wwPDB EM Validation Summary Report (i)

Dec 11, 2022 – 12:50 pm GMT

PDB ID	:	6SPC
EMDB ID	:	EMD-10281
Title	:	Pseudomonas aeruginosa 30s ribosome from an aminoglycoside resistant clinical isolate
Authors	:	Halfon, Y.; Jimenez-Fernande, A.; La Ros, R.; Espinos, R.; Krogh Johansen, H.; Matzov, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Belousoff, M.; Molin, S.; Yonath, A.
Deposited on	:	2019-09-01
Resolution	:	2.95 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

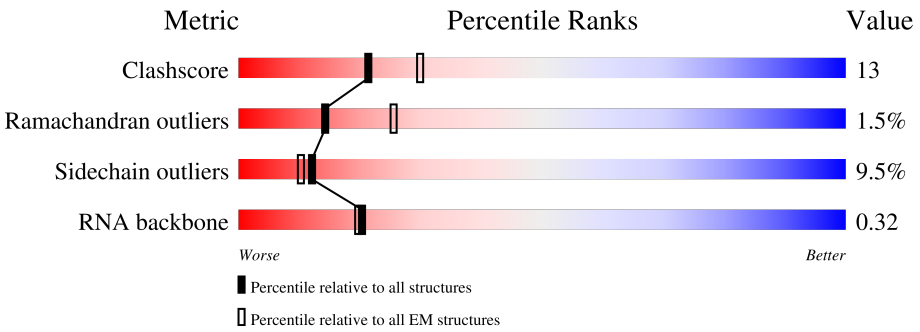
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.95 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 >=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	a	1519	• 47% 44% 10%
2	b	221	68% 31% •
3	c	203	37% 97% •
4	d	205	• 95% 5%
5	e	149	90% 9% •
6	f	100	92% 7% •
7	g	154	7% 62% 38% •

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Mol	Chain	Length	Quality of chain
8	h	125	75% 17% 6%
9	i	126	98%
10	j	96	18% 97%
11	k	115	95% 5%
12	l	120	84% 9% 6%
13	m	109	19% 94% 6%
14	n	98	28% 97%
15	o	87	97%
16	p	78	94% 6%
17	q	76	97%
18	r	56	96%
19	s	80	10% 94% 6%
20	t	86	97%
21	u	34	21% 100%

2 Entry composition (i)

There are 21 unique types of molecules in this entry. The entry contains 50569 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	a	1519	32595	14540	5985	10552	1518	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	2	A	-	conflict	GB 1359201046
a	?	-	C	deletion	GB 1359201046
a	?	-	G	deletion	GB 1359201046
a	72	A	G	conflict	GB 1359201046
a	101	A	G	conflict	GB 1359201046

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	b	221	1728	1088	316	314	10	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	?	-	THR	deletion	UNP A0A072ZPV8
b	?	-	PHE	deletion	UNP A0A072ZPV8
b	?	-	ASP	deletion	UNP A0A072ZPV8
b	?	-	LYS	deletion	UNP A0A072ZPV8
b	?	-	LEU	deletion	UNP A0A072ZPV8

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	c	203	1609	1017	303	284	5	0	0

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	d	205	1600	991	310	294	5	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	e	149	1092	687	202	197	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	?	-	ALA	deletion	UNP A0A241XG65

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	f	100	802	497	152	149	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	80	ALA	TYR	conflict	UNP A0A069Q263

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	g	154	1190	747	227	211	5	0	0

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	h	123	915	575	161	174	5	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	94	ALA	LYS	conflict	UNP E2RXT9
h	129	VAL	LEU	conflict	UNP E2RXT9

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	i	126	994	616	198	179	1	0	0

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	j	96	763	479	143	140	1	0	0

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	k	115	828	511	159	156	2	0	0

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	l	113	893	547	184	158	4	0	0

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	m	109	847	515	173	155	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	?	-	TYR	deletion	UNP E2RXU3

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	n	98	776	479	163	131	3	0	0

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	o	86	686	425	134	126	1	0	0

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	p	78	606	379	120	107	0	0

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	q	76	619	387	120	110	2	0	0

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	r	56	443	283	79	81	0	0

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	s	80	635	405	121	106	3	0	0

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	t	85	653	404	135	112	2	0	0

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	u	34	295	178	70	47	0	0

There is a discrepancy between the modelled and reference sequences:

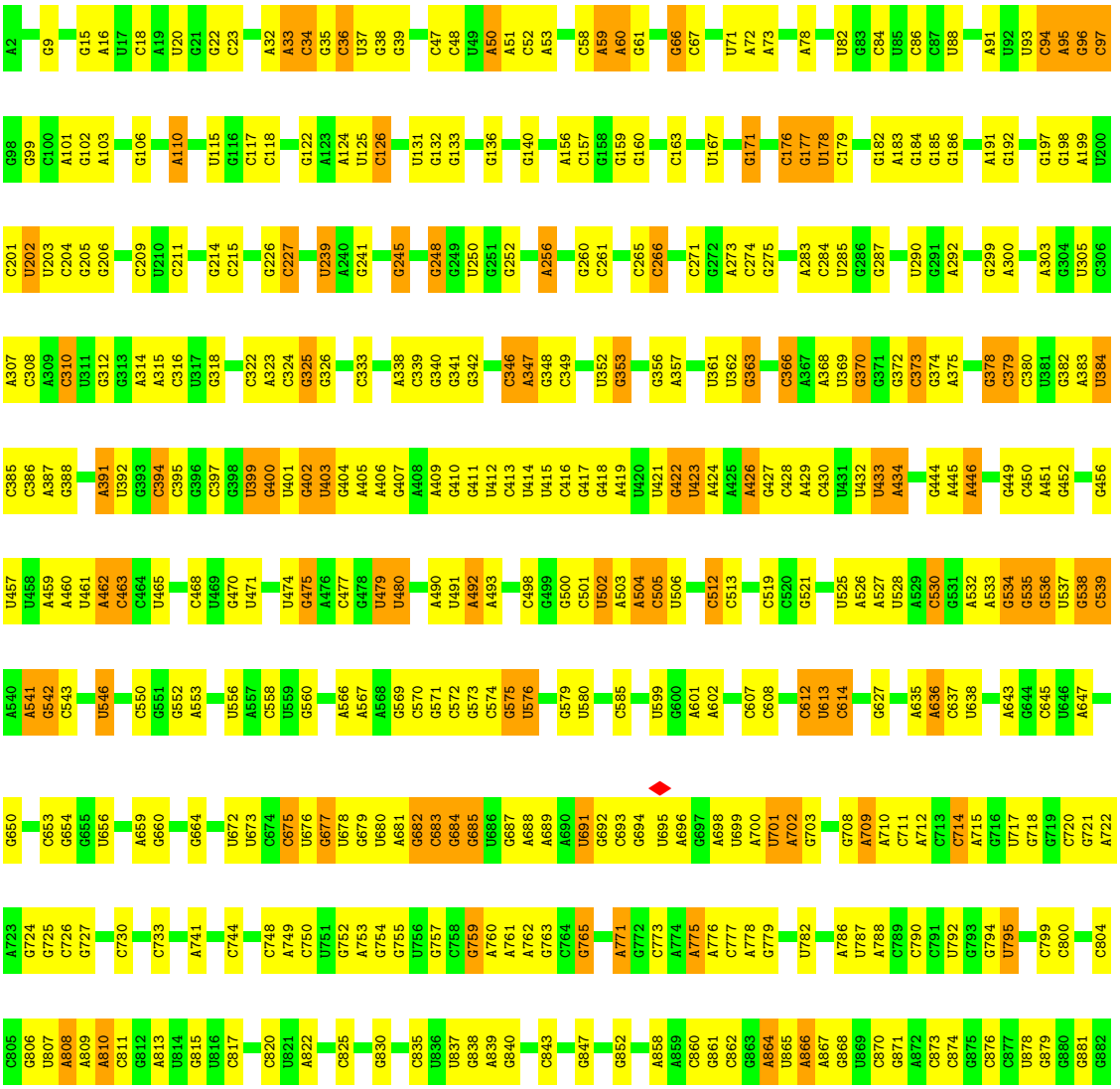
Chain	Residue	Modelled	Actual	Comment	Reference
u	46	ARG	LYS	conflict	UNP A0A069QC99

