



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2024 – 07:53 PM EST

PDB ID : 8UU4
EMDB ID : EMD-42554
Title : Cryo-EM structure of the *Listeria innocua* 70S ribosome in complex with HPF (structure I-A)
Authors : Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on : 2023-10-31
Resolution : 3.00 Å (reported)
Based on initial model : 7NHN

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:

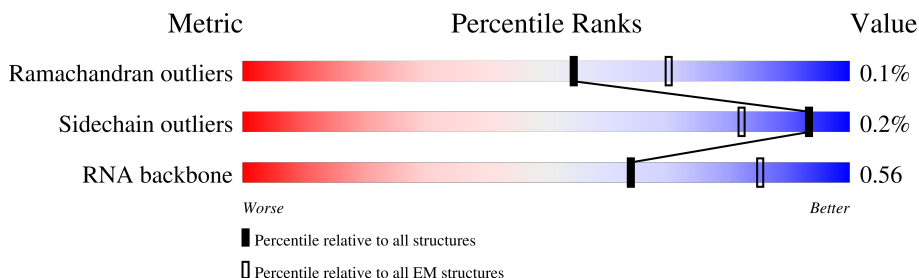
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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.



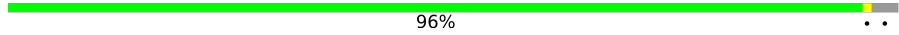
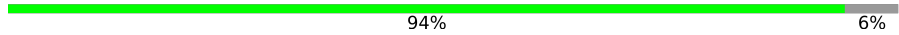

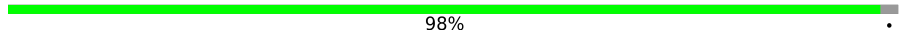

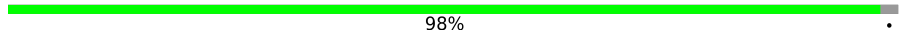
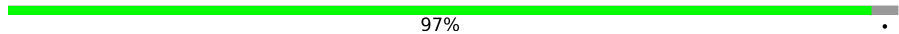
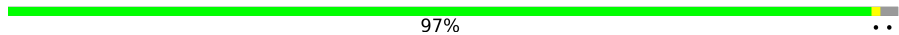



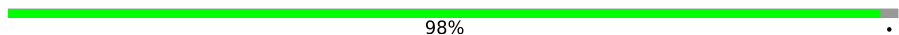



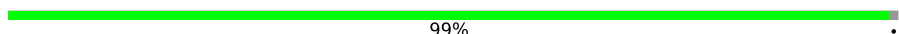
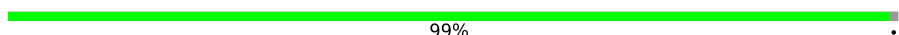
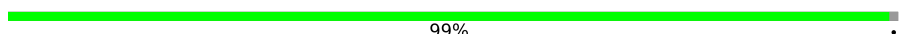
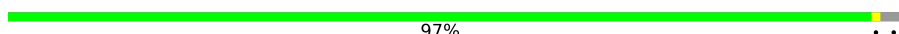
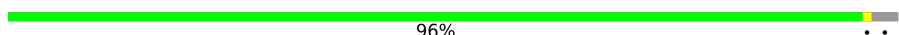
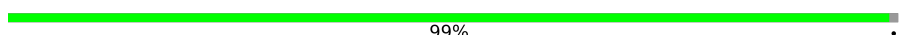
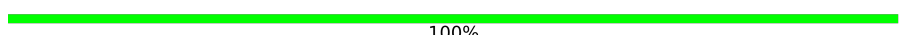
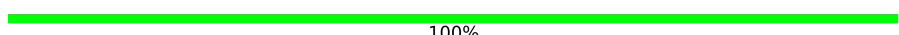


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1550	
2	b	249	
3	c	218	
4	d	200	
5	e	167	
6	f	97	
7	g	156	
8	h	132	


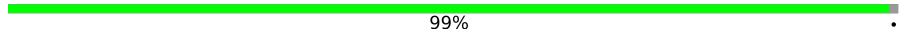
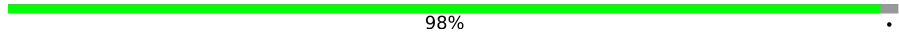
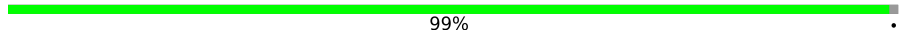
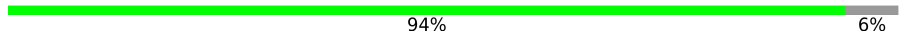
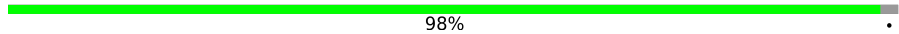
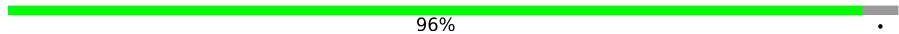

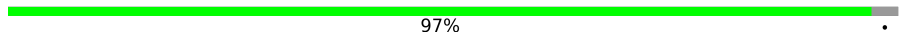
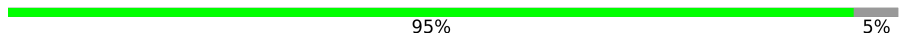
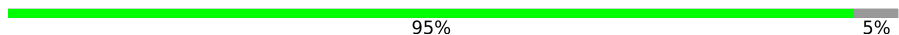
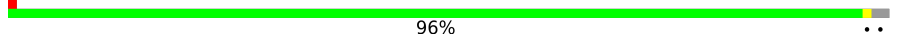

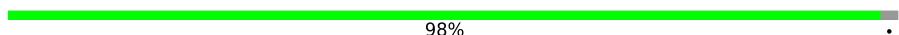
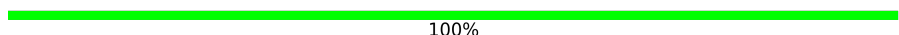
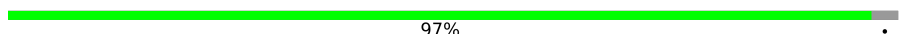
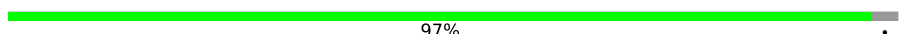
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Mol	Chain	Length	Quality of chain
9	i	130	 96%
10	j	102	 94%
11	k	129	 89%
12	l	137	 98%
13	m	121	 90%
14	n	61	 98%
15	o	89	 97%
16	p	90	 97%
17	q	87	 92%
18	r	79	 82%
19	s	92	 87%
20	t	84	 98%
21	w	187	 54%
22	A	2932	 82%
23	B	116	 88%
24	C	277	 99%
25	D	209	 99%
26	E	207	 99%
27	F	179	 97%
28	G	178	 96%
29	L	145	 99%
30	M	122	 100%
31	N	146	 100%
32	O	144	 93%
33	P	135	 90%

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Mol	Chain	Length	Quality of chain
34	Q	119	 100%
35	R	114	 99%
36	S	119	 98%
37	T	102	 99%
38	U	118	 94% 6%
39	V	94	 98%
40	W	103	 96%
41	Y	96	 79% 21%
42	Z	62	 97%
43	1	63	 95% 5%
44	2	59	 95% 5%
45	3	81	 96%
46	4	57	 93% 7%
47	5	49	 98%
48	6	44	 100%
49	7	66	 97%
50	8	37	 97%

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 139761 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
			Total	C	N	O	P		
1	a	1516	32515	14504	5960	10535	1516	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	b	221	1709	1087	301	314	7	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	c	204	1583	988	297	295	3	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	d	199	1499	938	282	277	2	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	e	156	1146	719	210	215	2	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	f	94	786	497	137	150	2	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	g	154	1167	728	220	210	9	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	h	131	1022	651	180	189	2	0	0

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	i	126	960	605	188	166	1	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	j	96	699	440	127	131	1	0	0

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	k	115	841	517	162	159	3	0	0

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	l	134	1040	645	209	184	2	0	0

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	m	109	767	471	155	140	1	0	0

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			490	313	97	75	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	86	Total	C	N	O	S	0	0
			722	448	145	127	2		

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	88	Total	C	N	O	S	0	0
			711	450	132	126	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			656	413	123	119	1		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	65	Total	C	N	O	S	0	0
			527	339	96	90	2		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	81	Total	C	N	O	S	0	0
			634	406	117	109	2		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	82	Total	C	N	O	S	0	0
			624	378	127	118	1		

- Molecule 21 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	102	Total	C	N	O	S	0	0
			847	536	150	160	1		

- Molecule 22 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	A	2903	Total	C	N	O	P	0	0
			62360	27830	11535	20092	2903		

- Molecule 23 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B	114	Total	C	N	O	P	0	0
			2428	1082	428	804	114		

- Molecule 24 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	273	Total	C	N	O	S	0	0
			2108	1307	415	379	7		

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	206	Total	C	N	O	S	0	0
			1583	995	291	293	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	E	204	Total	C	N	O	0	0
			1560	988	287	285		

- Molecule 27 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	174	Total	C	N	O	S	0	0
			1283	812	221	245	5		

- Molecule 28 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	G	172	1316	828	242	245	1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	L	143	1128	715	205	205	3	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	M	122	925	573	175	172	5	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	N	146	1112	687	216	208	1	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	O	134	1063	680	206	171	6	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	P	122	982	616	193	172	1	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Q	119	900	555	176	168	1	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	R	113	Total	C	N	O	S	0	0
			909	573	181	154	1		

- Molecule 36 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	S	117	Total	C	N	O	S	0	0
			944	599	186	155	4		

- Molecule 37 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	T	101	Total	C	N	O	S	0	0
			785	506	134	144	1		

- Molecule 38 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	U	111	Total	C	N	O	0	0
			855	539	161	155		

- Molecule 39 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	V	92	Total	C	N	O	S	0	0
			751	477	131	140	3		

- Molecule 40 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	W	99	Total	C	N	O	S	0	0
			752	476	139	134	3		

- Molecule 41 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Y	76	Total	C	N	O	S	0	0
			585	357	114	113	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	60	Total	C	N	O	S	0	0
			467	289	98	78	2		

- Molecule 43 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1	60	Total	C	N	O	S	0	0
			495	304	95	95	1		

- Molecule 44 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2	56	Total	C	N	O	S	0	0
			433	272	82	78	1		

- Molecule 45 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	3	79	Total	C	N	O	S	0	0
			491	308	89	93	1		

- Molecule 46 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	4	53	Total	C	N	O	S	0	0
			425	259	87	74	5		

- Molecule 47 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5	48	Total	C	N	O	S	0	0
			408	248	82	74	4		

- Molecule 48 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	6	44	Total	C	N	O	S	0	0
			370	225	89	54	2		

- Molecule 49 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	N	O			S
49	7	64	520	322	114	79	5	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	N	O			S
50	8	36	292	183	59	44	6	0	0

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	a	167	Total 167	Mg 167	0
51	A	280	Total 280	Mg 280	0
51	B	1	Total 1	Mg 1	0
51	C	1	Total 1	Mg 1	0

- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	n	1	Total 1	Zn 1	0
52	4	1	Total 1	Zn 1	0
52	5	1	Total 1	Zn 1	0
52	8	1	Total 1	Zn 1	0

- Molecule 53 is water.

