



wwPDB EM Validation Summary Report ⓘ

Nov 8, 2022 – 09:43 AM JST

PDB ID : 5ZEU
EMDB ID : EMD-6923
Title : M. smegmatis P/P state 30S ribosomal subunit
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on : 2018-02-28
Resolution : 3.70 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 ⓘ symbol.

The types of validation reports are described at

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

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

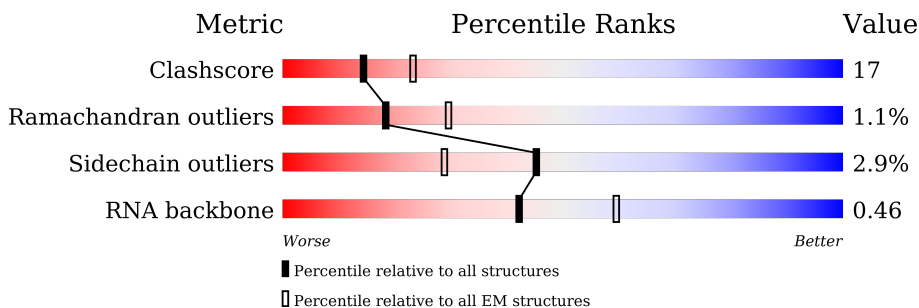
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 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.




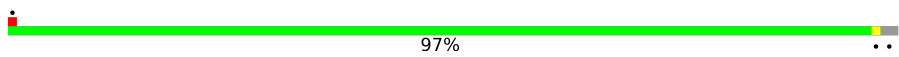
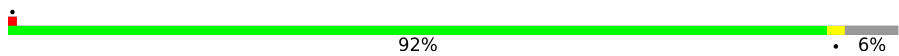


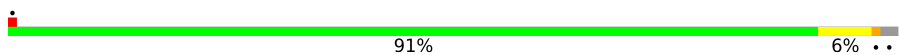

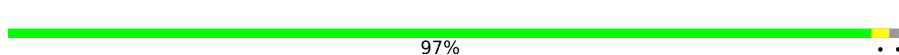

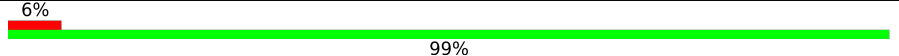
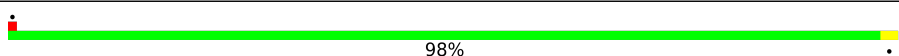
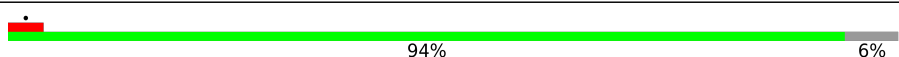

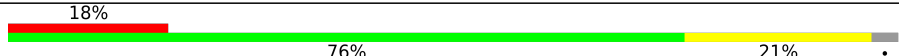
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	1528	68% 27% . .
2	c	275	69% . . 24%
3	e	214	12% 88% . 7%
4	g	156	96% .
5	h	132	93% 5% .
6	i	150	79% 5% . 16%
7	j	101	9% 89% 7% .

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Mol	Chain	Length	Quality of chain
8	k	138	 78% 7% 15%
9	l	124	 92% 6%
10	o	89	 97%
11	q	98	 92% 6%
12	r	84	 76% 24%
13	s	93	 80% 16%
14	t	86	 91% 6%
15	v	77	 8% 77% 23%
16	n	61	 97%
17	b	277	 45% 81% 18%
18	d	201	 6% 99%
19	f	96	 98%
20	m	124	 94% 6%
21	p	156	 72% 28%
22	u	33	 18% 76% 21%

2 Entry composition [i](#)

There are 22 unique types of molecules in this entry. The entry contains 52954 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	1506	32341	14404	5921	10510	1506	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	c	210	1672	1043	324	300	5	0	0

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	e	198	1433	885	282	262	4	0	0

- Molecule 4 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	g	156	1240	773	242	222	3	0	0

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	h	130	1003	629	188	185	1	0	0

- Molecule 6 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
6	i	126	994	630	194	170	0	0

- Molecule 7 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	j	97	775	488	143	141	3	0	0

- Molecule 8 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	k	117	871	539	173	158	1	0	0

- Molecule 9 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	l	122	958	594	197	165	2	0	0

- Molecule 10 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	o	87	709	443	143	123	0	0

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	q	92	730	458	138	132	2	0	0

- Molecule 12 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	r	64	512	319	102	88	3	0	0

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	s	78	630	405	117	107	1	0	0

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	t	84	Total	C	N	O	0	0
			655	399	138	118		

- Molecule 15 is a RNA chain called P-tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	v	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 17 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 18 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 20 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 21 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	p	113	891	570	162	159	0	0

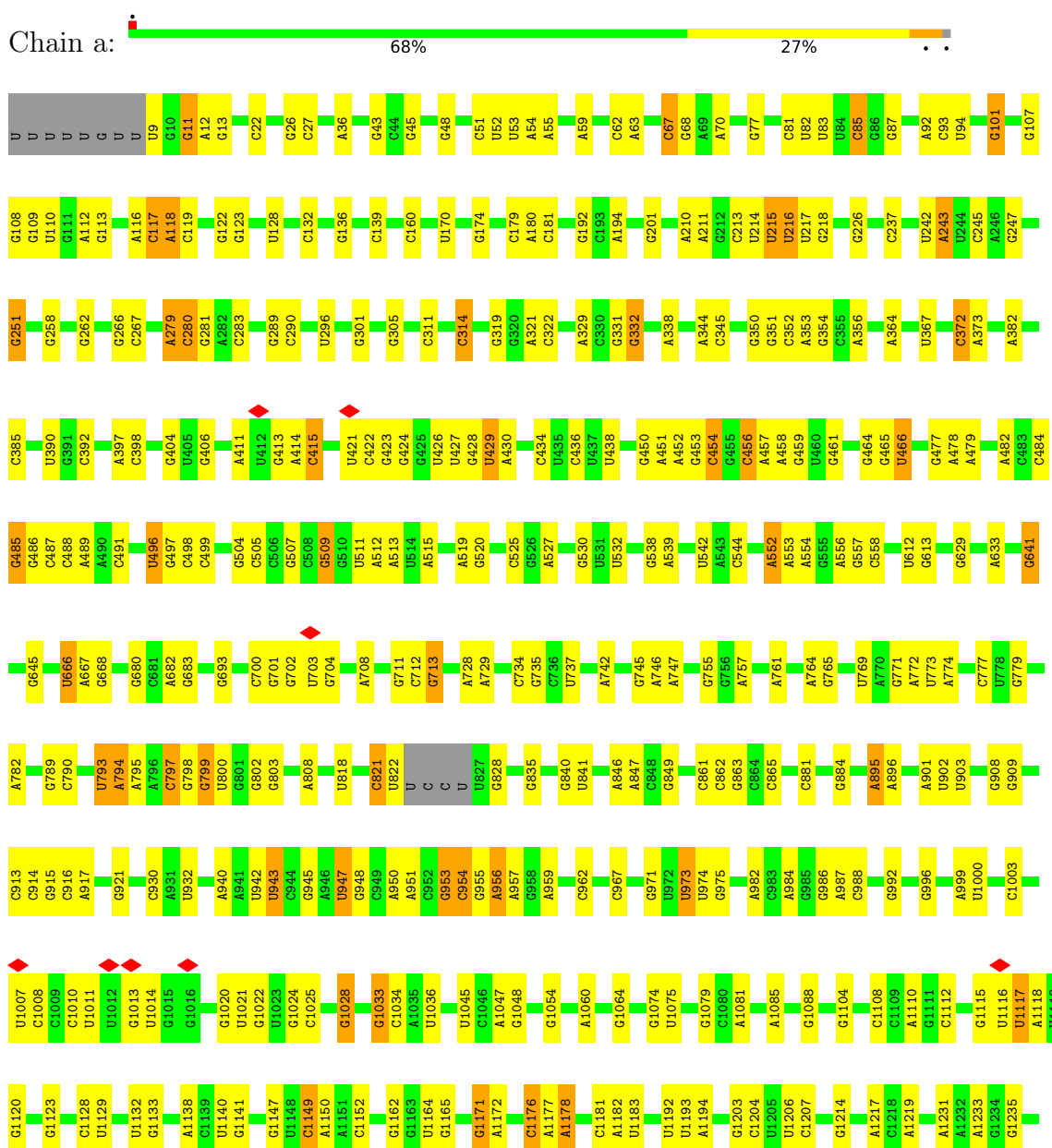
- Molecule 22 is a protein called Conserved domain protein.

