



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:44 AM UTC

PDB ID : 6SD2 / pdb_00006sd2
EMDB ID : EMD-10146
Title : Structure of the RBM2inner region of the Salmonella flagella MS-ring protein
FliF with 21-fold symmetry applied.
Authors : Johnson, S.; Fong, Y.H.; Deme, J.C.; Furlong, E.J.; Kuhlen, L.; Lea, S.M.
Deposited on : 2019-07-26
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

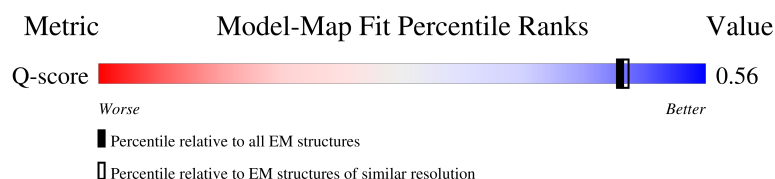
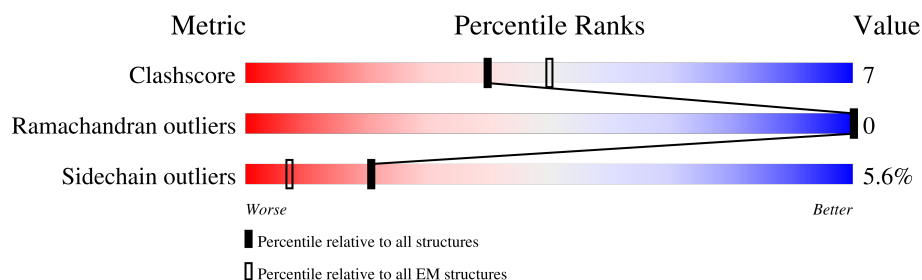
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



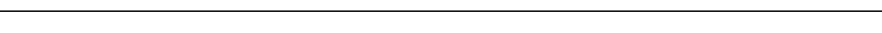
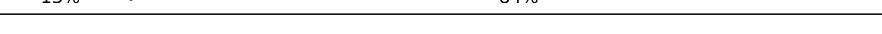
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	560	
1	C	560	
1	D	560	
1	F	560	

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Mol	Chain	Length	Quality of chain
1	G	560	 13% 84%
1	I	560	 12% 84%
1	J	560	 13% 84%
1	L	560	 12% 84%
1	N	560	 13% 84%
1	O	560	 13% 84%
1	Q	560	 13% 84%
1	R	560	 13% 84%
1	T	560	 13% 84%
1	U	560	 13% 84%
1	W	560	 13% 84%
1	Y	560	 13% 84%
1	Z	560	 13% 84%
1	b	560	 13% 84%
1	c	560	 13% 84%
1	e	560	 13% 84%
1	f	560	 13% 84%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13566 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	C	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	D	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	F	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	G	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	I	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	J	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	L	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	N	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	O	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	Q	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	R	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	T	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	U	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	W	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	Y	88	Total	C	N	O	S	0	0
			646	402	115	128	1		
1	Z	88	Total	C	N	O	S	0	0
			646	402	115	128	1		

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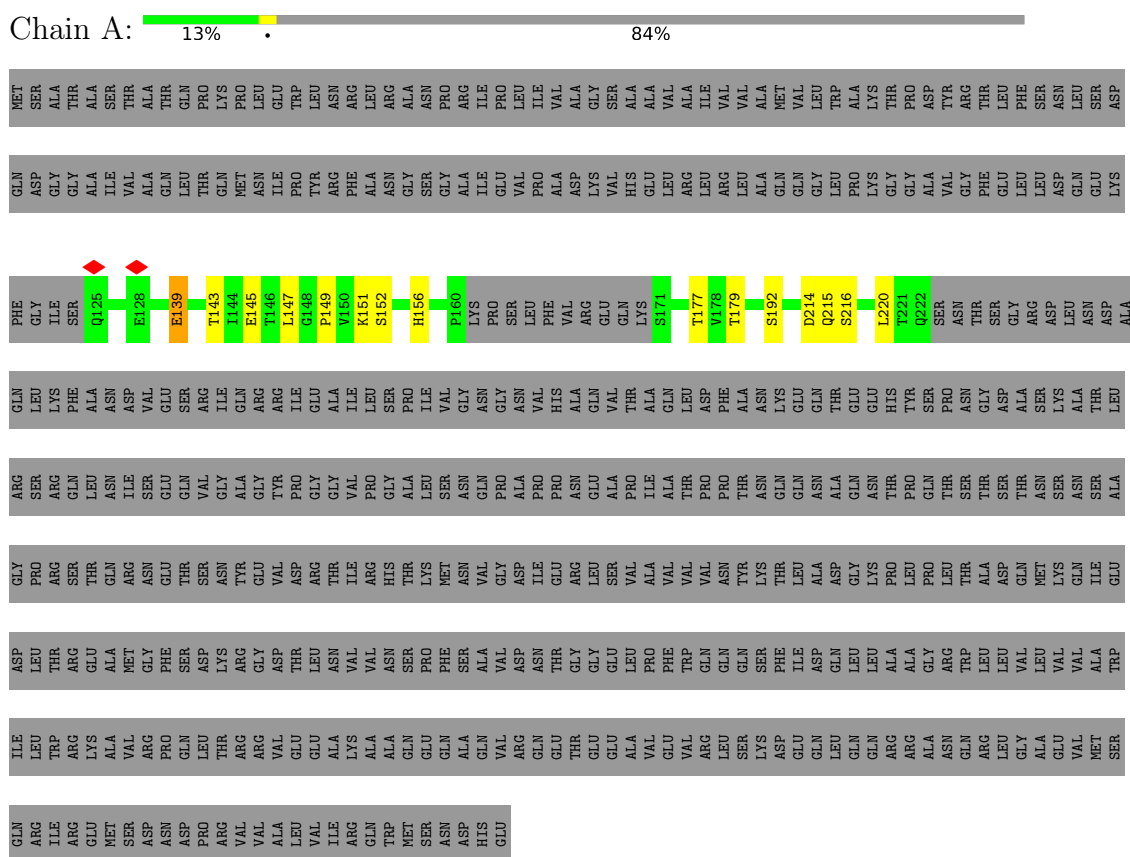
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	c	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	e	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	f	88	Total 646	C 402	N 115	O 128	S 1	0	0

3 Residue-property plots

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

• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein



MET SER GLN ARG ILE GLU MET SER ASP ASN PRO ARG VAL ALA VAL GLU VAL ILE ARG GLN TRP MET SER ASN HIS GLU	TRP	ALA	ILE	TRP	ARG	LYS	VAL	ARG	ASP	PRO	GLN	LEU	ARG	VAL	GLU	ALA	ALA	GLN	ALA	GLN	ALA	GLN	ALA	VAL	ARG	GLN	GLU	GLU	ALA	VAL	GLU	GLU	GLU	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
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● Molecule 1: Flagellar M-ring protein

Chain D: 13% 84%

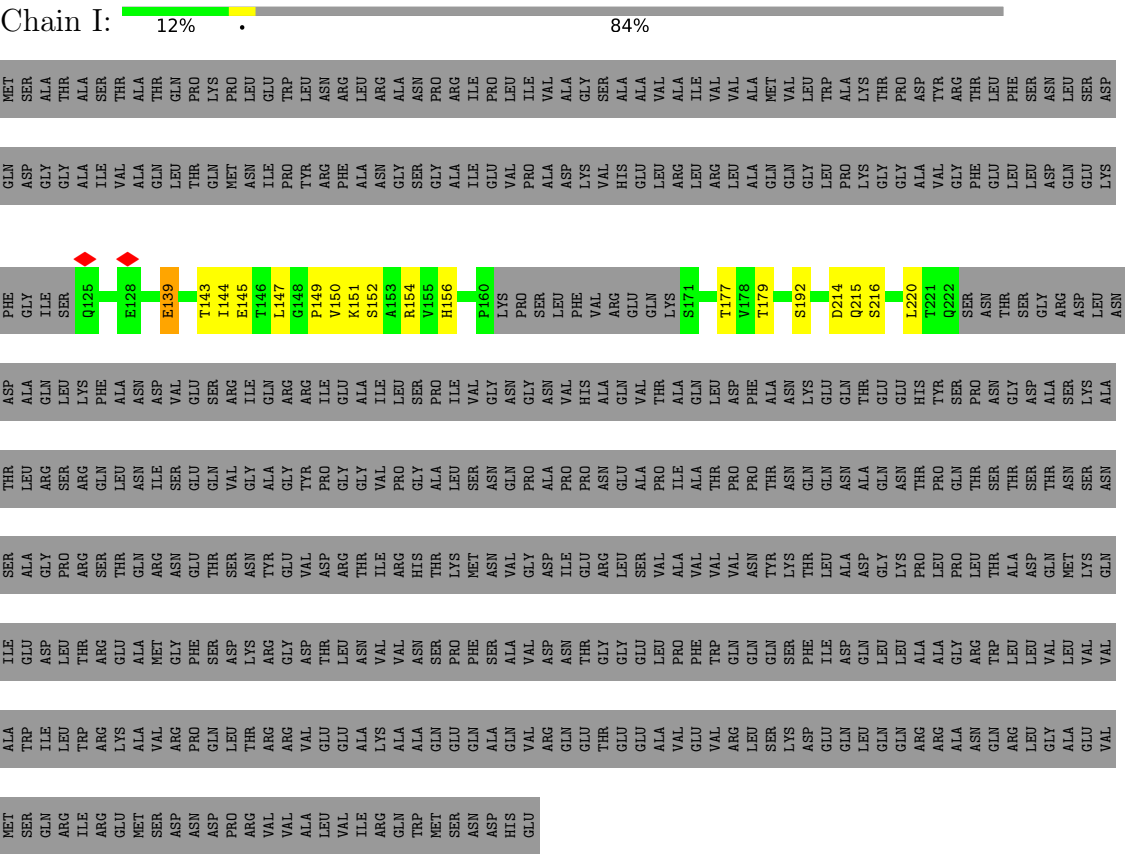
GLN	ARG	ILE	LEU	ASP	GLY	ARG	SER	GLN	THR	GLN	VAL	GLY	THR	ASP	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	GLY	THR	GLN	VAL	
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● Molecule 1: Flagellar M-ring protein

