



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 09:42 PM UTC

PDB ID : 9ATB / pdb_00009atb
EMDB ID : EMD-43829
Title : cryo-EM of Cupriavidus gilardii flagellum
Authors : Fields, J.L.; Zhang, H.; Halder, S.K.; Wu, H.; Wang, F.
Deposited on : 2024-02-26
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

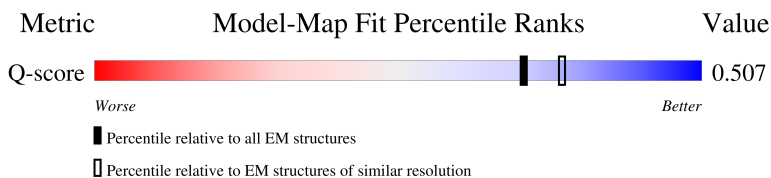
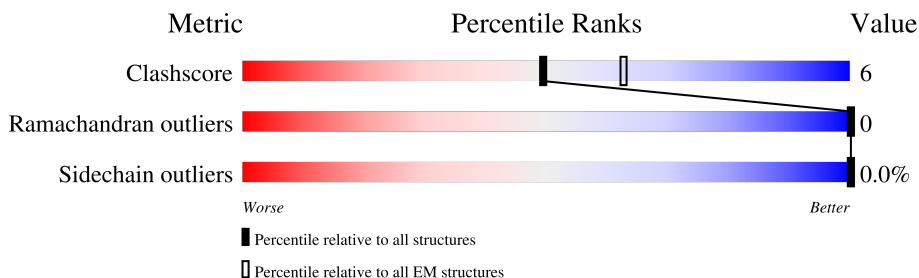
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



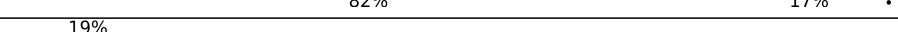
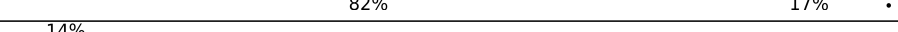
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	397	
1	B	397	
1	C	397	
1	D	397	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	397	 88% 11% .
1	F	397	 88% 12% .
1	G	397	 83% 17% .
1	H	397	 88% 11% .
1	I	397	 8% 82% 18% .
1	J	397	 22% 80% 19% .
1	K	397	 87% 13% .
1	a	397	 88% 11% .
1	b	397	 10% 86% 14% .
1	c	397	 92% 8% .
1	d	397	 90% 10% .
1	e	397	 87% 12% .
1	f	397	 5% 84% 15% .
1	g	397	 87% 13% .
1	h	397	 88% 11% .
1	i	397	 82% 17% .
1	j	397	 19% 82% 17% .
1	k	397	 14% 84% 16% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 63316 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 Flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	a	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	B	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	b	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	C	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	c	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	D	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	d	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	E	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	e	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	F	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	f	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	G	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	g	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	H	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	h	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	I	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	i	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	J	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	j	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	K	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		
1	k	395	Total	C	N	O	S	0	0
			2878	1748	513	614	3		

