



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 07:38 PM UTC

PDB ID : 6SD5 / pdb_00006sd5
EMDB ID : EMD-10149
Title : Structure of the RBM2 inner ring of Salmonella flagella MS-ring protein FljF with 22-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)
Based on initial model : 6SCN

This is a Full wwPDB EM Validation 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

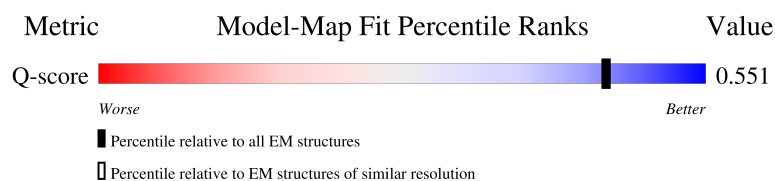
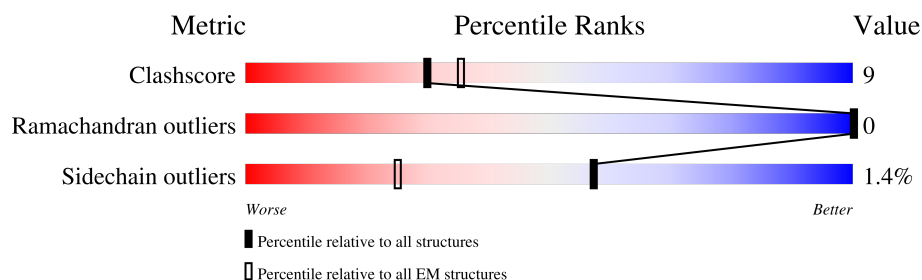
1 Overall quality at a glance

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.



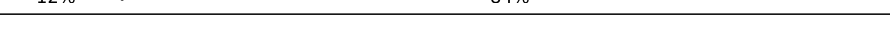
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	 12% 84%
1	I	560	 12% 84%
1	J	560	 12% 84%
1	L	560	 12% 84%
1	M	560	 12% 84%
1	O	560	 12% 84%
1	P	560	 13% 84%
1	R	560	 12% 84%
1	T	560	 12% 84%
1	U	560	 12% 84%
1	W	560	 12% 84%
1	X	560	 12% 84%
1	Z	560	 12% 84%
1	a	560	 12% 84%
1	c	560	 12% 84%
1	d	560	 12% 84%
1	f	560	 12% 84%
1	g	560	 12% 84%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14212 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	M	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	P	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	X	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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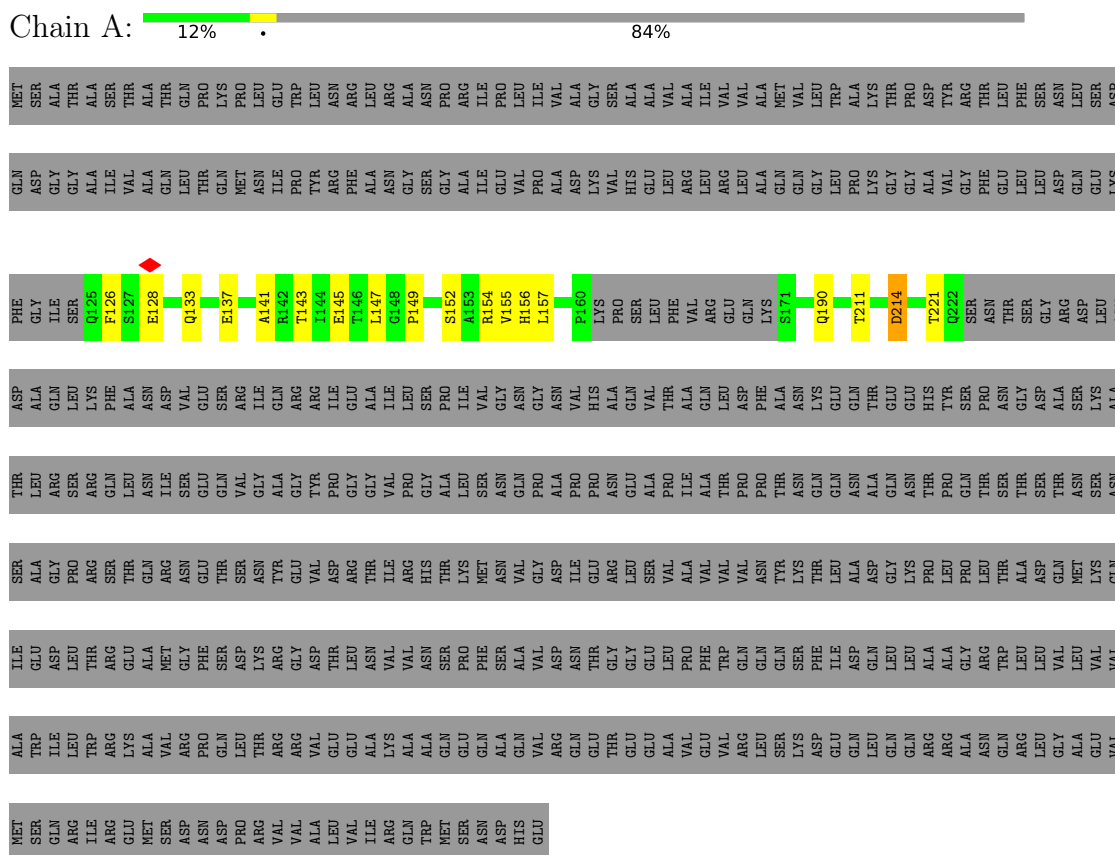
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	c	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	d	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	f	88	Total 646	C 402	N 115	O 128	S 1	0	0
1	g	88	Total 646	C 402	N 115	O 128	S 1	0	0

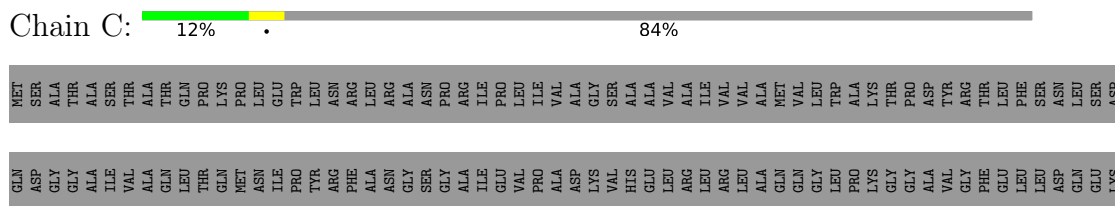
3 Residue-property plots

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





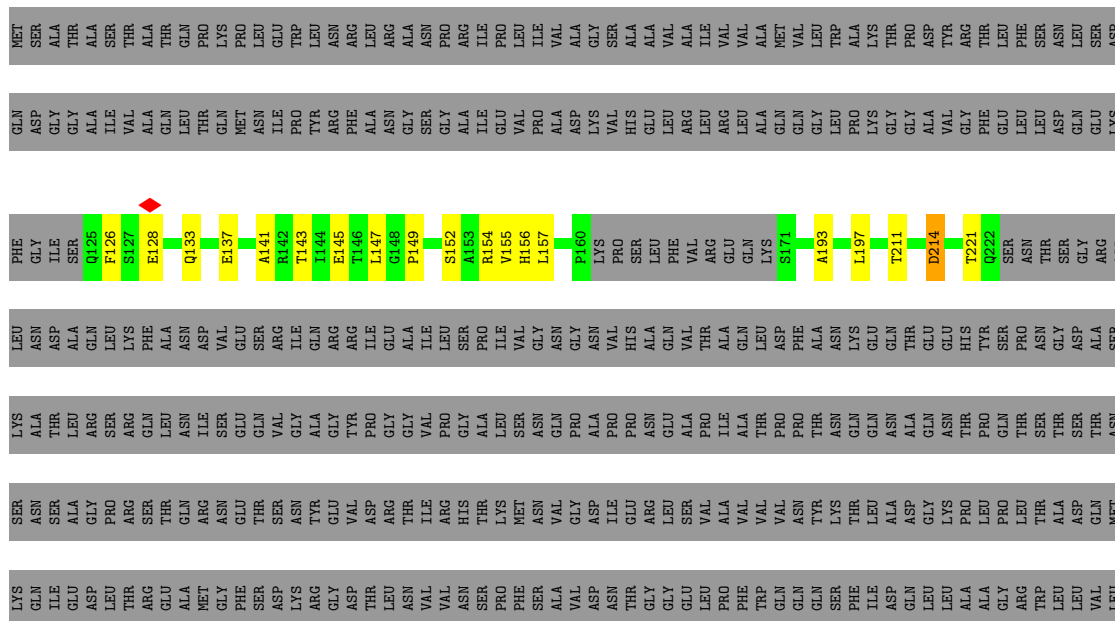
GLN	LEU	GLY	ASP	TRP	THR	SER	ASN	THR	PHE	GLN	MET
ARG	LEU	ASP	GLY	LEU	SER	THR	GLY	SER	GLY	ASP	SER
ALA	LEU	VAL	GLY	VAL	THR	ASN	ALA	ARG	ILE	GLY	ALA
GLU	LEU	MET	ASN	LEU	MET	THR	LYS	LEU	Q125	ALA	THR
VAL	VAL	VAL	GLN	ASN	ASN	SER	ALA	ASN	F126	ILE	SER
VAL	ALA	ILE	ILE	SER	ILE	SER	THR	ASP	S127	VAL	THR
GLN	GLN	TRP	TRP	ALA	GLU	ALA	LEU	ASP	E128	ALA	THR
ARG	GLN	ILE	ASP	GLY	ARG	GLY	ARG	GLN	Q133	LEU	THR
ILE	ARG	TRP	THR	PRO	SER	ARG	SER	LEU	ILE	THR	PRO
ARG	ARG	ARG	ARG	SER	SER	THR	GLN	LYS	E137	GLN	PRO
GLU	GLU	LYS	GLU	THR	THR	THR	LEU	PHE	ILE	MET	PRO
MET	MET	ALA	ALA	ALA	ASN	ASN	ASN	ASN	A141	ASN	LEU
SER	SER	VAL	ARG	ARG	MET	ARG	ILE	ASP	R142	ILE	GLU
ASN	ASN	PRO	GLY	ASN	GLY	ASN	SER	VAL	T143	PRO	TRP
ASP	ASP	GLN	SER	THR	THR	THR	GLU	GLU	E145	ARG	ASN
PRO	PRO	LEU	ASP	THR	ASP	SER	VAL	ARG	T146	PHE	ARG
ARG	ARG	THR	LYS	LYS	THR	THR	GLY	ILE	L147	ALA	LEU
VAL	VAL	ARG	ARG	TYR	THR	ALA	ALA	GLN	G148	ASN	ARG
VAL	VAL	ARG	GLY	GLY	GLY	GLY	ALA	ARG	P149	GLY	ALA
ALA	ALA	VAL	VAL	VAL	THR	VAL	TYR	ARG	S152	SER	ASN
LEU	LEU	GLU	THR	ASP	THR	ASP	PRO	ILE	A153	GLY	PRO
VAL	VAL	LEU	LEU	LEU	GLY	GLY	GLY	GLU	R154	ALA	ARG
ILE	ILE	ALA	ASN	THR	GLY	THR	GLY	ALA	V155	ILE	PRO
ARG	ARG	LYS	VAL	ILE	VAL	ILE	VAL	ILE	H156	VAL	LEU
GLN	GLN	ALA	VAL	VAL	ARG	ARG	PRO	LEU	L157	PRO	ILE
TRP	TRP	ALA	ASN	VAL	ASN	HIS	GLY	SER	ILE	ALA	VAL
MET	MET	GLN	SER	THR	SER	THR	ALA	PRO	P160	ASP	ALA
SER	SER	GLU	PHO	PHO	LYS	LYS	LEU	ILE	GLY	LYS	GLY
ASN	ASN	GLN	PHE	PHE	THR	MET	SER	VAL	PRO	VAL	GLY
ASP	ASP	ALA	SER	SER	ASN	ASN	ASN	GLY	SER	HIS	ALA
HIS	HIS	GLN	ALA	ALA	GLN	VAL	GLN	ASN	LEU	GLU	ALA
GLU	GLU	VAL	VAL	VAL	GLY	GLY	PRO	GLY	PHE	LEU	VAL
		ARG	ASP	ASP	ASN	ALA	ALA	ASN	VAL	ARG	ALA
		GLN	ASN	ILE	THR	ILE	PRO	VAL	ARG	LEU	ILE
		GLU	THR	THR	THR	GLU	PRO	HIS	GLU	ARG	ILE
		THR	GLY	GLY	ASN	ASN	GLY	ALA	GLN	VAL	VAL
		GLU	GLY	GLY	LEU	LEU	GLU	GLN	LYS	ALA	ALA
		GLU	GLU	SER	SER	SER	ALA	VAL	S171	GLN	MET
		ALA	LEU	VAL	VAL	VAL	PRO	THR	GLY	GLN	VAL
		VAL	PHO	ALA	ILE	ALA	ILE	ALA	D187	GLY	VAL
		GLU	THR	VAL	ALA	VAL	ALA	GLN	ILE	LEU	TRP
		VAL	PHE	VAL	THR	VAL	THR	LEU	Q190	PRO	ALA
		ARG	GLN	VAL	THR	VAL	PRO	ASP	I191	LYS	TRP
		LEU	GLN	GLN	PRO	PRO	PRO	PHE	S192	GLY	THR
		SER	GLN	THR	THR	THR	THR	ALA	A193	GLY	PRO
		LYS	SER	LYS	ASN	ASN	ASN	ASN	L197	VAL	TVR
		GLU	THR	THR	GLN	THR	GLN	LYS	ILE	GLY	ARG
		GLU	ILE	ILE	LEU	LEU	GLN	GLU	T211	PHE	THR
		LEU	GLN	ASP	ALA	ASN	ALA	THR	D214	GLU	LEU
		GLN	LEU	GLY	ALA	GLY	GLN	GLU	T221	LEU	PHE
		ARG	ALA	PRO	THR	PRO	THR	HIS	Q222	ASP	ASN
		ARG	ALA	LEU	THR	LEU	PRO	TYR	SER	GLN	SER
		ASN	ASN	THR	PRO	THR	GLN	PRO	GLY	GLY	VS

