



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 07:34 AM EDT

PDB ID : 9Q44 / pdb_00009q44
EMDB ID : EMD-72220
Title : Pseudomonas aeruginosa 50S ribosome bound to RsfS (L1 stalk in 'out' conformation and missing uL1 and tRNA)
Authors : Findlay, J.L.; Kanik, M.; Gauvin, C.C.; Franklin, M.J.; Lawrence, C.M.
Deposited on : 2025-08-19
Resolution : 2.29 Å (reported)
Based on initial models : ., 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:

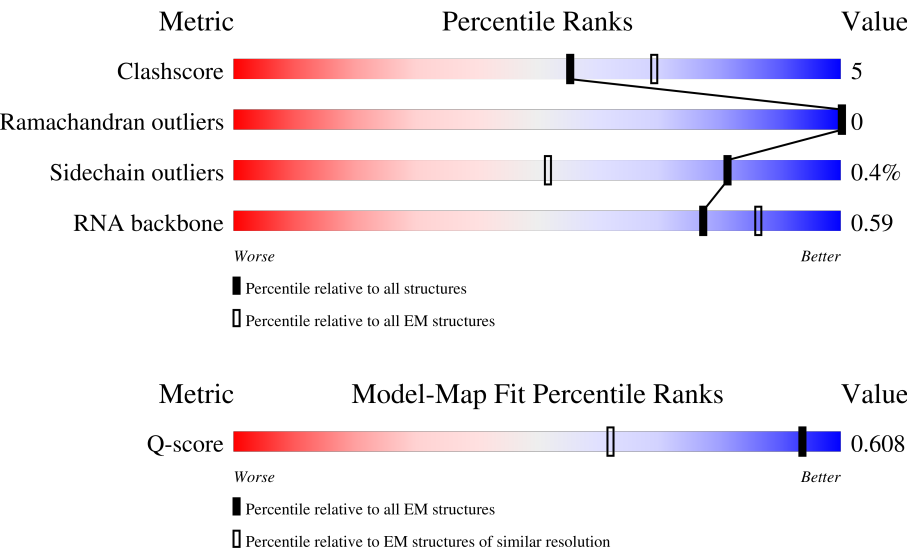
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.29 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.



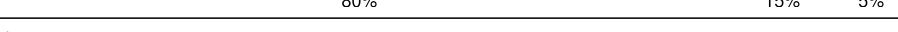
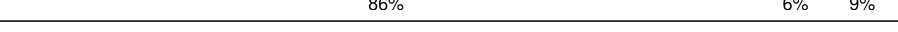
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3699 (1.79 - 2.79)

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	
2	B	121	
3	D	273	

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Mol	Chain	Length	Quality of chain
4	E	211	 85% 14%
5	F	200	 82% 18%
6	G	179	 82% 18%
7	H	177	 84% 15%
8	I	148	 43% 71% 7% 22%
9	L	142	 89% 11%
10	M	122	 83% 17%
11	N	144	 85% 15%
12	O	137	 78% 22%
13	P	129	 81% 12% 8%
14	Q	116	 80% 19%
15	R	116	 5% 84% 15%
16	S	118	 86% 13%
17	T	103	 85% 15%
18	U	110	 88% 12%
19	V	99	 80% 15% 5%
20	W	104	 86% 6% 9%
21	X	204	 80% 13% 7%
22	Y	85	 86% 5% 9%
23	Z	78	 86% 13%
24	1	63	 86% 11%
25	2	58	 93%
26	4	60	 80% 10% 10%
27	5	51	 8% 73% 25%
28	6	44	 73% 25%

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Mol	Chain	Length	Quality of chain
29	7	64	 84% 14% •
30	8	38	 84% 16%
31	9	118	 72% 16% 12% •
32	J	166	 6% 57% 10% 33%
33	K	143	 85% 15% •

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 96632 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 uL2.

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

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 8 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 11 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 13 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 15 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 16 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 17 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 20 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 21 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 22 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 23 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	56	Total	C	N	O	S	0	0
			440	275	86	77	2		

- Molecule 26 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	54	Total	C	N	O	S	0	0
			431	258	91	81	1		

- Molecule 27 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 28 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 29 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 30 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	8	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 31 is a protein called Ribosomal silencing factor RsfS.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	104	Total	C	N	O	S	0	0
			804	504	135	162	3		

- Molecule 32 is a protein called Large ribosomal subunit protein uL10.

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

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

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

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	A	195	Total	Mg	0
			195	195	
34	B	3	Total	Mg	0
			3	3	
34	D	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
34	E	1	Total 1	Mg 1	0
34	S	1	Total 1	Mg 1	0
34	4	1	Total 1	Mg 1	0

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	8	1	Total 1	Zn 1	0

- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	A	4039	Total 4039	O 4039	0
36	B	76	Total 76	O 76	0
36	D	91	Total 91	O 91	0
36	E	81	Total 81	O 81	0
36	F	49	Total 49	O 49	0
36	G	10	Total 10	O 10	0
36	H	4	Total 4	O 4	0
36	I	1	Total 1	O 1	0
36	L	31	Total 31	O 31	0
36	M	20	Total 20	O 20	0
36	N	64	Total 64	O 64	0
36	O	36	Total 36	O 36	0
36	P	32	Total 32	O 32	0

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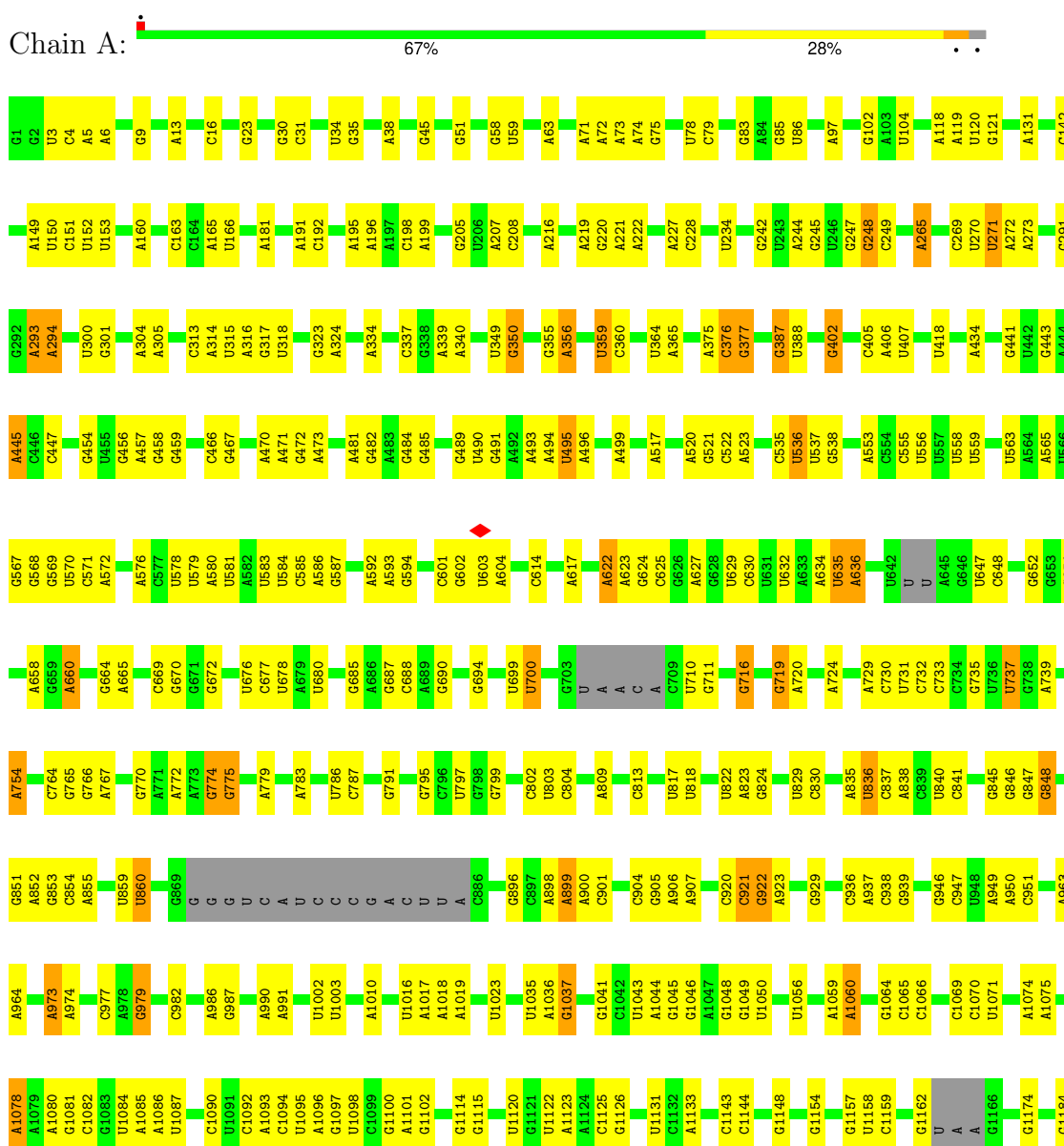
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Mol	Chain	Residues	Atoms		AltConf
36	Q	7	Total 7	O 7	0
36	R	26	Total 26	O 26	0
36	S	46	Total 46	O 46	0
36	T	35	Total 35	O 35	0
36	U	39	Total 39	O 39	0
36	V	30	Total 30	O 30	0
36	W	9	Total 9	O 9	0
36	X	22	Total 22	O 22	0
36	Y	25	Total 25	O 25	0
36	Z	21	Total 21	O 21	0
36	1	4	Total 4	O 4	0
36	2	18	Total 18	O 18	0
36	4	32	Total 32	O 32	0
36	5	3	Total 3	O 3	0
36	6	19	Total 19	O 19	0
36	7	24	Total 24	O 24	0
36	8	9	Total 9	O 9	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.