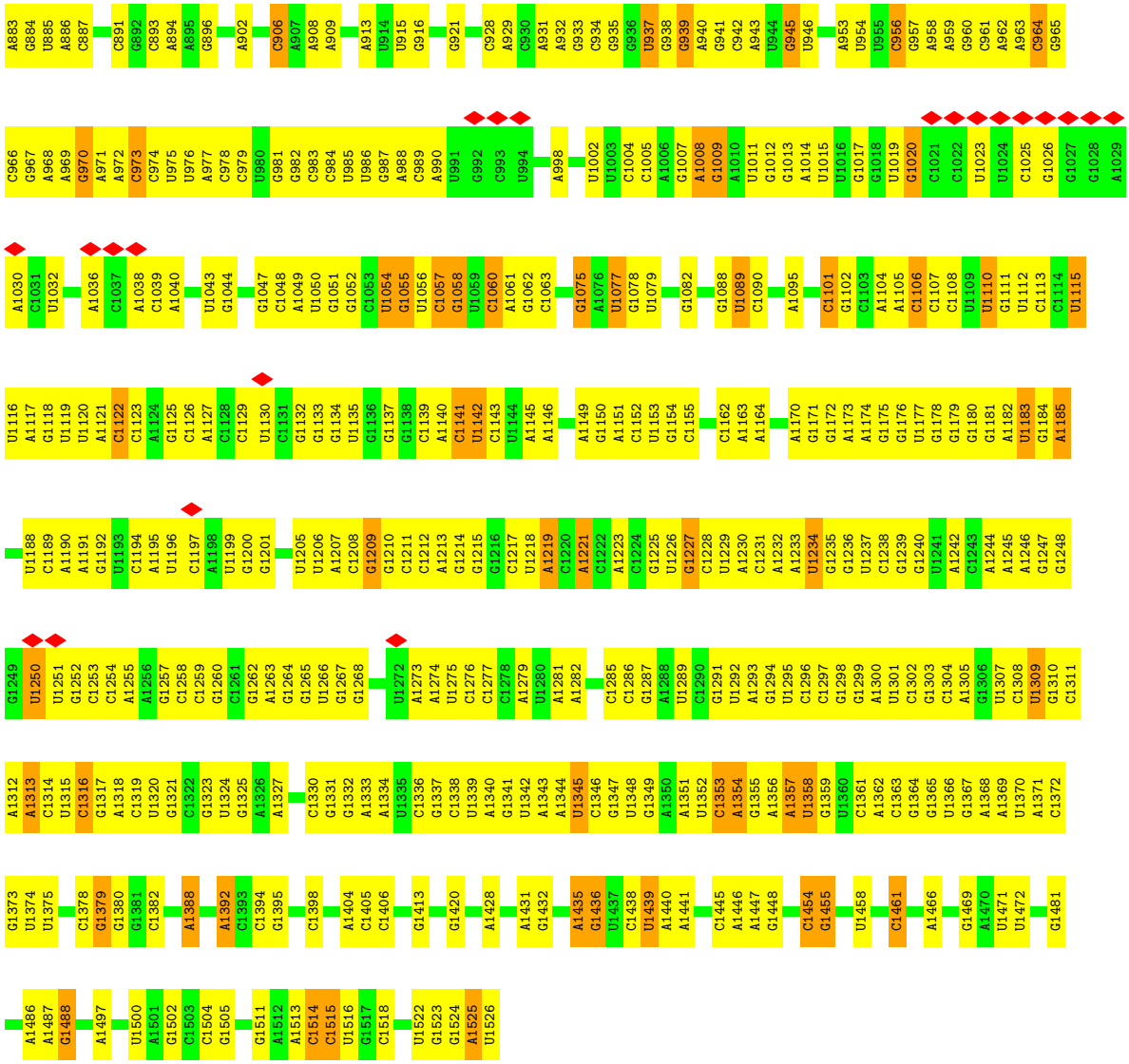
3 Residue-property plots (i)

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: 16S rRNA

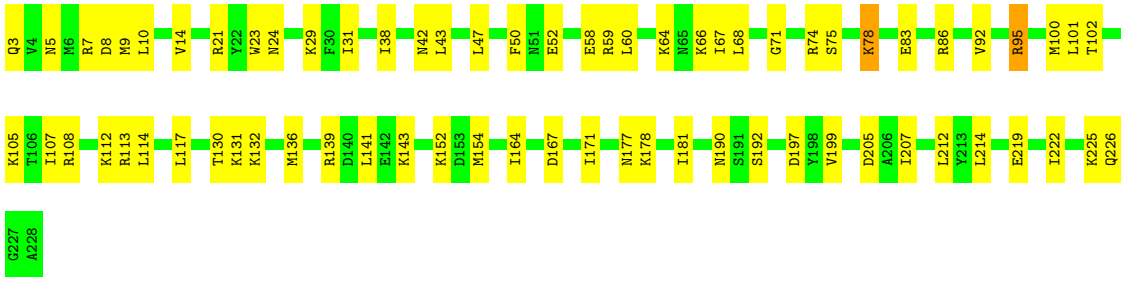
Chain a: 47% 44% 10%





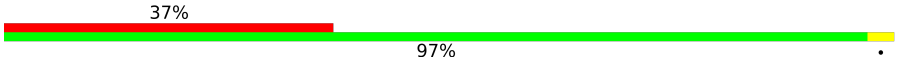
- Molecule 2: 30S ribosomal protein S2

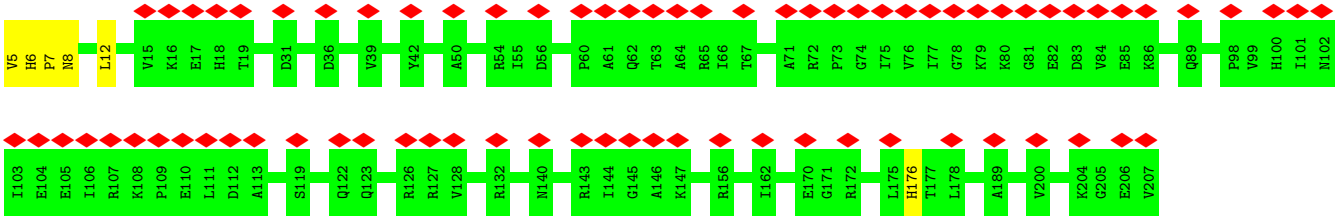
Chain b:



