



## wwPDB EM Validation Summary Report ⓘ

Apr 4, 2023 – 07:44 pm BST

PDB ID : 8C00  
EMDB ID : EMD-16347  
Title : Enp1TAP-S21\_A population of yeast small ribosomal subunit precursors depleted of rpS21/eS21  
Authors : Milkereit, P.; Poell, G.  
Deposited on : 2022-12-15  
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

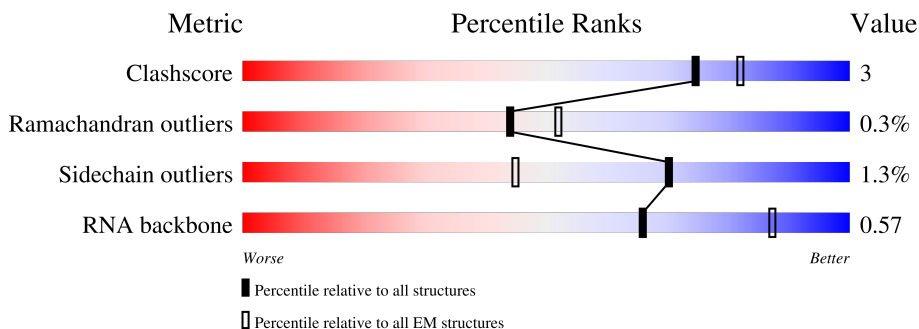
EMDB validation analysis : 0.0.1.dev50  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.2

# 1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 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.




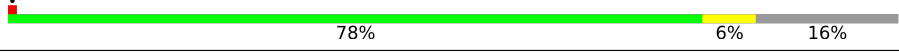
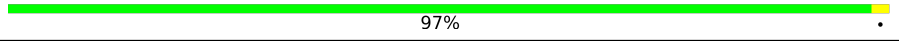
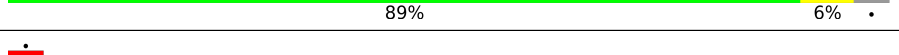
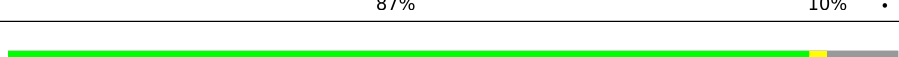
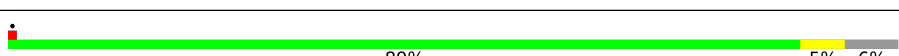

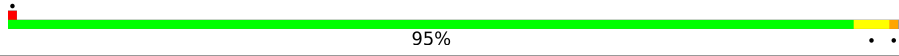
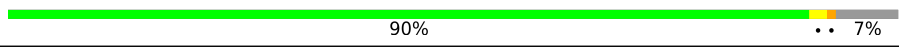
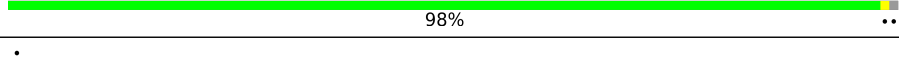
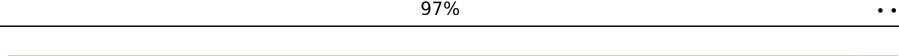
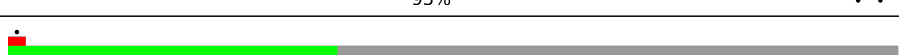
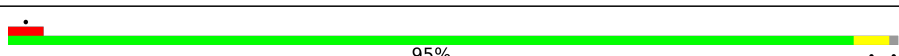






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	1800	57% 19% • 21%
2	B	225	82% 8% 11%
3	E	142	7% 77% • 20%
4	F	143	81% 6% 13%
5	H	146	74% 10% 16%
6	I	144	91% 7% •
7	K	108	56% 8% 36%

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Mol	Chain	Length	Quality of chain
8	L	67	 81% 9% 10%
9	Q	255	 78% 6% 16%
10	S	261	 97%
11	T	236	 89% 6%
12	U	190	 87% 10%
13	V	200	 90% 8%
14	W	197	 89% 5% 6%
15	X	156	 88% 10%
16	Y	151	 95%
17	Z	137	 90% 7%
18	b	130	 98%
19	c	145	 97%
20	d	135	 95%
21	e	483	 37% 63%
22	f	82	 95%
23	g	63	 46% 52%
24	p	274	 65% 34%
25	r	425	 11% 44% 55%
26	t	788	 6% 78% 21%

## 2 Entry composition [i](#)

There are 26 unique types of molecules in this entry. The entry contains 63117 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 18S rRNA precursor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1425	30408	13596	5424	9963	1425	0	0

- Molecule 2 is a protein called rpS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	201	1588	996	295	294	3	0	0

- Molecule 3 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	114	902	575	167	153	7	0	0

- Molecule 4 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	F	125	973	625	174	174	0	0

- Molecule 5 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	H	122	1009	636	193	178	2	0	0

- Molecule 6 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	I	141	1096	684	206	204	2	0	0

- Molecule 7 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	K	69	556	356	103	97	0	0

- Molecule 8 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L	60	471	290	93	87	1	0	0

- Molecule 9 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	Q	214	1709	1084	310	311	4	0	0

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	S	260	2068	1316	389	360	3	0	0

- Molecule 11 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	T	226	1813	1137	350	323	3	0	0

- Molecule 12 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	U	184	1481	951	265	265	0	0

- Molecule 13 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	V	185	1462	907	292	261	2	0	0

- Molecule 14 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	W	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 15 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	141	Total	C	N	O	S	0	0
			1137	730	216	188	3		

- Molecule 16 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 17 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Z	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 18 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 19 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 20 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	d	130	Total	C	N	O	0	0
			1046	662	203	181		

- Molecule 21 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	e	179	Total	C	N	O	0	0
			796	431	183	182		

- Molecule 22 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 23 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	30	Total	C	N	O	S	0	0
			257	164	55	37	1		

- Molecule 24 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	180	Total	C	N	O	S	0	0
			1425	911	257	253	4		

- Molecule 25 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	190	Total	C	N	O	S	0	0
			1574	1014	268	278	14		