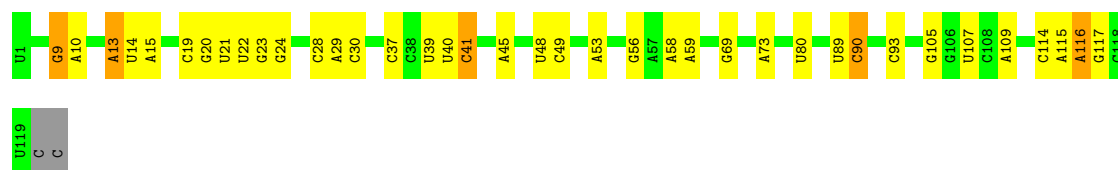
• Molecule 1: 23S rRNA



A2768	U2624	C2306	G2191	A2113	U2013	A	G1461	A1352	U1185
U2771	G2625	A2307	C2195	G2114	A2017	C	G1469	C1357	U1186
A2775	A2626	A2308	A2198	G2115	A2018	G	G1635	G1358	C1187
C2776	G2627	A2309	A2201	U2118	G2019	G1009	U1783	A1365	A1192
C2633	C2634	A2312	A2212	U2119	A2020	U1911	A1496	U1366	G1193
U2634	A2635	A2315	A2220	G2120	G2025	C1912	G1511	G1372	G1199
G2635	A2636	A2316	U2221	A2121	U2026	U1913	A1515	A1374	G1223
C2636	A2637	A2317	G2225	A2122	A2026	U1915	G1656	U1374	G1237
U2637	A2638	A2318	G2226	G2123	U2030	A1916	G1657	U1379	A1240
U2643	A2639	A2323	G2227	C2124	U2038	G1917	A1658	A1380	U1241
U2644	A2640	A2324	G2228	G2128	C2042	U1918	U	A1381	U1242
C2645	A2641	A2325	G2229	A2129	G2043	A1923	C	A1382	G1243
G2648	A2642	A2327	A2230	G2130	G2044	A1925	U	U1392	U1250
C2652	U2428	A2330	U2231	G2131	A2047	U1926	U	U1393	G1251
A2653	U2429	U2330	U2232	U2137	G2048	U1933	A	U1394	A1252
G2654	C2430	U2331	U2233	C2138	A2049	C1934	G	U1395	G1253
U2655	G2431	G2332	U2234	G2139	C2050	U1935	A	G1403	A1256
U2656	G2432	C2333	A2234	C2140	C2051	C1936	U	C1404	G1405
C2667	G2435	U2335	G2238	G2141	C2052	U1942	U	A1406	C1257
U2674	A2439	C2336	C2245	U2142	C2053	U1950	U	U1407	A1259
G2675	C2439	A2341	A2245	G2143	G2056	G1951	U	G1414	G1265
U2676	A2440	A2346	A2255	A2145	A2057	C1952	U	C1415	C1276
U2677	G2441	C2347	A2266	G2146	A2058	C1954	U	G1416	A1277
U2685	C2442	A2348	G2269	C2147	C2059	C1955	U	G1417	C1284
C2686	C2443	U2349	U2270	C2148	C2060	A1957	U	G1418	G1287
G2701	A2448	G2350	A2271	C2149	U2061	U1958	U	A1420	A1288
C2710	C2449	C2351	G2272	U2150	U2062	G1959	U	A1421	A1289
U2711	A2454	G2352	A2274	C2151	C2065	G1971	U	G1422	G1296
A2712	C2455	U2353	U2278	C2152	U2066	U1978	U	G1423	U1303
U2713	A2456	C2354	G2279	U2153	U2073	G1979	U	U1434	G1304
G2719	U2460	A2359	U2283	U2154	U2074	U1980	U	C1433	A1308
A2720	C2461	C2360	U2292	A2158	U2079	C1986	U	U1435	U1316
C2731	C2462	G2362	C2293	U2159	G2080	U1988	U	G1439	U1339
A2735	G2471	A2365	G2294	C2161	U2086	G1989	U	U1447	A1340
C2740	G2472	U2367	G2295	C2162	U2095	C1993	U	A1450	C1344
U2871	G2475	G2370	U2298	U2167	U2096	U1997	U	G1451	G1345
U2872	A2743	U2371	A2299	G2168	G2097	G1999	U	G1452	A1346
G2873	A2744	C2372	U2300	U2172	G2098	A2000	U	U1453	G1347
U2885	U2750	G2376	C2300	G2173	U2099	A2001	C	G1456	G1348
A2890	G2750	U2377	C2304	C2174	A2101	A2002	G	A1457	U1350
U2896	A2751	G2378	U2305	U2175	G2102	A2006	U	U1460	G1351
C2867	A2752	A2379	U2306	U2176	G2103	A2007	A		
U2871	U2760	U	U2307	A2177	A2104	A2008	C		
U2872	A2765	C2388	U2308	G2178	U2105	U2009	A		
G2873	U2766	U2389	U2309	A2179	A2106	G2011	U		
U2885	G2767	A2390	U2310	C2183	G2107	C2012	A		
A2890		U	U2311	U2184	G2108				
A		A	U2312	A2185					
				A2186					
				C2187					

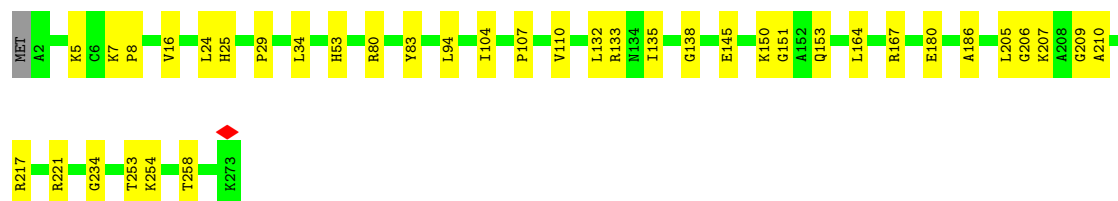
• Molecule 2: 5S rRNA

Chain B: 



- Molecule 3: Large ribosomal subunit protein uL2

Chain D: 



- Molecule 4: Large ribosomal subunit protein uL3

Chain E: 



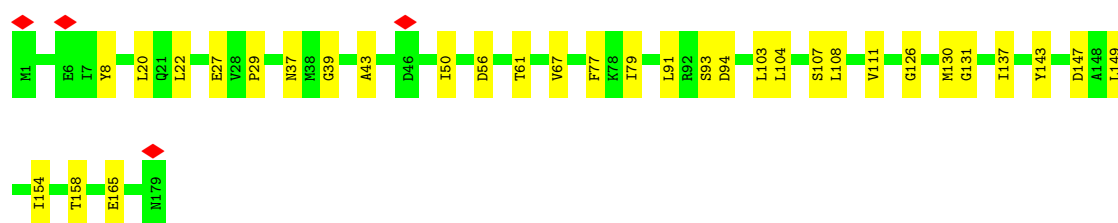
- Molecule 5: Large ribosomal subunit protein uL4

Chain F: 



- Molecule 6: Large ribosomal subunit protein uL5

Chain G: 



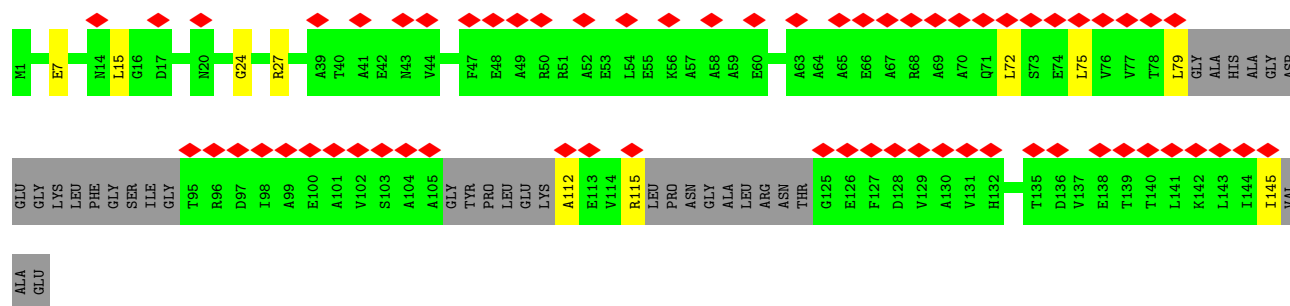
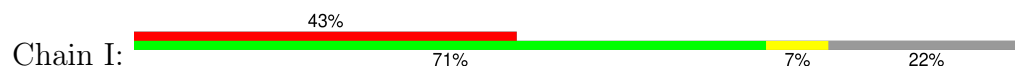
- Molecule 7: Large ribosomal subunit protein uL6

Chain H: 

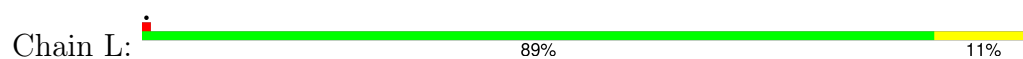




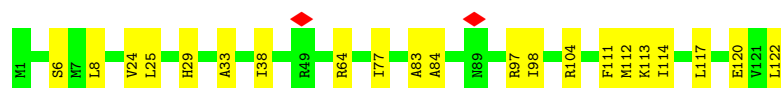
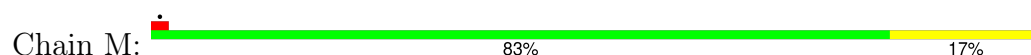
- Molecule 8: Large ribosomal subunit protein bL9



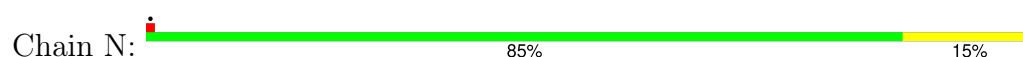
- Molecule 9: Large ribosomal subunit protein uL13



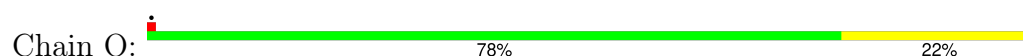
- Molecule 10: Large ribosomal subunit protein uL14



