



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:59 PM UTC

PDB ID : 7BGD / pdb_00007bgd
EMDB ID : EMD-12178
Title : Staphylococcus aureus 30S ribosomal subunit in presence of spermidine (body only)
Authors : Belinite, M.; Khusainov, I.; Marzi, S.; Romby, P.; Yusupov, M.; Hashem, Y.
Deposited on : 2021-01-06
Resolution : 3.20 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:

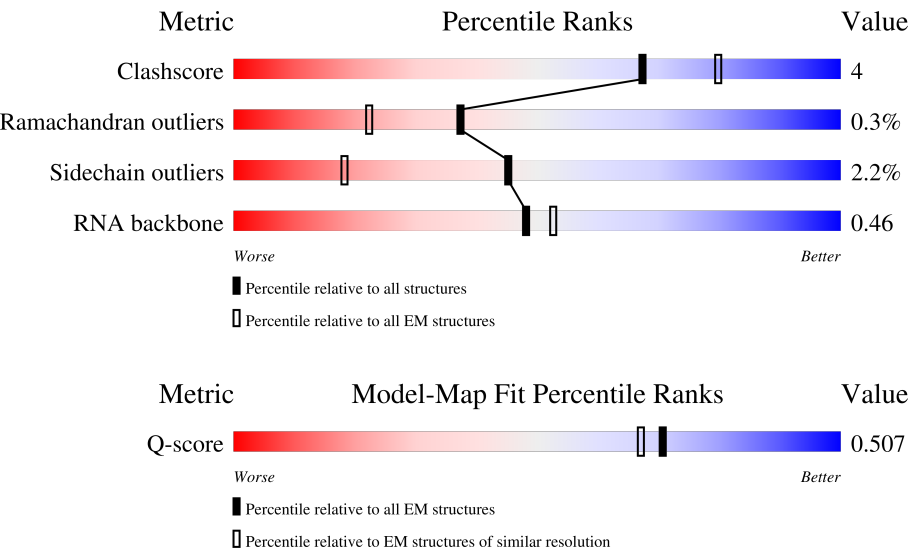
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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.



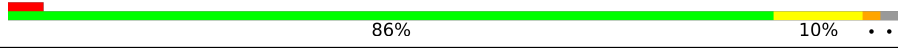
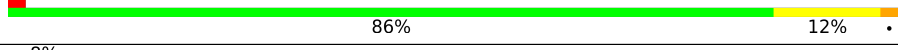
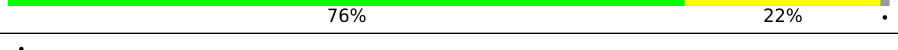
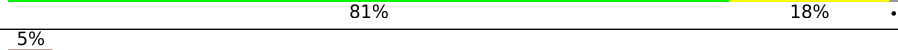
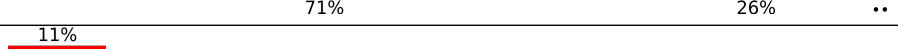
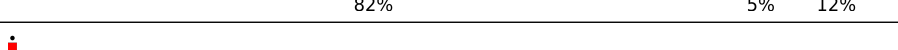
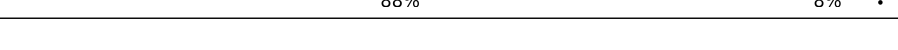
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	32	
2	a	1556	
3	b	255	

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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	166	
6	f	98	
7	h	132	
8	k	129	
9	l	137	
10	o	89	
11	p	91	
12	q	87	
13	r	80	
14	t	83	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 35364 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 mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	32	Total	C	N	O	P	0	0
			693	311	135	215	32		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	1096	Total	C	N	O	P	0	0
			23497	10487	4299	7615	1096		

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	163	Total	C	N	O	S	0	0
			1299	828	226	239	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	196	Total	C	N	O	S	0	0
			1595	1006	299	288	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	157	Total	C	N	O	S	0	0
			1169	735	214	218	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			798	503	139	153	3		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	118	Total	C	N	O	S	0	0
			880	543	169	165	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	135	Total	C	N	O	S	0	0
			1058	658	214	184	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	o	88	Total	C	N	O	S	0	0
			738	454	153	130	1		

- Molecule 11 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	p	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 12 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	q	86	Total	C	N	O	S	0	0
			707	447	126	133	1		

- Molecule 13 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	r	70	Total	C	N	O	S	0	0
			580	367	114	96	3		

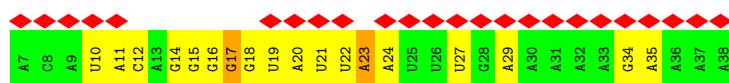
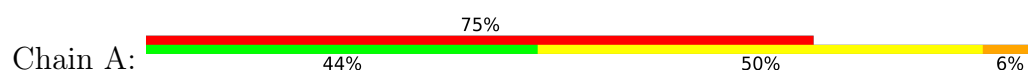
- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	t	80	606	367	119	118	2	0	0