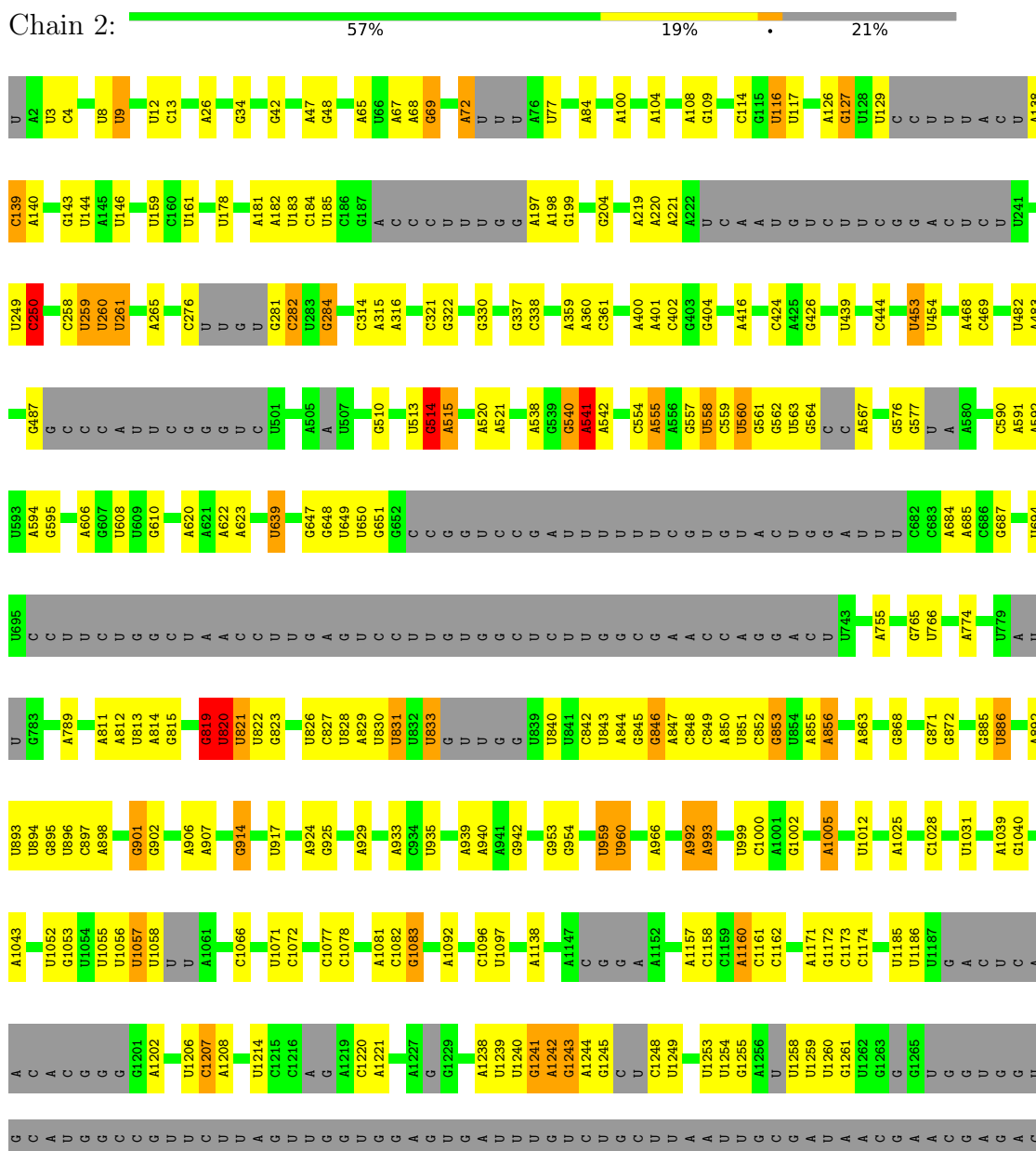
- Molecule 26 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	t	619	Total	C	N	O	S	0	0
			4982	3199	873	897	13		

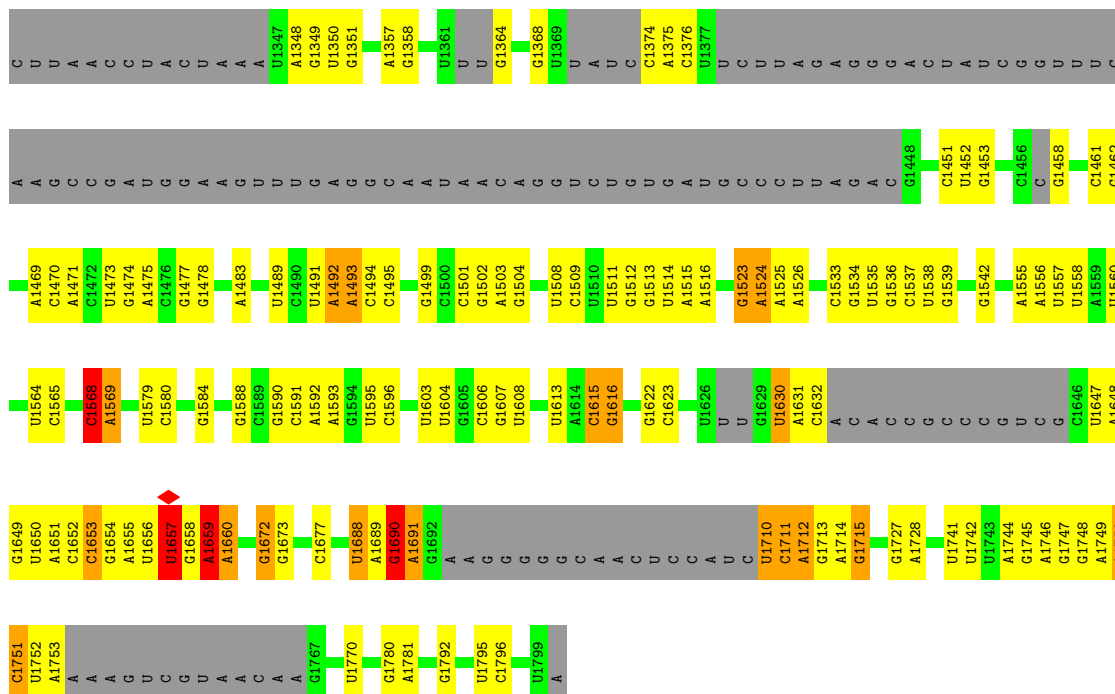
### 3 Residue-property plots

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.

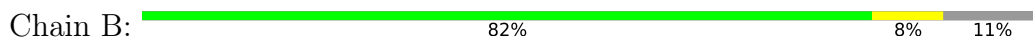
- Molecule 1: 18S rRNA precursor



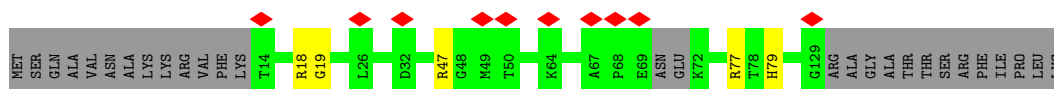
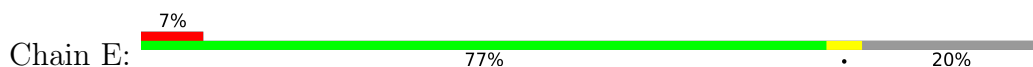




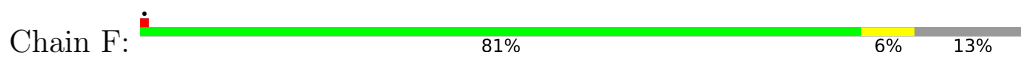
• Molecule 2: rpS5



• Molecule 3: 40S ribosomal protein S15



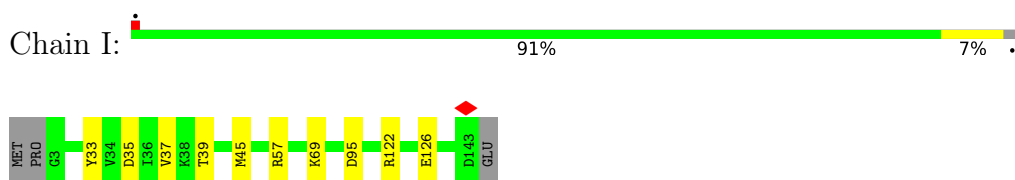
• Molecule 4: 40S ribosomal protein S16-A



