



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 05:16 PM UTC

PDB ID : 9I3N / pdb_00009i3n
EMDB ID : EMD-52601
Title : Csu pilus rod type 1 stack
Authors : Malmi, H.; Pakharukova, N.; Zavialov, A.V.
Deposited on : 2025-01-23
Resolution : 7.58 Å (reported)
Based on initial model : 7ZL4

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:

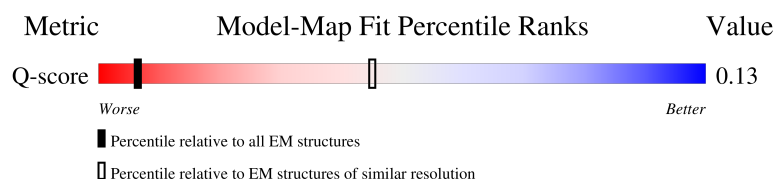
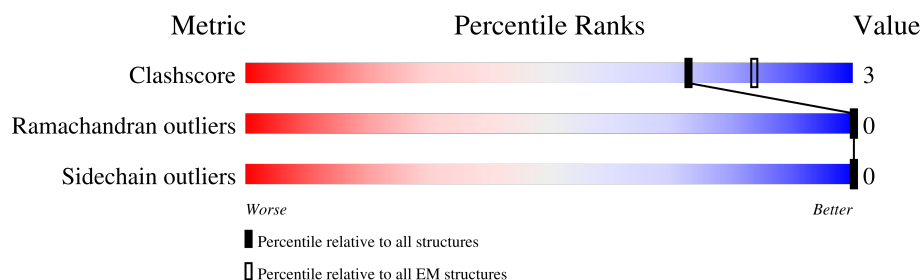
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.58 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.













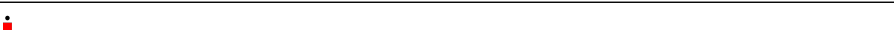

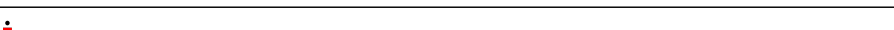
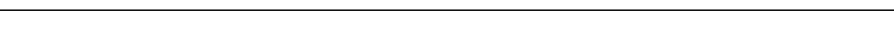

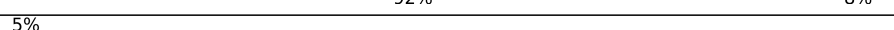

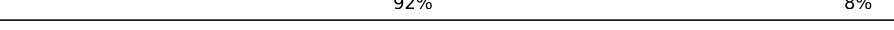
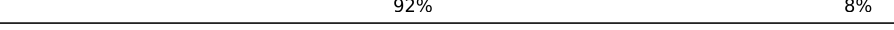






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	370 (7.08 - 8.04)

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	A1	155	
1	A2	155	
1	A3	155	
1	B1	155	

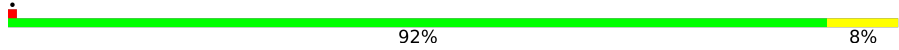
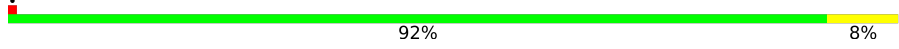
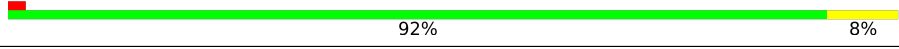
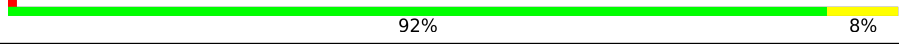
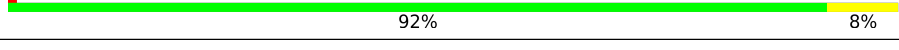
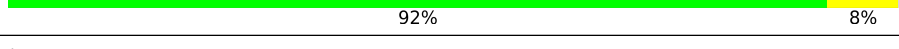
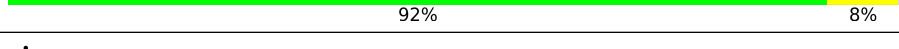
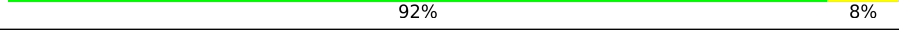
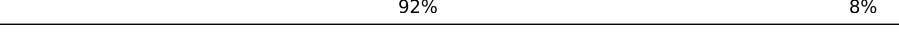
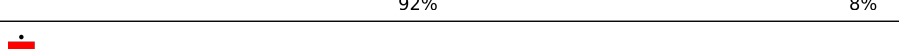
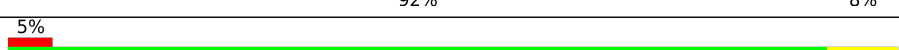
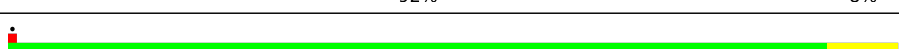
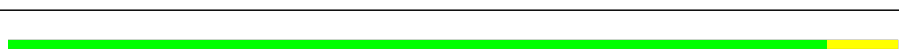
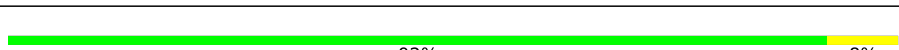
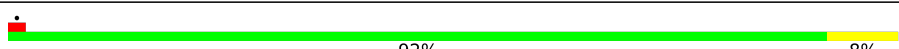


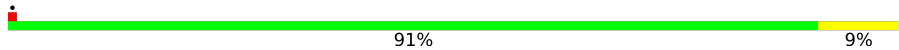
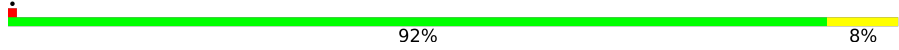

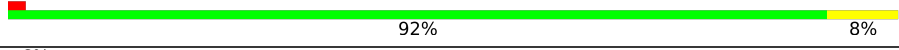
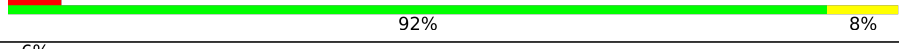
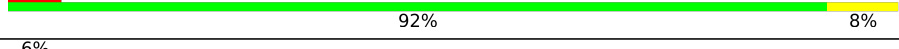
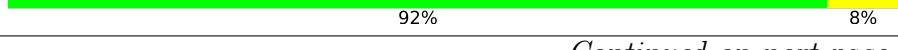

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Mol	Chain	Length	Quality of chain
1	B2	155	 93% 7%
1	B3	155	 91% 9%
1	C1	155	 92% 8%
1	C2	155	 91% 9%
1	C3	155	 92% 8%
1	D1	155	 92% 8%
1	D2	155	 92% 8%
1	D3	155	 92% 8%
1	E1	155	 92% 8%
1	E2	155	 92% 8%
1	E3	155	 92% 8%
1	F1	155	 92% 8%
1	F2	155	 92% 8%
1	F3	155	 92% 8%
1	G1	155	 92% 8%
1	G2	155	 5% 92% 8%
1	G3	155	 92% 8%
1	H1	155	 92% 8%
1	H2	155	 92% 8%
1	H3	155	 92% 8%
1	I1	155	 91% 9%
1	I2	155	 92% 8%
1	I3	155	 91% 9%
1	J1	155	 92% 8%
1	J2	155	 91% 9%

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Mol	Chain	Length	Quality of chain
1	J3	155	
1	K1	155	
1	K2	155	
1	K3	155	
1	L1	155	
1	L2	155	
1	L3	155	
1	M1	155	
1	M2	155	
1	M3	155	
1	N1	155	
1	N2	155	
1	N3	155	
1	O1	155	
1	O2	155	
1	O3	155	
1	P1	155	
1	P2	155	
1	P3	155	
1	Q1	155	
1	Q2	155	
1	Q3	155	
1	R1	155	
1	R2	155	
1	R3	155	

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Mol	Chain	Length	Quality of chain
1	S1	155	<div><div><div></div><div></div><div></div></div><div>6% .</div><div>91%</div></div>
1	S2	155	<div><div><div></div><div></div><div></div></div><div>7% .</div><div>91%</div></div>
1	S3	155	<div><div><div></div><div></div><div></div></div><div>6% .</div><div>91%</div></div>

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 120204 atoms, of which 59238 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 CsuA/B.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A1	141	Total 2017	C 634	H 988	N 177	O 215	S 3	0	0
1	B1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	C1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	D1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	E1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	F1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	G1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	H1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	I1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	J1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	K1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	L1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	M1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	N1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	O1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	P1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	Q1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	R1	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	S1	14	Total 209	C 62	H 109	N 17	O 21		0	0
1	A2	141	Total 2017	C 634	H 988	N 177	O 215	S 3	0	0
1	B2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	C2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	D2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	E2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	F2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	G2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	H2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	I2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	J2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	K2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	L2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	M2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	N2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	O2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	P2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	Q2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	R2	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	S2	14	Total 209	C 62	H 109	N 17	O 21		0	0