- Molecule 1: Flagellar M-ring protein

Chain G: 12% . 84%

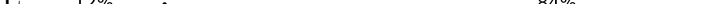
ARG	LEU	ALA	THR	GLY	SER	PHE	GLN	MET
ARG	LEU	ASP	THR	ASP	GLY	GLY	ASP	SER
LEU	VAL	GLN	SER	ALA	THR	ILE	GLY	GLY
GLU	VAL	MET	ASN	LEU	ASP	Q125	ALA	ALA
VAL	VAL	GLN	ASN	ALA	ASN	F126	ILE	SER
MET	ALA	ILE	SER	THR	ASP	S127	VAL	THR
SER	TRP	GLU	ALA	LEU	ALA	E128	ALA	THR
GLN	ILE	ASP	GLY	ARG	GLN		GLN	THR
ARG	LEU	LEU	PRO	SER	LEU	Q133	LEU	GLN
ILE	TRP	THR	ARG	ARG	LYS		THR	PRO
ARG	TRP	ARG	SER	GLN	PHE	E137	GLN	LYS
GLU	LYS	GLU	THR	LEU	ALA		MET	PRO
GLU	ALA	ALA	GLN	ASN	ASN	A141	ASN	LEU
MET	VAL	MET	ARG	ILE	ASP	R142	ILE	LEU
SER	ARG	GLY	ASN	SER	VAL	T143	PRO	TRP
ASN	PRO	PHE	GLU	GLU	GLY	I144	TYR	LEU
ASP	GLN	SER	THR	GLN	SER	E145	ARG	ASN
PRO	LEU	ASP	SER	VAL	ARG	T146	PHE	ARG
ARG	THR	LYS	ASN	GLY	ILE	L147	ALA	LEU
VAL	ARG	GLY	TYR	ALA	GLN	G148	ASN	ARG
VAL	ARG	GLY	GLU	GLY	ARG	P149	GLY	ALA
ALA	VAL	ASP	VAL	TYR	ARG		SER	ASN
LEU	GLU	THR	VAL	PRO	ILE	S152	GLY	PRO
VAL	GLU	LEU	ARG	GLY	GLU	A153	ALA	ARG
ILE	ALA	ASN	THR	GLY	ALA	R154	ILE	ILE
ARG	LYS	VAL	ILE	VAL	ILE	V155	GLU	PRO
GLN	ALA	VAL	ARG	PRO	LEU	H156	VAL	LEU
TRP	ALA	ASN	HIS	GLY	SER	L157	PRO	ILE
MET	ALA	SER	THR	ALA	PRO		ALA	VAL
GLU	GLN	PRO	LYS	LEU	ILE	P160	ASP	ALA
ASN	GLN	PHE	MET	SER	VAL	LYS	LYS	ALA
SER	ALA	SER	ASN	ASN	GLY	PRO	GLY	SER
HIS	GLN	ALA	VAL	GLN	ASN	SER	HIS	SER
GLU	VAL	VAL	GLY	PRO	GLY	LEU	GLU	ALA
ARG	GLN	ASN	ILE	ALA	ASN	PHE	LEU	VAL
GLU	GLU	ASN	GLU	PRO	VAL	VAL	ARG	ALA
THR	THR	GLY	GLU	ASN	HIS	ARG	ILE	ALA
GLU	GLU	GLY	LEU	ASN	ALA	GLU	ARG	VAL
ALA	GLU	GLU	SER	ALA	VAL	GLN	LEU	VAL
VAL	ALA	LEU	VAL	PRO	THR	LYS	ALA	VAL
GLU	VAL	PRO	ALA	ILE	ALA	S171	GLN	MET
GLU	GLU	PHE	VAL	ALA	GLN	S175	GLY	VAL
VAL	VAL	TRP	VAL	THR	LEU		LEU	LEU
ARG	ARG	GLN	VAL	PRO	ASP	A193	PRO	ALA
LEU	LEU	GLN	ASN	PRO	PHE		LYS	LYS
SER	SER	GLN	TYR	THR	ALA	L197	GLY	THR
LYS	LYS	SER	LYS	THR	ASN		GLY	PRO
ASP	ASP	PHE	THR	GLN	ASN	T211	ALA	ASP
GLU	GLU	ILE	THR	GLN	GLY		VAL	TYR
GLN	GLN	ASP	ALA	ASN	GLN	D214	GLY	ARG
LEU	LEU	GLN	ASP	ALA	THR		PHE	THR
GLN	GLN	LEU	GLY	GLN	GLU	G217	GLU	LEU
GLN	GLN	LEU	LYS	ASN	GLU		LEU	PHE
ARG	ARG	ALA	PRO	THR	HIS	T221	LEU	SER
ALA	ALA	ALA	PRO	THR	TYR	Q222	ASP	ASN
ALA	ALA	GLY	LEU	GLN	SER	SER	GLN	ASN
ASN	ASN	ARG	THR	SER	PRO	ASN	GLY	SER
GLN	GLN	TRP	LEU	THR	ASN		YS	YS

Chain I: 12% 1% 84%



[illegible]

- Molecule 1: Flagellar M-ring protein

Chain L:  12% 84%

MET	SER	ALA	THR	ALA	SER	THR	ALA	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	ARG	ARG	ASN	PRO	ARG	ILE	PRO	LEU	LEU	VAL	ALA	GLY	SER	ALA	ALA	VAL	VAL	ALA	ILE	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ALA	LYS	THR	PRO	TYP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	LEU	SER	SER
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[illegible]

PHE	Q125	P126	Q128	Q133	E137	A141	T143	E144	L146	G148	P149	S152	A153	R154	V155	H156	L157	P160	L160	PRO	PRO	SER	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	S171	D187	I191	S192	A193		L197	T211	D214	T221	D222	SER	ASN
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SER	GLY	ARG	ASP	LEU	ASN	ASP	ALA	GLN	LEU	LYS	PHE	ALA	ASN	ASP	VAL	GLU	SER	ARG	ILE	GLN	ARG	ARG	ILE	GLU	PRO	ILE	VAL	GLY	ASN	ASN	VAL	HIS	ALA	ALA	GLN	VAL	THR	THR	GLU	GLU	HIS	TYR	SER	SER	PRO	ASN
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GLY	ASP	ALA	ALA	SER	LYS	ALA	THR	LEU	ARG	ARG	GLN	LEU	ILE	ASN	SER	GLU	GLN	VAL	GLY	GLY	VAL	PRO	PRO	GLY	GLY	VAL	PRO	PRO	GLY	ALA	LEU	SER	ASN	GLN	ALA	PRO	PRO	PRO	GLU	ALA	PRO	PRO	THR	ASN	GLN	GLN	ASN	ALA	GLN	ASN	THR	PRO	GLN	THR	FER
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THR	SER	THR	ASN	SER	ASN	SER	ALA	GLY	PRO	ARG	SER	THR	GLN	ARG	ASN	GLU	THR	SER	ASN	TYR	GLU	VAL	ASP	ARG	THR	ILE	ARG	HIS	THR	LYS	MET	ASN	VAL	GLY	ASP	ILE	GLU	ARG	LEU	SER	VAL	ALA	TYR	LYS	THR	LEU	ALA	ASP	GLY	LYS	PRO	LEU	PRO	LEU	THR
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ALA	GLN	ASP	GLN	ILE	GLU	ASP	LEU	THR	ARG	GLU	ALA	MET	PHE	GLY	SER	ASP	LYS	ARG	GLY	ASP	THR	LEU	ASN	VAL	ASN	SER	PRO	PHE	SER	ALA	VAL	ASP	ASP	ASN	THR	GLY	GLU	GLY	LEU	PRO	PHE	TRP	GLN	GLN	GLN	SER	PHE	ILE	THR	ASP	ASP	GLN	LEU	LEU	ALA	ALA	GLY	GLY	ARG	ALA
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LEU LEU VAL VAL VAL VAL ALA TRP ILE LEU LEU TRP ARG LYS ALA VAL ARG PRO GLN LEU THR ARG ARG VAL GLU GLU ALA LYS ALA ALA ALA GLN GLU GLN GLN GLN VAL ARG GLN GLN THR THU GLU GLU ALA VAL VAL ARG GLU GLN GLN GLN LEU SER LYS ASP GLU GLN ARG ARG LEU LEU GLN GLN GLN ARG ARG ALA ASN

ARG	LEU	GLY	ALA	GLU	VAL	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
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- Molecule 1: Flagellar M-ring protein

Chain M: 12% 84%

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

PHE	GLY	ILE	SER	I125	F126	I127	I128	Q133	E137	A141	A142	T143	I144	E145	T146	L147	G148	P149	S152	A153	R154	V155	H156	L157	P160	L161	PRO	SER	SER	LEU	PHE	VAL	ARG	GLY	GLN	LYS	I171	S175	A193	L197	T211	D214	T221	Q222	ASN	THR	SER	SER
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ARG	ASP	LEU	ASN	ASP	ALA	GLN	LEU	LYS	PHE	ALA	ASN	ASP	GLU	VAL	GLN	ARG	ARG	LEU	LEU	ILE	ALA	ILE	GLY	ASN	GLY	ASN	VAL	HIS	ALA	GLN	THR	ALA	GLN	LEU	ASP	PHE	ALA	ASN	LYS	GLU	GLN	THR	GLU	GLU	HIS	TYR	SER	ASN	ASP	GLY
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ALA	SER	LYS	THR	ALA	THR	LEU	ARG	SER	SER	ARG	GLN	LEU	ASN	ILE	SER	GLU	GLY	VAL	GLN	GLY	ALA	GLY	TYR	PRO	PRO	GLY	GLY	GLY	VAL	PRO	GLY	ALA	ALA	ALA	PRO	PRO	ASN	ASN	GLU	ALA	ALA	PRO	PRO	ILE	ALA	THR	PRO	PRO	THR	THR	THR	GLN	GLN	ASN	ALA	ALA	GLN	ASN	GLN	THR	THR	SER	SER	THR	THR	SER
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[illegible]

- Molecule 1: Flagellar M-ring protein

Chain O: 12% . 84%

GLY	ALA	GLY	GLY	VAL	GLN	THR	ALA	ARG	PHE	GLN	MET
ALA	GLY	GLY	VAL	VAL	VAL	ASN	SER	ASP	GLY	ASP	SER
VAL	VAL	VAL	ALA	GLN	ASN	ASN	ALA	ASN	ILE	GLY	THR
MET	MET	ALA	ALA	ILE	SER	GLY	THR	ASP	Q125	ALA	SER
SER	SER	TRP	TRP	ASP	ALA	ALA	LEU	ALA	F126	VAL	THR
GLN	GLN	ILE	ILE	ASP	GLY	ARG	ARG	GLN	S127	VAL	THR
ILE	ILE	TRP	TRP	THR	PRO	SER	SER	LEU	E128	ALA	THR
ARG	ARG	ARG	ARG	ARG	GLN	GLN	GLN	PHE	Q133	LEU	THR
GLY	GLY	LYS	LYS	GLY	THR	THR	LEU	ALA	ILE	THR	PRO
MET	MET	ALA	ALA	ALA	ASN	ASN	ASN	ASN	E137	GLN	LYS
SER	SER	VAL	VAL	MET	ILE	ARG	ILE	ASP	ILE	MET	PRO
ASP	ASP	PRO	PRO	GLY	SER	GLY	SER	VAL	A141	ASN	LEU
ASN	ASN	ASN	ASN	PHE	GLU	GLU	GLU	GLU	R142	ILE	GLY
PRO	PRO	GLN	GLN	SER	THR	THR	GLN	SER	T143	PRO	TRP
PRO	PRO	LEU	LEU	ASP	VAL	ASN	VAL	ARG	I144	TYR	LEU
ARG	ARG	THR	THR	LYS	GLY	ASN	GLY	ILE	I145	ARG	ASN
VAL	VAL	ARG	ARG	ARG	ALA	THR	ALA	GLN	T146	PHE	ARG
VAL	ALA	VAL	VAL	GLY	GLY	VAL	GLY	ARG	L147	ALA	LEU
ALA	ALA	GLY	GLY	THR	TYR	VAL	TYR	ARG	G148	ASN	ARG
VAL	VAL	GLY	GLY	THR	PRO	PRO	GLY	ILE	P149	GLY	ASN
ILE	ILE	ALA	ALA	ASN	GLY	THR	GLY	GLU	S152	SER	ASN
ARG	ARG	LYS	VAL	VAL	ILE	ILE	VAL	ILE	A153	ALA	PRO
GLN	GLN	ALA	VAL	VAL	PRO	GLY	PRO	LEU	R154	ILE	ILE
TRP	TRP	ALA	ALA	ASN	HIS	HIS	GLY	SER	V155	GLY	PRO
MET	MET	GLN	GLN	SER	THR	THR	ALA	PRO	H156	VAL	LEU
SER	SER	GLY	GLY	PRO	LYS	LYS	LEU	ILE	L157	PRO	ILE
ASN	ASN	GLN	GLN	PHE	MET	MET	SER	VAL	ILE	ALA	VAL
ASP	ASP	ALA	ALA	SER	ASN	ASN	ASN	GLY	P160	ASP	ALA
GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLN	ASN	LYS	LYS	GLY
HIS	HIS	ARG	ARG	ASP	GLY	GLY	PRO	GLY	PRO	SER	ALA
GLY	GLY	GLN	GLN	ASN	ALA	ASN	ALA	ASN	SER	HIS	SER
ALA	ALA	ASN	ASN	ASN	PRO	ILE	PRO	VAL	LEU	GLY	ALA
VAL	VAL	THR	THR	THR	GLU	GLU	ASN	HIS	PHE	LEU	VAL
THR	THR	GLY	GLY	GLY	LEU	LEU	GLY	GLN	VAL	ARG	ILE
ALA	ALA	ALA	LEU	LEU	ALA	ALA	PRO	THR	GLN	LEU	VAL
VAL	VAL	VAL	PRO	PRO	ALA	ILE	ILE	ALA	LYS	ALA	ALA
GLY	GLY	PHE	PHE	THR	VAL	VAL	ALA	GLN	S171	GLN	MET
VAL	VAL	TRP	TRP	TRP	VAL	VAL	THR	ASP	ILE	GLN	VAL
ARG	ARG	GLN	GLN	GLN	VAL	VAL	PRO	ASP	S175	GLY	LEU
LEU	LEU	SER	SER	ASN	VAL	VAL	PRO	PHE	ILE	LEU	TRP
SER	SER	GLN	GLN	THR	THR	THR	THR	ALA	A193	PRO	ALA
LYS	LYS	SER	SER	LYS	ASN	ASN	ASN	ASN	L197	LYS	LYS
ASP	ASP	PHE	PHE	THR	THR	THR	GLN	LYS	THR	GLY	THR
GLY	GLY	ILE	ILE	LEU	LEU	LEU	GLN	GLY	T211	GLY	PRO
LEU	LEU	GLN	GLN	ALA	ALA	ALA	ASN	GLN	THR	VAL	TYR
GLN	GLN	LEU	LEU	GLY	GLY	GLY	GLN	GLU	D214	GLY	ARG
GLN	GLN	GLY	GLY	LYS	ASN	ASN	ASN	GLY	T221	PHE	THR
ARG	ARG	ALA	ALA	PRO	THR	THR	PRO	HIS	Q222	GLY	LEU
ALA	ALA	ALA	ALA	PRO	PRO	PRO	GLN	TYR	SER	LEU	PHE
ASN	ASN	GLY	GLY	THR	THR	THR	GLN	SER	THR	LEU	ASN
GLN	GLN	TRP	TRP	THR	SER	SER	ASN	ASN	THR	GLN	ASN
ARG	ARG	LEU	LEU	ASP	GLY	GLY	THR	GLY	SER	GLY	SER
ILE	ILE	THR	THR	LEU	THR	THR	SER	ASP	THR	YS	ASN

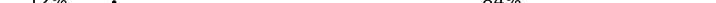
- Molecule 1: Flagellar M-ring protein

Chain P: 13% . 84%

PHE	GLY	Q125	SER	F126	S127	E128	Q133	E137	A141	A142	T143	I144	T146	L147	G148	P149	S152	A153	R154	V155	H156	L157	P160	LYS	PRO	SER	LEU	PHE	ARG	GLU	GLY	LYS	GLN	LEU	THR	ASP	GLY	ASP	GLN	THR	SER	MET												
ILE	ILE	Q125	GLY	GLY	VAL	GLN	THR	MET	ASN	ILE	PRO	TYR	ARG	PHE	ASN	GLY	SER	GLY	ILE	GLU	VAL	PRO	ILE	VAL	ALA	ASP	LYS	VAL	HIS	GLU	LEU	ARG	LEU	LEU	GLN	GLN	GLY	PRO	LEU	LYS	THR	PRO	ASP	TYR	THR	LEU	PHE	SER	ASN	LEU	LEU	GLN	GLY	ASP

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

- Molecule 1: Flagellar M-ring protein

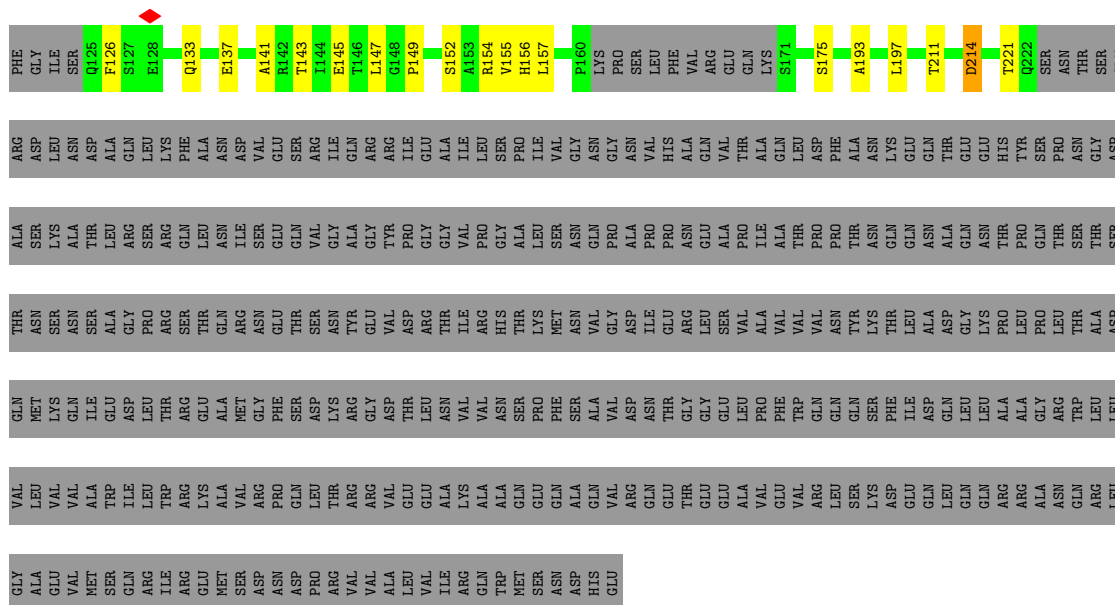
Chain R:  12% . 84%

[illegible]

