



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:58 PM UTC

PDB ID : 6VW2 / pdb_00006vw2
EMDB ID : EMD-21410
Title : Cryo-EM structure of human islet amyloid polypeptide (hIAPP, or amylin) fibrils
Authors : Cao, Q.; Boyer, D.R.; Sawaya, M.R.; Eisenberg, D.S.
Deposited on : 2020-02-18
Resolution : 3.40 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

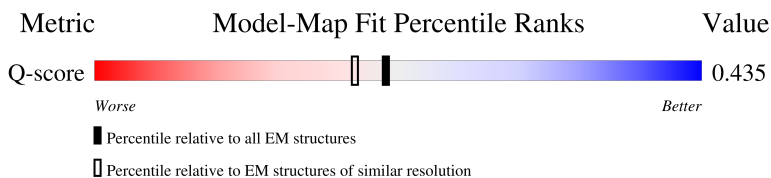
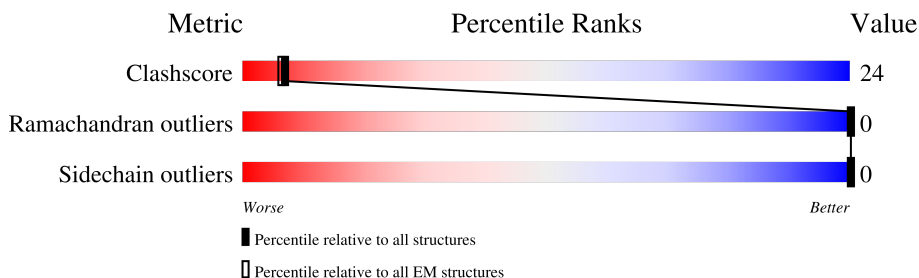
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	155	 10% 6% 85%
1	B	155	 9% 6% 85%
1	C	155	 10% 6% 85%
1	D	155	 9% 6% 85%

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Mol	Chain	Length	Quality of chain
1	E	155	 9% 6% 85%
1	F	155	 9% 6% 85%
1	G	155	 9% 6% 85%
1	H	155	 10% 6% 85%
1	I	155	 9% 6% 85%
1	J	155	 10% 6% 85%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1800 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 Islet amyloid polypeptide (SUMO-tagged).

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	24	Total	C	N	O	0	0
			180	111	31	38		
1	B	24	Total	C	N	O	0	0
			180	111	31	38		
1	C	24	Total	C	N	O	0	0
			180	111	31	38		
1	D	24	Total	C	N	O	0	0
			180	111	31	38		
1	E	24	Total	C	N	O	0	0
			180	111	31	38		
1	F	24	Total	C	N	O	0	0
			180	111	31	38		
1	G	24	Total	C	N	O	0	0
			180	111	31	38		
1	H	24	Total	C	N	O	0	0
			180	111	31	38		
1	I	24	Total	C	N	O	0	0
			180	111	31	38		
1	J	24	Total	C	N	O	0	0
			180	111	31	38		