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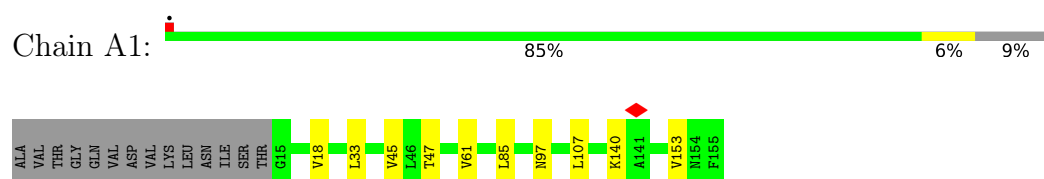
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Mol	Chain	Residues	Atoms						AltConf	Trace
1	A3	141	Total 2017	C 634	H 988	N 177	O 215	S 3	0	0
1	B3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	C3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	D3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	E3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	F3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	G3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	H3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	I3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	J3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	K3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	L3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	M3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	N3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	O3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	P3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	Q3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	R3	155	Total 2226	C 696	H 1097	N 194	O 236	S 3	0	0
1	S3	14	Total 209	C 62	H 109	N 17	O 21		0	0

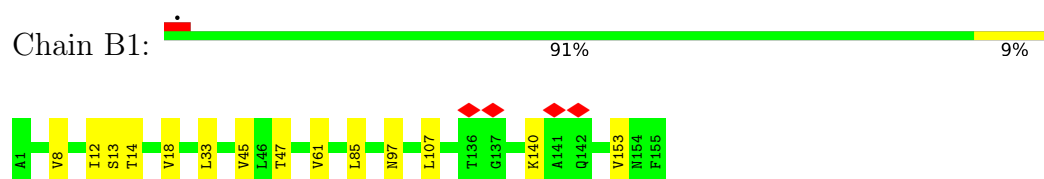
3 Residue-property plots

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.

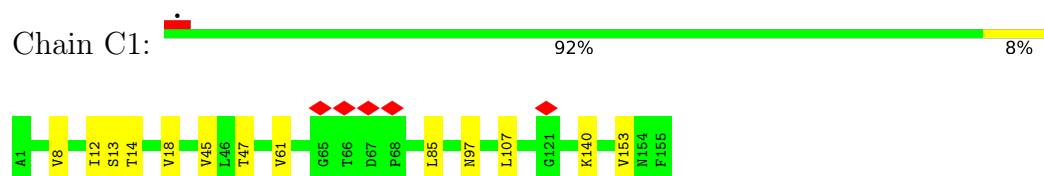
- Molecule 1: CsuA/B



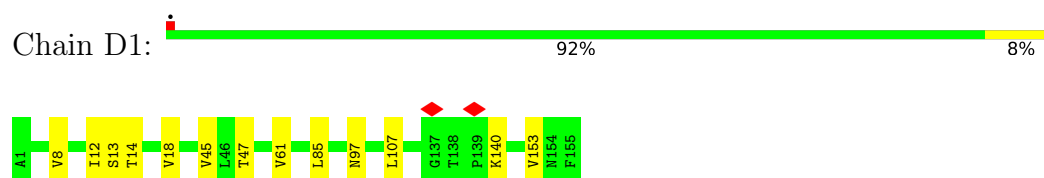
- Molecule 1: CsuA/B



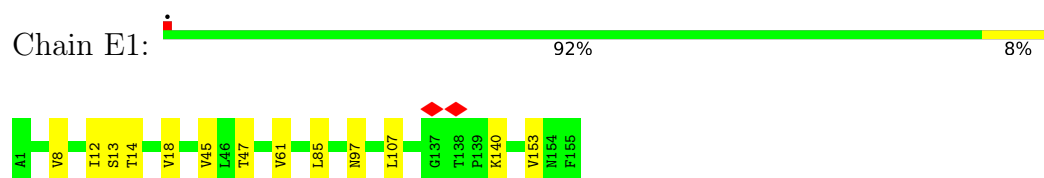
- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



● Molecule 1: CsuA/B

Chain F1:  92% 8%



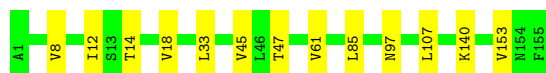
● Molecule 1: CsuA/B

Chain G1:  92% 8%




● Molecule 1: CsuA/B

Chain H1:  92% 8%



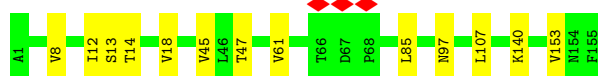
● Molecule 1: CsuA/B

Chain I1:  91% 9%



● Molecule 1: CsuA/B

Chain J1:  92% 8%



● Molecule 1: CsuA/B

Chain K1:  92% 8%

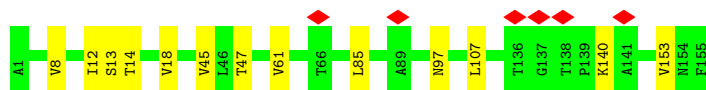


● Molecule 1: CsuA/B

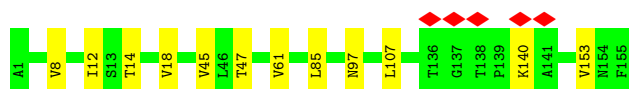
Chain L1:  92% 8%



- Molecule 1: CsuA/B



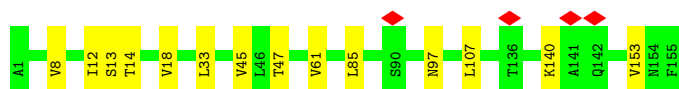
- Molecule 1: CsuA/B



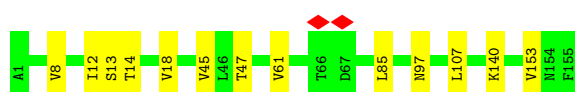
- Molecule 1: CsuA/B



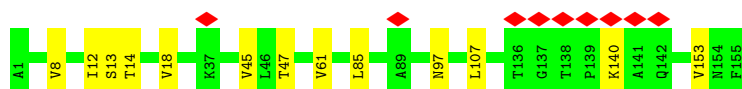
- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



