wwPDB EM Validation Summary Report (i)

Nov 30, 2021 – 05:35 pm GMT

PDB ID	:	7OHU
EMDB ID	:	EMD-12909
Title	:	Nog1-TAP associated immature ribosomal particles from S. cerevisiae after rpL2 expression shut down, population B
Authors	:	Milkereit, P.; Poell, G.
Deposited on	:	2021-05-11
Resolution	:	3.70 Å(reported)
Based on initial model	:	6EM1

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

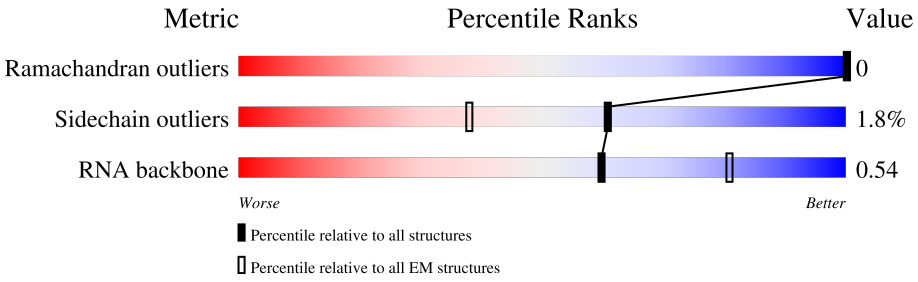
EMDB validation analysis	:	0.0.0.dev97
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.70 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 <=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	1	3396	38% 11% 50%
2	2	158	77% 17% 6%
3	B	387	84% 15%
4	C	362	7% 92% 7%
5	E	176	81% 18%
6	F	244	92% 8%
7	G	256	8% 60% 39%
8	H	191	6% 98%

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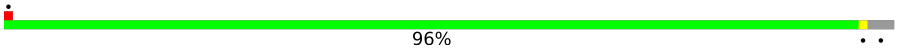
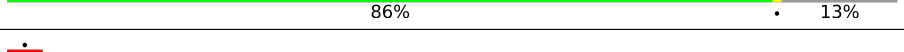
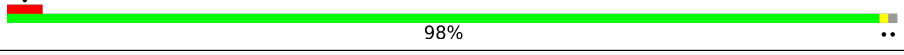
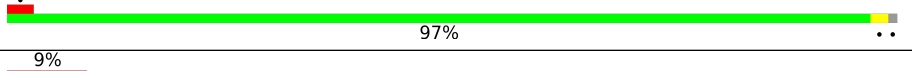
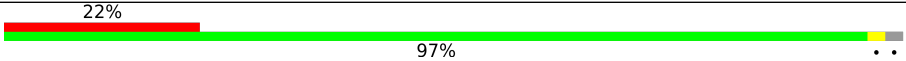
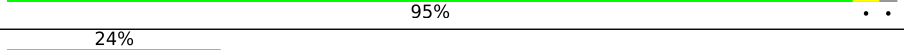
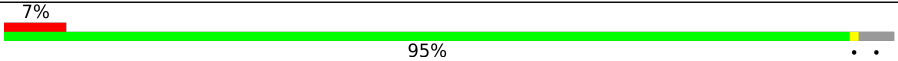
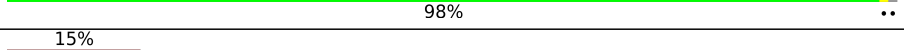
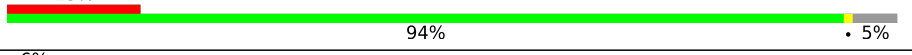
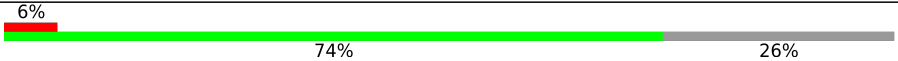
Mol	Chain	Length	Quality of chain
9	L	199	
10	M	138	
11	N	204	
12	O	199	
13	P	184	
14	Q	186	
15	S	172	
16	V	137	
17	W	236	
18	Y	127	
19	b	647	
20	e	130	
21	f	107	
22	h	120	
23	i	100	
24	j	88	
25	r	261	
26	u	199	
27	y	245	

2 Entry composition (i)

There are 28 unique types of molecules in this entry. The entry contains 127652 atoms, of which 54773 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 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	1	1692	54436	16178	18197	6560	11809	1692	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	2	148	4737	1407	1591	557	1034	148	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	B	330	5336	1669	2709	487	466	5	0	0

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	C	336	5260	1622	2688	489	458	3	0	0

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	144	2376	736	1235	206	198	1	0	0

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	225	3700	1166	1891	329	313	1	0	0

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	156	Total	C	H	N	O	S	0	0
			2488	784	1275	206	221	2		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	190	Total	C	H	N	O	S	0	0
			3086	957	1576	273	276	4		

- Molecule 9 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	108	Total	C	H	N	O	0	0
			1782	541	918	180	143		

- Molecule 10 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	M	134	Total	C	H	N	O	S	0	0
			2179	668	1138	197	174	2		

- Molecule 11 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	N	177	Total	C	H	N	O	S	0	0
			3079	948	1566	320	244	1		

- Molecule 12 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	O	197	Total	C	H	N	O	S	0	0
			3215	1003	1660	289	262	1		

- Molecule 13 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	108	Total	C	H	N	O	0	0
			1694	533	850	152	159		

- Molecule 14 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	Q	131	Total	C	H	N	O	S	0	0
			2101	645	1092	190	173	1		

- Molecule 15 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	S	170	Total	C	H	N	O	S	0	0
			2904	922	1472	265	242	3		

- Molecule 16 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	V	124	Total	C	H	N	O	S	0	0
			1890	578	970	173	162	7		

- Molecule 17 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	W	232	Total	C	H	N	O	S	0	0
			3773	1184	1903	321	360	5		

- Molecule 18 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	125	Total	C	H	N	O	0	0
			2060	620	1076	191	173		

- Molecule 19 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	b	411	Total	C	H	N	O	S	0	0
			6718	2131	3385	573	612	17		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	e	125	Total	C	H	N	O	S	0	0
			2090	641	1081	203	164	1		

- Molecule 21 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 22 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	h	114	Total	C	H	N	O	S	0	0
			1969	592	1038	178	160	1		

- Molecule 23 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	i	74	Total	C	H	N	O	S	0	0
			1236	367	642	125	101	1		

- Molecule 24 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	j	71	Total	C	H	N	O	S	0	0
			1137	344	571	123	94	5		

- Molecule 25 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	r	73	Total	C	H	N	O	S	0	0
			1288	388	660	133	106	1		

- Molecule 26 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	u	116	Total	C	H	N	O	S	0	0
			1987	612	1011	200	155	9		

- Molecule 27 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	y	225	Total	C	H	N	O	S	0	0
			3398	1056	1697	295	343	7		

- Molecule 28 is ZINC ION (three-letter code: ZN) (formula: Zn).

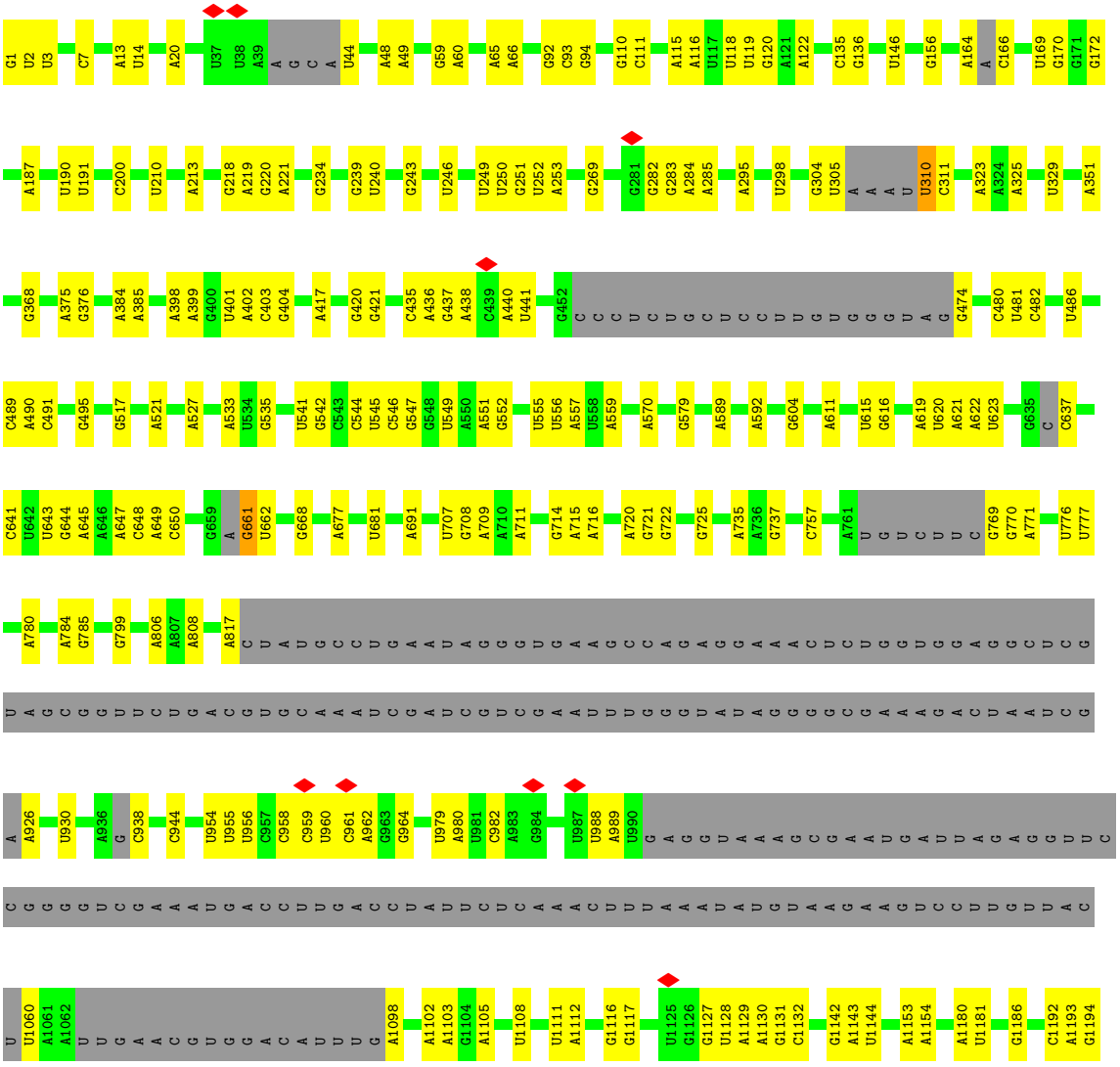
Mol	Chain	Residues	Atoms	AltConf
28	j	1	Total Zn 1 1	0
28	u	1	Total Zn 1 1	0

