



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2025 – 10:19 PM JST

PDB ID : 8YP6
EMDB ID : EMD-39462
Title : Cryo-EM map of 30S ribosomal subunit in complex with MetAP1c of Mycobacterium smegmatis
Authors : Banerjee, A.; Srinivasan, K.; Sengupta, J.
Deposited on : 2024-03-15
Resolution : 4.70 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.2

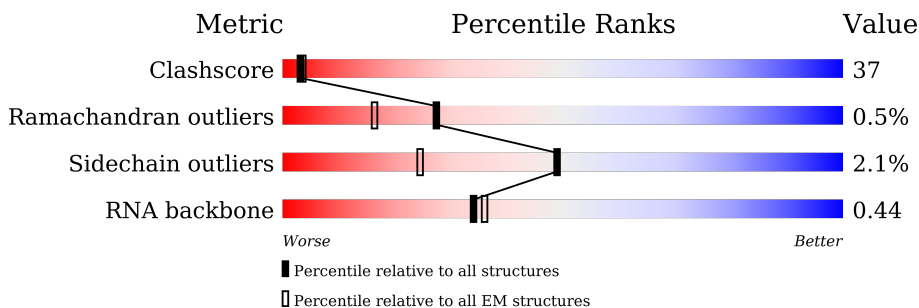
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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.



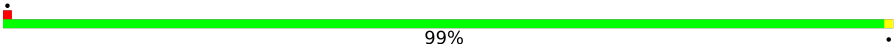
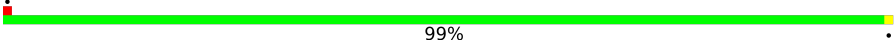
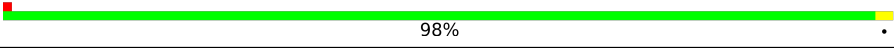
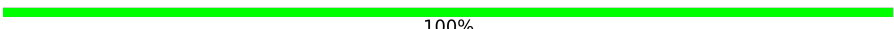
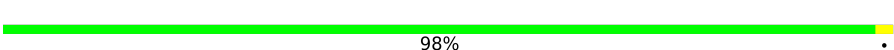
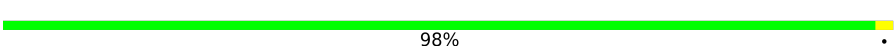
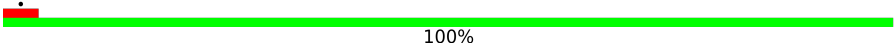
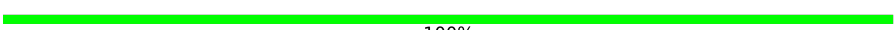
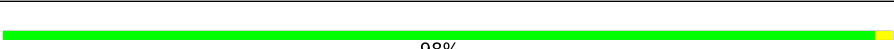

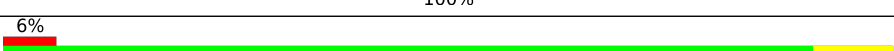

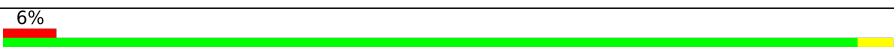
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1510	 69% 30% 18%
2	c	210	 96% 10%
3	d	200	 99% 11%
4	e	198	 98% 10%
5	f	96	 100% 11%
6	g	156	 99% 11%
7	h	130	 98% 11%

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Mol	Chain	Length	Quality of chain
8	i	126	 99%
9	j	97	 99%
10	k	117	 98%
11	l	122	 100%
12	n	60	 98%
13	o	87	 98%
14	p	113	 100%
15	q	92	 100%
16	r	64	 98%
17	t	84	 100%
18	s	80	 6% 91% 9%
19	A	296	 17% 48% 43% 5%
20	m	117	 6% 96%

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 51445 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
1	a	1506	Total	C	N	O	P	0	0
			32341	14404	5921	10510	1506		

- Molecule 2 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 3 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 5 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 6 is a protein called 30S ribosomal protein S7.

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

- Molecule 7 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 8 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 10 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 11 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS14B.

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

- Molecule 13 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 14 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 16 is a protein called Small ribosomal subunit protein bS18B.

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

- Molecule 17 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	s	80	Total	C	N	O	S	0
			647	417	120	109	1	0

- Molecule 19 is a protein called Methionine aminopeptidase.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	A	285	Total	C	N	O	S	0
			2185	1382	372	422	9	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	286	ALA	-	expression tag	UNP I7FJS2
A	287	ALA	-	expression tag	UNP I7FJS2
A	288	ALA	-	expression tag	UNP I7FJS2
A	289	LEU	-	expression tag	UNP I7FJS2
A	290	GLN	-	expression tag	UNP I7FJS2
A	291	HIS	-	expression tag	UNP I7FJS2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	292	HIS	-	expression tag	UNP I7FJS2
A	293	HIS	-	expression tag	UNP I7FJS2
A	294	HIS	-	expression tag	UNP I7FJS2
A	295	HIS	-	expression tag	UNP I7FJS2
A	296	HIS	-	expression tag	UNP I7FJS2

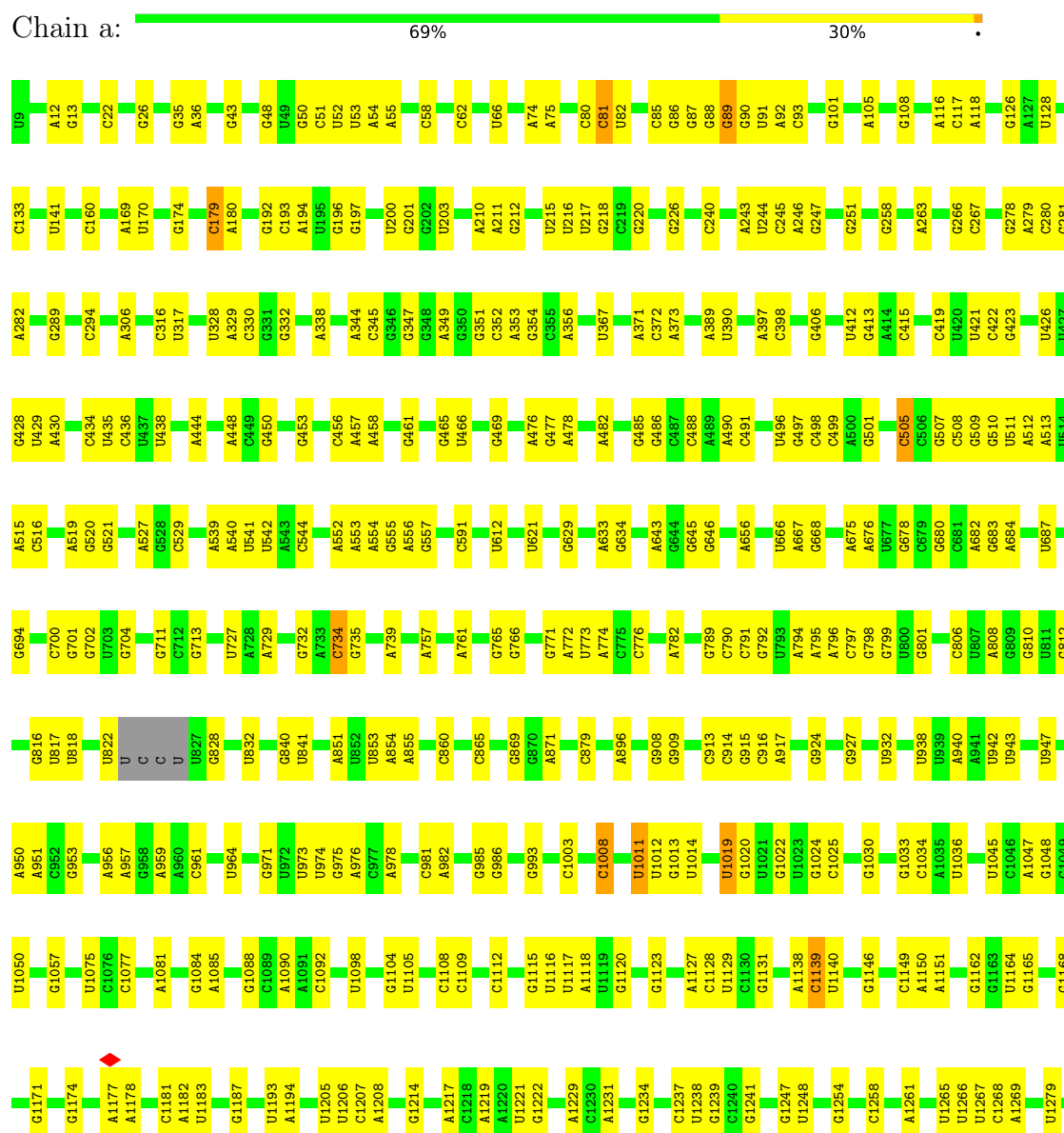
- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	117	Total	C	N	O	S	0	0
			940	575	192	170	3		