- Molecule 1: CsuA/B

- Molecule 1: CsuA/B

- Molecule 1: CsuA/B

- Molecule 1: CsuA/B

- Molecule 1: CsuA/B

- Molecule 1: CsuA/B

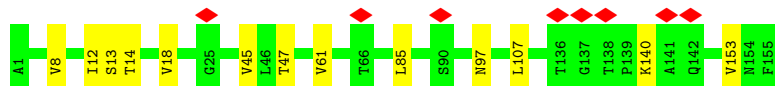
- Molecule 1: CsuA/B

Chain F2:  92% 8%



• Molecule 1: CsuA/B

Chain G2:  5% 92% 8%




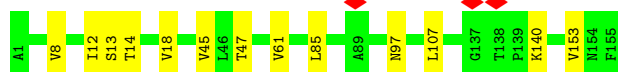
• Molecule 1: CsuA/B

Chain H2:  92% 8%




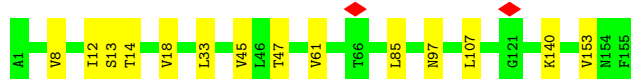
• Molecule 1: CsuA/B

Chain I2:  92% 8%



• Molecule 1: CsuA/B

Chain J2:  91% 9%



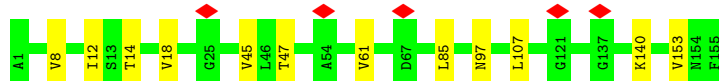
• Molecule 1: CsuA/B

Chain K2:  92% 8%



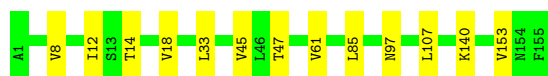
• Molecule 1: CsuA/B

Chain L2:  92% 8%



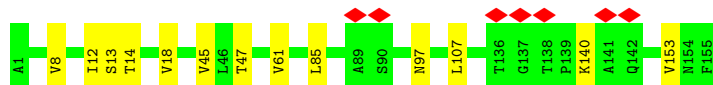
- Molecule 1: CsuA/B

Chain M2:  92% 8%



- Molecule 1: CsuA/B

Chain N2:  5% 92% 8%



- Molecule 1: CsuA/B

Chain O2:  92% 8%



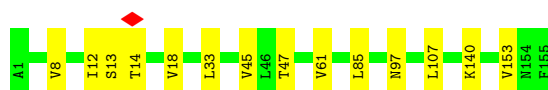
- Molecule 1: CsuA/B

Chain P2:  92% 8%



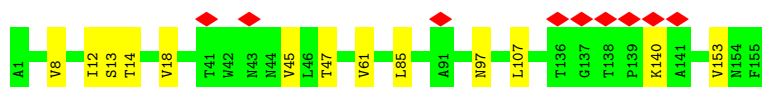
- Molecule 1: CsuA/B

Chain Q2:  91% 9%



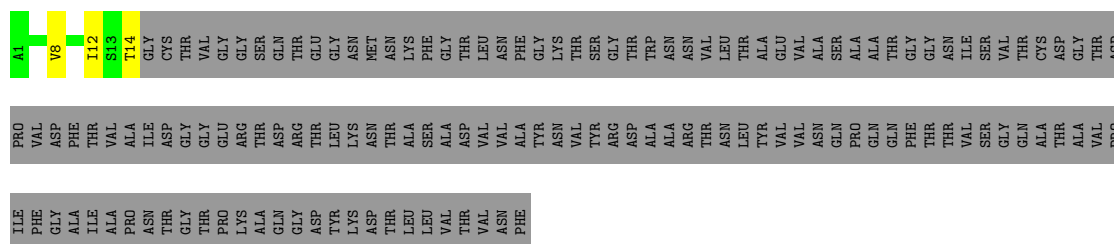
- Molecule 1: CsuA/B

Chain R2:  6% 92% 8%

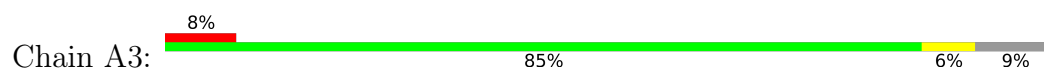


- Molecule 1: CsuA/B

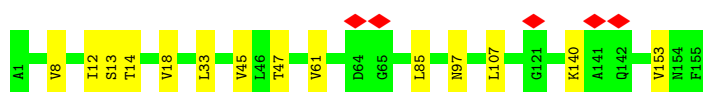
Chain S2:  7% 91%



● Molecule 1: CsuA/B



● Molecule 1: CsuA/B



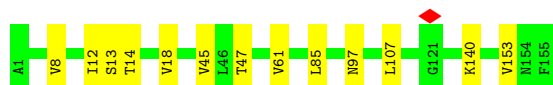
● Molecule 1: CsuA/B



● Molecule 1: CsuA/B

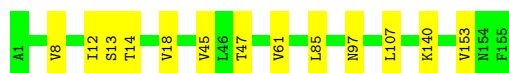


● Molecule 1: CsuA/B



● Molecule 1: CsuA/B

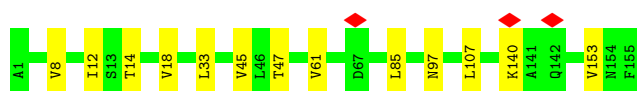




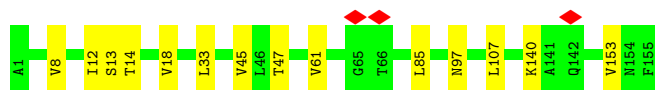
- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



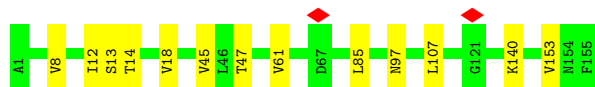
- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



- Molecule 1: CsuA/B



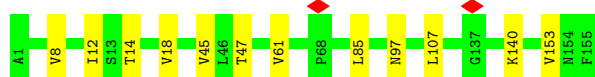
- Molecule 1: CsuA/B

Chain M3:  92% 8%



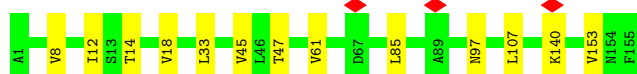
• Molecule 1: CsuA/B

Chain N3:  92% 8%




• Molecule 1: CsuA/B

Chain O3:  92% 8%



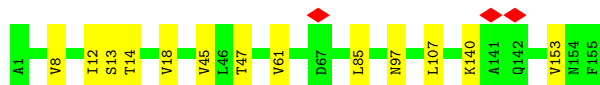
• Molecule 1: CsuA/B

Chain P3:  91% 9%



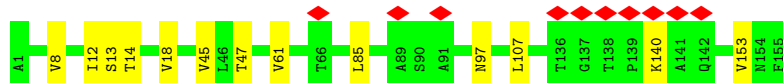
• Molecule 1: CsuA/B

Chain Q3:  92% 8%



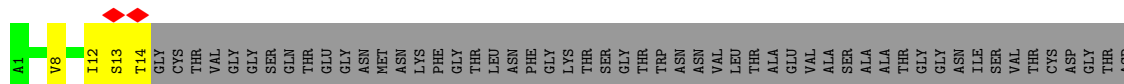
• Molecule 1: CsuA/B

Chain R3:  6% 92% 8%



• Molecule 1: CsuA/B

Chain S3:  6% 91%



PRO	VAL	ASP	PHE	THR	VAL	ALA	ILE	ASP	GLY	GLY	GLU	ARG	THR	ASP	THR	LEU	LYS	ASN	THR	ALA	SER	LEU	ALA	ASP	VAL	VAL	ALA	TYR	TYR	ARG	THR	ASN	VAL	TYR	ARG	ASP	ALA	ALA	ALA	ALA	ARG	ARG	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	504940	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 ($e^-/\text{\AA}^2$)	59.848	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.312	Depositor
Minimum map value	-0.137	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	91.36743, 171.21104, 511.16373	wwPDB
Map dimensions	621, 208, 111	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82313, 0.82313, 0.82313	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	A1	0.51	0/1045	0.89	0/1427
1	A2	0.51	0/1045	0.87	0/1427
1	A3	0.51	0/1045	0.89	0/1427
1	B1	0.52	0/1145	0.87	0/1564
1	B2	0.51	0/1145	0.87	0/1564
1	B3	0.52	0/1145	0.87	0/1564
1	C1	0.52	0/1145	0.87	0/1564
1	C2	0.52	0/1145	0.87	0/1564
1	C3	0.52	0/1145	0.87	0/1564
1	D1	0.52	0/1145	0.87	0/1564
1	D2	0.52	0/1145	0.87	0/1564
1	D3	0.52	0/1145	0.87	0/1564
1	E1	0.52	0/1145	0.87	0/1564
1	E2	0.52	0/1145	0.89	0/1564
1	E3	0.51	0/1145	0.87	0/1564
1	F1	0.52	0/1145	0.87	0/1564
1	F2	0.52	0/1145	0.89	0/1564
1	F3	0.51	0/1145	0.87	0/1564
1	G1	0.52	0/1145	0.89	0/1564
1	G2	0.51	0/1145	0.87	0/1564
1	G3	0.52	0/1145	0.89	0/1564
1	H1	0.52	0/1145	0.89	0/1564
1	H2	0.51	0/1145	0.87	0/1564
1	H3	0.52	0/1145	0.89	0/1564
1	I1	0.52	0/1145	0.87	0/1564
1	I2	0.52	0/1145	0.87	0/1564
1	I3	0.51	0/1145	0.87	0/1564
1	J1	0.51	0/1145	0.87	0/1564
1	J2	0.51	0/1145	0.87	0/1564
1	J3	0.51	0/1145	0.87	0/1564
1	K1	0.51	0/1145	0.87	0/1564
1	K2	0.52	0/1145	0.87	0/1564
1	K3	0.52	0/1145	0.87	0/1564
1	L1	0.51	0/1145	0.87	0/1564

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L2	0.52	0/1145	0.89	0/1564
1	L3	0.52	0/1145	0.87	0/1564
1	M1	0.52	0/1145	0.87	0/1564
1	M2	0.52	0/1145	0.89	0/1564
1	M3	0.51	0/1145	0.87	0/1564
1	N1	0.52	0/1145	0.89	0/1564
1	N2	0.52	0/1145	0.87	0/1564
1	N3	0.52	0/1145	0.89	0/1564
1	O1	0.52	0/1145	0.89	0/1564
1	O2	0.51	0/1145	0.87	0/1564
1	O3	0.52	0/1145	0.89	0/1564
1	P1	0.52	0/1145	0.87	0/1564
1	P2	0.52	0/1145	0.87	0/1564
1	P3	0.51	0/1145	0.87	0/1564
1	Q1	0.52	0/1145	0.87	0/1564
1	Q2	0.52	0/1145	0.87	0/1564
1	Q3	0.52	0/1145	0.87	0/1564
1	R1	0.52	0/1145	0.87	0/1564
1	R2	0.51	0/1145	0.87	0/1564
1	R3	0.51	0/1145	0.87	0/1564
1	S1	0.58	0/99	0.82	0/134
1	S2	0.59	0/99	0.83	0/134
1	S3	0.59	0/99	0.82	0/134
All	All	0.52	0/61827	0.88	0/84447