Mol	Chain	Residues	Atoms		AltConf
53	a	47	Total 47	O 47	0
53	d	1	Total 1	O 1	0
53	t	1	Total 1	O 1	0

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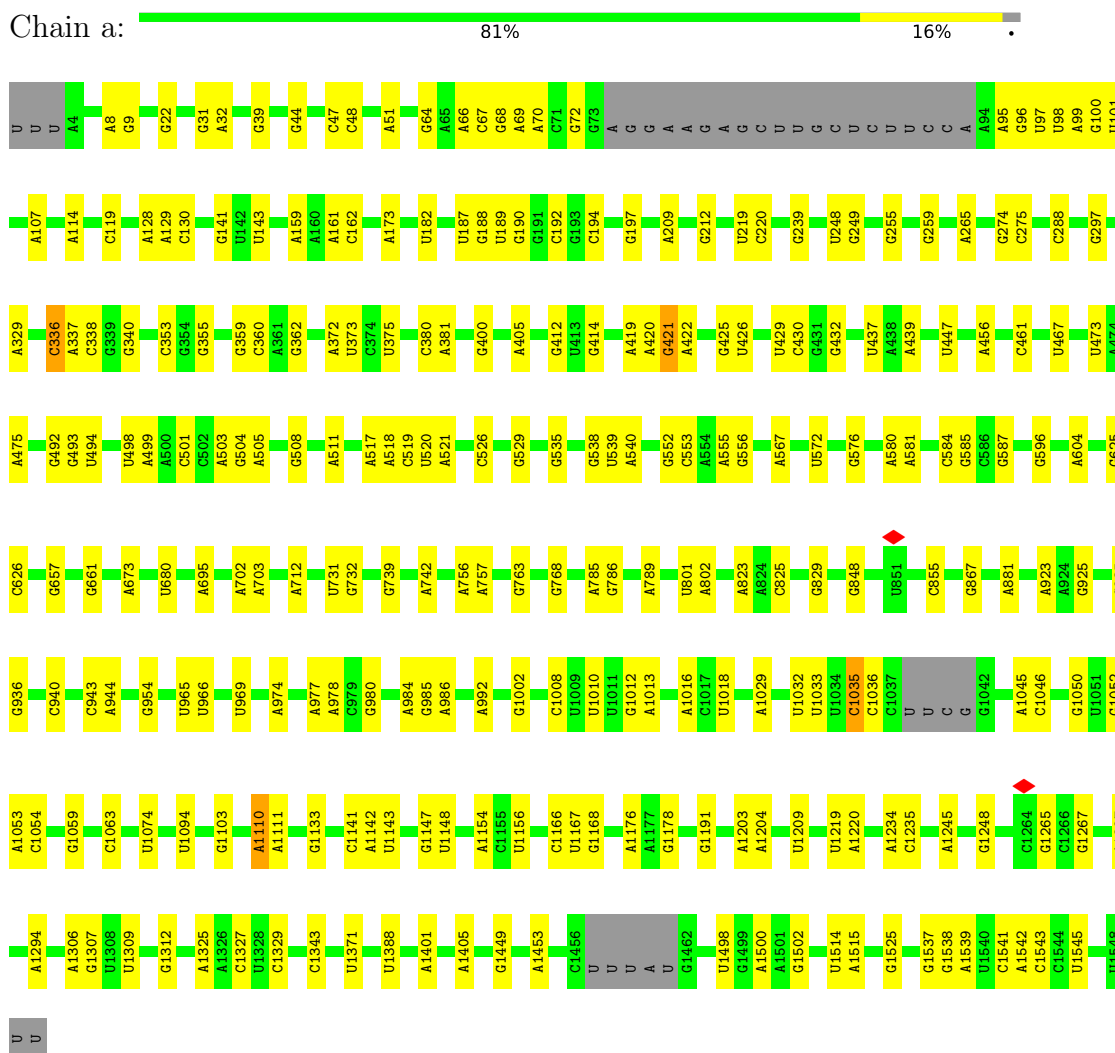
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Mol	Chain	Residues	Atoms	AltConf
53	A	80	Total O 80 80	0
53	E	1	Total O 1 1	0
53	N	1	Total O 1 1	0
53	3	1	Total O 1 1	0
53	6	1	Total O 1 1	0

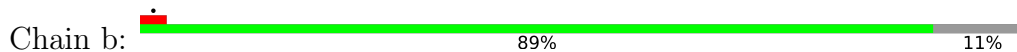
3 Residue-property plots

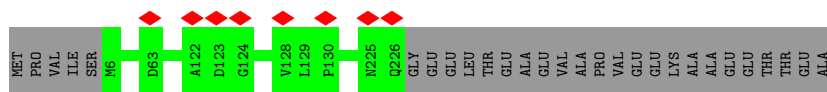
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S Ribosomal RNA

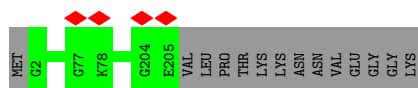


- Molecule 2: Small ribosomal subunit protein uS2





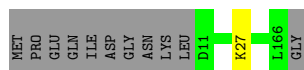
- Molecule 3: Small ribosomal subunit protein uS3



- Molecule 4: Small ribosomal subunit protein uS4



- Molecule 5: Small ribosomal subunit protein uS5



- Molecule 6: Small ribosomal subunit protein bS6



- Molecule 7: Small ribosomal subunit protein uS7

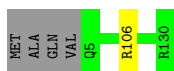


- Molecule 8: Small ribosomal subunit protein uS8



- Molecule 9: Small ribosomal subunit protein uS9

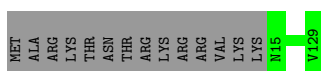
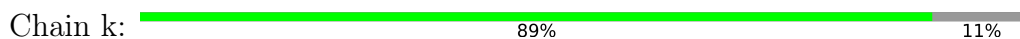




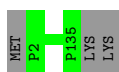
- Molecule 10: Small ribosomal subunit protein uS10



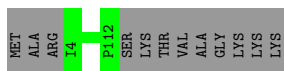
- Molecule 11: Small ribosomal subunit protein uS11



- Molecule 12: Small ribosomal subunit protein uS12



- Molecule 13: Small ribosomal subunit protein uS13



- Molecule 14: Small ribosomal subunit protein uS14

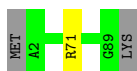


- Molecule 15: Small ribosomal subunit protein uS15

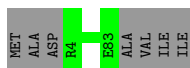


- Molecule 16: Small ribosomal subunit protein bS16

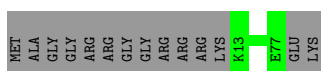
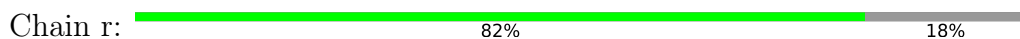




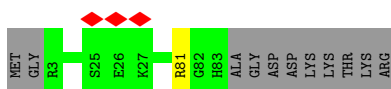
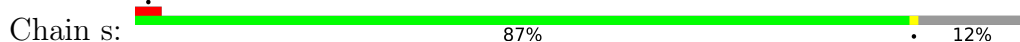
- Molecule 17: Small ribosomal subunit protein uS17



- Molecule 18: Small ribosomal subunit protein bS18



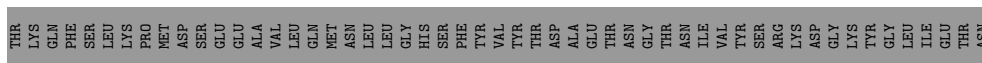
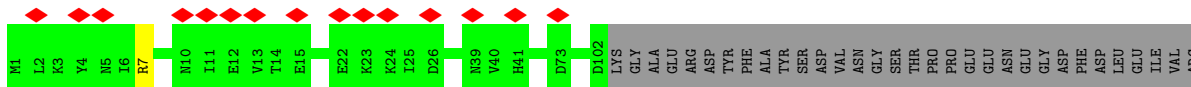
- Molecule 19: Small ribosomal subunit protein uS19



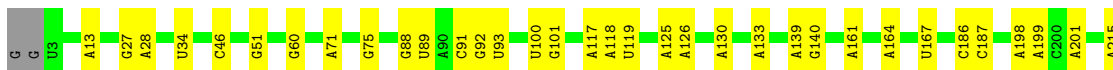
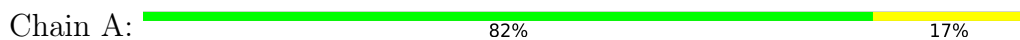
- Molecule 20: Small ribosomal subunit protein bS20