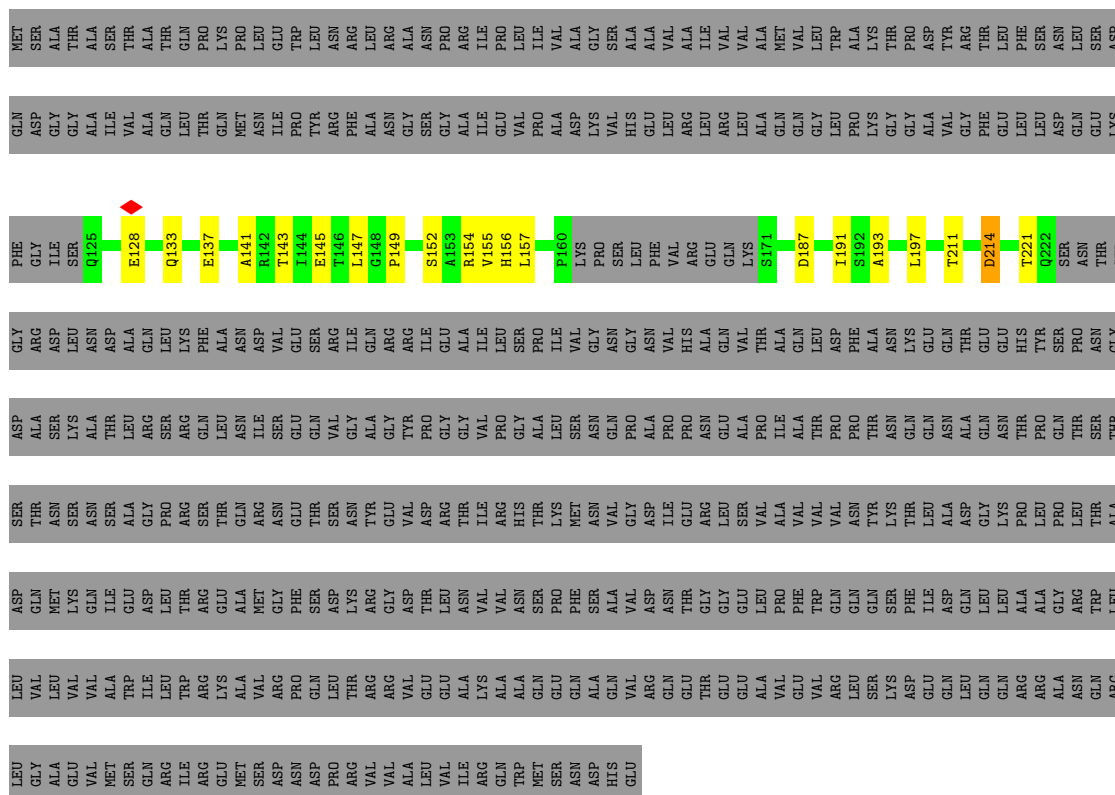
- Molecule 1: Flagellar M-ring protein

Chain T: 12% . 84%

[illegible]



- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein



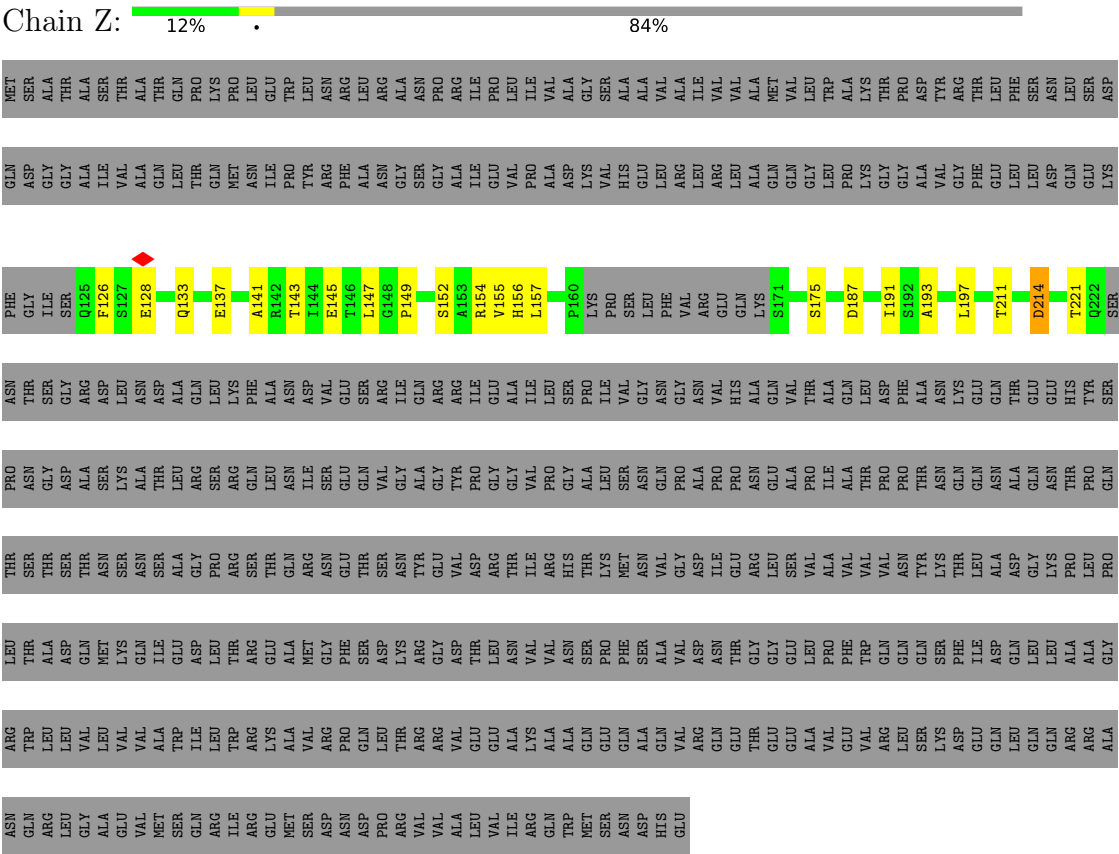
GLY	ALA	GLU	GLU	VAL	VAL	VAL	VAL	GLN	THR	ALA	ARG	PHE	GLN	MET
ALA	GLU	GLU	VAL	VAL	VAL	VAL	GLN	MET	ASN	SER	ASP	GLY	ASP	SER
VAL	VAL	VAL	ALA	ALA	ALA	ILE	GLN	GLY	ASN	THR	ASN	Q125	ALA	ALA
SER	SER	TRP	TRP	TRP	GLY	ASP	GLY	GLY	ALA	LEU	ALA	F126	VAL	SER
GLN	GLN	ILE	TRP	TRP	PRO	ASP	PRO	ARG	ARG	SER	GLN	S127	VAL	THR
ARG	ARG	LEU	TRP	TRP	THR	ARG	THR	ARG	LEU	SER	LEU	E128	ALA	THR
ILE	ILE	TRP	TRP	TRP	ARG	ARG	GLN	PHE	GLN	GLN	LYS	Q133	ALA	THR
GLU	GLU	LYS	LYS	LYS	THR	GLU	ASN	ALA	LEU	LEU	ALA	Q137	THR	PRO
MET	MET	ALA	ALA	ALA	GLY	MET	ILE	ASN	ILE	ASN	ASP	E137	GLN	LYS
SER	SER	VAL	VAL	VAL	GLY	ARG	SER	VAL	SER	VAL	VAL	A141	MET	PRO
ASN	ASN	ARG	PRO	PRO	PHE	GLY	GLU	GLU	GLU	GLU	GLU	R142	ASN	LEU
ASP	ASP	GLN	GLN	GLN	THR	THR	THR	GLN	SER	SER	SER	T143	PRO	TRP
PRO	PRO	LEU	LEU	LEU	ASP	ASP	VAL	VAL	ARG	ARG	ARG	E145	TYR	LEU
ARG	ARG	THR	THR	THR	LYS	ASN	TYR	GLY	ILE	ILE	ILE	T146	ARG	ASN
VAL	VAL	ARG	ARG	ARG	ARG	ARG	GLY	ALA	GLN	GLY	GLY	T147	PHE	ARG
ALA	ALA	VAL	VAL	VAL	ASP	VAL	TYR	GLY	ARG	ARG	ARG	G148	ALA	ARG
LEU	LEU	GLU	GLU	GLU	THR	THR	PRO	PRO	ILE	ILE	ILE	P149	ASN	ARG
VAL	VAL	GLU	GLU	GLU	LEU	LEU	GLY	GLY	GLU	GLU	GLU	S152	SER	ASN
ILE	ILE	ALA	ALA	ALA	ASN	THR	THR	GLY	ALA	ALA	ALA	A153	PRO	ASN
GLN	GLN	LYS	VAL	VAL	VAL	VAL	VAL	ILE	ILE	ILE	ILE	R154	ALA	ARG
TRP	TRP	ALA	ALA	ALA	ASN	ASN	PRO	GLY	LEU	LEU	SER	V155	GLY	PRO
MET	MET	GLN	GLN	GLN	SER	SER	THR	THR	ALA	ALA	PRO	H156	VAL	LEU
SER	SER	GLU	GLU	GLU	PRO	PRO	LYS	ILE	ILE	ILE	ILE	L157	PRO	ILE
ASN	ASN	GLN	GLN	GLN	PHE	PHE	MET	SER	VAL	VAL	VAL	Q160	ALA	VAL
ASP	ASP	ALA	ALA	ALA	SER	SER	ASN	ASN	GLY	GLY	GLY	L160	ASP	ALA
HIS	HIS	GLN	GLN	GLN	VAL	VAL	VAL	GLN	ASN	ASN	ASN	LYS	LYS	GLY
GLU	GLU	VAL	VAL	VAL	GLY	GLY	GLY	PRO	GLY	GLY	VAL	PRO	VAL	SER
		GLN	GLN	GLN	ASN	ASN	ILE	PRO	ALA	ASN	VAL	SER	HIS	ALA
		GLU	GLU	GLU	THR	THR	GLU	PRO	VAL	HIS	VAL	LEU	GLU	ALA
		THR	THR	THR	GLY	GLY	LEU	ASN	ALA	ASN	GLN	VAL	ARG	ILE
		TRP	TRP	TRP	LEU	LEU	LEU	GLN	VAL	VAL	THR	ARG	VAL	VAL
		ALA	ALA	ALA	THR	THR	ALA	ILE	ALA	ALA	GLN	LYS	ALA	ALA
		VAL	VAL	VAL	PHE	PHE	VAL	VAL	GLN	GLN	GLN	S171	GLN	MET
		GLU	GLU	GLU	TRP	TRP	TRP	THR	THR	THR	THR	S171	GLN	VAL
		ARG	ARG	ARG	GLN	GLN	VAL	PRO	ASP	PRO	PRO	S175	GLY	VAL
		LEU	LEU	LEU	GLN	GLN	VAL	ASN	PHE	PHE	PHE	Q175	LEU	TRP
		SER	SER	SER	GLN	GLN	TYR	THR	ALA	ALA	ALA	A193	PRO	LYS
		LYS	LYS	LYS	SER	SER	THR	ASN	ASN	ASN	ASN	L197	LYS	THR
		ASP	ASP	ASP	PHE	PHE	THR	GLN	LYS	LYS	LYS	L197	GLY	THR
		GLU	GLU	GLU	ILE	LEU	LEU	GLN	GLY	GLY	GLY	T211	VAL	PRO
		LEU	LEU	LEU	GLN	GLN	ASP	ALA	ALA	THR	THR	T211	VAL	TYR
		GLN	GLN	GLN	LEU	LEU	LYS	GLN	GLU	GLY	GLY	D214	ARG	THR
		GLN	GLN	GLN	LEU	LEU	PRO	ASN	GLU	GLY	GLY	T221	PHE	THR
		ARG	ARG	ARG	ALA	ALA	THR	HIS	GLY	GLY	GLY	T221	GLY	LEU
		ARG	ARG	ALA	ALA	ALA	LEU	TYR	THR	THR	SER	Q222	LEU	PHE
		ASN	ASN	ASN	GLY	GLY	PRO	SER	SER	SER	SER	Q222	LEU	ASN
		GLN	GLN	GLN	ARG	ARG	THR	PRO	PRO	PRO	ASN	THR	GLN	ASN
		TRP	TRP	TRP	THR	THR	THR	ASN	ASN	ASN	THR	THR	GLN	GLY
		ARG	ARG	ARG	LEU	LEU	ALA	GLY	GLY	GLY	SER	SER	GLY	SER
		TRP	TRP	TRP	THR	THR	THR	SER	SER	SER	ASN	SER	GLY	ASN
		VAL	VAL	VAL	LEU	LEU	THR	SER	SER	SER	GLY	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	GLY	ASN
		THR	THR	THR										

