



wwPDB EM Validation Summary Report ⓘ

Mar 31, 2025 – 06:27 PM JST

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:

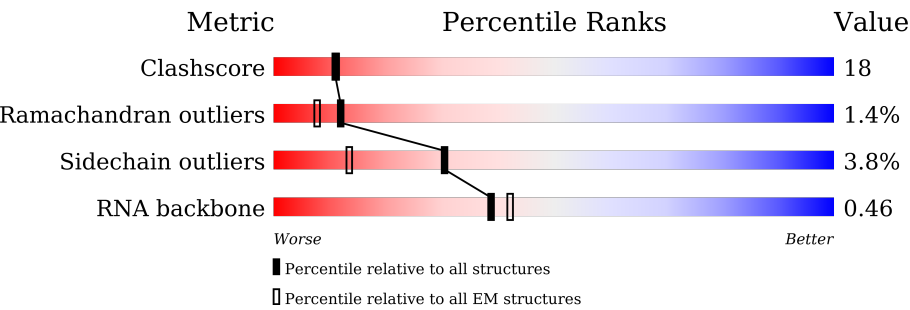
EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

1 Overall quality at a glance 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	C	278	<div><div>58%35%5%..</div></div>
2	D	217	<div><div>81%14%..</div></div>
3	E	215	<div><div>53%38%... </div></div>
4	F	187	<div><div>43%47%7%. </div></div>
5	G	179	<div><div>77%21%. </div></div>
6	H	151	<div><div>20%88%11%. </div></div>
7	I	175	<div><div>41%61%11%28%</div></div>

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Mol	Chain	Length	Quality of chain
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	
29	3	57	
30	4	55	
31	5	47	
32	6	64	

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Mol	Chain	Length	Quality of chain
33	7	37	<div><div></div><div>51%</div><div>46%</div><div></div></div>
34	8	24	<div><div></div><div>79%</div><div>17%</div><div></div></div>

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	0
			907	570	171	165	1		

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

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

- 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	0
			731	456	137	136	2		

- 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		

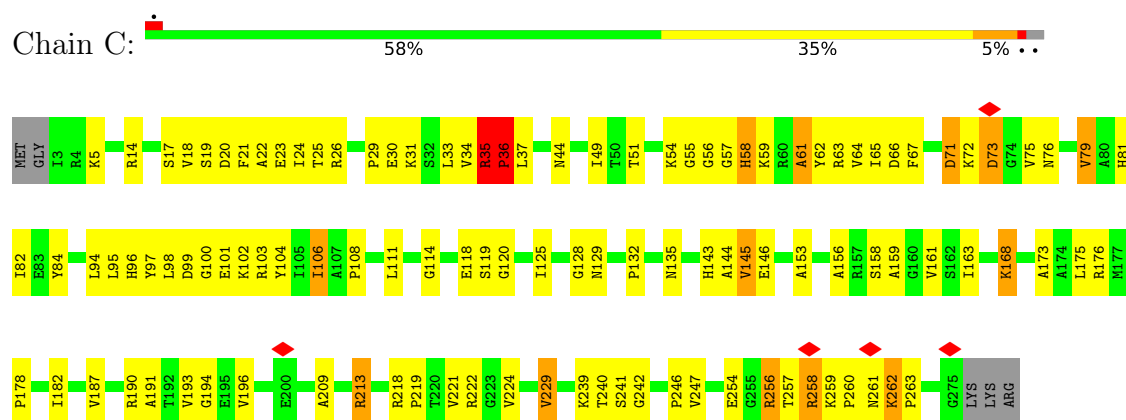
- Molecule 34 is a protein called Uncharacterized protein bL37.

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

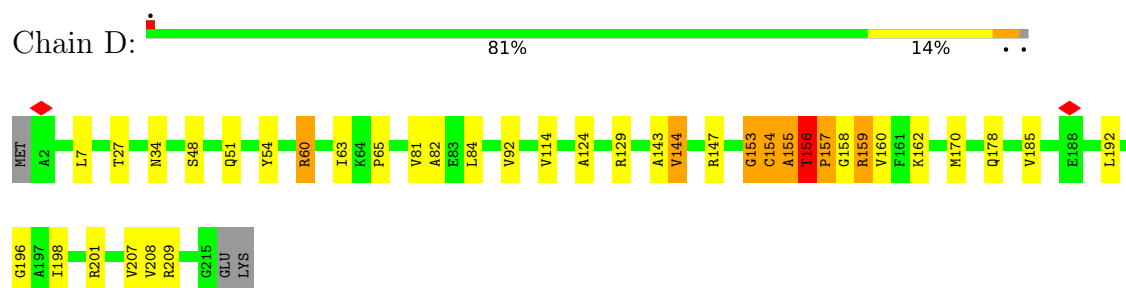
3 Residue-property plots

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.

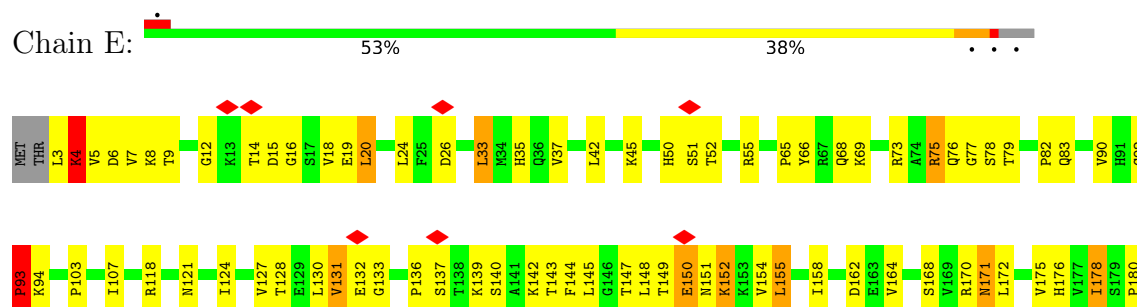
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3



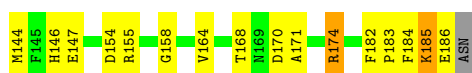
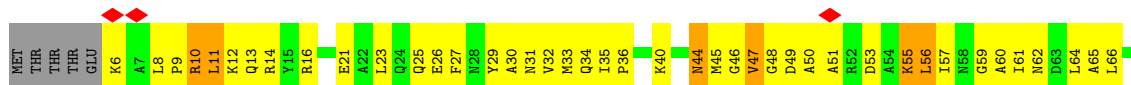
• Molecule 3: 50S ribosomal protein L4