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-117	MET	-	initiating methionine	UNP Q12306
A	-116	GLY	-	expression tag	UNP Q12306
A	-115	SER	-	expression tag	UNP Q12306
A	-114	SER	-	expression tag	UNP Q12306
A	-113	HIS	-	expression tag	UNP Q12306
A	-112	HIS	-	expression tag	UNP Q12306
A	-111	HIS	-	expression tag	UNP Q12306
A	-110	HIS	-	expression tag	UNP Q12306
A	-109	HIS	-	expression tag	UNP Q12306
A	-108	HIS	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-107	GLY	-	expression tag	UNP Q12306
A	-106	SER	-	expression tag	UNP Q12306
A	-105	GLY	-	expression tag	UNP Q12306
A	-104	LEU	-	expression tag	UNP Q12306
A	-103	VAL	-	expression tag	UNP Q12306
A	-102	PRO	-	expression tag	UNP Q12306
A	-101	ARG	-	expression tag	UNP Q12306
A	-100	GLY	-	expression tag	UNP Q12306
A	-99	SER	-	expression tag	UNP Q12306
A	-98	ALA	-	expression tag	UNP Q12306
A	-97	SER	-	expression tag	UNP Q12306
B	-117	MET	-	initiating methionine	UNP Q12306
B	-116	GLY	-	expression tag	UNP Q12306
B	-115	SER	-	expression tag	UNP Q12306
B	-114	SER	-	expression tag	UNP Q12306
B	-113	HIS	-	expression tag	UNP Q12306
B	-112	HIS	-	expression tag	UNP Q12306
B	-111	HIS	-	expression tag	UNP Q12306
B	-110	HIS	-	expression tag	UNP Q12306
B	-109	HIS	-	expression tag	UNP Q12306
B	-108	HIS	-	expression tag	UNP Q12306
B	-107	GLY	-	expression tag	UNP Q12306
B	-106	SER	-	expression tag	UNP Q12306
B	-105	GLY	-	expression tag	UNP Q12306
B	-104	LEU	-	expression tag	UNP Q12306
B	-103	VAL	-	expression tag	UNP Q12306
B	-102	PRO	-	expression tag	UNP Q12306
B	-101	ARG	-	expression tag	UNP Q12306
B	-100	GLY	-	expression tag	UNP Q12306
B	-99	SER	-	expression tag	UNP Q12306
B	-98	ALA	-	expression tag	UNP Q12306
B	-97	SER	-	expression tag	UNP Q12306
C	-117	MET	-	initiating methionine	UNP Q12306
C	-116	GLY	-	expression tag	UNP Q12306
C	-115	SER	-	expression tag	UNP Q12306
C	-114	SER	-	expression tag	UNP Q12306
C	-113	HIS	-	expression tag	UNP Q12306
C	-112	HIS	-	expression tag	UNP Q12306
C	-111	HIS	-	expression tag	UNP Q12306
C	-110	HIS	-	expression tag	UNP Q12306
C	-109	HIS	-	expression tag	UNP Q12306
C	-108	HIS	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-107	GLY	-	expression tag	UNP Q12306
C	-106	SER	-	expression tag	UNP Q12306
C	-105	GLY	-	expression tag	UNP Q12306
C	-104	LEU	-	expression tag	UNP Q12306
C	-103	VAL	-	expression tag	UNP Q12306
C	-102	PRO	-	expression tag	UNP Q12306
C	-101	ARG	-	expression tag	UNP Q12306
C	-100	GLY	-	expression tag	UNP Q12306
C	-99	SER	-	expression tag	UNP Q12306
C	-98	ALA	-	expression tag	UNP Q12306
C	-97	SER	-	expression tag	UNP Q12306
D	-117	MET	-	initiating methionine	UNP Q12306
D	-116	GLY	-	expression tag	UNP Q12306
D	-115	SER	-	expression tag	UNP Q12306
D	-114	SER	-	expression tag	UNP Q12306
D	-113	HIS	-	expression tag	UNP Q12306
D	-112	HIS	-	expression tag	UNP Q12306
D	-111	HIS	-	expression tag	UNP Q12306
D	-110	HIS	-	expression tag	UNP Q12306
D	-109	HIS	-	expression tag	UNP Q12306
D	-108	HIS	-	expression tag	UNP Q12306
D	-107	GLY	-	expression tag	UNP Q12306
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D	-99	SER	-	expression tag	UNP Q12306
D	-98	ALA	-	expression tag	UNP Q12306
D	-97	SER	-	expression tag	UNP Q12306
E	-117	MET	-	initiating methionine	UNP Q12306
E	-116	GLY	-	expression tag	UNP Q12306
E	-115	SER	-	expression tag	UNP Q12306
E	-114	SER	-	expression tag	UNP Q12306
E	-113	HIS	-	expression tag	UNP Q12306
E	-112	HIS	-	expression tag	UNP Q12306
E	-111	HIS	-	expression tag	UNP Q12306
E	-110	HIS	-	expression tag	UNP Q12306
E	-109	HIS	-	expression tag	UNP Q12306
E	-108	HIS	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-107	GLY	-	expression tag	UNP Q12306
E	-106	SER	-	expression tag	UNP Q12306
E	-105	GLY	-	expression tag	UNP Q12306
E	-104	LEU	-	expression tag	UNP Q12306
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E	-101	ARG	-	expression tag	UNP Q12306
E	-100	GLY	-	expression tag	UNP Q12306
E	-99	SER	-	expression tag	UNP Q12306
E	-98	ALA	-	expression tag	UNP Q12306
E	-97	SER	-	expression tag	UNP Q12306
F	-117	MET	-	initiating methionine	UNP Q12306
F	-116	GLY	-	expression tag	UNP Q12306
F	-115	SER	-	expression tag	UNP Q12306
F	-114	SER	-	expression tag	UNP Q12306
F	-113	HIS	-	expression tag	UNP Q12306
F	-112	HIS	-	expression tag	UNP Q12306
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F	-110	HIS	-	expression tag	UNP Q12306
F	-109	HIS	-	expression tag	UNP Q12306
F	-108	HIS	-	expression tag	UNP Q12306
F	-107	GLY	-	expression tag	UNP Q12306
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F	-99	SER	-	expression tag	UNP Q12306
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G	-117	MET	-	initiating methionine	UNP Q12306
G	-116	GLY	-	expression tag	UNP Q12306
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G	-113	HIS	-	expression tag	UNP Q12306
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G	-110	HIS	-	expression tag	UNP Q12306
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G	-107	GLY	-	expression tag	UNP Q12306
G	-106	SER	-	expression tag	UNP Q12306
G	-105	GLY	-	expression tag	UNP Q12306
G	-104	LEU	-	expression tag	UNP Q12306
G	-103	VAL	-	expression tag	UNP Q12306
G	-102	PRO	-	expression tag	UNP Q12306
G	-101	ARG	-	expression tag	UNP Q12306
G	-100	GLY	-	expression tag	UNP Q12306
G	-99	SER	-	expression tag	UNP Q12306
G	-98	ALA	-	expression tag	UNP Q12306
G	-97	SER	-	expression tag	UNP Q12306
H	-117	MET	-	initiating methionine	UNP Q12306
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J	-99	SER	-	expression tag	UNP Q12306
J	-98	ALA	-	expression tag	UNP Q12306
J	-97	SER	-	expression tag	UNP Q12306

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

ASN	THR	LYS
THR	ALA	THR
ALA	THR	ALA
CYS	PRO	CYS
LEU	ALA	LEU
THR	THR	THR
GLN	GLN	GLN
ARG	ARG	ARG
LEU	LEU	LEU
ALA	ALA	ALA
N14	N14	N14
V17	V17	V17
N22	N22	N22
I26	I26	I26
S29	S29	S29
T30	T30	T30
N31	N31	N31
V32	V32	V32
G33	G33	G33
S34	S34	S34
N35	N35	N35
T36	T36	T36
Y37	Y37	Y37

● Molecule 1: Islet amyloid polypeptide (SUMO-tagged)



MET	GLY	ASN	LYS
THR	SER	LYS	THR
ALA	SER	THR	ALA
THR	SER	THR	THR
CYS	PRO	THR	PRO
LEU	HIS	LEU	LEU
ALA	HIS	ALA	ARG
THR	HIS	THR	ARG
GLN	HIS	GLN	ARG
ARG	HIS	ARG	LEU
LEU	HIS	LEU	MET
MET	HIS	LEU	LEU
GLY	GLY	ALA	GLY
ALA	SER	ALA	SER
N14	GLY	PHE	GLY
V17	LEU	ALA	LEU
N21	VAL	LYS	VAL
N22	PRO	LYS	PRO
I26	ARG	GLN	ARG
S29	GLY	LYS	GLY
T30	LYS	GLU	LYS
N31	MET	GLU	MET
V32	ASP	ASP	ASP
G33	SER	SER	SER
S34	LEU	LEU	LEU
N35	ASP	PHE	ASP
T36	VAL	TYR	VAL
Y37	ASN	ASP	ASN
	GLN	GLY	GLN
	GLY	ILE	GLY
	ALA	ARG	ALA
	LYS	ILE	LYS
	PRO	ILE	PRO
	GLN	GLN	GLN
	VAL	VAL	VAL
	LYS	ASP	LYS
	PRO	GLN	PRO
	GLU	THR	GLU
	VAL	PRO	VAL
	LYS	GLU	LYS
	PRO	ASP	PRO
	LEU	LEU	LEU
	THR	ASP	THR
	HIS	MET	HIS
	ILE	GLU	ILE
	ASN	ASP	ASN
	LEU	LEU	LEU
	LYS	ASP	LYS
	VAL	ILE	VAL
	SER	ILE	SER
	ASP	GLU	ASP
	GLY	ALA	GLY
	HIS	ARG	HIS
	SER	ARG	SER
	GLU	GLU	GLU
	ILE	ILE	ILE
	PHE	GLN	PHE
	PHE	ILE	PHE
	LYS	GLY	LYS
	LYS	LYS	LYS
	ILE	ILE	ILE