- Molecule 1: Flagellar M-ring protein

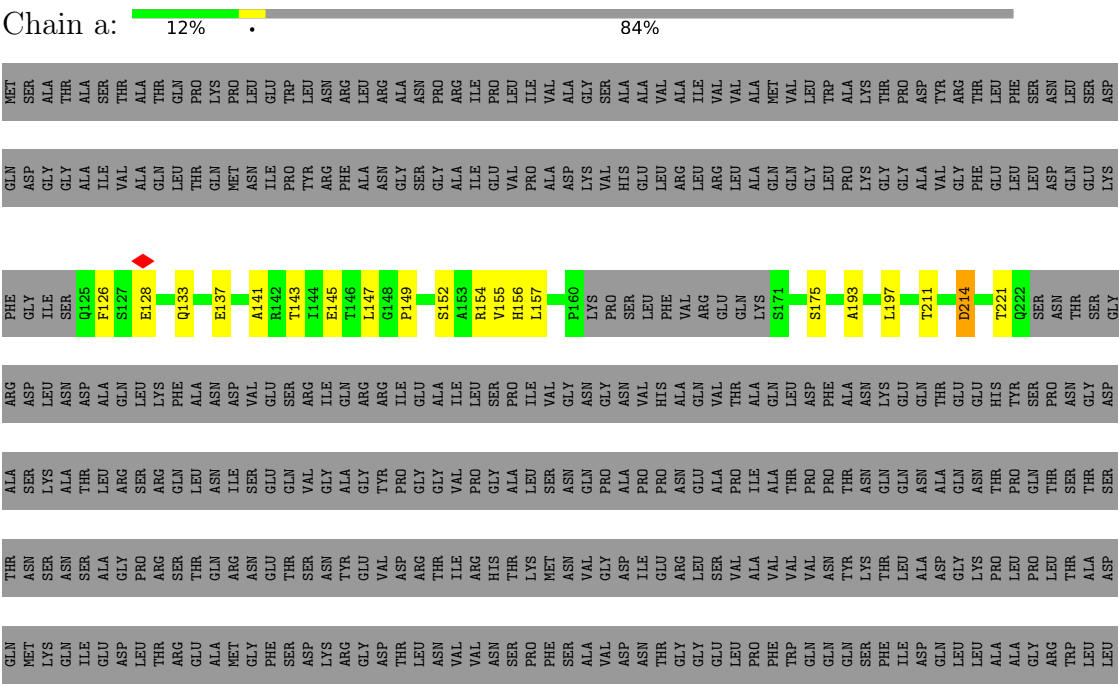
Chain X: 12% . 84%

GLY	ALA	GLY	GLY	VAL	GLN	THR	ALA	ARG	PHE	GLN	MET
ALA	GLY	VAL	VAL	VAL	GLN	ASN	SER	ASP	GLY	ASP	SER
VAL	VAL	VAL	ALA	ALA	ASN	ASN	ALA	ASN	ILE	GLY	THR
MET	MET	ALA	ILE	ILE	GLN	GLY	LEU	ASP	Q125	ALA	THR
SER	SER	THR	ASP	GLU	ALA	ALA	SER	ALA	F126	ILE	SER
GLN	GLN	ILE	ASP	ASP	GLN	GLN	GLN	GLN	S127	VAL	THR
ARG	ARG	THR	PRO	THR	ARG	ARG	SER	PHE	E128	ALA	THR
ILE	ILE	TRP	TRP	TRP	ARG	GLN	GLN	GLN	Q133	LEU	THR
GLY	GLY	LYS	GLY	GLY	THR	LEU	ALA	ALA		GLN	PRO
MET	MET	ALA	ALA	ALA	ASN	ASN	ASN	ASN	E137	GLN	LYS
SER	SER	VAL	MET	MET	ARG	ARG	ILE	ASP		MET	PRO
ASP	ASP	ARG	GLY	GLY	SER	SER	SER	VAL	A141	ASN	ASN
ASN	ASN	PRO	PHE	PHE	GLU	GLU	GLU	GLU	R142	ILE	LEU
ASP	ASP	GLN	SER	SER	THR	THR	GLN	SER	T143	TYR	TRP
PRO	PRO	LEU	ASP	ASP	GLY	GLY	VAL	ARG	I144	TYR	LEU
ARG	ARG	THR	LYS	LYS	ASN	ASN	GLY	ILE	E145	ARG	ASN
VAL	VAL	ARG	ARG	ARG	TTR	TTR	ALA	GLN	T146	PHE	ARG
VAL	VAL	ARG	GLY	GLY	VAL	VAL	GLY	ARG	L147	ALA	LEU
ALA	ALA	VAL	ASP	ASP	VAL	THR	TYR	ARG	G148	ASN	ARG
LEU	LEU	GLU	THR	THR	ASP	ASP	PRO	ILE	P149	GLY	ALA
VAL	VAL	GLU	LEU	LEU	ASN	THR	GLY	GLU		SER	ASN
ILE	ILE	ALA	ASN	ASN	THR	THR	GLY	ALA	S152	GLY	PRO
ARG	ARG	LYS	VAL	VAL	ILE	ILE	VAL	ILE	A153	ALA	ARG
GLN	GLN	ALA	VAL	VAL	GLU	GLU	PRO	LEU	R154	ILE	ILE
TRP	TRP	ALA	ASN	ASN	HIS	HIS	GLY	SER	V155	GLU	PRO
MET	MET	GLN	SER	SER	THR	THR	ALA	PRO	H156	VAL	LEU
SER	SER	GLU	PRO	PRO	LYS	LYS	LEU	ILE	L157	PRO	ILE
ASN	ASN	GLN	PHE	PHE	MET	MET	SER	VAL		ALA	VAL
ASP	ASP	ALA	SER	SER	ASN	ASN	GLN	GLY	P160	ASP	ALA
HIS	HIS	GLN	ALA	ALA	VAL	VAL	ASN	ASN	LYS	LYS	SER
GLY	GLY	ARG	VAL	VAL	GLY	GLY	PRO	GLY	PRO	VAL	ALA
		ARG	ASP	ASP	ASP	ASP	ALA	ASN	SER	HIS	SER
		GLN	ASN	ASN	ILE	ILE	PRO	VAL	LEU	GLU	ALA
		GLU	THR	THR	GLU	GLU	PRO	HIS	PHE	LEU	VAL
		THR	GLY	GLY	LEU	LEU	ASN	ALA	VAL	ARG	VAL
		GLU	GLY	GLY	LEU	LEU	GLU	GLN	ARG	LEU	ILE
		ALA	LEU	LEU	VAL	VAL	PRO	THR	GLN	ARG	VAL
		VAL	PRO	PRO	ALA	ALA	ILE	ALA	LYS	ALA	VAL
		GLU	PHE	PHE	VAL	VAL	ALA	GLN	S171	GLN	MET
		VAL	TRP	TRP	THR	THR	THR	LEU		GLN	VAL
		ARG	GLN	GLN	VAL	VAL	PRO	ASP	S175	GLY	LEU
		LEU	GLN	GLN	ASN	ASN	PRO	PHE		LEU	TRP
		SER	GLN	GLN	TTR	TTR	THR	ALA	A193	PRO	ALA
		LYS	SER	SER	LYS	LYS	ASN	ASN		LYS	LYS
		ASP	PHE	PHE	THR	THR	GLN	LYS	L197	GLY	THR
		GLU	ILE	ILE	LEU	LEU	GLN	GLU		GLY	PRO
		GLN	GLN	GLN	ALA	ALA	ASN	GLN	T211	VAL	TYR
		LEU	GLN	GLN	GLY	GLY	GLN	THR		ALA	ASP
		GLN	LEU	LEU	GLY	GLY	GLN	GLU	D214	GLY	ARG
		GLN	LEU	LEU	ASN	ASN	ASN	GLU		PHE	THR
		ARG	ALA	ALA	PRO	PRO	THR	HIS	T221	GLU	LEU
		ARG	ALA	ALA	PRO	PRO	PRO	TYR	Q222	LEU	PHE
		ALA	GLY	GLY	GLU	GLU	GLN	SER		LEU	SER
		ASN	ASN	ASN	ARG	ARG	THR	ASN	SER	ASN	ASN
		GLN	TRP	TRP	LEU	LEU	SER	ASN	THR	GLN	GLN
		ARG	LEU	LEU	THR	THR	THR	GLY	SER	YS	SER

● Molecule 1: Flagellar M-ring protein



● Molecule 1: Flagellar M-ring protein



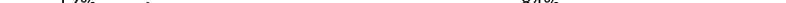
[illegible]

- Molecule 1: Flagellar M-ring protein

Chain c: 12% . 84%

ARG	LEU	ALA	THR	GLY	SER	PHE	GLN	MET
ARG	LEU	ASP	THR	ASP	GLY	GLY	ASP	SER
GLY	VAL	GLN	THR	ARG	ILE	ILE	GLY	ALA
ALA	LEU	MET	ASN	SER	SER	SER	THR	SER
GLU	VAL	LYS	ASN	LEU	Q125	Q125	ALA	ALA
VAL	VAL	GLN	ASN	ASN	F126	F126	ILE	SER
MET	ALA	ILE	SER	ASP	S127	S127	VAL	THR
SER	TRP	GLU	ALA	ASP	E128	E128	ALA	THR
GLN	ILE	ASP	GLY	ARG			GLN	THR
ARG	LEU	LEU	PRO	SER			LEU	GLN
ILE	TRP	THR	ARG	ARG	Q133	Q133	THR	PRO
ARG	LYS	ARG	SER	GLN	E137	E137	LYS	PRO
GLU	LYS	GLU	THR	LEU			MET	PRO
MET	ALA	ALA	GLN	ASP	A141	A141	ASN	LEU
SER	VAL	MET	ARG	ILE	R142	R142	ILE	LEU
ASP	PRO	PHE	ASN	VAL	T143	T143	PRO	TRP
ASN	ARG	GLY	GLU	GLU	I144	I144	TYR	LEU
ASP	GLN	SER	THR	SER	E145	E145	ASN	ASN
PRO	LEU	ASP	SER	VAL	T146	T146	ARG	ARG
ARG	THR	LYS	SER	GLY	L147	L147	LEU	LEU
VAL	ARG	ARG	TYR	ALA	G148	G148	ASN	ARG
VAL	ARG	GLY	GLU	GLY	P149	P149	GLY	ALA
ALA	VAL	ASP	VAL	TYR	ARG	ARG	ASN	ASN
LEU	GLU	THR	ASP	PRO	ILE	ILE	SER	PRO
VAL	GLU	LEU	ARG	GLY	ASP	S152	GLY	PRO
ILE	ALA	ASN	THR	GLY	A153	A153	ALA	ARG
ARG	LYS	VAL	ILE	ILE	R154	R154	ILE	GLY
GLN	ALA	VAL	ARG	PRO	V155	V155	VAL	PRO
TRP	ALA	ASN	HIS	GLY	H156	H156	LEU	ILE
MET	GLN	SER	THR	ALA	L157	L157	PRO	ILE
ASN	GLU	PRO	THR	LEU			ALA	ALA
SER	GLN	PHE	MET	SER	P160	P160	ASP	VAL
ASN	ALA	SER	GLY	VAL	LYS	LYS	LYS	GLY
ASP	GLN	ALA	ASN	ASN	PRO	PRO	SER	ALA
HIS	GLN	ALA	VAL	GLN	GLY	GLY	HIS	ALA
GLU	ARG	VAL	GLY	PRO	ILE	ILE	GLU	VAL
	ARG	ASP	ALA	ASN	ALA	ALA	LEU	VAL
	GLN	ASN	ILE	PRO	VAL	VAL	ARG	ALA
	THR	THR	GLU	PRO	VAL	VAL	LEU	ALA
	GLU	GLY	GLY	ASN	ALA	ALA	LEU	ILE
	GLU	GLY	LEU	GLN	VAL	VAL	LEU	VAL
	ALA	LEU	SER	ALA	LYS	LYS	ALA	ALA
	VAL	PRO	VAL	THR	S171	S171	GLN	MET
	GLU	VAL	ILE	ALA			GLN	VAL
	GLU	PHE	VAL	GLN	S175	S175	GLY	VAL
	VAL	TRP	THR	LEU			LEU	TRP
	ARG	GLN	VAL	PRO	Q190	Q190	PRO	ALA
	LEU	GLN	VAL	PRO	PHE	PHE	LYS	ALA
	SER	GLN	TYR	THR	ALA	ALA	GLY	THR
	LYS	GLN	LYS	ASN	A193	A193	GLY	PRO
	ASP	PHE	THR	ASN			ALA	THR
	GLU	THR	THR	GLN	L197	L197	VAL	TYR
	LEU	ILE	THR	ASN			VAL	ASP
	GLN	ASP	ALA	GLN	T211	T211	GLY	ARG
	LEU	GLN	GLY	ALA			PHE	THR
	GLN	LEU	GLY	GLU	D214	D214	GLU	LEU
	ARG	ALA	ASN	GLU			LEU	PHE
	ARG	ALA	PRO	HIS	T221	T221	LEU	SER
	ALA	GLY	PRO	TYR	Q222	Q222	ASP	ASN
	ARG	GLY	GLN	SER	SER	SER	GLN	LEU
	ASN	TRP	THR	PRO	ASN	ASN	GLU	SER
	GLN	TRP	THR	SER			LYS	ASP

- Molecule 1: Flagellar M-ring protein

Chain d:  12% . 84%

[illegible]

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain f: 12% . 84%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain g: 12% . 84%

PHE	GLY	ILE	Q125	F126	S127	E128	Q133	E137	A141	R142	T143	I144	T146	L147	G148	P149	S152	A153	R154	V155	H156	L157	P160	PRO	SER	PHE	VAL	ARG	GLY	LYS	S171	S175	A193	L197	T211	D214	T221	SER	THR	THR									
GLN	ASP	GLY	ALA	ILE	VAL	GLN	THR	GLN	ASN	ILE	TYR	ARG	PHE	ALA	ASN	GLY	GLY	ALA	ILE	GLY	VAL	PRO	ILE	VAL	ASP	GLY	SER	ALA	VAL	ALA	VAL	GLN	GLN	LEU	PRO	LYS	GLY	ALA	VAL	PHE	GLY	GLY	LEU	ASN	GLN	GLY			
MET	SER	THR	ALA	ALA	SER	THR	ALA	GLN	PRO	LEU	TRP	LEU	ASN	ARG	ALA	ASN	PRO	ARG	ILE	PRO	LEU	ILE	VAL	ALA	GLY	SER	ALA	VAL	ALA	VAL	VAL	ALA	MET	VAL	LEU	TRP	ALA	LYS	THR	PRO	ASP	TYR	THR	LEU	PHE	SER	ASN	LEU	SER

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C22	Depositor
Number of particles used	87107	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	0.079	Depositor
Minimum map value	-0.043	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	0.29	0/655	0.43	0/893
1	C	0.29	0/655	0.43	0/893
1	D	0.29	0/655	0.43	0/893
1	F	0.29	0/655	0.43	0/893
1	G	0.29	0/655	0.43	0/893
1	I	0.29	0/655	0.43	0/893
1	J	0.29	0/655	0.43	0/893
1	L	0.29	0/655	0.43	0/893
1	M	0.29	0/655	0.43	0/893
1	O	0.29	0/655	0.43	0/893
1	P	0.29	0/655	0.43	0/893
1	R	0.29	0/655	0.43	0/893
1	T	0.29	0/655	0.43	0/893
1	U	0.29	0/655	0.43	0/893
1	W	0.29	0/655	0.43	0/893
1	X	0.29	0/655	0.43	0/893
1	Z	0.29	0/655	0.43	0/893
1	a	0.29	0/655	0.43	0/893
1	c	0.29	0/655	0.43	0/893
1	d	0.29	0/655	0.43	0/893
1	f	0.29	0/655	0.43	0/893
1	g	0.29	0/655	0.43	0/893
All	All	0.29	0/14410	0.43	0/19646

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	646	0	652	14	0
1	C	646	0	652	16	0
1	D	646	0	652	15	0
1	F	646	0	652	16	0
1	G	646	0	652	16	0
1	I	646	0	652	15	0
1	J	646	0	652	14	0
1	L	646	0	652	15	0
1	M	646	0	652	15	0
1	O	646	0	652	15	0
1	P	646	0	652	12	0
1	R	646	0	652	14	0
1	T	646	0	652	14	0
1	U	646	0	652	14	0
1	W	646	0	652	15	0
1	X	646	0	652	15	0
1	Z	646	0	652	16	0
1	a	646	0	652	15	0
1	c	646	0	652	15	0
1	d	646	0	652	15	0
1	f	646	0	652	13	0
1	g	646	0	652	15	0
All	All	14212	0	14344	259	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 9.

