



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2025 – 03:56 am BST

PDB ID : 7AMY / pdb_00007amy
EMDB ID : EMD-11827
Title : Nonameric cytoplasmic domain of FlhA from *Vibrio parahaemolyticus*
Authors : Kuhlen, L.; Johnson, S.; Lea, S.
Deposited on : 2020-10-09
Resolution : 3.75 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

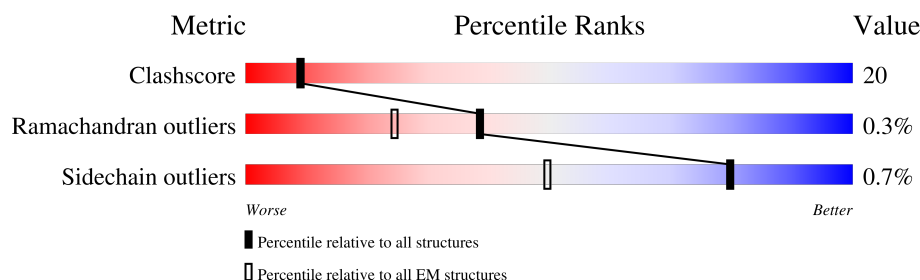
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 Å.

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



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

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	702	<div> <div>24%</div> <div>30% 20% 50%</div> </div>
1	B	702	<div> <div>23%</div> <div>30% 21% 50%</div> </div>
1	C	702	<div> <div>23%</div> <div>30% 20% 50%</div> </div>
1	D	702	<div> <div>23%</div> <div>30% 20% 50%</div> </div>
1	E	702	<div> <div>23%</div> <div>29% 21% 50%</div> </div>
1	F	702	<div> <div>23%</div> <div>30% 20% 50%</div> </div>
1	G	702	<div> <div>23%</div> <div>30% 20% 50%</div> </div>
1	H	702	<div> <div>23%</div> <div>30% 20% 50%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	I	702	<div><div><div></div><div></div><div></div><div></div></div><div>23%30%21%50%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 24849 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 Flagellar biosynthesis protein FlhA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	B	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	C	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	D	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	E	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	F	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	G	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	H	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	I	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	696	GLU	-	expression tag	UNP A0A0F5SXE4
A	697	ASN	-	expression tag	UNP A0A0F5SXE4
A	698	LEU	-	expression tag	UNP A0A0F5SXE4
A	699	TYR	-	expression tag	UNP A0A0F5SXE4
A	700	PHE	-	expression tag	UNP A0A0F5SXE4
A	701	GLN	-	expression tag	UNP A0A0F5SXE4
B	696	GLU	-	expression tag	UNP A0A0F5SXE4
B	697	ASN	-	expression tag	UNP A0A0F5SXE4
B	698	LEU	-	expression tag	UNP A0A0F5SXE4
B	699	TYR	-	expression tag	UNP A0A0F5SXE4
B	700	PHE	-	expression tag	UNP A0A0F5SXE4
B	701	GLN	-	expression tag	UNP A0A0F5SXE4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	696	GLU	-	expression tag	UNP A0A0F5SXE4
C	697	ASN	-	expression tag	UNP A0A0F5SXE4
C	698	LEU	-	expression tag	UNP A0A0F5SXE4
C	699	TYR	-	expression tag	UNP A0A0F5SXE4
C	700	PHE	-	expression tag	UNP A0A0F5SXE4
C	701	GLN	-	expression tag	UNP A0A0F5SXE4
D	696	GLU	-	expression tag	UNP A0A0F5SXE4
D	697	ASN	-	expression tag	UNP A0A0F5SXE4
D	698	LEU	-	expression tag	UNP A0A0F5SXE4
D	699	TYR	-	expression tag	UNP A0A0F5SXE4
D	700	PHE	-	expression tag	UNP A0A0F5SXE4
D	701	GLN	-	expression tag	UNP A0A0F5SXE4
E	696	GLU	-	expression tag	UNP A0A0F5SXE4
E	697	ASN	-	expression tag	UNP A0A0F5SXE4
E	698	LEU	-	expression tag	UNP A0A0F5SXE4
E	699	TYR	-	expression tag	UNP A0A0F5SXE4
E	700	PHE	-	expression tag	UNP A0A0F5SXE4
E	701	GLN	-	expression tag	UNP A0A0F5SXE4
F	696	GLU	-	expression tag	UNP A0A0F5SXE4
F	697	ASN	-	expression tag	UNP A0A0F5SXE4
F	698	LEU	-	expression tag	UNP A0A0F5SXE4
F	699	TYR	-	expression tag	UNP A0A0F5SXE4
F	700	PHE	-	expression tag	UNP A0A0F5SXE4
F	701	GLN	-	expression tag	UNP A0A0F5SXE4
G	696	GLU	-	expression tag	UNP A0A0F5SXE4
G	697	ASN	-	expression tag	UNP A0A0F5SXE4
G	698	LEU	-	expression tag	UNP A0A0F5SXE4
G	699	TYR	-	expression tag	UNP A0A0F5SXE4
G	700	PHE	-	expression tag	UNP A0A0F5SXE4
G	701	GLN	-	expression tag	UNP A0A0F5SXE4
H	696	GLU	-	expression tag	UNP A0A0F5SXE4
H	697	ASN	-	expression tag	UNP A0A0F5SXE4
H	698	LEU	-	expression tag	UNP A0A0F5SXE4
H	699	TYR	-	expression tag	UNP A0A0F5SXE4
H	700	PHE	-	expression tag	UNP A0A0F5SXE4
H	701	GLN	-	expression tag	UNP A0A0F5SXE4
I	696	GLU	-	expression tag	UNP A0A0F5SXE4
I	697	ASN	-	expression tag	UNP A0A0F5SXE4
I	698	LEU	-	expression tag	UNP A0A0F5SXE4
I	699	TYR	-	expression tag	UNP A0A0F5SXE4
I	700	PHE	-	expression tag	UNP A0A0F5SXE4
I	701	GLN	-	expression tag	UNP A0A0F5SXE4

Chain B:



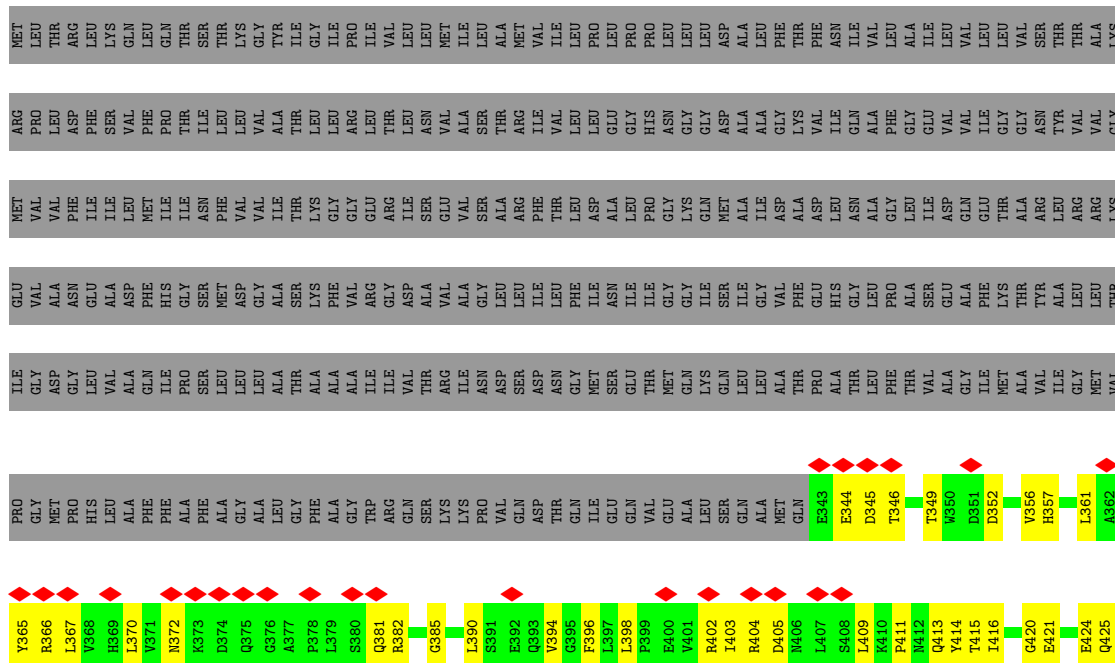
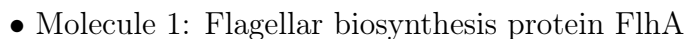
ILE	GLY	ASP	ALA	VAL	GLU	MET	VAL	VAL	MET	ARG	MET
GLY	ASP	ASN	ALA	ASP	ALA	VAL	PHE	ILE	LEU	PRO	LEU
GLY	LEU	LEU	ALA	PHE	GLU	ILE	ILE	ILE	ASP	ASP	ARG
VAL	ALA	ASP	ASP	ALA	ALA	ILE	ILE	LEU	SER	VAL	GLN
ALA	ALA	ASP	PHE	GLU	ASP	VAL	ILE	ILE	PHE	VAL	LEU
GLN	GLN	HIS	ILE	GLY	GLY	VAL	ILE	ILE	PRO	VAL	GLN
ILE	PRO	GLY	GLY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

