



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 08:03 PM UTC

PDB ID : 8WIC / pdb_00008wic
EMDB ID : EMD-37563
Title : Cryo- EM structure of Mycobacterium smegmatis 50S ribosomal subunit (body 1) of 70S ribosome, E- tRNA and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 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:

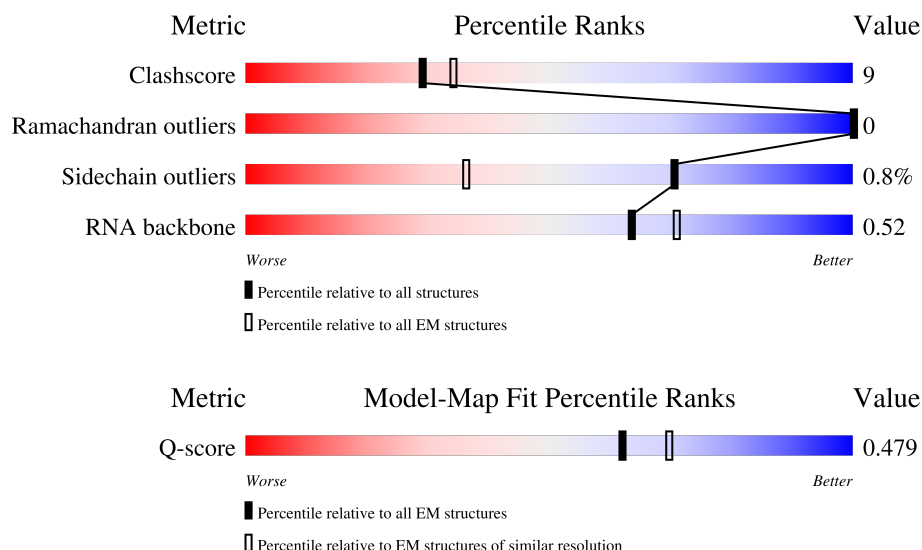
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	
2	F	217	
3	G	215	

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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	

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Mol	Chain	Length	Quality of chain
29	C	76	36% 46% 18%

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 91332 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	209	Total	C	N	O	S	0	0
			1563	969	305	285	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	208	Total	C	N	O	S	0	0
			1562	965	294	301	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	180	Total	C	N	O	S	0	0
			1428	897	267	258	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	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	125	Total	C	N	O	0	0
			951	583	198	170		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	S	112	Total	C	N	O	0	0
			899	565	170	164		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	123	Total	C	N	O	0	0
			982	610	202	170		

- 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	113	Total	C	N	O	0	0
			864	538	170	156		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	96	Total	C	N	O	0	0
			751	476	137	138		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	92	Total	C	N	O	S	0	0
			706	441	132	131	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	77	Total	C	N	O	0	0
			574	355	121	98		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	62	Total	C	N	O	S	0	0
			465	280	102	79	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	58	Total	C	N	O	0	0
			470	290	94	86		

- 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 L33A.

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	63	Total	C	N	O	0	0
			502	302	115	85		

- 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	3022	Total	C	N	O	P	0	0
			64906	28929	11938	21017	3022		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	117	Total	C	N	O	P	0	0
			2502	1117	465	803	117		

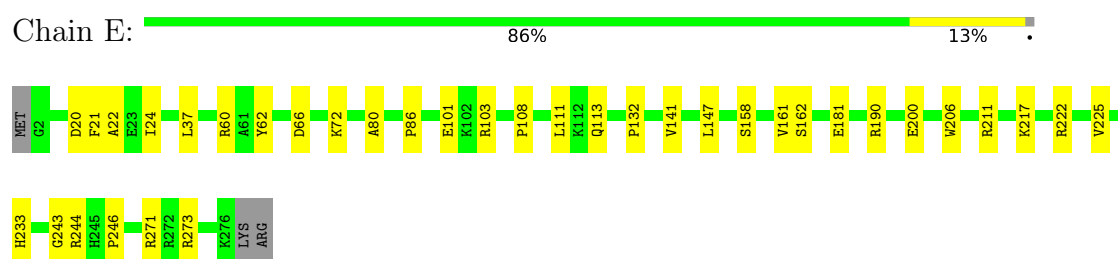
- Molecule 29 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	C	76	Total	C	N	O	P	0	0
			1622	723	294	529	76		

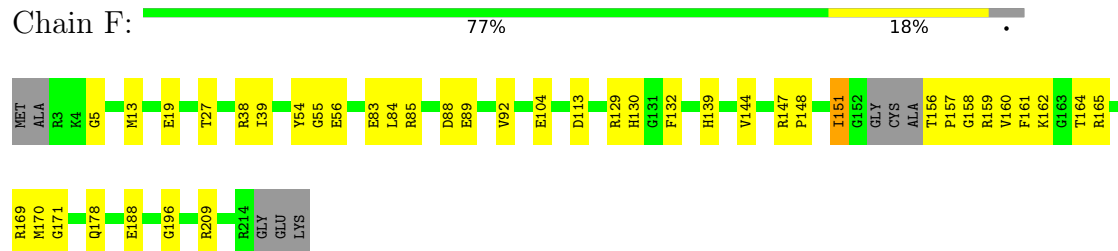
3 Residue-property plots [i](#)

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

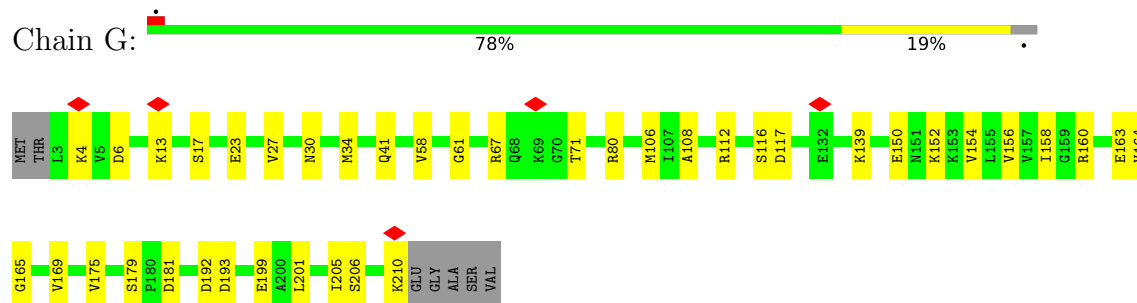
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4



- Molecule 4: 50S ribosomal protein L5





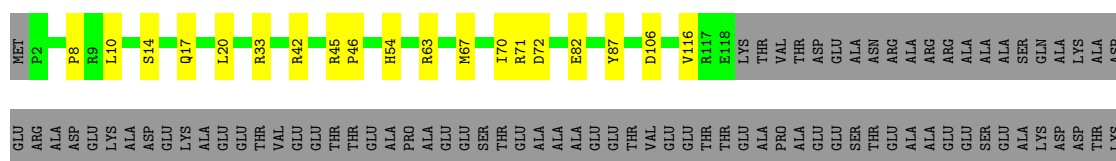
- Molecule 9: 50S ribosomal protein L15

Chain O: 82% 16%



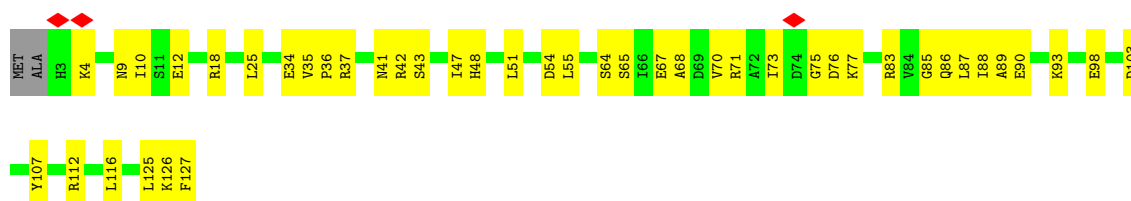
- Molecule 10: 50S ribosomal protein L17

Chain Q: 49% 10% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R: 64% 35%



- Molecule 12: 50S ribosomal protein L19

Chain S: 83% 16%



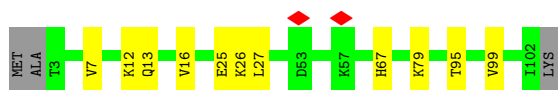
- Molecule 13: 50S ribosomal protein L20

Chain T: 76% 19% 5%



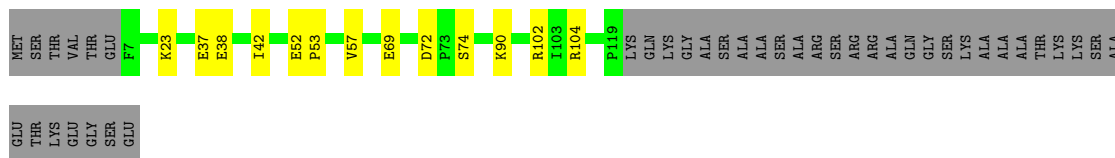
- Molecule 14: 50S ribosomal protein L21

Chain U: 86% 11%



- Molecule 15: 50S ribosomal protein L22

Chain V: 65% 8% 26%



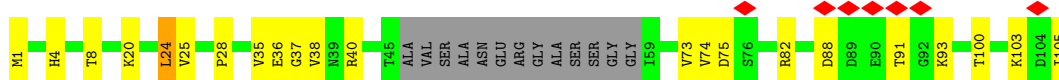
- Molecule 16: 50S ribosomal protein L23

Chain W: 83% 13% .