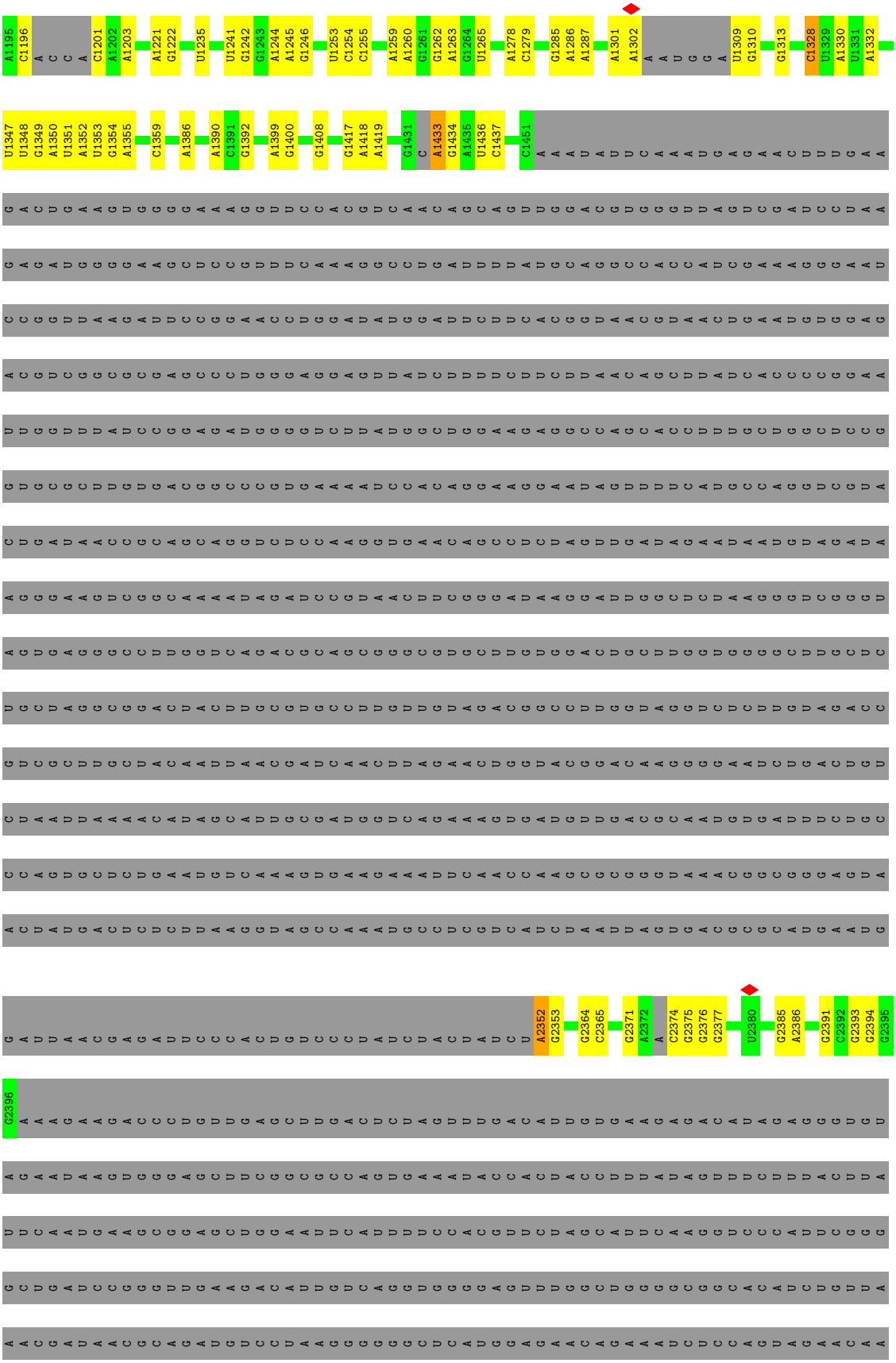
3 Residue-property plots (i)

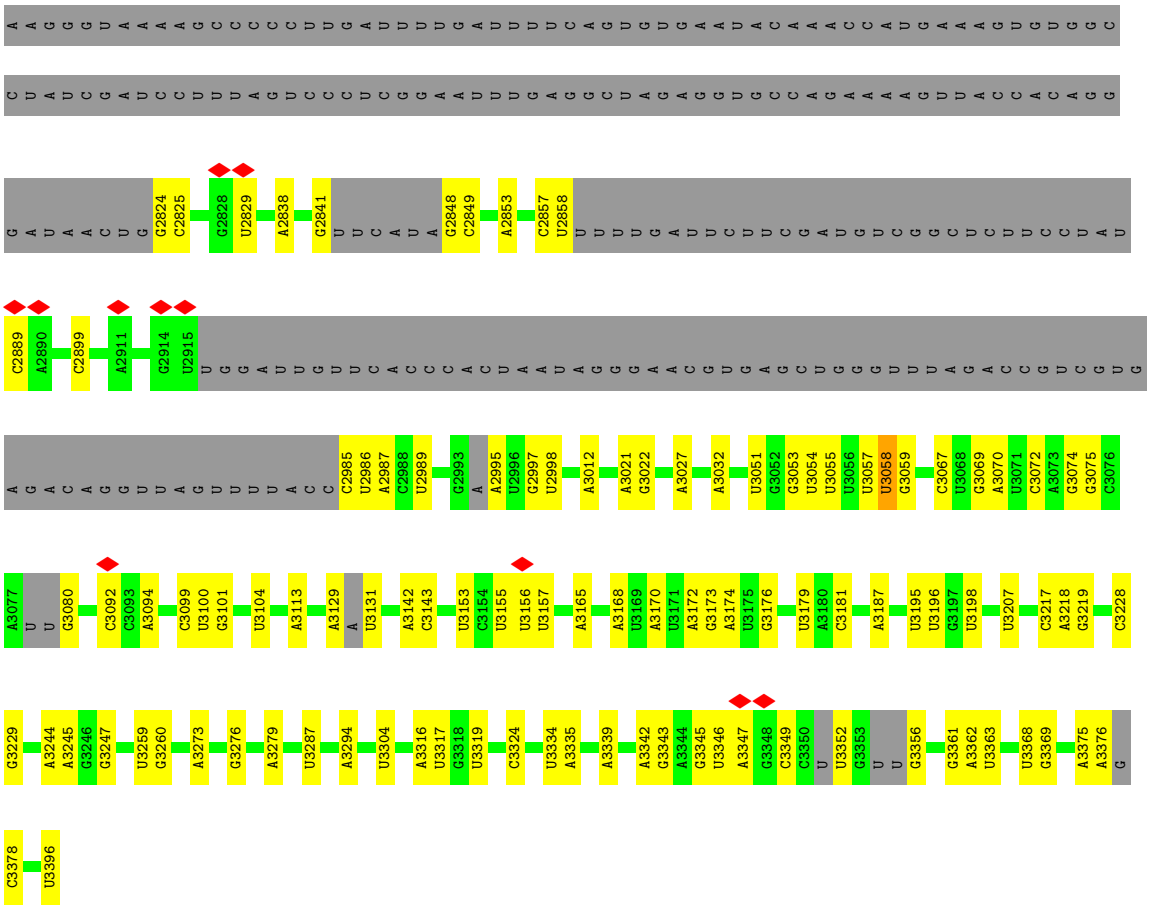
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 25S rRNA

Chain 1:

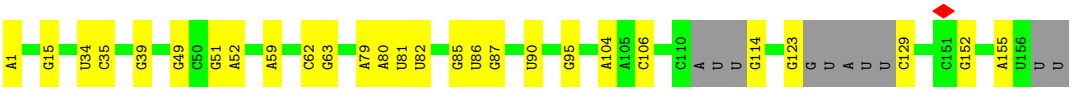






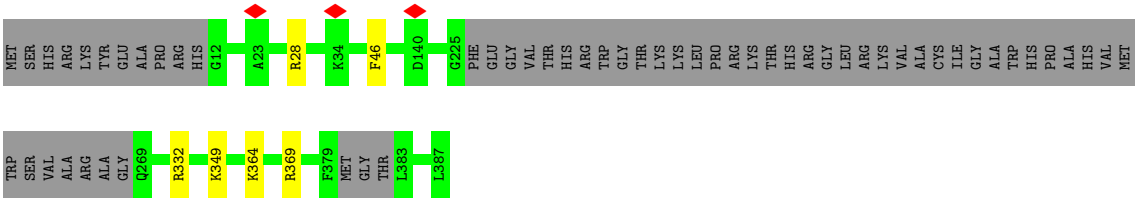
• Molecule 2: 5.8S rRNA

Chain 2:



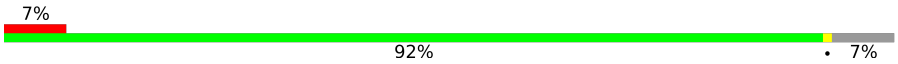
• Molecule 3: 60S ribosomal protein L3

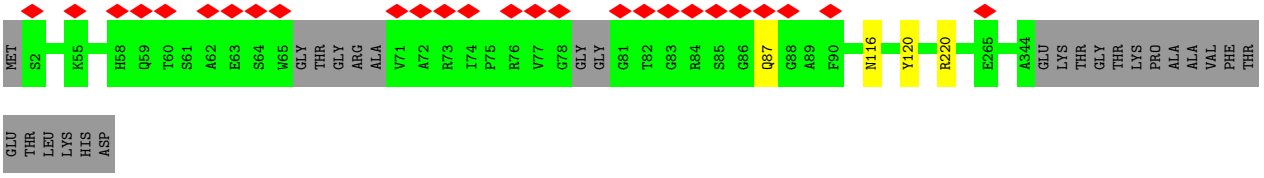
Chain B:



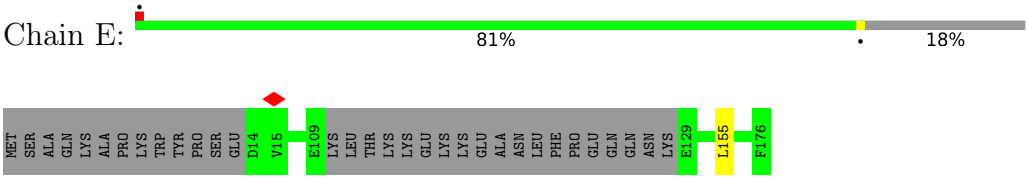
• Molecule 4: 60S ribosomal protein L4-A

Chain C:

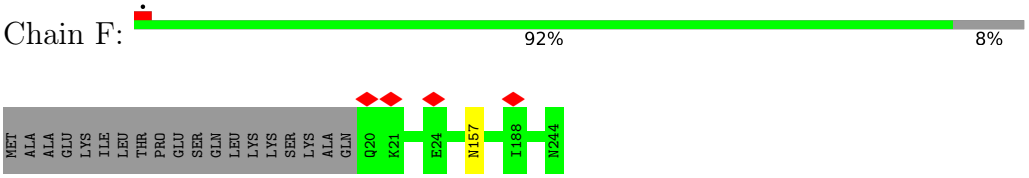




• Molecule 5: 60S ribosomal protein L6-A

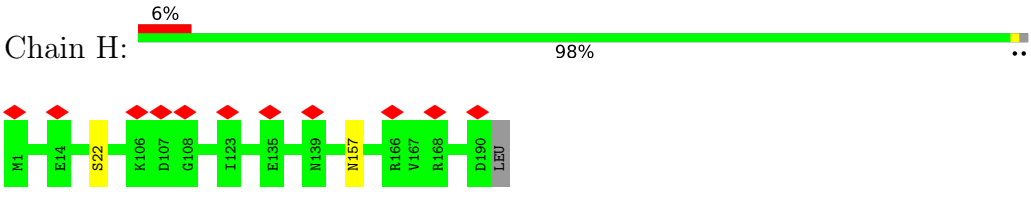


• Molecule 6: 60S ribosomal protein L7-A

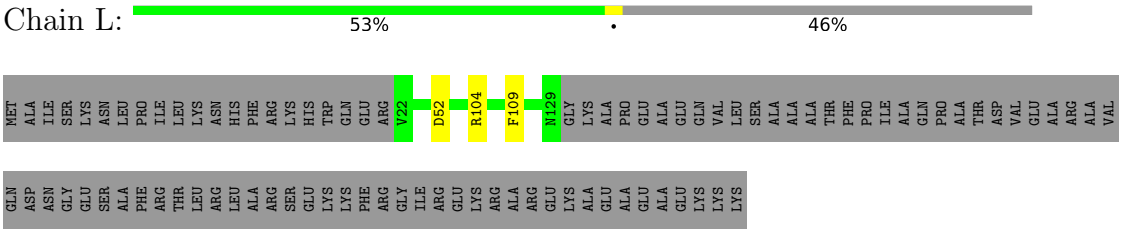


• Molecule 7: 60S ribosomal protein L8-A

• Molecule 8: 60S ribosomal protein L9-A

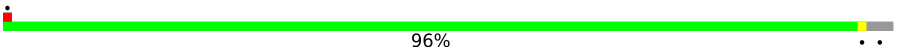


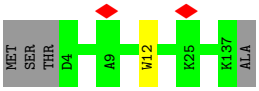
• Molecule 9: 60S ribosomal protein L13-A



• Molecule 10: 60S ribosomal protein L14-A

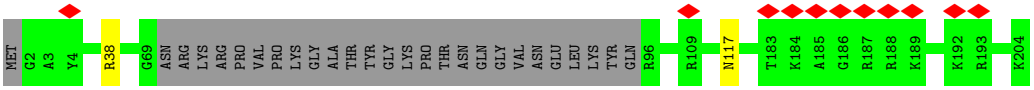
Chain M:





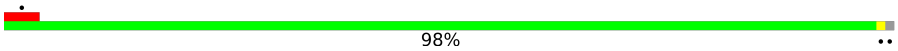
• Molecule 11: 60S ribosomal protein L15-A

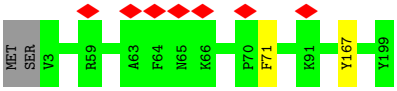
Chain N:



• Molecule 12: 60S ribosomal protein L16-A

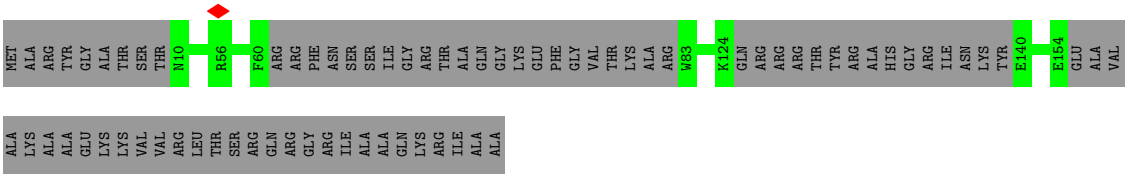
Chain O:





• Molecule 13: 60S ribosomal protein L17-A

Chain P:

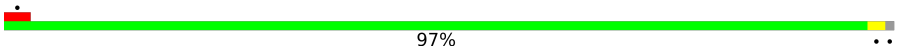


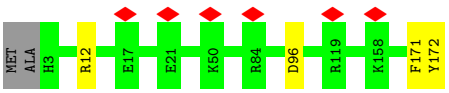
• Molecule 14: 60S ribosomal protein L18-A

Chain Q:

• Molecule 15: 60S ribosomal protein L20-A

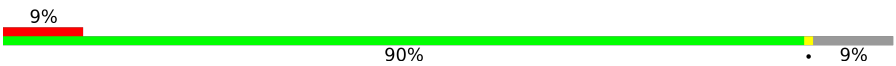
Chain S:

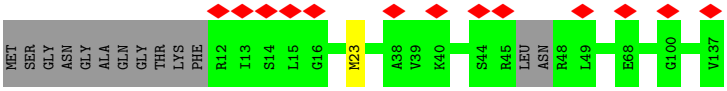




• Molecule 16: 60S ribosomal protein L23-A

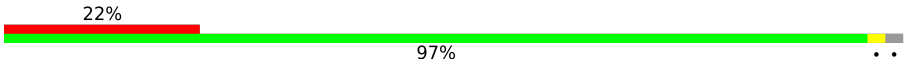
Chain V:

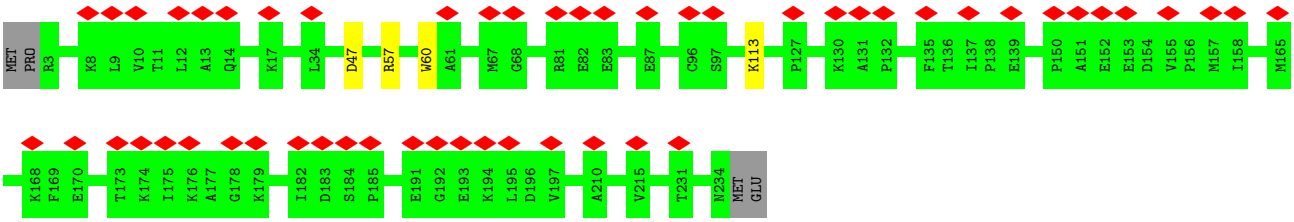




• Molecule 17: Ribosome assembly factor MRT4

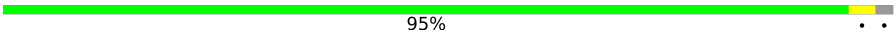
Chain W:

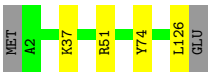




• Molecule 18: 60S ribosomal protein L26-A

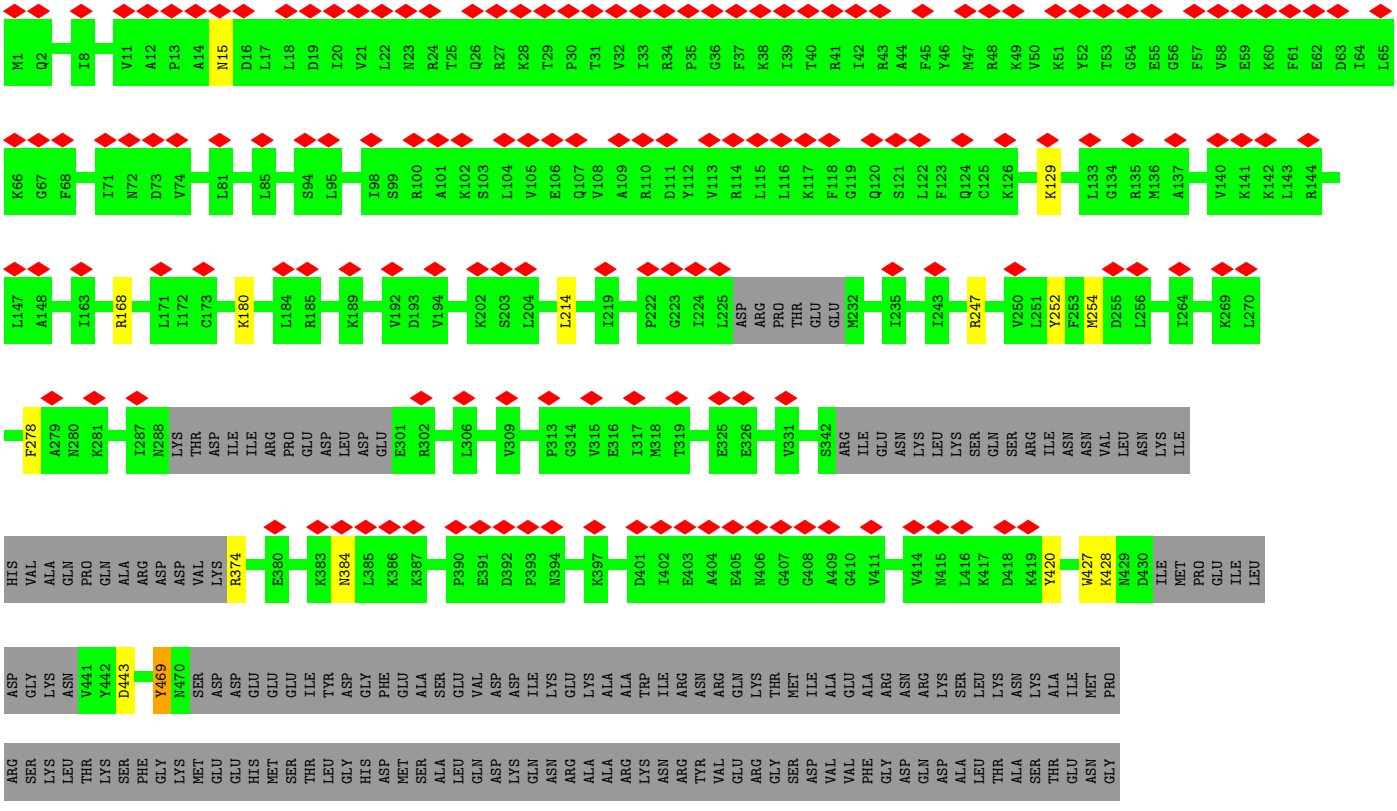
Chain Y:

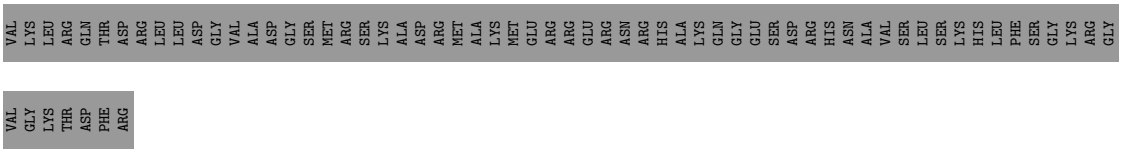




• Molecule 19: Nucleolar GTP-binding protein 1

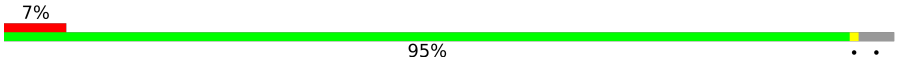
Chain b:

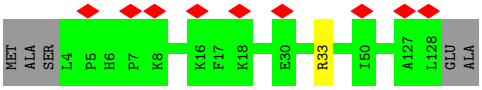




• Molecule 20: 60S ribosomal protein L32

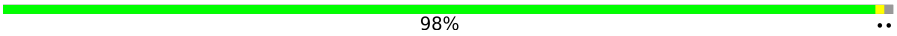
Chain e:

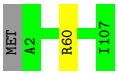




• Molecule 21: 60S ribosomal protein L33-A

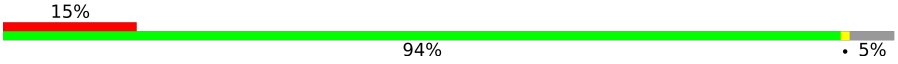
Chain f:

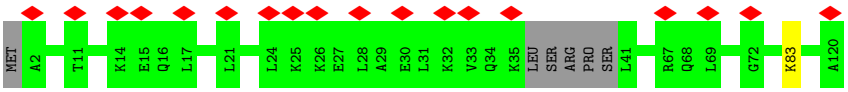




• Molecule 22: 60S ribosomal protein L35-A

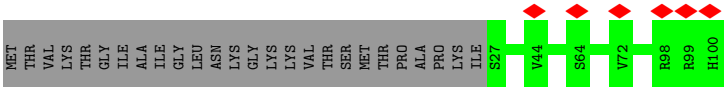
Chain h:





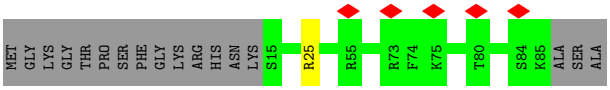
• Molecule 23: 60S ribosomal protein L36-A

Chain i:



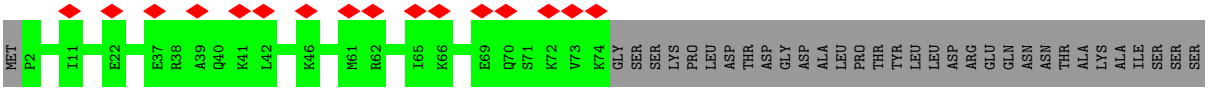
• Molecule 24: 60S ribosomal protein L37-A

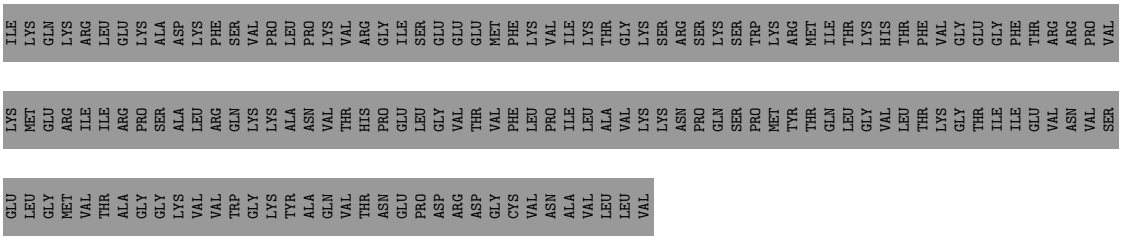
Chain j:



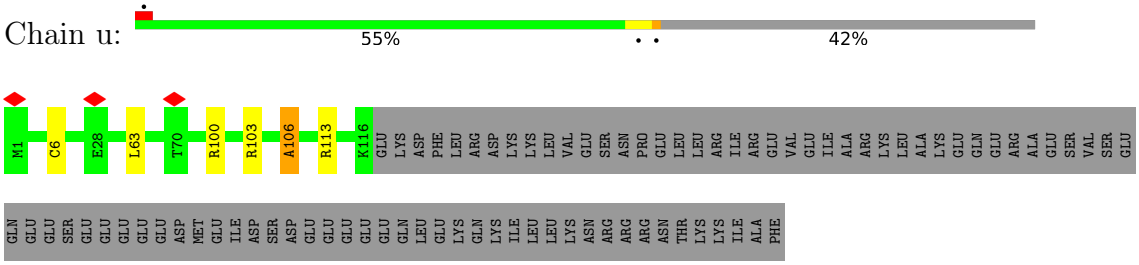
• Molecule 25: Ribosome biogenesis protein NSA2

Chain r:

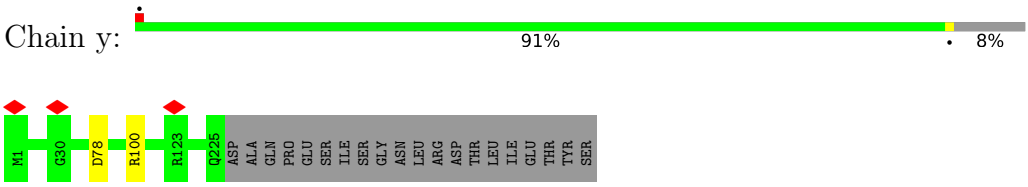




• Molecule 26: Ribosome biogenesis protein RLP24



• Molecule 27: Eukaryotic translation initiation factor 6



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48487	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 ($e^-/Å^2$)	86.45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.114	Depositor
Minimum map value	-0.031	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.021	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	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	1	0.16	0/40546	0.75	43/63168 (0.1%)
2	2	0.16	0/3514	0.76	4/5467 (0.1%)
3	B	0.24	0/2679	0.43	0/3598
4	C	0.24	0/2619	0.41	0/3544
5	E	0.24	0/1157	0.40	0/1553
6	F	0.24	0/1846	0.39	0/2484
7	G	0.24	0/1234	0.41	0/1671
8	H	0.23	0/1531	0.42	0/2062
9	L	0.24	0/877	0.40	0/1179
10	M	0.23	0/1056	0.39	0/1421
11	N	0.23	0/1544	0.39	0/2065
12	O	0.24	0/1585	0.39	0/2128
13	P	0.24	0/859	0.37	0/1160
14	Q	0.25	0/1024	0.41	0/1385
15	S	0.24	0/1468	0.41	0/1973
16	V	0.24	0/933	0.42	0/1254
17	W	0.23	0/1902	0.42	0/2564
18	Y	0.24	0/995	0.41	0/1329
19	b	2.02	6/3395 (0.2%)	0.42	1/4575 (0.0%)
20	e	0.23	0/1030	0.41	0/1379
21	f	0.25	0/868	0.43	0/1168
22	h	0.24	0/938	0.37	0/1245
23	i	0.24	0/599	0.38	0/793
24	j	0.24	0/578	0.42	0/767
25	r	0.23	0/638	0.36	0/837
26	u	0.38	1/996 (0.1%)	0.80	5/1324 (0.4%)
27	y	0.23	0/1722	0.44	0/2343
All	All	0.46	7/78133 (0.0%)	0.64	53/114436 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	1
26	u	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	b	469	TYR	CD2-CE2	65.71	2.38	1.39
19	b	469	TYR	CD1-CE1	62.55	2.33	1.39
19	b	469	TYR	CE2-CZ	43.94	1.95	1.38
19	b	469	TYR	CE1-CZ	40.76	1.91	1.38
19	b	469	TYR	CG-CD2	30.58	1.78	1.39

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	u	106	ALA	N-CA-CB	-16.41	87.12	110.10
26	u	106	ALA	CB-CA-C	12.52	128.88	110.10
26	u	106	ALA	O-C-N	-10.85	105.35	122.70
1	1	988	U	N3-C4-O4	-8.72	113.30	119.40
1	1	988	U	C5-C4-O4	7.25	130.25	125.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	22	SER	Peptide
26	u	106	ALA	Peptide

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	
3	B	324/387 (84%)	307 (95%)	17 (5%)	0	100	100
4	C	330/362 (91%)	310 (94%)	20 (6%)	0	100	100
5	E	140/176 (80%)	137 (98%)	3 (2%)	0	100	100
6	F	223/244 (91%)	214 (96%)	9 (4%)	0	100	100
7	G	152/256 (59%)	147 (97%)	5 (3%)	0	100	100
8	H	188/191 (98%)	181 (96%)	7 (4%)	0	100	100
9	L	106/199 (53%)	100 (94%)	6 (6%)	0	100	100
10	M	132/138 (96%)	131 (99%)	1 (1%)	0	100	100
11	N	173/204 (85%)	171 (99%)	2 (1%)	0	100	100
12	O	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
13	P	102/184 (55%)	102 (100%)	0	0	100	100
14	Q	129/186 (69%)	129 (100%)	0	0	100	100
15	S	168/172 (98%)	157 (94%)	11 (6%)	0	100	100
16	V	120/137 (88%)	118 (98%)	2 (2%)	0	100	100
17	W	230/236 (98%)	224 (97%)	6 (3%)	0	100	100
18	Y	123/127 (97%)	123 (100%)	0	0	100	100
19	b	401/647 (62%)	383 (96%)	18 (4%)	0	100	100
20	e	123/130 (95%)	121 (98%)	2 (2%)	0	100	100
21	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
22	h	110/120 (92%)	107 (97%)	3 (3%)	0	100	100
23	i	72/100 (72%)	67 (93%)	5 (7%)	0	100	100
24	j	69/88 (78%)	69 (100%)	0	0	100	100
25	r	71/261 (27%)	63 (89%)	8 (11%)	0	100	100
26	u	114/199 (57%)	105 (92%)	9 (8%)	0	100	100
27	y	223/245 (91%)	217 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	4122/5295 (78%)	3977 (96%)	145 (4%)	0	100 100

There are no Ramachandran outliers to report.

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
3	B	278/323 (86%)	272 (98%)	6 (2%)	52 72
4	C	271/289 (94%)	267 (98%)	4 (2%)	65 81
5	E	124/153 (81%)	123 (99%)	1 (1%)	81 89
6	F	189/205 (92%)	188 (100%)	1 (0%)	88 94
7	G	127/208 (61%)	125 (98%)	2 (2%)	62 80
8	H	170/171 (99%)	169 (99%)	1 (1%)	86 93
9	L	87/159 (55%)	84 (97%)	3 (3%)	37 64
10	M	106/109 (97%)	105 (99%)	1 (1%)	78 88
11	N	153/176 (87%)	151 (99%)	2 (1%)	69 83
12	O	160/162 (99%)	158 (99%)	2 (1%)	69 83
13	P	89/146 (61%)	89 (100%)	0	100 100
14	Q	107/151 (71%)	106 (99%)	1 (1%)	78 88
15	S	155/156 (99%)	151 (97%)	4 (3%)	46 69
16	V	96/105 (91%)	95 (99%)	1 (1%)	76 86
17	W	209/213 (98%)	205 (98%)	4 (2%)	57 76
18	Y	108/110 (98%)	104 (96%)	4 (4%)	34 61
19	b	368/573 (64%)	352 (96%)	16 (4%)	29 58
20	e	108/111 (97%)	107 (99%)	1 (1%)	78 88
21	f	90/91 (99%)	89 (99%)	1 (1%)	73 85
22	h	99/105 (94%)	98 (99%)	1 (1%)	76 86
23	i	61/82 (74%)	61 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
24	j	59/71 (83%)	58 (98%)	1 (2%)	60 79
25	r	65/229 (28%)	65 (100%)	0	100 100
26	u	101/180 (56%)	96 (95%)	5 (5%)	24 55
27	y	193/211 (92%)	191 (99%)	2 (1%)	76 86
All	All	3573/4489 (80%)	3509 (98%)	64 (2%)	61 77

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	u	6	CYS
26	u	100	ARG
15	S	12	ARG
14	Q	145	ASN
26	u	103	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
19	b	217	GLN
27	y	83	HIS
8	H	51	GLN
11	N	182	ASN
11	N	195	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1669/3396 (49%)	337 (20%)	35 (2%)
2	2	145/158 (91%)	24 (16%)	0
All	All	1814/3554 (51%)	361 (19%)	35 (1%)

5 of 361 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	3	U
1	1	7	C
1	1	14	U
1	1	20	A

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2857	C
1	1	2986	U
1	1	3218	A
1	1	649	A
1	1	644	G

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 (i)

Of 2 ligands modelled in this entry, 2 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.

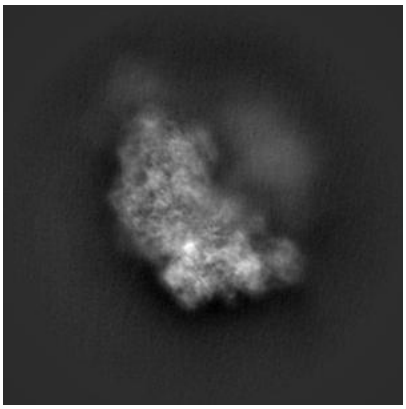
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12909. These allow visual inspection of the internal detail of the map and identification of artifacts.

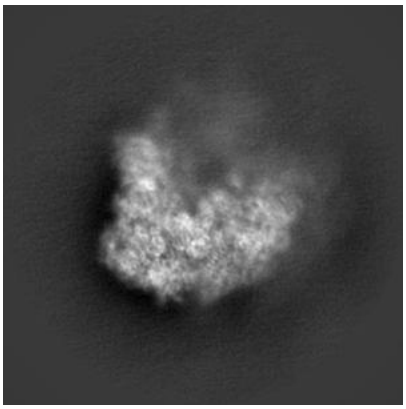
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