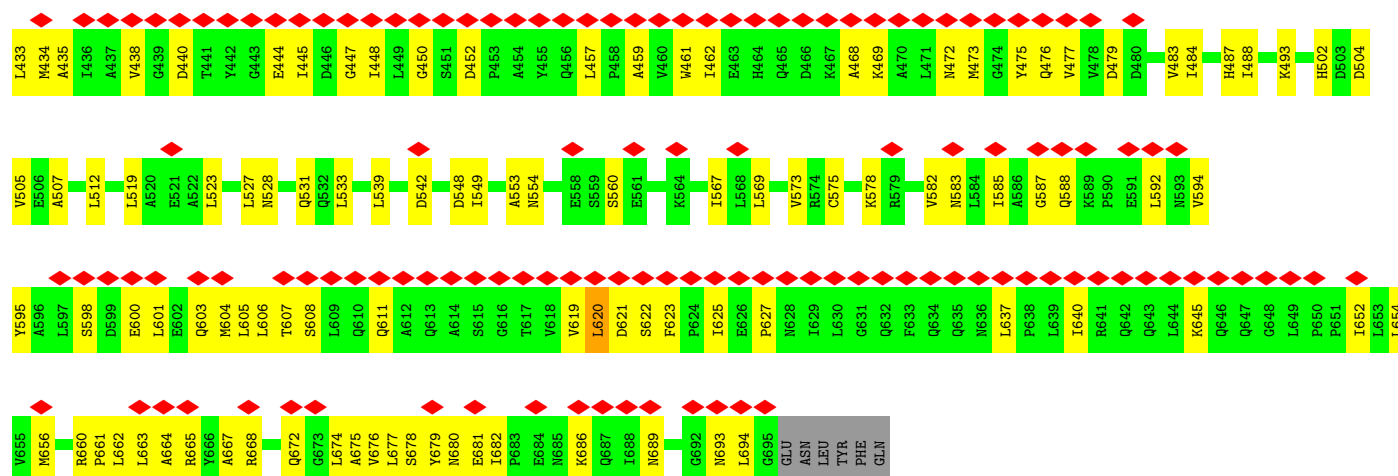
PRO	GLY	MET	PRO	HIS	LEU	PHE	PHE	PHE	ALA	GLY	GLY	LEU	GLY	PHE	ALA	GLY	TRP	ARG	SER	LYS	PRO	VAL	ASP	THR	GLN	ILE	GLU	GLN	VAL	GLU	ALA	LEU	SER	GLN	ALA	MET	GLN	E343	E344	D345	T346	P347	L348	T349	W350	D351	D352	V356	H357	L361	A362	L363																																																																																																				
																																																					G364	Y365	R366	L367	V368	H369	L370	V371	K372	N373	D374	Q375	G376	A377	P378	L379	Q381	R382	G385	L390	S391	E392	Q393	V394	G395	F396	L397	L398	R402	I403	R404	D405	M406	L407	S408	K410	P411	N412	Q413	Y414	T415	I416	G420	E421	E424	Q425	G426	F427	I428	E429	P430	E431	R432																																															
																																																					L433	M434	A435	I436	A437	V438	G439	D440	T441	Y442	G443	E444	I445	D446	G447	I448	L449	G450	S451	D452	P453	A454	Y455	Q456	L457	P458	A459	Y460	N461	I462	H464	Q465	D466	K467	A468	K469	A470	L471	M472	N473	G474	Y475	Q476	V477	W478	D479	D480	Y483	I484	H487	I488	K493	L496	H502																																														
																																																					B503	D504	V505	E506	A507	L512	L519	A520	E521	A522	L523	L527	N528	Q531	Q532	L533	L539	L540	L541	D542	D548	I549	A553	N554	E556	S559	S560	E561	I567	L568	V573	R574	C575	K578	R579	V582	N583	L584	L585	A586	G587	Q588	K589	P590	E591	L592	N593	V594	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654
																																																					Y595	A596	L597	S598	D599	E500	L601	E602	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654																																								
																																																					B503	D504	V505	E506	A507	L512	L519	A520	E521	A522	L523	L527	N528	Q531	Q532	L533	L539	L540	L541	D542	D548	I549	A553	N554	E556	S559	S560	E561	I567	L568	V573	R574	C575	K578	R579	V582	N583	L584	L585	A586	G587	Q588	K589	P590	E591	L592	N593	V594	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654
																																																					Y595	A596	L597	S598	D599	E500	L601	E602	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654																																								
																																																					B503	D504	V505	E506	A507	L512	L519	A520	E521	A522	L523	L527	N528	Q531	Q532	L533	L539	L540	L541	D542	D548	I549	A553	N554	E556	S559	S560	E561	I567	L568	V573	R574	C575	K578	R579	V582	N583	L584	L585	A586	G587	Q588	K589	P590	E591	L592	N593	V594	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654
																																																					Y595	A596	L597	S598	D599	E500	L601	E602	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654																																								
																																																					B503	D504	V505	E506	A507	L512	L519	A520	E521	A522	L523	L527	N528	Q531	Q532	L533	L539	L540	L541	D542	D548	I549	A553	N554	E556	S559	S560	E561	I567	L568	V573	R574	C575	K578	R579	V582	N583	L584	L585	A586	G587	Q588	K589	P590	E591	L592	N593	V594	Q603	N604	L605	L606	T607	S608	L609	Q610	Q611	A612	Q613	A614	S615	G616	T617	V618	V619	L620	D621	S622	F623	P624	I625	E626	P627	N628	T629	L630	G631	Q632	F633	Q634	Q635	N636	L637	P638	L639	T640	R641	Q642	Q643	L644	K645	Q646	Q647	G648	L649	P650	P651	T652	L653	L654

Chain C:

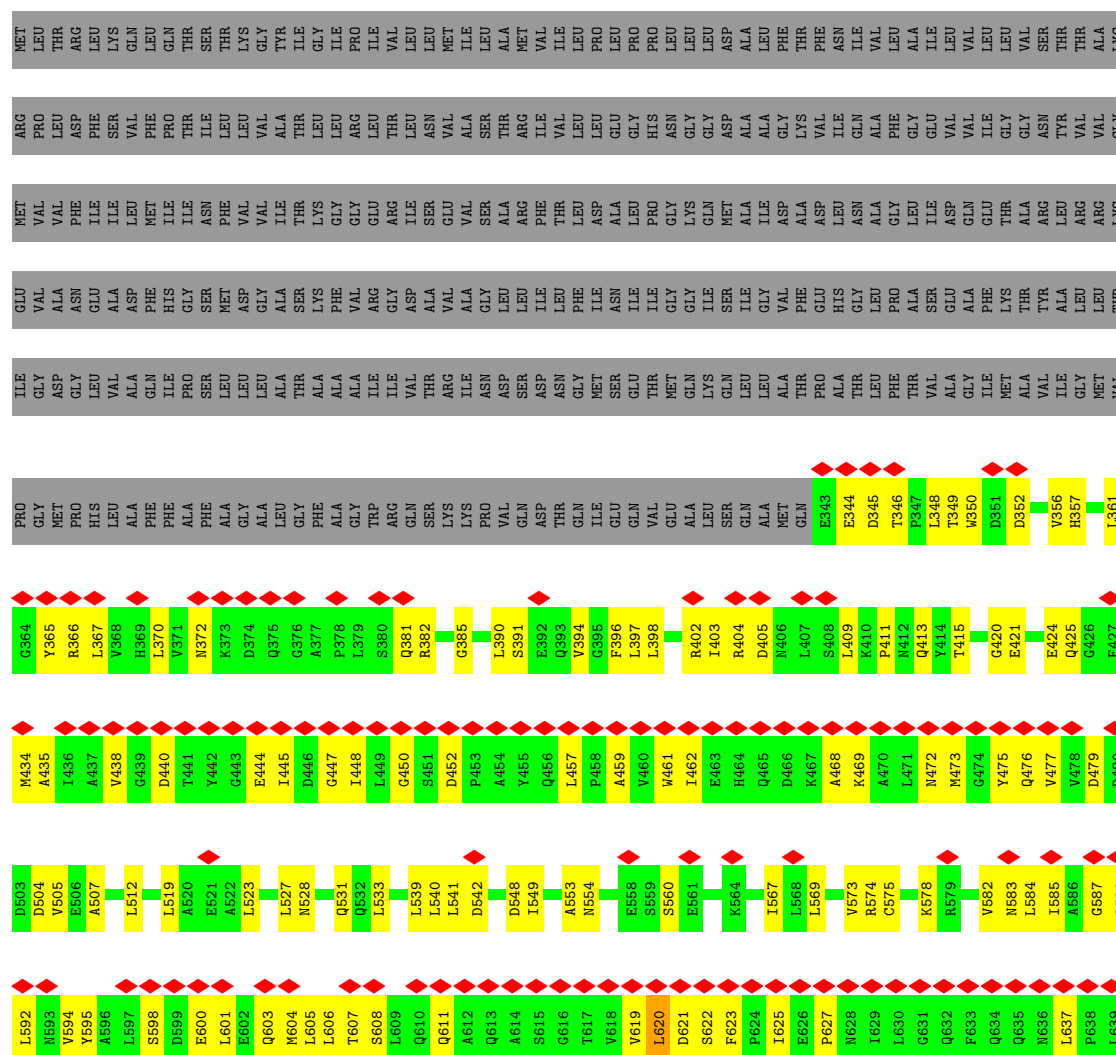
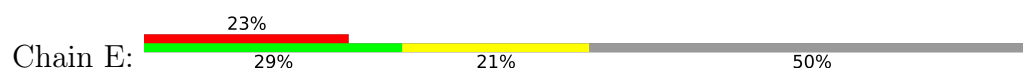