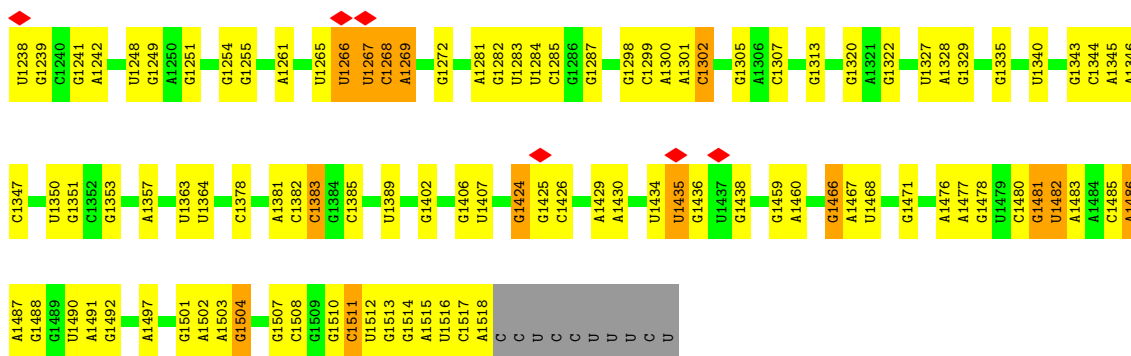
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	u	32	280	172	71	36	1	0	0

3 Residue-property plots [i](#)

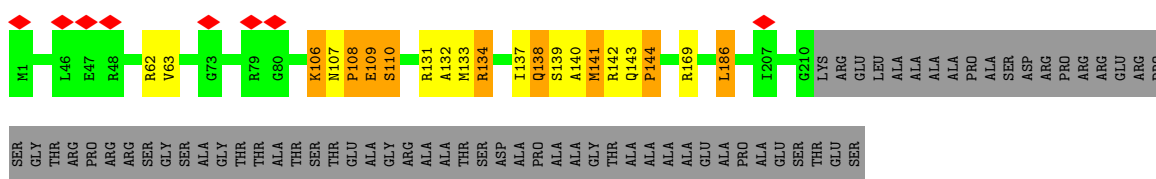
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

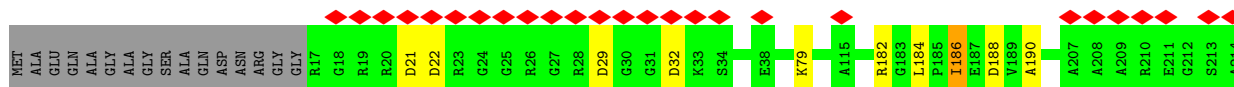
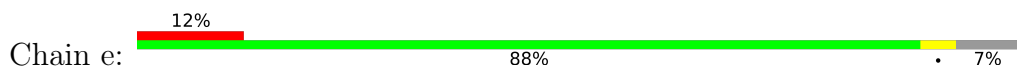




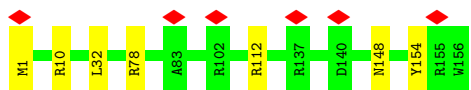
• Molecule 2: 30S ribosomal protein S3



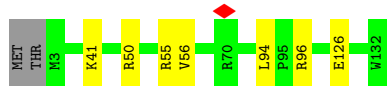
• Molecule 3: 30S ribosomal protein S5



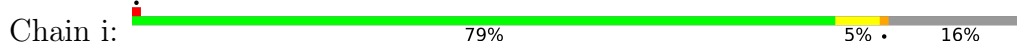
• Molecule 4: 30S ribosomal protein S7

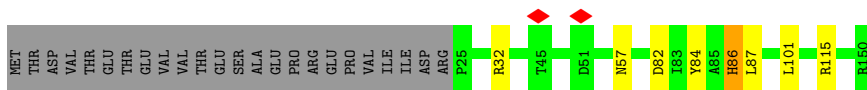


• Molecule 5: 30S ribosomal protein S8

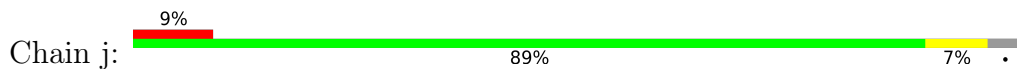


• Molecule 6: 30S ribosomal protein S9

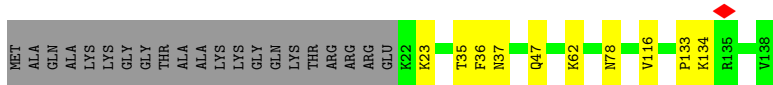
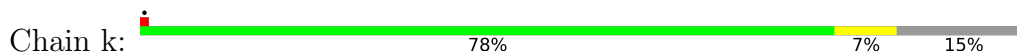




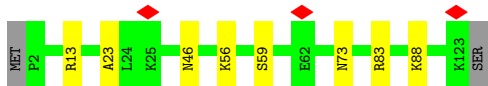
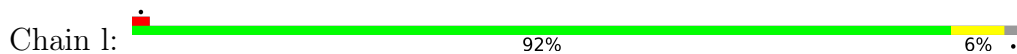
• Molecule 7: 30S ribosomal protein S10