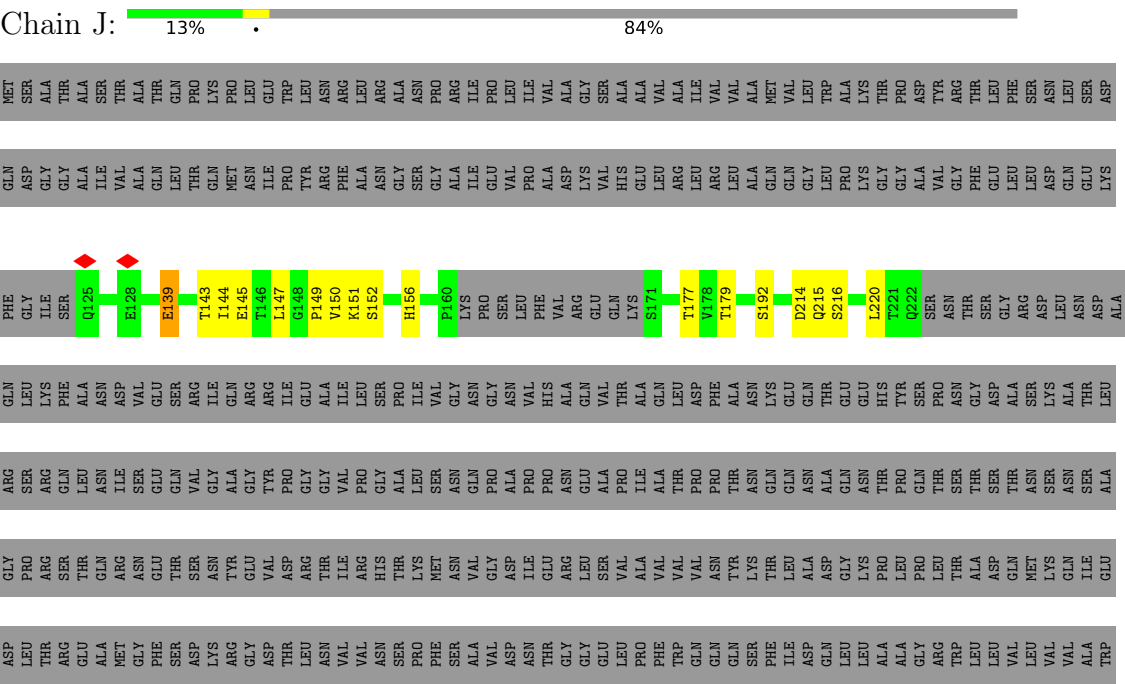
Chain F: 13% 84%



● Molecule 1: Flagellar M-ring protein



● Molecule 1: Flagellar M-ring protein



[illegible]

- Molecule 1: Flagellar M-ring protein

Chain L: 12% 2% 84%

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

PHE	GLY	ILE	SER	Q125	E128	E139	T143	I144	E145	T146	I147	G148	P149	V150	K151	S152	A153	R154	V155	H156	P160	LYS	PRO	SER	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	S171	T177	V178	T179	S192	D214	Q215	Q216	L220	T221	Q222	SER	ASN	THR	THR	GLY	ARG	ASP	LEU
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ASP	ALA	GLN	LEU	LYS	PHE	ALA	ASN	ASP	VAL	GLU	SER	ARG	ILE	GLN	ARG	ARG	ILE	GLU	ALA	LEU	SER	PRO	GLY	ASN	ASN	VAL	HIS	ALA	GLN	GLN	VAL	THR	ALA	GLN	LEU	LEU	ASP	PHE	ASP	ALA	ASN	LYS	GLU	GLN	THR	GLU	GLU	HIS	TYR	SER	PRO	SER	ASN	GLY	ASP	ALA	SER	SER	LYS	ALA
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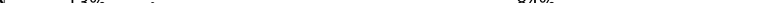
SER	ALA	GLY	GLY	PRO	ARG	SER	THR	GLN	ARG	ASN	GLU	THR	SER	ASP	VAL	GLY	ASP	ILE	GLU	LEU	ARG	LEU	SER	SER	VAL	ALA	VAL	VAL	VAL	VAL	ASN	TYR	LYS	THR	HIS	ARG	THR	ILE	THR	ARG	THR	ARG	ASP	VAL	GLU	TYR
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MET SER GLN ARG ILE ARG GLU MET SER ASP ASN ASP PRO ARG VAL VAL ALA LEU VAL ILE ARG GLN TRP MET SER ASN ASP HIS GLU

- Molecule 1: Flagellar M-ring protein

Chain N:  13% 84%

MET	ALA	THR	SER	THR	ALA	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	LEU	ALA	ARG	ASN	PRO	ARG	ILE	LEU	ILE	VAL	ALA	GLY	SER	ALA	ALA	VAL	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ALA	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	STR
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Gln Asp Gly Ile Val Ala Ala Leu Thr Gln Met Asn Ile Tyr Arg Phe Ala Ala Asn Ser Gly Ala Ile Glu Val Val Pro Pro Ala Asp Lys Val Val His Glu Leu Arg Leu Arg Leu Ala Ala Gln Gln Gly Leu Leu Pro Pro Lys Gly Gly Ala Val Val Phe Glu Leu Leu Leu Asp Gln Gln Lys

PHE	GLY	ILE	SER	Q125	E128	E139	T143	E144	E145	T146	L147	G148	P149	K151	S152	H156	P160	PRO	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	T177	V178	T179	S192	D214	Q215	S216	L220	T221	Q222	SER	ASN	THR	THR	SER	GLY	ARG	ASP	LEU	ASN	ASP
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ARG	SER	ARG	GLN	LEU	ASN	ILE	SER	SER	GLU	GLN	VAL	GLY	ALA	GLY	TYR	PRO	GLY	GLY	VAL	PRO	PRO	GLY	ALA	ALA	PRO	PRO	ASN	GLU	GLU	PRO	PRO	ASN	ILE	ALA	THR	PRO	PRO	THR	THR	ASN	GLN	GLN	ASN	ASN	ALA	GLN	ASN	ASN	THR	ASN	PRO	GLN	THR	SER	SER	THR	ASN	SER	ALA
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[illegible]