3 Residue-property plots

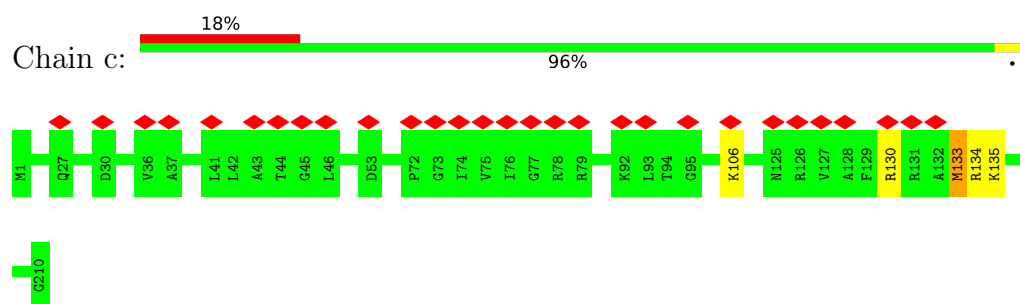
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA

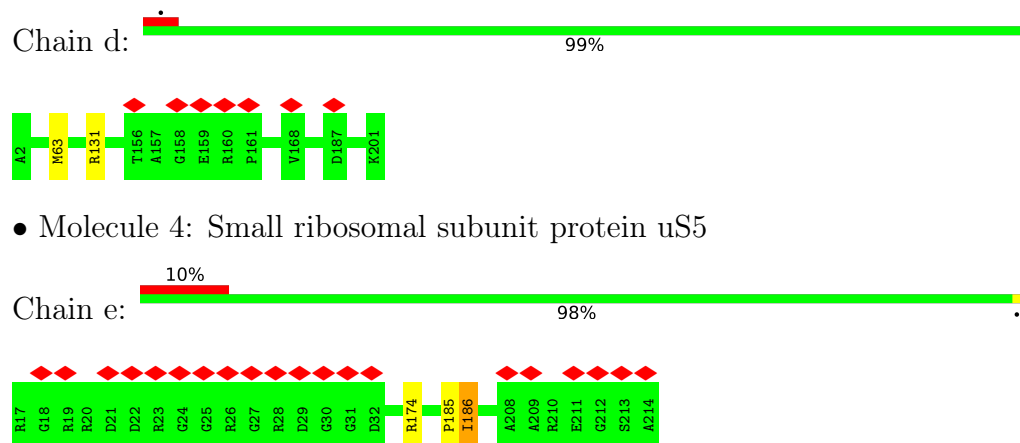




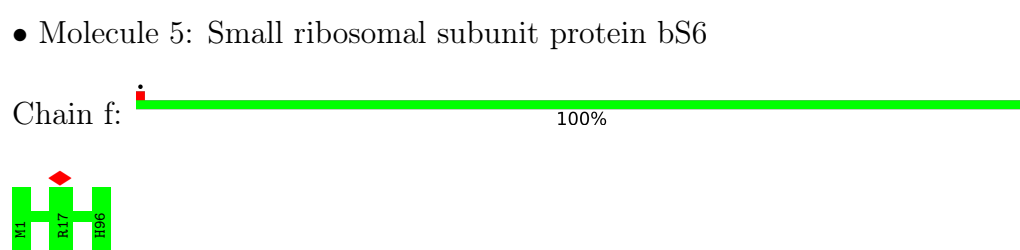
- Molecule 2: Small ribosomal subunit protein uS3



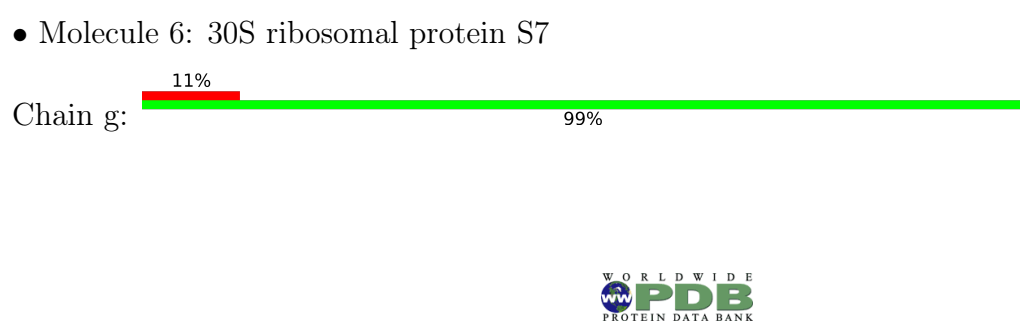
- Molecule 3: Small ribosomal subunit protein uS4



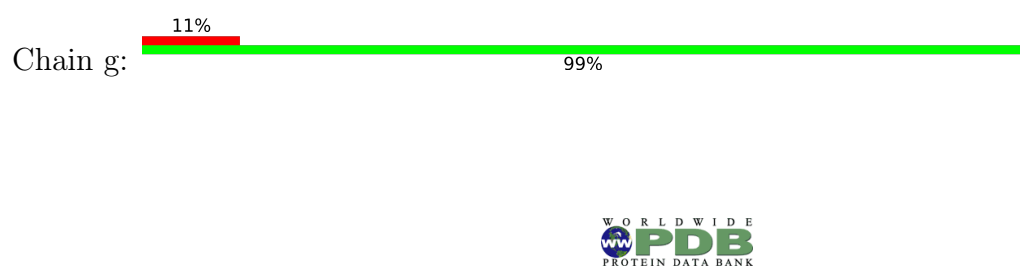
- Molecule 4: Small ribosomal subunit protein uS5

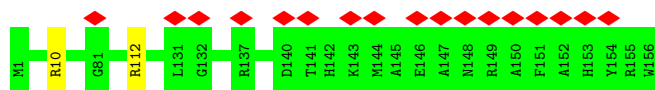


- Molecule 5: Small ribosomal subunit protein bS6



- Molecule 6: 30S ribosomal protein S7





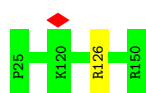
- Molecule 7: Small ribosomal subunit protein uS8

Chain h: 98%



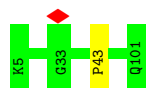
- Molecule 8: Small ribosomal subunit protein uS9

Chain i: 99%



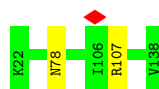
- Molecule 9: Small ribosomal subunit protein uS10

Chain j: 99%



- Molecule 10: Small ribosomal subunit protein uS11

Chain k: 98%



- Molecule 11: Small ribosomal subunit protein uS12

Chain l: 100%

There are no outlier residues recorded for this chain.

- Molecule 12: Small ribosomal subunit protein uS14B

Chain n: 98%



- Molecule 13: Small ribosomal subunit protein uS15

Chain o: 98%



- Molecule 14: Small ribosomal subunit protein bS16

Chain p: 100%



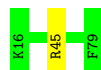
- Molecule 15: Small ribosomal subunit protein uS17

Chain q: 100%

There are no outlier residues recorded for this chain.

- Molecule 16: Small ribosomal subunit protein bS18B

Chain r: 98%



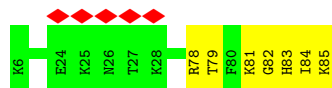
- Molecule 17: Small ribosomal subunit protein bS20

Chain t: 100%

There are no outlier residues recorded for this chain.