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	A1	1029	988	987	7	0
1	A2	1029	988	987	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A3	1029	988	987	7	0
1	B1	1129	1097	1097	10	0
1	B2	1129	1097	1097	8	0
1	B3	1129	1097	1097	10	0
1	C1	1129	1097	1097	9	0
1	C2	1129	1097	1097	10	0
1	C3	1129	1097	1097	9	0
1	D1	1129	1097	1097	9	0
1	D2	1129	1097	1097	9	0
1	D3	1129	1097	1097	9	0
1	E1	1129	1097	1097	9	0
1	E2	1129	1097	1097	9	0
1	E3	1129	1097	1097	9	0
1	F1	1129	1097	1097	9	0
1	F2	1129	1097	1097	10	0
1	F3	1129	1097	1097	9	0
1	G1	1129	1097	1097	9	0
1	G2	1129	1097	1097	9	0
1	G3	1129	1097	1097	9	0
1	H1	1129	1097	1097	10	0
1	H2	1129	1097	1097	9	0
1	H3	1129	1097	1097	10	0
1	I1	1129	1097	1097	10	0
1	I2	1129	1097	1097	9	0
1	I3	1129	1097	1097	10	0
1	J1	1129	1097	1097	9	0
1	J2	1129	1097	1097	10	0
1	J3	1129	1097	1097	9	0
1	K1	1129	1097	1097	9	0
1	K2	1129	1097	1097	9	0
1	K3	1129	1097	1097	9	0
1	L1	1129	1097	1097	9	0
1	L2	1129	1097	1097	9	0
1	L3	1129	1097	1097	9	0
1	M1	1129	1097	1097	9	0
1	M2	1129	1097	1097	10	0
1	M3	1129	1097	1097	9	0
1	N1	1129	1097	1097	9	0
1	N2	1129	1097	1097	9	0
1	N3	1129	1097	1097	9	0
1	O1	1129	1097	1097	10	0
1	O2	1129	1097	1097	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O3	1129	1097	1097	10	0
1	P1	1129	1097	1097	10	0
1	P2	1129	1097	1097	9	0
1	P3	1129	1097	1097	10	0
1	Q1	1129	1097	1097	9	0
1	Q2	1129	1097	1097	10	0
1	Q3	1129	1097	1097	9	0
1	R1	1129	1097	1097	9	0
1	R2	1129	1097	1097	9	0
1	R3	1129	1097	1097	9	0
1	S1	100	109	109	3	0
1	S2	100	109	109	3	0
1	S3	100	109	109	3	0
All	All	60966	59238	59235	394	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 3.

The worst 5 of 394 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:R3:45:VAL:HG12	1:R3:47:THR:HG23	1.87	0.57
1:D1:45:VAL:HG12	1:D1:47:THR:HG23	1.87	0.57
1:K1:45:VAL:HG12	1:K1:47:THR:HG23	1.87	0.57
1:K3:45:VAL:HG12	1:K3:47:THR:HG23	1.87	0.57
1:M1:45:VAL:HG12	1:M1:47:THR:HG23	1.87	0.57

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	
1	A1	139/155 (90%)	138 (99%)	1 (1%)	0	100	100
1	A2	139/155 (90%)	138 (99%)	1 (1%)	0	100	100
1	A3	139/155 (90%)	138 (99%)	1 (1%)	0	100	100
1	B1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	B2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	B3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	C1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	C2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	C3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	D1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	D2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	D3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	E1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	E2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	E3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	F1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	F2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	F3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	G1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	G2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	G3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	H1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	H2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	H3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	I1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	I2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	I3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	J1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	J2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	J3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	K1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	K2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	L1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	L2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	L3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	M1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	M2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	M3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	N1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	N2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	N3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	O1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	O2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	O3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	P1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	P2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	P3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	Q1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	Q2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	Q3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	R1	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	R2	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	R3	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
1	S1	12/155 (8%)	11 (92%)	1 (8%)	0	100	100
1	S2	12/155 (8%)	11 (92%)	1 (8%)	0	100	100
1	S3	12/155 (8%)	11 (92%)	1 (8%)	0	100	100
All	All	8256/8835 (93%)	8097 (98%)	159 (2%)	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	A1	110/122 (90%)	110 (100%)	0	100	100
1	A2	110/122 (90%)	110 (100%)	0	100	100
1	A3	110/122 (90%)	110 (100%)	0	100	100
1	B1	122/122 (100%)	122 (100%)	0	100	100
1	B2	122/122 (100%)	122 (100%)	0	100	100
1	B3	122/122 (100%)	122 (100%)	0	100	100
1	C1	122/122 (100%)	122 (100%)	0	100	100
1	C2	122/122 (100%)	122 (100%)	0	100	100
1	C3	122/122 (100%)	122 (100%)	0	100	100
1	D1	122/122 (100%)	122 (100%)	0	100	100
1	D2	122/122 (100%)	122 (100%)	0	100	100
1	D3	122/122 (100%)	122 (100%)	0	100	100
1	E1	122/122 (100%)	122 (100%)	0	100	100
1	E2	122/122 (100%)	122 (100%)	0	100	100
1	E3	122/122 (100%)	122 (100%)	0	100	100
1	F1	122/122 (100%)	122 (100%)	0	100	100
1	F2	122/122 (100%)	122 (100%)	0	100	100
1	F3	122/122 (100%)	122 (100%)	0	100	100
1	G1	122/122 (100%)	122 (100%)	0	100	100
1	G2	122/122 (100%)	122 (100%)	0	100	100
1	G3	122/122 (100%)	122 (100%)	0	100	100
1	H1	122/122 (100%)	122 (100%)	0	100	100
1	H2	122/122 (100%)	122 (100%)	0	100	100
1	H3	122/122 (100%)	122 (100%)	0	100	100
1	I1	122/122 (100%)	122 (100%)	0	100	100
1	I2	122/122 (100%)	122 (100%)	0	100	100
1	I3	122/122 (100%)	122 (100%)	0	100	100
1	J1	122/122 (100%)	122 (100%)	0	100	100
1	J2	122/122 (100%)	122 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J3	122/122 (100%)	122 (100%)	0	100	100
1	K1	122/122 (100%)	122 (100%)	0	100	100
1	K2	122/122 (100%)	122 (100%)	0	100	100
1	K3	122/122 (100%)	122 (100%)	0	100	100
1	L1	122/122 (100%)	122 (100%)	0	100	100
1	L2	122/122 (100%)	122 (100%)	0	100	100
1	L3	122/122 (100%)	122 (100%)	0	100	100
1	M1	122/122 (100%)	122 (100%)	0	100	100
1	M2	122/122 (100%)	122 (100%)	0	100	100
1	M3	122/122 (100%)	122 (100%)	0	100	100
1	N1	122/122 (100%)	122 (100%)	0	100	100
1	N2	122/122 (100%)	122 (100%)	0	100	100
1	N3	122/122 (100%)	122 (100%)	0	100	100
1	O1	122/122 (100%)	122 (100%)	0	100	100
1	O2	122/122 (100%)	122 (100%)	0	100	100
1	O3	122/122 (100%)	122 (100%)	0	100	100
1	P1	122/122 (100%)	122 (100%)	0	100	100
1	P2	122/122 (100%)	122 (100%)	0	100	100
1	P3	122/122 (100%)	122 (100%)	0	100	100
1	Q1	122/122 (100%)	122 (100%)	0	100	100
1	Q2	122/122 (100%)	122 (100%)	0	100	100
1	Q3	122/122 (100%)	122 (100%)	0	100	100
1	R1	122/122 (100%)	122 (100%)	0	100	100
1	R2	122/122 (100%)	122 (100%)	0	100	100
1	R3	122/122 (100%)	122 (100%)	0	100	100
1	S1	12/122 (10%)	12 (100%)	0	100	100
1	S2	12/122 (10%)	12 (100%)	0	100	100
1	S3	12/122 (10%)	12 (100%)	0	100	100
All	All	6588/6954 (95%)	6588 (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 54

such sidechains are listed below:

Mol	Chain	Res	Type
1	K2	26	ASN
1	R2	26	ASN
1	N3	26	ASN
1	L2	26	ASN
1	O2	26	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-52601. 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](#)

