



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:17 PM UTC

PDB ID : 7SPC / pdb_00007spc
EMDB ID : EMD-24770
Title : Models for C17 reconstruction of Outer Membrane Core Complex (OMCC) of Type IV Secretion System (T4SS) encoded by F-plasmid (pED208).
Authors : Liu, X.; Khara, P.; Baker, M.L.; Christie, P.J.; Hu, B.
Deposited on : 2021-11-02
Resolution : 2.95 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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:

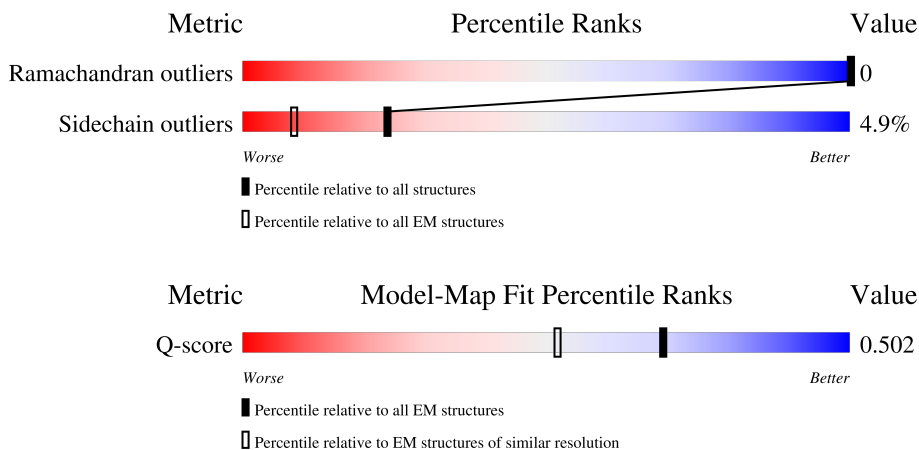
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.95 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.
















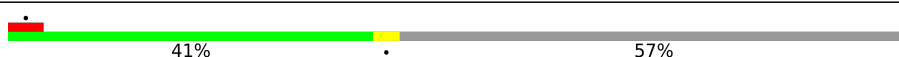
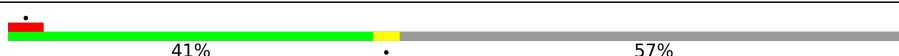
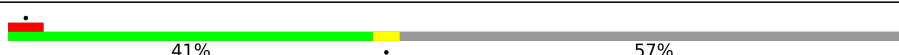
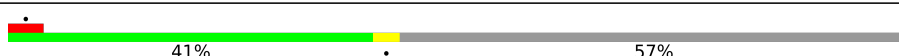







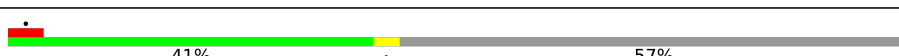
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13114 (2.45 - 3.45)

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	AB1	204	18% 82%
1	AB10	204	18% 82%
1	AB11	204	18% 82%
1	AB12	204	18% 82%
1	AB13	204	18% 82%


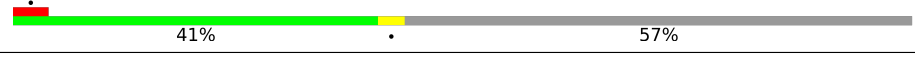


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Mol	Chain	Length	Quality of chain
1	AB14	204	 18% 82%
1	AB15	204	 18% 82%
1	AB16	204	 18% 82%
1	AB17	204	 18% 82%
1	AB2	204	 18% 82%
1	AB3	204	 18% 82%
1	AB4	204	 18% 82%
1	AB5	204	 18% 82%
1	AB6	204	 18% 82%
1	AB7	204	 18% 82%
1	AB8	204	 18% 82%
1	AB9	204	 18% 82%
2	EF1	453	 41% 57%
2	EF10	453	 41% 57%
2	EF11	453	 41% 57%
2	EF12	453	 41% 57%
2	EF13	453	 41% 57%
2	EF14	453	 41% 57%
2	EF15	453	 41% 57%
2	EF16	453	 41% 57%
2	EF17	453	 41% 57%
2	EF2	453	 41% 57%
2	EF3	453	 41% 57%
2	EF4	453	 41% 57%
2	EF5	453	 41% 57%

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Mol	Chain	Length	Quality of chain
2	EF6	453	 41% 57%
2	EF7	453	 41% 57%
2	EF8	453	 41% 57%
2	EF9	453	 41% 57%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 29716 atoms, of which 0 are hydrogens and 0 are deuteriums.

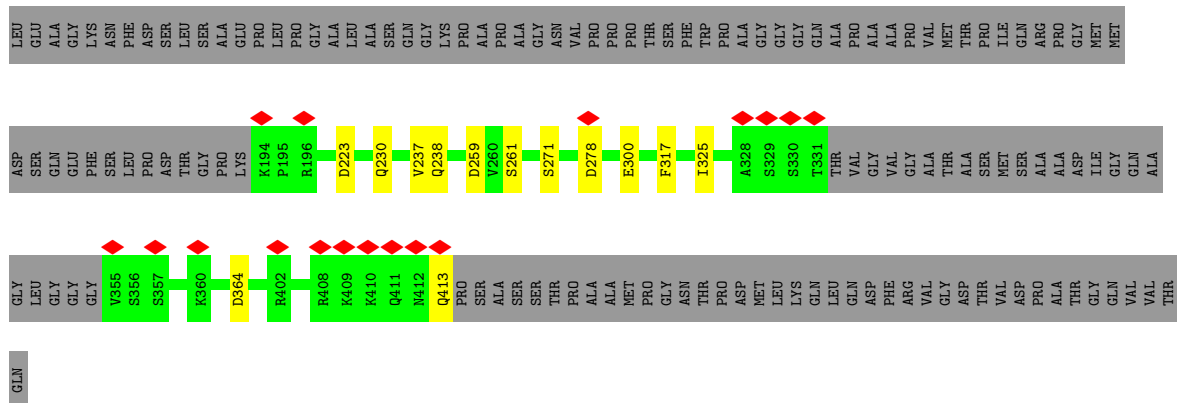
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called TraV.