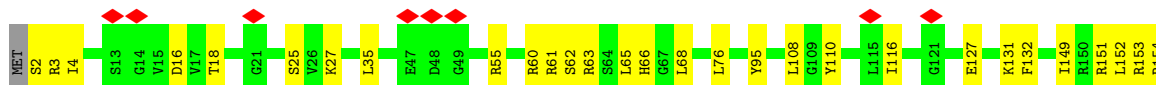
• Molecule 4: 50S ribosomal protein L5

Chain F: 43% 47% 7%



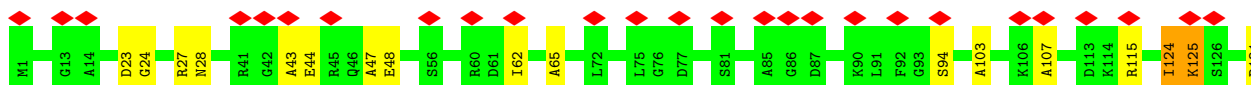
• Molecule 5: 50S ribosomal protein L6

Chain G: 77% 21%



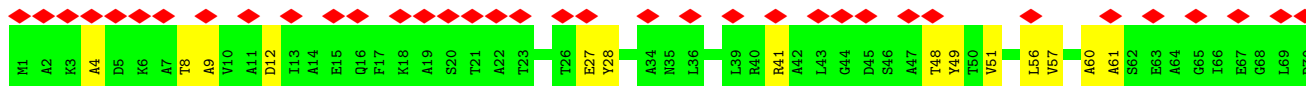
• Molecule 6: 50S ribosomal protein L9

Chain H: 20% 88% 11%



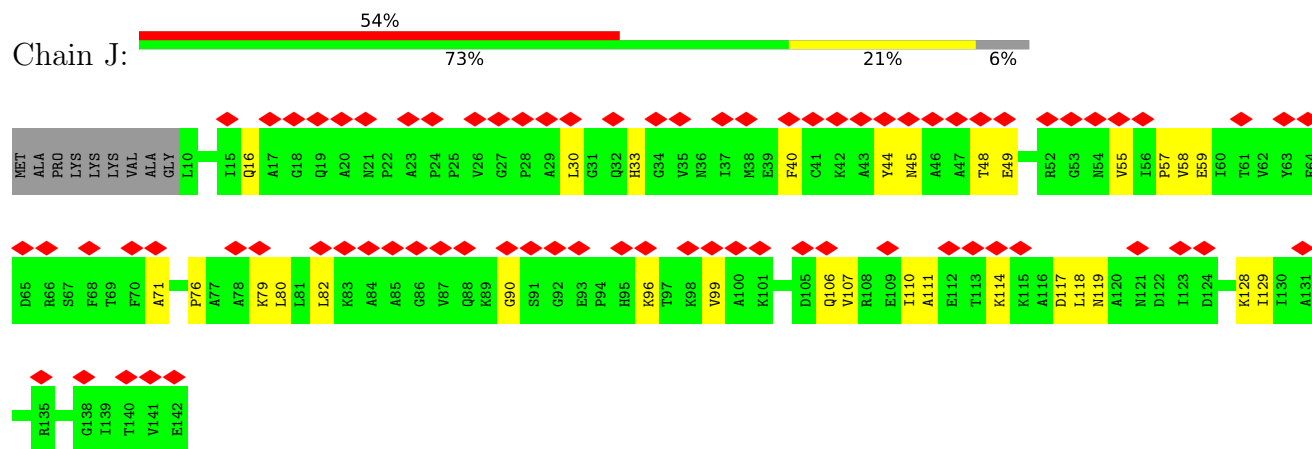
• Molecule 7: 50S ribosomal protein L10

Chain I: 41% 61% 11% 28%

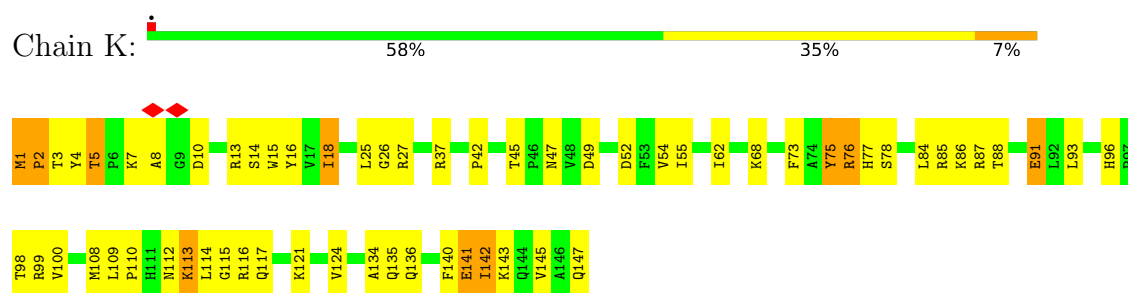


GLY
ALA
MET
LYS
GLY
ASN
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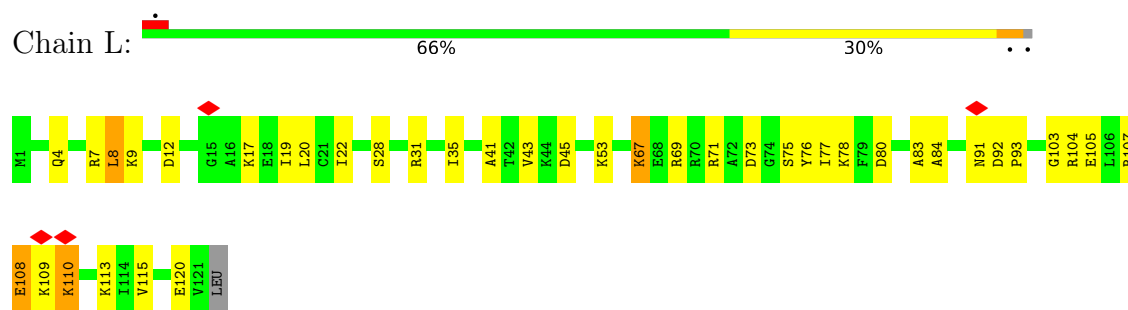
• Molecule 8: 50S ribosomal protein L11



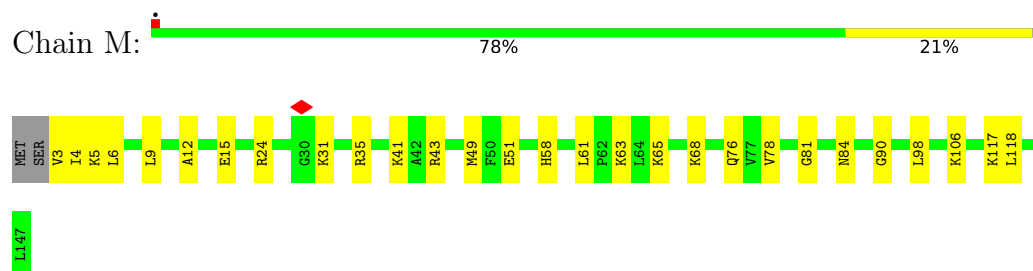
• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

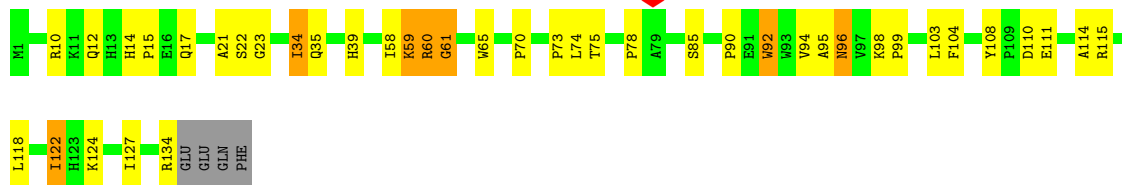


• Molecule 11: 50S ribosomal protein L15



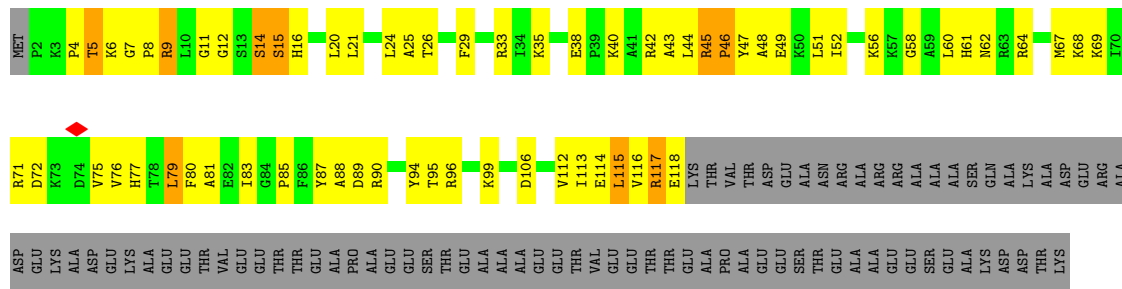
• Molecule 12: 50S ribosomal protein L16

Chain N: 67% 25% 5%



- Molecule 13: 50S ribosomal protein L17

Chain 0:



- Molecule 14: 50S ribosomal protein L18

Chain P: 77% 22%

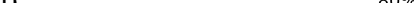


- Molecule 15: 50S ribosomal protein L19

Chain Q:  71% 28%



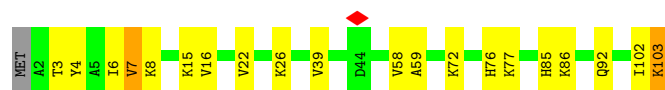
- Molecule 16: 50S ribosomal protein L20

Chain R:  80% 16% .

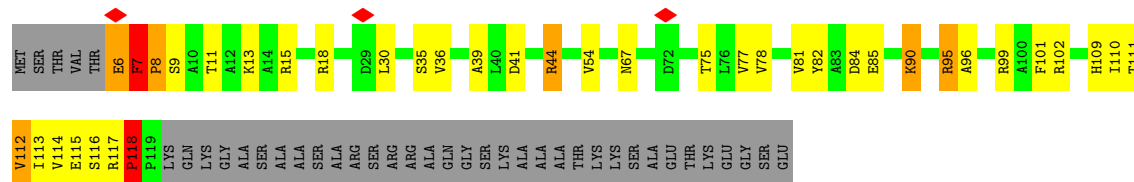


- Molecule 17: 50S ribosomal protein L21

Chain S: 80% 17% ..



