wwPDB EM Validation Summary Report

Nov 24, 2025 – 01:25 PM 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:

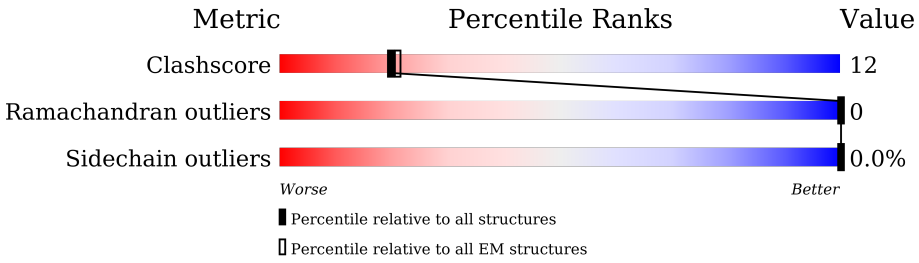
EMDB validation analysis	:	0.0.1.dev129
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

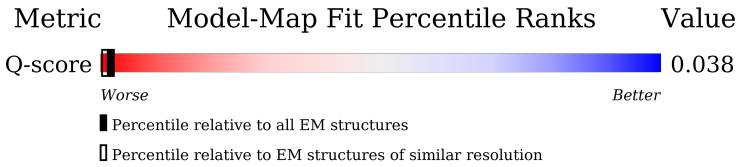
1 Overall quality at a glance (i)

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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
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 <=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	35% 8% 58%
1	B	992	11% 27% 14% 59%
1	C	992	35% 7% 58%
1	D	992	12% 28% 13% 59%

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Mol	Chain	Length	Quality of chain
1	E	992	6% 35% 8% 58%
1	F	992	13% 28% 13% 59%
1	G	992	6% 35% 7% 58%
1	H	992	12% 26% 15% 59%
1	I	992	5% 35% 7% 58%
1	J	992	11% 27% 14% 59%

2 Entry composition (i)

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

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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

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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

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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

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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

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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

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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

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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

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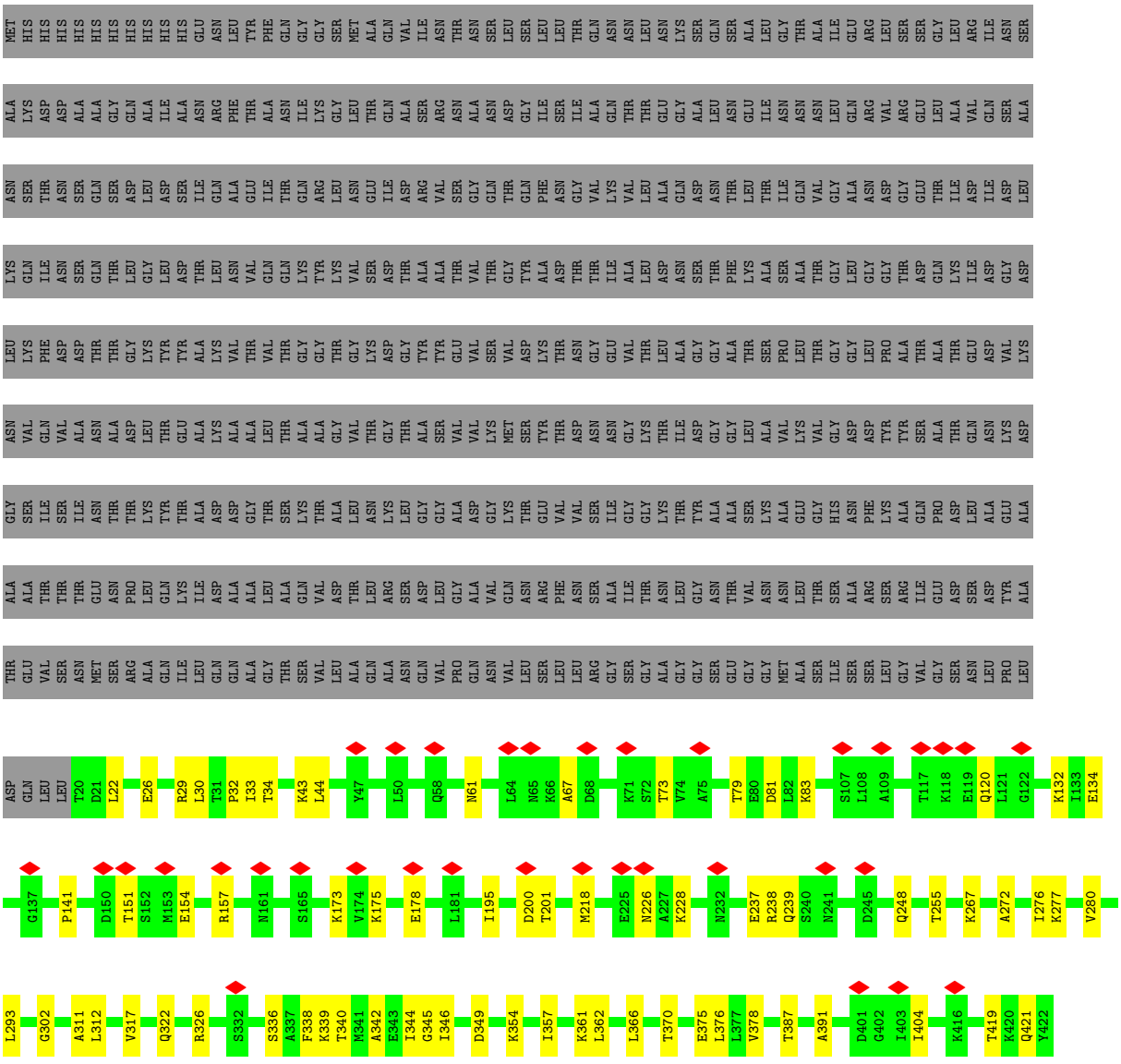
Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLN	-	expression tag	UNP P06179
J	-2	GLY	-	expression tag	UNP P06179
J	-1	GLY	-	expression tag	UNP P06179
J	0	SER	-	expression tag	UNP P06179
J	496	GLY	-	linker	UNP P06179
J	497	SER	-	linker	UNP P06179
J	498	GLY	-	linker	UNP P06179
J	499	ALA	-	linker	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 (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.

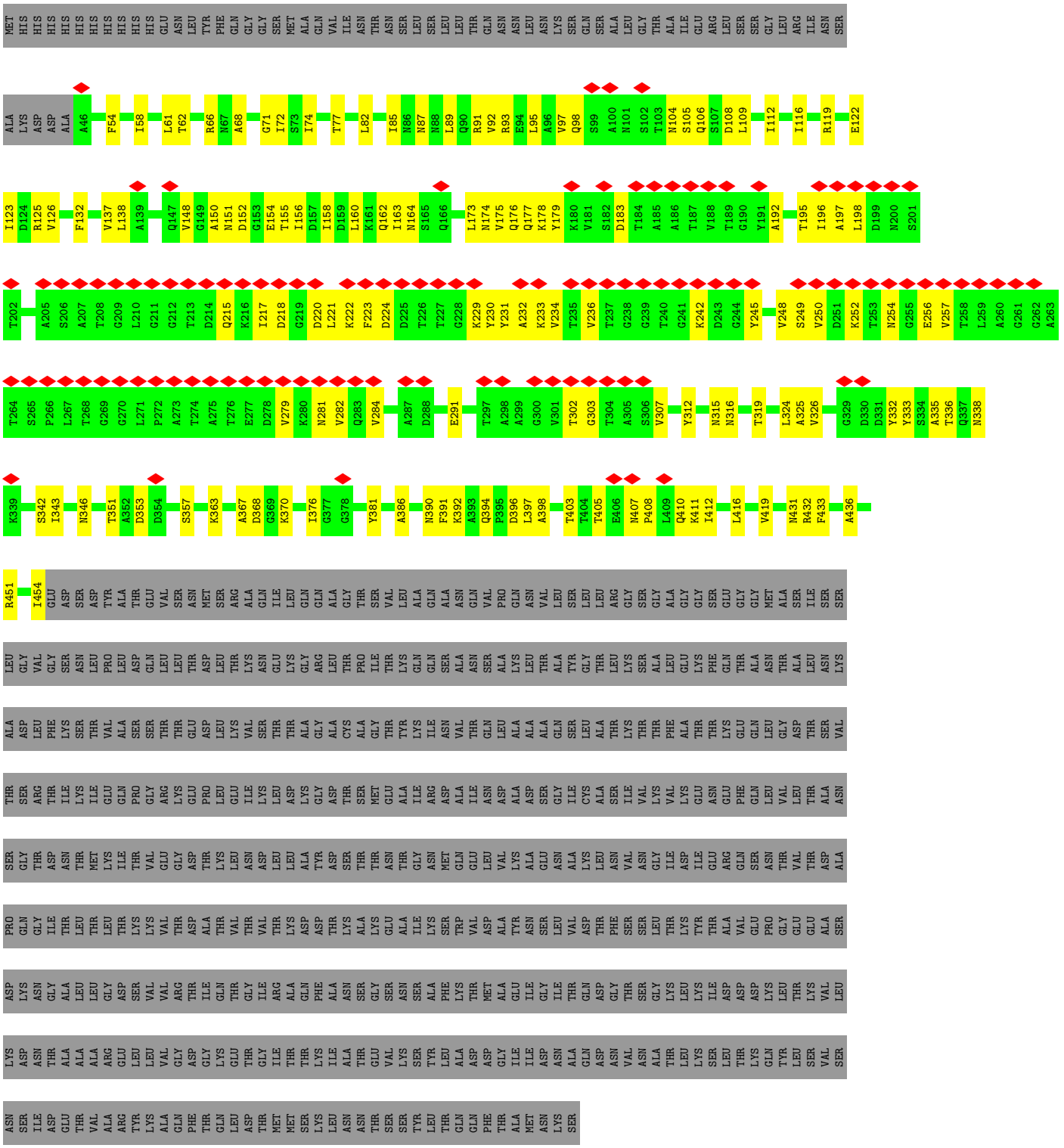
- Molecule 1: Flagellin,Flagellar hook-associated protein 2

Chain A:



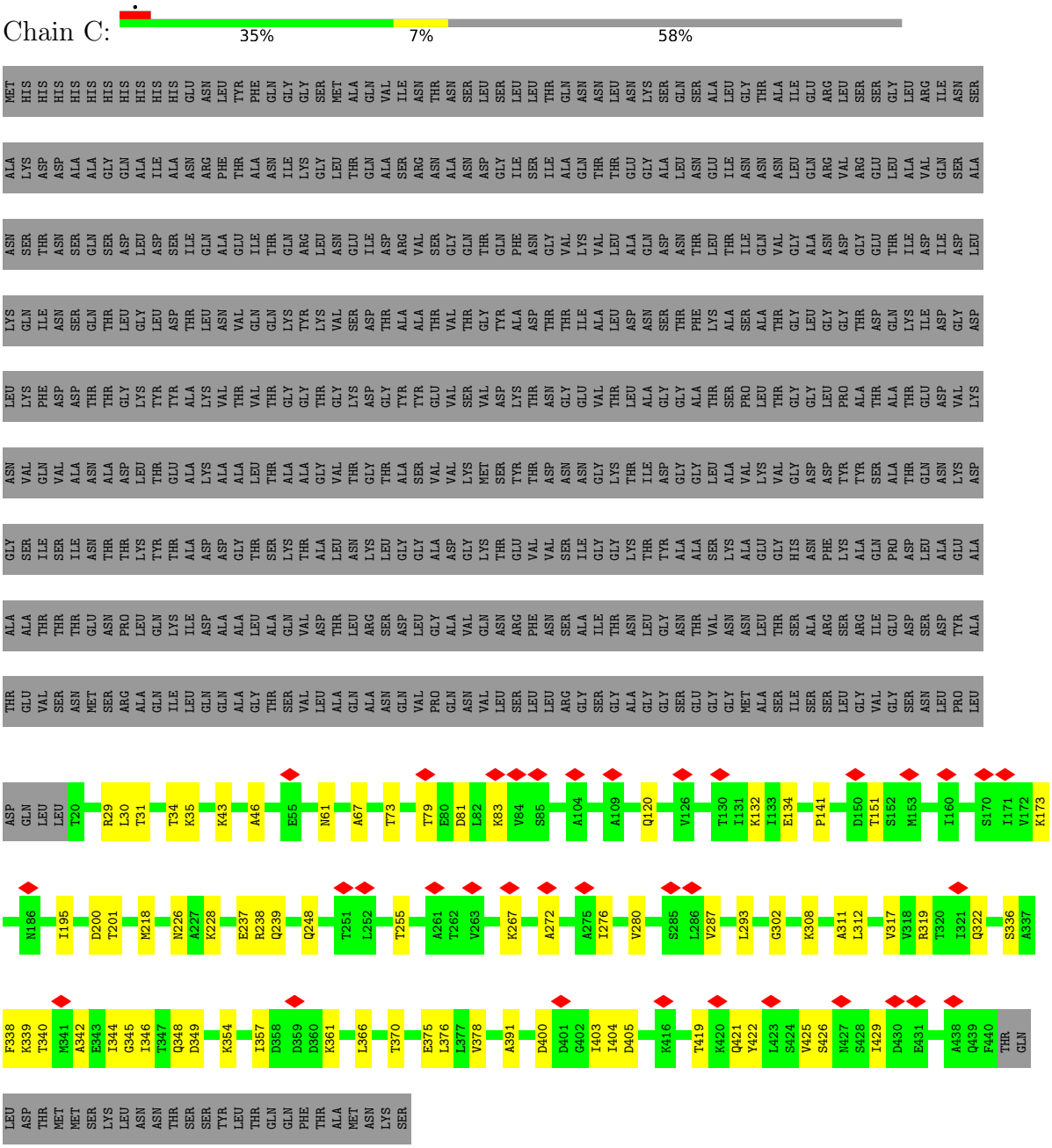
• Molecule 1: Flagellin,Flagellar hook-associated protein 2

Chain B:



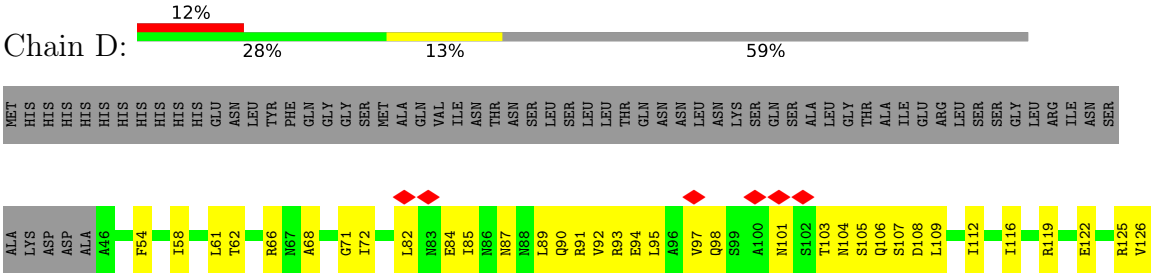
• Molecule 1: Flagellin,Flagellar hook-associated protein 2

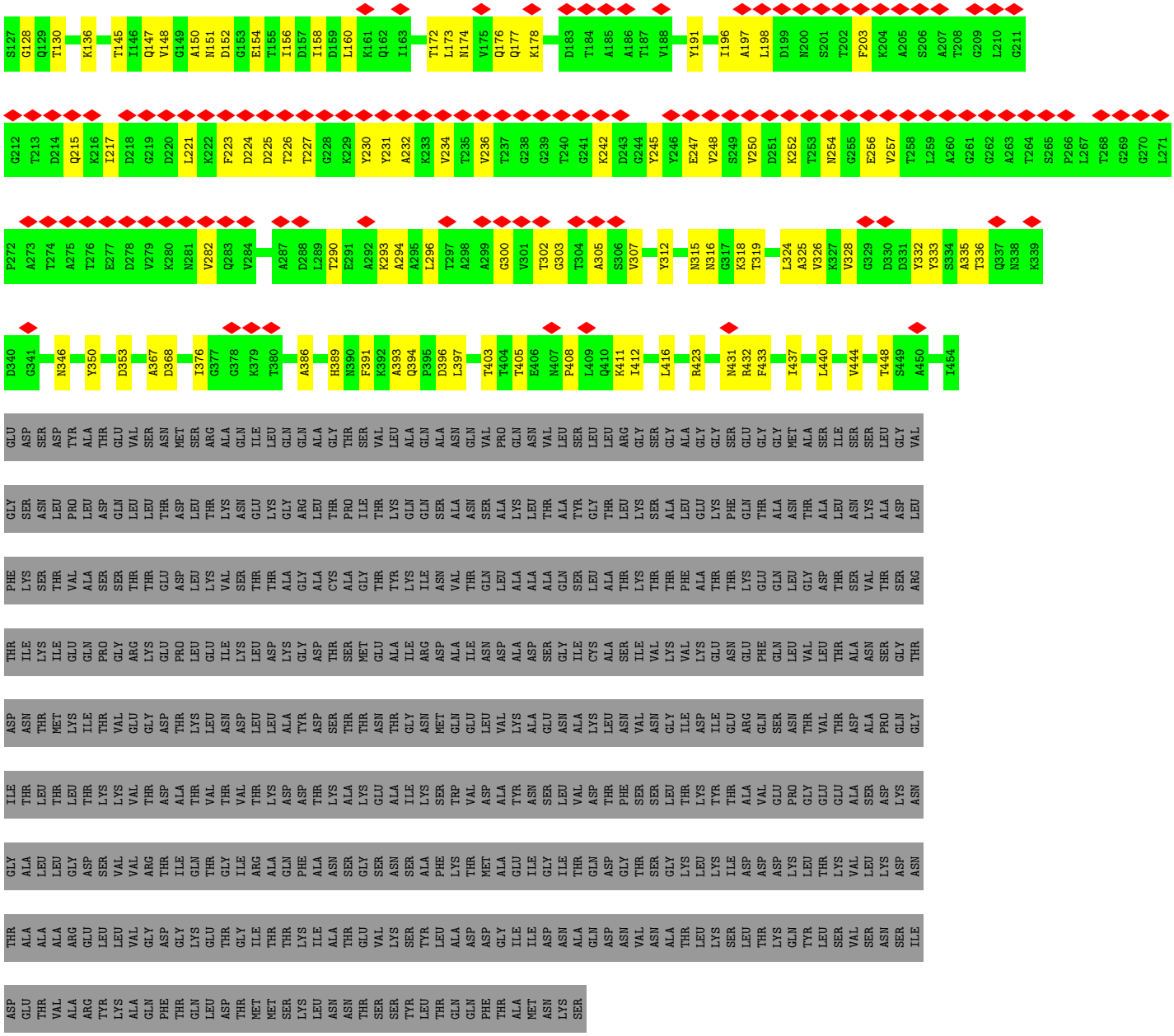
Chain C:



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

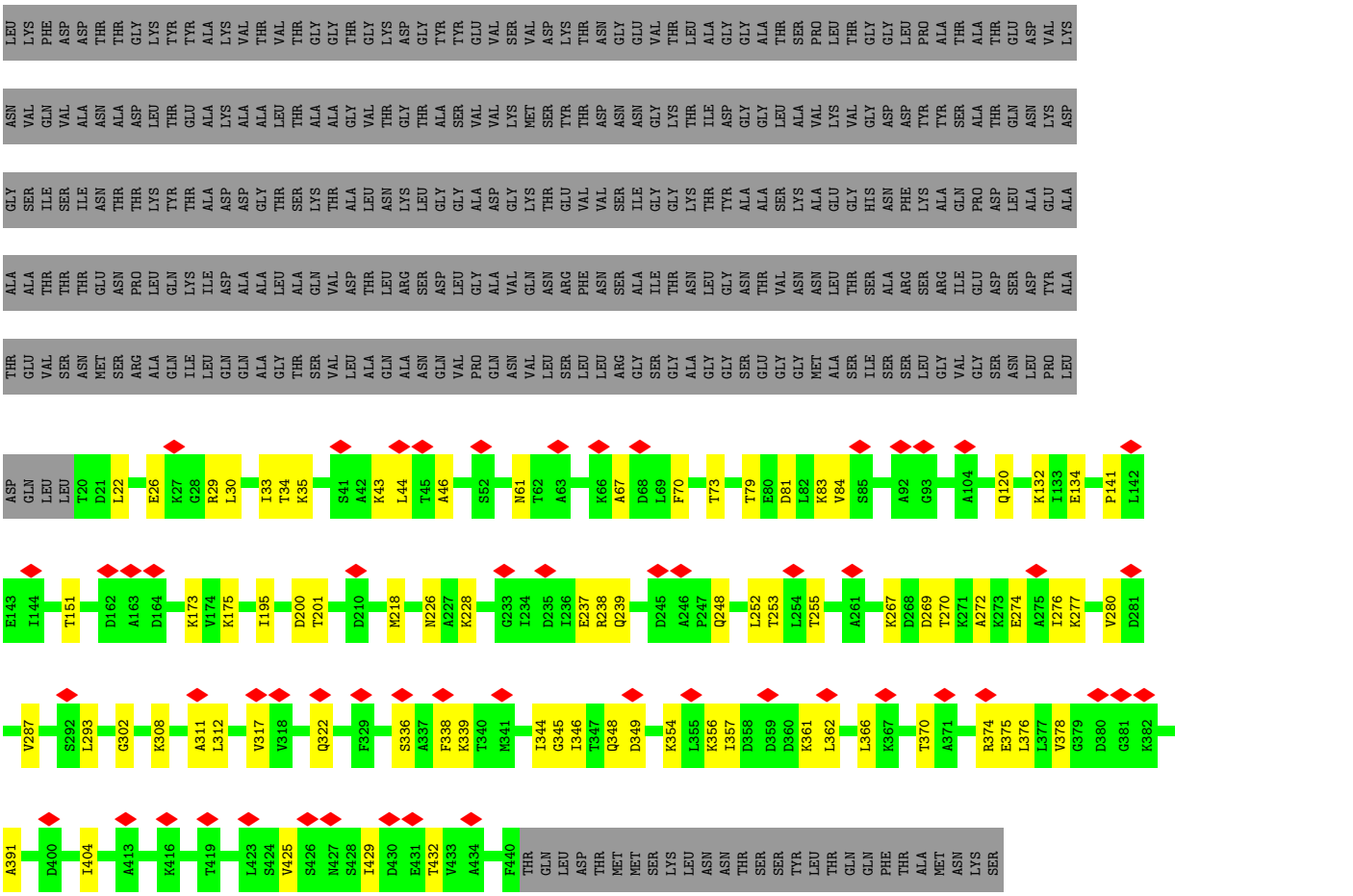
Chain D:





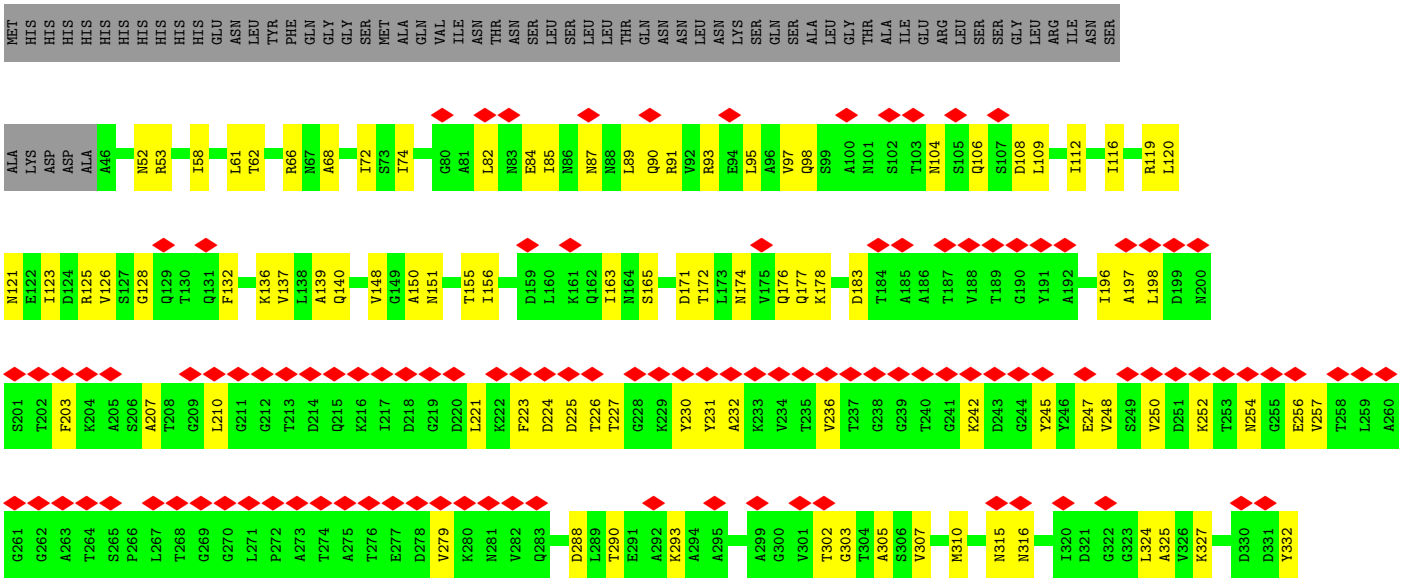
• Molecule 1: Flagellin,Flagellar hook-associated protein 2

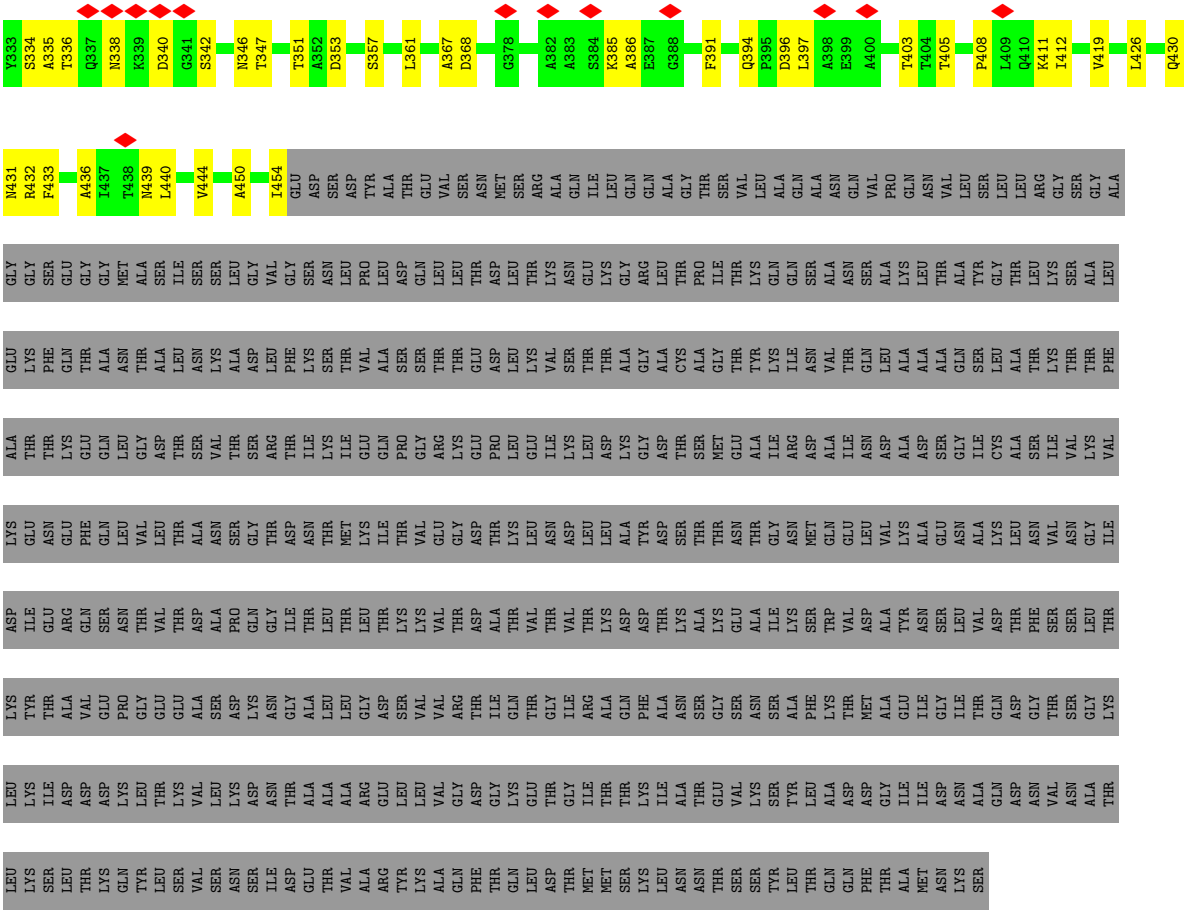
Chain E:



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

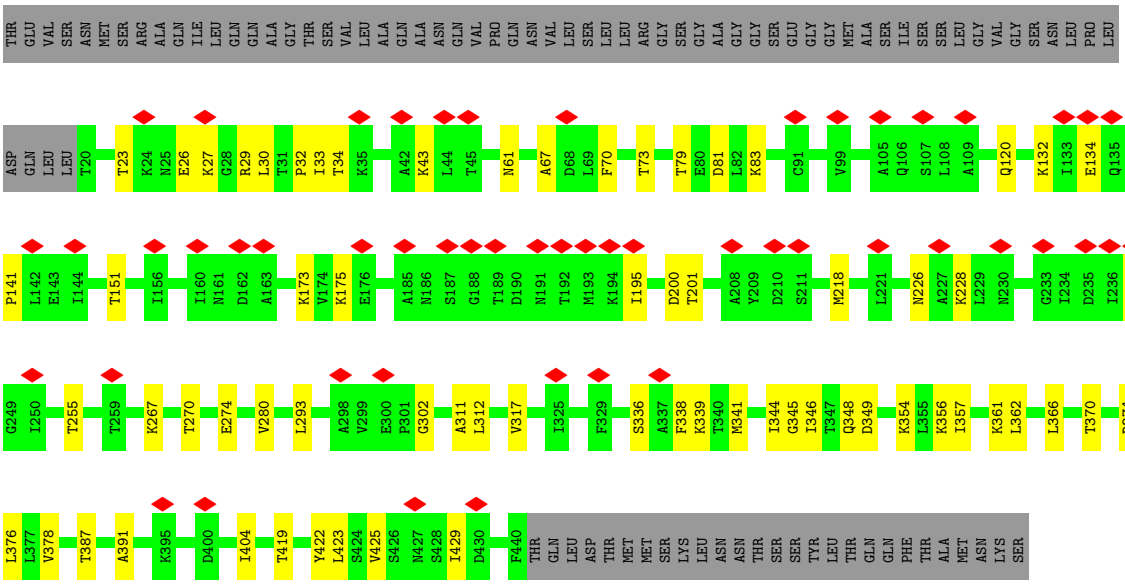
Chain F:




Y333 S334 A335 T336 Q337 N338 K339 D340 G341 S342 N346 T347 T351 A352 D353 S357 L361 A367 D368 G378 A382 A383 S384 K385 A386 E387 G388 F391 Q394 P395 D396 L397 A398 E399 A400 T403 T404 T405 P408 L409 Q410 K411 I412 V419 L426 Q430
N431 R432 F433 A436 I437 T438 N439 L440 V444 A450 T454 GLU ASP SER ASP TYR ALA THR GLU VAL SER ASN MET SER ARG ALA GLN ILE LEU GLN GLN ALA GLY THR SER VAL LEU ALA GLN VAL PRO GLN ASN VAL LEU SER LEU LEU ARG GLY SER GLY ALA
GLY GLY SER GLU GLY GLY MET ALA SER ILE SER SER LEU GLY VAL GLY SER ASN LEU PRO LEU ASP GLN LEU LEU THR ASP LEU THR LYS ASN GLU LYS GLY ARG ALA GLN ILE LEU LEU GLN GLN ALA GLY THR PRO ILE THR LYS GLN GLN ALA ASN SER ALA LYS LEU GLN THR ALA TYR GLY LEU THR LEU LYS SER
GLU LYS PHE GLN THR ALA ASN THR ALA LEU ASN LYS ALA ASP LEU PHE LYS SER THR VAL ALA SER SER THR THR GLU ASP LEU LYS VAL SER THR THR ALA GLY ALA CYS ALA GLY THR TYR LYS ILE ASN VAL THR GLN LEU ALA ALA ASP ALA ALA GLN LEU ALA LEU LYS THR PHE
ALA THR THR LYS GLU GLN LEU GLY ASP THR SER VAL THR SER ARG THR ILE LYS ILE GLU GLN PRO GLY ARG LYS GLU PRO LEU GLU GLU ILE LYS LEU ASP LYS GLY ASP THR SER MET GLU ALA ILE ARG ASP ALA ILE ASN ASP ALA ASP SER GLY ILE CYS ALA SER ILE VAL LYS VAL
LYS GLU ASN GLU PHE GLN LEU VAL LEU THR ALA ASN SER GLY THR ASP ASN THR MET LYS ILE THR VAL GLU GLY ASP THR LYS LEU LEU ASN ASP LEU LEU LEU ALA TYR ASP SER THR THR ASN THR GLY ASN MET GLN GLU LEU VAL LYS ALA GLU ASN ALA ALA LYS LEU ASN VAL ASN GLY ILE
ASP ILE GLU ARG GLN SER ASN THR VAL THR ASP ALA PRO GLN GLY ILE THR LEU THR LEU THR LYS LYS VAL THR ASP ALA THR VAL THR VAL THR LYS ASP ASP THR LYS ALA LYS GLU ALA ILE LYS SER TRP VAL ASP ALA TYR ASN SER LEU VAL ASP THR PHE SER SER LEU THR
LYS TYR THR ALA VAL GLU PRO GLY GLU GLU ALA SER ASP LYS ASN GLY ALA LEU LEU GLY ASP SER VAL VAL ARG THR ILE GLN THR GLY ILE ARG ALA GLN PHE ALA ASN SER GLY SER ASN SER ALA PHE LYS THR MET ALA GLU ILE GLY ILE THR GLN ASP GLY THR SER GLY LYS
LEU LYS ILE ASP ASP LYS LEU THR LYS VAL LEU LYS ASP ASN THR ALA ALA ALA ARG GLU LEU LEU VAL GLY ASP GLY LYS GLU THR GLY ILE THR THR LYS ILE ALA THR GLU VAL LYS SER TYR LEU ALA ASP ASP GLY ILE ILE ASP ASN ALA GLN ASP ASN VAL ASN ALA THR
LEU LYS SER LEU THR LYS GLN TYR LEU SER VAL SER ASN SER ILE ASP GLU THR VAL ALA ARG TYR LYS ALA GLN PHE THR GLN LEU ASP THR MET MET SER LYS LEU ASN ASN THR SER SER TYR LEU THR GLN GLN PHE THR ALA MET ASN LYS SER

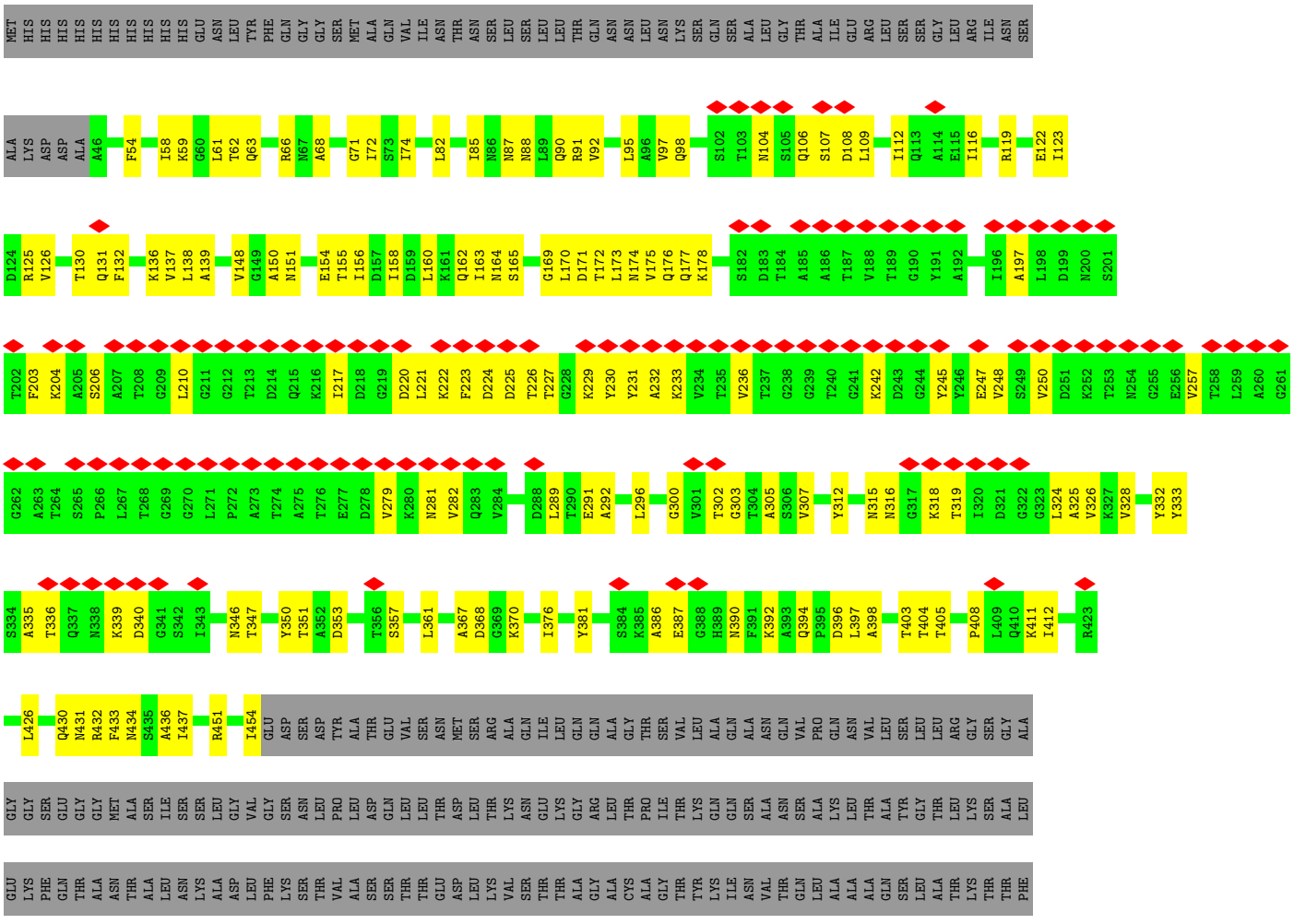
• Molecule 1: Flagellin,Flagellar hook-associated protein 2

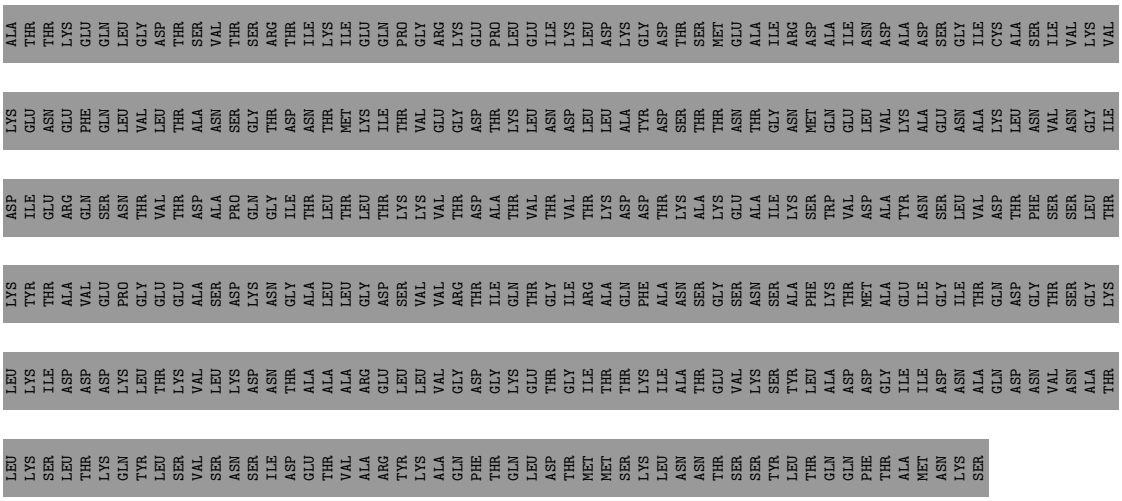
Chain G:



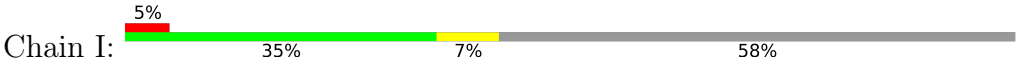
• Molecule 1: Flagellin,Flagellar hook-associated protein 2

