



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 11:51 AM UTC

PDB ID : 8WI8 / pdb_00008wi8
EMDB ID : EMD-37560
Title : Cryo- EM structure of Mycobacterium smegmatis 50S ribosomal subunit (body 1) of 70S ribosome, bS1 and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 2.70 Å(reported)
Based on initial model : 8WHX

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:

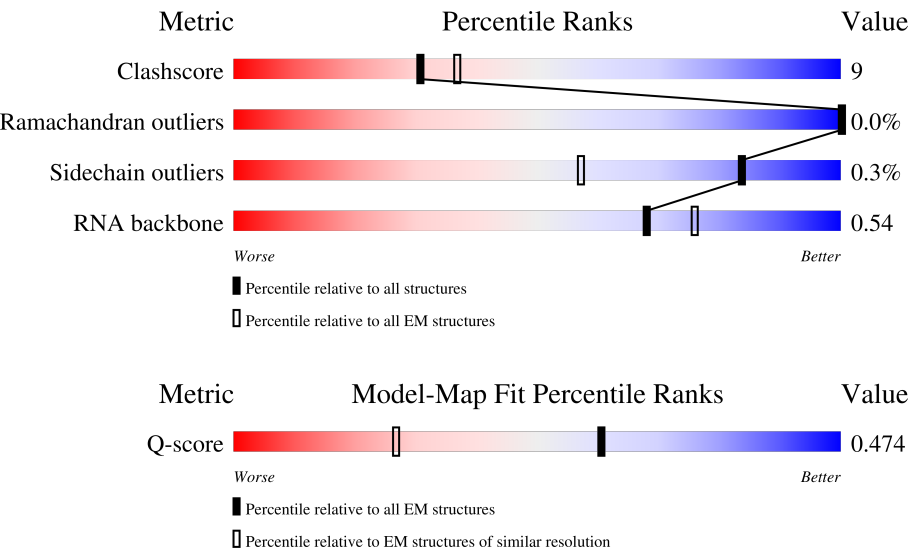
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.70 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	10327 (2.20 - 3.20)

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	E	278	83%16%.
2	F	217	85%13%.
3	G	215	85%12%.

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

2 Entry composition [i](#)

There are 28 unique types of molecules in this entry. The entry contains 89877 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	E	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

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

- Molecule 8 is a protein called 50S ribosomal protein L14.

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

- Molecule 9 is a protein called 50S ribosomal protein L15.

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

- Molecule 10 is a protein called 50S ribosomal protein L17.

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

- Molecule 11 is a protein called 50S ribosomal protein L18.

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

- Molecule 12 is a protein called 50S ribosomal protein L19.

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

- Molecule 13 is a protein called 50S ribosomal protein L20.

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

- Molecule 14 is a protein called 50S ribosomal protein L21.

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

- Molecule 15 is a protein called 50S ribosomal protein L22.

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

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	95	Total	C	N	O	0	0
			747	474	136	137		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	93	Total	C	N	O	S	0	0
			710	443	133	132	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	76	Total	C	N	O	0	0
			568	352	120	96		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	62	Total	C	N	O	0	0
			498	300	114	84		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3025	Total	C	N	O	P	0	0
			64965	28956	11946	21038	3025		

- Molecule 28 is a RNA chain called 5S rRNA.

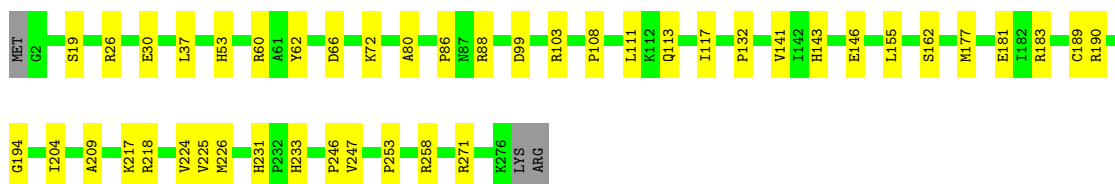
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
28	B	118	2522	1126	468	810	118	0	0

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

Chain E: 



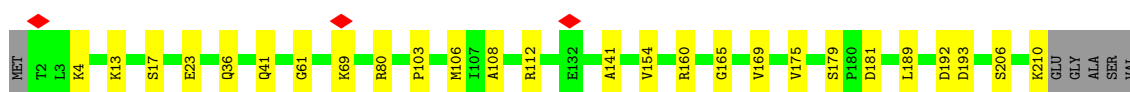
- Molecule 2: 50S ribosomal protein L3

Chain F: 



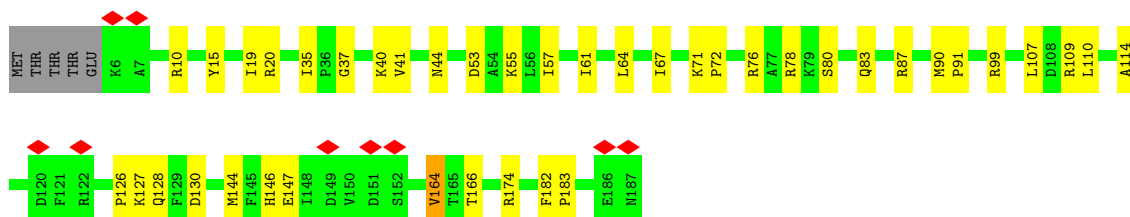
- Molecule 3: 50S ribosomal protein L4

Chain G: 



- Molecule 4: 50S ribosomal protein L5

Chain H: 



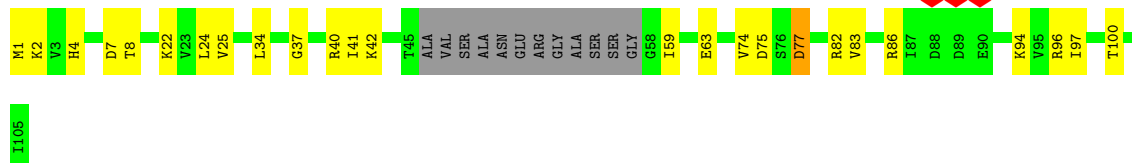
- Molecule 5: 50S ribosomal protein L6

Chain W:  87% 8% 5%



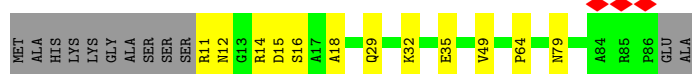
- Molecule 17: 50S ribosomal protein L24

Chain X:  65% 23% 11%



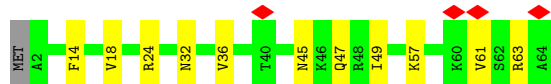
- Molecule 18: 50S ribosomal protein L27

Chain Z:  73% 14% 14%



- Molecule 19: 50S ribosomal protein L28

Chain 1:  6% 81% 17%



- Molecule 20: 50S ribosomal protein L29

Chain 2:  60% 23% 17%



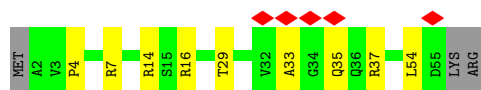
- Molecule 21: 50S ribosomal protein L30

Chain 3:  72% 25%

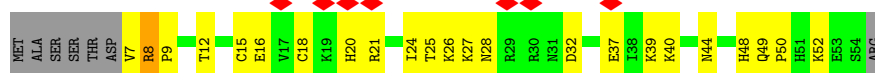
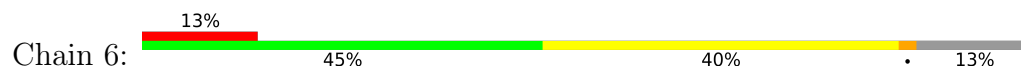


- Molecule 22: 50S ribosomal protein L32

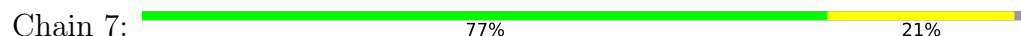
Chain 5:  9% 79% 16% 5%



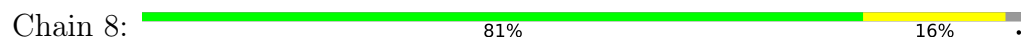
- Molecule 23: 50S ribosomal protein L33