- Molecule 1: Flagellar M-ring protein

Chain 0: 13% 84%

Met	Ser	Gln	Trp	Ala	Ile	Ser	Thr	Asp	Phe	Gln	Met
Ser	Gln	Ala	Trp	Ala	Glu	Ala	Leu	Ala	Gly	Asp	Ser
Arg	Arg	Gly	Leu	Gln	Leu	Pro	Ser	Leu	Ile	Gly	Arg
Arg	Ile	Trp	Arg	Arg	Thr	Thr	Gln	Phe	Ala	Ile	Ser
Glu	Glu	Lys	Lys	Glu	Glu	Leu	Leu	Ala	Val	Val	Thr
Met	Met	Ala	Ala	Ala	Ala	Ala	Asn	Asn	Ala	Ala	Thr
Ser	Ser	Val	Val	Arg	Gly	Arg	Ile	Val	E128	Gln	Thr
Asn	Asn	Pro	Pro	Phe	Phe	Glu	Gln	Glu	E139	Leu	Pro
Asp	Asp	Gln	Gln	Ser	Thr	Thr	Val	Ser	T143	Lys	Lys
Pro	Pro	Leu	Leu	Asp	Asp	Ser	Val	Arg	T144	Gln	Pro
Arg	Arg	Thr	Thr	Lys	Lys	Ser	Gly	Ile	E145	Met	Pro
Val	Val	Arg	Arg	Arg	Arg	Tyr	Ala	Gln	T146	Asn	Leu
Val	Val	Arg	Gly	Glu	Glu	Glu	Tyr	Arg	L147	Glu	Trp
Ala	Ala	Val	Val	Asp	Val	Val	Gly	Arg	G148	Tyr	Leu
Val	Val	Glu	Thr	Thr	Thr	Pro	Pro	Ile	P149	Arg	Asn
Val	Val	Glu	Glu	Leu	Leu	Arg	Gly	Glu	V150	Phe	Arg
Ile	Ile	Ala	Ala	Asn	Ala	Thr	Gly	Ala	K151	Ala	Leu
Arg	Arg	Lys	Val	Val	Val	Ile	Val	Ile	S152	Asn	Arg
Gln	Gln	Lys	Ala	Asn	Val	Arg	Pro	Val	A153	Gly	Ala
Trp	Trp	Ala	Ala	Asn	Ala	His	Gly	Ser	R154	Ser	Asn
Met	Met	Gln	Ser	Ser	Ser	Thr	Ala	Pro	V155	Gly	Pro
Ser	Ser	Glu	Pro	Pro	Pro	Lys	Leu	Ile	H156	Ala	Arg
Asn	Asn	Gln	Gln	Phe	Phe	Met	Ser	Val	+	Ile	Ile
Asp	Asp	Ala	Ser	Ser	Ala	Val	Asn	Gly	P160	Glu	Pro
His	His	Val	Val	Ala	Ala	Gln	Gln	Asn	Lys	Leu	Ile
Glu	Glu	Val	Val	Val	Val	Gly	Pro	Gly	Pro	Pro	Ile
		Arg	Asp	Asp	Asp	Asp	Ala	Asn	Ser	Val	Val
		Gln	Gln	Gln	Gln	Glu	Pro	Val	Leu	Ala	Ala
		Thr	Thr	Thr	Thr	Ile	Pro	Val	Phe	Asp	Ala
		Glu	Gly	Gly	Gly	Arg	Asn	Ala	Val	Lys	Ser
		Glu	Glu	Glu	Glu	Leu	Glu	Gln	Gln	His	Ala
		Glu	Glu	Glu	Ser	Ser	Ala	Val	Gln	Glu	Ala
		Ala	Leu	Val	Val	Val	Pro	Thr	Lys	Leu	Val
		Val	Val	Pro	Pro	Ala	Ile	Ala	S171	Arg	Ala
		Glu	Phe	Phe	Val	Val	Ala	Gln	+	Leu	Ile
		Val	Trp	Trp	Trp	Val	Thr	Leu	T177	Val	Val
		Gln	Gln	Gln	Val	Val	Pro	Asp	V178	Leu	Val
		Leu	Leu	Asn	Asn	Pro	Pro	Phe	+	Ala	Ala
		Ser	Ser	Tyr	Tyr	Thr	Thr	Ala	T179	Gln	Met
		Lys	Lys	Gln	Gln	Ser	Asn	Asn	+	Gln	Val
		Asp	Phe	Phe	Thr	Thr	Gln	Lys	S192	Gly	Val
		Gln	Ile	Ile	Ile	Leu	Gln	Gln	+	Gly	Leu
		Gln	Asp	Asp	Ala	Ala	Asn	Gln	D214	Pro	Trp
		Leu	Gln	Gln	Gln	Gly	Ala	Thr	Q215	Lys	Lys
		Gln	Leu	Leu	Leu	Asp	Gln	Glu	S216	Gly	Thr
		Gln	Leu	Leu	Leu	Lys	Asn	Glu	+	Gly	Pro
		Arg	Ala	Ala	Pro	Pro	Thr	His	L220	Ala	Asp
		Ala	Gly	Gly	Leu	Leu	Gln	Tyr	T221	Val	Tyr
		Asn	Ala	Ala	Pro	Pro	Gln	Ser	Q222	Gly	Arg
		Asn	Arg	Arg	Leu	Leu	Thr	Pro	+	Phe	Thr
		Gln	Gln	Gln	Arg	Thr	Ser	Asn	+	Glu	Leu
		Arg	Leu	Leu	Trp	Ala	Thr	Asn	Lys	Thr	Phe
		Gly	Leu	Leu	Val	Ala	Thr	Gly	Glu	Leu	Leu
		Ala	Ala	Leu	Val	Met	Thr	Ala	Arg	Leu	Leu
		Val	Val	Val	Val	Gln	Ser	Lys	Leu	Gln	Ser
		Glu	Glu	Glu	Glu	Asn	Asn	Ala	+	Val	Ser

- Molecule 1: Flagellar M-ring protein

Chain Q: 13% . 84%

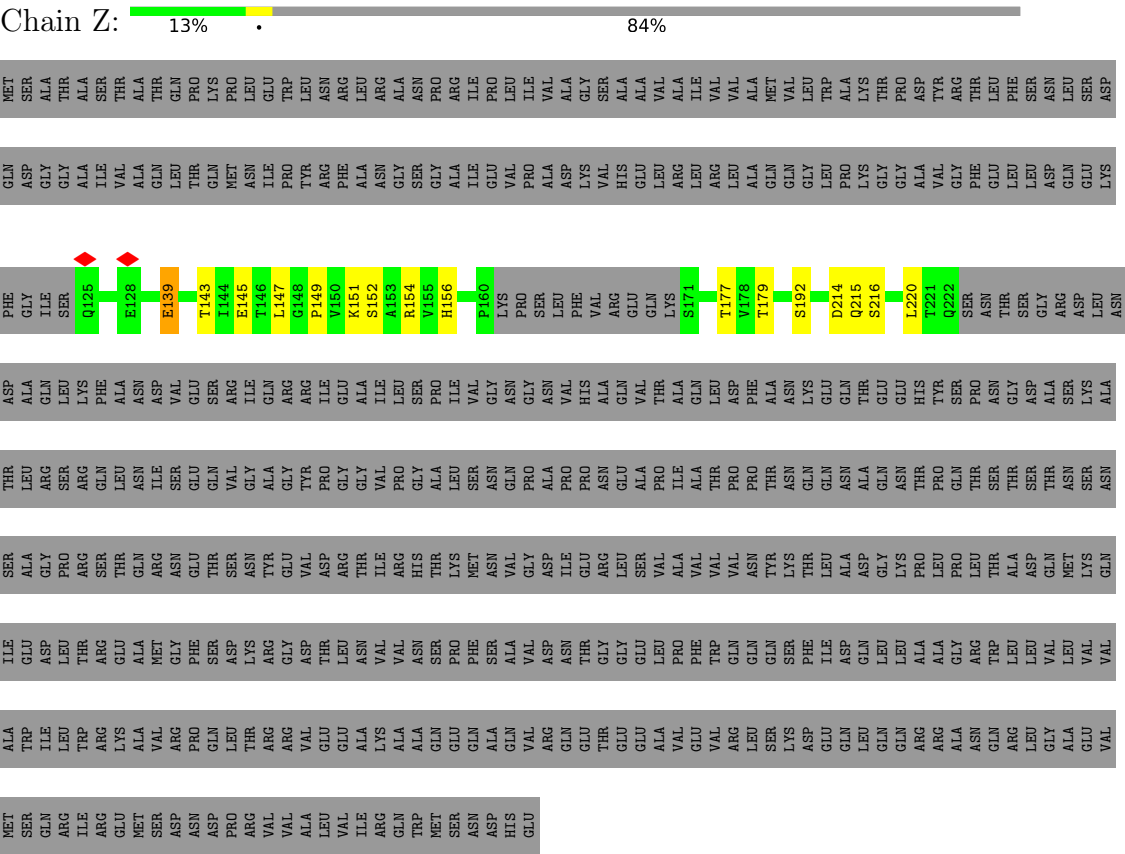
PHE	GLY	ILE	SER	Q125	E128	E139	T143	I144	E145	T146	L147	G148	P149	V150	K151	S152	A153	R154	V155	H156	P160	LYS	PRO	SER	LEU	PHE	VAL	ARG	GLN	GLN	LYS	S171	T177	Q215	S216	L220	T221	Q222	SER	ASN	THR	ASN	GLY	ARG	ASP	LEU			
THR	ALA	THR	THR	ALA	VAL	GLN	THR	GLN	ASN	ILE	TRP	LEU	TYR	ARG	PHE	ALA	GLY	SER	GLY	ALA	ILE	GLU	VAL	PRO	ALA	ASP	VAL	GLY	GLY	GLN	GLN	GLY	LEU	PRO	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	
MET	SER	ALA	THR	ALA	SER	THR	ALA	ILE	VAL	GLN	ASP	GLY	ARG	ASN	ARG	ALA	GLY	ASN	SER	GLY	ALA	ILE	PRO	LEU	ILE	VAL	ALA	GLY	SER	ALA	ALA	VAL	ILE	VAL	VAL	ALA	ALA	MET	THR	VAL	LEU	TRP	ALA	LYS	THR	PRO	ASP	TYR	SER