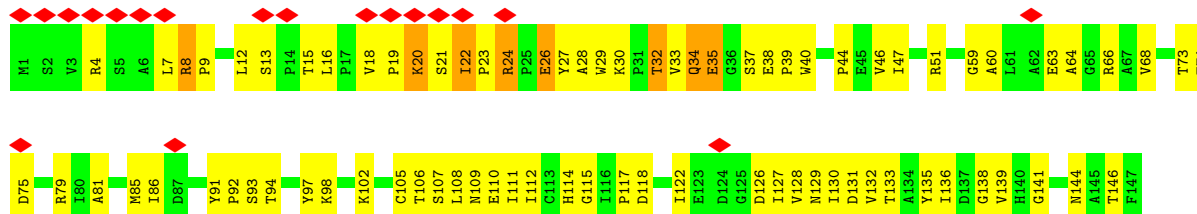
- Molecule 18: Small ribosomal subunit protein uS19

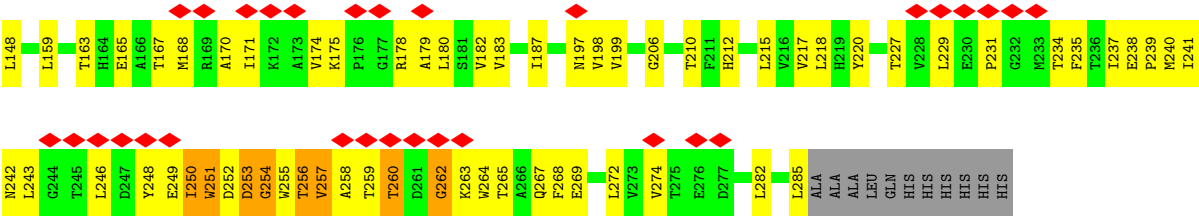
Chain s: 6% 91% 9%



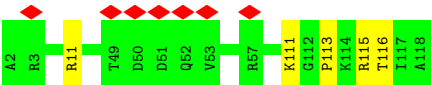
- Molecule 19: Methionine aminopeptidase

Chain A: 17% 48% 43% 5%





• Molecule 20: Small ribosomal subunit protein uS13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50296	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20.7	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.005	Depositor
Map size (\AA)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	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	0.37	0/36201	0.92	42/56488 (0.1%)
2	c	0.25	0/1696	0.53	0/2276
3	d	0.26	0/1672	0.55	0/2251
4	e	0.28	0/1449	0.58	0/1949
5	f	0.29	0/782	0.55	0/1059
6	g	0.26	0/1260	0.53	0/1701
7	h	0.28	0/1018	0.57	0/1375
8	i	0.26	0/1012	0.56	0/1362
9	j	0.24	0/789	0.57	0/1069
10	k	0.27	0/889	0.54	0/1201
11	l	0.27	0/969	0.65	0/1294
12	n	0.24	0/488	0.53	0/650
13	o	0.26	0/718	0.57	1/963 (0.1%)
14	p	0.26	0/908	0.53	0/1226
15	q	0.29	0/741	0.62	0/993
16	r	0.25	0/517	0.57	0/691
17	t	0.27	0/658	0.55	0/875
18	s	0.28	0/664	0.55	0/893
19	A	0.26	0/2237	0.51	0/3057
20	m	0.29	0/947	0.65	0/1267
All	All	0.33	0/55615	0.82	43/82640 (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
3	d	0	1
7	h	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	330	C	N1-C2-O2	15.17	128.00	118.90
1	a	330	C	N3-C2-O2	-12.61	113.07	121.90
1	a	108	G	N3-C2-N2	9.33	126.43	119.90
1	a	80	C	N3-C2-O2	-9.14	115.50	121.90
1	a	179	C	N1-C2-O2	8.65	124.09	118.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	d	63	MET	Peptide
7	h	55	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	16271	0	0
2	c	1672	0	1722	0	0
3	d	1641	0	1668	0	0
4	e	1433	0	1490	0	0
5	f	771	0	797	0	0
6	g	1240	0	1293	0	0
7	h	1003	0	1039	0	0
8	i	994	0	1050	0	0
9	j	775	0	808	0	0
10	k	871	0	885	0	0
11	l	958	0	1045	0	0
12	n	477	0	503	0	0
13	o	709	0	747	0	0
14	p	891	0	935	0	0
15	q	730	0	774	0	0
16	r	512	0	543	0	0
17	t	655	0	707	0	0
18	s	647	0	664	0	0
19	A	2185	0	2139	139	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	m	940	0	989	0	0
All	All	51445	0	36069	139	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 37.

The worst 5 of 139 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)
19:A:37:SER:HB2	19:A:40:TRP:CZ2	1.79	1.17
19:A:37:SER:HB2	19:A:40:TRP:HZ2	1.04	1.15
19:A:37:SER:HA	19:A:210:THR:HG21	1.50	0.92
19:A:37:SER:CB	19:A:40:TRP:CZ2	2.57	0.86
19:A:115:GLY:HA2	19:A:256:THR:HA	1.59	0.85

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	208/210 (99%)	180 (86%)	25 (12%)	3 (1%)	9	40
3	d	198/200 (99%)	185 (93%)	13 (7%)	0	100	100
4	e	196/198 (99%)	172 (88%)	22 (11%)	2 (1%)	13	49
5	f	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
6	g	154/156 (99%)	148 (96%)	6 (4%)	0	100	100
7	h	128/130 (98%)	112 (88%)	15 (12%)	1 (1%)	16	54
8	i	124/126 (98%)	111 (90%)	13 (10%)	0	100	100
9	j	95/97 (98%)	88 (93%)	6 (6%)	1 (1%)	12	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	k	115/117 (98%)	99 (86%)	16 (14%)	0	100	100
11	l	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
12	n	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
13	o	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
14	p	111/113 (98%)	107 (96%)	4 (4%)	0	100	100
15	q	90/92 (98%)	79 (88%)	11 (12%)	0	100	100
16	r	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
17	t	82/84 (98%)	79 (96%)	3 (4%)	0	100	100
18	s	78/80 (98%)	65 (83%)	11 (14%)	2 (3%)	4	26
19	A	283/296 (96%)	256 (90%)	25 (9%)	2 (1%)	19	56
20	m	115/117 (98%)	100 (87%)	13 (11%)	2 (2%)	7	36
All	All	2396/2445 (98%)	2164 (90%)	219 (9%)	13 (0%)	27	64

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	144	PRO
4	e	186	ILE
19	A	254	GLY
20	m	116	THR
2	c	133	MET

5.3.2 Protein sidechains ⓘ

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	171/171 (100%)	164 (96%)	7 (4%)	26	48
3	d	175/175 (100%)	174 (99%)	1 (1%)	84	88
4	e	139/139 (100%)	137 (99%)	2 (1%)	62	76
5	f	85/85 (100%)	85 (100%)	0	100	100
6	g	132/132 (100%)	130 (98%)	2 (2%)	60	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	h	106/106 (100%)	105 (99%)	1 (1%)	75	83
8	i	102/102 (100%)	101 (99%)	1 (1%)	73	82
9	j	88/88 (100%)	88 (100%)	0	100	100
10	k	91/91 (100%)	89 (98%)	2 (2%)	47	66
11	l	103/103 (100%)	103 (100%)	0	100	100
12	n	49/49 (100%)	48 (98%)	1 (2%)	50	69
13	o	75/75 (100%)	74 (99%)	1 (1%)	65	77
14	p	92/92 (100%)	92 (100%)	0	100	100
15	q	78/78 (100%)	78 (100%)	0	100	100
16	r	55/55 (100%)	54 (98%)	1 (2%)	54	71
17	t	69/69 (100%)	69 (100%)	0	100	100
18	s	71/71 (100%)	66 (93%)	5 (7%)	12	33
19	A	234/242 (97%)	218 (93%)	16 (7%)	13	34
20	m	99/99 (100%)	96 (97%)	3 (3%)	36	56
All	All	2014/2022 (100%)	1971 (98%)	43 (2%)	49	67

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	A	24	ARG
19	A	251	TRP
19	A	26	GLU
19	A	34	GLN
19	A	256	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
20	m	92	HIS
19	A	129	ASN
18	s	83	HIS
18	s	52	HIS
19	A	34	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1504/1510 (99%)	452 (30%)	0

5 of 452 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	12	A
1	a	13	G
1	a	22	C
1	a	26	G
1	a	35	G

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 oligosaccharides 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.