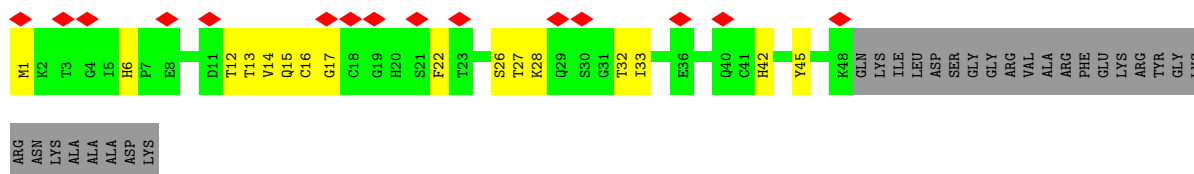
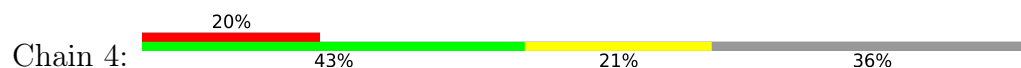
- Molecule 24: 50S ribosomal protein L34



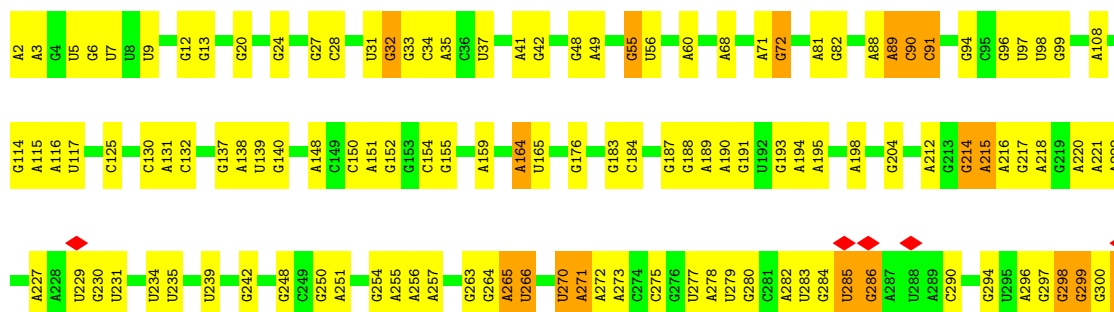
- Molecule 25: 50S ribosomal protein L35



- Molecule 26: 50S ribosomal protein L31

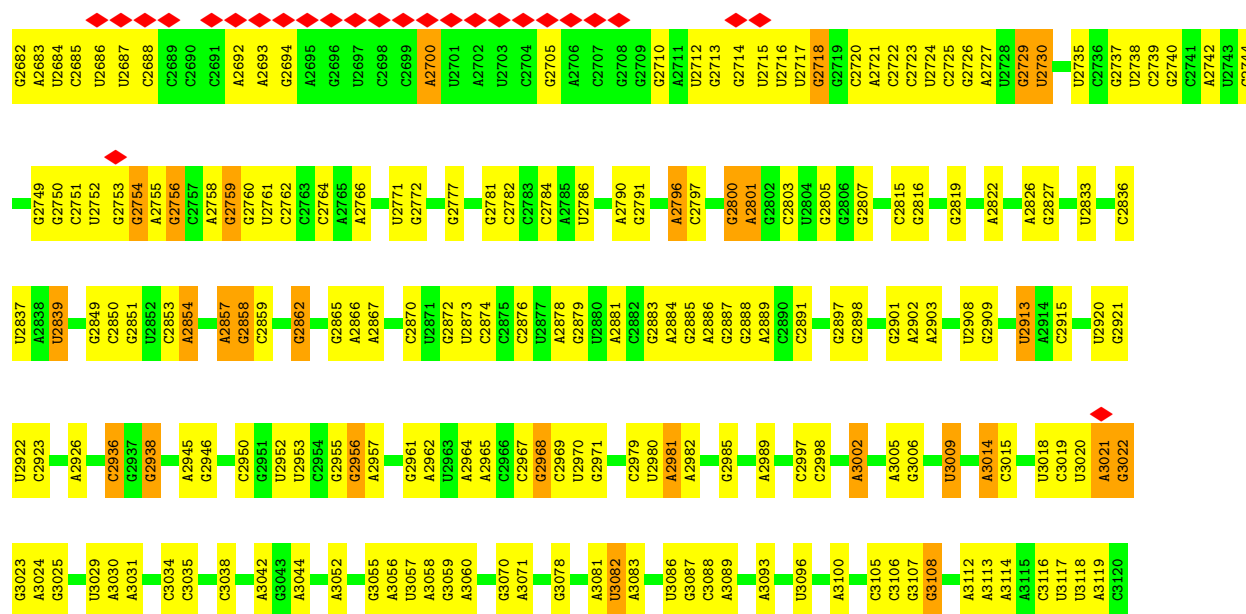


- Molecule 27: 23S rRNA

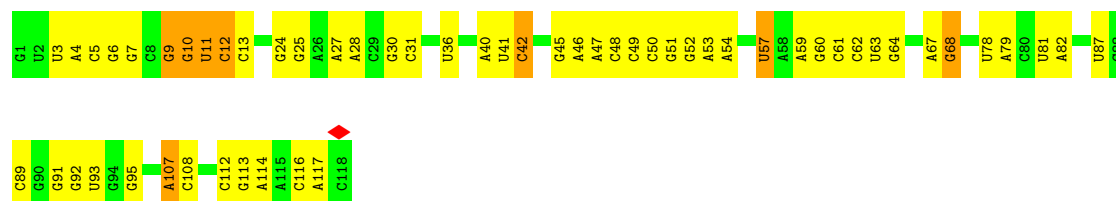




A2600	A2601	A2602	G2603	G2604	G2605	G2606	G2607	G2608	G2609	G2610	G2613	G2614	G2615	G2616	G2622	G2623	G2624	G2625	G2626	G2627	A2630	G2634	A2635	A2636	G2639	G2640	G2641	G2642	G2643	G2647	G2648	A2649	A2650	G2651	G2652	G2653	A2654	G2655	A2659	G2665	G2671	A2672	G2673	A2674	A2677	G2678	G2679	G2680	G2681									
A2512	U2515	U2516	G2527	G2528	A2529	G2530	G2531	G2532	U2536	C2537	A2538	G2539	G2540	U2541	U2544	G2545	U2548	G2549	A2552	G2553	G2556	A2557	C2558	A2559	A2560	G2563	A2564	G2569	A2570	C2571	C2574	A2578	G2581	C2582	C2583	U2584	G2585	U2587	C2588	G2589	A2593	G2594	G2595	G2599														
A2434	U2435	A2436	G2439	G2440	G2441	U2442	U2443	G2444	G2447	G2448	A2449	G2450	A2451	U2457	G2458	G2459	U2460	G2461	G2462	G2463	U2464	A2465	G2466	U2467	U2468	A2469	A2470	A2471	G2472	U2473	G2474	G2480	U2481	U2482	U2486	G2487	G2488	U2489	A2490	A2491	A2492	A2493	U2494	G2495	G2501	A2502	G2503	G2506	C2507	A2510	A2511							
C2368	C2369	A2370	G2371	U2372	G2373	U2374	G2375	G2376	G2377	U2378	G2379	G2380	A2381	G2382	U2383	C2384	G2385	U2386	U2387	G2388	U2389	U2390	G2391	A2392	A2393	A2394	U2395	A2396	G2397	C2398	A2399	U2400	U2401	C2402	U2403	G2404	A2405	U2406	G2407	G2408	A2409	A2410	U2411	U2412	G2413	G2414	G2415	C2416	U2420	A2421	A2422	U2425	G2426	G2427	C2431			
U2298	C2299	A2303	C2304	A2305	A2313	U2314	U2315	G2316	C2320	U2321	C2322	G2323	A2324	U2325	A2326	C2327	G2328	G2329	U2330	U2331	U2332	G2333	U2334	G2335	U2336	A2337	G2338	G2339	A2340	U2341	A2342	G2343	G2344	U2345	G2346	G2347	G2348	G2349	G2350	A2351	C2352	U2353	G2354	U2355	G2356	A2357	U2358	G2359	C2360	U2361	G2362	A2363	C2364	A2365	C2366	G2367		
U2215	G2216	U2217	C2220	A2221	C2224	C2235	G2236	A2237	A2238	A2239	U2240	A2244	C2245	U2246	A2247	G2248	G2249	A2250	G2251	A2254	A2255	G2256	A2257	U2258	U2261	C2262	G2263	U2264	U2265	A2266	C2267	C2271	G2272	G2275	G2276	G2279	G2280	A2283	A2284	G2285	A2286	C2287	C2288	C2289	A2294	C2295	G2296	U2297										
A2084	C2085	U2086	C2087	C2088	C2089	U2090	U2091	U2092	G2093	G2094	G2095	G2096	G2097	U2098	G2099	A2106	G2107	A2108	A2109	G2130	G2131	A2137	U2141	U2147	C2148	A2151	A2152	G2153	G2154	A2160	A2161	A2162	U2163	U2170	C2171	A2176	U2179	A2190	C2191	A2194	U2195	G2196	C2211	A2212														
A1975	U1981	G1982	C1988	G1989	A1990	C1991	U1992	U1996	A2001	A2002	A2003	A2004	C2005	A2006	C2007	A1896	A1897	A1898	G1899	A1899	U2011	C2012	G2016	C2017	G2018	C2025	A2026	A2029	C2030	U2033	G2034	C2042	C2043	A2046	C2047	G2048	U2061	A1948	G1950	G1951	A1955	A2070	A2071	G2074	G2075	C2079	G2080	U2081										
G1740	G1754	A1755	G1756	U1757	A1758	A1759	G1762	G1763	U1767	G1770	G1771	G1786	A1787	G1788	A1789	A1790	A1791	A1792	U1798	A1803	G1804	G1805	G1815	A1816	G1822	C1825	A1826	A1827	A1828	G1829	C1830	A1831	A1832	G1840	G1849	A1850	G1851	A1852	A1853	U1854	A1855	A1859	G1736	U1737	G1738	A1739												
A1652	G1653	A1656	G1657	C1658	U1659	A1660	U1665	A1666	U1667	U1670	A1673	G1674	U1675	G1676	G1677	A1678	A1679	A1680	U1681	G1613	G1614	G1615	A1616	C1617	U1618	U1619	U1620	A1621	G1622	U1623	U1624	G1625	G1626	U1627	A1628	G1629	U1630	A1631	U1632	U1633	C1634	A1635	A1636	U1637	C1638	G1639	A1640	U1641	G1642	U1645	U1646	G1647	U1648	G1649	G1650	G1651		
C1531	G1532	U1533	C1534	C1535	A1536	U1537	G1538	A1539	U1540	A1541	A1542	A1543	U1544	C1545	A1546	G1547	G1608	G1609	C1610	A1611	U1612	G1613	G1614	G1615	A1616	C1617	U1618	U1619	U1620	A1621	G1622	U1623	U1624	G1625	G1626	U1627	A1628	G1629	U1630	A1631	U1632	U1633	C1634	A1635	A1636	U1637	C1638	G1639	A1640	U1641	G1642	U1645	U1646	G1647	U1648	G1649	G1650	G1651



