



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2026 – 04:26 PM EDT

PDB ID : 9YPH / pdb_00009yph
EMDB ID : EMD-73298
Title : Pseudomonas aeruginosa 50S ribosome (L1 stalk 'in' conformation)
Authors : Findlay, J.L.; Kanik, M.; Gauvin, C.C.; Franklin, M.J.; Lawrence, C.M.
Deposited on : 2025-10-14
Resolution : 2.25 Å (reported)
Based on initial model : 7UNW

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:

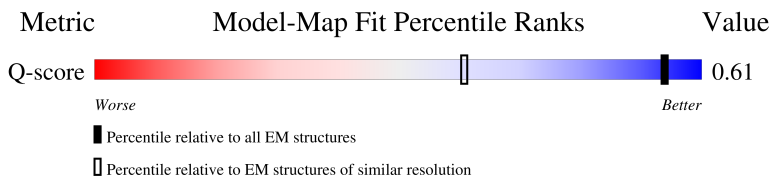
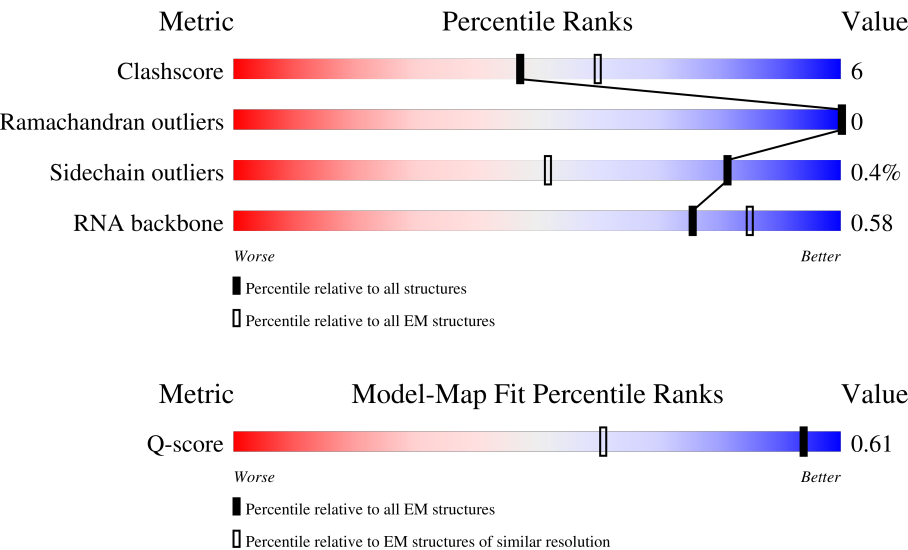
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 2.25 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	3458 (1.75 - 2.75)

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	A	2892	62%32%••
2	B	121	61%31%6%•
3	C	231	5%40%19%41%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	273	
5	E	211	
6	F	200	
7	G	179	
8	H	177	
9	I	148	
10	L	142	
11	M	122	
12	N	144	
13	O	137	
14	P	129	
15	Q	116	
16	R	116	
17	S	118	
18	T	103	
19	U	110	
20	V	99	
21	W	104	
22	X	204	
23	Y	85	
24	Z	78	
25	1	63	
26	2	58	
27	4	60	
28	5	51	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	6	44	 84%16%
30	7	64	 81%17%
31	8	38	 89%11%
32	v	76	 47%46%7%13%
33	J	166	 13%51%16%33%
34	K	143	 20%83%17%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 98470 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2837	Total	C	N	O	P	0	0
			60895	27173	11178	19708	2836		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	119	Total	C	N	O	P	0	0
			2535	1132	452	832	119		

- Molecule 3 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	136	Total	C	N	O	S	0	0
			1040	658	185	196	1		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	272	Total	C	N	O	S	0	0
			2072	1276	426	364	6		

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	208	Total	C	N	O	S	0	0
			1564	968	298	293	5		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	200	Total	C	N	O	S	0	0
			1521	955	283	280	3		

- Molecule 7 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	179	Total	C	N	O	S	0	0
			1435	914	256	260	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	174	Total	C	N	O	S	0	0
			1314	828	242	242	2		

- Molecule 9 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	115	Total	C	N	O	S	0	0
			858	539	152	166	1		

- Molecule 10 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	142	Total	C	N	O	S	0	0
			1130	718	206	202	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 12 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	137	Total	C	N	O	S	0	0
			1085	689	211	181	4		

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	119	Total	C	N	O	S	0	0
			952	595	191	161	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	115	Total	C	N	O	S	0	0
			881	544	174	161	2		

- Molecule 16 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	114	Total	C	N	O	S	0	0
			901	567	171	162	1		

- Molecule 17 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	117	Total	C	N	O	S	0	0
			936	592	196	148			

- Molecule 18 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	103	Total	C	N	O	S	0	0
			822	521	156	143	2		

- Molecule 19 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	110	Total	C	N	O	S	0	0
			833	515	161	153	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	94	Total	C	N	O	S	0	0
			739	472	134	132	1		

- Molecule 21 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	95	Total	C	N	O	S	0	0
			738	466	142	129	1		

- Molecule 22 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	190	Total	C	N	O	S	0	0
			1445	915	262	265	3		

- Molecule 23 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	77	Total	C	N	O	S	0	0
			581	367	112	102			

- Molecule 24 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 26 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2	56	Total	C	N	O	S	0	0
			440	275	86	77	2		

- Molecule 27 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	54	Total	C	N	O	S	0	0
			431	258	91	81	1		

- Molecule 28 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 29 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 30 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	7	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 31 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	8	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 32 is a RNA chain called tRNA-Ala.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	v	76	Total	C	N	O	P	0	0
			1623	723	289	535	76		

- Molecule 33 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	J	111	Total	C	N	O	S	0	0
			840	533	151	155	1		

- Molecule 34 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	K	143	Total	C	N	O	S	0	0
			1046	655	186	201	4		

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	A	196	Total 196	Mg 196	0
35	B	3	Total 3	Mg 3	0
35	D	1	Total 1	Mg 1	0
35	E	1	Total 1	Mg 1	0
35	4	1	Total 1	Mg 1	0

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	8	1	Total 1	Zn 1	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		AltConf
37	A	4032	Total 4032	O 4032	0
37	B	76	Total 76	O 76	0
37	D	89	Total 89	O 89	0
37	E	78	Total 78	O 78	0
37	F	47	Total 47	O 47	0
37	G	12	Total 12	O 12	0
37	H	3	Total 3	O 3	0
37	I	1	Total 1	O 1	0
37	L	34	Total 34	O 34	0
37	M	18	Total 18	O 18	0
37	N	64	Total 64	O 64	0
37	O	37	Total 37	O 37	0

Continued on next page...

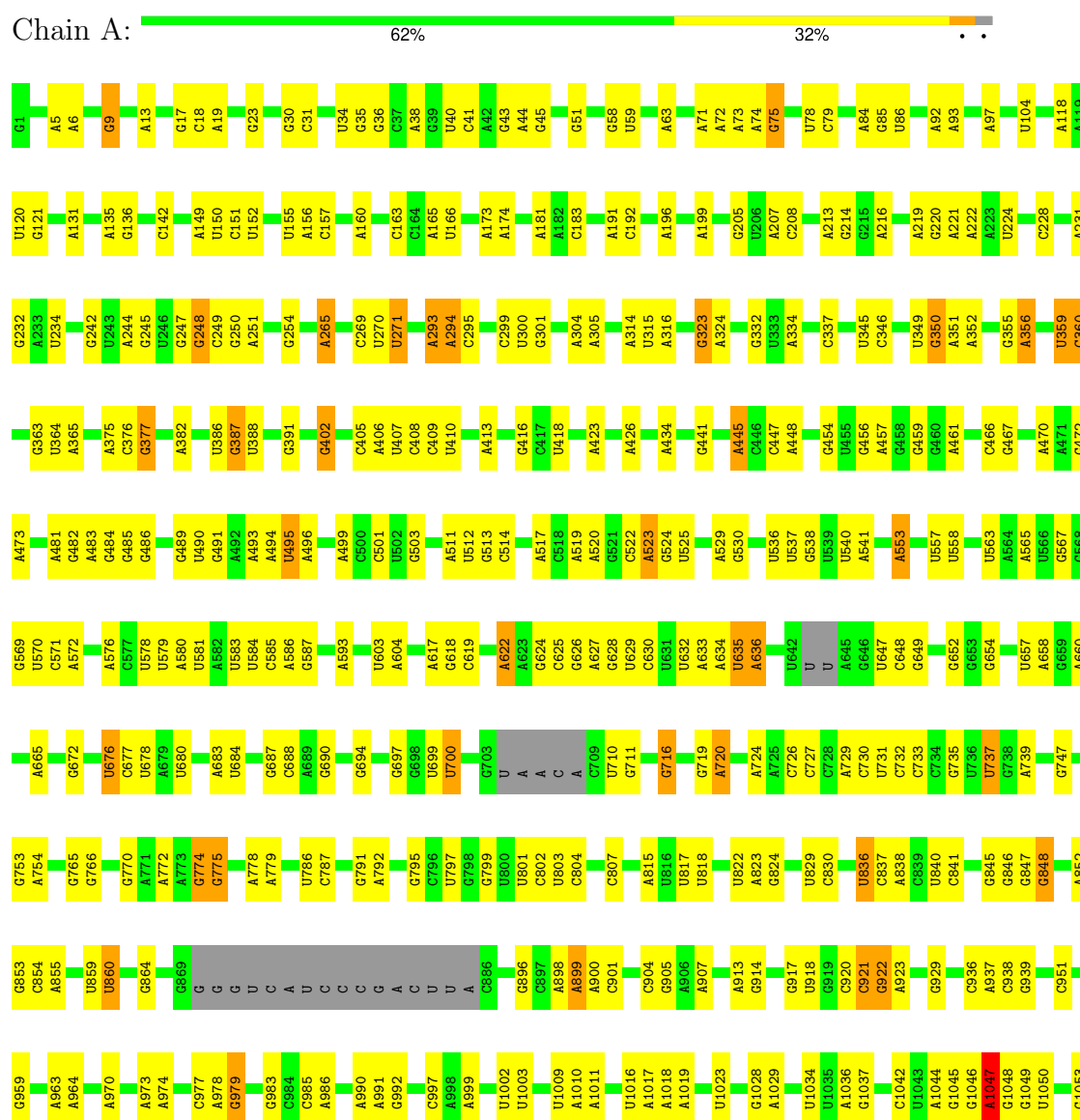
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
37	P	36	Total 36	O 36	0
37	Q	6	Total 6	O 6	0
37	R	25	Total 25	O 25	0
37	S	44	Total 44	O 44	0
37	T	32	Total 32	O 32	0
37	U	40	Total 40	O 40	0
37	V	26	Total 26	O 26	0
37	W	11	Total 11	O 11	0
37	X	22	Total 22	O 22	0
37	Y	24	Total 24	O 24	0
37	Z	20	Total 20	O 20	0
37	1	3	Total 3	O 3	0
37	2	16	Total 16	O 16	0
37	4	32	Total 32	O 32	0
37	5	1	Total 1	O 1	0
37	6	23	Total 23	O 23	0
37	7	22	Total 22	O 22	0
37	8	8	Total 8	O 8	0

