



## wwPDB EM Validation Summary Report ⓘ

Nov 10, 2024 – 10:03 PM EST

PDB ID : 8FMW  
EMDB ID : EMD-29298  
Title : The structure of a hibernating ribosome in the Lyme disease pathogen  
Authors : Sharma, M.R.; Manjari, S.R.; Agrawal, E.K.; Keshavan, P.; Koripella, R.K.;  
Majumdar, S.; Marcinkiewicz, A.L.; Lin, Y.P.; Agrawal, R.K.; Banavali, N.K.  
Deposited on : 2022-12-25  
Resolution : 2.86 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

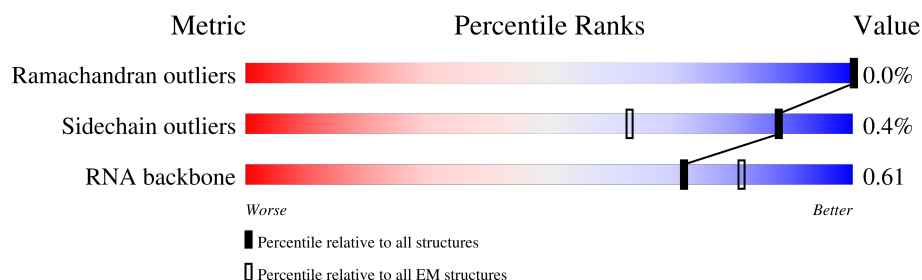
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.86 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.



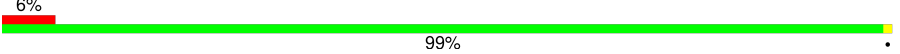
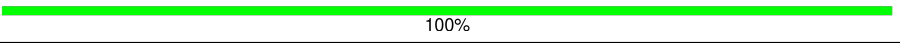
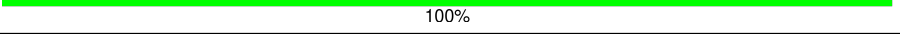
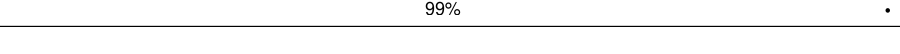
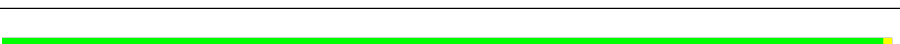

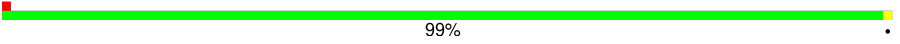
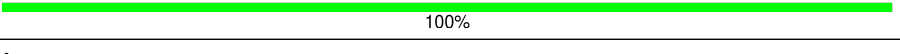
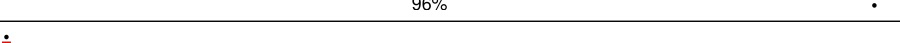
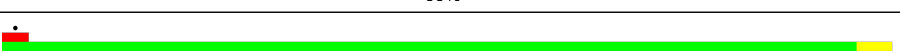
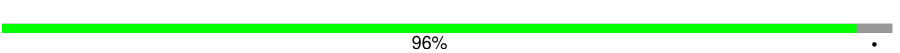
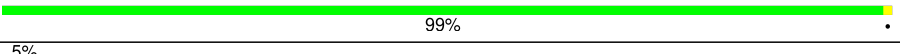

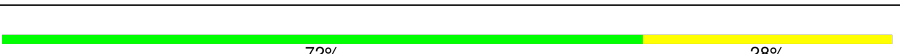

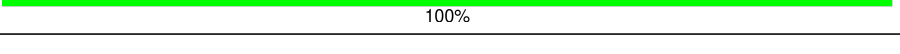
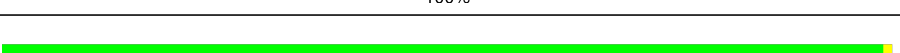
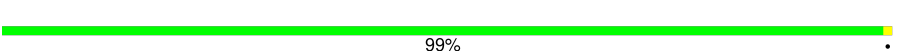
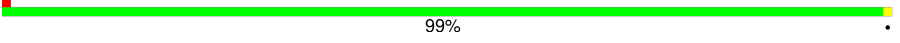
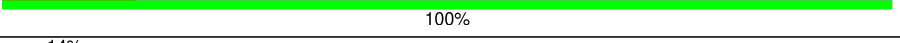
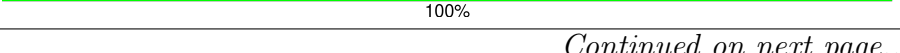



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1529	
2	C	206	
3	D	208	
4	E	158	
5	F	97	
6	G	157	
7	H	132	
8	I	131	

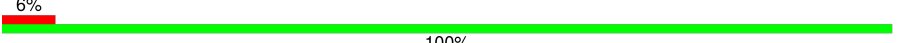
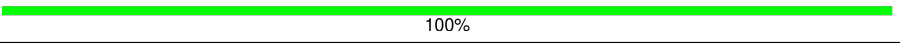
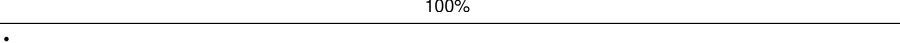

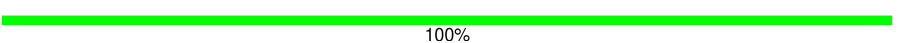
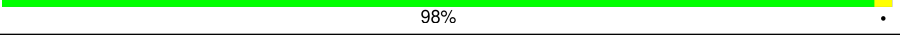
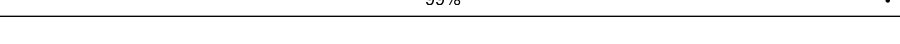
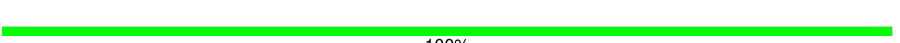
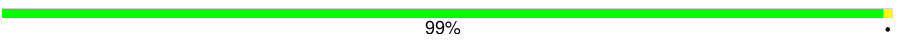
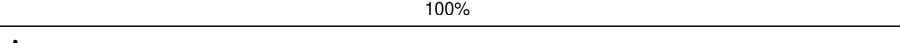


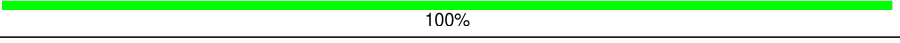
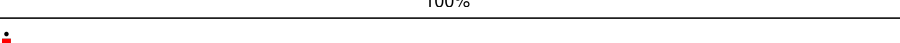

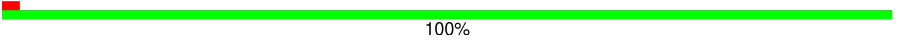
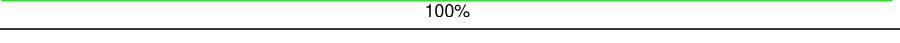






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Mol	Chain	Length	Quality of chain
9	J	102	 6% 99%
10	K	117	 100%
11	L	124	 100%
12	M	114	 99%
13	N	60	 100%
14	O	88	 99%
15	P	83	 100%
16	Q	82	 99%
17	R	63	 100%
18	S	84	 96%
19	T	85	 99%
20	U	69	 96%
21	V	28	 96%
22	W	97	 99%
23	X	76	 5% 75% 25%
24	AA	2929	 80% 19%
25	AB	112	 72% 28%
26	AC	221	 21% 100%
27	AD	277	 100%
28	AE	206	 100%
29	AF	209	 99%
30	AG	182	 99%
31	AH	180	 99%
32	AI	148	 15% 100%
33	AJ	162	14% 100%

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Mol	Chain	Length	Quality of chain
34	AK	139	 100%
35	AL	145	 100%
36	AM	122	 100%
37	AN	145	 99%
38	AO	138	 98%
39	AP	121	 100%
40	AQ	119	 98%
41	AR	117	 99%
42	AS	114	 99%
43	AT	103	 100%
44	AU	115	 99%
45	AV	98	 100%
46	AW	101	 97%
47	AX	181	 99%
48	AY	74	 100%
49	AZ	91	 100%
50	Aa	65	 100%
51	Ab	100	 100%
52	Ac	81	 98%
53	Ad	59	 100%
54	Ae	51	 100%
55	Af	50	 100%
56	Ag	66	 98%
57	Ah	37	 100%
58	Ai	46	 85% 13%

## 2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 147910 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1529	Total	C	N	O	P	0	0
			32780	14645	5986	10621	1528		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	206	Total	C	N	O	S	0	0
			1646	1066	294	284	2		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	208	Total	C	N	O	S	0	0
			1689	1069	321	296	3		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	158	Total	C	N	O	S	0	0
			1196	763	222	206	5		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	97	Total	C	N	O	S	0	0
			814	529	137	144	4		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	157	Total	C	N	O	S	0	0
			1282	809	235	231	7		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	132	Total	C	N	O	S	0	0
			1039	662	183	188	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	131	Total	C	N	O	S	0	0
			1043	651	201	188	3		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	102	Total	C	N	O	S	0	0
			817	524	145	145	3		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	117	Total	C	N	O	S	0	0
			876	551	163	159	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	124	Total	C	N	O	S	0	0
			968	601	198	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	114	Total	C	N	O	S	0	0
			901	554	181	161	5		

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	60	Total	C	N	O	S	0	0
			491	309	99	76	7		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	88	Total	C	N	O	S	0	0
			718	455	135	126	2		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	83	Total	C	N	O	S	0	0
			676	425	127	119	5		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	82	Total	C	N	O	S	0	0
			678	436	122	118	2		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	63	Total	C	N	O	S	0	0
			521	337	95	86	3		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	84	Total	C	N	O	S	0	0
			669	435	114	119	1		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	85	Total	C	N	O	S	0	0
			697	439	143	112	3		

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	69	Total	C	N	O	S	0	0
			603	382	119	100	2		

- Molecule 21 is a protein called 30S ribosomal protein bS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	27	Total	C	N	O	S	0	0
			240	147	61	31	1		

- Molecule 22 is a protein called Ribosomal subunit interface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	97	Total	C	N	O	S	0	0
			818	528	145	144	1		

- Molecule 23 is a RNA chain called E-site t-RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	76	Total	C	N	O	P	0	0
			1618	722	284	536	76		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	?	-	U	deletion	GB AE000783.1
X	74	C	U	conflict	GB AE000783.1
X	75	C	U	conflict	GB AE000783.1

- Molecule 24 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AA	2929	Total	C	N	O	P	0	0
			62816	28077	11503	20307	2929		

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AB	112	Total	C	N	O	P	0	0
			2398	1071	434	781	112		

- Molecule 26 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	AC	221	Total	C	N	O	0	0
			884	442	221	221		

- Molecule 27 is a protein called 50S ribosomal protein L2.