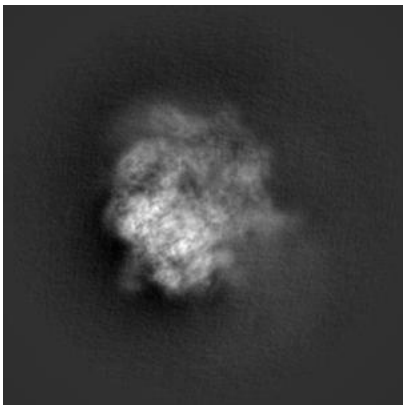
6.1.1 Primary map



X

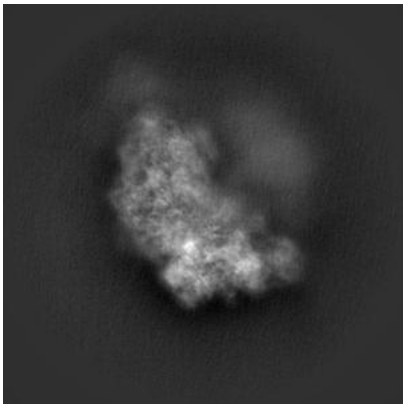


Y

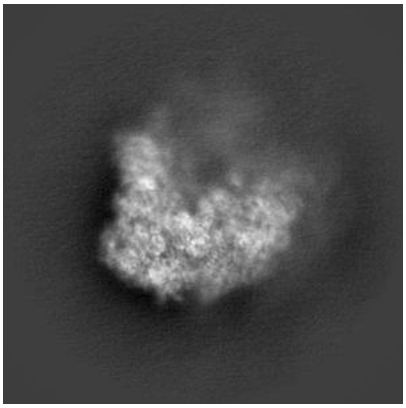


Z

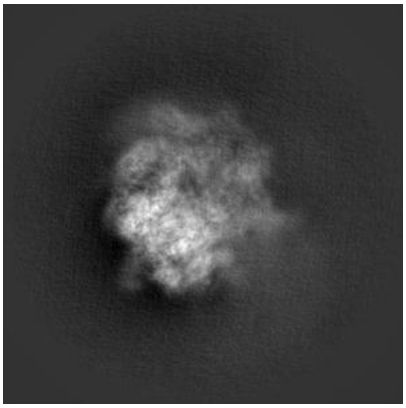
6.1.2 Raw map



X



Y

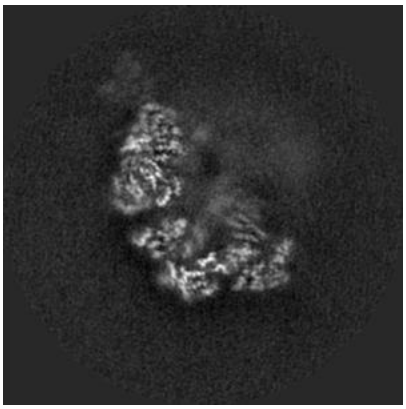


Z

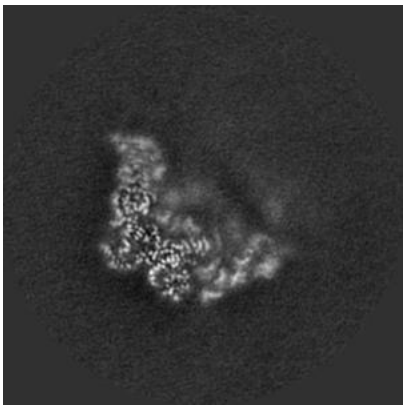
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

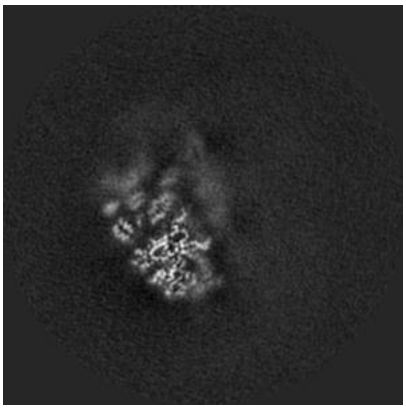
6.2.1 Primary map



X Index: 200

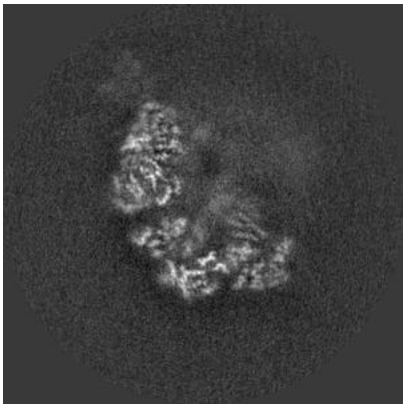


Y Index: 200

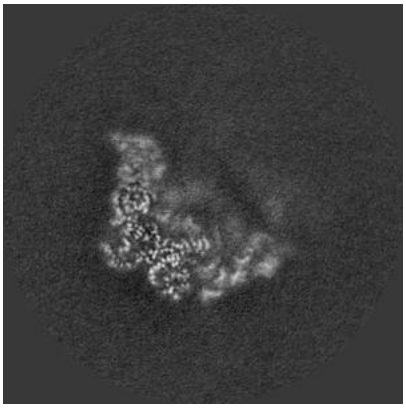


Z Index: 200

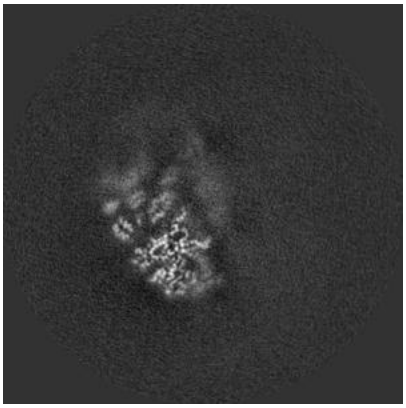
6.2.2 Raw map



X Index: 200



Y Index: 200

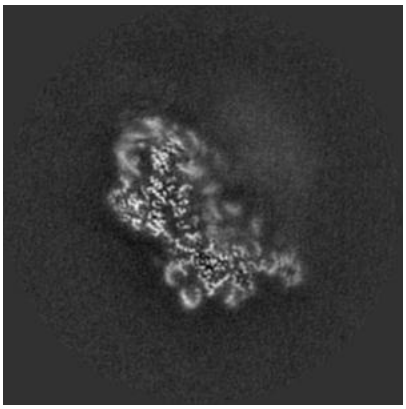


Z Index: 200

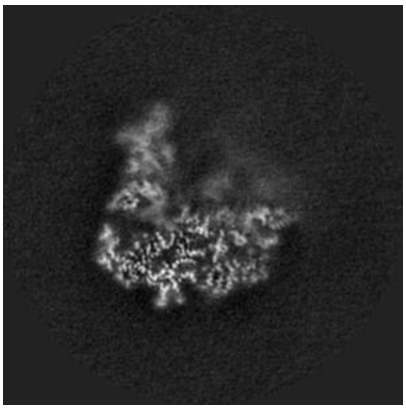
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

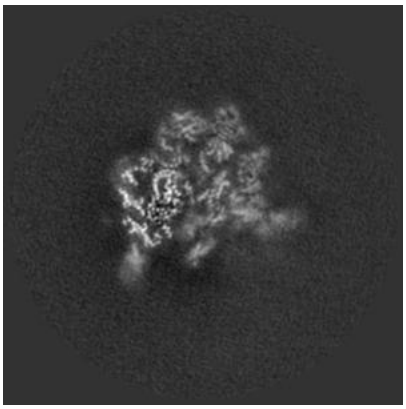
6.3.1 Primary map



X Index: 169

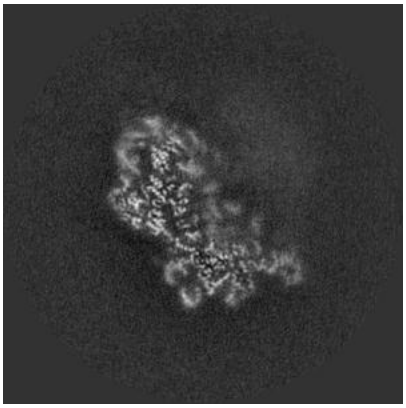


Y Index: 184

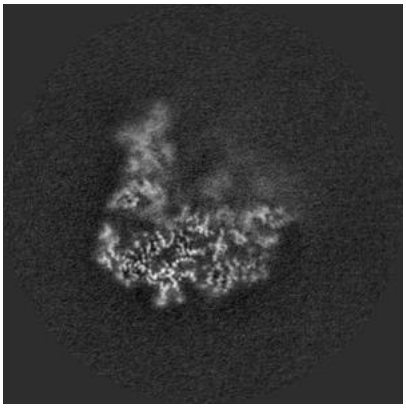


Z Index: 150

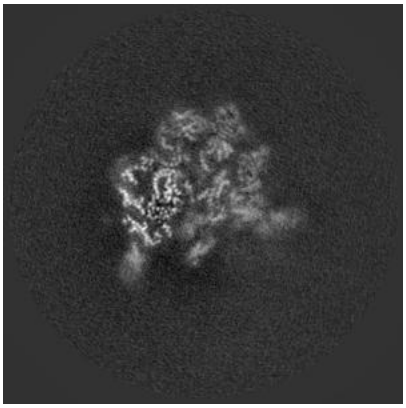
6.3.2 Raw map



X Index: 169



Y Index: 184



Z Index: 150

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

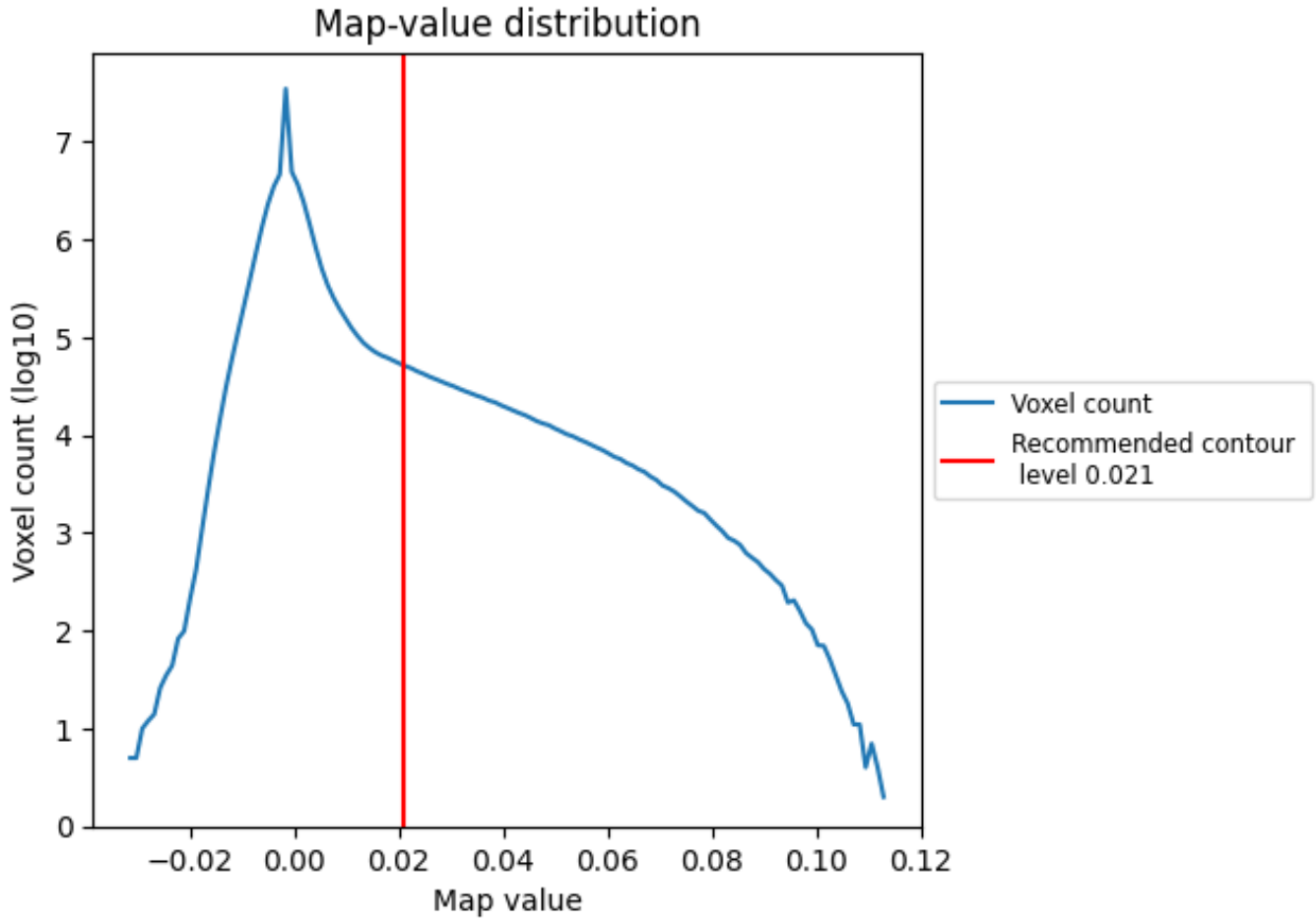
6.5 Mask visualisation (i)