ASN	THR	LYS
THR	ALA	THR
ALA	THR	ALA
CYS	PRO	CYS
LEU	ALA	LEU
THR	THR	THR
GLN	GLN	GLN
ARG	ARG	ARG
LEU	LEU	LEU
ALA	ALA	ALA
N14	N14	N14
V17	V17	V17
N21	N21	N21
N22	N22	N22
I26	I26	I26
S29	S29	S29
T30	T30	T30
N31	N31	N31
V32	V32	V32
G33	G33	G33
S34	S34	S34
N35	N35	N35
T36	T36	T36
Y37	Y37	Y37

● Molecule 1: Islet amyloid polypeptide (SUMO-tagged)



MET	GLY	ASN	LYS
THR	SER	LYS	THR
ALA	SER	THR	ALA
THR	SER	THR	THR
CYS	PRO	THR	PRO
LEU	HIS	LEU	LEU
ALA	HIS	ALA	ARG
THR	HIS	THR	ARG
GLN	HIS	GLN	ARG
ARG	HIS	ARG	LEU
LEU	HIS	LEU	MET
MET	HIS	LEU	LEU
GLY	GLY	ALA	GLY
ALA	SER	ALA	SER
N14	GLY	PHE	GLY
V17	LEU	ALA	LEU
N22	VAL	LYS	VAL
I26	PRO	LYS	PRO
S29	ARG	GLN	ARG
T30	GLY	LYS	GLY
N31	LYS	GLU	LYS
V32	MET	GLU	MET
G33	ASP	ASP	ASP
S34	SER	SER	SER
N35	LEU	LEU	LEU
I36	ASP	PHE	ASP
Y37	VAL	TYR	VAL
	ASN	ASP	ASN
	GLN	GLY	GLN
	GLY	ILE	GLY
	ALA	ARG	ALA
	LYS	ILE	LYS
	PRO	ILE	PRO
	GLN	GLN	GLN
	VAL	VAL	VAL
	LYS	ASP	LYS
	PRO	GLN	PRO
	GLU	THR	GLU
	VAL	PRO	VAL
	LYS	GLU	LYS
	PRO	ASP	PRO
	LEU	LEU	LEU
	THR	ASP	THR
	HIS	MET	HIS
	ILE	GLU	ILE
	ASN	ASP	ASN
	LEU	LEU	LEU
	LYS	ASP	LYS
	VAL	ILE	VAL
	SER	ILE	SER
	ASP	GLU	ASP
	GLY	ALA	GLY
	HIS	ARG	HIS
	SER	ARG	SER
	GLU	GLU	GLU
	ILE	ILE	ILE
	PHE	GLN	PHE
	PHE	ILE	PHE
	LYS	GLY	LYS
	LYS	LYS	LYS
	ILE	ILE	ILE

ASN	THR	LYS
THR	ALA	THR
ALA	THR	ALA
CYS	PRO	CYS
LEU	ALA	LEU
THR	THR	THR
GLN	GLN	GLN
ARG	ARG	ARG
LEU	LEU	LEU
ALA	ALA	ALA
N14	N14	N14
V17	V17	V17
N22	N22	N22
I26	I26	I26
S29	S29	S29
T30	T30	T30
N31	N31	N31
V32	V32	V32
G33	G33	G33
S34	S34	S34
N35	N35	N35
I36	I36	I36
Y37	Y37	Y37

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=179.42°, rise=2.406 Å, axial sym=C1	Depositor
Number of segments used	25767	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 ($e^-/\text{Å}^2$)	44	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	14.139	Depositor
Minimum map value	-8.656	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	136.192, 136.192, 136.192	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	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	0.33	0/183	0.71	0/247
1	B	0.33	0/183	0.71	0/247
1	C	0.33	0/183	0.71	0/247
1	D	0.33	0/183	0.71	0/247
1	E	0.33	0/183	0.71	0/247
1	F	0.33	0/183	0.71	0/247
1	G	0.33	0/183	0.71	0/247
1	H	0.33	0/183	0.71	0/247
1	I	0.33	0/183	0.71	0/247
1	J	0.33	0/183	0.71	0/247
All	All	0.33	0/1830	0.71	0/2470

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	180	0	164	14	0
1	B	180	0	164	16	0
1	C	180	0	164	15	0
1	D	180	0	164	15	0
1	E	180	0	164	16	0
1	F	180	0	164	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	180	0	164	10	0
1	H	180	0	164	9	0
1	I	180	0	164	10	0
1	J	180	0	164	9	0
All	All	1800	0	1640	83	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 24.

The worst 5 of 83 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)
1:H:34:SER:HB2	1:H:37:TYR:OH	1.74	0.88
1:D:34:SER:HB2	1:D:37:TYR:OH	1.74	0.87
1:A:34:SER:HB2	1:A:37:TYR:OH	1.74	0.87
1:J:34:SER:HB2	1:J:37:TYR:OH	1.74	0.87
1:E:34:SER:HB2	1:E:37:TYR:OH	1.74	0.87

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	
1	A	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	B	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	C	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	D	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	E	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	F	22/155 (14%)	16 (73%)	6 (27%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	H	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	I	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
1	J	22/155 (14%)	16 (73%)	6 (27%)	0	100	100
All	All	220/1550 (14%)	160 (73%)	60 (27%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	21/135 (16%)	21 (100%)	0	100	100
1	B	21/135 (16%)	21 (100%)	0	100	100
1	C	21/135 (16%)	21 (100%)	0	100	100
1	D	21/135 (16%)	21 (100%)	0	100	100
1	E	21/135 (16%)	21 (100%)	0	100	100
1	F	21/135 (16%)	21 (100%)	0	100	100
1	G	21/135 (16%)	21 (100%)	0	100	100
1	H	21/135 (16%)	21 (100%)	0	100	100
1	I	21/135 (16%)	21 (100%)	0	100	100
1	J	21/135 (16%)	21 (100%)	0	100	100
All	All	210/1350 (16%)	210 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	21	ASN

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Mol	Chain	Res	Type
1	J	21	ASN
1	J	31	ASN
1	J	14	ASN
1	E	21	ASN

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.

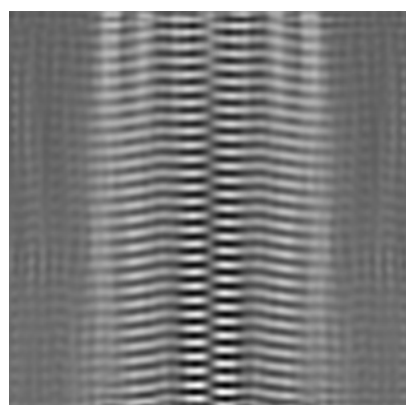
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21410. These allow visual inspection of the internal detail of the map and identification of artifacts.