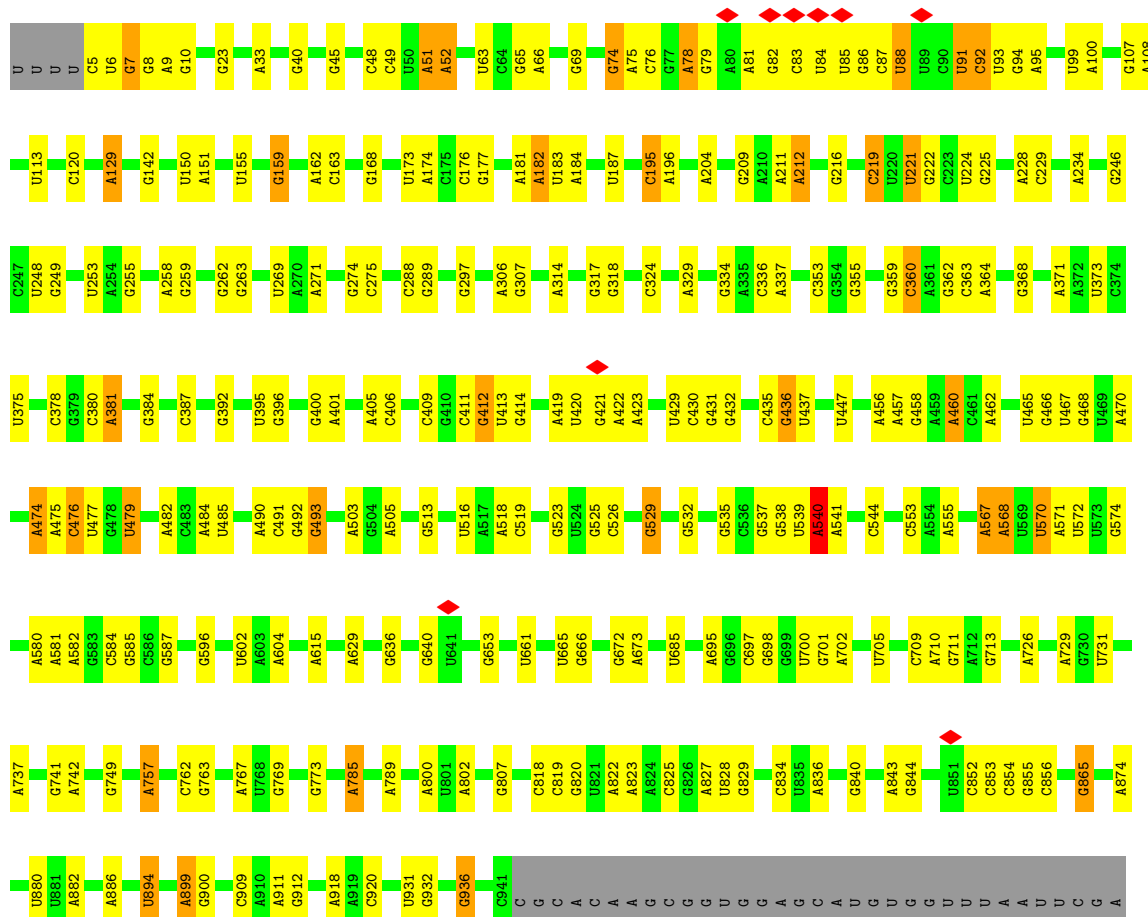
3 Residue-property plots

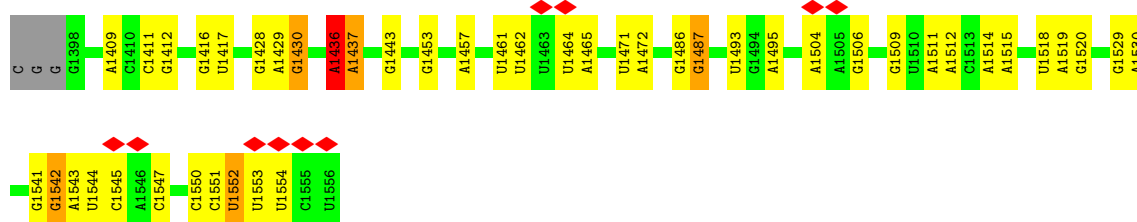
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

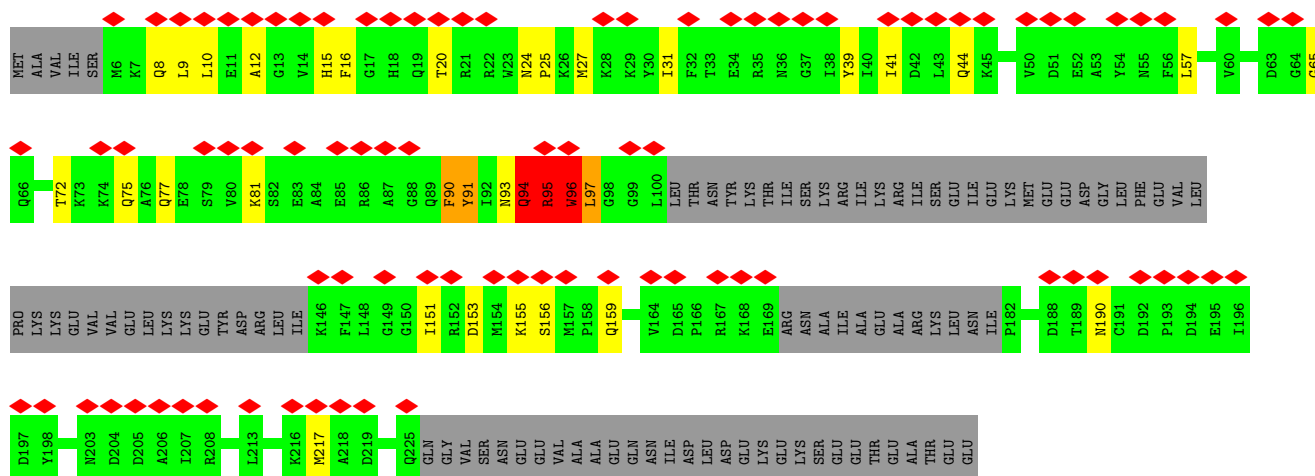


• Molecule 2: 16S ribosomal RNA

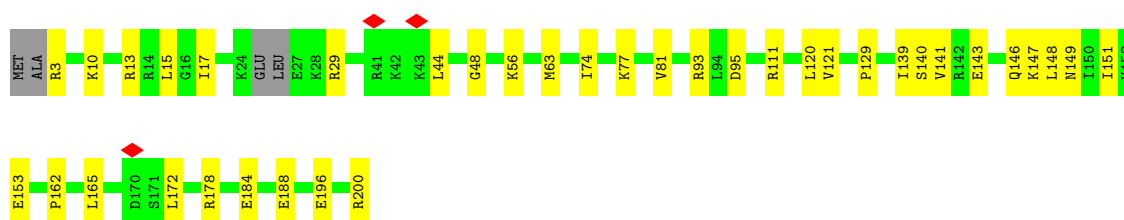




Chain b:

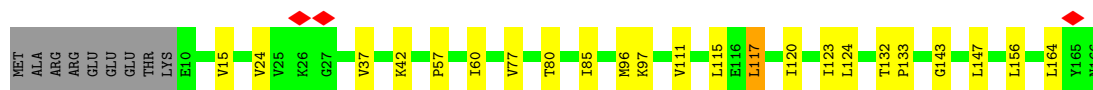


Chain d:



- Molecule 5: 30S ribosomal protein S5

Chain e:  81% 13% 5%



- Molecule 6: 30S ribosomal protein S6

Chain f:  86% 10% ..