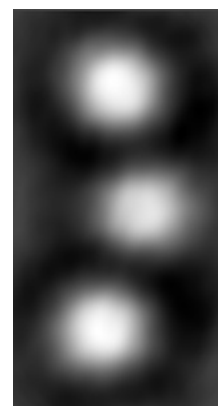
6.1.1 Primary map



X

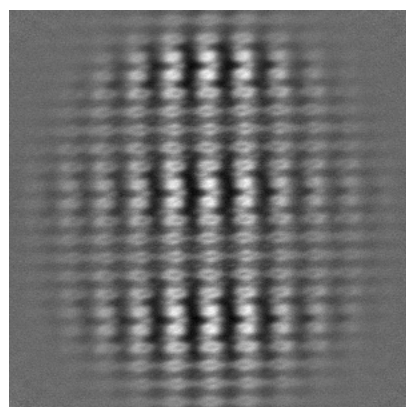


Y

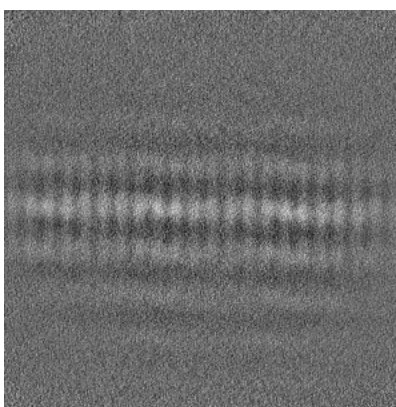


Z

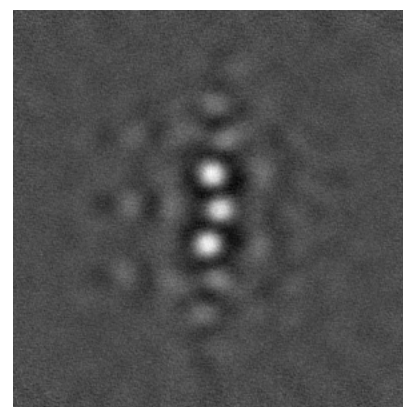
6.1.2 Raw map



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:
55

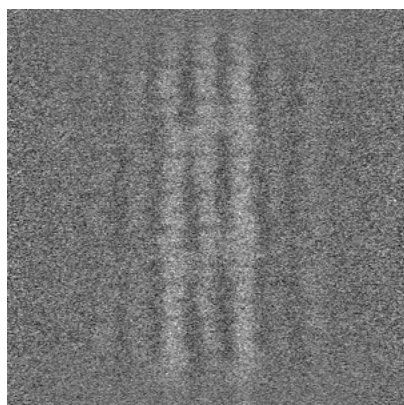


Y Index: 104

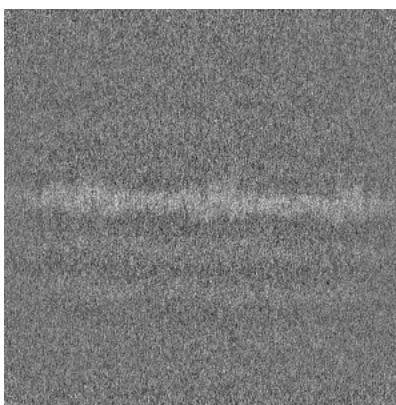


Z Index: 310

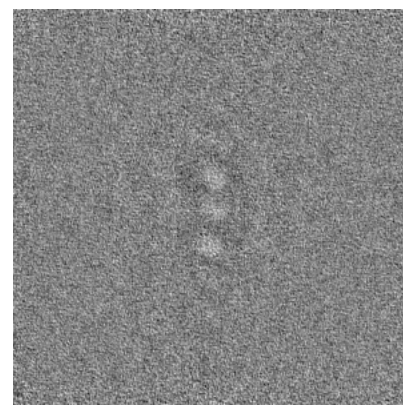
6.2.2 Raw map



X Index: 360



Y Index: 360



Z Index: 360

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:
47

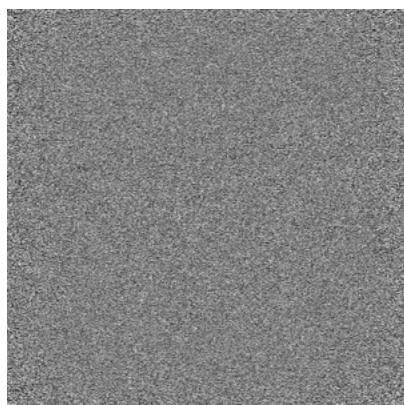


Y Index: 43

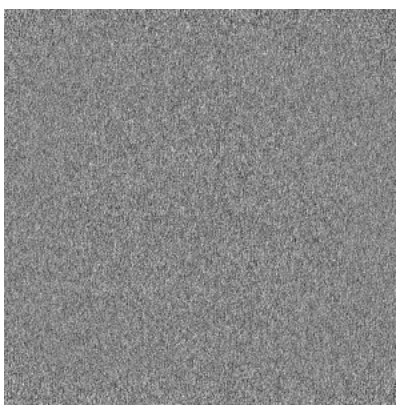


Z Index: 322

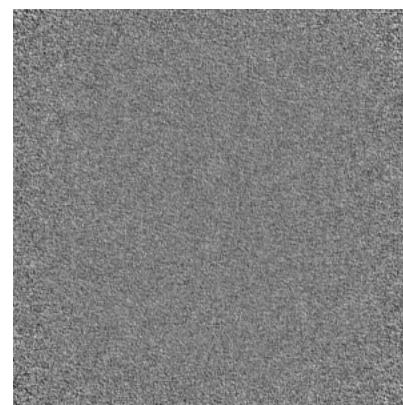
6.3.2 Raw map



X Index: 0



Y Index: 0

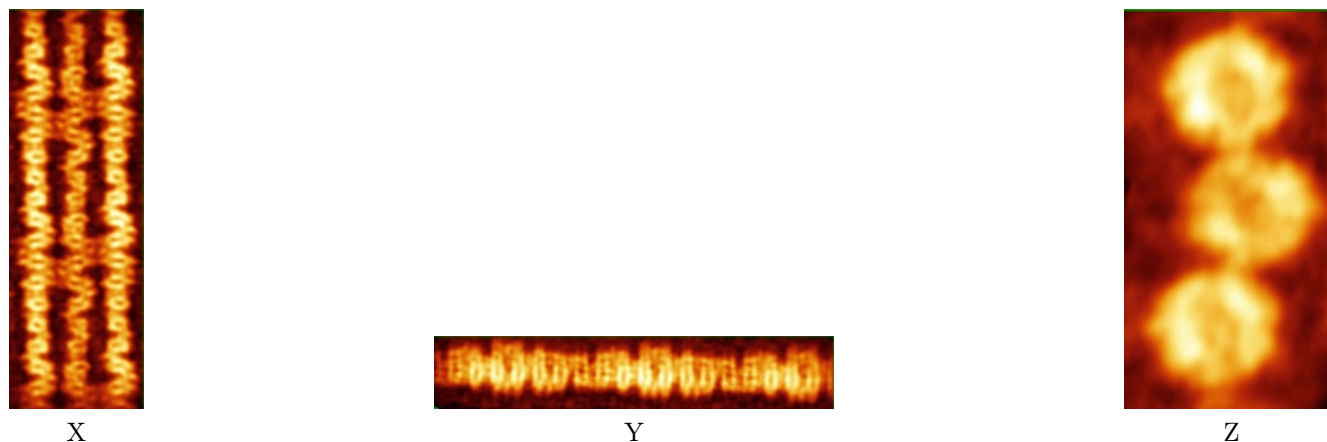


Z Index: 0

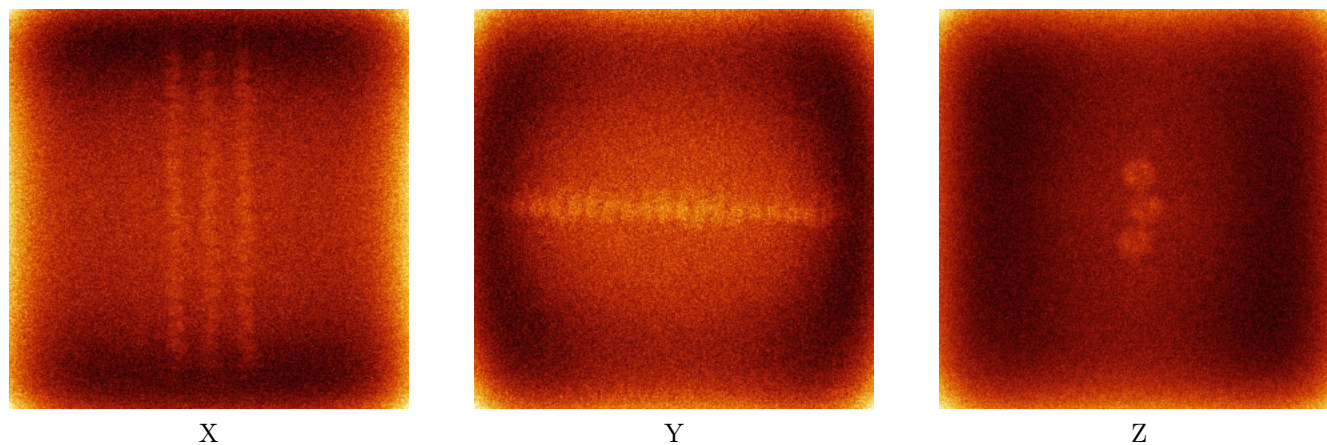
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