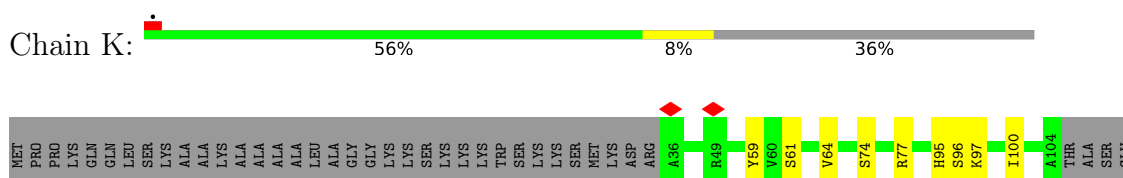
• Molecule 5: 40S ribosomal protein S18-A



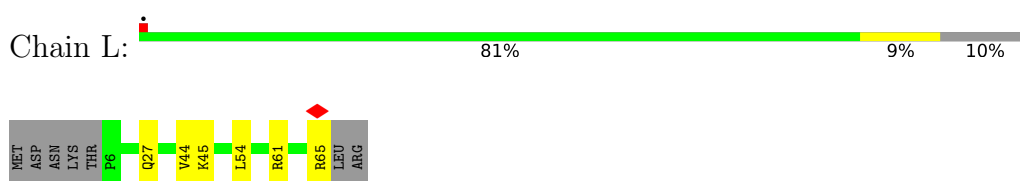
- Molecule 6: 40S ribosomal protein S19-A



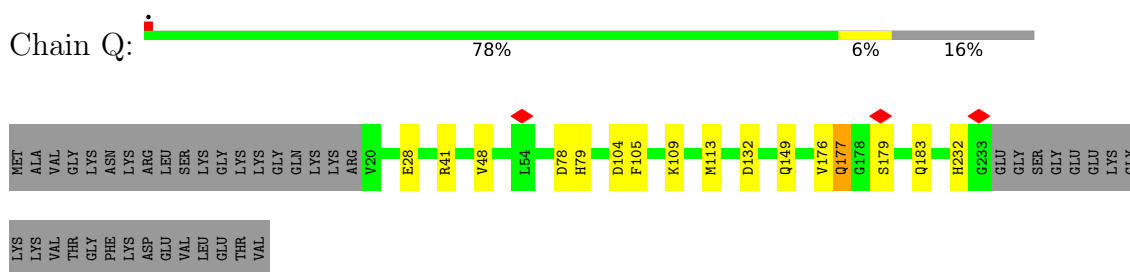
- Molecule 7: 40S ribosomal protein S25-A



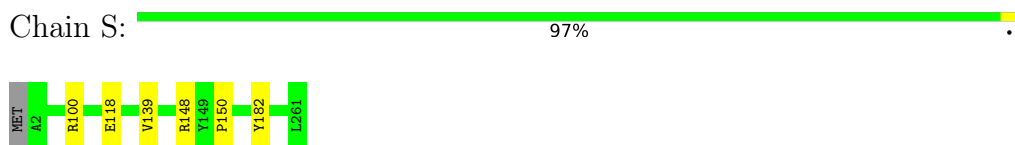
- Molecule 8: 40S ribosomal protein S28-A



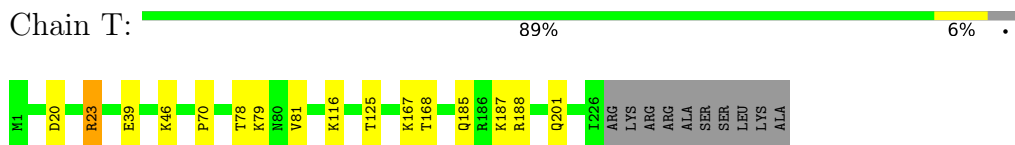
- Molecule 9: 40S ribosomal protein S1-A



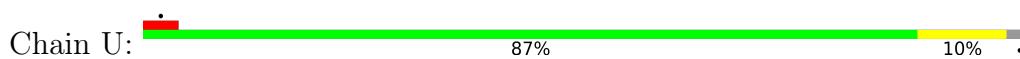
- Molecule 10: 40S ribosomal protein S4-A



- Molecule 11: 40S ribosomal protein S6-A



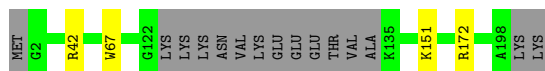
- Molecule 12: 40S ribosomal protein S7-A





- Molecule 13: 40S ribosomal protein S8-A

Chain V: 90% 8%



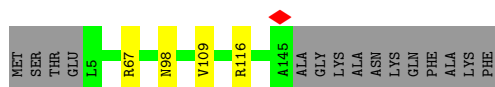
- Molecule 14: 40S ribosomal protein S9-A

Chain W: 89% 5% 6%



- Molecule 15: 40S ribosomal protein S11-A

Chain X: 88% 5% 10%



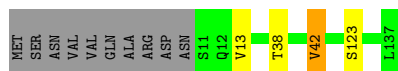
- Molecule 16: 40S ribosomal protein S13

Chain Y: 95% 5% 2%



- Molecule 17: 40S ribosomal protein S14-A

Chain Z: 90% 5% 7%



- Molecule 18: 40S ribosomal protein S22-A

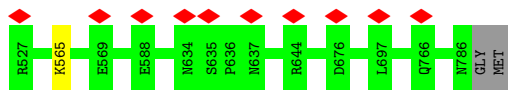
Chain b: 98% 2% 2%



- Molecule 19: 40S ribosomal protein S23-A







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	132563	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 200	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	50000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.048	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	387.2, 387.2, 387.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.96800005, 0.96800005, 0.96800005	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	2	0.79	0/33998	1.01	55/52913 (0.1%)
2	B	0.28	0/1607	0.55	0/2172
3	E	0.29	0/921	0.54	0/1236
4	F	0.30	0/990	0.53	0/1335
5	H	0.28	0/1027	0.54	0/1383
6	I	0.30	0/1113	0.56	0/1494
7	K	0.26	0/564	0.51	0/758
8	L	0.30	0/473	0.64	0/634
9	Q	0.33	0/1735	0.57	0/2335
10	S	0.43	0/2109	0.61	0/2839
11	T	0.36	0/1837	0.60	0/2455
12	U	0.33	0/1506	0.56	0/2028
13	V	0.43	0/1487	0.64	0/1988
14	W	0.41	0/1519	0.60	0/2035
15	X	0.47	0/1163	0.58	0/1568
16	Y	0.40	0/1215	0.56	0/1638
17	Z	0.34	0/937	0.62	0/1261
18	b	0.44	0/1038	0.58	0/1395
19	c	0.38	0/1139	0.58	0/1518
20	d	0.43	0/1060	0.58	0/1412
21	e	0.23	0/807	0.42	0/1025
22	f	0.35	0/620	0.54	0/838
23	g	0.43	0/262	0.64	0/346
24	p	0.32	0/1451	0.57	0/1955
25	r	0.26	0/1605	0.50	0/2141
26	t	0.28	0/5092	0.52	0/6868
All	All	0.61	0/67275	0.84	55/97570 (0.1%)

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
6	I	0	1
9	Q	0	1
10	S	0	1
16	Y	0	1
26	t	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	453	U	C2-N1-C1'	8.69	128.13	117.70
1	2	558	U	C2-N1-C1'	8.40	127.78	117.70
1	2	1657	U	C2-N1-C1'	8.34	127.71	117.70
1	2	1659	A	O4'-C1'-N9	7.88	114.51	108.20
1	2	514	G	P-O3'-C3'	7.85	129.12	119.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	I	57	ARG	Sidechain
9	Q	132	ASP	Peptide
10	S	148	ARG	Sidechain
16	Y	3	ARG	Sidechain
26	t	253	ARG	Sidechain