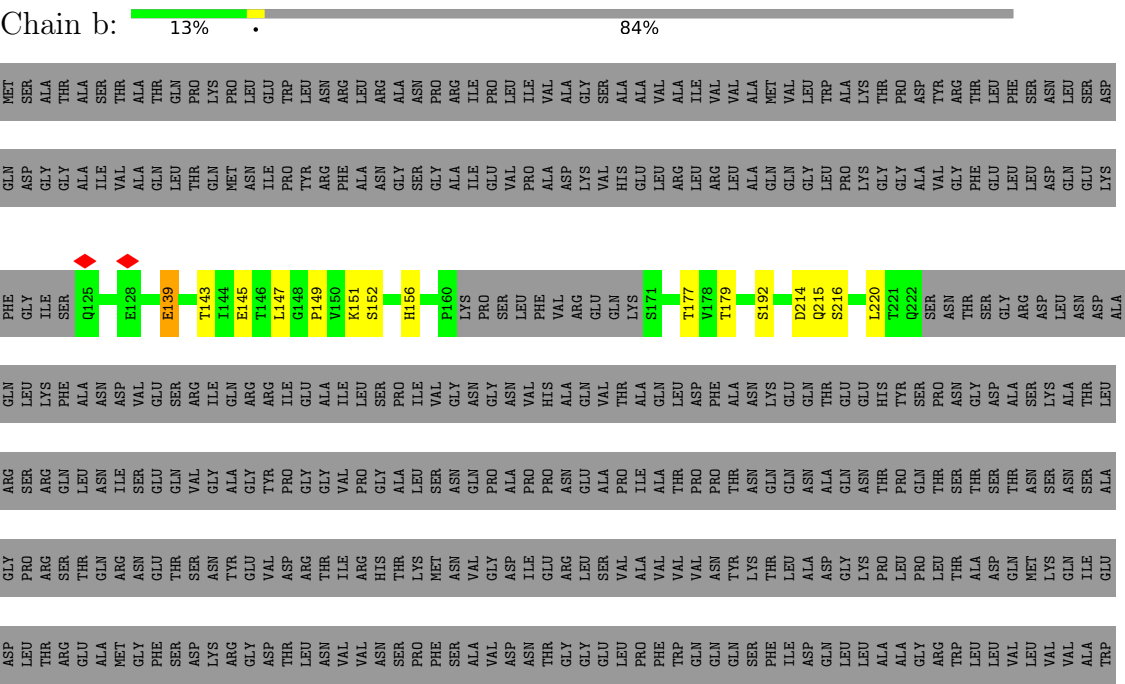




● Molecule 1: Flagellar M-ring protein

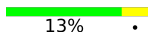


● Molecule 1: Flagellar M-ring protein



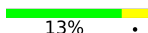
ILE	TRP	ARG	LYS	VAL	ARG	PRO	GLN	LEU	THR	ARG	VAL	LEU	GLU	ALA	GLN	VAL	ARG	ASN	GLN	ARG	LEU	SER	ASP	GLY	LEU	ASP	GLN	ARG	THR	GLY	LEU	ALA	GLU	VAL	SER	MET	LYS	
GLN	ARG	ILE	ARG	GLY	GLU	MET	SER	ASP	ASN	PRO	THR	ARG	VAL	VAL	ALA	LEU	VAL	GLU	ILE	ALA	GLN	TRP	MET	GLY	ASN	PRO	ARG	ILE	ALA	ASP	HIS	GLU						

• Molecule 1: Flagellar M-ring protein

Chain c:  13%  84%

MET	GLN	PHE	THR	ASP	THR	SER	GLY	ILE	ASP	GLY	THR	GLN	ASP	GLN	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR	GLN	ASP	GLY	THR
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• Molecule 1: Flagellar M-ring protein

Chain e:  13%  84%

THR	LEU	ARG	SER	GLN	ARG	ILE	ASN	ASN	SER	GLU	GLN	VAL	GLY	ALA	TYR	PRO	GLY	GLY	ALA	GLY	LEU	ASN	SER	ASN	THR	ALA	GLN	THR	ASN	THR	THR	SER	THR	GLY	ASP	ALA	ASN	LYS	ALA											
ASP	ALA	GLN	LEU	LYS	PHE	ALA	ASN	ASP	VAL	GLU	SER	ARG	ILE	GLN	ARG	ILE	GLU	ILE	PRO	THR	GLN	VAL	ASN	GLY	THR	ALA	GLN	THR	ASN	THR	THR	GLY	ASP	ALA	LYS	LYS	ALA													
PHE	GLY	ILE	SER	Q125	E128	E139	T143	I144	E145	T146	L147	G148	P149	V150	K151	S152	A153	R154	V155	H156	F160	LYS	PRO	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	S171	T177	Q215	S216	L220	T221	Q222	SER	ASN	THR	ASN	SER	GLY	ARG	ASP	LEU			
GLN	ASP	GLY	GLY	ILE	VAL	THR	THR	GLN	GLN	THR	GLN	MET	ASN	ILE	PRO	ARG	ASN	SER	GLY	ILE	GLU	PRO	VAL	ALA	GLY	VAL	ARG	HIS	GLU	LEU	ARG	GLN	GLY	GLY	ALA	ASP	VAL	GLY	PHE	THR	LEU	LEU	ASP	GLN	GLY	THR	ASP	GLN		
MET	SER	ALA	THR	ALA	SER	THR	PRO	LYS	PRO	LYS	LYS	VAL	ARG	ASN	ASN	ARG	ASN	ASN	ASN	PRO	ARG	ILE	PRO	LEU	LEU	VAL	ALA	VAL	LEU	ARG	ILE	VAL	VAL	GLN	GLY	ASP	THR	ARG	THR	LEU	PHE	SER	ASN	GLN	LEU	LEU	ASP	GLN	THR	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C21	Depositor
Number of particles used	84797	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.081	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	355.104, 355.104, 355.104	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/655	0.52	0/893
1	C	0.39	0/655	0.52	0/893
1	D	0.39	0/655	0.52	0/893
1	F	0.39	0/655	0.52	0/893
1	G	0.39	0/655	0.52	0/893
1	I	0.39	0/655	0.52	0/893
1	J	0.39	0/655	0.52	0/893
1	L	0.39	0/655	0.52	0/893
1	N	0.39	0/655	0.52	0/893
1	O	0.39	0/655	0.52	0/893
1	Q	0.39	0/655	0.52	0/893
1	R	0.39	0/655	0.52	0/893
1	T	0.39	0/655	0.52	0/893
1	U	0.39	0/655	0.52	0/893
1	W	0.39	0/655	0.52	0/893
1	Y	0.39	0/655	0.52	0/893
1	Z	0.39	0/655	0.52	0/893
1	b	0.39	0/655	0.52	0/893
1	c	0.39	0/655	0.52	0/893
1	e	0.39	0/655	0.52	0/893
1	f	0.39	0/655	0.52	0/893
All	All	0.39	0/13755	0.52	0/18753

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	646	0	652	12	0
1	C	646	0	652	13	0
1	D	646	0	652	11	0
1	F	646	0	652	11	0
1	G	646	0	652	12	0
1	I	646	0	652	12	0
1	J	646	0	652	11	0
1	L	646	0	652	12	0
1	N	646	0	652	11	0
1	O	646	0	652	11	0
1	Q	646	0	652	10	0
1	R	646	0	652	11	0
1	T	646	0	652	13	0
1	U	646	0	652	10	0
1	W	646	0	652	10	0
1	Y	646	0	652	12	0
1	Z	646	0	652	10	0
1	b	646	0	652	10	0
1	c	646	0	652	13	0
1	e	646	0	652	11	0
1	f	646	0	652	9	0
All	All	13566	0	13692	194	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 7.