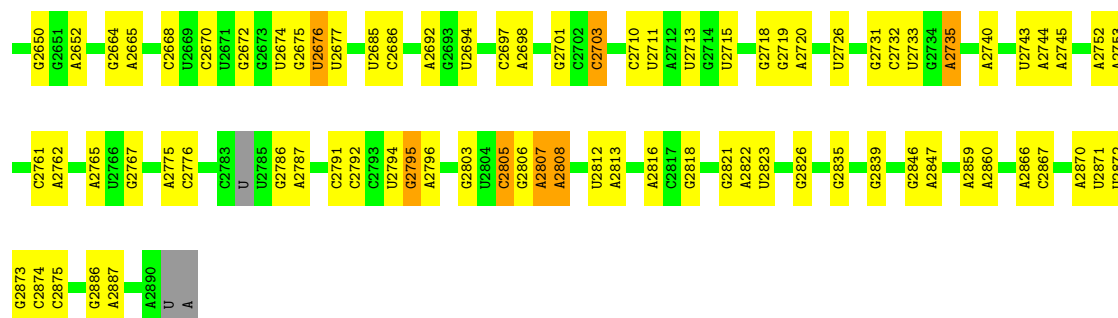
3 Residue-property plots

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: 23S rRNA

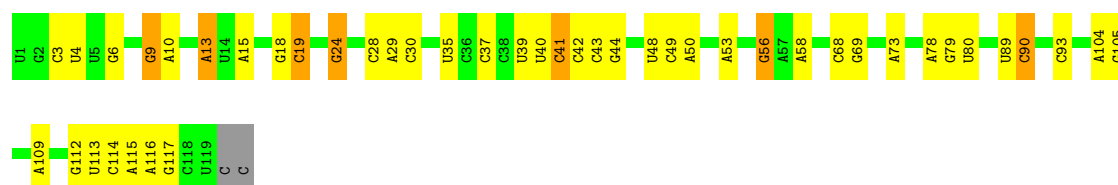


A2559	U2460	U2359	U2278	G2089	A2001	C1782	A1658	A	G	C1302	A	C1054
C2563	U2461	A2360	G2279	U2182	A2002	U1783	G1664	A	A	U1303	A	G1058
A2564	C2462	C2361	U2283	C2183	A2006	C1784	U1670	U	U	G1304	U1167	A1059
A2565	U2464	A2362	U2284	U2184	A2007	U1785	G1671	A	G	C1307	U1168	A1060
C2566	A2363	A2363	A2287	A2186	U2008	C1786	G1672	U	U	A1308	A1169	G1061
G2569	A2364	A2364	C2288	G2191	U2009	U1787	A1788	U	A	A1309	U1180	C1062
C2570	A2365	A2365	C2289	G2192	C2010	A1789	A1674	A	A	C1310	U1185	A1063
C2571	G2370	G2370	U2292	C2195	G2011	A1790	A1674	C	C	U1316	U1186	C1064
C2572	U2371	U2371	C2293	A2198	U2012	A1791	A1680	U	U	U1316	U1187	C1065
C2573	U2372	U2372	C2294	A2199	U2013	A1792	A1681	U	U	C1320	U1188	U1066
C2574	U2373	U2373	G2295	U2210	U2014	A1793	C1681	U	U	G1321	U1189	C1067
C2575	G2376	G2376	G2296	G2111	A2017	U1910	U1687	U	U	G1325	U1193	C1068
C2576	U2377	U2377	A2298	G2112	A2018	C1911	A1688	U	U	U1328	A1211	U1070
C2577	U2378	U2378	U2299	A2113	A2019	G1916	A1689	U	U	U1339	A1212	U1071
C2578	A2379	A2379	C2300	G2114	A2020	U1917	U1692	U	U	A1341	A1214	A1074
C2579	G2380	G2380	G2301	U2117	U2024	U1918	U1692	U	U	G1344	G1223	G1077
C2580	U2381	U2381	A2302	G2120	G2025	U1919	U1692	U	U	G1345	G1235	U1084
C2581	C2382	C2382	C2303	A2121	U2026	U1920	U1692	U	U	U1348	G1237	U1085
C2582	U2383	U2383	G2304	G2122	U2027	A1923	U1708	U	U	C1349	C1238	A1086
C2583	A2384	A2384	G2305	A2123	A2028	A1924	U1709	U	U	G1350	G1239	U1087
C2584	U2385	U2385	C2306	G2124	U2029	A1925	A1710	U	U	G1351	A1241	U1088
C2585	A2386	A2386	A2307	U2128	U2030	U1926	A1711	U	U	A1352	U1242	G1097
C2586	U2387	U2387	G2308	A2129	U2031	U1927	A1712	U	U	G1353	G1243	C1099
C2587	A2388	A2388	A2309	U2136	U2032	U1928	U1713	U	U	U1357	U1250	G1100
C2588	U2389	U2389	U2310	U2137	U2033	U1929	U1714	U	U	A1101	G1102	G1101
C2589	A2390	A2390	U2311	G2138	U2034	U1930	U1715	U	U	U1358	G1251	G1102
C2590	U2391	U2391	G2312	C2139	A2047	U1931	U1716	U	U	G1359	G1252	G1115
C2591	A2392	A2392	A2313	G2140	U2048	U1932	U1717	U	U	A1365	A1116	A1116
C2592	U2393	U2393	A2314	G2141	U2049	U1933	U1718	U	U	U1366	U1120	U1120
C2593	A2394	A2394	U2315	G2142	U2050	U1934	U1719	U	U	A1372	G1121	G1121
C2594	U2395	U2395	G2316	A2143	U2051	U1935	U1720	U	U	A1373	U1122	U1122
C2595	A2396	A2396	U2317	G2144	U2052	U1936	U1721	U	U	A1374	A1123	A1123
C2596	U2397	U2397	A2318	A2145	U2053	U1937	U1722	U	U	U1379	C1124	C1124
C2597	A2398	A2398	U2319	G2146	U2054	U1938	U1723	U	U	A1380	G1125	G1125
C2598	U2399	U2399	G2320	C2147	U2055	U1939	U1724	U	U	U1381	U1276	U1276
C2599	A2399	A2399	U2321	G2148	U2056	U1940	U1725	U	U	A1382	A1277	U1131
C2600	U2400	U2400	U2322	A2149	U2057	U1941	U1726	U	U	U1383	A1281	A1133
C2601	A2401	A2401	G2323	C2152	U2058	U1942	U1727	U	U	U1384	C1284	U1140
C2602	U2402	U2402	U2324	G2155	U2059	U1943	U1728	U	U	U1385	C1285	A1140
C2603	A2403	A2403	C2325	A2156	U2060	U1944	U1729	U	U	U1386	C1286	C1141
C2604	U2404	U2404	U2326	G2157	U2061	U1945	U1730	U	U	U1387	A1287	A1288
C2605	A2405	A2405	A2327	A2158	U2062	U1946	U1731	U	U	U1388	C1144	C1144
C2606	U2406	U2406	G2328	U2159	U2063	U1947	U1732	U	U	U1389	U1289	U1289
C2607	A2407	A2407	U2329	G2162	U2064	U1948	U1733	U	U	U1390	G1298	G1298
C2608	U2408	U2408	U2330	A2163	U2065	U1949	U1734	U	U	U1391	U1299	U1299
C2609	A2409	A2409	G2331	C2164	U2066	U1950	U1735	U	U	U1392	U1300	U1300
C2610	U2410	U2410	U2332	G2165	U2067	U1951	U1736	U	U	U1393	G1403	G1403
C2611	A2411	A2411	U2333	C2166	U2068	U1952	U1737	U	U	U1394	C1404	C1404
C2612	U2412	U2412	G2334	U2168	U2069	U1953	U1738	U	U	U1395	G1405	G1405
C2613	A2413	A2413	U2335	G2169	U2070	U1954	U1739	U	U	U1396	U1406	U1406
C2614	U2414	U2414	A2336	A2171	U2071	U1955	U1740	U	U	U1397	G1407	G1407
C2615	A2415	A2415	U2337	U2172	U2072	U1956	U1741	U	U	U1398	U1408	U1408
C2616	U2416	U2416	G2338	G2173	U2073	U1957	U1742	U	U	U1399	G1409	G1409
C2617	A2417	A2417	U2339	A2178	U2074	U1958	U1743	U	U	U1400	U1410	U1410
C2618	U2418	U2418	G2340	U2179	U2075	U1959	U1744	U	U	U1401	G1411	G1411
C2619	A2419	A2419	U2341	C2179	U2076	U1960	U1745	U	U	U1402	U1412	U1412
C2620	U2420	U2420	G2342	G2180	U2077	U1961	U1746	U	U	U1403	U1413	U1413
C2621	A2421	A2421	U2343	U2181	U2078	U1962	U1747	U	U	U1404	U1414	U1414
C2622	U2422	U2422	U2344	G2182	U2079	U1963	U1748	U	U	U1405	U1415	U1415
C2623	A2423	A2423	G2345	A2183	U2080	U1964	U1749	U	U	U1406	U1416	U1416
C2624	U2424	U2424	U2346	U2184	U2081	U1965	U1750	U	U	U1407	U1417	U1417
C2625	A2425	A2425	A2347	G2185	U2082	U1966	U1751	U	U	U1408	U1418	U1418
C2626	U2426	U2426	U2348	U2186	U2083	U1967	U1752	U	U	U1409	U1419	U1419
C2627	A2427	A2427	G2349	G2187	U2084	U1968	U1753	U	U	U1410	U1420	U1420
C2628	U2428	U2428	U2350	U2188	U2085	U1969	U1754	U	U	U1411	U1421	U1421
C2629	A2429	A2429	G2351	A2189	U2086	U1970	U1755	U	U	U1412	U1422	U1422
C2630	U2430	U2430	U2352	U2190	U2087	U1971	U1756	U	U	U1413	U1423	U1423
C2631	A2431	A2431	G2353	G2191	U2088	U1972	U1757	U	U	U1414	U1424	U1424
C2632	U2432	U2432	U2354	U2192	U2089	U1973	U1758	U	U	U1415	U1425	U1425
C2633	A2433	A2433	A2341	A2193	U2090	U1974	U1759	U	U	U1416	U1426	U1426
C2634	U2434	U2434	G2346	U2194	U2091	U1975	U1760	U	U	U1417	U1427	U1427
C2635	A2435	A2435	A2347	G2195	U2092	U1976	U1761	U	U	U1418	U1428	U1428
C2636	U2436	U2436	U2348	U2196	U2093	U1977	U1762	U	U	U1419	U1429	U1429
C2637	A2437	A2437	G2349	G2197	U2094	U1978	U1763	U	U	U1420	U1430	U1430
C2638	U2438	U2438	U2350	U2198	U2095	U1979	U1764	U	U	U1421	U1431	U1431
C2639	A2439	A2439	A2341	A2199	U2096	U1980	U1765	U	U	U1422	U1432	U1432
C2640	U2440	U2440	G2346	U2200	U2097	U1981	U1766	U	U	U1423	U1433	U1433
C2641	A2441	A2441	A2347	G2201	U2098	U1982	U1767	U	U	U1424	U1434	U1434
C2642	U2442	U2442	U2348	U2202	U2099	U1983	U1768	U	U	U1425	U1435	U1435
C2643	A2443	A2443	G2349	G2203	U2100	U1984	U1769	U	U	U1426	U1436	U1436
C2644	U2444	U2444	U2350	U2204	U2101	U1985	U1770	U	U	U1427	U1437	U1437
C2645	A2445	A2445	A2341	U2205	U2102	U1986	U1771	U	U	U1428	U1438	U1438
C2646	U2446	U2446	G2346	G2206	U2103	U1987	U1772	U	U	U1429	U1439	U1439
C2647	A2447	A2447	A2347	U2207	U2104	U1988	U1773	U	U	U1430	U1440	U1440
C2648	U2448	U2448	U2348	U2208	U2105	U1989	U1774	U	U	U1431	U1441	U1441
C2649	A2449	A2449	G2349	G2209	U2106	U1990	U1775	U	U	U1432	U1442	U1442
C2650	U2450	U2450	U2350	U2210	U2107	U1991	U1776	U	U	U1433	U1443	U1443
C2651	A2451	A2451	A2341	G2211	U2108	U1992	U1777	U	U	U1434	U1444	U1444
C2652	U2452	U2452	G2346	U2212	U2109	U1993	U1778	U	U	U1435	U1445	U1445
C2653	A2453	A2453	A2347	G2213	U2110	U1994	U1779	U	U	U1436	U1446	U1446
C2654	U2454	U2454	U2348	U2214	U2111	U1995	U1780	U	U	U1437	U1447	U1447
C2655	A2455	A2455	G2349	G2215	U2112	U1996	U1781	U	U	U1438	U1448	U1448
C2656	U2456	U2456	U2350	U2216	U2113	U1997	U1782	U	U	U1439	U1449	U1449
C2657	A2457	A2457	A2341	U2217	U2114	U1998	U1783	U	U	U1440	U1450	U1450
C2658	U2458	U2458	G2346	U2218	U2115	U1999	U1784	U	U	U1441	U1451	U1451
C2659	A2459	A2459	A2347	G2219	U2116	U2000	U1785	U	U	U1442	U1452	U1452
C2660	U2460	U2460	U2348	U2220	U2117	U2001	U1786	U	U	U1443	U1453	U1453
C2661	A2461	A2461	G2349	U2221	U2118	U2002	U1787	U	U	U1444	U1454	U1454
C2662	U2462	U2462	U2350	G2222	U2119	U2003	U1788	U	U	U1445	U1455	U1455
C2663	A2463	A2463	A2341	U2223	U							