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

7 Map analysis

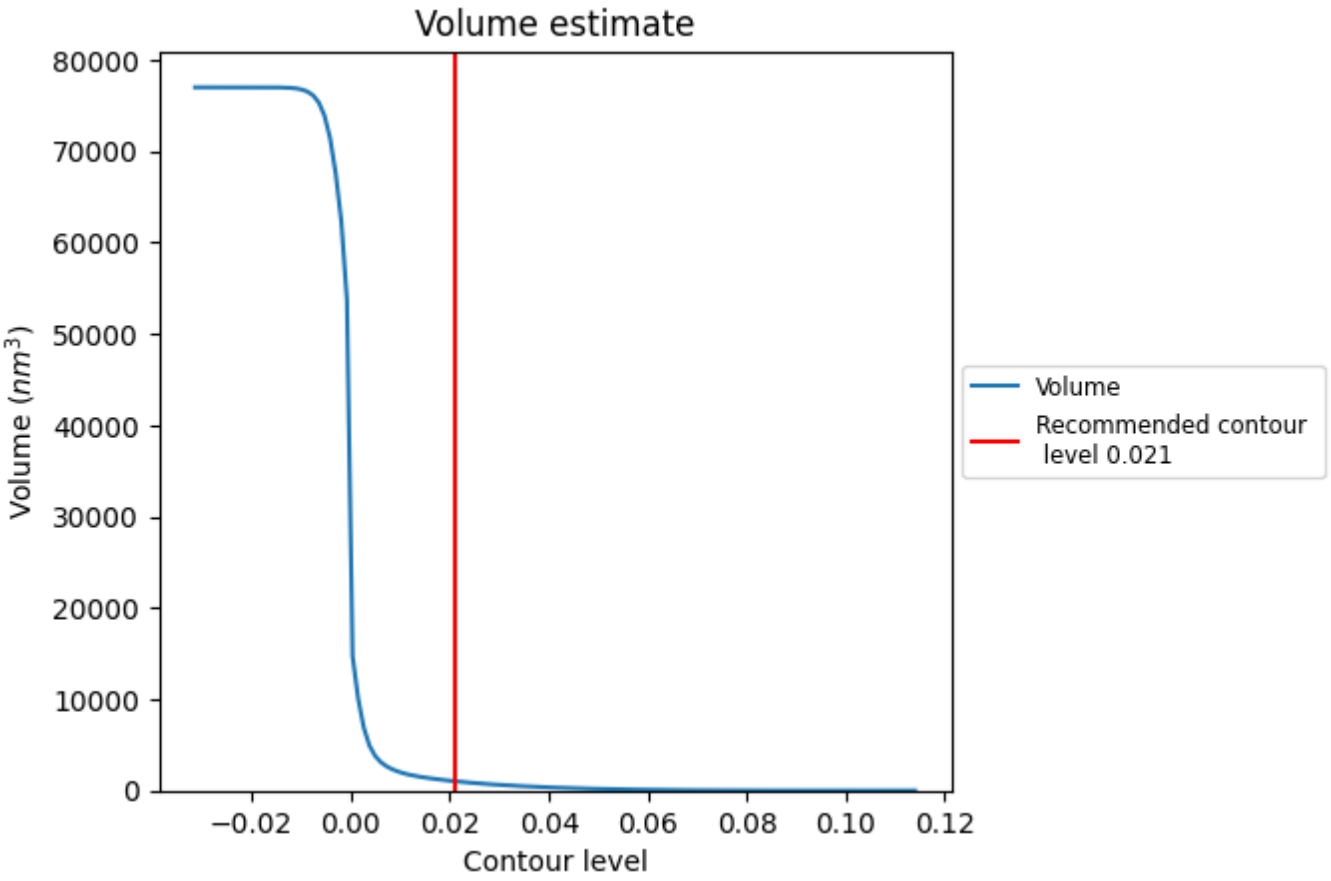
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

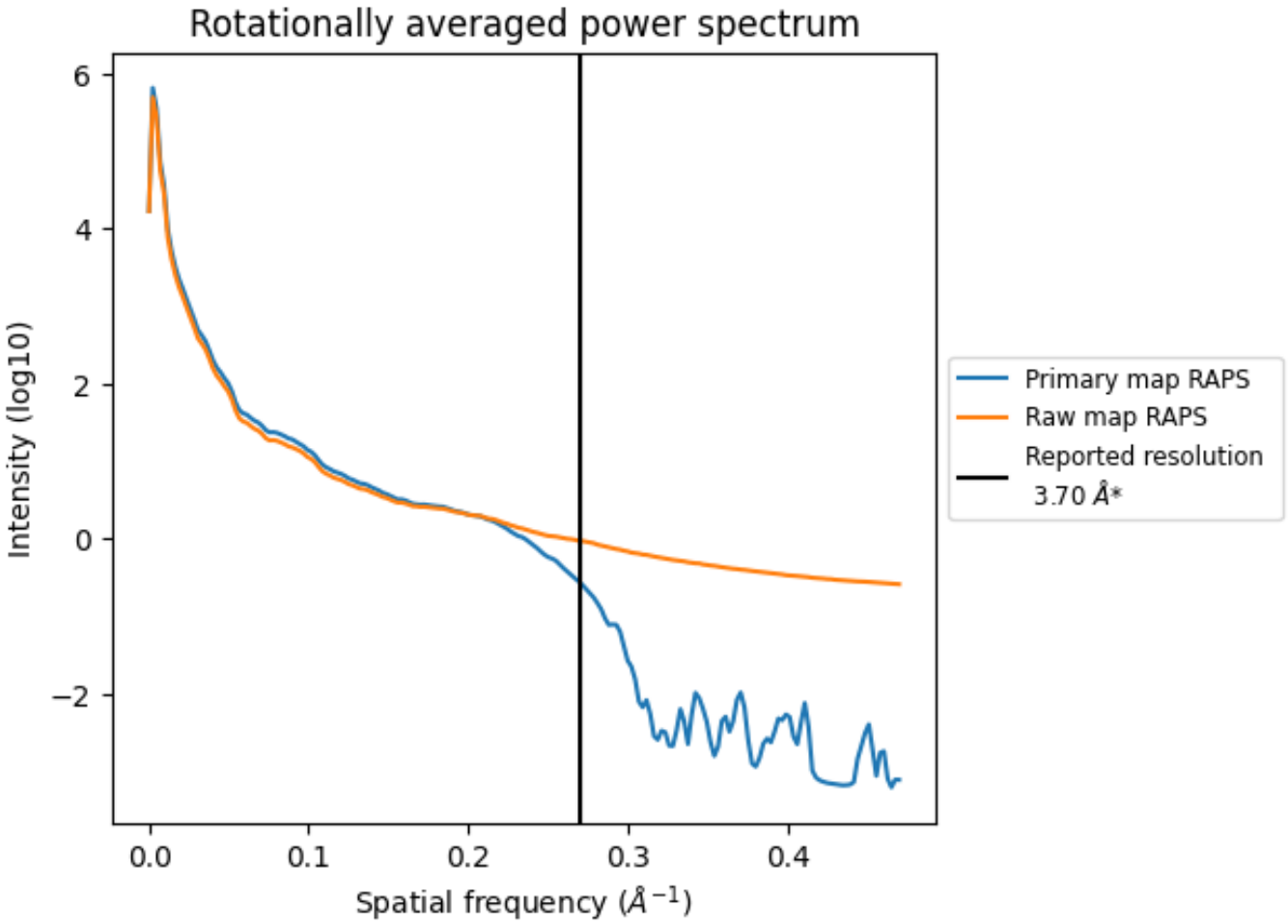
7.2 Volume estimate (i)



The volume at the recommended contour level is 1023 nm^3; this corresponds to an approximate mass of 924 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)