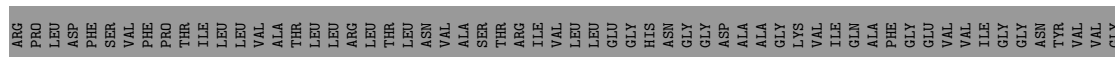
NET	VAL	VAL	PHE	ILE	LEU	MET	ILE	ILE	ASN	PHE	VAL	VAL	VAL	ILE	THR	THR	LYS	GLY	ILE	GLY	PRO	ILE	VAL	LEU	LEU	ASN	THR	VAL	GLY	LYS	THR	THR	GLN	GLN	ARG	THR	LEU	MET
ARG	VAL	VAL	PHE	ILE	LEU	MET	ILE	ILE	ASN	PHE	VAL	VAL	VAL	ILE	THR	THR	LYS	GLY	ILE	GLY	PRO	ILE	VAL	LEU	LEU	ASN	THR	VAL	GLY	LYS	THR	THR	GLN	GLN	ARG	THR	LEU	MET

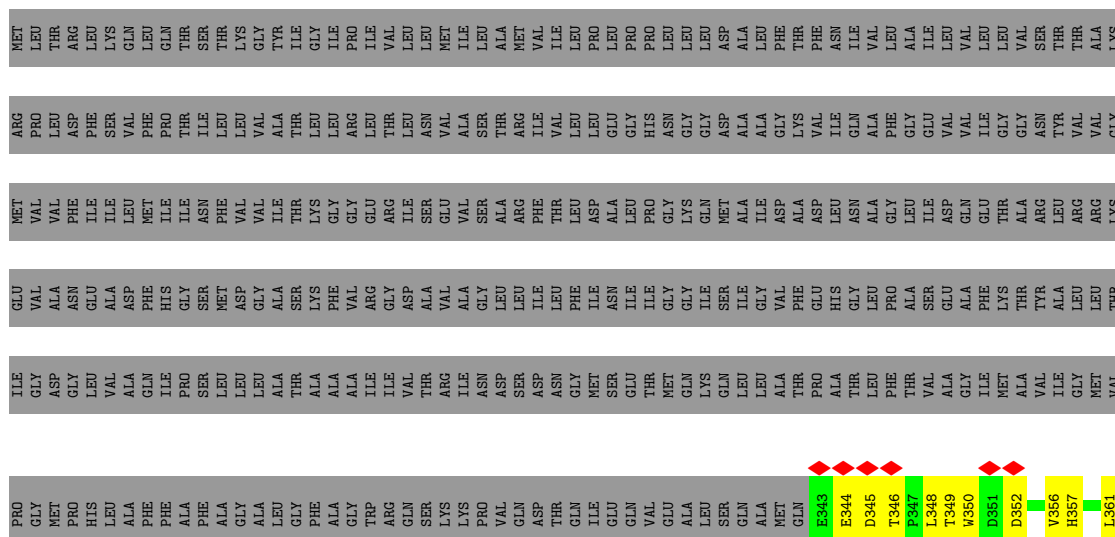
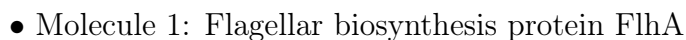


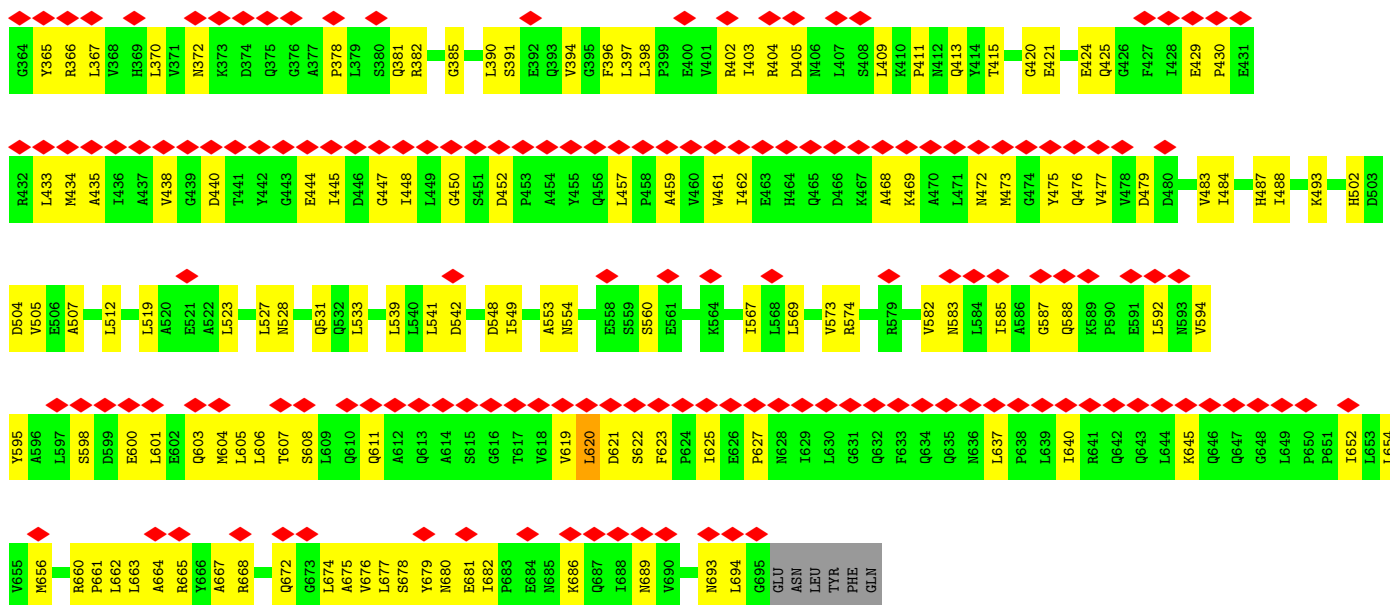


• Molecule 1: Flagellar biosynthesis protein FlhA

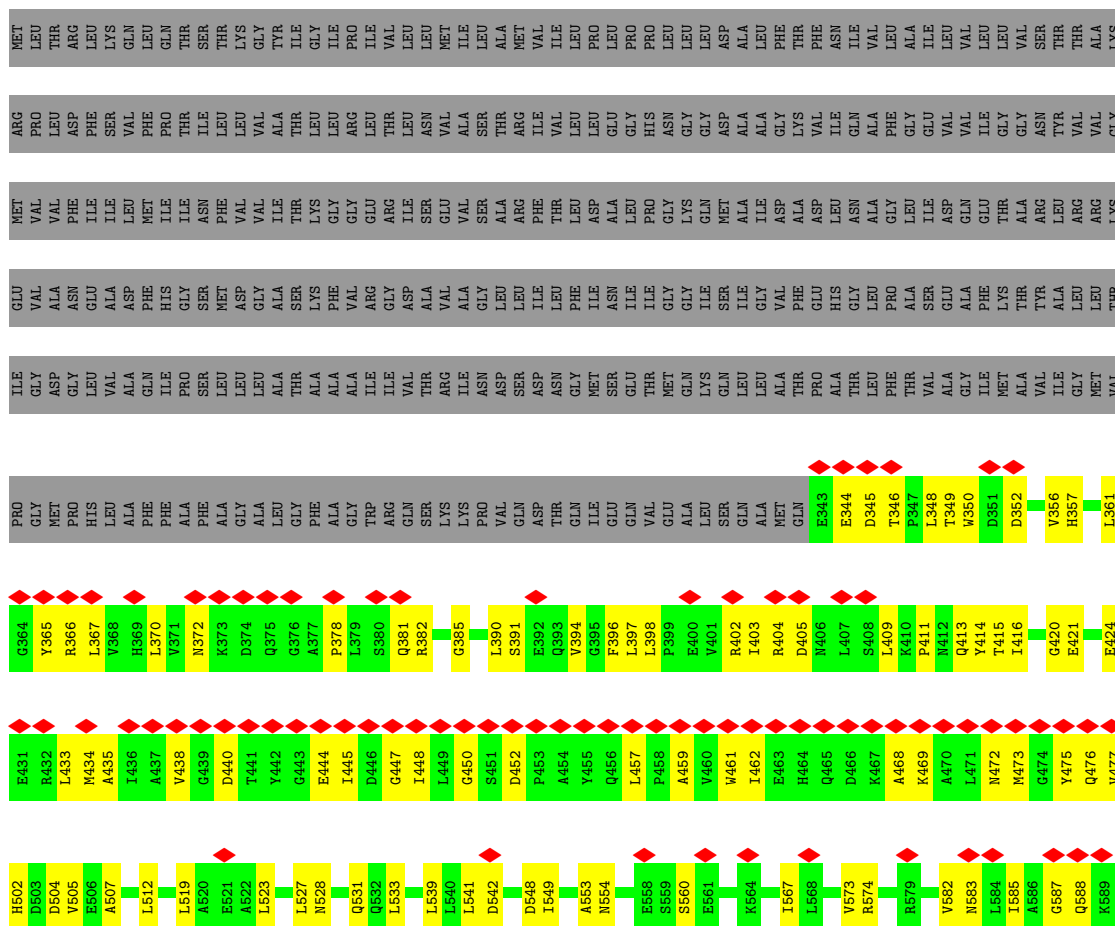
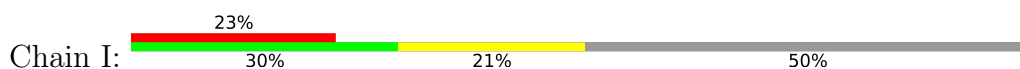








• Molecule 1: Flagellar biosynthesis protein FlhA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C9	Depositor
Number of particles used	9756	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 ($e^-/\text{\AA}^2$)	48	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	0.048	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0146	Depositor
Map size (Å)	348.528, 348.528, 348.528	wwPDB
Map dimensions	424, 424, 424	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	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	0.43	0/2806	0.50	1/3819 (0.0%)
1	B	0.43	0/2806	0.50	1/3819 (0.0%)
1	C	0.43	0/2806	0.50	1/3819 (0.0%)
1	D	0.43	0/2806	0.50	1/3819 (0.0%)
1	E	0.43	0/2806	0.50	1/3819 (0.0%)
1	F	0.43	0/2806	0.50	1/3819 (0.0%)
1	G	0.43	0/2806	0.50	1/3819 (0.0%)
1	H	0.43	0/2806	0.50	1/3819 (0.0%)
1	I	0.43	0/2806	0.50	1/3819 (0.0%)
All	All	0.43	0/25254	0.50	9/34371 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	345	ASP	N-CA-C	-6.45	106.14	112.97
1	G	345	ASP	N-CA-C	-6.44	106.14	112.97
1	I	345	ASP	N-CA-C	-6.42	106.17	112.97
1	B	345	ASP	N-CA-C	-6.42	106.17	112.97
1	E	345	ASP	N-CA-C	-6.40	106.19	112.97

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	2761	0	2832	120	0
1	B	2761	0	2832	117	0
1	C	2761	0	2832	113	0
1	D	2761	0	2832	111	0
1	E	2761	0	2832	123	0
1	F	2761	0	2832	115	0
1	G	2761	0	2832	118	0
1	H	2761	0	2832	118	0
1	I	2761	0	2832	118	0
All	All	24849	0	25488	1020	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 20.