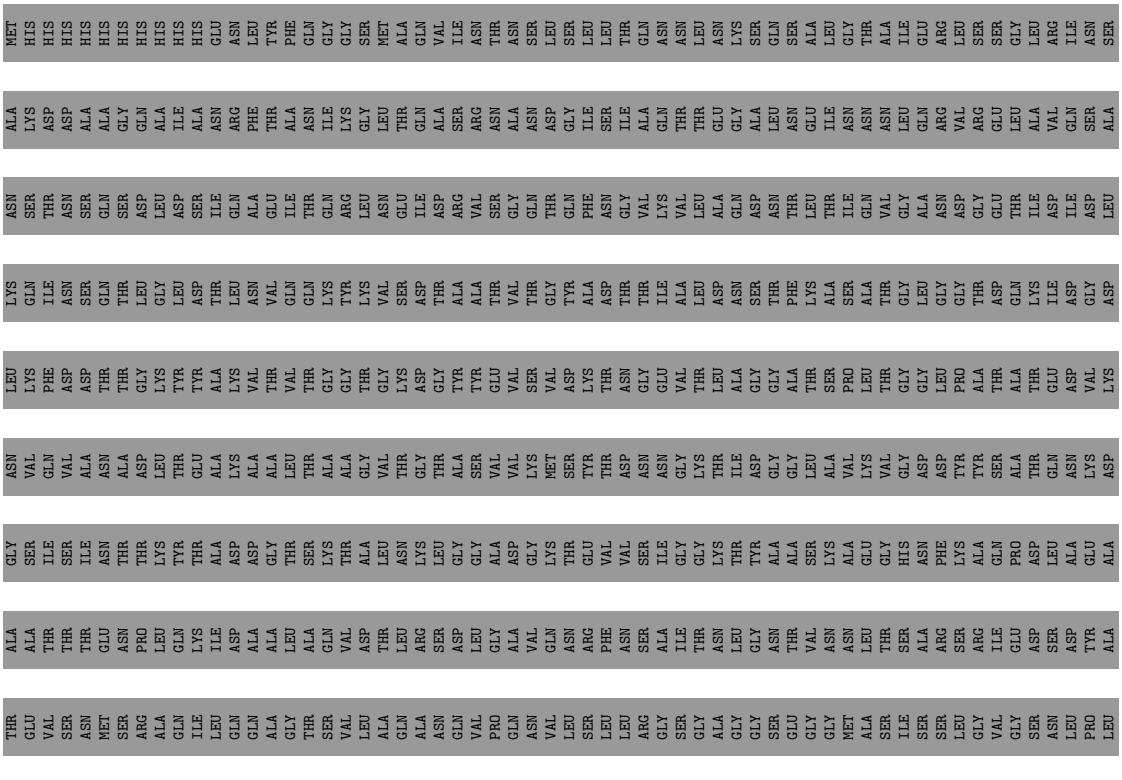
Chain H:

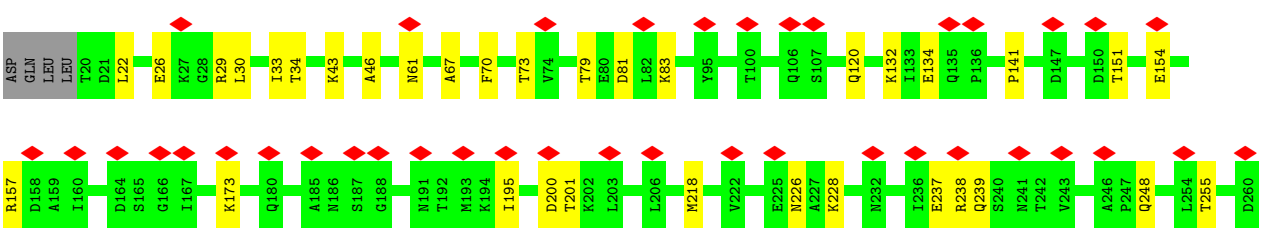


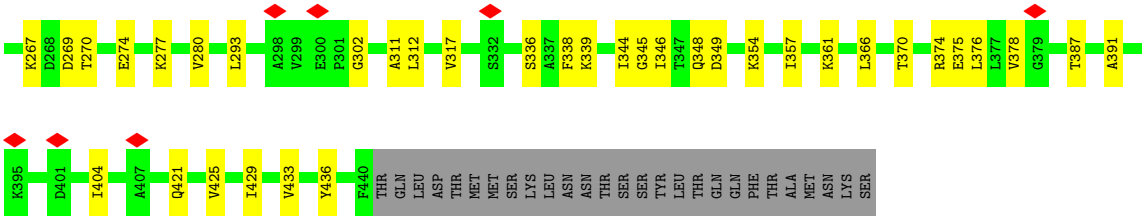


• Molecule 1: Flagellin,Flagellar hook-associated protein 2

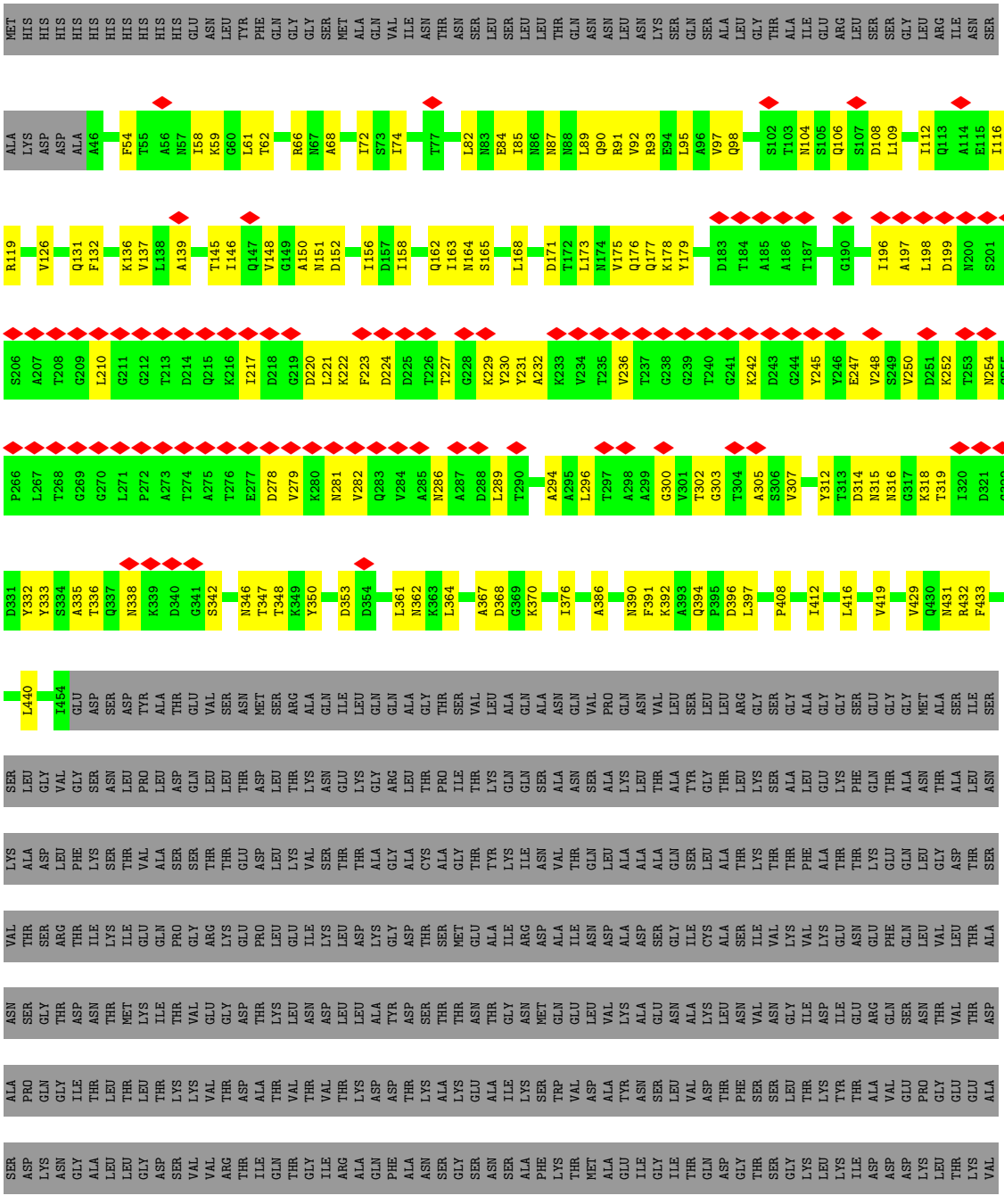








• Molecule 1: Flagellin,Flagellar hook-associated protein 2



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

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

4 Experimental information (i)

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 ($e^-/Å^2$)	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

5.1 Standard geometry

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

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

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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

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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 (i)

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%)	91	95
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

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

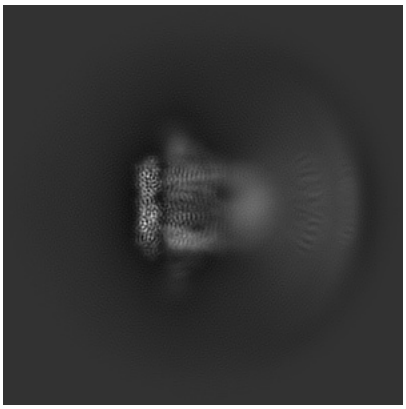
This section contains visualisations of the EMDB entry EMD-63660. These allow visual inspection of the internal detail of the map and identification of artifacts.

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.