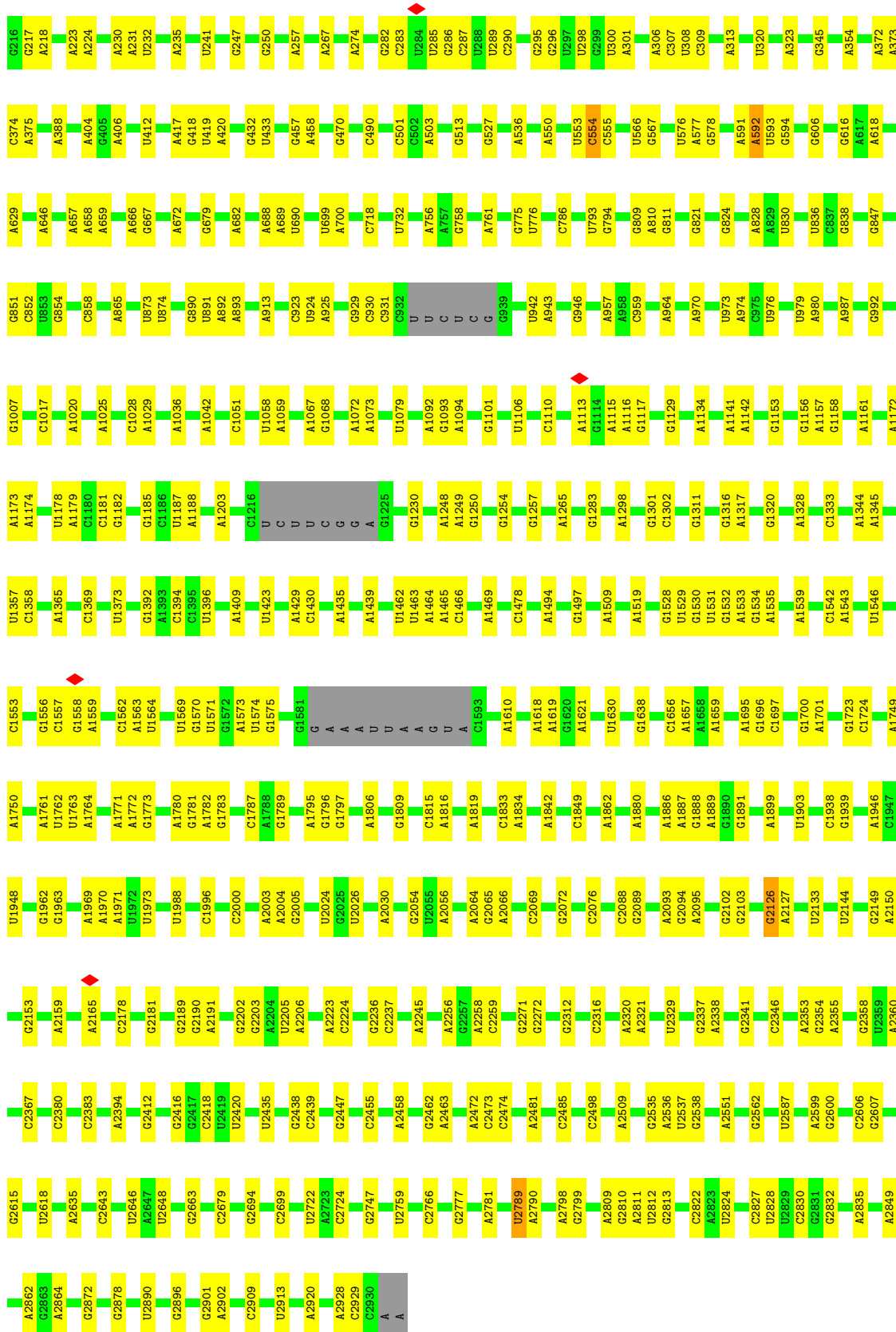


- Molecule 21: Ribosome hibernation promoting factor




- Molecule 22: 23S Ribosomal RNA





• Molecule 23: 5S Ribosomal RNA

Chain B:  88% 10%



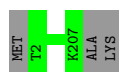
- Molecule 24: Large ribosomal subunit protein uL2

Chain C:  99%



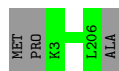
- Molecule 25: Large ribosomal subunit protein uL3

Chain D:  99%



- Molecule 26: Large ribosomal subunit protein uL4

Chain E:  99%



- Molecule 27: Large ribosomal subunit protein uL5

Chain F:  97%



- Molecule 28: Large ribosomal subunit protein uL6

Chain G:  96%



- Molecule 29: Large ribosomal subunit protein uL13

Chain L:  99%



- Molecule 30: Large ribosomal subunit protein uL14

Chain M:  100%

There are no outlier residues recorded for this chain.

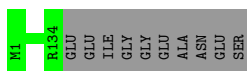
- Molecule 31: Large ribosomal subunit protein uL15

Chain N:  100%


There are no outlier residues recorded for this chain.

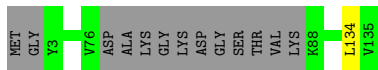
- Molecule 32: Large ribosomal subunit protein uL16

Chain O:  93% 7%



- Molecule 33: Large ribosomal subunit protein bL17

Chain P:  90% 10%



- Molecule 34: Large ribosomal subunit protein uL18

Chain Q:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: Large ribosomal subunit protein bL19

Chain R:  99%



- Molecule 36: Large ribosomal subunit protein bL20

Chain S:  98%



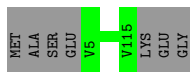
- Molecule 37: Large ribosomal subunit protein bL21

Chain T:  99%



- Molecule 38: Large ribosomal subunit protein uL22

Chain U:  94% 6%



- Molecule 39: Large ribosomal subunit protein uL23

Chain V:  98% .



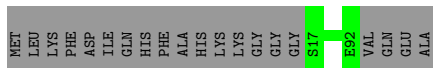
- Molecule 40: Large ribosomal subunit protein uL24

Chain W:  96% .



- Molecule 41: Large ribosomal subunit protein bL27

Chain Y:  79% 21%



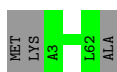
- Molecule 42: Large ribosomal subunit protein bL28

Chain Z:  97% .



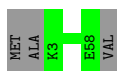
- Molecule 43: Large ribosomal subunit protein uL29

Chain 1:  95% 5%



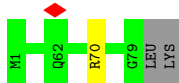
- Molecule 44: Large ribosomal subunit protein uL30

Chain 2:  95% 5%



- Molecule 45: Large ribosomal subunit protein bL31B

Chain 3:  96%



- Molecule 46: Large ribosomal subunit protein bL32

Chain 4:  93% 7%



- Molecule 47: Large ribosomal subunit protein bL33

Chain 5:  98%



- Molecule 48: Large ribosomal subunit protein bL34

Chain 6:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: Large ribosomal subunit protein bL35

Chain 7:  97%



- Molecule 50: Large ribosomal subunit protein bL36

Chain 8:  97%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	303270	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.498	Depositor
Minimum map value	-0.520	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.078	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.43	0/36403	0.79	10/56778 (0.0%)
2	b	0.27	0/1736	0.49	0/2341
3	c	0.27	0/1608	0.55	0/2173
4	d	0.28	0/1526	0.51	0/2065
5	e	0.29	0/1159	0.52	0/1565
6	f	0.31	0/798	0.56	0/1069
7	g	0.25	0/1182	0.52	0/1591
8	h	0.30	0/1035	0.54	0/1392
9	i	0.26	0/978	0.55	0/1321
10	j	0.25	0/709	0.47	0/962
11	k	0.27	0/855	0.55	0/1155
12	l	0.30	0/1056	0.59	0/1418
13	m	0.26	0/773	0.55	0/1046
14	n	0.28	0/500	0.56	0/664
15	o	0.29	0/732	0.55	0/980
16	p	0.28	0/724	0.53	0/970
17	q	0.28	0/665	0.54	0/889
18	r	0.30	0/535	0.54	0/716
19	s	0.26	0/650	0.49	0/878
20	t	0.25	0/627	0.49	0/835
21	w	0.27	0/859	0.56	0/1157
22	A	0.69	0/69865	0.83	11/108989 (0.0%)
23	B	0.38	0/2711	0.75	0/4224
24	C	0.41	0/2144	0.59	0/2875
25	D	0.41	0/1605	0.58	0/2156
26	E	0.37	0/1580	0.56	0/2129
27	F	0.29	0/1298	0.55	0/1758
28	G	0.28	0/1338	0.51	0/1807
29	L	0.38	0/1151	0.51	0/1546
30	M	0.41	0/932	0.59	0/1248
31	N	0.36	0/1123	0.57	0/1492
32	O	0.35	0/1085	0.55	0/1449

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	P	0.38	0/993	0.63	1/1328 (0.1%)
34	Q	0.28	0/908	0.55	0/1214
35	R	0.39	0/921	0.61	0/1234
36	S	0.43	0/957	0.54	0/1273
37	T	0.41	0/798	0.52	0/1071
38	U	0.38	0/865	0.57	0/1170
39	V	0.39	0/760	0.61	0/1017
40	W	0.32	0/762	0.49	0/1017
41	Y	0.39	0/592	0.60	0/788
42	Z	0.37	0/472	0.58	0/626
43	1	0.30	0/496	0.55	0/662
44	2	0.33	0/436	0.58	0/585
45	3	0.25	0/498	0.48	0/681
46	4	0.44	0/433	0.62	0/577
47	5	0.35	0/412	0.61	0/551
48	6	0.43	0/373	0.70	0/486
49	7	0.36	0/527	0.61	0/685
50	8	0.35	0/295	0.62	0/387
All	All	0.55	0/151440	0.76	22/226990 (0.0%)

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1036	C	N3-C2-O2	-7.39	116.73	121.90
22	A	1028	C	N3-C2-O2	-7.35	116.76	121.90
1	a	336	C	C2-N1-C1'	6.44	125.89	118.80
22	A	1357	U	C2-N1-C1'	6.38	125.36	117.70
22	A	1110	C	N1-C2-O2	6.32	122.69	118.90