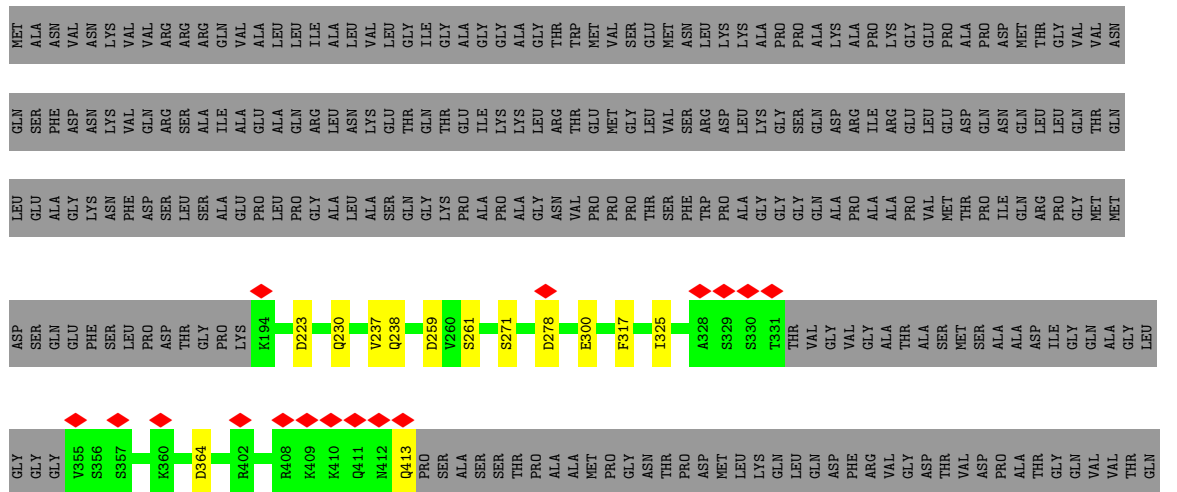
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	AB1	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB2	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB3	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB4	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB5	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB6	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB7	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB8	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB9	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB10	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB11	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB12	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB13	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB14	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB15	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB16	37	Total 261	C 153	N 47	O 56	S 5	0	0
1	AB17	37	Total 261	C 153	N 47	O 56	S 5	0	0

- Molecule 2 is a protein called TraB.

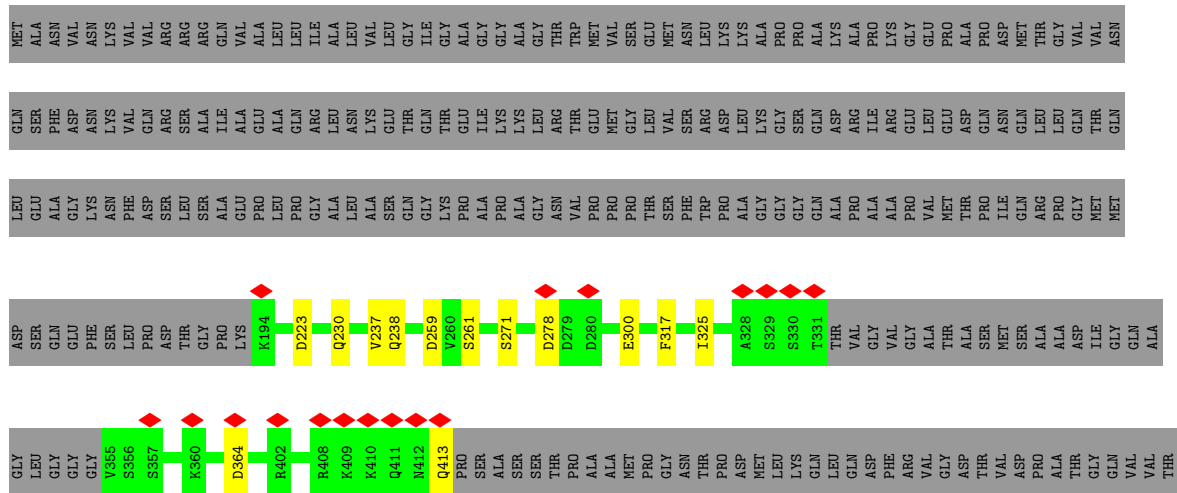
Mol	Chain	Residues	Atoms					AltConf	Trace
2	EF1	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF2	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF3	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF4	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF5	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF6	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF7	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF8	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF9	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF10	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF11	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF12	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF13	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF14	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF15	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF16	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		
2	EF17	197	Total	C	N	O	S	0	0
			1487	930	260	291	6		



• Molecule 2: TraB



• Molecule 2: TraB



THR
GLN

• Molecule 2: TraB

Chain EF17: 41% 57%

MET ALA THR
SER ASN
GLY VAL
ASP ASN
LYS ASN
VAL VAL
VAL VAL
ARG ARG
SER ARG
GLN ARG
VAL VAL
ALA VAL
LEU ALA
LEU LEU
LEU LEU
ILE ILE
ALA ALA
LEU LEU
VAL VAL
GLY LEU
GLY LEU
ILE ILE
GLY THR
GLY THR
ALA ALA
GLY GLY
GLY GLY
GLY GLY
THR THR
MET MET
VAL VAL

GLN SER
PHE ASP
ASN ASN
LYS VAL
VAL VAL
GLN VAL
ARG ARG
SER ARG
SER ALA
ILE ILE
ALA ALA
GLU GLU
LEU LEU
ALA ALA
LEU LEU
ARG ARG
LEU LEU
ASN ASN
LYS LYS
THR THR
GLN GLN
ILE ILE
THR THR
GLU GLU
ILE ILE
LYS LYS
LEU LEU
THR THR
ILE ILE
ALA ALA
GLY GLY
GLN GLN
ASP ASP
MET MET
THR THR
GLY GLY
VAL VAL
GLN GLN