There are 550 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	LYS	ARG	conflict	UNP A0A849B394
A	196	THR	ALA	conflict	UNP A0A849B394
A	199	ASN	GLN	conflict	UNP A0A849B394
A	202	THR	GLY	conflict	UNP A0A849B394
A	206	THR	SER	conflict	UNP A0A849B394
A	208	SER	ALA	conflict	UNP A0A849B394
A	209	SER	ASN	conflict	UNP A0A849B394
A	211	ASN	GLY	conflict	UNP A0A849B394
A	212	ALA	ASP	conflict	UNP A0A849B394
A	215	GLY	SER	conflict	UNP A0A849B394
A	221	ASN	ALA	conflict	UNP A0A849B394
A	234	ASP	GLU	conflict	UNP A0A849B394
A	239	TYR	PHE	conflict	UNP A0A849B394
A	247	GLY	ALA	conflict	UNP A0A849B394
A	248	SER	ASP	conflict	UNP A0A849B394
A	264	ASN	ALA	conflict	UNP A0A849B394
A	265	GLY	THR	conflict	UNP A0A849B394
A	281	VAL	LEU	conflict	UNP A0A849B394
A	282	THR	SER	conflict	UNP A0A849B394
A	284	THR	PRO	conflict	UNP A0A849B394
A	285	ALA	THR	conflict	UNP A0A849B394
A	286	GLY	-	insertion	UNP A0A849B394
A	287	THR	SER	conflict	UNP A0A849B394
A	319	ALA	SER	conflict	UNP A0A849B394
A	320	ASP	SER	conflict	UNP A0A849B394
a	59	LYS	ARG	conflict	UNP A0A849B394
a	196	THR	ALA	conflict	UNP A0A849B394
a	199	ASN	GLN	conflict	UNP A0A849B394
a	202	THR	GLY	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
a	206	THR	SER	conflict	UNP A0A849B394
a	208	SER	ALA	conflict	UNP A0A849B394
a	209	SER	ASN	conflict	UNP A0A849B394
a	211	ASN	GLY	conflict	UNP A0A849B394
a	212	ALA	ASP	conflict	UNP A0A849B394
a	215	GLY	SER	conflict	UNP A0A849B394
a	221	ASN	ALA	conflict	UNP A0A849B394
a	234	ASP	GLU	conflict	UNP A0A849B394
a	239	TYR	PHE	conflict	UNP A0A849B394
a	247	GLY	ALA	conflict	UNP A0A849B394
a	248	SER	ASP	conflict	UNP A0A849B394
a	264	ASN	ALA	conflict	UNP A0A849B394
a	265	GLY	THR	conflict	UNP A0A849B394
a	281	VAL	LEU	conflict	UNP A0A849B394
a	282	THR	SER	conflict	UNP A0A849B394
a	284	THR	PRO	conflict	UNP A0A849B394
a	285	ALA	THR	conflict	UNP A0A849B394
a	286	GLY	-	insertion	UNP A0A849B394
a	287	THR	SER	conflict	UNP A0A849B394
a	319	ALA	SER	conflict	UNP A0A849B394
a	320	ASP	SER	conflict	UNP A0A849B394
B	59	LYS	ARG	conflict	UNP A0A849B394
B	196	THR	ALA	conflict	UNP A0A849B394
B	199	ASN	GLN	conflict	UNP A0A849B394
B	202	THR	GLY	conflict	UNP A0A849B394
B	206	THR	SER	conflict	UNP A0A849B394
B	208	SER	ALA	conflict	UNP A0A849B394
B	209	SER	ASN	conflict	UNP A0A849B394
B	211	ASN	GLY	conflict	UNP A0A849B394
B	212	ALA	ASP	conflict	UNP A0A849B394
B	215	GLY	SER	conflict	UNP A0A849B394
B	221	ASN	ALA	conflict	UNP A0A849B394
B	234	ASP	GLU	conflict	UNP A0A849B394
B	239	TYR	PHE	conflict	UNP A0A849B394
B	247	GLY	ALA	conflict	UNP A0A849B394
B	248	SER	ASP	conflict	UNP A0A849B394
B	264	ASN	ALA	conflict	UNP A0A849B394
B	265	GLY	THR	conflict	UNP A0A849B394
B	281	VAL	LEU	conflict	UNP A0A849B394
B	282	THR	SER	conflict	UNP A0A849B394
B	284	THR	PRO	conflict	UNP A0A849B394
B	285	ALA	THR	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	286	GLY	-	insertion	UNP A0A849B394
B	287	THR	SER	conflict	UNP A0A849B394
B	319	ALA	SER	conflict	UNP A0A849B394
B	320	ASP	SER	conflict	UNP A0A849B394
b	59	LYS	ARG	conflict	UNP A0A849B394
b	196	THR	ALA	conflict	UNP A0A849B394
b	199	ASN	GLN	conflict	UNP A0A849B394
b	202	THR	GLY	conflict	UNP A0A849B394
b	206	THR	SER	conflict	UNP A0A849B394
b	208	SER	ALA	conflict	UNP A0A849B394
b	209	SER	ASN	conflict	UNP A0A849B394
b	211	ASN	GLY	conflict	UNP A0A849B394
b	212	ALA	ASP	conflict	UNP A0A849B394
b	215	GLY	SER	conflict	UNP A0A849B394
b	221	ASN	ALA	conflict	UNP A0A849B394
b	234	ASP	GLU	conflict	UNP A0A849B394
b	239	TYR	PHE	conflict	UNP A0A849B394
b	247	GLY	ALA	conflict	UNP A0A849B394
b	248	SER	ASP	conflict	UNP A0A849B394
b	264	ASN	ALA	conflict	UNP A0A849B394
b	265	GLY	THR	conflict	UNP A0A849B394
b	281	VAL	LEU	conflict	UNP A0A849B394
b	282	THR	SER	conflict	UNP A0A849B394
b	284	THR	PRO	conflict	UNP A0A849B394
b	285	ALA	THR	conflict	UNP A0A849B394
b	286	GLY	-	insertion	UNP A0A849B394
b	287	THR	SER	conflict	UNP A0A849B394
b	319	ALA	SER	conflict	UNP A0A849B394
b	320	ASP	SER	conflict	UNP A0A849B394
C	59	LYS	ARG	conflict	UNP A0A849B394
C	196	THR	ALA	conflict	UNP A0A849B394
C	199	ASN	GLN	conflict	UNP A0A849B394
C	202	THR	GLY	conflict	UNP A0A849B394
C	206	THR	SER	conflict	UNP A0A849B394
C	208	SER	ALA	conflict	UNP A0A849B394
C	209	SER	ASN	conflict	UNP A0A849B394
C	211	ASN	GLY	conflict	UNP A0A849B394
C	212	ALA	ASP	conflict	UNP A0A849B394
C	215	GLY	SER	conflict	UNP A0A849B394
C	221	ASN	ALA	conflict	UNP A0A849B394
C	234	ASP	GLU	conflict	UNP A0A849B394
C	239	TYR	PHE	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	247	GLY	ALA	conflict	UNP A0A849B394
C	248	SER	ASP	conflict	UNP A0A849B394
C	264	ASN	ALA	conflict	UNP A0A849B394
C	265	GLY	THR	conflict	UNP A0A849B394
C	281	VAL	LEU	conflict	UNP A0A849B394
C	282	THR	SER	conflict	UNP A0A849B394
C	284	THR	PRO	conflict	UNP A0A849B394
C	285	ALA	THR	conflict	UNP A0A849B394
C	286	GLY	-	insertion	UNP A0A849B394
C	287	THR	SER	conflict	UNP A0A849B394
C	319	ALA	SER	conflict	UNP A0A849B394
C	320	ASP	SER	conflict	UNP A0A849B394
c	59	LYS	ARG	conflict	UNP A0A849B394
c	196	THR	ALA	conflict	UNP A0A849B394
c	199	ASN	GLN	conflict	UNP A0A849B394
c	202	THR	GLY	conflict	UNP A0A849B394
c	206	THR	SER	conflict	UNP A0A849B394
c	208	SER	ALA	conflict	UNP A0A849B394
c	209	SER	ASN	conflict	UNP A0A849B394
c	211	ASN	GLY	conflict	UNP A0A849B394
c	212	ALA	ASP	conflict	UNP A0A849B394
c	215	GLY	SER	conflict	UNP A0A849B394
c	221	ASN	ALA	conflict	UNP A0A849B394
c	234	ASP	GLU	conflict	UNP A0A849B394
c	239	TYR	PHE	conflict	UNP A0A849B394
c	247	GLY	ALA	conflict	UNP A0A849B394
c	248	SER	ASP	conflict	UNP A0A849B394
c	264	ASN	ALA	conflict	UNP A0A849B394
c	265	GLY	THR	conflict	UNP A0A849B394
c	281	VAL	LEU	conflict	UNP A0A849B394
c	282	THR	SER	conflict	UNP A0A849B394
c	284	THR	PRO	conflict	UNP A0A849B394
c	285	ALA	THR	conflict	UNP A0A849B394
c	286	GLY	-	insertion	UNP A0A849B394
c	287	THR	SER	conflict	UNP A0A849B394
c	319	ALA	SER	conflict	UNP A0A849B394
c	320	ASP	SER	conflict	UNP A0A849B394
D	59	LYS	ARG	conflict	UNP A0A849B394
D	196	THR	ALA	conflict	UNP A0A849B394
D	199	ASN	GLN	conflict	UNP A0A849B394
D	202	THR	GLY	conflict	UNP A0A849B394
D	206	THR	SER	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	208	SER	ALA	conflict	UNP A0A849B394
D	209	SER	ASN	conflict	UNP A0A849B394
D	211	ASN	GLY	conflict	UNP A0A849B394
D	212	ALA	ASP	conflict	UNP A0A849B394
D	215	GLY	SER	conflict	UNP A0A849B394
D	221	ASN	ALA	conflict	UNP A0A849B394
D	234	ASP	GLU	conflict	UNP A0A849B394
D	239	TYR	PHE	conflict	UNP A0A849B394
D	247	GLY	ALA	conflict	UNP A0A849B394
D	248	SER	ASP	conflict	UNP A0A849B394
D	264	ASN	ALA	conflict	UNP A0A849B394
D	265	GLY	THR	conflict	UNP A0A849B394
D	281	VAL	LEU	conflict	UNP A0A849B394
D	282	THR	SER	conflict	UNP A0A849B394
D	284	THR	PRO	conflict	UNP A0A849B394
D	285	ALA	THR	conflict	UNP A0A849B394
D	286	GLY	-	insertion	UNP A0A849B394
D	287	THR	SER	conflict	UNP A0A849B394
D	319	ALA	SER	conflict	UNP A0A849B394
D	320	ASP	SER	conflict	UNP A0A849B394
d	59	LYS	ARG	conflict	UNP A0A849B394
d	196	THR	ALA	conflict	UNP A0A849B394
d	199	ASN	GLN	conflict	UNP A0A849B394
d	202	THR	GLY	conflict	UNP A0A849B394
d	206	THR	SER	conflict	UNP A0A849B394
d	208	SER	ALA	conflict	UNP A0A849B394
d	209	SER	ASN	conflict	UNP A0A849B394
d	211	ASN	GLY	conflict	UNP A0A849B394
d	212	ALA	ASP	conflict	UNP A0A849B394
d	215	GLY	SER	conflict	UNP A0A849B394
d	221	ASN	ALA	conflict	UNP A0A849B394
d	234	ASP	GLU	conflict	UNP A0A849B394
d	239	TYR	PHE	conflict	UNP A0A849B394
d	247	GLY	ALA	conflict	UNP A0A849B394
d	248	SER	ASP	conflict	UNP A0A849B394
d	264	ASN	ALA	conflict	UNP A0A849B394
d	265	GLY	THR	conflict	UNP A0A849B394
d	281	VAL	LEU	conflict	UNP A0A849B394
d	282	THR	SER	conflict	UNP A0A849B394
d	284	THR	PRO	conflict	UNP A0A849B394
d	285	ALA	THR	conflict	UNP A0A849B394
d	286	GLY	-	insertion	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
d	287	THR	SER	conflict	UNP A0A849B394
d	319	ALA	SER	conflict	UNP A0A849B394
d	320	ASP	SER	conflict	UNP A0A849B394
E	59	LYS	ARG	conflict	UNP A0A849B394
E	196	THR	ALA	conflict	UNP A0A849B394
E	199	ASN	GLN	conflict	UNP A0A849B394
E	202	THR	GLY	conflict	UNP A0A849B394
E	206	THR	SER	conflict	UNP A0A849B394
E	208	SER	ALA	conflict	UNP A0A849B394
E	209	SER	ASN	conflict	UNP A0A849B394
E	211	ASN	GLY	conflict	UNP A0A849B394
E	212	ALA	ASP	conflict	UNP A0A849B394
E	215	GLY	SER	conflict	UNP A0A849B394
E	221	ASN	ALA	conflict	UNP A0A849B394
E	234	ASP	GLU	conflict	UNP A0A849B394
E	239	TYR	PHE	conflict	UNP A0A849B394
E	247	GLY	ALA	conflict	UNP A0A849B394
E	248	SER	ASP	conflict	UNP A0A849B394
E	264	ASN	ALA	conflict	UNP A0A849B394
E	265	GLY	THR	conflict	UNP A0A849B394
E	281	VAL	LEU	conflict	UNP A0A849B394
E	282	THR	SER	conflict	UNP A0A849B394
E	284	THR	PRO	conflict	UNP A0A849B394
E	285	ALA	THR	conflict	UNP A0A849B394
E	286	GLY	-	insertion	UNP A0A849B394
E	287	THR	SER	conflict	UNP A0A849B394
E	319	ALA	SER	conflict	UNP A0A849B394
E	320	ASP	SER	conflict	UNP A0A849B394
e	59	LYS	ARG	conflict	UNP A0A849B394
e	196	THR	ALA	conflict	UNP A0A849B394
e	199	ASN	GLN	conflict	UNP A0A849B394
e	202	THR	GLY	conflict	UNP A0A849B394
e	206	THR	SER	conflict	UNP A0A849B394
e	208	SER	ALA	conflict	UNP A0A849B394
e	209	SER	ASN	conflict	UNP A0A849B394
e	211	ASN	GLY	conflict	UNP A0A849B394
e	212	ALA	ASP	conflict	UNP A0A849B394
e	215	GLY	SER	conflict	UNP A0A849B394
e	221	ASN	ALA	conflict	UNP A0A849B394
e	234	ASP	GLU	conflict	UNP A0A849B394
e	239	TYR	PHE	conflict	UNP A0A849B394
e	247	GLY	ALA	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
e	248	SER	ASP	conflict	UNP A0A849B394
e	264	ASN	ALA	conflict	UNP A0A849B394
e	265	GLY	THR	conflict	UNP A0A849B394
e	281	VAL	LEU	conflict	UNP A0A849B394
e	282	THR	SER	conflict	UNP A0A849B394
e	284	THR	PRO	conflict	UNP A0A849B394
e	285	ALA	THR	conflict	UNP A0A849B394
e	286	GLY	-	insertion	UNP A0A849B394
e	287	THR	SER	conflict	UNP A0A849B394
e	319	ALA	SER	conflict	UNP A0A849B394
e	320	ASP	SER	conflict	UNP A0A849B394
F	59	LYS	ARG	conflict	UNP A0A849B394
F	196	THR	ALA	conflict	UNP A0A849B394
F	199	ASN	GLN	conflict	UNP A0A849B394
F	202	THR	GLY	conflict	UNP A0A849B394
F	206	THR	SER	conflict	UNP A0A849B394
F	208	SER	ALA	conflict	UNP A0A849B394
F	209	SER	ASN	conflict	UNP A0A849B394
F	211	ASN	GLY	conflict	UNP A0A849B394
F	212	ALA	ASP	conflict	UNP A0A849B394
F	215	GLY	SER	conflict	UNP A0A849B394
F	221	ASN	ALA	conflict	UNP A0A849B394
F	234	ASP	GLU	conflict	UNP A0A849B394
F	239	TYR	PHE	conflict	UNP A0A849B394
F	247	GLY	ALA	conflict	UNP A0A849B394
F	248	SER	ASP	conflict	UNP A0A849B394
F	264	ASN	ALA	conflict	UNP A0A849B394
F	265	GLY	THR	conflict	UNP A0A849B394
F	281	VAL	LEU	conflict	UNP A0A849B394
F	282	THR	SER	conflict	UNP A0A849B394
F	284	THR	PRO	conflict	UNP A0A849B394
F	285	ALA	THR	conflict	UNP A0A849B394
F	286	GLY	-	insertion	UNP A0A849B394
F	287	THR	SER	conflict	UNP A0A849B394
F	319	ALA	SER	conflict	UNP A0A849B394
F	320	ASP	SER	conflict	UNP A0A849B394
f	59	LYS	ARG	conflict	UNP A0A849B394
f	196	THR	ALA	conflict	UNP A0A849B394
f	199	ASN	GLN	conflict	UNP A0A849B394
f	202	THR	GLY	conflict	UNP A0A849B394
f	206	THR	SER	conflict	UNP A0A849B394
f	208	SER	ALA	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
f	209	SER	ASN	conflict	UNP A0A849B394
f	211	ASN	GLY	conflict	UNP A0A849B394
f	212	ALA	ASP	conflict	UNP A0A849B394
f	215	GLY	SER	conflict	UNP A0A849B394
f	221	ASN	ALA	conflict	UNP A0A849B394
f	234	ASP	GLU	conflict	UNP A0A849B394
f	239	TYR	PHE	conflict	UNP A0A849B394
f	247	GLY	ALA	conflict	UNP A0A849B394
f	248	SER	ASP	conflict	UNP A0A849B394
f	264	ASN	ALA	conflict	UNP A0A849B394
f	265	GLY	THR	conflict	UNP A0A849B394
f	281	VAL	LEU	conflict	UNP A0A849B394
f	282	THR	SER	conflict	UNP A0A849B394
f	284	THR	PRO	conflict	UNP A0A849B394
f	285	ALA	THR	conflict	UNP A0A849B394
f	286	GLY	-	insertion	UNP A0A849B394
f	287	THR	SER	conflict	UNP A0A849B394
f	319	ALA	SER	conflict	UNP A0A849B394
f	320	ASP	SER	conflict	UNP A0A849B394
G	59	LYS	ARG	conflict	UNP A0A849B394
G	196	THR	ALA	conflict	UNP A0A849B394
G	199	ASN	GLN	conflict	UNP A0A849B394
G	202	THR	GLY	conflict	UNP A0A849B394
G	206	THR	SER	conflict	UNP A0A849B394
G	208	SER	ALA	conflict	UNP A0A849B394
G	209	SER	ASN	conflict	UNP A0A849B394
G	211	ASN	GLY	conflict	UNP A0A849B394
G	212	ALA	ASP	conflict	UNP A0A849B394
G	215	GLY	SER	conflict	UNP A0A849B394
G	221	ASN	ALA	conflict	UNP A0A849B394
G	234	ASP	GLU	conflict	UNP A0A849B394
G	239	TYR	PHE	conflict	UNP A0A849B394
G	247	GLY	ALA	conflict	UNP A0A849B394
G	248	SER	ASP	conflict	UNP A0A849B394
G	264	ASN	ALA	conflict	UNP A0A849B394
G	265	GLY	THR	conflict	UNP A0A849B394
G	281	VAL	LEU	conflict	UNP A0A849B394
G	282	THR	SER	conflict	UNP A0A849B394
G	284	THR	PRO	conflict	UNP A0A849B394
G	285	ALA	THR	conflict	UNP A0A849B394
G	286	GLY	-	insertion	UNP A0A849B394
G	287	THR	SER	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	319	ALA	SER	conflict	UNP A0A849B394
G	320	ASP	SER	conflict	UNP A0A849B394
g	59	LYS	ARG	conflict	UNP A0A849B394
g	196	THR	ALA	conflict	UNP A0A849B394
g	199	ASN	GLN	conflict	UNP A0A849B394
g	202	THR	GLY	conflict	UNP A0A849B394
g	206	THR	SER	conflict	UNP A0A849B394
g	208	SER	ALA	conflict	UNP A0A849B394
g	209	SER	ASN	conflict	UNP A0A849B394
g	211	ASN	GLY	conflict	UNP A0A849B394
g	212	ALA	ASP	conflict	UNP A0A849B394
g	215	GLY	SER	conflict	UNP A0A849B394
g	221	ASN	ALA	conflict	UNP A0A849B394
g	234	ASP	GLU	conflict	UNP A0A849B394
g	239	TYR	PHE	conflict	UNP A0A849B394
g	247	GLY	ALA	conflict	UNP A0A849B394
g	248	SER	ASP	conflict	UNP A0A849B394
g	264	ASN	ALA	conflict	UNP A0A849B394
g	265	GLY	THR	conflict	UNP A0A849B394
g	281	VAL	LEU	conflict	UNP A0A849B394
g	282	THR	SER	conflict	UNP A0A849B394
g	284	THR	PRO	conflict	UNP A0A849B394
g	285	ALA	THR	conflict	UNP A0A849B394
g	286	GLY	-	insertion	UNP A0A849B394
g	287	THR	SER	conflict	UNP A0A849B394
g	319	ALA	SER	conflict	UNP A0A849B394
g	320	ASP	SER	conflict	UNP A0A849B394
H	59	LYS	ARG	conflict	UNP A0A849B394
H	196	THR	ALA	conflict	UNP A0A849B394
H	199	ASN	GLN	conflict	UNP A0A849B394
H	202	THR	GLY	conflict	UNP A0A849B394
H	206	THR	SER	conflict	UNP A0A849B394
H	208	SER	ALA	conflict	UNP A0A849B394
H	209	SER	ASN	conflict	UNP A0A849B394
H	211	ASN	GLY	conflict	UNP A0A849B394
H	212	ALA	ASP	conflict	UNP A0A849B394
H	215	GLY	SER	conflict	UNP A0A849B394
H	221	ASN	ALA	conflict	UNP A0A849B394
H	234	ASP	GLU	conflict	UNP A0A849B394
H	239	TYR	PHE	conflict	UNP A0A849B394
H	247	GLY	ALA	conflict	UNP A0A849B394
H	248	SER	ASP	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
H	264	ASN	ALA	conflict	UNP A0A849B394
H	265	GLY	THR	conflict	UNP A0A849B394
H	281	VAL	LEU	conflict	UNP A0A849B394
H	282	THR	SER	conflict	UNP A0A849B394
H	284	THR	PRO	conflict	UNP A0A849B394
H	285	ALA	THR	conflict	UNP A0A849B394
H	286	GLY	-	insertion	UNP A0A849B394
H	287	THR	SER	conflict	UNP A0A849B394
H	319	ALA	SER	conflict	UNP A0A849B394
H	320	ASP	SER	conflict	UNP A0A849B394
h	59	LYS	ARG	conflict	UNP A0A849B394
h	196	THR	ALA	conflict	UNP A0A849B394
h	199	ASN	GLN	conflict	UNP A0A849B394
h	202	THR	GLY	conflict	UNP A0A849B394
h	206	THR	SER	conflict	UNP A0A849B394
h	208	SER	ALA	conflict	UNP A0A849B394
h	209	SER	ASN	conflict	UNP A0A849B394
h	211	ASN	GLY	conflict	UNP A0A849B394
h	212	ALA	ASP	conflict	UNP A0A849B394
h	215	GLY	SER	conflict	UNP A0A849B394
h	221	ASN	ALA	conflict	UNP A0A849B394
h	234	ASP	GLU	conflict	UNP A0A849B394
h	239	TYR	PHE	conflict	UNP A0A849B394
h	247	GLY	ALA	conflict	UNP A0A849B394
h	248	SER	ASP	conflict	UNP A0A849B394
h	264	ASN	ALA	conflict	UNP A0A849B394
h	265	GLY	THR	conflict	UNP A0A849B394
h	281	VAL	LEU	conflict	UNP A0A849B394
h	282	THR	SER	conflict	UNP A0A849B394
h	284	THR	PRO	conflict	UNP A0A849B394
h	285	ALA	THR	conflict	UNP A0A849B394
h	286	GLY	-	insertion	UNP A0A849B394
h	287	THR	SER	conflict	UNP A0A849B394
h	319	ALA	SER	conflict	UNP A0A849B394
h	320	ASP	SER	conflict	UNP A0A849B394
I	59	LYS	ARG	conflict	UNP A0A849B394
I	196	THR	ALA	conflict	UNP A0A849B394
I	199	ASN	GLN	conflict	UNP A0A849B394
I	202	THR	GLY	conflict	UNP A0A849B394
I	206	THR	SER	conflict	UNP A0A849B394
I	208	SER	ALA	conflict	UNP A0A849B394
I	209	SER	ASN	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	211	ASN	GLY	conflict	UNP A0A849B394
I	212	ALA	ASP	conflict	UNP A0A849B394
I	215	GLY	SER	conflict	UNP A0A849B394
I	221	ASN	ALA	conflict	UNP A0A849B394
I	234	ASP	GLU	conflict	UNP A0A849B394
I	239	TYR	PHE	conflict	UNP A0A849B394
I	247	GLY	ALA	conflict	UNP A0A849B394
I	248	SER	ASP	conflict	UNP A0A849B394
I	264	ASN	ALA	conflict	UNP A0A849B394
I	265	GLY	THR	conflict	UNP A0A849B394
I	281	VAL	LEU	conflict	UNP A0A849B394
I	282	THR	SER	conflict	UNP A0A849B394
I	284	THR	PRO	conflict	UNP A0A849B394
I	285	ALA	THR	conflict	UNP A0A849B394
I	286	GLY	-	insertion	UNP A0A849B394
I	287	THR	SER	conflict	UNP A0A849B394
I	319	ALA	SER	conflict	UNP A0A849B394
I	320	ASP	SER	conflict	UNP A0A849B394
i	59	LYS	ARG	conflict	UNP A0A849B394
i	196	THR	ALA	conflict	UNP A0A849B394
i	199	ASN	GLN	conflict	UNP A0A849B394
i	202	THR	GLY	conflict	UNP A0A849B394
i	206	THR	SER	conflict	UNP A0A849B394
i	208	SER	ALA	conflict	UNP A0A849B394
i	209	SER	ASN	conflict	UNP A0A849B394
i	211	ASN	GLY	conflict	UNP A0A849B394
i	212	ALA	ASP	conflict	UNP A0A849B394
i	215	GLY	SER	conflict	UNP A0A849B394
i	221	ASN	ALA	conflict	UNP A0A849B394
i	234	ASP	GLU	conflict	UNP A0A849B394
i	239	TYR	PHE	conflict	UNP A0A849B394
i	247	GLY	ALA	conflict	UNP A0A849B394
i	248	SER	ASP	conflict	UNP A0A849B394
i	264	ASN	ALA	conflict	UNP A0A849B394
i	265	GLY	THR	conflict	UNP A0A849B394
i	281	VAL	LEU	conflict	UNP A0A849B394
i	282	THR	SER	conflict	UNP A0A849B394
i	284	THR	PRO	conflict	UNP A0A849B394
i	285	ALA	THR	conflict	UNP A0A849B394
i	286	GLY	-	insertion	UNP A0A849B394
i	287	THR	SER	conflict	UNP A0A849B394
i	319	ALA	SER	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
i	320	ASP	SER	conflict	UNP A0A849B394
J	59	LYS	ARG	conflict	UNP A0A849B394
J	196	THR	ALA	conflict	UNP A0A849B394
J	199	ASN	GLN	conflict	UNP A0A849B394
J	202	THR	GLY	conflict	UNP A0A849B394
J	206	THR	SER	conflict	UNP A0A849B394
J	208	SER	ALA	conflict	UNP A0A849B394
J	209	SER	ASN	conflict	UNP A0A849B394
J	211	ASN	GLY	conflict	UNP A0A849B394
J	212	ALA	ASP	conflict	UNP A0A849B394
J	215	GLY	SER	conflict	UNP A0A849B394
J	221	ASN	ALA	conflict	UNP A0A849B394
J	234	ASP	GLU	conflict	UNP A0A849B394
J	239	TYR	PHE	conflict	UNP A0A849B394
J	247	GLY	ALA	conflict	UNP A0A849B394
J	248	SER	ASP	conflict	UNP A0A849B394
J	264	ASN	ALA	conflict	UNP A0A849B394
J	265	GLY	THR	conflict	UNP A0A849B394
J	281	VAL	LEU	conflict	UNP A0A849B394
J	282	THR	SER	conflict	UNP A0A849B394
J	284	THR	PRO	conflict	UNP A0A849B394
J	285	ALA	THR	conflict	UNP A0A849B394
J	286	GLY	-	insertion	UNP A0A849B394
J	287	THR	SER	conflict	UNP A0A849B394
J	319	ALA	SER	conflict	UNP A0A849B394
J	320	ASP	SER	conflict	UNP A0A849B394
j	59	LYS	ARG	conflict	UNP A0A849B394
j	196	THR	ALA	conflict	UNP A0A849B394
j	199	ASN	GLN	conflict	UNP A0A849B394
j	202	THR	GLY	conflict	UNP A0A849B394
j	206	THR	SER	conflict	UNP A0A849B394
j	208	SER	ALA	conflict	UNP A0A849B394
j	209	SER	ASN	conflict	UNP A0A849B394
j	211	ASN	GLY	conflict	UNP A0A849B394
j	212	ALA	ASP	conflict	UNP A0A849B394
j	215	GLY	SER	conflict	UNP A0A849B394
j	221	ASN	ALA	conflict	UNP A0A849B394
j	234	ASP	GLU	conflict	UNP A0A849B394
j	239	TYR	PHE	conflict	UNP A0A849B394
j	247	GLY	ALA	conflict	UNP A0A849B394
j	248	SER	ASP	conflict	UNP A0A849B394
j	264	ASN	ALA	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
j	265	GLY	THR	conflict	UNP A0A849B394
j	281	VAL	LEU	conflict	UNP A0A849B394
j	282	THR	SER	conflict	UNP A0A849B394
j	284	THR	PRO	conflict	UNP A0A849B394
j	285	ALA	THR	conflict	UNP A0A849B394
j	286	GLY	-	insertion	UNP A0A849B394
j	287	THR	SER	conflict	UNP A0A849B394
j	319	ALA	SER	conflict	UNP A0A849B394
j	320	ASP	SER	conflict	UNP A0A849B394
K	59	LYS	ARG	conflict	UNP A0A849B394
K	196	THR	ALA	conflict	UNP A0A849B394
K	199	ASN	GLN	conflict	UNP A0A849B394
K	202	THR	GLY	conflict	UNP A0A849B394
K	206	THR	SER	conflict	UNP A0A849B394
K	208	SER	ALA	conflict	UNP A0A849B394
K	209	SER	ASN	conflict	UNP A0A849B394
K	211	ASN	GLY	conflict	UNP A0A849B394
K	212	ALA	ASP	conflict	UNP A0A849B394
K	215	GLY	SER	conflict	UNP A0A849B394
K	221	ASN	ALA	conflict	UNP A0A849B394
K	234	ASP	GLU	conflict	UNP A0A849B394
K	239	TYR	PHE	conflict	UNP A0A849B394
K	247	GLY	ALA	conflict	UNP A0A849B394
K	248	SER	ASP	conflict	UNP A0A849B394
K	264	ASN	ALA	conflict	UNP A0A849B394
K	265	GLY	THR	conflict	UNP A0A849B394
K	281	VAL	LEU	conflict	UNP A0A849B394
K	282	THR	SER	conflict	UNP A0A849B394
K	284	THR	PRO	conflict	UNP A0A849B394
K	285	ALA	THR	conflict	UNP A0A849B394
K	286	GLY	-	insertion	UNP A0A849B394
K	287	THR	SER	conflict	UNP A0A849B394
K	319	ALA	SER	conflict	UNP A0A849B394
K	320	ASP	SER	conflict	UNP A0A849B394
k	59	LYS	ARG	conflict	UNP A0A849B394
k	196	THR	ALA	conflict	UNP A0A849B394
k	199	ASN	GLN	conflict	UNP A0A849B394
k	202	THR	GLY	conflict	UNP A0A849B394
k	206	THR	SER	conflict	UNP A0A849B394
k	208	SER	ALA	conflict	UNP A0A849B394
k	209	SER	ASN	conflict	UNP A0A849B394
k	211	ASN	GLY	conflict	UNP A0A849B394