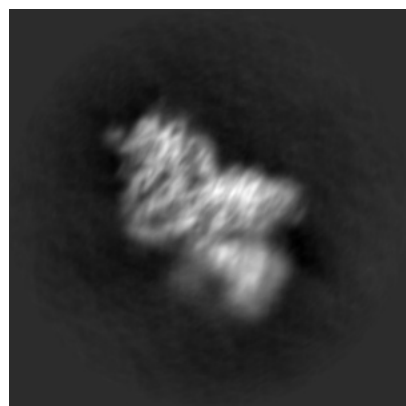
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39462. These allow visual inspection of the internal detail of the map and identification of artifacts.

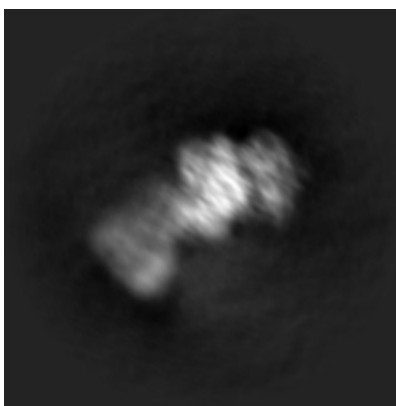
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

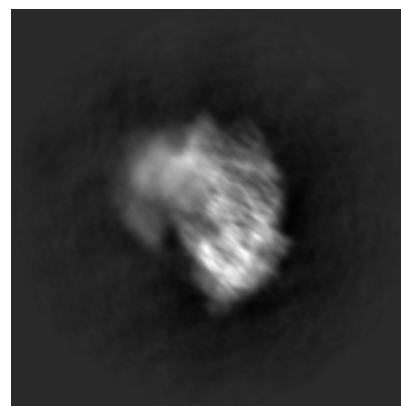
6.1.1 Primary map



X

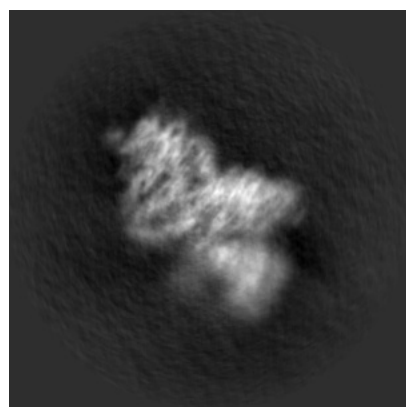


Y

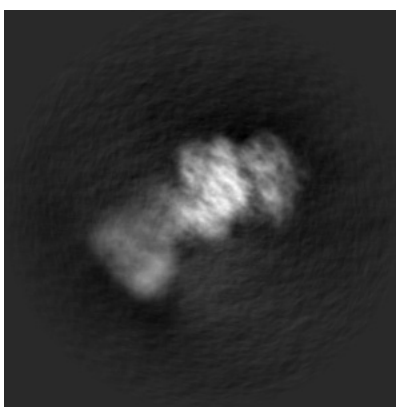


Z

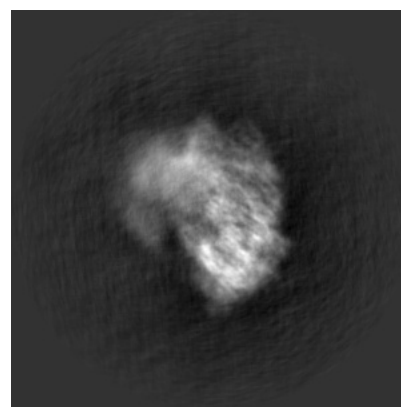
6.1.2 Raw map



X



Y

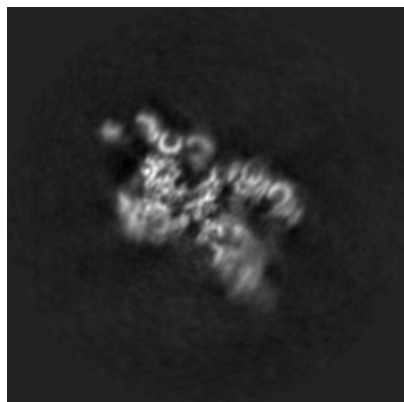


Z

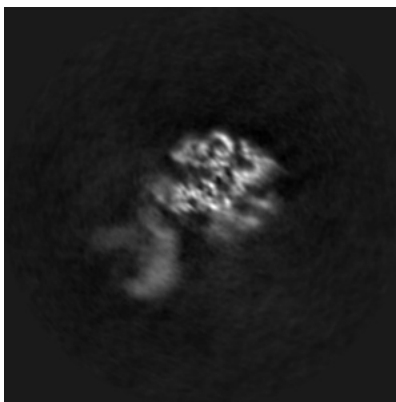
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

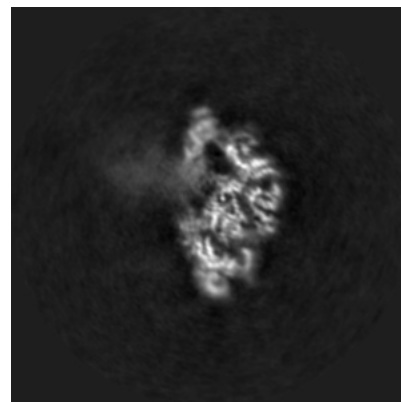
6.2.1 Primary map



X Index: 175

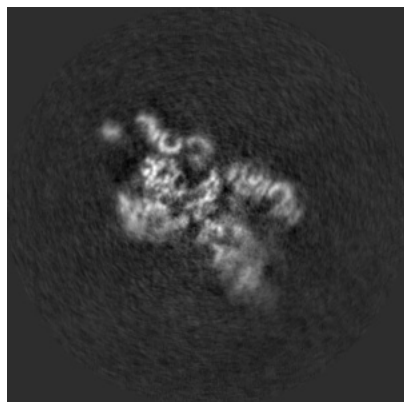


Y Index: 175

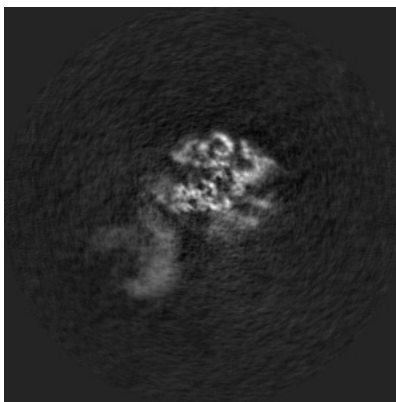


Z Index: 175

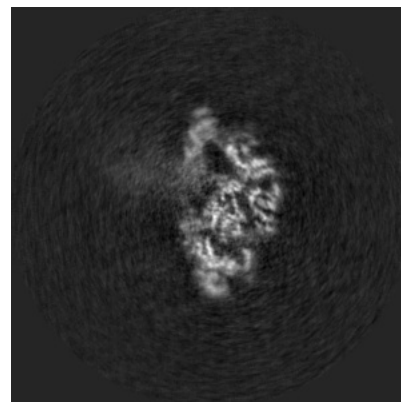
6.2.2 Raw map



X Index: 175



Y Index: 175

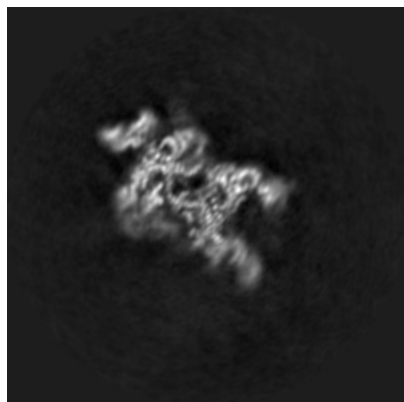


Z Index: 175

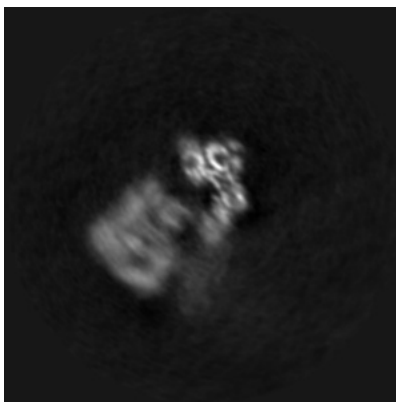
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