- Molecule 17: 50S ribosomal protein L24

Chain X: 7% 67% 20% . 12%



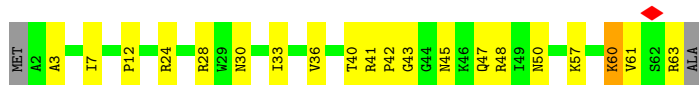
- Molecule 18: 50S ribosomal protein L27

Chain Z: 74% 14% 13%



- Molecule 19: 50S ribosomal protein L28

Chain 1: 66% 30% . .



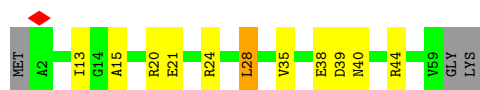
- Molecule 20: 50S ribosomal protein L29

Chain 2: 58% 23% 18%



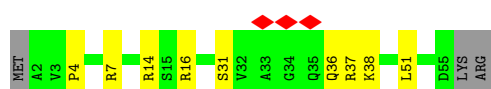
- Molecule 21: 50S ribosomal protein L30

Chain 3:  77% 16% 5%



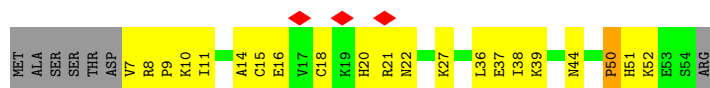
- Molecule 22: 50S ribosomal protein L32

Chain 5:  79% 16% 5%



- Molecule 23: 50S ribosomal protein L33A

Chain 6:  49% 36% 13%



- Molecule 24: 50S ribosomal protein L34

Chain 7:  74% 23% 3%

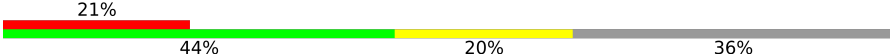


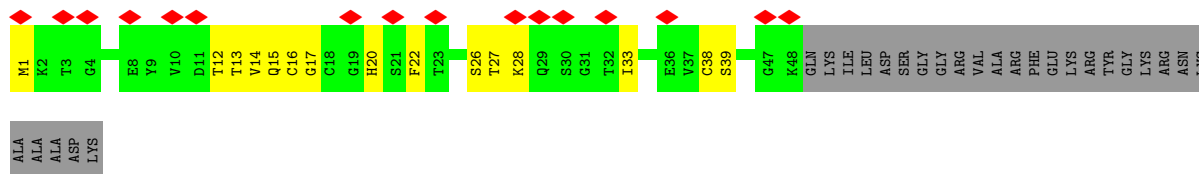
- Molecule 25: 50S ribosomal protein L35

Chain 8:  81% 17% 2%



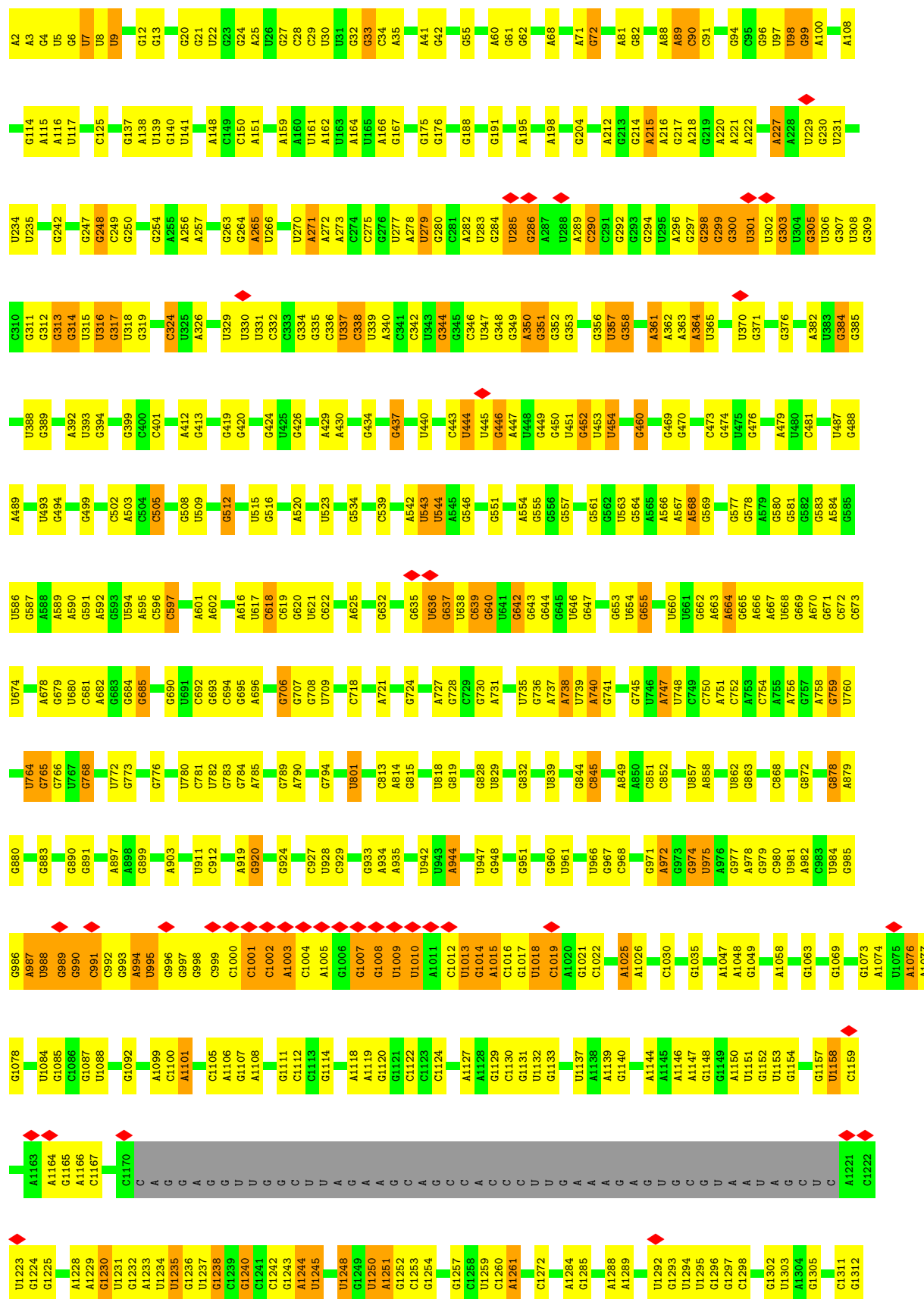
- Molecule 26: 50S ribosomal protein L31