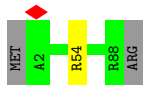
• Molecule 8: 30S ribosomal protein S11



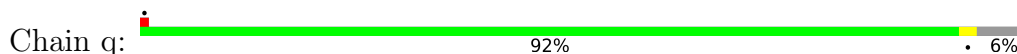
• Molecule 9: 30S ribosomal protein S12



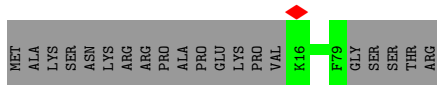
• Molecule 10: 30S ribosomal protein S15



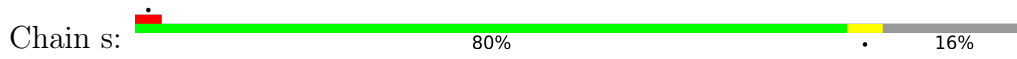
• Molecule 11: 30S ribosomal protein S17



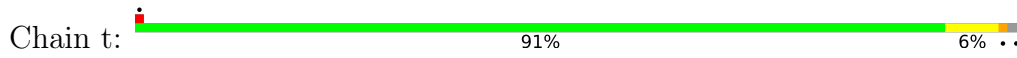
• Molecule 12: 30S ribosomal protein S18 2



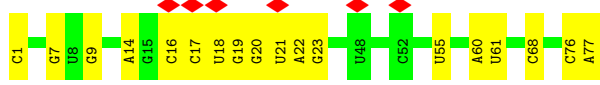
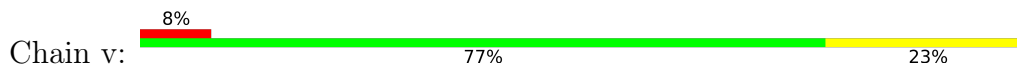
• Molecule 13: 30S ribosomal protein S19



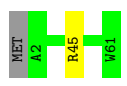
• Molecule 14: 30S ribosomal protein S20



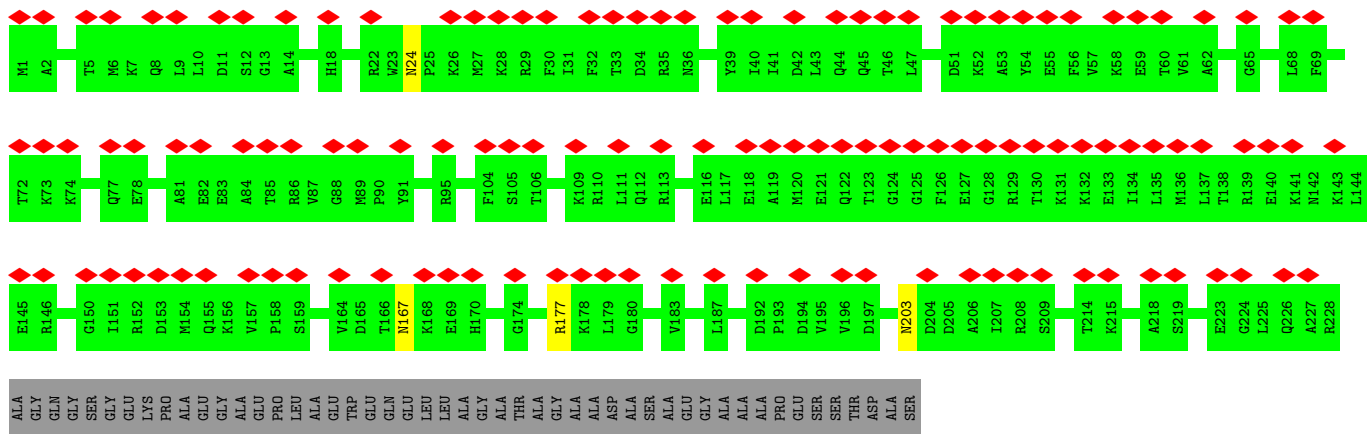
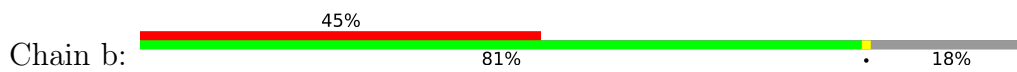
• Molecule 15: P-tRNA^{fMet}



• Molecule 16: 30S ribosomal protein S14 type Z

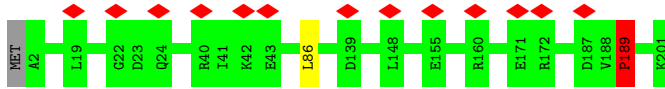


• Molecule 17: 30S ribosomal protein S2

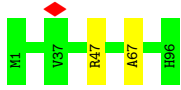


• Molecule 18: 30S ribosomal protein S4

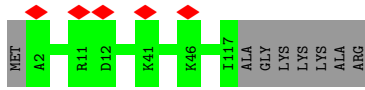




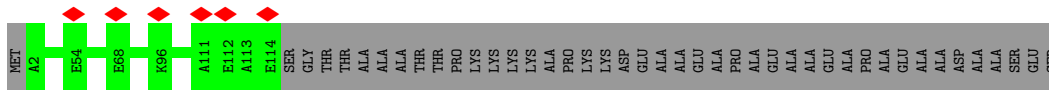
- Molecule 19: 30S ribosomal protein S6



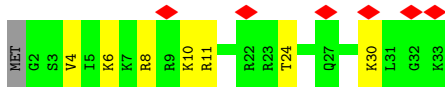
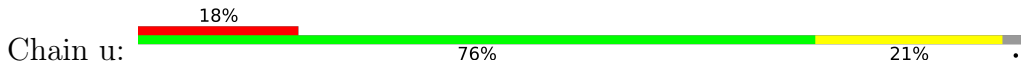
- Molecule 20: 30S ribosomal protein S13



- Molecule 21: 30S ribosomal protein S16



- Molecule 22: Conserved domain protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	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	0.643	Depositor
Minimum map value	-0.383	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	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	0.81	23/36201 (0.1%)	1.27	216/56488 (0.4%)
2	c	0.37	0/1696	0.64	1/2276 (0.0%)
3	e	0.39	0/1449	0.67	5/1949 (0.3%)
4	g	0.35	0/1260	0.58	0/1701
5	h	0.42	0/1018	0.71	2/1375 (0.1%)
6	i	0.38	0/1012	0.73	2/1362 (0.1%)
7	j	0.40	0/789	0.62	0/1069
8	k	0.31	0/889	0.57	0/1201
9	l	0.38	0/969	0.76	0/1294
10	o	0.34	0/718	0.58	0/963
11	q	0.39	0/741	0.67	1/993 (0.1%)
12	r	0.35	0/517	0.59	0/691
13	s	0.34	0/647	0.64	0/871
14	t	0.35	0/658	0.56	0/875
15	v	0.40	1/1835 (0.1%)	0.79	0/2857
16	n	0.53	0/488	0.57	0/650
17	b	0.31	0/1822	0.55	0/2457
18	d	0.38	0/1672	0.61	1/2251 (0.0%)
19	f	0.38	0/782	0.62	1/1059 (0.1%)
20	m	0.36	0/942	0.62	0/1260
21	p	0.42	0/908	0.60	0/1226
22	u	0.49	0/280	0.67	0/359
All	All	0.69	24/57293 (0.0%)	1.10	229/85227 (0.3%)