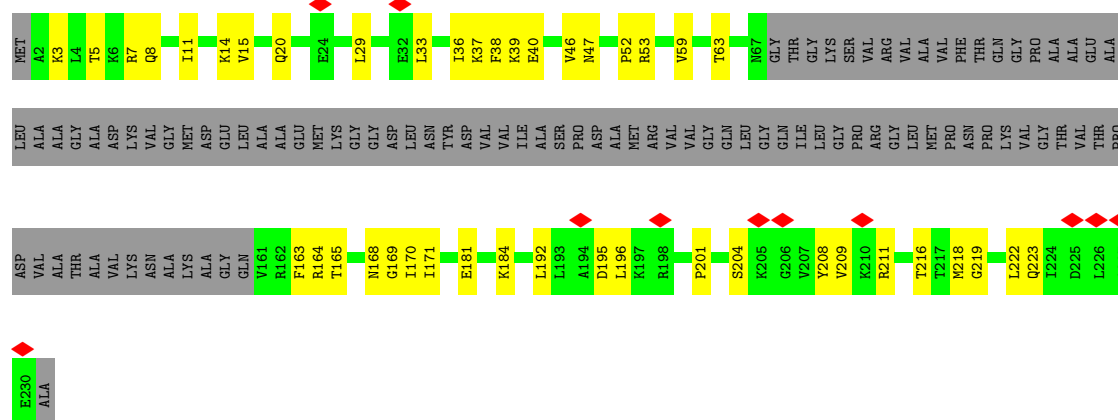
- Molecule 2: 5S rRNA

Chain B: 61% 31% 6%



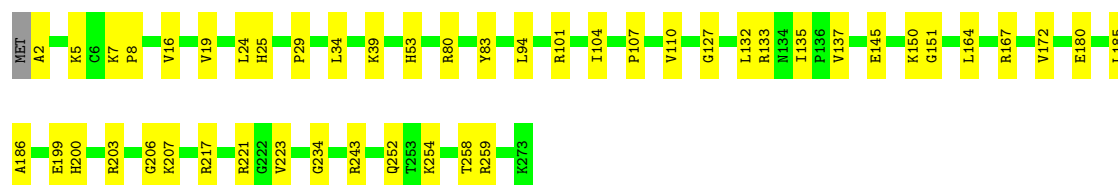
- Molecule 3: Large ribosomal subunit protein uL1

Chain C: 5% 40% 19% 41%



- Molecule 4: Large ribosomal subunit protein uL2

Chain D: 82% 17%



- Molecule 5: Large ribosomal subunit protein uL3

Chain E:  87% 11%



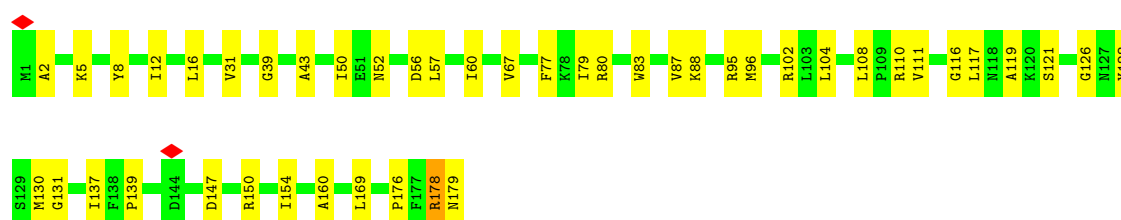
- Molecule 6: Large ribosomal subunit protein uL4

Chain F:  85% 14%



- Molecule 7: Large ribosomal subunit protein uL5

Chain G:  75% 25%



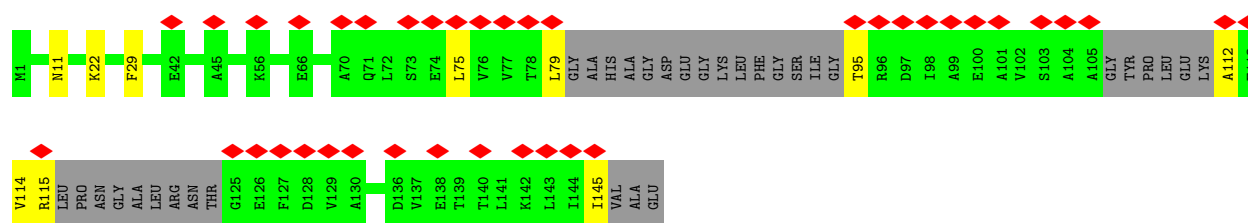
- Molecule 8: Large ribosomal subunit protein uL6

Chain H:  83% 15%



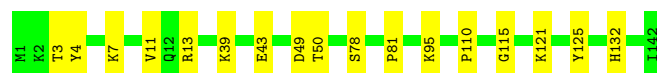
- Molecule 9: Large ribosomal subunit protein bL9

Chain I:  26% 71% 7% 22%



- Molecule 10: Large ribosomal subunit protein uL13

Chain L:  88% 12%



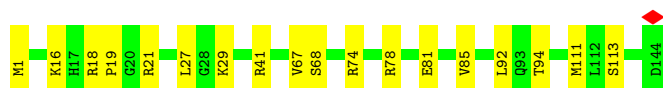
- Molecule 11: Large ribosomal subunit protein uL14

Chain M:  86% 14%



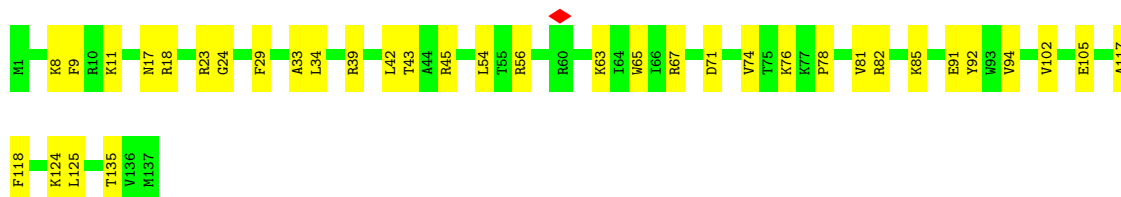
- Molecule 12: Large ribosomal subunit protein uL15

Chain N:  88% 12%



- Molecule 13: Large ribosomal subunit protein uL16

Chain O:  74% 26%



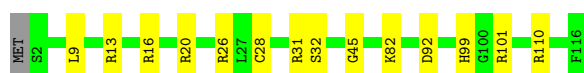
- Molecule 14: Large ribosomal subunit protein bL17

Chain P:  80% 12% 8%



- Molecule 15: Large ribosomal subunit protein uL18

Chain Q:  87% 12%



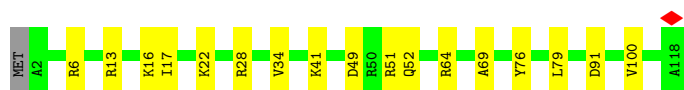
- Molecule 16: Large ribosomal subunit protein bL19

Chain R:  5% 84% 14%



- Molecule 17: Large ribosomal subunit protein bL20

Chain S:  85% 14%



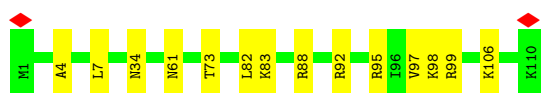
- Molecule 18: Large ribosomal subunit protein bL21

Chain T: 89% 11%



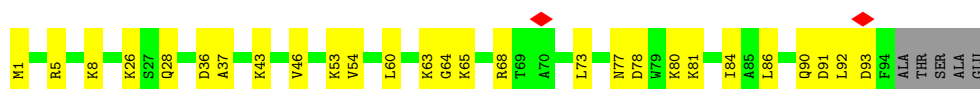
- Molecule 19: Large ribosomal subunit protein uL22

Chain U: 87% 13%



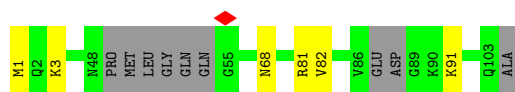
- Molecule 20: Large ribosomal subunit protein uL23

Chain V: 68% 27% 5%



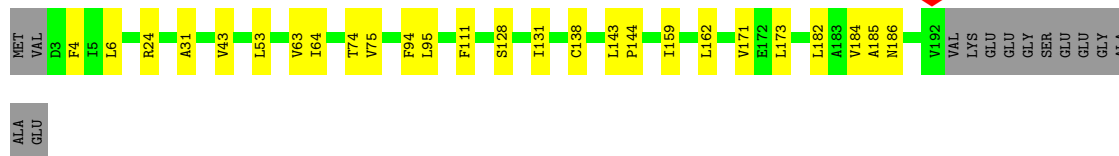
- Molecule 21: Large ribosomal subunit protein uL24

Chain W: 86% 6% 9%



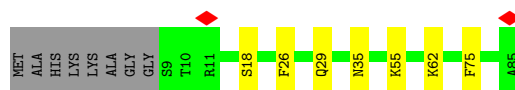
- Molecule 22: Large ribosomal subunit protein bL25

Chain X: 80% 13% 7%



- Molecule 23: Large ribosomal subunit protein bL27

Chain Y: 82% 8% 9%



- Molecule 24: Large ribosomal subunit protein bL28

Chain Z:  85% 14%



- Molecule 25: Large ribosomal subunit protein uL29

Chain 1:  86% 11%



- Molecule 26: Large ribosomal subunit protein uL30

Chain 2:  93%



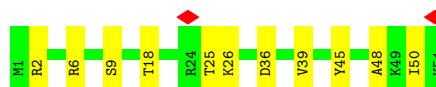
- Molecule 27: Large ribosomal subunit protein bL32

Chain 4:  75% 15% 10%



- Molecule 28: Large ribosomal subunit protein bL33

Chain 5:  78% 22%



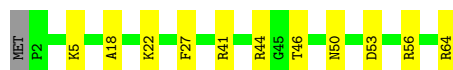
- Molecule 29: Large ribosomal subunit protein bL34

Chain 6:  84% 16%



- Molecule 30: Large ribosomal subunit protein bL35

Chain 7:  81% 17%

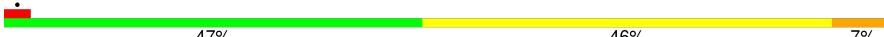


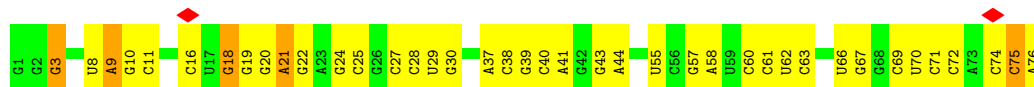
- Molecule 31: Large ribosomal subunit protein bL36A