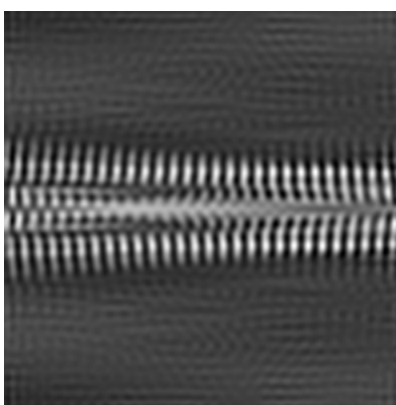
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

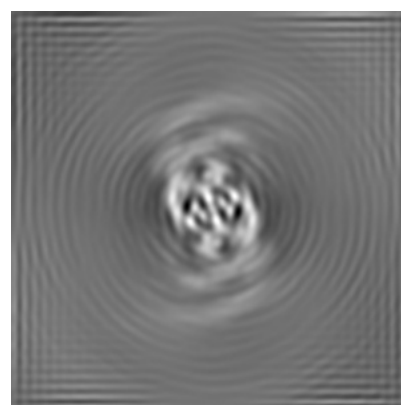
6.1.1 Primary map



X



Y

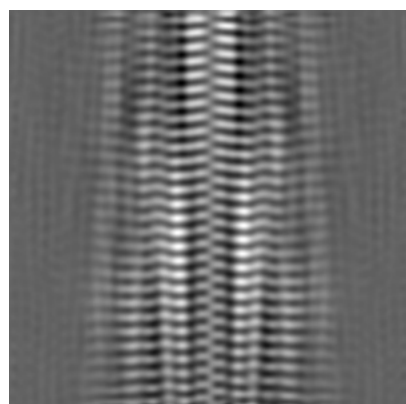


Z

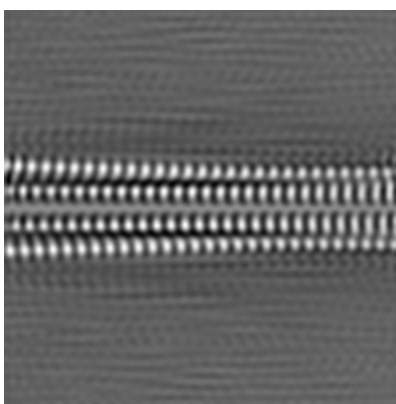
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

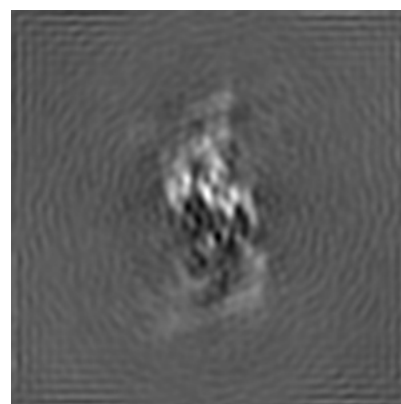
6.2.1 Primary map



X Index: 64



Y Index: 64

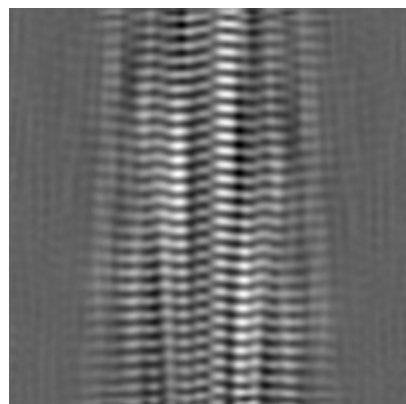


Z Index: 64

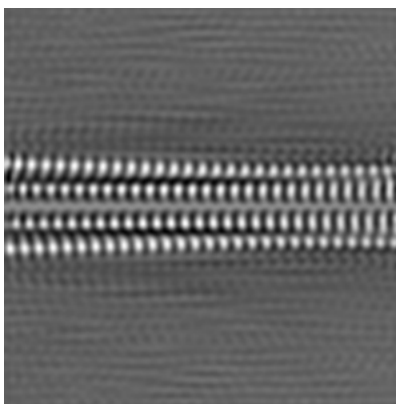
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

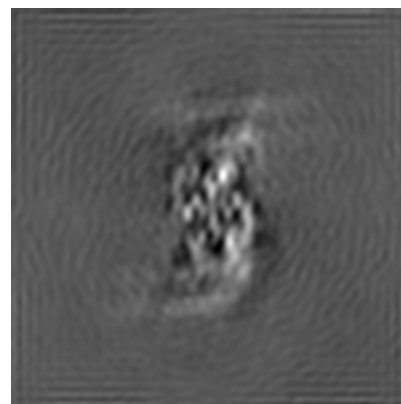
6.3.1 Primary map



X Index: 63



Y Index: 64

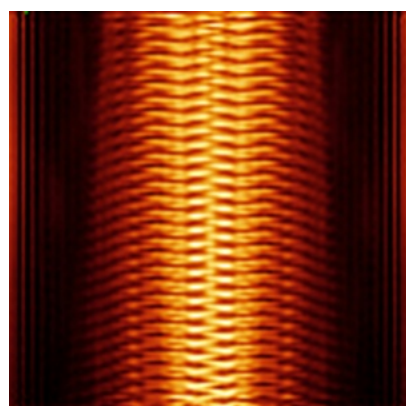


Z Index: 126

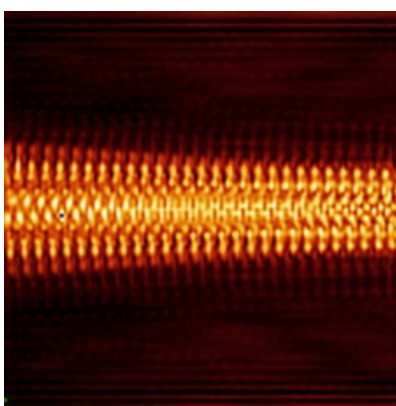
The images above show the largest variance slices of the map in three orthogonal directions.