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
2	c	0	8
3	e	0	1
4	g	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	h	0	2
6	i	0	2
7	j	0	2
8	k	0	2
9	l	0	2
11	q	0	1
13	s	0	2
14	t	0	1
18	d	0	1
All	All	0	26

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	v	1	C	OP3-P	-10.55	1.48	1.61
1	a	861	C	N1-C6	-7.30	1.32	1.37
1	a	552	A	N9-C4	-7.15	1.33	1.37
1	a	552	A	N3-C4	-6.70	1.30	1.34
1	a	746	A	N3-C4	-6.28	1.31	1.34

The worst 5 of 229 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	h	94	LEU	N-CA-C	-9.60	85.08	111.00
1	a	1482	U	P-O3'-C3'	9.53	131.14	119.70
1	a	101	G	C8-N9-C4	-9.51	102.60	106.40
6	i	101	LEU	CB-CG-CD2	-9.26	95.25	111.00
1	a	70	A	N1-C2-N3	9.15	133.88	129.30

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	106	LYS	Peptide
2	c	107	ASN	Peptide
2	c	108	PRO	Peptide
2	c	110	SER	Peptide
2	c	62	ARG	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	32341	0	16267	0	0
2	c	1672	0	1722	0	0
3	e	1433	0	1485	0	0
4	g	1240	0	1293	0	0
5	h	1003	0	1039	0	0
6	i	994	0	1049	0	0
7	j	775	0	808	0	0
8	k	871	0	885	0	0
9	l	958	0	1045	0	0
10	o	709	0	747	0	0
11	q	730	0	772	0	0
12	r	512	0	543	0	0
13	s	630	0	639	0	0
14	t	655	0	703	0	0
15	v	1643	0	833	0	0
16	n	477	0	501	0	0
17	b	1793	0	1839	0	0
18	d	1641	0	1668	0	0
19	f	771	0	797	0	0
20	m	935	0	986	0	0
21	p	891	0	933	0	0
22	u	280	0	342	0	0
All	All	52954	0	36896	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 17.

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	c	208/275 (76%)	175 (84%)	19 (9%)	14 (7%)	1	16
3	e	196/214 (92%)	176 (90%)	19 (10%)	1 (0%)	29	66
4	g	154/156 (99%)	144 (94%)	9 (6%)	1 (1%)	25	62
5	h	128/132 (97%)	119 (93%)	8 (6%)	1 (1%)	19	56
6	i	124/150 (83%)	110 (89%)	13 (10%)	1 (1%)	19	56
7	j	95/101 (94%)	83 (87%)	10 (10%)	2 (2%)	7	38
8	k	115/138 (83%)	103 (90%)	10 (9%)	2 (2%)	9	42
9	l	120/124 (97%)	94 (78%)	25 (21%)	1 (1%)	19	56
10	o	85/89 (96%)	81 (95%)	4 (5%)	0	100	100
11	q	90/98 (92%)	78 (87%)	12 (13%)	0	100	100
12	r	62/84 (74%)	55 (89%)	7 (11%)	0	100	100
13	s	76/93 (82%)	68 (90%)	8 (10%)	0	100	100
14	t	82/86 (95%)	77 (94%)	3 (4%)	2 (2%)	6	35
16	n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
17	b	226/277 (82%)	212 (94%)	14 (6%)	0	100	100
18	d	198/201 (98%)	185 (93%)	12 (6%)	1 (0%)	29	66
19	f	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
20	m	114/124 (92%)	102 (90%)	12 (10%)	0	100	100
21	p	111/156 (71%)	104 (94%)	7 (6%)	0	100	100
22	u	30/33 (91%)	28 (93%)	2 (7%)	0	100	100
All	All	2366/2688 (88%)	2137 (90%)	203 (9%)	26 (1%)	18	50

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	108	PRO
2	c	109	GLU
2	c	110	SER
2	c	132	ALA
2	c	133	MET

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	c	171/212 (81%)	164 (96%)	7 (4%)	30	59
3	e	139/147 (95%)	135 (97%)	4 (3%)	42	66
4	g	132/132 (100%)	128 (97%)	4 (3%)	41	66
5	h	106/108 (98%)	103 (97%)	3 (3%)	43	67
6	i	102/125 (82%)	98 (96%)	4 (4%)	32	60
7	j	88/90 (98%)	85 (97%)	3 (3%)	37	64
8	k	91/105 (87%)	85 (93%)	6 (7%)	16	48
9	l	103/105 (98%)	98 (95%)	5 (5%)	25	56
10	o	75/77 (97%)	74 (99%)	1 (1%)	69	83
11	q	78/83 (94%)	78 (100%)	0	100	100
12	r	55/72 (76%)	55 (100%)	0	100	100
13	s	69/84 (82%)	67 (97%)	2 (3%)	42	66
14	t	69/70 (99%)	65 (94%)	4 (6%)	20	52
16	n	49/50 (98%)	48 (98%)	1 (2%)	55	74
17	b	191/218 (88%)	187 (98%)	4 (2%)	53	74
18	d	175/176 (99%)	174 (99%)	1 (1%)	86	93
19	f	85/85 (100%)	84 (99%)	1 (1%)	71	84
20	m	99/104 (95%)	99 (100%)	0	100	100
21	p	92/118 (78%)	92 (100%)	0	100	100
22	u	30/31 (97%)	23 (77%)	7 (23%)	1	6
All	All	1999/2192 (91%)	1942 (97%)	57 (3%)	45	66

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	k	62	LYS
22	u	24	THR
9	l	83	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
22	u	11	ARG
19	f	47	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
8	k	47	GLN
18	d	49	GLN
8	k	78	ASN
19	f	80	ASN
17	b	24	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1504/1528 (98%)	392 (26%)	0
15	v	76/77 (98%)	17 (22%)	0
All	All	1580/1605 (98%)	409 (25%)	0

5 of 409 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	11	G
1	a	12	A
1	a	13	G
1	a	26	G
1	a	36	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](#)

There are no chain breaks in this entry.