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

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	30408	0	15313	243	0
2	B	1588	0	1657	9	0
3	E	902	0	934	5	0
4	F	973	0	1029	3	0
5	H	1009	0	1029	8	0
6	I	1096	0	1110	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	K	556	0	596	5	0
8	L	471	0	505	4	0
9	Q	1709	0	1784	8	0
10	S	2068	0	2154	2	0
11	T	1813	0	1905	11	0
12	U	1481	0	1572	10	0
13	V	1462	0	1486	3	0
14	W	1494	0	1573	5	0
15	X	1137	0	1207	0	0
16	Y	1192	0	1255	4	0
17	Z	926	0	950	2	0
18	b	1021	0	1060	0	0
19	c	1121	0	1196	0	0
20	d	1046	0	1112	0	0
21	e	796	0	296	0	0
22	f	610	0	633	0	0
23	g	257	0	281	0	0
24	p	1425	0	1502	0	0
25	r	1574	0	1545	0	0
26	t	4982	0	4954	0	0
All	All	63117	0	48638	298	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 298 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1690:G:H21	1:2:1712:A:N6	1.52	1.05
1:2:1690:G:N2	1:2:1712:A:H61	1.57	1.02
1:2:1588:G:H1	1:2:1608:U:H3	1.03	0.94
1:2:1690:G:H21	1:2:1712:A:H61	0.90	0.89
1:2:1081:A:N3	1:2:1082:C:N4	2.28	0.80

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	197/225 (88%)	189 (96%)	7 (4%)	1 (0%)	29	61
3	E	110/142 (78%)	102 (93%)	8 (7%)	0	100	100
4	F	123/143 (86%)	115 (94%)	7 (6%)	1 (1%)	19	51
5	H	120/146 (82%)	110 (92%)	10 (8%)	0	100	100
6	I	139/144 (96%)	136 (98%)	2 (1%)	1 (1%)	22	54
7	K	67/108 (62%)	64 (96%)	2 (3%)	1 (2%)	10	34
8	L	58/67 (87%)	55 (95%)	3 (5%)	0	100	100
9	Q	212/255 (83%)	208 (98%)	4 (2%)	0	100	100
10	S	258/261 (99%)	250 (97%)	8 (3%)	0	100	100
11	T	224/236 (95%)	219 (98%)	4 (2%)	1 (0%)	34	66
12	U	182/190 (96%)	172 (94%)	9 (5%)	1 (0%)	29	61
13	V	181/200 (90%)	175 (97%)	6 (3%)	0	100	100
14	W	183/197 (93%)	178 (97%)	4 (2%)	1 (0%)	29	61
15	X	139/156 (89%)	135 (97%)	4 (3%)	0	100	100
16	Y	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
17	Z	125/137 (91%)	119 (95%)	4 (3%)	2 (2%)	9	32
18	b	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
19	c	142/145 (98%)	134 (94%)	8 (6%)	0	100	100
20	d	128/135 (95%)	124 (97%)	4 (3%)	0	100	100
21	e	167/483 (35%)	162 (97%)	4 (2%)	1 (1%)	25	58
22	f	79/82 (96%)	77 (98%)	1 (1%)	1 (1%)	12	37
23	g	26/63 (41%)	24 (92%)	2 (8%)	0	100	100
24	p	178/274 (65%)	174 (98%)	4 (2%)	0	100	100
25	r	174/425 (41%)	166 (95%)	8 (5%)	0	100	100
26	t	607/788 (77%)	587 (97%)	19 (3%)	1 (0%)	47	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	4094/5283 (78%)	3941 (96%)	141 (3%)	12 (0%)	44 71

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	K	96	SER
17	Z	42	VAL
12	U	98	ILE
14	W	118	LEU
26	t	96	ASP

### 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	173/191 (91%)	171 (99%)	2 (1%)	71 91
3	E	95/118 (80%)	95 (100%)	0	100 100
4	F	105/119 (88%)	102 (97%)	3 (3%)	42 76
5	H	109/129 (84%)	106 (97%)	3 (3%)	43 76
6	I	113/116 (97%)	110 (97%)	3 (3%)	44 77
7	K	60/89 (67%)	60 (100%)	0	100 100
8	L	53/60 (88%)	53 (100%)	0	100 100
9	Q	191/224 (85%)	190 (100%)	1 (0%)	88 96
10	S	221/222 (100%)	220 (100%)	1 (0%)	88 96
11	T	191/201 (95%)	189 (99%)	2 (1%)	76 92
12	U	165/170 (97%)	163 (99%)	2 (1%)	71 91
13	V	147/161 (91%)	146 (99%)	1 (1%)	84 95
14	W	158/166 (95%)	157 (99%)	1 (1%)	86 96
15	X	126/137 (92%)	122 (97%)	4 (3%)	39 73
16	Y	127/128 (99%)	127 (100%)	0	100 100
17	Z	91/105 (87%)	90 (99%)	1 (1%)	73 92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	b	110/111 (99%)	109 (99%)	1 (1%)	78	93
19	c	119/120 (99%)	116 (98%)	3 (2%)	47	78
20	d	109/113 (96%)	107 (98%)	2 (2%)	59	85
21	e	17/424 (4%)	17 (100%)	0	100	100
22	f	70/71 (99%)	68 (97%)	2 (3%)	42	76
23	g	27/54 (50%)	26 (96%)	1 (4%)	34	68
24	p	157/238 (66%)	154 (98%)	3 (2%)	57	84
25	r	171/384 (44%)	167 (98%)	4 (2%)	50	80
26	t	535/703 (76%)	529 (99%)	6 (1%)	73	92
All	All	3440/4554 (76%)	3394 (99%)	46 (1%)	70	90

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	d	121	THR
24	p	245	GLU
20	d	132	ARG
23	g	54	ARG
25	r	152	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
14	W	48	GLN
19	c	27	ASN
26	t	237	ASN
18	b	12	ASN
20	d	110	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1397/1800 (77%)	165 (11%)	51 (3%)

5 of 165 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	U
1	2	4	C
1	2	26	A
1	2	34	G
1	2	42	G

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1158	C
1	2	1537	C
1	2	1750	A
1	2	1241	G
1	2	1491	U

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

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

#### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

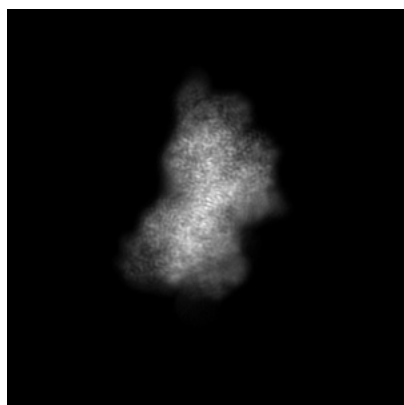
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16347. These allow visual inspection of the internal detail of the map and identification of artifacts.