The worst 5 of 194 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:R:143:THR:HG21	1:T:156:HIS:NE2	1.94	0.82
1:W:143:THR:HG21	1:Y:156:HIS:NE2	2.02	0.73
1:F:143:THR:HG21	1:G:156:HIS:NE2	2.04	0.73
1:L:143:THR:HG21	1:N:156:HIS:NE2	2.04	0.72
1:A:143:THR:HG21	1:C:156:HIS:NE2	2.04	0.72

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	C	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	D	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	F	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	G	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	I	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	J	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	L	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	N	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	O	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	Q	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	R	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	T	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	U	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	W	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	Y	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	Z	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	b	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	c	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	e	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
1	f	84/560 (15%)	78 (93%)	6 (7%)	0	100	100
All	All	1764/11760 (15%)	1636 (93%)	128 (7%)	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	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	C	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	D	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	F	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	G	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	I	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	J	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	L	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	N	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	O	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	Q	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	R	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	T	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	U	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	W	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	Y	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	Z	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	b	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	c	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	e	72/467 (15%)	68 (94%)	4 (6%)	19	49
1	f	72/467 (15%)	68 (94%)	4 (6%)	19	49
All	All	1512/9807 (15%)	1428 (94%)	84 (6%)	21	49

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	W	177	THR
1	b	216	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	W	216	SER
1	Z	177	THR
1	c	216	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	196	HIS
1	Y	196	HIS
1	W	196	HIS
1	Z	196	HIS
1	I	196	HIS

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.

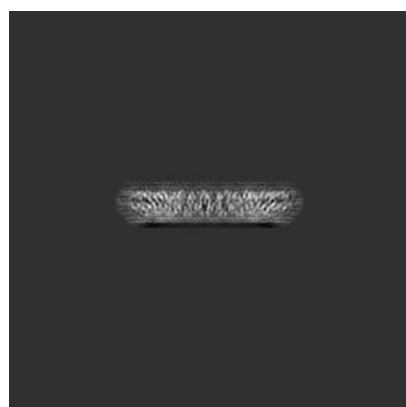
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10146. These allow visual inspection of the internal detail of the map and identification of artifacts.

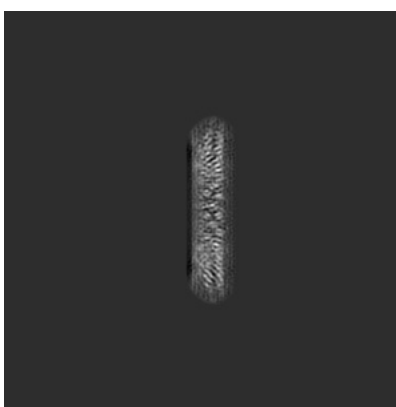
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

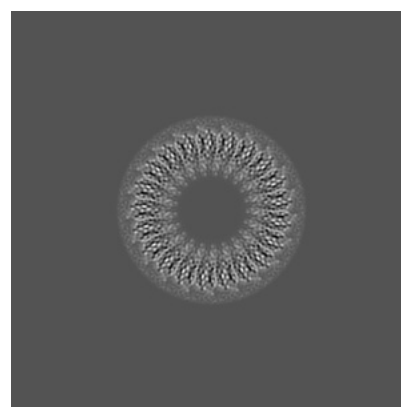
6.1.1 Primary map



X



Y

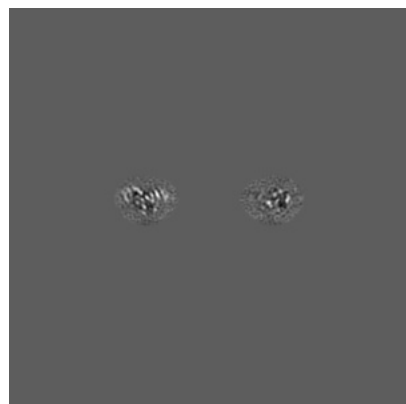


Z

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

6.2 Central slices [i](#)

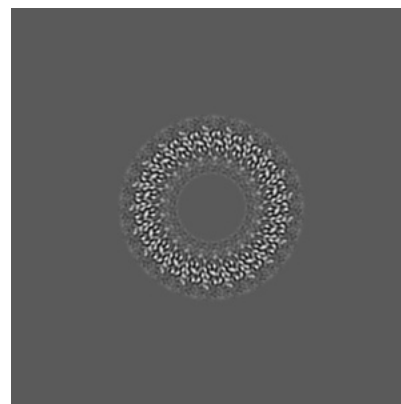
6.2.1 Primary map



X Index: 216



Y Index: 216

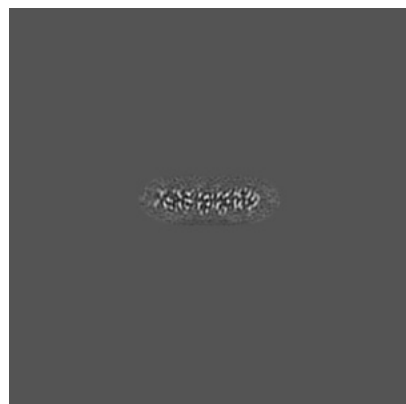


Z Index: 216

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

6.3 Largest variance slices [i](#)

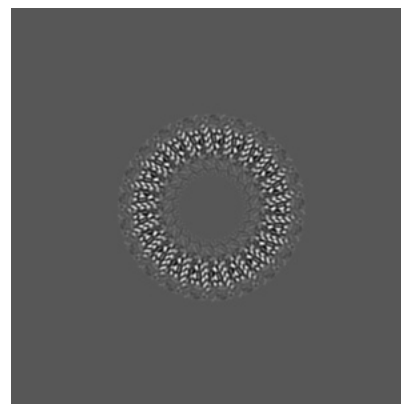
6.3.1 Primary map



X Index: 283



Y Index: 151

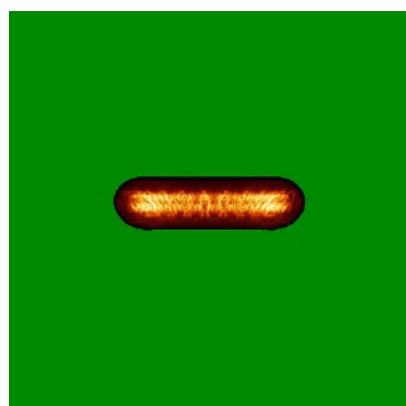


Z Index: 220

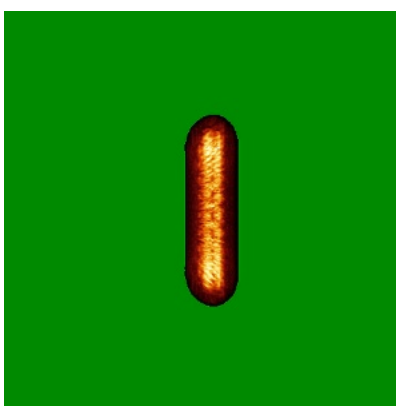
The images above show the largest variance slices of the map in three orthogonal directions.

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

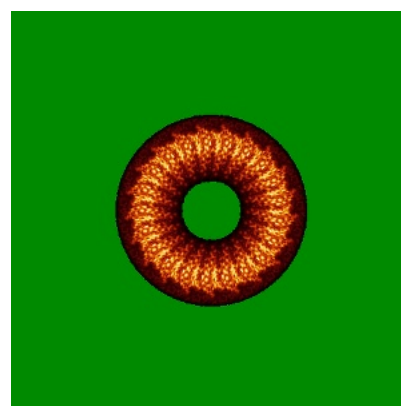
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

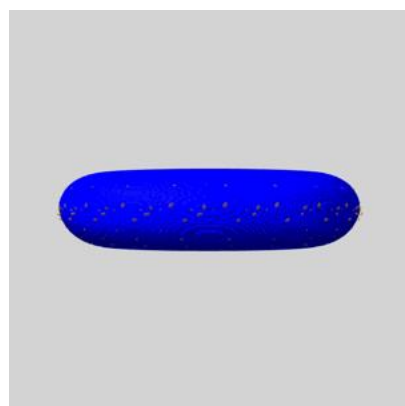
6.6 Mask visualisation [i](#)

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

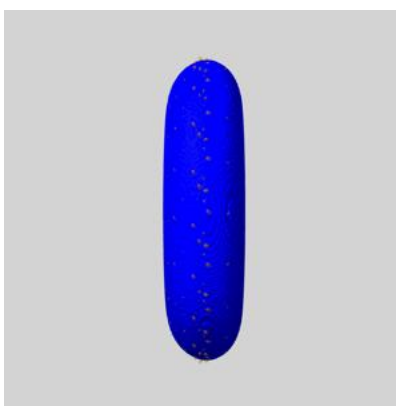
A mask typically either:

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

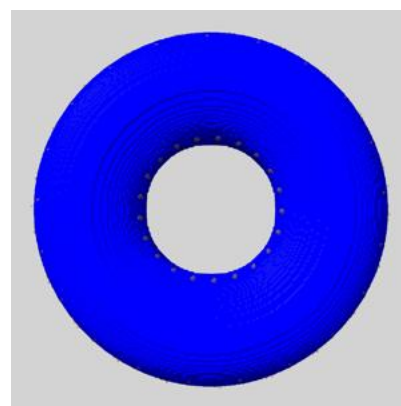
6.6.1 emd_10146_msk_1.map [i](#)



X



Y

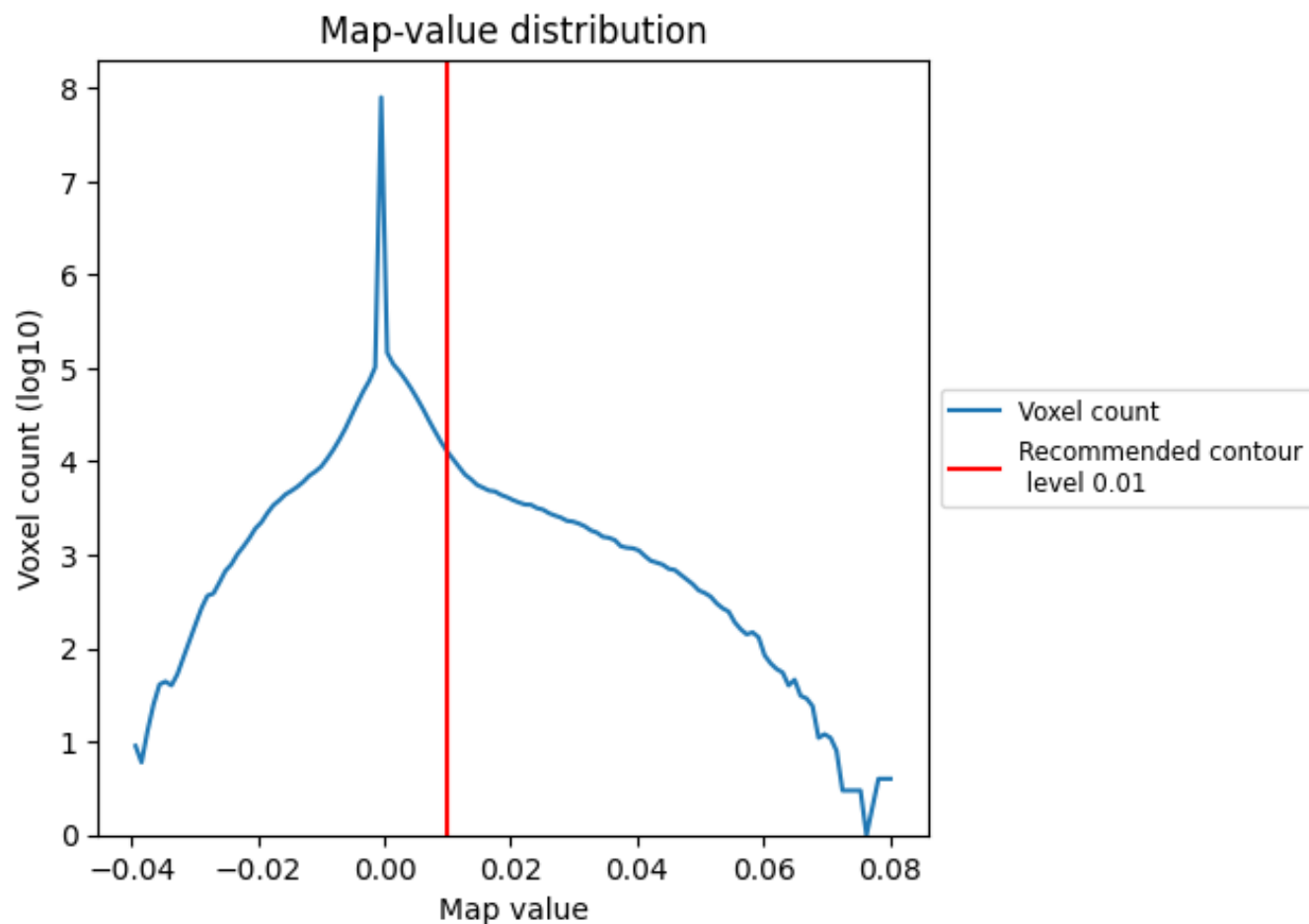


Z

7 Map analysis [i](#)

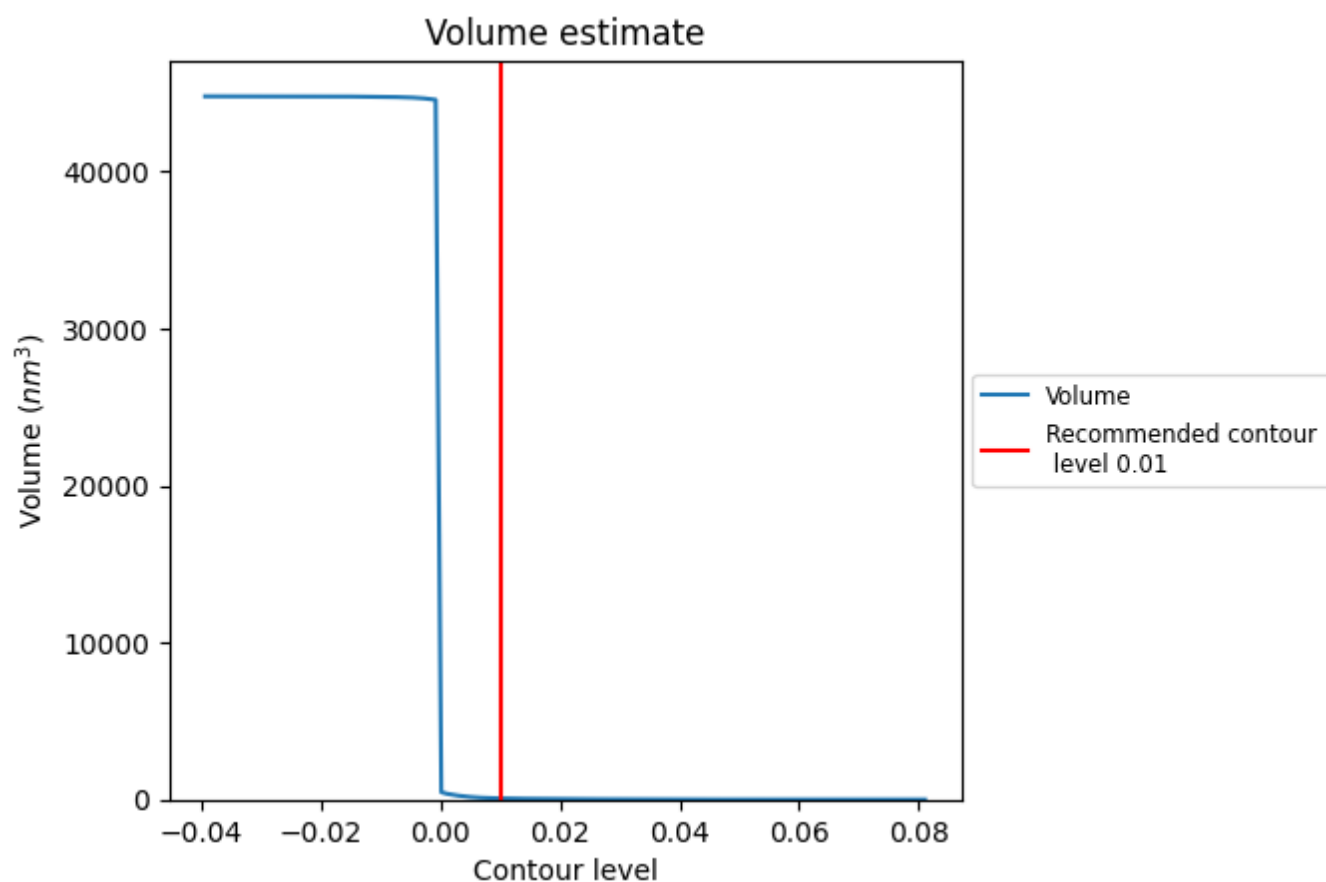
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