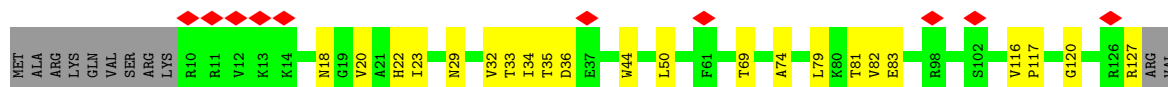
- Molecule 7: 30S ribosomal protein S8

Chain h:  86% 12% ..



- Molecule 8: 30S ribosomal protein S11

Chain k:  8% 74% 17% 9%



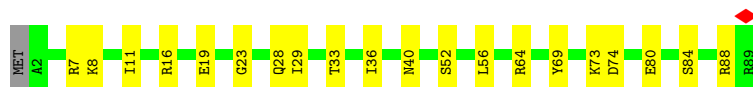
- Molecule 9: 30S ribosomal protein S12

Chain l:  80% 18% ..



- Molecule 10: 30S ribosomal protein S15

Chain o:  76% 22% .

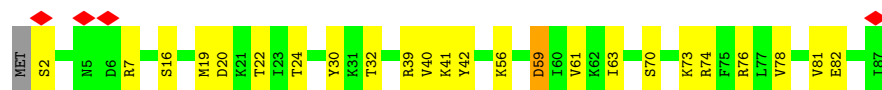


- Molecule 11: 30S ribosomal protein S16

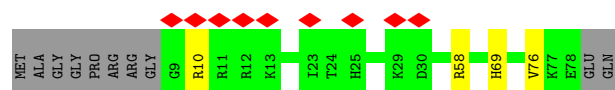
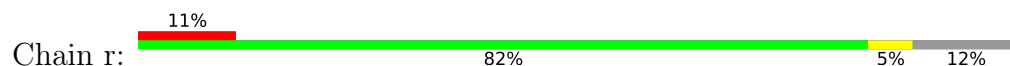
Chain p:  81% 18% .



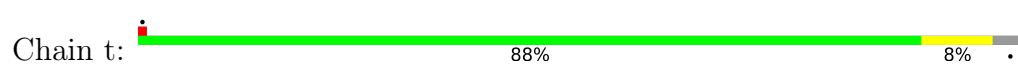
- Molecule 12: 30S ribosomal protein S17



- Molecule 13: 30S ribosomal protein S18



- Molecule 14: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	529602	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.297	Depositor
Minimum map value	-0.138	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0357	Depositor
Map size (Å)	321.30002, 321.30002, 321.30002	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	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	0.28	0/779	0.60	1/1213 (0.1%)
2	a	0.41	0/26310	0.57	5/41033 (0.0%)
3	b	0.43	2/1320 (0.2%)	0.86	9/1771 (0.5%)
4	d	0.46	0/1624	0.84	1/2178 (0.0%)
5	e	0.42	0/1183	0.82	1/1595 (0.1%)
6	f	0.30	0/809	0.64	0/1085
7	h	0.45	0/1044	0.85	1/1401 (0.1%)
8	k	0.31	0/895	0.66	0/1207
9	l	0.69	2/1075 (0.2%)	1.04	8/1439 (0.6%)
10	o	0.40	0/747	0.78	0/996
11	p	0.44	0/723	0.82	2/971 (0.2%)
12	q	0.38	0/715	0.81	0/955
13	r	0.39	0/589	0.82	0/785
14	t	0.39	0/606	0.77	0/810
All	All	0.42	4/38419 (0.0%)	0.65	28/57439 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	l	118	SER	C-N	12.47	1.44	1.33
9	l	117	THR	C-N	10.81	1.49	1.33
3	b	90	PHE	C-N	8.47	1.46	1.33
3	b	91	TYR	C-N	6.46	1.42	1.33

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	l	118	SER	CA-C-N	10.47	129.97	119.92
9	l	118	SER	C-N-CA	10.47	129.97	119.92
9	l	128	SER	N-CA-C	-7.81	102.70	111.14
9	l	118	SER	O-C-N	-7.52	114.44	123.16
2	a	540	A	P-O3'-C3'	7.01	130.72	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	693	0	346	1	0
2	a	23497	0	11823	82	0
3	b	1299	0	1318	30	0
4	d	1595	0	1623	22	0
5	e	1169	0	1229	12	0
6	f	798	0	794	8	0
7	h	1032	0	1082	10	0
8	k	880	0	899	12	0
9	l	1058	0	1130	21	0
10	o	738	0	769	11	0
11	p	712	0	744	8	0
12	q	707	0	749	13	0
13	r	580	0	622	3	0
14	t	606	0	650	5	0
All	All	35364	0	23778	206	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 4.