● Molecule 28: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.213	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	E	0.12	0/2153	0.27	0/2895
2	F	0.17	0/1609	0.41	0/2165
3	G	0.12	0/1592	0.27	0/2153
4	H	0.13	0/1467	0.35	0/1973
5	I	0.13	0/1281	0.35	0/1733
6	J	0.21	0/311	0.46	0/419
7	M	0.14	0/1157	0.32	0/1567
8	N	0.12	0/946	0.29	0/1268
9	O	0.13	0/1091	0.37	0/1457
10	Q	0.13	0/945	0.30	0/1267
11	R	0.15	0/966	0.43	0/1298
12	S	0.14	0/921	0.34	0/1236
13	T	0.14	0/1000	0.29	0/1341
14	U	0.15	0/764	0.30	0/1030
15	V	0.13	0/887	0.30	0/1204
16	W	0.15	0/757	0.33	0/1018
17	X	0.14	0/716	0.35	0/957
18	Z	0.14	0/577	0.31	0/774
19	1	0.11	0/478	0.30	0/641
20	2	0.13	0/534	0.32	0/713
21	3	0.15	0/477	0.32	0/640
22	5	0.13	0/427	0.28	0/572
23	6	0.19	0/405	0.47	0/542
24	7	0.11	0/380	0.29	0/500
25	8	0.10	0/503	0.27	0/667
26	4	0.14	0/372	0.37	0/503
27	A	0.12	0/72743	0.26	0/113499
28	B	0.11	0/2821	0.24	0/4396
All	All	0.12	0/98280	0.28	0/148428

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	30	0
2	F	1587	0	1630	24	0
3	G	1569	0	1607	20	0
4	H	1445	0	1476	33	0
5	I	1260	0	1300	48	0
6	J	308	0	323	11	0
7	M	1130	0	1167	19	0
8	N	938	0	1000	15	0
9	O	1078	0	1151	22	0
10	Q	928	0	972	14	0
11	R	956	0	991	19	0
12	S	907	0	938	14	0
13	T	988	0	1038	14	0
14	U	754	0	802	11	0
15	V	873	0	909	12	0
16	W	747	0	794	7	0
17	X	710	0	760	20	0
18	Z	568	0	586	12	0
19	1	470	0	484	9	0
20	2	531	0	541	11	0
21	3	474	0	500	10	0
22	5	423	0	463	9	0
23	6	397	0	407	22	0
24	7	377	0	411	7	0
25	8	498	0	538	8	0
26	4	364	0	352	14	0
27	A	64965	0	32687	939	0
28	B	2522	0	1285	38	0
All	All	89877	0	57277	1281	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 9.

The worst 5 of 1281 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)
27:A:2971:G:H21	27:A:2981:A:N6	1.45	1.14
27:A:2971:G:N2	27:A:2981:A:H62	1.52	1.05
27:A:1610:C:H2'	27:A:1611:A:C8	1.96	0.99
27:A:1547:G:H1	27:A:1623:U:H3	1.01	0.96
27:A:1550:G:H1	27:A:1620:U:H3	1.13	0.96

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	E	273/278 (98%)	265 (97%)	8 (3%)	0	100	100
2	F	212/217 (98%)	204 (96%)	7 (3%)	1 (0%)	24	48
3	G	207/215 (96%)	205 (99%)	2 (1%)	0	100	100
4	H	180/187 (96%)	173 (96%)	7 (4%)	0	100	100
5	I	163/179 (91%)	162 (99%)	1 (1%)	0	100	100
6	J	39/151 (26%)	39 (100%)	0	0	100	100
7	M	144/147 (98%)	141 (98%)	3 (2%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	131 (92%)	12 (8%)	0	100	100
10	Q	116/199 (58%)	114 (98%)	2 (2%)	0	100	100
11	R	124/127 (98%)	124 (100%)	0	0	100	100
12	S	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
13	T	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
14	U	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
15	V	112/153 (73%)	111 (99%)	1 (1%)	0	100	100
16	W	93/100 (93%)	92 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	X	89/105 (85%)	88 (99%)	1 (1%)	0	100	100
18	Z	74/88 (84%)	71 (96%)	3 (4%)	0	100	100
19	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
20	2	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
21	3	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
23	6	46/55 (84%)	42 (91%)	4 (9%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	60/64 (94%)	58 (97%)	2 (3%)	0	100	100
26	4	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
All	All	2848/3260 (87%)	2771 (97%)	76 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	156	THR

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	E	215/218 (99%)	215 (100%)	0	100	100
2	F	160/163 (98%)	158 (99%)	2 (1%)	61	83
3	G	169/173 (98%)	169 (100%)	0	100	100
4	H	151/156 (97%)	150 (99%)	1 (1%)	76	90
5	I	139/150 (93%)	138 (99%)	1 (1%)	76	90
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	119 (100%)	0	100	100
8	N	100/100 (100%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	O	112/114 (98%)	112 (100%)	0	100	100
10	Q	97/158 (61%)	97 (100%)	0	100	100
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	100/100 (100%)	100 (100%)	0	100	100
13	T	97/99 (98%)	97 (100%)	0	100	100
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	90/117 (77%)	90 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	78 (99%)	1 (1%)	61	83
18	Z	55/63 (87%)	55 (100%)	0	100	100
19	1	50/51 (98%)	50 (100%)	0	100	100
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	52 (100%)	0	100	100
22	5	43/46 (94%)	43 (100%)	0	100	100
23	6	46/52 (88%)	45 (98%)	1 (2%)	45	74
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	43/63 (68%)	43 (100%)	0	100	100
All	All	2351/2617 (90%)	2345 (100%)	6 (0%)	84	94

