



Full wwPDB EM Validation Report ⓘ

May 12, 2024 – 08:05 am BST

PDB ID : 6SD1
EMDB ID : EMD-10145
Title : Structure of the RBM3/collar region of the Salmonella flagella MS-ring protein
FliF with 33-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 : 2.60 Å(reported)

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

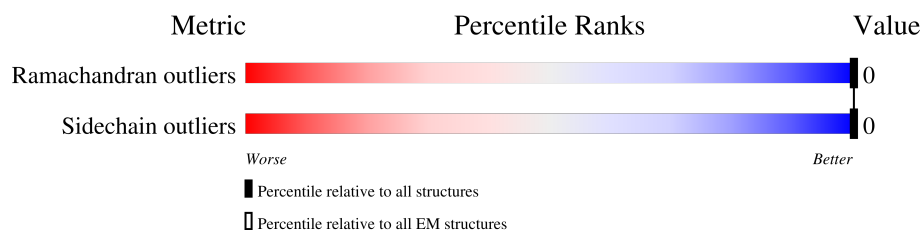
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY










The reported resolution of this entry is 2.60 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.













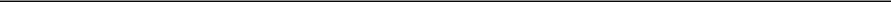

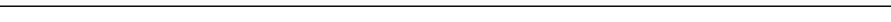











Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	 27% 73%
1	B	560	 27% 73%
1	C	560	 27% 73%
1	D	560	 27% 73%
1	E	560	 27% 73%
1	F	560	 27% 73%
1	G	560	 27% 73%
1	H	560	 27% 73%
1	I	560	 27% 73%

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Mol	Chain	Length	Quality of chain	
1	J	560		
1	K	560		
1	L	560		
1	M	560		
1	N	560		
1	O	560		
1	P	560		
1	Q	560		
1	R	560		
1	S	560		
1	T	560		
1	U	560		
1	V	560		
1	W	560		
1	X	560		
1	Y	560		
1	Z	560		
1	a	560		
1	b	560		
1	c	560		
1	d	560		
1	e	560		
1	f	560		
1	g	560		

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 39369 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	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	B	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	C	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	D	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	E	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	F	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	G	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	H	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	I	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	J	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	K	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	L	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	M	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	N	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	O	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	P	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	Q	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		

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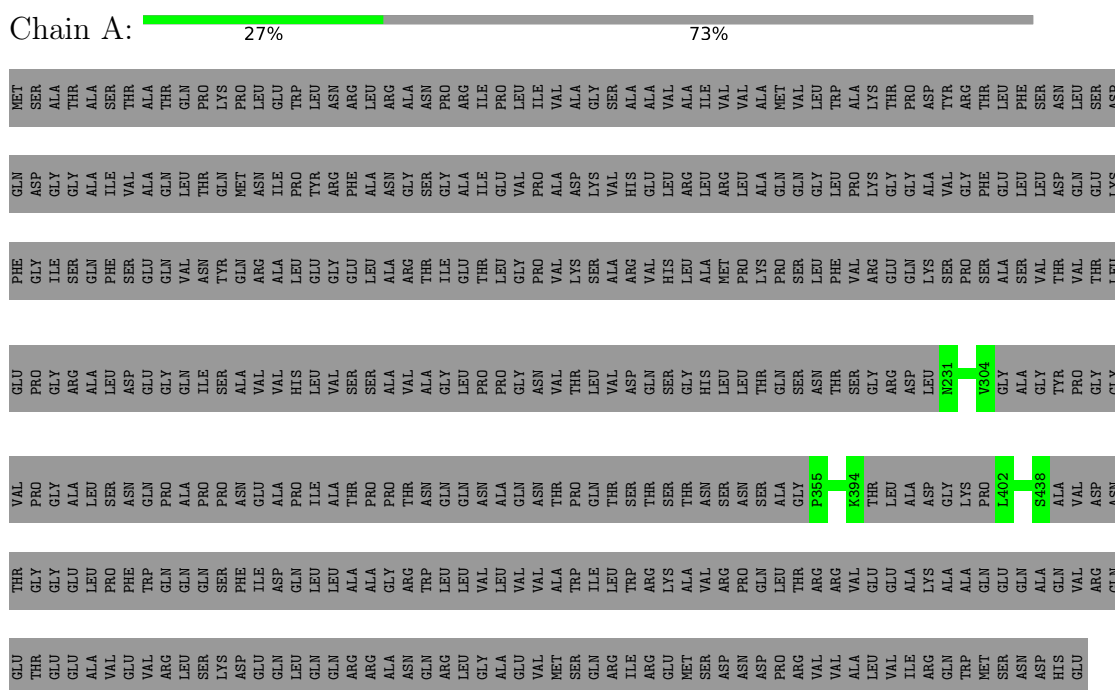
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	S	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	T	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	U	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	V	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	W	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	X	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	Y	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	Z	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	a	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	b	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	c	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	d	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	e	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	f	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	g	151	Total 1193	C 726	N 223	O 241	S 3	0	0