All (259) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:HIS:NE2	1:g:143:THR:HG21	2.05	0.72
1:C:143:THR:HG21	1:D:156:HIS:NE2	2.05	0.71
1:G:143:THR:HG21	1:I:156:HIS:NE2	2.07	0.69
1:M:143:THR:HG21	1:O:156:HIS:NE2	2.10	0.66
1:O:143:THR:HG21	1:P:156:HIS:NE2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:143:THR:HG21	1:G:156:HIS:NE2	2.11	0.65
1:J:143:THR:HG21	1:L:156:HIS:NE2	2.11	0.65
1:R:143:THR:HG21	1:T:156:HIS:NE2	2.11	0.65
1:Z:143:THR:HG21	1:a:156:HIS:NE2	2.12	0.65
1:P:143:THR:HG21	1:R:156:HIS:NE2	2.12	0.64
1:L:143:THR:HG21	1:M:156:HIS:NE2	2.12	0.64
1:X:143:THR:HG21	1:Z:156:HIS:NE2	2.13	0.64
1:U:143:THR:HG21	1:W:156:HIS:NE2	2.13	0.63
1:A:143:THR:HG21	1:C:156:HIS:NE2	2.14	0.63
1:W:143:THR:HG21	1:X:156:HIS:NE2	2.15	0.61
1:c:143:THR:HG21	1:d:156:HIS:NE2	2.15	0.61
1:T:143:THR:HG21	1:U:156:HIS:NE2	2.15	0.61
1:P:145:GLU:HG2	1:P:152:SER:HA	1.82	0.61
1:C:145:GLU:HG2	1:C:152:SER:HA	1.82	0.61
1:O:145:GLU:HG2	1:O:152:SER:HA	1.82	0.61
1:R:145:GLU:HG2	1:R:152:SER:HA	1.82	0.61
1:T:145:GLU:HG2	1:T:152:SER:HA	1.82	0.61
1:f:145:GLU:HG2	1:f:152:SER:HA	1.82	0.61
1:A:145:GLU:HG2	1:A:152:SER:HA	1.82	0.61
1:g:145:GLU:HG2	1:g:152:SER:HA	1.82	0.61
1:L:145:GLU:HG2	1:L:152:SER:HA	1.82	0.61
1:M:145:GLU:HG2	1:M:152:SER:HA	1.82	0.61
1:U:145:GLU:HG2	1:U:152:SER:HA	1.82	0.61
1:W:145:GLU:HG2	1:W:152:SER:HA	1.82	0.61
1:c:145:GLU:HG2	1:c:152:SER:HA	1.82	0.61
1:M:214:ASP:OD1	1:M:214:ASP:N	2.34	0.60
1:X:145:GLU:HG2	1:X:152:SER:HA	1.82	0.60
1:F:145:GLU:HG2	1:F:152:SER:HA	1.82	0.60
1:d:145:GLU:HG2	1:d:152:SER:HA	1.82	0.60
1:C:214:ASP:N	1:C:214:ASP:OD1	2.34	0.60
1:D:145:GLU:HG2	1:D:152:SER:HA	1.82	0.60
1:d:143:THR:HG21	1:f:156:HIS:NE2	2.17	0.60
1:A:143:THR:HG22	1:C:154:ARG:HG2	1.83	0.60
1:A:214:ASP:OD1	1:A:214:ASP:N	2.34	0.60
1:G:145:GLU:HG2	1:G:152:SER:HA	1.82	0.60
1:J:145:GLU:HG2	1:J:152:SER:HA	1.82	0.60
1:R:214:ASP:OD1	1:R:214:ASP:N	2.34	0.60
1:a:145:GLU:HG2	1:a:152:SER:HA	1.82	0.60
1:f:214:ASP:OD1	1:f:214:ASP:N	2.34	0.60
1:O:214:ASP:N	1:O:214:ASP:OD1	2.34	0.60
1:f:143:THR:HG21	1:g:156:HIS:NE2	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:214:ASP:OD1	1:G:214:ASP:N	2.34	0.60
1:P:214:ASP:OD1	1:P:214:ASP:N	2.34	0.60
1:U:214:ASP:OD1	1:U:214:ASP:N	2.34	0.60
1:I:145:GLU:HG2	1:I:152:SER:HA	1.82	0.60
1:c:214:ASP:OD1	1:c:214:ASP:N	2.34	0.60
1:Z:145:GLU:HG2	1:Z:152:SER:HA	1.82	0.59
1:X:214:ASP:OD1	1:X:214:ASP:N	2.34	0.59
1:g:214:ASP:N	1:g:214:ASP:OD1	2.34	0.59
1:L:214:ASP:N	1:L:214:ASP:OD1	2.34	0.59
1:Z:214:ASP:OD1	1:Z:214:ASP:N	2.34	0.59
1:a:214:ASP:OD1	1:a:214:ASP:N	2.35	0.59
1:d:214:ASP:OD1	1:d:214:ASP:N	2.34	0.59
1:W:214:ASP:OD1	1:W:214:ASP:N	2.34	0.59
1:T:214:ASP:N	1:T:214:ASP:OD1	2.34	0.59
1:D:214:ASP:OD1	1:D:214:ASP:N	2.34	0.58
1:a:143:THR:HG22	1:c:154:ARG:HG2	1.85	0.58
1:I:143:THR:HG21	1:J:156:HIS:NE2	2.18	0.58
1:F:143:THR:HG22	1:G:154:ARG:HG2	1.86	0.58
1:I:214:ASP:OD1	1:I:214:ASP:N	2.34	0.57
1:D:143:THR:HG21	1:F:156:HIS:NE2	2.20	0.57
1:a:141:ALA:HB2	1:a:155:VAL:HG12	1.87	0.57
1:O:141:ALA:HB2	1:O:155:VAL:HG12	1.87	0.57
1:U:141:ALA:HB2	1:U:155:VAL:HG12	1.87	0.57
1:X:141:ALA:HB2	1:X:155:VAL:HG12	1.87	0.57
1:c:141:ALA:HB2	1:c:155:VAL:HG12	1.87	0.57
1:R:141:ALA:HB2	1:R:155:VAL:HG12	1.87	0.57
1:T:141:ALA:HB2	1:T:155:VAL:HG12	1.87	0.57
1:W:141:ALA:HB2	1:W:155:VAL:HG12	1.87	0.57
1:d:141:ALA:HB2	1:d:155:VAL:HG12	1.87	0.57
1:A:141:ALA:HB2	1:A:155:VAL:HG12	1.87	0.56
1:P:141:ALA:HB2	1:P:155:VAL:HG12	1.87	0.56
1:Z:141:ALA:HB2	1:Z:155:VAL:HG12	1.87	0.56
1:L:141:ALA:HB2	1:L:155:VAL:HG12	1.87	0.56
1:f:141:ALA:HB2	1:f:155:VAL:HG12	1.87	0.56
1:D:143:THR:HG22	1:F:154:ARG:HG2	1.87	0.56
1:J:214:ASP:N	1:J:214:ASP:OD1	2.34	0.56
1:c:143:THR:HG22	1:d:154:ARG:HG2	1.88	0.56
1:g:141:ALA:HB2	1:g:155:VAL:HG12	1.87	0.56
1:D:141:ALA:HB2	1:D:155:VAL:HG12	1.87	0.56
1:F:214:ASP:OD1	1:F:214:ASP:N	2.34	0.56
1:I:141:ALA:HB2	1:I:155:VAL:HG12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:141:ALA:HB2	1:M:155:VAL:HG12	1.87	0.56
1:R:143:THR:HG22	1:T:154:ARG:HG2	1.88	0.56
1:G:141:ALA:HB2	1:G:155:VAL:HG12	1.87	0.56
1:a:143:THR:HG21	1:c:156:HIS:NE2	2.21	0.56
1:I:143:THR:HG22	1:J:154:ARG:HG2	1.89	0.55
1:C:141:ALA:HB2	1:C:155:VAL:HG12	1.87	0.55
1:F:141:ALA:HB2	1:F:155:VAL:HG12	1.87	0.55
1:J:141:ALA:HB2	1:J:155:VAL:HG12	1.87	0.55
1:f:143:THR:HG22	1:g:154:ARG:HG2	1.89	0.55
1:F:133:GLN:NE2	1:F:137:GLU:OE2	2.40	0.55
1:d:143:THR:HG22	1:f:154:ARG:HG2	1.89	0.55
1:R:133:GLN:NE2	1:R:137:GLU:OE2	2.41	0.54
1:g:133:GLN:NE2	1:g:137:GLU:OE2	2.40	0.54
1:L:133:GLN:NE2	1:L:137:GLU:OE2	2.41	0.54
1:P:133:GLN:NE2	1:P:137:GLU:OE2	2.40	0.54
1:A:133:GLN:NE2	1:A:137:GLU:OE2	2.41	0.54
1:G:133:GLN:NE2	1:G:137:GLU:OE2	2.40	0.54
1:f:133:GLN:NE2	1:f:137:GLU:OE2	2.40	0.54
1:D:133:GLN:NE2	1:D:137:GLU:OE2	2.41	0.54
1:J:133:GLN:NE2	1:J:137:GLU:OE2	2.41	0.54
1:M:133:GLN:NE2	1:M:137:GLU:OE2	2.41	0.54
1:T:133:GLN:NE2	1:T:137:GLU:OE2	2.41	0.54
1:U:143:THR:HG22	1:W:154:ARG:HG2	1.90	0.54
1:X:133:GLN:NE2	1:X:137:GLU:OE2	2.41	0.54
1:Z:133:GLN:NE2	1:Z:137:GLU:OE2	2.41	0.54
1:a:133:GLN:NE2	1:a:137:GLU:OE2	2.40	0.54
1:W:143:THR:HG22	1:X:154:ARG:HG2	1.90	0.54
1:L:143:THR:HG22	1:M:154:ARG:HG2	1.90	0.54
1:W:133:GLN:NE2	1:W:137:GLU:OE2	2.41	0.54
1:A:154:ARG:HG2	1:g:143:THR:HG22	1.89	0.53
1:O:133:GLN:NE2	1:O:137:GLU:OE2	2.41	0.53
1:X:143:THR:HG22	1:Z:154:ARG:HG2	1.90	0.53
1:d:133:GLN:NE2	1:d:137:GLU:OE2	2.41	0.53
1:C:133:GLN:NE2	1:C:137:GLU:OE2	2.41	0.53
1:U:133:GLN:NE2	1:U:137:GLU:OE2	2.41	0.53
1:I:133:GLN:NE2	1:I:137:GLU:OE2	2.41	0.53
1:f:128:GLU:HG2	1:g:126:PHE:CD2	2.44	0.52
1:c:133:GLN:NE2	1:c:137:GLU:OE2	2.41	0.52
1:J:143:THR:HG22	1:L:154:ARG:HG2	1.92	0.52
1:M:143:THR:HG22	1:O:154:ARG:HG2	1.92	0.52
1:J:147:LEU:O	1:J:149:PRO:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:147:LEU:O	1:G:149:PRO:HD2	2.11	0.51
1:O:147:LEU:O	1:O:149:PRO:HD2	2.11	0.51
1:F:147:LEU:O	1:F:149:PRO:HD2	2.11	0.51
1:M:147:LEU:O	1:M:149:PRO:HD2	2.11	0.51
1:T:147:LEU:O	1:T:149:PRO:HD2	2.11	0.51
1:U:147:LEU:O	1:U:149:PRO:HD2	2.11	0.51
1:P:147:LEU:O	1:P:149:PRO:HD2	2.11	0.51
1:R:147:LEU:O	1:R:149:PRO:HD2	2.11	0.51
1:Z:147:LEU:O	1:Z:149:PRO:HD2	2.11	0.51
1:X:147:LEU:O	1:X:149:PRO:HD2	2.11	0.51
1:L:147:LEU:O	1:L:149:PRO:HD2	2.11	0.51
1:T:143:THR:HG22	1:U:154:ARG:HG2	1.92	0.51
1:A:147:LEU:O	1:A:149:PRO:HD2	2.11	0.51
1:D:147:LEU:O	1:D:149:PRO:HD2	2.11	0.51
1:d:147:LEU:O	1:d:149:PRO:HD2	2.11	0.51
1:I:147:LEU:O	1:I:149:PRO:HD2	2.11	0.50
1:a:147:LEU:O	1:a:149:PRO:HD2	2.11	0.50
1:c:147:LEU:O	1:c:149:PRO:HD2	2.11	0.50
1:g:147:LEU:O	1:g:149:PRO:HD2	2.11	0.50
1:W:147:LEU:O	1:W:149:PRO:HD2	2.11	0.50
1:F:128:GLU:HG2	1:G:126:PHE:CD2	2.47	0.50
1:C:147:LEU:O	1:C:149:PRO:HD2	2.11	0.50
1:F:211:THR:HA	1:F:221:THR:HG21	1.94	0.50
1:C:211:THR:HA	1:C:221:THR:HG21	1.94	0.49
1:P:211:THR:HA	1:P:221:THR:HG21	1.94	0.49
1:T:211:THR:HA	1:T:221:THR:HG21	1.94	0.49
1:U:211:THR:HA	1:U:221:THR:HG21	1.94	0.49
1:G:143:THR:HG22	1:I:154:ARG:HG2	1.94	0.49
1:I:211:THR:HA	1:I:221:THR:HG21	1.94	0.49
1:O:143:THR:HG22	1:P:154:ARG:HG2	1.94	0.49
1:O:211:THR:HA	1:O:221:THR:HG21	1.94	0.49
1:P:143:THR:HG22	1:R:154:ARG:HG2	1.94	0.49
1:D:211:THR:HA	1:D:221:THR:HG21	1.94	0.49
1:J:211:THR:HA	1:J:221:THR:HG21	1.94	0.49
1:M:211:THR:HA	1:M:221:THR:HG21	1.94	0.49
1:R:211:THR:HA	1:R:221:THR:HG21	1.94	0.49
1:W:211:THR:HA	1:W:221:THR:HG21	1.94	0.49
1:X:211:THR:HA	1:X:221:THR:HG21	1.94	0.49
1:a:128:GLU:HG2	1:c:126:PHE:CD2	2.47	0.49
1:f:147:LEU:O	1:f:149:PRO:HD2	2.11	0.49
1:f:211:THR:HA	1:f:221:THR:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:THR:HA	1:A:221:THR:HG21	1.95	0.49
1:G:211:THR:HA	1:G:221:THR:HG21	1.94	0.49
1:a:211:THR:HA	1:a:221:THR:HG21	1.94	0.49
1:L:211:THR:HA	1:L:221:THR:HG21	1.95	0.49
1:g:211:THR:HA	1:g:221:THR:HG21	1.94	0.49
1:c:211:THR:HA	1:c:221:THR:HG21	1.94	0.49
1:Z:143:THR:HG22	1:a:154:ARG:HG2	1.95	0.49
1:d:211:THR:HA	1:d:221:THR:HG21	1.94	0.49
1:Z:211:THR:HA	1:Z:221:THR:HG21	1.94	0.49
1:D:128:GLU:HG2	1:F:126:PHE:CD2	2.48	0.48
1:g:175:SER:O	1:g:175:SER:OG	2.32	0.48
1:C:175:SER:O	1:C:175:SER:OG	2.32	0.47
1:c:175:SER:O	1:c:175:SER:OG	2.32	0.47
1:J:128:GLU:HG2	1:L:126:PHE:CD2	2.49	0.47
1:A:126:PHE:CD2	1:g:128:GLU:HG2	2.51	0.47
1:X:175:SER:O	1:X:175:SER:OG	2.32	0.46
1:M:128:GLU:HG2	1:O:126:PHE:CD2	2.51	0.46
1:T:175:SER:O	1:T:175:SER:OG	2.32	0.46
1:a:175:SER:O	1:a:175:SER:OG	2.32	0.45
1:R:128:GLU:HG2	1:T:126:PHE:CD2	2.50	0.45
1:D:175:SER:O	1:D:175:SER:OG	2.32	0.45
1:O:175:SER:O	1:O:175:SER:OG	2.32	0.45
1:O:128:GLU:HG2	1:P:126:PHE:CD2	2.52	0.45
1:A:128:GLU:HG2	1:C:126:PHE:CD2	2.52	0.44
1:W:128:GLU:HG2	1:X:126:PHE:CD2	2.51	0.44
1:W:175:SER:O	1:W:175:SER:OG	2.32	0.44
1:G:175:SER:O	1:G:175:SER:OG	2.32	0.44
1:d:175:SER:O	1:d:175:SER:OG	2.32	0.44
1:Z:128:GLU:HG2	1:a:126:PHE:CD2	2.53	0.43
1:G:128:GLU:HG2	1:I:126:PHE:CD2	2.53	0.43
1:L:137:GLU:HG2	1:L:157:LEU:HG	2.02	0.42
1:P:137:GLU:HG2	1:P:157:LEU:HG	2.02	0.42
1:R:175:SER:O	1:R:175:SER:OG	2.32	0.42
1:U:137:GLU:HG2	1:U:157:LEU:HG	2.02	0.42
1:Z:137:GLU:HG2	1:Z:157:LEU:HG	2.02	0.42
1:a:137:GLU:HG2	1:a:157:LEU:HG	2.02	0.42
1:J:137:GLU:HG2	1:J:157:LEU:HG	2.01	0.42
1:L:128:GLU:HG2	1:M:126:PHE:CD2	2.55	0.42
1:W:137:GLU:HG2	1:W:157:LEU:HG	2.02	0.42
1:R:137:GLU:HG2	1:R:157:LEU:HG	2.02	0.42
1:U:128:GLU:HG2	1:W:126:PHE:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:137:GLU:HG2	1:M:157:LEU:HG	2.02	0.42
1:F:137:GLU:HG2	1:F:157:LEU:HG	2.02	0.42
1:f:137:GLU:HG2	1:f:157:LEU:HG	2.02	0.42
1:C:143:THR:HG22	1:D:154:ARG:HG2	2.01	0.42
1:g:137:GLU:HG2	1:g:157:LEU:HG	2.02	0.42
1:D:137:GLU:HG2	1:D:157:LEU:HG	2.02	0.41
1:O:137:GLU:HG2	1:O:157:LEU:HG	2.02	0.41
1:G:137:GLU:HG2	1:G:157:LEU:HG	2.02	0.41
1:D:193:ALA:O	1:D:197:LEU:HB2	2.21	0.41
1:I:128:GLU:HG2	1:J:126:PHE:CD2	2.55	0.41
1:T:137:GLU:HG2	1:T:157:LEU:HG	2.02	0.41
1:T:193:ALA:O	1:T:197:LEU:HB2	2.21	0.41
1:Z:175:SER:O	1:Z:175:SER:OG	2.32	0.41
1:L:193:ALA:O	1:L:197:LEU:HB2	2.21	0.41
1:X:137:GLU:HG2	1:X:157:LEU:HG	2.02	0.41
1:c:137:GLU:HG2	1:c:157:LEU:HG	2.02	0.41
1:F:193:ALA:O	1:F:197:LEU:HB2	2.21	0.41
1:U:193:ALA:O	1:U:197:LEU:HB2	2.21	0.41
1:d:137:GLU:HG2	1:d:157:LEU:HG	2.02	0.41
1:A:137:GLU:HG2	1:A:157:LEU:HG	2.01	0.41
1:J:193:ALA:O	1:J:197:LEU:HB2	2.21	0.41
1:M:193:ALA:O	1:M:197:LEU:HB2	2.21	0.41
1:R:193:ALA:O	1:R:197:LEU:HB2	2.21	0.41
1:Z:193:ALA:O	1:Z:197:LEU:HB2	2.21	0.41
1:C:193:ALA:O	1:C:197:LEU:HB2	2.21	0.41
1:W:193:ALA:O	1:W:197:LEU:HB2	2.21	0.41
1:X:193:ALA:O	1:X:197:LEU:HB2	2.21	0.41
1:a:193:ALA:O	1:a:197:LEU:HB2	2.21	0.41
1:c:193:ALA:O	1:c:197:LEU:HB2	2.21	0.41
1:f:193:ALA:O	1:f:197:LEU:HB2	2.21	0.41
1:M:175:SER:O	1:M:175:SER:OG	2.32	0.41
1:d:193:ALA:O	1:d:197:LEU:HB2	2.21	0.41
1:g:193:ALA:O	1:g:197:LEU:HB2	2.21	0.41
1:A:190:GLN:HG3	1:C:217:GLY:HA3	2.03	0.40
1:C:128:GLU:HG2	1:D:126:PHE:CD2	2.56	0.40
1:F:187:ASP:O	1:F:191:ILE:HG12	2.21	0.40
1:I:187:ASP:O	1:I:191:ILE:HG12	2.21	0.40
1:Z:187:ASP:O	1:Z:191:ILE:HG12	2.21	0.40
1:I:137:GLU:HG2	1:I:157:LEU:HG	2.02	0.40
1:C:137:GLU:HG2	1:C:157:LEU:HG	2.02	0.40
1:G:193:ALA:O	1:G:197:LEU:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:187:ASP:O	1:L:191:ILE:HG12	2.21	0.40
1:O:193:ALA:O	1:O:197:LEU:HB2	2.21	0.40
1:I:193:ALA:O	1:I:197:LEU:HB2	2.21	0.40
1:F:190:GLN:HG3	1:G:217:GLY:HA3	2.03	0.40
1:U:187:ASP:O	1:U:191:ILE:HG12	2.21	0.40
1:X:128:GLU:HG2	1:Z:126:PHE:CD2	2.56	0.40
1:c:190:GLN:HG3	1:d:217:GLY:HA3	2.04	0.40
1:d:187:ASP:O	1:d:191:ILE:HG12	2.21	0.40