LEU GLU
ALA ALA
GLY GLY
LYS LYS
ASN ASN
PHE PHE
ASP ASP
SER SER
LEU LEU
THR THR
SER SER
GLY GLY
ALA ALA
GLU GLU
PRO PRO
LEU LEU
PRO PRO
GLY GLY
LEU LEU
ALA ALA
LEU LEU
SER SER
GLY GLY
THR THR
LYS LYS
PRO PRO
ALA ALA
PRO PRO
LYS LYS
ALA ALA
LEU LEU
SER SER
GLY GLY
THR THR
VAL VAL
PRO PRO
PRO PRO
THR THR
SER SER
PHE PHE
TRP TRP
ARG ARG
ASP ASP
LEU LEU
LYS LYS
ALA ALA
GLY GLY
GLY GLY
SER SER
GLN GLN
ALA ALA
PRO PRO
VAL VAL
ALA ALA
ILE ILE
ARG ARG
THR THR
MET MET
ILE ILE
GLN GLN
PRO PRO
ARG ARG
LEU LEU
THR THR
GLY GLY
VAL VAL
MET MET

ASP SER
GLN GLU
PHE PHE
SER SER
LEU LEU
PRO PRO
THR THR
GLY GLY
PRO PRO
LYS LYS
K194
P195
R196
D223
Q230
V237
Q238
D259
V260
S261
S271
D278
E300
F317
I325
A328
S329
S330
T331
THR VAL
GLY GLY
VAL VAL
GLY GLY
ALA ALA
THR THR
ALA ALA
SER SER
MET MET
SER SER
ALA ALA
ALA ALA
ASP ASP
ILE ILE
GLY GLY
GLN GLN
ALA ALA

GLY LEU
GLY GLY
GLY GLY
V355
S356
S357
K360
D364
R402
R408
K409
K410
Q411
M412
Q413
PRO SER
SER ALA
SER SER
SER SER
THR THR
PRO PRO
ALA ALA
ALA ALA
MET MET
PRO PRO
GLY GLY
ASN ASN
THR THR
PRO PRO
ASP ASP
MET MET
LEU LEU
LYS LYS
GLN GLN
LEU LEU
GLN GLN
ASP ASP
PHE PHE
ARG ARG
VAL VAL
GLY GLY
ASP ASP
THR THR
VAL VAL
VAL VAL
PRO PRO
ALA ALA
ALA ALA
THR THR
GLY GLY
ILE ILE
VAL VAL
GLN GLN
VAL VAL
THR THR

GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C17	Depositor
Number of particles used	70700	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.196	Depositor
Minimum map value	-4.361	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.122	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	426.08, 426.08, 426.08	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0652, 1.0652, 1.0652	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	AB1	0.86	0/261	0.78	0/348
1	AB10	0.86	0/261	0.78	0/348
1	AB11	0.86	0/261	0.78	0/348
1	AB12	0.86	0/261	0.78	0/348
1	AB13	0.86	0/261	0.78	0/348
1	AB14	0.86	0/261	0.78	0/348
1	AB15	0.86	0/261	0.78	0/348
1	AB16	0.86	0/261	0.78	0/348
1	AB17	0.86	0/261	0.78	0/348
1	AB2	0.86	0/261	0.78	0/348
1	AB3	0.86	0/261	0.78	0/348
1	AB4	0.86	0/261	0.78	0/348
1	AB5	0.86	0/261	0.78	0/348
1	AB6	0.86	0/261	0.78	0/348
1	AB7	0.86	0/261	0.78	0/348
1	AB8	0.86	0/261	0.78	0/348
1	AB9	0.86	0/261	0.78	0/348
2	EF1	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF10	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF11	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF12	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF13	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF14	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF15	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF16	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF17	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF2	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF3	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF4	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF5	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF6	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF7	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF8	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)
2	EF9	0.65	2/1509 (0.1%)	0.81	4/2031 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.69	34/30090 (0.1%)	0.81	68/40443 (0.2%)

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	EF12	237	VAL	CA-C	-5.35	1.46	1.52
2	EF16	237	VAL	CA-C	-5.35	1.46	1.52
2	EF8	237	VAL	CA-C	-5.35	1.46	1.52
2	EF7	237	VAL	CA-C	-5.33	1.46	1.52
2	EF17	237	VAL	CA-C	-5.32	1.46	1.52

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	EF10	325	ILE	N-CA-C	-9.90	103.88	111.90
2	EF14	325	ILE	N-CA-C	-9.89	103.89	111.90
2	EF4	325	ILE	N-CA-C	-9.89	103.89	111.90
2	EF7	325	ILE	N-CA-C	-9.89	103.89	111.90
2	EF17	325	ILE	N-CA-C	-9.89	103.89	111.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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
1	AB1	35/204 (17%)	34 (97%)	1 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AB10	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB11	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB12	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB13	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB14	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB15	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB16	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB17	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB2	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB3	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB4	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB5	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB6	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB7	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB8	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
1	AB9	35/204 (17%)	34 (97%)	1 (3%)	0	100	100
2	EF1	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF10	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF11	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF12	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF13	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF14	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF15	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF16	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF17	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF2	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF3	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF4	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF5	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF6	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF7	193/453 (43%)	184 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	EF8	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
2	EF9	193/453 (43%)	184 (95%)	9 (5%)	0	100	100
All	All	3876/11169 (35%)	3706 (96%)	170 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	AB1	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB10	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB11	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB12	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB13	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB14	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB15	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB16	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB17	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB2	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB3	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB4	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB5	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB6	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB7	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB8	28/168 (17%)	27 (96%)	1 (4%)	31	56
1	AB9	28/168 (17%)	27 (96%)	1 (4%)	31	56
2	EF1	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF10	156/353 (44%)	148 (95%)	8 (5%)	21	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	EF11	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF12	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF13	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF14	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF15	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF16	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF17	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF2	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF3	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF4	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF5	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF6	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF7	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF8	156/353 (44%)	148 (95%)	8 (5%)	21	47
2	EF9	156/353 (44%)	148 (95%)	8 (5%)	21	47
All	All	3128/8857 (35%)	2975 (95%)	153 (5%)	24	48

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	EF13	259	ASP
2	EF16	364	ASP
2	EF13	364	ASP
2	EF15	230	GLN
2	EF17	300	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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.

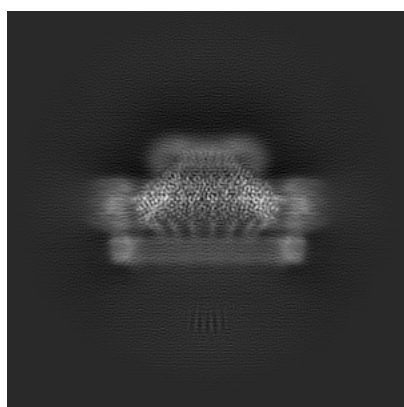
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24770. These allow visual inspection of the internal detail of the map and identification of artifacts.