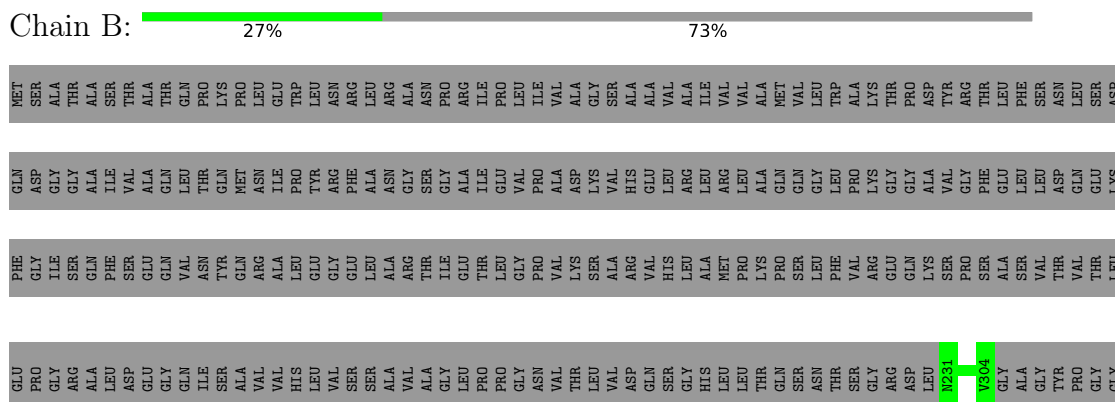
3 Residue-property plots

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



- Molecule 1: Flagellar M-ring protein

Chain E:  27% 73%

MET	SER	ALA	THR	SER	ALA	THR	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	LEU	ARG	ALA	ALA	ASN	PRO	ARG	ILE	PRO	LEU	ILE	VAL	GLY	ALA	SER	ALA	ALA	VAL	VAL	ALA	ALA	VAL	VAL	VAL	VAL	MET	VAL	LEU	TRP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	TRP
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GLN	ASP	GLY	GLY	ALA	VAL	GLN	THR	GLN	MET	ASN	ASN	PRO	TYR	ARG	ALA	ALA	ASN	GLY	GLY	GLY	ALA	ALA	GLU	VAL	PRO	PRO	ALA	ASP	LYS	VAL	VAL	HIS	LEU	ARG	LEU	GLU	GLU	LEU	ALA	ALA	GLN	GLN	GLY	GLY	PRO	LEU	LYS	GLY	GLY	ALA	VAL	VAL	GLY	GLU	ASP	GLN	GLN	GLY	TYR
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GLU PRO GLY ARG ALA LEU ASP GLU GLN ILE SER ALA VAL VAL HIS LEU VAL SER SER ALA VAL VAL ASP ASP THR THR GLM SER ASN THR THR GLY GLY HIS LEU LEU THR GLM SER ASN THR THR GLY ASP ARG N231 N234

[illegible]

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

Chain F:  27% 73%

MET	SER	ALA	ALA	THR	ALA	SER	THR	ALA	ALA	THR	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	LEU	ALA	ARG	ALA	ASN	PRO	PRO	ARG	ILE	PRO	LEU	ILE	VAL	ALA	GLY	SER	ALA	ALA	VAL	VAL	ALA	ALA	ALA	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ASP	TYR	ARG	THR	LYS	ALA	ALA	PRO	THR	LEU	PHE	SER	ASN	ASN	LEU	SER	SER
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GLN	ASP	GLY	ALA	ILE	VAL	ALA	GLN	LEU	THR	GLN	MET	ASN	ILE	PRO	TYR	ARG	PHE	ALA	ALA	ASN	GLY	SER	GLY	ALA	GLU	VAL	PRO	ALA	ASP	LYS	VAL	HIS	GLU	LEU	ARG	LEU	ARG	LEU	ALA	GLN	GLN	GLY	LEU	PRO	LYS	GLY	PHE	GLY	VAL	GLU	LEU	ASP	GLN	GLY	LYS
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GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	ALA	GLY	LEU	PRO	PRO	GLY	ASN	VAL	THR	LEU	VAL	ASP	GLN	SER	GLY	HIS	LEU	LEU	THR	GLN	SER	ASN	THR	SER	GLY	ARG	ASP	LEU	N231	N2304	GLY	ALA	GLY	TYR	PRO	PRO	GLY	GLY
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[illegible]