Chain 4:  44% 20% 36%

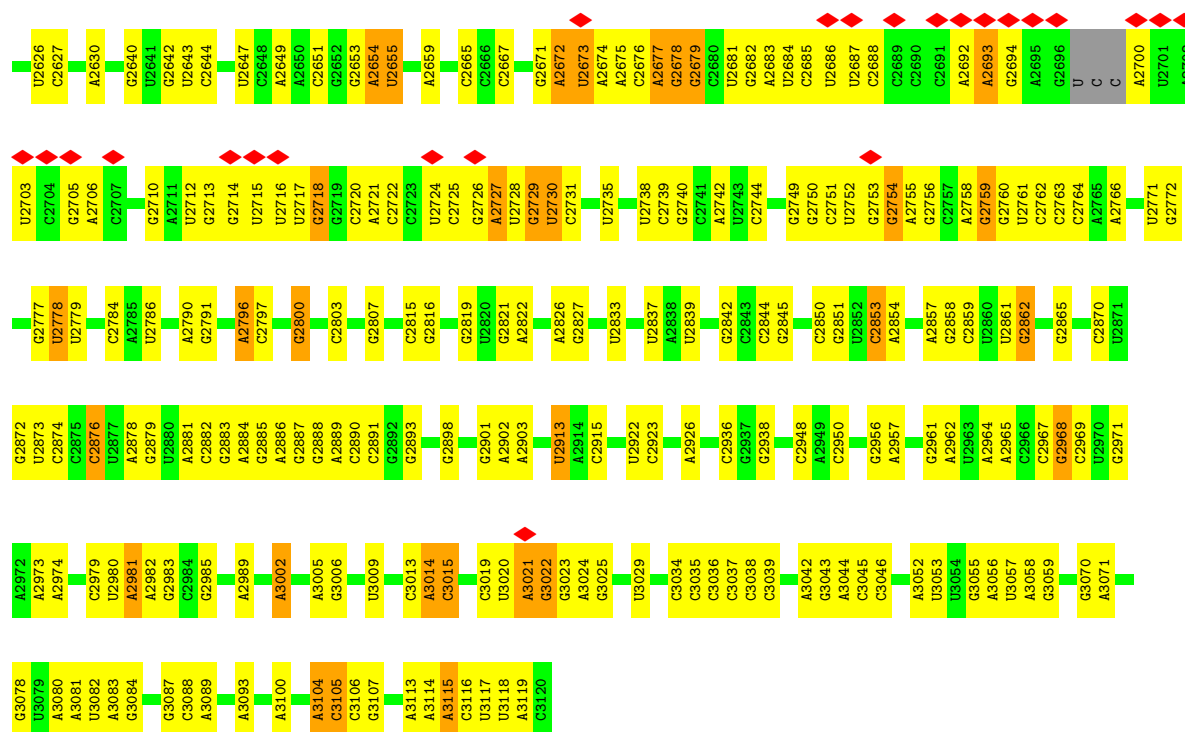


- Molecule 27: 23S rRNA

Chain A:  55% 34% 8%

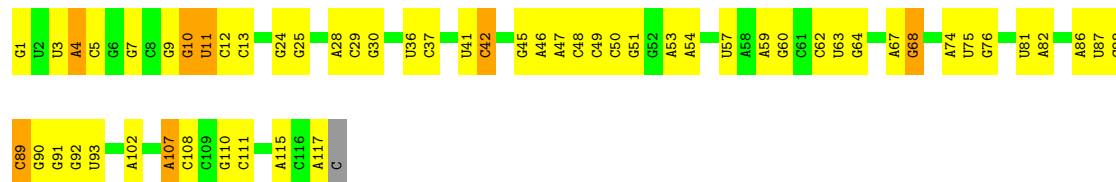


U2541	U2542	U2543	U2544	U2545	U2546	U2547	U2548	U2549	U2550	U2551	U2552	U2553	U2554	U2558	U2559	U2560	U2561	U2562	U2563	U2564	U2567	U2568	U2569	U2570	U2571	U2572	U2573	U2574	U2580	U2581	U2582	U2583	U2584	U2585	U2593	U2599	U2600	U2601	U2602	U2603	U2604	U2605	U2606	U2607	U2608	U2609	U2613	U2614	U2618	U2622	U2623				
A2436	U2443	U2443	U2444	U2445	U2447	U2448	U2448	U2449	U2457	U2458	U2459	U2462	U2463	U2464	U2465	U2466	U2467	U2468	U2469	U2470	U2471	U2472	U2473	U2474	U2482	U2488	U2493	U2494	U2495	U2501	U2502	U2503	U2504	U2507	U2510	U2511	U2512	U2515	U2516	U2527	U2528	U2529	U2530	U2531	U2532	U2536	U2537	U2538	U2539	U2540					
C2369	A2370	U2371	U2372	U2373	U2374	U2375	U2376	U2377	U2378	U2379	U2380	A2381	U2382	U2383	U2384	U2385	U2386	U2387	U2388	U2389	U2390	U2391	U2392	U2393	U2394	U2395	U2396	U2399	U2400	U2401	U2402	U2403	U2404	U2405	U2406	U2407	U2408	U2409	U2410	U2411	U2412	U2413	U2417	U2418	U2419	U2420	U2421	U2422	U2425	U2426	U2427	U2431	U2434	U2435	
A2294	U2295	U2299	U2311	U2315	U2316	U2317	U2318	U2319	U2320	U2321	U2322	U2323	U2324	U2325	U2326	U2327	U2328	U2329	U2330	U2331	U2332	U2333	U2334	U2335	U2336	U2337	U2338	U2339	U2340	U2341	U2342	U2343	U2344	U2347	U2348	U2349	U2350	U2351	U2352	U2353	U2354	U2355	U2356	U2357	U2358	U2359	U2360	U2361	U2362	U2363	U2364	U2365	U2366	U2367	U2368
C2191	U2195	U2196	U2211	U2212	U2215	U2216	U2217	U2221	U2230	U2232	U2233	U2234	U2235	U2236	U2237	U2238	U2239	U2240	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257	U2258	U2261	U2262	U2263	U2264	U2265	U2266	U2267	U2275	U2276	U2279	U2280	U2284	U2285	U2286	U2287	U2288	U2289					
G2074	U2075	U2084	U2085	U2086	U2087	U2088	U2089	U2090	U2091	U2092	U2093	U2094	U2095	U2096	U2097	U2098	U2099	A2106	U2107	U2108	U2109	U2110	U2111	U2113	U2114	U2130	U2137	U2141	U2142	U2143	U2144	U2147	U2148	U2152	U2153	U2154	U2160	U2161	U2162	U2163	U2170	U2171	U2176	U2179	U2188										
U1938	U1939	U1946	U1947	U1948	U1949	U1950	U1955	U1973	U1974	U1975	U1981	U1985	U1986	U1987	U1988	U1989	U1991	U1992	U1996	A2001	A2002	A2003	A2004	U2005	A2006	A2007	A2008	G2016	C2017	G2018	A2019	A2020	A2026	A2029	C2030	U2033	C2043	U2044	U2045	U2046	G2056	U2061	U2062	U2063	U2065	A2070	A2071								
A1792	U1798	U1803	U1804	U1805	U1806	U1807	U1825	U1826	U1840	U1854	U1855	U1859	U1860	U1864	U1865	U1866	U1867	U1870	U1871	U1872	U1876	U1877	U1885	U1888	U1892	U1895	U1896	U1897	U1900	U1901	U1906	U1917	U1918	U1921	U1922	U1923	U1927	U1933	U1937																
G1674	U1675	U1676	U1677	U1678	U1679	U1680	U1681	U1684	U1685	U1690	U1691	U1703	U1704	U1705	U1706	U1707	U1710	U1711	U1714	U1715	U1716	U1717	U1724	U1725	U1726	U1728	U1729	U1730	U1731	U1732	U1733	U1734	U1737	U1738	U1739	U1754	U1755	U1756	U1757	U1758	U1759	U1767	U1786	U1787	U1788	U1789	U1790	U1791							
U	U	G	G	U	U	G	G	G1606	C1607	U1608	C1609	C1610	A1611	U1612	G1613	G1614	A1615	A1616	C1617	U1618	U1619	U1620	C1621	G1622	U1623	U1624	G1625	U1626	U1627	A1628	G1629	U1630	A1631	U1632	U1633	C1634	G1639	U1640	U1641	G1642	G1645	U1646	U1647	U1648	C1649	G1650	C1651	A1656	U1657	U1658	U1659	U1660	G1670	A1673	
G1538	A1539	U1540	G1541	A1542	A1543	U1544	C1545	A1546	U1547	C1548	G1549	U1550	U1551	A1552	C1553	U1554	A1555	U1556	C1557	C1558	U1559	U1560	C1561	C	A	A	A	A	C	C	A	C	C	G	U	G	A	C	C	C	U	U	C	G	G	U	U	U	G	C	G				
G1438	U1444	G1448	C1449	G1452	U1453	U1454	U1455	U1456	U1465	C1466	U1467	A1468	A1469	G1470	G1471	C1472	U1476	C1477	A1480	C1485	U1486	U1487	A1493	U1494	A1499	A1500	C1501	G1502	G1507	A1508	U1509	A1510	U1511	A1518	G1522	U1523	G1524	G1528	U1529	G1530	C1531	G1426	U1533	C1534	C1435	A1536	U1537								



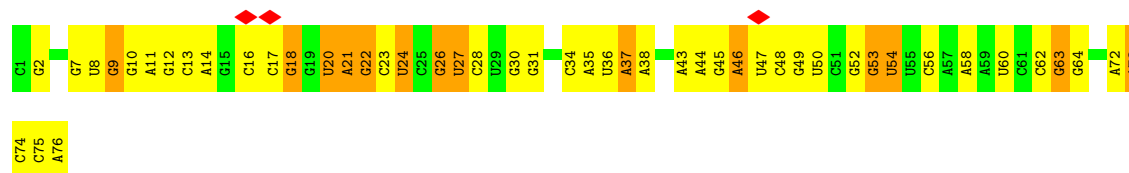
• Molecule 28: 5S rRNA

Chain B: 52% 42% 6%



• Molecule 29: E-tRNA

Chain C: 36% 46% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44299	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE; CTF correction in Relion	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	0.218	Depositor
Minimum map value	-0.037	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	0.32	0/2153	0.34	0/2895
2	F	0.31	0/1584	0.46	1/2130 (0.0%)
3	G	0.32	0/1585	0.47	0/2143
4	H	0.23	0/1450	0.40	0/1951
5	I	0.18	0/1281	0.45	0/1733
6	J	0.31	0/311	0.49	0/419
7	M	0.31	0/1157	0.35	0/1567
8	N	0.30	0/946	0.37	0/1268
9	O	0.29	0/1091	0.39	0/1457
10	Q	0.31	0/936	0.42	0/1256
11	R	0.27	0/961	0.53	0/1291
12	S	0.30	0/913	0.44	0/1226
13	T	0.33	0/994	0.38	0/1333
14	U	0.31	0/764	0.36	0/1030
15	V	0.30	0/878	0.38	0/1192
16	W	0.31	0/761	0.37	0/1023
17	X	0.27	0/712	0.45	0/952
18	Z	0.30	0/583	0.34	0/782
19	1	0.32	0/473	0.52	0/634
20	2	0.28	0/530	0.48	0/708
21	3	0.35	0/473	0.43	0/635
22	5	0.23	0/427	0.32	0/572
23	6	0.39	0/405	0.84	1/542 (0.2%)
24	7	0.35	0/380	0.38	0/500
25	8	0.26	0/507	0.31	0/672
26	4	0.23	0/372	0.47	0/503
27	A	0.31	0/72677	0.31	0/113395
28	B	0.28	0/2799	0.33	0/4362
29	C	0.16	0/1812	0.35	0/2821
All	All	0.30	0/99915	0.34	2/150992 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	6	50	PRO	CA-N-CD	-9.63	98.52	112.00
2	F	151	ILE	N-CA-C	-6.85	106.82	113.53