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	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	C	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	D	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	F	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	G	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	I	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	J	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	L	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	M	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	O	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	P	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	R	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	T	84/560 (15%)	77 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	U	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	W	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	X	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	Z	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	a	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	c	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	d	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	f	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
1	g	84/560 (15%)	77 (92%)	7 (8%)	0	100	100
All	All	1848/12320 (15%)	1694 (92%)	154 (8%)	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%)	71 (99%)	1 (1%)	59	76
1	C	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	D	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	F	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	G	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	I	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	J	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	L	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	M	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	O	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	P	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	R	72/467 (15%)	71 (99%)	1 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	T	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	U	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	W	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	X	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	Z	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	a	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	c	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	d	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	f	72/467 (15%)	71 (99%)	1 (1%)	59	76
1	g	72/467 (15%)	71 (99%)	1 (1%)	59	76
All	All	1584/10274 (15%)	1562 (99%)	22 (1%)	57	76

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	214	ASP
1	C	214	ASP
1	D	214	ASP
1	F	214	ASP
1	G	214	ASP
1	I	214	ASP
1	J	214	ASP
1	L	214	ASP
1	M	214	ASP
1	O	214	ASP
1	P	214	ASP
1	R	214	ASP
1	T	214	ASP
1	U	214	ASP
1	W	214	ASP
1	X	214	ASP
1	Z	214	ASP
1	a	214	ASP
1	c	214	ASP
1	d	214	ASP
1	f	214	ASP
1	g	214	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	196	HIS
1	C	196	HIS
1	D	196	HIS
1	F	196	HIS
1	G	196	HIS
1	I	196	HIS
1	J	196	HIS
1	L	196	HIS
1	M	196	HIS
1	O	196	HIS
1	P	196	HIS
1	R	196	HIS
1	T	196	HIS
1	U	196	HIS
1	W	196	HIS
1	X	196	HIS
1	Z	196	HIS
1	a	196	HIS
1	c	196	HIS
1	d	196	HIS
1	f	196	HIS
1	g	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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

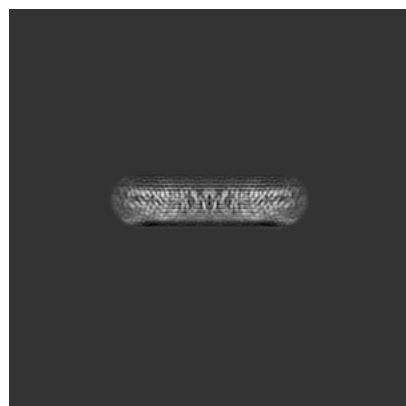
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10149. These allow visual inspection of the internal detail of the map and identification of artifacts.

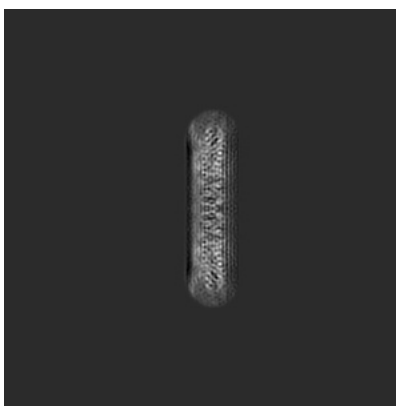
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

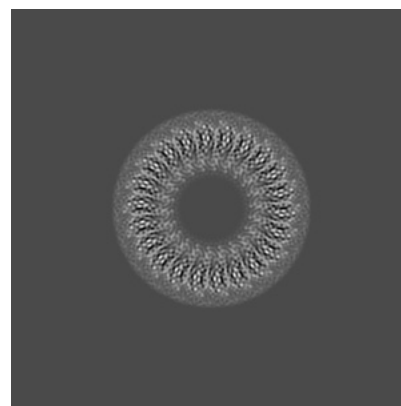
6.1.1 Primary map



X

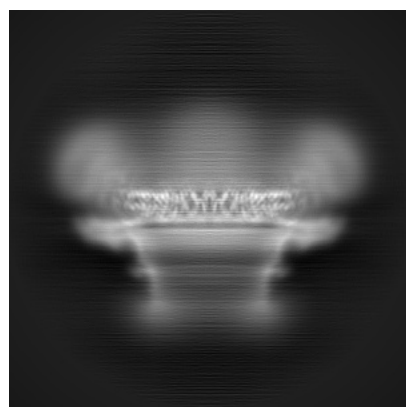


Y

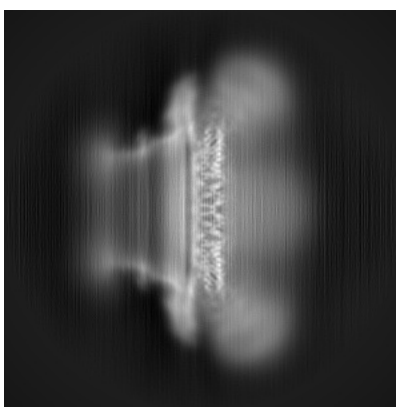


Z

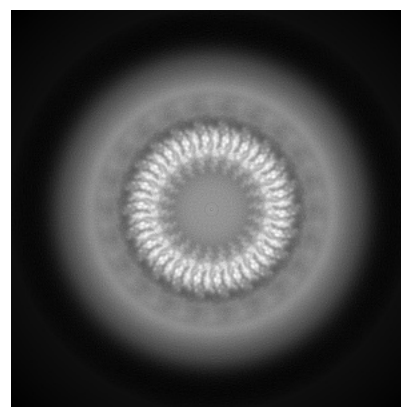
6.1.2 Raw map



X



Y



Z

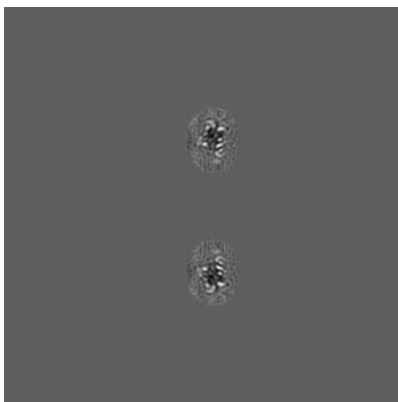
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

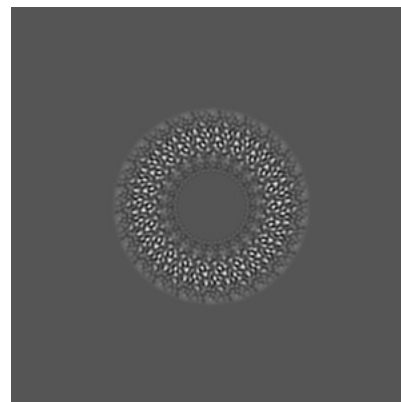
6.2.1 Primary map



X Index: 216

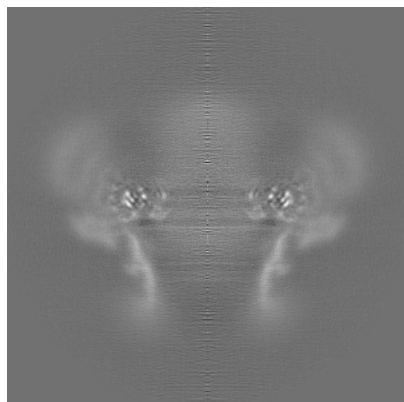


Y Index: 216

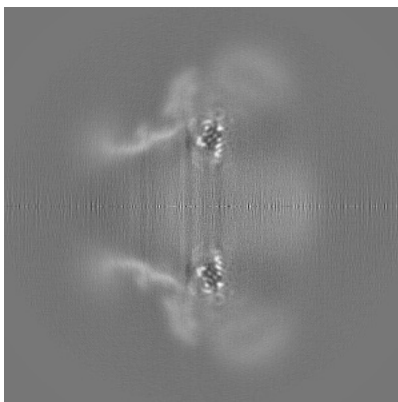


Z Index: 216

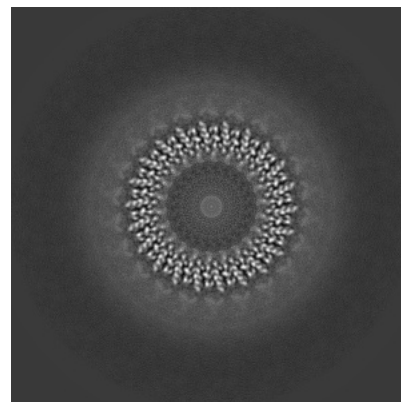
6.2.2 Raw map



X Index: 216



Y Index: 216

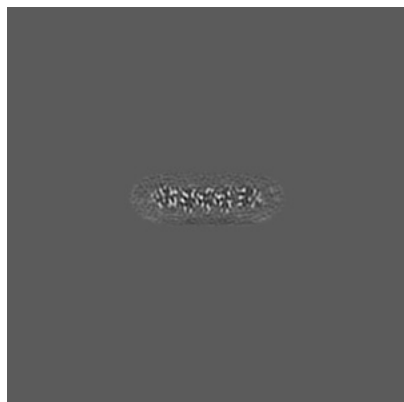


Z Index: 216

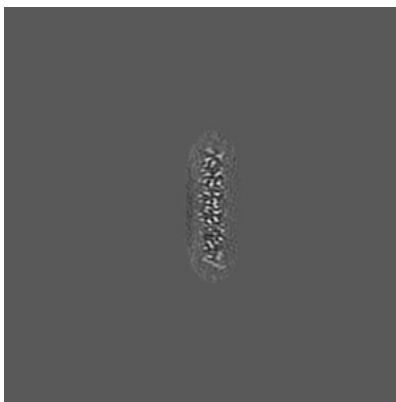
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

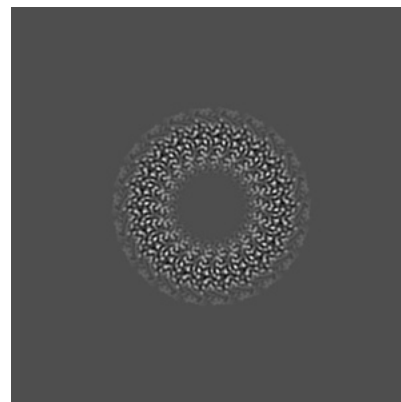
6.3.1 Primary map



X Index: 149

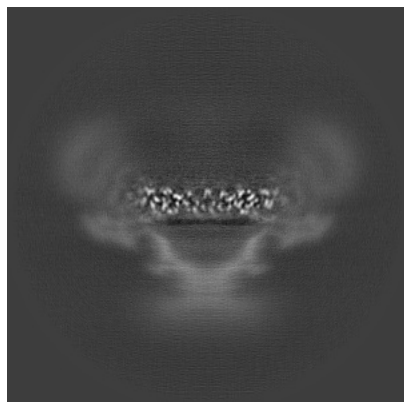


Y Index: 285

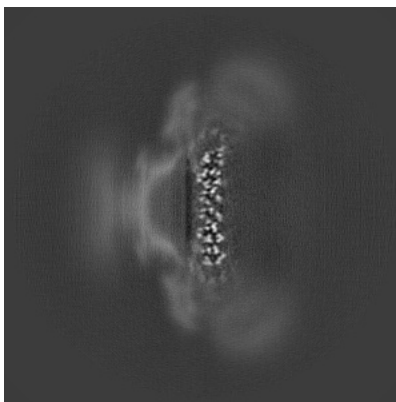


Z Index: 230

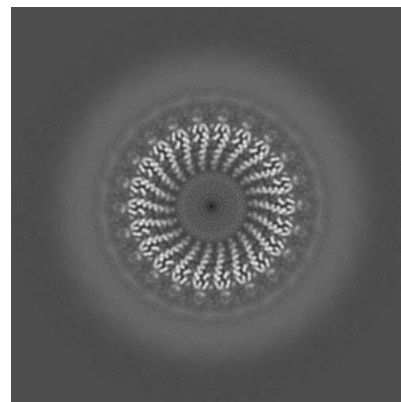
6.3.2 Raw map



X Index: 277



Y Index: 151

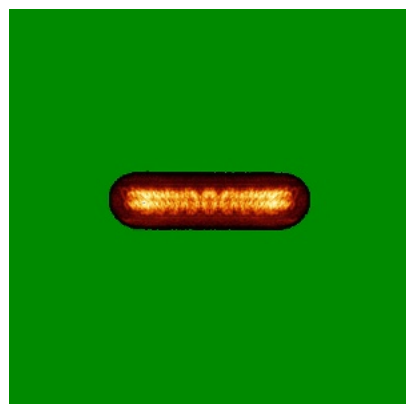


Z Index: 232

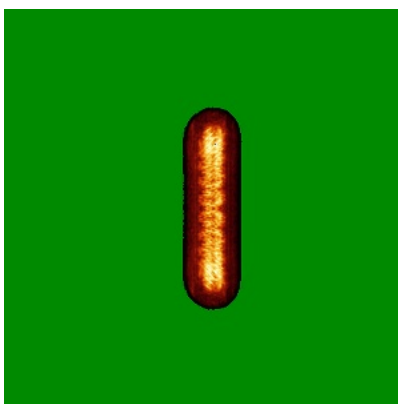
The images above show the largest variance slices of the map in three orthogonal directions.