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

Chain G:  27% 73%

GLU	THR	GLU	THR	VAL	GLU	PHE	GLN	MET
THR	GLY	GLY	PRO	PRO	PRO	GLY	ASP	SER
GLU	GLY	GLY	ALA	ALA	ALA	ILE	GLY	ILE
ALA	ALA	ALA	LEU	LEU	ARG	GLN	ALA	ALA
VAL	PRO	PHE	SER	SER	LEU	PHE	ILE	SER
GLU	PHE	ASN	ASN	ASN	ASP	SER	VAL	THR
VAL	TRP	GLN	GLN	GLN	GLY	GLU	ALA	ALA
ARG	GLN	GLN	PRO	PRO	GLY	THR	GLN	THR
LEU	GLN	GLN	ALA	ALA	VAL	VAL	LEU	GLN
SER	GLN	ILE	ILE	ILE	VAL	GLY	THR	PRO
LYS	SER	PRO	PRO	PRO	SER	TYR	GLN	LYS
ASP	PHE	ASN	ASN	ASN	ALA	GLN	MET	PRO
GLU	ILE	GLU	GLU	VAL	VAL	ARG	ASN	LEU
GLN	ASP	ALA	ALA	ALA	ALA	ALA	ILE	GLU
LEU	GLN	LEU	PRO	PRO	HIS	VAL	PRO	TRP
SER	GLN	LEU	PRO	PRO	GLN	VAL	LEU	GLN
GLN	LEU	ILE	ILE	ILE	VAL	GLY	TYR	THR
GLN	ALA	ALA	ALA	THR	SER	GLY	ARG	ASN
ARG	ALA	THR	THR	THR	SER	GLU	PHE	ARG
ARG	ALA	ALA	PRO	PRO	SER	LEU	ALA	ALA
ARG	GLY	GLY	PRO	PRO	ALA	ARG	ASN	ARG
ASN	ASN	THR	THR	THR	VAL	THR	GLY	ASN
ARG	GLN	TRP	ASN	ASN	ALA	THR	SER	ASN
LEU	LEU	LEU	GLN	GLN	GLY	ILE	GLY	PRO
GLY	VAL	VAL	ASN	ASN	LEU	GLU	ALA	ARG
ALA	LEU	ALA	ALA	ALA	PRO	THR	ILE	PRO
GLU	VAL	GLU	GLN	GLN	GLY	GLY	VAL	LEU
VAL	VAL	VAL	ASN	ASN	ASN	PRO	PRO	ILE
MET	MET	ALA	THR	THR	VAL	VAL	ALA	VAL
SER	TRP	TRP	PRO	PRO	THR	LYS	ASP	ALA
GLN	ILE	GLN	GLN	GLN	LEU	SER	GLY	GLY
ARG	LEU	TRP	THR	THR	VAL	ALA	HIS	SER
ARG	ARG	ARG	THR	THR	GLN	VAL	GLU	ALA
GLU	LYS	GLY	SER	SER	SER	HIS	LEU	VAL
MET	ALA	ALA	THR	THR	GLY	LEU	ARG	ALA
SER	VAL	ASN	ASN	ASN	HIS	ALA	ILE	VAL
ASP	ARG	SER	SER	SER	LEU	MET	ARG	VAL
ASN	PRO	PRO	ASN	ASN	LEU	PRO	LEU	VAL
ASP	GLN	ASN	SER	SER	THR	LYS	ALA	ALA
PRO	LEU	ALA	ALA	ALA	GLN	PRO	GLN	MET
ARG	THR	GLY	GLY	SER	SER	SER	GLN	VAL
VAL	ARG	P355	GLY	ASN	ASN	GLY	GLY	VAL
VAL	ARG	GLY	THR	THR	THR	PHE	LEU	TRP
VAL	VAL	K394	ALA	ALA	SER	VAL	PRO	LYS
LEU	LEU	THR	LEU	ALA	ARG	GLY	GLY	THR
VAL	ILE	ALA	ALA	LEU	GLU	GLN	GLY	PRO
ARG	GLN	LYS	ASP	ASP	ASP	LYS	ALA	ASP
GLN	ALA	ALA	GLY	GLY	SER	VAL	VAL	TYR
TRP	ALA	LYS	LYS	PRO	PRO	GLY	GLY	ARG
MET	MET	GLN	GLN	PRO	GLY	SER	PHE	THR
SER	SER	GLU	GLU	PRO	GLY	ALA	GLU	LEU
ASN	ASN	GLN	GLN	ALA	SER	SER	LEU	PHE
ASP	ASP	ALA	GLY	ALA	VAL	VAL	LEU	SER
HIS	GLN	GLN	TYR	TYR	THR	THR	ASP	ASN
GLU	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN
	ARG	ASN	ASN	ASN	GLY	THR	GLY	ASN

- Molecule 1: Flagellar M-ring protein

Chain H: 27% 73%

GLU	THR	GLU	THR	VAL	GLU	PHE	GLN	MET
THR	GLY	PRO	GLY	PRO	PRO	GLY	ASP	SER
GLU	GLY	ALA	GLY	ALA	ARG	ILE	GLY	ALA
ALA	LEU	LEU	ALA	ALA	ALA	GLN	ALA	ALA
VAL	PRO	SER	PHE	ASN	LEU	PHE	ILE	SER
GLU	PHE	ASN	ASP	ASP	ASP	SER	VAL	THR
VAL	TRP	GLN	TRP	GLN	GLU	GLU	ALA	ALA
LEU	GLN	PRO	GLN	PRO	GLN	GLN	GLN	THR
SER	GLN	PRO	ILE	ILE	ILE	ASN	LEU	GLN
LYS	SER	PRO	SER	SER	SER	TYR	GLN	LYS
ASP	PHE	ASN	ALA	ALA	ALA	GLN	MET	PRO
GLN	ILE	GLU	ASP	VAL	VAL	ARG	ASN	LEU
LEU	GLN	PRO	GLN	PRO	HIS	LEU	TRP	GLU
GLN	LEU	ILE	VAL	VAL	VAL	GLY	TYR	LEU
GLN	ALA	ALA	ASN	ASN	ASN	GLY	ARG	ASN
ARG	ALA	THR	ALA	THR	SER	GLU	PHE	ARG
ARG	ALA	PRO	ALA	PRO	SER	LEU	ALA	ARG
ALA	GLY	PRO	GLY	ALA	ALA	ALA	ASN	ALA
ASN	ARG	THR	THR	VAL	VAL	ARG	GLY	ALA
GLN	TRP	ASN	LEU	ASN	ALA	THR	SER	ASN
ARG	LEU	GLN	LEU	GLN	GLY	ILE	GLY	PRO
LEU	VAL	ASN	VAL	GLN	LEU	GLU	ALA	ARG
GLY	VAL	ASN	GLY	ASN	PRO	THR	ILE	ILE
ALA	LEU	ALA	LEU	ALA	PRO	LEU	GLU	PRO
GLU	VAL	GLN	VAL	GLN	GLY	GLY	VAL	LEU
VAL	VAL	ASN	VAL	ASN	ASN	PRO	PRO	ILE
MET	ALA	THR	ALA	THR	VAL	VAL	ALA	VAL
SER	TRP	PRO	TRP	PRO	THR	LYS	ASP	ALA
GLN	ILE	GLN	ILE	GLN	LEU	SER	GLY	ALA
ARG	LEU	THR	LEU	THR	VAL	ALA	VAL	SER
ARG	ARG	THR	ARG	THR	ASN	VAL	GLU	ALA
GLU	LYS	SER	LYS	SER	SER	HIS	LEU	VAL
MET	ALA	THR	ALA	THR	GLY	LEU	ARG	ALA
SER	VAL	ASN	VAL	ASN	LEU	ALA	LEU	ALA
ASP	ARG	SER	VAL	SER	MET	MET	ARG	VAL
ASN	PRO	ASN	PRO	ASN	LEU	PRO	LEU	ALA
ASP	GLN	SER	GLN	SER	THR	LYS	ALA	ALA
PRO	LEU	ALA	LEU	ALA	GLN	PRO	GLN	MET
ARG	THR	GLY	THR	ARG	ASN	SER	GLN	VAL
VAL	ARG	P355	ARG	P355	ASN	LEU	GLY	LEU
VAL	VAL	K394	THR	K394	THR	PHE	LEU	TRP
ALA	ALA	THR	GLY	THR	GLY	VAL	PRO	LYS
LEU	VAL	LEU	ARG	LEU	ARG	GLU	GLY	THR
ILE	ALA	ALA	ALA	ALA	ASP	GLN	GLY	LYS
GLN	ARG	GLY	ALA	GLY	LEU	SER	VAL	TYR
TRP	ALA	LYS	ALA	LYS	PRO	PRO	GLY	ARG
MET	GLN	PRO	GLN	PRO	K304	SER	PHE	THR
SER	GLU	L402	GLU	L402	GLY	ALA	GLU	LEU
ASN	GLN	ALA	GLN	ALA	ALA	SER	LEU	PHE
ASP	ASP	S438	ALA	S438	GLY	VAL	LEU	SER
HIS	GLN	ALA	GLN	ALA	TYR	THR	ASP	ASN
GLU	VAL	VAL	VAL	VAL	PRO	VAL	GLN	GLU
	ARG	ASP	ARG	ASP	GLY	THR	LEU	SER
	GLN	ASN	GLN	ASN	GLY	ILE	LYS	ASN

