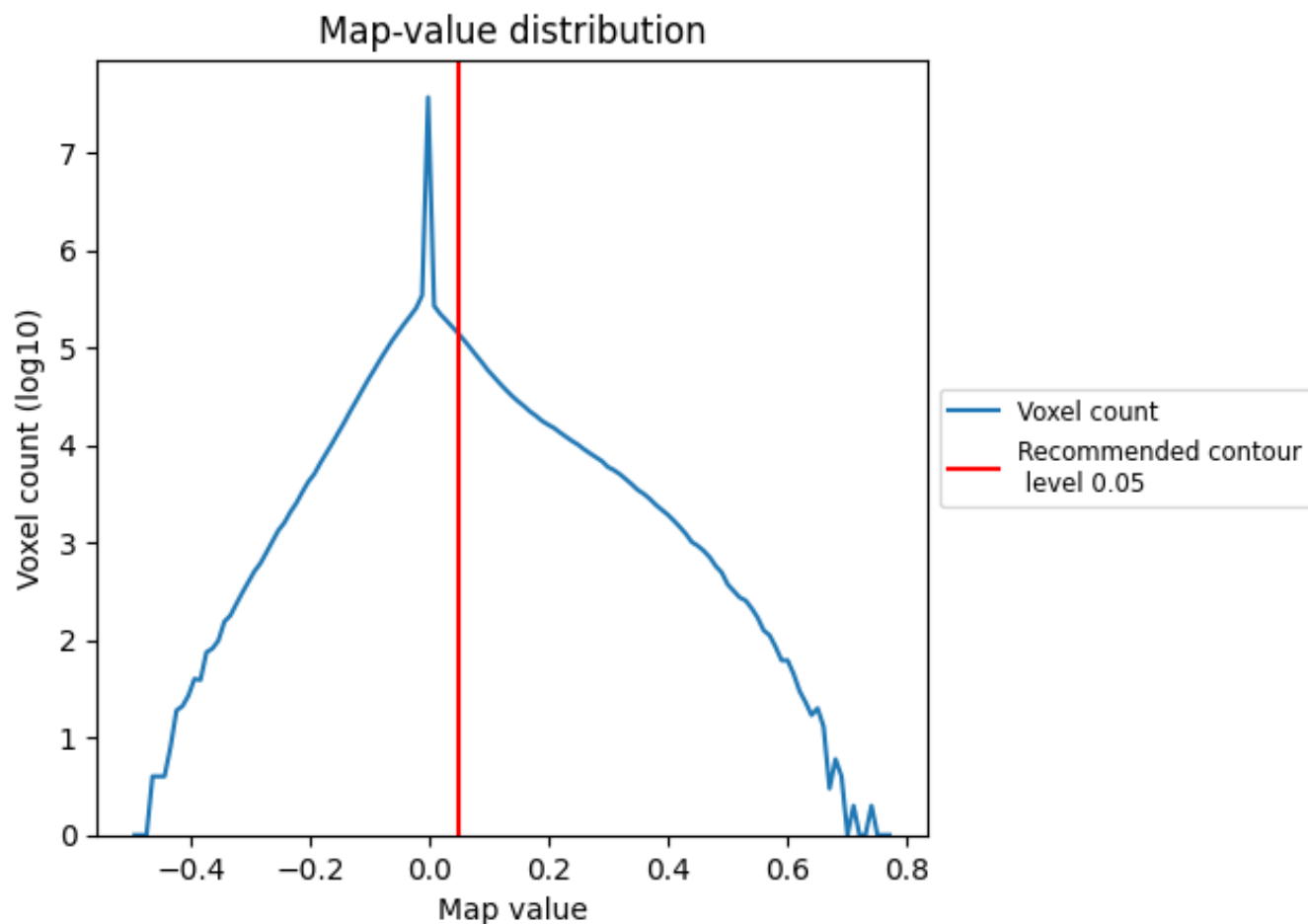
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