The worst 5 of 206 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)
9:l:127:ARG:HG2	9:l:132:THR:HG23	1.27	1.15
3:b:72:THR:HG23	3:b:94:GLN:CB	1.76	1.15
9:l:127:ARG:HG2	9:l:132:THR:CG2	1.89	1.02
3:b:72:THR:HG23	3:b:94:GLN:HB3	1.46	0.96
9:l:123:ARG:HB2	9:l:132:THR:HG21	1.50	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	b	157/255 (62%)	142 (90%)	14 (9%)	1 (1%)	21	56
4	d	192/200 (96%)	172 (90%)	19 (10%)	1 (0%)	24	59
5	e	155/166 (93%)	144 (93%)	11 (7%)	0	100	100
6	f	94/98 (96%)	88 (94%)	6 (6%)	0	100	100
7	h	129/132 (98%)	122 (95%)	7 (5%)	0	100	100
8	k	116/129 (90%)	109 (94%)	7 (6%)	0	100	100
9	l	133/137 (97%)	115 (86%)	16 (12%)	2 (2%)	8	37
10	o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
11	p	88/91 (97%)	78 (89%)	10 (11%)	0	100	100
12	q	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
13	r	68/80 (85%)	62 (91%)	6 (9%)	0	100	100
14	t	78/83 (94%)	75 (96%)	3 (4%)	0	100	100
All	All	1380/1547 (89%)	1266 (92%)	110 (8%)	4 (0%)	37	68

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	l	131	GLY
3	b	96	TRP
4	d	143	GLU
9	l	57	LYS

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	
3	b	138/221 (62%)	135 (98%)	3 (2%)	45	71
4	d	172/175 (98%)	171 (99%)	1 (1%)	78	84
5	e	123/131 (94%)	120 (98%)	3 (2%)	43	70
6	f	84/86 (98%)	82 (98%)	2 (2%)	43	70
7	h	112/113 (99%)	109 (97%)	3 (3%)	39	68
8	k	94/104 (90%)	93 (99%)	1 (1%)	65	79
9	l	117/119 (98%)	113 (97%)	4 (3%)	32	64
10	o	80/81 (99%)	80 (100%)	0	100	100
11	p	76/77 (99%)	73 (96%)	3 (4%)	28	62
12	q	81/82 (99%)	76 (94%)	5 (6%)	16	49
13	r	62/68 (91%)	61 (98%)	1 (2%)	55	75
14	t	67/69 (97%)	67 (100%)	0	100	100
All	All	1206/1326 (91%)	1180 (98%)	26 (2%)	45	71

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	l	120	VAL
11	p	3	VAL
12	q	78	VAL
9	l	132	THR
11	p	21	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
6	f	53	ASN
14	t	69	ASN
9	l	5	ASN
11	p	62	ASN
7	h	122	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	31/32 (96%)	17 (54%)	2 (6%)
2	a	1094/1556 (70%)	237 (21%)	0
All	All	1125/1588 (70%)	254 (22%)	2 (0%)

5 of 254 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	U
1	A	11	A
1	A	12	C
1	A	14	G
1	A	15	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	17	G
1	A	22	U

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

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

5.5 Carbohydrates [i](#)

There are no 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.

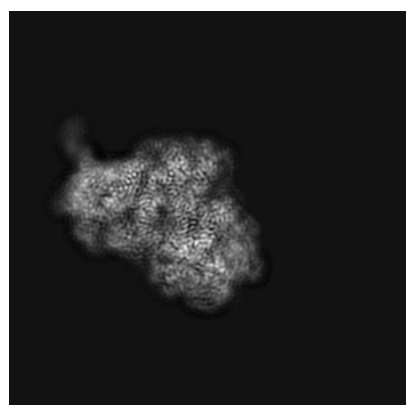
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12178. These allow visual inspection of the internal detail of the map and identification of artifacts.

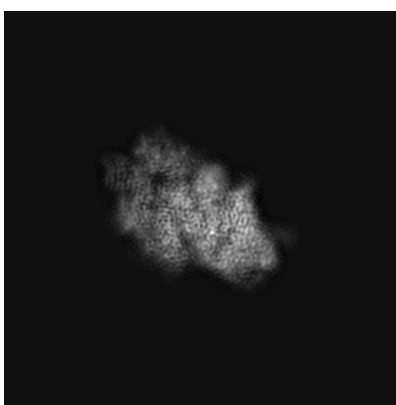
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

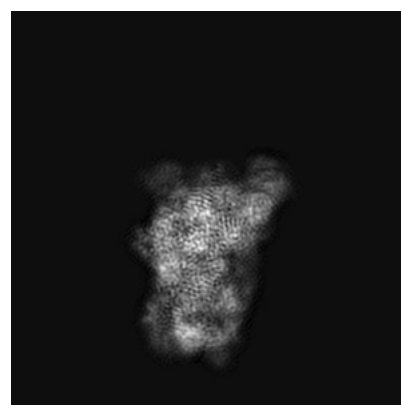
6.1.1 Primary map



X



Y

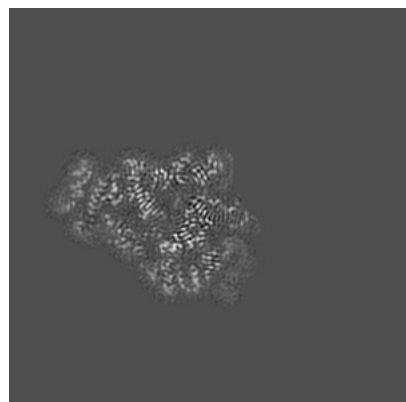


Z

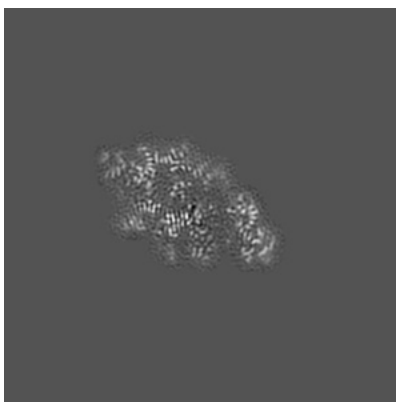
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