Continued on next page...

Continued from previous page...

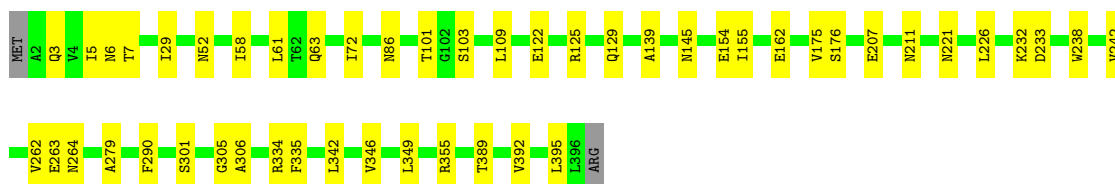
Chain	Residue	Modelled	Actual	Comment	Reference
k	212	ALA	ASP	conflict	UNP A0A849B394
k	215	GLY	SER	conflict	UNP A0A849B394
k	221	ASN	ALA	conflict	UNP A0A849B394
k	234	ASP	GLU	conflict	UNP A0A849B394
k	239	TYR	PHE	conflict	UNP A0A849B394
k	247	GLY	ALA	conflict	UNP A0A849B394
k	248	SER	ASP	conflict	UNP A0A849B394
k	264	ASN	ALA	conflict	UNP A0A849B394
k	265	GLY	THR	conflict	UNP A0A849B394
k	281	VAL	LEU	conflict	UNP A0A849B394
k	282	THR	SER	conflict	UNP A0A849B394
k	284	THR	PRO	conflict	UNP A0A849B394
k	285	ALA	THR	conflict	UNP A0A849B394
k	286	GLY	-	insertion	UNP A0A849B394
k	287	THR	SER	conflict	UNP A0A849B394
k	319	ALA	SER	conflict	UNP A0A849B394
k	320	ASP	SER	conflict	UNP A0A849B394

3 Residue-property plots [i](#)

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.

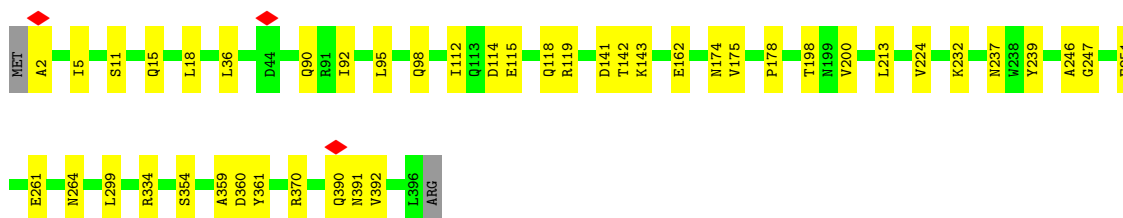
- Molecule 1: Flagellin

Chain A: 



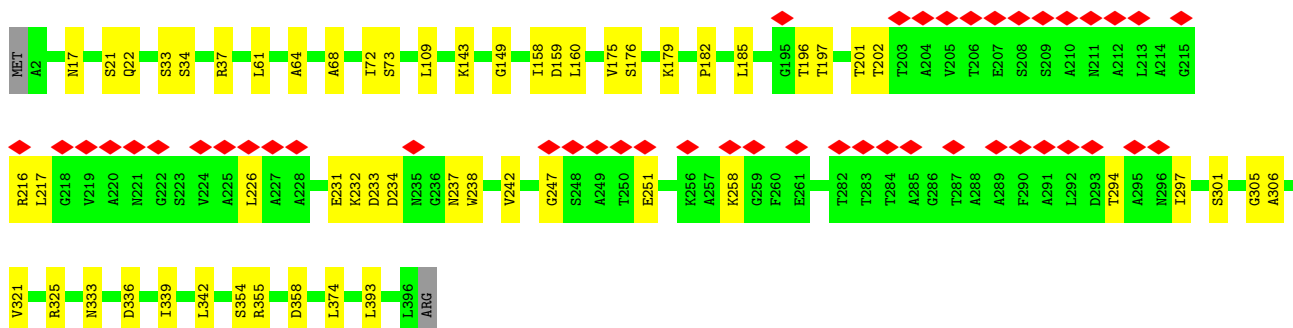
- Molecule 1: Flagellin

Chain a: 

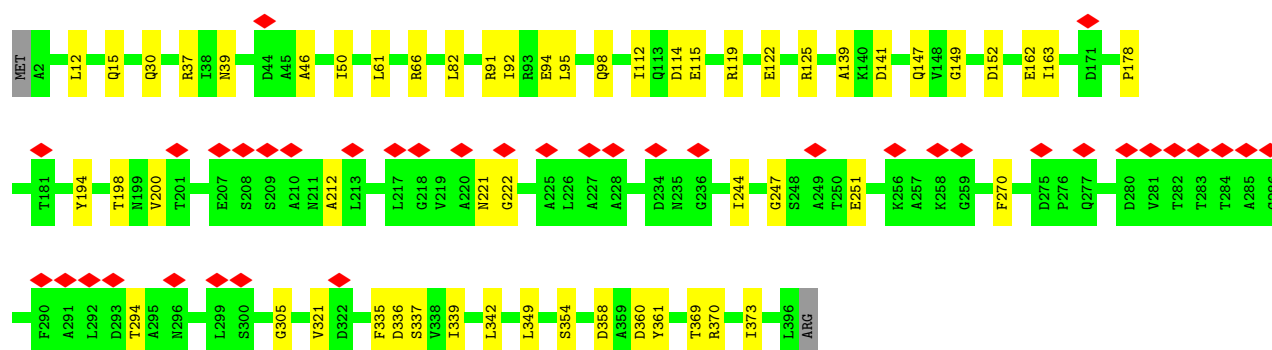
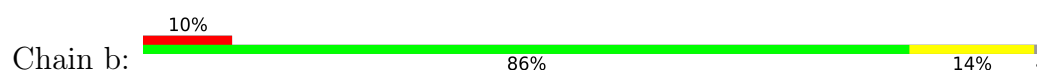


- Molecule 1: Flagellin

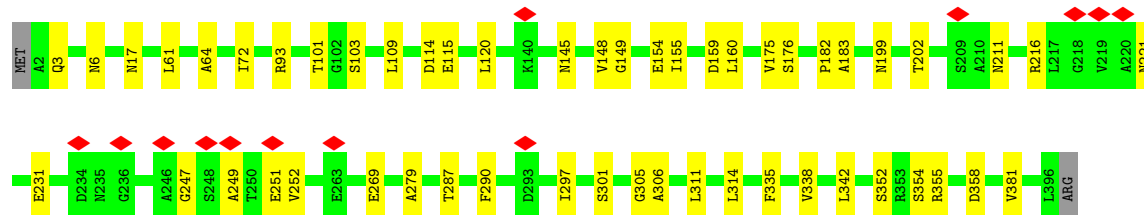
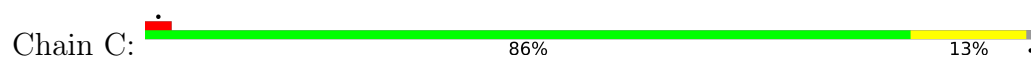
Chain B: 