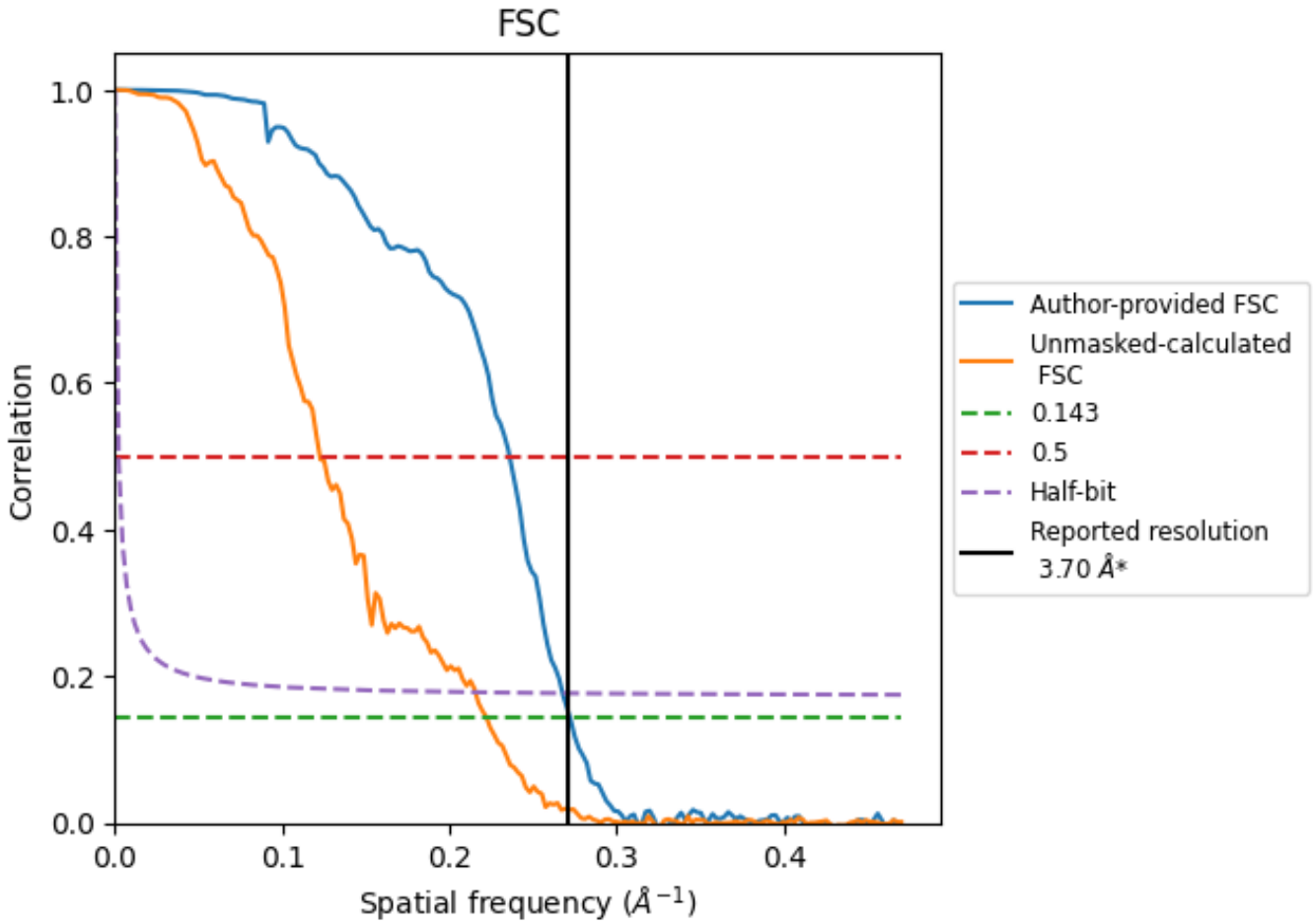


*Reported resolution corresponds to spatial frequency of 0.270 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

8.2 Resolution estimates (i)

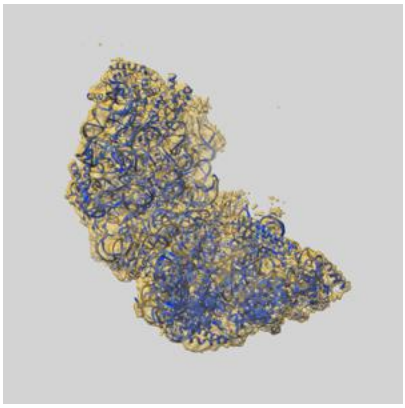
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.68	4.24	3.74
Unmasked-calculated*	4.50	8.16	4.64

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.50 differs from the reported value 3.7 by more than 10 %

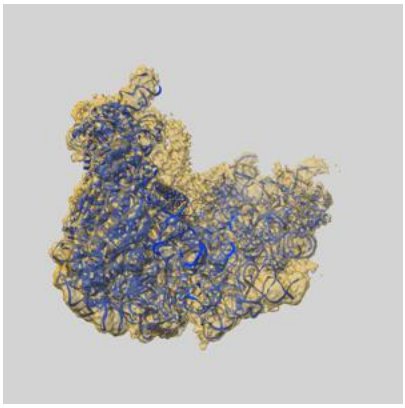
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12909 and PDB model 7OHU. Per-residue inclusion information can be found in section 3 on page 9.

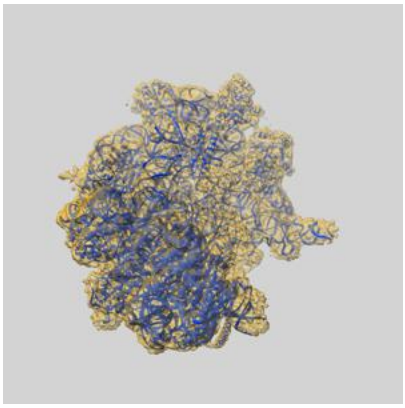
9.1 Map-model overlay



X



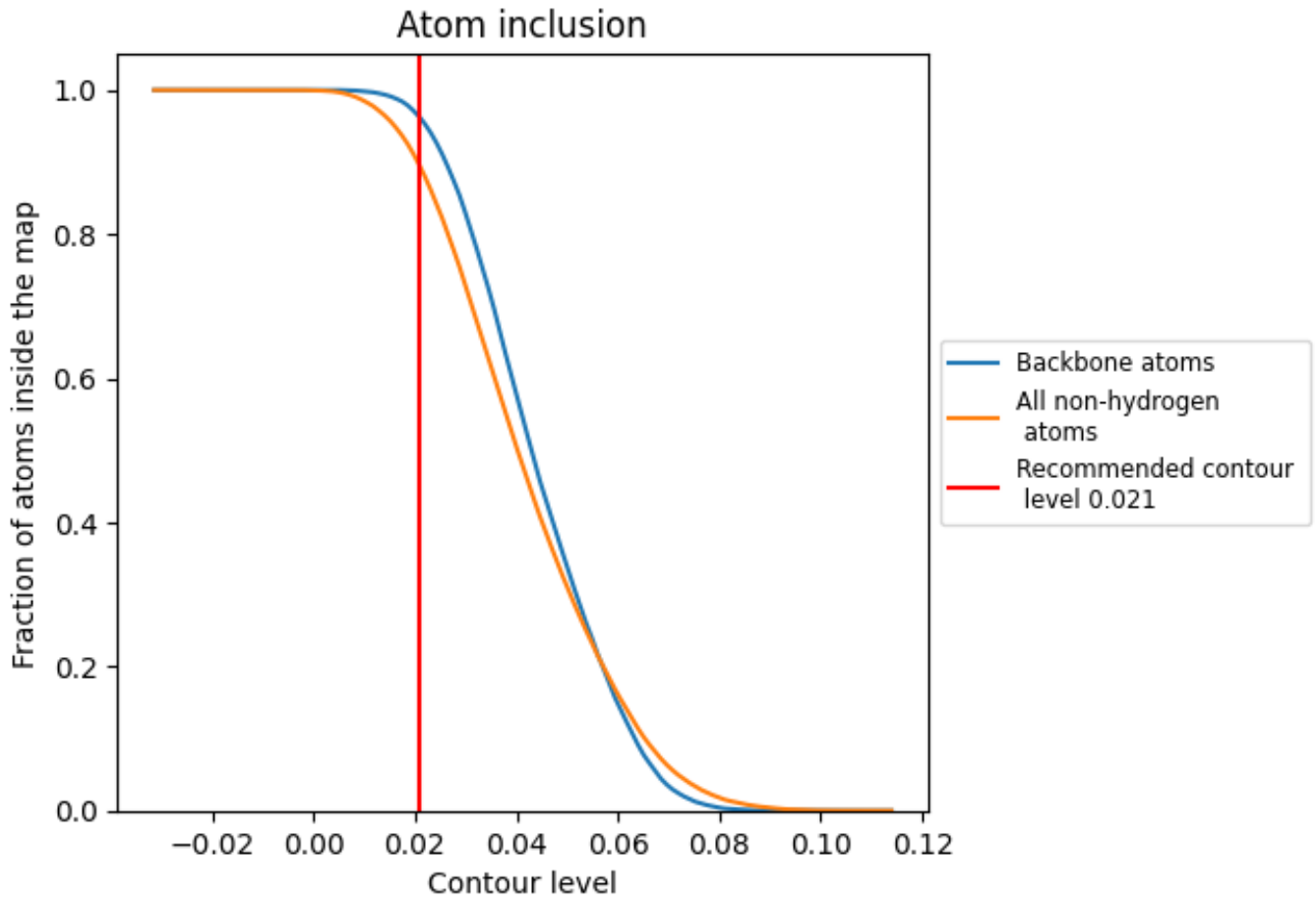
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.021 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 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.