- Molecule 3: 30S ribosomal protein S3

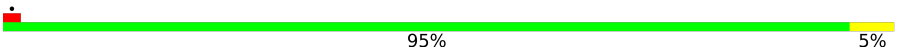
Chain c:

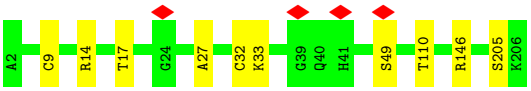




• Molecule 4: 30S ribosomal protein S4

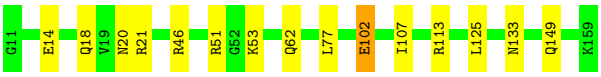
Chain d:





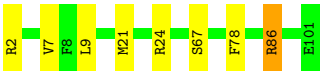
• Molecule 5: 30S ribosomal protein S5

Chain e:



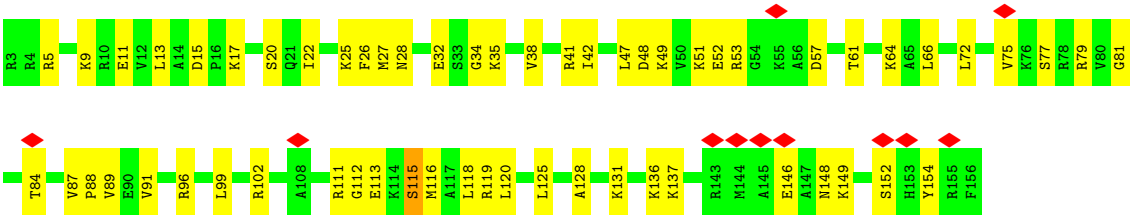
• Molecule 6: 30S ribosomal protein S6

Chain f:



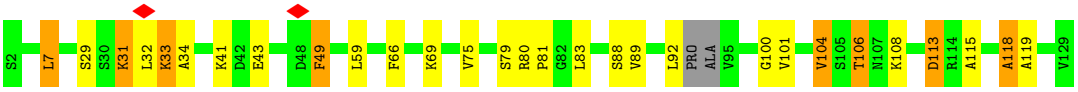
• Molecule 7: 30S ribosomal protein S7

Chain g:



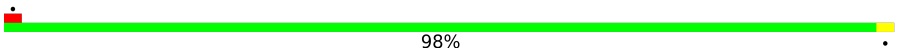
• Molecule 8: 30S ribosomal protein S8

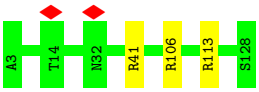
Chain h:



• Molecule 9: 30S ribosomal protein S9

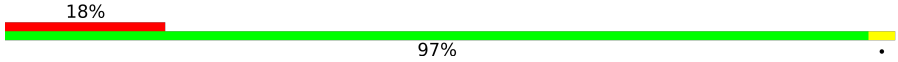
Chain i:

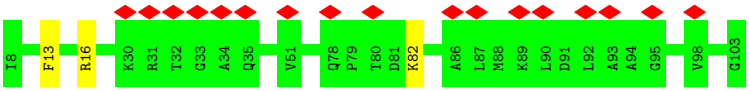




• Molecule 10: 30S ribosomal protein S10

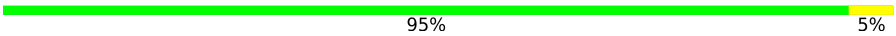
Chain j:

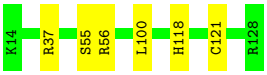




• Molecule 11: 30S ribosomal protein S11

Chain k:



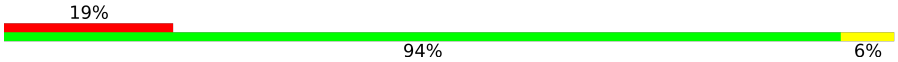


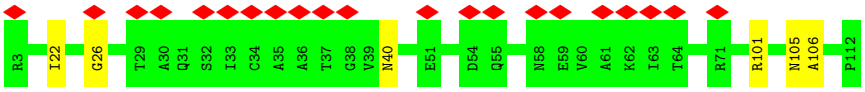
• Molecule 12: 30S ribosomal protein S12

Chain l:

• Molecule 13: 30S ribosomal protein S13

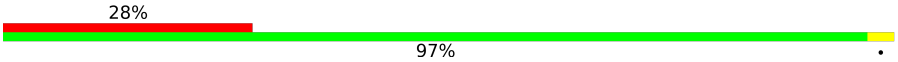
Chain m:

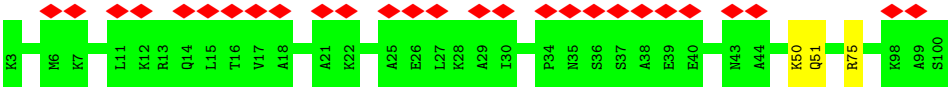




• Molecule 14: 30S ribosomal protein S14

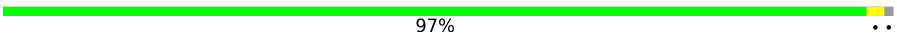
Chain n:

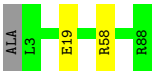




• Molecule 15: 30S ribosomal protein S15

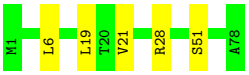
Chain o:





- Molecule 16: 30S ribosomal protein S16

Chain p: 94% 6%

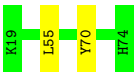


- Molecule 17: 30S ribosomal protein S17

Chain q: 97%

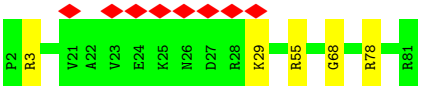
- Molecule 18: 30S ribosomal protein S18

Chain r: 96%



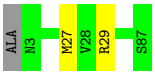
- Molecule 19: 30S ribosomal protein S19