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

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	
2	b	219/249 (88%)	198 (90%)	21 (10%)	0	100	100
3	c	202/218 (93%)	190 (94%)	12 (6%)	0	100	100
4	d	197/200 (98%)	182 (92%)	15 (8%)	0	100	100
5	e	154/167 (92%)	148 (96%)	5 (3%)	1 (1%)	25	64
6	f	92/97 (95%)	87 (95%)	5 (5%)	0	100	100
7	g	152/156 (97%)	139 (91%)	10 (7%)	3 (2%)	7	34
8	h	129/132 (98%)	127 (98%)	2 (2%)	0	100	100
9	i	124/130 (95%)	116 (94%)	8 (6%)	0	100	100
10	j	94/102 (92%)	84 (89%)	10 (11%)	0	100	100
11	k	113/129 (88%)	108 (96%)	5 (4%)	0	100	100
12	l	132/137 (96%)	125 (95%)	7 (5%)	0	100	100
13	m	107/121 (88%)	99 (92%)	8 (8%)	0	100	100
14	n	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
15	o	84/89 (94%)	83 (99%)	1 (1%)	0	100	100
16	p	86/90 (96%)	82 (95%)	4 (5%)	0	100	100
17	q	78/87 (90%)	75 (96%)	3 (4%)	0	100	100
18	r	63/79 (80%)	62 (98%)	1 (2%)	0	100	100
19	s	79/92 (86%)	74 (94%)	5 (6%)	0	100	100
20	t	80/84 (95%)	80 (100%)	0	0	100	100
21	w	100/187 (54%)	93 (93%)	7 (7%)	0	100	100
24	C	271/277 (98%)	260 (96%)	11 (4%)	0	100	100
25	D	204/209 (98%)	189 (93%)	15 (7%)	0	100	100
26	E	202/207 (98%)	186 (92%)	16 (8%)	0	100	100
27	F	172/179 (96%)	160 (93%)	12 (7%)	0	100	100
28	G	170/178 (96%)	156 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	L	141/145 (97%)	137 (97%)	4 (3%)	0	100	100
30	M	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
31	N	144/146 (99%)	134 (93%)	10 (7%)	0	100	100
32	O	132/144 (92%)	130 (98%)	2 (2%)	0	100	100
33	P	118/135 (87%)	110 (93%)	8 (7%)	0	100	100
34	Q	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
35	R	111/114 (97%)	102 (92%)	9 (8%)	0	100	100
36	S	115/119 (97%)	113 (98%)	2 (2%)	0	100	100
37	T	99/102 (97%)	94 (95%)	5 (5%)	0	100	100
38	U	109/118 (92%)	104 (95%)	5 (5%)	0	100	100
39	V	90/94 (96%)	81 (90%)	9 (10%)	0	100	100
40	W	97/103 (94%)	93 (96%)	4 (4%)	0	100	100
41	Y	74/96 (77%)	66 (89%)	8 (11%)	0	100	100
42	Z	58/62 (94%)	54 (93%)	4 (7%)	0	100	100
43	1	58/63 (92%)	55 (95%)	3 (5%)	0	100	100
44	2	54/59 (92%)	52 (96%)	2 (4%)	0	100	100
45	3	77/81 (95%)	57 (74%)	19 (25%)	1 (1%)	12	45
46	4	51/57 (90%)	47 (92%)	4 (8%)	0	100	100
47	5	46/49 (94%)	46 (100%)	0	0	100	100
48	6	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
49	7	62/66 (94%)	57 (92%)	5 (8%)	0	100	100
50	8	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
All	All	5311/5732 (93%)	4980 (94%)	326 (6%)	5 (0%)	54	85

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	e	27	LYS
45	3	70	ARG
7	g	17	ILE
7	g	61	VAL
7	g	3	ARG

5.3.2 Protein sidechains [i](#)

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	b	172/214 (80%)	172 (100%)	0	100	100
3	c	156/177 (88%)	156 (100%)	0	100	100
4	d	142/170 (84%)	141 (99%)	1 (1%)	84	94
5	e	122/131 (93%)	122 (100%)	0	100	100
6	f	83/85 (98%)	82 (99%)	1 (1%)	71	90
7	g	116/130 (89%)	115 (99%)	1 (1%)	78	92
8	h	109/110 (99%)	109 (100%)	0	100	100
9	i	91/102 (89%)	90 (99%)	1 (1%)	73	90
10	j	66/93 (71%)	66 (100%)	0	100	100
11	k	86/100 (86%)	86 (100%)	0	100	100
12	l	115/118 (98%)	115 (100%)	0	100	100
13	m	66/102 (65%)	66 (100%)	0	100	100
14	n	51/52 (98%)	51 (100%)	0	100	100
15	o	79/81 (98%)	79 (100%)	0	100	100
16	p	78/80 (98%)	77 (99%)	1 (1%)	69	89
17	q	73/78 (94%)	73 (100%)	0	100	100
18	r	58/67 (87%)	58 (100%)	0	100	100
19	s	64/78 (82%)	63 (98%)	1 (2%)	62	86
20	t	64/66 (97%)	64 (100%)	0	100	100
21	w	96/170 (56%)	95 (99%)	1 (1%)	76	91
24	C	221/225 (98%)	221 (100%)	0	100	100
25	D	169/171 (99%)	169 (100%)	0	100	100
26	E	168/174 (97%)	168 (100%)	0	100	100
27	F	130/155 (84%)	129 (99%)	1 (1%)	81	93
28	G	140/147 (95%)	139 (99%)	1 (1%)	84	94
29	L	120/121 (99%)	120 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	M	101/101 (100%)	101 (100%)	0	100	100
31	N	115/115 (100%)	115 (100%)	0	100	100
32	O	106/113 (94%)	106 (100%)	0	100	100
33	P	102/111 (92%)	102 (100%)	0	100	100
34	Q	91/97 (94%)	91 (100%)	0	100	100
35	R	98/99 (99%)	98 (100%)	0	100	100
36	S	95/97 (98%)	95 (100%)	0	100	100
37	T	82/82 (100%)	82 (100%)	0	100	100
38	U	92/97 (95%)	92 (100%)	0	100	100
39	V	82/84 (98%)	82 (100%)	0	100	100
40	W	84/88 (96%)	84 (100%)	0	100	100
41	Y	61/76 (80%)	61 (100%)	0	100	100
42	Z	50/53 (94%)	50 (100%)	0	100	100
43	1	53/55 (96%)	53 (100%)	0	100	100
44	2	50/52 (96%)	50 (100%)	0	100	100
45	3	29/73 (40%)	29 (100%)	0	100	100
46	4	47/50 (94%)	47 (100%)	0	100	100
47	5	47/48 (98%)	47 (100%)	0	100	100
48	6	39/39 (100%)	39 (100%)	0	100	100
49	7	54/56 (96%)	54 (100%)	0	100	100
50	8	35/35 (100%)	35 (100%)	0	100	100
All	All	4348/4818 (90%)	4339 (100%)	9 (0%)	93	98

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	F	78	ARG
28	G	69	ARG
9	i	106	ARG
16	p	71	ARG
19	s	81	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
41	Y	58	ASN
42	Z	23	ASN
47	5	26	ASN
16	p	61	HIS
15	o	28	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1512/1550 (97%)	255 (16%)	0
22	A	2899/2932 (98%)	474 (16%)	30 (1%)
23	B	113/116 (97%)	12 (10%)	0
All	All	4524/4598 (98%)	741 (16%)	30 (0%)

5 of 741 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	A
1	a	9	G
1	a	22	G
1	a	31	G
1	a	32	A

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	A	1248	A
22	A	2535	G
22	A	1528	G
22	A	2809	A
22	A	2320	A

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 453 ligands modelled in this entry, 453 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

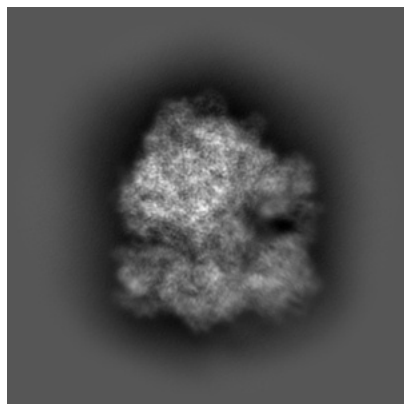
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42554. These allow visual inspection of the internal detail of the map and identification of artifacts.

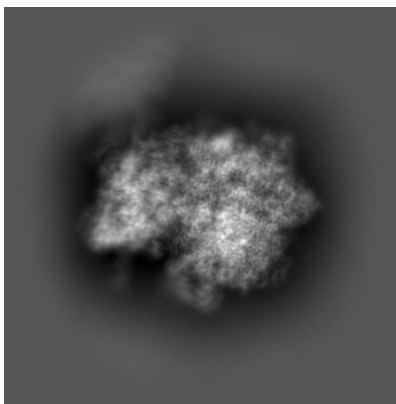
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