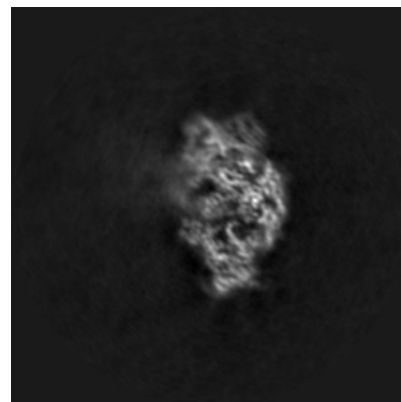
6.3.1 Primary map



X Index: 185

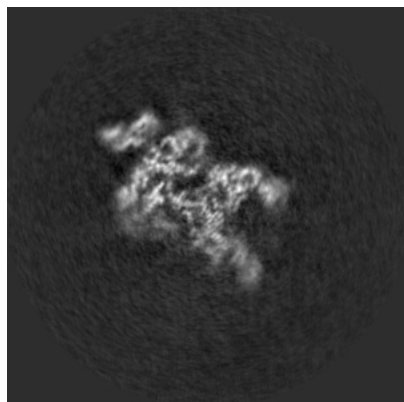


Y Index: 209

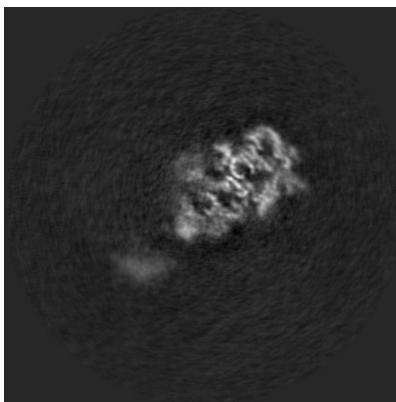


Z Index: 190

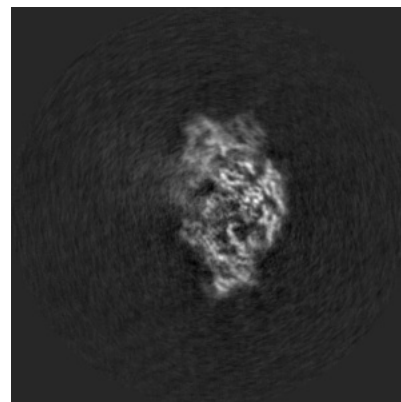
6.3.2 Raw map



X Index: 184



Y Index: 148

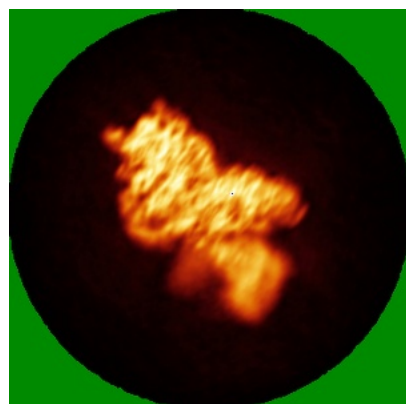


Z Index: 189

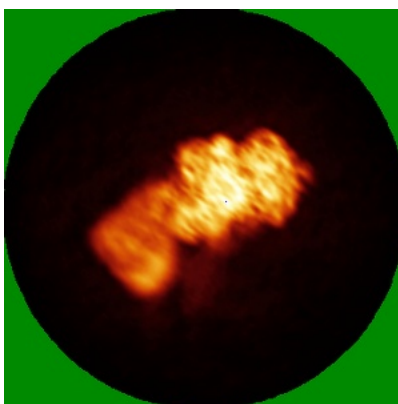
The images above show the largest variance slices of the map in three orthogonal directions.

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

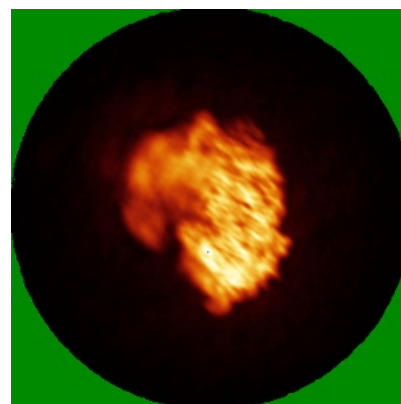
6.4.1 Primary map



X

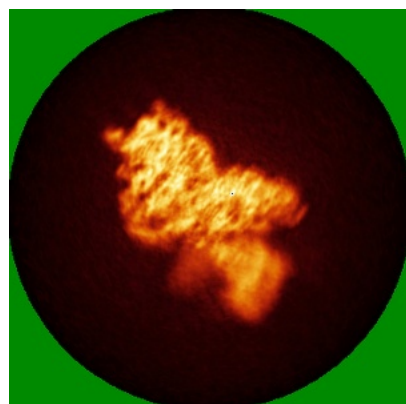


Y

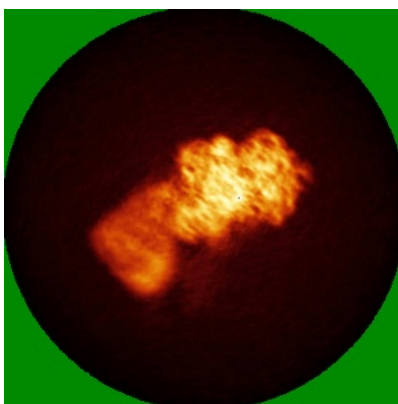


Z

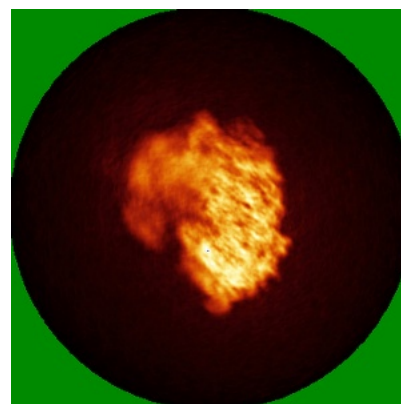
6.4.2 Raw map



X



Y



Z

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

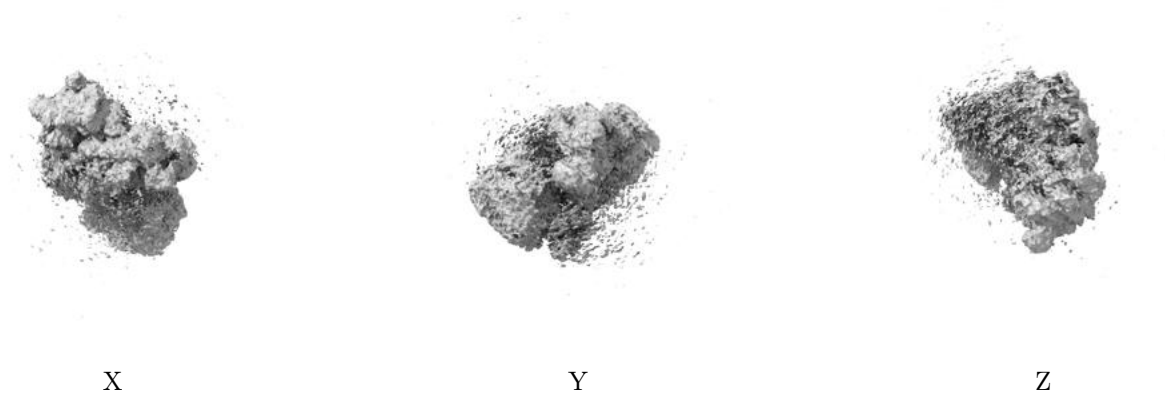
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