- Molecule 1: Flagellar M-ring protein

Chain I:  27% 73%

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

GLU	THR	THR	VAL	GLU	PRO	PHE
GLU	GLY	GLY	GLY	PRO	GLY	ILE
GLU	GLU	GLU	ALA	ALA	ARG	SER
ALA	GLU	LEU	LEU	LEU	ALA	GLN
VAL	VAL	PRO	SER	SER	ASP	PHE
GLU	THR	PHE	ASN	ASN	ASP	SER
ARG	GLN	TRP	GLN	GLN	GLU	GLU
GLN	GLN	GLN	PRO	PRO	GLY	VAL
LEU	LEU	GLN	ALA	ALA	GLN	ASN
SER	SER	GLN	PRO	ILE	ILE	TYR
LYS	ASP	SER	PRO	SER	SER	GLN
ASP	ILE	PHE	ASN	ASN	ALA	ARG
GLU	GLN	ILE	GLU	VAL	VAL	ALA
GLN	ASP	GLN	ALA	PRO	HIS	LEU
ARG	ALA	GLY	THR	SER	VAL	GLY
ALA	ASN	ARG	THR	VAL	VAL	ARG
ASN	GLN	TRP	ASN	ALA	ALA	THR
ARG	LEU	LEU	GLN	GLY	GLY	ILE
LEU	VAL	VAL	GLN	LEU	LEU	GLU
GLY	GLY	VAL	ASN	PRO	PRO	THR
ALA	ALA	VAL	ALA	GLY	GLY	LEU
VAL	VAL	VAL	ASN	ASN	ASN	PRO
MET	MET	ALA	THR	VAL	VAL	VAL
SER	SER	TRP	PRO	THR	THR	LYS
GLN	GLN	ILE	GLN	GLN	LEU	SER
ARG	ARG	LEU	THR	THR	HIS	ALA
GLU	GLU	LYS	SER	SER	LEU	ALA
MET	MET	ALA	THR	THR	GLY	MET
SER	ASP	ARG	SER	SER	LEU	PRO
ASN	ASN	PRO	ASN	ASN	LEU	PRO
ASP	ASP	GLN	SER	SER	THR	LYS
PRO	PRO	LEU	ALA	GLN	GLN	PRO
ARG	ARG	THR	GLY	SER	SER	SER
VAL	VAL	ARG	P355	ASN	ASN	PHE
ALA	ALA	VAL	K394	THR	THR	VAL
LEU	LEU	GLU	THR	GLY	ARG	ARG
VAL	GLU	GLU	LEU	ARG	GLY	GLU
ILE	ILE	ALA	ALA	ALA	ARG	GLN
ARG	ARG	LYS	ASP	ASP	LEU	GLN
GLN	GLN	ALA	GLY	GLY	LEU	SER
TRP	TRP	ALA	LYS	LYS	M231	PRO
MET	MET	GLN	PRO	PRO	V504	SER
SER	SER	GLU	L402	GLY	ALA	ALA
ASN	ASN	GLN	S438	ALA	SER	VAL
ASP	ASP	ALA	ALA	TYR	THR	THR
HIS	HIS	GLN	VAL	PRO	VAL	VAL
GLU	GLU	ARG	ASP	GLY	THR	THR
		GLN	ASN	GLY	GLY	LEU

- Molecule 1: Flagellar M-ring protein

Chain J: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain K:  27% 73%

[illegible]

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain L: 27% 73%

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

- Molecule 1: Flagellar M-ring protein

Chain M: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain N:  27% 73%

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

GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	VAL	GLY	ASN	VAL	THR	LEU	VAL	ASP	GLN	SER	GLY	HIS	LEU	LEU	THR	GLN	SER	ASN	THR	SER	GLY	ARG	ASP	LEU	221	230	GLY	ALA	GLY	TYR	PRO	GLY
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[illegible]