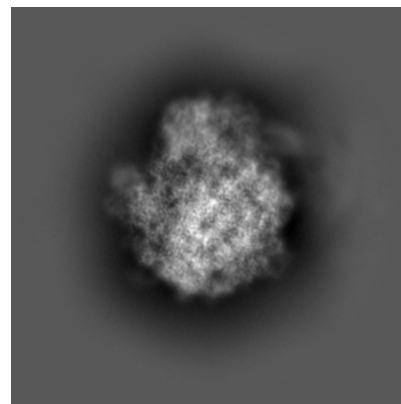
6.1.1 Primary map



X

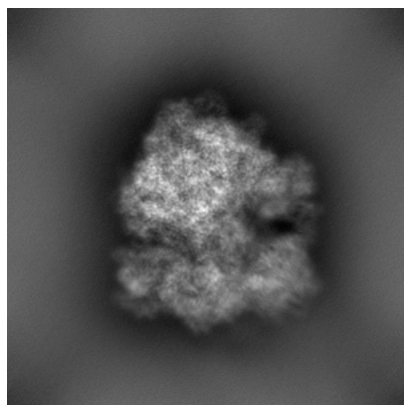


Y

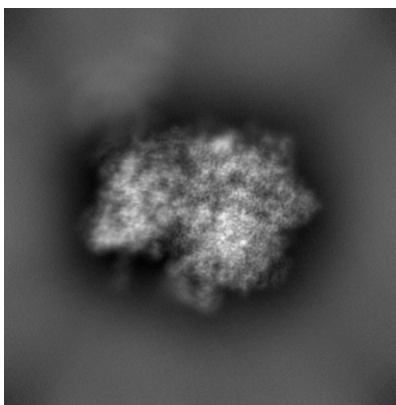


Z

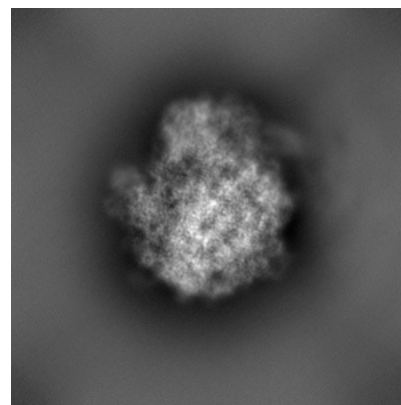
6.1.2 Raw map



X



Y

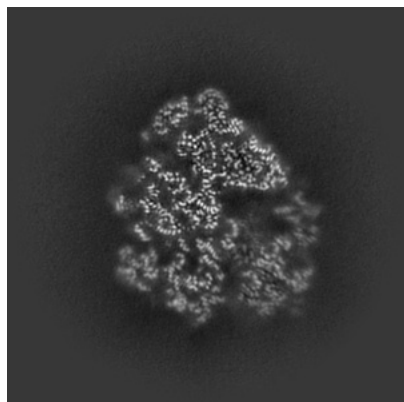


Z

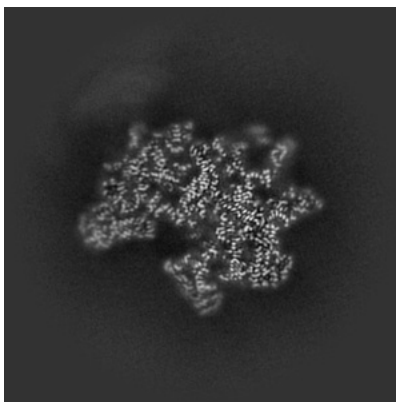
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

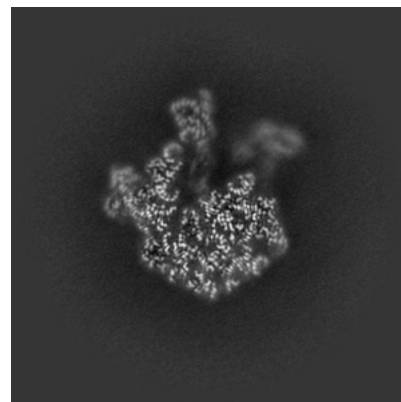
6.2.1 Primary map



X Index: 256

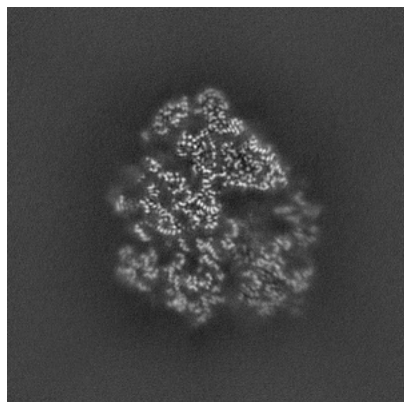


Y Index: 256

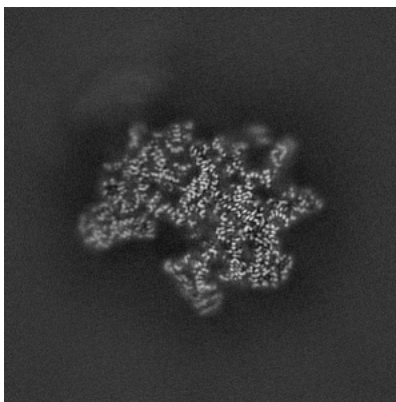


Z Index: 256

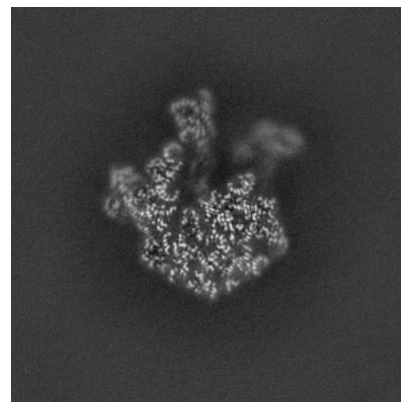
6.2.2 Raw map



X Index: 256



Y Index: 256

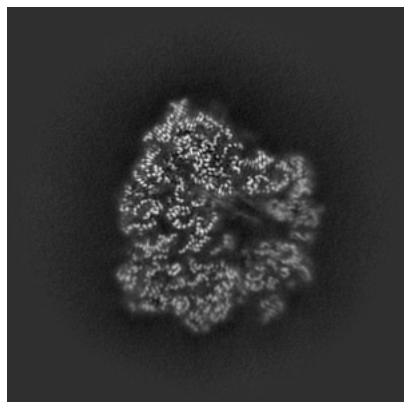


Z Index: 256

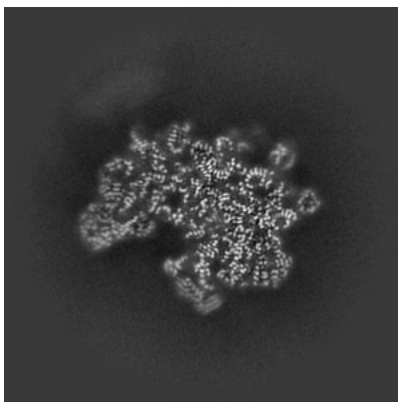
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

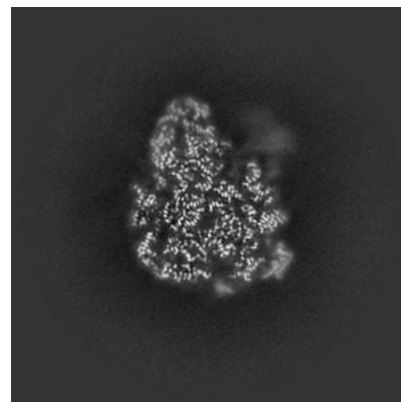
6.3.1 Primary map



X Index: 240

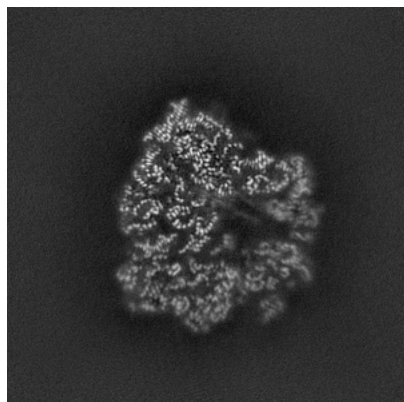


Y Index: 251

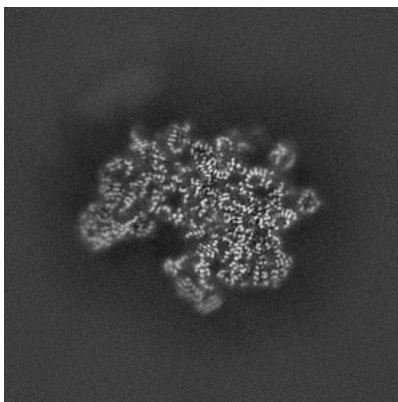


Z Index: 288

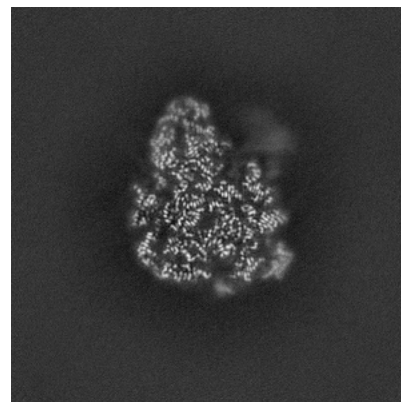
6.3.2 Raw map



X Index: 240



Y Index: 251

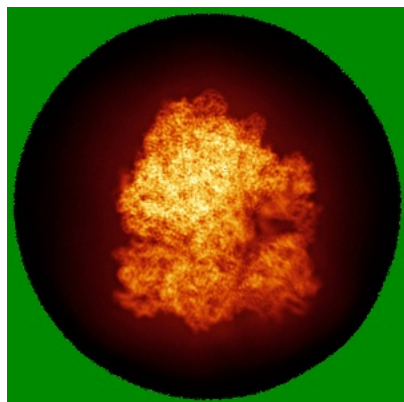


Z Index: 288

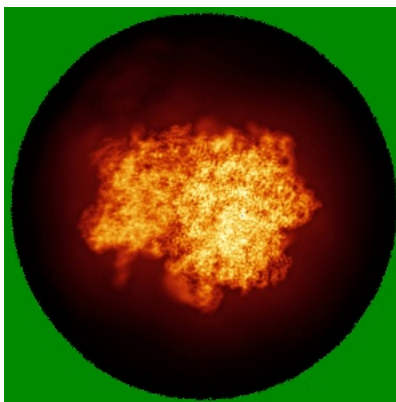
The images above show the largest variance slices of the map in three orthogonal directions.