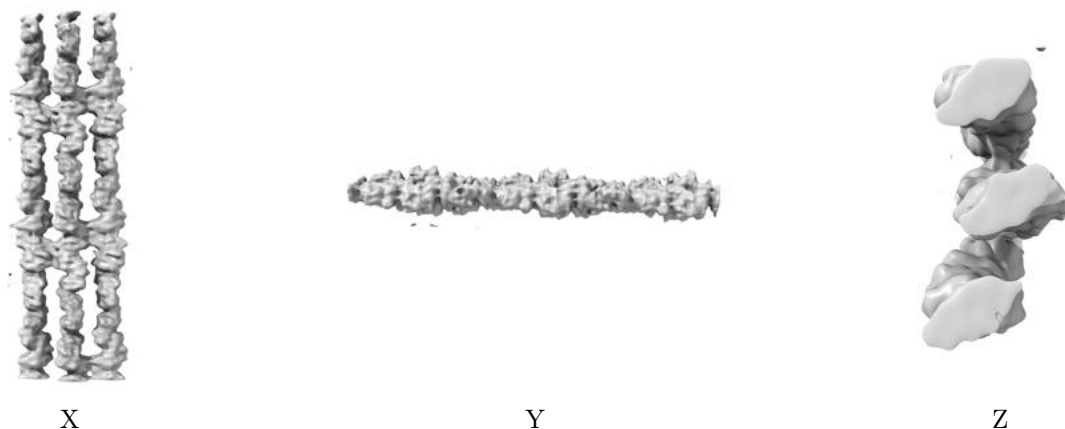
6.4.2 Raw map



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.

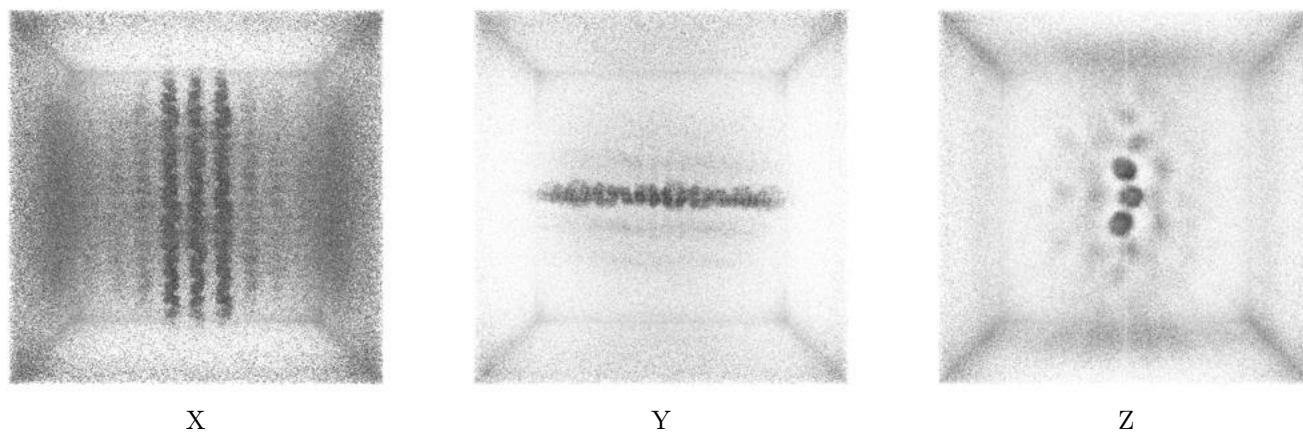
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. 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.

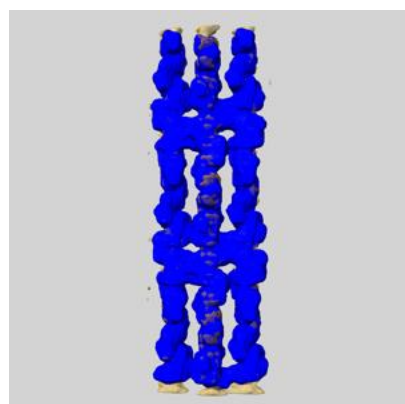
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

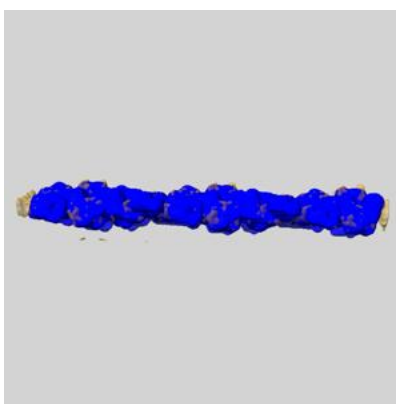
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

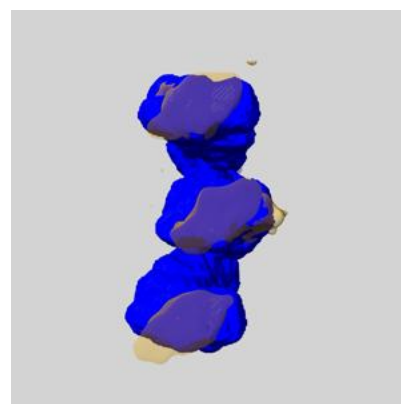
6.6.1 emd_52601_msk_1.map [i](#)