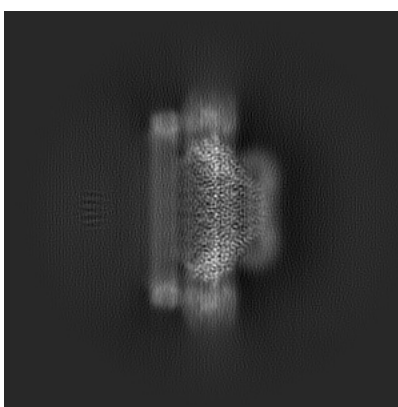
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

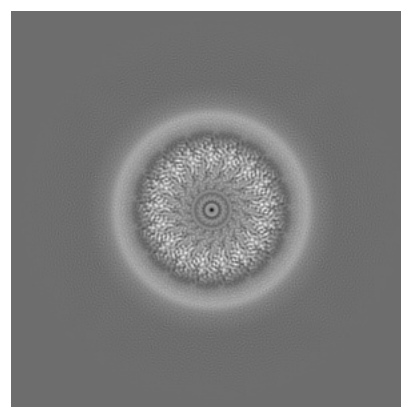
6.1.1 Primary map



X



Y

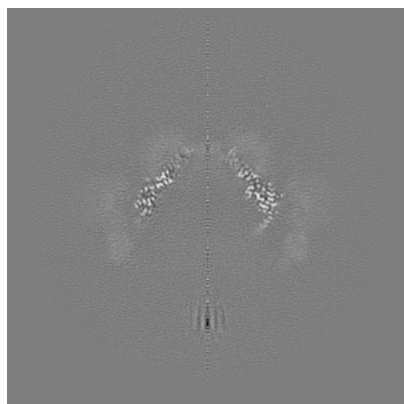


Z

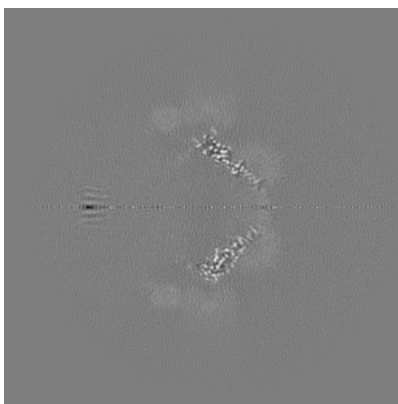
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

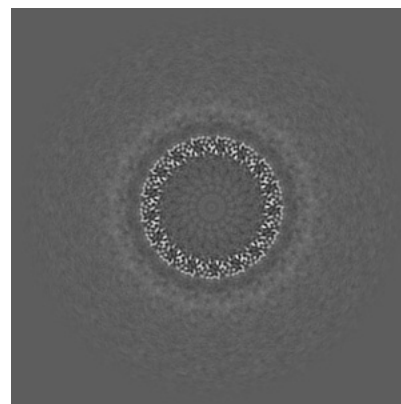
6.2.1 Primary map



X Index: 200



Y Index: 200

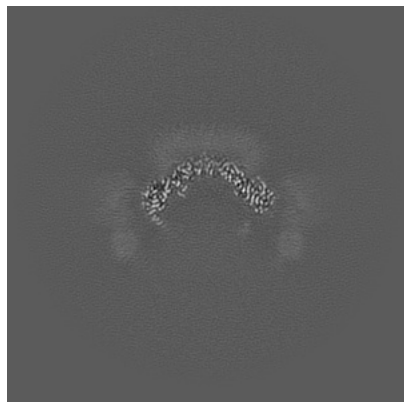


Z Index: 200

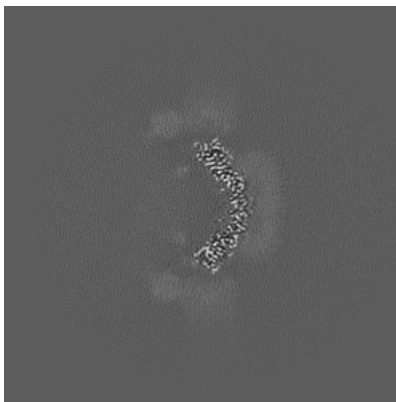
The images above show central slices of the map in three orthogonal directions.

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

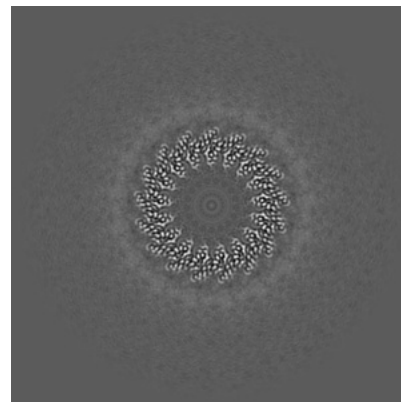
6.3.1 Primary map



X Index: 169



Y Index: 235

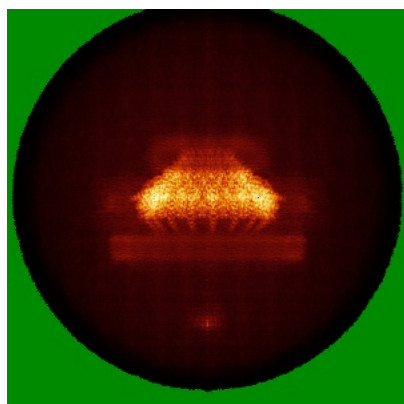


Z Index: 211

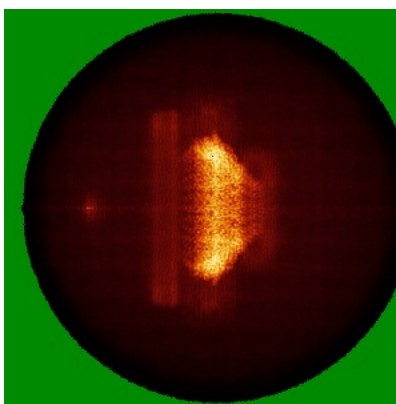
The images above show the largest variance slices of the map in three orthogonal directions.