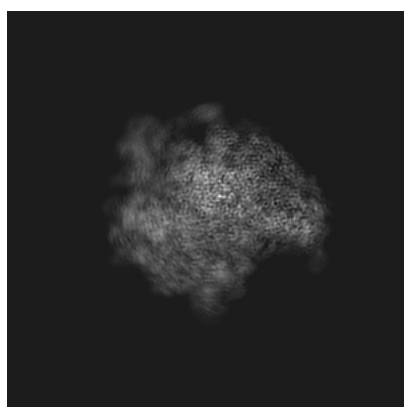
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6923. These allow visual inspection of the internal detail of the map and identification of artifacts.

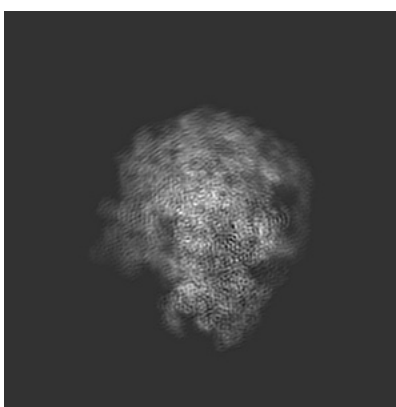
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

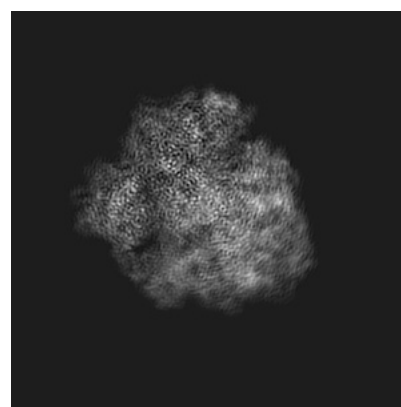
6.1.1 Primary map



X



Y

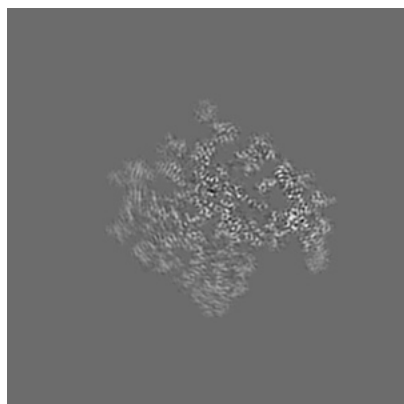


Z

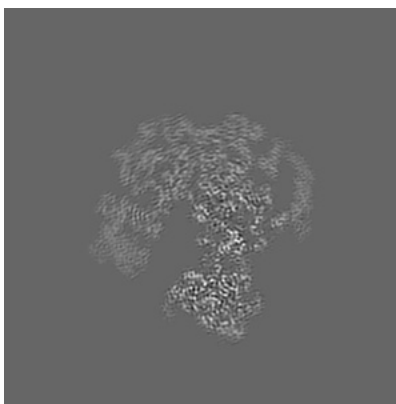
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

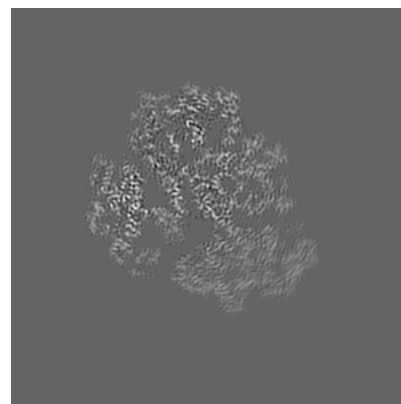
6.2.1 Primary map



X Index: 200



Y Index: 200

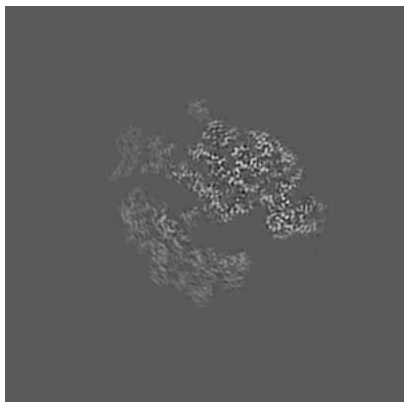


Z Index: 200

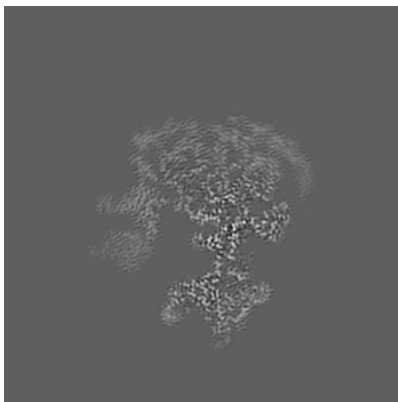
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