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

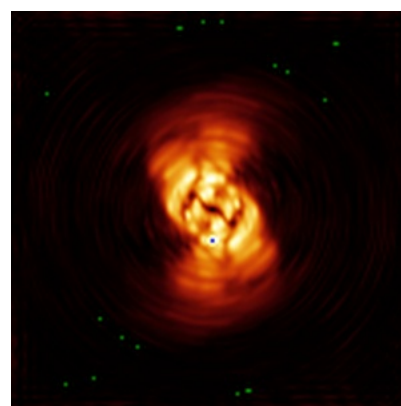
6.4.1 Primary map



X



Y

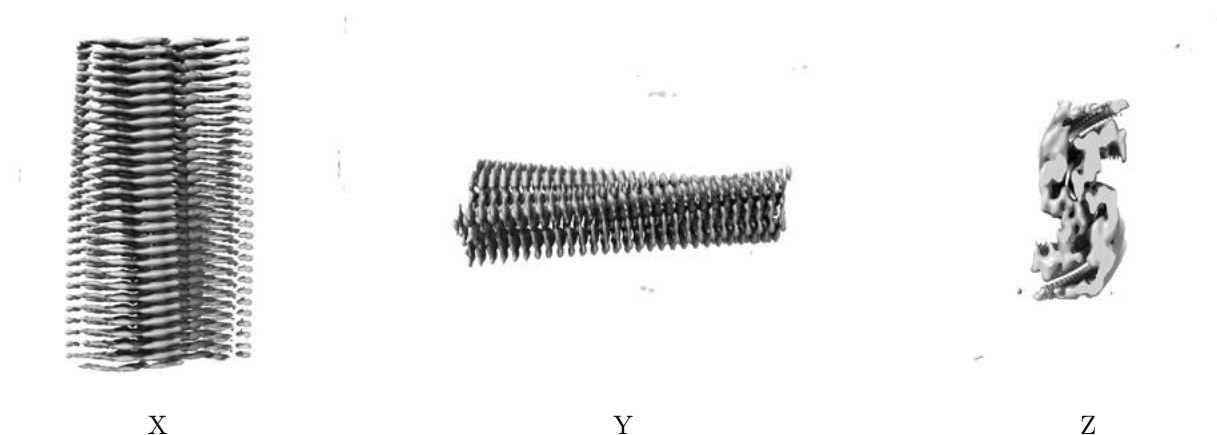


Z

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

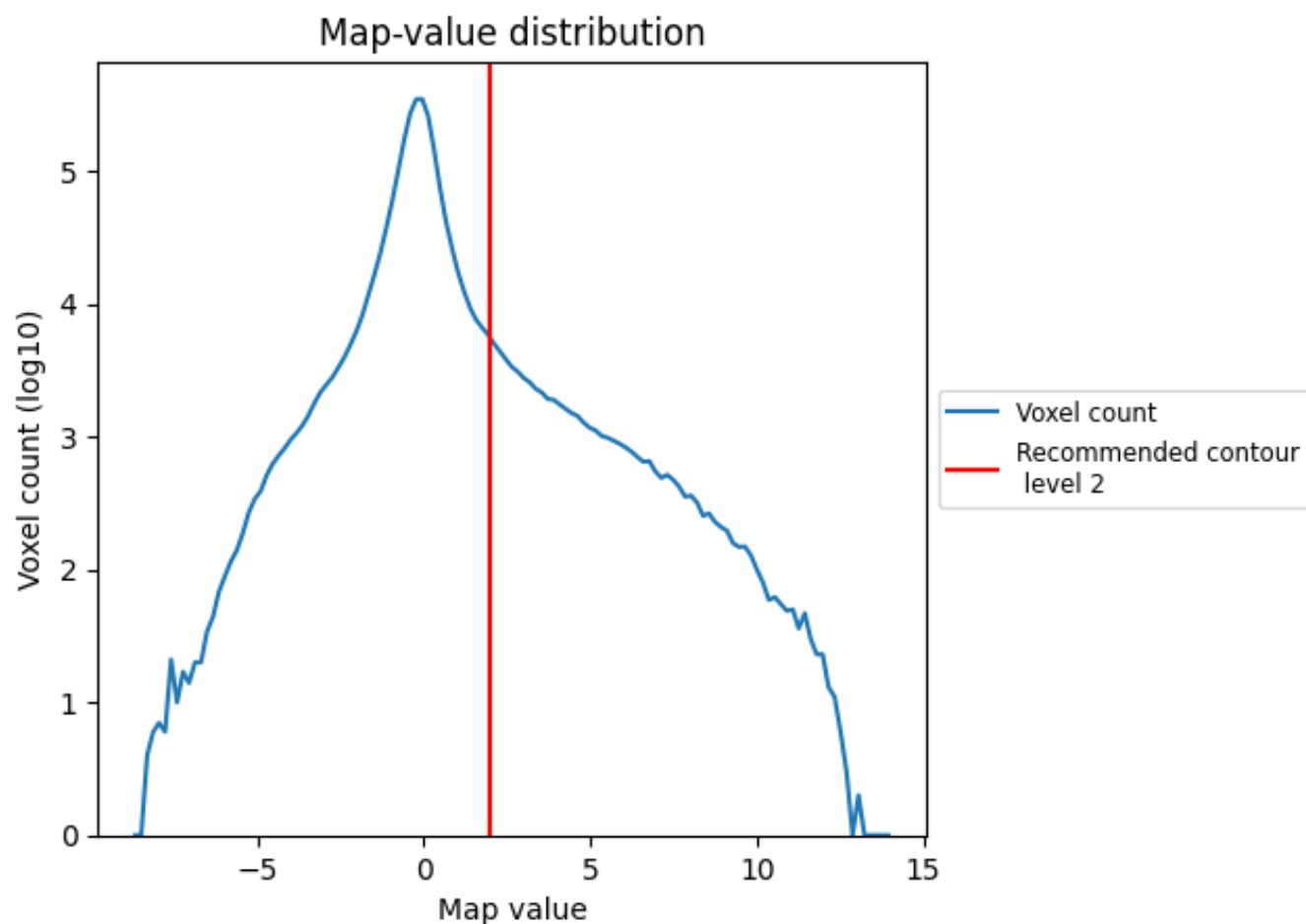
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