The worst 5 of 1020 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:A:409:LEU:HB2	1:A:413:GLN:HE21	1.34	0.93
1:B:409:LEU:HB2	1:B:413:GLN:HE21	1.34	0.92
1:I:409:LEU:HB2	1:I:413:GLN:HE21	1.34	0.91
1:C:409:LEU:HB2	1:C:413:GLN:HE21	1.34	0.91
1:E:409:LEU:HB2	1:E:413:GLN:HE21	1.34	0.91

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	A	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	37	68
1	B	351/702 (50%)	301 (86%)	49 (14%)	1 (0%)	37	68
1	C	351/702 (50%)	301 (86%)	49 (14%)	1 (0%)	37	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	37	68
1	E	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	37	68
1	F	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	37	68
1	G	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	37	68
1	H	351/702 (50%)	301 (86%)	49 (14%)	1 (0%)	37	68
1	I	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	37	68
All	All	3159/6318 (50%)	2715 (86%)	435 (14%)	9 (0%)	38	68

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	420	GLY
1	B	420	GLY
1	C	420	GLY
1	D	420	GLY
1	E	420	GLY

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	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	B	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	C	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	D	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	E	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	F	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	G	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	H	305/584 (52%)	303 (99%)	2 (1%)	81	88
1	I	305/584 (52%)	303 (99%)	2 (1%)	81	88
All	All	2745/5256 (52%)	2727 (99%)	18 (1%)	80	88

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	488	ILE
1	I	620	LEU
1	I	488	ILE
1	E	488	ILE
1	G	620	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	413	GLN
1	I	646	GLN
1	H	425	GLN
1	I	413	GLN
1	D	413	GLN

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 ⓘ

There are no chain breaks in this entry.

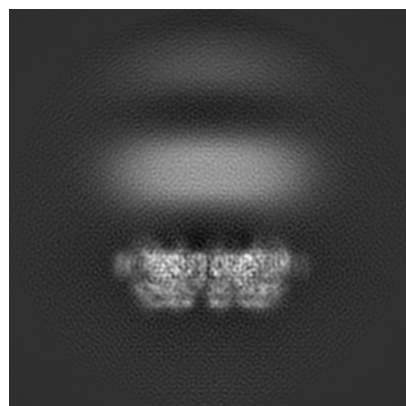
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11827. These allow visual inspection of the internal detail of the map and identification of artifacts.

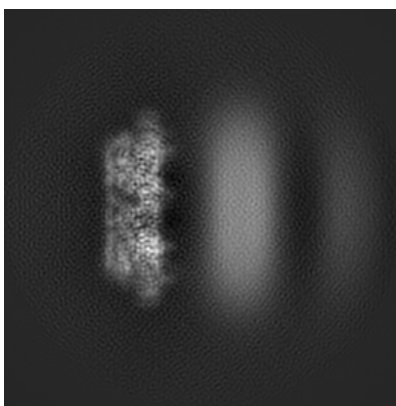
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

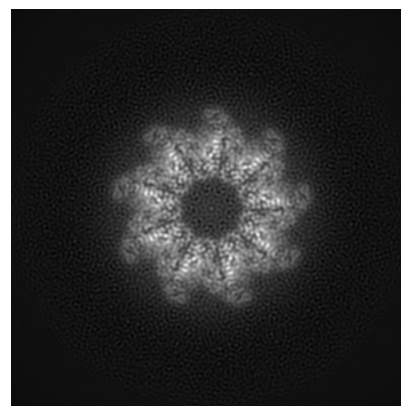
6.1.1 Primary map



X

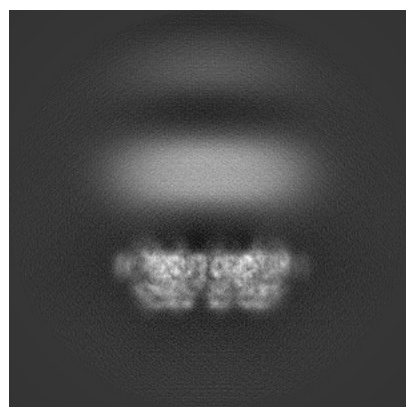


Y

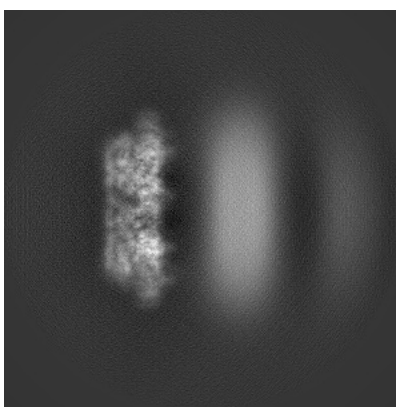


Z

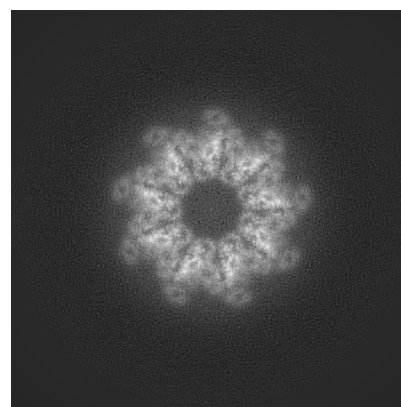
6.1.2 Raw map



X



Y

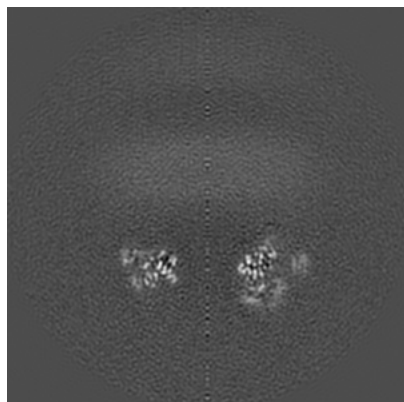


Z

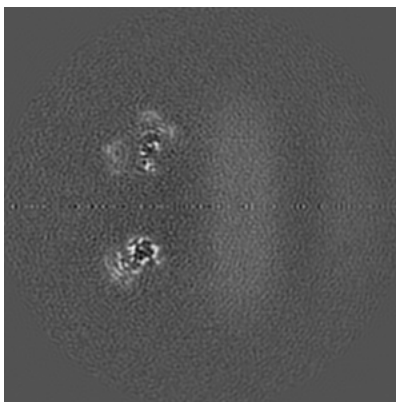
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