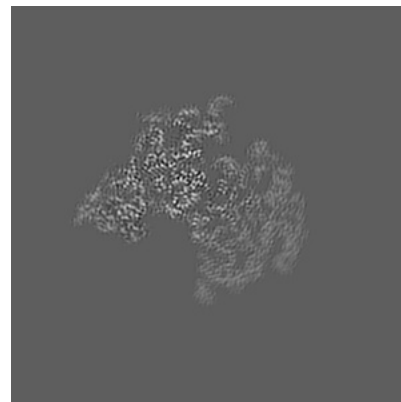
6.3.1 Primary map



X Index: 186



Y Index: 212



Z Index: 232

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

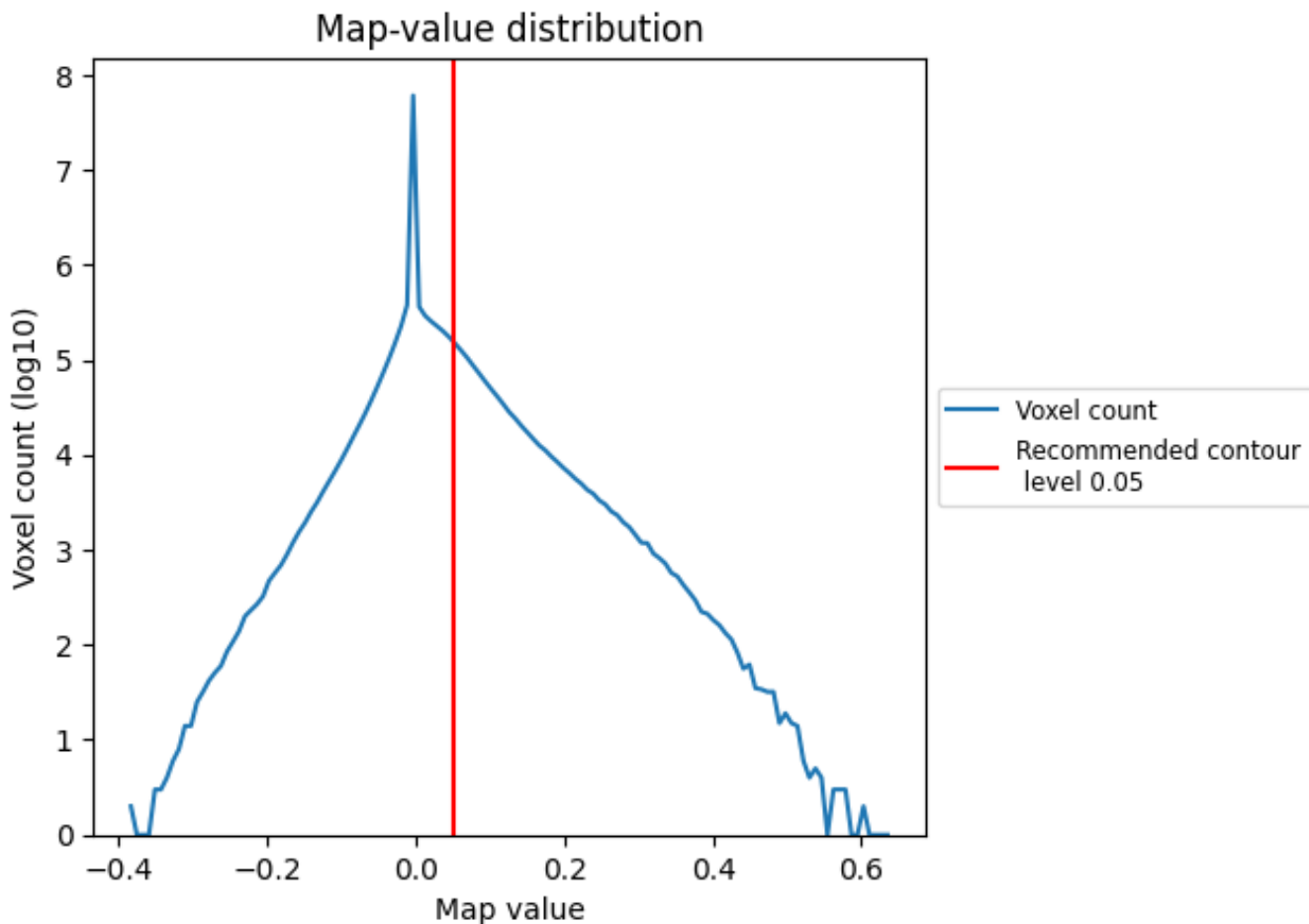
6.5 Mask visualisation

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

7 Map analysis [i](#)

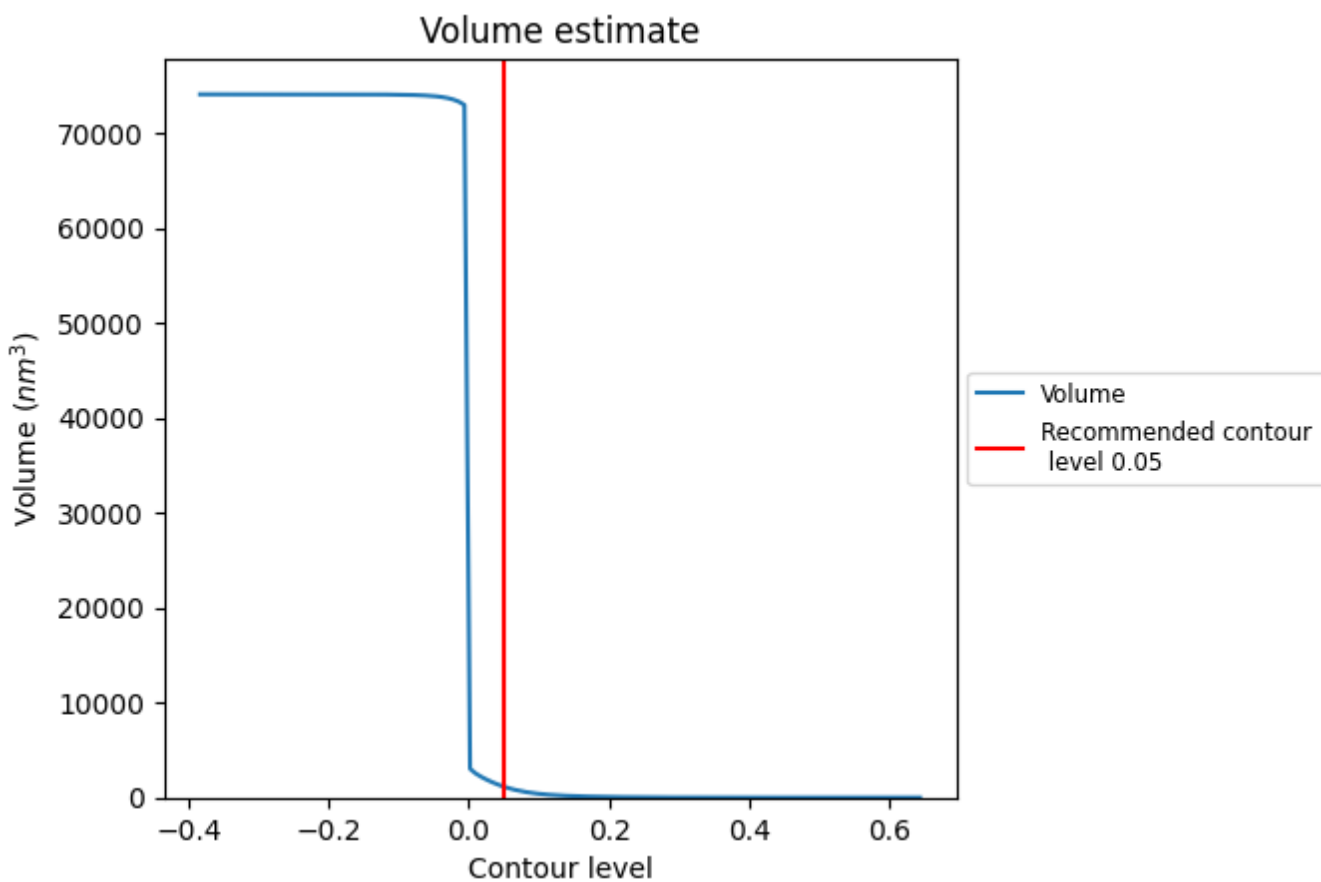
This section contains the results of statistical analysis of the map.

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.