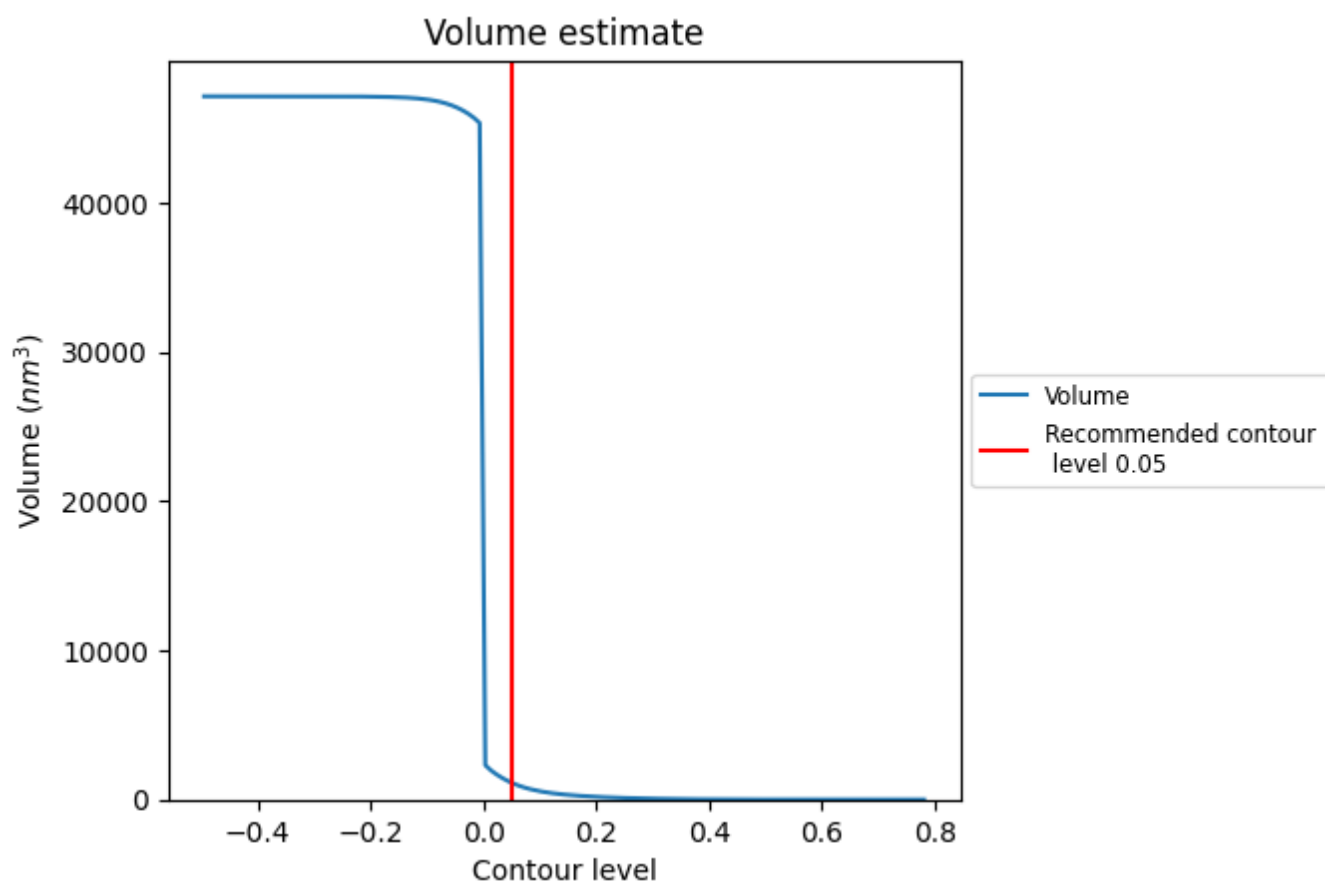
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