Chain s: 10% 94% 6%



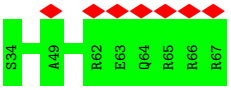
- Molecule 20: 30S ribosomal protein S20

Chain t: 97%



- Molecule 21: 30S ribosomal protein S21

Chain u: 21% 100%



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	319022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.603	Depositor
Minimum map value	-0.352	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.00936	Depositor
Map size (Å)	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	a	1.40	78/36497 (0.2%)	1.83	689/56927 (1.2%)
2	b	0.35	0/1754	0.57	0/2355
3	c	0.30	0/1638	0.60	0/2209
4	d	0.48	1/1619 (0.1%)	0.76	1/2168 (0.0%)
5	e	0.53	0/1106	0.72	0/1488
6	f	0.49	0/815	0.71	1/1098 (0.1%)
7	g	0.24	0/1207	0.50	0/1616
8	h	0.73	1/924 (0.1%)	1.14	6/1243 (0.5%)
9	i	0.32	0/1006	0.68	0/1347
10	j	0.29	0/773	0.63	0/1045
11	k	0.47	0/844	0.66	1/1148 (0.1%)
12	l	0.57	0/906	0.91	2/1215 (0.2%)
13	m	0.31	0/853	0.71	0/1144
14	n	0.31	0/786	0.68	0/1047
15	o	0.61	0/693	0.75	0/926
16	p	0.77	0/617	0.89	2/832 (0.2%)
17	q	0.59	0/627	0.67	0/844
18	r	0.62	0/450	0.76	1/608 (0.2%)
19	s	4.73	1/649 (0.2%)	0.75	1/874 (0.1%)
20	t	0.56	0/660	0.67	0/880
21	u	0.43	0/298	0.60	0/391
All	All	1.28	81/54722 (0.1%)	1.58	704/81405 (0.9%)

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
3	c	0	2
4	d	0	2
8	h	0	15
11	k	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
12	l	0	6
13	m	0	4
14	n	0	2
16	p	0	1
All	All	0	34

The worst 5 of 81 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	s	3	ARG	CB-CG	120.10	4.76	1.52
1	a	1313	A	N3-C4	57.70	1.69	1.34
1	a	1313	A	C6-N1	51.87	1.71	1.35
1	a	1219	A	N9-C4	44.11	1.64	1.37
1	a	1313	A	C5-C4	41.51	1.67	1.38

The worst 5 of 704 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	a	1219	A	N7-C8-N9	-144.78	41.41	113.80
1	a	1219	A	C4-C5-N7	-137.11	42.15	110.70
1	a	1219	A	C8-N9-C4	-133.34	52.46	105.80
1	a	1219	A	C5-N7-C8	57.27	132.53	103.90
1	a	1219	A	C6-C5-N7	38.34	159.14	132.30

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	c	12	LEU	Peptide
3	c	176	HIS	Peptide
4	d	205	SER	Peptide
4	d	49	SER	Peptide
8	h	29	SER	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32595	0	16400	0	0
2	b	1728	0	1766	0	0
3	c	1609	0	1636	0	0
4	d	1600	0	1620	0	0
5	e	1092	0	1139	0	0
6	f	802	0	769	0	0
7	g	1190	0	1227	0	0
8	h	915	0	952	0	0
9	i	994	0	1031	0	0
10	j	763	0	801	0	0
11	k	828	0	808	0	0
12	l	893	0	932	0	0
13	m	847	0	888	0	0
14	n	776	0	818	0	0
15	o	686	0	709	0	0
16	p	606	0	606	0	0
17	q	619	0	659	0	0
18	r	443	0	460	0	0
19	s	635	0	662	0	0
20	t	653	0	699	0	0
21	u	295	0	313	0	0
All	All	50569	0	34895	0	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 13.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	b	217/221 (98%)	179 (82%)	34 (16%)	4 (2%)	8 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	c	201/203 (99%)	170 (85%)	29 (14%)	2 (1%)	15	48
4	d	203/205 (99%)	161 (79%)	39 (19%)	3 (2%)	10	38
5	e	147/149 (99%)	130 (88%)	15 (10%)	2 (1%)	11	39
6	f	98/100 (98%)	86 (88%)	10 (10%)	2 (2%)	7	30
7	g	152/154 (99%)	115 (76%)	27 (18%)	10 (7%)	1	5
8	h	121/125 (97%)	84 (69%)	29 (24%)	8 (7%)	1	5
9	i	124/126 (98%)	104 (84%)	20 (16%)	0	100	100
10	j	94/96 (98%)	82 (87%)	12 (13%)	0	100	100
11	k	113/115 (98%)	93 (82%)	20 (18%)	0	100	100
12	l	111/120 (92%)	91 (82%)	18 (16%)	2 (2%)	8	33
13	m	105/109 (96%)	86 (82%)	19 (18%)	0	100	100
14	n	96/98 (98%)	80 (83%)	16 (17%)	0	100	100
15	o	84/87 (97%)	79 (94%)	4 (5%)	1 (1%)	13	43
16	p	76/78 (97%)	64 (84%)	12 (16%)	0	100	100
17	q	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
18	r	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
19	s	78/80 (98%)	63 (81%)	15 (19%)	0	100	100
20	t	83/86 (96%)	83 (100%)	0	0	100	100
21	u	32/34 (94%)	25 (78%)	7 (22%)	0	100	100
All	All	2263/2318 (98%)	1898 (84%)	331 (15%)	34 (2%)	14	38

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	c	8	ASN
4	d	14	ARG
4	d	33	LYS
5	e	14	GLU
6	f	86	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	182/183 (100%)	114 (63%)	68 (37%)	0	0
3	c	163/169 (96%)	161 (99%)	2 (1%)	71	88
4	d	166/173 (96%)	162 (98%)	4 (2%)	49	77
5	e	108/109 (99%)	94 (87%)	14 (13%)	4	16
6	f	81/85 (95%)	75 (93%)	6 (7%)	13	41
7	g	116/120 (97%)	66 (57%)	50 (43%)	0	0
8	h	98/103 (95%)	90 (92%)	8 (8%)	11	36
9	i	102/102 (100%)	99 (97%)	3 (3%)	42	73
10	j	85/85 (100%)	82 (96%)	3 (4%)	36	68
11	k	82/87 (94%)	79 (96%)	3 (4%)	34	66
12	l	100/104 (96%)	97 (97%)	3 (3%)	41	72
13	m	91/91 (100%)	89 (98%)	2 (2%)	52	79
14	n	78/80 (98%)	77 (99%)	1 (1%)	69	87
15	o	73/73 (100%)	72 (99%)	1 (1%)	67	86
16	p	60/63 (95%)	58 (97%)	2 (3%)	38	70
17	q	70/70 (100%)	68 (97%)	2 (3%)	42	73
18	r	46/48 (96%)	45 (98%)	1 (2%)	52	79
19	s	69/71 (97%)	66 (96%)	3 (4%)	29	62
20	t	67/68 (98%)	65 (97%)	2 (3%)	41	72
21	u	28/28 (100%)	28 (100%)	0	100	100
All	All	1865/1912 (98%)	1687 (90%)	178 (10%)	12	29

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	g	61	THR
7	g	154	TYR
7	g	75	VAL
7	g	113	GLU
8	h	106	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
14	n	71	HIS
15	o	42	HIS
19	s	14	HIS
5	e	123	ASN
5	e	90	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1514/1519 (99%)	677 (44%)	0

5 of 677 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	9	G
1	a	15	G
1	a	22	G
1	a	32	A
1	a	33	A

There are no RNA pucker outliers to report.