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

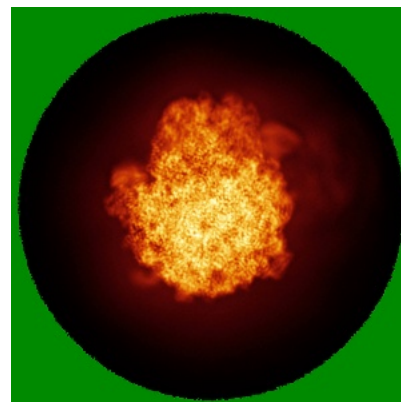
6.4.1 Primary map



X

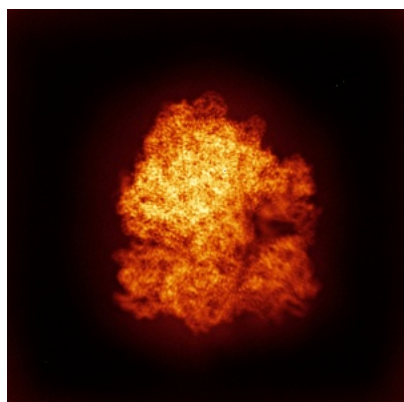


Y

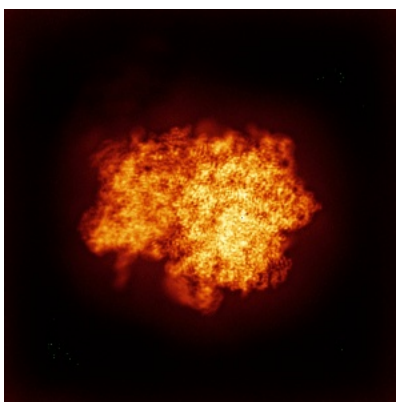


Z

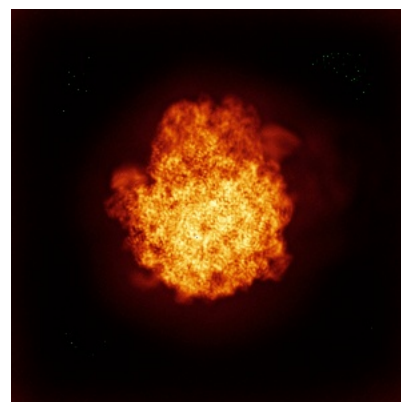
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

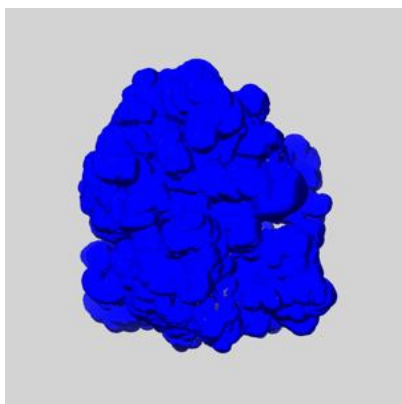
6.6 Mask visualisation [i](#)

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

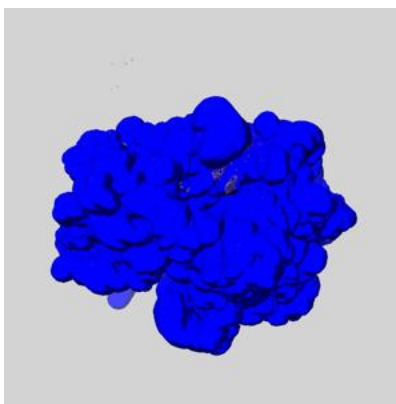
A mask typically either:

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

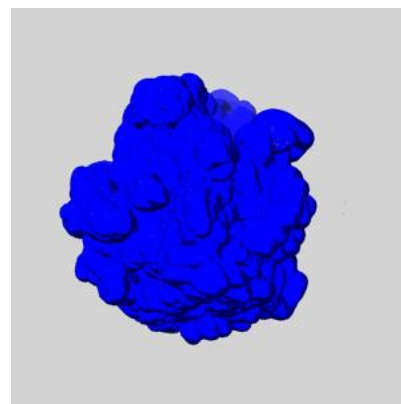
6.6.1 emd_42554_msk_1.map [i](#)



X



Y

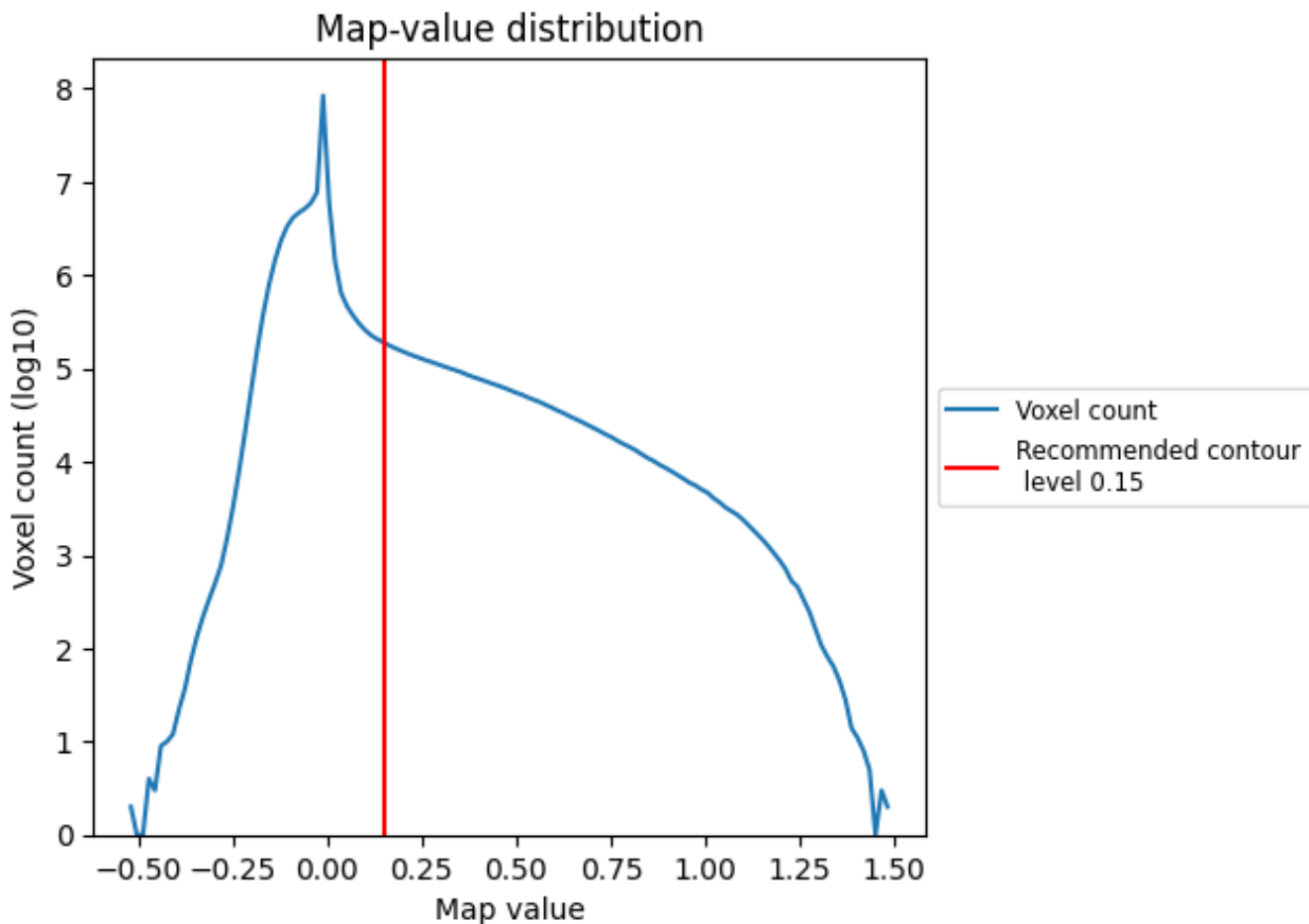


Z

7 Map analysis [i](#)

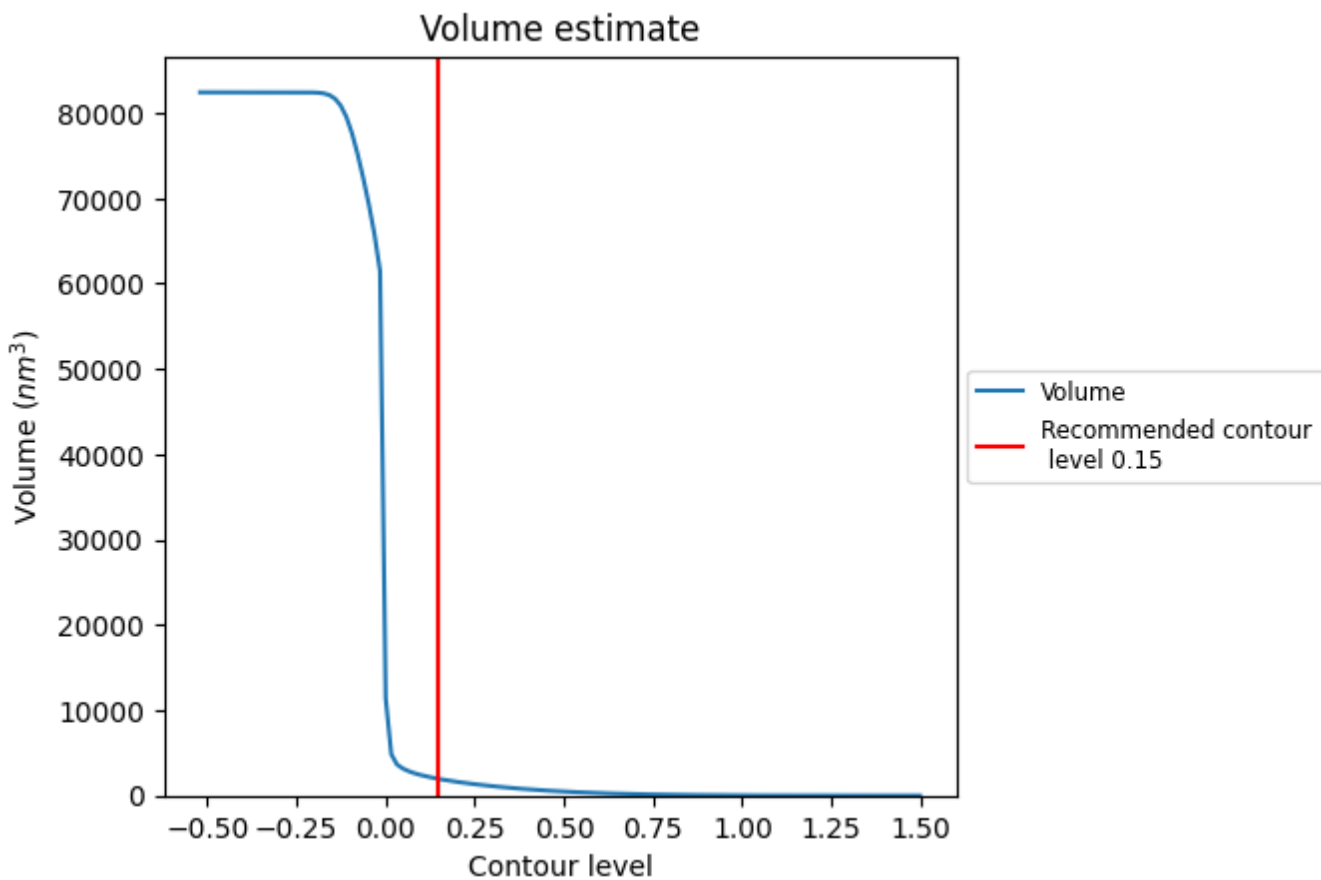
This section contains the results of statistical analysis of the map.