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	26	0
2	F	1563	0	1608	33	0
3	G	1562	0	1600	33	0
4	H	1428	0	1457	59	0
5	I	1260	0	1300	66	0
6	J	308	0	323	14	0
7	M	1130	0	1167	21	0
8	N	938	0	1000	11	0
9	O	1078	0	1151	20	0
10	Q	919	0	959	16	0
11	R	951	0	986	37	0
12	S	899	0	926	12	0
13	T	982	0	1033	19	0
14	U	754	0	802	9	0
15	V	864	0	903	10	0
16	W	751	0	797	10	0
17	X	706	0	757	15	0
18	Z	574	0	591	11	0
19	1	465	0	479	16	0
20	2	527	0	538	12	0
21	3	470	0	497	8	0
22	5	423	0	463	9	0
23	6	397	0	407	16	0
24	7	377	0	411	6	0
25	8	502	0	541	8	0
26	4	364	0	352	12	0
27	A	64906	0	32656	883	0
28	B	2502	0	1274	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	C	1622	0	825	31	0
All	All	91332	0	57968	1351	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 1351 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	1.55	1.04
27:A:1550:G:H1	27:A:1620:U:H3	1.04	1.04
27:A:2086:U:H3	27:A:2096:G:H1	1.01	0.97
27:A:1754:G:H1	27:A:1759:A:H61	1.13	0.97
27:A:2971:G:N2	27:A:2981:A:H62	1.61	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%)	267 (98%)	6 (2%)	0	100	100
2	F	205/217 (94%)	200 (98%)	5 (2%)	0	100	100
3	G	206/215 (96%)	199 (97%)	7 (3%)	0	100	100
4	H	178/187 (95%)	173 (97%)	5 (3%)	0	100	100
5	I	163/179 (91%)	159 (98%)	4 (2%)	0	100	100
6	J	39/151 (26%)	37 (95%)	2 (5%)	0	100	100
7	M	144/147 (98%)	143 (99%)	1 (1%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	O	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
10	Q	115/199 (58%)	112 (97%)	3 (3%)	0	100	100
11	R	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
12	S	110/113 (97%)	104 (94%)	6 (6%)	0	100	100
13	T	121/129 (94%)	120 (99%)	1 (1%)	0	100	100
14	U	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
15	V	111/153 (72%)	109 (98%)	2 (2%)	0	100	100
16	W	94/100 (94%)	93 (99%)	1 (1%)	0	100	100
17	X	88/105 (84%)	86 (98%)	2 (2%)	0	100	100
18	Z	75/88 (85%)	71 (95%)	4 (5%)	0	100	100
19	1	60/64 (94%)	56 (93%)	4 (7%)	0	100	100
20	2	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
21	3	56/61 (92%)	54 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	52 (100%)	0	0	100	100
23	6	46/55 (84%)	43 (94%)	3 (6%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
26	4	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
All	All	2832/3260 (87%)	2754 (97%)	78 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	159/163 (98%)	155 (98%)	4 (2%)	42	63
3	G	168/173 (97%)	168 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	149/156 (96%)	148 (99%)	1 (1%)	76	78
5	I	139/150 (93%)	137 (99%)	2 (1%)	59	71
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	117 (98%)	2 (2%)	53	70
8	N	100/100 (100%)	99 (99%)	1 (1%)	68	75
9	O	112/114 (98%)	111 (99%)	1 (1%)	70	76
10	Q	96/158 (61%)	95 (99%)	1 (1%)	68	75
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	99/100 (99%)	99 (100%)	0	100	100
13	T	96/99 (97%)	95 (99%)	1 (1%)	68	75
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	89/117 (76%)	89 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	77 (98%)	2 (2%)	42	63
18	Z	56/63 (89%)	56 (100%)	0	100	100
19	1	50/51 (98%)	48 (96%)	2 (4%)	28	54
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	51 (98%)	1 (2%)	50	68
22	5	43/46 (94%)	42 (98%)	1 (2%)	44	64
23	6	46/52 (88%)	46 (100%)	0	100	100
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	2344/2617 (90%)	2325 (99%)	19 (1%)	70	77

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	X	24	LEU
21	3	28	LEU
22	5	37	ARG
19	1	61	VAL
7	M	138	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
22	5	12	ASN
25	8	25	GLN
26	4	42	HIS
23	6	31	ASN
10	Q	54	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3018/3119 (96%)	553 (18%)	15 (0%)
28	B	116/118 (98%)	17 (14%)	1 (0%)
29	C	75/76 (98%)	29 (38%)	3 (4%)
All	All	3209/3313 (96%)	599 (18%)	19 (0%)

5 of 599 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	9	U
27	A	12	G
27	A	20	G
27	A	29	C

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	2729	G
29	C	20	U
29	C	53	G
29	C	17	C
27	A	1002	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 [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.

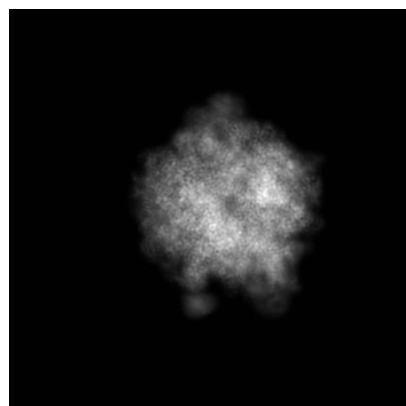
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37563. These allow visual inspection of the internal detail of the map and identification of artifacts.

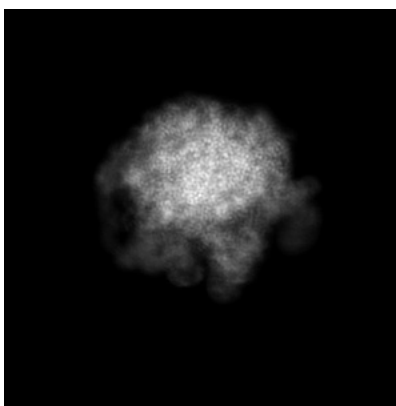
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

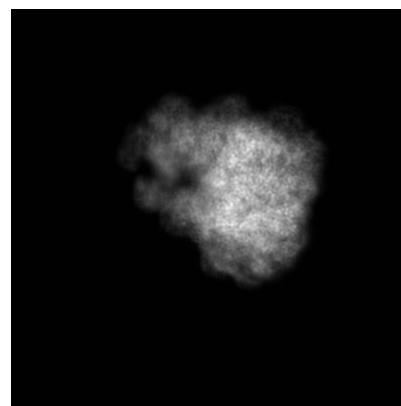
6.1.1 Primary map



X

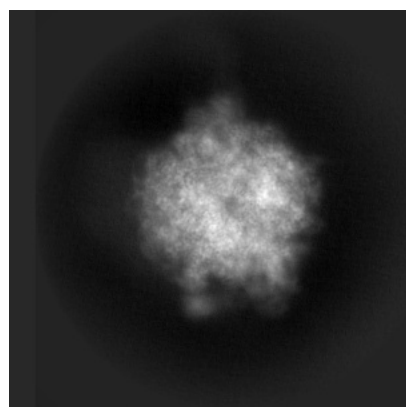


Y

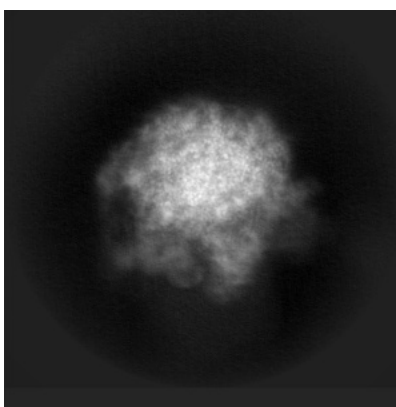


Z

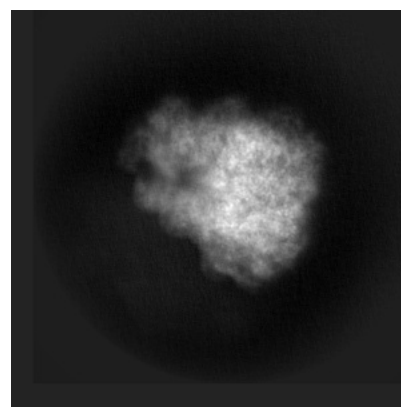
6.1.2 Raw map



X



Y

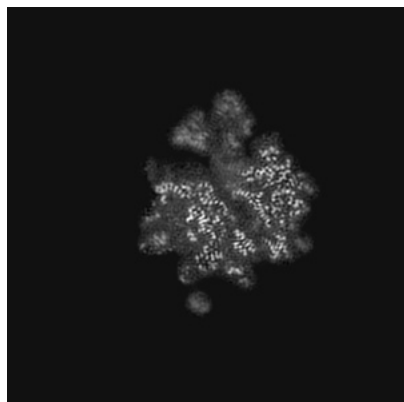


Z

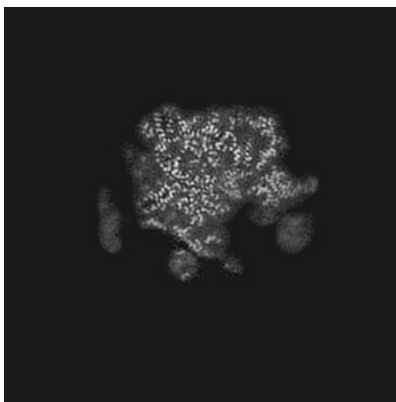
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