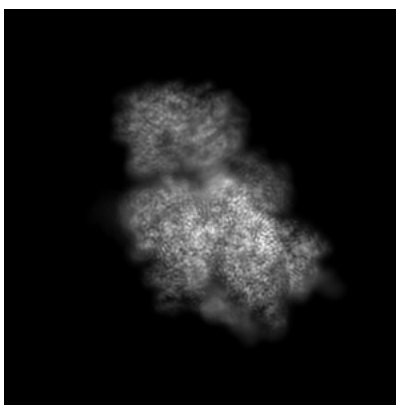
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

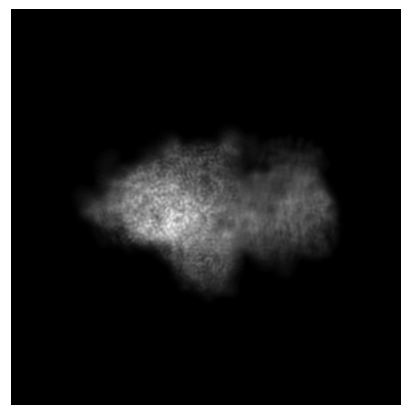
#### 6.1.1 Primary map



X



Y

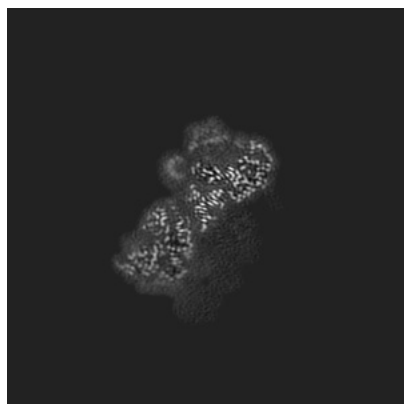


Z

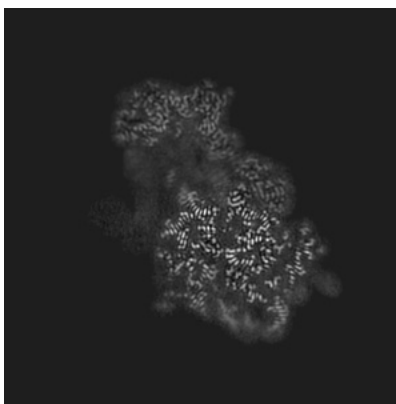
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

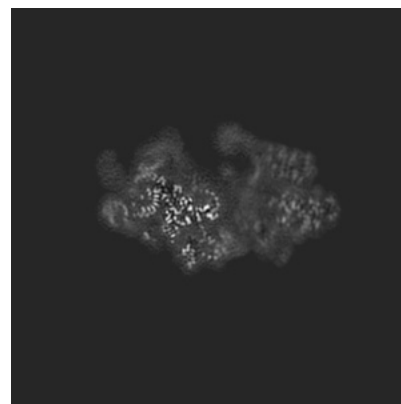
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

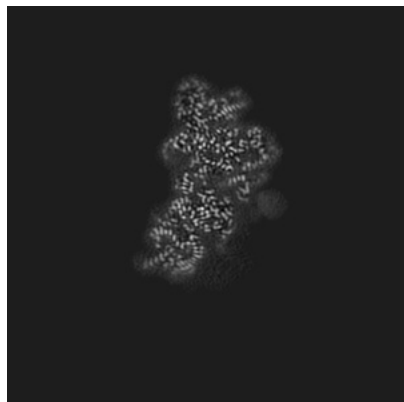


Z Index: 200

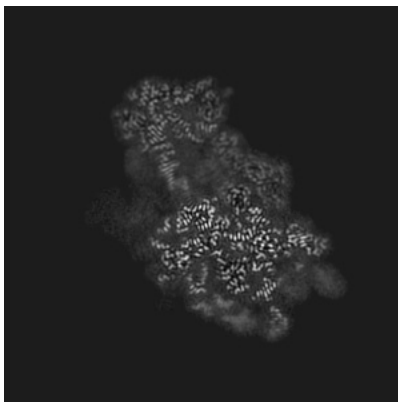
The images above show central slices of the map in three orthogonal directions.

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

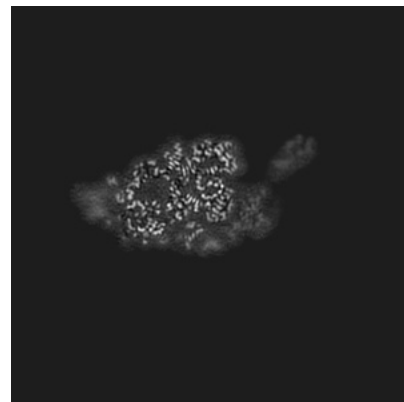
### 6.3.1 Primary map



X Index: 161



Y Index: 193

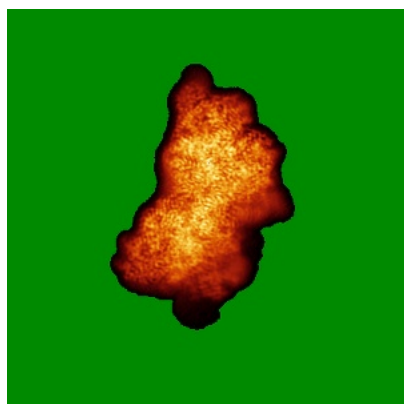


Z Index: 240

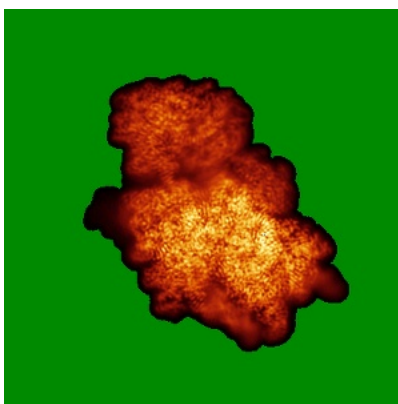
The images above show the largest variance slices of the map in three orthogonal directions.