Mol	Chain	Residues	Atoms					AltConf	Trace
27	AD	277	Total	C	N	O	S	0	0
			2156	1354	414	383	5		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AE	206	Total	C	N	O	S	0	0
			1564	995	278	286	5		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AF	209	Total	C	N	O	S	0	0
			1658	1056	301	299	2		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AG	182	Total	C	N	O	S	0	0
			1439	930	240	265	4		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AH	180	Total	C	N	O	S	0	0
			1405	895	249	259	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AI	148	Total	C	N	O	S	0	0
			751	423	161	166	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	AJ	162	Total	C	N	O	0	0
			648	324	162	162		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	AK	139	Total	C	N	O	0	0
			556	278	139	139		

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	AL	145	Total	C	N	O	S	0
			1171	756	211	202	2	0

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	AM	122	Total	C	N	O	S	0
			942	593	174	170	5	0

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	AN	145	Total	C	N	O	S	0
			1129	716	210	201	2	0

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	AO	138	Total	C	N	O	S	0
			1092	693	204	188	7	0

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	AP	121	Total	C	N	O	S	0
			1004	643	193	164	4	0

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	AQ	119	Total	C	N	O	S	0
			968	613	184	170	1	0

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AR	117	Total	C	N	O	S	0	0
			951	613	174	161	3		

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AS	114	Total	C	N	O	S	0	0
			943	597	189	155	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS	40	ARG	UNK	conflict	UNP O51206

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AT	103	Total	C	N	O	S	0	0
			859	552	148	157	2		

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AU	115	Total	C	N	O	S	0	0
			918	574	180	158	6		

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AV	98	Total	C	N	O	S	0	0
			784	507	134	140	3		

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AW	101	Total	C	N	O	S	0	0
			800	501	155	140	4		

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AX	181	Total	C	N	O	S	0	0
			1432	912	245	273	2		

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AY	74	Total	C	N	O		0	0
			571	359	112	100			

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AZ	91	Total	C	N	O	S	0	0
			705	452	135	115	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Aa	65	Total	C	N	O	S	0	0
			553	352	102	95	4		

- Molecule 51 is a protein called 50S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ab	100	Total	C	N	O	S	0	0
			814	518	158	133	5		

- Molecule 52 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ac	81	Total	C	N	O	S	0	0
			656	419	114	121	2		

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ad	59	Total	C	N	O	S	0	0
			484	300	99	80	5		

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Ae	51	Total	C	N	O	S	0	0
			425	266	80	76	3		

- Molecule 55 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Af	50	Total	C	N	O	S	0	0
			422	260	95	64	3		

- Molecule 56 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ag	66	Total	C	N	O	S	0	0
			548	346	111	88	3		

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ah	37	Total	C	N	O	S	0	0
			305	192	63	46	4		

- Molecule 58 is a protein called 50S ribosomal protein bL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ai	46	Total	C	N	O	S	0	0
			375	236	72	65	2		

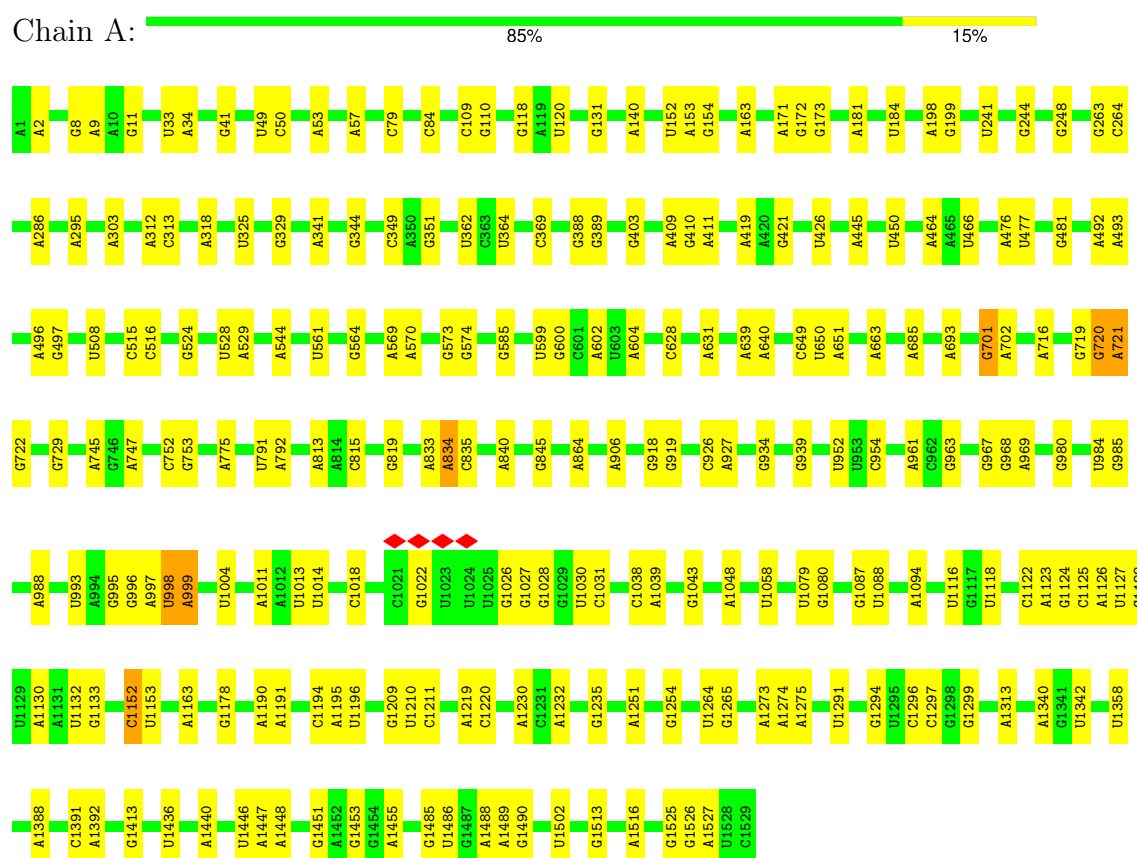
- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
59	N	1	Total	Zn	0
			1	1	
59	R	1	Total	Zn	0
			1	1	
59	Ad	1	Total	Zn	0
			1	1	
59	Ah	1	Total	Zn	0
			1	1	

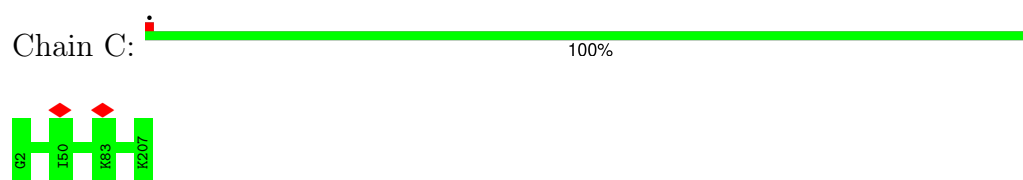
### 3 Residue-property plots

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: 16S ribosomal RNA



#### • Molecule 2: 30S ribosomal protein S3



#### • Molecule 3: 30S ribosomal protein S4





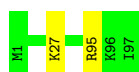
- Molecule 4: 30S ribosomal protein S5

Chain E:  99%



- Molecule 5: 30S ribosomal protein S6

Chain F:  98%



- Molecule 6: 30S ribosomal protein S7

Chain G:  99%



- Molecule 7: 30S ribosomal protein S8

Chain H:  100%



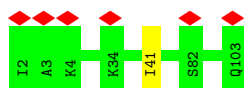
- Molecule 8: 30S ribosomal protein S9

Chain I:  99%



- Molecule 9: 30S ribosomal protein S10

Chain J:  99%



- Molecule 10: 30S ribosomal protein S11

Chain K:  100%

There are no outlier residues recorded for this chain.

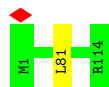
- Molecule 11: 30S ribosomal protein S12

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: 30S ribosomal protein S13

Chain M:  99%



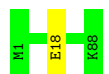
- Molecule 13: 30S ribosomal protein S14 type Z

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 14: 30S ribosomal protein S15

Chain O:  99%



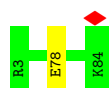
- Molecule 15: 30S ribosomal protein S16

Chain P:  100%



- Molecule 16: 30S ribosomal protein S17

Chain Q:  99%



- Molecule 17: 30S ribosomal protein S18

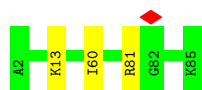
Chain R:  100%

There are no outlier residues recorded for this chain.

- Molecule 18: 30S ribosomal protein S19

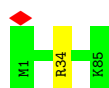


Chain S:  96%



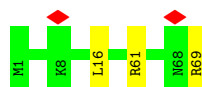
- Molecule 19: 30S ribosomal protein S20

Chain T:  99%



- Molecule 20: 30S ribosomal protein S21

Chain U:  96%



- Molecule 21: 30S ribosomal protein bS22

Chain V:  96%




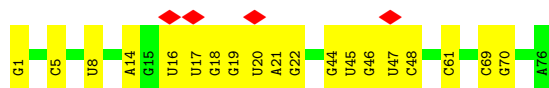
- Molecule 22: Ribosomal subunit interface protein