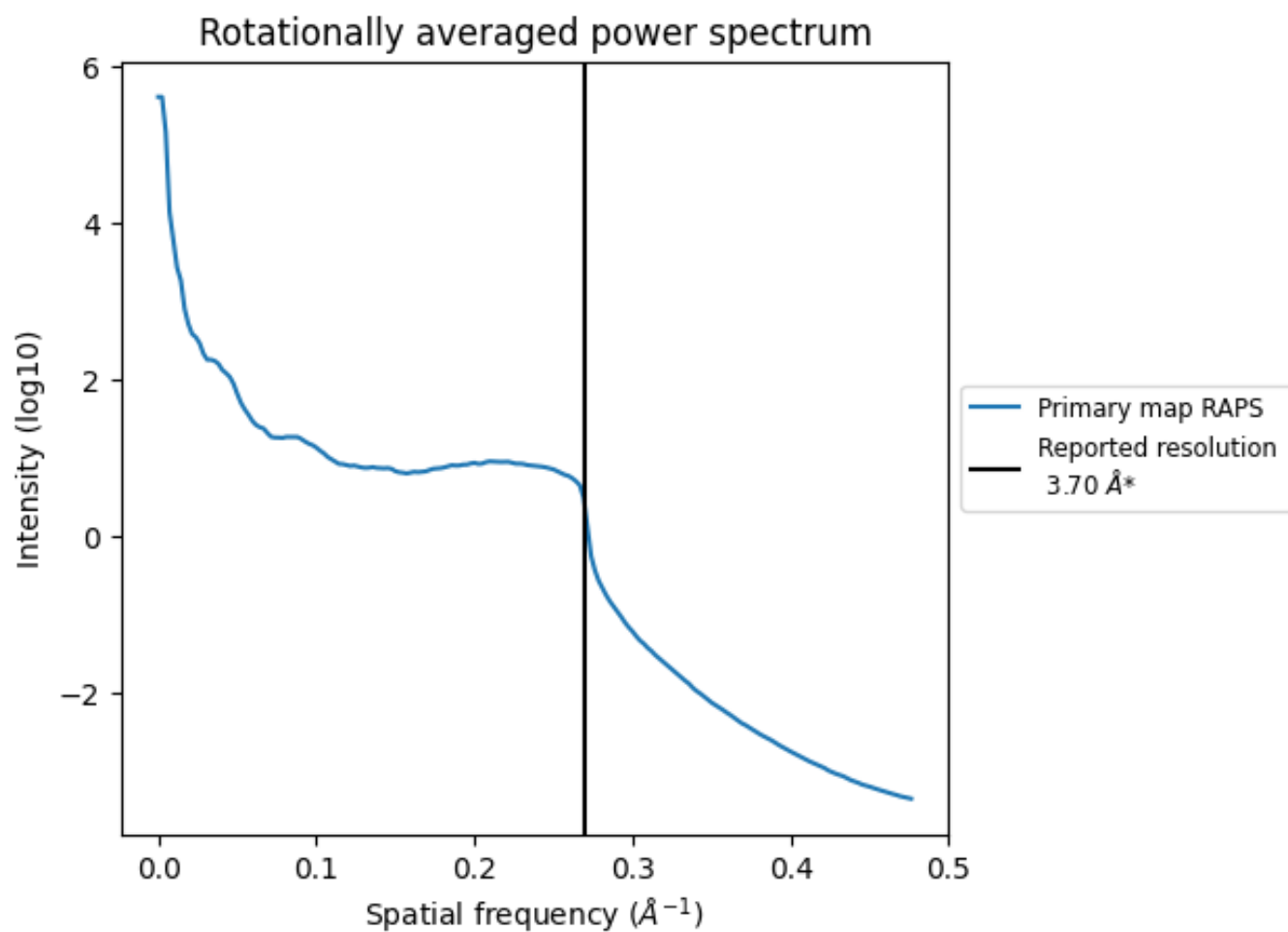
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1146 nm³; this corresponds to an approximate mass of 1036 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\AA^{-1}

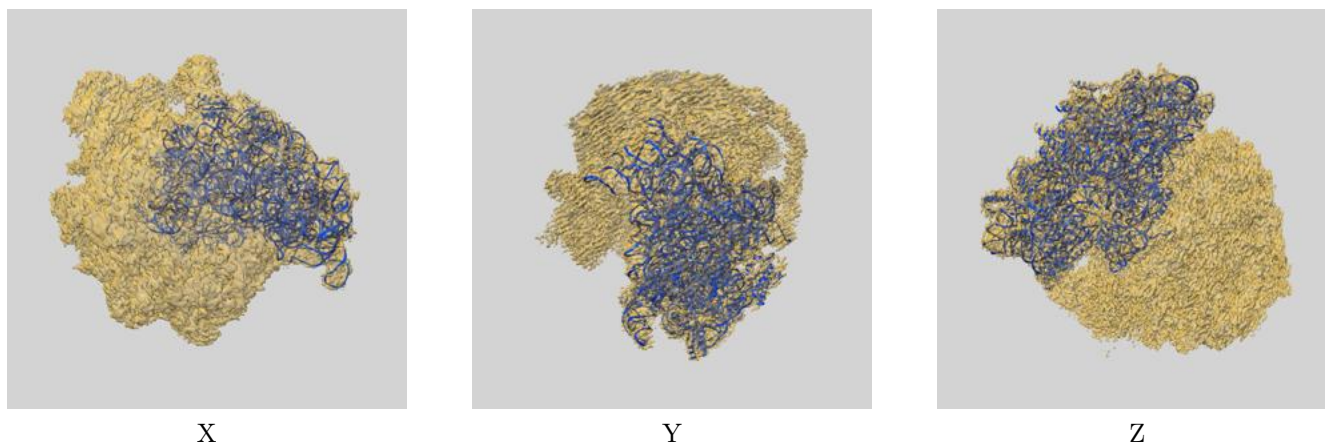
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

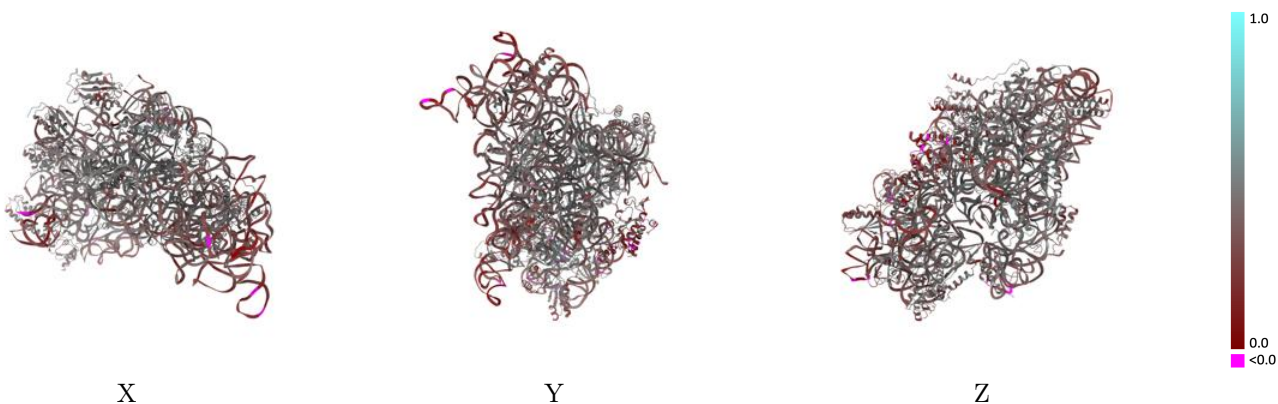
This section contains information regarding the fit between EMDB map EMD-6923 and PDB model 5ZEU. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