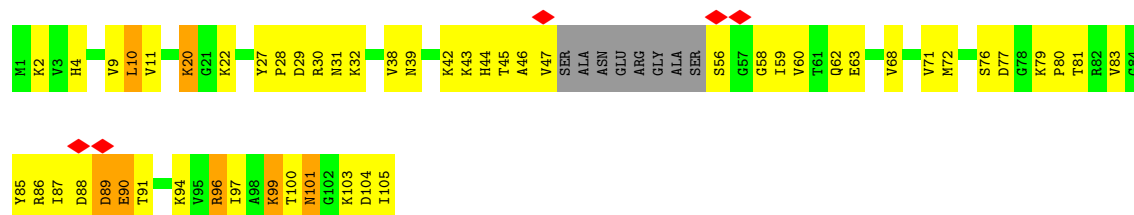
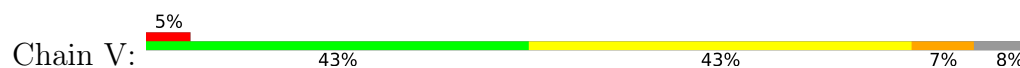
• Molecule 18: 50S ribosomal protein L22



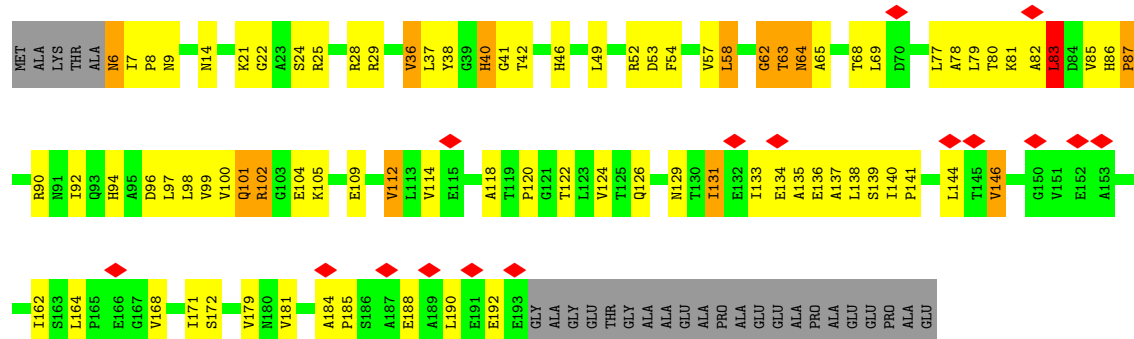
• Molecule 19: 50S ribosomal protein L23



• Molecule 20: 50S ribosomal protein L24

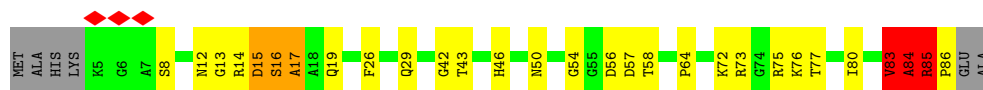


• Molecule 21: 50S ribosomal protein L25




- Molecule 22: 50S ribosomal protein L27

Chain X: 



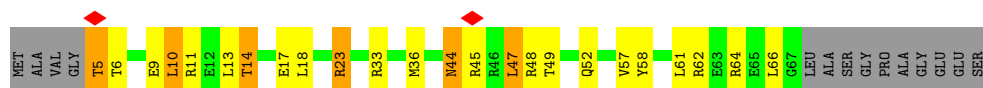
- Molecule 23: 50S ribosomal protein L28

Chain Y: 




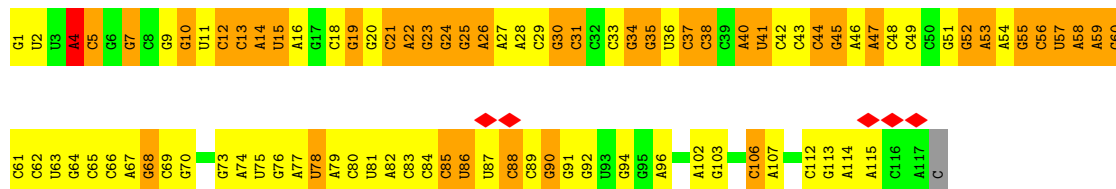
- Molecule 24: 50S ribosomal protein L29

Chain Z: 



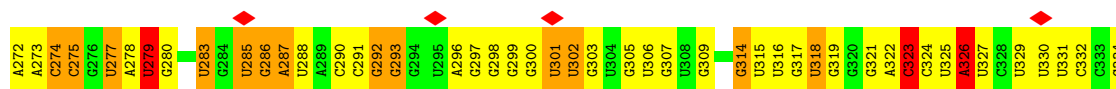
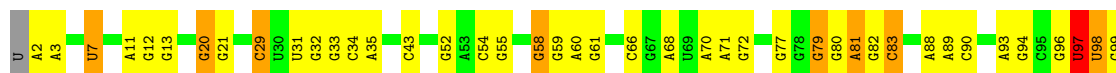
- Molecule 25: P-tRNA^{fMet}

Chain B: 

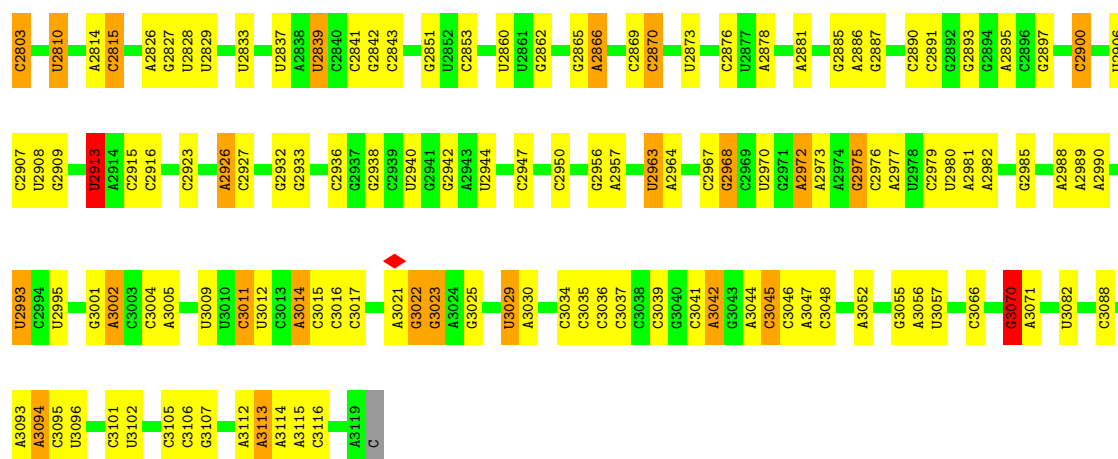


- Molecule 26: 23S rRNA

Chain A: 