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

Chain O:  27% 73%

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

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

[illegible][illegible]

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

- Molecule 1: Flagellar M-ring protein

Chain P: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain Q: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain R:  27% 73%

[illegible]

GLU	THR	THR	VAL	GLU	PRO	PHE
GLU	GLY	GLY	GLY	PRO	GLY	ILE
GLU	GLU	GLU	ALA	ALA	ARG	SER
ALA	GLU	LEU	LEU	LEU	ALA	GLN
VAL	VAL	PRO	SER	SER	ASP	PHE
GLU	THR	PHE	ASN	ASN	ASP	SER
VAL	THR	TRP	GLN	GLN	GLU	GLU
ARG	GLN	GLN	PRO	PRO	GLY	VAL
LEU	GLN	GLN	ALA	ALA	GLN	GLN
SER	SER	GLN	PRO	PRO	ILE	ASN
LYS	LYS	SER	PRO	SER	SER	TYR
ASP	ASP	PHE	ASN	ASN	ALA	GLN
GLU	GLU	ILE	GLU	GLU	VAL	ARG
GLN	ASP	ASP	ALA	ALA	VAL	ALA
LEU	LEU	GLN	ILE	LEU	HIS	LEU
GLN	GLN	LEU	ALA	VAL	VAL	GLY
ARG	ALA	LEU	THR	SER	SER	GLY
ARG	ALA	ALA	THR	SER	GLU	GLU
ARG	ALA	LEU	GLN	GLN	LEU	THR
LEU	LEU	VAL	ASN	PRO	PRO	GLY
GLY	GLY	VAL	ALA	ALA	GLY	GLY
GLU	VAL	VAL	GLN	GLN	ASN	PRO
VAL	VAL	VAL	ASN	ASN	VAL	VAL
MET	MET	ALA	THR	THR	VAL	LYS
SER	SER	TRP	PRO	PRO	THR	SER
GLN	GLN	ILE	GLN	GLN	LEU	LYS
ARG	ARG	LEU	THR	THR	VAL	ALA
ILE	ILE	TRP	SER	SER	VAL	ARG
ARG	ARG	ARG	THR	THR	GLN	VAL
GLU	GLU	LYS	SER	SER	SER	HIS
MET	MET	ALA	THR	THR	GLY	LEU
SER	SER	VAL	ASN	SER	LEU	ALA
ASP	ASP	ARG	SER	SER	MET	PRO
ASN	ASN	PRO	ASN	ASN	LEU	LYS
ASP	ASP	GLN	SER	SER	THR	PRO
PRO	PRO	LEU	ALA	ALA	GLN	LYS
ARG	ARG	THR	GLY	GLY	SER	SER
VAL	VAL	ARG	P355	VAL	ASN	THR
ALA	ALA	VAL	K394	THR	SER	PHE
LEU	LEU	GLU	THR	GLY	ARG	VAL
VAL	VAL	GLU	LEU	ALA	GLY	ARG
ILE	ILE	ALA	ALA	ASP	ARG	GLU
ARG	ARG	LYS	ALA	ASP	THR	GLN
GLN	GLN	ALA	GLY	GLY	LEU	GLN
TRP	TRP	ALA	LYS	LYS	M231	SER
MET	MET	GLN	PRO	PRO	V504	PRO
SER	SER	GLU	L402	GLY	ALA	ALA
ASN	ASN	GLN	S438	ALA	SER	SER
ASP	ASP	ALA	ALA	GLY	VAL	VAL
HIS	HIS	GLN	VAL	TRP	THR	THR
GLU	GLU	VAL	VAL	PRO	VAL	VAL
		ARG	ASP	GLY	THR	THR
		GLN	ASN	GLY	GLY	LEU

- Molecule 1: Flagellar M-ring protein

Chain S: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain T:  27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