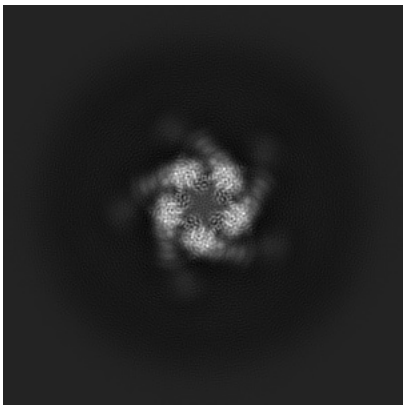
6.1 Orthogonal projections

6.1.1 Primary map

X

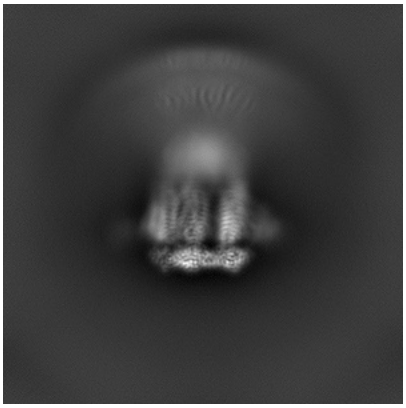


Y

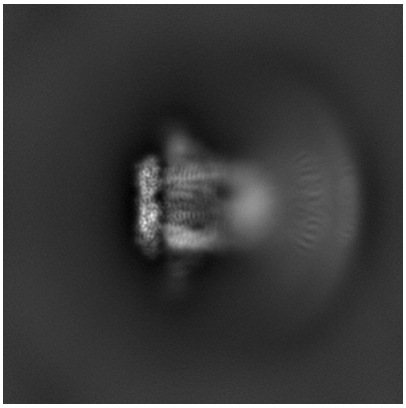


Z

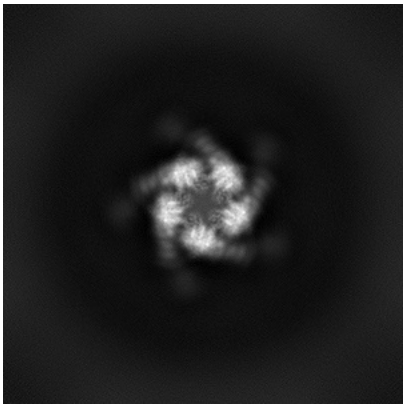
6.1.2 Raw map



X



Y



Z

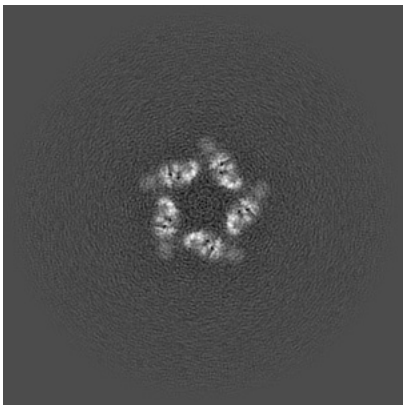
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

X Index: 300

Y Index: 300

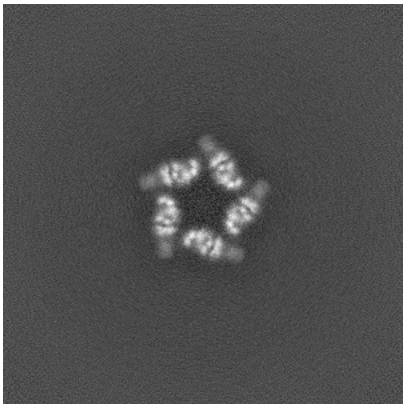


Z Index: 300

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

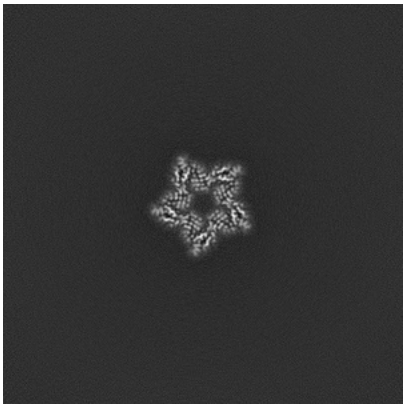
Y Index: 341

Z Index: 212

6.3.2 Raw map

X Index: 341

Y Index: 288

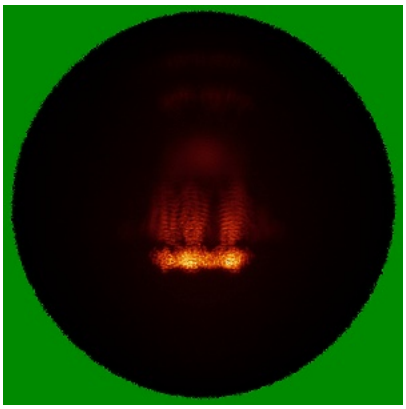


Z Index: 212

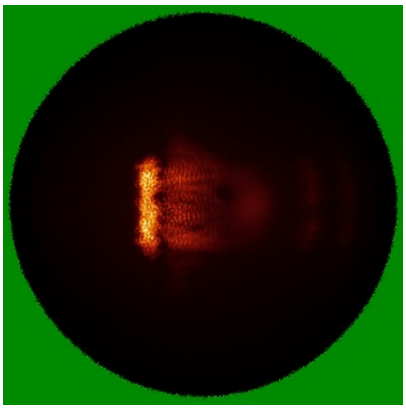
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

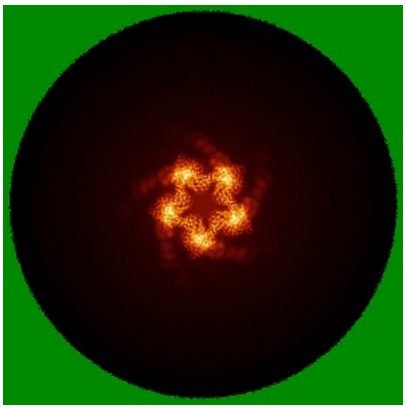
6.4.1 Primary map



X

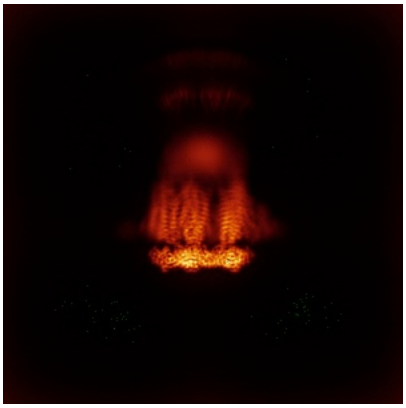


Y

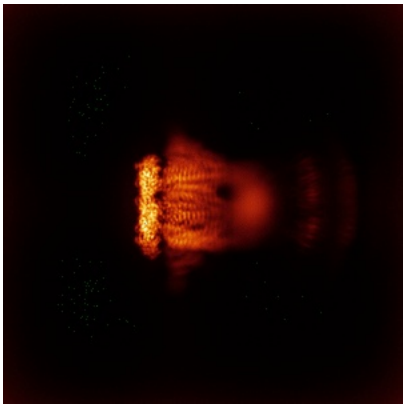


Z

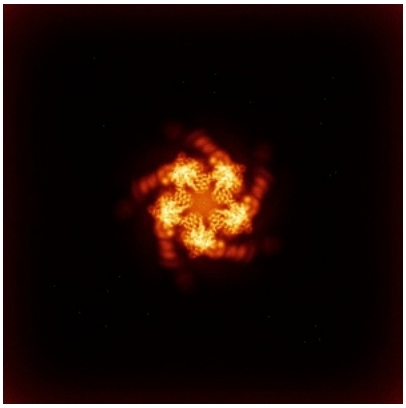
6.4.2 Raw map



X



Y



Z

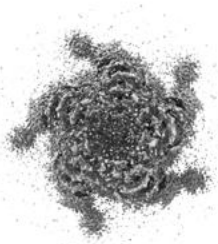
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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.

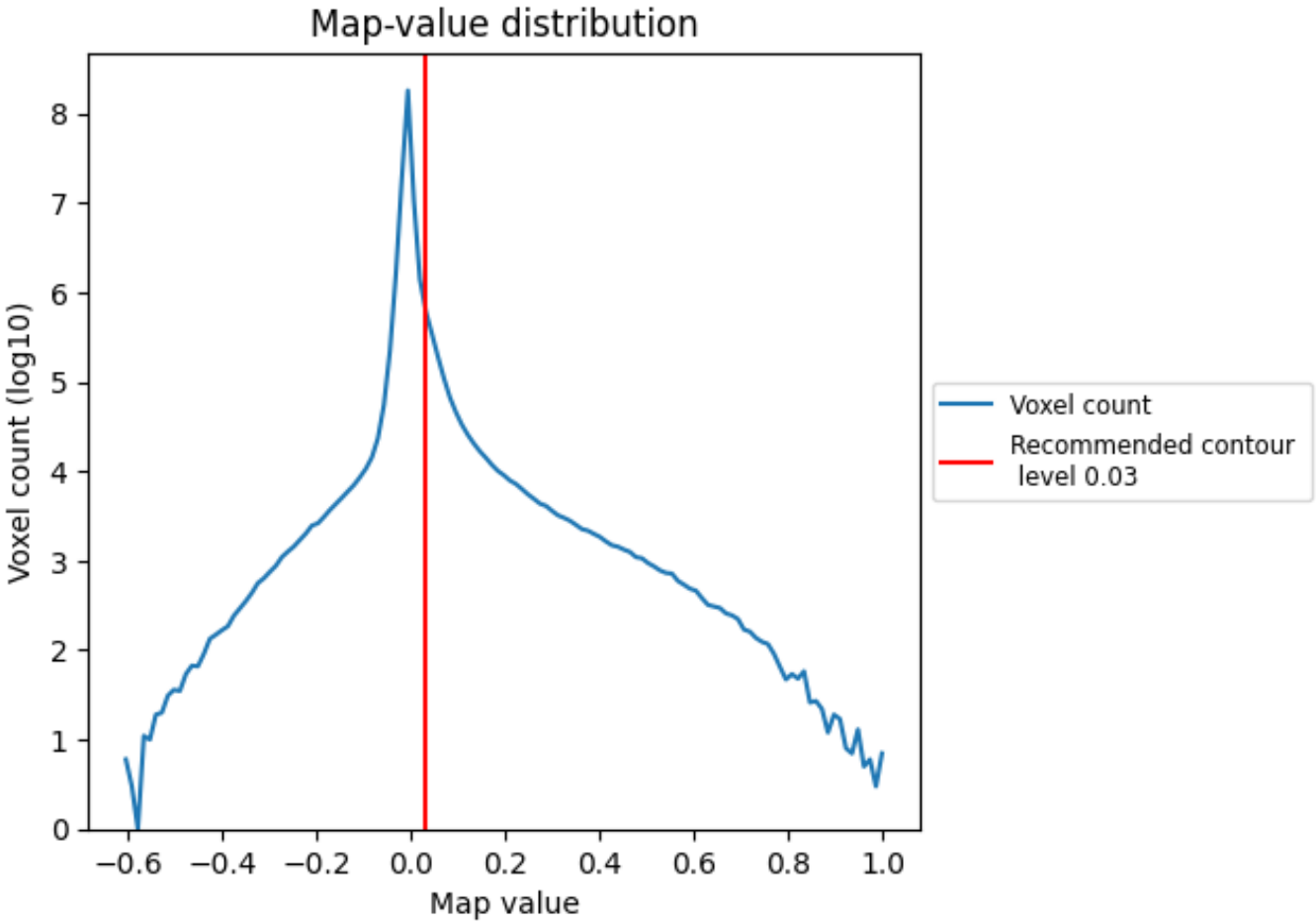
6.6 Mask visualisation (i)