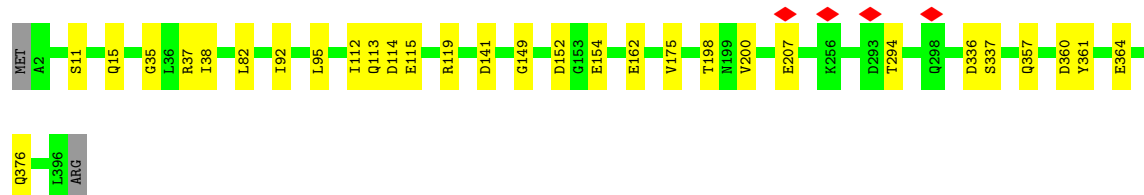
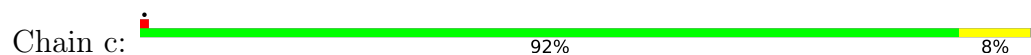
- Molecule 1: Flagellin



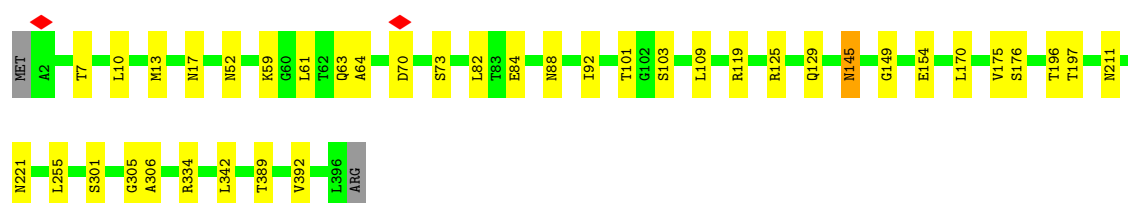
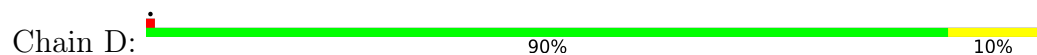
• Molecule 1: Flagellin



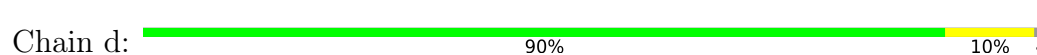
• Molecule 1: Flagellin

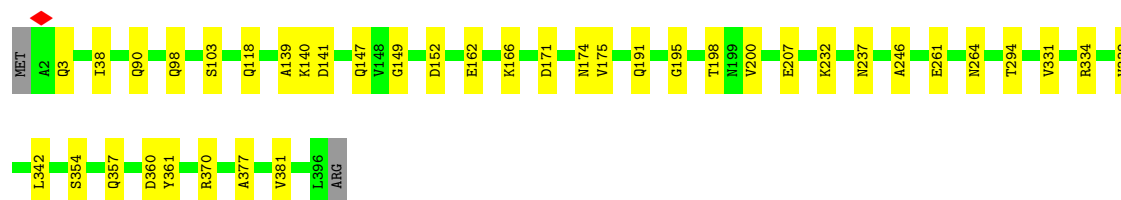


• Molecule 1: Flagellin



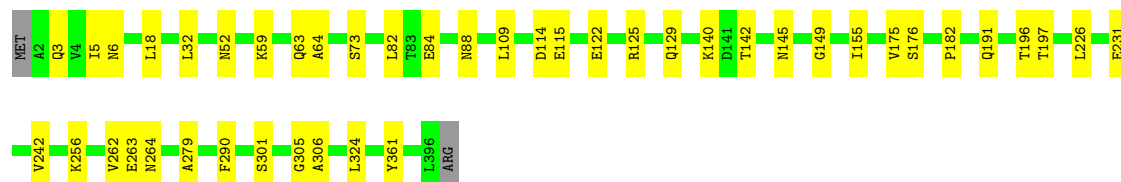
• Molecule 1: Flagellin





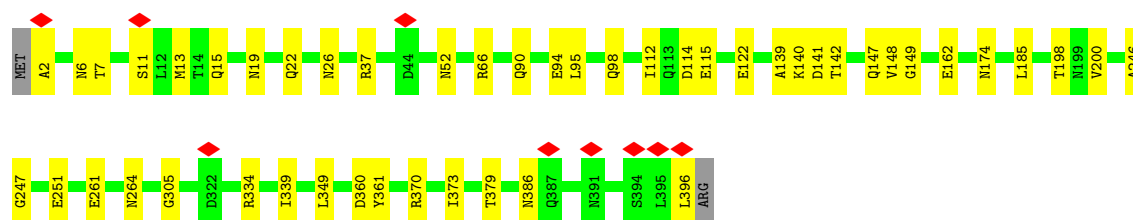
• Molecule 1: Flagellin

Chain E: 88% 11%



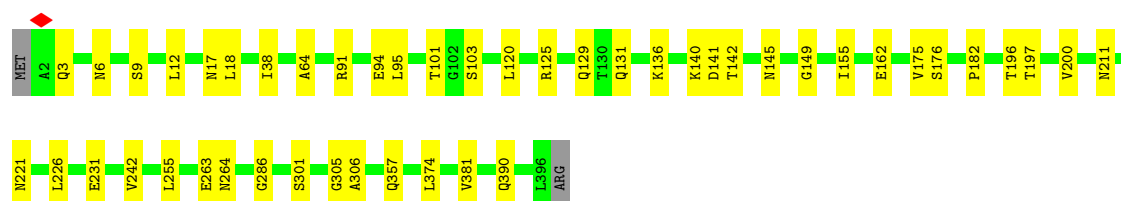
• Molecule 1: Flagellin

Chain e: 87% 12%



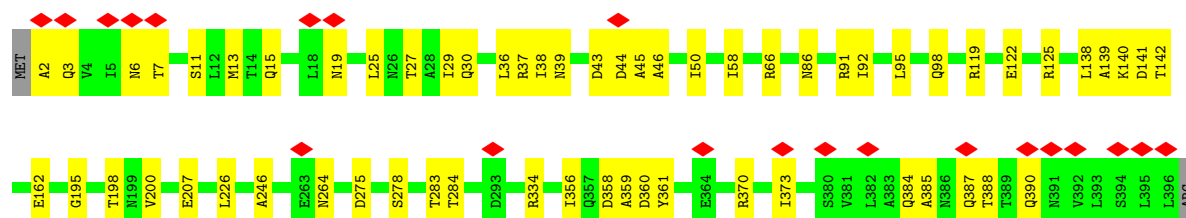
• Molecule 1: Flagellin

Chain F: 88% 12%



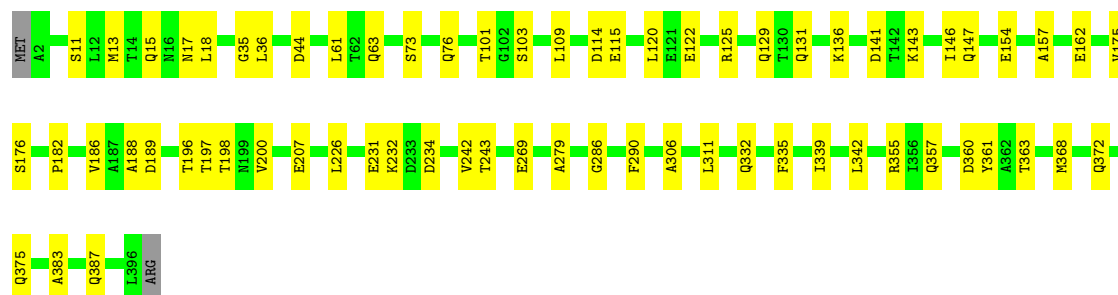
• Molecule 1: Flagellin

Chain f: 5% 84% 15%



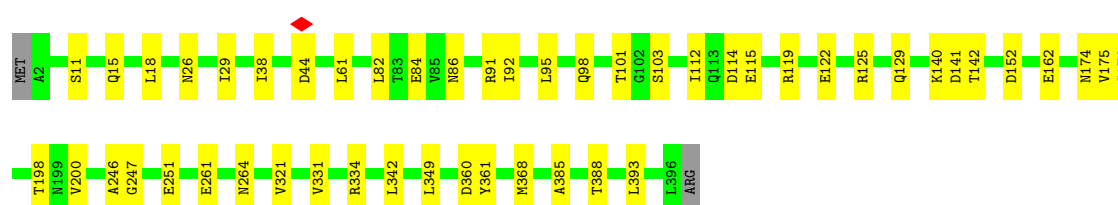
- Molecule 1: Flagellin

Chain G:  83% 17%



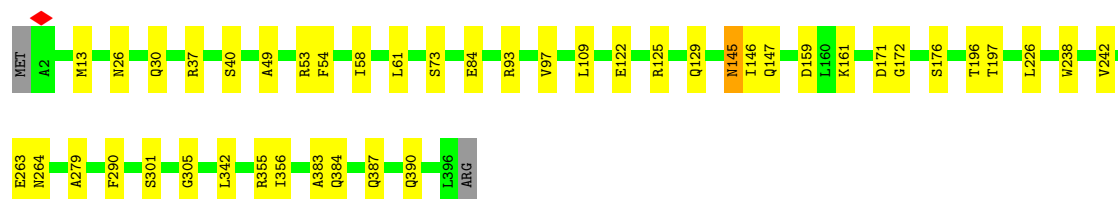
- Molecule 1: Flagellin

Chain g:  87% 13%



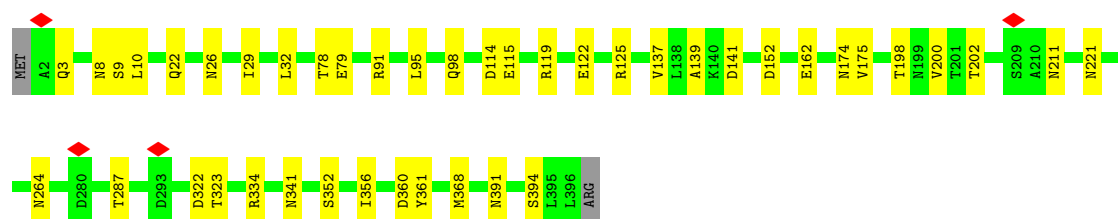
- Molecule 1: Flagellin

Chain H:  88% 11%



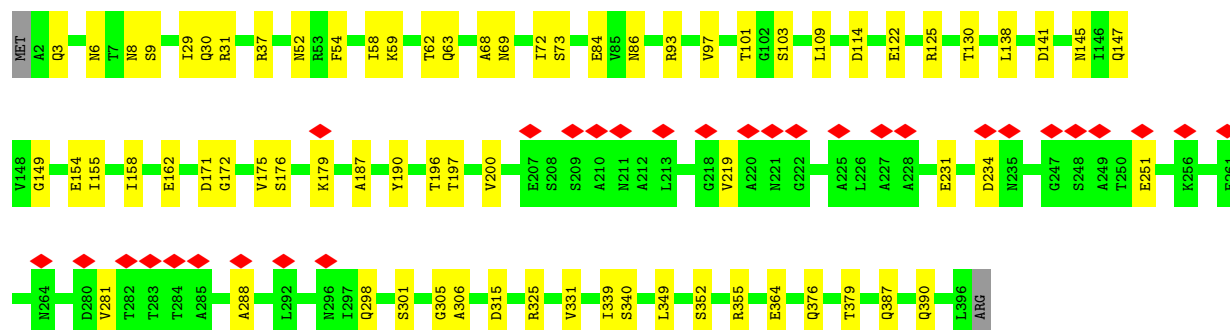
- Molecule 1: Flagellin

Chain h:  88% 11%

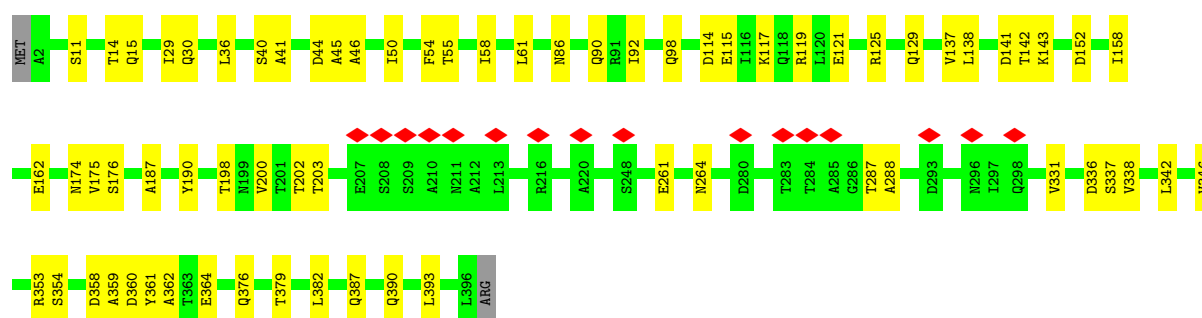
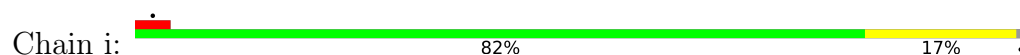