Chain W:  99%




- Molecule 23: E-site t-RNA

Chain X:  5% 75% 25%



- Molecule 24: 23S ribosomal RNA

Chain AA:  80% 19%



G2791	A2475	G2236	G2110	U1862	U1456	C1214	G1100	G697	U313	A166
A2795	A2476	G2244	A2114	G1665	A1460	G1215	A1104	A708	A314	U167
A2805	A2487	G2245	A2115	G1666	A1469	A1221	A1104	A718	A169	A168
G2808	A2494	U2249	U2122	U1668	A1472	A1230	G1111	A726	U322	G177
G2813	G2250	G1927	G2123	G1669	A1473	G1241	A1124	A727	A323	A178
A2825	U2251	U1936	U2130	G1670	U1473	G1241	A1125	A728	G325	U179
U2826	A2252	G1937	U2143	U1671	C1484	A1261	A1126	A732	A329	A180
G2827	A2253	U1941	G2149	U1672	U1485	A1286	C1127	A733	G330	C181
U2831	G2256	U1942	G2143	A1674	A1485	A1287	A1135	A734	A336	A194
U2832	G2257	U1942	G2143	A1675	G1490	A1288	A1139	A735	A337	A197
U2836	G2258	U1966	U2152	A1676	U1491	G1289	U1139	A736	A340	A211
U2837	G2270	U1967	U2153	A1677	U1492	G1289	U1143	A737	A344	A214
U2838	A2271	U1968	G2154	G1678	C1494	U1294	C1142	A738	A347	A219
U2855	G2284	U1971	A2158	G1679	U1497	U1299	G1146	A751	A348	A220
U2863	G2285	U1971	A2158	G1680	G1498	G1300	A1147	A752	A349	A225
G2864	G2286	G1984	U2161	A1691	U1499	G1301	A1148	A753	A351	G227
A2865	G2325	U1984	A2162	A1697	A1500	G1304	G1149	A754	A352	A228
U2891	G2329	C2329	U2163	A1698	G1501	U1307	C1150	A755	A353	
A2897	A2333	U1983	G2164	A1699	G1505	U1307	G1151	A756	A358	
G2902	U2351	U2009	A2171	U1703	U1519	G1313	A1155	A757	A361	
A2903	G2352	G2046	G2174	U1704	A1520	G1313	A1156	A758	A362	C270
G2904	G2353	U2047	A2180	G1709	C1521	G1315	A1157	A759	A372	U271
C2910	G2354	A2051	U2185	A1799	U1522	G1315	A1158	A797	A373	U273
A2913	A2355	A2073	U2186	G1736	C1523	G1327	C1158	A803	U374	A274
U2914	G2371	G2075	U2187	A1737	C1524	U1330	U1162	A804	A384	
A2916	U2379	U2076	G2197	G1621	U1530	A1330	A1163	A805	A403	
C2917	U2380	A2077	G2198	G1622	A1531	G1333	A1164	A822	A415	
U2921	A2381	G2081	G2199	G1623	U1532	G1333	A1167	A829	A425	
A2922	A2382	A2084	C2200	G1626	U1536	G1348	G1168	A835	A428	
U2923	A2383	A2085	A2201	A1628	G1537	A1349	U1169	A839	A435	
	C2393	G2086	A2202	A1629	U1538	A1350	A1174	A845	A436	
	U2396	A2087	G2203	U1630	C1539	A1377	A1175	A846	A439	
G2734	G2429	A2452	G2211	G1631	U1552	A1378	U1176	A847	A440	
U2735	U2430	A2452	G2212	U1632	U1553	A1378	G1025	A855	A443	
G2748	G2431	A2452	G2213	G1633	A1554	U1380	G1032	A856	A449	
G2755	G2437	A2452	A2217	G1634	U1558	U1390	U1187	A857	A461	
A2756	U2447	A2452	U2218	G1635	G1559	A1398	A1038	A862	A462	
A2758	G2448	A2452	C2219	U1636	U1560	C1410	G1040	A863	A463	
G2759	A2452	A2452	A2223	U1637	U1561	U1418	G1053	A864		
U2760	A2452	A2452	A2224	G1643	U1562	C1426	A1062	A865		
G2761	A2452	A2452	A2225	G1644	U1563	U1429	A1069	A866		
C2773	U2469	A2471	U2226	A1649	U1564	U1429	A1075	A867		
A2780	U2470	A2471	A2227	A1652	U1565	A1442	A1090	A868		
	A2472	A2472	C2228	U1655	A1571	A1455	A1091	A871		
			C2232	G1903	G1572		U1211			
							A1212			
							A1213			

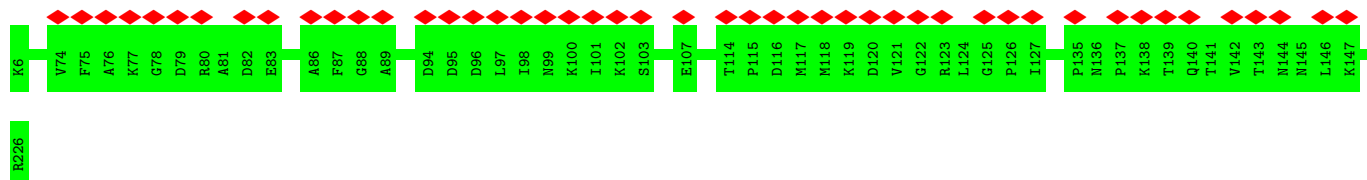
- Molecule 25: 5S ribosomal RNA

Chain AB:  72% 28%



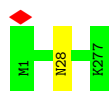
- Molecule 26: 50S ribosomal protein L1

Chain AC:  21% 100%



- Molecule 27: 50S ribosomal protein L2

Chain AD:  100%



- Molecule 28: 50S ribosomal protein L3

Chain AE:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: 50S ribosomal protein L4

Chain AF:  99%



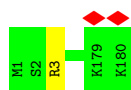
- Molecule 30: 50S ribosomal protein L5

Chain AG:  99%



- Molecule 31: 50S ribosomal protein L6

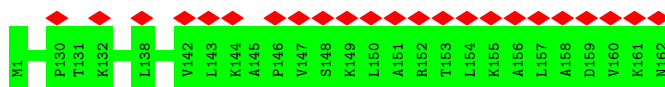
Chain AH:  99%



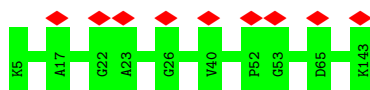
- Molecule 32: 50S ribosomal protein L9



- Molecule 33: 50S ribosomal protein L10



- Molecule 34: 50S ribosomal protein L11



- Molecule 35: 50S ribosomal protein L13



There are no outlier residues recorded for this chain.

- Molecule 36: 50S ribosomal protein L14



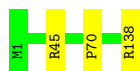
There are no outlier residues recorded for this chain.

- Molecule 37: 50S ribosomal protein L15



- Molecule 38: 50S ribosomal protein L16





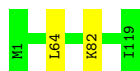
- Molecule 39: 50S ribosomal protein L17

Chain AP:  100%

There are no outlier residues recorded for this chain.

- Molecule 40: 50S ribosomal protein L18

Chain AQ:  98%



- Molecule 41: 50S ribosomal protein L19

Chain AR:  99%



- Molecule 42: 50S ribosomal protein L20

Chain AS:  99%



- Molecule 43: 50S ribosomal protein L21

Chain AT:  100%

There are no outlier residues recorded for this chain.

- Molecule 44: 50S ribosomal protein L22

Chain AU:  99%



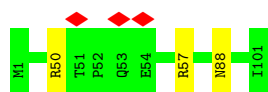
- Molecule 45: 50S ribosomal protein L23

Chain AV:  100%

There are no outlier residues recorded for this chain.

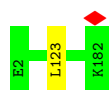
- Molecule 46: 50S ribosomal protein L24

Chain AW:  97%



- Molecule 47: 50S ribosomal protein L25

Chain AX:  99%



- Molecule 48: 50S ribosomal protein L27

Chain AY:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L28

Chain AZ:  100%

There are no outlier residues recorded for this chain.

- Molecule 50: 50S ribosomal protein L29

Chain Aa:  100%

There are no outlier residues recorded for this chain.

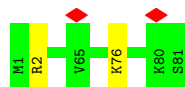
- Molecule 51: 50S ribosomal protein uL30

Chain Ab:  100%



- Molecule 52: 50S ribosomal protein L31 type B

Chain Ac:  98%



- Molecule 53: 50S ribosomal protein L32

Chain Ad:  100%



- Molecule 54: 50S ribosomal protein L33

Chain Ae: 100%

There are no outlier residues recorded for this chain.

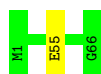
- Molecule 55: 50S ribosomal protein L34

Chain Af: 100%

There are no outlier residues recorded for this chain.

- Molecule 56: 50S ribosomal protein L35

Chain Ag: 98%



- Molecule 57: 50S ribosomal protein L36

Chain Ah: 100%

There are no outlier residues recorded for this chain.

- Molecule 58: 50S ribosomal protein bL38

Chain Ai: 85% 13%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	288776	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	67.527	Depositor
Minimum defocus (nm)	820	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.084	Depositor
Minimum map value	-0.439	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	493.245, 493.245, 493.245	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	0.25	0/36721	0.79	28/57268 (0.0%)
2	C	0.39	0/1673	0.53	0/2240
3	D	0.36	0/1716	0.55	1/2298 (0.0%)
4	E	0.42	0/1215	0.56	0/1626
5	F	0.38	0/826	0.62	0/1098
6	G	0.32	0/1302	0.55	0/1734
7	H	0.46	0/1053	0.58	0/1406
8	I	0.32	0/1056	0.50	0/1405
9	J	0.36	0/828	0.59	1/1108 (0.1%)
10	K	0.42	0/891	0.56	0/1201
11	L	0.39	0/983	0.52	0/1318
12	M	0.33	0/907	0.69	2/1208 (0.2%)
13	N	0.37	0/500	0.55	0/662
14	O	0.40	0/724	0.57	1/956 (0.1%)
15	P	0.36	0/685	0.48	0/913
16	Q	0.52	1/686 (0.1%)	0.61	0/910
17	R	0.39	0/532	0.54	0/705
18	S	0.33	0/683	0.79	5/917 (0.5%)
19	T	0.39	0/700	0.68	1/918 (0.1%)
20	U	0.34	0/609	0.74	3/800 (0.4%)
21	V	0.38	0/242	0.45	0/307
22	W	0.37	0/832	0.58	1/1110 (0.1%)
23	X	0.34	1/1807 (0.1%)	0.77	0/2812
24	AA	0.33	0/70389	0.83	156/109770 (0.1%)
25	AB	0.27	0/2684	0.72	0/4183
26	AC	0.24	0/883	0.45	0/1102
27	AD	0.54	0/2196	0.59	1/2935 (0.0%)
28	AE	0.52	0/1588	0.54	0/2122
29	AF	0.50	0/1682	0.54	1/2249 (0.0%)
30	AG	0.35	0/1460	0.53	1/1955 (0.1%)
31	AH	0.38	0/1422	0.50	0/1903
32	AI	0.30	0/756	0.51	0/973

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	AJ	0.23	0/647	0.43	0/807
34	AK	0.25	0/555	0.46	0/692
35	AL	0.54	0/1197	0.54	0/1612
36	AM	0.56	0/951	0.59	0/1276
37	AN	0.49	0/1142	0.59	0/1515
38	AO	0.51	0/1110	0.68	1/1480 (0.1%)
39	AP	0.52	0/1020	0.54	0/1353
40	AQ	0.38	0/979	0.62	2/1299 (0.2%)
41	AR	0.61	1/962 (0.1%)	0.65	0/1280
42	AS	0.59	0/954	0.60	0/1264
43	AT	0.56	0/872	0.53	0/1163
44	AU	0.53	0/931	0.57	0/1245
45	AV	0.47	0/796	0.54	0/1065
46	AW	0.40	0/803	0.55	0/1059
47	AX	0.38	0/1451	0.52	1/1955 (0.1%)
48	AY	0.53	0/577	0.52	0/760
49	AZ	0.45	0/713	0.53	0/943
50	Aa	0.41	0/559	0.58	0/739
51	Ab	0.47	0/818	0.55	0/1079
52	Ac	0.31	0/669	0.52	0/893
53	Ad	0.55	0/492	0.51	0/654
54	Ae	0.44	0/429	0.68	0/568
55	Af	0.53	0/425	0.57	0/551
56	Ag	0.57	0/554	0.61	2/726 (0.3%)
57	Ah	0.49	0/306	0.54	0/400
58	Ai	0.72	1/381 (0.3%)	1.31	7/502 (1.4%)
All	All	0.35	4/160524 (0.0%)	0.76	215/238992 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	X	1	G	OP3-P	-10.73	1.48	1.61
16	Q	78	GLU	CG-CD	-5.97	1.43	1.51
58	Ai	40	GLU	CD-OE2	-5.81	1.19	1.25
41	AR	33	GLU	CB-CG	-5.18	1.42	1.52