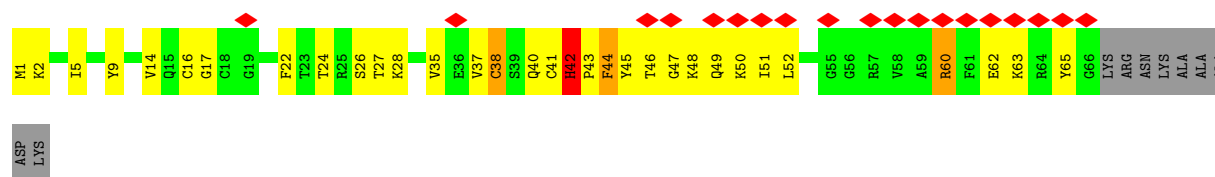
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G2713	G2653	G2545	U2453	U2378	U2309	C2211	U2111	G2014	G1917	C1818	A1729	G1650	C1586	
G2714	A2634	A2546	U2457	G2379	A2212	A2212	U2112	U2015	G1917	G1819	U1730	G1651	G1587	
U2715	A2635	G2547	G2458	G2380	U2315	U2215	C2116	G2017	G1921	C1822	A1731	G1654	G1588	
U2716	G2640	U2548	G2462	A2381	G2316	G2216	G2117	A2019	G1922	A1826	C1734	G1658	G1589	
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G2737	U2655	C2571	U2482	A2392	G2328	A2239	C2138	U2046	U	A1853	U	A1674	U1599	
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U2743	A2659	G2575	U2486	U2395	G2335	A2244	U2140	G2052	U	U1854	A1759	U1676	G1601	
C2745	C2745	A2578	C2487	A2396	U2336	A2245	U2141	G2052	A	A1855	G1760	G1676	U1602	
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G2747	C2667	A2582	A2497	U2403	G2338	A2247	C2144	C2060	C1954	A1858	G1763	A1680	G1604	
G2750	G2668	U2585	A2498	G2404	G2339	A2248	U2147	G2062	A1955	C1862	A1765	A1681	G1605	
C2751	G2669	G2586	G2499	A2405	A2340	C2248	A2151	G2063	A1956	G1863	U1767	U1688	G1606	
G2752	G2670	G2590	G2500	U2406	U2341	C2248	A2152	G2064	G1957	U1864	C1768	A1690	C1607	
G2753	C2671	G2593	G2501	C2407	A2342	C2248	A2160	C2064	C1958	A1865	G1769	A1691	U1608	
G2754	A2672	G2594	G2502	G2408	G2343	C2255	A2161	C2077	G1967	C1866	U1774	C1692	C1610	
A2755	U2673	G2594	G2503	U2409	G2346	A2257	G2153	A2070	G1970	C1869	C1775	C1693	U1611	
G2756	G2676	G2595	A2510	U2410	G2347	A2257	U2155	A2071	C1971	U1870	U1778	U1695	A1612	
C2757	A2677	G2596	A2511	U2411	G2348	C2260	G2158	G2073	C1972	A1871	U1779	G1696	G1613	
U2758	G2678	A2601	C2507	U2412	G2349	U2261	G2159	G2075	A1972	A1872	U1780	U1697	U1614	
G2759	G2679	A2602	C2508	G2414	G2350	G2262	A2160	A2076	A1974	U1875	C1785	G1703	A1616	
C2764	C2680	G2607	C2509	A2351	A2351	G2263	A2162	C2077	A1975	U1877	G1786	C1705	C1617	
C2780	U2681	G2608	A2510	U2418	G2352	C2267	U2163	U2081	A1976	G1878	A1787	U1704	U1618	
G2781	G2682	A2609	A2512	U2419	U2353	G2268	G2166	A2083	C1977	U1877	G1788	U1710	U1619	
C2782	U2686	C2610	G2611	U2420	G2354	C2269	U2167	U2084	U1981	C1882	G1788	U1710	U1620	
U2786	U2687	U2611	U2515	A2421	U2355	C2274	A2176	C2085	A1990	A1885	A1790	G1711	C1621	
U2787	C2688	G2612	U2516	A2422	G2356	A2275	A2176	U2086	C1991	G1886	A1791	G1712	G1622	
A2788	C2689	G2613	C2517	C2423	A2357	G2276	A2176	C2087	U1992	A1887	U1792	U1713	U1623	
G2789	C2690	U2614	C2521	G2424	A2357	C2276	U2179	C2088	U1996	U1887	C1798	A1715	U1624	
U2790	C2691	G2615	G2522	C2427	A2358	G2280	U2180	C2089	A1997	G1892	U1798	A1716	G1625	
G2791	A2692	U2616	A2522	G2427	G2359	C2280	C2181	U2090	C1998	C1893	C1801	U1717	G1626	
C2792	G2694	C2618	G2527	C2430	U2361	A2284	A2190	U2091	U1999	G1893	G1802	C1718	U1627	
G2793	U2697	C2622	G2528	G2432	C2362	A2285	C2191	U2092	C2000	U1898	A1803	C1719	A1628	
C2794	C2698	U2433	A2530	U2433	A2363	A2286	G2093	G2093	A2001	C1903	G1804	G1720	G1629	
A2796	C2699	G2531	G2531	A2434	C2364	C2287	A2194	G2094	C2005	C1904	G1805	U1721	U1630	
C2797	U2700	U2626	G2532	U2435	A2365	C2288	U2195	G2095	A2006	C2005	A1806	G1724	A1631	
G2798	U2701	C2627	U2536	U2437	C2366	C2289	G2196	G2096	C2007	G1985	C1813	C1726	G1632	
C2799	A2702	U2658	C2537	G2438	G2367	C2290	G2197	G2097	C2007	U1906	C1813	C1726	U1633	
G2800	G2705	A2801	G2538	G2446	C2368	C2295	C2198	A2106	C2012	G1913	C1816	A1727	C1634	
G2802	C2449	C2450	A2451	U2371	G2371	C2295	C2198	G2107	C2012	G1913	C1816	A1727	A1635	
				U2374	U2374								A1636	
				G2375	G2375								C1637	
				G2376	G2376								C1638	
													C1639	
													C1640	
													U1641	
													G1642	
													A1648	



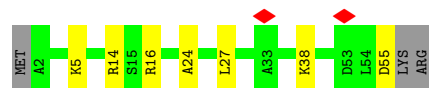
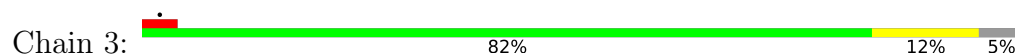
- Molecule 27: 50S ribosomal protein L30



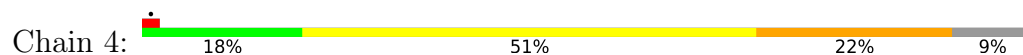
- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S ribosomal protein L33 1

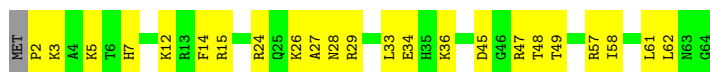


- Molecule 31: 50S ribosomal protein L34





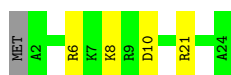
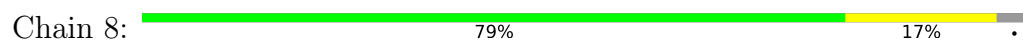
- Molecule 32: 50S ribosomal protein L35



- Molecule 33: 50S ribosomal protein L36



- Molecule 34: Uncharacterized protein bL37



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 (\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 (\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	5/2140 (0.2%)	0.94	5/2879 (0.2%)
2	D	0.55	0/1609	0.66	2/2165 (0.1%)
3	E	0.84	1/1576 (0.1%)	0.87	4/2132 (0.2%)
4	F	0.59	0/1459	0.79	0/1962
5	G	0.36	0/1369	0.57	0/1848
6	H	0.33	0/1027	0.61	1/1398 (0.1%)
7	I	0.29	0/925	0.52	0/1246
8	J	0.29	0/1006	0.60	0/1364
9	K	0.76	1/1165 (0.1%)	0.88	4/1578 (0.3%)
10	L	0.92	0/938	0.95	4/1257 (0.3%)
11	M	0.53	0/1091	0.65	0/1457
12	N	0.91	1/1100 (0.1%)	0.91	2/1482 (0.1%)
13	O	0.75	0/936	0.94	4/1256 (0.3%)
14	P	0.43	0/966	0.57	0/1298
15	Q	0.51	0/921	0.60	1/1236 (0.1%)
16	R	0.55	0/1000	0.58	0/1341
17	S	0.48	0/778	0.57	0/1048
18	T	0.96	1/887 (0.1%)	0.93	3/1204 (0.2%)
19	U	0.74	0/749	0.83	2/1006 (0.2%)
20	V	0.65	0/737	0.78	1/987 (0.1%)
21	W	0.53	0/1422	0.81	4/1941 (0.2%)
22	X	0.94	0/613	0.85	1/821 (0.1%)
23	Y	0.55	0/478	0.70	0/641
24	Z	0.69	0/530	0.75	0/708
25	B	0.56	1/2797 (0.0%)	1.13	18/4357 (0.4%)
26	A	1.00	1/74597 (0.0%)	1.24	633/116386 (0.5%)
27	1	0.80	0/486	0.89	0/651
28	2	0.37	0/520	0.60	1/698 (0.1%)
29	3	0.55	0/427	0.61	0/572
30	4	0.73	1/424 (0.2%)	0.78	2/567 (0.4%)
31	5	0.85	0/375	1.00	1/493 (0.2%)
32	6	0.91	0/507	0.94	2/672 (0.3%)
33	7	0.83	0/302	0.80	0/401
34	8	0.44	0/191	0.60	0/247

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.92	12/106048 (0.0%)	1.14	695/159299 (0.4%)