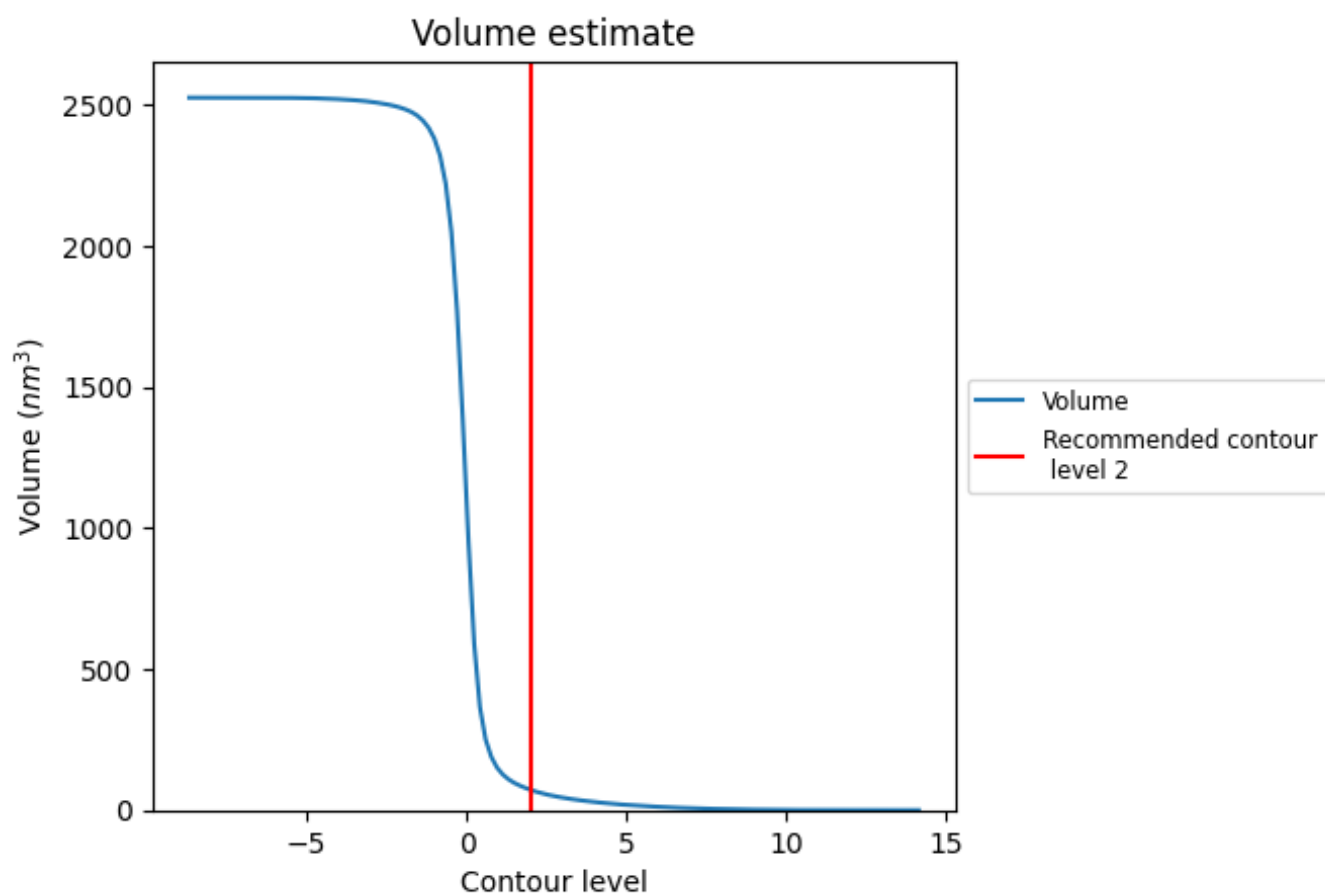
This section contains the results of statistical analysis of the map.

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.

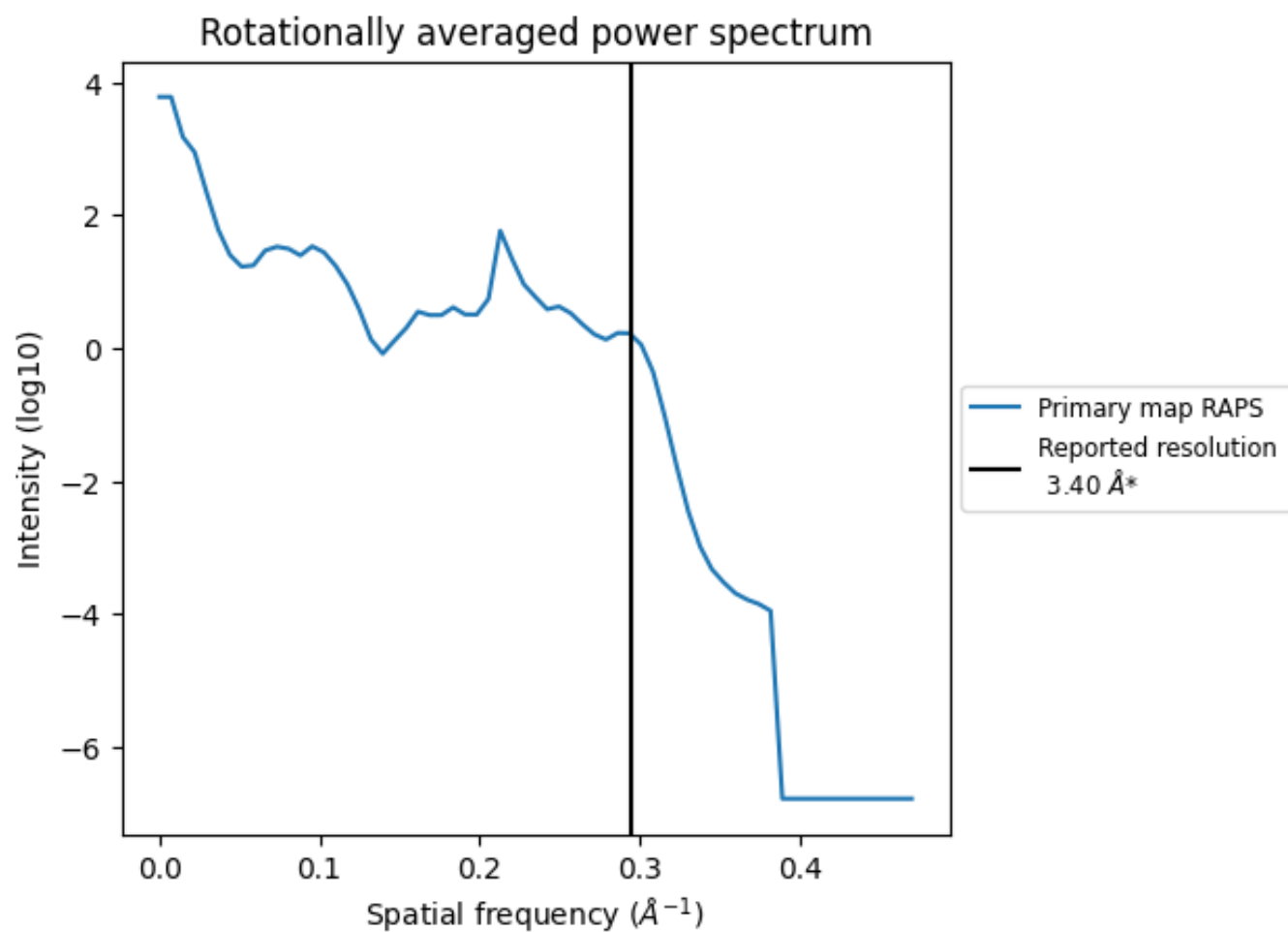
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 72 nm³; this corresponds to an approximate mass of 65 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 ⓘ