- Molecule 11: Large ribosomal subunit protein uL15



- Molecule 12: Large ribosomal subunit protein uL16



- Molecule 13: Large ribosomal subunit protein bL17

Chain P:  81% 12% 8%



- Molecule 14: Large ribosomal subunit protein uL18

Chain Q:  80% 19%



- Molecule 15: Large ribosomal subunit protein bL19

Chain R:  5% 84% 15%



- Molecule 16: Large ribosomal subunit protein bL20

Chain S:  86% 13%



- Molecule 17: Large ribosomal subunit protein bL21

Chain T:  85% 15%



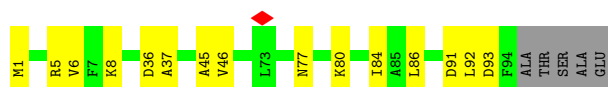
- Molecule 18: Large ribosomal subunit protein uL22

Chain U:  88% 12%



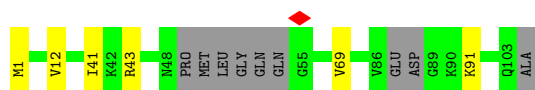
- Molecule 19: Large ribosomal subunit protein uL23

Chain V:  80% 15% 5%



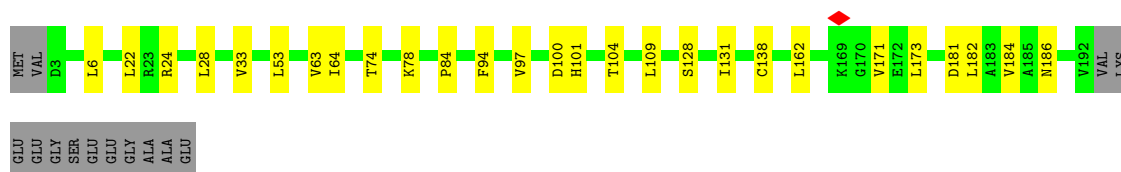
- Molecule 20: Large ribosomal subunit protein uL24

Chain W: 



- Molecule 21: Large ribosomal subunit protein bL25

Chain X: 



- Molecule 22: Large ribosomal subunit protein bL27

Chain Y: 



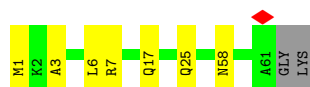
- Molecule 23: Large ribosomal subunit protein bL28

Chain Z: 

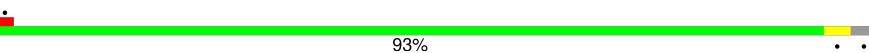


- Molecule 24: Large ribosomal subunit protein uL29

Chain 1: 



- Molecule 25: Large ribosomal subunit protein uL30

Chain 2: 



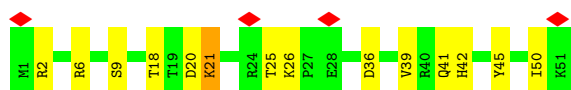
- Molecule 26: Large ribosomal subunit protein bL32

Chain 4:  80% 10% 10%



- Molecule 27: Large ribosomal subunit protein bL33

Chain 5:  8% 73% 25%



- Molecule 28: Large ribosomal subunit protein bL34

Chain 6:  73% 25%



- Molecule 29: Large ribosomal subunit protein bL35

Chain 7:  84% 14%



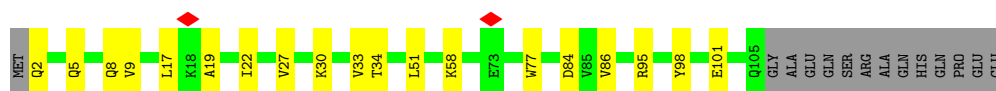
- Molecule 30: Large ribosomal subunit protein bL36A

Chain 8:  84% 16%



- Molecule 31: Ribosomal silencing factor RsfS

Chain 9:  72% 16% 12%



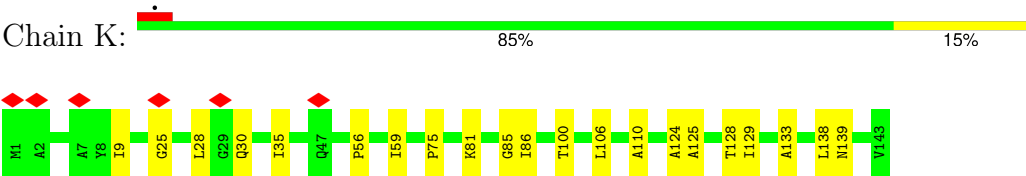
- Molecule 32: Large ribosomal subunit protein uL10

Chain J:  6% 57% 10% 33%



ILE
ASP
VAL
LEU
ALA
SER
LEU
PRO
THR
TYR
ASP
GLU
ALA
VAL
SER
GLN
LEU
MET
SER
VAL
ILE
GLN
GLY
ALA
THR
SER
LYS
LEU
ALA
ARG
THR
LEU
ALA
ALA
ILE
ARG
ASP
GLN
LYS
GLU
ALA
ALA
ALA

● Molecule 33: Large ribosomal subunit protein uL10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	452165	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	66.579	Depositor
Minimum map value	-43.550	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.055	Depositor
Recommended contour level	3.5	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: 5MC, 7MG, 5MU, 6MZ, OMC, 2MG, MG, 1MG, OMG, OMU, ZN, 2MA

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	0.23	0/67882	0.26	0/105870
2	B	0.12	0/2833	0.21	0/4413
3	D	0.16	0/2108	0.29	0/2831
4	E	0.17	0/1587	0.31	0/2138
5	F	0.09	0/1541	0.23	0/2075
6	G	0.13	0/1456	0.26	0/1953
7	H	0.10	0/1332	0.22	0/1794
8	I	0.14	0/861	0.30	0/1159
9	L	0.12	0/1156	0.28	0/1559
10	M	0.10	0/947	0.26	0/1268
11	N	0.08	0/1078	0.23	0/1436
12	O	0.08	0/1105	0.21	0/1476
13	P	0.17	0/968	0.36	0/1294
14	Q	0.18	0/888	0.23	0/1183
15	R	0.20	0/910	0.32	0/1218
16	S	0.16	0/946	0.31	0/1257
17	T	0.09	0/835	0.21	0/1117
18	U	0.10	0/837	0.22	0/1114
19	V	0.08	0/749	0.23	0/1002
20	W	0.09	0/743	0.27	0/988
21	X	0.13	0/1468	0.26	0/1987
22	Y	0.13	0/589	0.37	0/782
23	Z	0.15	0/641	0.25	0/854
24	1	0.14	0/491	0.23	0/654
25	2	0.19	0/444	0.27	0/597
26	4	0.09	0/437	0.23	0/583
27	5	0.12	0/433	0.27	0/576
28	6	0.18	0/368	0.36	0/482
29	7	0.15	0/511	0.34	0/668
30	8	0.09	0/308	0.19	0/404
31	9	0.17	0/813	0.35	0/1103
32	J	0.08	0/850	0.22	0/1142

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	K	0.08	0/1061	0.23	0/1435
All	All	0.21	0/99176	0.26	0/148412

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 [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	30645	483	0
2	B	2535	0	1283	20	0
3	D	2072	0	2152	26	0
4	E	1564	0	1575	21	0
5	F	1521	0	1581	27	0
6	G	1435	0	1504	21	0
7	H	1314	0	1373	15	0
8	I	858	0	890	6	0
9	L	1130	0	1160	11	0
10	M	938	0	1012	16	0
11	N	1066	0	1112	15	0
12	O	1085	0	1157	21	0
13	P	952	0	996	11	0
14	Q	881	0	920	14	0
15	R	901	0	958	14	0
16	S	936	0	1025	13	0
17	T	822	0	858	11	0
18	U	833	0	897	8	0
19	V	739	0	788	10	0
20	W	738	0	806	4	0
21	X	1445	0	1486	18	0
22	Y	581	0	603	3	0
23	Z	630	0	653	8	0
24	1	490	0	520	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	2	440	0	469	2	0
26	4	431	0	424	6	0
27	5	426	0	457	10	0
28	6	365	0	409	10	0
29	7	506	0	569	11	0
30	8	307	0	342	4	0
31	9	804	0	809	13	0
32	J	840	0	867	10	0
33	K	1046	0	1089	14	0
34	4	1	0	0	0	0
34	A	195	0	0	0	0
34	B	3	0	0	0	0
34	D	1	0	0	0	0
34	E	1	0	0	0	0
34	S	1	0	0	0	0
35	8	1	0	0	0	0
36	1	4	0	0	0	0
36	2	18	0	0	0	0
36	4	32	0	0	1	0
36	5	3	0	0	1	0
36	6	19	0	0	1	0
36	7	24	0	0	1	0
36	8	9	0	0	0	0
36	A	4039	0	0	16	0
36	B	76	0	0	1	0
36	D	91	0	0	1	0
36	E	81	0	0	0	0
36	F	49	0	0	1	0
36	G	10	0	0	0	0
36	H	4	0	0	0	0
36	I	1	0	0	0	0
36	L	31	0	0	0	0
36	M	20	0	0	0	0
36	N	64	0	0	0	0
36	O	36	0	0	0	0
36	P	32	0	0	0	0
36	Q	7	0	0	0	0
36	R	26	0	0	1	0
36	S	46	0	0	2	0
36	T	35	0	0	0	0
36	U	39	0	0	1	0
36	V	30	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	W	9	0	0	1	0
36	X	22	0	0	0	0
36	Y	25	0	0	0	0
36	Z	21	0	0	1	0
All	All	96632	0	61389	753	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 5.