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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	B	1	G	OP3-P	-10.43	1.48	1.61
1	C	79	VAL	CB-CG2	-6.92	1.38	1.52
18	T	112	VAL	CB-CG2	-6.68	1.38	1.52
1	C	224	VAL	CB-CG2	-6.23	1.39	1.52
12	N	92	TRP	CB-CG	-6.01	1.39	1.50

The worst 5 of 695 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	323	C	N1-C2-O2	11.55	125.83	118.90
26	A	1130	C	N1-C2-O2	11.20	125.62	118.90
26	A	2245	C	N1-C2-O2	11.08	125.55	118.90
26	A	2245	C	C2-N1-C1'	10.64	130.51	118.80
26	A	323	C	C2-N1-C1'	10.56	130.42	118.80

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
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	211	0
2	D	1587	0	1629	66	0
3	E	1553	0	1586	145	0
4	F	1437	0	1463	210	0
5	G	1348	0	1399	27	0
6	H	1018	0	988	12	0
7	I	918	0	959	14	0
8	J	990	0	1021	28	0
9	K	1138	0	1174	115	0
10	L	930	0	989	57	0
11	M	1078	0	1151	46	0
12	N	1074	0	1116	63	0
13	O	919	0	959	151	0
14	P	956	0	989	41	0
15	Q	907	0	938	30	0
16	R	988	0	1038	19	0
17	S	768	0	820	46	0
18	T	873	0	909	57	0
19	U	739	0	777	119	0
20	V	731	0	782	114	0
21	W	1407	0	1423	155	0
22	X	604	0	622	56	0
23	Y	470	0	484	9	0
24	Z	527	0	537	54	0
25	B	2501	0	1269	297	0
26	A	66623	0	33514	1028	0
27	1	483	0	513	22	0
28	2	510	0	497	61	0
29	3	423	0	463	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	4	416	0	421	95	0
31	5	372	0	406	41	0
32	6	502	0	541	32	0
33	7	298	0	320	25	0
34	8	189	0	205	4	0
All	All	97374	0	64049	2838	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 2838 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 ⓘ

5.3.1 Protein backbone ⓘ

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%)	7	35
2	D	212/217 (98%)	199 (94%)	11 (5%)	2 (1%)	14	49
3	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	24
4	F	179/187 (96%)	162 (90%)	15 (8%)	2 (1%)	12	44
5	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	19	54
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	27
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%)	13	47
18	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	26
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	30
21	W	186/215 (86%)	171 (92%)	10 (5%)	5 (3%)	4	26
22	X	80/88 (91%)	61 (76%)	13 (16%)	6 (8%)	1	6
23	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
24	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	8	37
27	1	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
28	2	64/75 (85%)	61 (95%)	2 (3%)	1 (2%)	8	37
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%)	12	40

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	58	HIS

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Mol	Chain	Res	Type
1	C	145	VAL
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%)	207 (97%)	7 (3%)	33	64
2	D	160/163 (98%)	155 (97%)	5 (3%)	35	66
3	E	167/173 (96%)	158 (95%)	9 (5%)	18	51
4	F	150/156 (96%)	137 (91%)	13 (9%)	8	32
5	G	148/150 (99%)	148 (100%)	0	100	100
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	64
10	L	99/100 (99%)	97 (98%)	2 (2%)	50	75
11	M	112/114 (98%)	111 (99%)	1 (1%)	75	89
12	N	112/116 (97%)	107 (96%)	5 (4%)	23	56
13	O	96/158 (61%)	91 (95%)	5 (5%)	19	52
14	P	93/94 (99%)	93 (100%)	0	100	100
15	Q	100/100 (100%)	99 (99%)	1 (1%)	73	87
16	R	97/99 (98%)	96 (99%)	1 (1%)	73	87
17	S	82/83 (99%)	81 (99%)	1 (1%)	67	85
18	T	90/117 (77%)	86 (96%)	4 (4%)	24	57
19	U	82/85 (96%)	71 (87%)	11 (13%)	3	15
20	V	81/86 (94%)	75 (93%)	6 (7%)	11	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	W	154/168 (92%)	139 (90%)	15 (10%)	6	27
22	X	59/63 (94%)	58 (98%)	1 (2%)	56	78
23	Y	50/51 (98%)	50 (100%)	0	100	100
24	Z	58/66 (88%)	53 (91%)	5 (9%)	8	33
27	1	53/54 (98%)	51 (96%)	2 (4%)	28	60
28	2	57/63 (90%)	54 (95%)	3 (5%)	19	52
29	3	43/46 (94%)	43 (100%)	0	100	100
30	4	48/52 (92%)	40 (83%)	8 (17%)	2	9
31	5	35/36 (97%)	33 (94%)	2 (6%)	17	50
32	6	53/54 (98%)	53 (100%)	0	100	100
33	7	35/35 (100%)	33 (94%)	2 (6%)	17	50
34	8	18/19 (95%)	18 (100%)	0	100	100
All	All	2947/3183 (93%)	2834 (96%)	113 (4%)	30	60

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	T	118	PRO
31	5	27	THR
20	V	39	ASN
31	5	6	ARG
28	2	44	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
30	4	20	HIS
30	4	49	GLN
34	8	17	ASN
10	L	4	GLN
9	K	135	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	B	116/118 (98%)	42 (36%)	3 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	A	3096/3120 (99%)	788 (25%)	44 (1%)
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 ⓘ

There are no chain breaks in this entry.

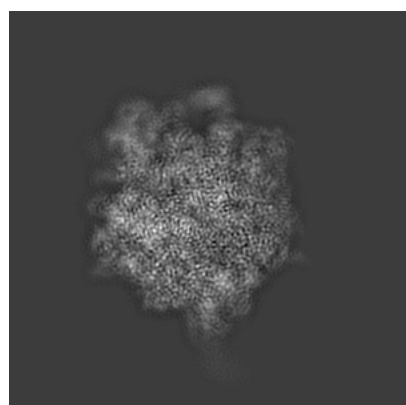
6 Map visualisation [i](#)

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.

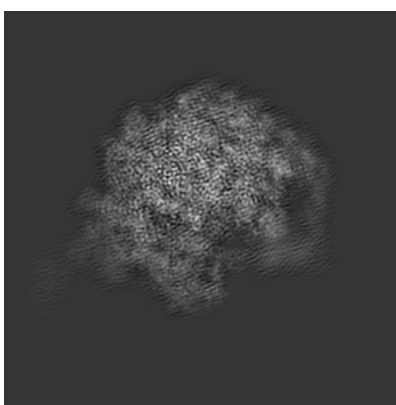
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

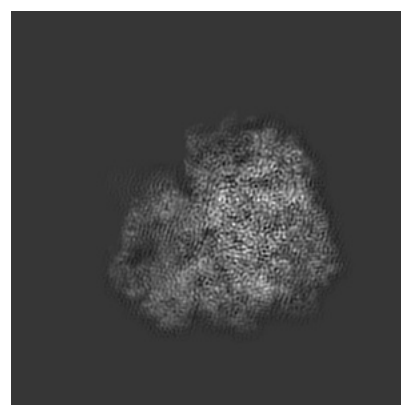
6.1.1 Primary map



X



Y

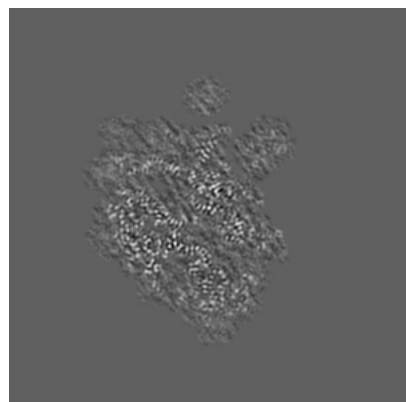


Z

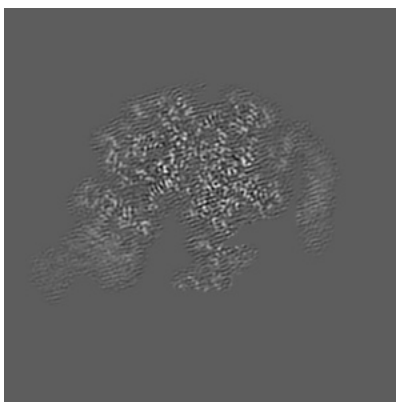
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

