



wwPDB EM Validation Summary Report ⓘ

Jul 23, 2026 – 07:46 AM JST

PDB ID : 9M67 / pdb_00009m67
EMDB ID : EMD-63660
Title : the flagellar filament cap FliD in complex with FliC
Authors : Xing, Q.; Cheng, X.Q.; Jiang, W.X.
Deposited on : 2025-03-07
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.dev133
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) : 2.50

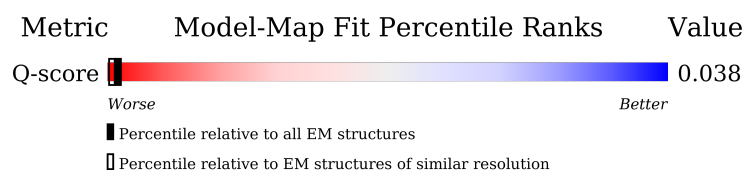
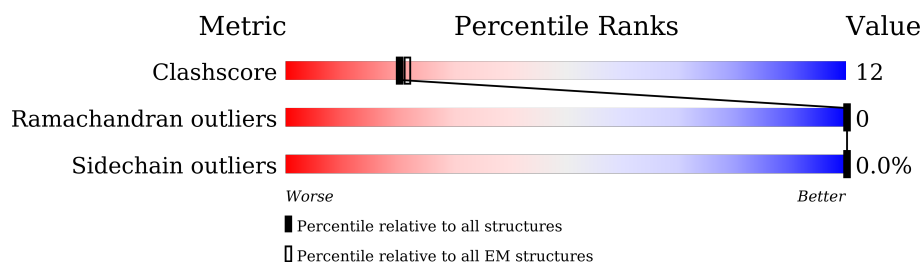
1 Overall quality at a glance

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	992	 11% 35% 8% 58%
1	B	992	 27% 14% 59%
1	C	992	 12% 35% 7% 58%
1	D	992	 28% 13% 59%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	992	
1	F	992	
1	G	992	
1	H	992	
1	I	992	
1	J	992	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 30640 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,Flagellar hook-associated protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	421	Total	C	N	O	S	0	0
			3147	1937	533	673	4		
1	B	409	Total	C	N	O	S	0	0
			2981	1809	523	648	1		
1	C	421	Total	C	N	O	S	0	0
			3147	1937	533	673	4		
1	D	409	Total	C	N	O	S	0	0
			2981	1809	523	648	1		
1	E	421	Total	C	N	O	S	0	0
			3147	1937	533	673	4		
1	F	409	Total	C	N	O	S	0	0
			2981	1809	523	648	1		
1	G	421	Total	C	N	O	S	0	0
			3147	1937	533	673	4		
1	H	409	Total	C	N	O	S	0	0
			2981	1809	523	648	1		
1	I	421	Total	C	N	O	S	0	0
			3147	1937	533	673	4		
1	J	409	Total	C	N	O	S	0	0
			2981	1809	523	648	1		

There are 320 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-524	MET	-	initiating methionine	UNP P06179
A	-523	HIS	-	expression tag	UNP P06179
A	-522	HIS	-	expression tag	UNP P06179
A	-521	HIS	-	expression tag	UNP P06179
A	-520	HIS	-	expression tag	UNP P06179
A	-519	HIS	-	expression tag	UNP P06179
A	-518	HIS	-	expression tag	UNP P06179
A	-517	HIS	-	expression tag	UNP P06179
A	-516	HIS	-	expression tag	UNP P06179
A	-515	HIS	-	expression tag	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-514	HIS	-	expression tag	UNP P06179
A	-513	GLU	-	expression tag	UNP P06179
A	-512	ASN	-	expression tag	UNP P06179
A	-511	LEU	-	expression tag	UNP P06179
A	-510	TYR	-	expression tag	UNP P06179
A	-509	PHE	-	expression tag	UNP P06179
A	-508	GLN	-	expression tag	UNP P06179
A	-507	GLY	-	expression tag	UNP P06179
A	-506	GLY	-	expression tag	UNP P06179
A	-505	SER	-	expression tag	UNP P06179
A	-9	GLY	-	linker	UNP P06179
A	-8	SER	-	linker	UNP P06179
A	-7	GLY	-	linker	UNP P06179
A	-6	ALA	-	linker	UNP P06179
A	-5	GLY	-	linker	UNP P06179
A	-4	GLY	-	linker	UNP P06179
A	-3	SER	-	linker	UNP P06179
A	-2	GLU	-	linker	UNP P06179
A	-1	GLY	-	linker	UNP P06179
A	0	GLY	-	linker	UNP P06179
A	91	CYS	ALA	conflict	UNP P16328
A	168	CYS	ALA	conflict	UNP P16328
B	-19	MET	-	initiating methionine	UNP P06179
B	-18	HIS	-	expression tag	UNP P06179
B	-17	HIS	-	expression tag	UNP P06179
B	-16	HIS	-	expression tag	UNP P06179
B	-15	HIS	-	expression tag	UNP P06179
B	-14	HIS	-	expression tag	UNP P06179
B	-13	HIS	-	expression tag	UNP P06179
B	-12	HIS	-	expression tag	UNP P06179
B	-11	HIS	-	expression tag	UNP P06179
B	-10	HIS	-	expression tag	UNP P06179
B	-9	HIS	-	expression tag	UNP P06179
B	-8	GLU	-	expression tag	UNP P06179
B	-7	ASN	-	expression tag	UNP P06179
B	-6	LEU	-	expression tag	UNP P06179
B	-5	TYR	-	expression tag	UNP P06179
B	-4	PHE	-	expression tag	UNP P06179
B	-3	GLN	-	expression tag	UNP P06179
B	-2	GLY	-	expression tag	UNP P06179
B	-1	GLY	-	expression tag	UNP P06179
B	0	SER	-	expression tag	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	496	GLY	-	linker	UNP P06179
B	497	SER	-	linker	UNP P06179
B	498	GLY	-	linker	UNP P06179
B	499	ALA	-	linker	UNP P06179
B	500	GLY	-	linker	UNP P06179
B	501	GLY	-	linker	UNP P06179
B	502	SER	-	linker	UNP P06179
B	503	GLU	-	linker	UNP P06179
B	504	GLY	-	linker	UNP P06179
B	505	GLY	-	linker	UNP P06179
B	596	CYS	ALA	conflict	UNP P16328
B	673	CYS	ALA	conflict	UNP P16328
C	-524	MET	-	initiating methionine	UNP P06179
C	-523	HIS	-	expression tag	UNP P06179
C	-522	HIS	-	expression tag	UNP P06179
C	-521	HIS	-	expression tag	UNP P06179
C	-520	HIS	-	expression tag	UNP P06179
C	-519	HIS	-	expression tag	UNP P06179
C	-518	HIS	-	expression tag	UNP P06179
C	-517	HIS	-	expression tag	UNP P06179
C	-516	HIS	-	expression tag	UNP P06179
C	-515	HIS	-	expression tag	UNP P06179
C	-514	HIS	-	expression tag	UNP P06179
C	-513	GLU	-	expression tag	UNP P06179
C	-512	ASN	-	expression tag	UNP P06179
C	-511	LEU	-	expression tag	UNP P06179
C	-510	TYR	-	expression tag	UNP P06179
C	-509	PHE	-	expression tag	UNP P06179
C	-508	GLN	-	expression tag	UNP P06179
C	-507	GLY	-	expression tag	UNP P06179
C	-506	GLY	-	expression tag	UNP P06179
C	-505	SER	-	expression tag	UNP P06179
C	-9	GLY	-	linker	UNP P06179
C	-8	SER	-	linker	UNP P06179
C	-7	GLY	-	linker	UNP P06179
C	-6	ALA	-	linker	UNP P06179
C	-5	GLY	-	linker	UNP P06179
C	-4	GLY	-	linker	UNP P06179
C	-3	SER	-	linker	UNP P06179
C	-2	GLU	-	linker	UNP P06179
C	-1	GLY	-	linker	UNP P06179
C	0	GLY	-	linker	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	91	CYS	ALA	conflict	UNP P16328
C	168	CYS	ALA	conflict	UNP P16328
D	-19	MET	-	initiating methionine	UNP P06179
D	-18	HIS	-	expression tag	UNP P06179
D	-17	HIS	-	expression tag	UNP P06179
D	-16	HIS	-	expression tag	UNP P06179
D	-15	HIS	-	expression tag	UNP P06179
D	-14	HIS	-	expression tag	UNP P06179
D	-13	HIS	-	expression tag	UNP P06179
D	-12	HIS	-	expression tag	UNP P06179
D	-11	HIS	-	expression tag	UNP P06179
D	-10	HIS	-	expression tag	UNP P06179
D	-9	HIS	-	expression tag	UNP P06179
D	-8	GLU	-	expression tag	UNP P06179
D	-7	ASN	-	expression tag	UNP P06179
D	-6	LEU	-	expression tag	UNP P06179
D	-5	TYR	-	expression tag	UNP P06179
D	-4	PHE	-	expression tag	UNP P06179
D	-3	GLN	-	expression tag	UNP P06179
D	-2	GLY	-	expression tag	UNP P06179
D	-1	GLY	-	expression tag	UNP P06179
D	0	SER	-	expression tag	UNP P06179
D	496	GLY	-	linker	UNP P06179
D	497	SER	-	linker	UNP P06179
D	498	GLY	-	linker	UNP P06179
D	499	ALA	-	linker	UNP P06179
D	500	GLY	-	linker	UNP P06179
D	501	GLY	-	linker	UNP P06179
D	502	SER	-	linker	UNP P06179
D	503	GLU	-	linker	UNP P06179
D	504	GLY	-	linker	UNP P06179
D	505	GLY	-	linker	UNP P06179
D	596	CYS	ALA	conflict	UNP P16328
D	673	CYS	ALA	conflict	UNP P16328
E	-524	MET	-	initiating methionine	UNP P06179
E	-523	HIS	-	expression tag	UNP P06179
E	-522	HIS	-	expression tag	UNP P06179
E	-521	HIS	-	expression tag	UNP P06179
E	-520	HIS	-	expression tag	UNP P06179
E	-519	HIS	-	expression tag	UNP P06179
E	-518	HIS	-	expression tag	UNP P06179
E	-517	HIS	-	expression tag	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-516	HIS	-	expression tag	UNP P06179
E	-515	HIS	-	expression tag	UNP P06179
E	-514	HIS	-	expression tag	UNP P06179
E	-513	GLU	-	expression tag	UNP P06179
E	-512	ASN	-	expression tag	UNP P06179
E	-511	LEU	-	expression tag	UNP P06179
E	-510	TYR	-	expression tag	UNP P06179
E	-509	PHE	-	expression tag	UNP P06179
E	-508	GLN	-	expression tag	UNP P06179
E	-507	GLY	-	expression tag	UNP P06179
E	-506	GLY	-	expression tag	UNP P06179
E	-505	SER	-	expression tag	UNP P06179
E	-9	GLY	-	linker	UNP P06179
E	-8	SER	-	linker	UNP P06179
E	-7	GLY	-	linker	UNP P06179
E	-6	ALA	-	linker	UNP P06179
E	-5	GLY	-	linker	UNP P06179
E	-4	GLY	-	linker	UNP P06179
E	-3	SER	-	linker	UNP P06179
E	-2	GLU	-	linker	UNP P06179
E	-1	GLY	-	linker	UNP P06179
E	0	GLY	-	linker	UNP P06179
E	91	CYS	ALA	conflict	UNP P16328
E	168	CYS	ALA	conflict	UNP P16328
F	-19	MET	-	initiating methionine	UNP P06179
F	-18	HIS	-	expression tag	UNP P06179
F	-17	HIS	-	expression tag	UNP P06179
F	-16	HIS	-	expression tag	UNP P06179
F	-15	HIS	-	expression tag	UNP P06179
F	-14	HIS	-	expression tag	UNP P06179
F	-13	HIS	-	expression tag	UNP P06179
F	-12	HIS	-	expression tag	UNP P06179
F	-11	HIS	-	expression tag	UNP P06179
F	-10	HIS	-	expression tag	UNP P06179
F	-9	HIS	-	expression tag	UNP P06179
F	-8	GLU	-	expression tag	UNP P06179
F	-7	ASN	-	expression tag	UNP P06179
F	-6	LEU	-	expression tag	UNP P06179
F	-5	TYR	-	expression tag	UNP P06179
F	-4	PHE	-	expression tag	UNP P06179
F	-3	GLN	-	expression tag	UNP P06179
F	-2	GLY	-	expression tag	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	GLY	-	expression tag	UNP P06179
F	0	SER	-	expression tag	UNP P06179
F	496	GLY	-	linker	UNP P06179
F	497	SER	-	linker	UNP P06179
F	498	GLY	-	linker	UNP P06179
F	499	ALA	-	linker	UNP P06179
F	500	GLY	-	linker	UNP P06179
F	501	GLY	-	linker	UNP P06179
F	502	SER	-	linker	UNP P06179
F	503	GLU	-	linker	UNP P06179
F	504	GLY	-	linker	UNP P06179
F	505	GLY	-	linker	UNP P06179
F	596	CYS	ALA	conflict	UNP P16328
F	673	CYS	ALA	conflict	UNP P16328
G	-524	MET	-	initiating methionine	UNP P06179
G	-523	HIS	-	expression tag	UNP P06179
G	-522	HIS	-	expression tag	UNP P06179
G	-521	HIS	-	expression tag	UNP P06179
G	-520	HIS	-	expression tag	UNP P06179
G	-519	HIS	-	expression tag	UNP P06179
G	-518	HIS	-	expression tag	UNP P06179
G	-517	HIS	-	expression tag	UNP P06179
G	-516	HIS	-	expression tag	UNP P06179
G	-515	HIS	-	expression tag	UNP P06179
G	-514	HIS	-	expression tag	UNP P06179
G	-513	GLU	-	expression tag	UNP P06179
G	-512	ASN	-	expression tag	UNP P06179
G	-511	LEU	-	expression tag	UNP P06179
G	-510	TYR	-	expression tag	UNP P06179
G	-509	PHE	-	expression tag	UNP P06179
G	-508	GLN	-	expression tag	UNP P06179
G	-507	GLY	-	expression tag	UNP P06179
G	-506	GLY	-	expression tag	UNP P06179
G	-505	SER	-	expression tag	UNP P06179
G	-9	GLY	-	linker	UNP P06179
G	-8	SER	-	linker	UNP P06179
G	-7	GLY	-	linker	UNP P06179
G	-6	ALA	-	linker	UNP P06179
G	-5	GLY	-	linker	UNP P06179
G	-4	GLY	-	linker	UNP P06179
G	-3	SER	-	linker	UNP P06179
G	-2	GLU	-	linker	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	GLY	-	linker	UNP P06179
G	0	GLY	-	linker	UNP P06179
G	91	CYS	ALA	conflict	UNP P16328
G	168	CYS	ALA	conflict	UNP P16328
H	-19	MET	-	initiating methionine	UNP P06179
H	-18	HIS	-	expression tag	UNP P06179
H	-17	HIS	-	expression tag	UNP P06179
H	-16	HIS	-	expression tag	UNP P06179
H	-15	HIS	-	expression tag	UNP P06179
H	-14	HIS	-	expression tag	UNP P06179
H	-13	HIS	-	expression tag	UNP P06179
H	-12	HIS	-	expression tag	UNP P06179
H	-11	HIS	-	expression tag	UNP P06179
H	-10	HIS	-	expression tag	UNP P06179
H	-9	HIS	-	expression tag	UNP P06179
H	-8	GLU	-	expression tag	UNP P06179
H	-7	ASN	-	expression tag	UNP P06179
H	-6	LEU	-	expression tag	UNP P06179
H	-5	TYR	-	expression tag	UNP P06179
H	-4	PHE	-	expression tag	UNP P06179
H	-3	GLN	-	expression tag	UNP P06179
H	-2	GLY	-	expression tag	UNP P06179
H	-1	GLY	-	expression tag	UNP P06179
H	0	SER	-	expression tag	UNP P06179
H	496	GLY	-	linker	UNP P06179
H	497	SER	-	linker	UNP P06179
H	498	GLY	-	linker	UNP P06179
H	499	ALA	-	linker	UNP P06179
H	500	GLY	-	linker	UNP P06179
H	501	GLY	-	linker	UNP P06179
H	502	SER	-	linker	UNP P06179
H	503	GLU	-	linker	UNP P06179
H	504	GLY	-	linker	UNP P06179
H	505	GLY	-	linker	UNP P06179
H	596	CYS	ALA	conflict	UNP P16328
H	673	CYS	ALA	conflict	UNP P16328
I	-524	MET	-	initiating methionine	UNP P06179
I	-523	HIS	-	expression tag	UNP P06179
I	-522	HIS	-	expression tag	UNP P06179
I	-521	HIS	-	expression tag	UNP P06179
I	-520	HIS	-	expression tag	UNP P06179
I	-519	HIS	-	expression tag	UNP P06179