The worst 5 of 215 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	999	A	O5'-P-OP1	-31.82	72.51	110.70
24	AA	1559	G	O5'-P-OP1	-31.12	73.36	110.70
24	AA	1967	A	O5'-P-OP1	-31.07	73.41	110.70

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AA	1677	A	O5'-P-OP1	-31.06	73.43	110.70
1	A	1265	G	O5'-P-OP1	-29.81	74.93	110.70

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
3	D	206/208 (99%)	196 (95%)	10 (5%)	0	100	100
4	E	156/158 (99%)	147 (94%)	9 (6%)	0	100	100
5	F	95/97 (98%)	88 (93%)	7 (7%)	0	100	100
6	G	155/157 (99%)	138 (89%)	17 (11%)	0	100	100
7	H	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
8	I	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
9	J	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
10	K	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
11	L	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
12	M	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
13	N	58/60 (97%)	57 (98%)	1 (2%)	0	100	100
14	O	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
15	P	81/83 (98%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
17	R	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
18	S	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
19	T	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
20	U	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
21	V	25/28 (89%)	24 (96%)	1 (4%)	0	100	100
22	W	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
26	AC	219/221 (99%)	211 (96%)	8 (4%)	0	100	100
27	AD	275/277 (99%)	259 (94%)	16 (6%)	0	100	100
28	AE	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
29	AF	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
30	AG	180/182 (99%)	168 (93%)	12 (7%)	0	100	100
31	AH	178/180 (99%)	170 (96%)	8 (4%)	0	100	100
32	AI	146/148 (99%)	134 (92%)	12 (8%)	0	100	100
33	AJ	160/162 (99%)	153 (96%)	7 (4%)	0	100	100
34	AK	137/139 (99%)	131 (96%)	6 (4%)	0	100	100
35	AL	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
36	AM	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
37	AN	143/145 (99%)	116 (81%)	27 (19%)	0	100	100
38	AO	136/138 (99%)	118 (87%)	17 (12%)	1 (1%)	19	36
39	AP	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
40	AQ	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
41	AR	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
42	AS	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
43	AT	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
44	AU	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
45	AV	96/98 (98%)	92 (96%)	4 (4%)	0	100	100
46	AW	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
47	AX	179/181 (99%)	168 (94%)	11 (6%)	0	100	100
48	AY	72/74 (97%)	69 (96%)	3 (4%)	0	100	100
49	AZ	89/91 (98%)	86 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	Aa	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
51	Ab	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
52	Ac	79/81 (98%)	67 (85%)	12 (15%)	0	100	100
53	Ad	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
54	Ae	49/51 (96%)	42 (86%)	7 (14%)	0	100	100
55	Af	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
56	Ag	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
57	Ah	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
58	Ai	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
All	All	6239/6348 (98%)	5831 (94%)	407 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	AO	70	PRO

### 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	
2	C	179/179 (100%)	179 (100%)	0	100	100
3	D	184/184 (100%)	184 (100%)	0	100	100
4	E	125/125 (100%)	124 (99%)	1 (1%)	79	90
5	F	88/88 (100%)	86 (98%)	2 (2%)	45	70
6	G	136/136 (100%)	135 (99%)	1 (1%)	81	91
7	H	115/115 (100%)	115 (100%)	0	100	100
8	I	113/113 (100%)	112 (99%)	1 (1%)	75	88
9	J	93/93 (100%)	93 (100%)	0	100	100
10	K	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	L	106/106 (100%)	106 (100%)	0	100	100
12	M	99/99 (100%)	99 (100%)	0	100	100
13	N	53/53 (100%)	53 (100%)	0	100	100
14	O	79/79 (100%)	79 (100%)	0	100	100
15	P	75/75 (100%)	75 (100%)	0	100	100
16	Q	79/79 (100%)	79 (100%)	0	100	100
17	R	56/56 (100%)	56 (100%)	0	100	100
18	S	76/76 (100%)	76 (100%)	0	100	100
19	T	75/75 (100%)	75 (100%)	0	100	100
20	U	65/65 (100%)	64 (98%)	1 (2%)	60	81
21	V	26/27 (96%)	26 (100%)	0	100	100
22	W	91/91 (100%)	91 (100%)	0	100	100
27	AD	229/229 (100%)	229 (100%)	0	100	100
28	AE	168/168 (100%)	168 (100%)	0	100	100
29	AF	181/181 (100%)	180 (99%)	1 (1%)	84	92
30	AG	155/155 (100%)	154 (99%)	1 (1%)	84	92
31	AH	156/156 (100%)	155 (99%)	1 (1%)	84	92
32	AI	34/134 (25%)	34 (100%)	0	100	100
35	AL	127/127 (100%)	127 (100%)	0	100	100
36	AM	103/103 (100%)	103 (100%)	0	100	100
37	AN	124/124 (100%)	123 (99%)	1 (1%)	79	90
38	AO	115/115 (100%)	114 (99%)	1 (1%)	75	88
39	AP	110/110 (100%)	110 (100%)	0	100	100
40	AQ	104/104 (100%)	103 (99%)	1 (1%)	73	87
41	AR	103/103 (100%)	103 (100%)	0	100	100
42	AS	99/99 (100%)	98 (99%)	1 (1%)	73	87
43	AT	96/96 (100%)	96 (100%)	0	100	100
44	AU	100/100 (100%)	99 (99%)	1 (1%)	73	87
45	AV	88/88 (100%)	88 (100%)	0	100	100
46	AW	89/89 (100%)	86 (97%)	3 (3%)	32	57
47	AX	163/163 (100%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	AY	60/60 (100%)	60 (100%)	0	100	100
49	AZ	76/76 (100%)	76 (100%)	0	100	100
50	Aa	61/61 (100%)	61 (100%)	0	100	100
51	Ab	93/93 (100%)	93 (100%)	0	100	100
52	Ac	73/73 (100%)	71 (97%)	2 (3%)	40	65
53	Ad	54/54 (100%)	54 (100%)	0	100	100
54	Ae	48/48 (100%)	48 (100%)	0	100	100
55	Af	44/44 (100%)	44 (100%)	0	100	100
56	Ag	61/61 (100%)	61 (100%)	0	100	100
57	Ah	36/36 (100%)	36 (100%)	0	100	100
58	Ai	40/40 (100%)	37 (92%)	3 (8%)	11	24
All	All	4994/5095 (98%)	4972 (100%)	22 (0%)	88	95

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	AW	50	ARG
52	Ac	2	ARG
46	AW	88	ASN
52	Ac	76	LYS
29	AF	21	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
39	AP	31	HIS
40	AQ	69	ASN
52	Ac	75	ASN
46	AW	88	ASN
36	AM	110	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1528/1529 (99%)	217 (14%)	17 (1%)
23	X	75/76 (98%)	18 (24%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	AA	2928/2929 (99%)	524 (17%)	42 (1%)
25	AB	111/112 (99%)	31 (27%)	4 (3%)
All	All	4642/4646 (99%)	790 (17%)	64 (1%)

5 of 790 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	9	A
1	A	11	G
1	A	33	U
1	A	34	A

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	AA	2831	U
24	AA	2922	A
24	AA	372	A
24	AA	350	U
25	AB	31	U

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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.

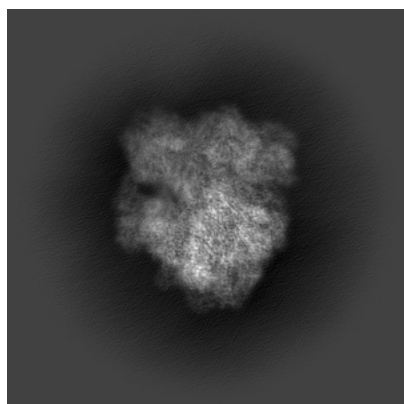
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29298. These allow visual inspection of the internal detail of the map and identification of artifacts.

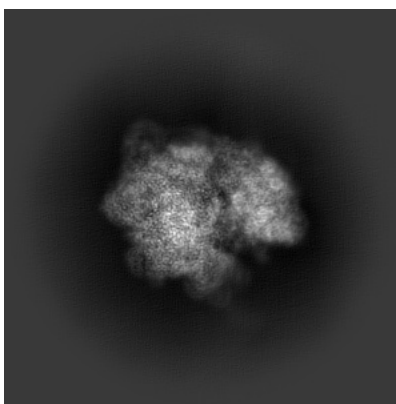
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

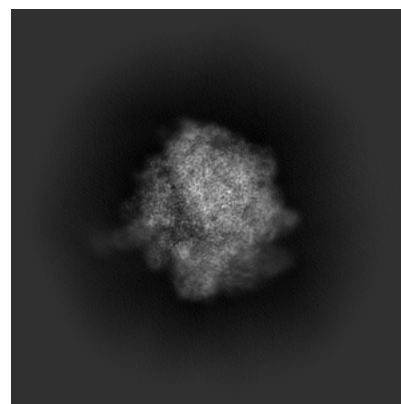
#### 6.1.1 Primary map



X

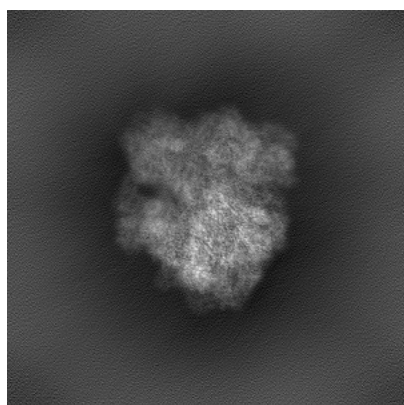


Y

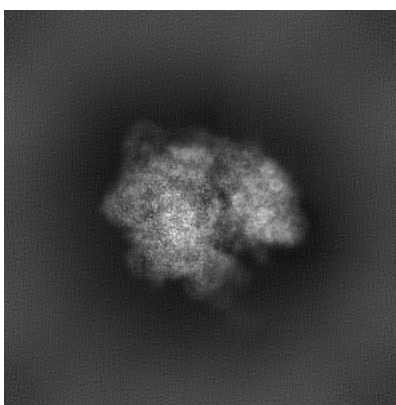


Z

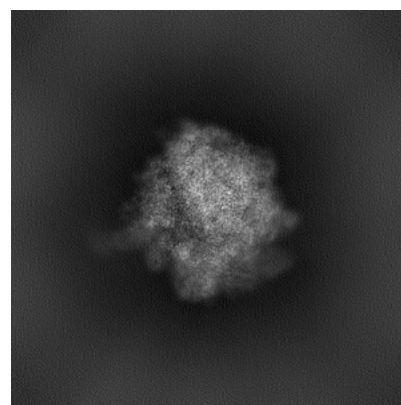
#### 6.1.2 Raw map



X



Y

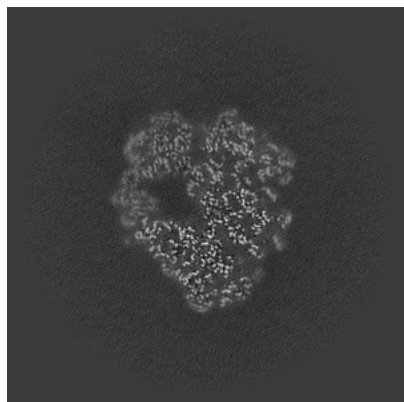


Z

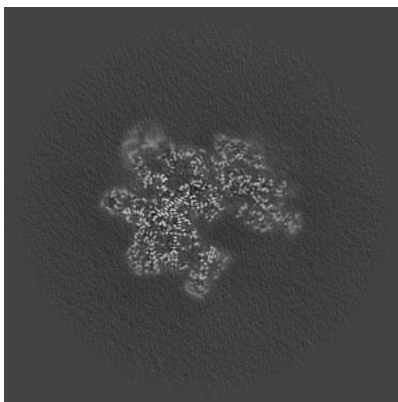
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