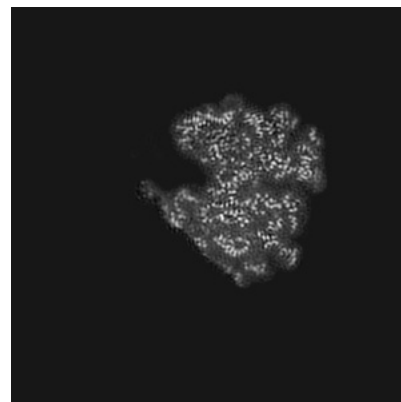
6.2.1 Primary map



X Index: 190

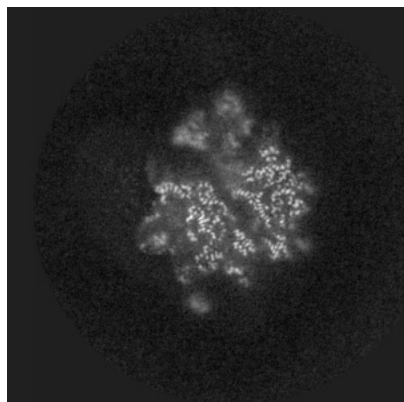


Y Index: 190

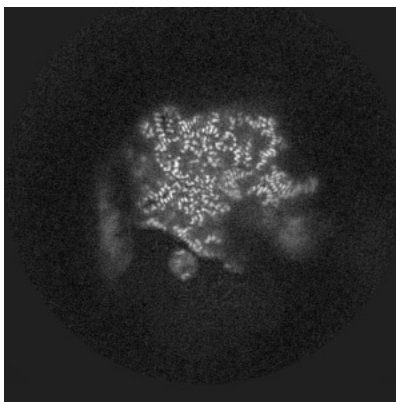


Z Index: 190

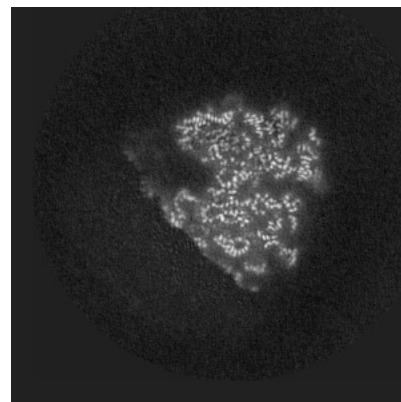
6.2.2 Raw map



X Index: 190



Y Index: 190

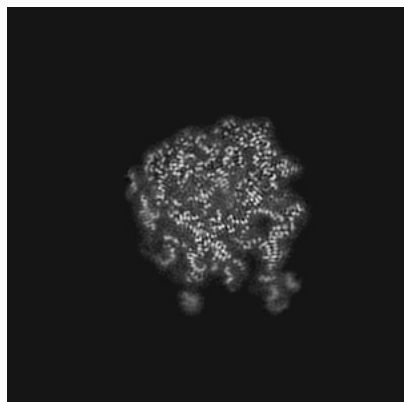


Z Index: 190

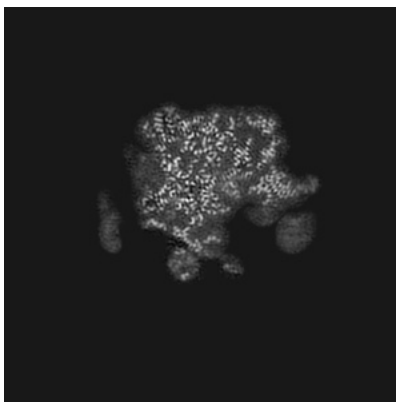
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

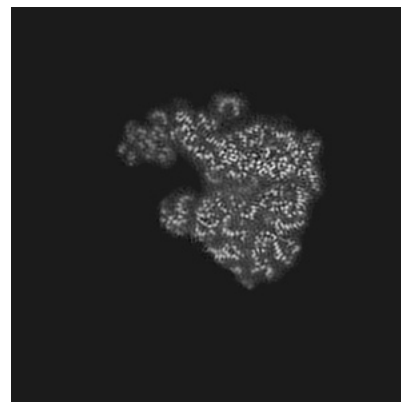
6.3.1 Primary map



X Index: 230

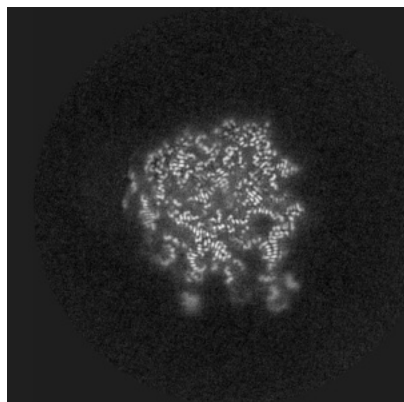


Y Index: 191

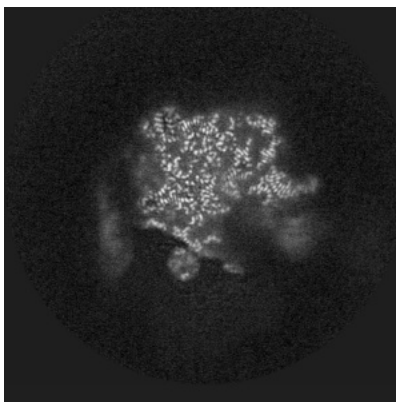


Z Index: 200

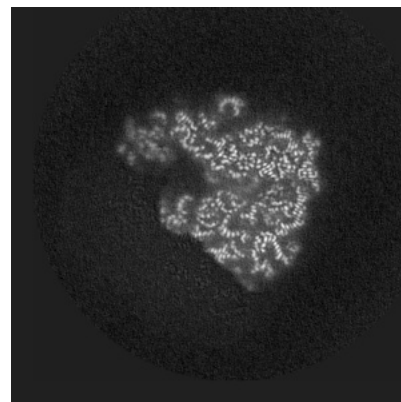
6.3.2 Raw map



X Index: 230



Y Index: 191

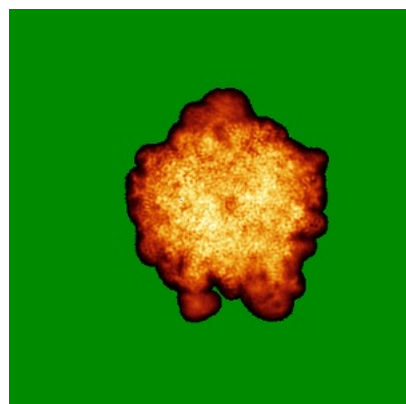


Z Index: 199

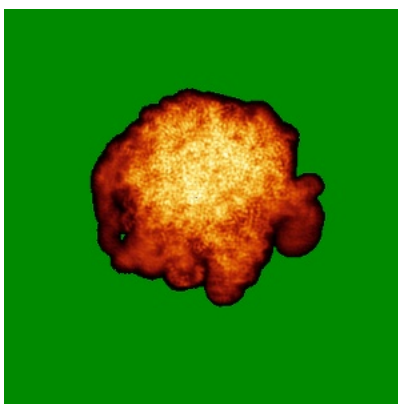
The images above show the largest variance slices of the map in three orthogonal directions.