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.

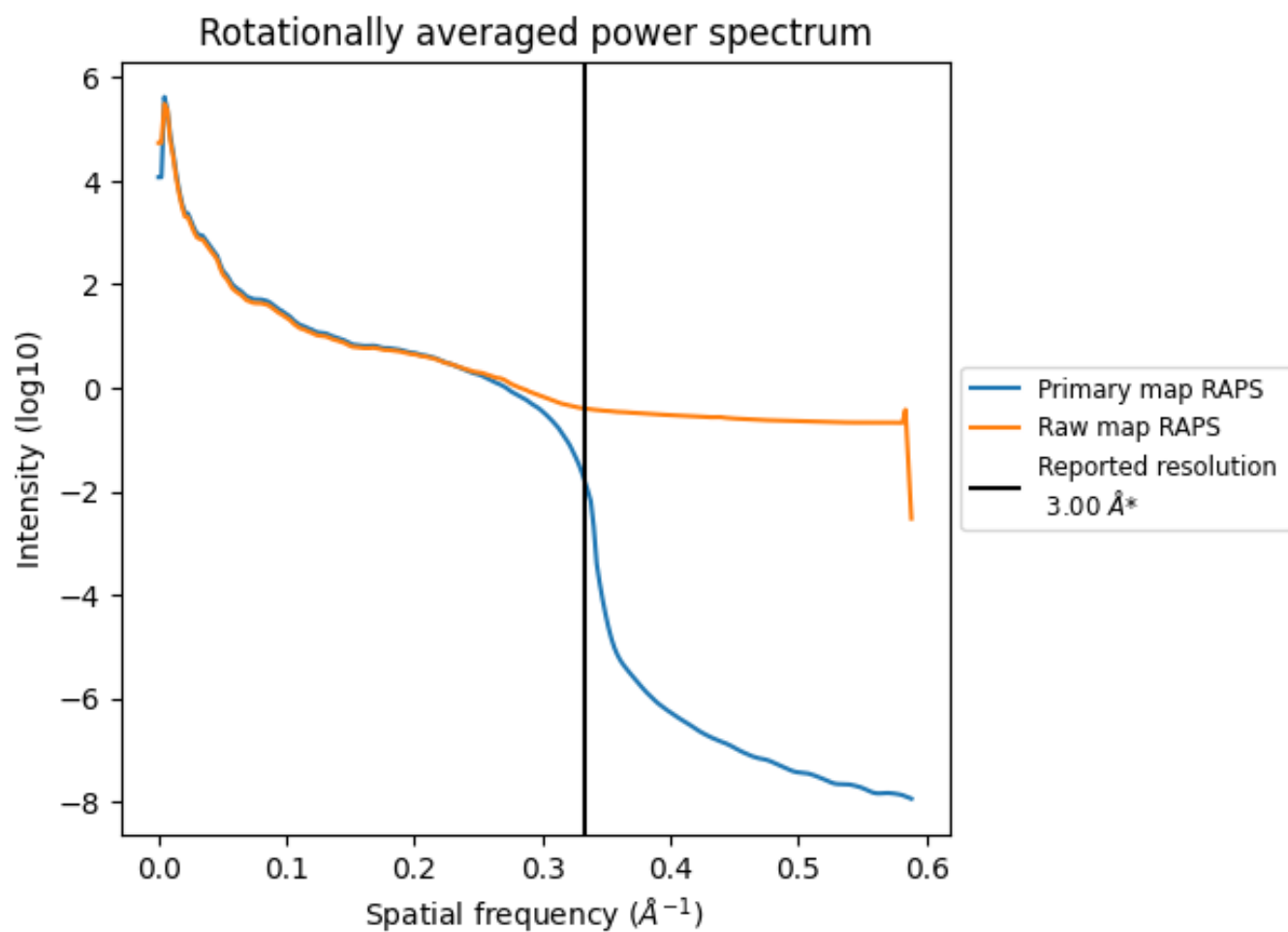
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1950 nm^3 ; this corresponds to an approximate mass of 1761 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 [i](#)

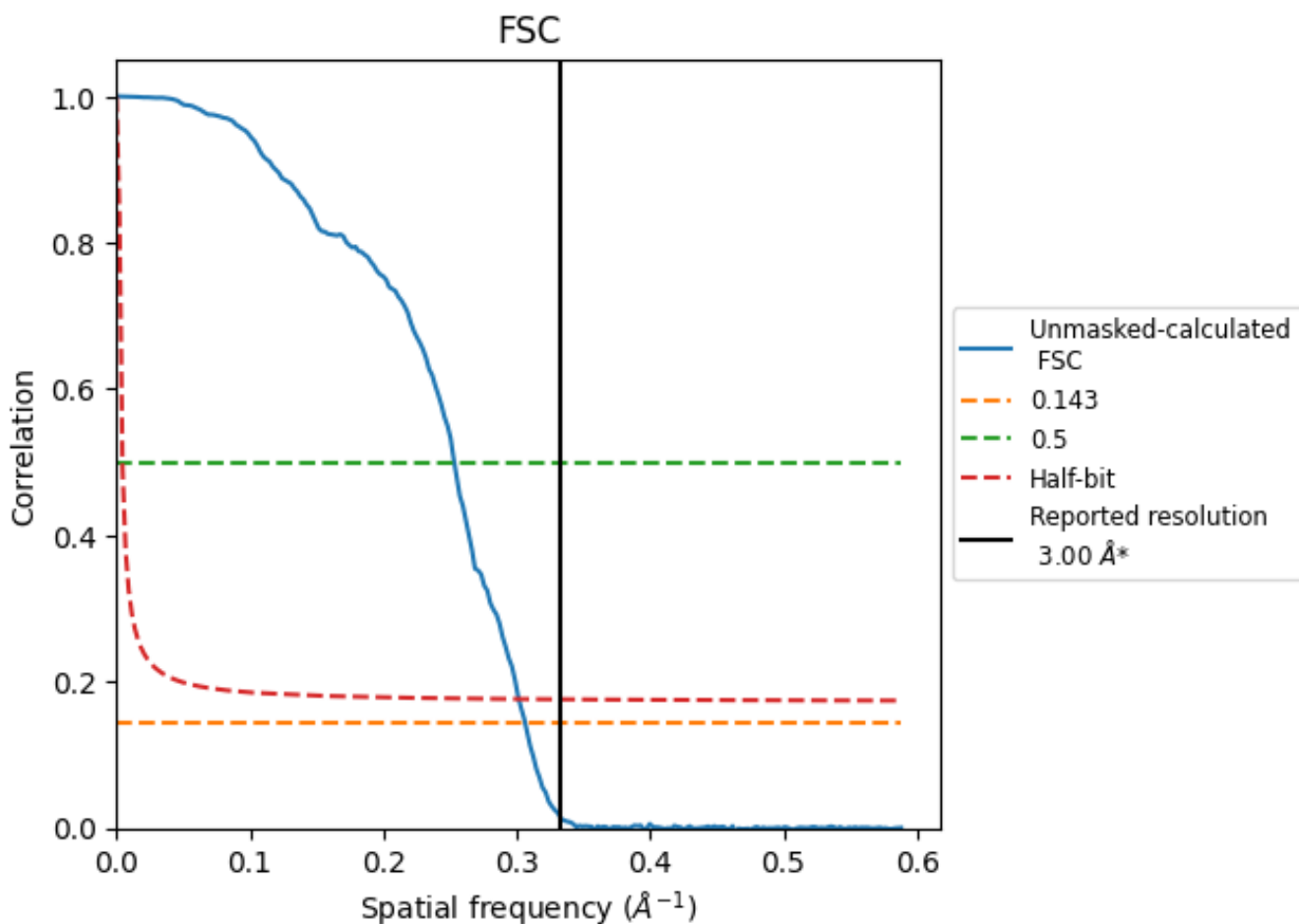


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

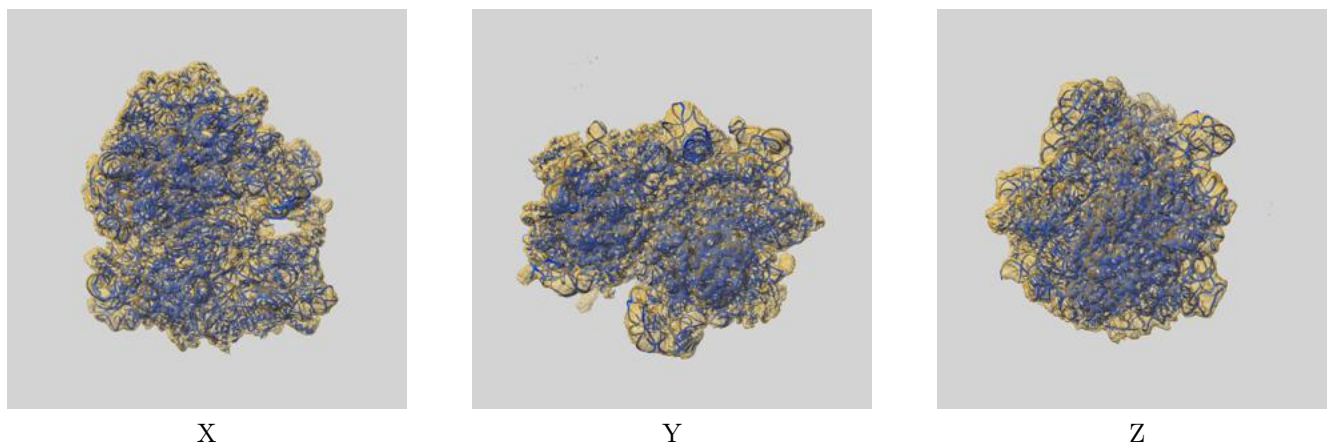
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.26	3.95	3.32