The worst 5 of 753 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)
1:A:79:C:HO2'	1:A:340:A:H8	1.25	0.81
7:H:16:GLU:HB2	7:H:27:LYS:HB3	1.71	0.72
1:A:1692:G:N7	36:A:3104:HOH:O	2.22	0.72
1:A:558:U:H1'	1:A:2017:6MZ:H9C1	1.73	0.70
1:A:1046:G:O2'	1:A:1093:A:N6	2.25	0.69

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	D	270/273 (99%)	265 (98%)	5 (2%)	0	100	100
4	E	206/211 (98%)	200 (97%)	6 (3%)	0	100	100
5	F	198/200 (99%)	198 (100%)	0	0	100	100
6	G	177/179 (99%)	175 (99%)	2 (1%)	0	100	100
7	H	172/177 (97%)	171 (99%)	1 (1%)	0	100	100
8	I	107/148 (72%)	104 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	L	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
10	M	120/122 (98%)	120 (100%)	0	0	100	100
11	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
12	O	135/137 (98%)	134 (99%)	1 (1%)	0	100	100
13	P	117/129 (91%)	115 (98%)	2 (2%)	0	100	100
14	Q	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
15	R	112/116 (97%)	109 (97%)	3 (3%)	0	100	100
16	S	115/118 (98%)	115 (100%)	0	0	100	100
17	T	101/103 (98%)	101 (100%)	0	0	100	100
18	U	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
19	V	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
20	W	89/104 (86%)	87 (98%)	2 (2%)	0	100	100
21	X	188/204 (92%)	187 (100%)	1 (0%)	0	100	100
22	Y	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
23	Z	75/78 (96%)	75 (100%)	0	0	100	100
24	1	59/63 (94%)	59 (100%)	0	0	100	100
25	2	54/58 (93%)	53 (98%)	1 (2%)	0	100	100
26	4	52/60 (87%)	52 (100%)	0	0	100	100
27	5	49/51 (96%)	49 (100%)	0	0	100	100
28	6	42/44 (96%)	42 (100%)	0	0	100	100
29	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
30	8	36/38 (95%)	36 (100%)	0	0	100	100
31	9	102/118 (86%)	100 (98%)	2 (2%)	0	100	100
32	J	109/166 (66%)	105 (96%)	4 (4%)	0	100	100
33	K	141/143 (99%)	136 (96%)	5 (4%)	0	100	100
All	All	3557/3800 (94%)	3506 (99%)	51 (1%)	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	D	212/213 (100%)	211 (100%)	1 (0%)	81	90
4	E	160/162 (99%)	160 (100%)	0	100	100
5	F	157/158 (99%)	157 (100%)	0	100	100
6	G	153/153 (100%)	153 (100%)	0	100	100
7	H	137/141 (97%)	137 (100%)	0	100	100
8	I	85/107 (79%)	84 (99%)	1 (1%)	63	79
9	L	119/119 (100%)	118 (99%)	1 (1%)	73	86
10	M	102/102 (100%)	102 (100%)	0	100	100
11	N	106/106 (100%)	105 (99%)	1 (1%)	70	84
12	O	110/110 (100%)	110 (100%)	0	100	100
13	P	98/104 (94%)	98 (100%)	0	100	100
14	Q	86/87 (99%)	86 (100%)	0	100	100
15	R	96/98 (98%)	96 (100%)	0	100	100
16	S	87/88 (99%)	86 (99%)	1 (1%)	65	81
17	T	86/86 (100%)	86 (100%)	0	100	100
18	U	87/87 (100%)	87 (100%)	0	100	100
19	V	79/82 (96%)	79 (100%)	0	100	100
20	W	81/88 (92%)	81 (100%)	0	100	100
21	X	154/164 (94%)	153 (99%)	1 (1%)	78	89
22	Y	57/61 (93%)	57 (100%)	0	100	100
23	Z	66/67 (98%)	66 (100%)	0	100	100
24	1	54/55 (98%)	53 (98%)	1 (2%)	50	69
25	2	48/49 (98%)	48 (100%)	0	100	100
26	4	47/52 (90%)	47 (100%)	0	100	100
27	5	47/47 (100%)	46 (98%)	1 (2%)	47	66
28	6	37/37 (100%)	35 (95%)	2 (5%)	20	29
29	7	54/55 (98%)	54 (100%)	0	100	100
30	8	34/34 (100%)	34 (100%)	0	100	100
31	9	90/101 (89%)	89 (99%)	1 (1%)	65	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	J	82/122 (67%)	82 (100%)	0	100	100
33	K	110/110 (100%)	110 (100%)	0	100	100
All	All	2921/3045 (96%)	2910 (100%)	11 (0%)	81	92

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

Mol	Chain	Res	Type
27	5	21	LYS
28	6	41	ARG
31	9	8	GLN
28	6	42	LEU
16	S	6	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
23	Z	34	GLN
33	K	30	GLN
24	1	39	GLN
28	6	26	ASN
10	M	91	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2827/2892 (97%)	315 (11%)	6 (0%)
2	B	118/121 (97%)	14 (11%)	0
All	All	2945/3013 (97%)	329 (11%)	6 (0%)

5 of 329 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	1871	G
1	A	2516	G
1	A	2743	U
1	A	635	U
1	A	221	A

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

12 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$
1	5MU	A	1926	1	19,22,23	0.46	0	27,32,35	0.62	0
1	2MG	A	2432	1	23,26,27	0.57	0	33,38,41	0.50	0
1	2MG	A	1822	1	23,26,27	0.49	0	33,38,41	0.49	0
1	OMU	A	2539	1	19,22,23	2.97	7 (36%)	25,31,34	1.83	5 (20%)
1	6MZ	A	1608	1	22,25,26	2.40	4 (18%)	29,36,39	2.36	10 (34%)
1	2MA	A	2490	1,34	22,25,26	1.70	5 (22%)	32,37,40	3.47	13 (40%)
1	5MC	A	1949	1	19,22,23	0.58	0	26,32,35	0.61	0
1	OMC	A	2485	1,34	19,22,23	0.56	0	25,31,34	0.68	0
1	1MG	A	735	1	23,26,27	3.05	8 (34%)	33,39,42	1.85	8 (24%)
1	7MG	A	2056	1	23,26,27	1.12	1 (4%)	27,39,42	0.92	2 (7%)
1	6MZ	A	2017	1	22,25,26	2.36	5 (22%)	29,36,39	2.32	12 (41%)
1	OMG	A	2238	1	23,26,27	0.52	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
1	5MU	A	1926	1	-	0/7/25/26	0/2/2/2
1	2MG	A	2432	1	-	2/9/27/28	0/3/3/3
1	2MG	A	1822	1	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	2MA	A	2490	1,34	-	1/7/25/26	0/3/3/3
1	5MC	A	1949	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2485	1,34	-	0/9/27/28	0/2/2/2
1	1MG	A	735	1	-	0/7/25/26	0/3/3/3
1	7MG	A	2056	1	-	0/7/37/38	0/3/3/3
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 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1608	6MZ	C6-N6	9.41	1.45	1.34
1	A	735	1MG	C2-N3	9.25	1.48	1.33
1	A	2017	6MZ	C6-N6	9.04	1.44	1.34
1	A	2539	OMU	C2-N1	7.65	1.50	1.38
1	A	735	1MG	C4-N3	6.68	1.49	1.34

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2490	2MA	C5-C4-N3	-8.74	117.97	127.18
1	A	2490	2MA	N6-C6-N1	-8.58	105.46	117.03
1	A	2490	2MA	CM2-C2-N3	7.73	128.70	117.13
1	A	2017	6MZ	N1-C2-N3	-5.88	119.69	128.58
1	A	1608	6MZ	N1-C2-N3	-5.82	119.77	128.58

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

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

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1926	5MU	1	0
1	A	2432	2MG	1	0
1	A	1822	2MG	1	0
1	A	2017	6MZ	1	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 [i](#)

There are no chain breaks in this entry.

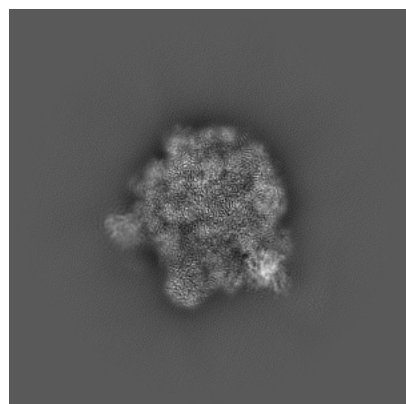
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72220. These allow visual inspection of the internal detail of the map and identification of artifacts.

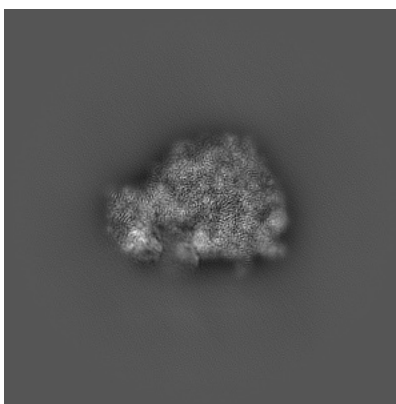
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