Chain 8:  89% 11%



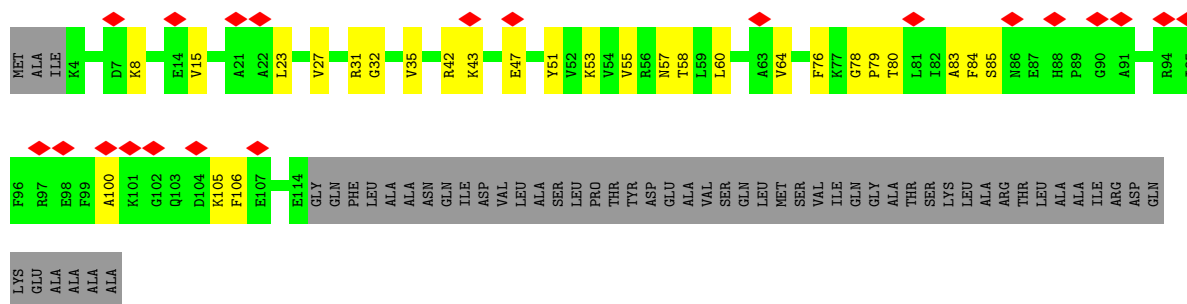
- Molecule 32: tRNA-Ala

Chain v:  47% 46% 7%



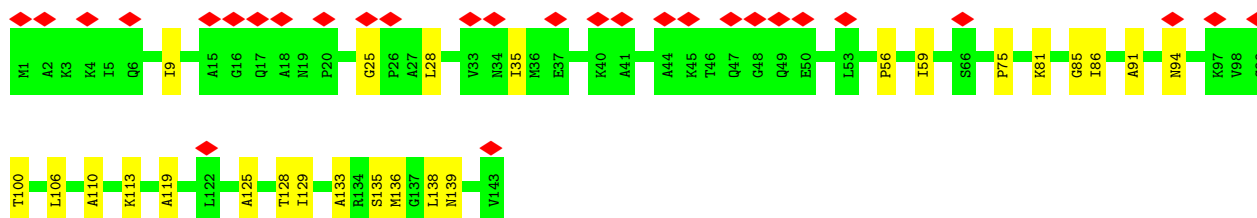
- Molecule 33: Large ribosomal subunit protein uL10

Chain J:  13% 51% 16% 33%



- Molecule 34: Large ribosomal subunit protein uL10

Chain K:  20% 83% 17%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	642285	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54.3	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	81.301	Depositor
Minimum map value	-59.207	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.069	Depositor
Recommended contour level	3	Depositor
Map size (Å)	468.408, 468.408, 468.408	wwPDB
Map dimensions	696, 696, 696	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.673, 0.673, 0.673	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 2MA, ZN, OMG, PSU, 6MZ, 5MU, 1MG, OMU, 2MG, 5MC, 7MG, OMC

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	A	0.28	0/67882	0.74	17/105870 (0.0%)
2	B	0.31	0/2833	0.67	1/4413 (0.0%)
3	C	0.15	0/1050	0.35	0/1411
4	D	0.15	0/2108	0.27	0/2831
5	E	0.20	0/1587	0.34	0/2138
6	F	0.17	0/1541	0.28	0/2075
7	G	0.25	0/1456	0.37	0/1953
8	H	0.09	0/1332	0.22	0/1794
9	I	0.11	0/861	0.24	0/1159
10	L	0.24	0/1156	0.38	0/1559
11	M	0.11	0/947	0.27	0/1268
12	N	0.11	0/1078	0.28	0/1436
13	O	0.12	0/1105	0.26	0/1476
14	P	0.19	0/968	0.31	0/1294
15	Q	0.18	0/888	0.29	0/1183
16	R	0.16	0/910	0.34	0/1218
17	S	0.14	0/946	0.30	0/1257
18	T	0.09	0/835	0.23	0/1117
19	U	0.09	0/837	0.23	0/1114
20	V	0.08	0/749	0.22	0/1002
21	W	0.09	0/743	0.24	0/988
22	X	0.09	0/1468	0.21	0/1987
23	Y	0.09	0/589	0.24	0/782
24	Z	0.16	0/641	0.23	0/854
25	1	0.17	0/491	0.31	0/654
26	2	0.08	0/444	0.23	0/597
27	4	0.31	0/437	0.55	0/583
28	5	0.09	0/433	0.24	0/576
29	6	0.16	0/368	0.36	0/482
30	7	0.16	0/511	0.27	0/668
31	8	0.08	0/308	0.22	0/404
32	v	0.35	0/1767	0.71	0/2752

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	J	0.48	0/850	0.63	0/1142
34	K	0.33	0/1061	0.42	0/1435
All	All	0.26	0/101180	0.66	18/151472 (0.0%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1911	C	C2-N1-C1'	-7.12	110.97	118.80
1	A	1097	G	N3-C4-N9	-6.80	121.92	126.00
1	A	9	G	O4'-C1'-N9	6.40	113.32	108.20
1	A	503	G	O4'-C1'-N9	6.11	113.09	108.20
1	A	1071	U	N3-C2-O2	-6.06	117.96	122.20

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	A	60895	0	30644	596	0
2	B	2535	0	1283	30	0
3	C	1040	0	1107	28	0
4	D	2072	0	2152	38	0
5	E	1564	0	1575	19	0
6	F	1521	0	1581	26	0
7	G	1435	0	1504	30	0
8	H	1314	0	1373	17	0
9	I	858	0	890	7	0
10	L	1130	0	1160	15	0
11	M	938	0	1012	12	0
12	N	1066	0	1112	14	0
13	O	1085	0	1157	26	0
14	P	952	0	996	11	0
15	Q	881	0	920	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	R	901	0	958	10	0
17	S	936	0	1025	17	0
18	T	822	0	858	7	0
19	U	833	0	897	10	0
20	V	739	0	788	18	0
21	W	738	0	806	5	0
22	X	1445	0	1486	18	0
23	Y	581	0	603	6	0
24	Z	630	0	653	8	0
25	1	490	0	520	5	0
26	2	440	0	469	2	0
27	4	431	0	424	7	0
28	5	426	0	457	8	0
29	6	365	0	409	6	0
30	7	506	0	569	10	0
31	8	307	0	342	3	0
32	v	1623	0	824	20	0
33	J	840	0	867	21	0
34	K	1046	0	1089	23	0
35	4	1	0	0	0	0
35	A	196	0	0	0	0
35	B	3	0	0	0	0
35	D	1	0	0	0	0
35	E	1	0	0	0	0
36	8	1	0	0	0	0
37	1	3	0	0	0	0
37	2	16	0	0	0	0
37	4	32	0	0	1	0
37	5	1	0	0	0	0
37	6	23	0	0	1	0
37	7	22	0	0	0	0
37	8	8	0	0	0	0
37	A	4032	0	0	29	0
37	B	76	0	0	2	0
37	D	89	0	0	1	0
37	E	78	0	0	0	0
37	F	47	0	0	3	0
37	G	12	0	0	0	0
37	H	3	0	0	0	0
37	I	1	0	0	0	0
37	L	34	0	0	0	0
37	M	18	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	N	64	0	0	0	0
37	O	37	0	0	3	0
37	P	36	0	0	0	0
37	Q	6	0	0	1	0
37	R	25	0	0	0	0
37	S	44	0	0	2	0
37	T	32	0	0	0	0
37	U	40	0	0	1	0
37	V	26	0	0	0	0
37	W	11	0	0	0	0
37	X	22	0	0	2	0
37	Y	24	0	0	0	0
37	Z	20	0	0	0	0
All	All	98470	0	62510	917	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 6.

The worst 5 of 917 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)
33:J:43:LYS:HG2	33:J:47:GLU:OE1	1.80	0.82
7:G:119:ALA:HB3	7:G:179:ASN:HB2	1.64	0.80
1:A:558:U:H1'	1:A:2017:6MZ:H9C1	1.68	0.76
1:A:1045:G:H5'	33:J:32:GLY:HA2	1.70	0.73
1:A:1097:G:O2'	33:J:78:GLY:HA2	1.89	0.73

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	
3	C	132/231 (57%)	130 (98%)	2 (2%)	0	100	100
4	D	270/273 (99%)	266 (98%)	4 (2%)	0	100	100
5	E	206/211 (98%)	201 (98%)	5 (2%)	0	100	100
6	F	198/200 (99%)	198 (100%)	0	0	100	100
7	G	177/179 (99%)	174 (98%)	3 (2%)	0	100	100
8	H	172/177 (97%)	172 (100%)	0	0	100	100
9	I	107/148 (72%)	103 (96%)	4 (4%)	0	100	100
10	L	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
11	M	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
12	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
13	O	135/137 (98%)	134 (99%)	1 (1%)	0	100	100
14	P	117/129 (91%)	115 (98%)	2 (2%)	0	100	100
15	Q	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
16	R	112/116 (97%)	108 (96%)	4 (4%)	0	100	100
17	S	115/118 (98%)	115 (100%)	0	0	100	100
18	T	101/103 (98%)	101 (100%)	0	0	100	100
19	U	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
20	V	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
21	W	89/104 (86%)	87 (98%)	2 (2%)	0	100	100
22	X	188/204 (92%)	185 (98%)	3 (2%)	0	100	100
23	Y	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
24	Z	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	1	59/63 (94%)	59 (100%)	0	0	100	100
26	2	54/58 (93%)	53 (98%)	1 (2%)	0	100	100
27	4	52/60 (87%)	51 (98%)	1 (2%)	0	100	100
28	5	49/51 (96%)	49 (100%)	0	0	100	100
29	6	42/44 (96%)	42 (100%)	0	0	100	100
30	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
31	8	36/38 (95%)	36 (100%)	0	0	100	100
33	J	109/166 (66%)	105 (96%)	4 (4%)	0	100	100
34	K	141/143 (99%)	135 (96%)	6 (4%)	0	100	100
All	All	3587/3913 (92%)	3530 (98%)	57 (2%)	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	
3	C	115/180 (64%)	114 (99%)	1 (1%)	70	79
4	D	212/213 (100%)	212 (100%)	0	100	100
5	E	160/162 (99%)	160 (100%)	0	100	100
6	F	157/158 (99%)	156 (99%)	1 (1%)	78	84
7	G	153/153 (100%)	151 (99%)	2 (1%)	61	72
8	H	137/141 (97%)	137 (100%)	0	100	100
9	I	85/107 (79%)	84 (99%)	1 (1%)	63	74
10	L	119/119 (100%)	119 (100%)	0	100	100
11	M	102/102 (100%)	102 (100%)	0	100	100
12	N	106/106 (100%)	105 (99%)	1 (1%)	70	79
13	O	110/110 (100%)	110 (100%)	0	100	100
14	P	98/104 (94%)	98 (100%)	0	100	100
15	Q	86/87 (99%)	86 (100%)	0	100	100
16	R	96/98 (98%)	95 (99%)	1 (1%)	68	77
17	S	87/88 (99%)	86 (99%)	1 (1%)	65	75
18	T	86/86 (100%)	86 (100%)	0	100	100
19	U	87/87 (100%)	87 (100%)	0	100	100
20	V	79/82 (96%)	79 (100%)	0	100	100
21	W	81/88 (92%)	81 (100%)	0	100	100
22	X	154/164 (94%)	154 (100%)	0	100	100
23	Y	57/61 (93%)	57 (100%)	0	100	100
24	Z	66/67 (98%)	66 (100%)	0	100	100
25	1	54/55 (98%)	53 (98%)	1 (2%)	50	61
26	2	48/49 (98%)	48 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	4	47/52 (90%)	46 (98%)	1 (2%)	47	58
28	5	47/47 (100%)	47 (100%)	0	100	100
29	6	37/37 (100%)	37 (100%)	0	100	100
30	7	54/55 (98%)	54 (100%)	0	100	100
31	8	34/34 (100%)	34 (100%)	0	100	100
33	J	82/122 (67%)	81 (99%)	1 (1%)	63	74
34	K	110/110 (100%)	110 (100%)	0	100	100
All	All	2946/3124 (94%)	2935 (100%)	11 (0%)	81	89