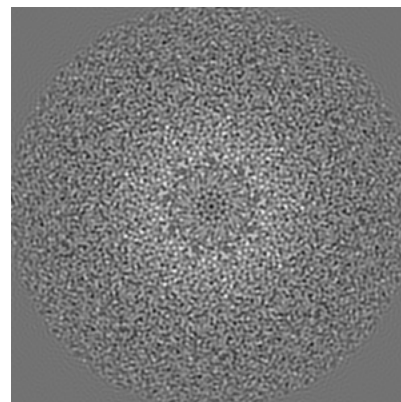
6.2.1 Primary map



X Index: 212

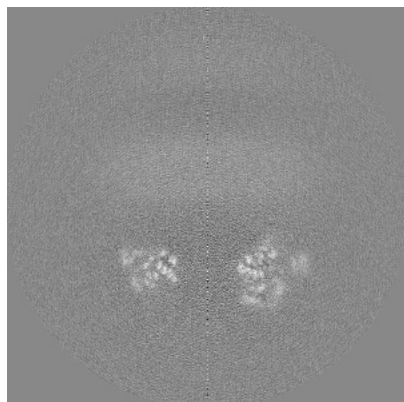


Y Index: 212

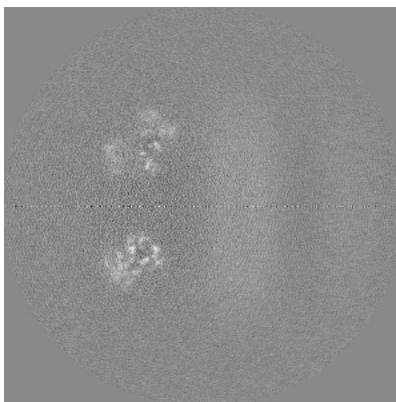


Z Index: 212

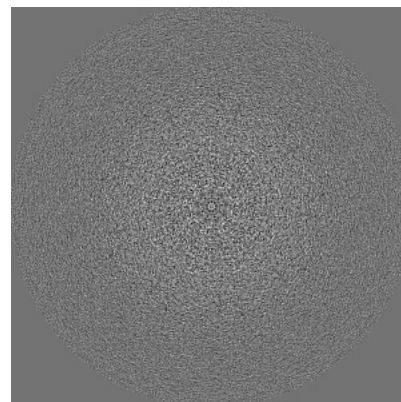
6.2.2 Raw map



X Index: 212



Y Index: 212

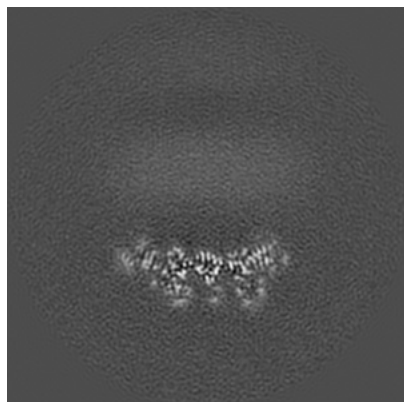


Z Index: 212

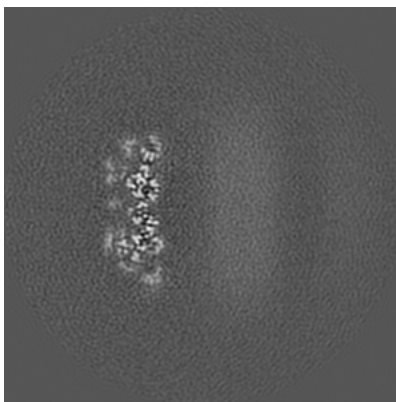
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

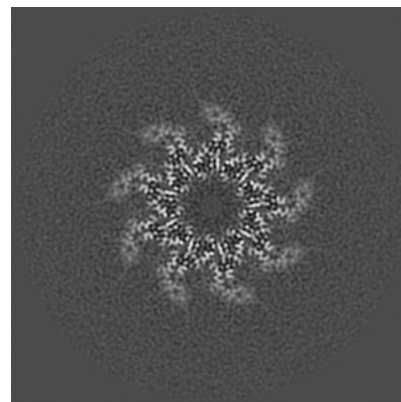
6.3.1 Primary map



X Index: 168

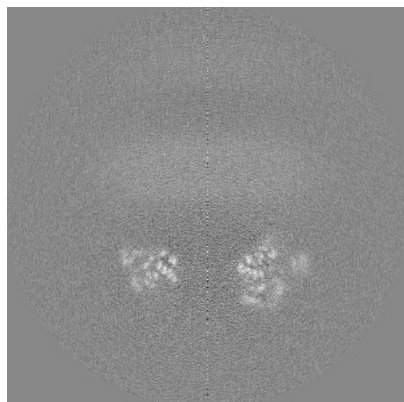


Y Index: 250

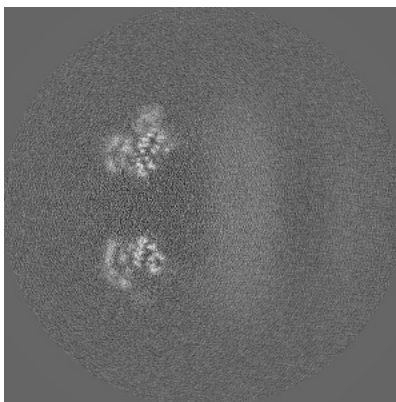


Z Index: 152

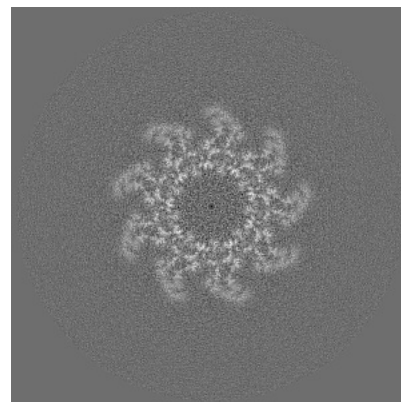
6.3.2 Raw map



X Index: 212



Y Index: 219

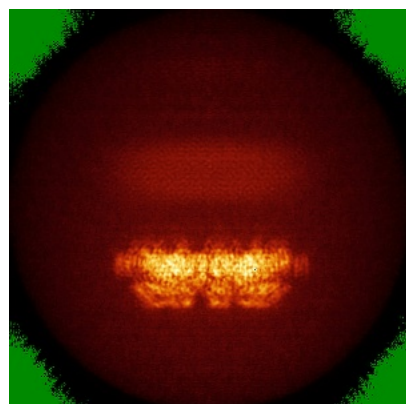


Z Index: 158

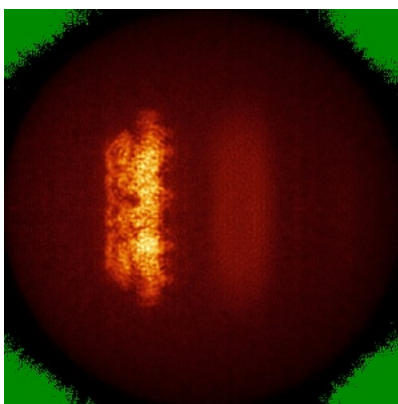
The images above show the largest variance slices of the map in three orthogonal directions.

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

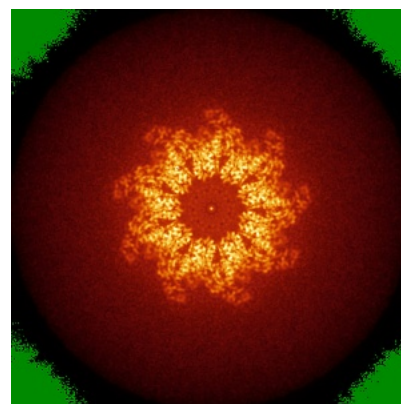
6.4.1 Primary map



X

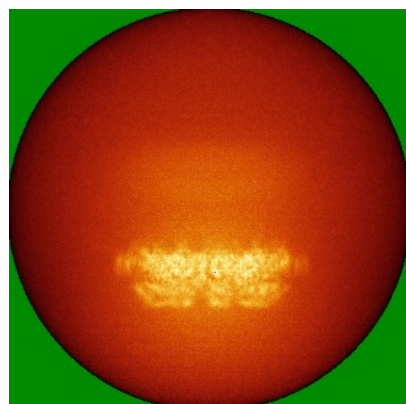


Y

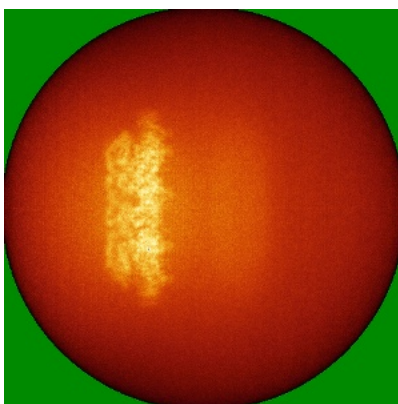


Z

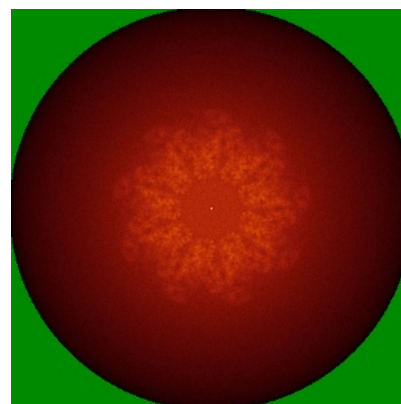
6.4.2 Raw map



X



Y

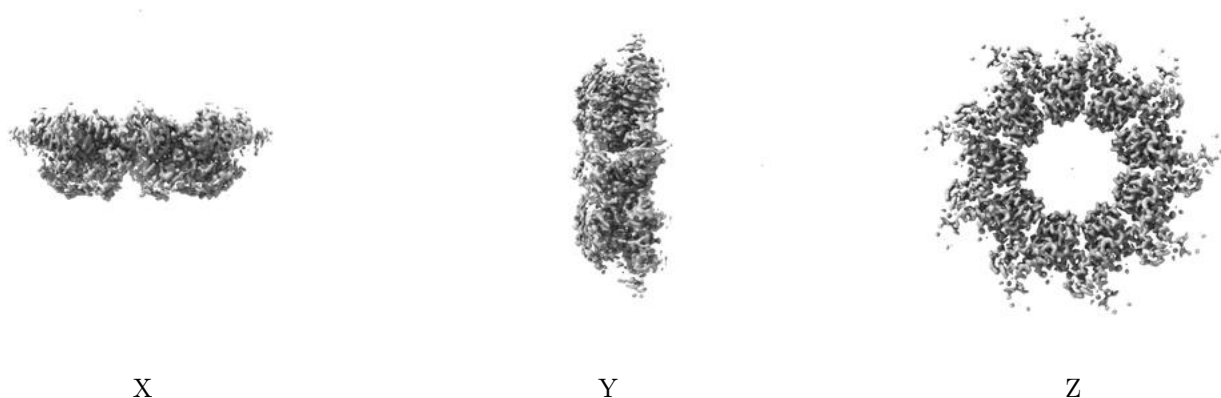


Z

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

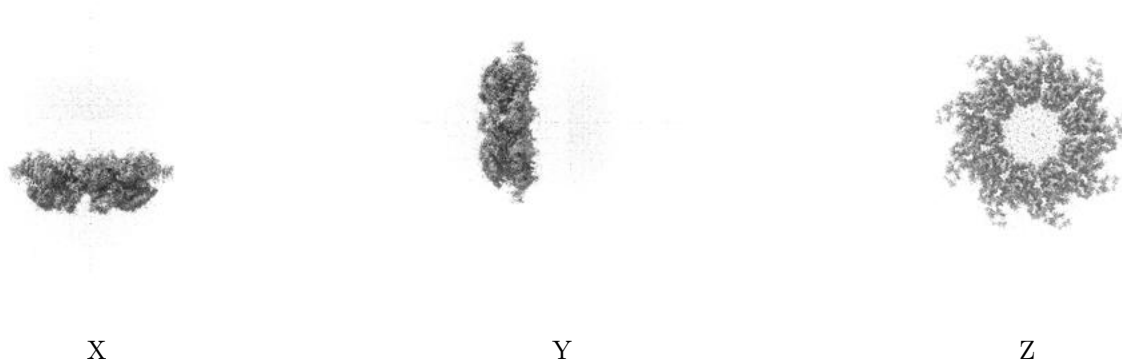
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0146. 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.