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	-518	HIS	-	expression tag	UNP P06179
I	-517	HIS	-	expression tag	UNP P06179
I	-516	HIS	-	expression tag	UNP P06179
I	-515	HIS	-	expression tag	UNP P06179
I	-514	HIS	-	expression tag	UNP P06179
I	-513	GLU	-	expression tag	UNP P06179
I	-512	ASN	-	expression tag	UNP P06179
I	-511	LEU	-	expression tag	UNP P06179
I	-510	TYR	-	expression tag	UNP P06179
I	-509	PHE	-	expression tag	UNP P06179
I	-508	GLN	-	expression tag	UNP P06179
I	-507	GLY	-	expression tag	UNP P06179
I	-506	GLY	-	expression tag	UNP P06179
I	-505	SER	-	expression tag	UNP P06179
I	-9	GLY	-	linker	UNP P06179
I	-8	SER	-	linker	UNP P06179
I	-7	GLY	-	linker	UNP P06179
I	-6	ALA	-	linker	UNP P06179
I	-5	GLY	-	linker	UNP P06179
I	-4	GLY	-	linker	UNP P06179
I	-3	SER	-	linker	UNP P06179
I	-2	GLU	-	linker	UNP P06179
I	-1	GLY	-	linker	UNP P06179
I	0	GLY	-	linker	UNP P06179
I	91	CYS	ALA	conflict	UNP P16328
I	168	CYS	ALA	conflict	UNP P16328
J	-19	MET	-	initiating methionine	UNP P06179
J	-18	HIS	-	expression tag	UNP P06179
J	-17	HIS	-	expression tag	UNP P06179
J	-16	HIS	-	expression tag	UNP P06179
J	-15	HIS	-	expression tag	UNP P06179
J	-14	HIS	-	expression tag	UNP P06179
J	-13	HIS	-	expression tag	UNP P06179
J	-12	HIS	-	expression tag	UNP P06179
J	-11	HIS	-	expression tag	UNP P06179
J	-10	HIS	-	expression tag	UNP P06179
J	-9	HIS	-	expression tag	UNP P06179
J	-8	GLU	-	expression tag	UNP P06179
J	-7	ASN	-	expression tag	UNP P06179
J	-6	LEU	-	expression tag	UNP P06179
J	-5	TYR	-	expression tag	UNP P06179
J	-4	PHE	-	expression tag	UNP P06179

Continued on next page...

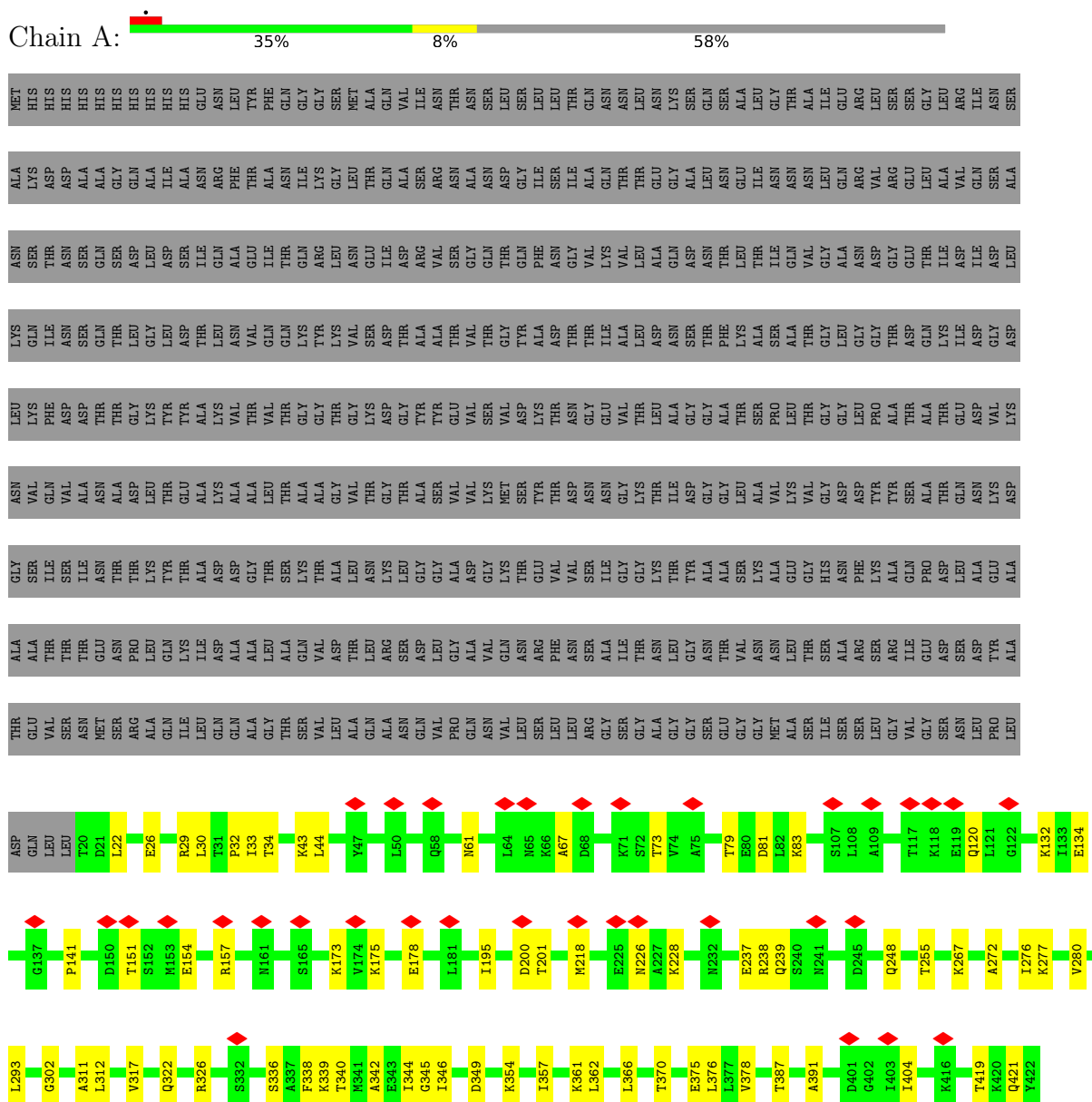
Continued from previous page...