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	I	76	LEU
17	X	77	ASP
23	6	8	ARG
2	F	156	THR
2	F	154	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
10	Q	61	HIS
22	5	12	ASN
12	S	28	HIS

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Mol	Chain	Res	Type
23	6	20	HIS
14	U	93	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3022/3119 (96%)	539 (17%)	16 (0%)
28	B	117/118 (99%)	16 (13%)	1 (0%)
All	All	3139/3237 (96%)	555 (17%)	17 (0%)

5 of 555 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	12	G
27	A	20	G
27	A	31	U
27	A	32	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	2381	A
28	B	10	G
27	A	974	G
27	A	1002	C
27	A	1004	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

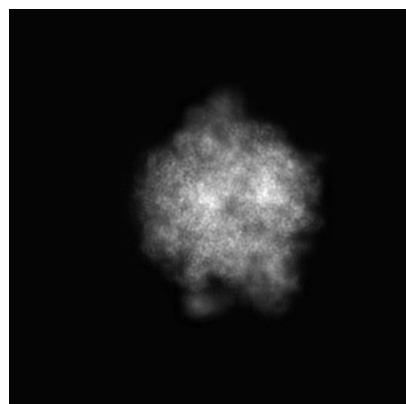
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37560. These allow visual inspection of the internal detail of the map and identification of artifacts.

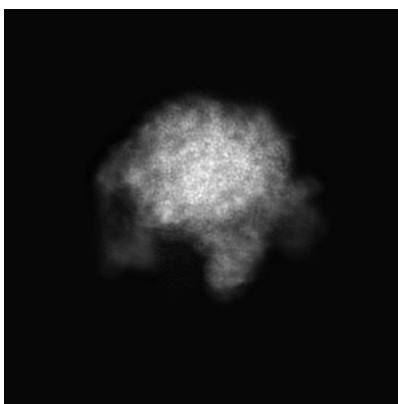
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

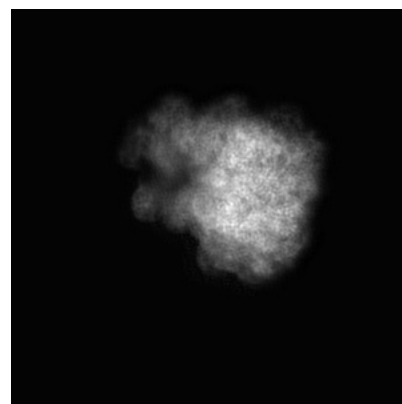
6.1.1 Primary map



X

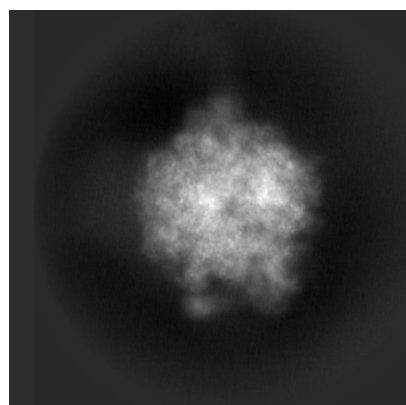


Y

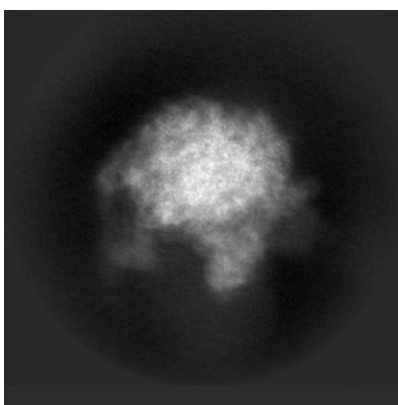


Z

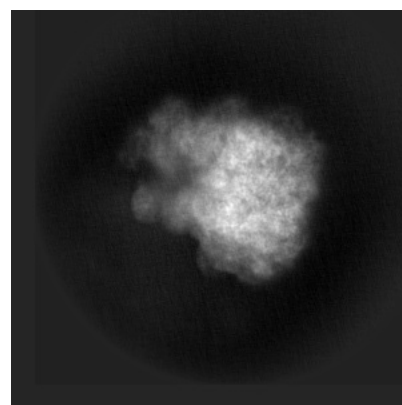
6.1.2 Raw map



X



Y

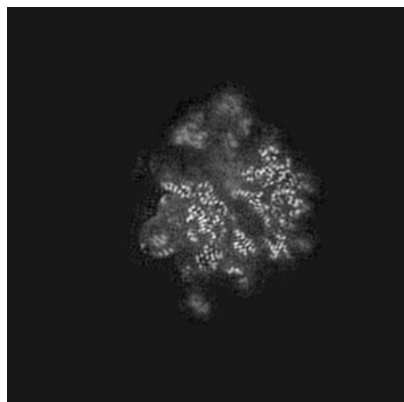


Z

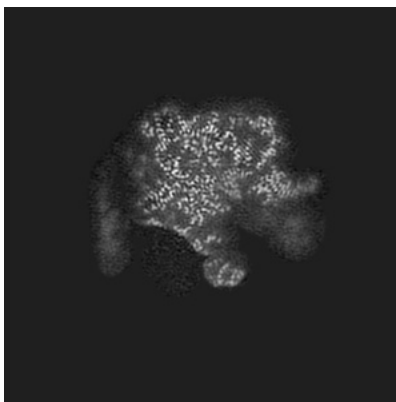
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

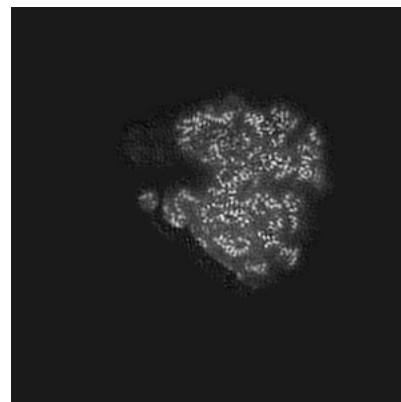
6.2.1 Primary map



X Index: 190

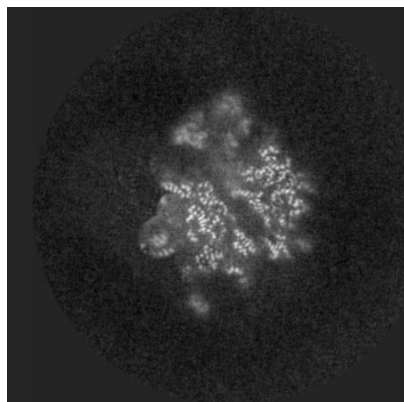


Y Index: 190

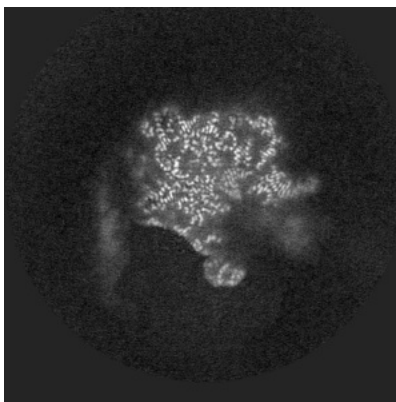


Z Index: 190

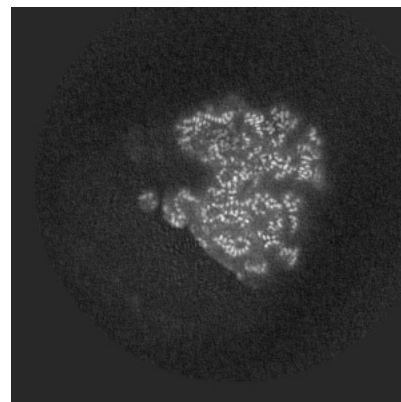
6.2.2 Raw map



X Index: 190



Y Index: 190

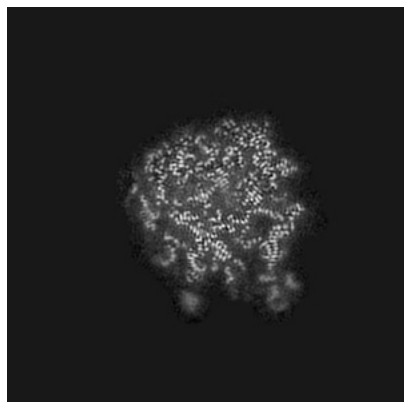


Z Index: 190

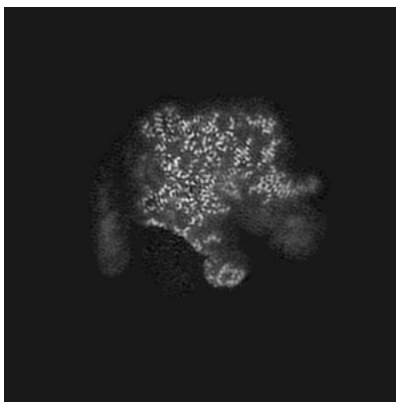
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