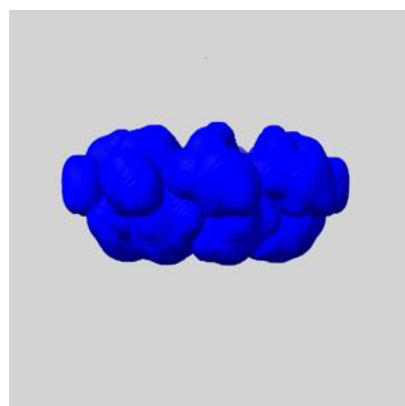
6.6 Mask visualisation [i](#)

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

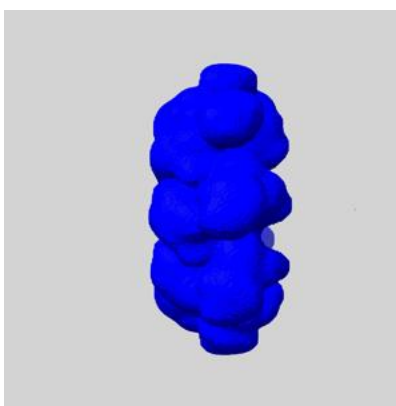
A mask typically either:

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

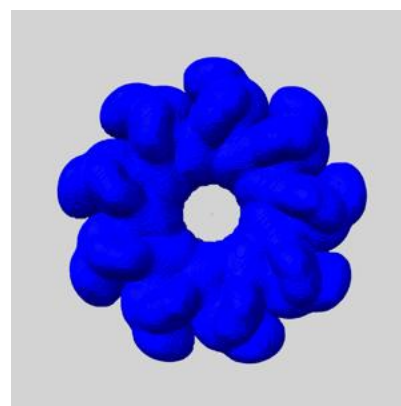
6.6.1 emd_11827_msk_1.map [i](#)



X



Y

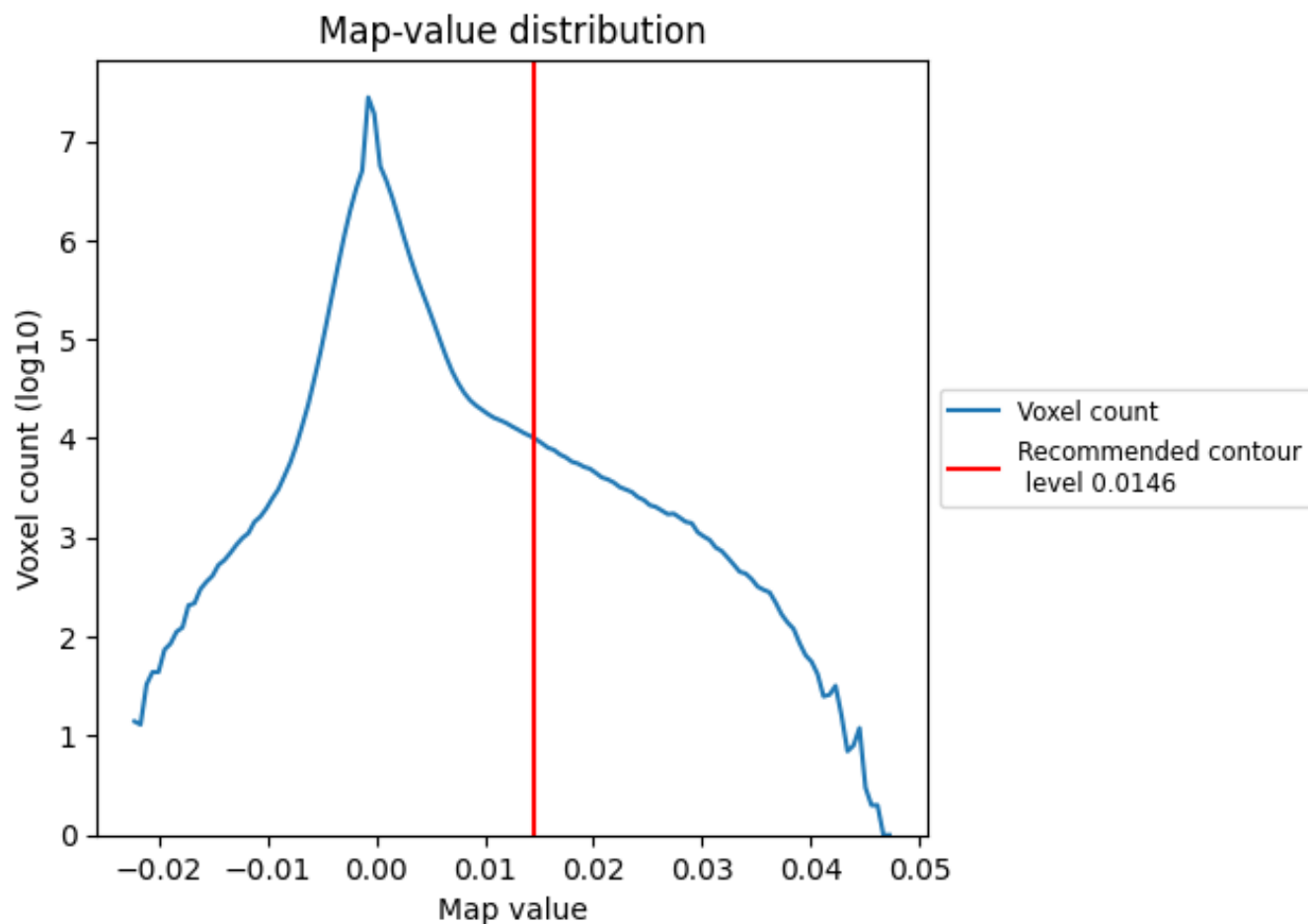


Z

7 Map analysis [i](#)

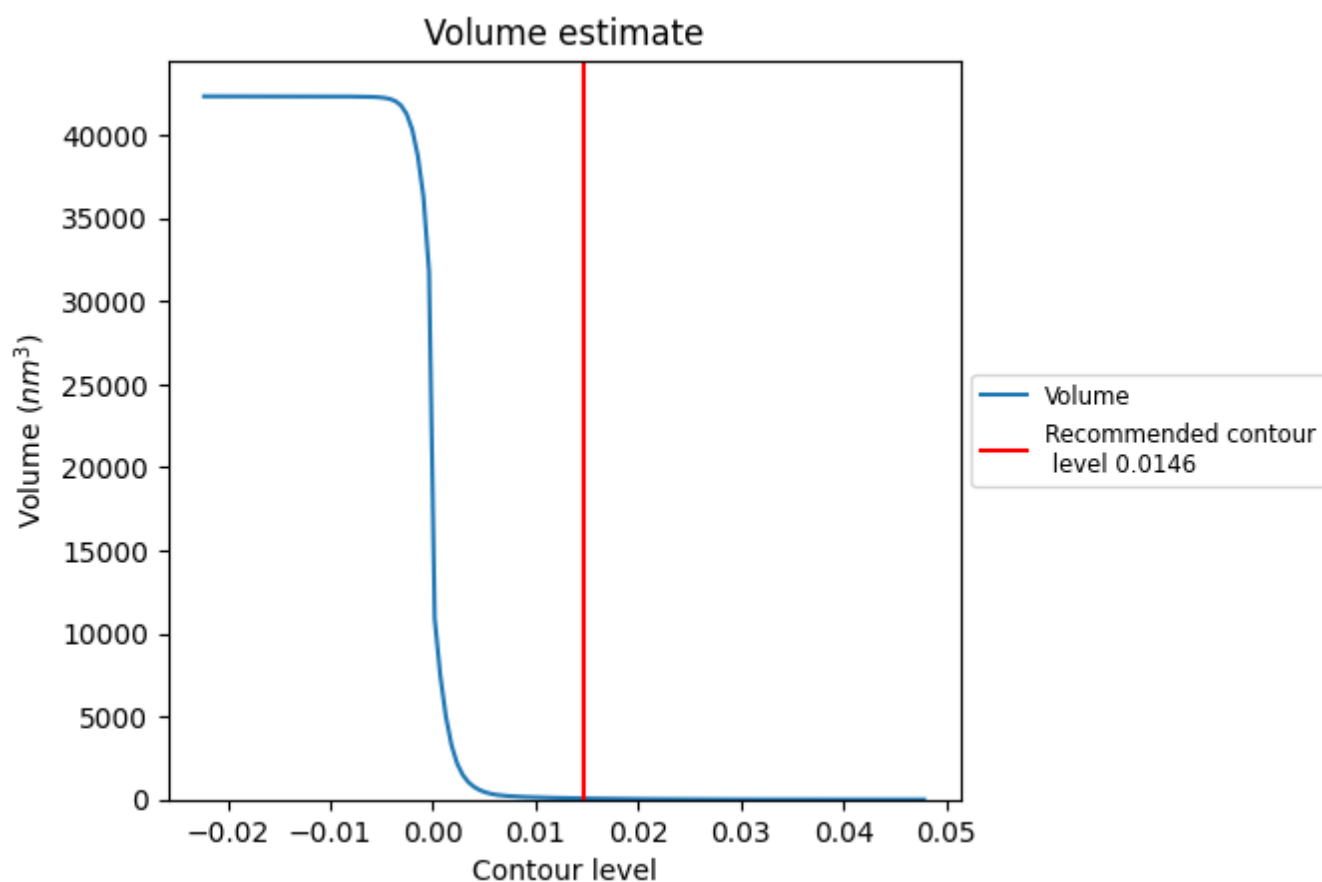
This section contains the results of statistical analysis of the map.