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

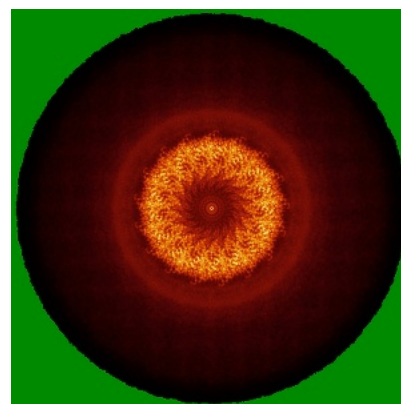
6.4.1 Primary map



X



Y

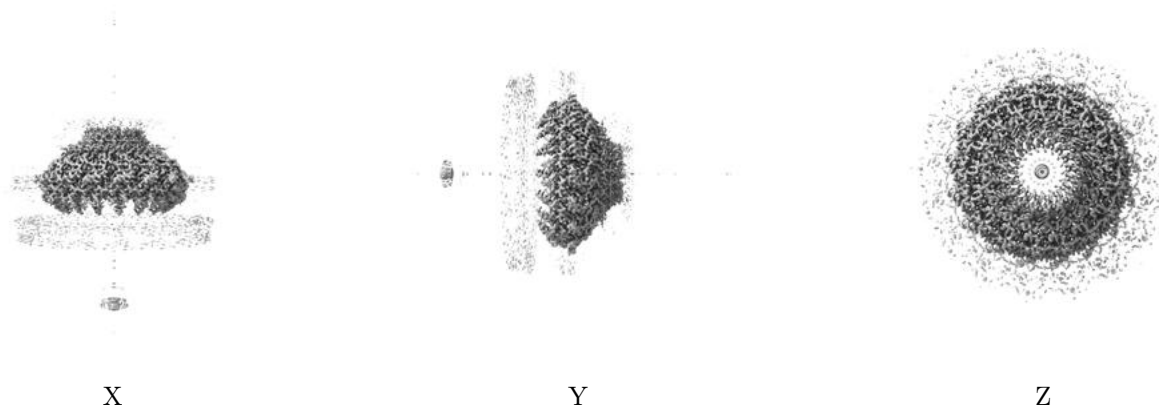


Z

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

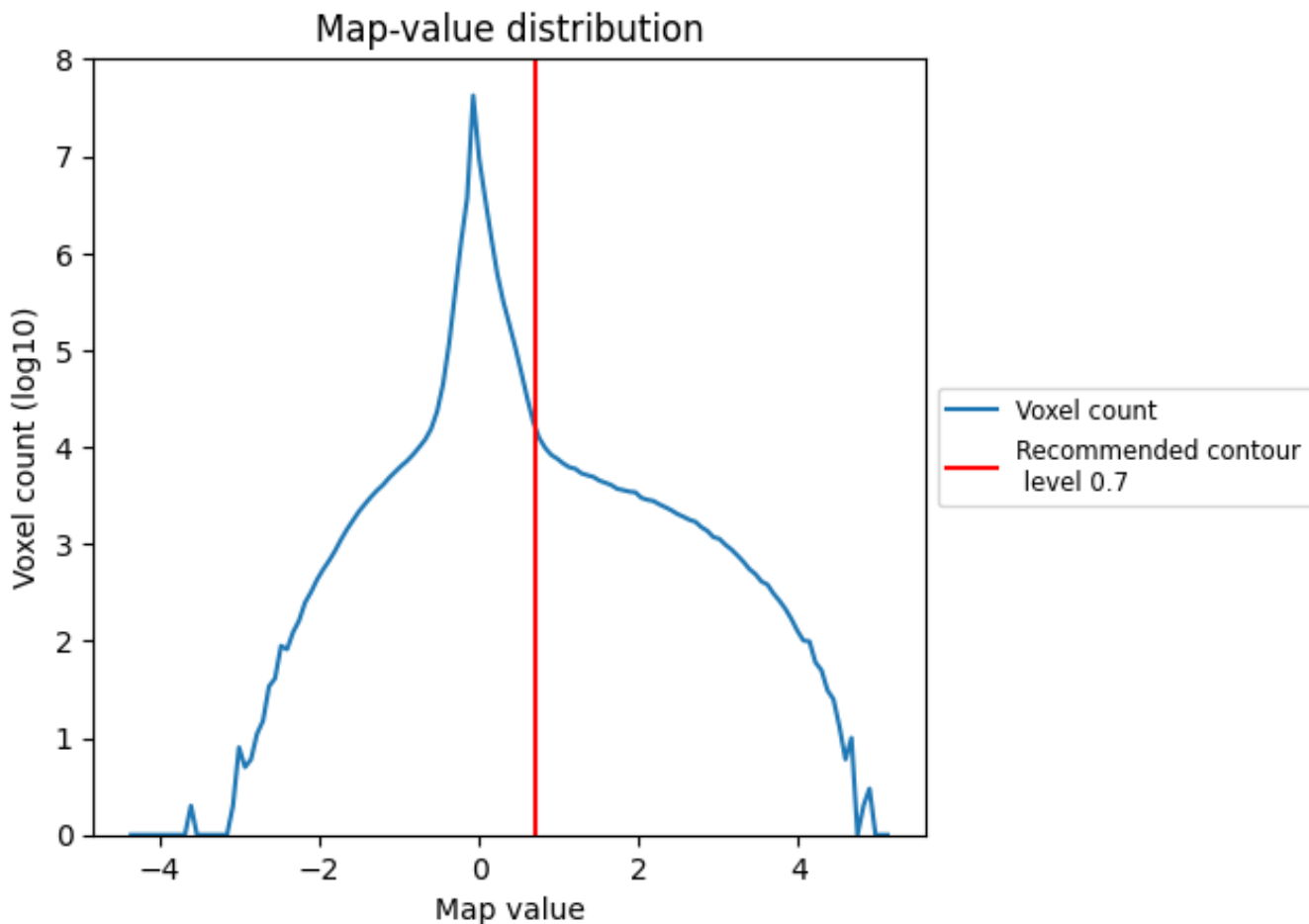
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