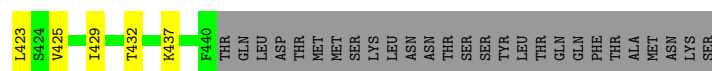
Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLN	-	expression tag	UNP P06179
J	-2	GLY	-	expression tag	UNP P06179
J	-1	GLY	-	expression tag	UNP P06179
J	0	SER	-	expression tag	UNP P06179
J	496	GLY	-	linker	UNP P06179
J	497	SER	-	linker	UNP P06179
J	498	GLY	-	linker	UNP P06179
J	499	ALA	-	linker	UNP P06179
J	500	GLY	-	linker	UNP P06179
J	501	GLY	-	linker	UNP P06179
J	502	SER	-	linker	UNP P06179
J	503	GLU	-	linker	UNP P06179
J	504	GLY	-	linker	UNP P06179
J	505	GLY	-	linker	UNP P06179
J	596	CYS	ALA	conflict	UNP P16328
J	673	CYS	ALA	conflict	UNP P16328

3 Residue-property plots

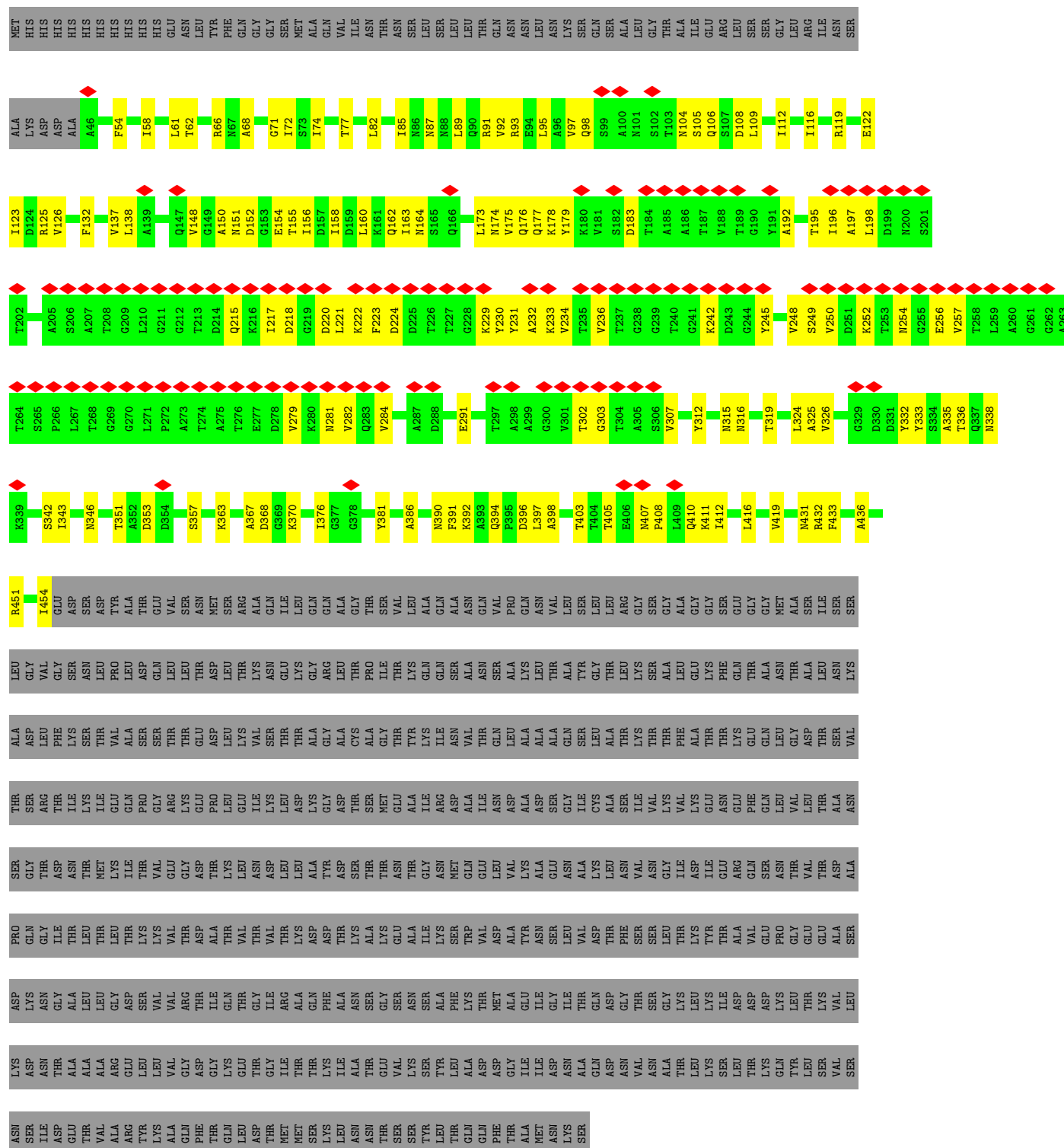
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Flagellin,Flagellar hook-associated protein 2

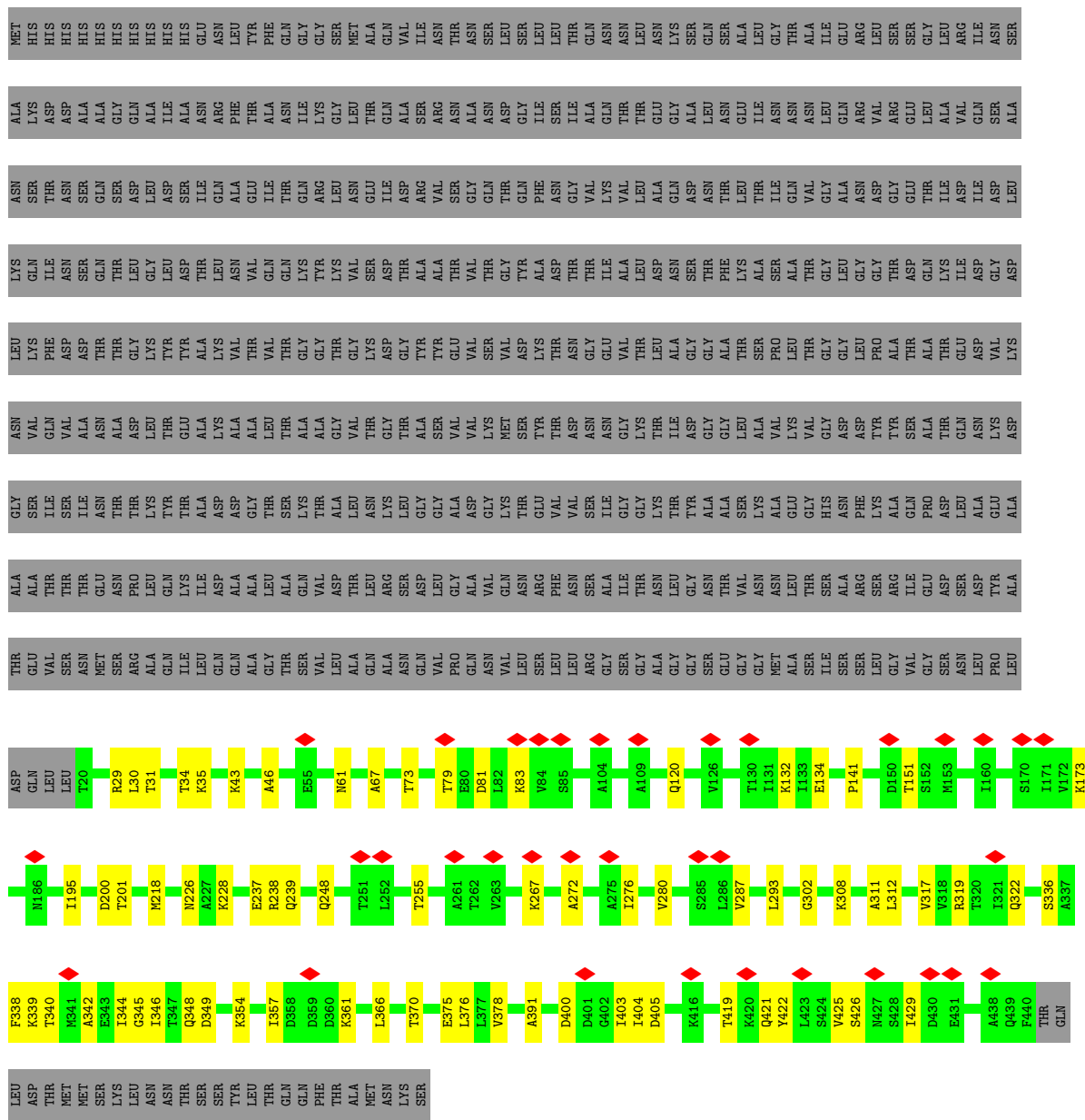




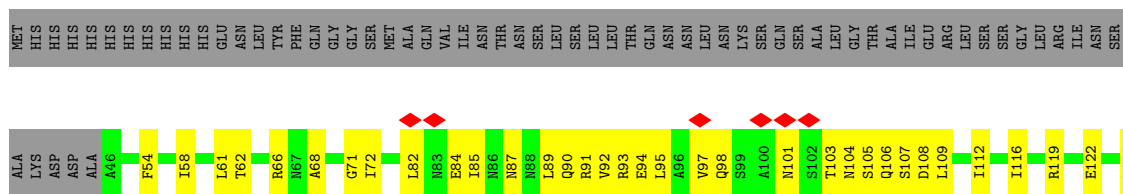
● Molecule 1: Flagellin, Flagellar hook-associated protein 2