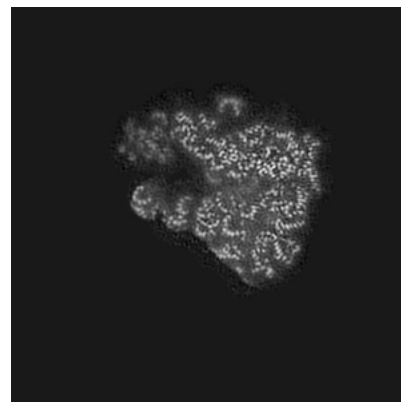
6.3.1 Primary map



X Index: 230

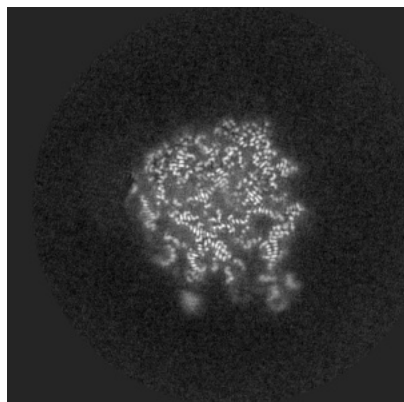


Y Index: 191

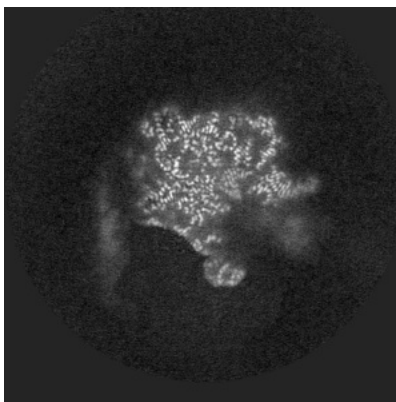


Z Index: 200

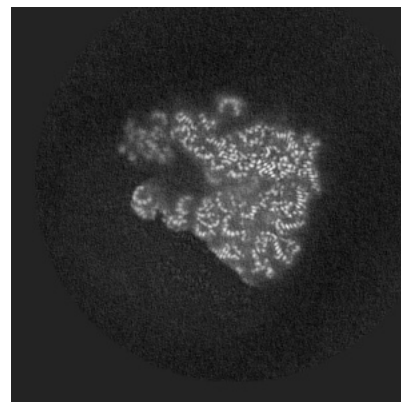
6.3.2 Raw map



X Index: 230



Y Index: 190

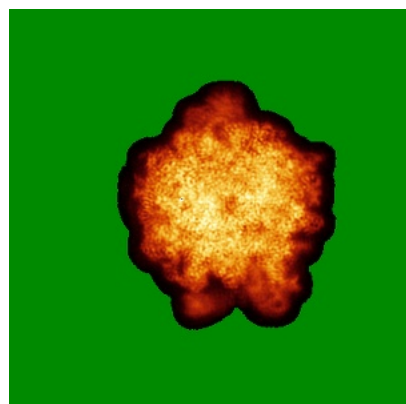


Z Index: 200

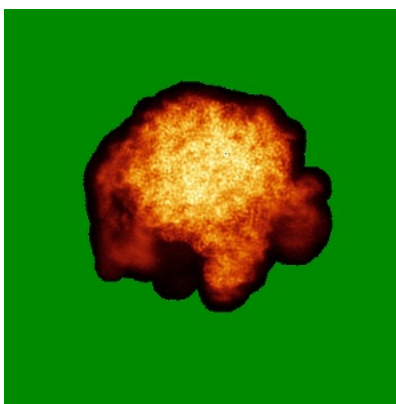
The images above show the largest variance slices of the map in three orthogonal directions.

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

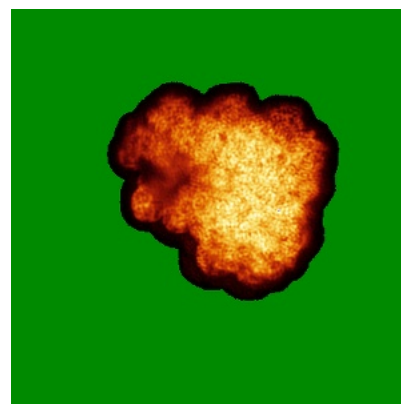
6.4.1 Primary map



X

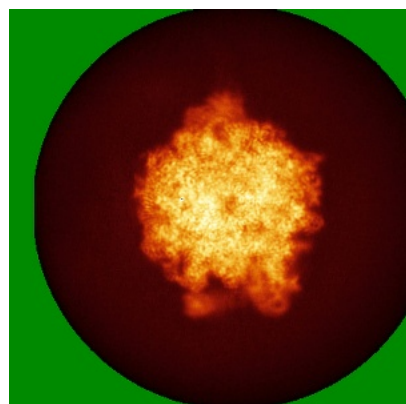


Y

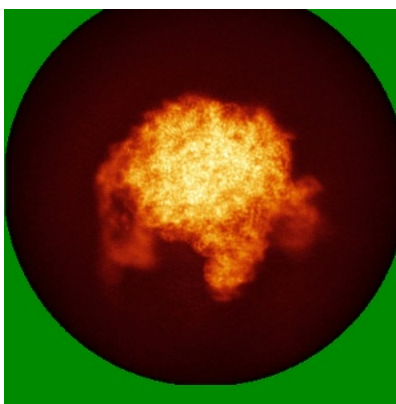


Z

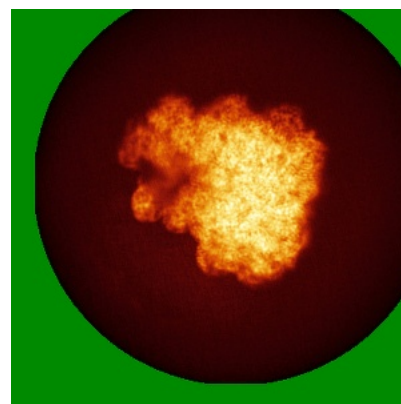
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

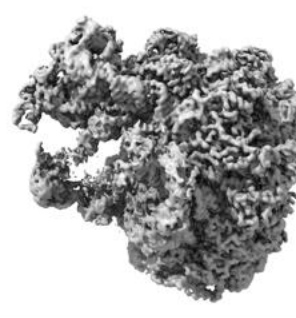
6.5.1 Primary map



X



Y



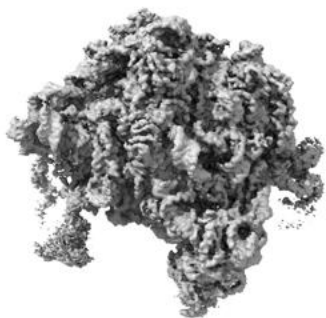
Z

The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

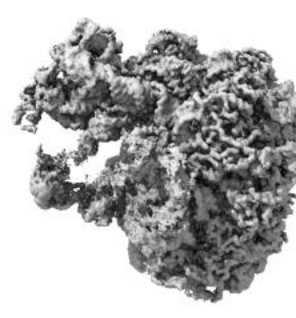
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