- Molecule 1: Flagellin

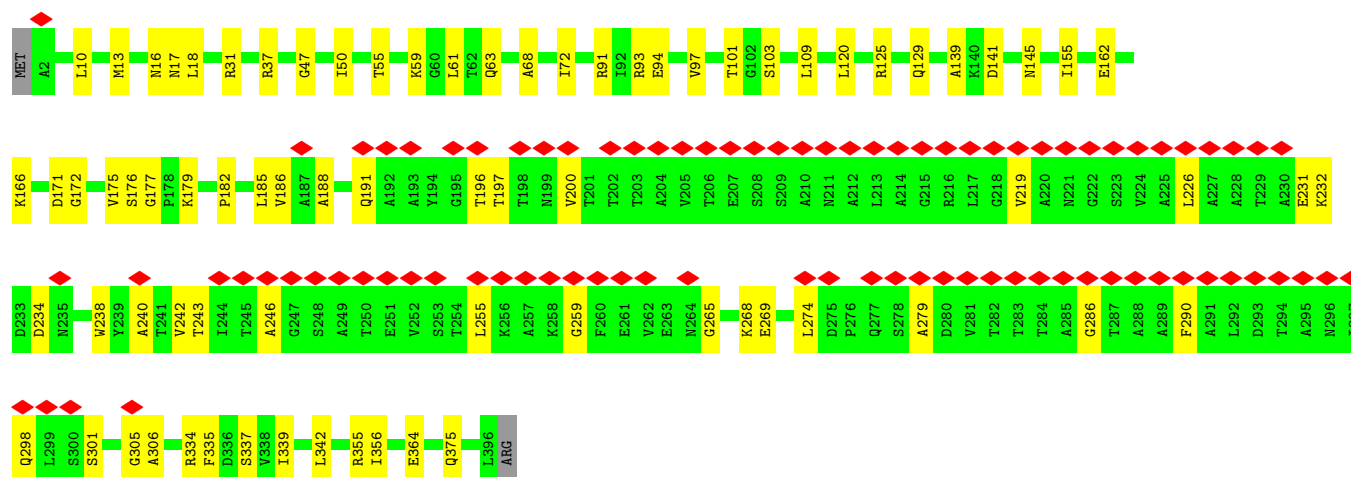
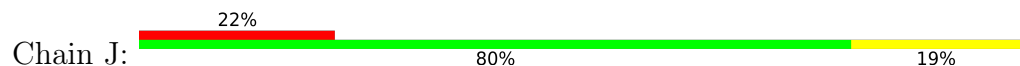
Chain I:  8% 82% 18%



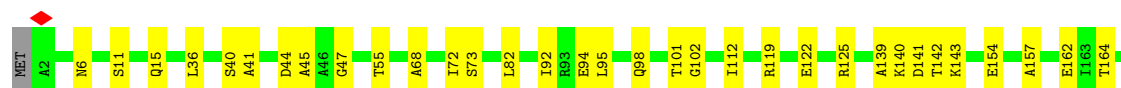
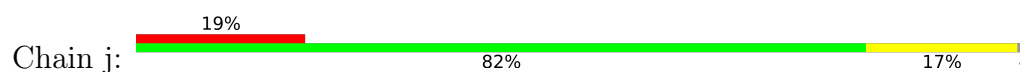
• Molecule 1: Flagellin

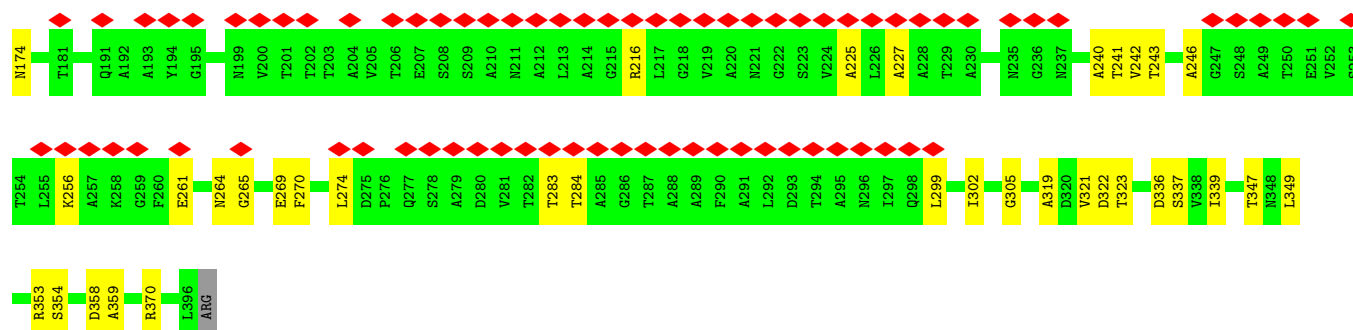


• Molecule 1: Flagellin

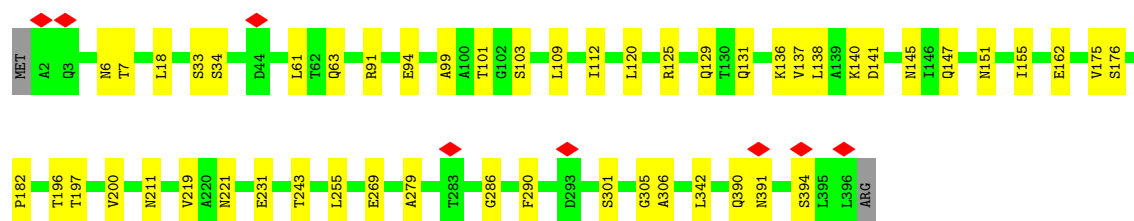
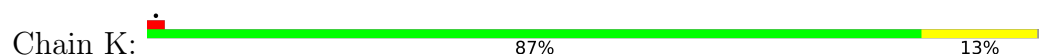


• Molecule 1: Flagellin

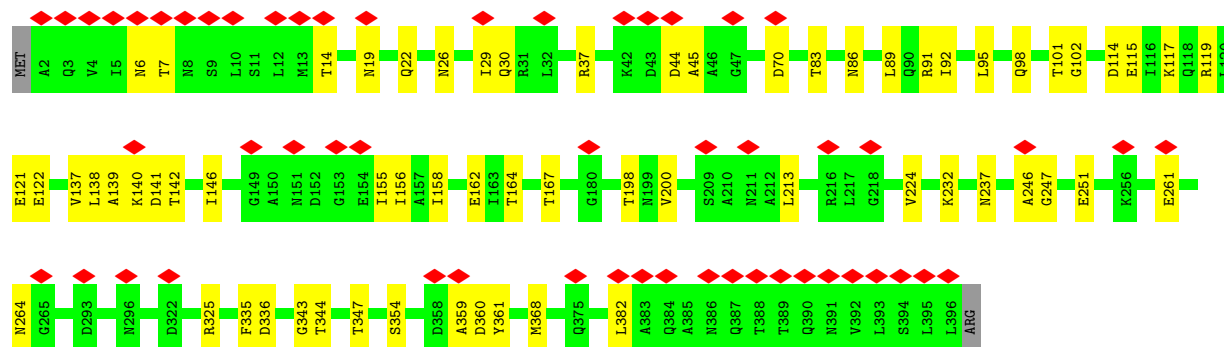
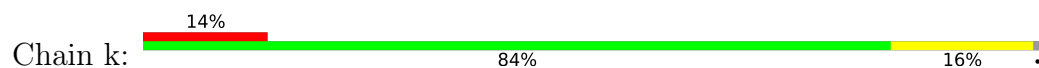




• Molecule 1: Flagellin



• Molecule 1: Flagellin



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-0.61°, rise=110.25 Å, axial sym=C1	Depositor
Number of segments used	223582	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.951	Depositor
Minimum map value	-0.479	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.215	Depositor
Map size (Å)	710.4, 710.4, 710.4	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.11, 1.11, 1.11	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	0.42	0/2895	0.52	0/3938
1	B	0.35	0/2895	0.48	0/3938
1	C	0.37	0/2895	0.51	0/3938
1	D	0.41	0/2895	0.51	0/3938
1	E	0.43	0/2895	0.55	0/3938
1	F	0.41	0/2895	0.53	0/3938
1	G	0.38	0/2895	0.51	0/3938
1	H	0.34	0/2895	0.48	0/3938
1	I	0.32	0/2895	0.48	0/3938
1	J	0.33	0/2895	0.50	0/3938
1	K	0.36	0/2895	0.53	0/3938
1	a	0.38	0/2895	0.48	0/3938
1	b	0.37	0/2895	0.53	0/3938
1	c	0.40	0/2895	0.53	0/3938
1	d	0.41	0/2895	0.51	0/3938
1	e	0.37	0/2895	0.49	0/3938
1	f	0.34	0/2895	0.48	1/3938 (0.0%)
1	g	0.39	0/2895	0.50	0/3938
1	h	0.38	0/2895	0.50	0/3938
1	i	0.35	0/2895	0.49	0/3938
1	j	0.35	0/2895	0.52	0/3938
1	k	0.30	0/2895	0.47	0/3938
All	All	0.37	0/63690	0.50	1/86636 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	f	58	ILE	N-CA-C	5.30	115.51	110.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2878	0	2869	37	0
1	B	2878	0	2869	37	0
1	C	2878	0	2869	37	0
1	D	2878	0	2869	29	0
1	E	2878	0	2869	36	0
1	F	2878	0	2869	35	0
1	G	2878	0	2869	40	0
1	H	2878	0	2869	29	0
1	I	2878	0	2869	57	0
1	J	2878	0	2869	54	0
1	K	2878	0	2869	33	0
1	a	2878	0	2869	29	0
1	b	2878	0	2869	33	0
1	c	2878	0	2869	21	0
1	d	2878	0	2869	27	0
1	e	2878	0	2869	41	0
1	f	2878	0	2869	43	0
1	g	2878	0	2869	34	0
1	h	2878	0	2869	29	0
1	i	2878	0	2869	48	0
1	j	2878	0	2869	43	0
1	k	2878	0	2869	45	0
All	All	63316	0	63118	722	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 6.

The worst 5 of 722 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:K:61:LEU:HD22	1:K:342:LEU:HD11	1.55	0.89
1:h:139:ALA:HA	1:h:162:GLU:HG2	1.53	0.88
1:J:246:ALA:HB3	1:J:265:GLY:H	1.43	0.83
1:E:3:GLN:HE22	1:F:18:LEU:HD21	1.44	0.82
1:I:30:GLN:HG2	1:J:13:MET:HE2	1.65	0.79

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	393/397 (99%)	372 (95%)	21 (5%)	0	100	100
1	B	393/397 (99%)	376 (96%)	17 (4%)	0	100	100
1	C	393/397 (99%)	379 (96%)	14 (4%)	0	100	100
1	D	393/397 (99%)	371 (94%)	22 (6%)	0	100	100
1	E	393/397 (99%)	372 (95%)	21 (5%)	0	100	100
1	F	393/397 (99%)	369 (94%)	24 (6%)	0	100	100
1	G	393/397 (99%)	376 (96%)	17 (4%)	0	100	100
1	H	393/397 (99%)	372 (95%)	21 (5%)	0	100	100
1	I	393/397 (99%)	373 (95%)	20 (5%)	0	100	100
1	J	393/397 (99%)	376 (96%)	17 (4%)	0	100	100
1	K	393/397 (99%)	373 (95%)	20 (5%)	0	100	100
1	a	393/397 (99%)	384 (98%)	9 (2%)	0	100	100
1	b	393/397 (99%)	378 (96%)	15 (4%)	0	100	100
1	c	393/397 (99%)	377 (96%)	16 (4%)	0	100	100
1	d	393/397 (99%)	379 (96%)	14 (4%)	0	100	100
1	e	393/397 (99%)	382 (97%)	11 (3%)	0	100	100
1	f	393/397 (99%)	378 (96%)	15 (4%)	0	100	100
1	g	393/397 (99%)	379 (96%)	14 (4%)	0	100	100
1	h	393/397 (99%)	384 (98%)	9 (2%)	0	100	100
1	i	393/397 (99%)	379 (96%)	14 (4%)	0	100	100
1	j	393/397 (99%)	377 (96%)	16 (4%)	0	100	100
1	k	393/397 (99%)	380 (97%)	13 (3%)	0	100	100
All	All	8646/8734 (99%)	8286 (96%)	360 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	309/311 (99%)	309 (100%)	0	100	100
1	B	309/311 (99%)	309 (100%)	0	100	100
1	C	309/311 (99%)	308 (100%)	1 (0%)	86	84
1	D	309/311 (99%)	308 (100%)	1 (0%)	86	84
1	E	309/311 (99%)	309 (100%)	0	100	100
1	F	309/311 (99%)	309 (100%)	0	100	100
1	G	309/311 (99%)	309 (100%)	0	100	100
1	H	309/311 (99%)	308 (100%)	1 (0%)	86	84
1	I	309/311 (99%)	309 (100%)	0	100	100
1	J	309/311 (99%)	309 (100%)	0	100	100
1	K	309/311 (99%)	309 (100%)	0	100	100
1	a	309/311 (99%)	309 (100%)	0	100	100
1	b	309/311 (99%)	309 (100%)	0	100	100
1	c	309/311 (99%)	309 (100%)	0	100	100
1	d	309/311 (99%)	309 (100%)	0	100	100
1	e	309/311 (99%)	309 (100%)	0	100	100
1	f	309/311 (99%)	309 (100%)	0	100	100
1	g	309/311 (99%)	309 (100%)	0	100	100
1	h	309/311 (99%)	309 (100%)	0	100	100
1	i	309/311 (99%)	309 (100%)	0	100	100
1	j	309/311 (99%)	309 (100%)	0	100	100
1	k	309/311 (99%)	309 (100%)	0	100	100
All	All	6798/6842 (99%)	6795 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	199	ASN
1	D	145	ASN
1	H	145	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	63	GLN
1	h	86	ASN
1	K	387	GLN
1	G	357	GLN
1	H	63	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 [i](#)

There are no chain breaks in this entry.

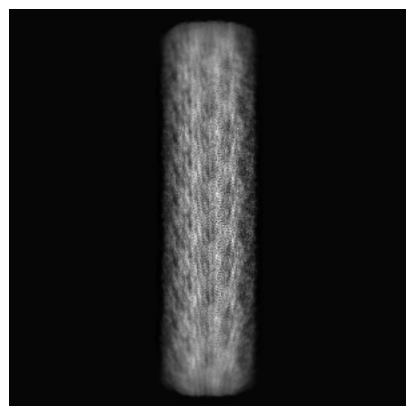
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43829. These allow visual inspection of the internal detail of the map and identification of artifacts.