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	S	6	ARG
25	1	7	ARG
33	J	60	LEU
27	4	51	ARG
9	I	75	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
18	T	69	HIS
22	X	175	GLN
19	U	23	GLN
20	V	87	GLN
24	Z	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2827/2892 (97%)	311 (11%)	6 (0%)
2	B	118/121 (97%)	17 (14%)	0
32	v	75/76 (98%)	14 (18%)	0
All	All	3020/3089 (97%)	342 (11%)	6 (0%)

5 of 342 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	34	U
1	A	45	G
1	A	51	G
1	A	63	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1046	G
1	A	1307	C
1	A	2743	U
1	A	635	U
1	A	221	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

14 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
32	PSU	v	55	32	18,21,22	1.12	1 (5%)	21,30,33	1.95	5 (23%)
1	2MG	A	2432	1	23,26,27	0.49	0	33,38,41	0.49	0
1	5MC	A	1949	1	19,22,23	0.54	0	26,32,35	0.63	0
1	OMC	A	2485	1,35	19,22,23	0.48	0	25,31,34	0.64	0
1	7MG	A	2056	1	23,26,27	1.13	1 (4%)	27,39,42	0.86	1 (3%)
32	5MU	v	54	32	19,22,23	0.37	0	27,32,35	0.62	0
1	2MA	A	2490	1,35	22,25,26	1.70	5 (22%)	32,37,40	3.65	12 (37%)
1	2MG	A	1822	1	23,26,27	0.43	0	33,38,41	0.47	0
1	OMU	A	2539	1	19,22,23	3.10	8 (42%)	25,31,34	1.82	4 (16%)
1	6MZ	A	1608	1	22,25,26	2.39	4 (18%)	29,36,39	2.33	9 (31%)
1	1MG	A	735	1	23,26,27	3.16	8 (34%)	33,39,42	1.84	9 (27%)
1	5MU	A	1926	1	19,22,23	0.42	0	27,32,35	0.58	0
1	6MZ	A	2017	1	22,25,26	2.34	5 (22%)	29,36,39	2.50	11 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	A	2238	1	23,26,27	0.44	0	32,38,41	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	PSU	v	55	32	-	0/7/25/26	0/2/2/2
1	2MG	A	2432	1	-	2/9/27/28	0/3/3/3
1	5MC	A	1949	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2485	1,35	-	0/9/27/28	0/2/2/2
1	7MG	A	2056	1	-	1/7/37/38	0/3/3/3
32	5MU	v	54	32	-	0/7/25/26	0/2/2/2
1	2MA	A	2490	1,35	-	1/7/25/26	0/3/3/3
1	2MG	A	1822	1	-	2/9/27/28	0/3/3/3
1	OMU	A	2539	1	-	0/9/27/28	0/2/2/2
1	6MZ	A	1608	1	-	0/9/27/28	0/3/3/3
1	1MG	A	735	1	-	0/7/25/26	0/3/3/3
1	5MU	A	1926	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	2017	1	-	2/9/27/28	0/3/3/3
1	OMG	A	2238	1	-	1/9/27/28	0/3/3/3

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1608	6MZ	C6-N6	9.73	1.45	1.34
1	A	735	1MG	C2-N3	9.65	1.48	1.33
1	A	2017	6MZ	C6-N6	9.35	1.44	1.34
1	A	2539	OMU	C2-N1	8.09	1.51	1.38
1	A	735	1MG	C4-N3	6.95	1.50	1.34

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2490	2MA	N6-C6-N1	-9.23	104.58	117.03
1	A	2490	2MA	CM2-C2-N3	9.13	130.79	117.13
1	A	2490	2MA	C5-C4-N3	-8.59	118.13	127.18
1	A	2017	6MZ	C9-N6-C6	-6.95	116.40	122.85
1	A	2490	2MA	N3-C4-N9	6.36	135.06	126.99

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2238	OMG	C1'-C2'-O2'-CM2
1	A	1822	2MG	C3'-C4'-C5'-O5'
1	A	2432	2MG	C3'-C4'-C5'-O5'
1	A	1822	2MG	O4'-C4'-C5'-O5'
1	A	2017	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	2432	2MG	1	0
1	A	1822	2MG	1	0
1	A	2017	6MZ	2	0
1	A	2238	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 203 ligands modelled in this entry, 203 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

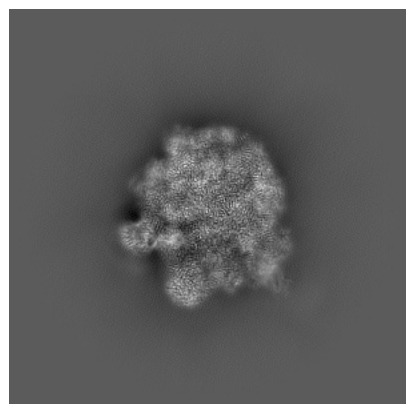
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73298. These allow visual inspection of the internal detail of the map and identification of artifacts.

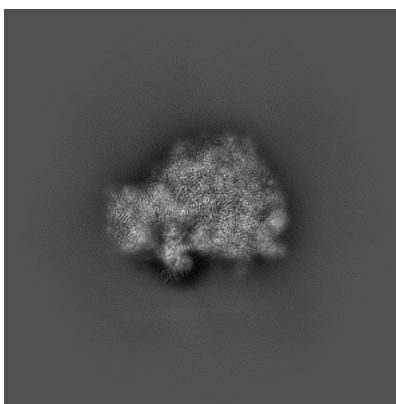
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

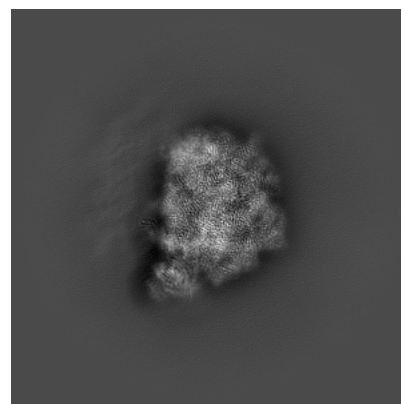
6.1.1 Primary map



X

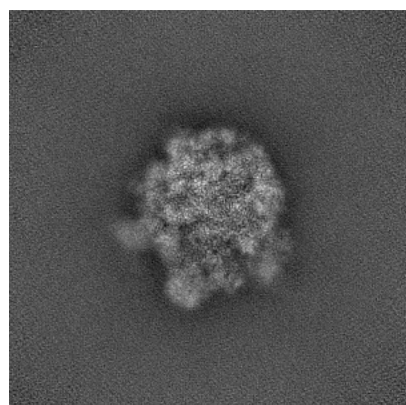


Y

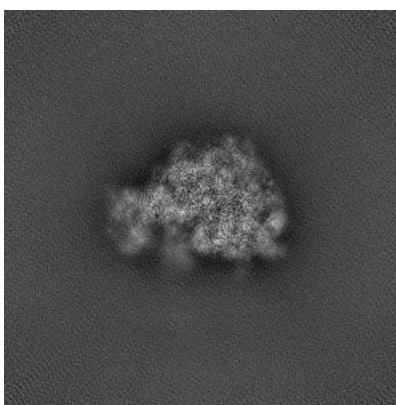


Z

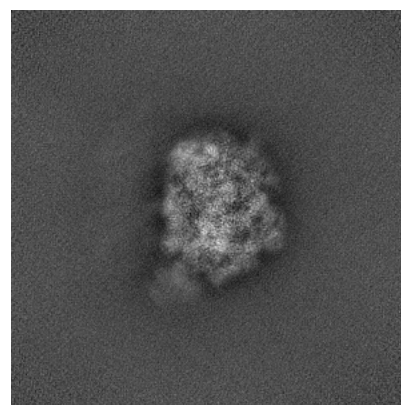
6.1.2 Raw map



X



Y

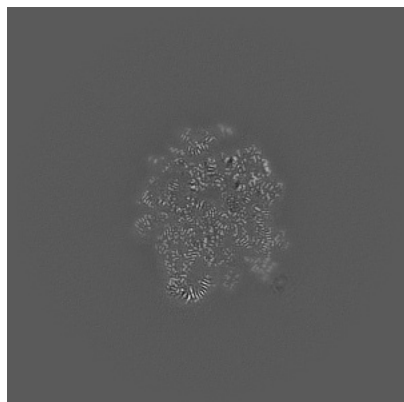


Z

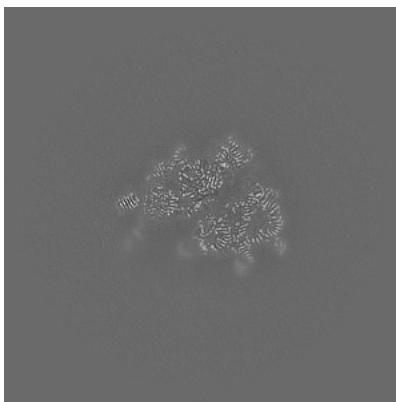
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

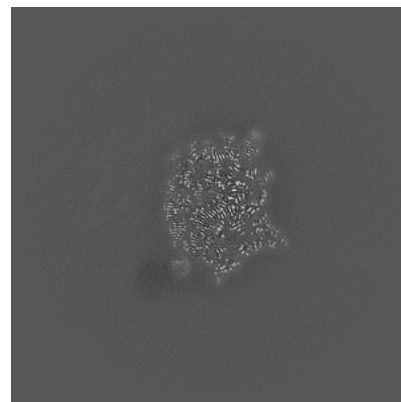
6.2.1 Primary map



X Index: 348

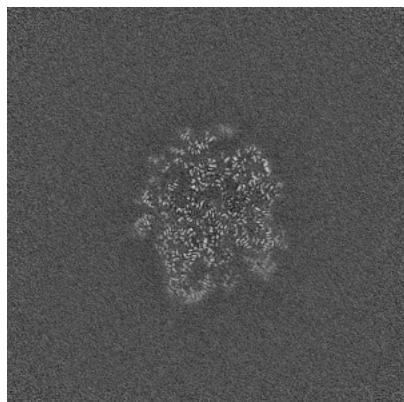


Y Index: 348

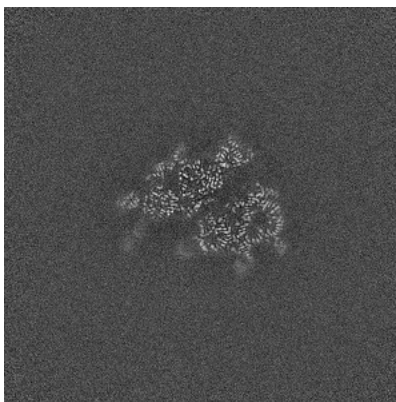


Z Index: 348

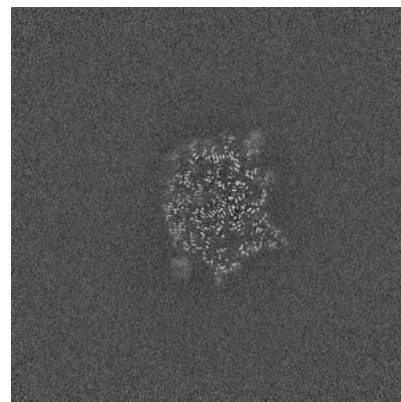
6.2.2 Raw map



X Index: 348



Y Index: 348

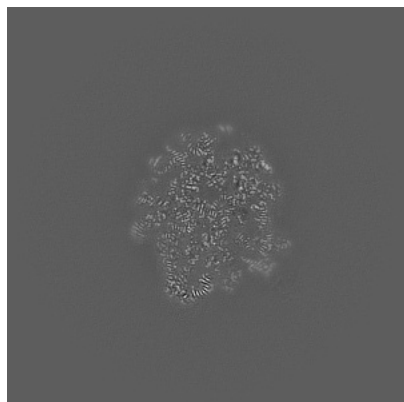


Z Index: 348

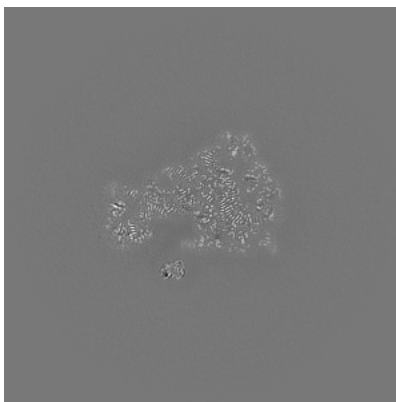
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