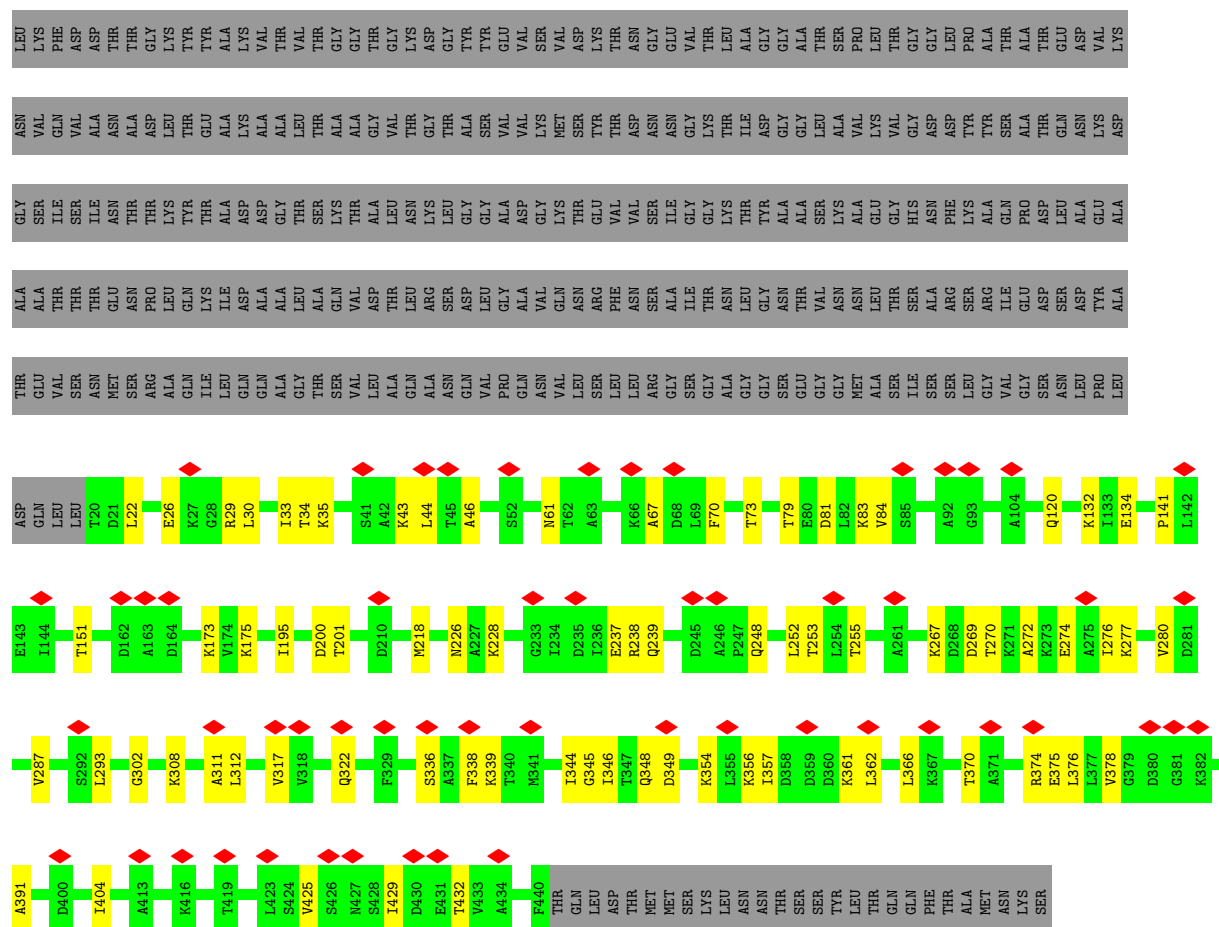
Chain C:



Chain D:





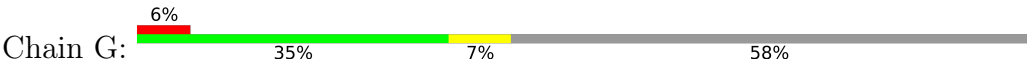


• Molecule 1: Flagellin, Flagellar hook-associated protein 2

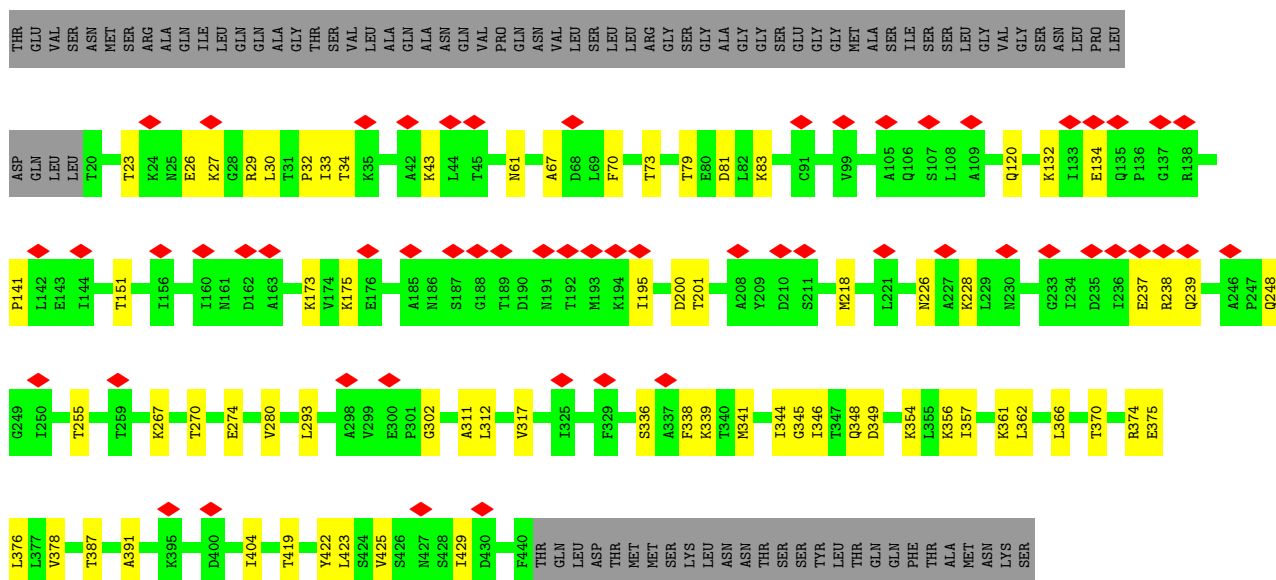


LEU	LYS	LEU	LEU	LEU	LYS	TYR	THR	LYS	ASP	ILE	GLU	THR	GLY	GLU	LYS	THR	THR	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

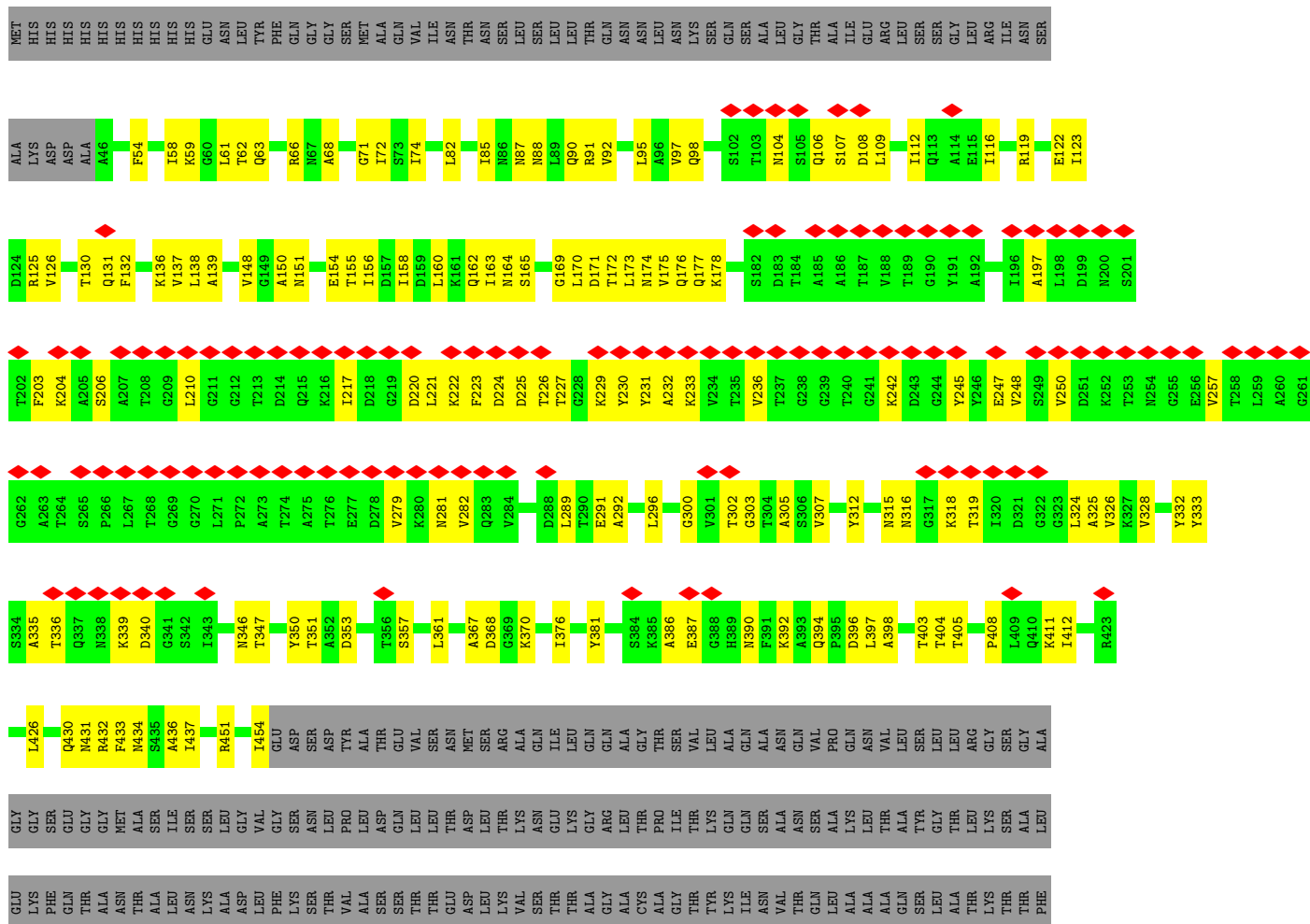
● Molecule 1: Flagellin,Flagellar hook-associated protein 2

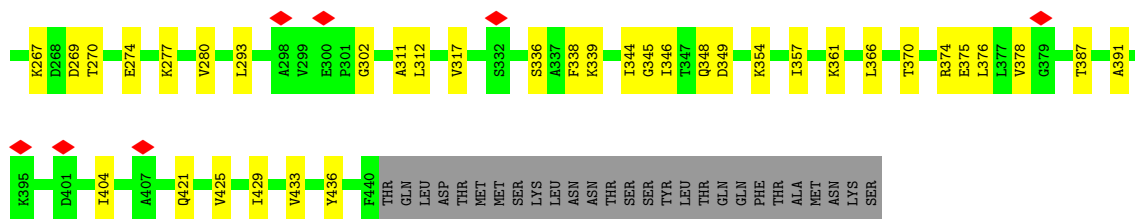


MET	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	GLU	ASN	LEU	TYR	PHE	GLN	GLY	GLY	SER	ILE	ASN	THR	THR	GLN	GLY	LEU	LEU	THR	GLY	ASN	LYS	SER	GLY	GLY	ALA	LEU	GLY	ARG	THR	LEU	ARG	ILE	SER		
ALA	LYS	ASP	ASN	ASP	ALA	ALA	GLY	GLN	GLY	ASN	ARG	PHE	THR	ALA	THR	ILE	GLY	GLY	LEU	VAL	ARG	THR	GLY	GLY	LEU	THR	THR	GLY	ILE	ASN	GLY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