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

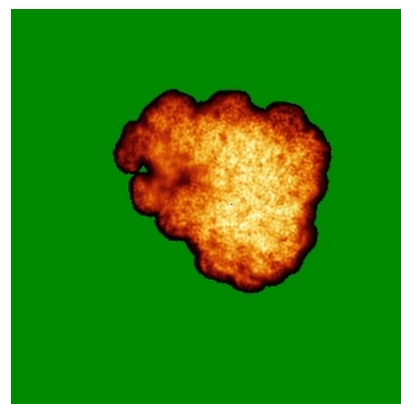
6.4.1 Primary map



X

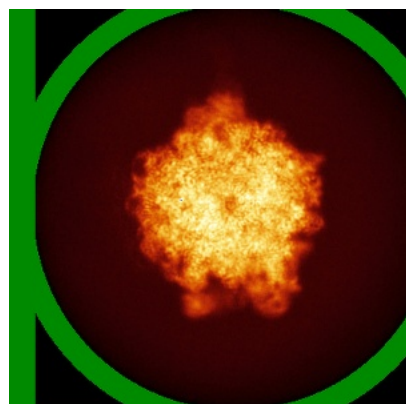


Y



Z

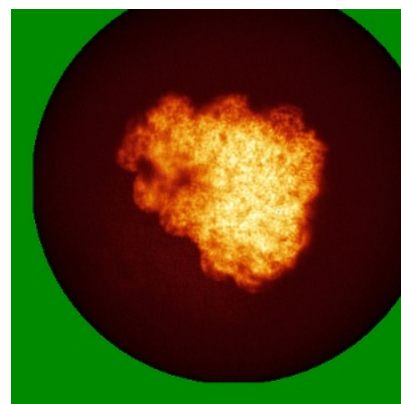
6.4.2 Raw map



X



Y

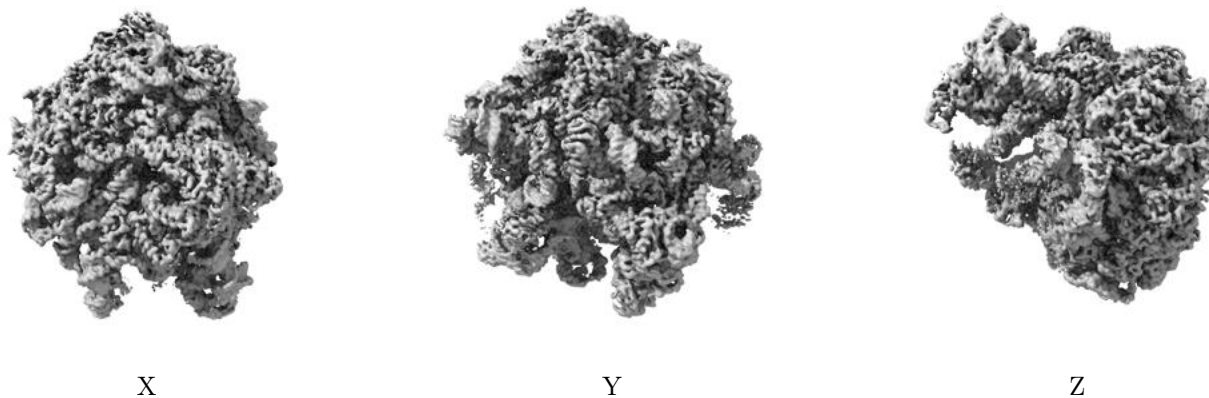


Z

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

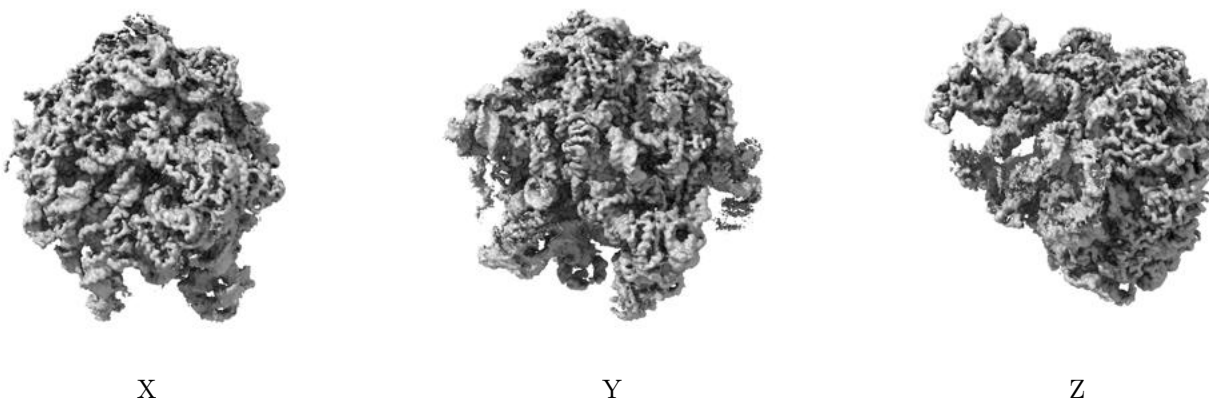
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. 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



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.

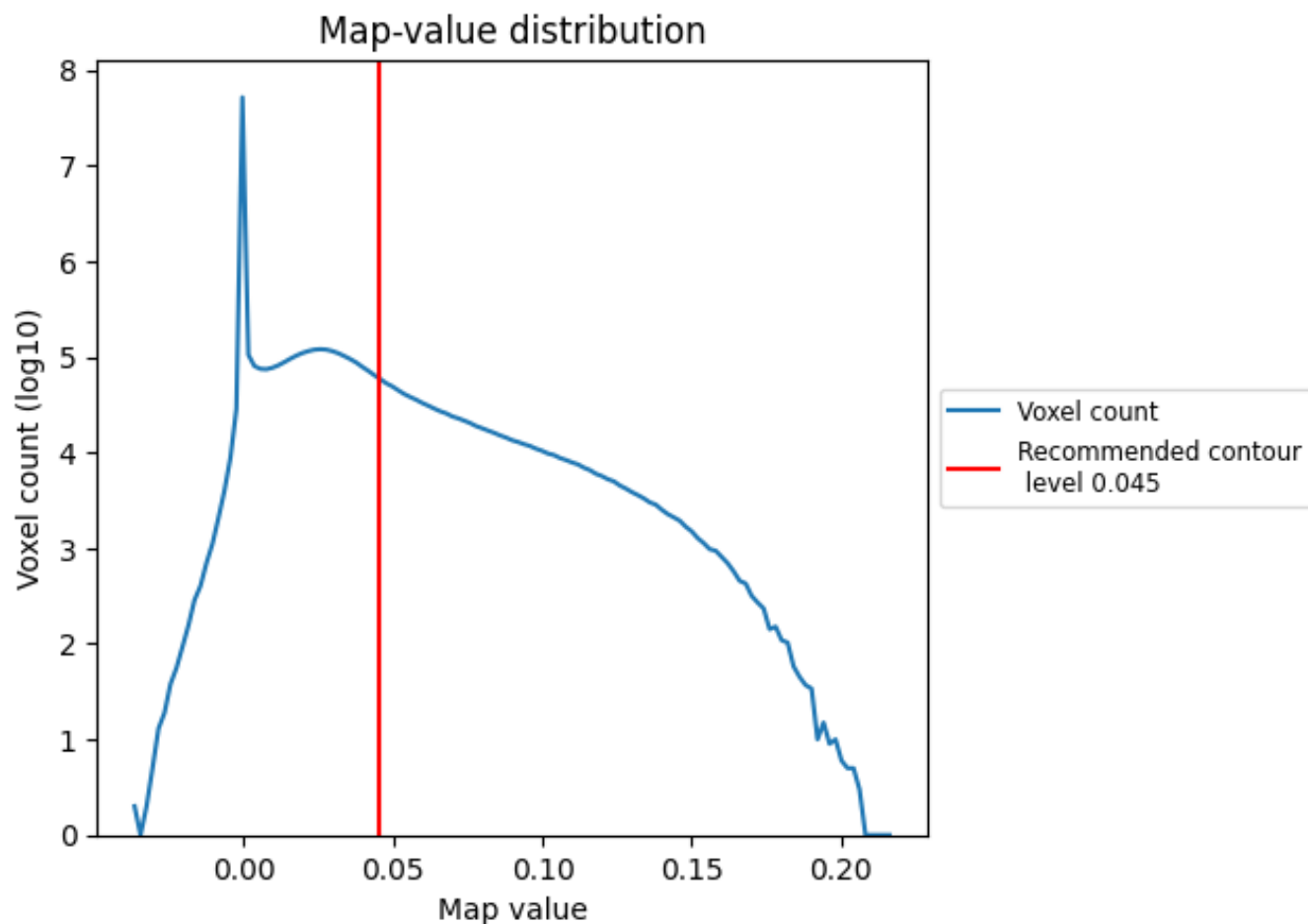
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

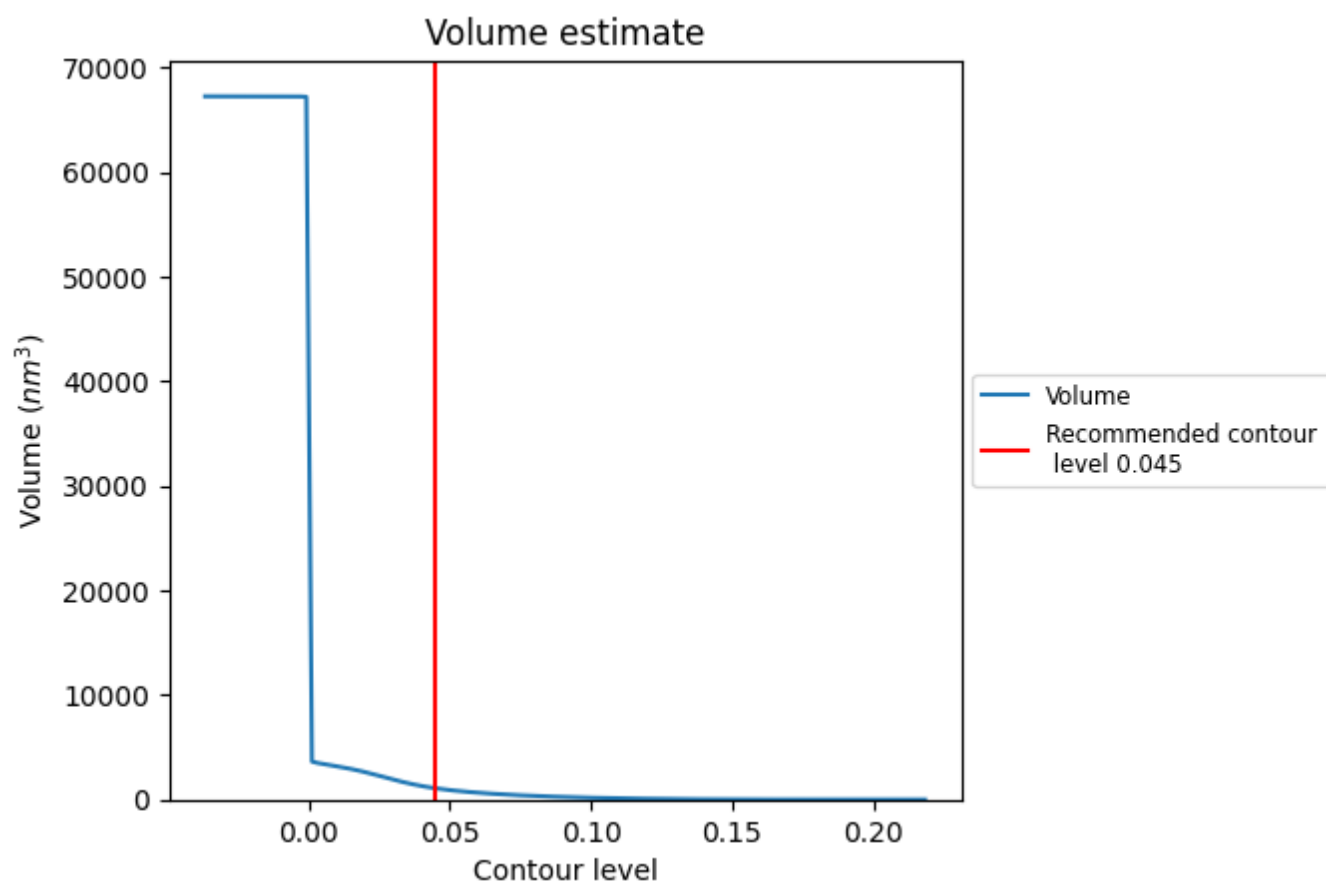
This section contains the results of statistical analysis of the map.