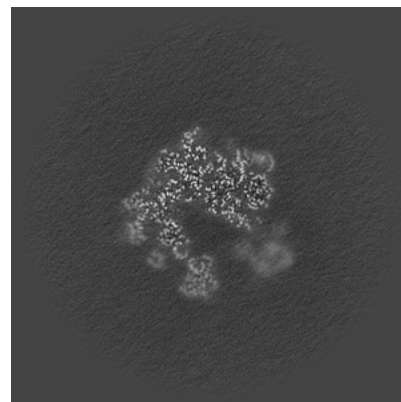
### 6.2.1 Primary map



X Index: 225

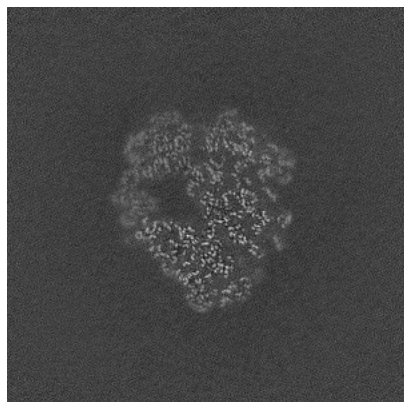


Y Index: 225

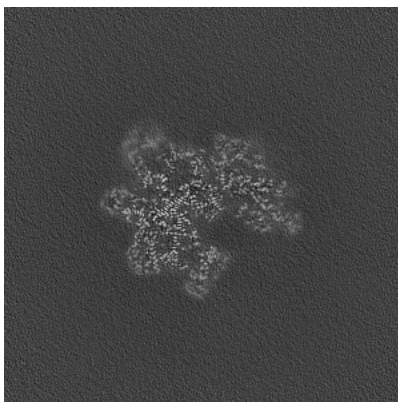


Z Index: 225

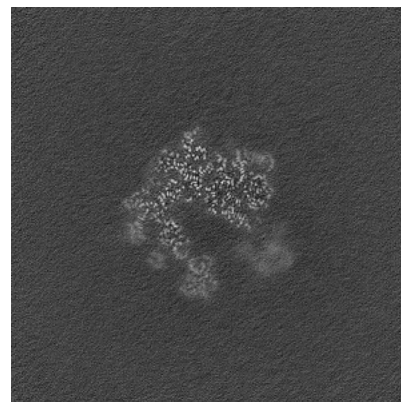
### 6.2.2 Raw map



X Index: 225



Y Index: 225

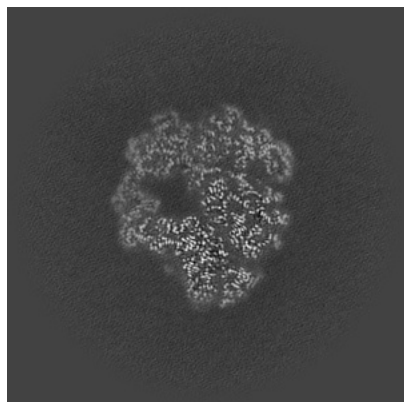


Z Index: 225

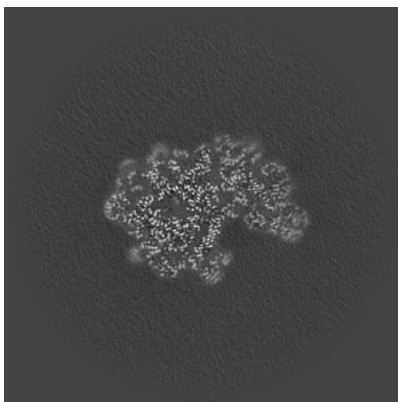
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