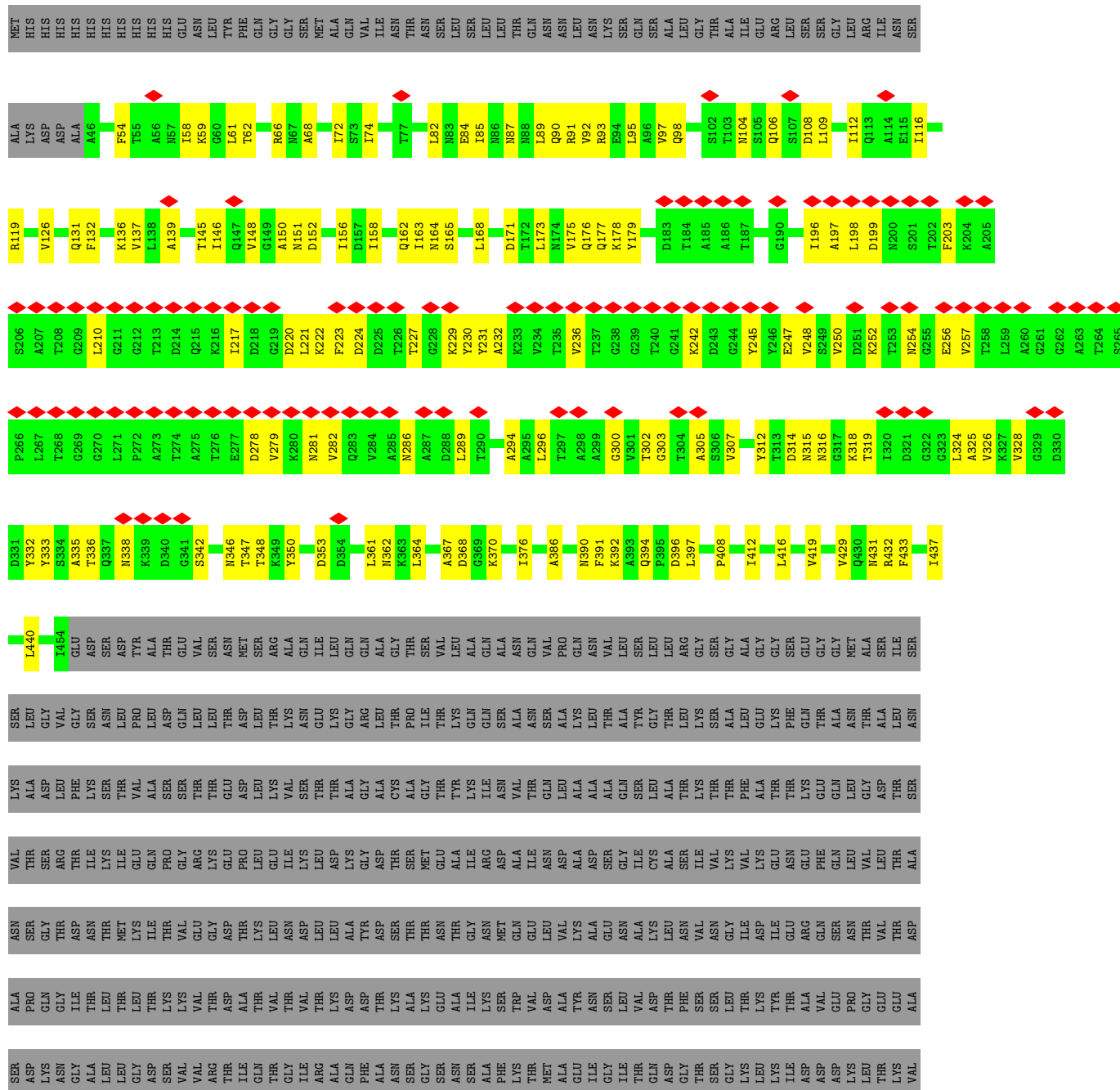


• Molecule 1: Flagellin, Flagellar hook-associated protein 2





• Molecule 1: Flagellin,Flagellar hook-associated protein 2



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

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	903918	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	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	1.011	Depositor
Minimum map value	-0.604	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	456.0, 456.0, 456.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.76, 0.76, 0.76	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	0.16	0/3169	0.31	0/4289
1	B	0.13	0/3002	0.33	0/4076
1	C	0.16	0/3169	0.28	0/4289
1	D	0.13	0/3002	0.33	0/4076
1	E	0.16	0/3169	0.30	0/4289
1	F	0.13	0/3002	0.35	0/4076
1	G	0.16	0/3169	0.29	0/4289
1	H	0.14	0/3002	0.34	0/4076
1	I	0.15	0/3169	0.29	0/4289
1	J	0.13	0/3002	0.33	0/4076
All	All	0.15	0/30855	0.31	0/41825

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3147	0	3189	49	0
1	B	2981	0	2935	107	0
1	C	3147	0	3189	47	0
1	D	2981	0	2935	99	0
1	E	3147	0	3189	52	0
1	F	2981	0	2935	100	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	3147	0	3189	47	0
1	H	2981	0	2935	113	0
1	I	3147	0	3189	47	0
1	J	2981	0	2935	108	0
All	All	30640	0	30620	747	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 12.

The worst 5 of 747 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:I:30:LEU:O	1:I:34:THR:N	2.15	0.76
1:J:109:LEU:HD13	1:J:177:GLN:HG2	1.67	0.76
1:A:22:LEU:HD13	1:A:432:THR:HB	1.68	0.76
1:F:198:LEU:HD23	1:F:252:LYS:HB3	1.69	0.75
1:A:30:LEU:O	1:A:34:THR:N	2.16	0.74

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	419/992 (42%)	407 (97%)	12 (3%)	0	100	100
1	B	407/992 (41%)	394 (97%)	13 (3%)	0	100	100
1	C	419/992 (42%)	408 (97%)	11 (3%)	0	100	100
1	D	407/992 (41%)	392 (96%)	15 (4%)	0	100	100
1	E	419/992 (42%)	408 (97%)	11 (3%)	0	100	100
1	F	407/992 (41%)	395 (97%)	12 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	419/992 (42%)	409 (98%)	10 (2%)	0	100	100
1	H	407/992 (41%)	389 (96%)	18 (4%)	0	100	100
1	I	419/992 (42%)	407 (97%)	12 (3%)	0	100	100
1	J	407/992 (41%)	390 (96%)	17 (4%)	0	100	100
All	All	4130/9920 (42%)	3999 (97%)	131 (3%)	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	349/805 (43%)	349 (100%)	0	100	100
1	B	318/805 (40%)	318 (100%)	0	100	100
1	C	349/805 (43%)	349 (100%)	0	100	100
1	D	318/805 (40%)	317 (100%)	1 (0%)	86	84
1	E	349/805 (43%)	349 (100%)	0	100	100
1	F	318/805 (40%)	318 (100%)	0	100	100
1	G	349/805 (43%)	349 (100%)	0	100	100
1	H	318/805 (40%)	318 (100%)	0	100	100
1	I	349/805 (43%)	349 (100%)	0	100	100
1	J	318/805 (40%)	318 (100%)	0	100	100
All	All	3335/8050 (41%)	3334 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	147	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	215	GLN
1	H	162	GLN
1	F	390	ASN
1	G	248	GLN
1	H	338	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

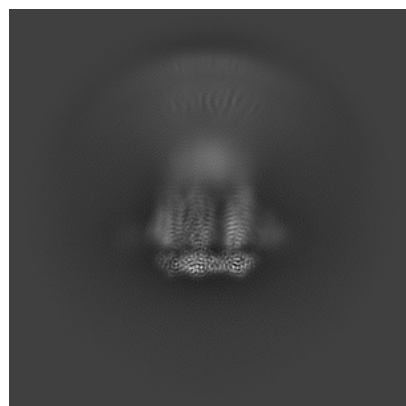
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63660. These allow visual inspection of the internal detail of the map and identification of artifacts.

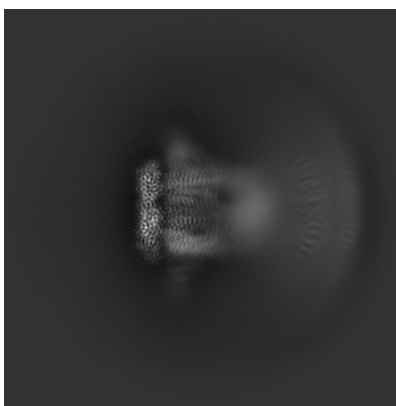
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

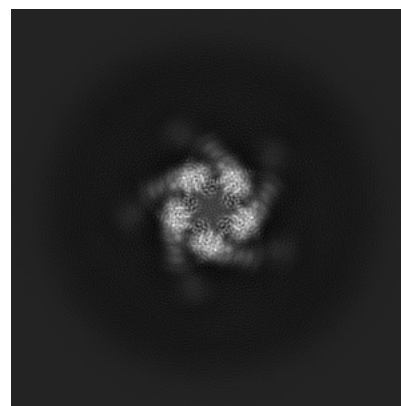
6.1.1 Primary map



X

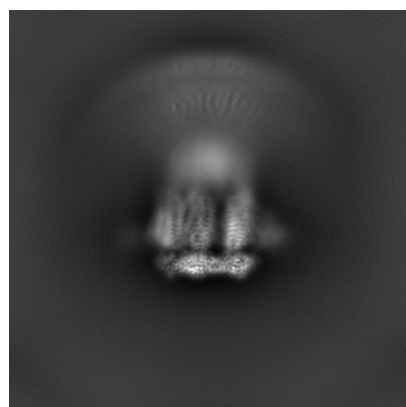


Y

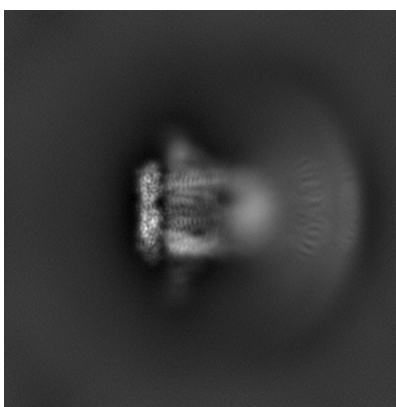


Z

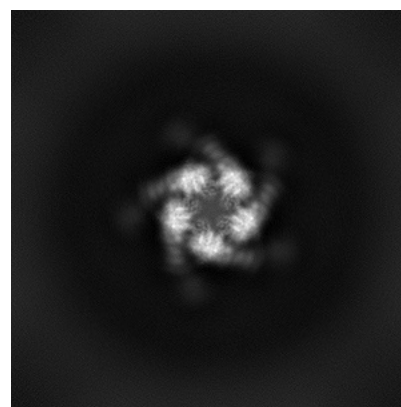
6.1.2 Raw map



X



Y

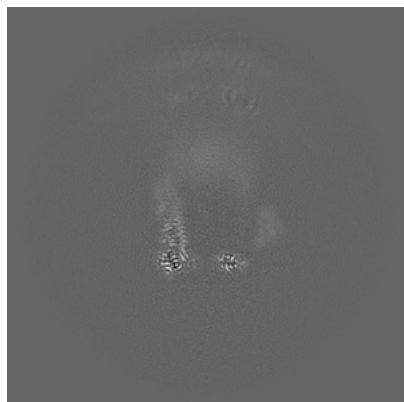


Z

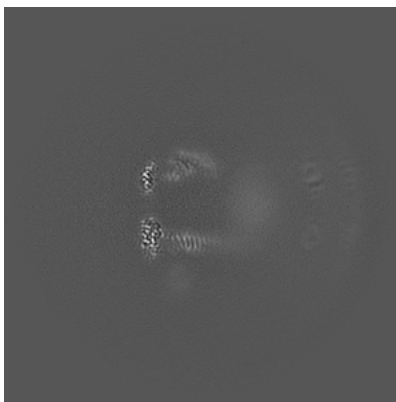
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