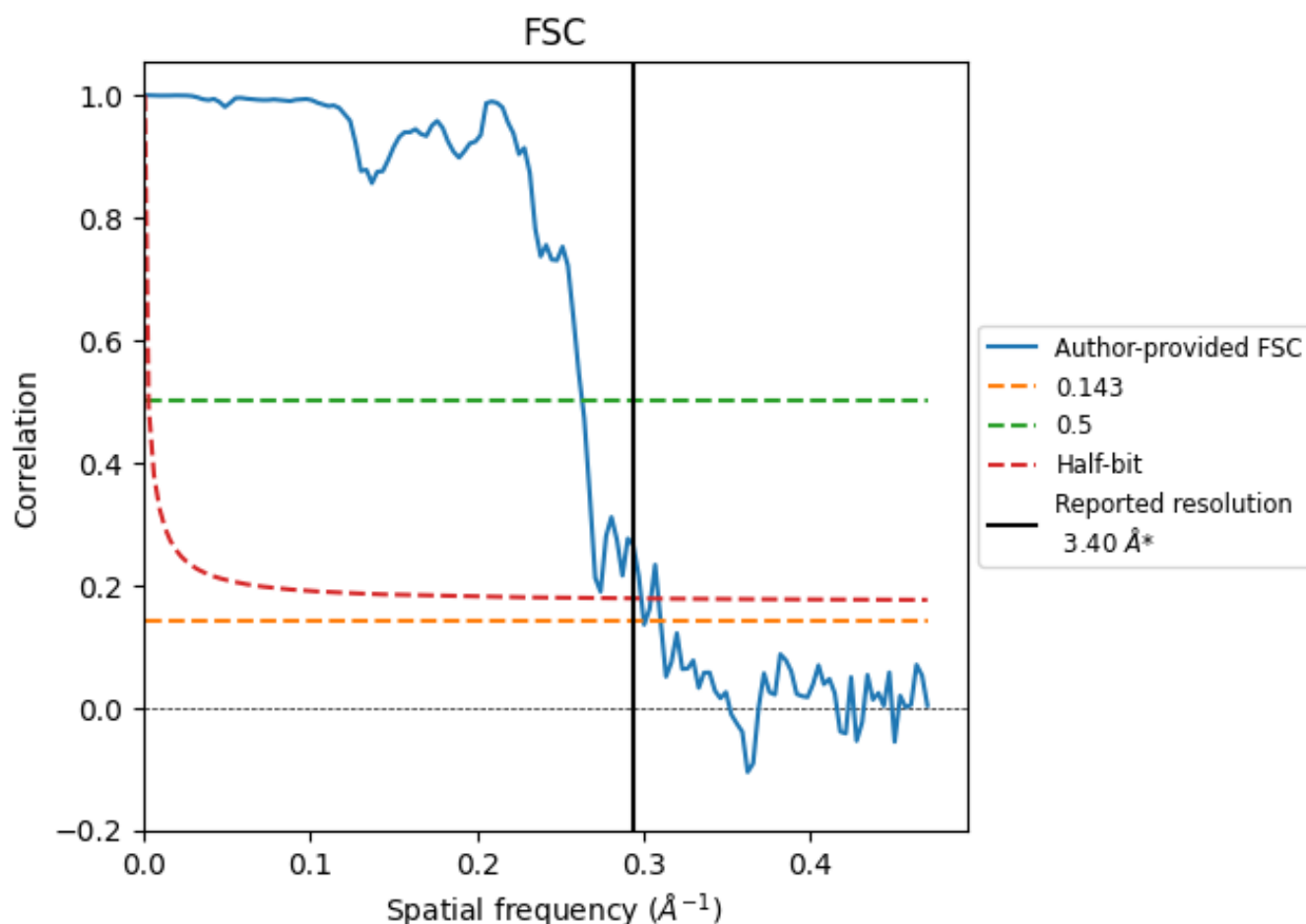


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

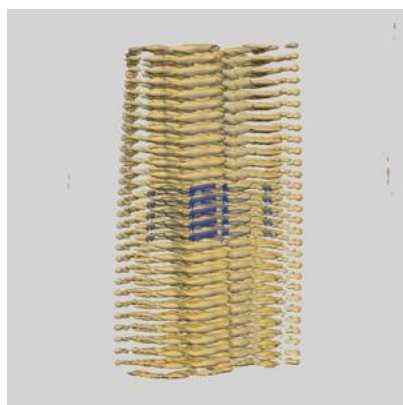
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.33	3.80	3.35
Unmasked-calculated*	-	-	-

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

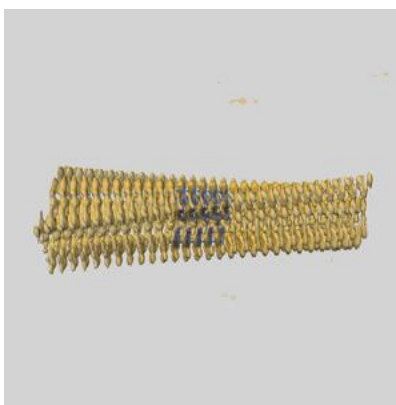
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21410 and PDB model 6VW2. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