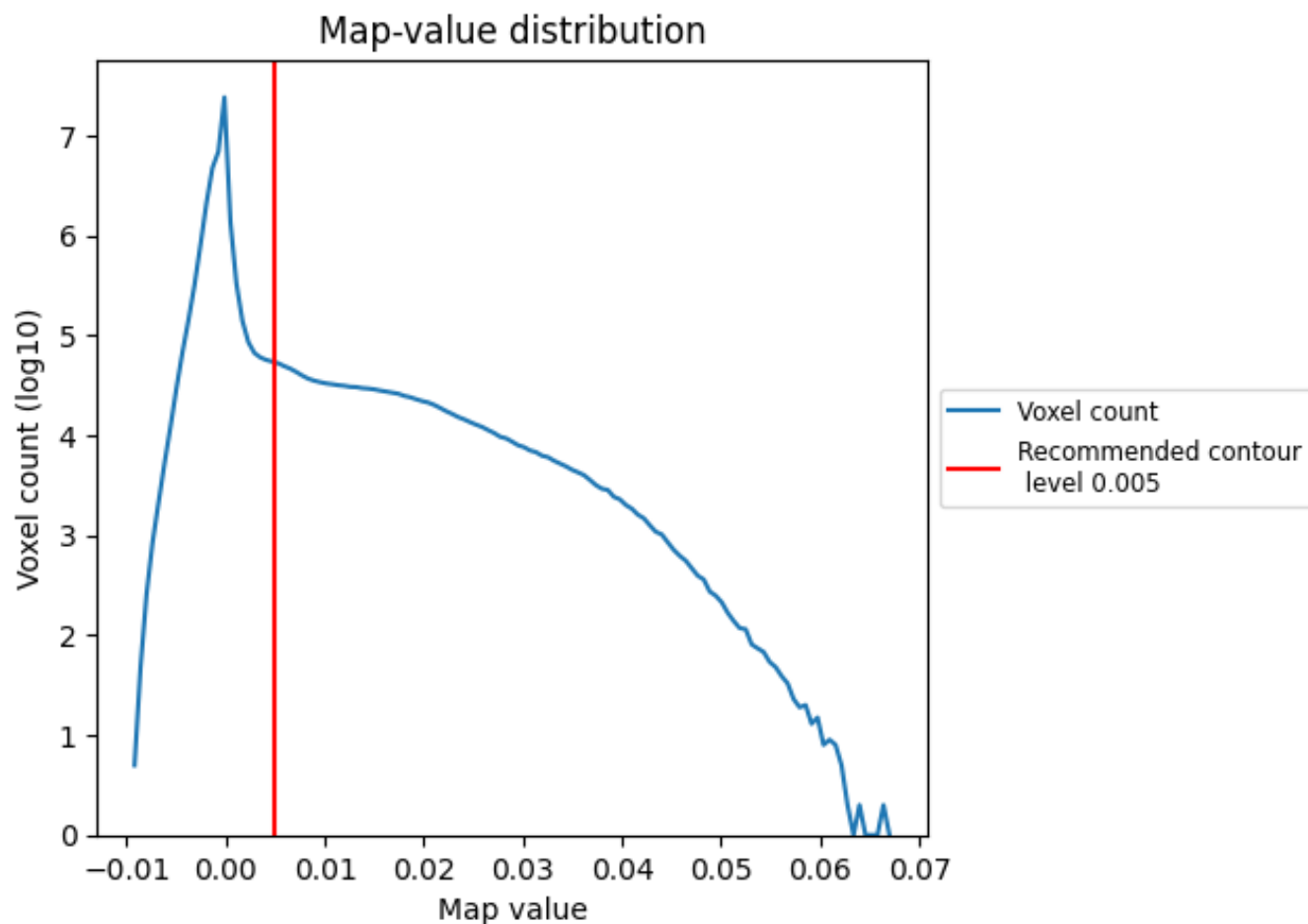
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

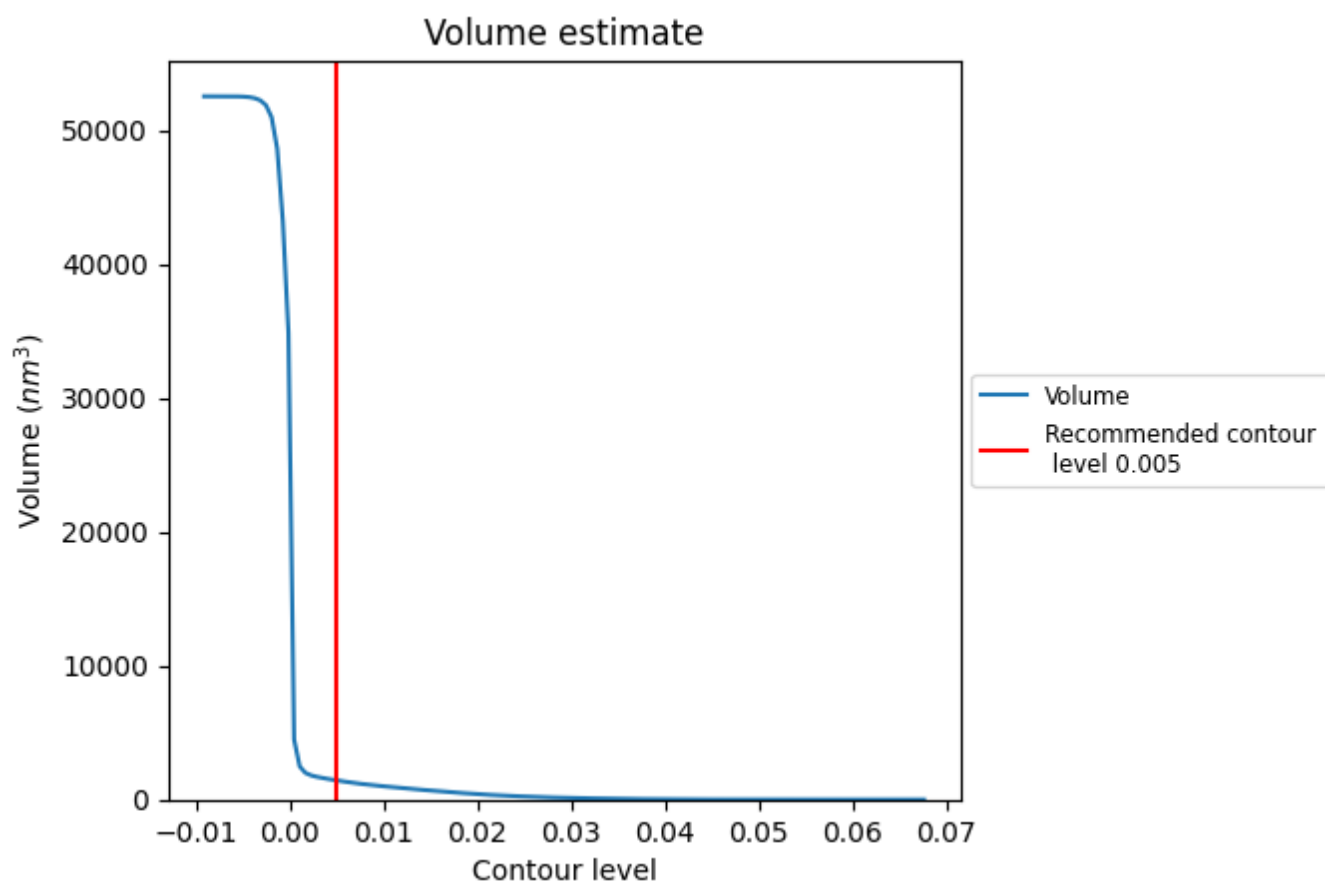
This section contains the results of statistical analysis of the map.

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.