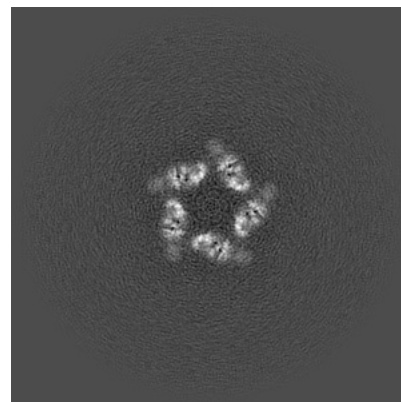
6.2.1 Primary map



X Index: 300

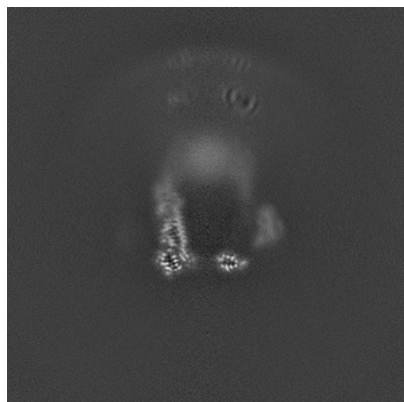


Y Index: 300

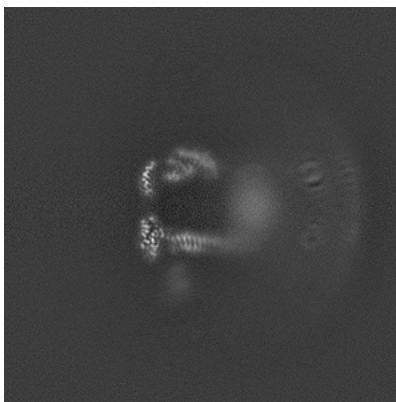


Z Index: 300

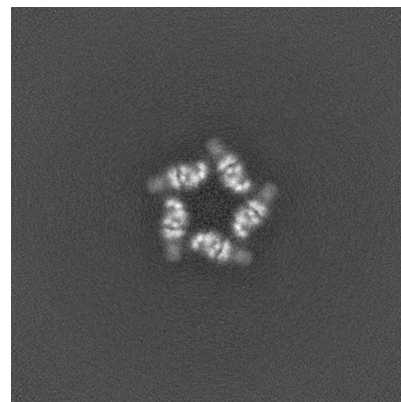
6.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

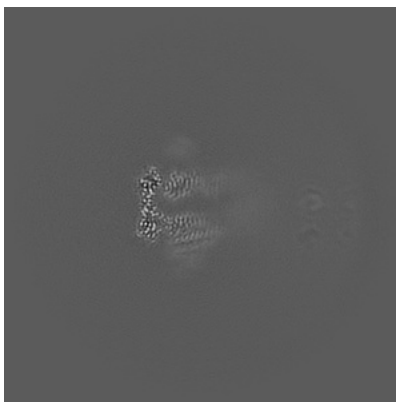
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

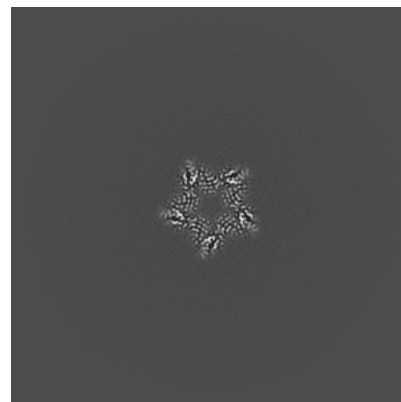
6.3.1 Primary map



X Index: 341



Y Index: 341

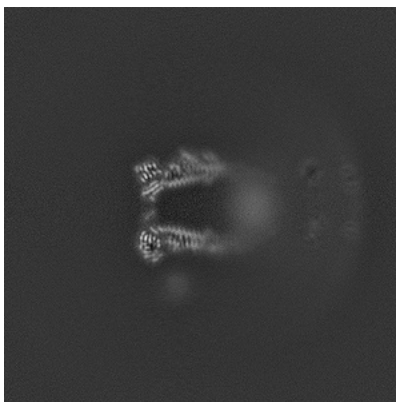


Z Index: 212

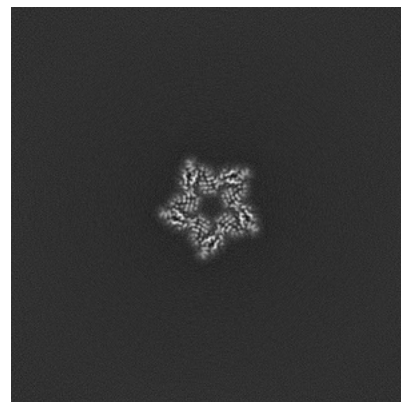
6.3.2 Raw map



X Index: 341



Y Index: 288

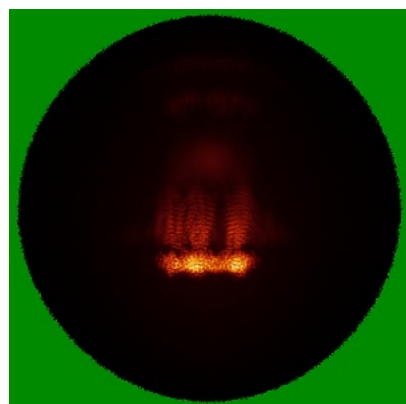


Z Index: 212

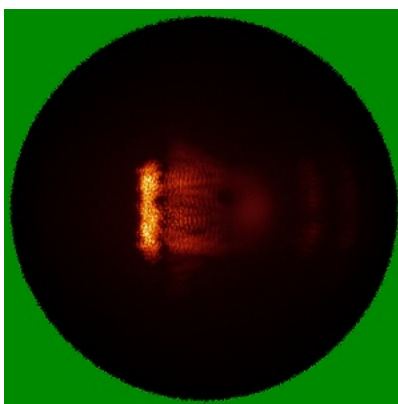
The images above show the largest variance slices of the map in three orthogonal directions.

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

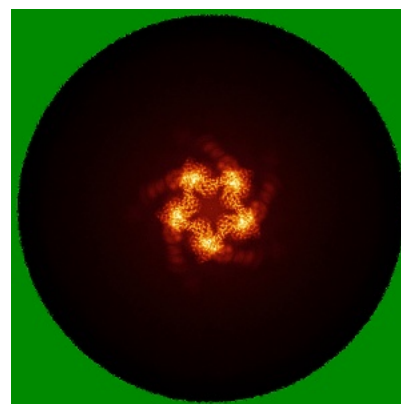
6.4.1 Primary map



X

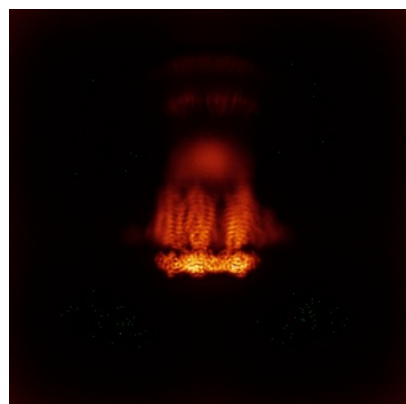


Y

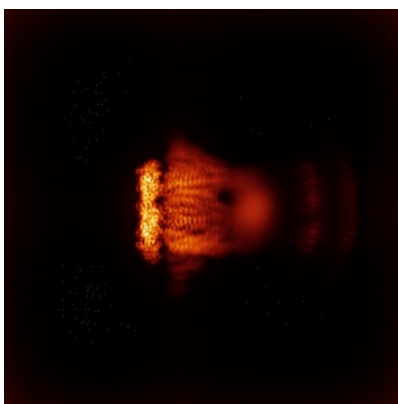


Z

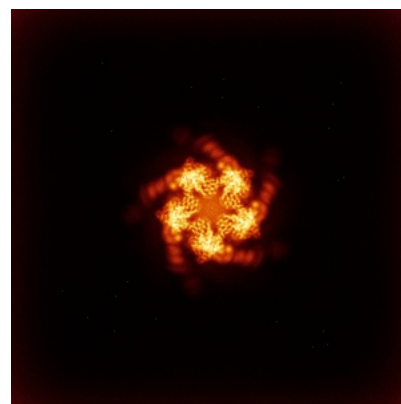
6.4.2 Raw map



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](#)

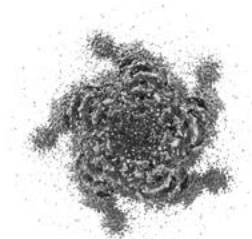
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

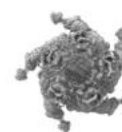
6.5.2 Raw map



X



Y



Z

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.

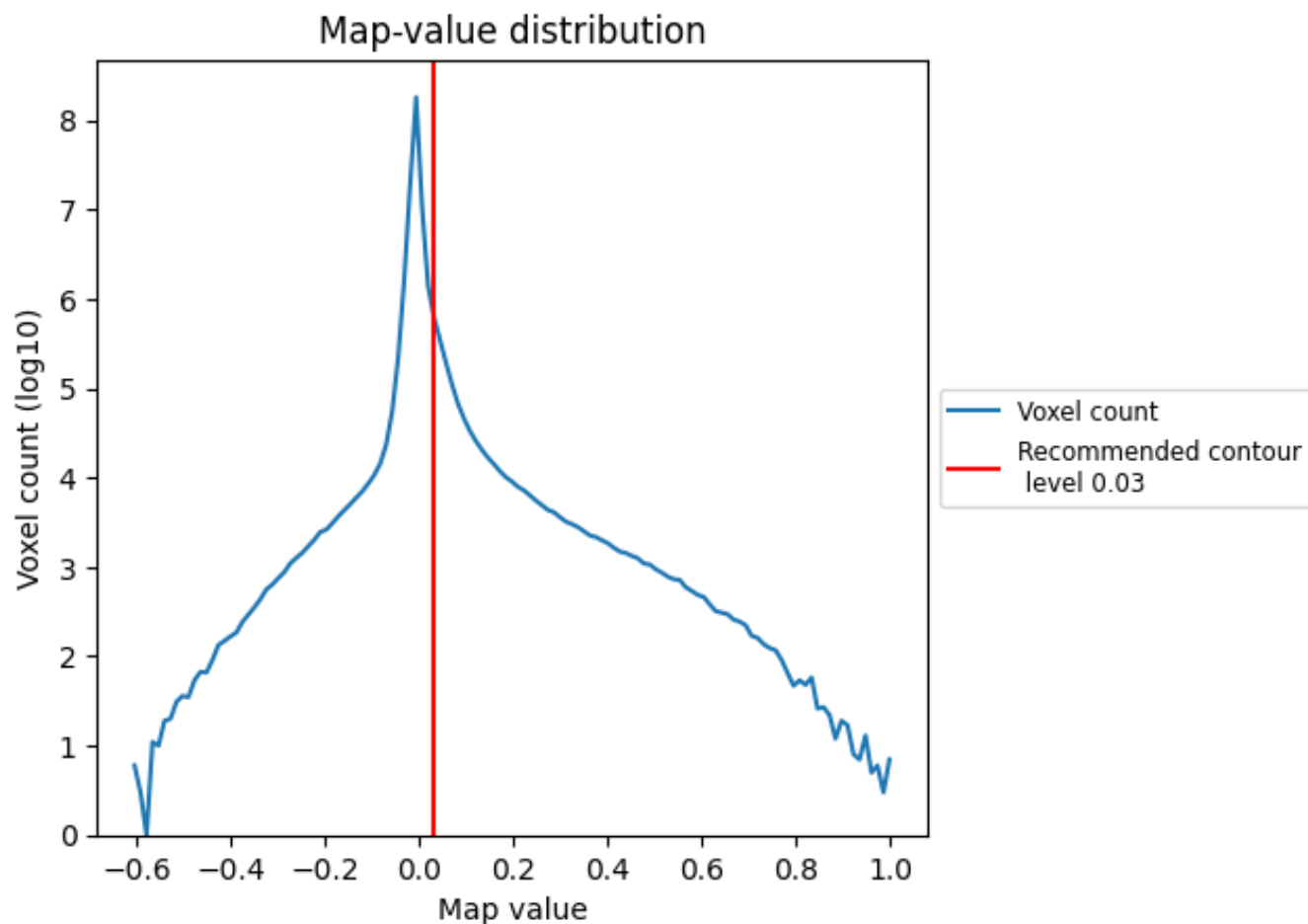
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