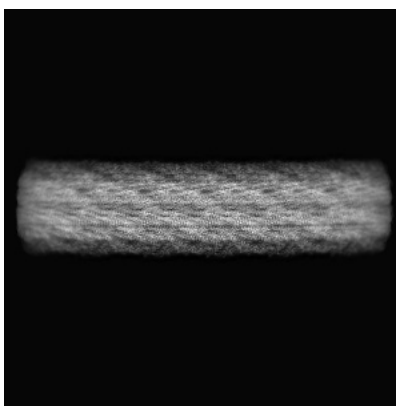
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

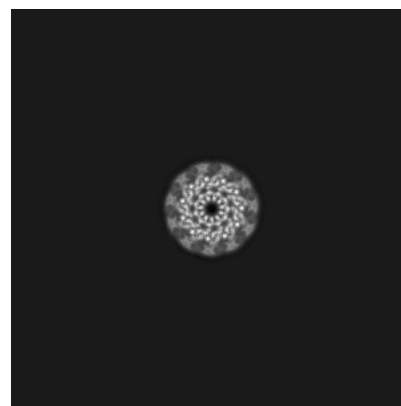
6.1.1 Primary map



X

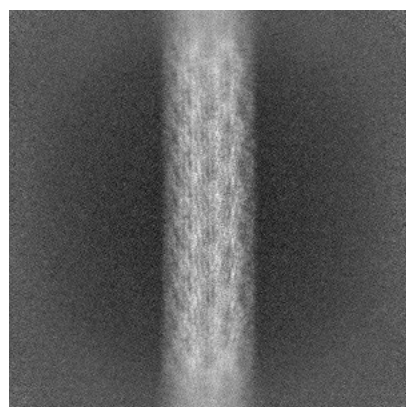


Y

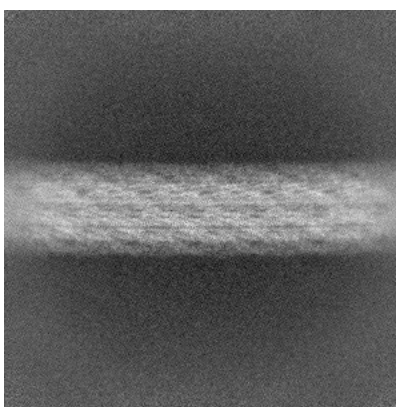


Z

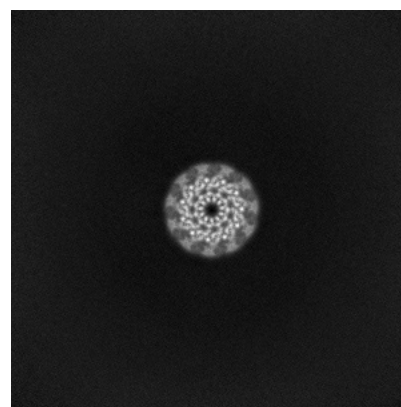
6.1.2 Raw map



X



Y

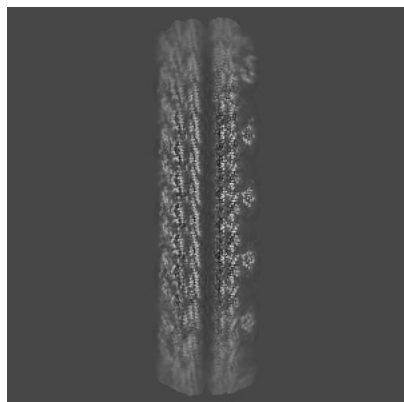


Z

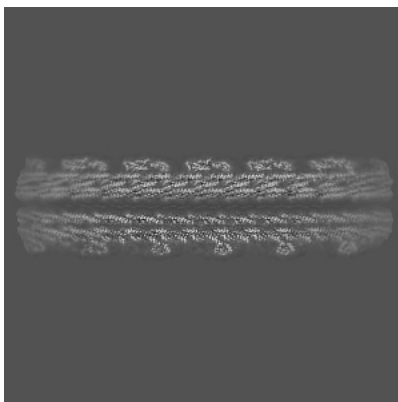
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

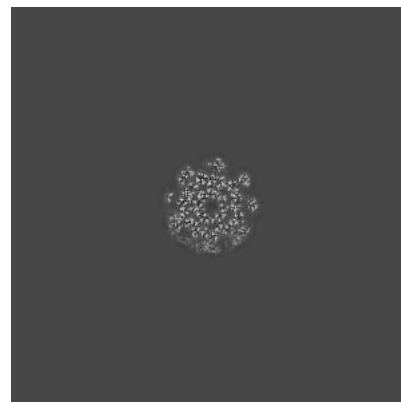
6.2.1 Primary map



X Index: 320

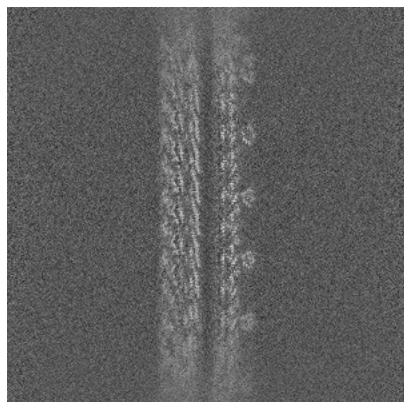


Y Index: 320

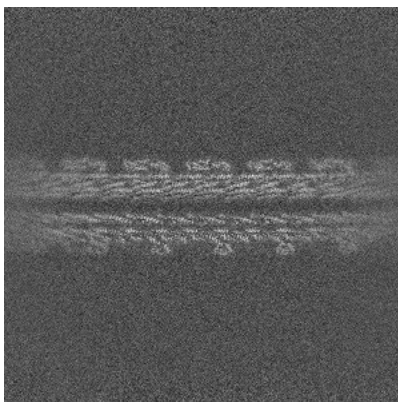


Z Index: 320

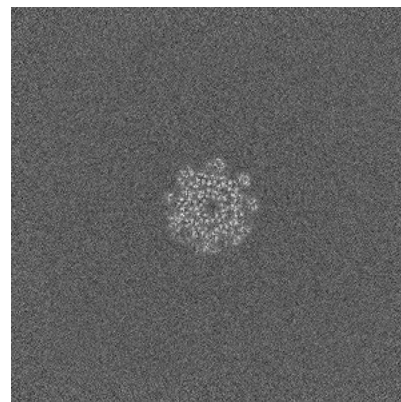
6.2.2 Raw map



X Index: 320



Y Index: 320

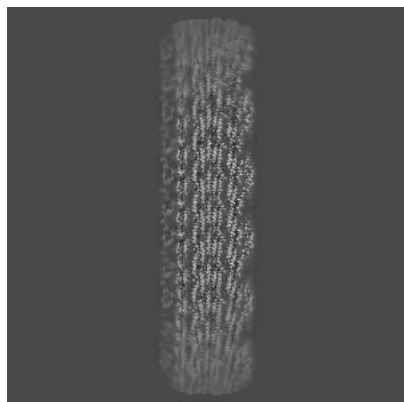


Z Index: 320

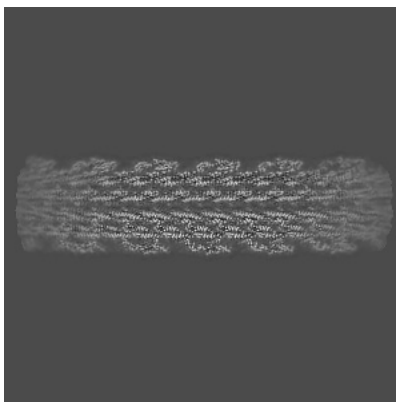
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

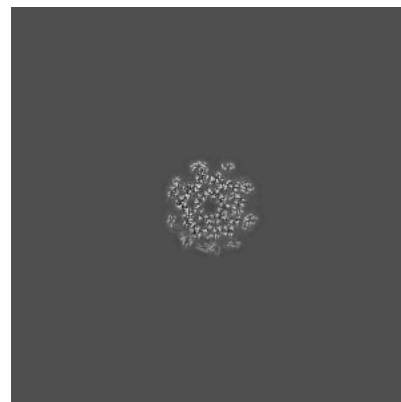
6.3.1 Primary map



X Index: 304

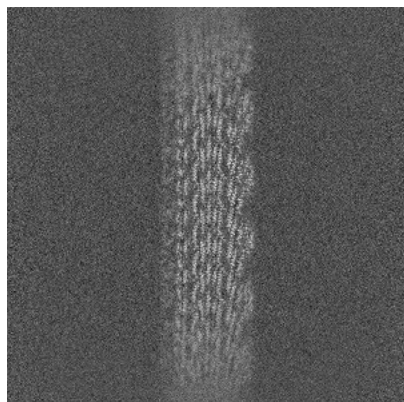


Y Index: 331

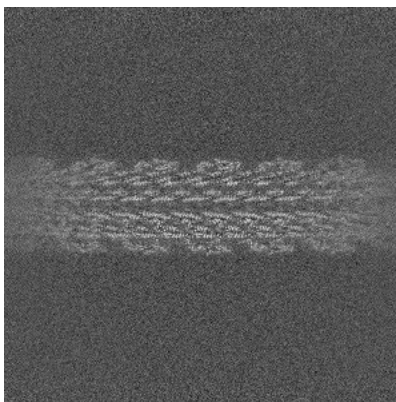


Z Index: 284

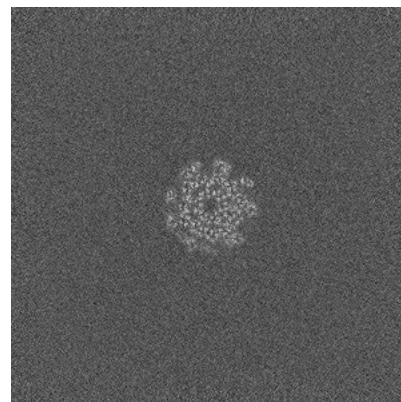
6.3.2 Raw map



X Index: 304



Y Index: 331

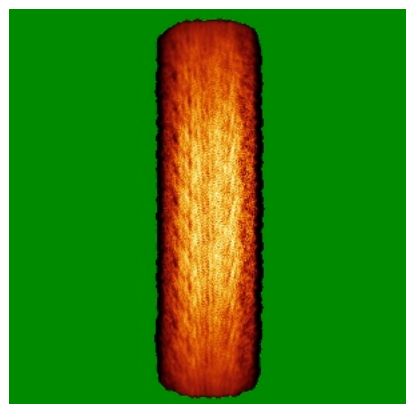


Z Index: 306

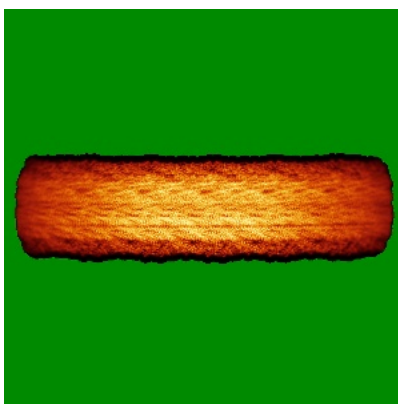
The images above show the largest variance slices of the map in three orthogonal directions.

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

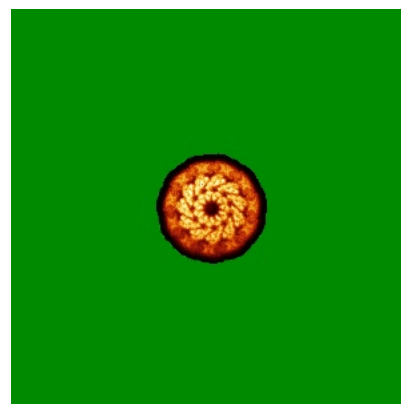
6.4.1 Primary map



X

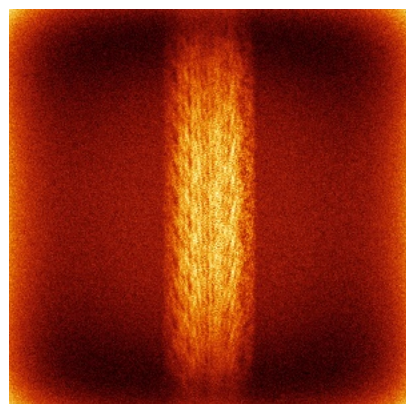


Y

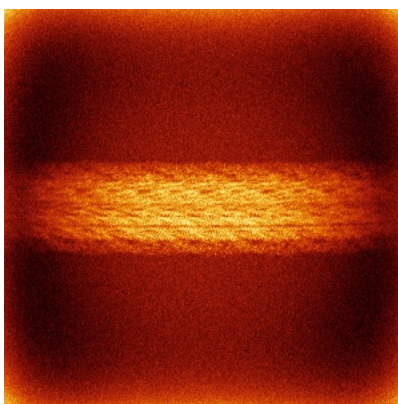


Z

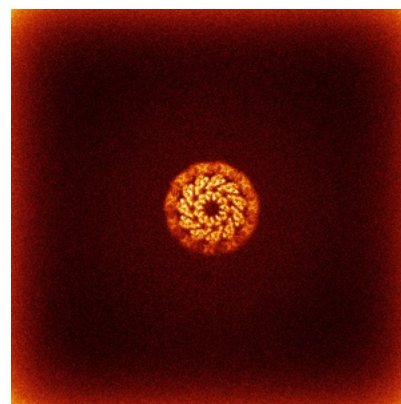
6.4.2 Raw map



X



Y

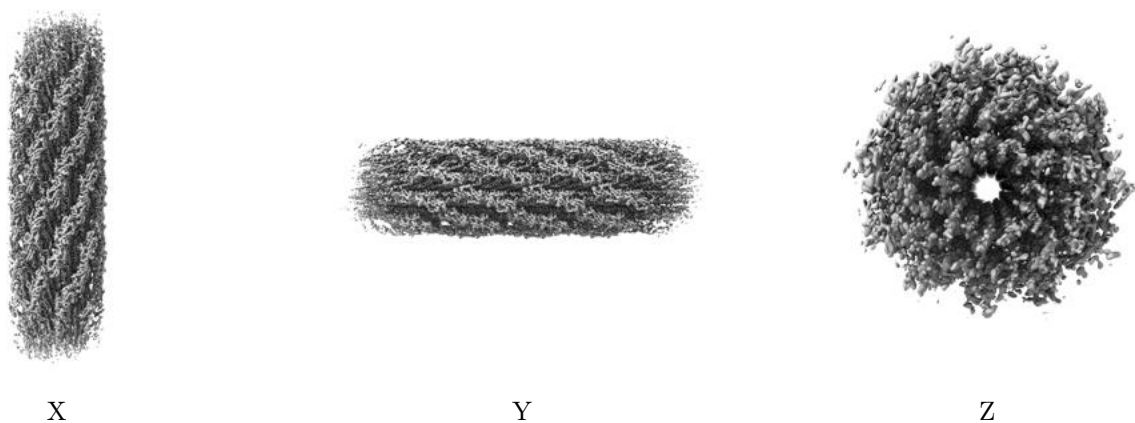


Z

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.