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

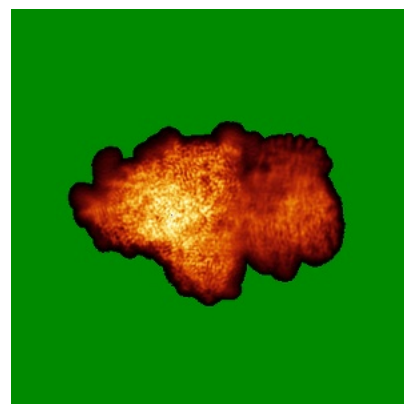
### 6.4.1 Primary map



X



Y



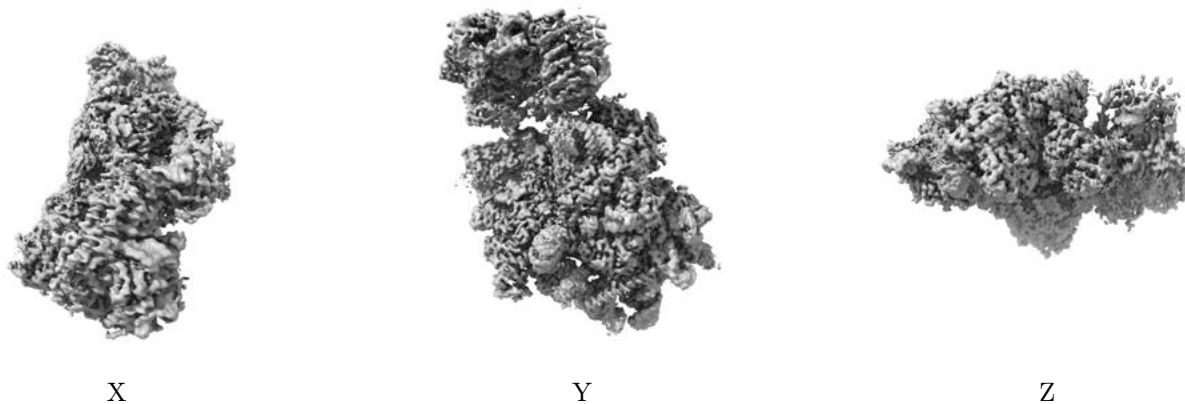
Z

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



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

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

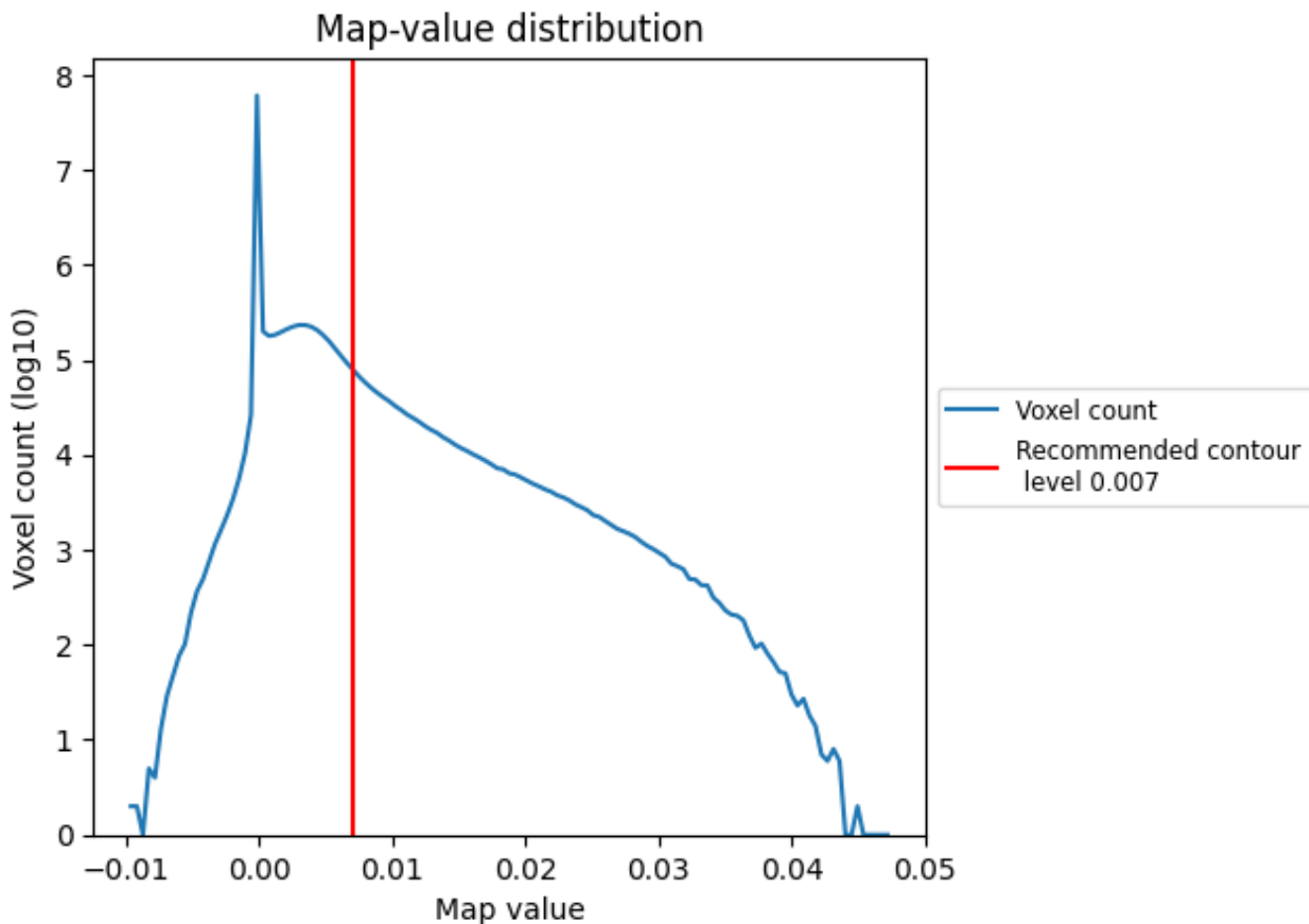
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

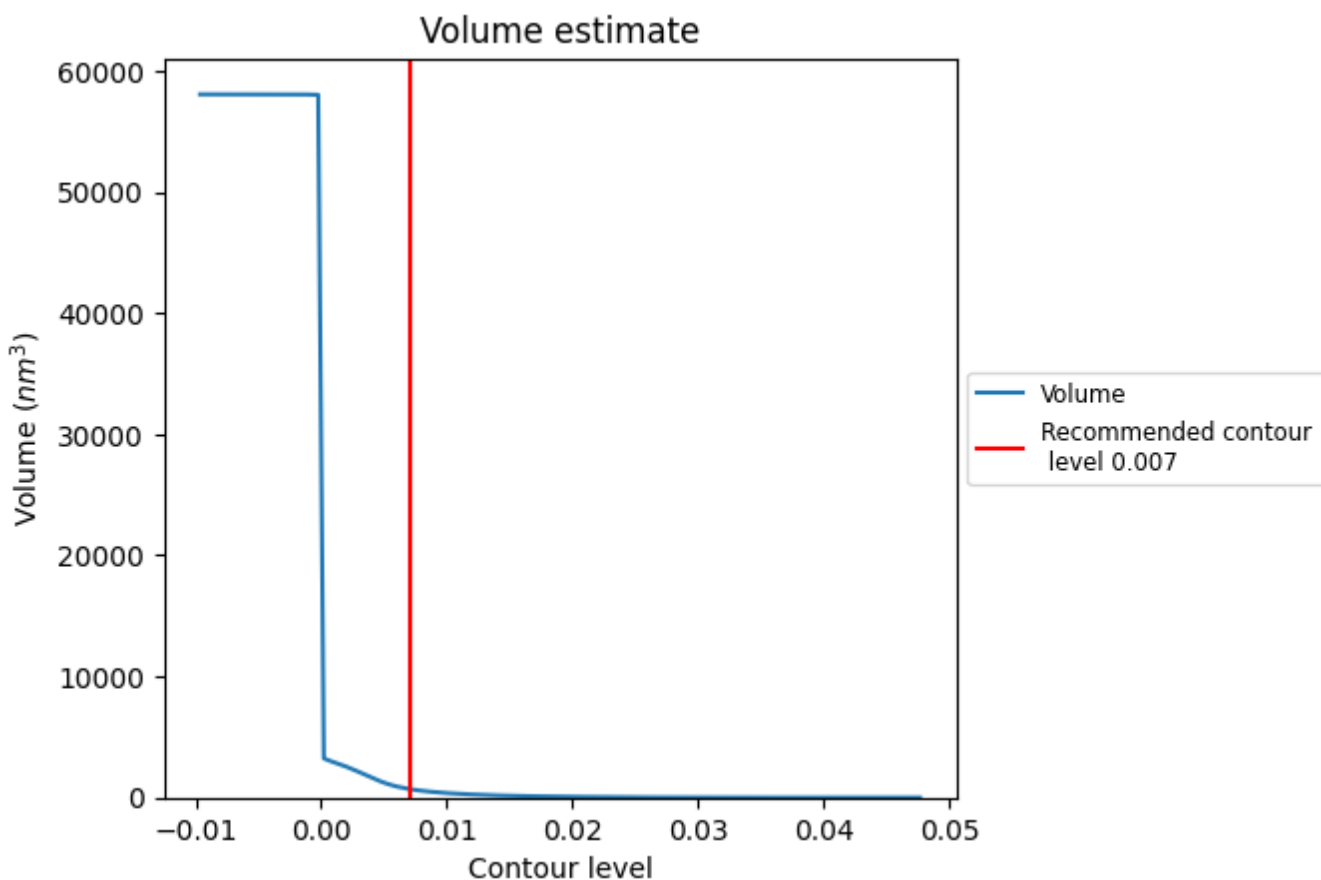
This section contains the results of statistical analysis of the map.