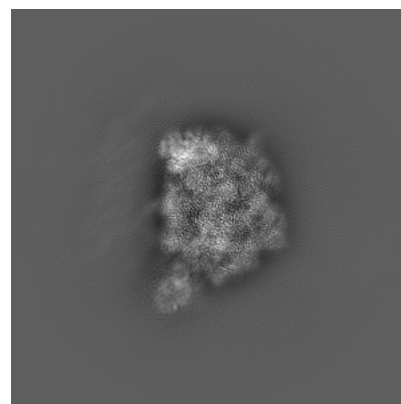
6.1.1 Primary map



X

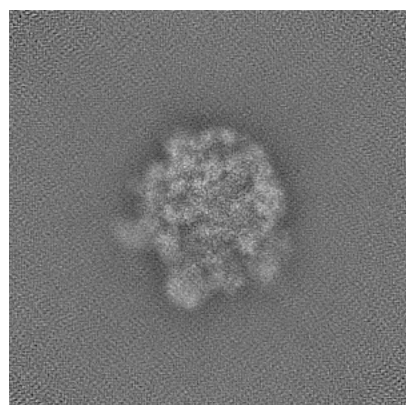


Y

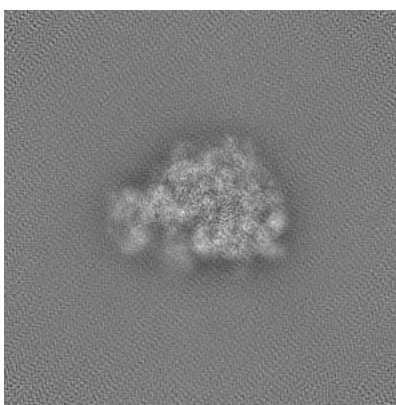


Z

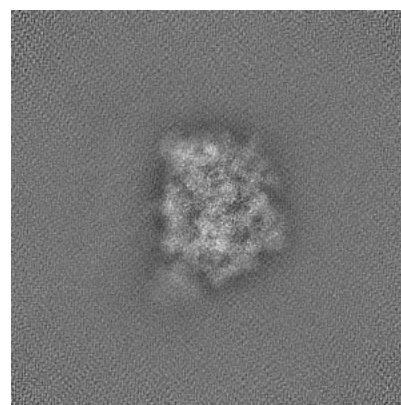
6.1.2 Raw map



X



Y

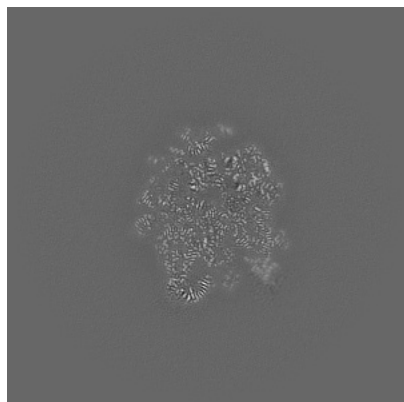


Z

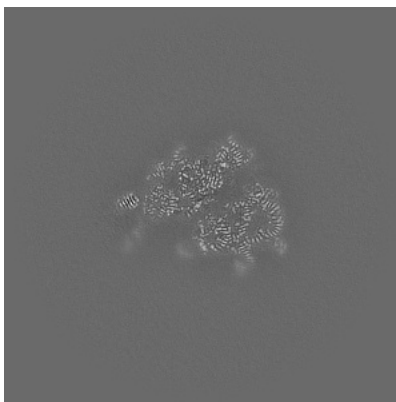
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

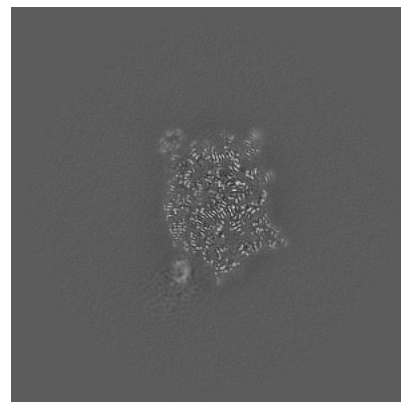
6.2.1 Primary map



X Index: 348

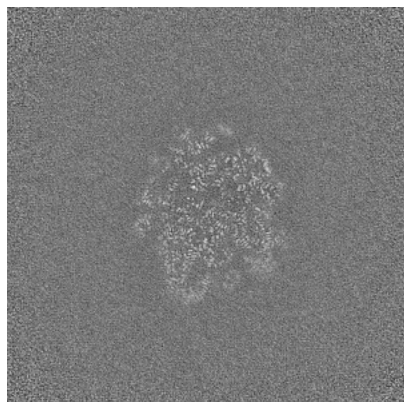


Y Index: 348

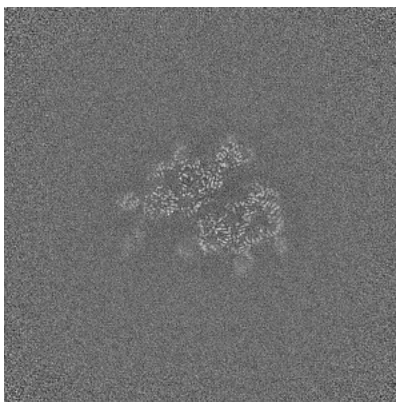


Z Index: 348

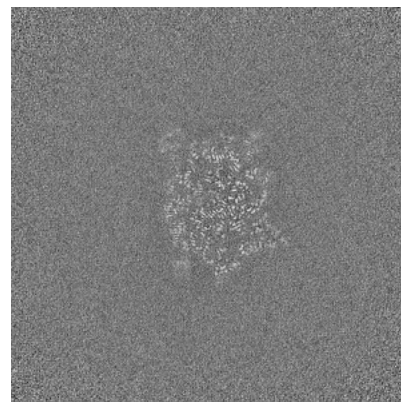
6.2.2 Raw map



X Index: 348



Y Index: 348

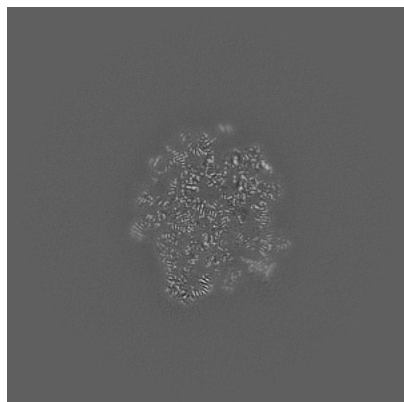


Z Index: 348

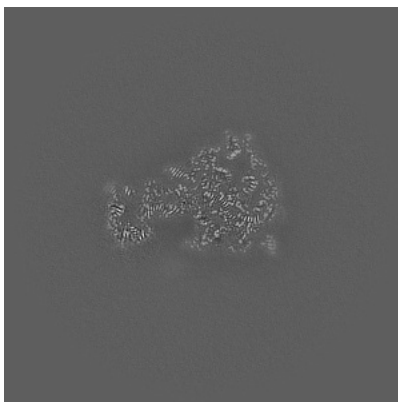
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

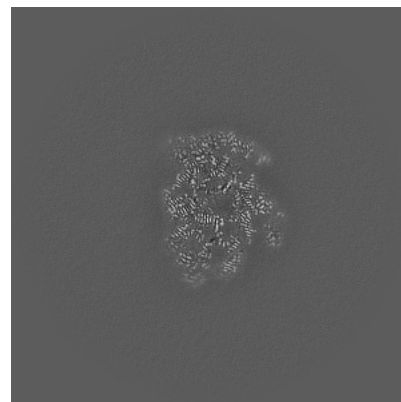
6.3.1 Primary map



X Index: 353

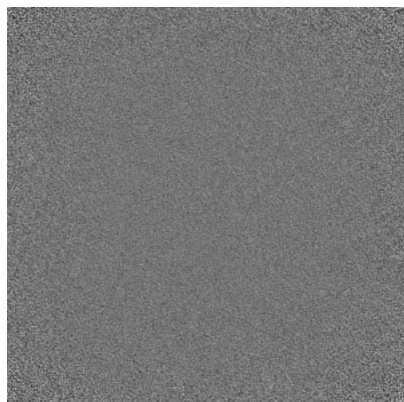


Y Index: 319

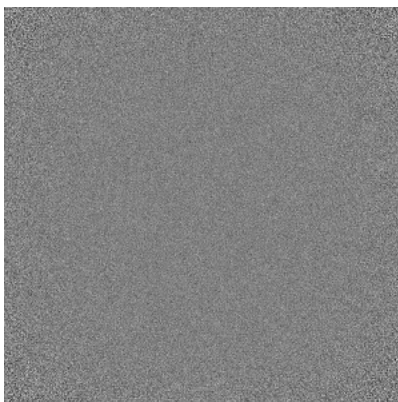


Z Index: 380

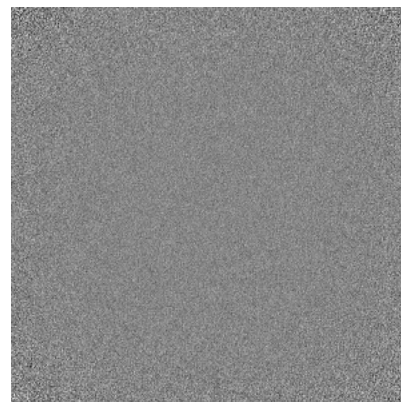
6.3.2 Raw map



X Index: 0



Y Index: 0

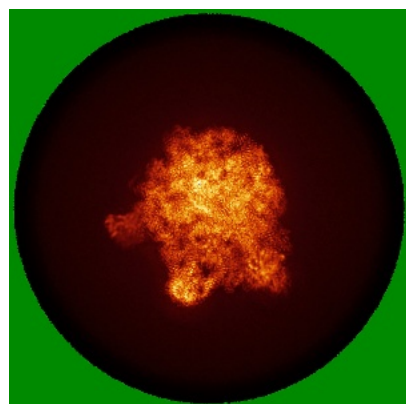


Z Index: 0

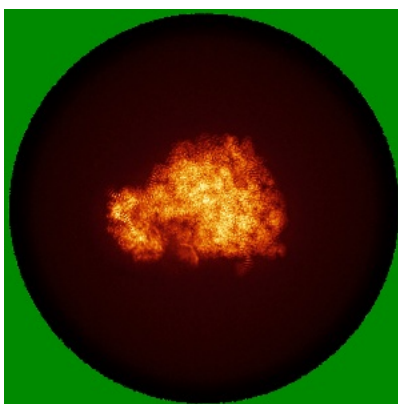
The images above show the largest variance slices of the map in three orthogonal directions.