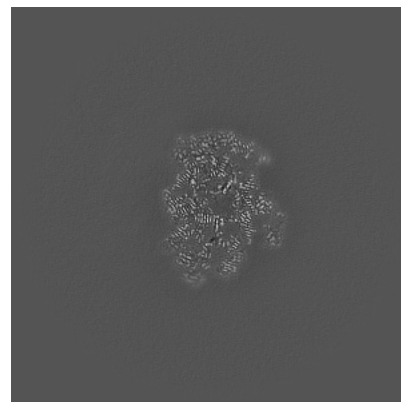
6.3.1 Primary map



X Index: 353

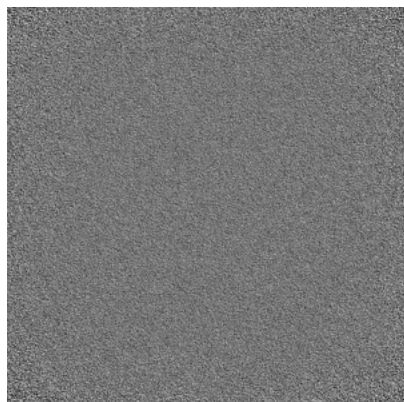


Y Index: 323

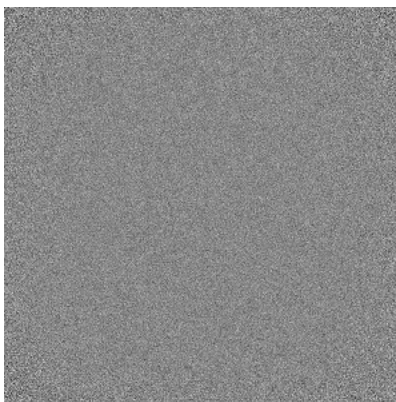


Z Index: 380

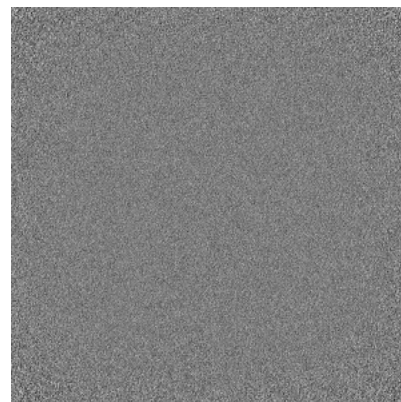
6.3.2 Raw map



X Index: 0



Y Index: 0

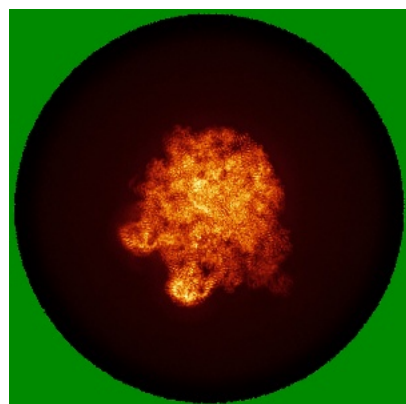


Z Index: 0

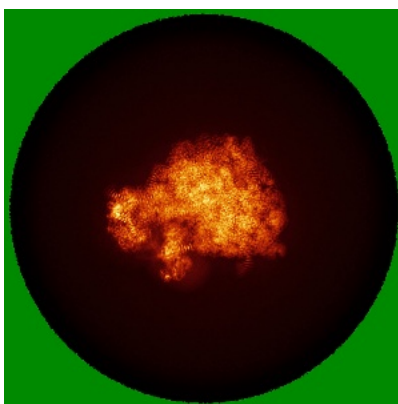
The images above show the largest variance slices of the map in three orthogonal directions.

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

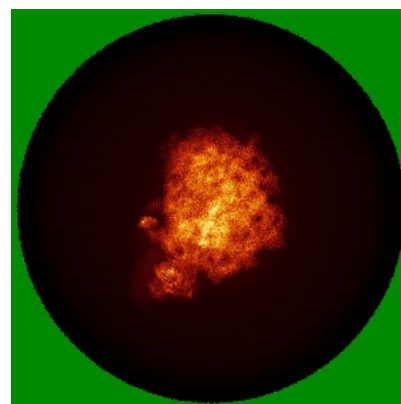
6.4.1 Primary map



X

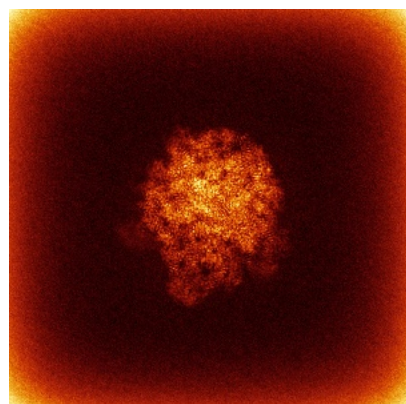


Y

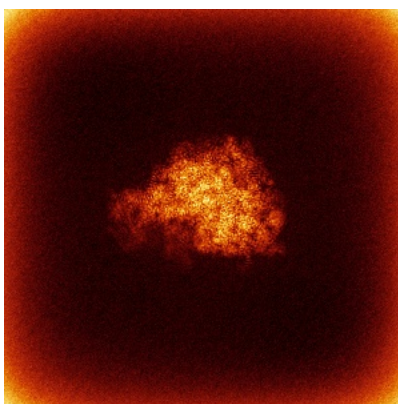


Z

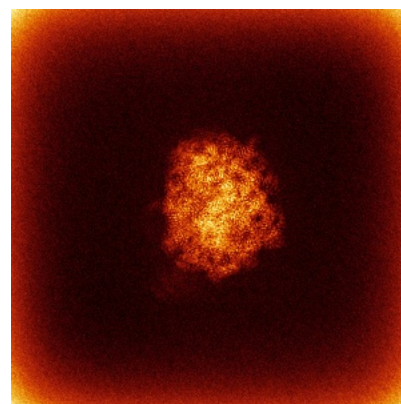
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



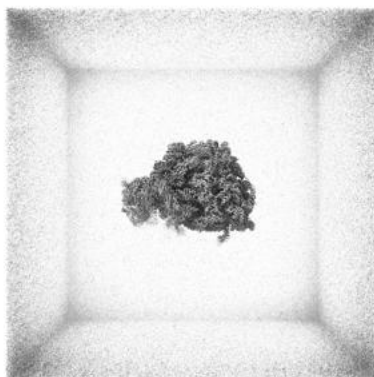
Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

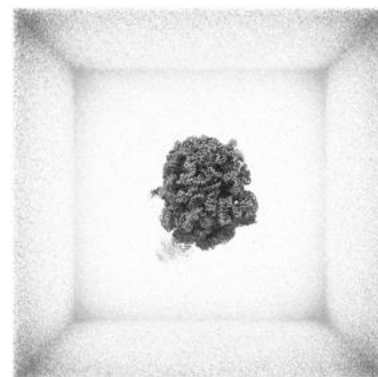
6.5.2 Raw map



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.

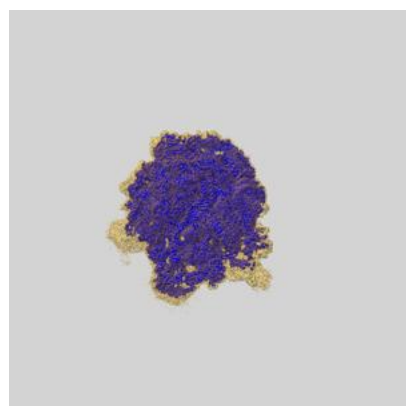
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

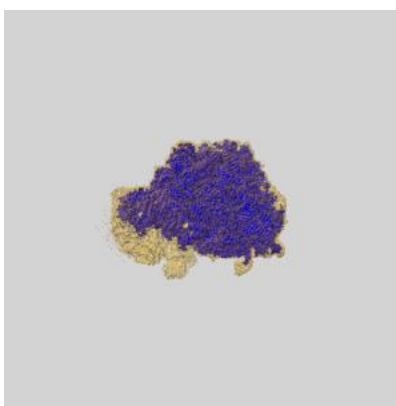
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

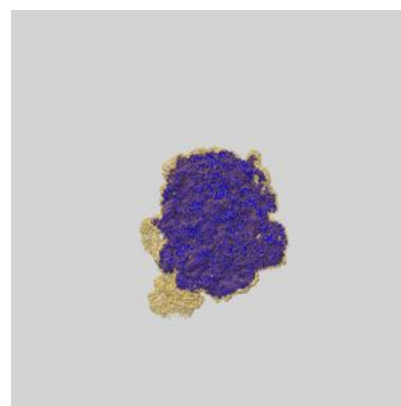
6.6.1 emd_73298_msk_1.map [i](#)