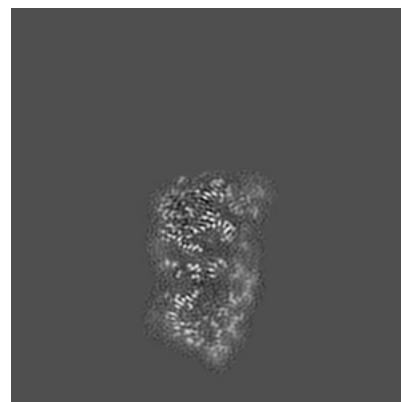
6.2.1 Primary map



X Index: 135



Y Index: 135

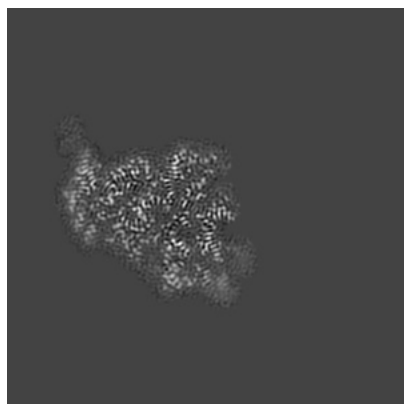


Z Index: 135

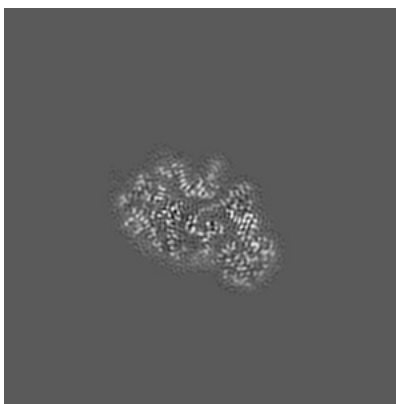
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

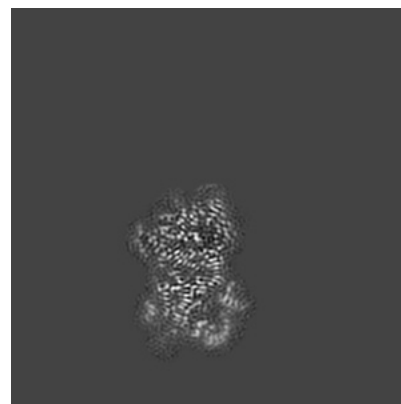
6.3.1 Primary map



X Index: 126



Y Index: 113

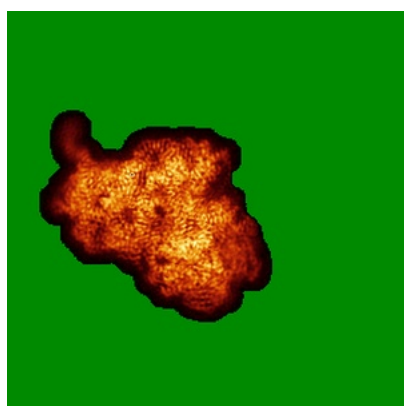


Z Index: 158

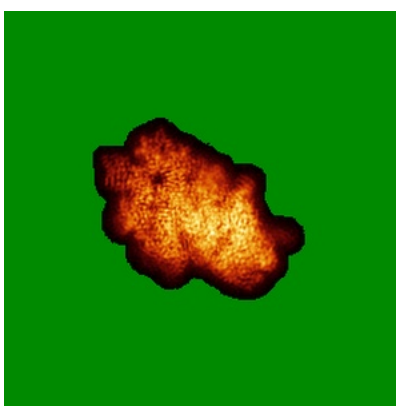
The images above show the largest variance slices of the map in three orthogonal directions.

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

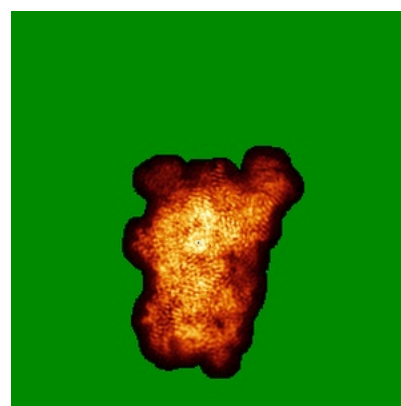
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0357. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

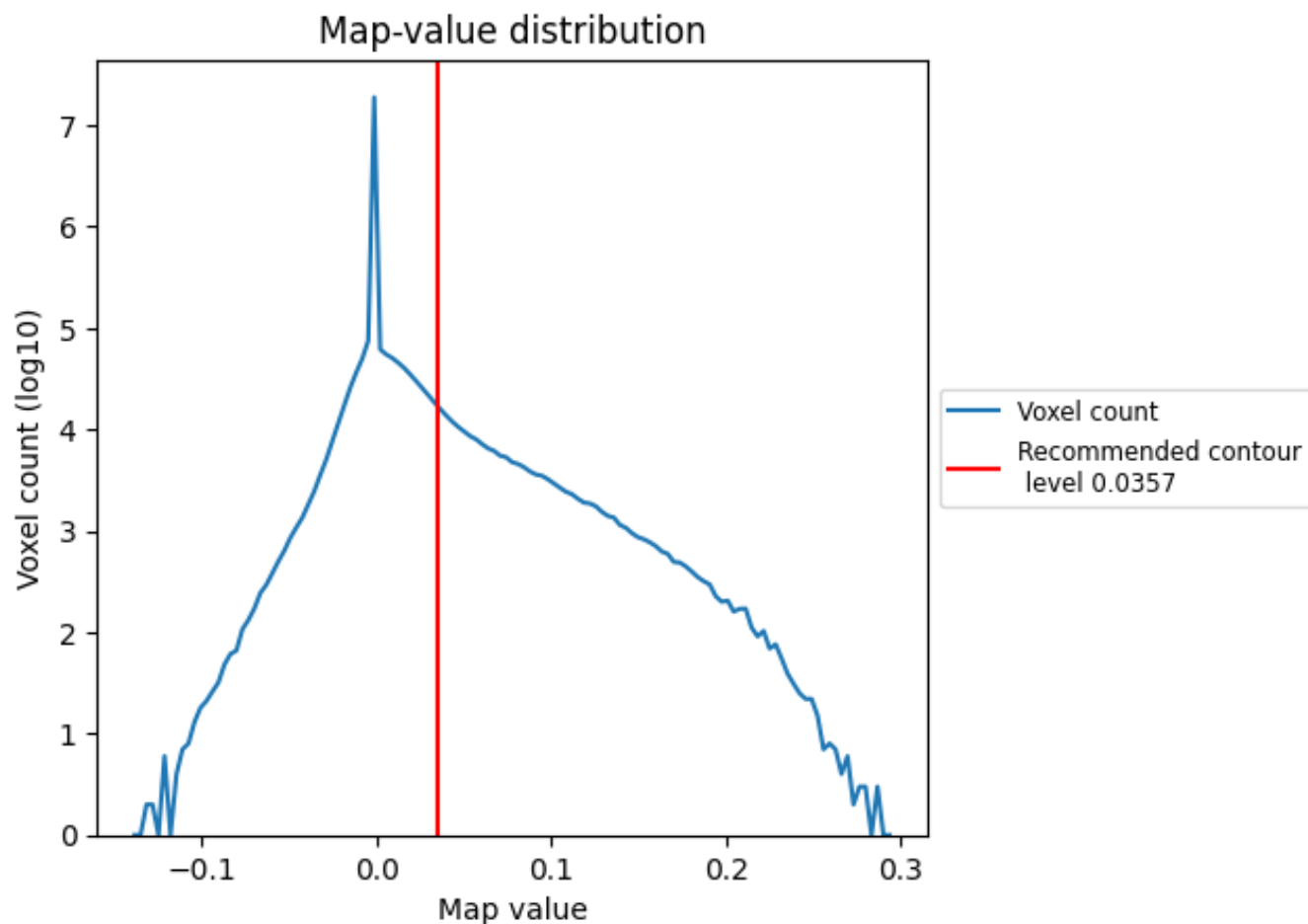
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