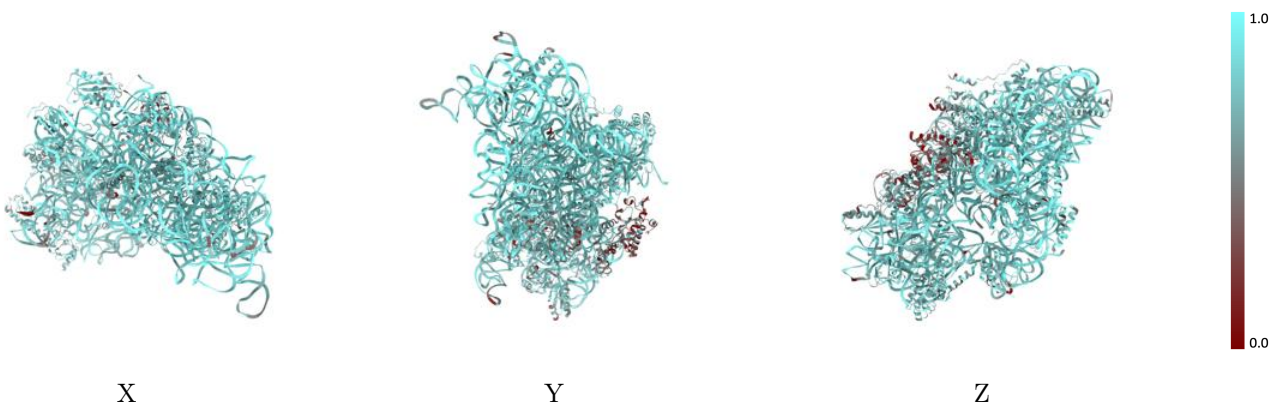
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



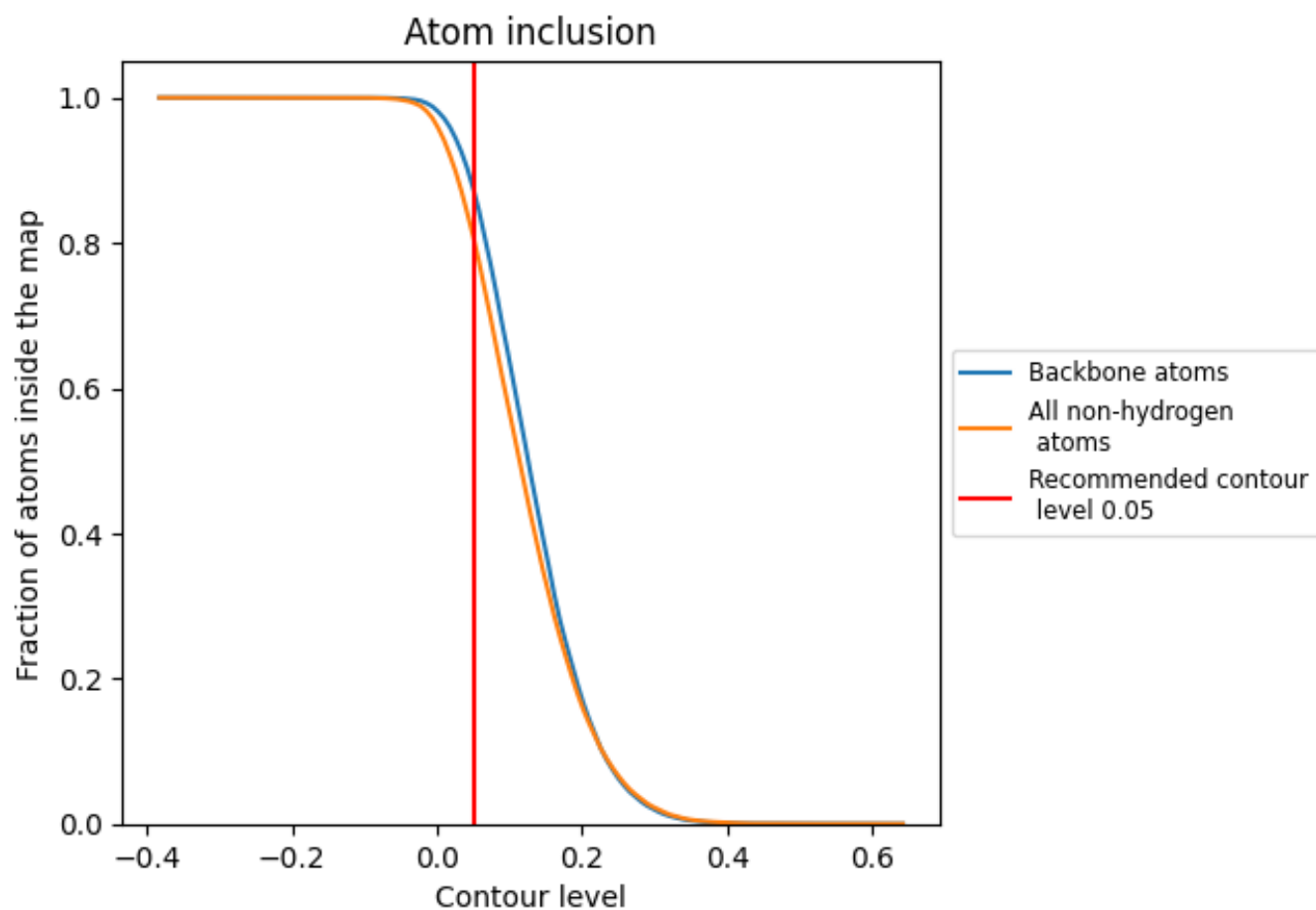
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8089	 0.3810
a	 0.8547	 0.3690
b	 0.3915	 0.2790
c	 0.7581	 0.4210
d	 0.7373	 0.3820
e	 0.7081	 0.3980
f	 0.7744	 0.4120
g	 0.7642	 0.4230
h	 0.8165	 0.4510
i	 0.8191	 0.4300
j	 0.7374	 0.4000
k	 0.7728	 0.4270
l	 0.7879	 0.4460
m	 0.7693	 0.4100
n	 0.8788	 0.4990
o	 0.8538	 0.4720
p	 0.8018	 0.4380
q	 0.7924	 0.4480
r	 0.8158	 0.4340
s	 0.7552	 0.3970
t	 0.8031	 0.4290
u	 0.5687	 0.3480
v	 0.7109	 0.2970