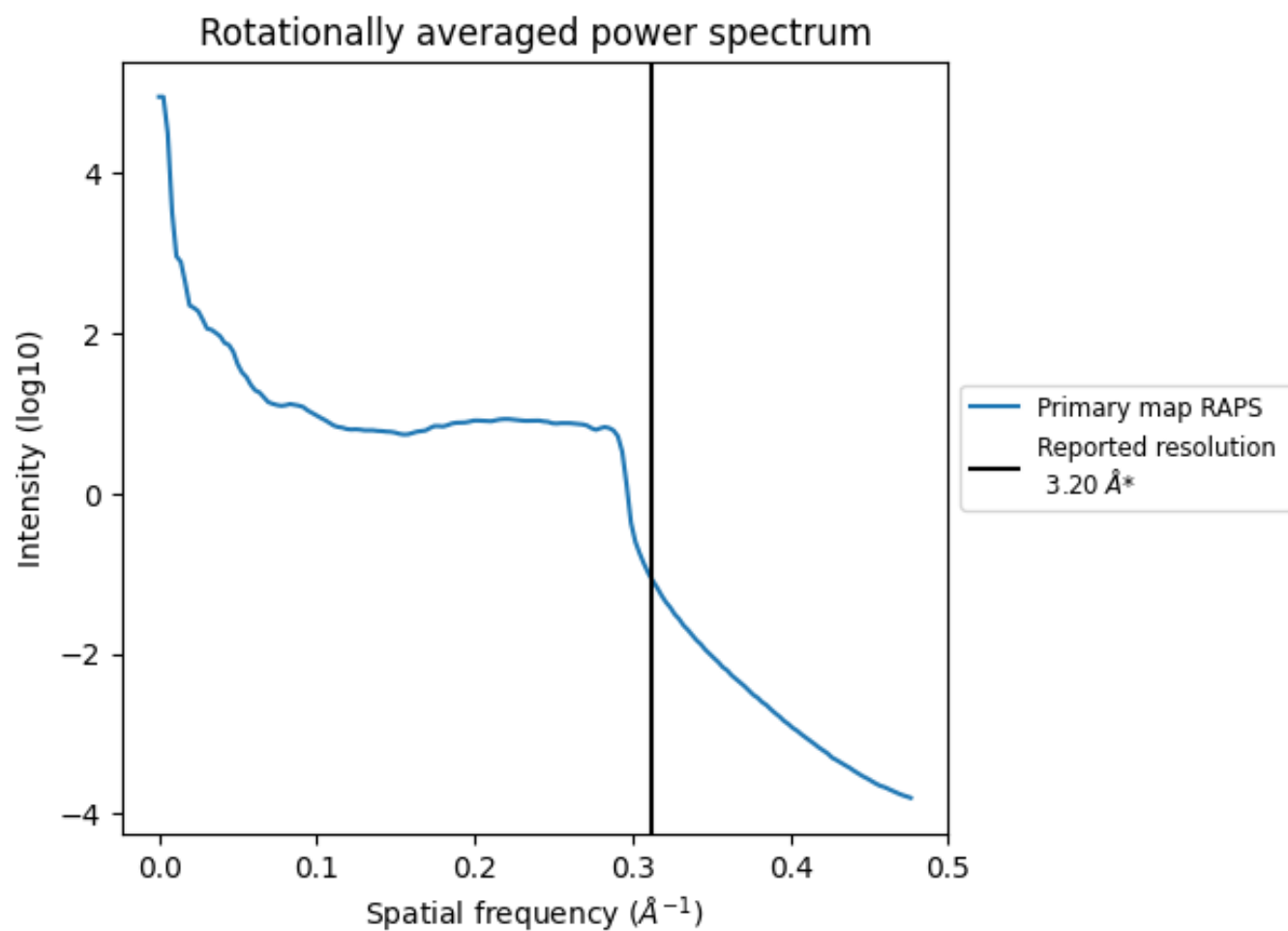
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1134 nm³; this corresponds to an approximate mass of 1024 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

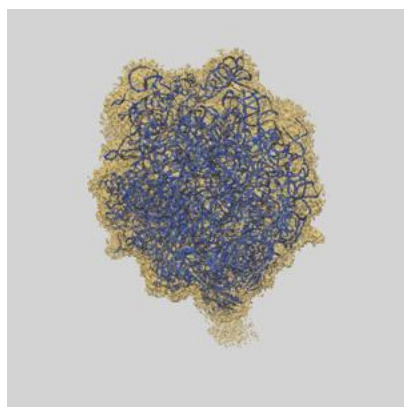
8 Fourier-Shell correlation

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

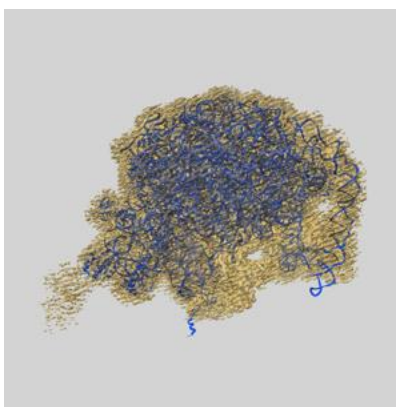
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6922 and PDB model 5ZET. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

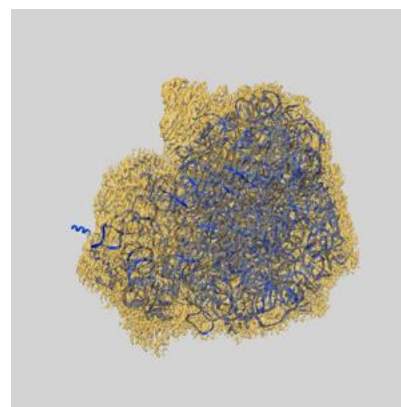
9.1 Map-model overlay [i](#)