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	a	4
2	b	1
13	m	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	2:A	O3'	7:A	P	21.37
1	a	63:C	O3'	65:A	P	7.46
1	b	124:GLY	C	130:THR	N	5.42
1	m	20:THR	C	22:ILE	N	3.27
1	a	1376:C	O3'	1377:C	P	3.24

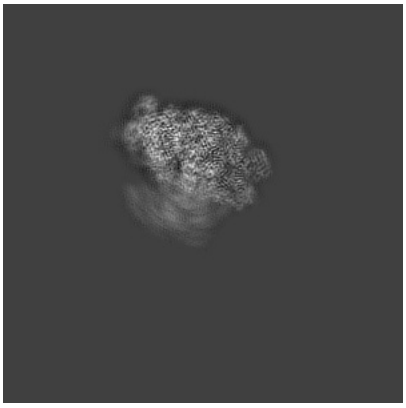
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-10281. These allow visual inspection of the internal detail of the map and identification of artifacts.

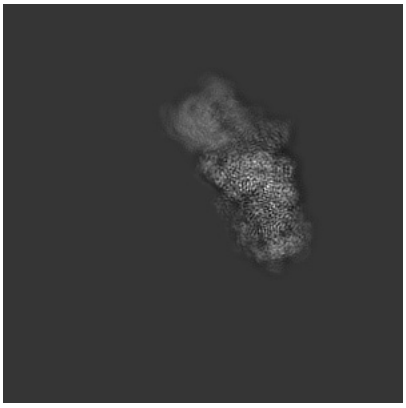
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

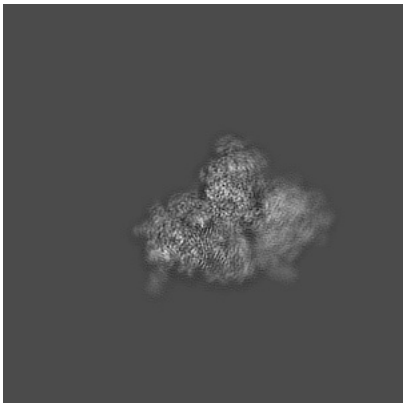
6.1.1 Primary map



X



Y



Z

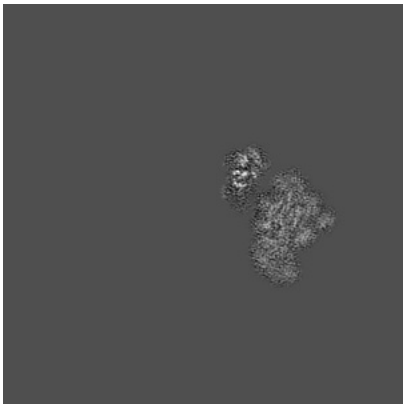
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

X Index: 200

Y Index: 200

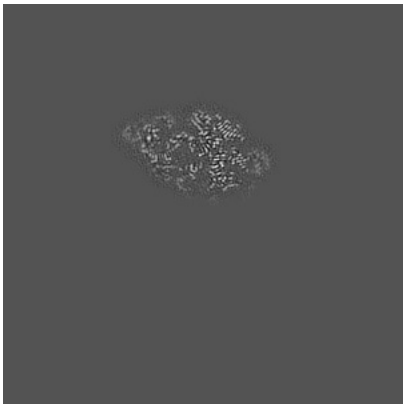


Z Index: 200

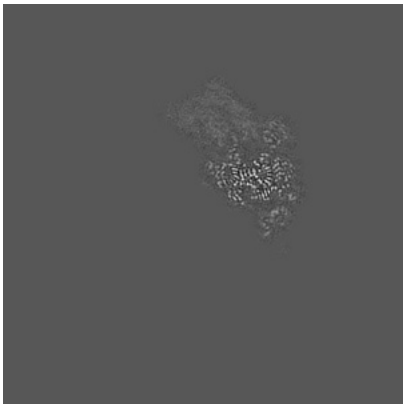
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

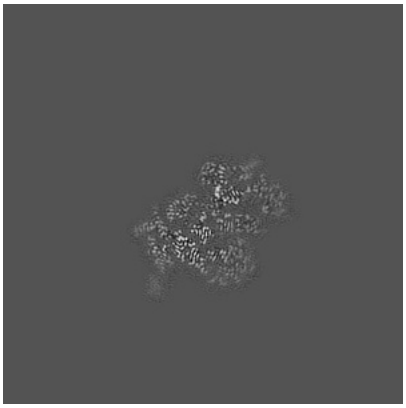
6.3.1 Primary map



X Index: 218



Y Index: 207

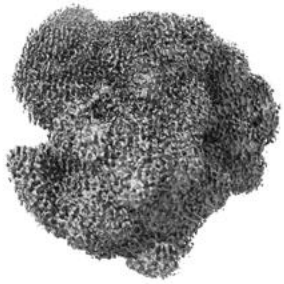


Z Index: 268

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 0.00936. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