### 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.

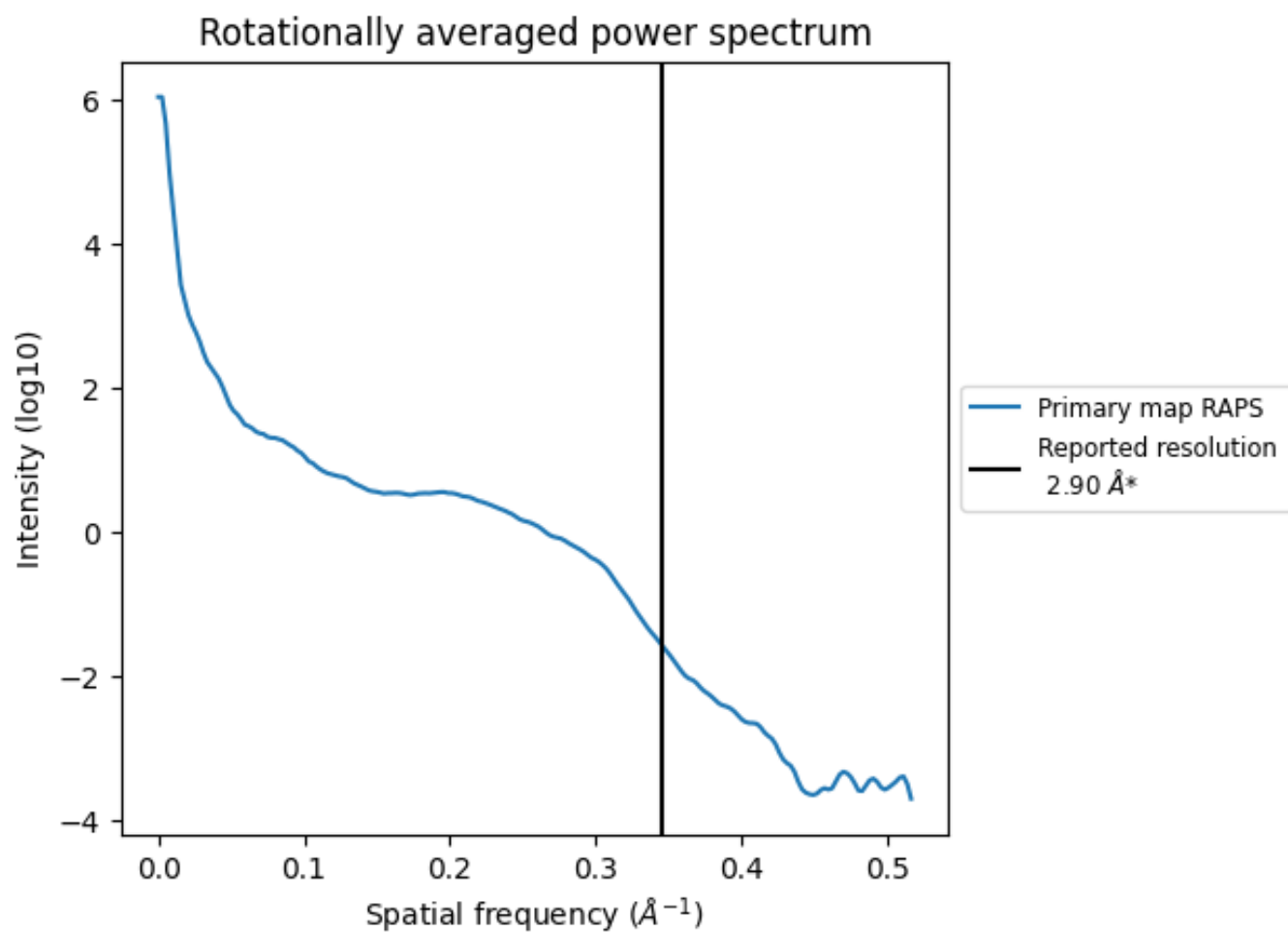
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 706 nm<sup>3</sup>; this corresponds to an approximate mass of 638 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  $0.345 \text{ \AA}^{-1}$

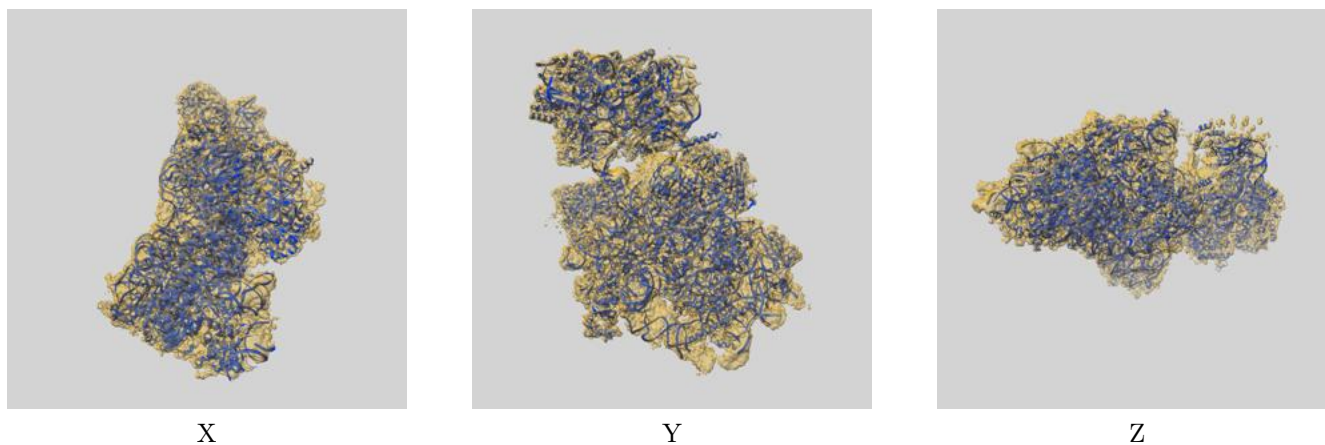
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

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

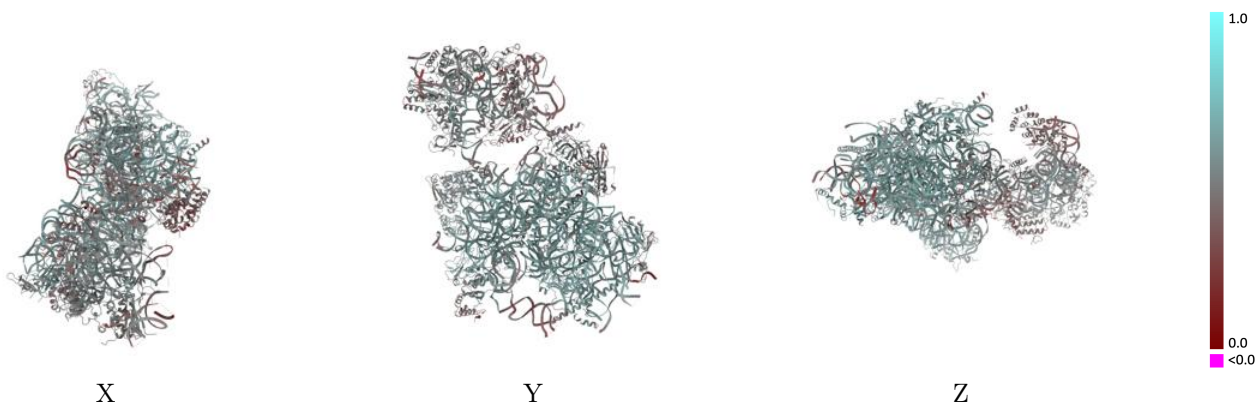
This section contains information regarding the fit between EMDB map EMD-16347 and PDB model 8C00. Per-residue inclusion information can be found in section [3](#) on page [8](#).