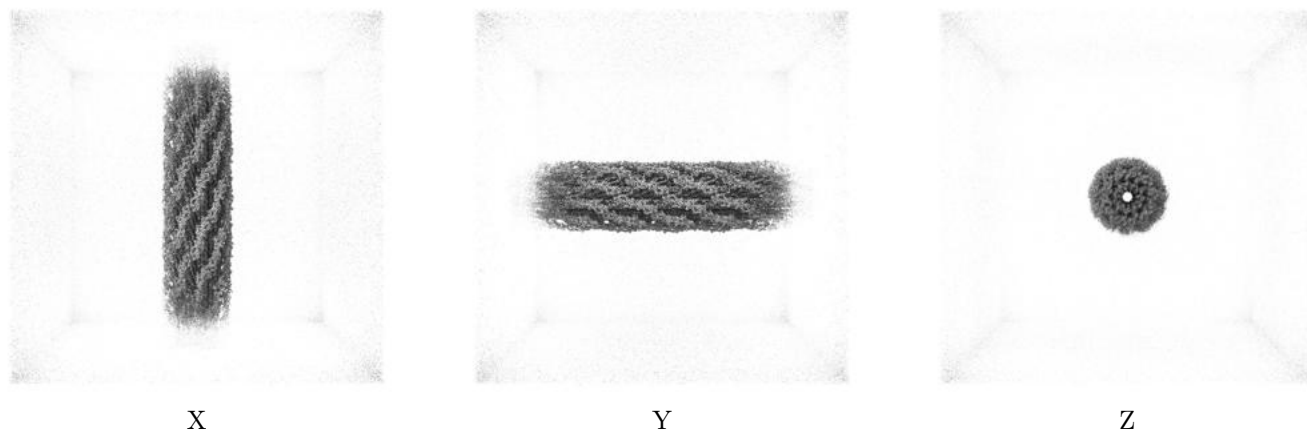
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.215. 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.

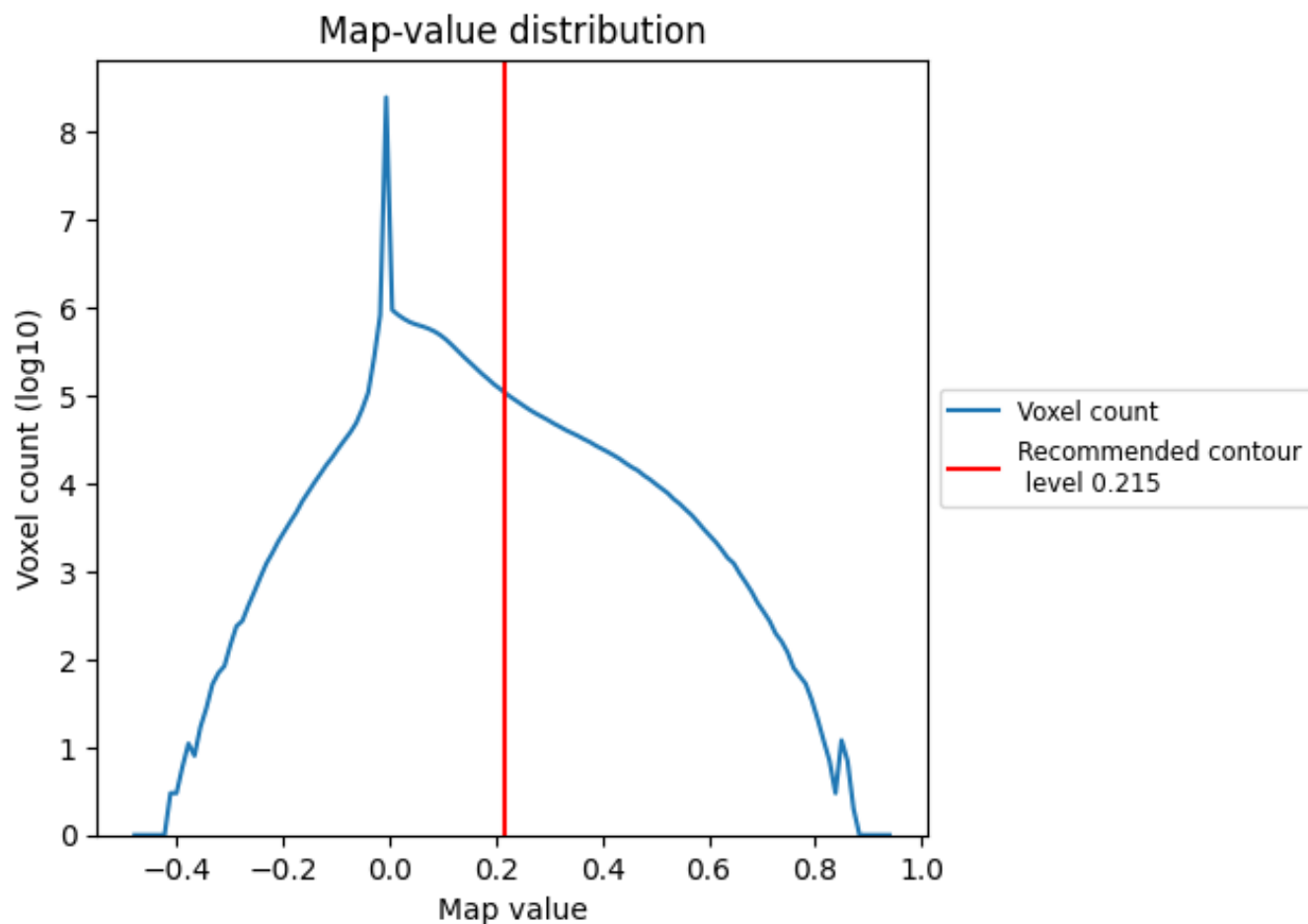
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

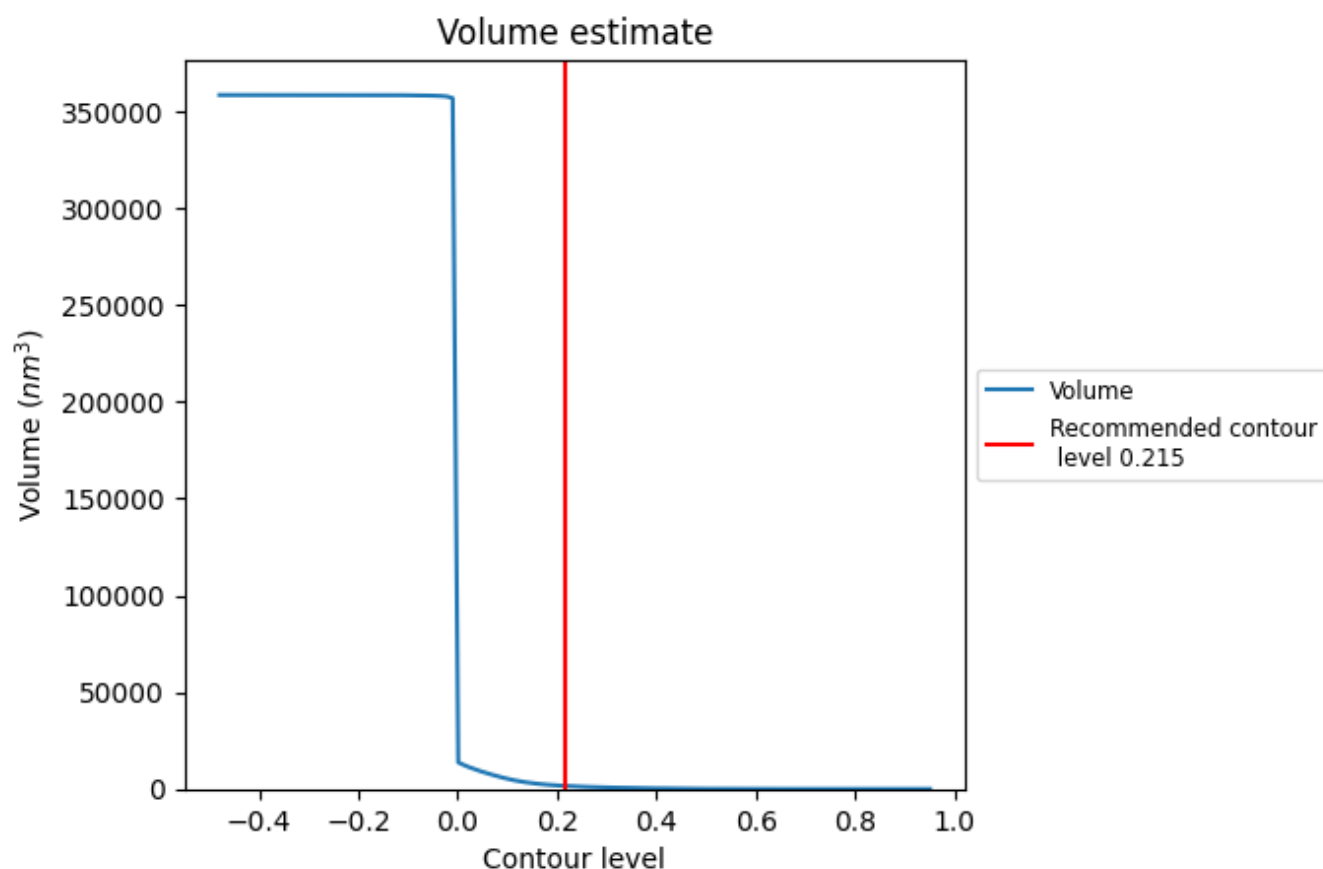
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

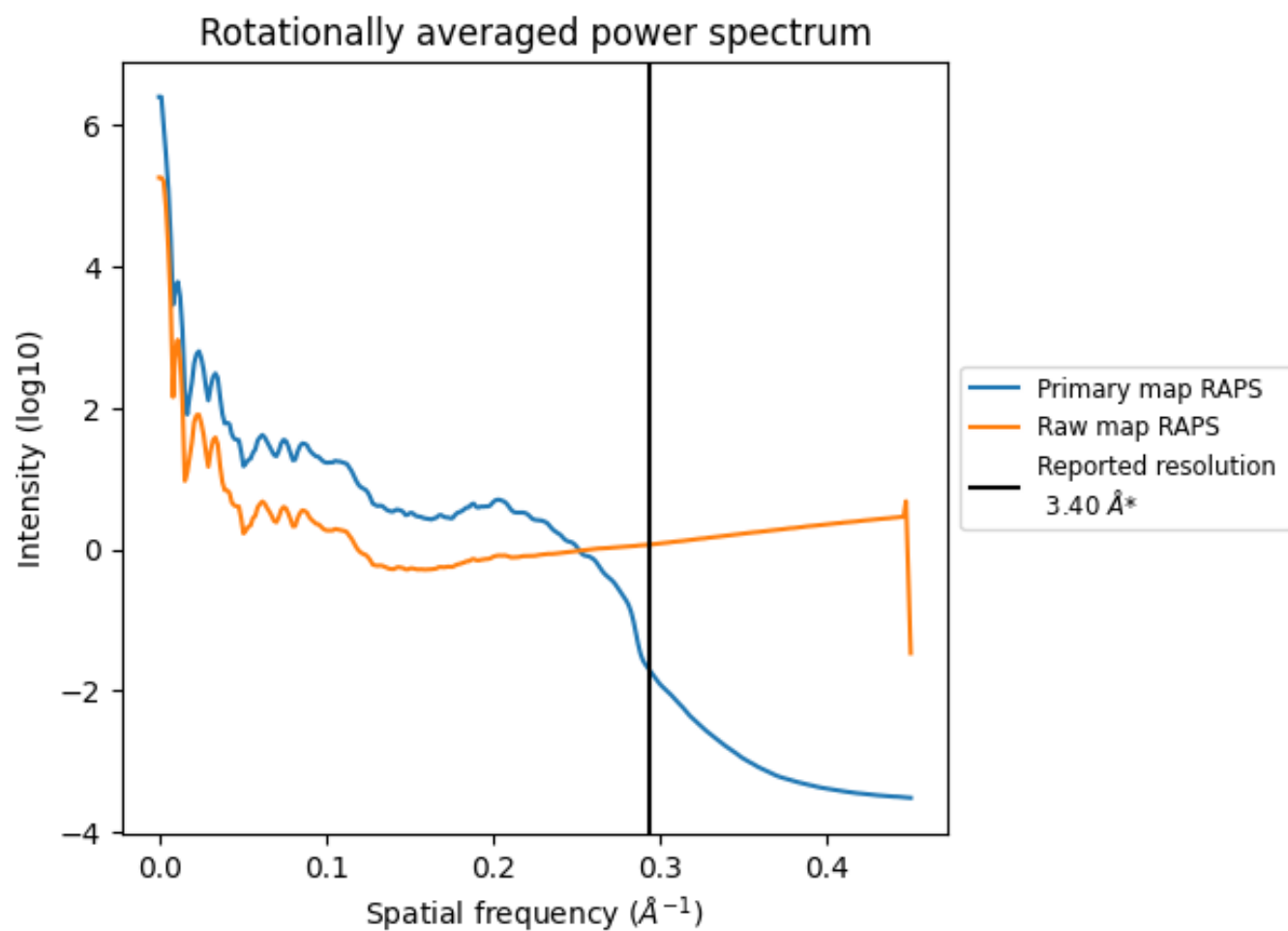
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1598 nm^3 ; this corresponds to an approximate mass of 1443 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