X



Y

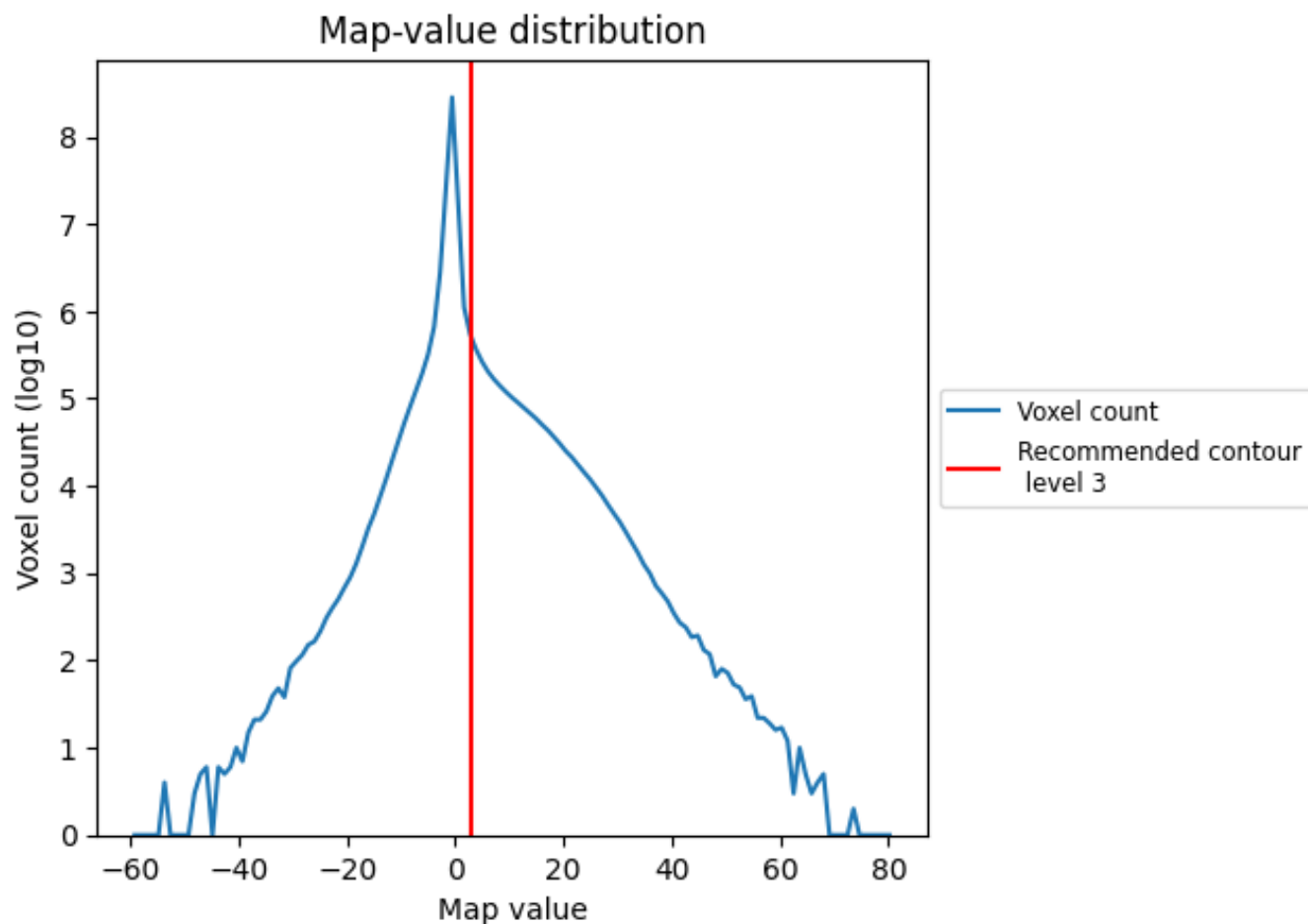


Z

7 Map analysis [i](#)

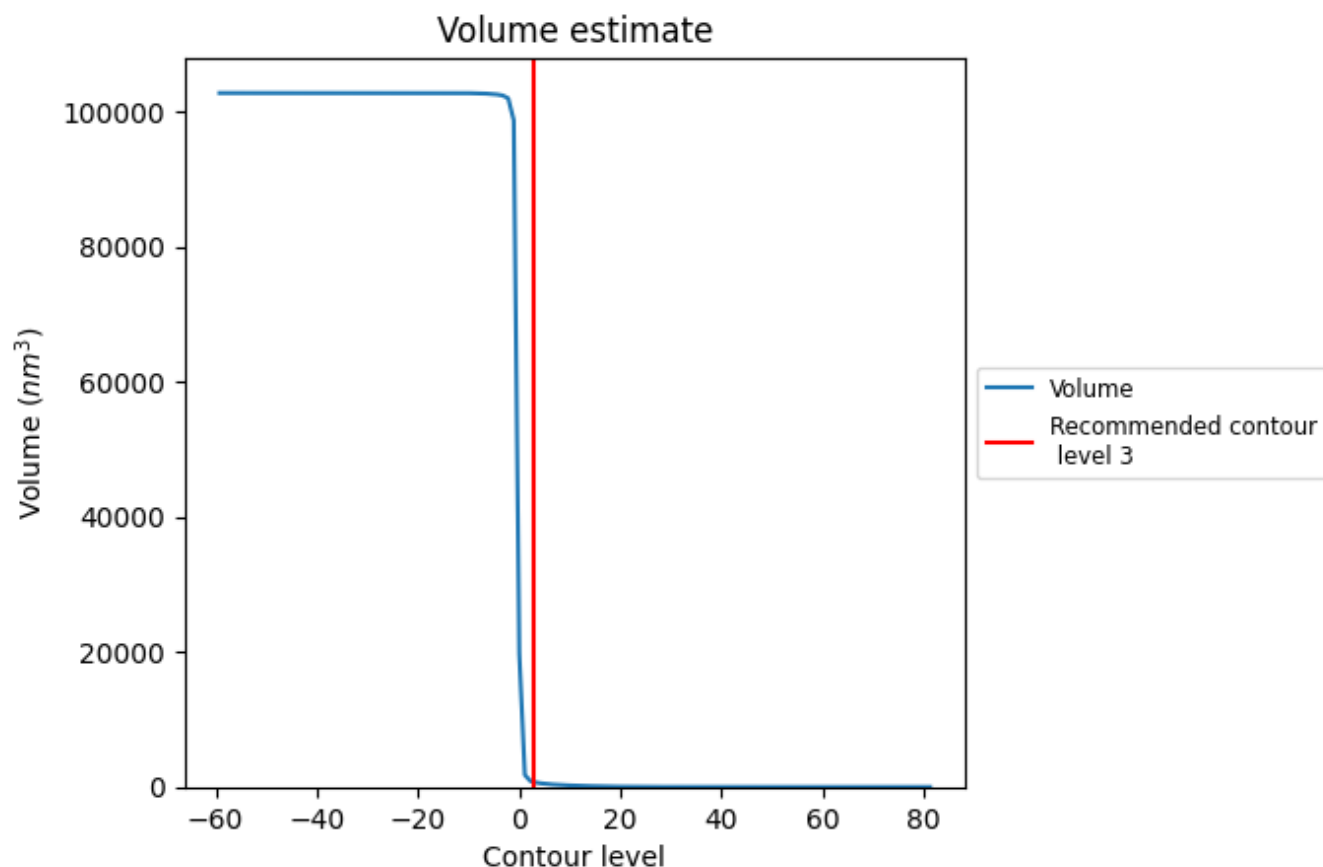
This section contains the results of statistical analysis of the map.

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.

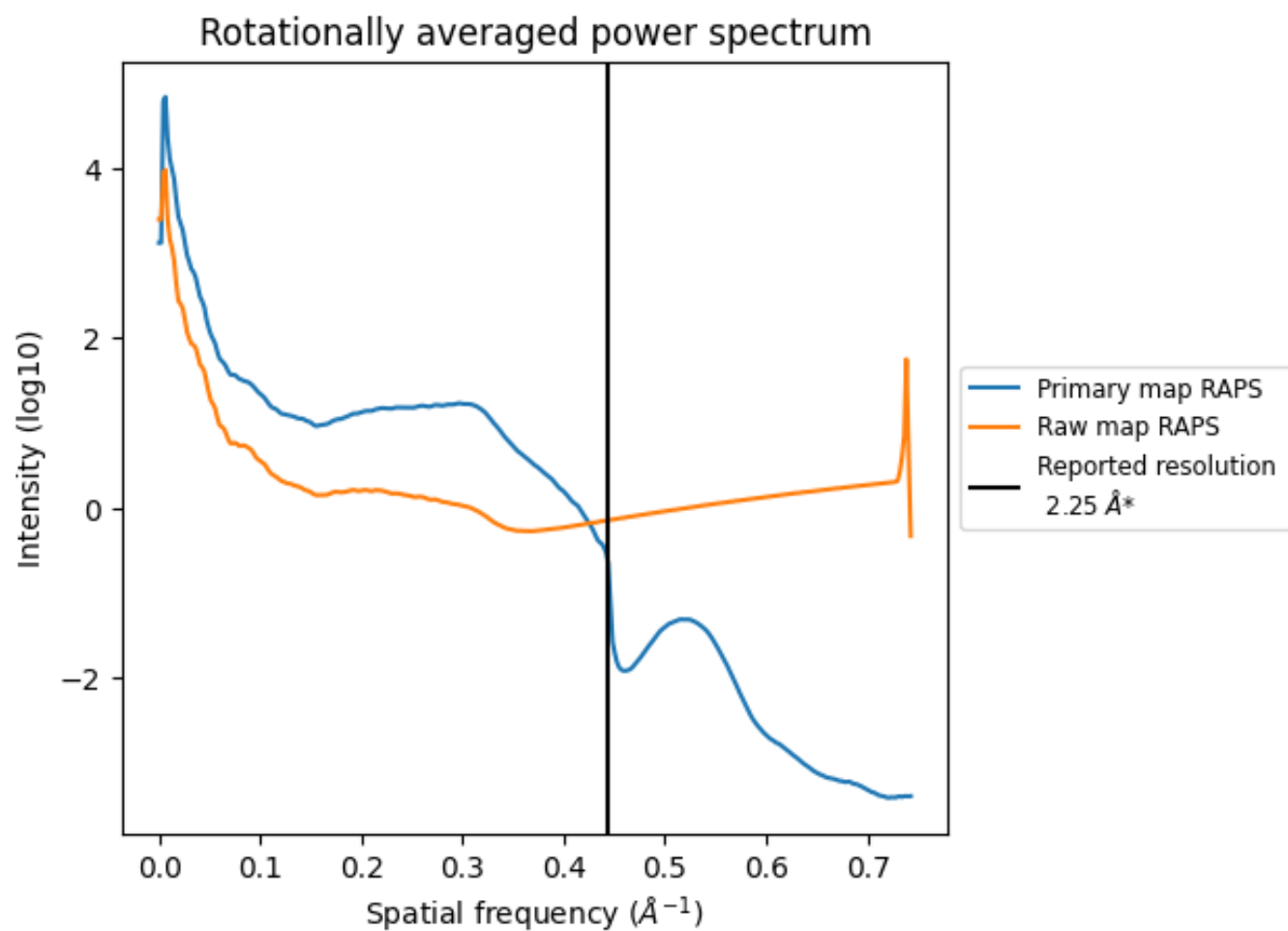
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 728 nm^3 ; this corresponds to an approximate mass of 658 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 ⓘ

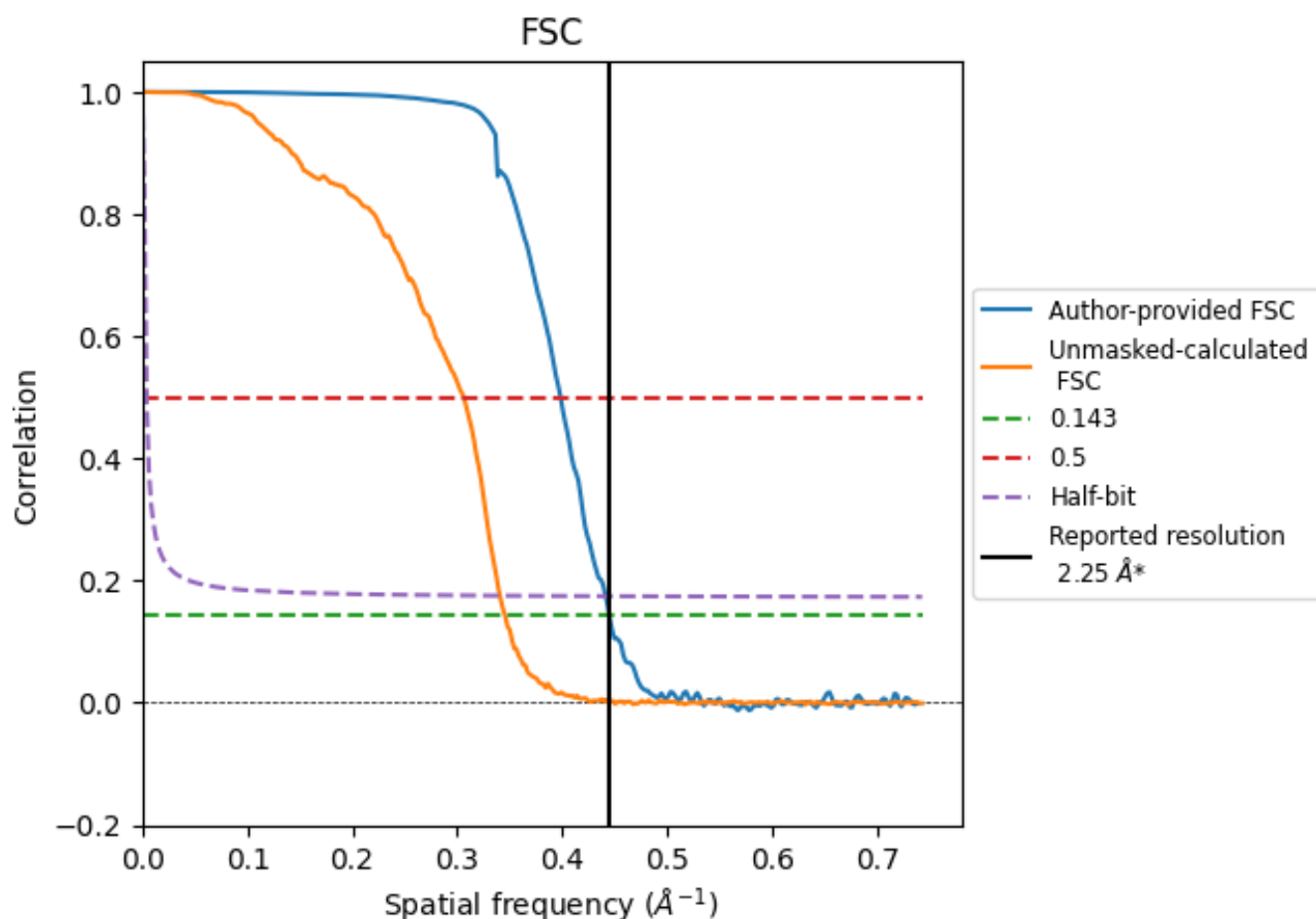


*Reported resolution corresponds to spatial frequency of $0.444 \text{ \AA}^{-1}$