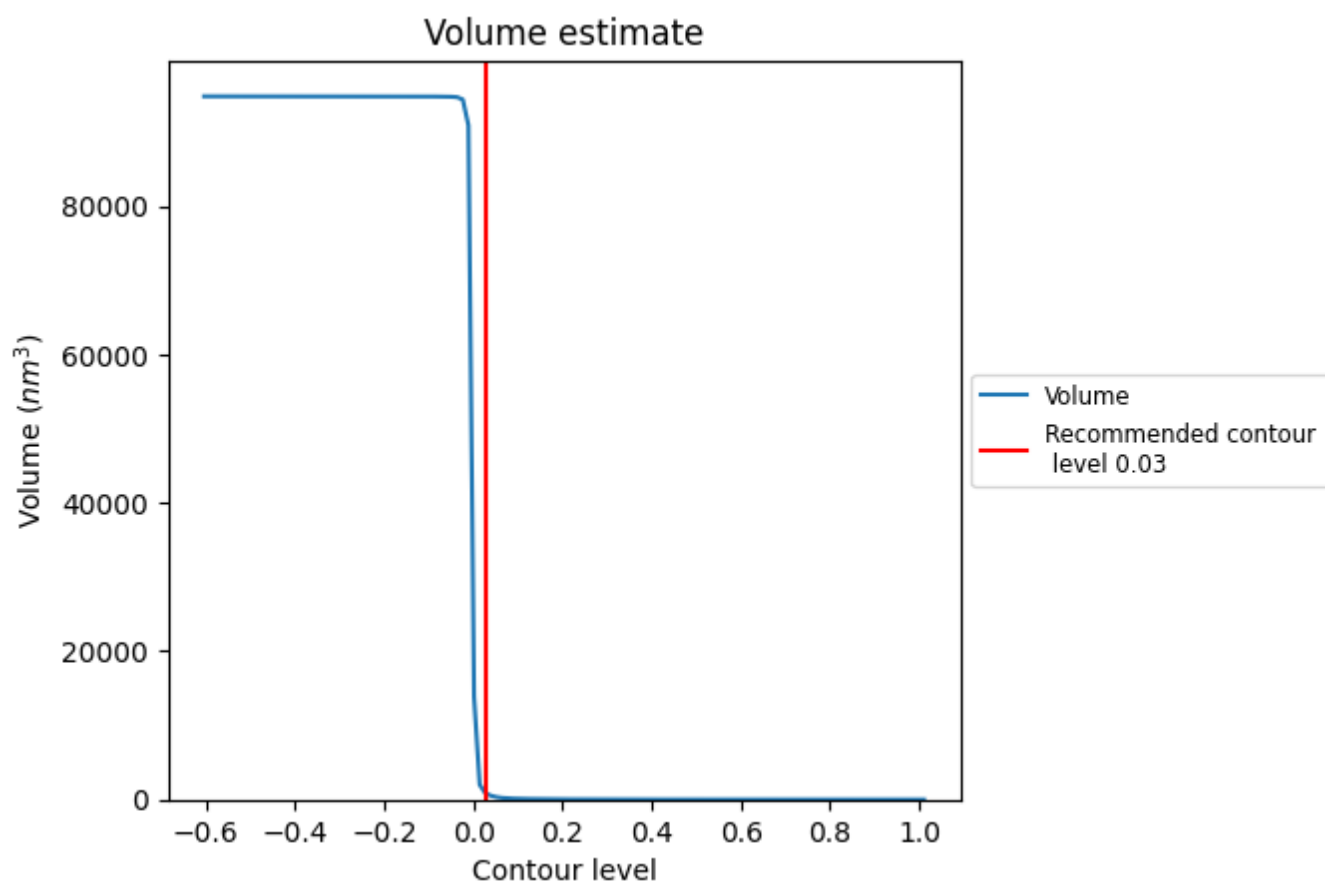
This section contains the results of statistical analysis of the map.

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.

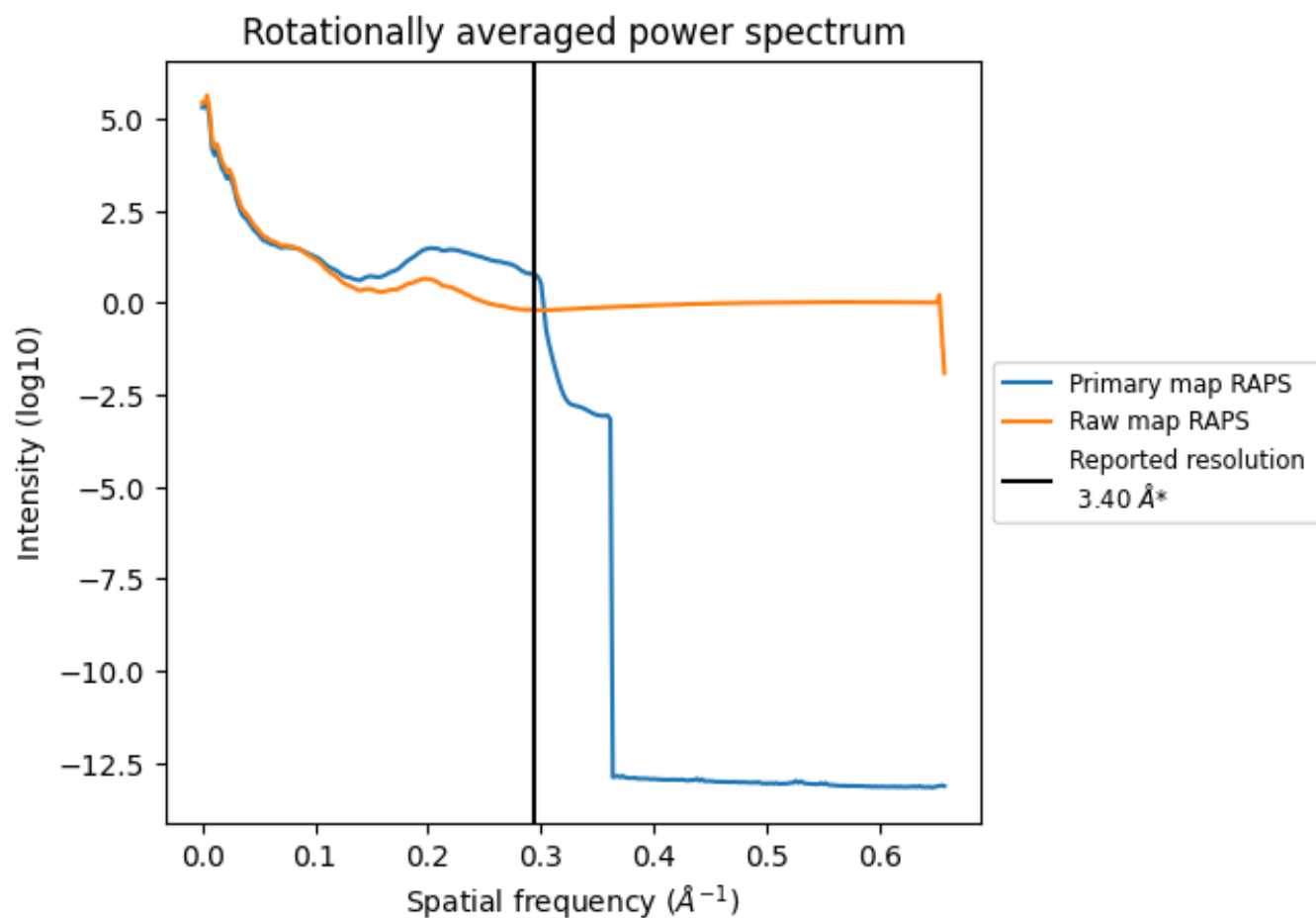
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 780 nm^3 ; this corresponds to an approximate mass of 705 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 ⓘ

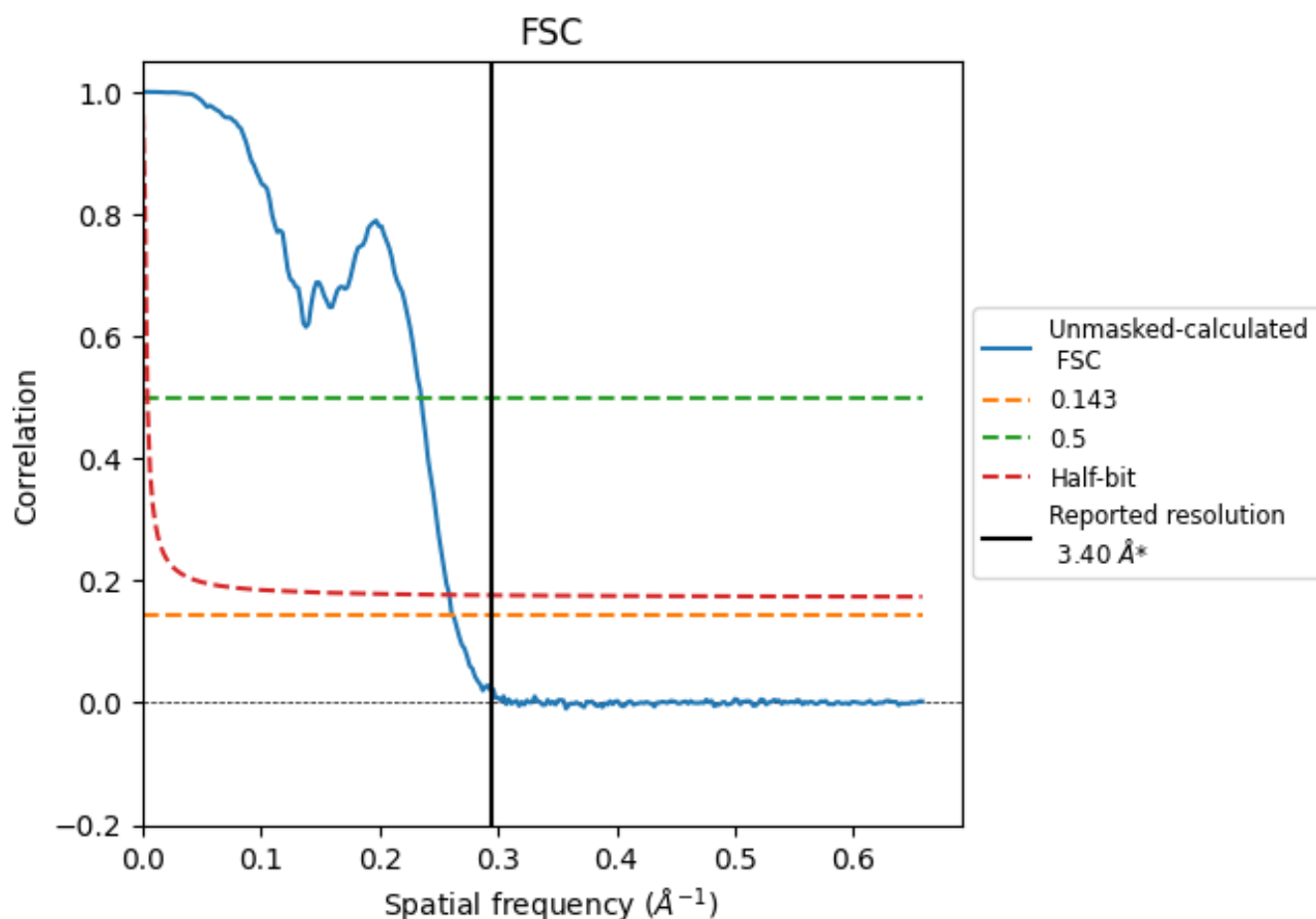


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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](#)