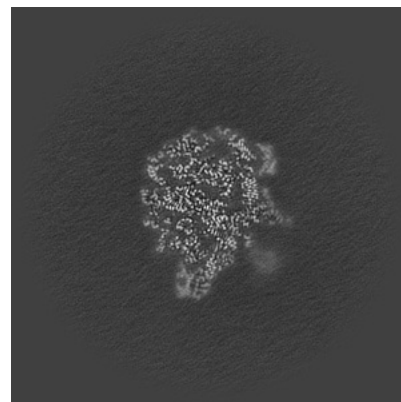
### 6.3.1 Primary map



X Index: 220

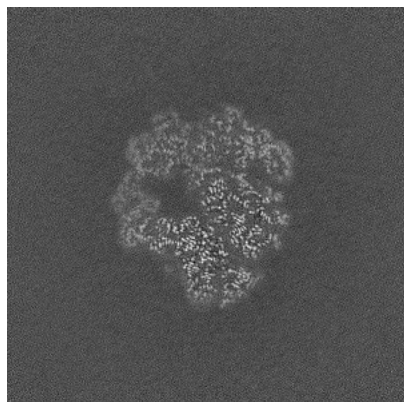


Y Index: 243

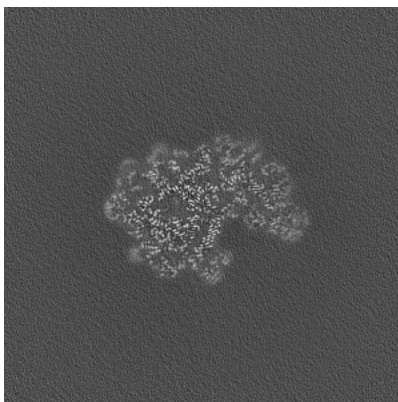


Z Index: 191

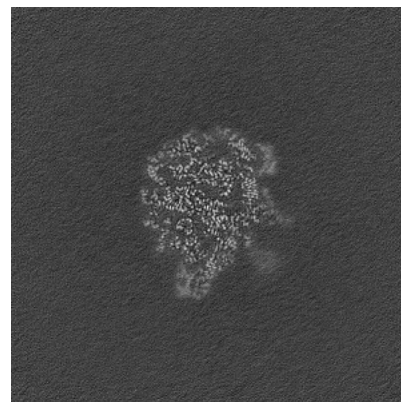
### 6.3.2 Raw map



X Index: 220



Y Index: 243



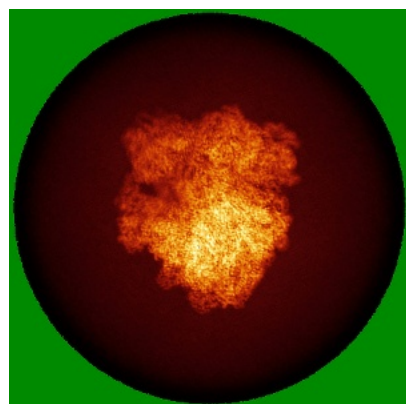
Z Index: 191

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

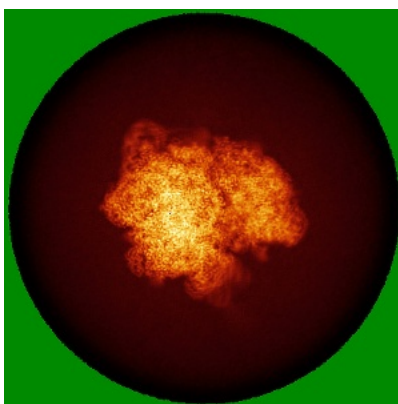


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

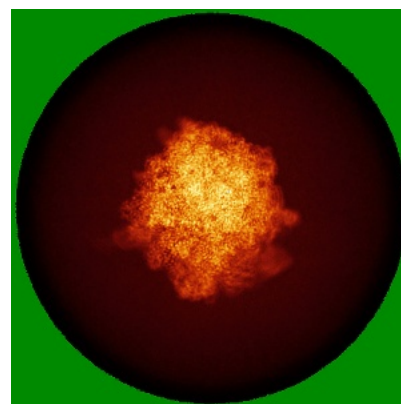
### 6.4.1 Primary map



X

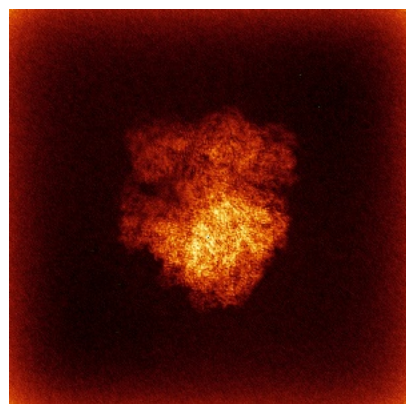


Y

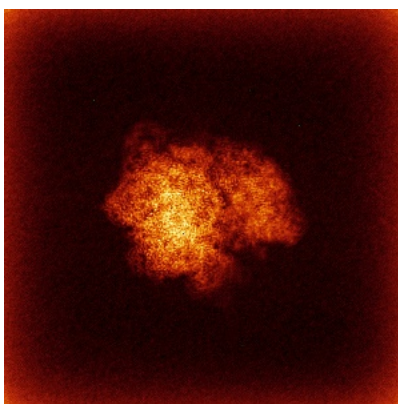


Z

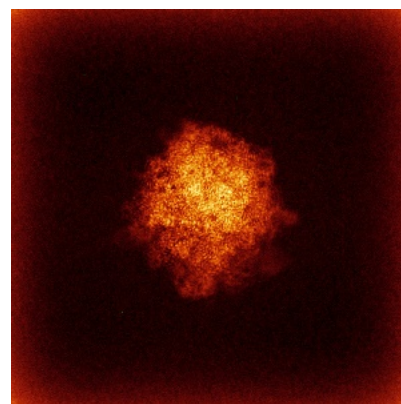
### 6.4.2 Raw map



X



Y

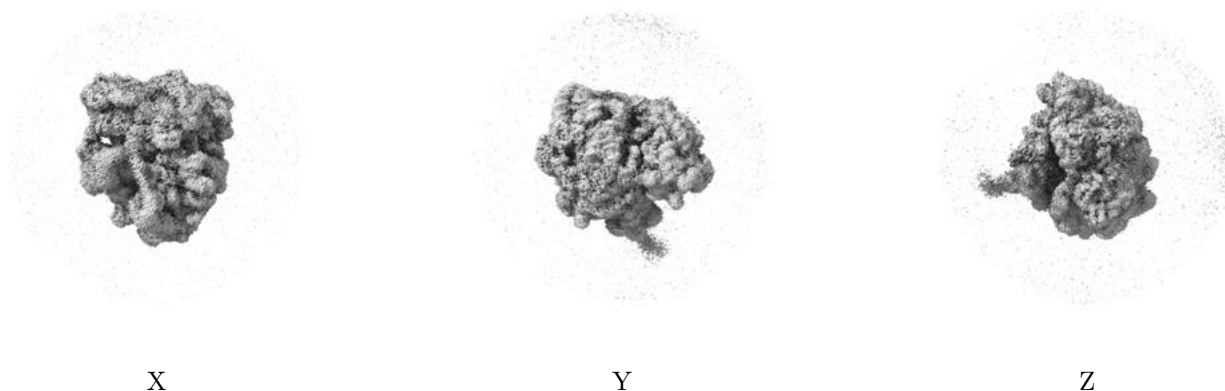


Z

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

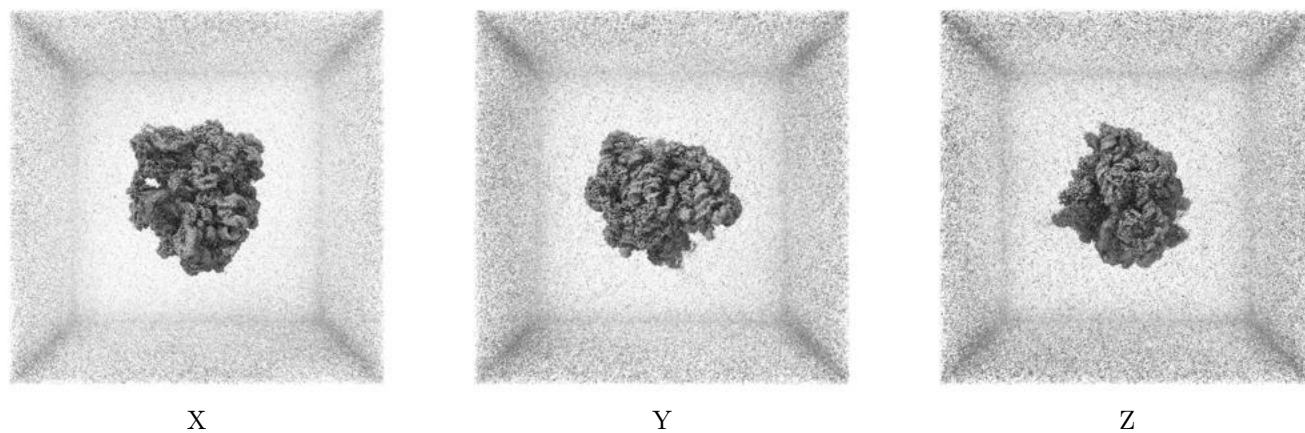
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

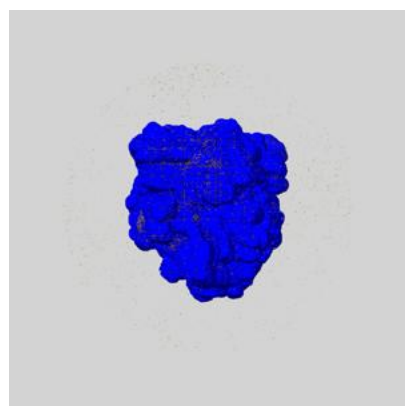
## 6.6 Mask visualisation [i](#)

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

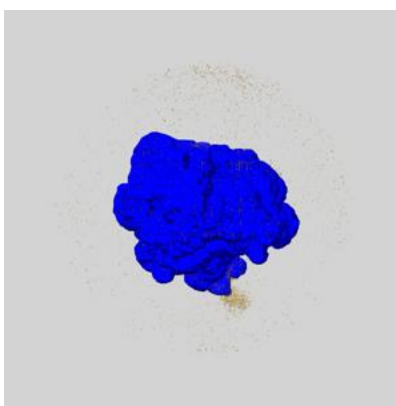
A mask typically either:

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

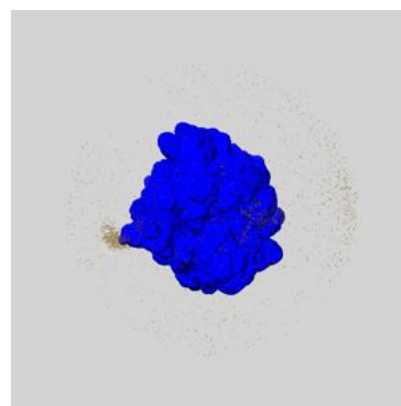
### 6.6.1 emd\_29298\_msk\_1.map [i](#)