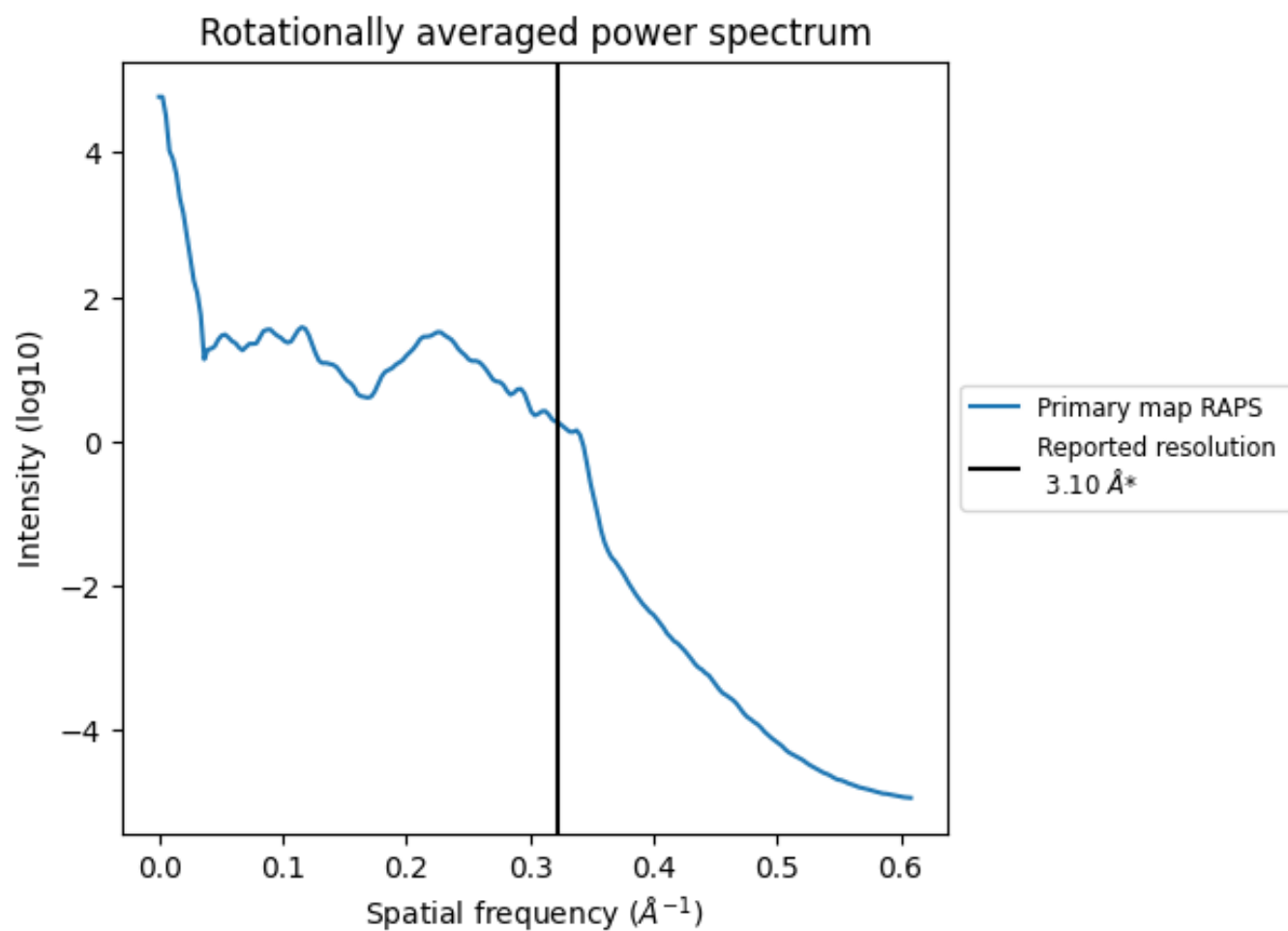
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 75 nm³; this corresponds to an approximate mass of 67 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 ⓘ

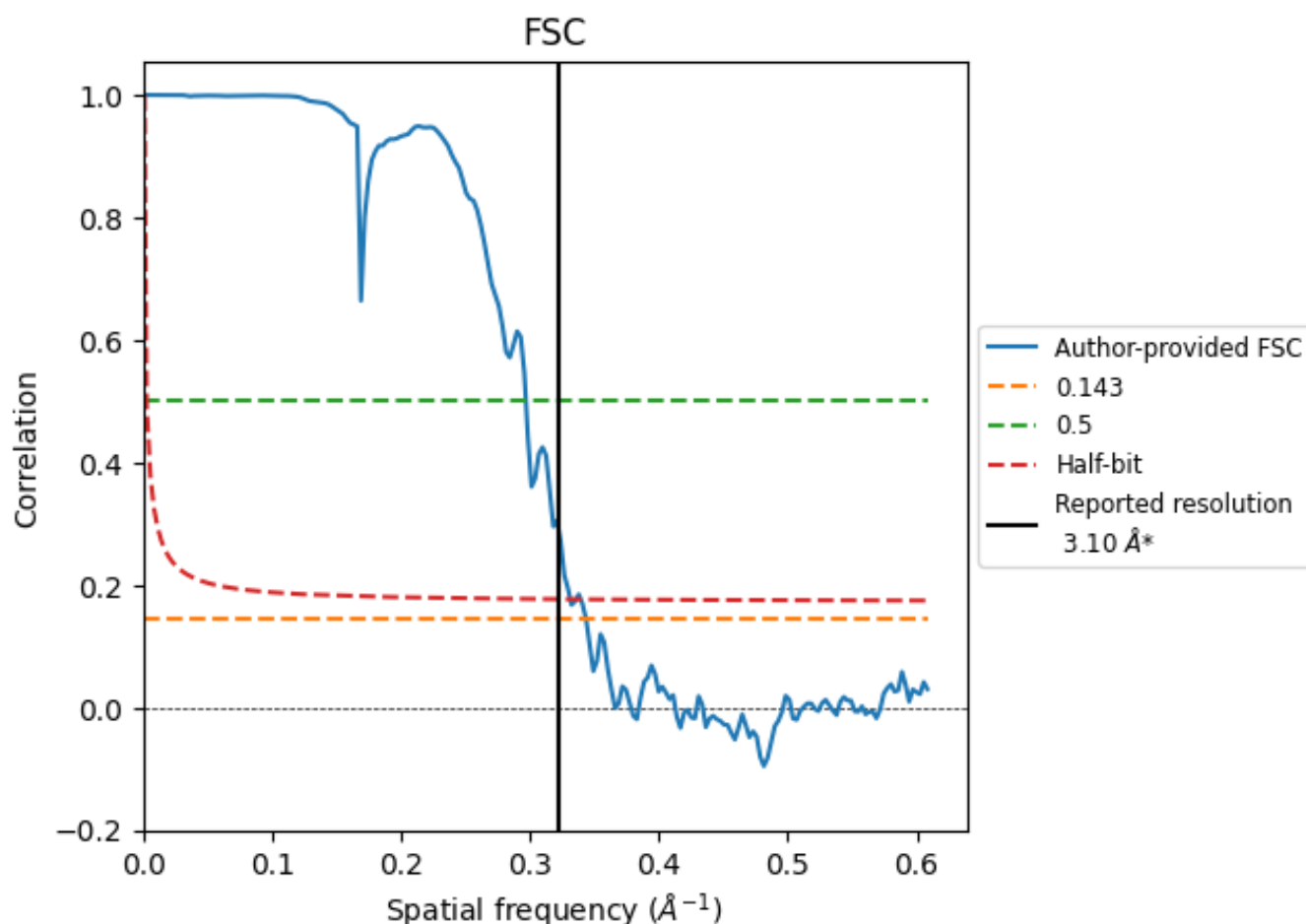


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

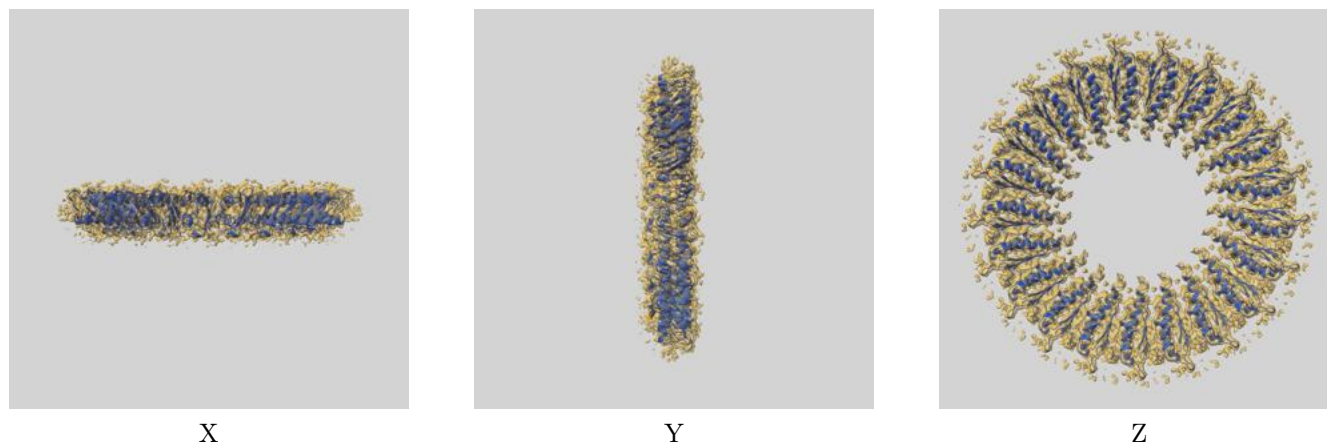
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	2.91	3.37	3.02
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