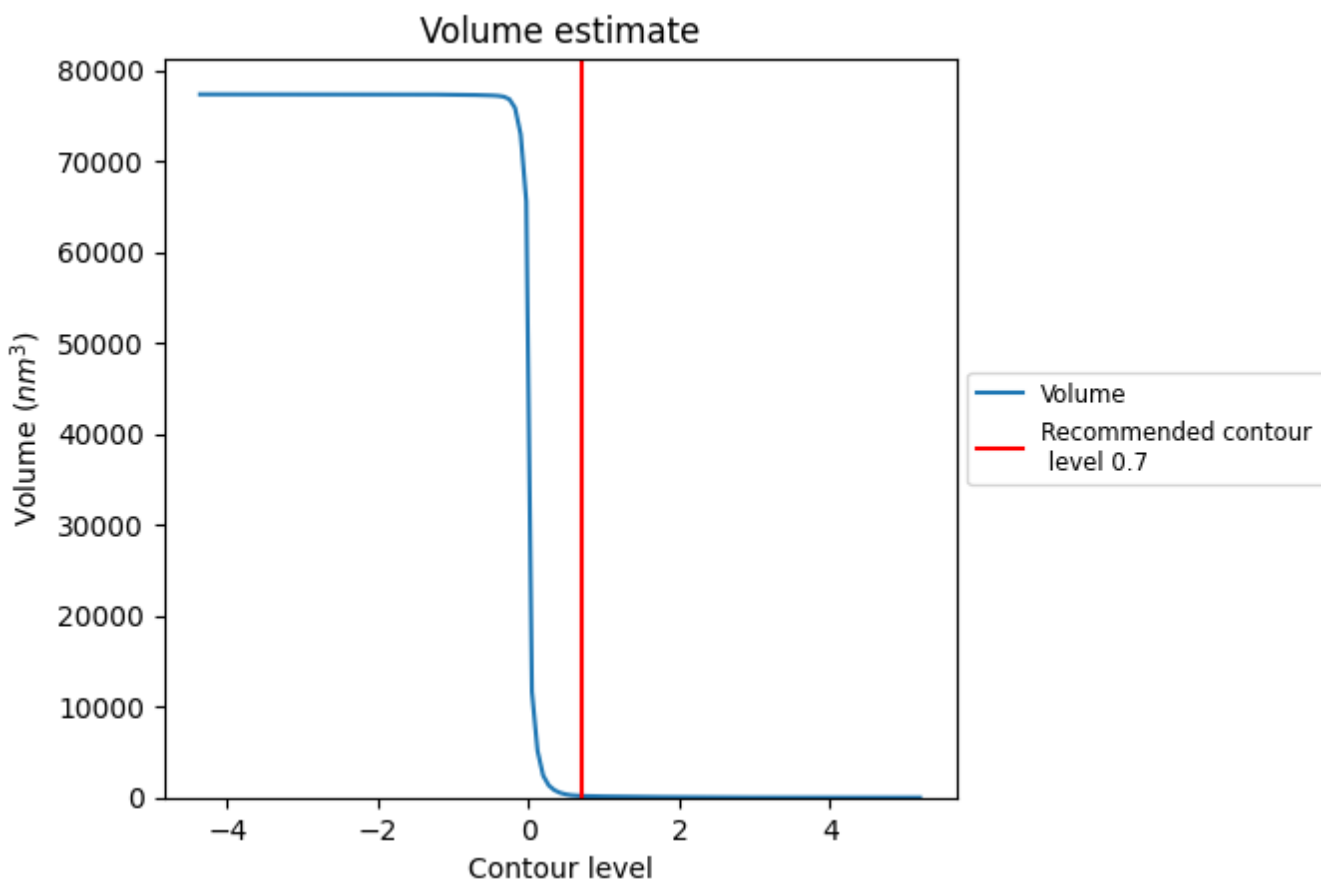
This section contains the results of statistical analysis of the map.

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.

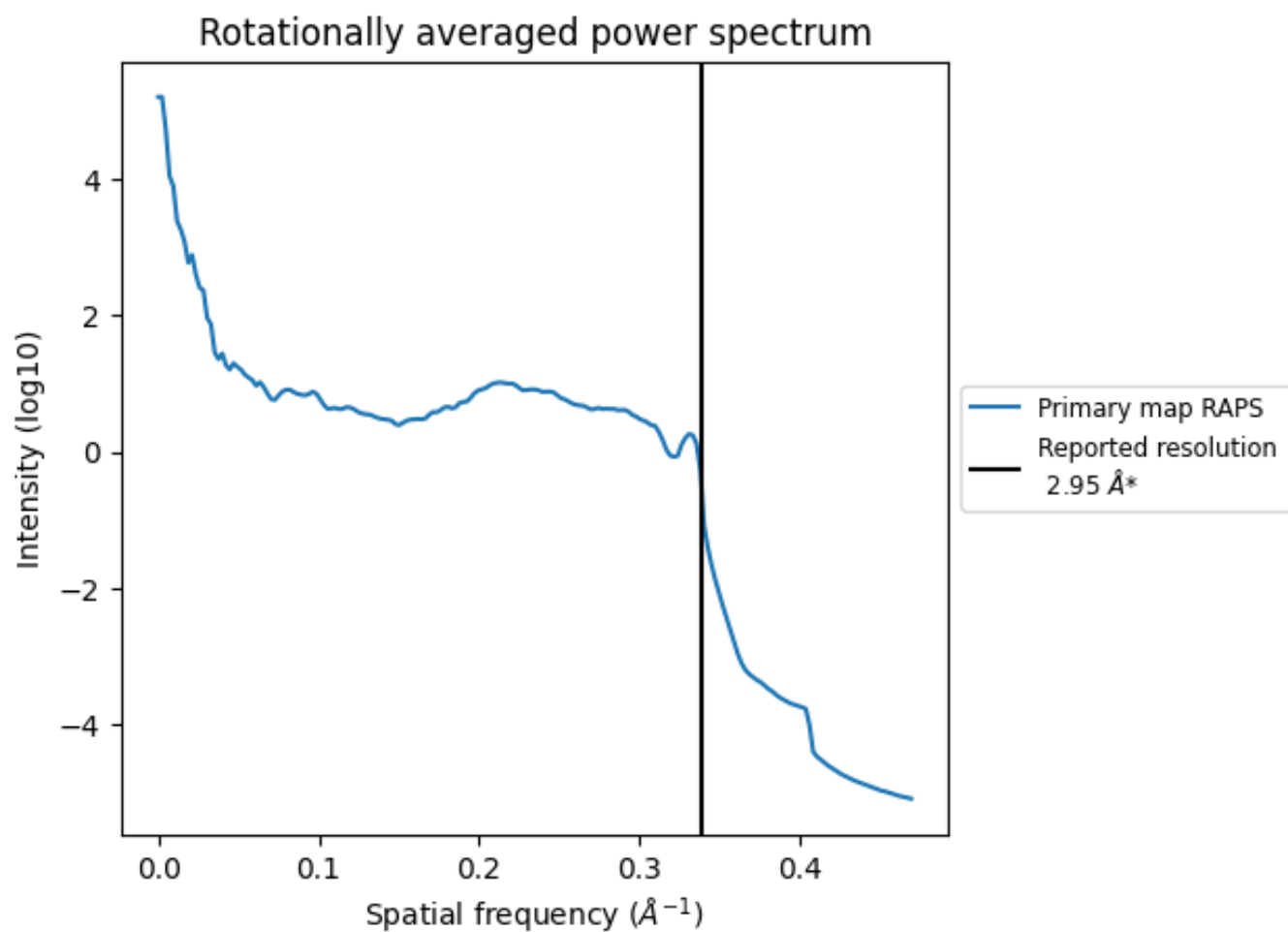
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm³; this corresponds to an approximate mass of 162 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.339 Å⁻¹