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

9 Map-model fit [i](#)

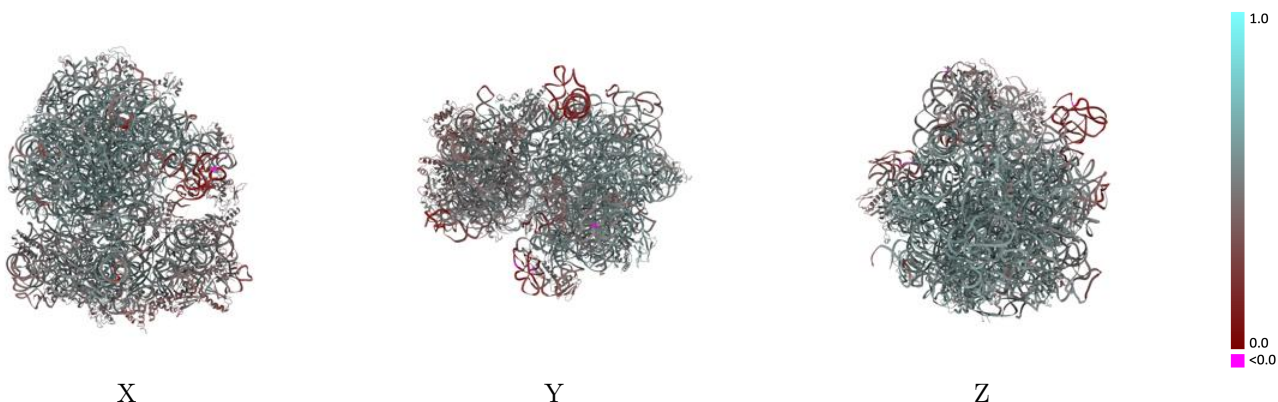
This section contains information regarding the fit between EMDB map EMD-42554 and PDB model 8UU4. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



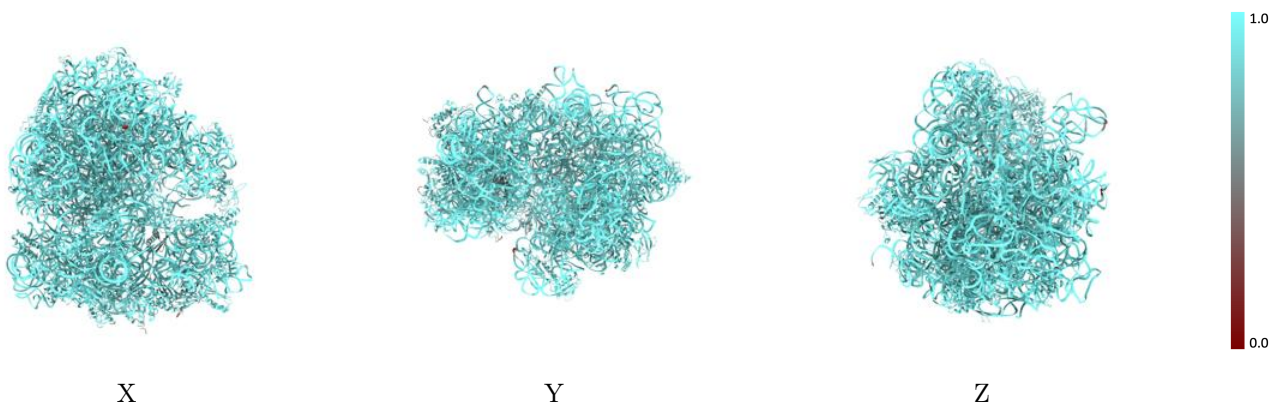
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



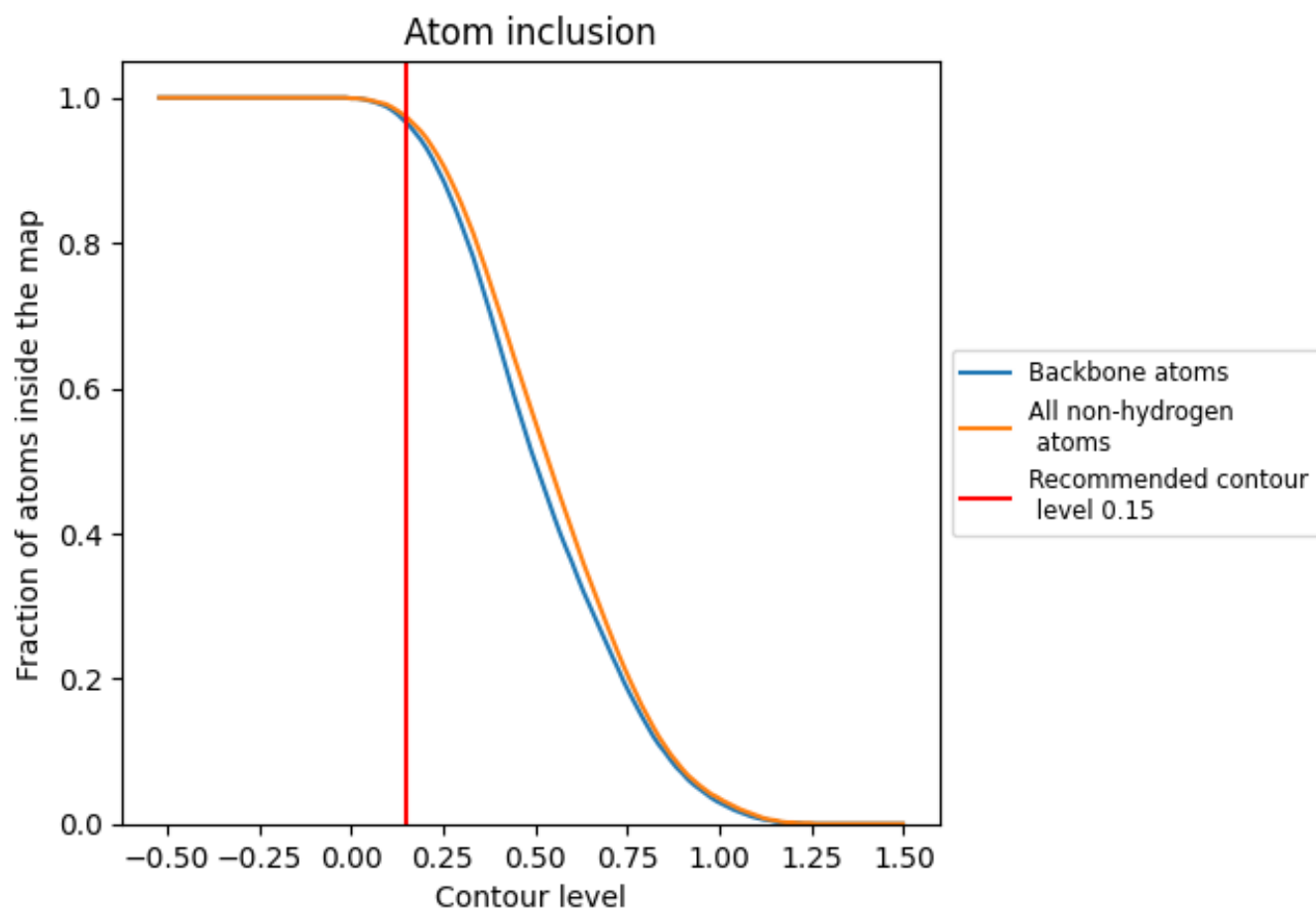
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9740	 0.5080
1	 0.9270	 0.4940
2	 0.9620	 0.5450
3	 0.9280	 0.4080
4	 0.9680	 0.5580
5	 0.9390	 0.5390
6	 0.9910	 0.5830
7	 0.9780	 0.5870
8	 0.9720	 0.5510
A	 0.9910	 0.5250
B	 0.9980	 0.4730
C	 0.9780	 0.5740
D	 0.9670	 0.5610
E	 0.9650	 0.5370
F	 0.9160	 0.4230
G	 0.9470	 0.4310
L	 0.9710	 0.5590
M	 0.9510	 0.5580
N	 0.9580	 0.5250
O	 0.9810	 0.5510
P	 0.9730	 0.5520
Q	 0.9590	 0.4660
R	 0.9550	 0.5570
S	 0.9790	 0.5620
T	 0.9670	 0.5570
U	 0.9760	 0.5610
V	 0.9580	 0.5390
W	 0.9150	 0.5000
Y	 0.9730	 0.5630
Z	 0.9850	 0.5540
a	 0.9930	 0.4850
b	 0.8180	 0.4100
c	 0.8480	 0.4510
d	 0.9400	 0.4670
e	 0.9090	 0.5050



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.9280	 0.4860
g	 0.9250	 0.4230
h	 0.9320	 0.4960
i	 0.9360	 0.4400
j	 0.9180	 0.4420
k	 0.9330	 0.4740
l	 0.9190	 0.5080
m	 0.9500	 0.4450
n	 0.9070	 0.4810
o	 0.9610	 0.5000
p	 0.9390	 0.4680
q	 0.8980	 0.4720
r	 0.9280	 0.5080
s	 0.8830	 0.4430
t	 0.9340	 0.4600
w	 0.6900	 0.4350