- Molecule 1: Flagellar M-ring protein

- Molecule 1: Flagellar M-ring protein



GLU	THR	GLU	THR	VAL	GLU	PHE	GLN	MET
THR	GLY	GLY	PRO	PRO	PRO	GLY	ASP	SER
GLU	GLY	GLY	ALA	ALA	ALA	ILE	GLY	ILE
ALA	ALA	ALA	LEU	LEU	ARG	GLN	ALA	ALA
VAL	PRO	PHE	SER	SER	LEU	PHE	ILE	SER
GLU	THR	THR	ASN	ASN	ASP	SER	VAL	THR
VAL	GLN	GLN	GLN	GLN	GLY	GLU	ALA	ALA
ARG	GLN	GLN	PRO	PRO	GLY	THR	LEU	GLN
LEU	GLN	GLN	ALA	ALA	VAL	VAL	GLN	THR
SER	GLN	GLN	ILE	ILE	LEU	GLY	ASN	PRO
LYS	SER	SER	PRO	PRO	VAL	GLY	THR	LYS
ASP	PHE	ASN	ASN	ASN	ALA	GLN	MET	PRO
GLU	ILE	GLU	GLU	VAL	VAL	ALA	ASN	LEU
GLN	ASP	ASP	ALA	ALA	VAL	ALA	ILE	GLU
LEU	GLN	GLN	PRO	PRO	HIS	VAL	PRO	TRP
SER	GLN	LEU	PRO	PRO	LEU	GLY	LEU	GLN
GLN	LEU	LEU	ILE	ILE	VAL	VAL	THR	ASN
GLN	ALA	ALA	ALA	ALA	SER	GLY	ARG	ASN
ARG	ALA	THR	THR	THR	SER	GLU	PHE	ARG
ARG	ALA	ALA	PRO	PRO	SER	LEU	ALA	ARG
ARG	GLY	GLY	PRO	PRO	ALA	ALA	ASN	ARG
ASN	ARG	THR	THR	THR	VAL	THR	GLY	ASN
GLN	TRP	TRP	ASN	ASN	ALA	THR	SER	ASN
ARG	LEU	LEU	GLN	GLN	GLY	ILE	GLY	PRO
LEU	LEU	VAL	GLN	GLN	LEU	GLU	ALA	ARG
GLY	VAL	VAL	ASN	ASN	PRO	THR	ILE	LEU
ALA	VAL	VAL	VAL	VAL	VAL	VAL	ALA	VAL
MET	MET	MET	THR	THR	LYS	LYS	ASP	ALA
SER	GLN	GLN	PRO	PRO	THR	THR	GLY	GLY
ARG	LEU	LEU	THR	THR	HIS	ALA	ILE	SER
GLN	VAL	VAL	ASN	ASN	LEU	MET	ARG	VAL
ASP	ARG	ASP	SER	SER	LEU	PRO	LEU	VAL
ASN	PRO	ASN	ASN	THR	THR	LYS	ALA	ALA
ASP	GLN	GLN	SER	SER	THR	PRO	GLN	MET
PRO	LEU	ALA	ALA	GLY	GLN	SER	GLN	VAL
ARG	THR	P355	GLY	SER	ASN	SER	GLY	VAL
VAL	ARG	GLY	THR	THR	THR	THR	GLY	THR
VAL	ARG	K394	THR	THR	SER	PHE	LEU	TRP
LEU	GLU	THR	LEU	ALA	GLY	ARG	LYS	LYS
VAL	ILE	ALA	ALA	ALA	ASP	GLU	GLY	THR
ARG	GLN	LYS	LYS	ASP	LEU	GLN	GLY	PRO
GLN	TRP	ALA	ALA	GLY	THR	SER	VAL	TYR
MET	MET	GLN	GLN	LYS	THR	PRO	GLY	THR
SER	SER	GLU	GLU	PRO	GLY	ALA	PHE	LEU
ASN	ASN	GLN	GLN	ALA	ALA	SER	GLU	LEU
ASP	ASP	ALA	ALA	GLY	GLY	VAL	LEU	PHE
HIS	GLN	GLN	VAL	TYR	THR	THR	ASP	ASN
GLU	THR	VAL	VAL	PRO	VAL	VAL	GLN	ASN
THR	ARG	ASN	ASN	ASN	GLN	THR	GLY	SER
ASN	GLN	GLN	GLN	GLY	THR	THR	LYS	THR

- Molecule 1: Flagellar M-ring protein

Chain Z: 27% 73%

GLU	THR	GLY	GLY	THR	VAL	GLU	PHE	GLN	MET	GLN	MET
THR	GLY	GLY	GLY	GLY	PRO	PRO	GLY	ASP	GLY	ASP	SER
GLU	GLU	GLU	GLU	ALA	ALA	ALA	ALA	GLY	ALA	GLY	THR
ALA	ALA	ALA	ALA	LEU	LEU	SER	PHE	ALA	ALA	ALA	SER
VAL	VAL	PRO	PRO	ASN	ASN	ASP	SER	VAL	VAL	VAL	THR
GLU	THR	THR	THR	GLN	GLN	GLN	GLU	ALA	ALA	ALA	THR
ARG	GLN	GLN	GLN	PRO	PRO	GLY	GLU	THR	THR	THR	GLN
SER	GLN	GLN	GLN	ALA	ALA	ILE	LEU	LEU	VAL	LEU	GLN
LYS	SER	SER	SER	PRO	PRO	ILE	ASN	THR	ASN	THR	PRO
ASP	PHE	PHE	PHE	ASN	ASN	ALA	GLN	MET	GLN	MET	LYS
GLU	ILE	ILE	ILE	VAL	VAL	VAL	ARG	ASN	ASN	ASN	PRO
GLN	ASP	ASP	ASP	ALA	ALA	HIS	ALA	ALA	ILE	ILE	LEU
LEU	GLN	GLN	GLN	PRO	PRO	LEU	LEU	PRO	VAL	VAL	TRP
LEU	LEU	LEU	LEU	ILE	ILE	VAL	GLY	VAL	VAL	VAL	GLN
GLN	LEU	LEU	LEU	ALA	ALA	GLY	GLY	THR	GLY	THR	ASN
ARG	ALA	ALA	ALA	THR	THR	SER	GLU	ARG	PHE	ARG	ARG
ARG	ALA	ALA	ALA	THR	THR	SER	GLU	ALA	ALA	ALA	ASN
ALA	GLY	GLY	GLY	PRO	PRO	ALA	LEU	ASN	GLY	GLY	ARG
ASN	ARG	ARG	ARG	THR	THR	VAL	THR	VAL	ASN	ASN	ASN
GLN	TRP	TRP	TRP	ASN	ASN	ALA	ILE	PRO	THR	PRO	PRO
LEU	LEU	LEU	LEU	GLN	GLN	GLY	GLU	GLY	ALA	ALA	LEU
ARG	LEU	LEU	LEU	GLN	GLN	GLY	THR	VAL	VAL	VAL	VAL
LEU	VAL	VAL	VAL	ALA	ALA	VAL	VAL	PRO	PRO	PRO	ILE
MET	VAL	VAL	VAL	THR	THR	VAL	VAL	ASN	ASN	ASN	ILE
SER	TRP	TRP	TRP	PRO	PRO	THR	THR	THR	LYS	LYS	ALA
GLN	ILE	ILE	ILE	GLN	GLN	LEU	SER	ASP	GLY	GLY	ALA
ARG	VAL	VAL	VAL	THR	THR	THR	ALA	VAL	HIS	HIS	ALA
ASP	VAL	VAL	VAL	SER	SER	THR	GLY	GLY	LEU	LEU	ALA
ASN	PRO	PRO	PRO	ASN	ASN	LEU	LEU	ARG	MET	MET	VAL
ASP	ASN	ASN	ASN	SER	SER	THR	LYS	ALA	PRO	PRO	ALA
PRO	LEU	LEU	LEU	ALA	ALA	THR	PRO	GLN	LYS	LYS	ALA
ARG	THR	THR	THR	GLY	GLY	ASN	SER	GLN	PRO	PRO	MET
VAL	ARG	ARG	ARG	P355	P355	VAL	SER	GLN	VAL	VAL	VAL
VAL	VAL	VAL	VAL	K394	K394	THR	PHE	GLY	LEU	LEU	TRP
LEU	LEU	LEU	LEU	THR	THR	GLY	ARG	LYS	ARG	LYS	LYS
ILE	ILE	ILE	ILE	ALA	ALA	ASP	GLU	GLY	GLY	GLY	THR
VAL	VAL	VAL	VAL	LEU	LEU	ASP	GLN	ALA	GLY	GLY	PRO
GLN	GLN	GLN	GLN	GLY	GLY	GLY	SER	VAL	SER	VAL	TYR
TRP	TRP	TRP	TRP	ALA	ALA	LYS	PRO	GLY	PRO	GLY	THR
MET	MET	MET	MET	PRO	PRO	PRO	ALA	PHE	SER	PHE	THR
SER	SER	SER	SER	GLU	GLU	GLU	ALA	GLY	ALA	GLY	LEU
ASN	ASN	ASN	ASN	GLN	GLN	ALA	SER	LEU	SER	LEU	PHE
ASP	ASP	ASP	ASP	ALA	ALA	GLY	VAL	LEU	VAL	LEU	ASP
HIS	HIS	HIS	HIS	GLN	GLN	TYR	THR	ASN	ASN	ASN	ASN
GLU	GLU	GLU	GLU	VAL	VAL	VAL	VAL	GLN	VAL	GLN	GLY
THR	THR	THR	THR	ASN	ASN	ASN	THR	GLY	THR	GLY	SER
ASN	ASN	ASN	ASN	GLN	GLN	GLN	LEU	LYS	LEU	LYS	THR
VAL	VAL	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR