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

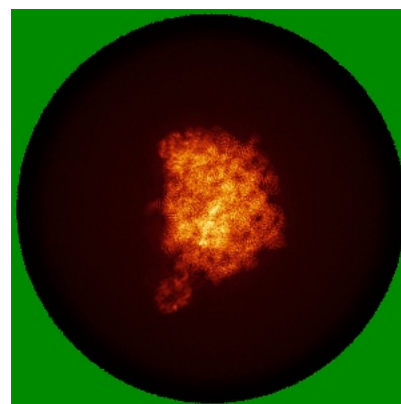
6.4.1 Primary map



X

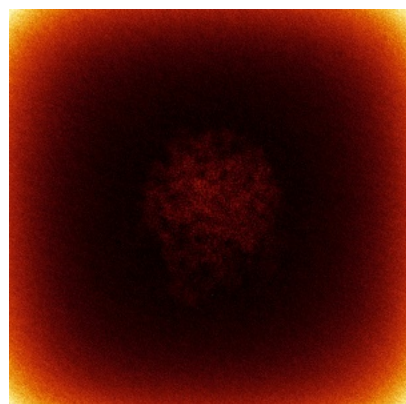


Y

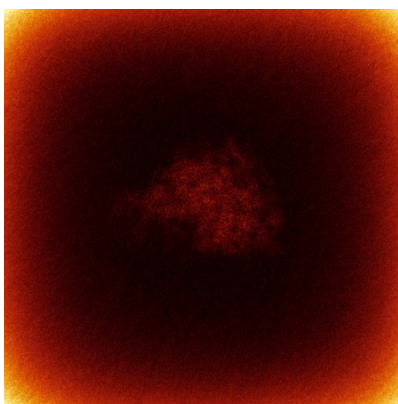


Z

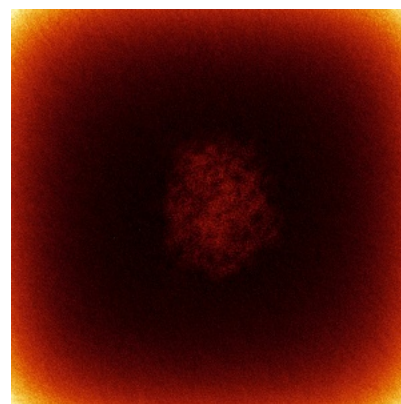
6.4.2 Raw map



X



Y

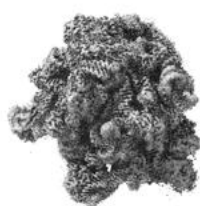


Z

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



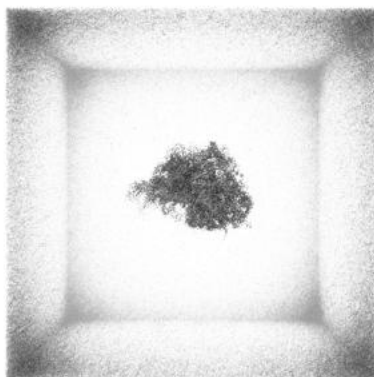
Z

The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

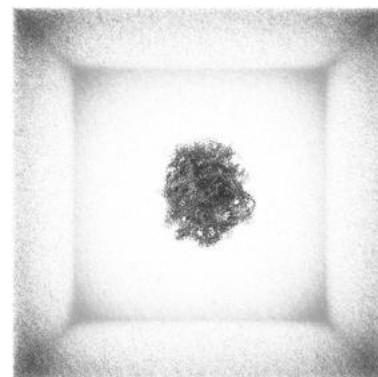
6.5.2 Raw map



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.

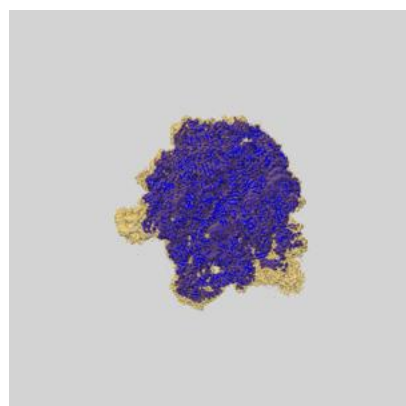
6.6 Mask visualisation [i](#)

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

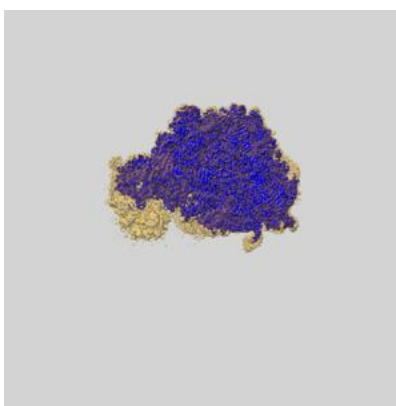
A mask typically either:

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

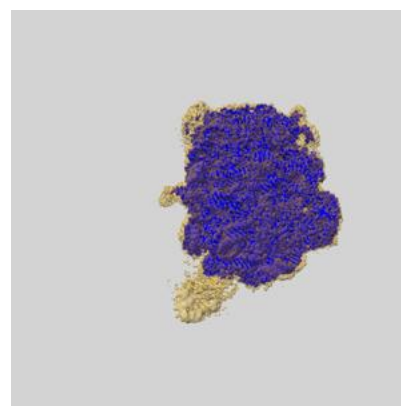
6.6.1 emd_72220_msk_1.map [i](#)



X



Y

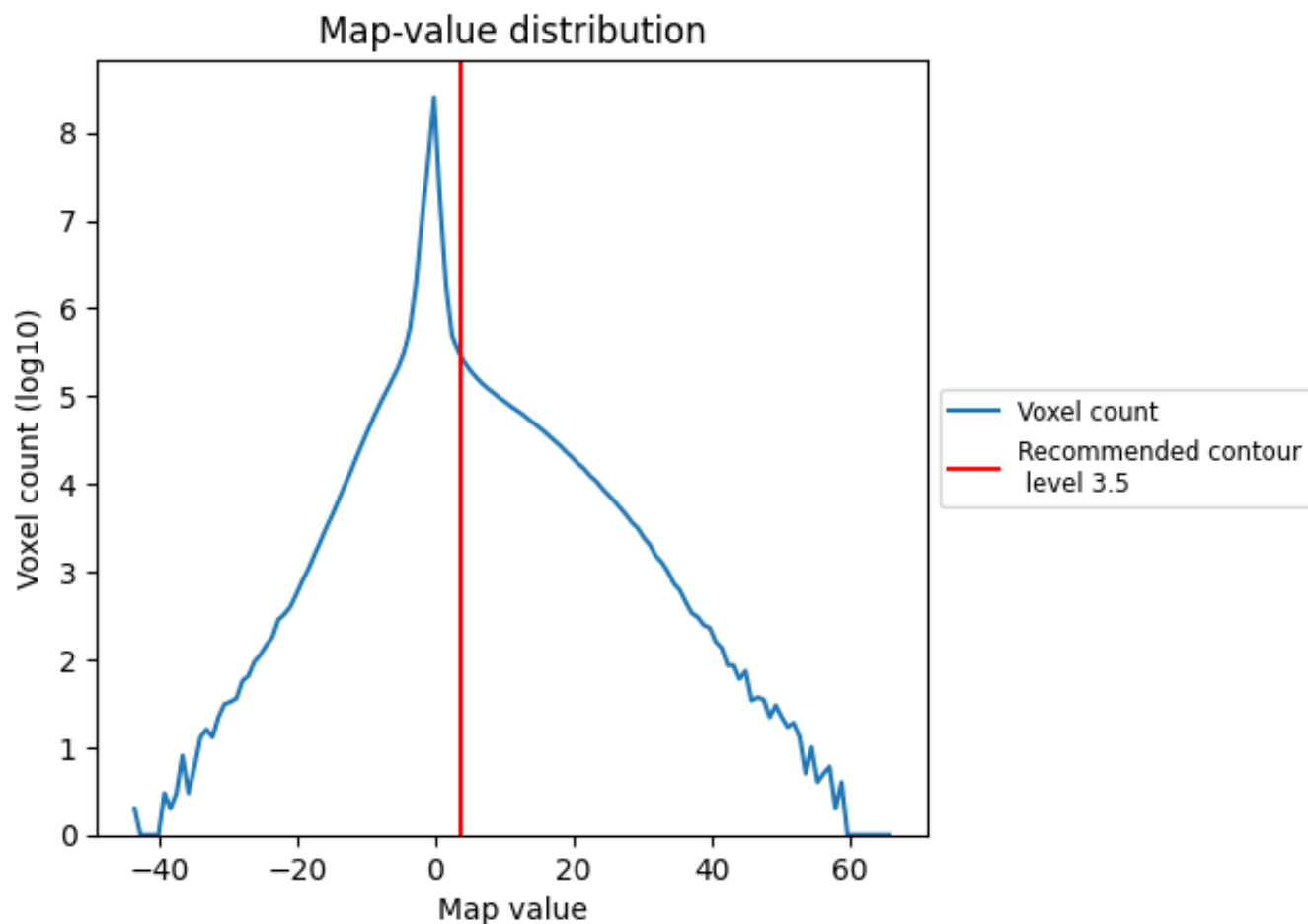


Z

7 Map analysis [i](#)

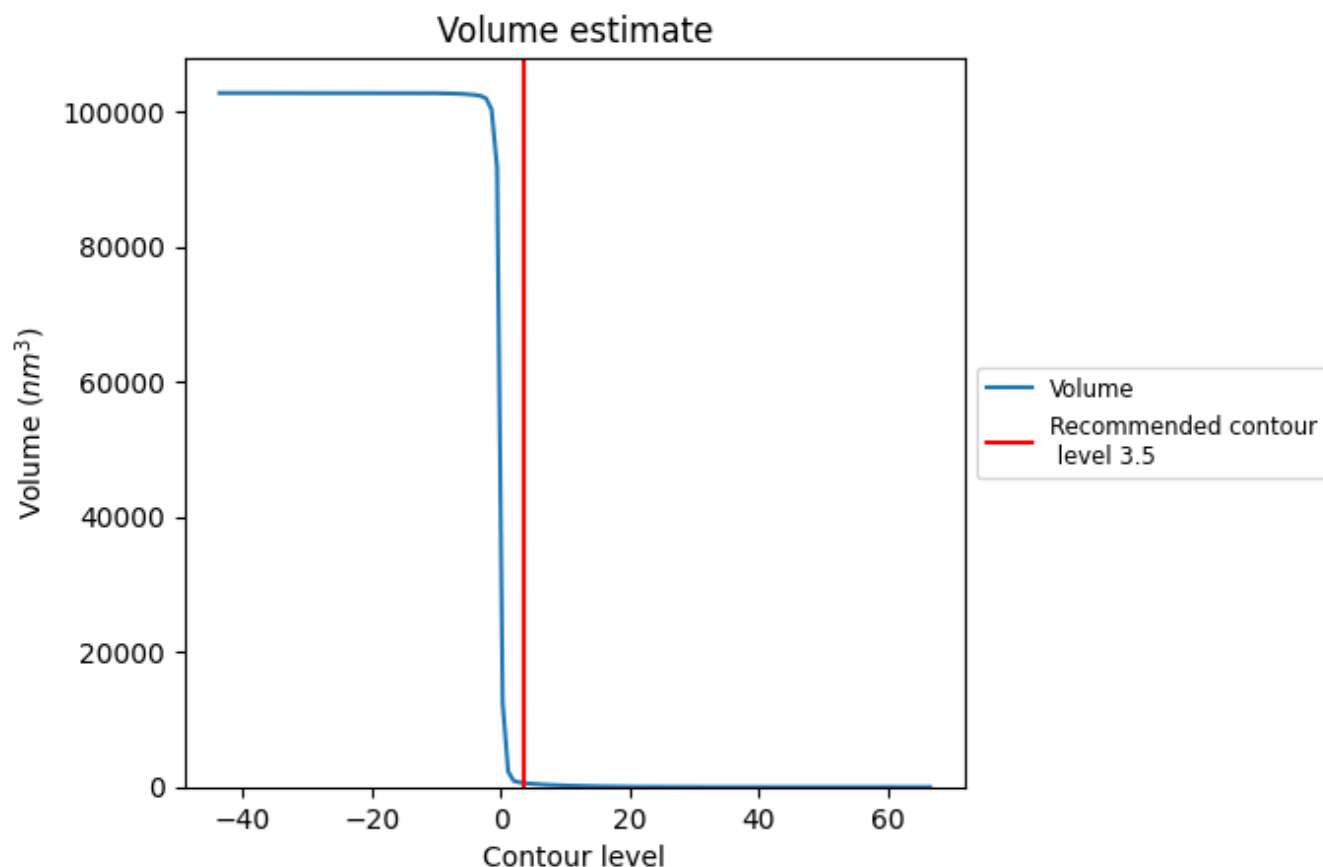
This section contains the results of statistical analysis of the map.