X



Y

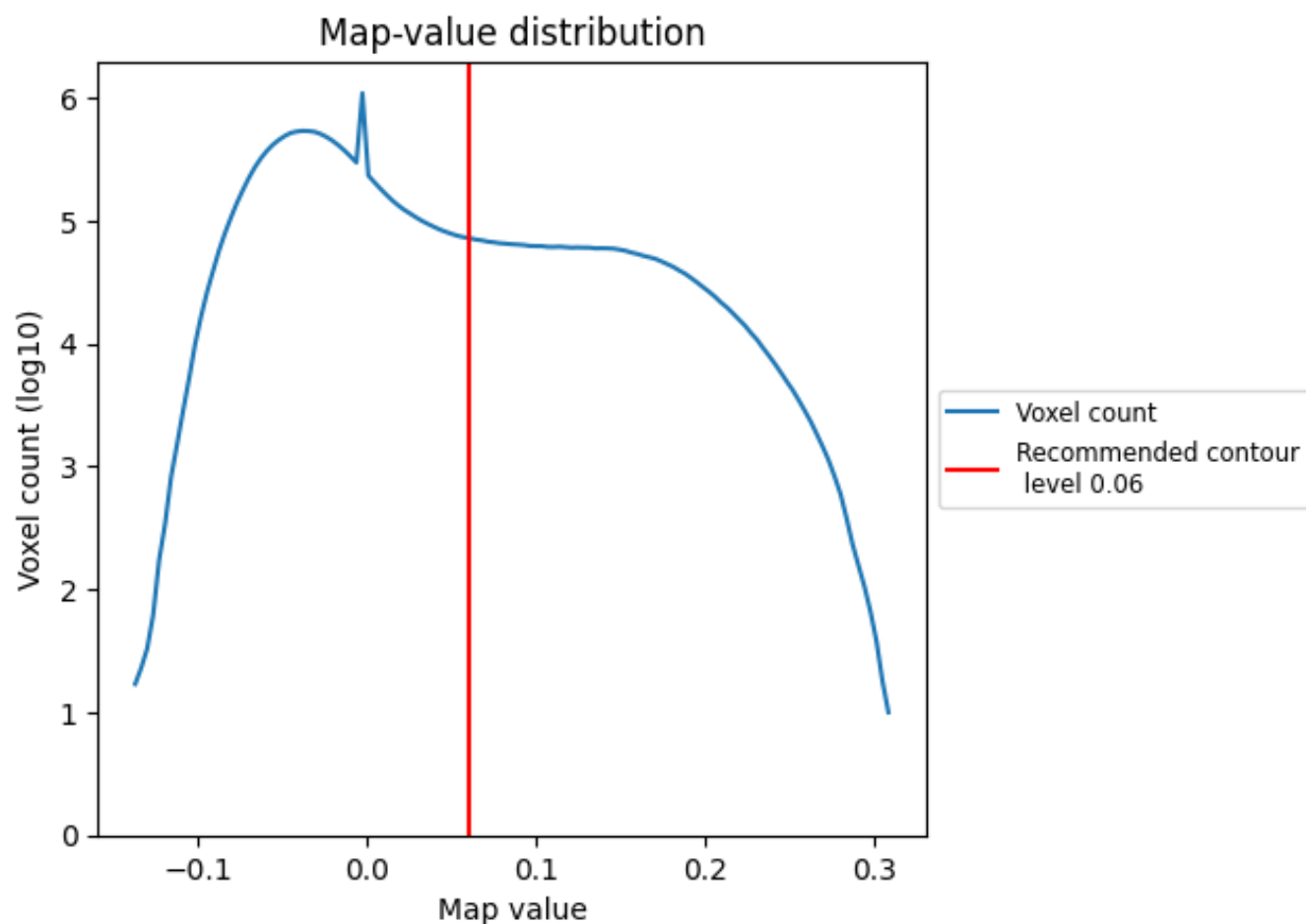


Z

7 Map analysis [i](#)

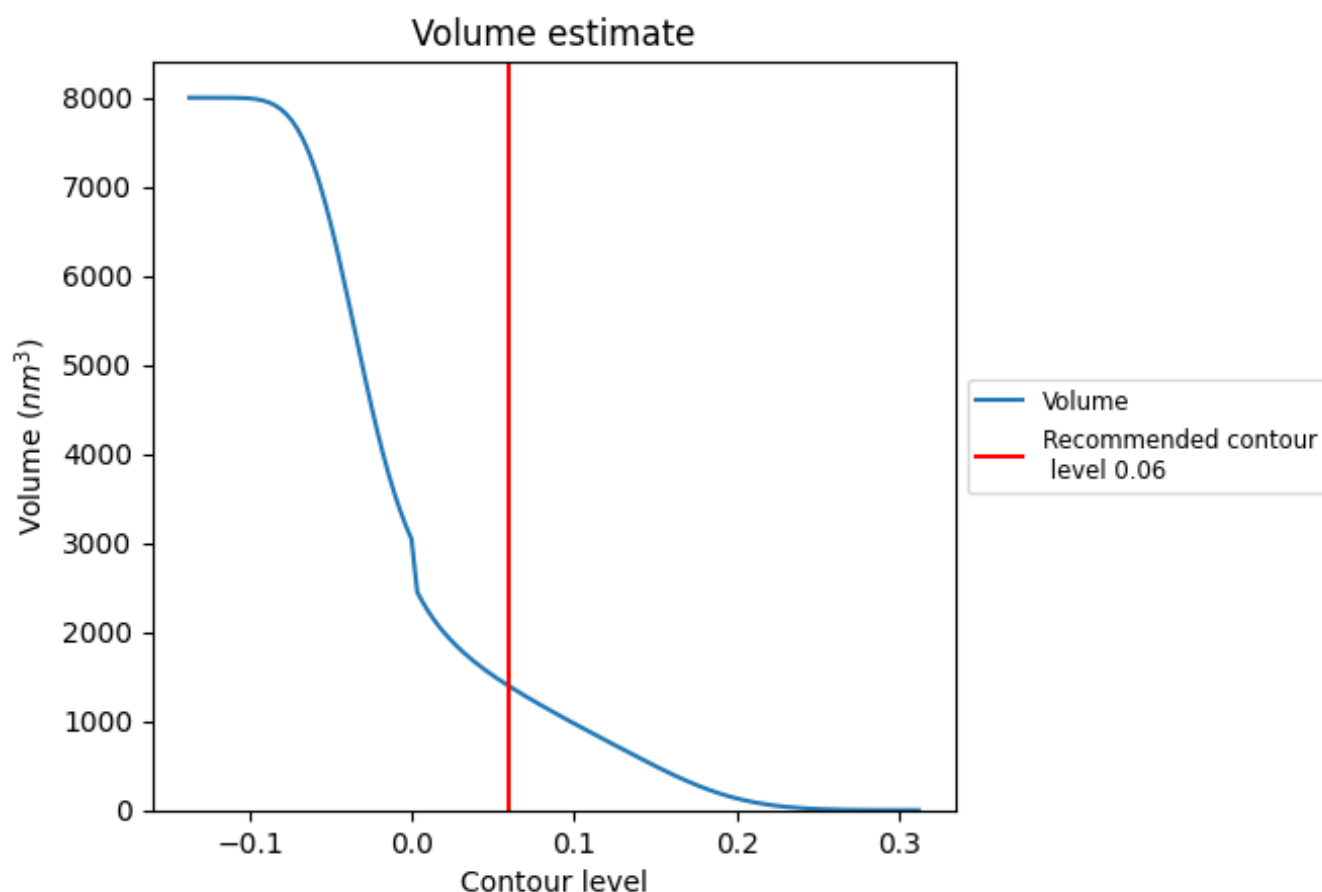
This section contains the results of statistical analysis of the map.

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 1389 nm³; this corresponds to an approximate mass of 1255 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.

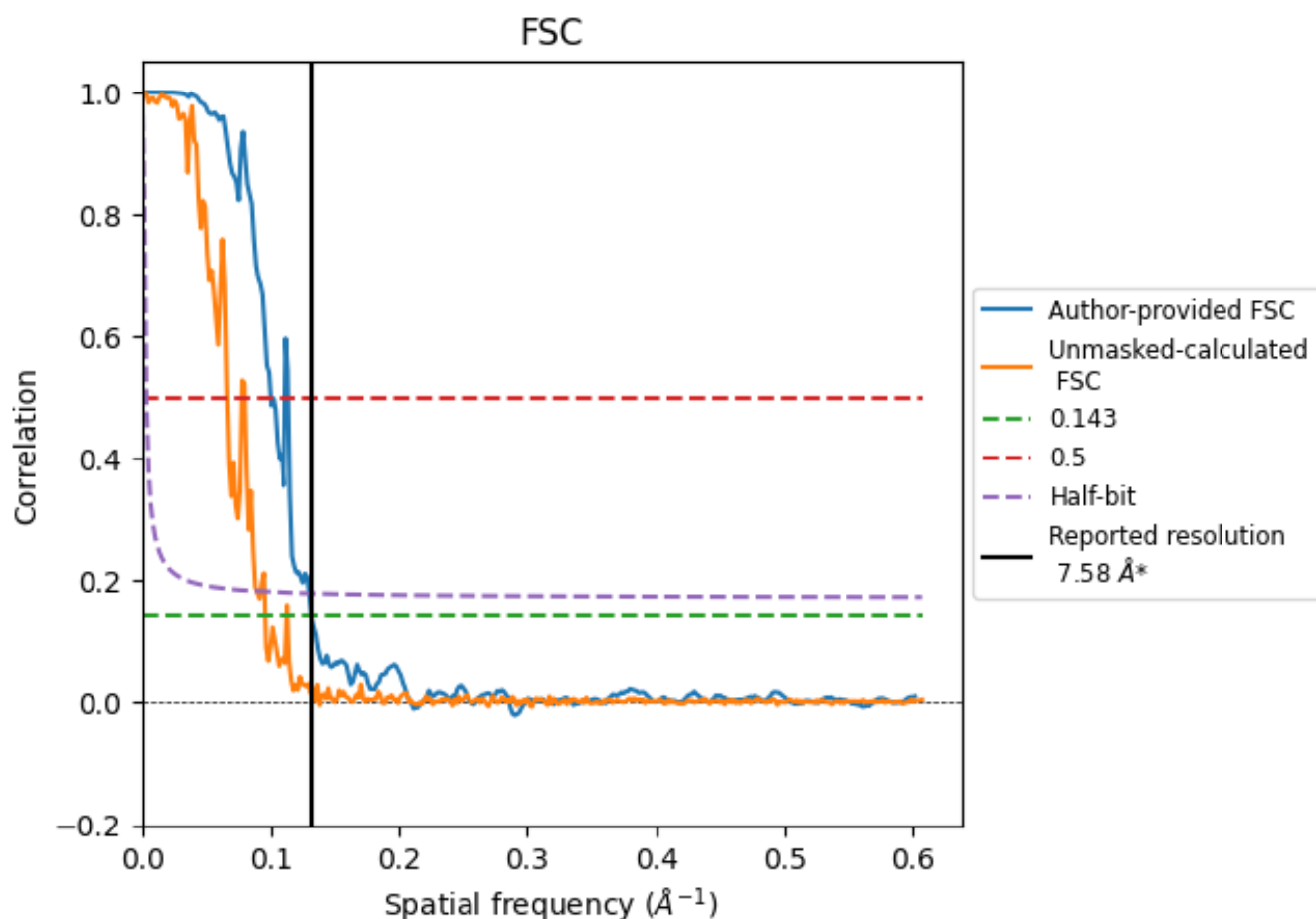
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

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 0.132 Å⁻¹

8.2 Resolution estimates [i](#)

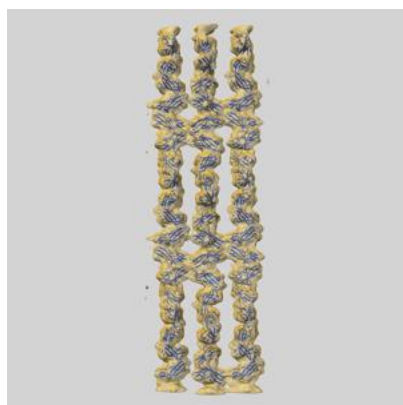
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.58	-	-
Author-provided FSC curve	7.58	10.02	7.67
Unmasked-calculated*	10.48	15.15	11.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.48 differs from the reported value 7.58 by more than 10 %

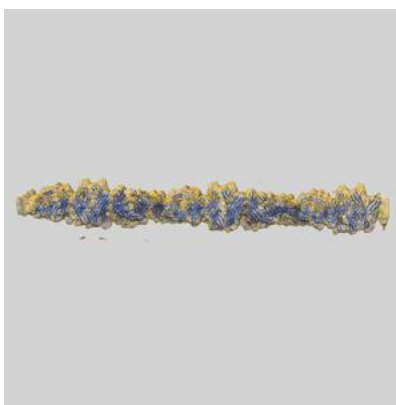
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52601 and PDB model 9I3N. Per-residue inclusion information can be found in section [3](#) on page [9](#).