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.

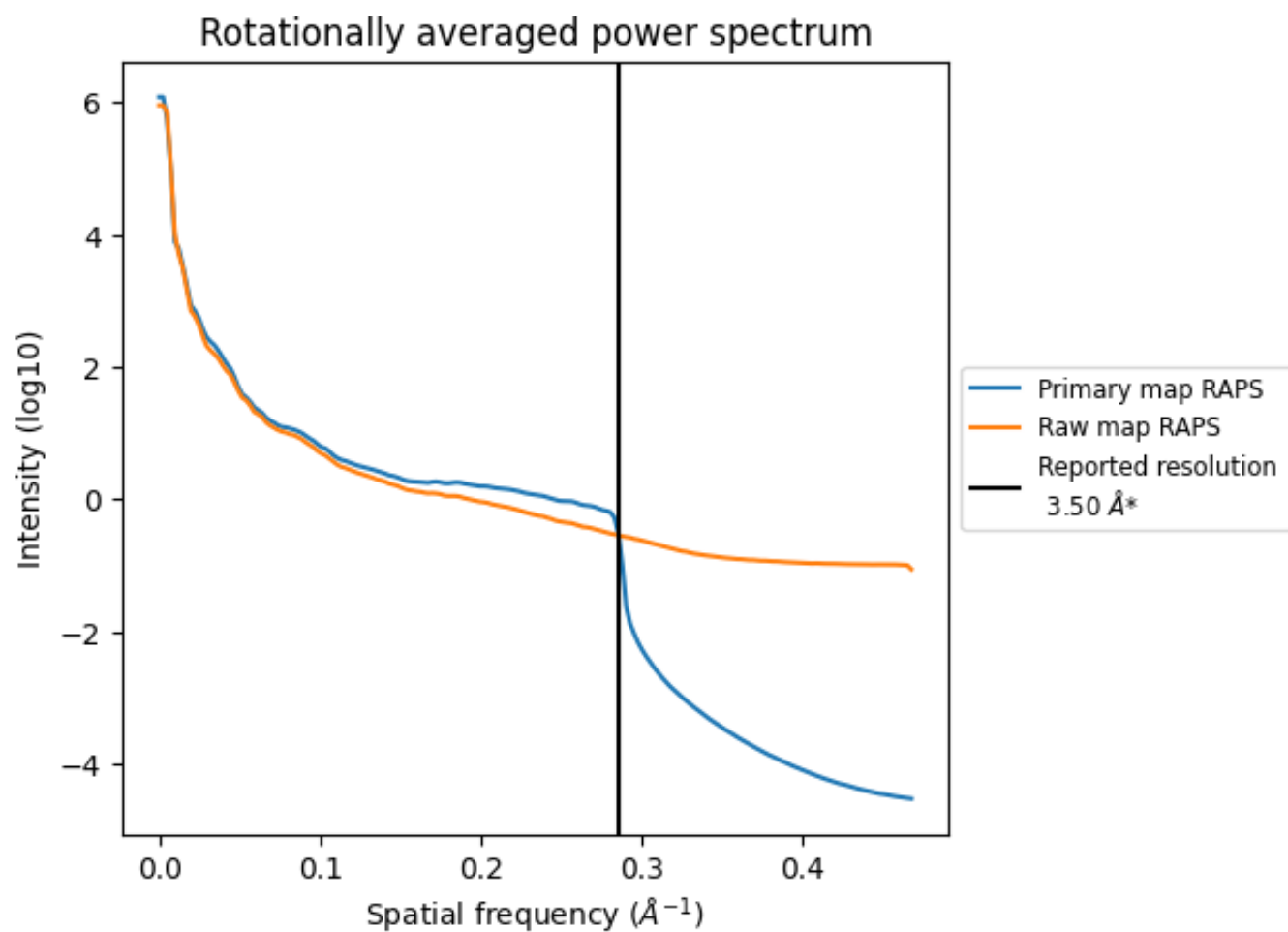
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1077 nm³; this corresponds to an approximate mass of 973 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 ⓘ

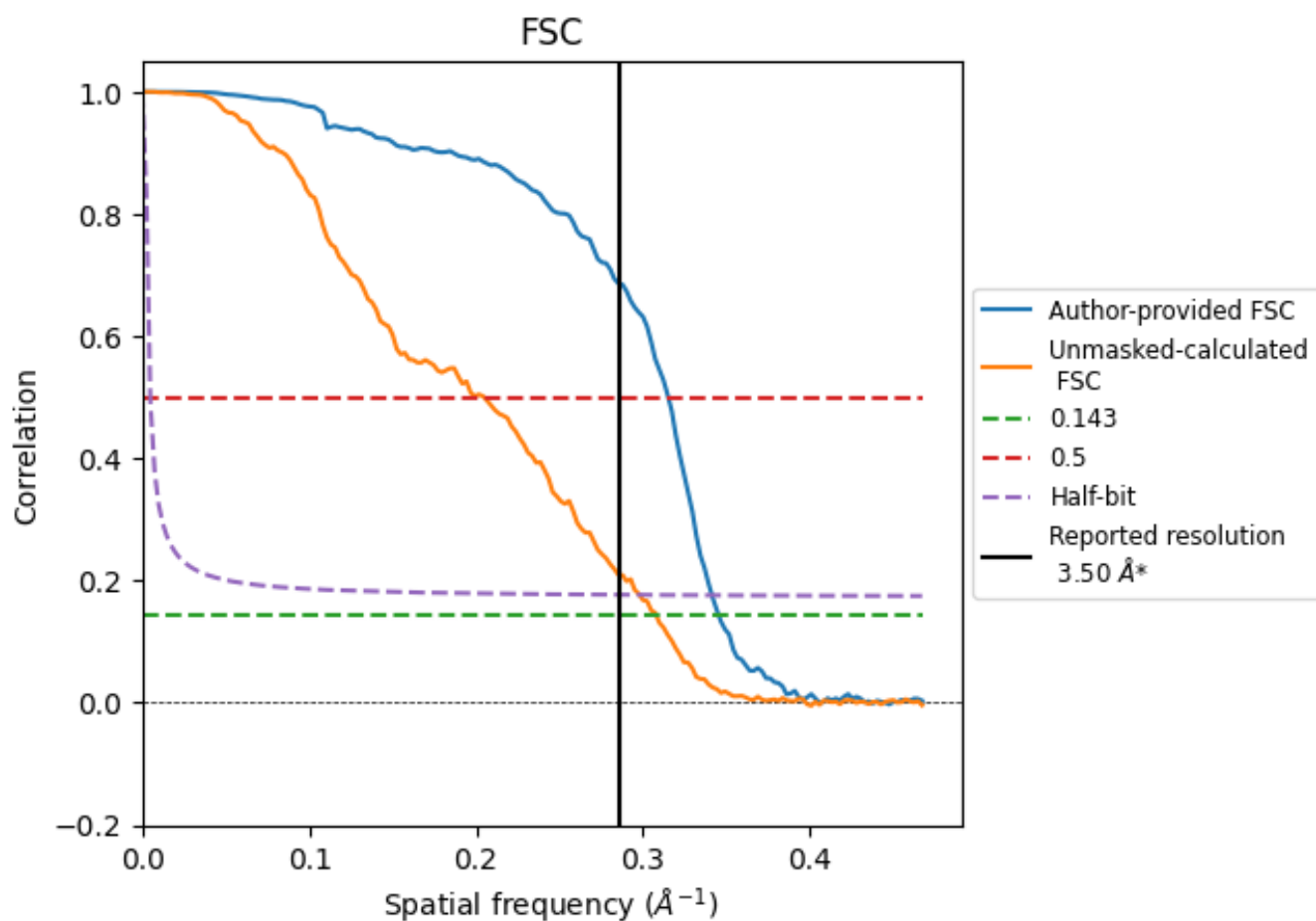


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

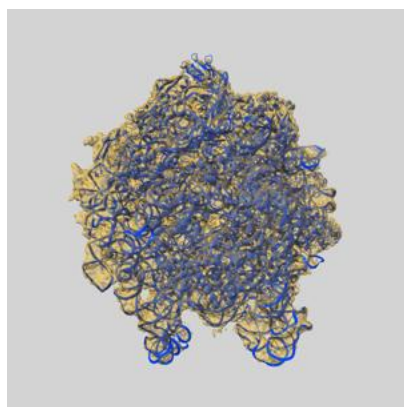
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.50
Author-provided FSC curve	2.90	3.17	2.93	-
Unmasked-calculated*	3.25	4.89	3.36	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

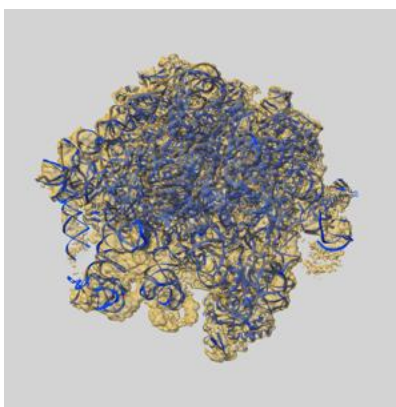
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37563 and PDB model 8WIC. Per-residue inclusion information can be found in section 3 on page 10.