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.

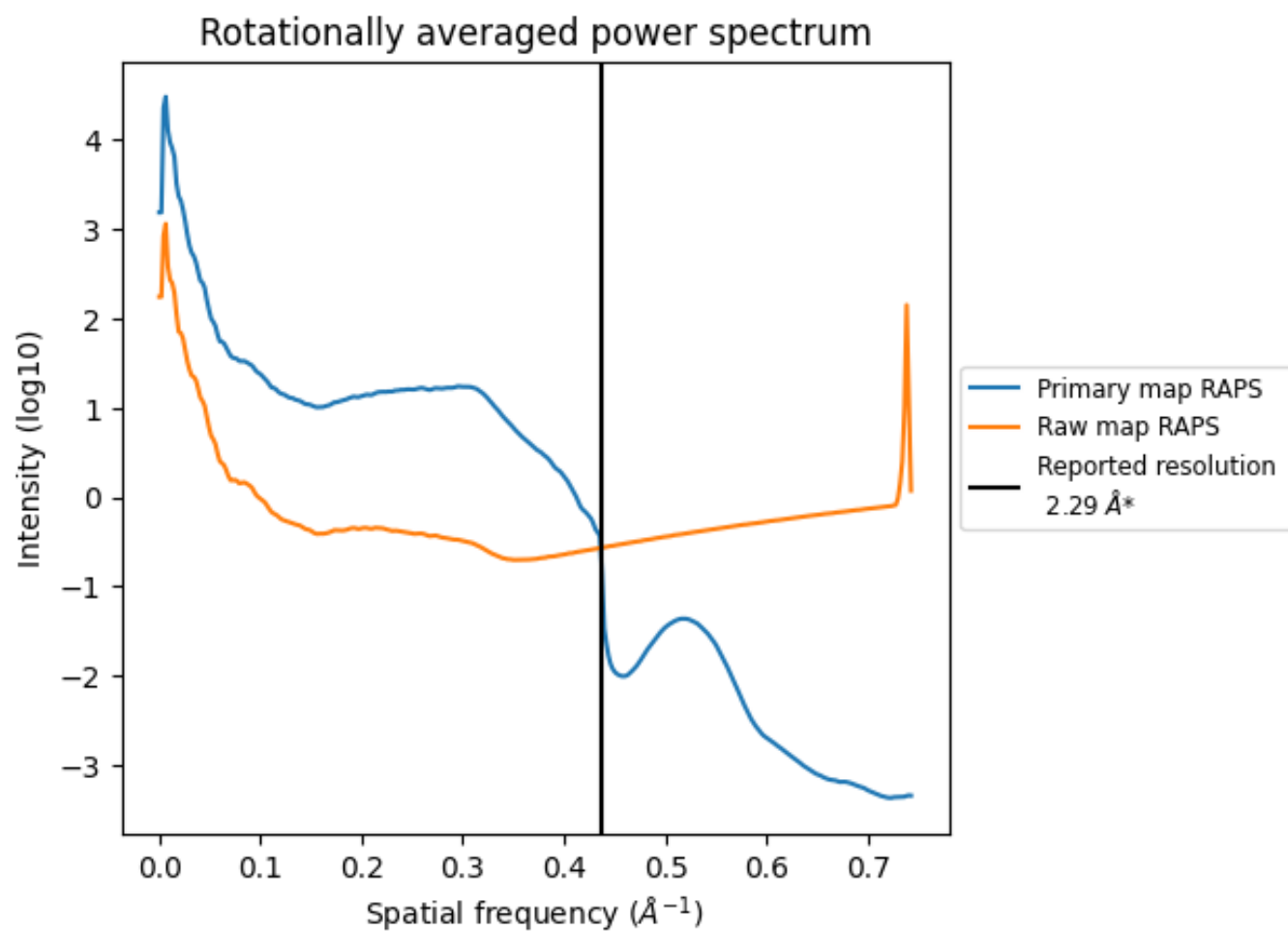
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 606 nm^3 ; this corresponds to an approximate mass of 548 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 ⓘ

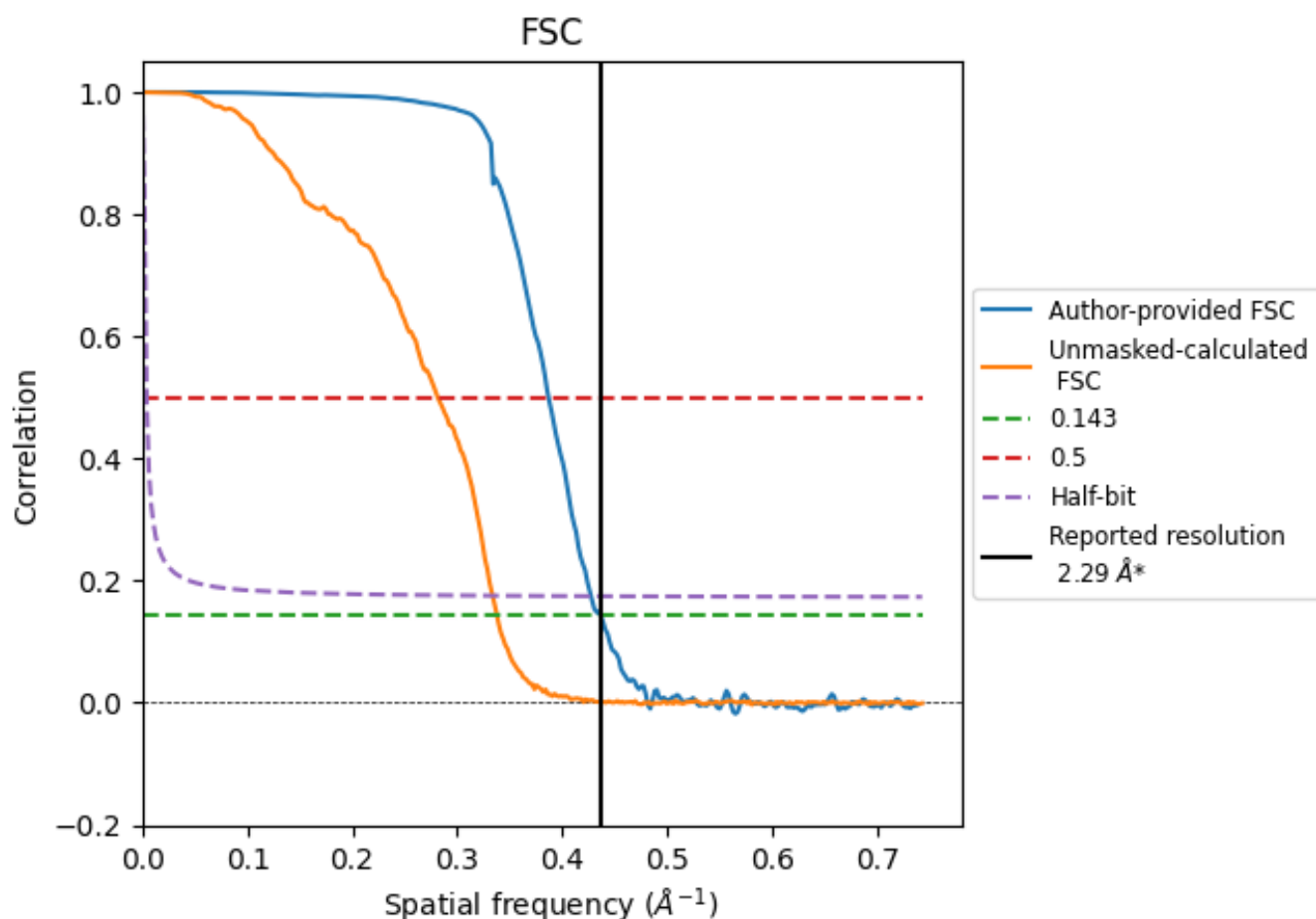


*Reported resolution corresponds to spatial frequency of 0.437 Å⁻¹

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 0.437 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