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



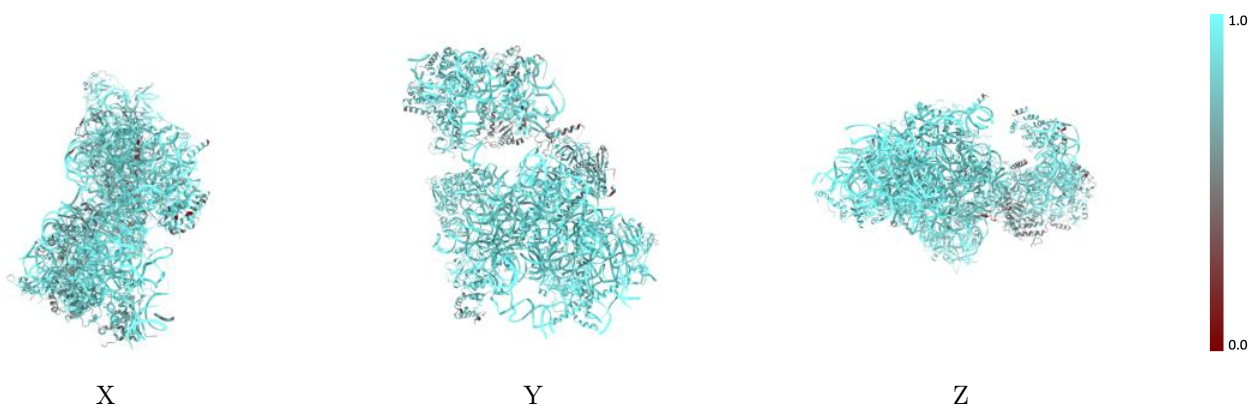
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



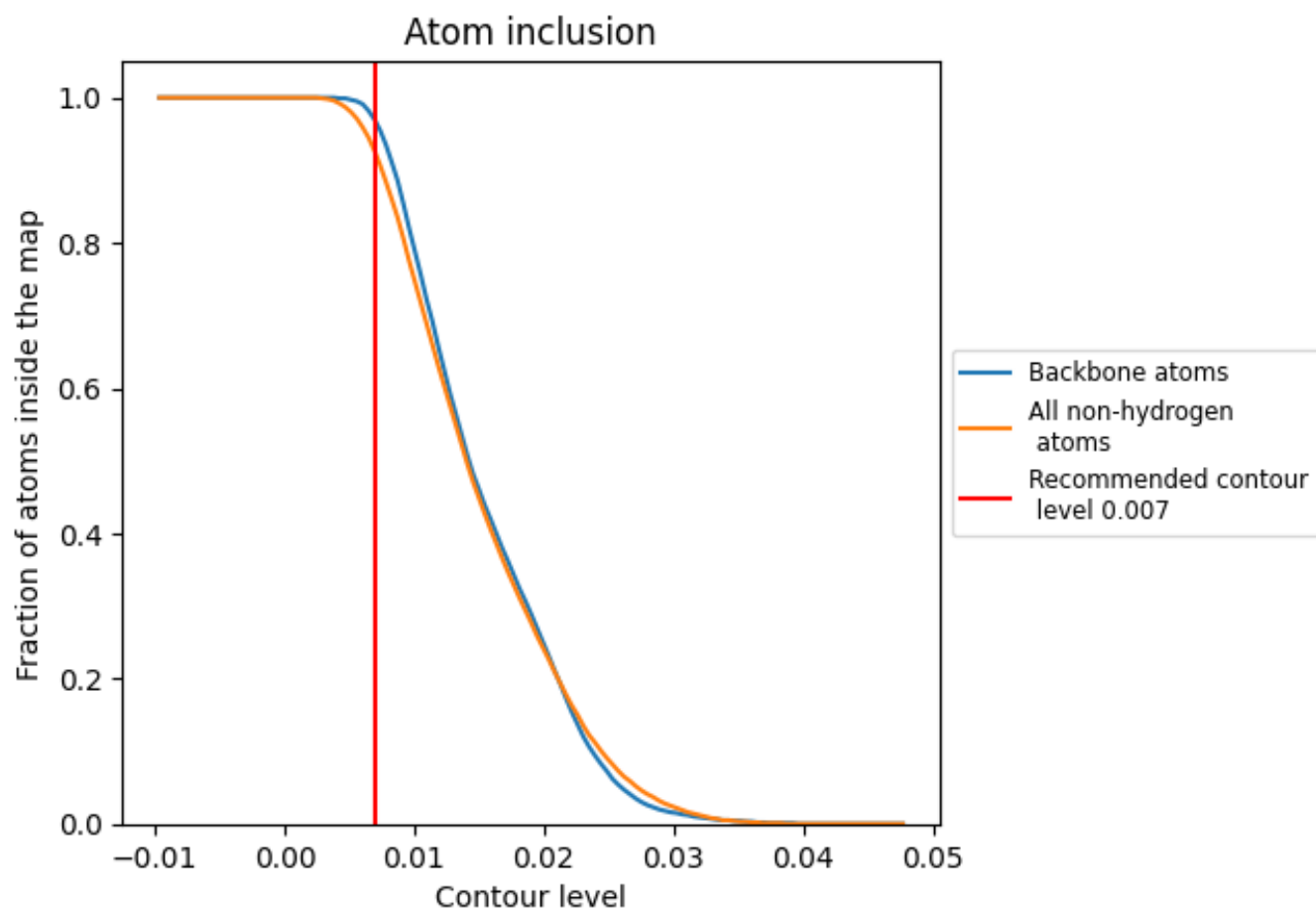
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

## 9.4 Atom inclusion [i](#)

























































At the recommended contour level, 97% of all backbone atoms, 92% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9240	 0.5350
2	 0.9860	 0.5560
B	 0.8480	 0.4820
E	 0.7600	 0.4720
F	 0.8080	 0.4630
H	 0.7810	 0.4740
I	 0.8560	 0.4940
K	 0.6830	 0.4670
L	 0.8210	 0.4510
Q	 0.9080	 0.5350
S	 0.9720	 0.5970
T	 0.9280	 0.5450
U	 0.8290	 0.5030
V	 0.9690	 0.5940
W	 0.9530	 0.5790
X	 0.9670	 0.5940
Y	 0.9470	 0.5690
Z	 0.9580	 0.5460
b	 0.9740	 0.5900
c	 0.9240	 0.5530
d	 0.9530	 0.5770
e	 0.8410	 0.4080
f	 0.9100	 0.5460
g	 0.9300	 0.5570
p	 0.9040	 0.5130
r	 0.5590	 0.3870
t	 0.7810	 0.4640