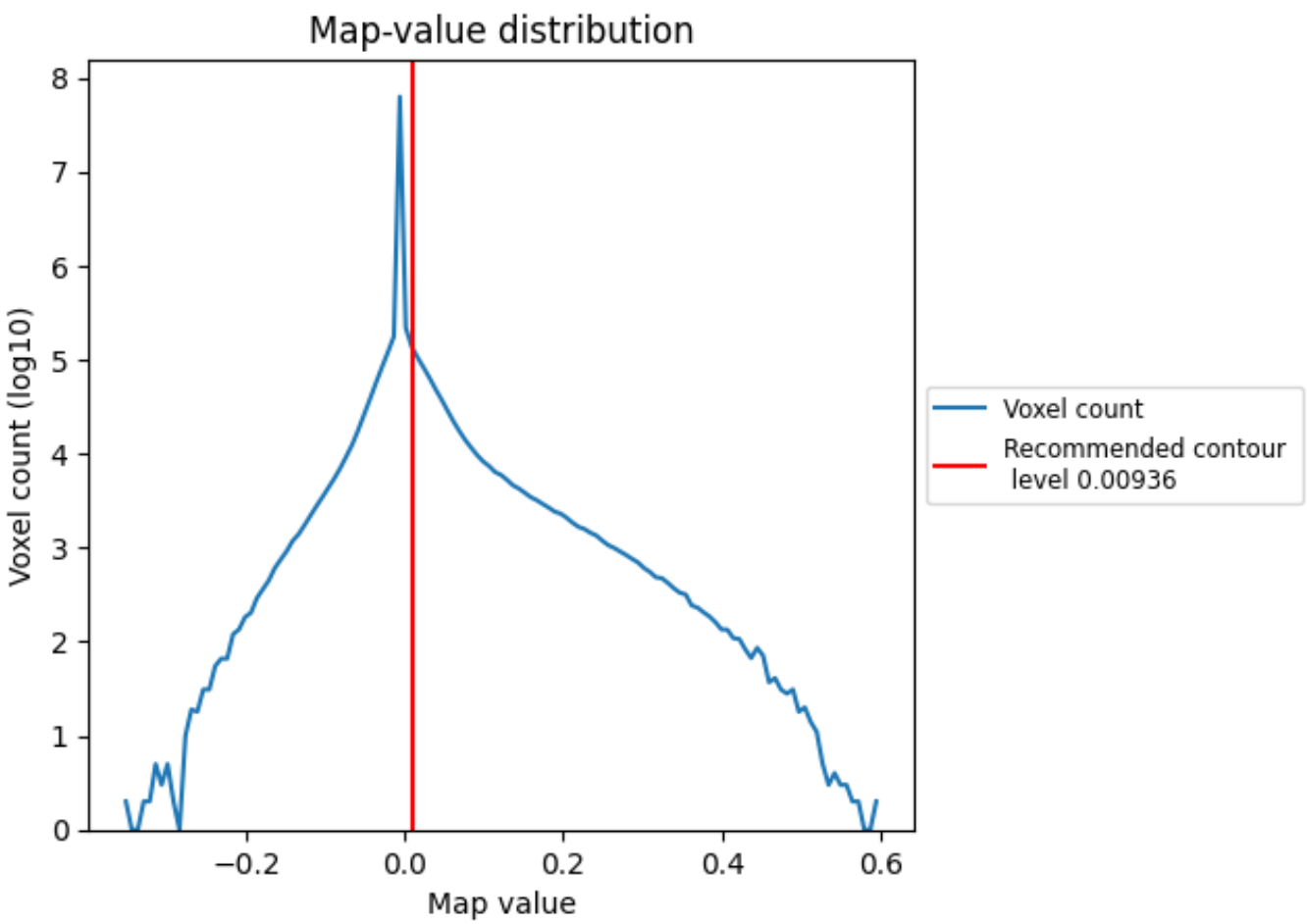
6.5 Mask visualisation (i)

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

7 Map analysis (i)

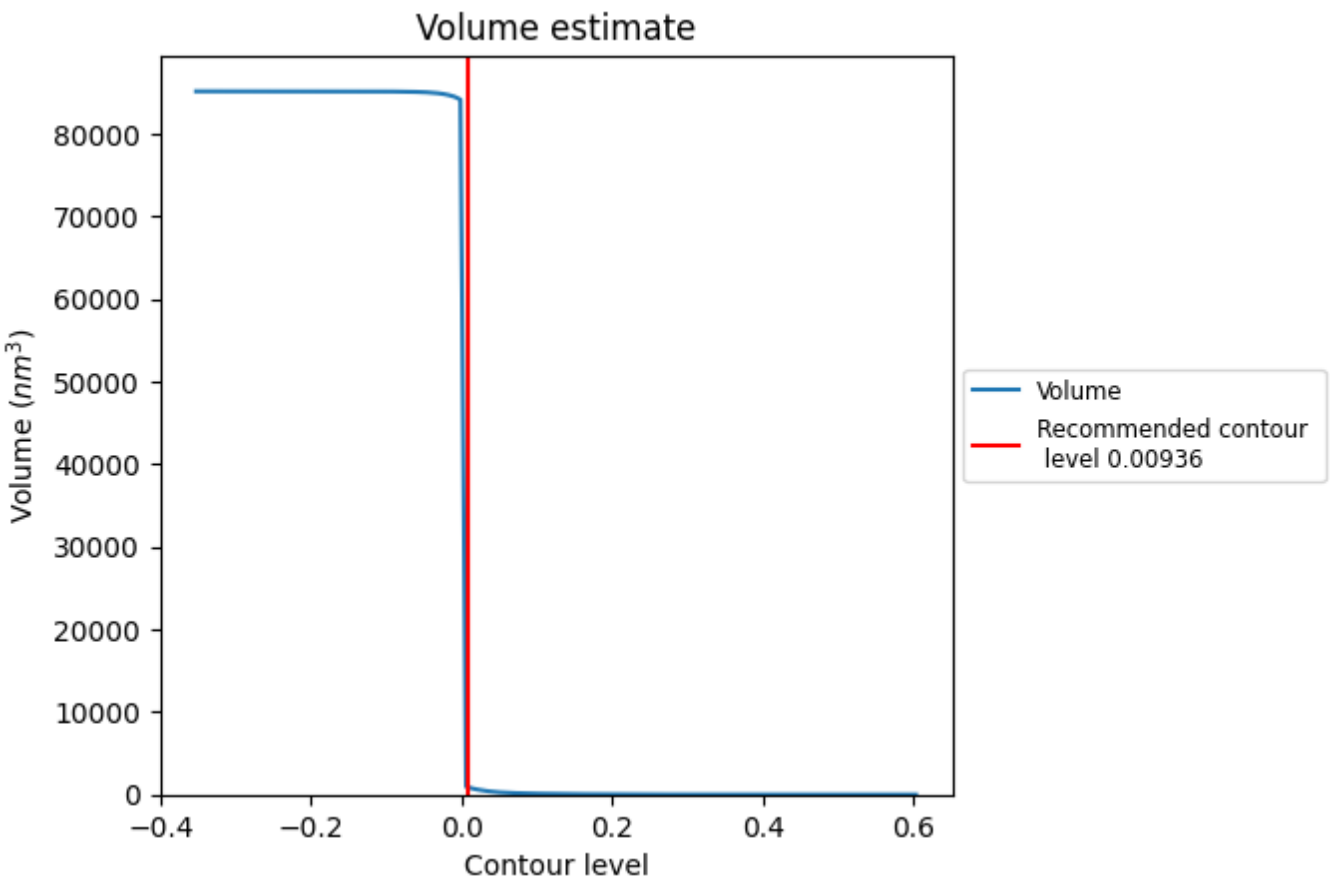
This section contains the results of statistical analysis of the map.

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.