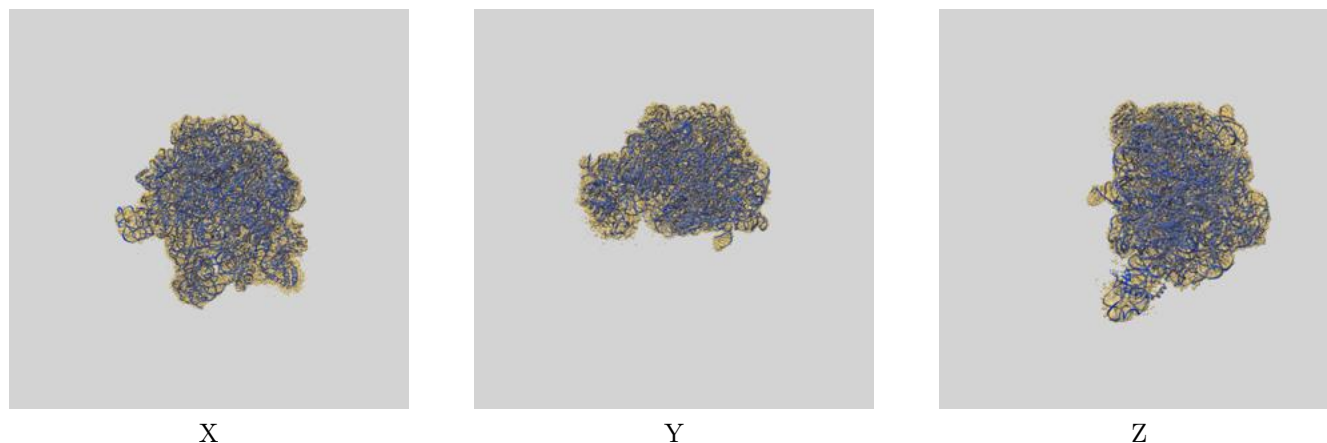
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.29	-	-
Author-provided FSC curve	2.29	2.58	2.34
Unmasked-calculated*	2.96	3.55	3.00

*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 2.96 differs from the reported value 2.29 by more than 10 %

9 Map-model fit [i](#)

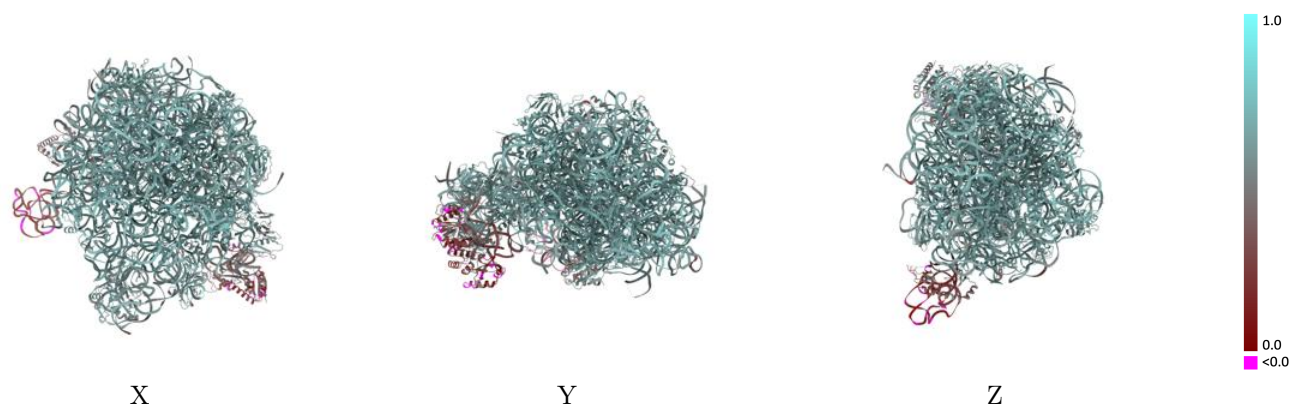
This section contains information regarding the fit between EMDB map EMD-72220 and PDB model 9Q44. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



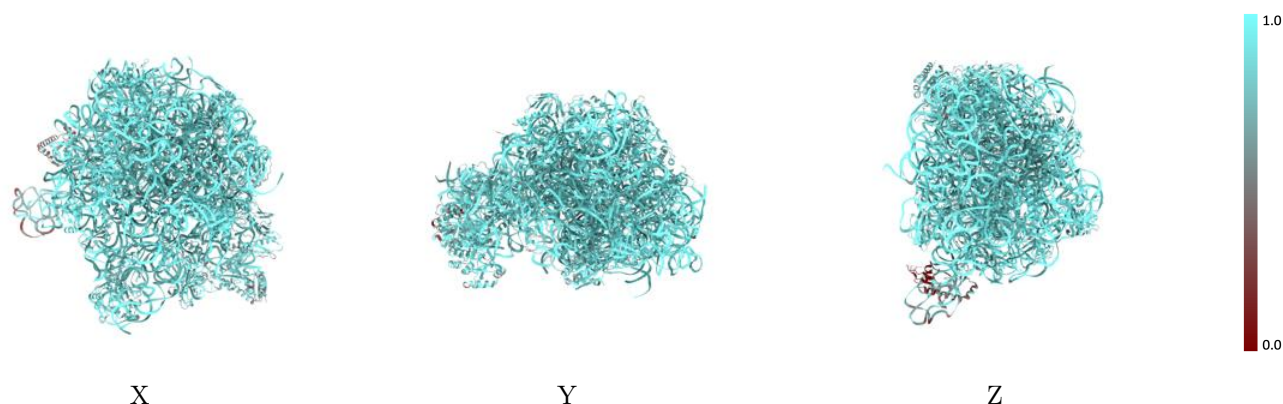
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



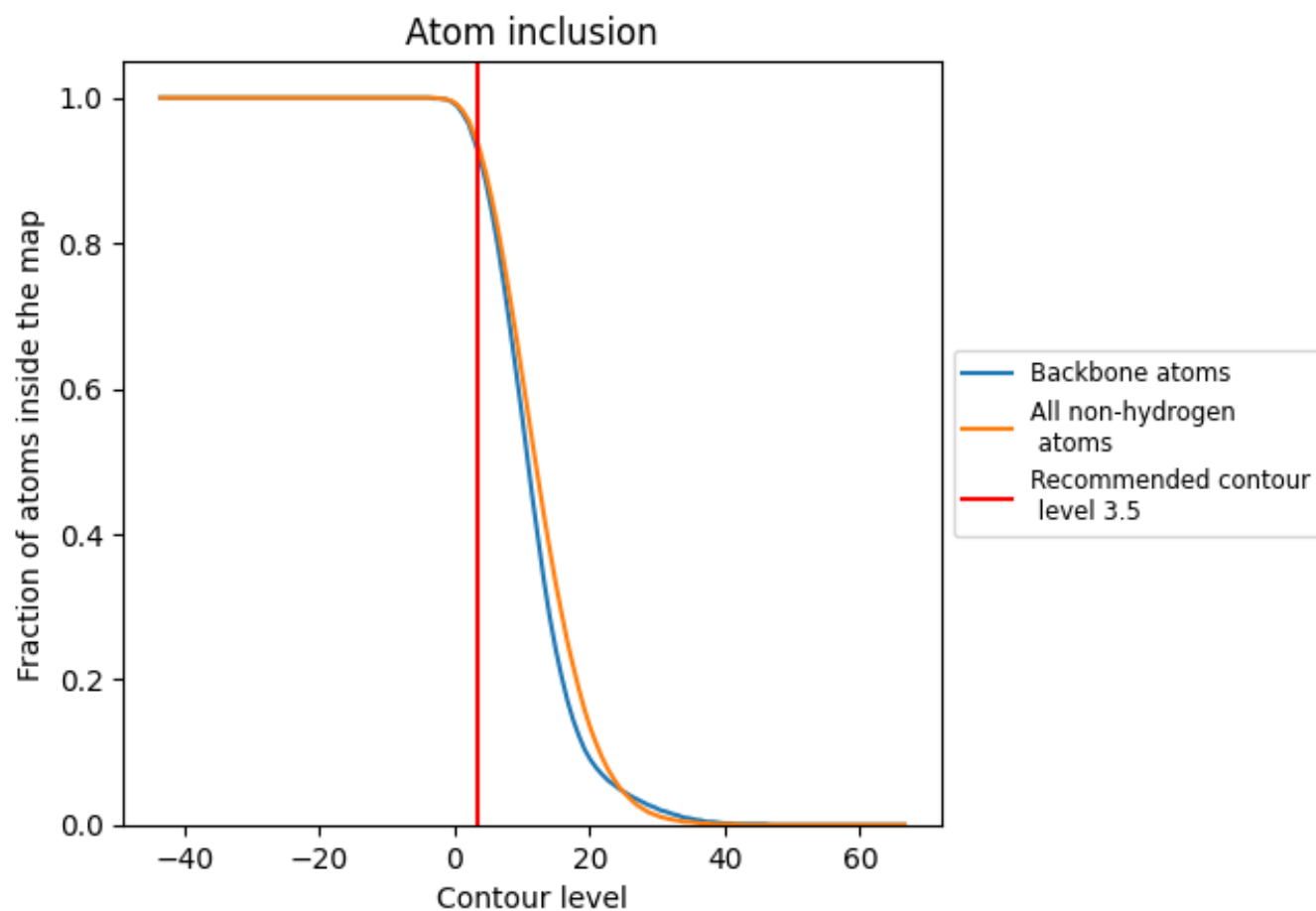
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 93% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.6080
1	 0.8900	 0.6060
2	 0.9320	 0.6350
4	 0.9110	 0.6280
5	 0.8020	 0.5860
6	 0.9390	 0.6590
7	 0.9370	 0.6570
8	 0.9290	 0.6230
9	 0.7700	 0.4890
A	 0.9610	 0.6210
B	 0.9540	 0.6000
D	 0.9420	 0.6540
E	 0.9320	 0.6450
F	 0.9200	 0.6260
G	 0.8470	 0.5260
H	 0.8350	 0.5540
I	 0.4070	 0.4090
J	 0.7440	 0.2420
K	 0.8280	 0.2000
L	 0.9290	 0.6450
M	 0.8870	 0.6210
N	 0.9240	 0.6400
O	 0.8970	 0.6370
P	 0.9510	 0.6530
Q	 0.9000	 0.5930
R	 0.8700	 0.6190
S	 0.9530	 0.6540
T	 0.9220	 0.6220
U	 0.8880	 0.6340
V	 0.8800	 0.6060
W	 0.8760	 0.5790
X	 0.8490	 0.5760
Y	 0.9190	 0.6410
Z	 0.9040	 0.6400