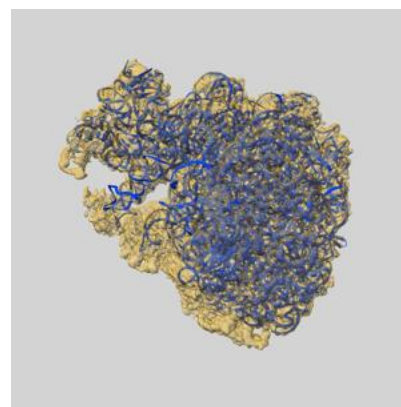
9.1 Map-model overlay [i](#)



X



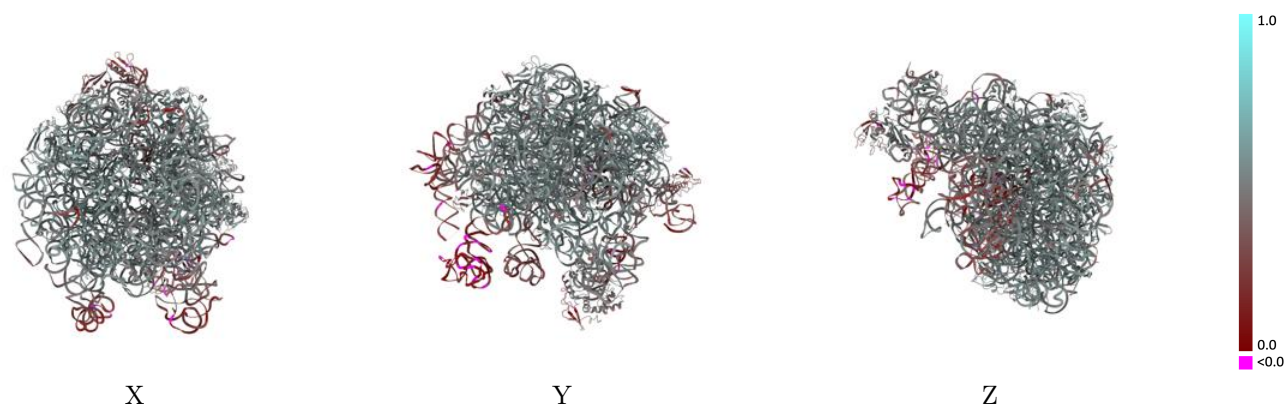
Y



Z

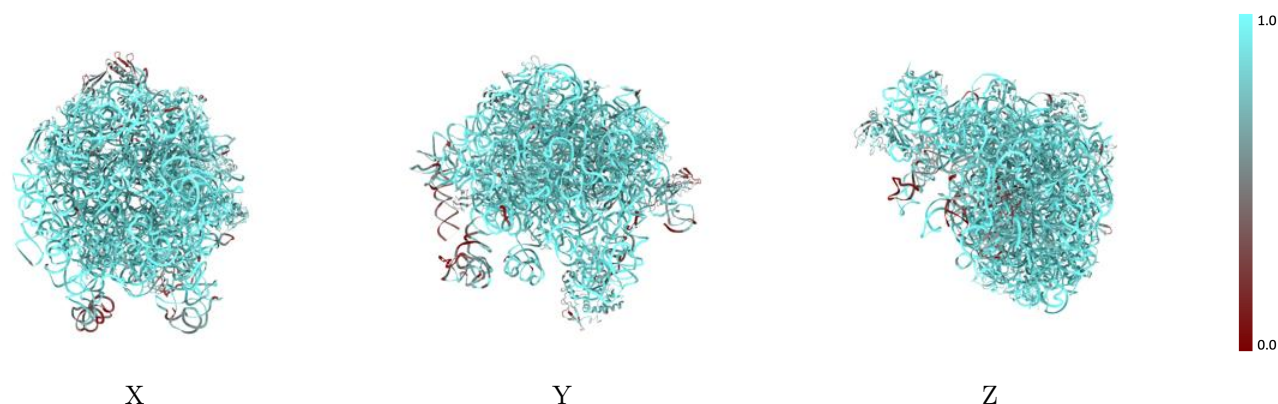
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



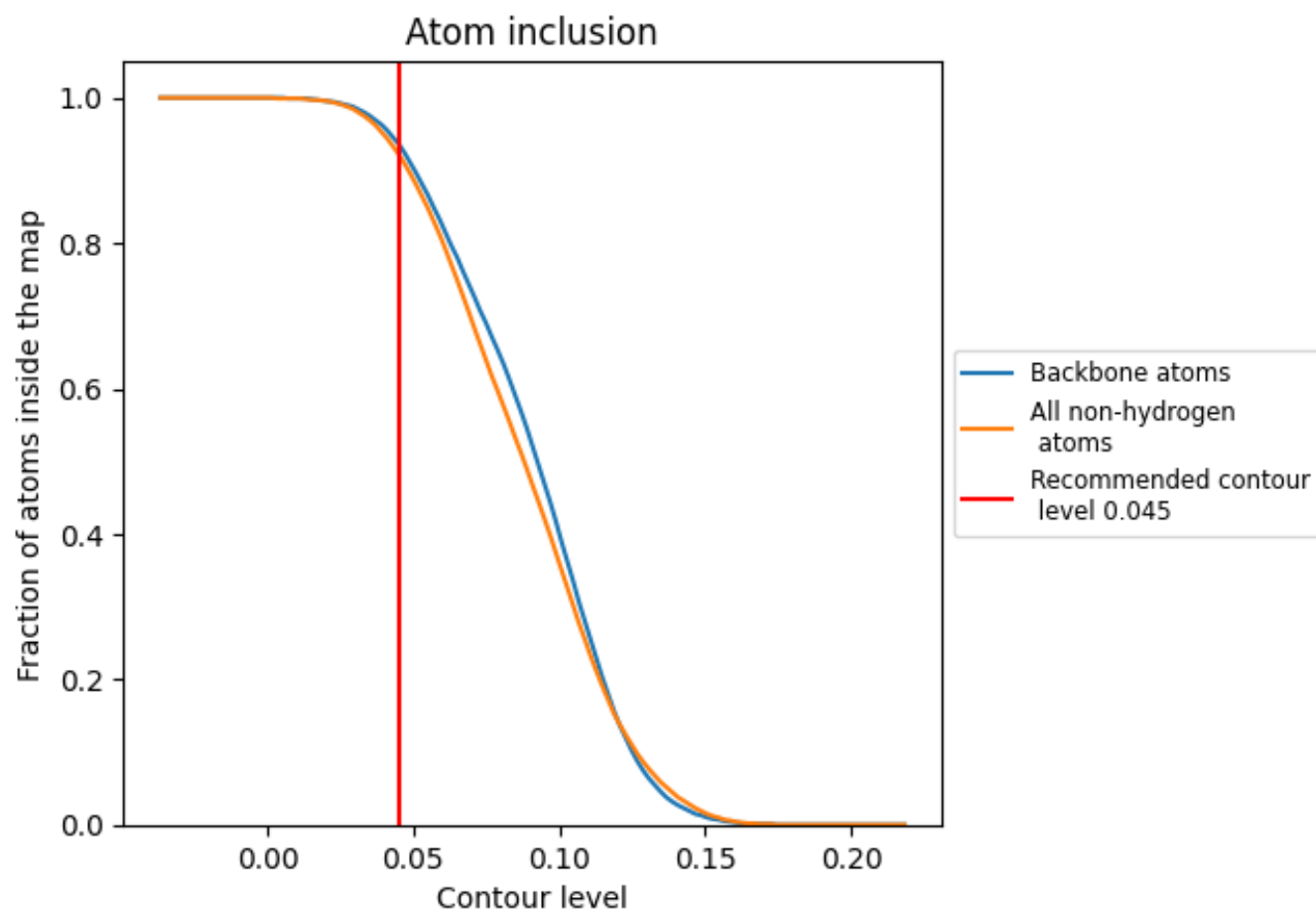
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 94% 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	 0.9220	 0.4790
1	 0.9330	 0.5030
2	 0.8750	 0.5020
3	 0.9080	 0.5350
4	 0.5750	 0.2580
5	 0.8580	 0.5330
6	 0.8320	 0.4410
7	 0.9940	 0.5520
8	 0.9540	 0.5470
A	 0.9350	 0.4760
B	 0.9700	 0.4650
C	 0.8740	 0.2920
E	 0.9700	 0.5510
F	 0.9260	 0.5370
G	 0.8770	 0.5180
H	 0.8110	 0.4510
I	 0.5250	 0.2920
J	 0.6430	 0.3650
M	 0.9310	 0.5380
N	 0.9420	 0.5390
O	 0.9030	 0.5340
Q	 0.9620	 0.5480
R	 0.8480	 0.4800
S	 0.9210	 0.5280
T	 0.9510	 0.5440
U	 0.8850	 0.5530
V	 0.9540	 0.5450
W	 0.9060	 0.5270
X	 0.8140	 0.4930
Z	 0.9370	 0.5390