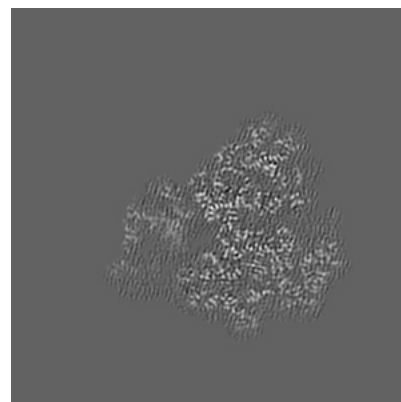
6.2.1 Primary map



X Index: 172



Y Index: 172

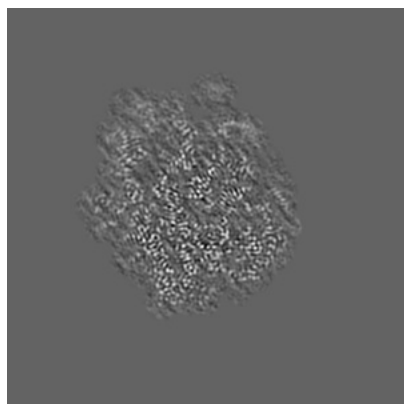


Z Index: 172

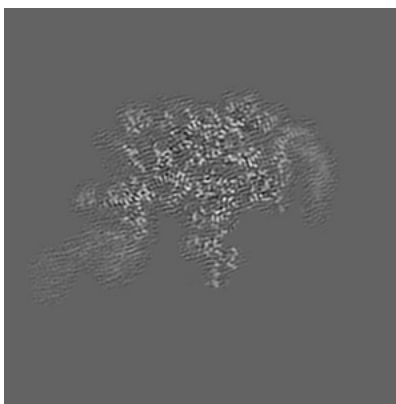
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

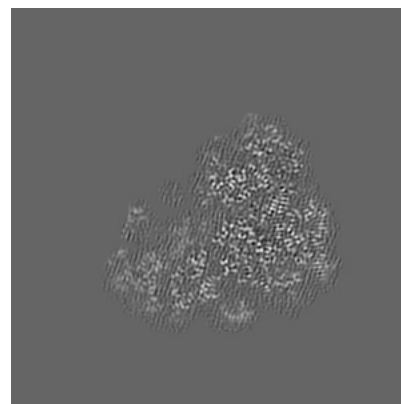
6.3.1 Primary map



X Index: 205



Y Index: 181

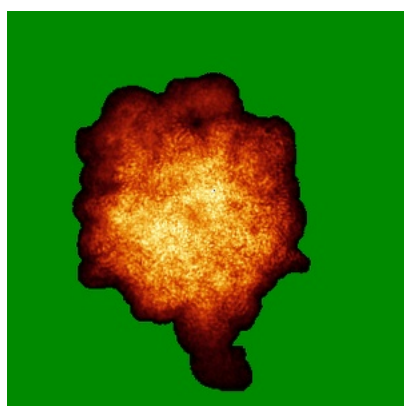


Z Index: 154

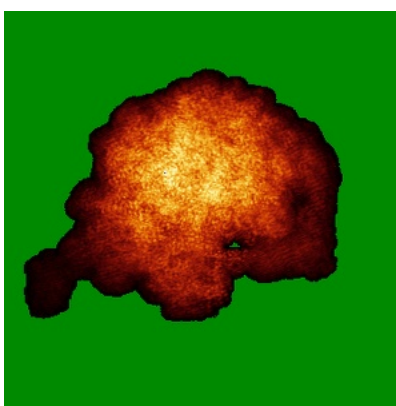
The images above show the largest variance slices of the map in three orthogonal directions.

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

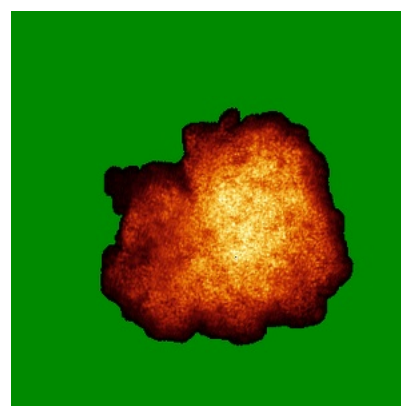
6.4.1 Primary map



X



Y

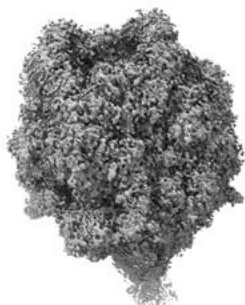


Z

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](#)

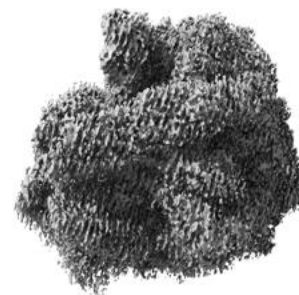
6.5.1 Primary map



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.

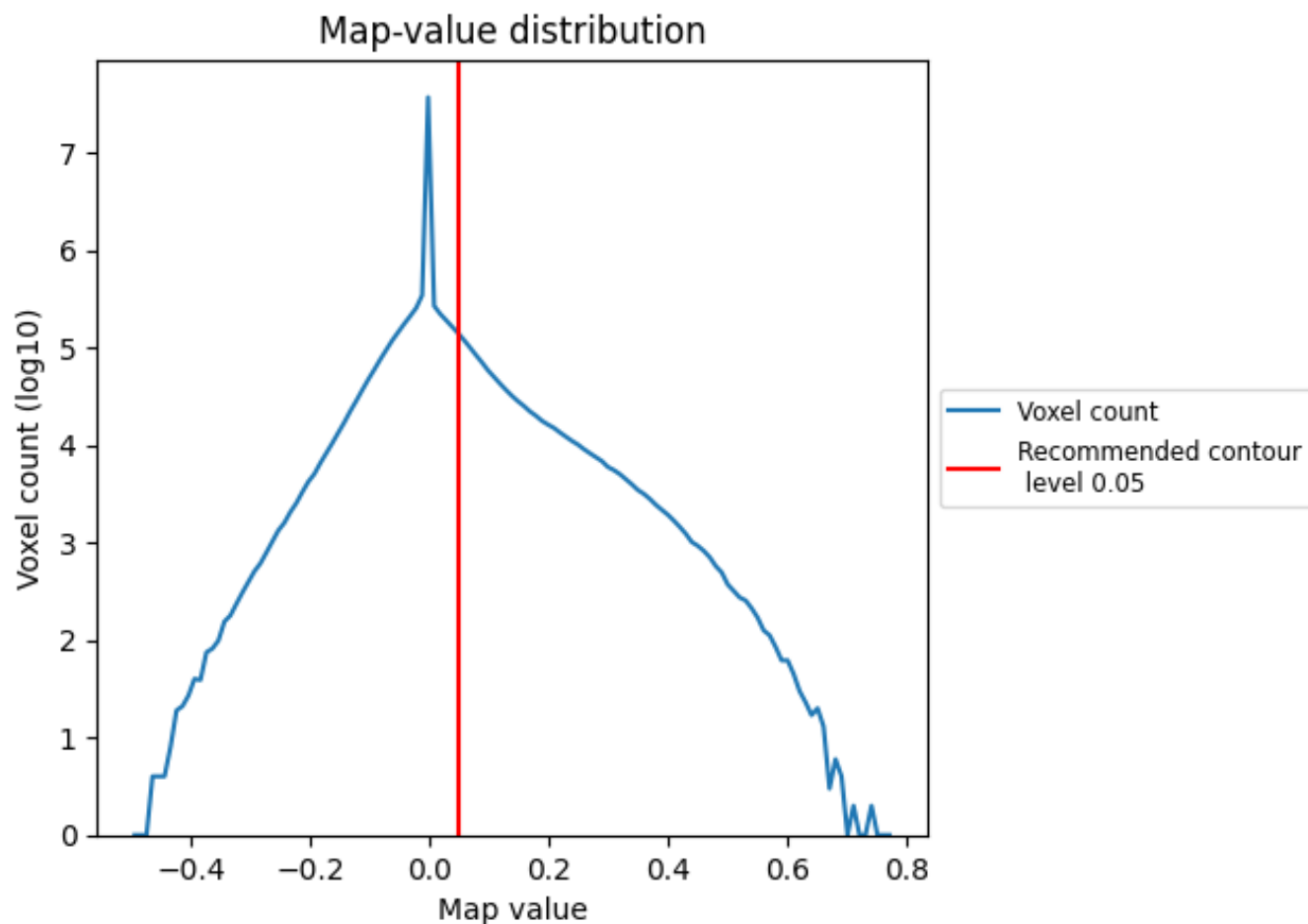
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