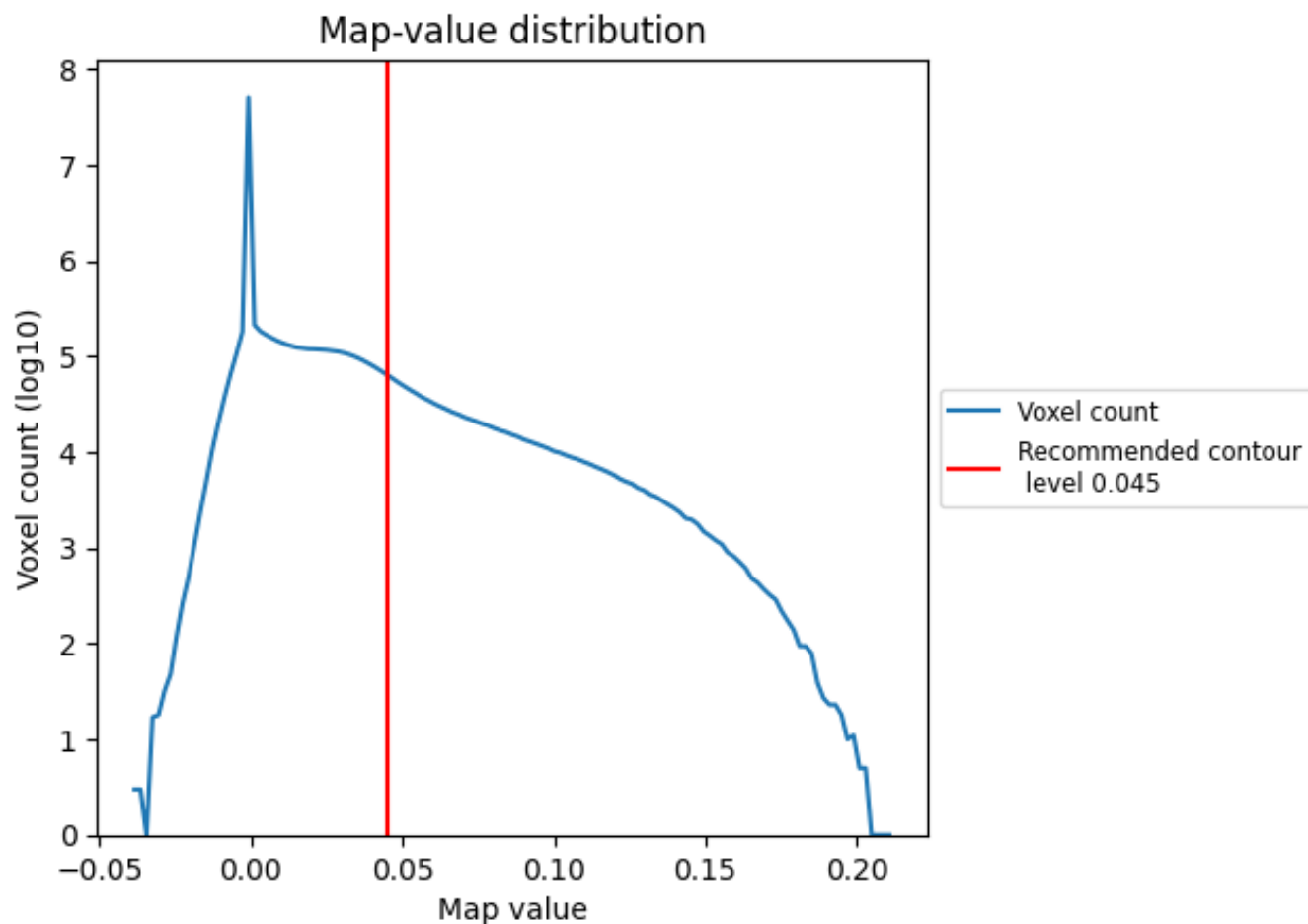
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

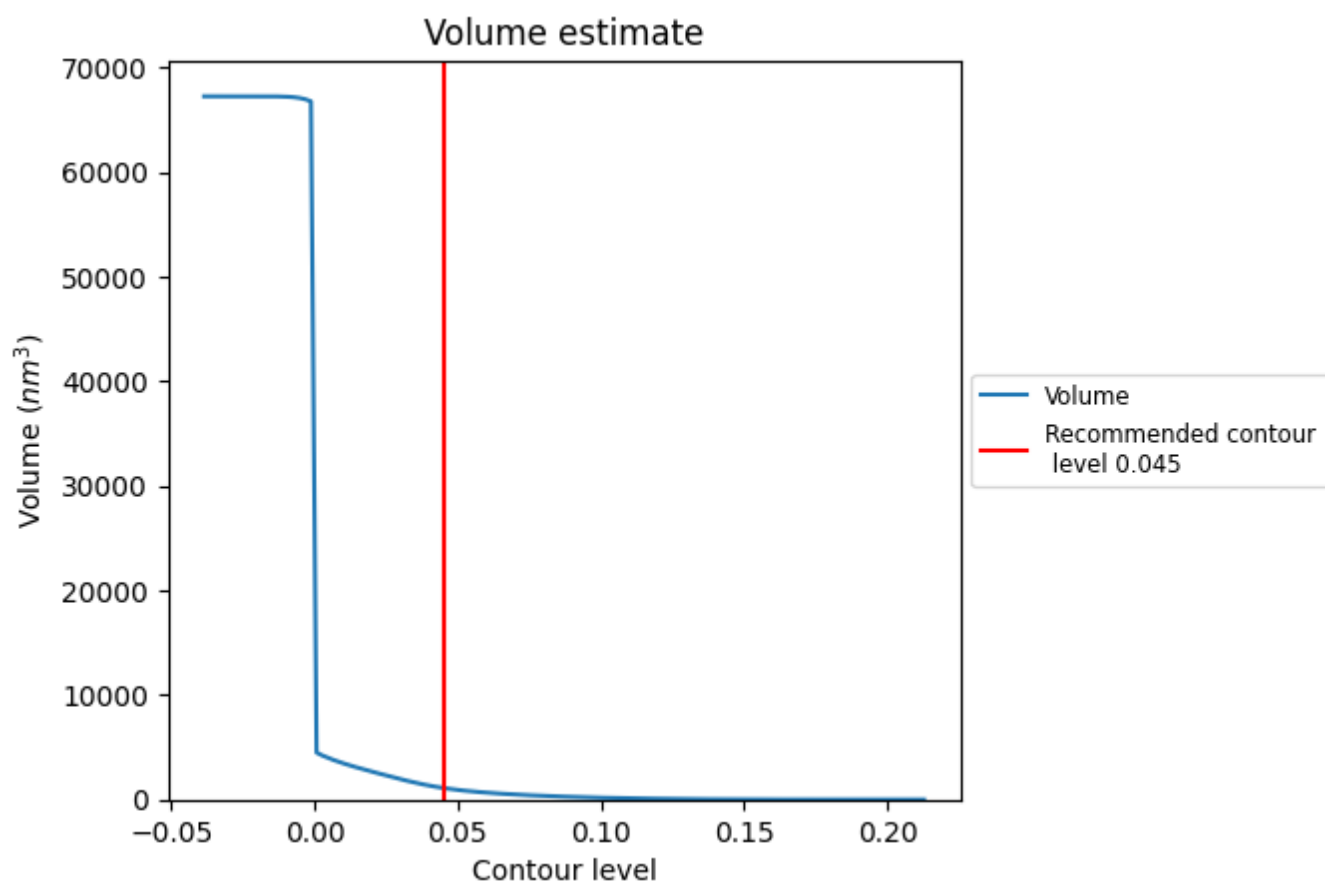
This section contains the results of statistical analysis of the map.

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.