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

7 Map analysis

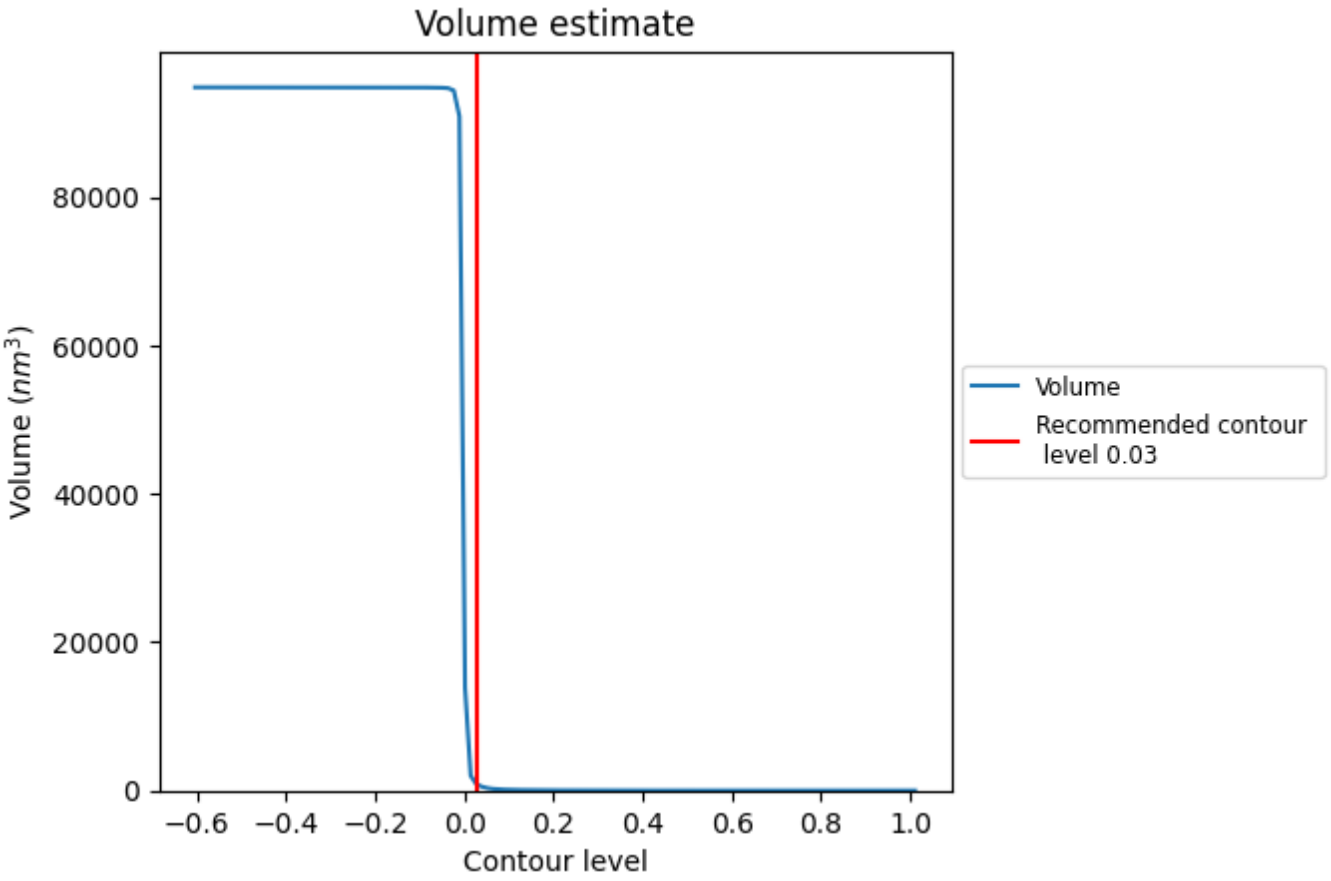
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

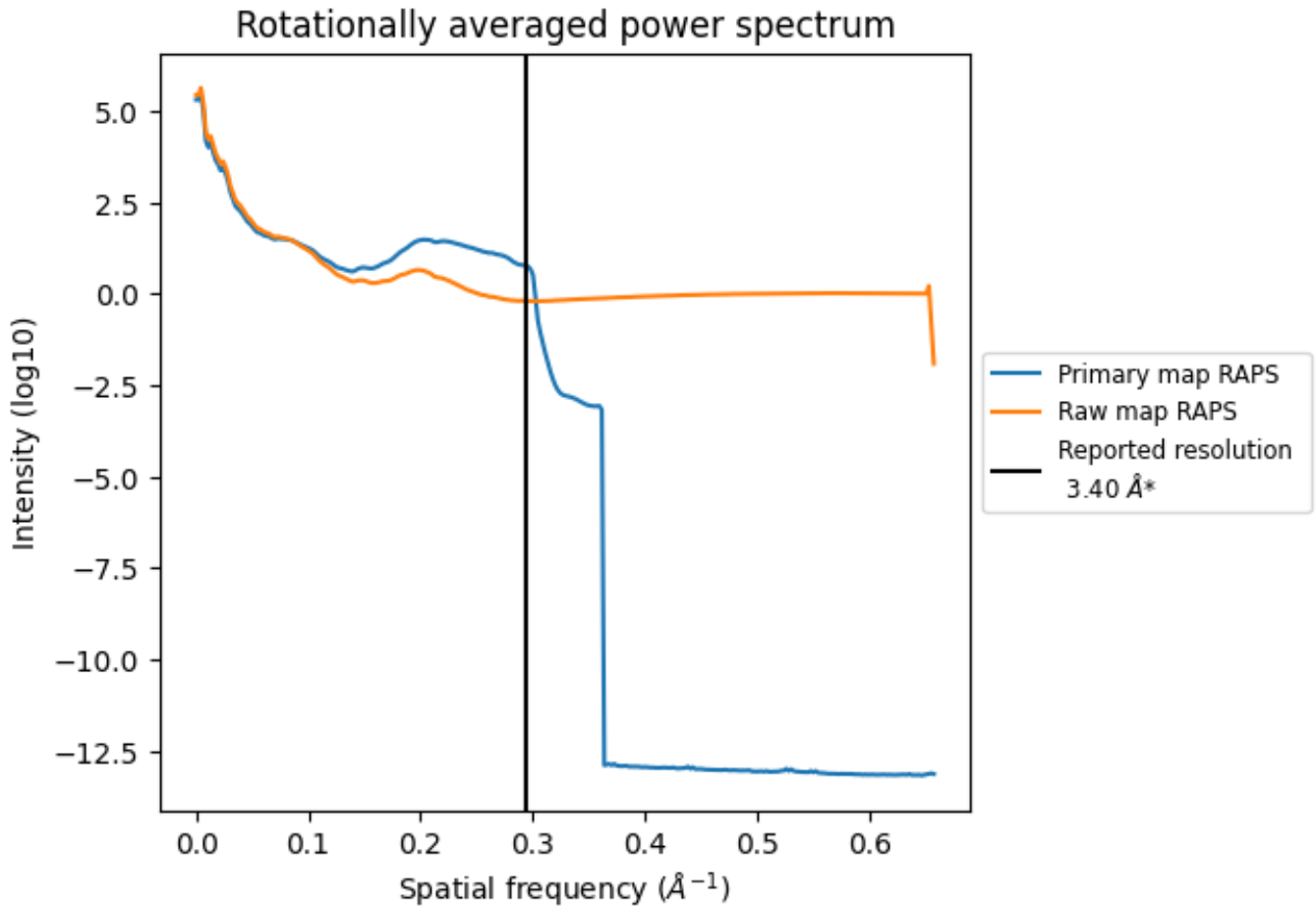
7.2 Volume estimate (i)



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 (i)