X



Y

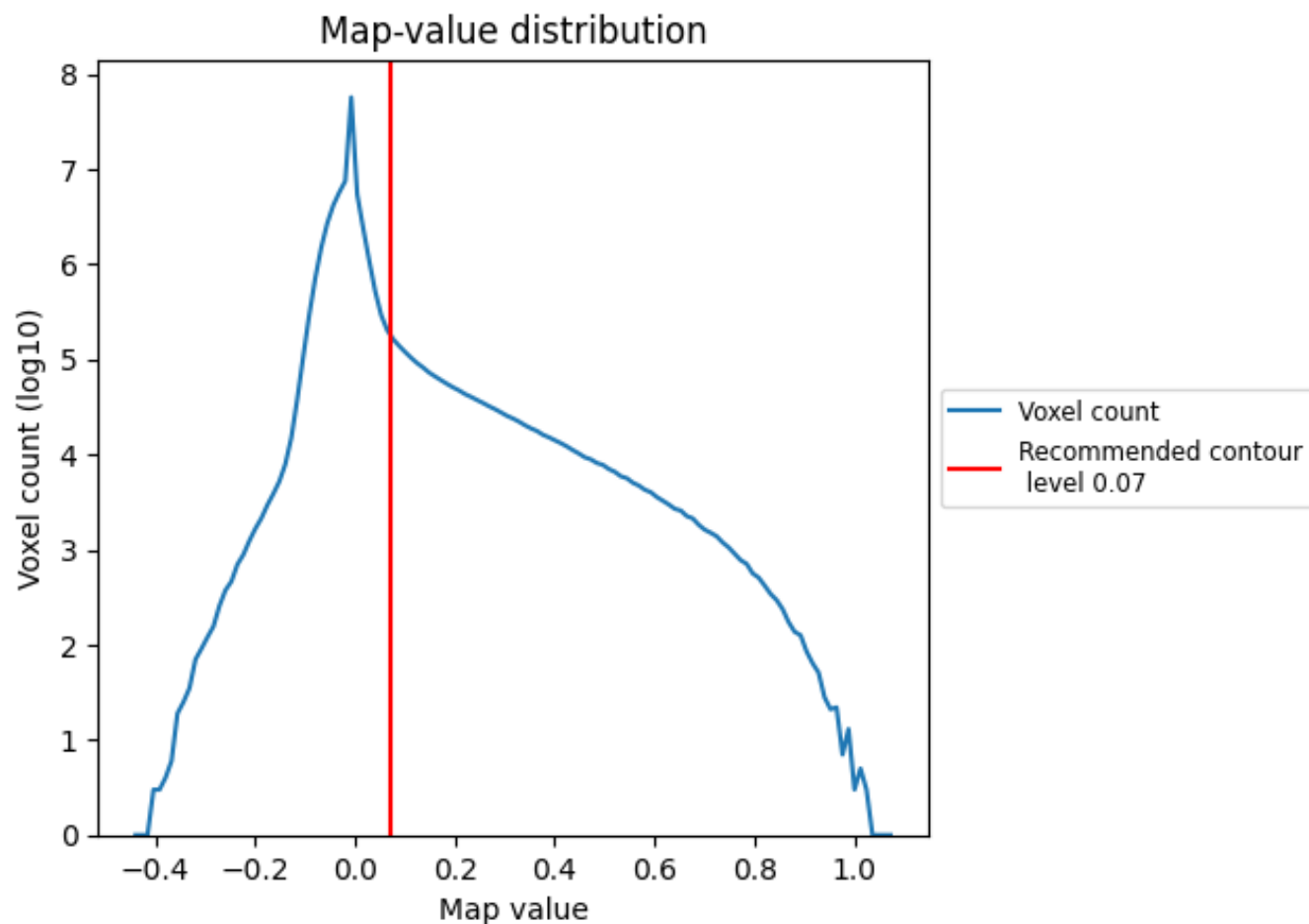


Z

## 7 Map analysis [i](#)

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

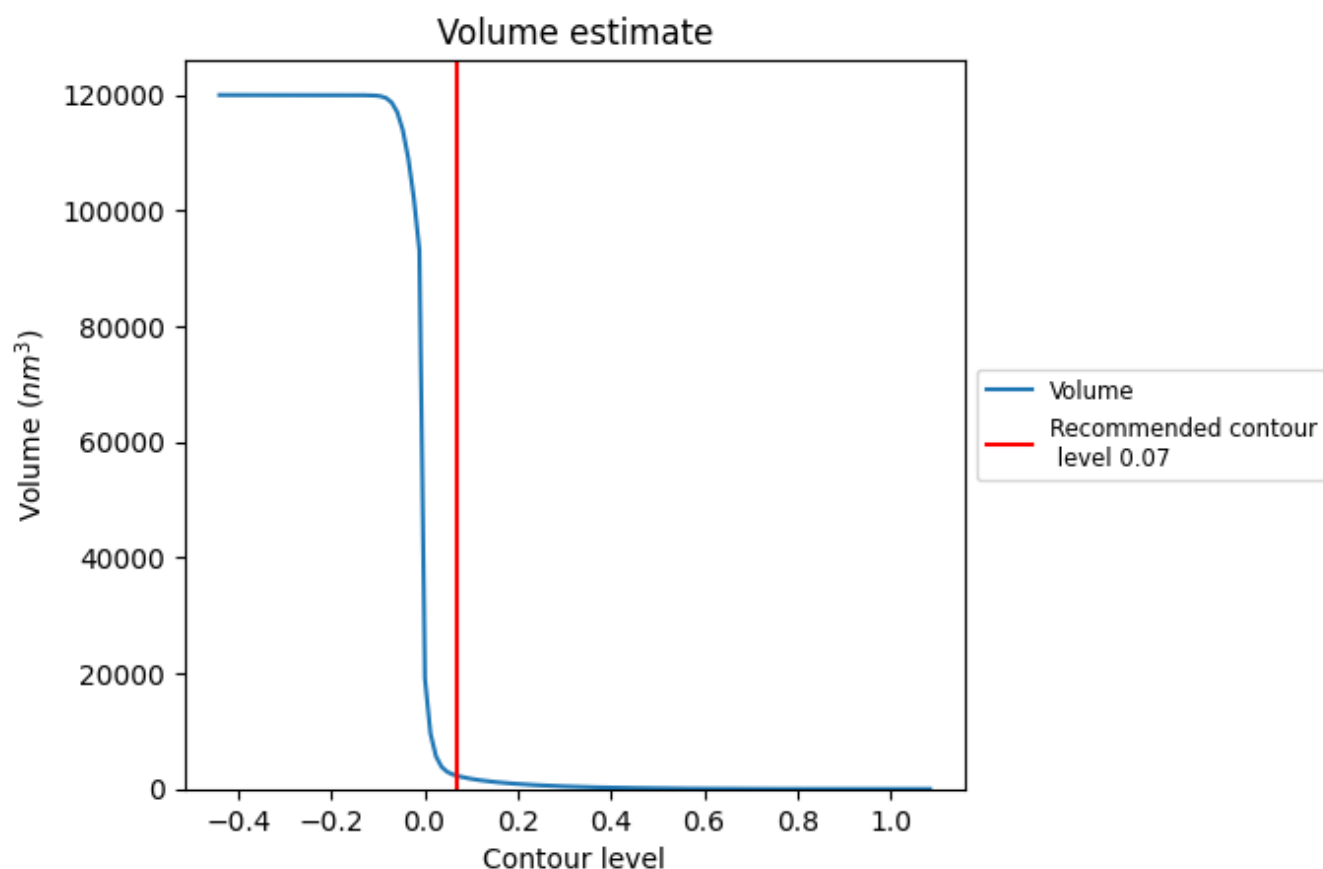
### 7.1 Map-value distribution [i](#)



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.



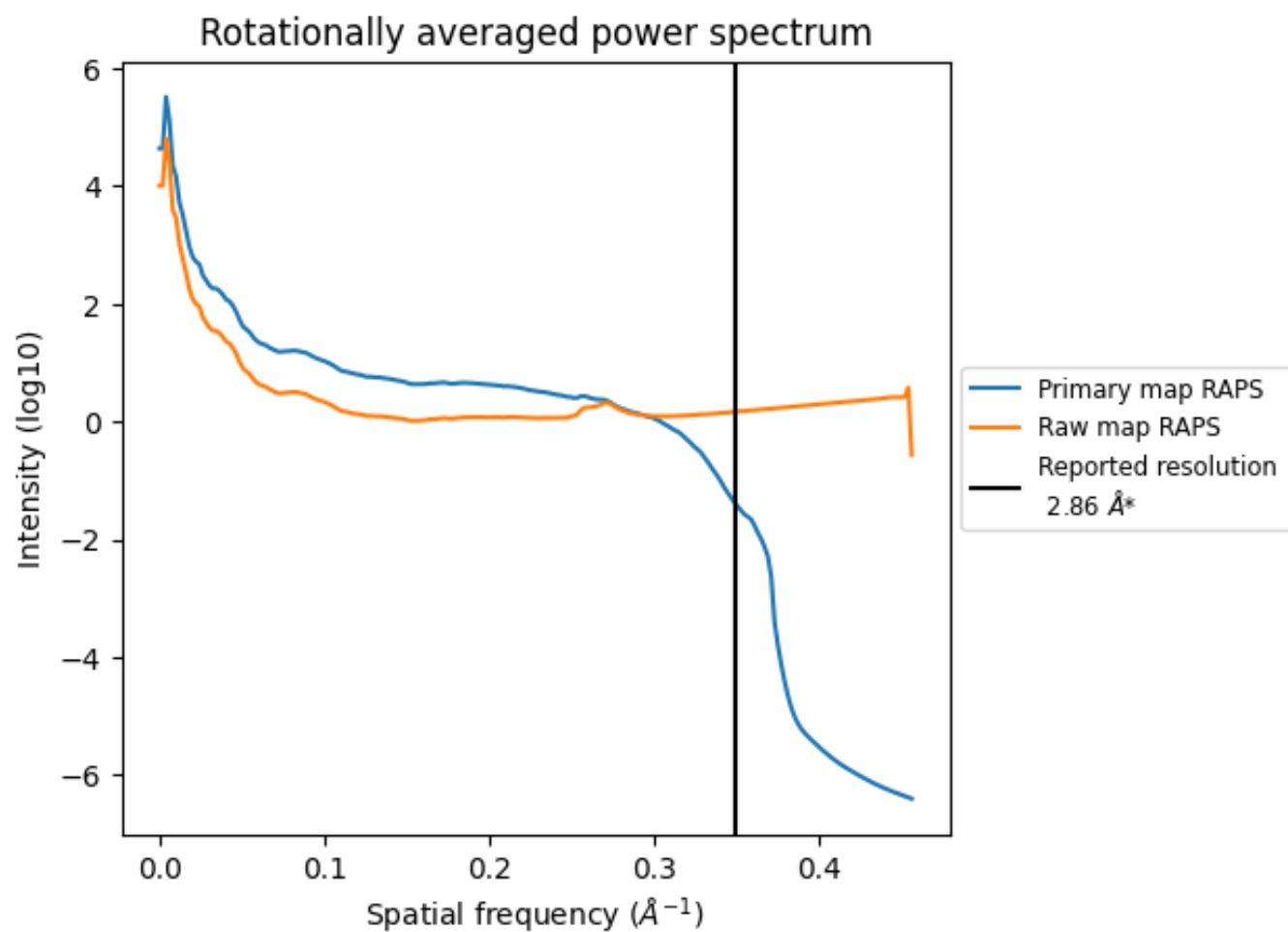
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2290  $\text{nm}^3$ ; this corresponds to an approximate mass of 2069 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 ⓘ

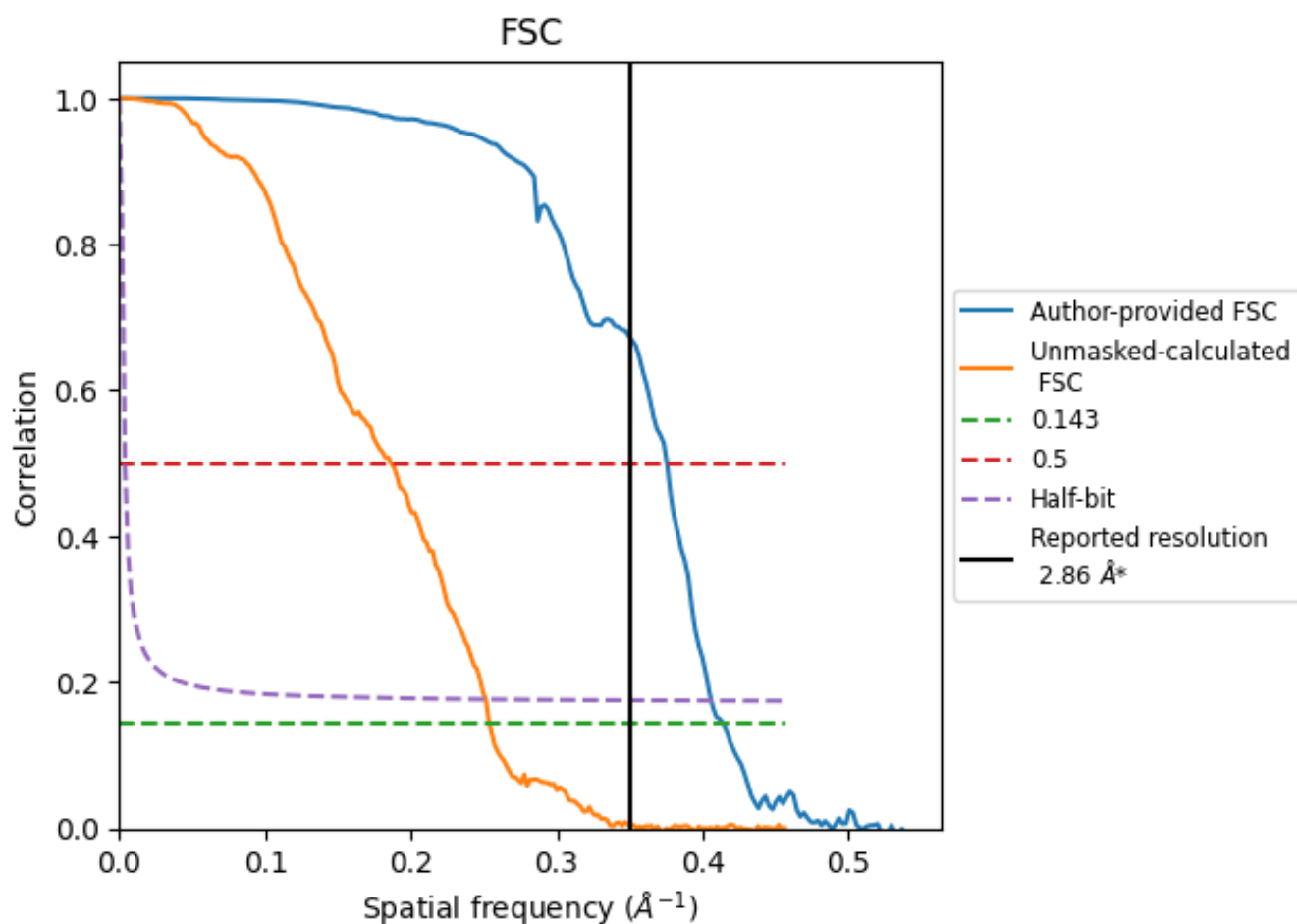


\*Reported resolution corresponds to spatial frequency of 0.350 Å<sup>-1</sup>

## 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 0.350  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.41	2.66	2.46
Unmasked-calculated*	3.94	5.36	3.98