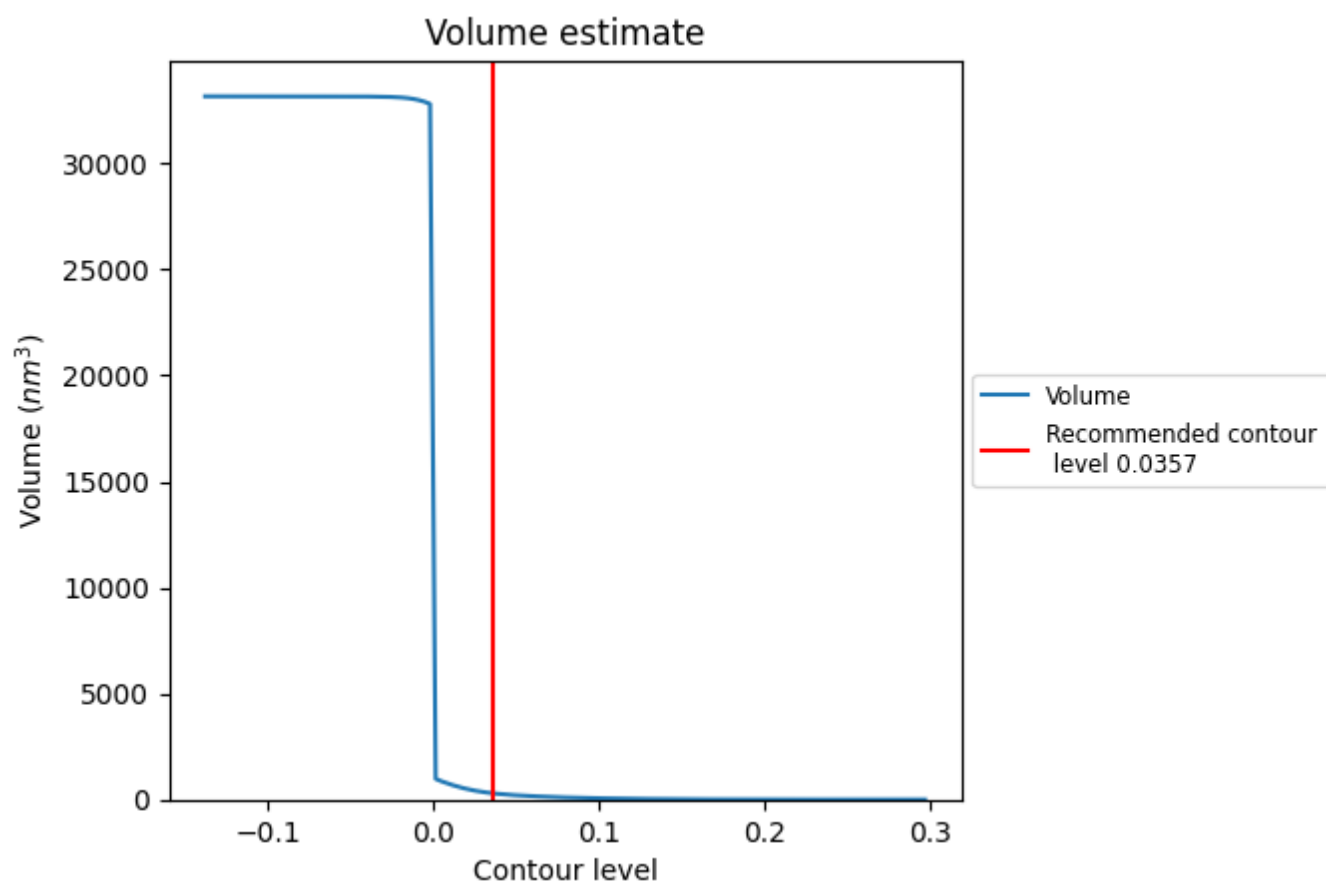
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