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

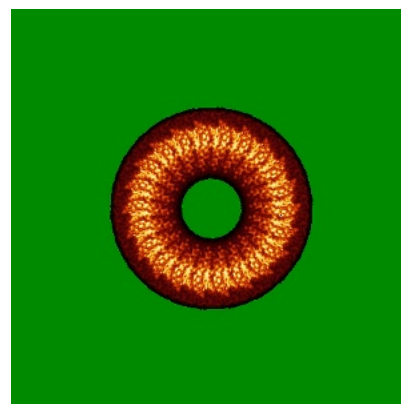
6.4.1 Primary map



X

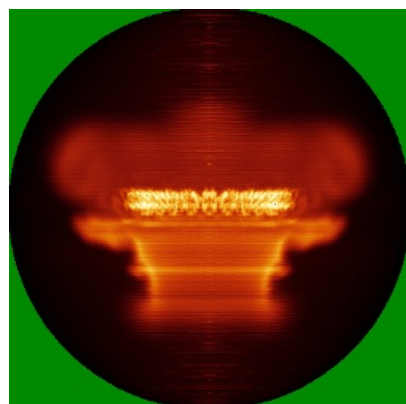


Y

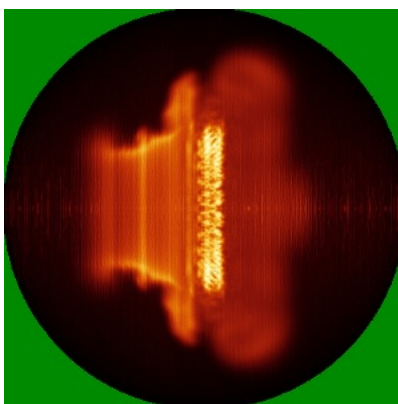


Z

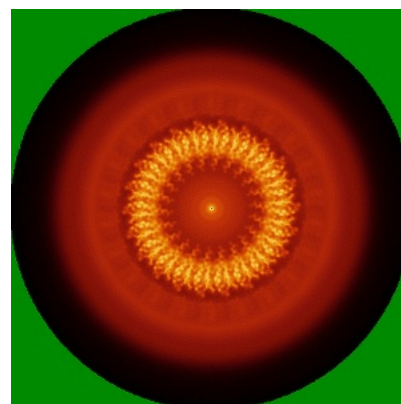
6.4.2 Raw map



X



Y

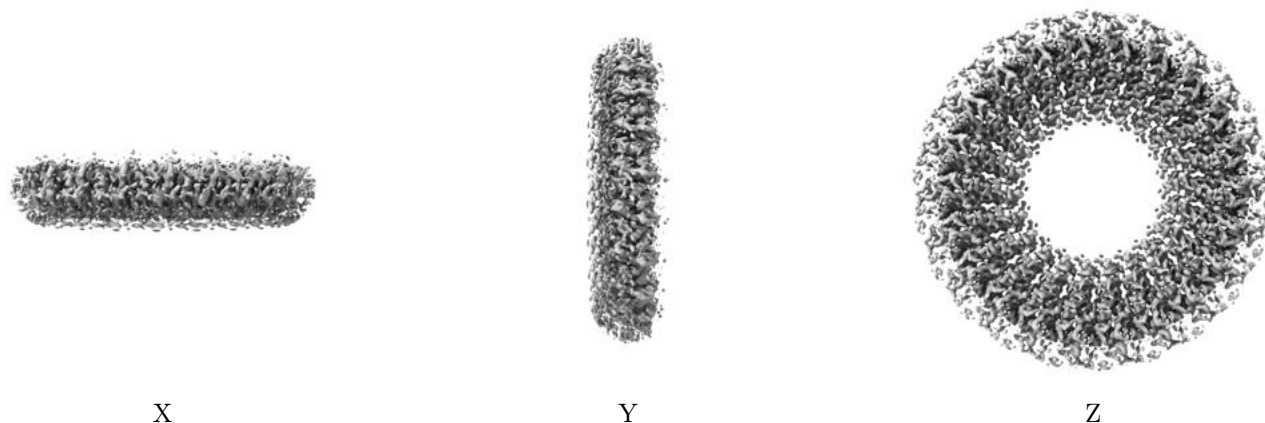


Z

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

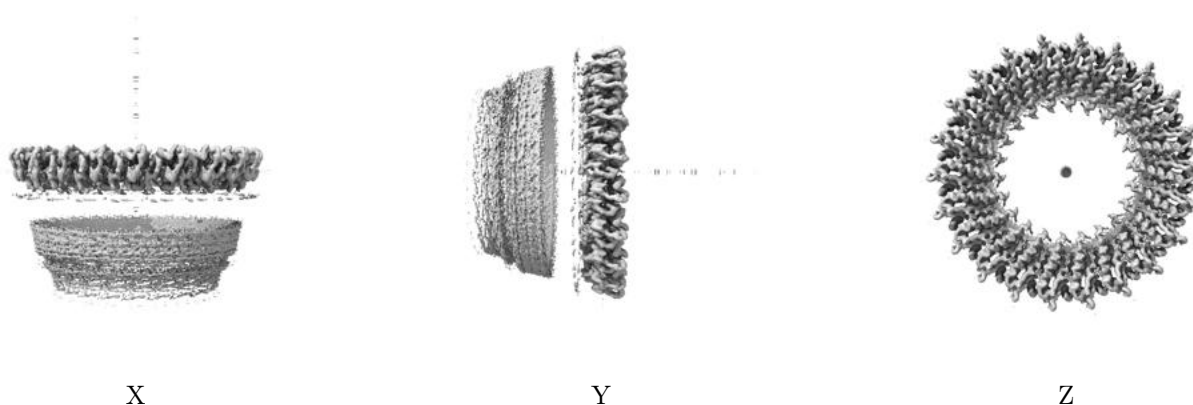
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

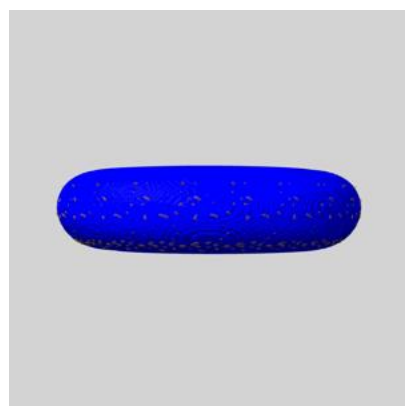
6.6 Mask visualisation [i](#)

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

A mask typically either:

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

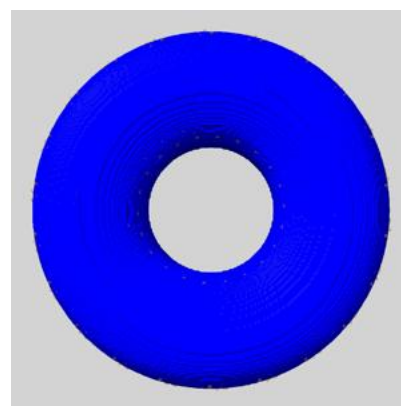
6.6.1 emd_10149_msk_1.map [i](#)



X



Y

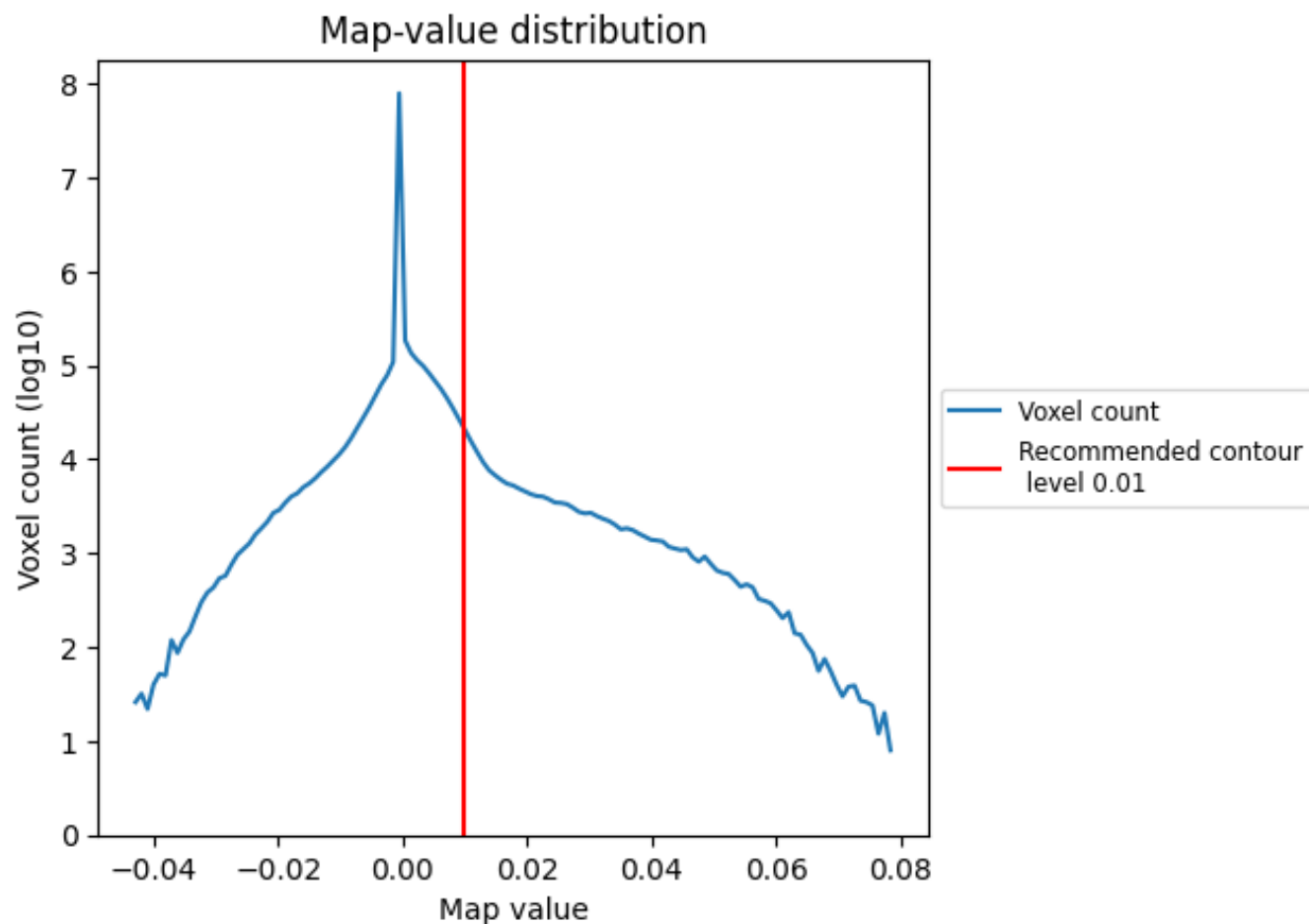


Z

7 Map analysis [i](#)

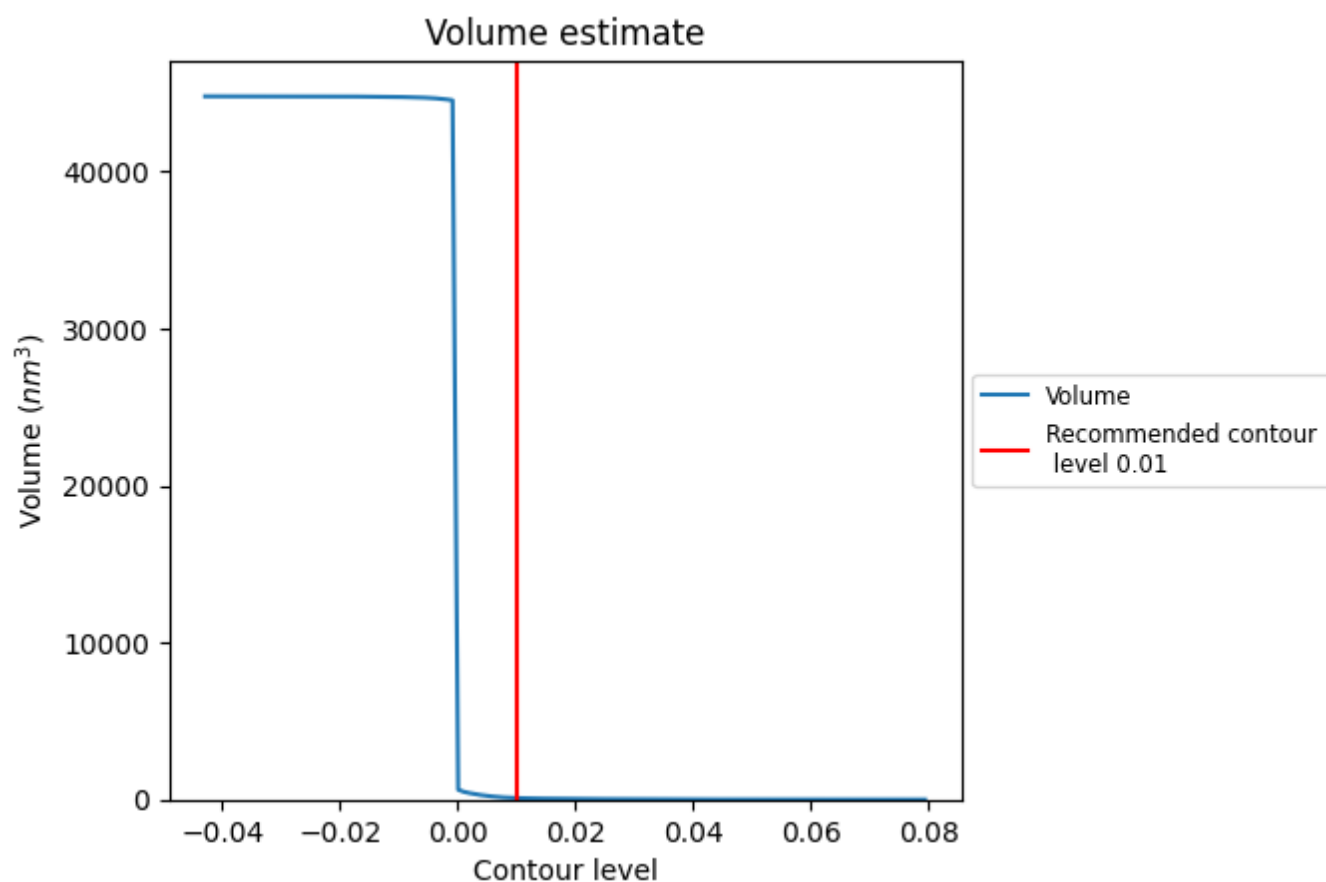
This section contains the results of statistical analysis of the map.

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.