- Molecule 1: Flagellar M-ring protein

Chain a:  27% 73%

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

GLU	THR	THR	VAL	GLU	PRO	PHE
GLU	GLY	GLY	GLY	PRO	GLY	ILE
GLU	GLU	GLU	ALA	ALA	ARG	SER
ALA	GLU	LEU	LEU	LEU	ALA	GLN
VAL	VAL	PRO	SER	SER	ASP	PHE
GLU	THR	PHE	ASN	ASN	ASP	SER
VAL	THR	TRP	GLN	GLN	GLU	GLU
ARG	GLN	GLN	PRO	PRO	GLY	VAL
LEU	GLN	GLN	ALA	ALA	GLN	GLN
SER	SER	GLN	PRO	ILE	ILE	ASN
LYS	LYS	SER	PRO	SER	SER	TYR
ASP	ASP	PHE	ASN	ASN	ALA	GLN
GLU	GLU	ILE	GLU	VAL	VAL	ARG
GLN	ASP	ASP	ALA	ALA	VAL	ALA
LEU	LEU	GLN	ILE	LEU	HIS	LEU
GLN	GLN	LEU	ALA	VAL	VAL	GLY
ARG	ALA	ALA	THR	SER	SER	GLY
ARG	ALA	LEU	ALA	THR	GLY	GLU
ARG	GLN	TRP	ASN	GLN	LEU	THR
LEU	LEU	LEU	GLN	GLN	PRO	GLU
GLY	VAL	VAL	ASN	ASN	PRO	THR
ALA	VAL	VAL	ALA	ALA	GLY	GLY
VAL	VAL	VAL	ASN	ASN	ASN	PRO
MET	MET	ALA	THR	VAL	VAL	VAL
SER	SER	TRP	PRO	THR	THR	LYS
GLN	GLN	ILE	GLN	GLN	LEU	SER
ARG	ARG	LEU	THR	THR	VAL	ALA
ILE	ILE	TRP	SER	SER	ASP	ARG
ARG	ARG	ARG	THR	THR	GLN	VAL
GLU	GLU	LYS	SER	SER	SER	HIS
MET	MET	ALA	THR	GLY	GLY	LEU
SER	SER	VAL	ASN	SER	LEU	ALA
ASP	ASP	ARG	SER	SER	MET	MET
ASN	ASN	PRO	ASN	ASN	PRO	PRO
ASP	ASP	GLN	SER	SER	THR	LYS
PRO	PRO	LEU	ALA	GLN	PRO	PRO
ARG	ARG	THR	GLY	SER	SER	SER
VAL	VAL	ARG	P355	ASN	THR	PHE
ALA	ALA	VAL	K394	THR	SER	VAL
LEU	LEU	GLU	THR	GLY	ARG	ARG
VAL	VAL	GLU	GLU	ARG	GLY	GLU
ILE	ILE	ALA	ALA	ASP	ARG	GLN
ARG	ARG	LYS	ALA	ASP	LEU	GLN
GLN	GLN	ALA	GLY	GLY	M231	SER
TRP	TRP	ALA	LYS	LYS	THR	PRO
MET	MET	GLN	PRO	PRO	V504	PRO
SER	SER	GLU	L402	GLY	ALA	ALA
ASN	ASN	GLN	L438	ALA	SER	SER
ASP	ASP	ALA	ALA	GLY	VAL	VAL
HIS	HIS	GLN	VAL	TYR	THR	THR
GLU	GLU	VAL	VAL	PRO	VAL	VAL
		ARG	ASP	GLY	THR	THR
		GLN	ASN	GLY	GLY	LEU