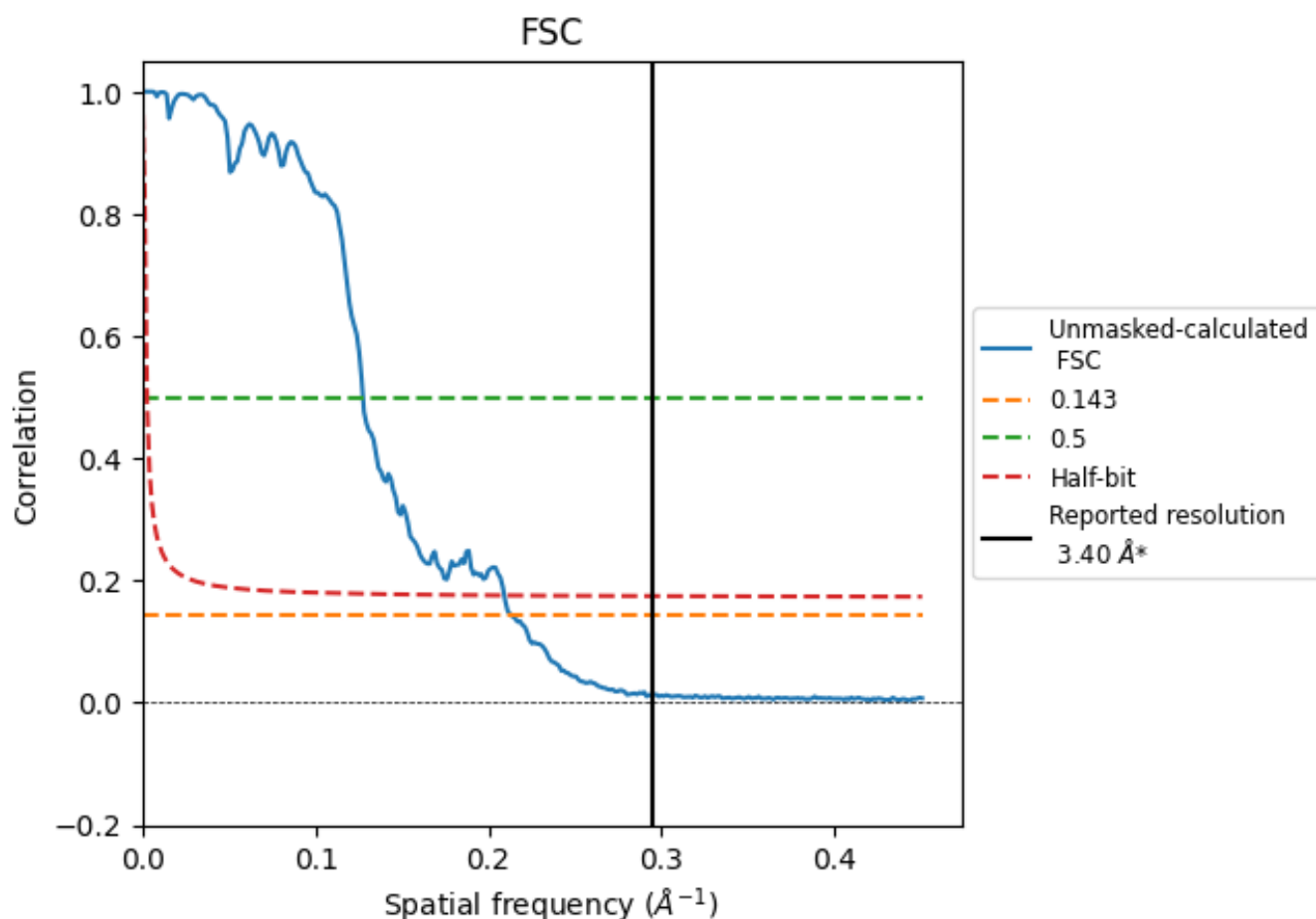


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

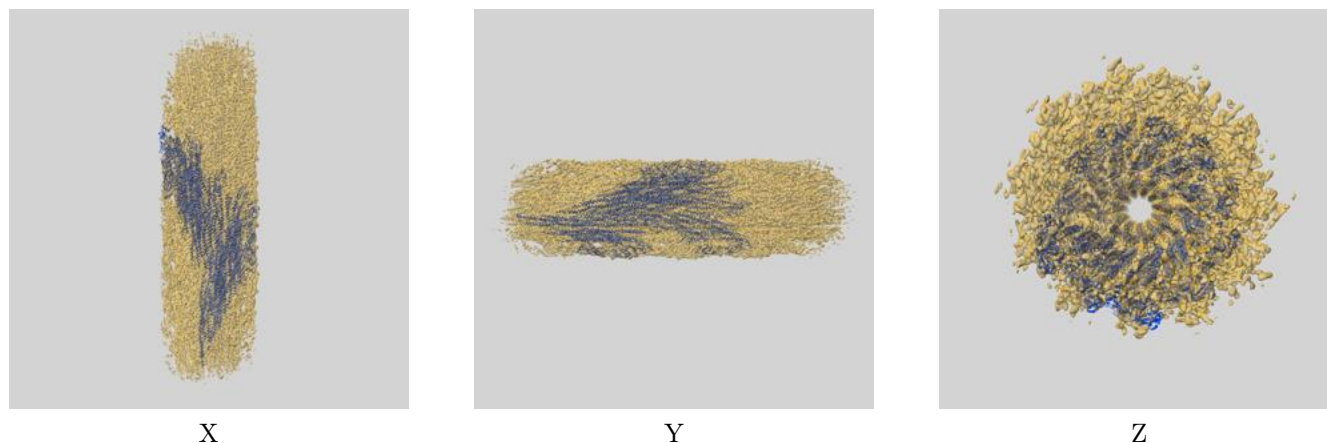
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.69	7.84	4.78

*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 4.69 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

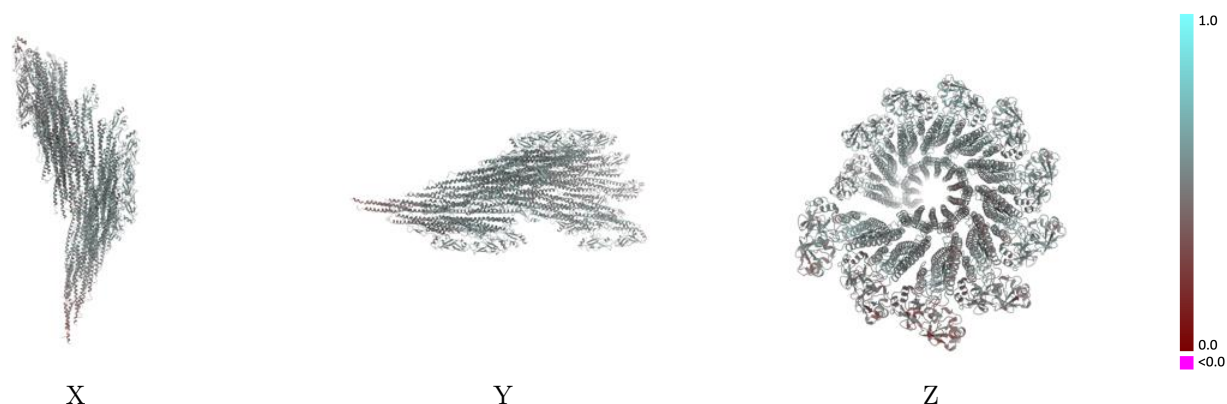
This section contains information regarding the fit between EMDB map EMD-43829 and PDB model 9ATB. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



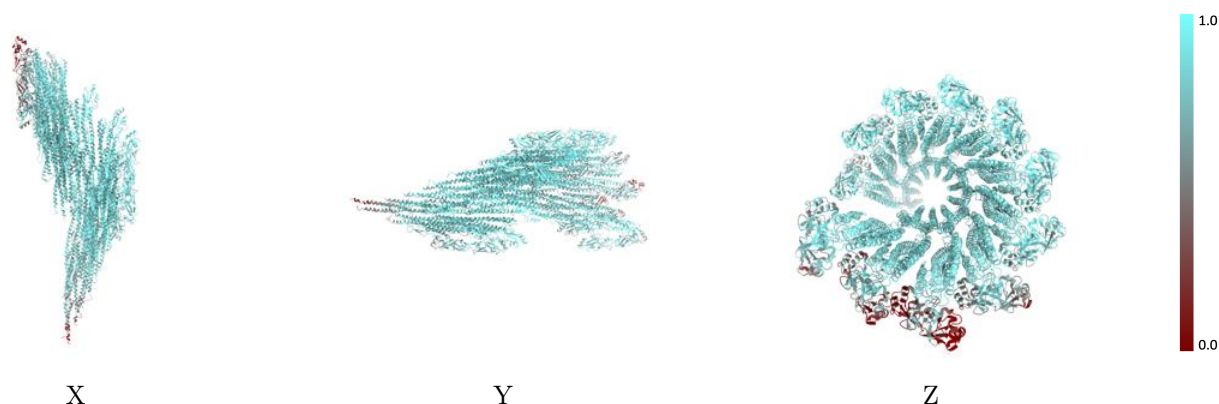
The images above show the 3D surface view of the map at the recommended contour level 0.215 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



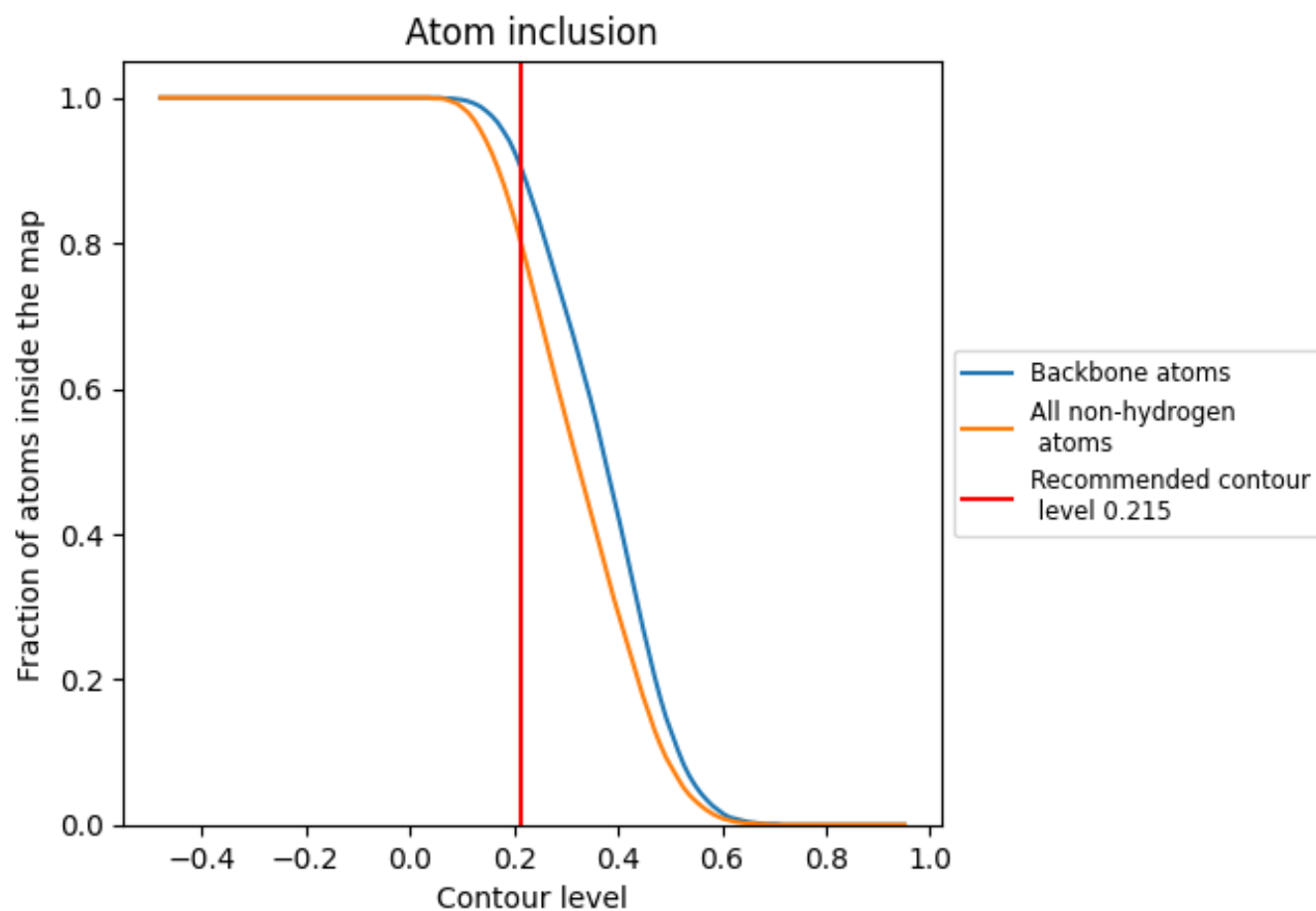
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.215).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 80% 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 (0.215) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7960	 0.5070
A	 0.8960	 0.5450
B	 0.7450	 0.4980
C	 0.8030	 0.5120
D	 0.8760	 0.5330
E	 0.8810	 0.5340
F	 0.8530	 0.5320
G	 0.8530	 0.5200
H	 0.8230	 0.5020
I	 0.7530	 0.4850
J	 0.6600	 0.4680
K	 0.8070	 0.5140
a	 0.8410	 0.5280
b	 0.7530	 0.4990
c	 0.8110	 0.5180
d	 0.8490	 0.5260
e	 0.8100	 0.5090
f	 0.7380	 0.4940
g	 0.8420	 0.5220
h	 0.8200	 0.5040
i	 0.7740	 0.4870
j	 0.6700	 0.4710
k	 0.6560	 0.4580