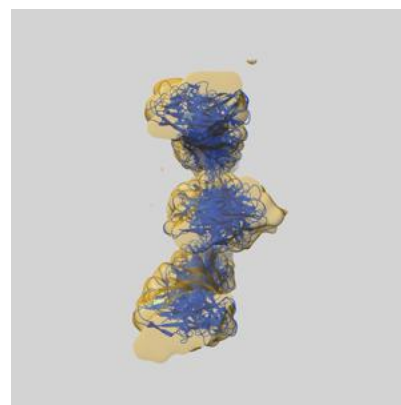
9.1 Map-model overlay [i](#)



X



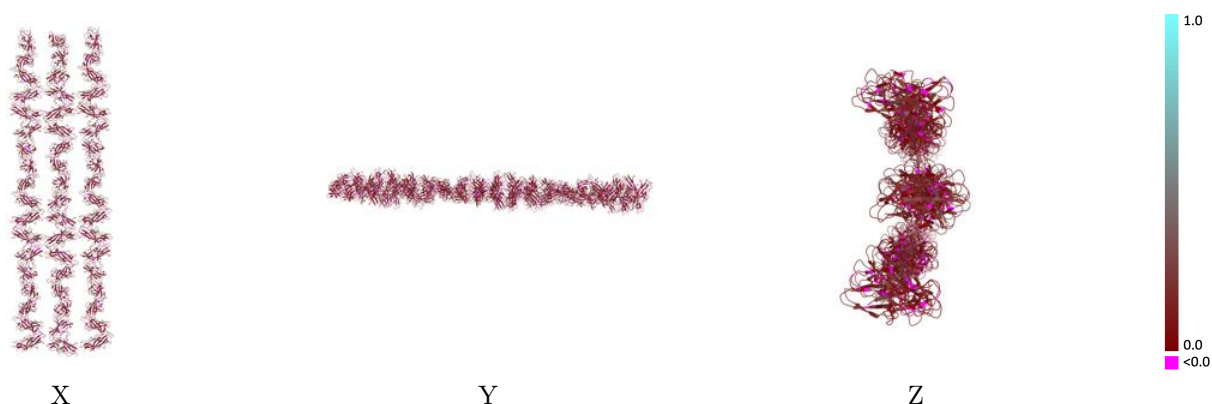
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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](#)



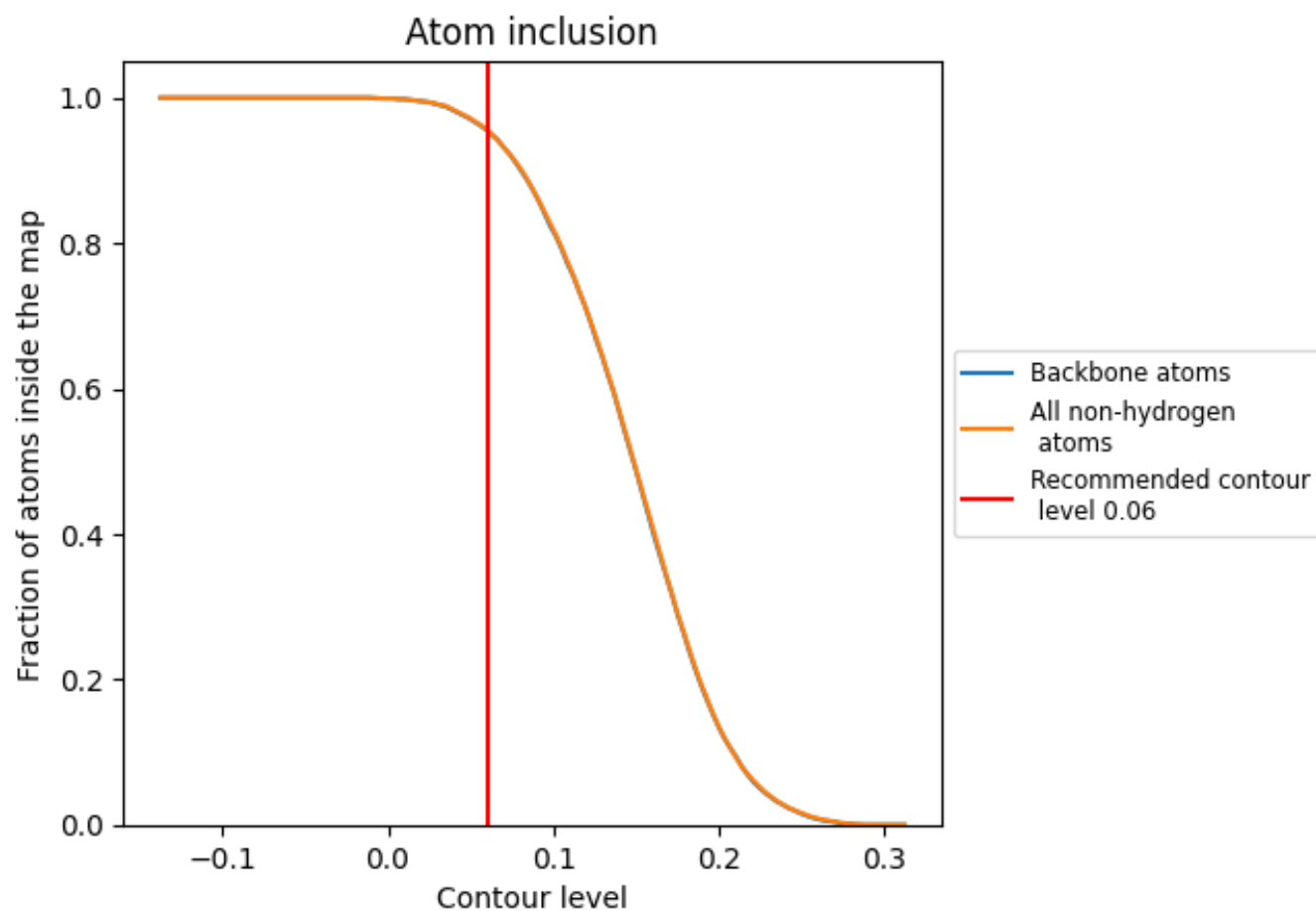
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9560	 0.1300
A1	 0.9650	 0.1340
A2	 0.9430	 0.1390
A3	 0.9000	 0.1250
B1	 0.9560	 0.1300
B2	 0.9780	 0.1400
B3	 0.9540	 0.1260
C1	 0.9630	 0.1250
C2	 0.9490	 0.1290
C3	 0.9750	 0.1300
D1	 0.9670	 0.1380
D2	 0.9370	 0.1320
D3	 0.9620	 0.1330
E1	 0.9570	 0.1310
E2	 0.9400	 0.1220
E3	 0.9710	 0.1260
F1	 0.9380	 0.1330
F2	 0.9500	 0.1410
F3	 0.9750	 0.1320
G1	 0.9480	 0.1260
G2	 0.9260	 0.1290
G3	 0.9680	 0.1340
H1	 0.9840	 0.1320
H2	 0.9690	 0.1310
H3	 0.9560	 0.1240
I1	 0.9620	 0.1280
I2	 0.9660	 0.1390
I3	 0.9630	 0.1320
J1	 0.9680	 0.1230
J2	 0.9590	 0.1270
J3	 0.9790	 0.1290
K1	 0.9700	 0.1340
K2	 0.9460	 0.1370
K3	 0.9600	 0.1320
L1	 0.9600	 0.1340



Continued on next page...

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Chain	Atom inclusion	Q-score
L2	 0.9480	 0.1270
L3	 0.9650	 0.1280
M1	 0.9360	 0.1230
M2	 0.9440	 0.1410
M3	 0.9710	 0.1330
N1	 0.9480	 0.1280
N2	 0.9260	 0.1330
N3	 0.9660	 0.1330
O1	 0.9790	 0.1320
O2	 0.9700	 0.1350
O3	 0.9500	 0.1320
P1	 0.9610	 0.1290
P2	 0.9670	 0.1330
P3	 0.9630	 0.1280
Q1	 0.9660	 0.1170
Q2	 0.9530	 0.1270
Q3	 0.9630	 0.1260
R1	 0.9220	 0.1310
R2	 0.8960	 0.1280
R3	 0.9170	 0.1210
S1	 0.8900	 0.1020
S2	 0.9200	 0.0890
S3	 0.8700	 0.1020