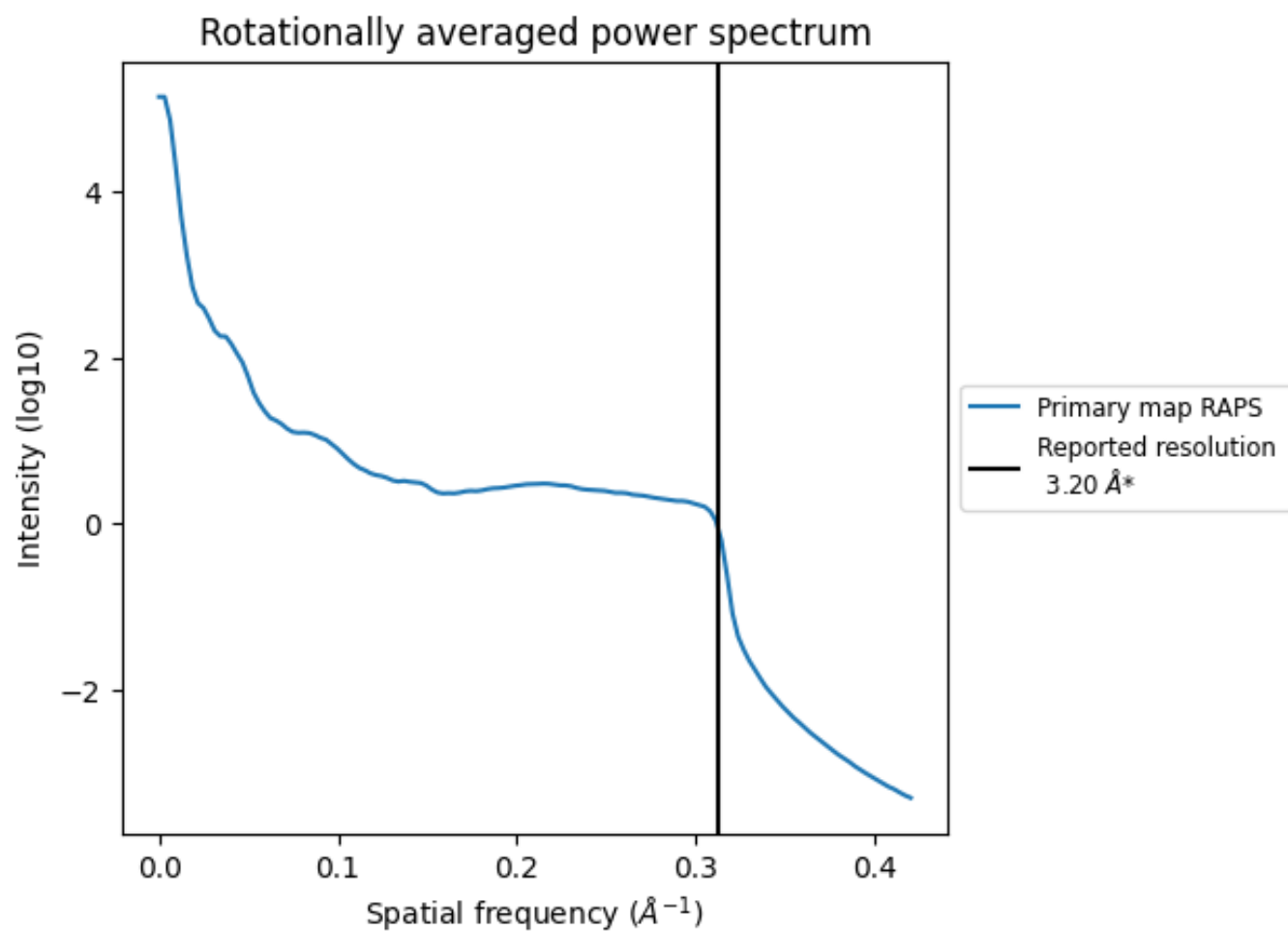
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 298 nm³; this corresponds to an approximate mass of 269 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 0.312 Å⁻¹

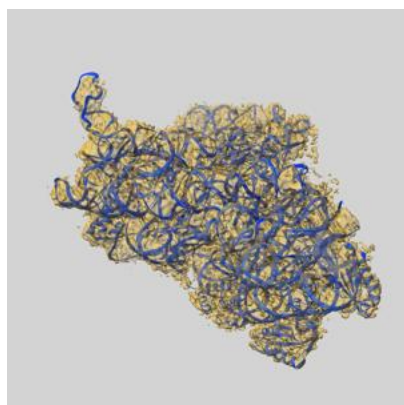
8 Fourier-Shell correlation

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

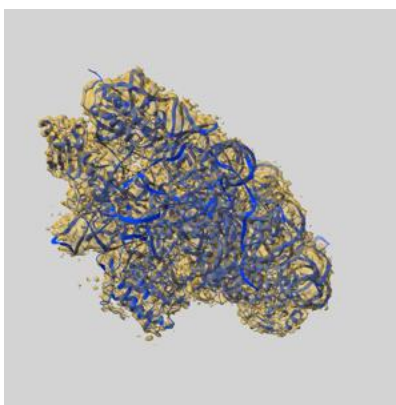
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12178 and PDB model 7BGD. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

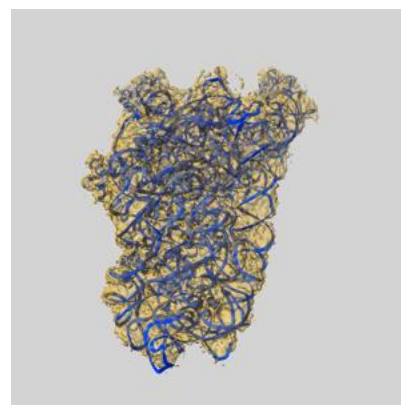
9.1 Map-model overlay [i](#)