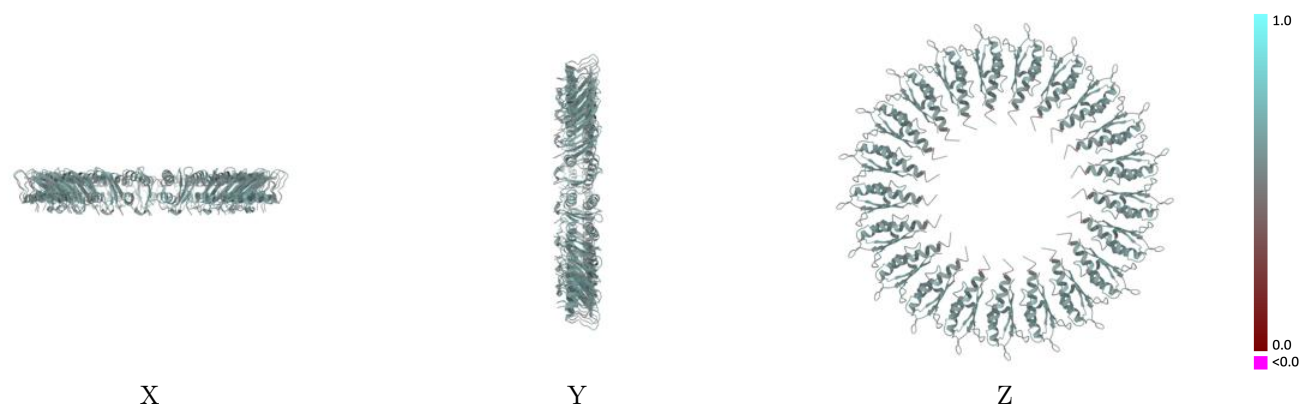
This section contains information regarding the fit between EMDB map EMD-10146 and PDB model 6SD2. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



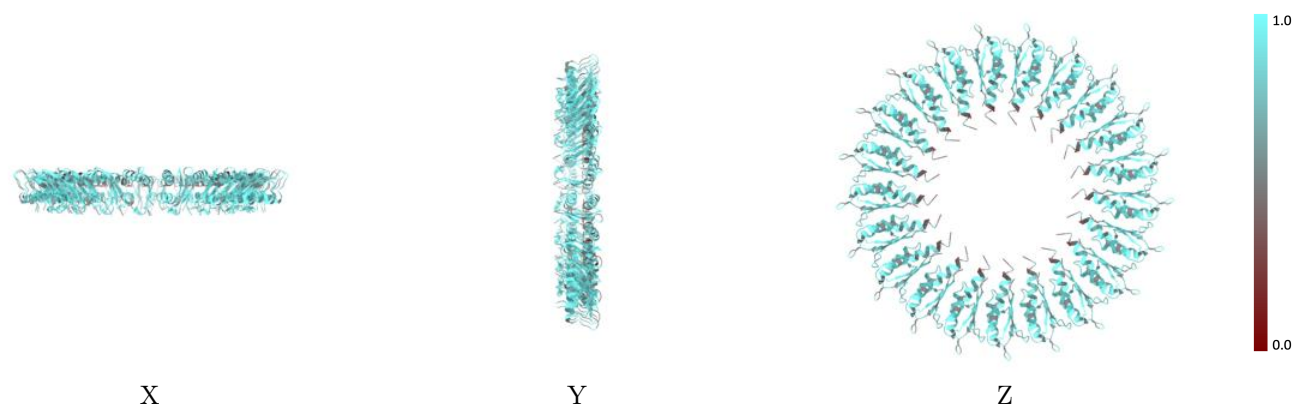
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



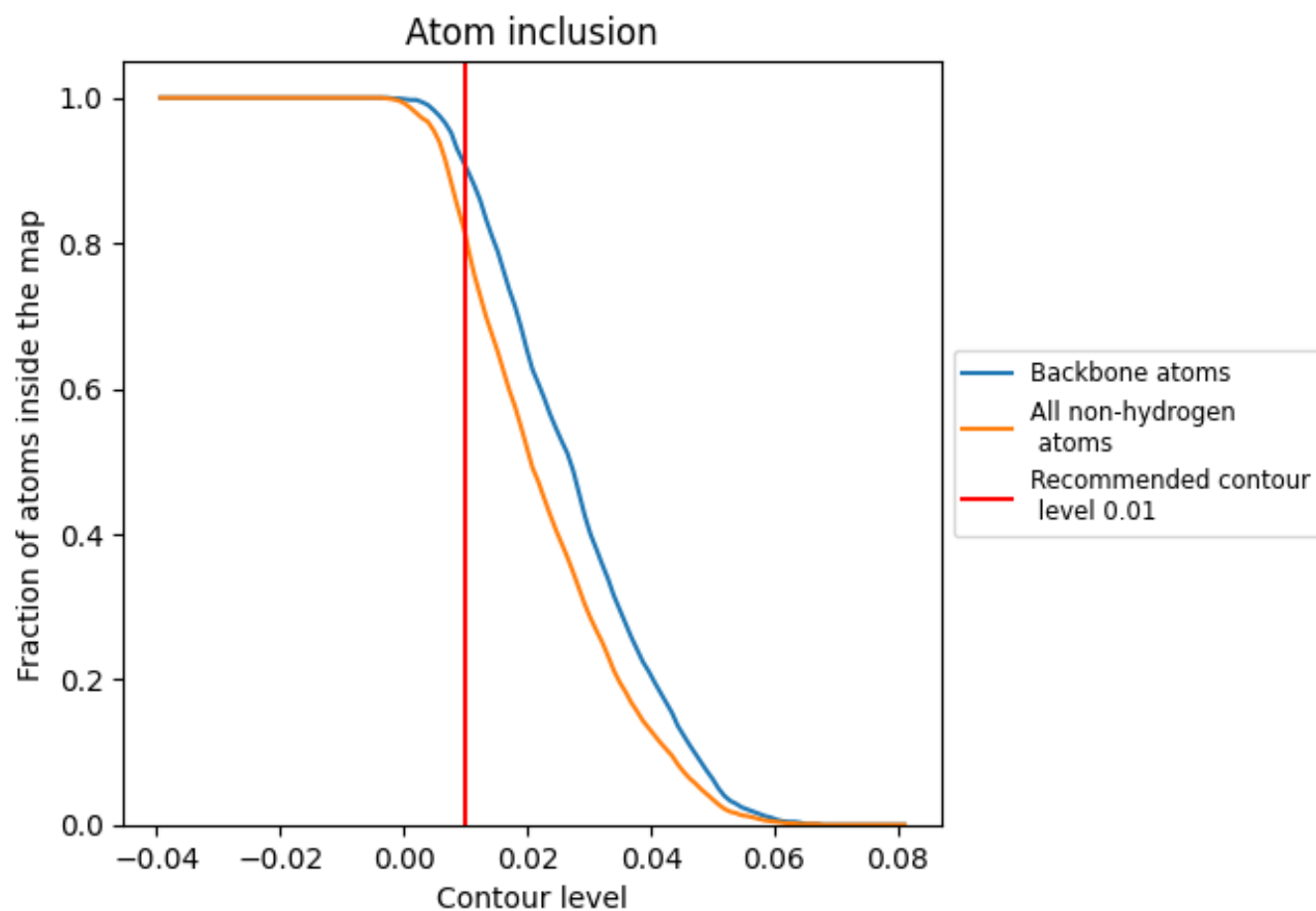
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 81% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8110	 0.5600
A	 0.8150	 0.5570
C	 0.8150	 0.5580
D	 0.8160	 0.5600
F	 0.8150	 0.5590
G	 0.8200	 0.5620
I	 0.8070	 0.5600
J	 0.8020	 0.5590
L	 0.8050	 0.5590
N	 0.8010	 0.5590
O	 0.8070	 0.5610
Q	 0.8130	 0.5620
R	 0.8100	 0.5620
T	 0.8100	 0.5630
U	 0.8020	 0.5590
W	 0.8130	 0.5610
Y	 0.8080	 0.5590
Z	 0.8130	 0.5600
b	 0.8120	 0.5580
c	 0.8120	 0.5570
e	 0.8130	 0.5580
f	 0.8150	 0.5570