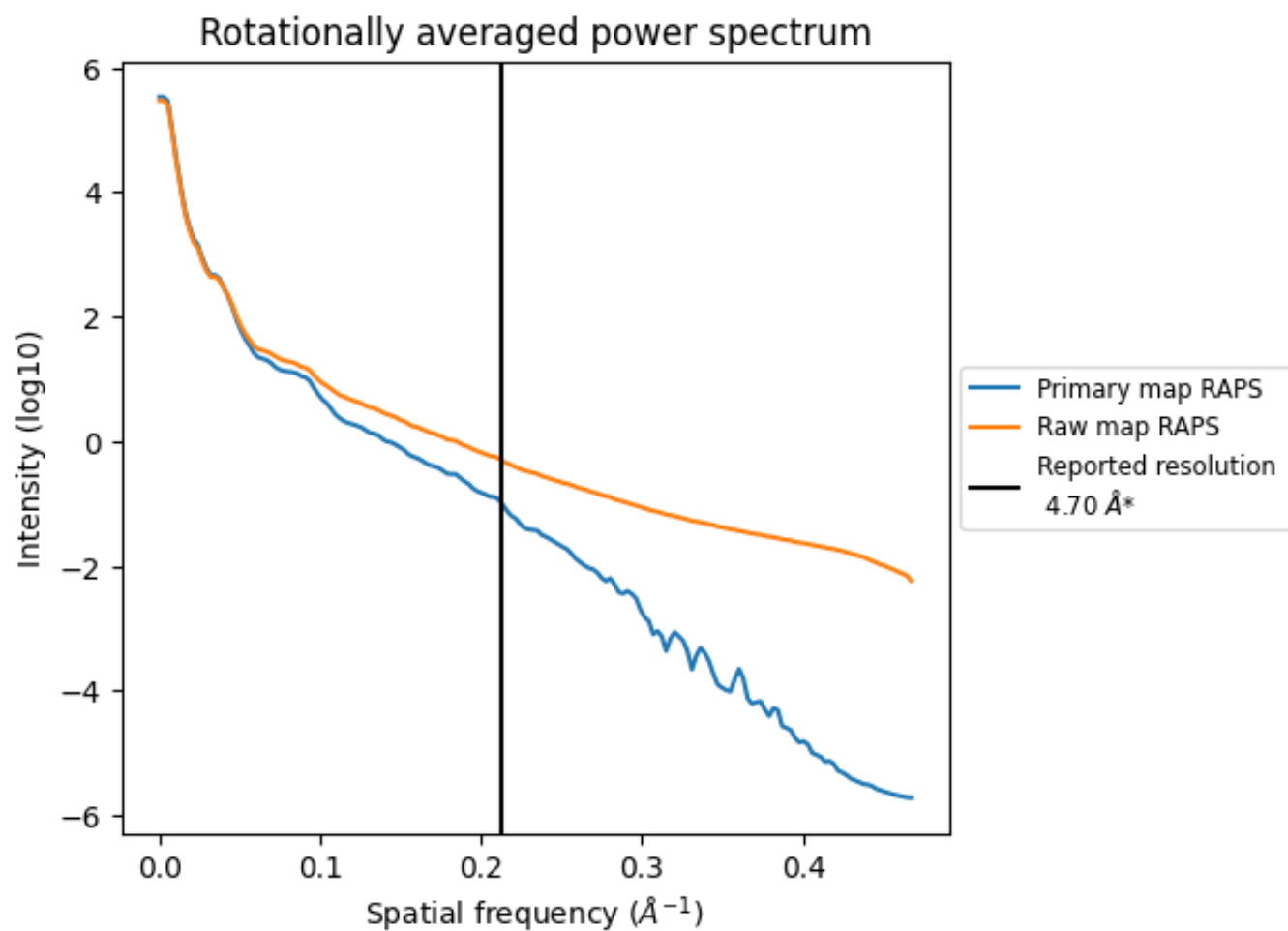
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1429 nm³; this corresponds to an approximate mass of 1291 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 ⓘ

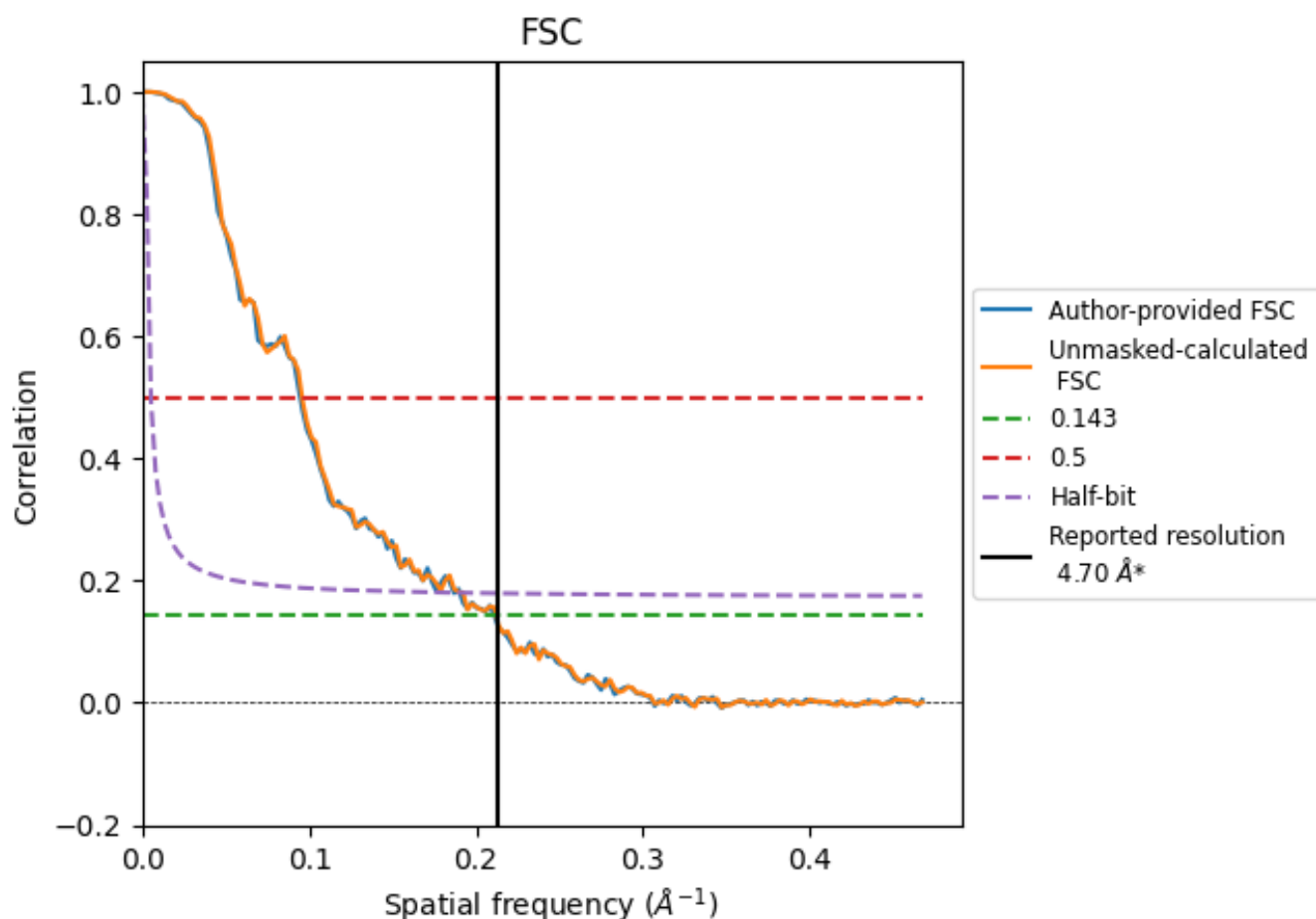


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

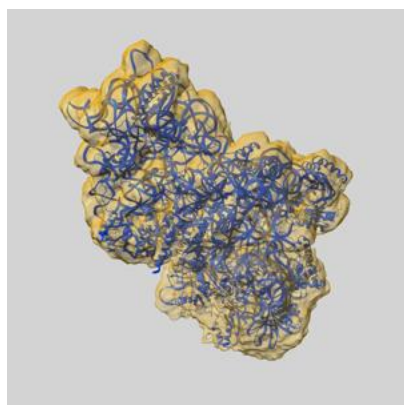
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.74	10.57	5.35
Unmasked-calculated*	4.71	10.44	5.21

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

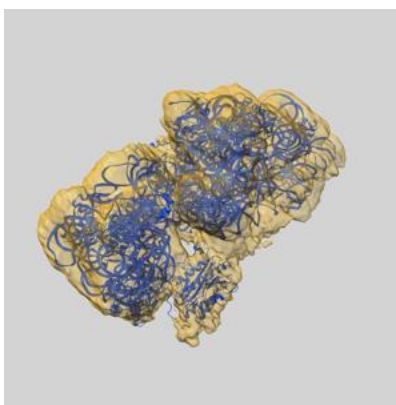
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39462 and PDB model 8YP6. Per-residue inclusion information can be found in section [3](#) on page [8](#).