X



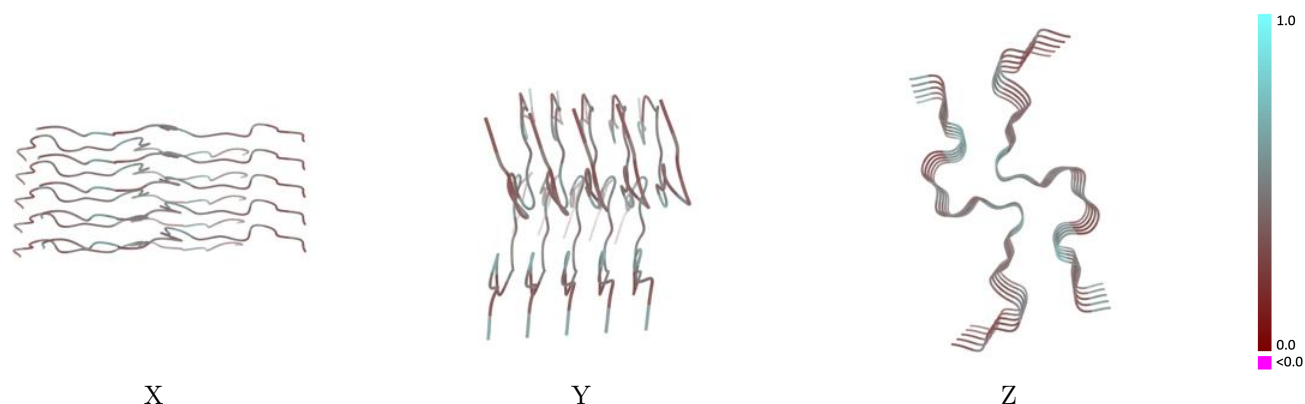
Y



Z

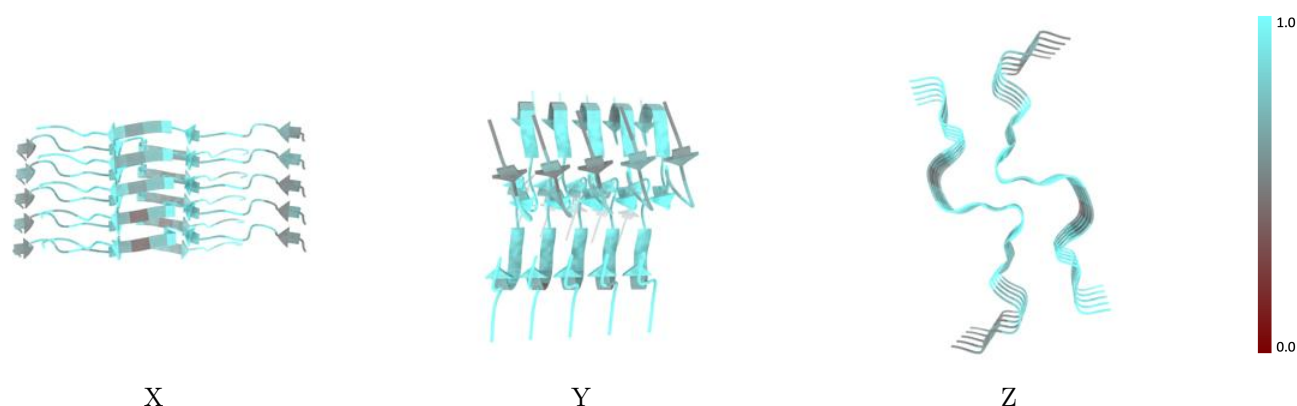
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



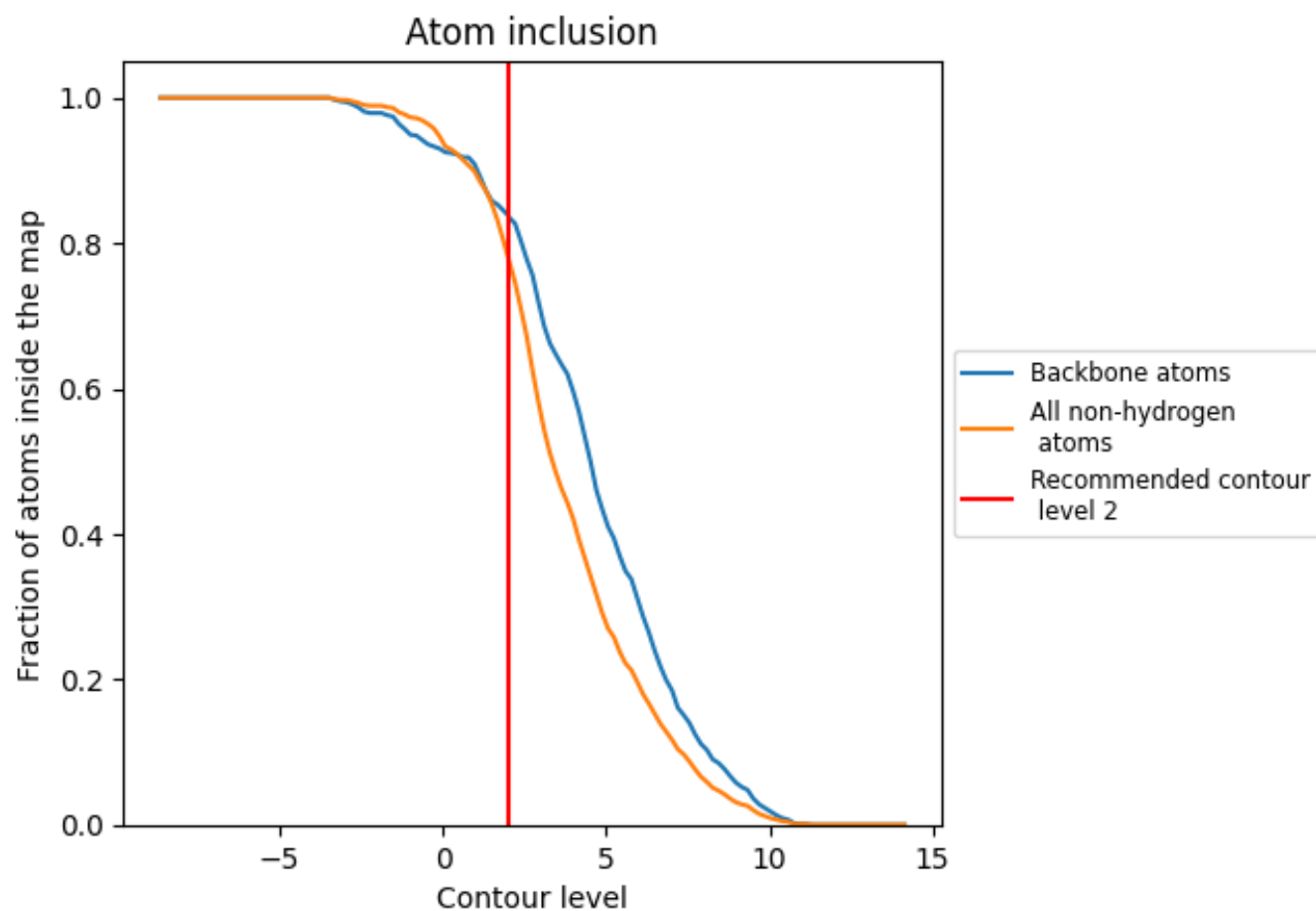
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7800	0.4350
A	0.7880	0.4360
B	0.7820	0.4310
C	0.7650	0.4380
D	0.7710	0.4400
E	0.7650	0.4400
F	0.7880	0.4350
G	0.7760	0.4290
H	0.7820	0.4370
I	0.7930	0.4340
J	0.7880	0.4340

1.0

0.0

<0.0