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.

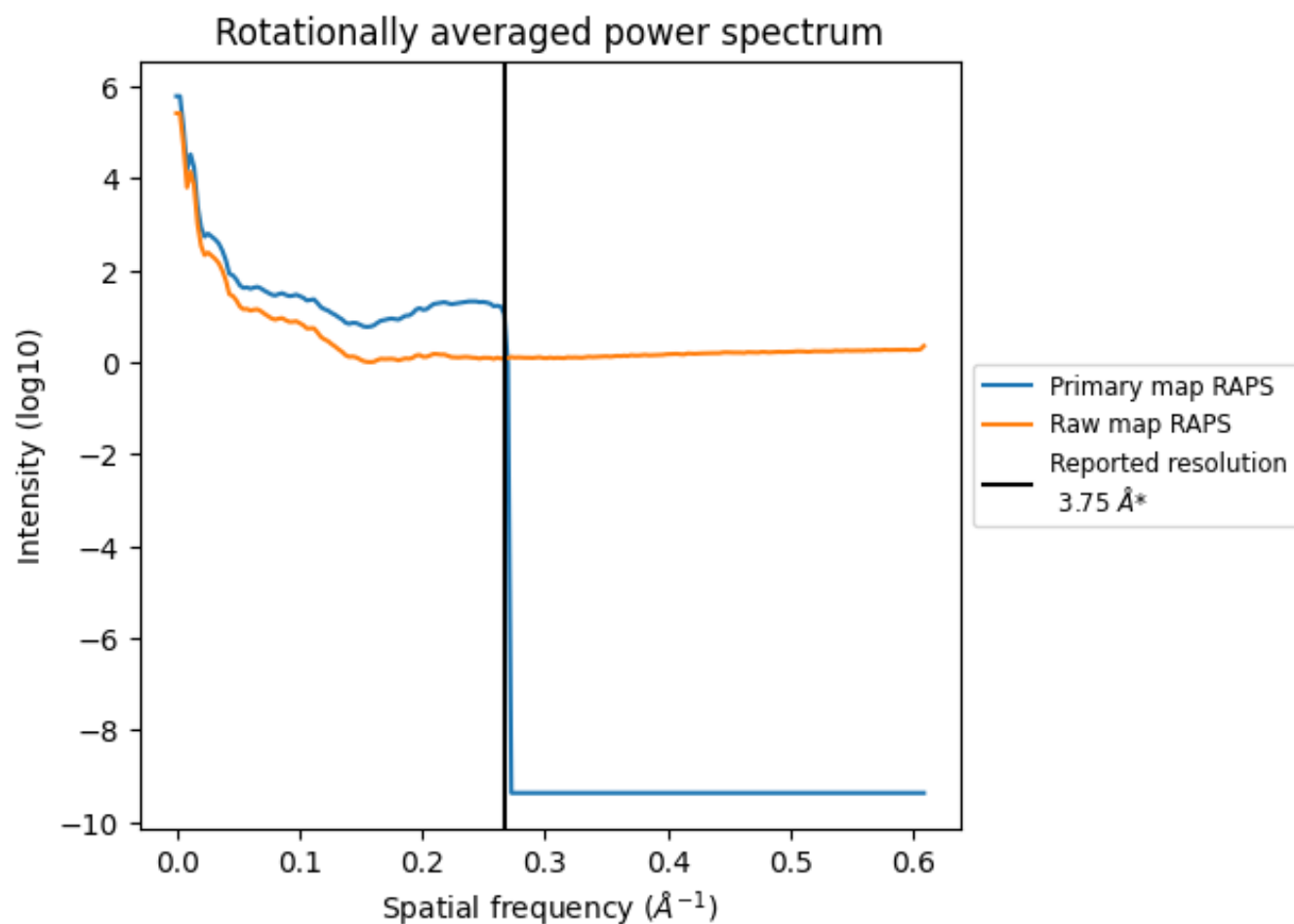
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 69 nm³; this corresponds to an approximate mass of 62 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 ⓘ

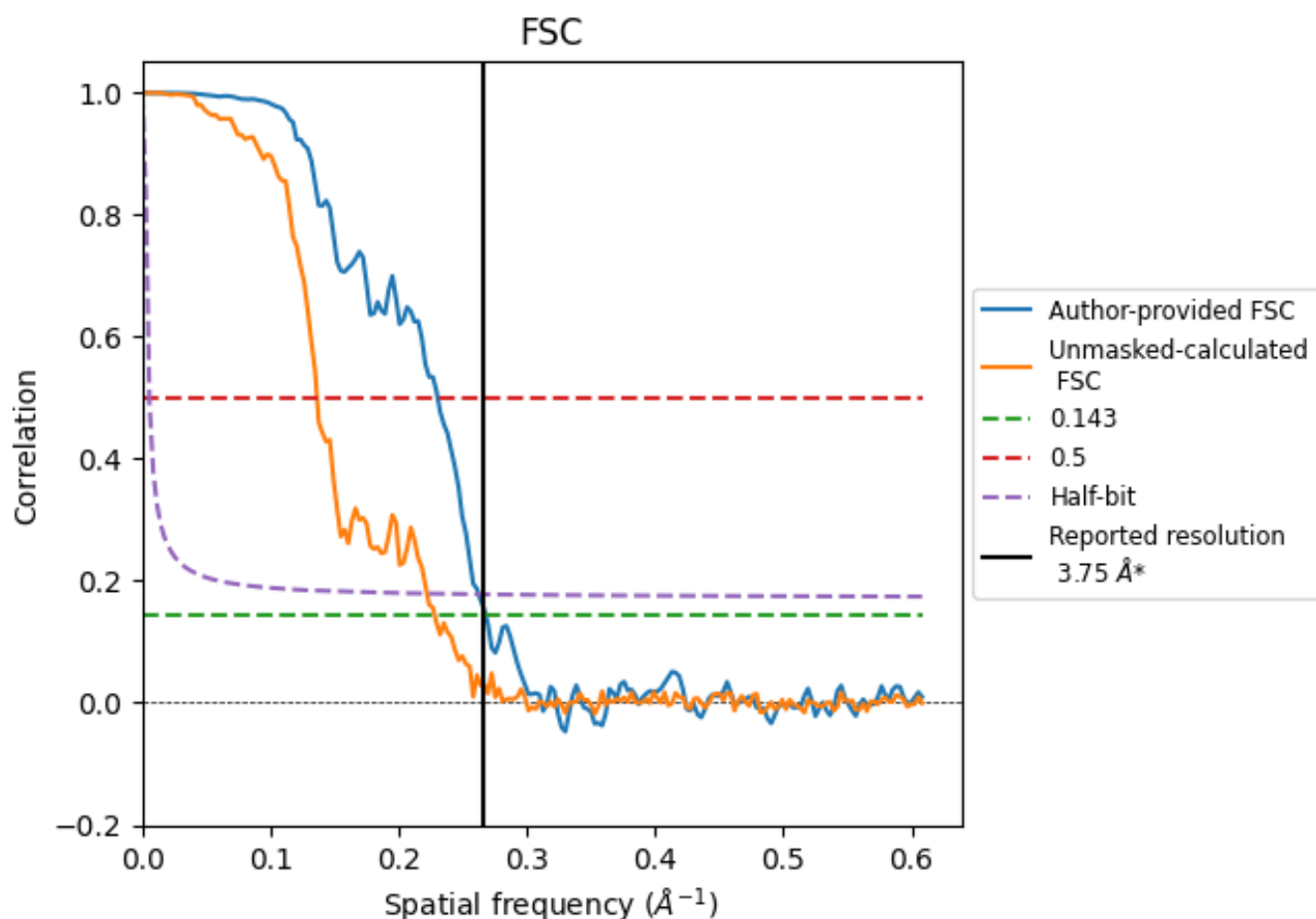


*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

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 0.267 \AA^{-1}

8.2 Resolution estimates [i](#)

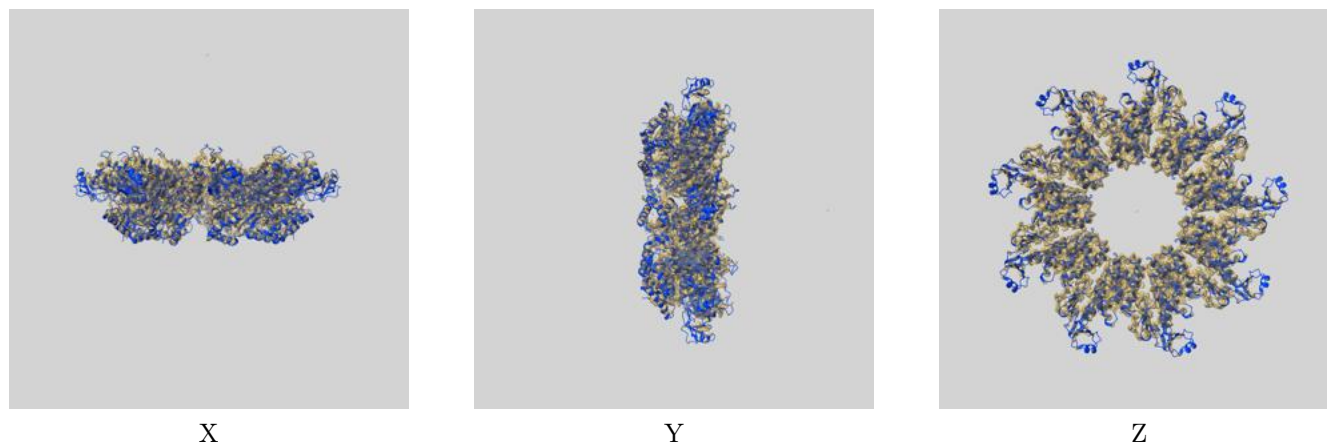
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.75	-	-
Author-provided FSC curve	3.73	4.34	3.81
Unmasked-calculated*	4.38	7.34	4.50