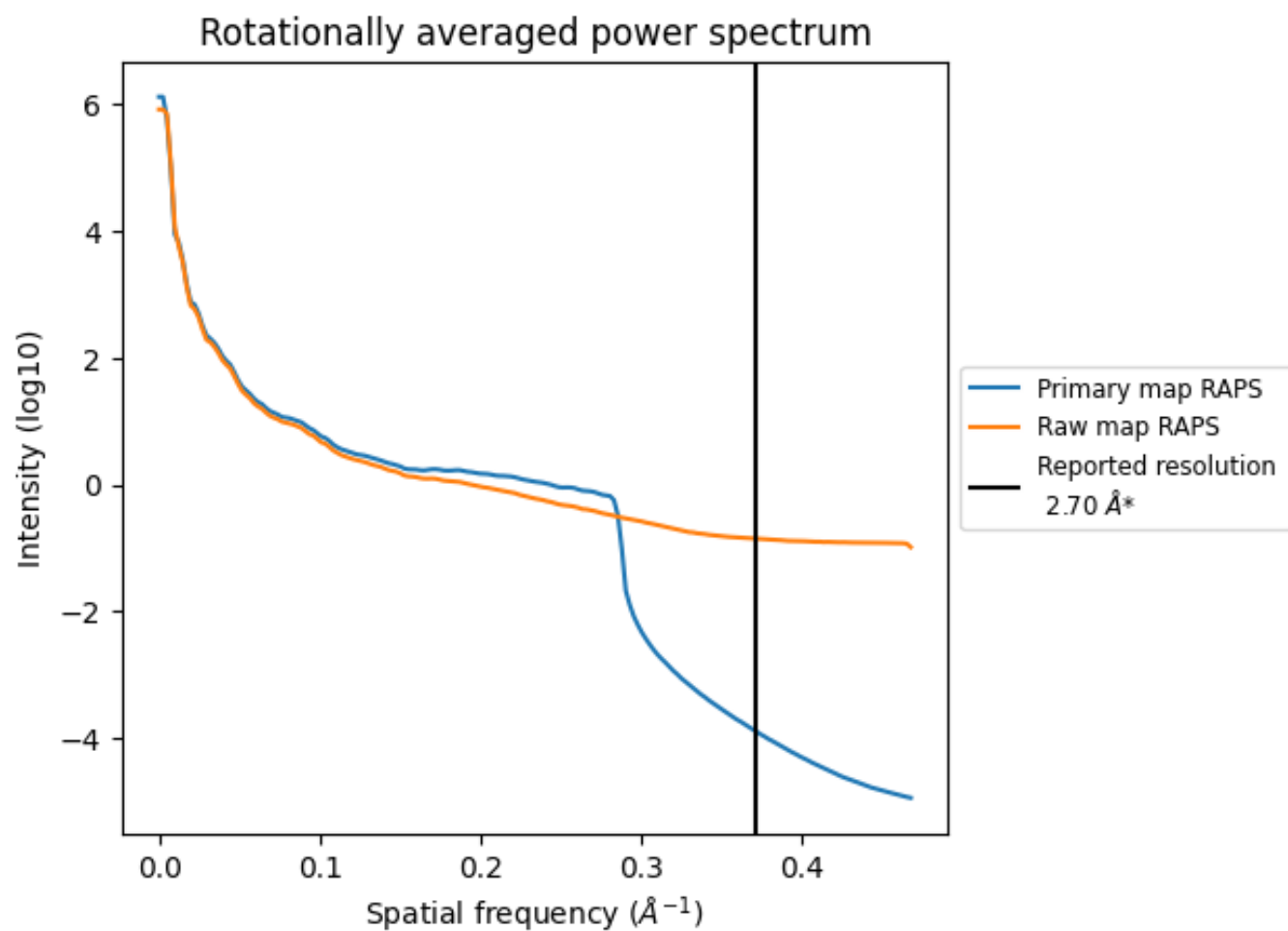
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1110 nm³; this corresponds to an approximate mass of 1002 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 ⓘ

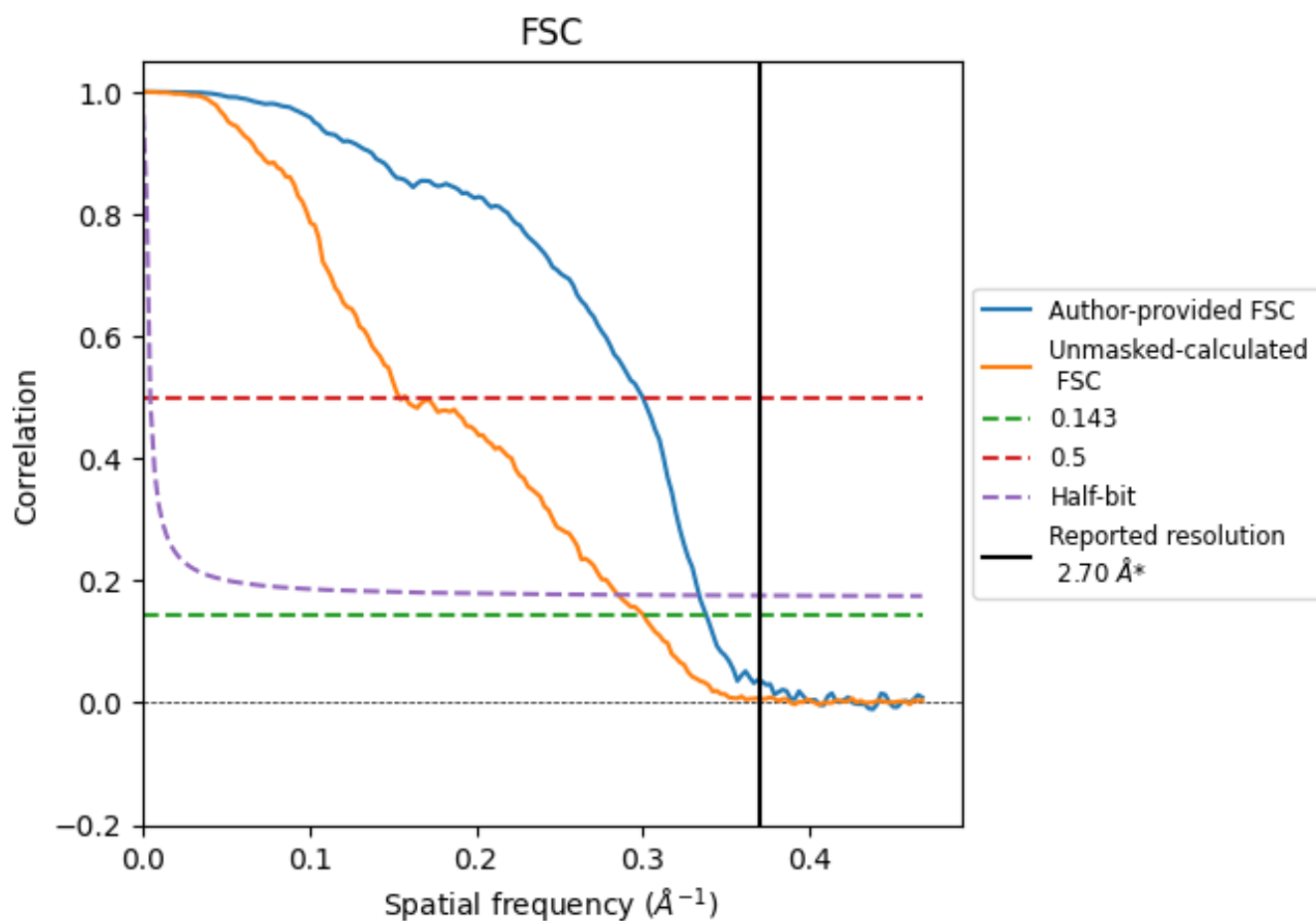


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

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 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

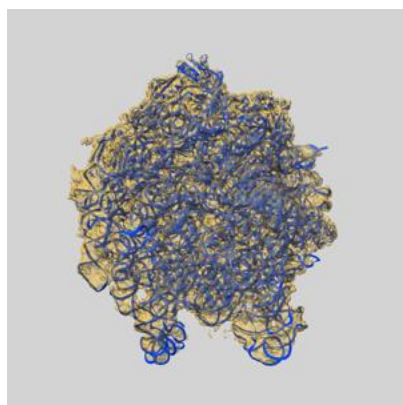
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.96	3.33	3.00
Unmasked-calculated*	3.33	6.49	3.51

*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 3.33 differs from the reported value 2.7 by more than 10 %

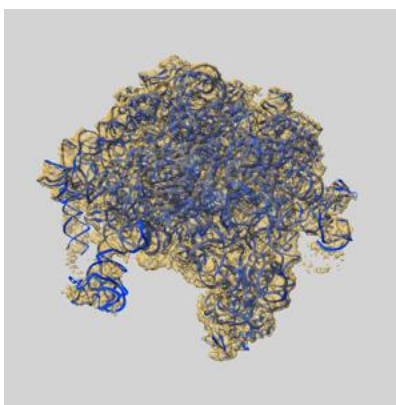
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37560 and PDB model 8WI8. Per-residue inclusion information can be found in section [3](#) on page [9](#).