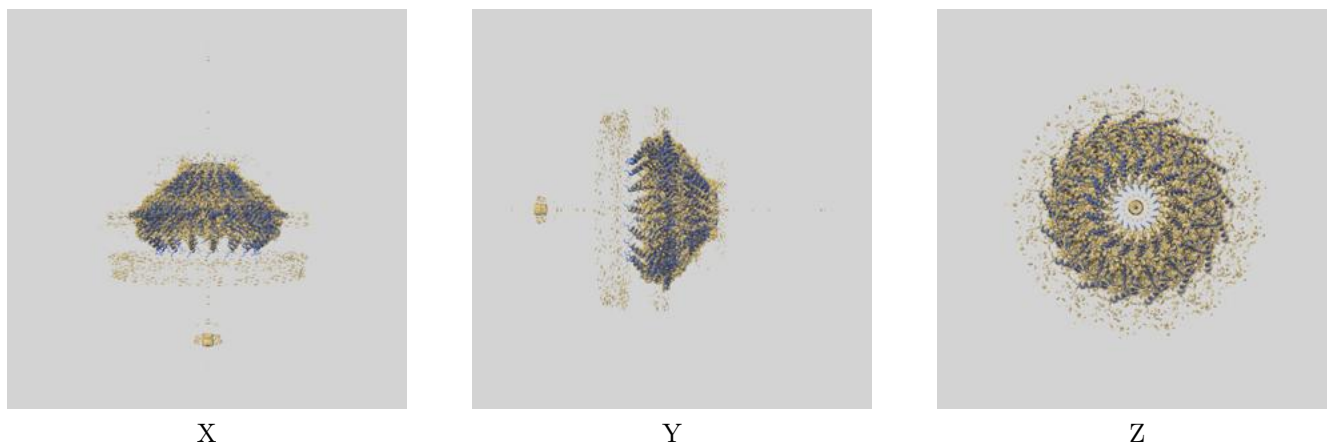
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

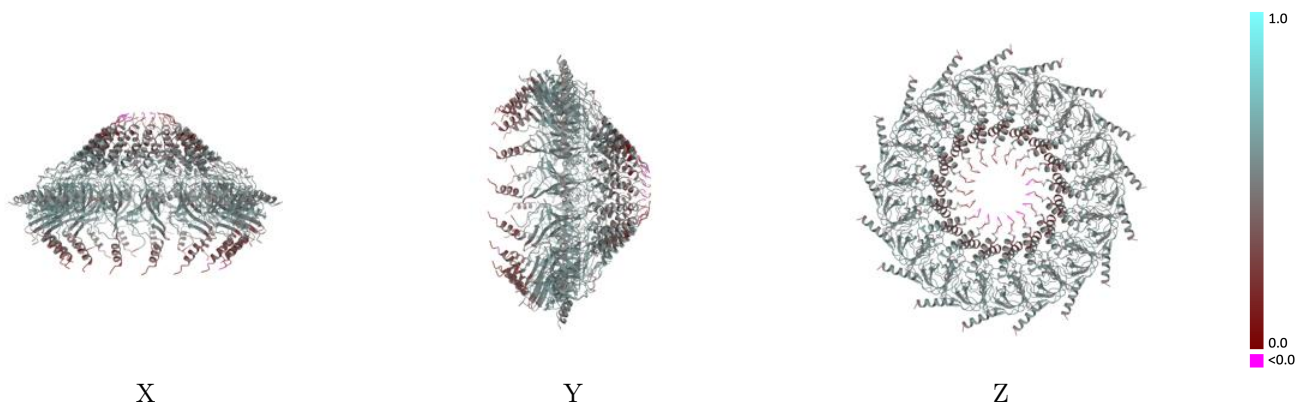
This section contains information regarding the fit between EMDB map EMD-24770 and PDB model 7SPC. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