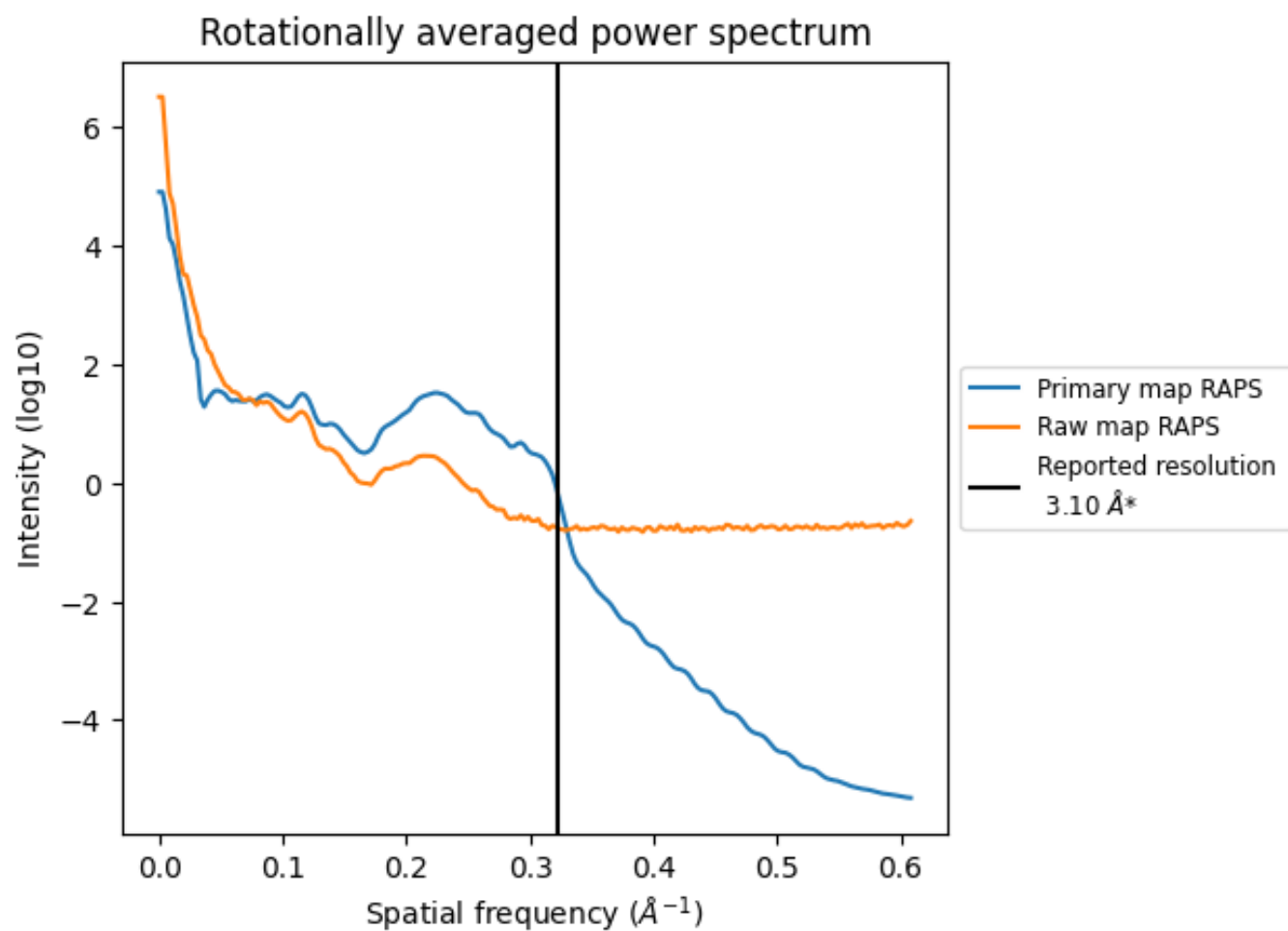
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 96 nm³; this corresponds to an approximate mass of 87 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 ⓘ

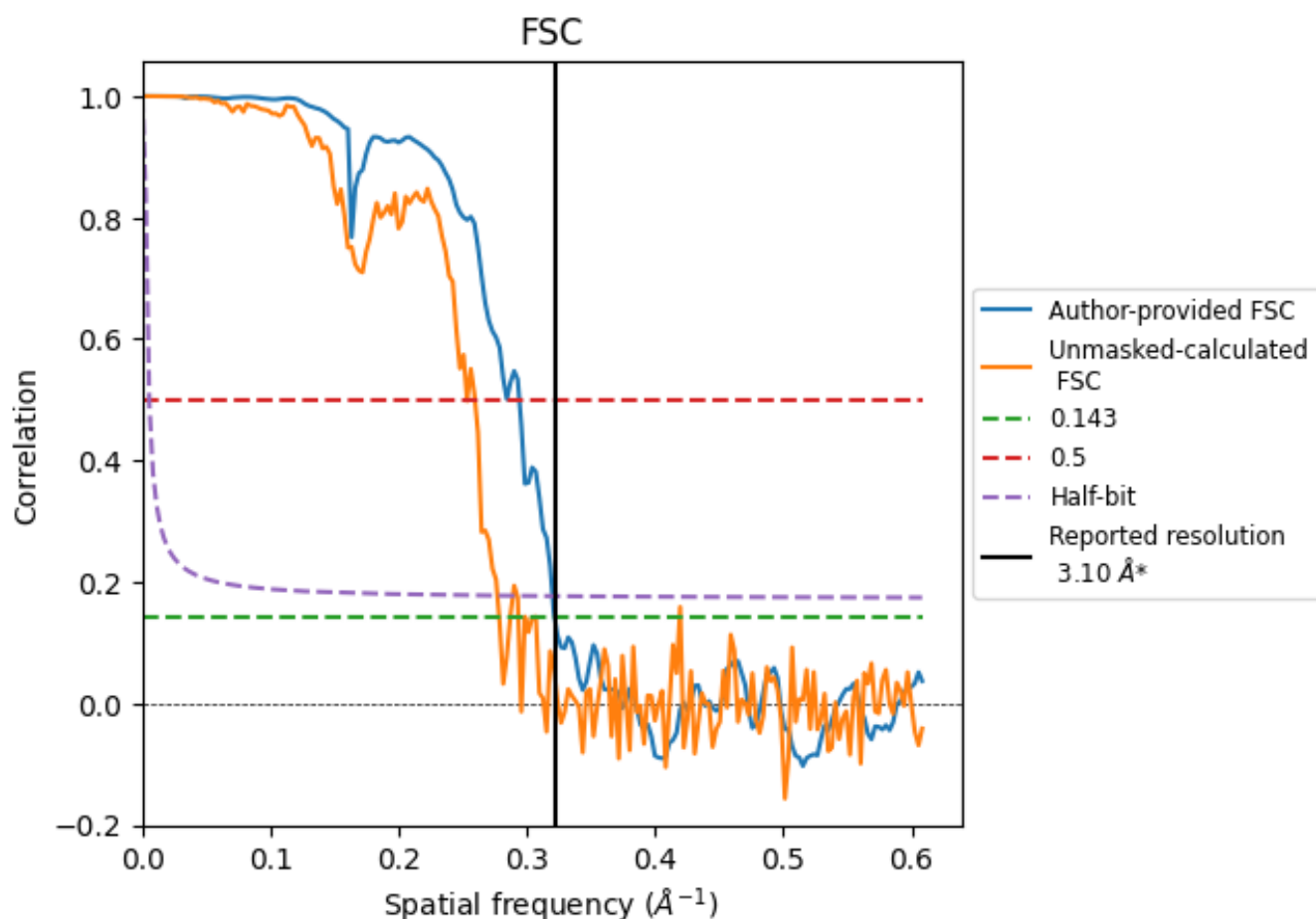


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

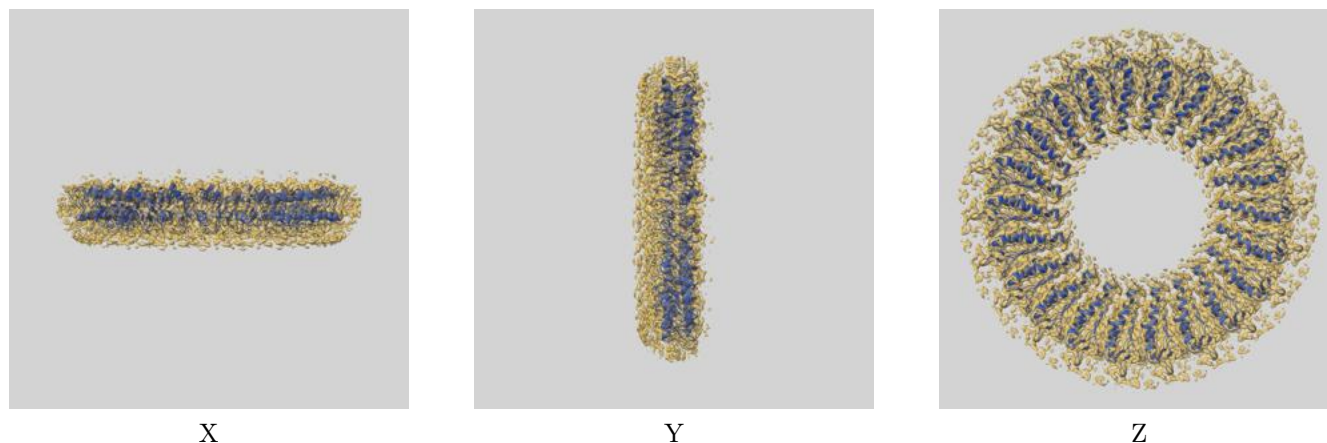
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	3.40	3.12
Unmasked-calculated*	3.59	3.95	3.61

*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 3.59 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

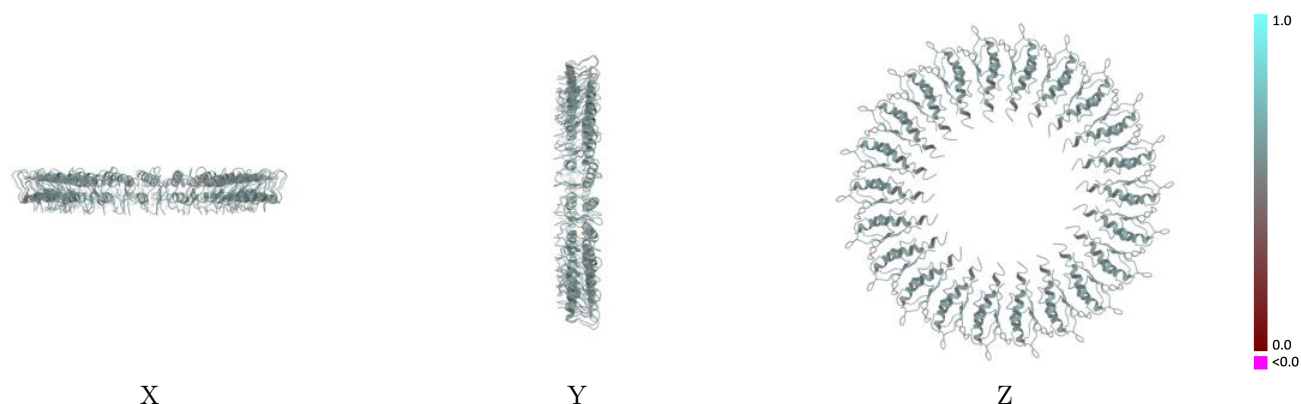
This section contains information regarding the fit between EMDB map EMD-10149 and PDB model 6SD5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



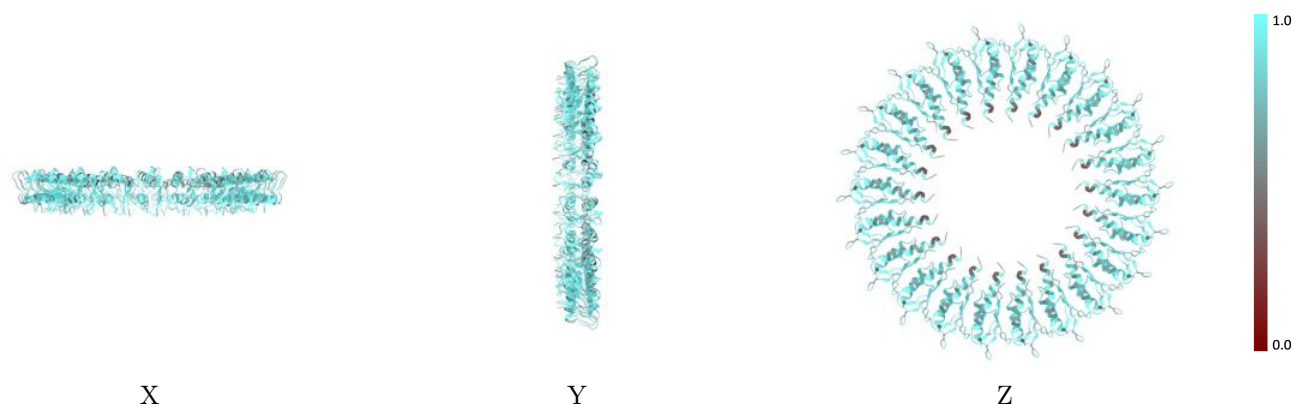
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



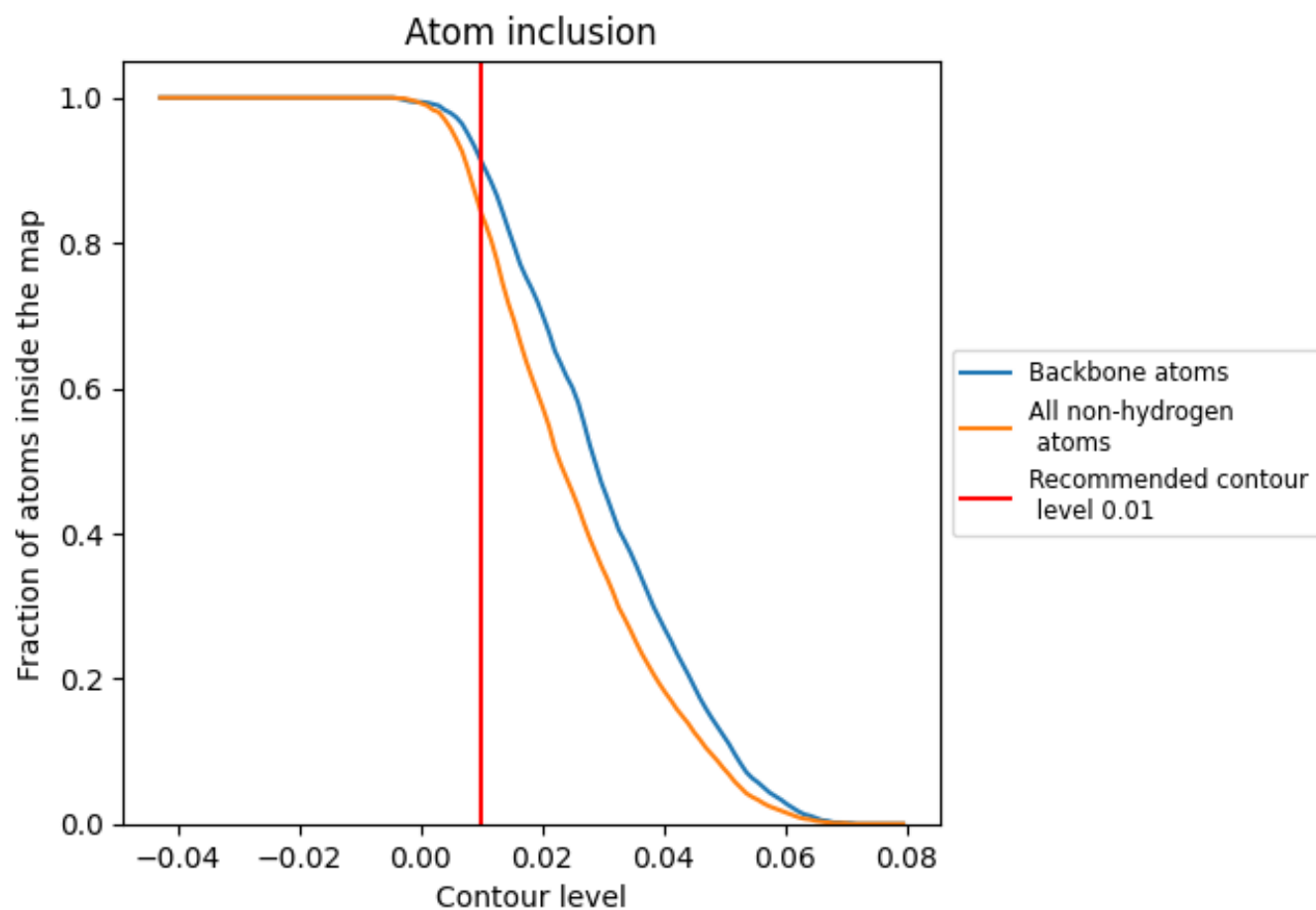
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% 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	 0.8390	 0.5510
A	 0.8370	 0.5520
C	 0.8460	 0.5510
D	 0.8400	 0.5520
F	 0.8370	 0.5510
G	 0.8350	 0.5510
I	 0.8350	 0.5500
J	 0.8380	 0.5490
L	 0.8430	 0.5490
M	 0.8370	 0.5510
O	 0.8430	 0.5500
P	 0.8380	 0.5500
R	 0.8350	 0.5500
T	 0.8410	 0.5500
U	 0.8490	 0.5520
W	 0.8380	 0.5530
X	 0.8370	 0.5520
Z	 0.8350	 0.5520
a	 0.8430	 0.5520
c	 0.8450	 0.5520
d	 0.8400	 0.5520
f	 0.8410	 0.5500
g	 0.8340	 0.5500