X



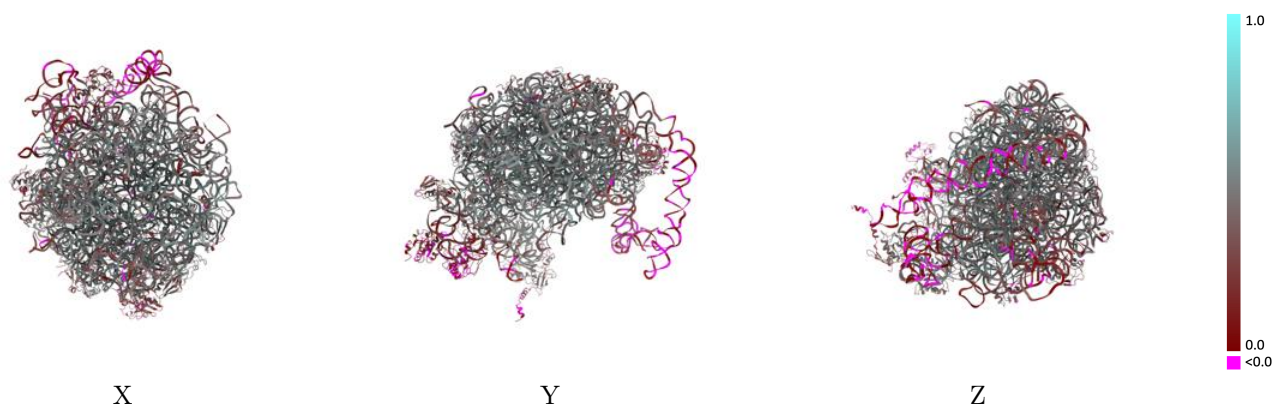
Y



Z

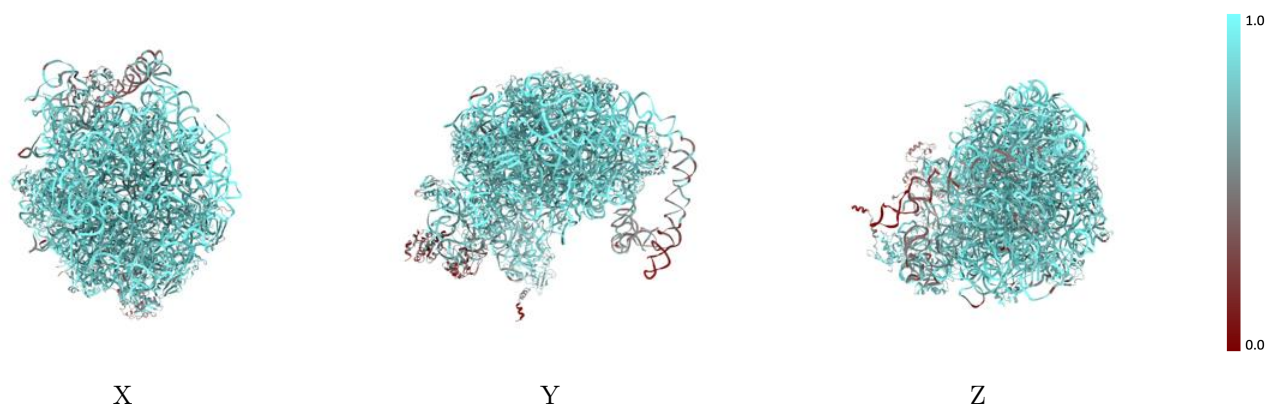
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