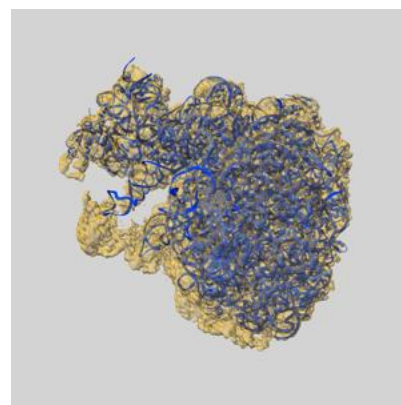
9.1 Map-model overlay [i](#)



X



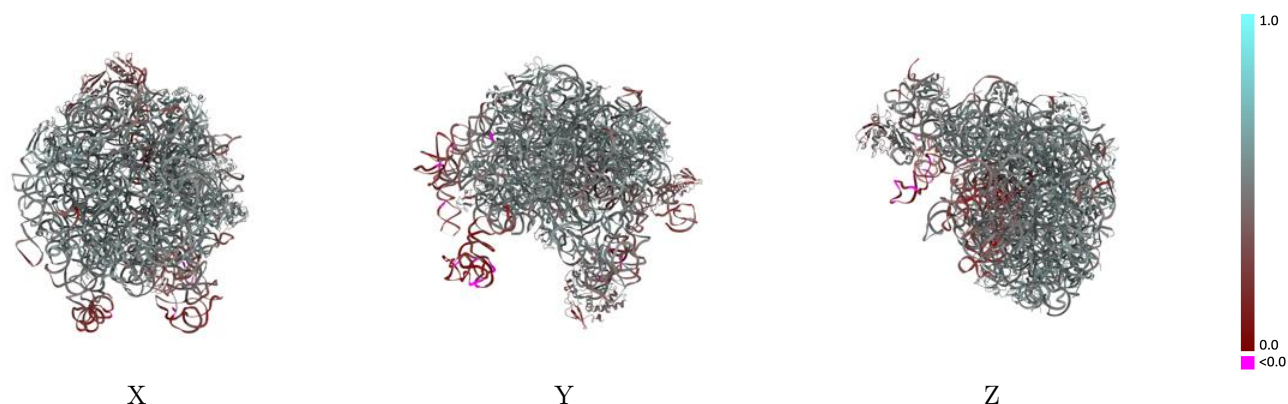
Y



Z

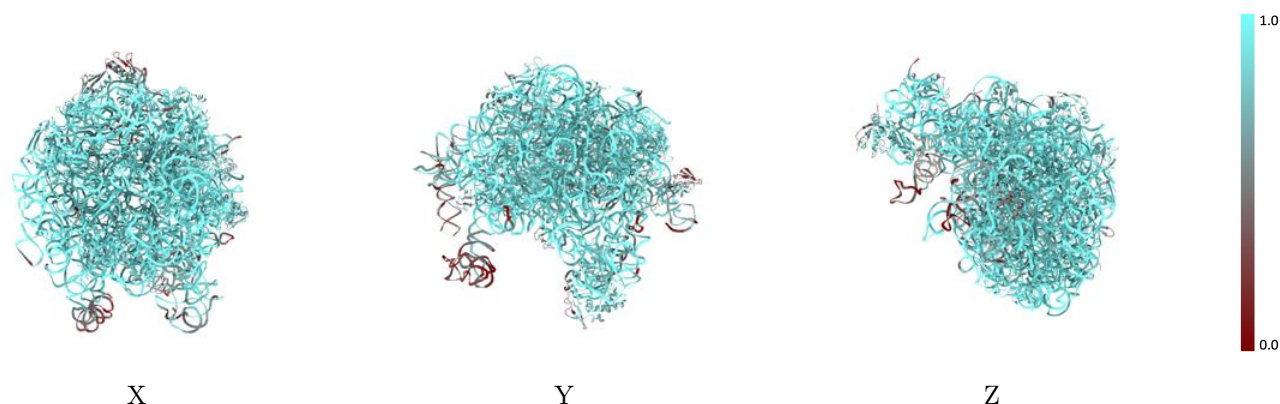
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



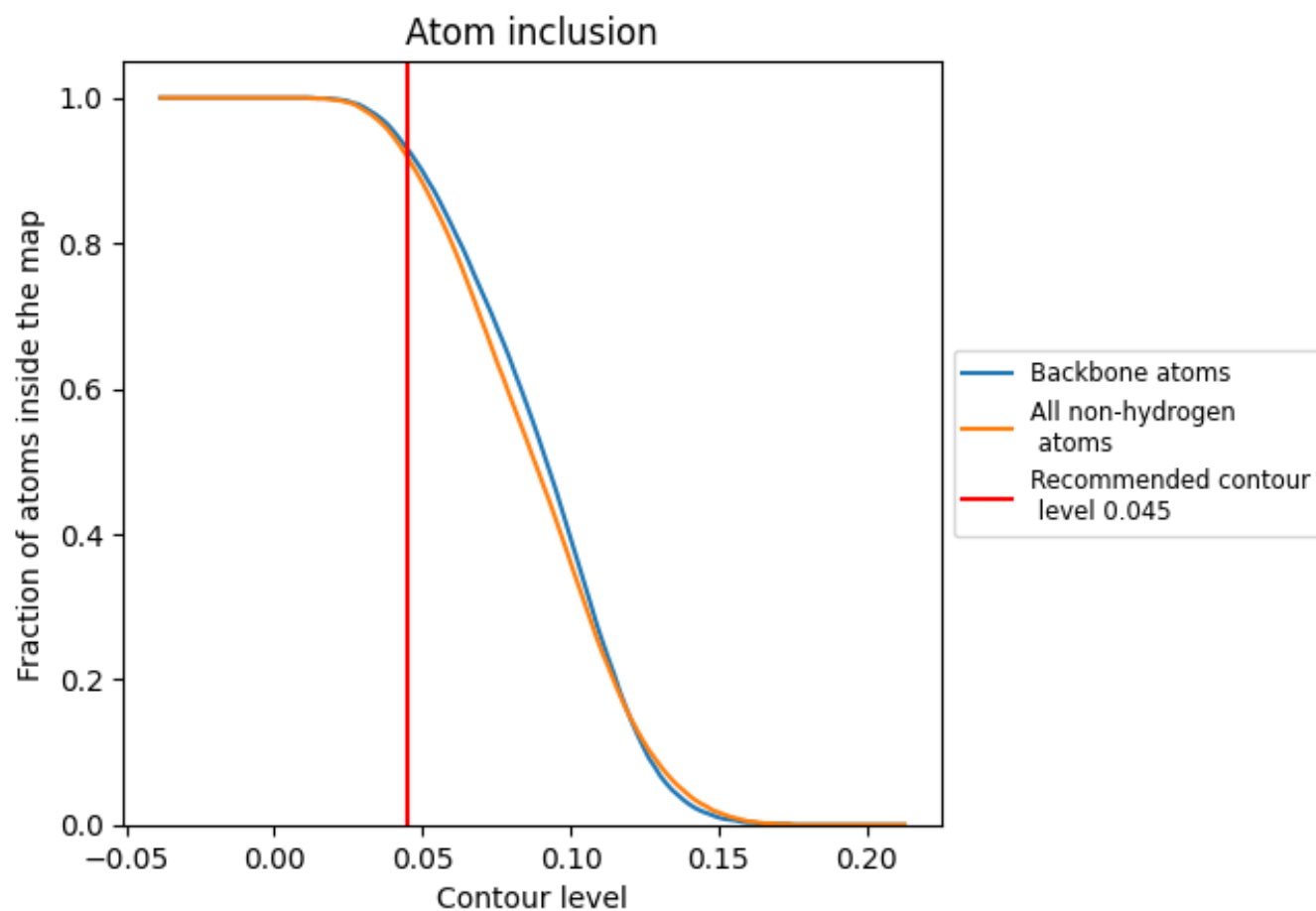
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.4740
1	 0.8980	 0.4910
2	 0.8470	 0.4960
3	 0.9060	 0.5350
4	 0.5580	 0.2870
5	 0.8480	 0.5190
6	 0.7050	 0.4680
7	 0.9970	 0.5480
8	 0.9080	 0.5400
A	 0.9290	 0.4650
B	 0.9560	 0.4540
E	 0.9730	 0.5470
F	 0.9340	 0.5390
G	 0.8950	 0.5170
H	 0.8070	 0.4310
I	 0.5430	 0.3030
J	 0.6970	 0.4270
M	 0.9410	 0.5370
N	 0.9500	 0.5350
O	 0.8930	 0.5270
Q	 0.9700	 0.5470
R	 0.8190	 0.4670
S	 0.9330	 0.5260
T	 0.9540	 0.5340
U	 0.8940	 0.5500
V	 0.9690	 0.5430
W	 0.9060	 0.5270
X	 0.8350	 0.4990
Z	 0.9530	 0.5360