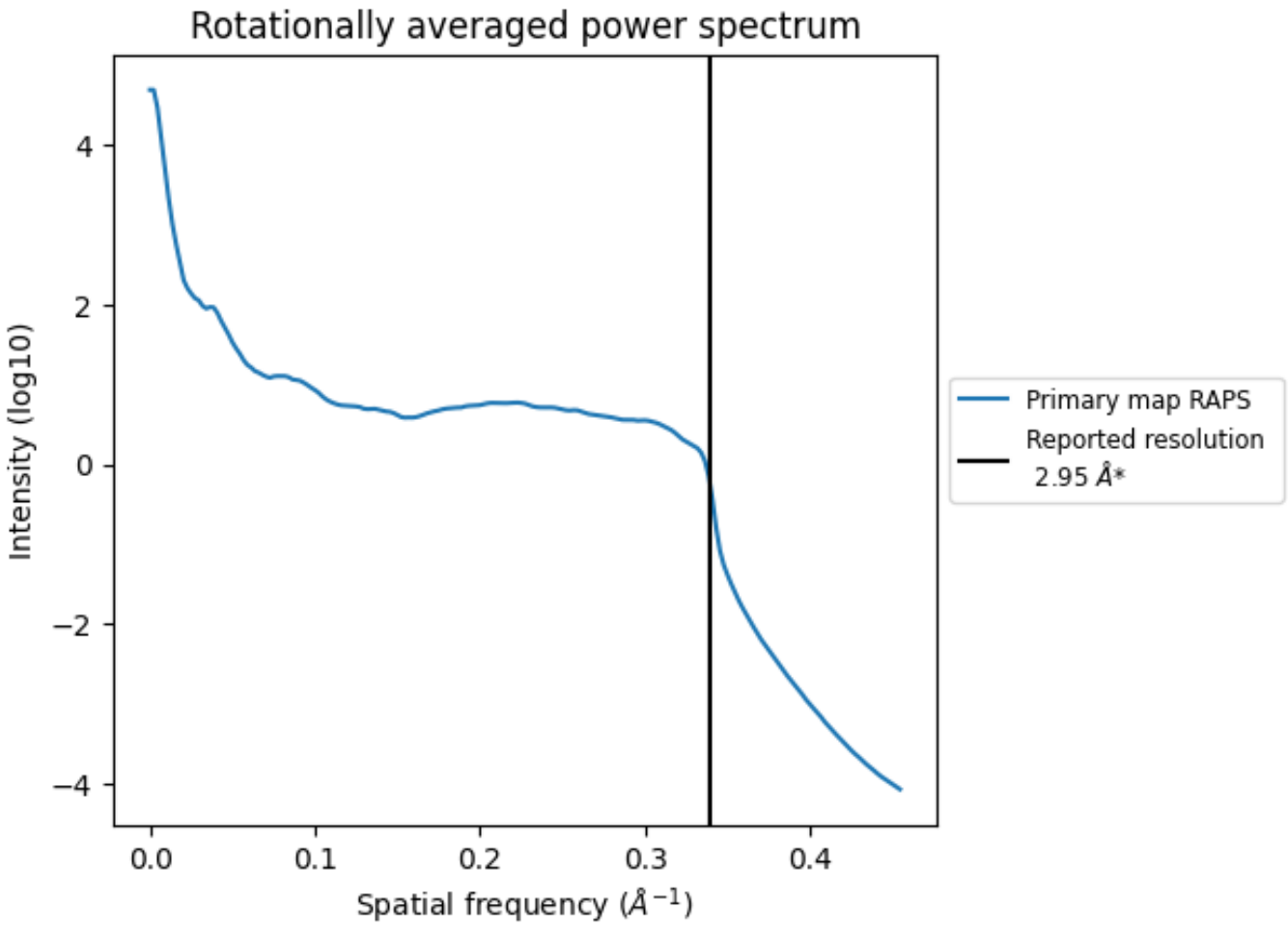
7.2 Volume estimate (i)



The volume at the recommended contour level is 868 nm^3; this corresponds to an approximate mass of 784 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 0.339 Å^{-1}

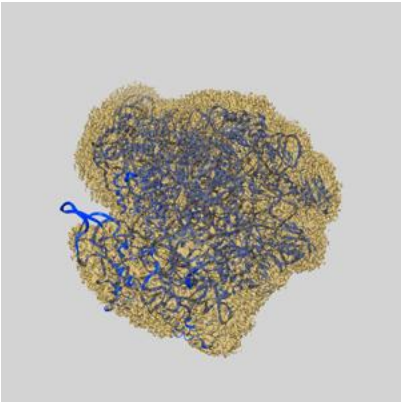
8 Fourier-Shell correlation (i)

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

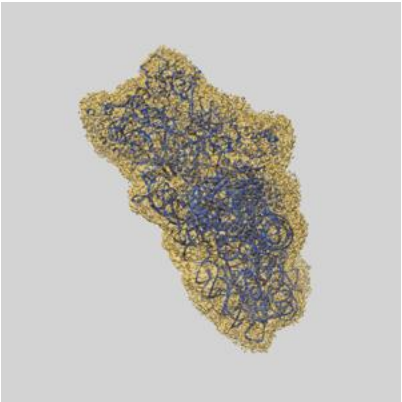
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-10281 and PDB model 6SPC. Per-residue inclusion information can be found in section 3 on page 9.

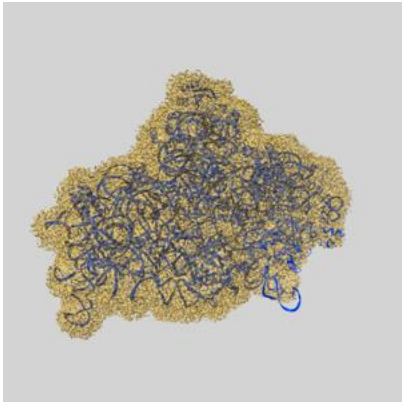
9.1 Map-model overlay (i)