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 $0.444 \text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

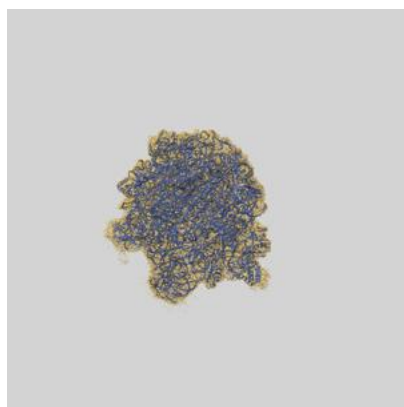
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.25	-	-
Author-provided FSC curve	2.25	2.51	2.27
Unmasked-calculated*	2.89	3.27	2.94

*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 2.89 differs from the reported value 2.25 by more than 10 %

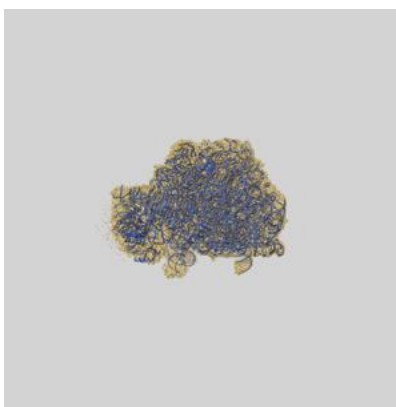
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73298 and PDB model 9YPH. Per-residue inclusion information can be found in section [3](#) on page [12](#).

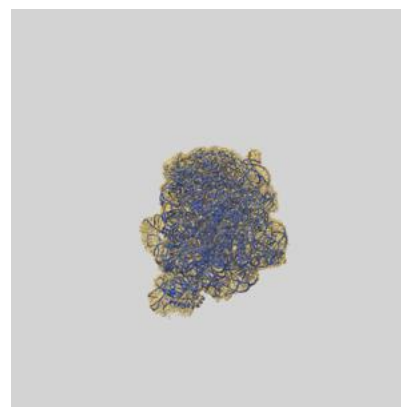
9.1 Map-model overlay [i](#)



X



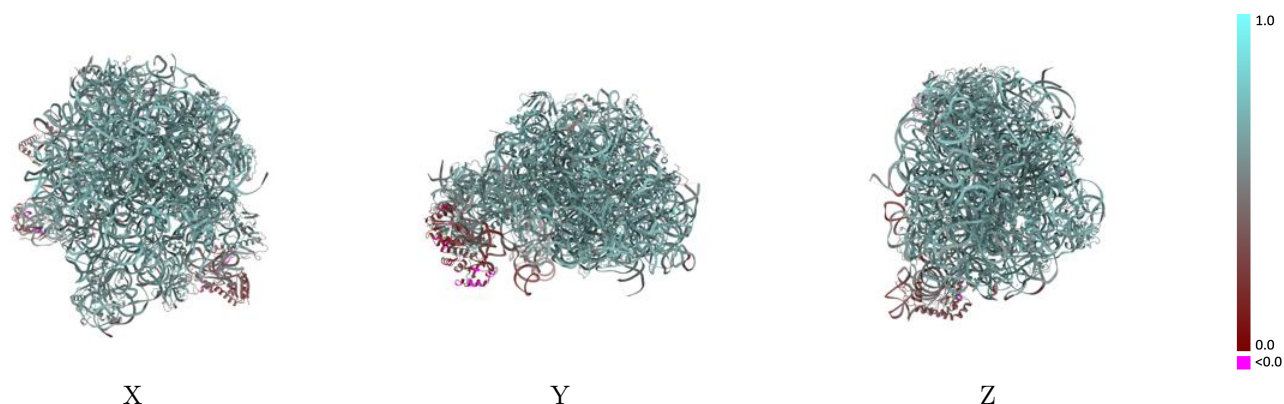
Y



Z

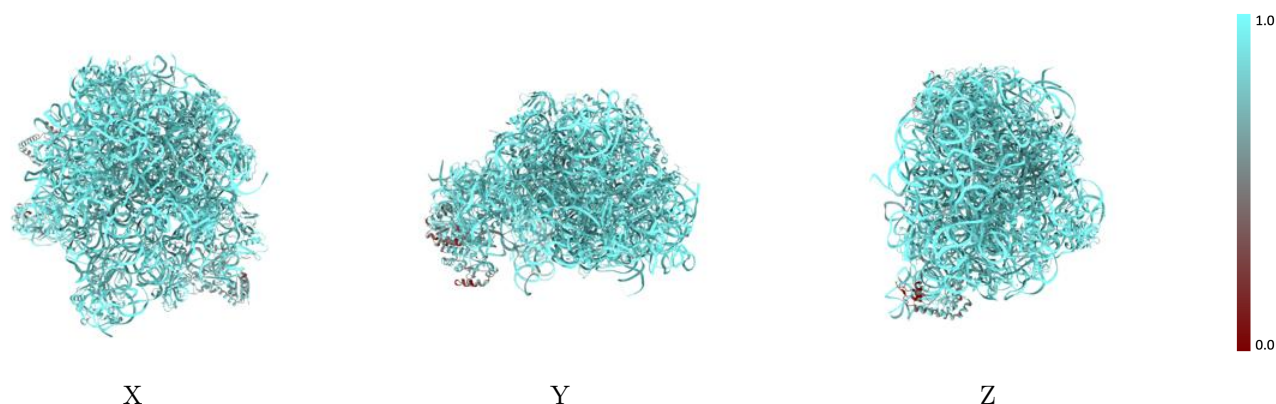
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



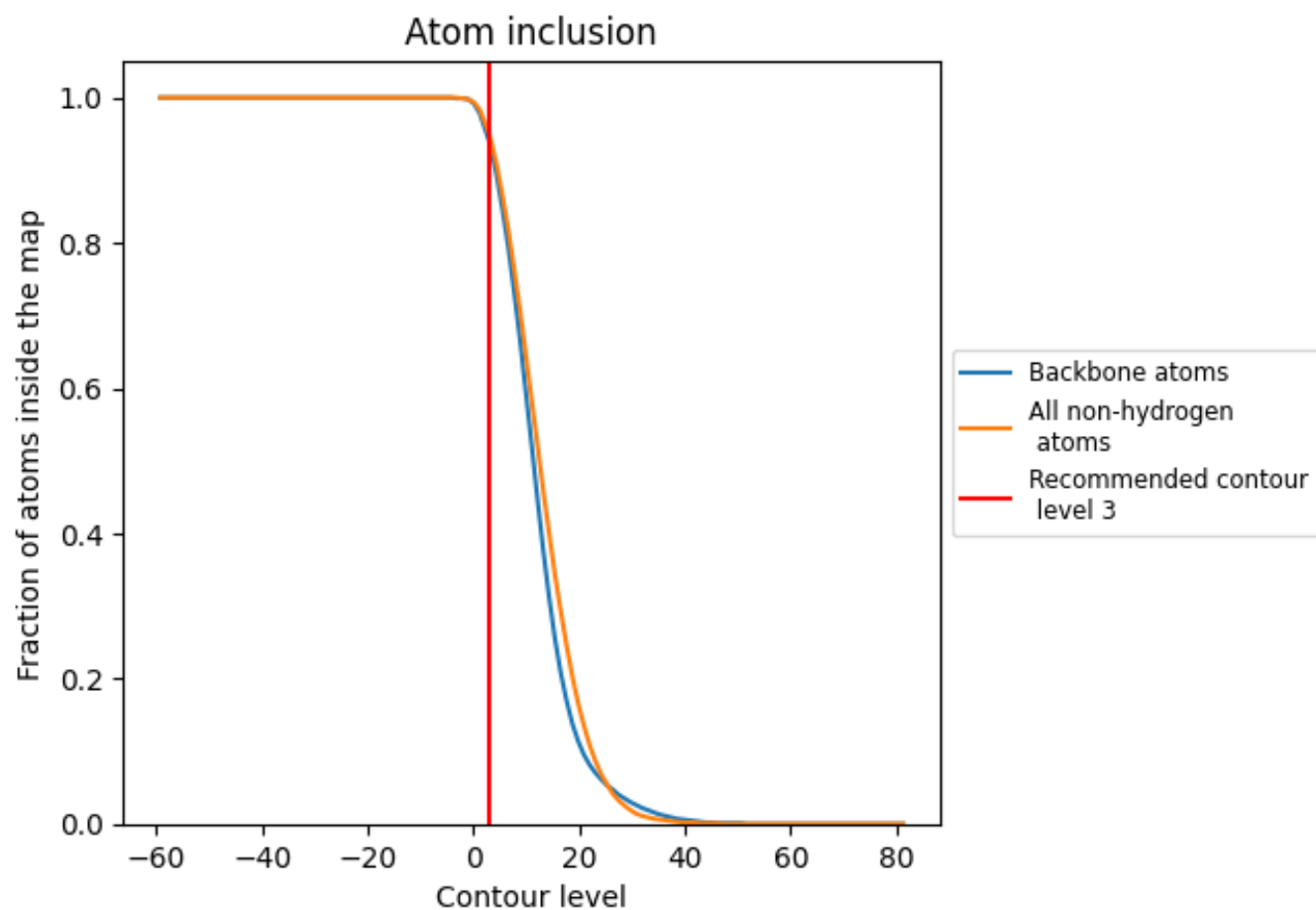
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 95% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.6100
1	 0.9170	 0.6020
2	 0.9530	 0.6460
4	 0.9330	 0.6200
5	 0.8410	 0.5760
6	 0.9450	 0.6690
7	 0.9610	 0.6660
8	 0.9490	 0.6450
A	 0.9790	 0.6340
B	 0.9780	 0.6050
C	 0.7920	 0.3080
D	 0.9570	 0.6600
E	 0.9500	 0.6510
F	 0.9480	 0.6400
G	 0.8940	 0.5280
H	 0.8950	 0.5500
I	 0.5460	 0.3930
J	 0.5940	 0.2320
K	 0.6240	 0.1980
L	 0.9450	 0.6470
M	 0.9080	 0.6140
N	 0.9470	 0.6500
O	 0.9250	 0.6440
P	 0.9670	 0.6580
Q	 0.9400	 0.6040
R	 0.8900	 0.6040
S	 0.9660	 0.6630
T	 0.9320	 0.6240
U	 0.9150	 0.6390
V	 0.9090	 0.6040
W	 0.9090	 0.5780
X	 0.8860	 0.5720
Y	 0.9290	 0.6490
Z	 0.9350	 0.6430
v	 0.8780	 0.3310