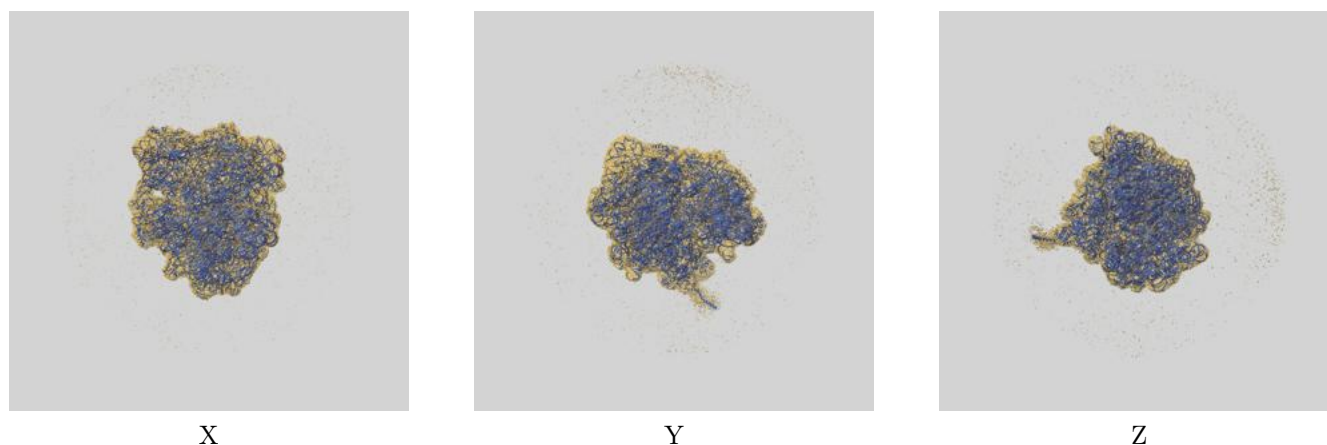
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.41 differs from the reported value 2.86 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.94 differs from the reported value 2.86 by more than 10 %

## 9 Map-model fit [i](#)

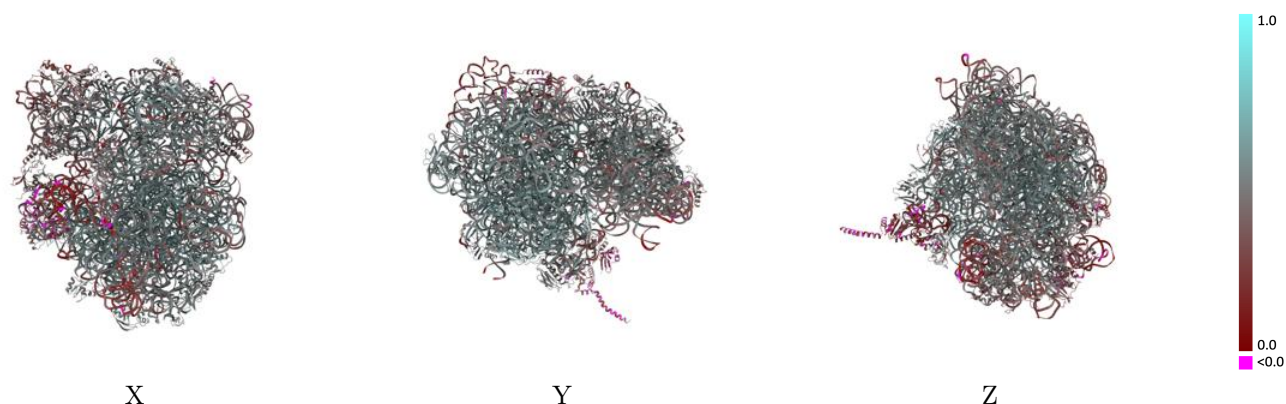
This section contains information regarding the fit between EMDB map EMD-29298 and PDB model 8FMW. Per-residue inclusion information can be found in section 3 on page 14.

### 9.1 Map-model overlay [i](#)



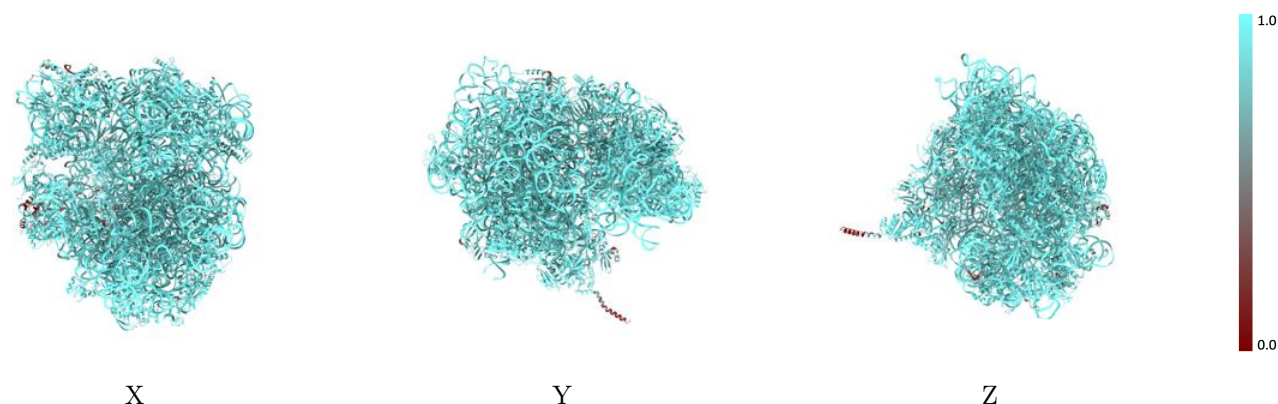
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



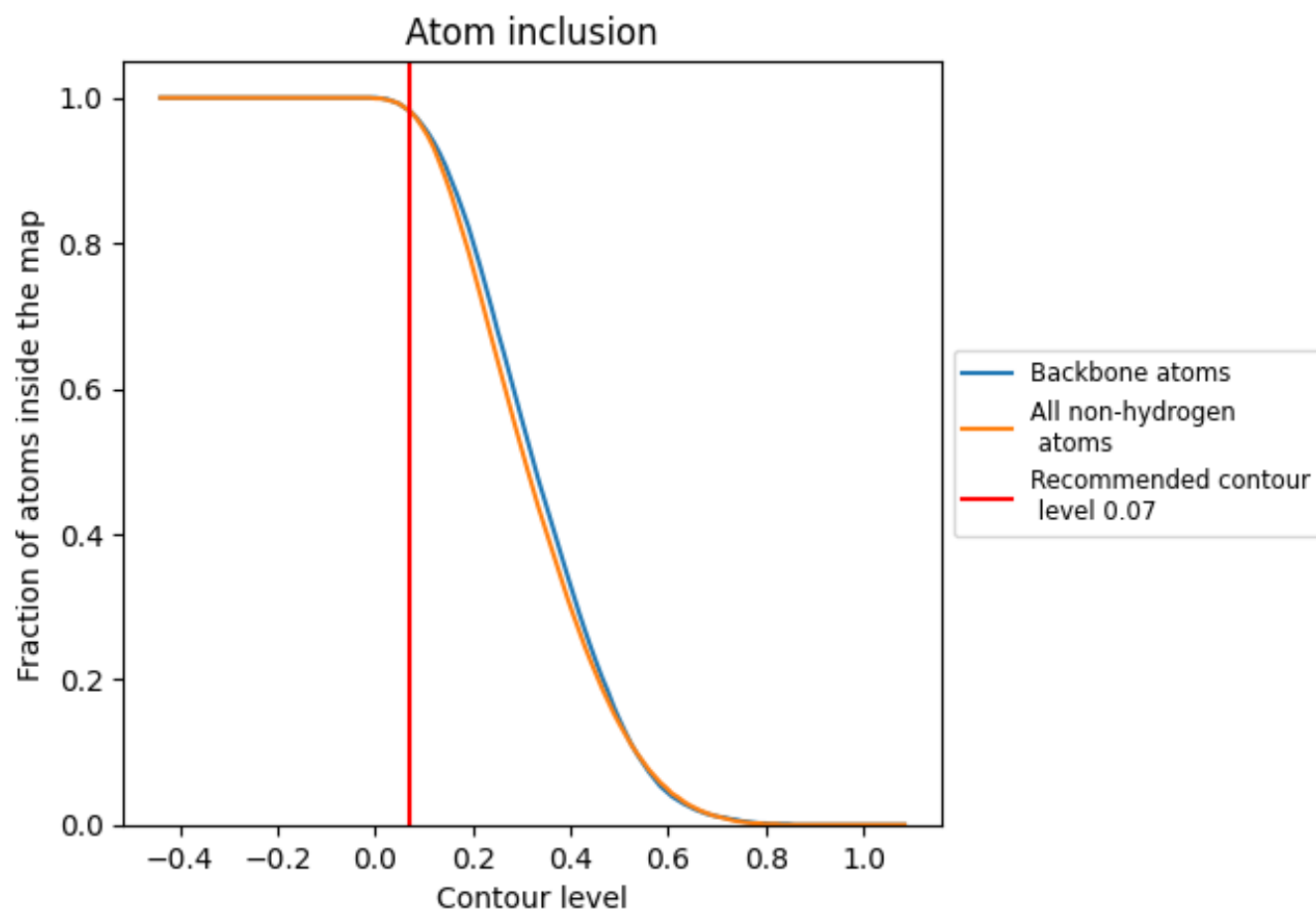
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

















































Chain	Atom inclusion	Q-score
All	 0.9820	 0.4840
A	 0.9910	 0.4700
AA	 0.9930	 0.5000
AB	 0.9970	 0.4510
AC	 0.7340	 0.1960
AD	 0.9880	 0.5780
AE	 0.9940	 0.5670
AF	 0.9970	 0.5480
AG	 0.9860	 0.4340
AH	 0.9800	 0.4740
AI	 0.8320	 0.3580
AJ	 0.8300	 0.2170
AK	 0.8880	 0.2360
AL	 0.9930	 0.5710
AM	 0.9880	 0.5760
AN	 0.9730	 0.5120
AO	 0.9830	 0.5420
AP	 0.9890	 0.5660
AQ	 0.9870	 0.4750
AR	 0.9910	 0.5480
AS	 0.9820	 0.5510
AT	 0.9850	 0.5370
AU	 0.9880	 0.5640
AV	 0.9790	 0.5270
AW	 0.9400	 0.4880
AX	 0.9780	 0.4350
AY	 0.9980	 0.5920
AZ	 0.9860	 0.5530
Aa	 0.9760	 0.4790
Ab	 0.9910	 0.5640
Ac	 0.9290	 0.3210
Ad	 0.9810	 0.5560
Ae	 0.9810	 0.5340
Af	 0.9980	 0.5930
Ag	 0.9910	 0.5820



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Chain	Atom inclusion	Q-score
Ah	 0.9770	 0.5590
Ai	 0.9640	 0.3980
C	 0.9450	 0.4380
D	 0.9760	 0.4510
E	 0.9750	 0.5080
F	 0.9750	 0.4180
G	 0.9620	 0.3930
H	 0.9820	 0.4960
I	 0.9670	 0.3780
J	 0.8770	 0.3970
K	 0.9840	 0.4780
L	 0.9820	 0.5340
M	 0.9460	 0.4190
N	 0.9550	 0.4430
O	 0.9870	 0.4820
P	 0.9880	 0.4870
Q	 0.9850	 0.5020
R	 0.9880	 0.4800
S	 0.9620	 0.3940
T	 0.9440	 0.4220
U	 0.8830	 0.3720
V	 0.9830	 0.5760
W	 0.9490	 0.5020
X	 0.8620	 0.2780