X



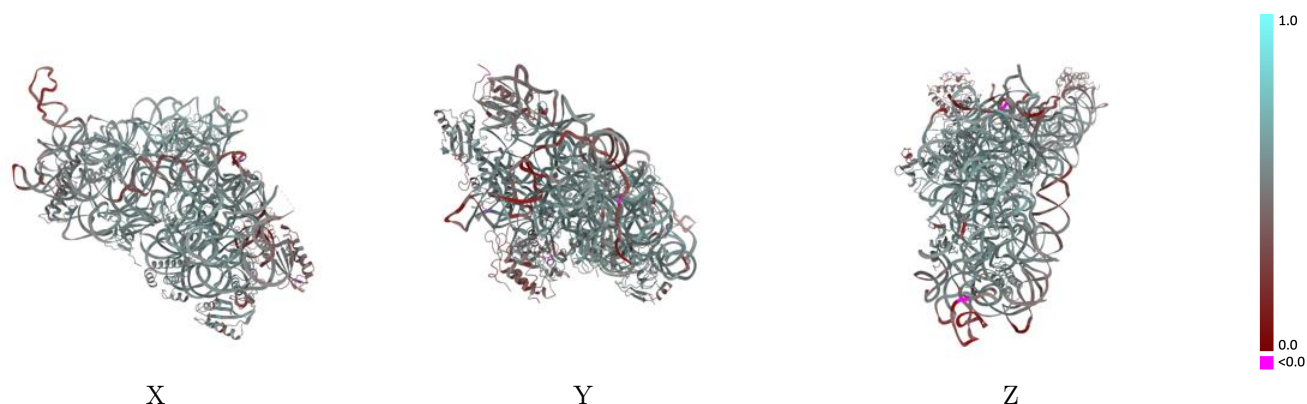
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0357 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](#)



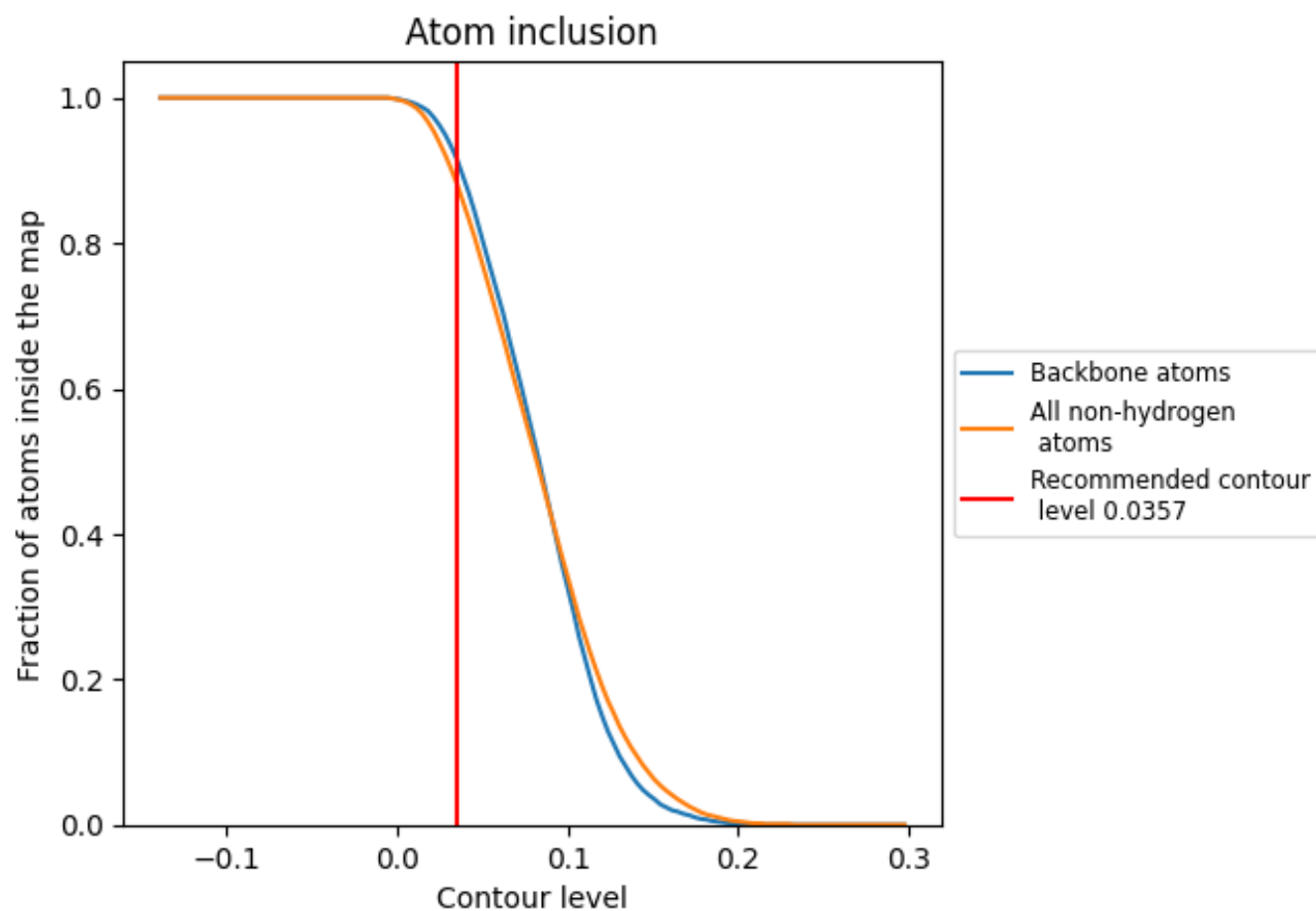
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0357).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.0357) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8790	 0.5070
A	 0.2110	 0.2120
a	 0.9470	 0.5220
b	 0.3730	 0.3670
d	 0.8690	 0.5260
e	 0.8270	 0.5250
f	 0.7420	 0.4890
h	 0.8730	 0.5390
k	 0.6690	 0.4300
l	 0.8810	 0.5390
o	 0.8910	 0.4980
p	 0.8420	 0.5280
q	 0.8330	 0.5170
r	 0.7610	 0.4750
t	 0.8460	 0.5140