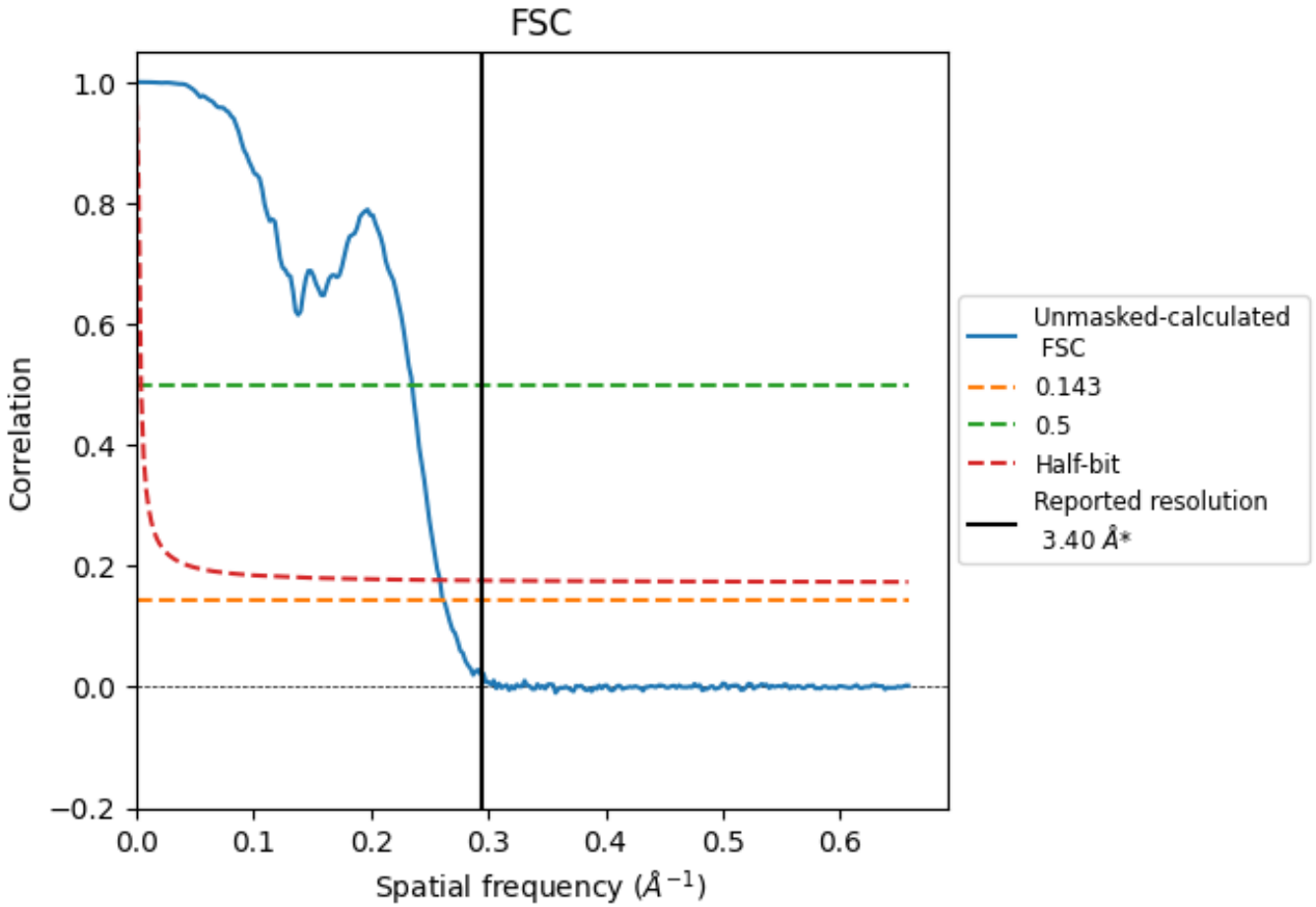


*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

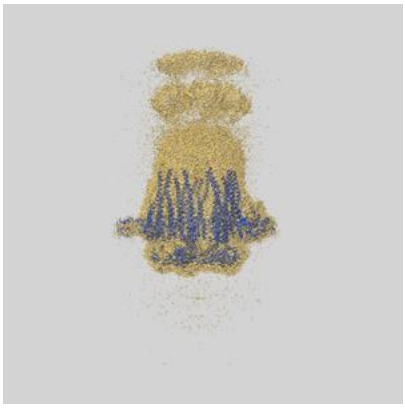
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	4.25	3.86

*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 %

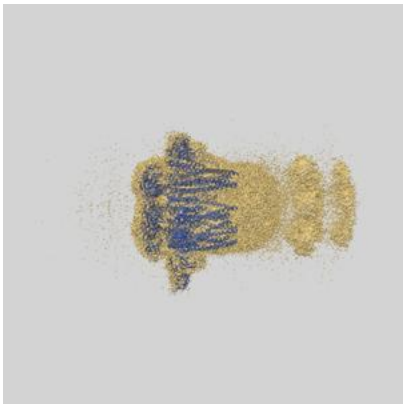
9 Map-model fit

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.

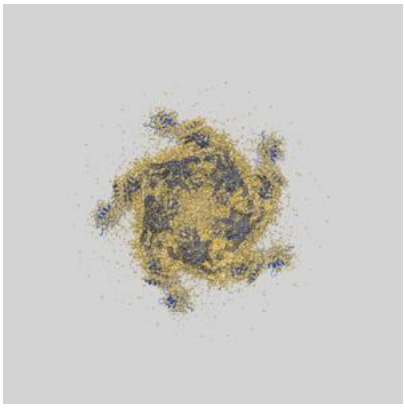
9.1 Map-model overlay



X



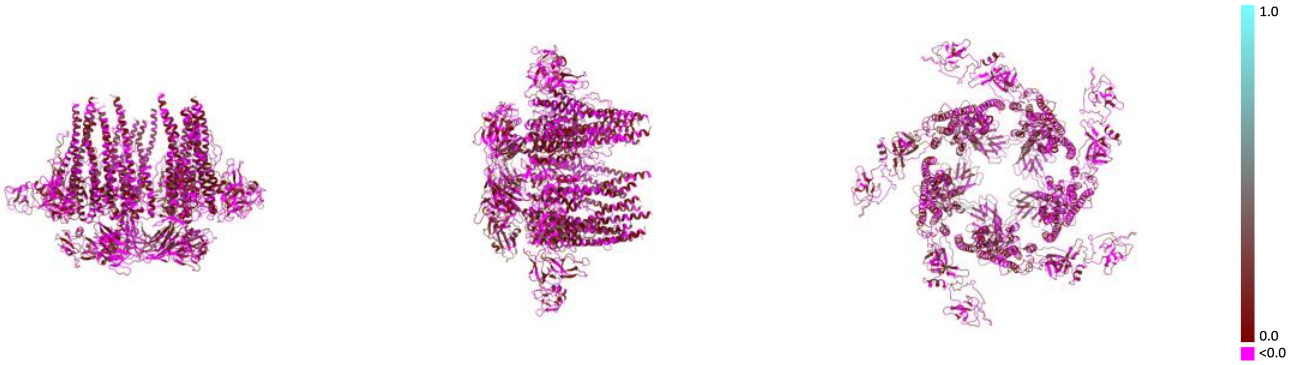
Y



Z

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.

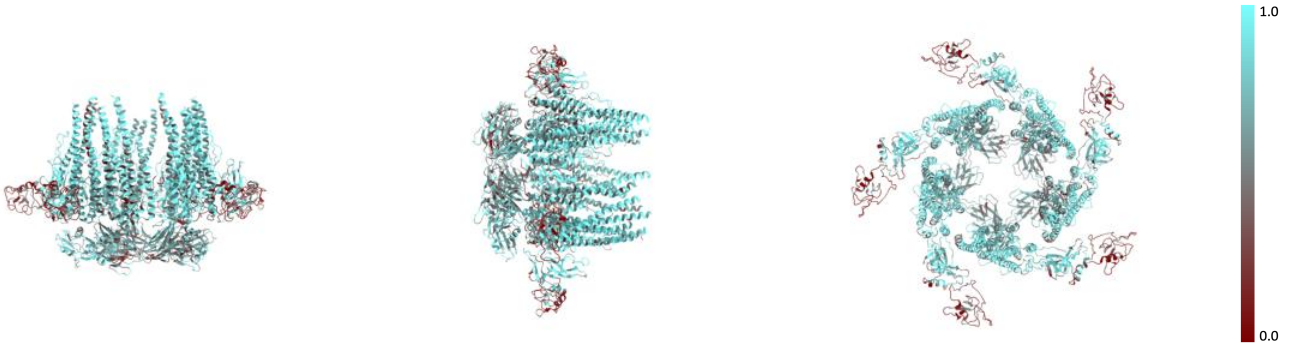
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

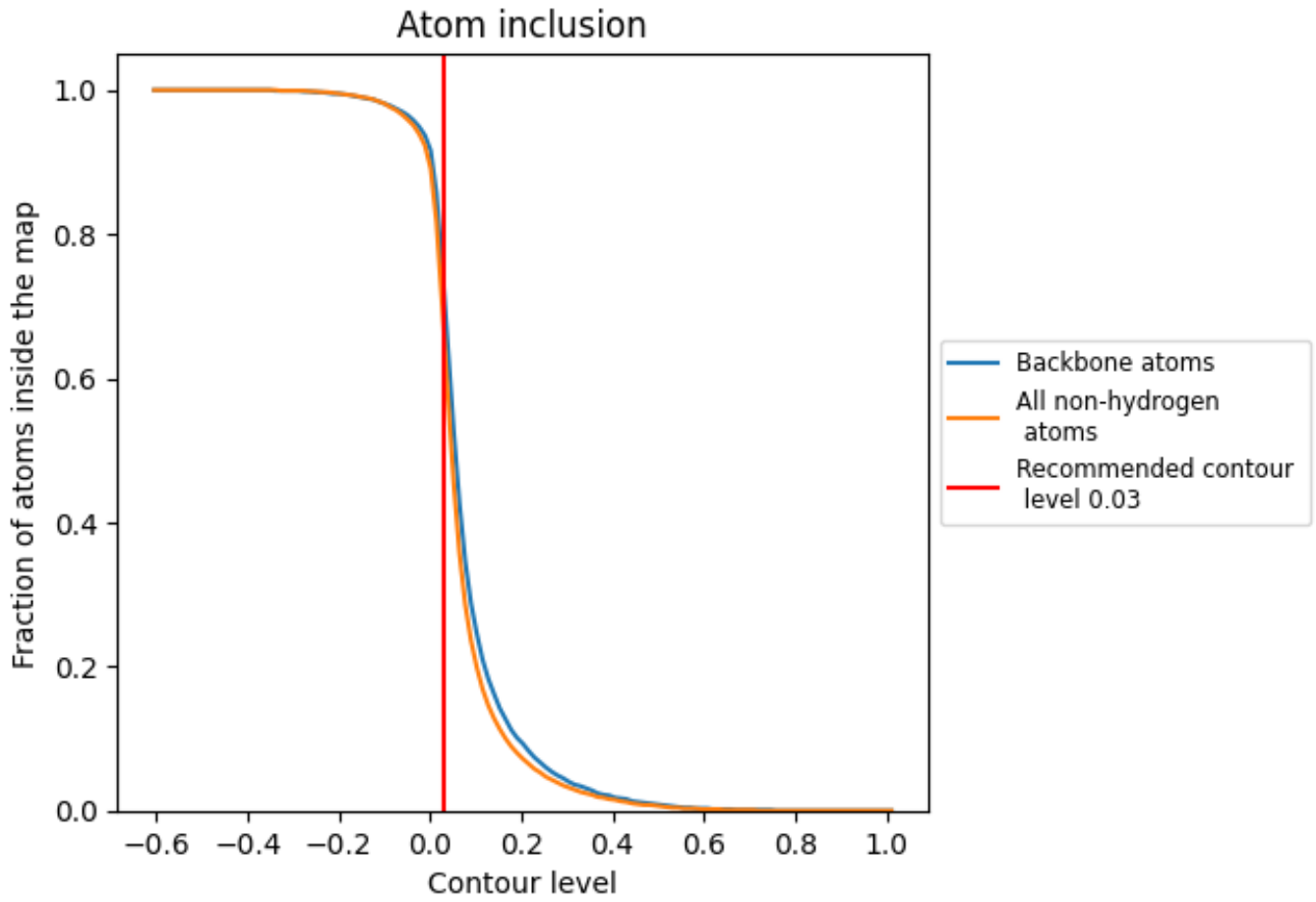
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (i)



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