*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 4.38 differs from the reported value 3.75 by more than 10 %

9 Map-model fit [i](#)

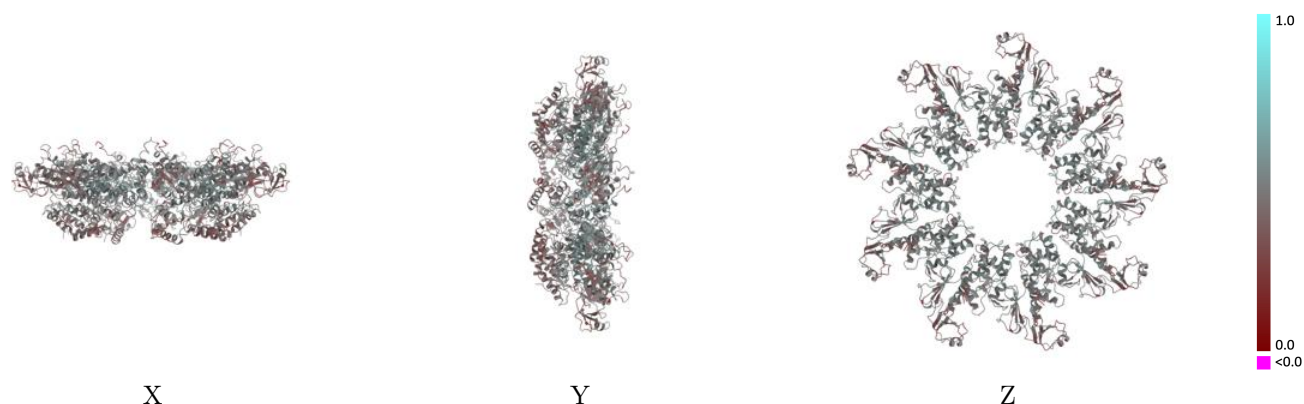
This section contains information regarding the fit between EMDB map EMD-11827 and PDB model 7AMY. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



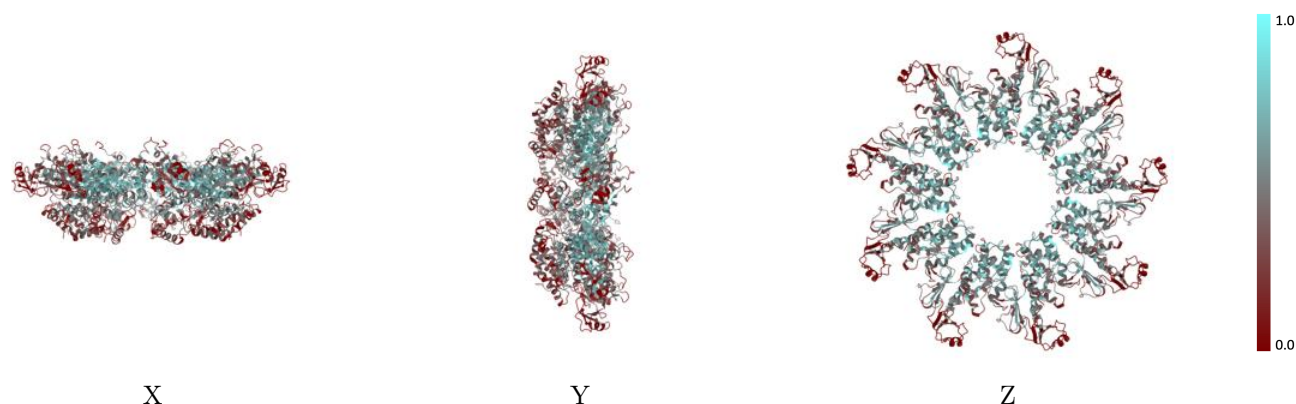
The images above show the 3D surface view of the map at the recommended contour level 0.0146 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



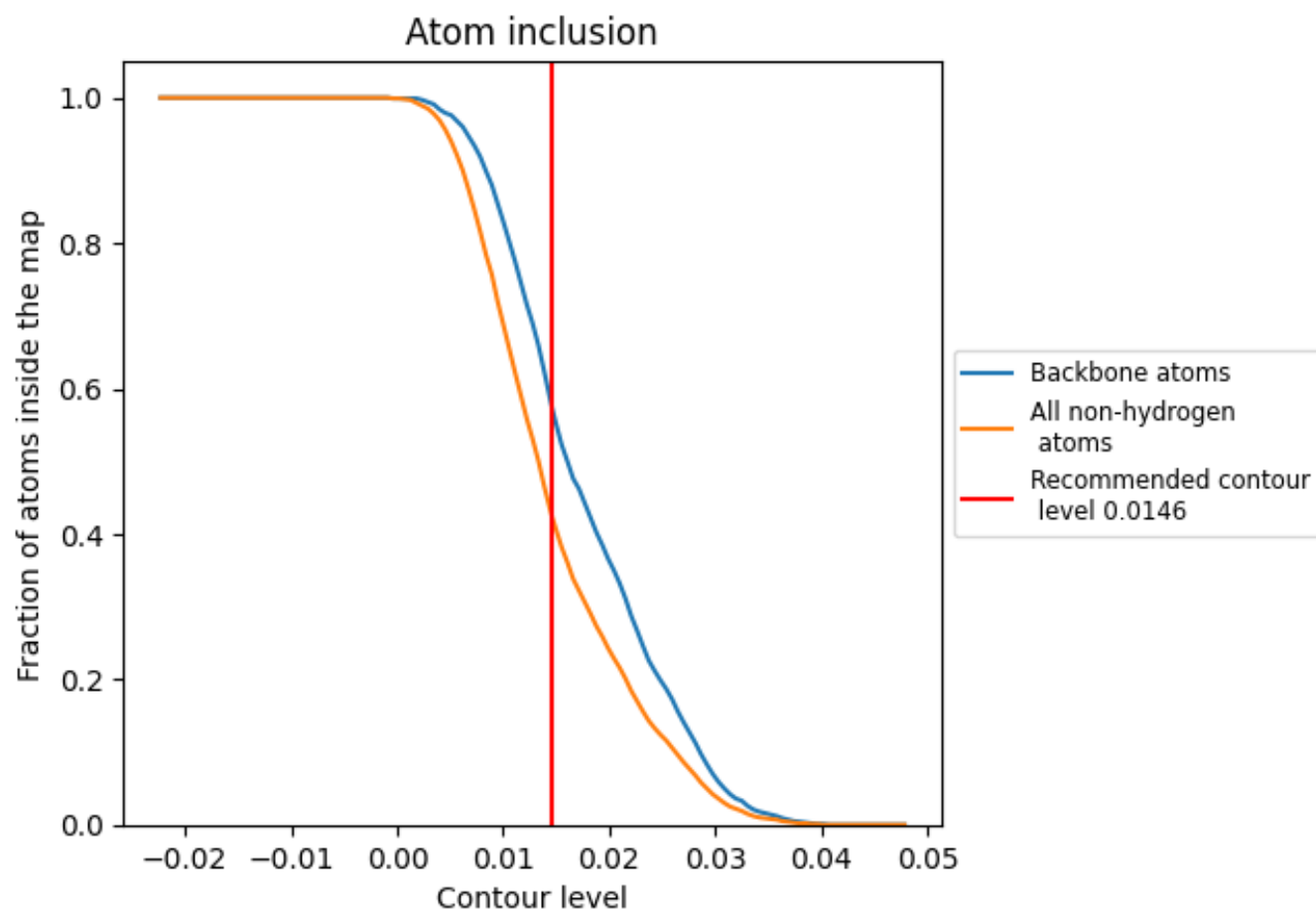
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0146).

9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 42% 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 (0.0146) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.4240	<div><div></div></div> 0.4560
A	<div><div></div></div> 0.4220	<div><div></div></div> 0.4560
B	<div><div></div></div> 0.4240	<div><div></div></div> 0.4560
C	<div><div></div></div> 0.4220	<div><div></div></div> 0.4550
D	<div><div></div></div> 0.4270	<div><div></div></div> 0.4560
E	<div><div></div></div> 0.4240	<div><div></div></div> 0.4560
F	<div><div></div></div> 0.4220	<div><div></div></div> 0.4560
G	<div><div></div></div> 0.4220	<div><div></div></div> 0.4560
H	<div><div></div></div> 0.4240	<div><div></div></div> 0.4560
I	<div><div></div></div> 0.4230	<div><div></div></div> 0.4570

1.0

0.0

<0.0