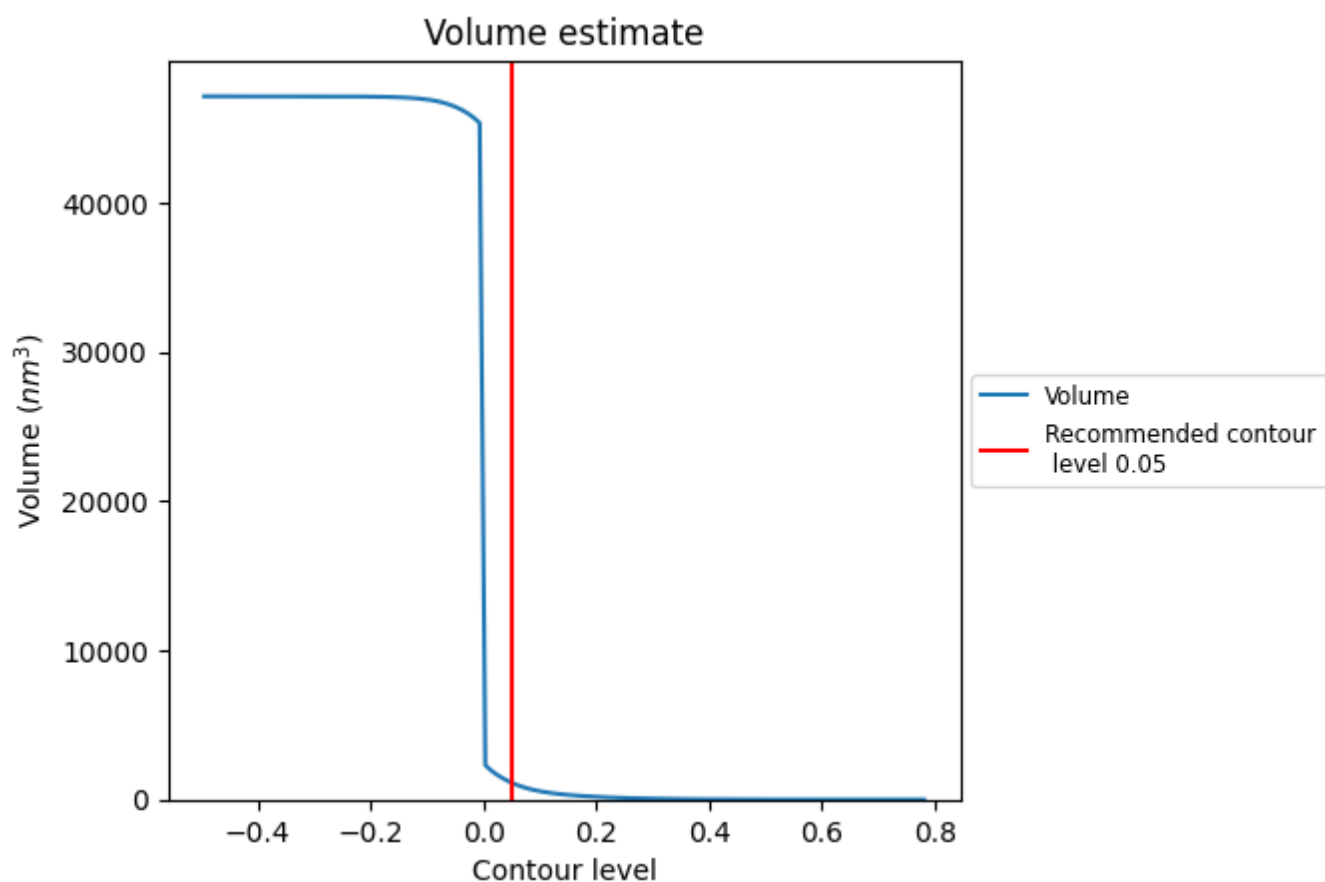
This section contains the results of statistical analysis of the map.

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.

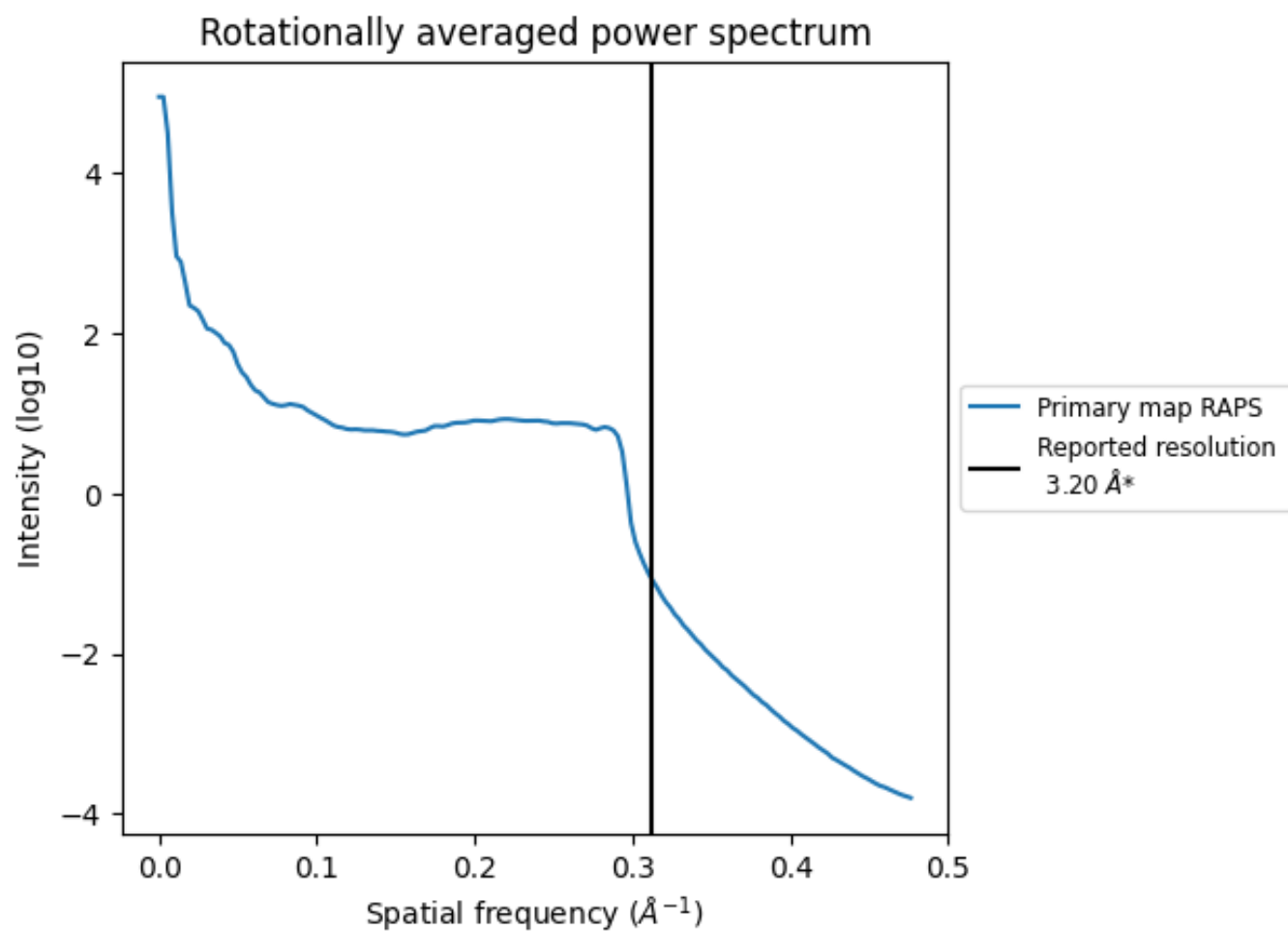
7.2 Volume estimate [i](#)



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

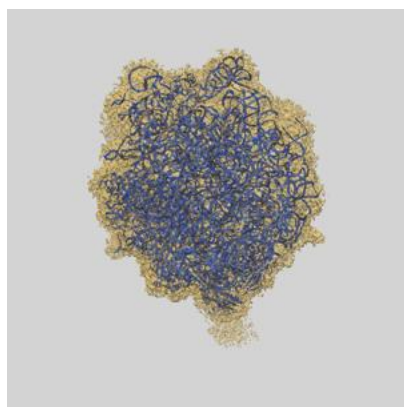
8 Fourier-Shell correlation

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

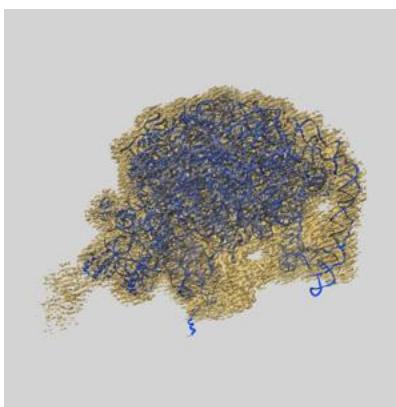
9 Map-model fit [i](#)

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](#).