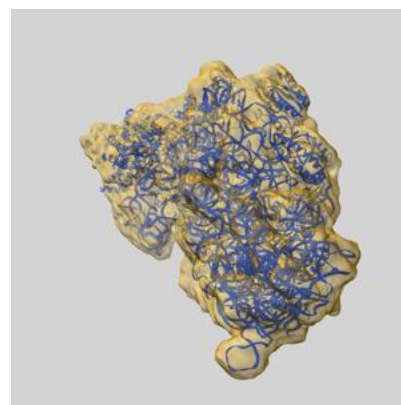
9.1 Map-model overlay [i](#)



X



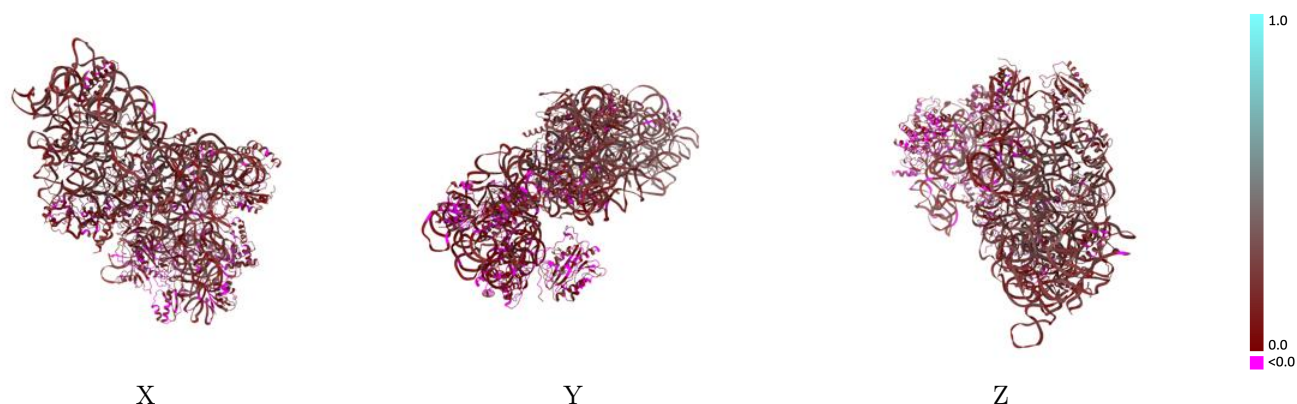
Y



Z

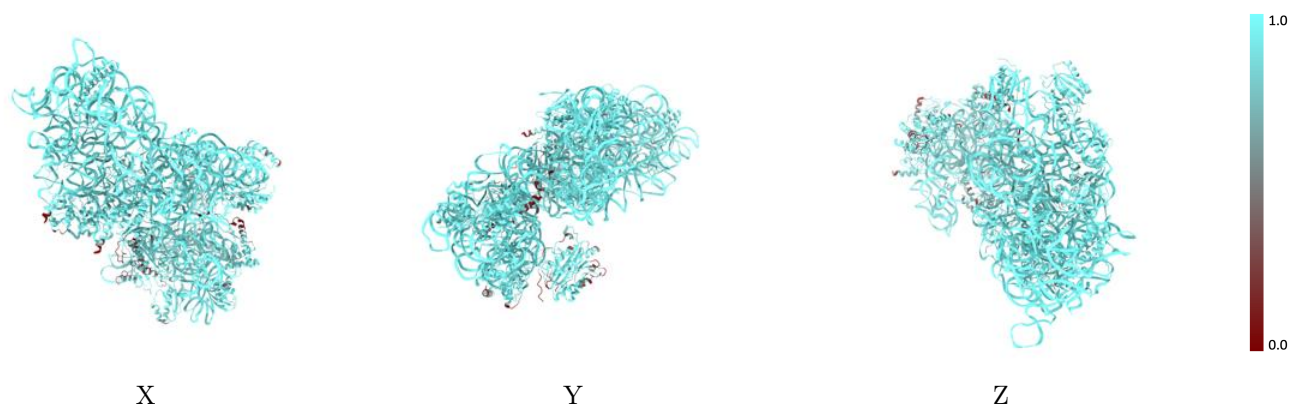
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



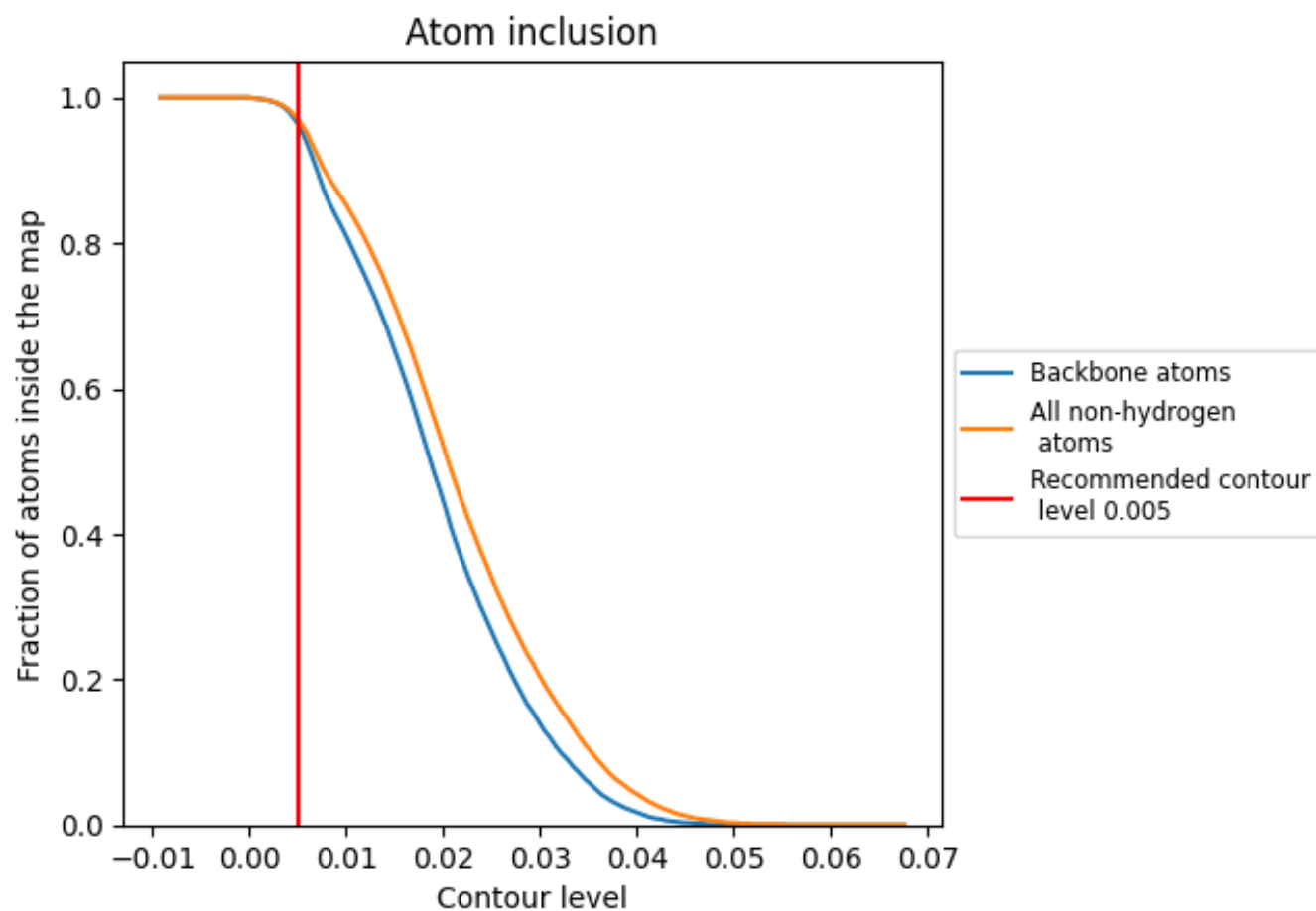
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.1660
A	 0.8000	 0.0580
a	 0.9970	 0.1940
c	 0.7840	 0.0750
d	 0.9410	 0.0870
e	 0.8940	 0.1760
f	 0.9610	 0.1940
g	 0.8860	 0.0780
h	 0.9960	 0.2110
i	 0.9870	 0.0690
j	 0.9590	 0.0210
k	 0.9700	 0.1180
l	 0.9880	 0.2020
m	 0.9320	 0.0550
n	 1.0000	 0.0530
o	 1.0000	 0.2060
p	 0.9560	 0.1840
q	 0.9920	 0.2210
r	 0.9960	 0.1670
s	 0.9230	 0.0490
t	 0.9980	 0.2010