X



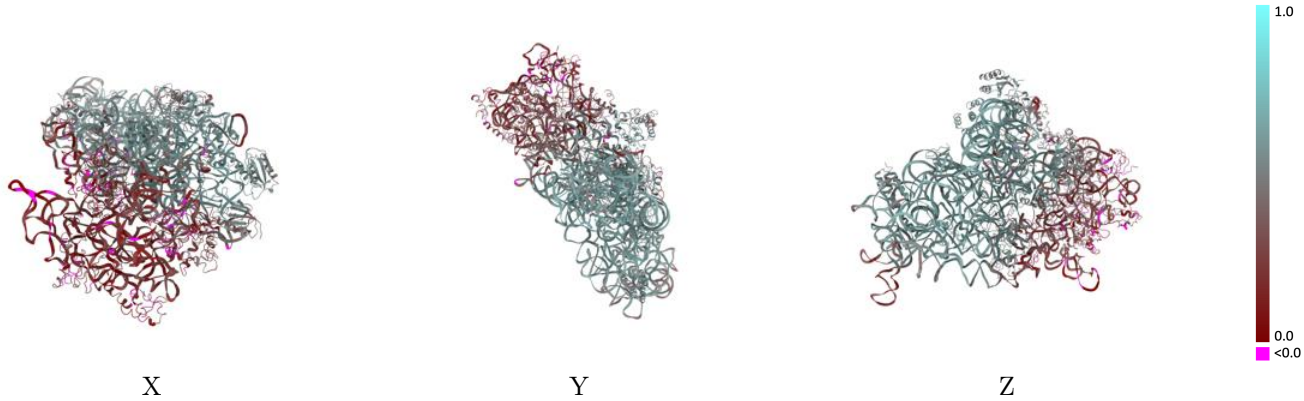
Y



Z

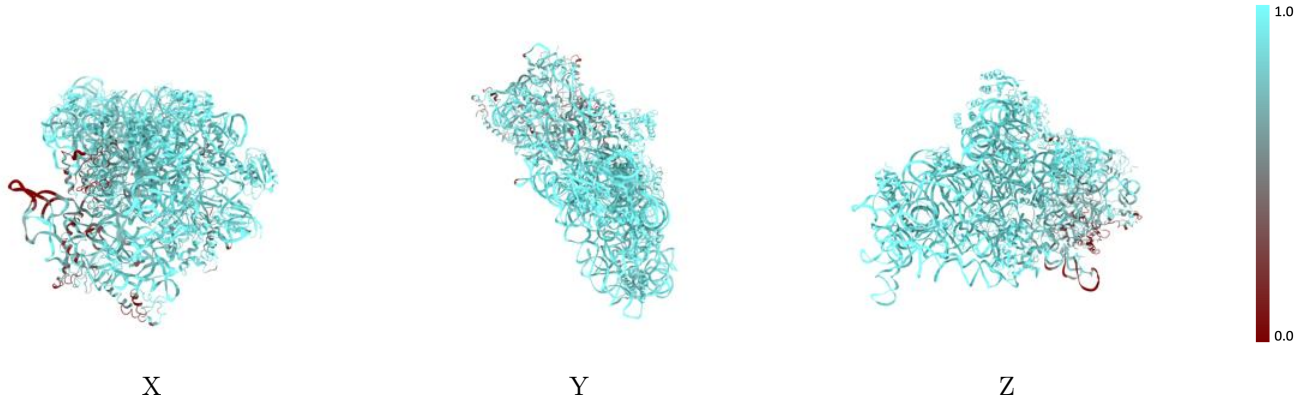
The images above show the 3D surface view of the map at the recommended contour level 0.00936 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



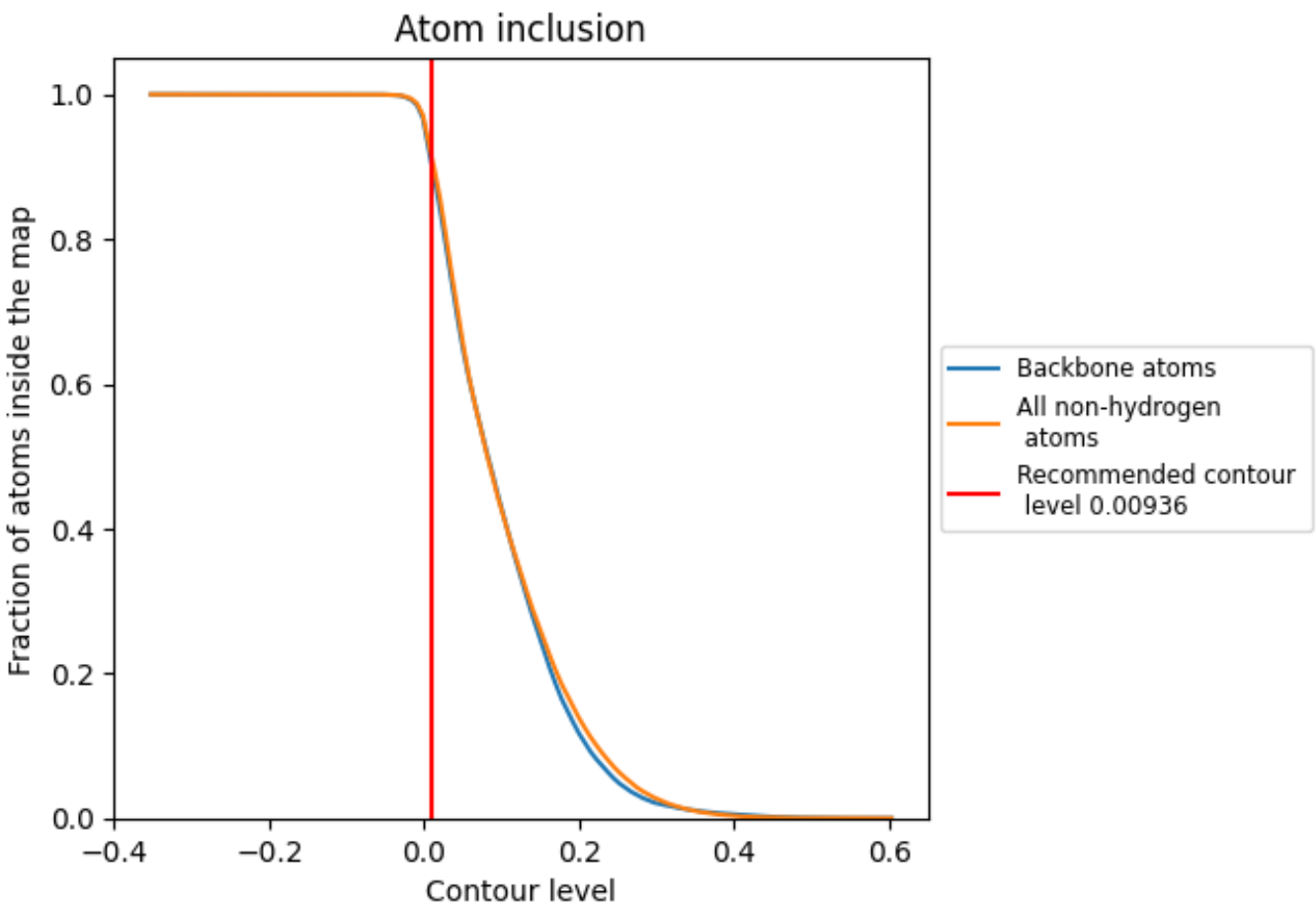
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00936).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.00936) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9146	0.4440
a	0.9445	0.4710
b	0.9769	0.5140
c	0.5423	0.1890
d	0.9276	0.4220
e	0.9729	0.5630
f	0.9820	0.5190
g	0.8147	0.3130
h	0.8831	0.4250
i	0.8249	0.1150
j	0.7151	0.2080
k	0.9679	0.4590
l	0.9406	0.5120
m	0.7197	0.1780
n	0.6121	0.2090
o	0.9955	0.5860
p	0.9880	0.5980
q	0.9766	0.5740
r	0.9860	0.5670
s	0.7617	0.2050
t	0.9890	0.5810
u	0.7283	0.4130