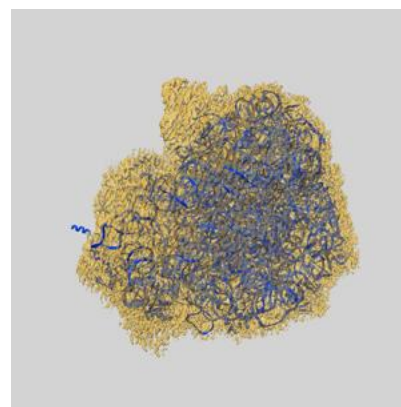
9.1 Map-model overlay [i](#)



X



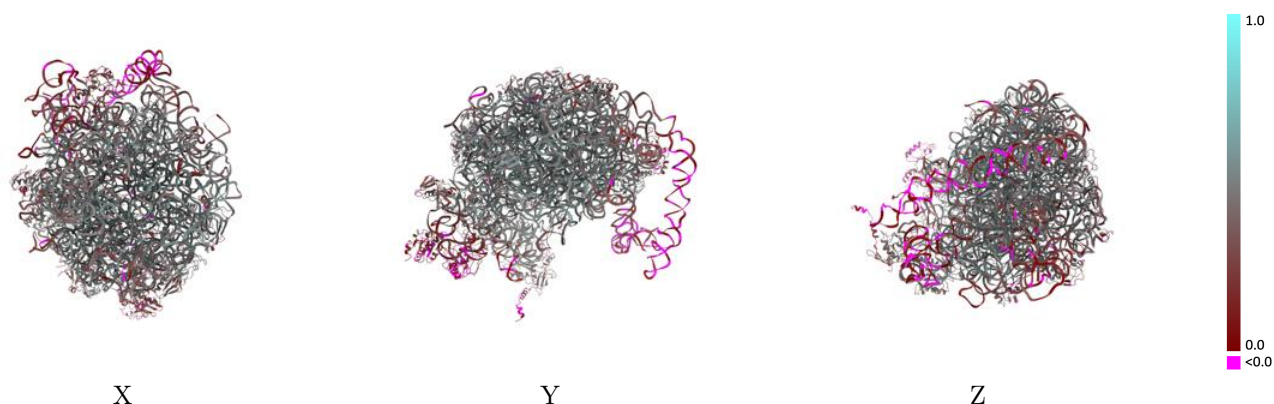
Y



Z

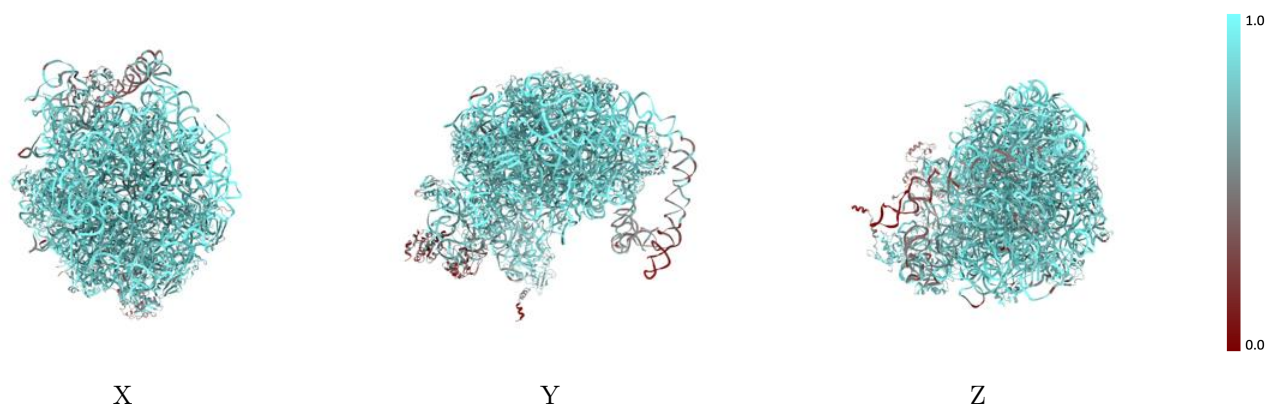
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



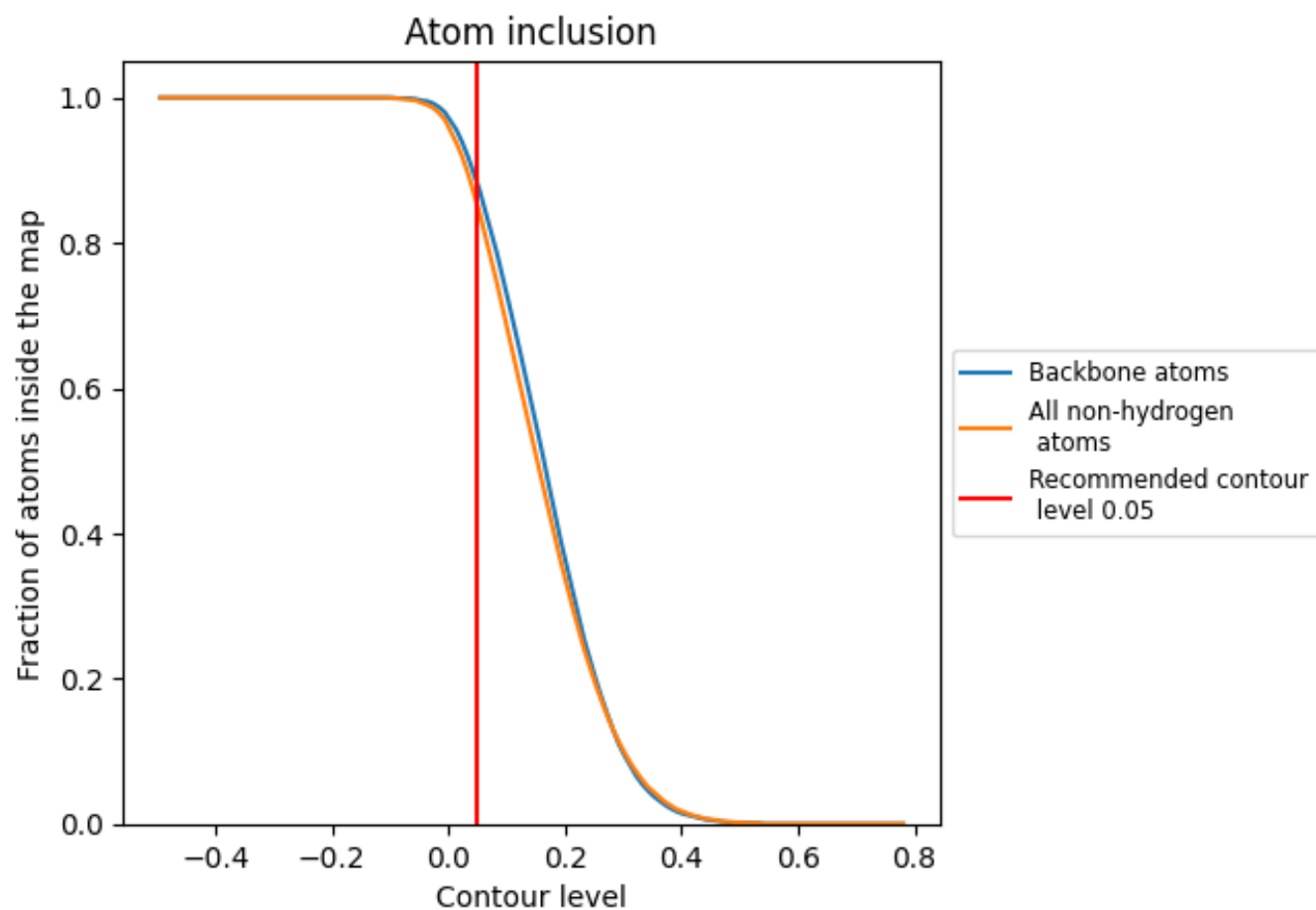
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