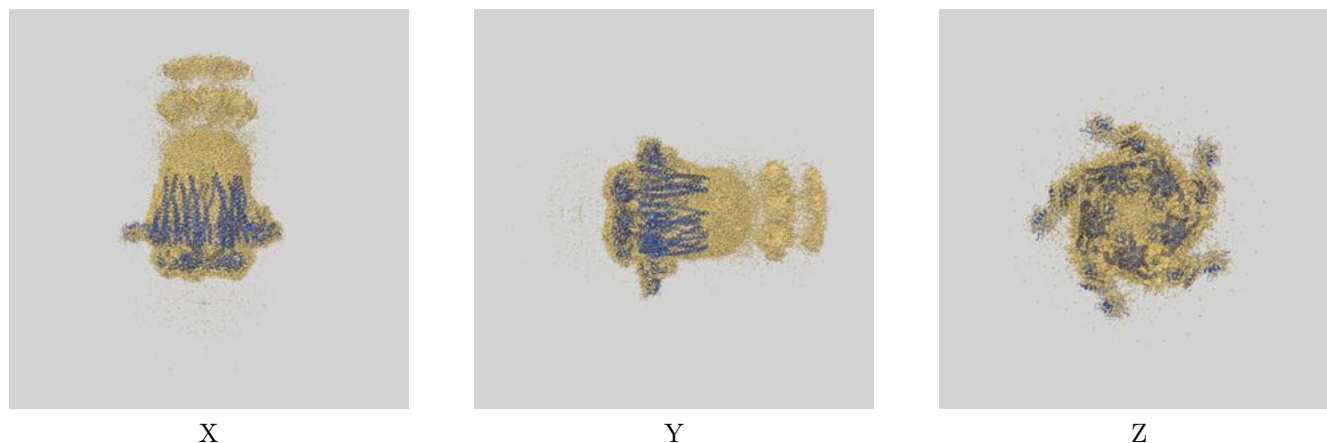
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	4.25	3.86

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

9 Map-model fit [i](#)

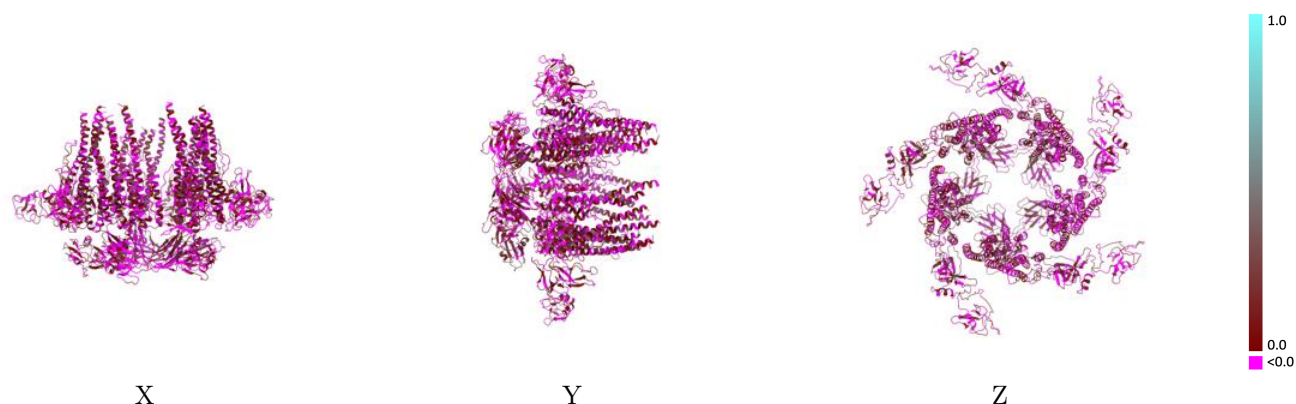
This section contains information regarding the fit between EMDB map EMD-63660 and PDB model 9M67. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



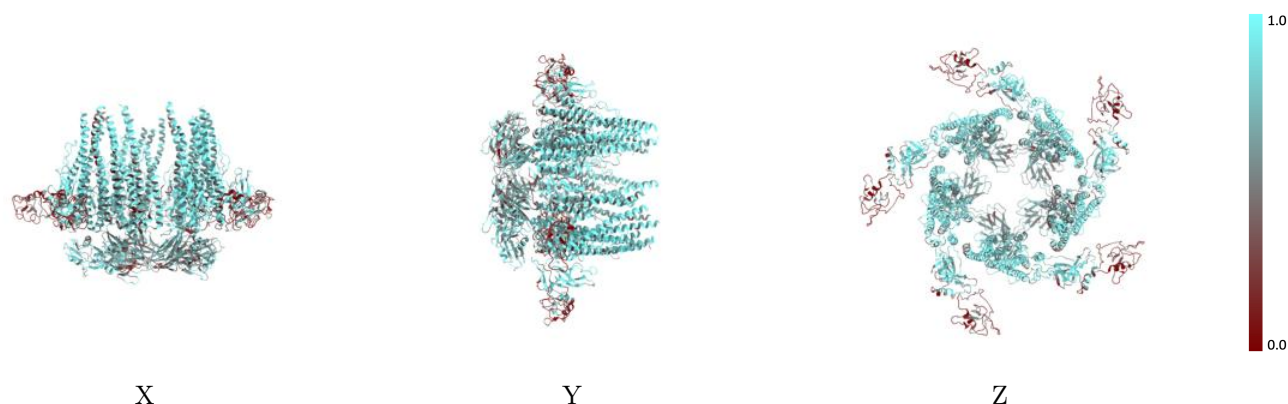
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



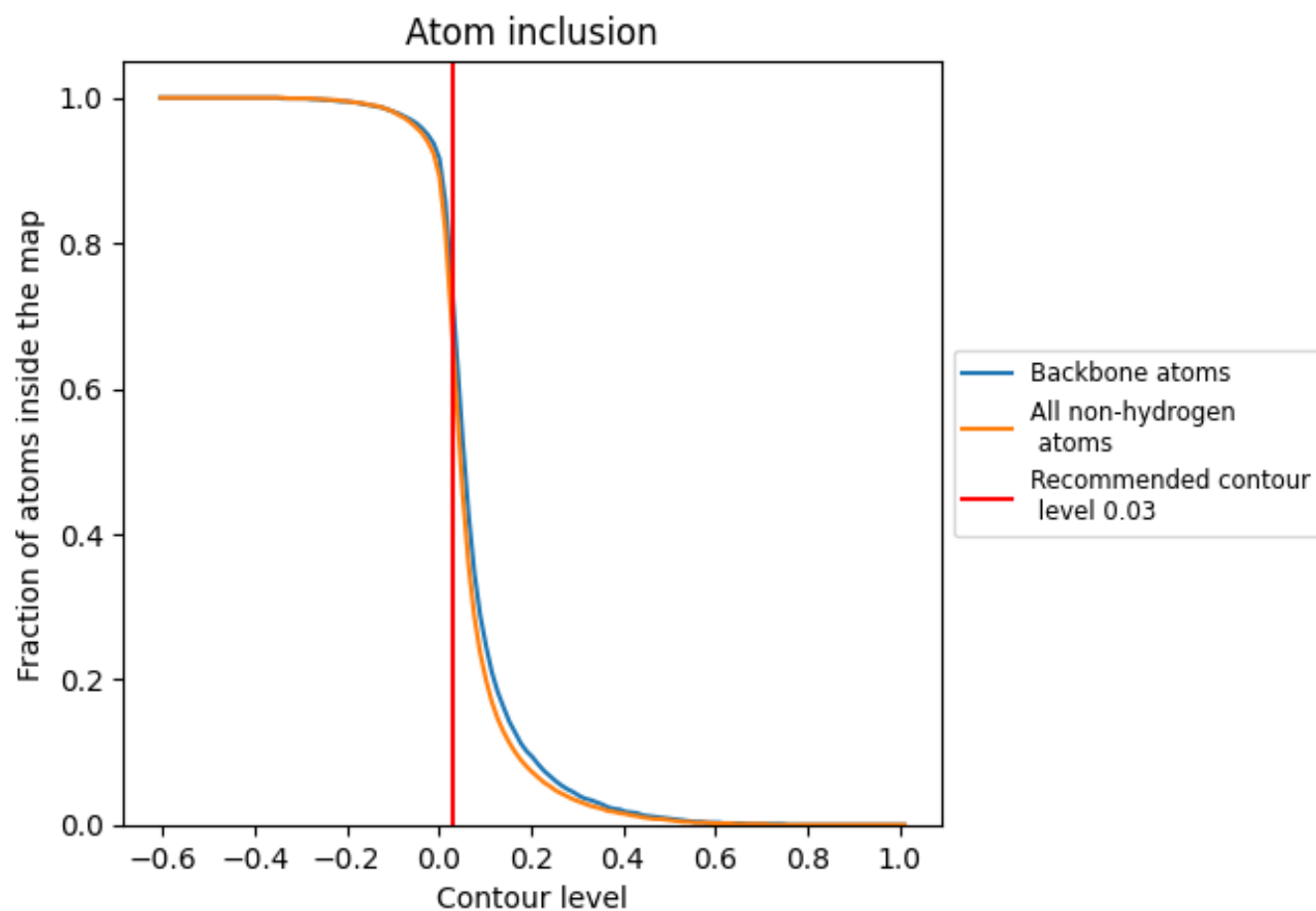
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion ⓘ



At the recommended contour level, 73% of all backbone atoms, 67% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6710	0.0380
A	0.7160	0.0540
B	0.6650	0.0670
C	0.7300	0.0730
D	0.6310	0.0340
E	0.6920	0.0400
F	0.6080	-0.0200
G	0.6840	0.0320
H	0.6410	0.0230
I	0.6750	0.0170
J	0.6600	0.0620

1.0
0.0
<0.0