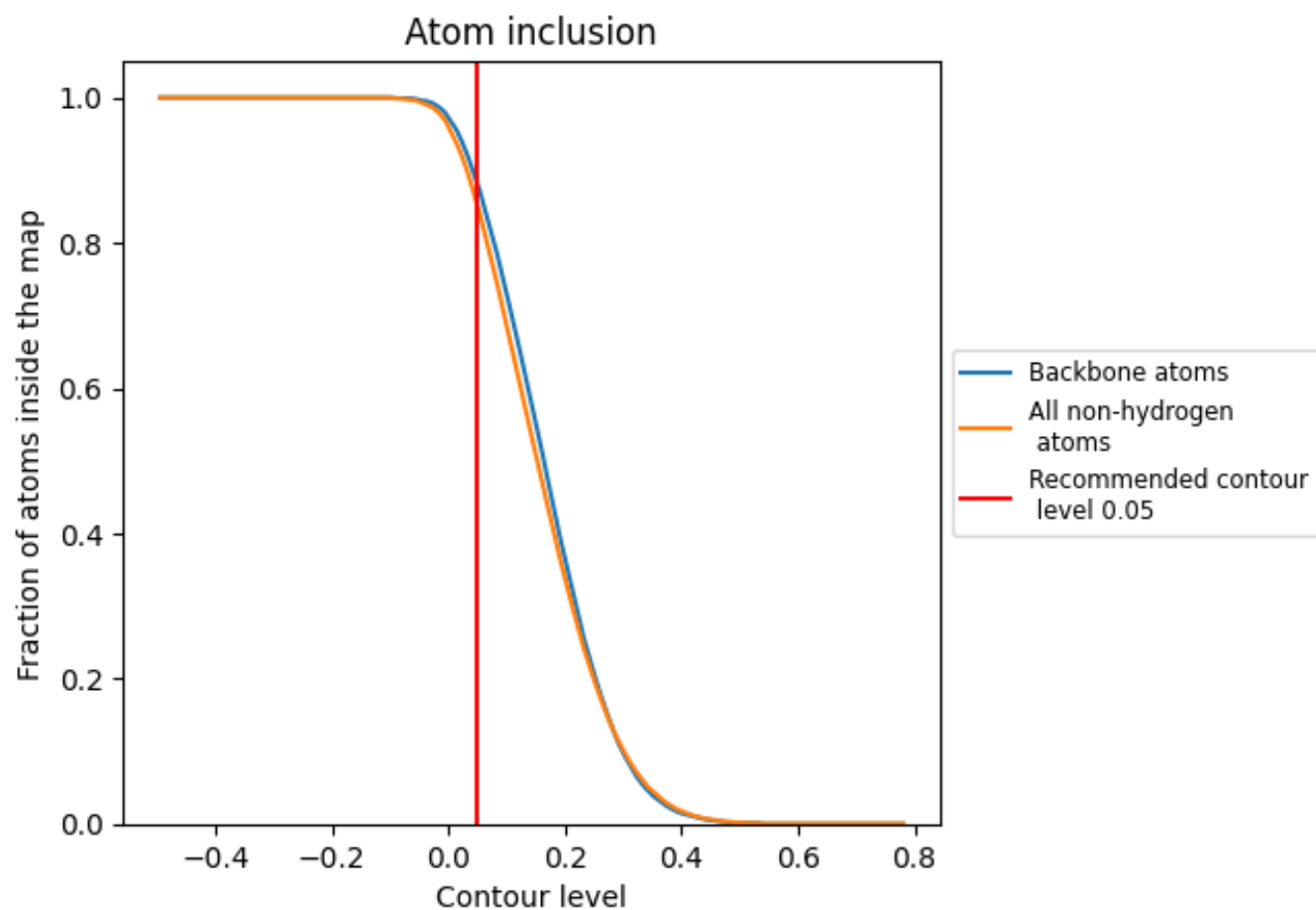
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.4220
1	 0.8210	 0.4500
2	 0.5390	 0.1850
3	 0.8360	 0.4500
4	 0.8040	 0.3790
5	 0.8610	 0.4740
6	 0.8690	 0.4850
7	 0.8810	 0.4790
8	 0.7930	 0.4410
A	 0.8820	 0.4320
B	 0.8620	 0.3920
C	 0.8530	 0.4810
D	 0.8520	 0.4720
E	 0.8200	 0.4230
F	 0.7930	 0.3790
G	 0.7670	 0.3570
H	 0.6300	 0.3000
I	 0.3450	 0.1310
J	 0.3720	 0.0990
K	 0.8400	 0.4650
L	 0.8260	 0.4500
M	 0.8220	 0.4320
N	 0.8410	 0.4600
O	 0.8220	 0.4380
P	 0.8330	 0.4300
Q	 0.8040	 0.4390
R	 0.8670	 0.4750
S	 0.8390	 0.4340
T	 0.8120	 0.4440
U	 0.7910	 0.4080
V	 0.7680	 0.3650
W	 0.6950	 0.3140
X	 0.8340	 0.4650
Y	 0.8370	 0.4520
Z	 0.8180	 0.4000