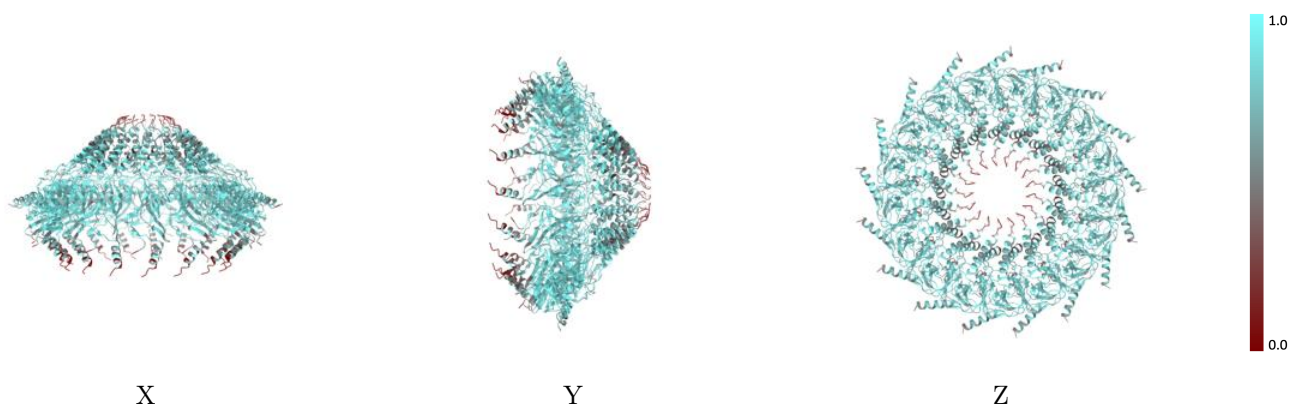
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



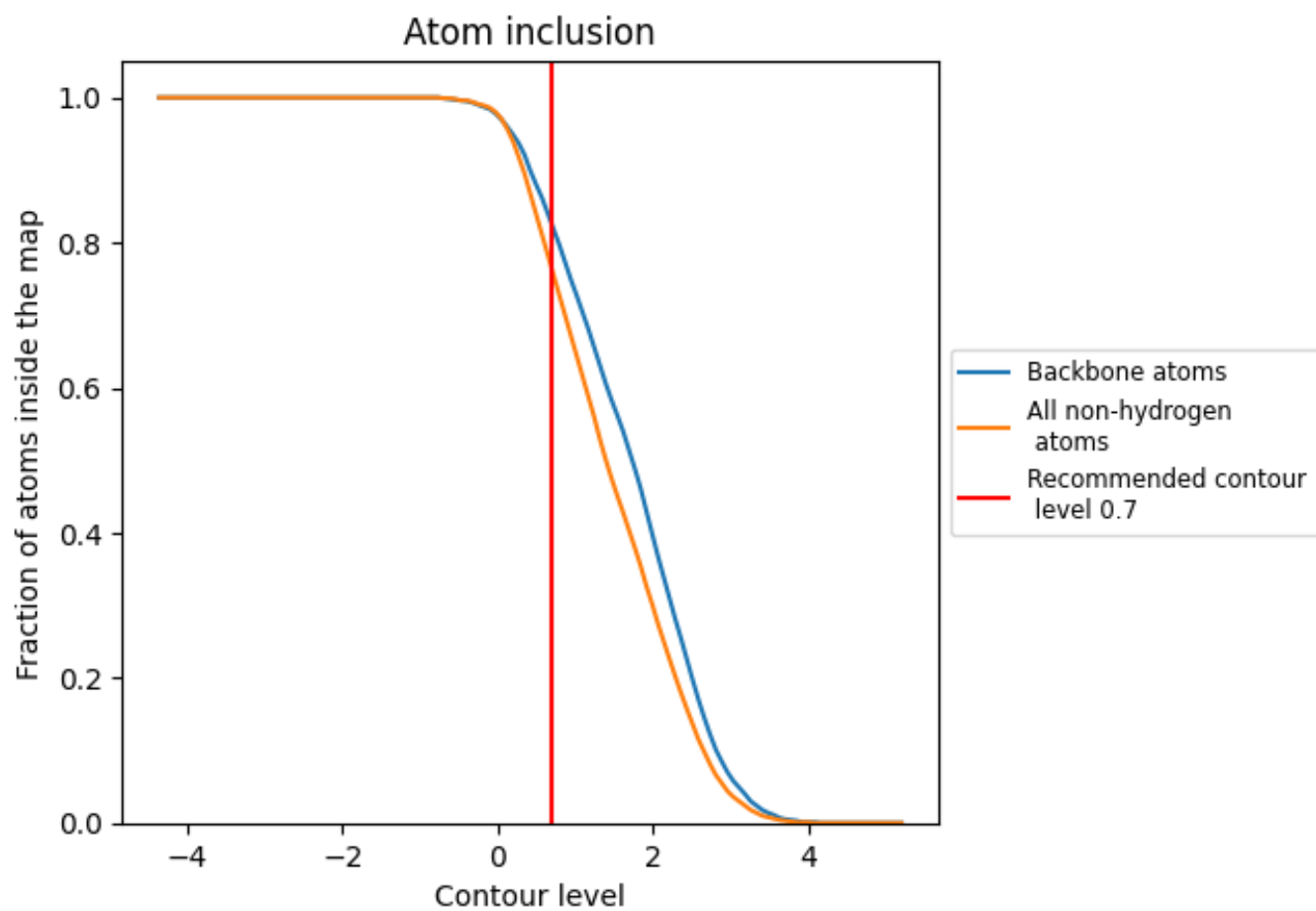
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 76% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7610	 0.5020
AB1	 0.7380	 0.5280
AB10	 0.7840	 0.5010
AB11	 0.7840	 0.5040
AB12	 0.7880	 0.5070
AB13	 0.7800	 0.5160
AB14	 0.7610	 0.5200
AB15	 0.7570	 0.5270
AB16	 0.7530	 0.5280
AB17	 0.7450	 0.5270
AB2	 0.7610	 0.5210
AB3	 0.7570	 0.5150
AB4	 0.7570	 0.5110
AB5	 0.7450	 0.5040
AB6	 0.7800	 0.5020
AB7	 0.7530	 0.5030
AB8	 0.7640	 0.4990
AB9	 0.7530	 0.4950
EF1	 0.7740	 0.5110
EF10	 0.7460	 0.4900
EF11	 0.7590	 0.4930
EF12	 0.7630	 0.5000
EF13	 0.7680	 0.5080
EF14	 0.7710	 0.5140
EF15	 0.7770	 0.5150
EF16	 0.7790	 0.5200
EF17	 0.7810	 0.5160
EF2	 0.7700	 0.5060
EF3	 0.7590	 0.5010
EF4	 0.7550	 0.4950
EF5	 0.7460	 0.4890
EF6	 0.7450	 0.4870
EF7	 0.7340	 0.4820
EF8	 0.7520	 0.4850
EF9	 0.7470	 0.4850