- Molecule 1: Flagellar M-ring protein

Chain b: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain c:  27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

- Molecule 1: Flagellar M-ring protein

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C33	Depositor
Number of particles used	77849	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	0.100	Depositor
Minimum map value	-0.057	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	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	0.26	0/1205	0.42	0/1624
1	B	0.26	0/1205	0.42	0/1624
1	C	0.26	0/1205	0.42	0/1624
1	D	0.26	0/1205	0.42	0/1624
1	E	0.26	0/1205	0.43	0/1624
1	F	0.26	0/1205	0.43	0/1624
1	G	0.26	0/1205	0.42	0/1624
1	H	0.26	0/1205	0.42	0/1624
1	I	0.26	0/1205	0.42	0/1624
1	J	0.26	0/1205	0.42	0/1624
1	K	0.26	0/1205	0.42	0/1624
1	L	0.26	0/1205	0.43	0/1624
1	M	0.26	0/1205	0.42	0/1624
1	N	0.26	0/1205	0.42	0/1624
1	O	0.26	0/1205	0.42	0/1624
1	P	0.26	0/1205	0.42	0/1624
1	Q	0.26	0/1205	0.42	0/1624
1	R	0.26	0/1205	0.43	0/1624
1	S	0.26	0/1205	0.42	0/1624
1	T	0.26	0/1205	0.43	0/1624
1	U	0.26	0/1205	0.42	0/1624
1	V	0.26	0/1205	0.42	0/1624
1	W	0.26	0/1205	0.42	0/1624
1	X	0.26	0/1205	0.42	0/1624
1	Y	0.26	0/1205	0.42	0/1624
1	Z	0.26	0/1205	0.43	0/1624
1	a	0.26	0/1205	0.42	0/1624
1	b	0.26	0/1205	0.42	0/1624
1	c	0.26	0/1205	0.42	0/1624
1	d	0.26	0/1205	0.43	0/1624
1	e	0.26	0/1205	0.42	0/1624
1	f	0.26	0/1205	0.42	0/1624
1	g	0.26	0/1205	0.42	0/1624
All	All	0.26	0/39765	0.42	0/53592

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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	B	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	C	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	D	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	E	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	F	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	G	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	H	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	I	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	J	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	K	145/560 (26%)	136 (94%)	9 (6%)	0	100	100
1	L	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	M	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	N	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	O	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	P	145/560 (26%)	139 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	R	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	S	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	T	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	U	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	V	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	W	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	X	145/560 (26%)	137 (94%)	8 (6%)	0	100	100
1	Y	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	Z	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	a	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	b	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	c	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	d	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	e	145/560 (26%)	138 (95%)	7 (5%)	0	100	100
1	f	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
1	g	145/560 (26%)	139 (96%)	6 (4%)	0	100	100
All	All	4785/18480 (26%)	4579 (96%)	206 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	134/467 (29%)	134 (100%)	0	100	100
1	B	134/467 (29%)	134 (100%)	0	100	100
1	C	134/467 (29%)	134 (100%)	0	100	100
1	D	134/467 (29%)	134 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	134/467 (29%)	134 (100%)	0	100	100
1	F	134/467 (29%)	134 (100%)	0	100	100
1	G	134/467 (29%)	134 (100%)	0	100	100
1	H	134/467 (29%)	134 (100%)	0	100	100
1	I	134/467 (29%)	134 (100%)	0	100	100
1	J	134/467 (29%)	134 (100%)	0	100	100
1	K	134/467 (29%)	134 (100%)	0	100	100
1	L	134/467 (29%)	134 (100%)	0	100	100
1	M	134/467 (29%)	134 (100%)	0	100	100
1	N	134/467 (29%)	134 (100%)	0	100	100
1	O	134/467 (29%)	134 (100%)	0	100	100
1	P	134/467 (29%)	134 (100%)	0	100	100
1	Q	134/467 (29%)	134 (100%)	0	100	100
1	R	134/467 (29%)	134 (100%)	0	100	100
1	S	134/467 (29%)	134 (100%)	0	100	100
1	T	134/467 (29%)	134 (100%)	0	100	100
1	U	134/467 (29%)	134 (100%)	0	100	100
1	V	134/467 (29%)	134 (100%)	0	100	100
1	W	134/467 (29%)	134 (100%)	0	100	100
1	X	134/467 (29%)	134 (100%)	0	100	100
1	Y	134/467 (29%)	134 (100%)	0	100	100
1	Z	134/467 (29%)	134 (100%)	0	100	100
1	a	134/467 (29%)	134 (100%)	0	100	100
1	b	134/467 (29%)	134 (100%)	0	100	100
1	c	134/467 (29%)	134 (100%)	0	100	100
1	d	134/467 (29%)	134 (100%)	0	100	100
1	e	134/467 (29%)	134 (100%)	0	100	100
1	f	134/467 (29%)	134 (100%)	0	100	100
1	g	134/467 (29%)	134 (100%)	0	100	100
All	All	4422/15411 (29%)	4422 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (126) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	261	ASN
1	A	263	HIS
1	A	365	ASN
1	A	434	ASN
1	B	261	ASN
1	B	263	HIS
1	B	434	ASN
1	C	261	ASN
1	C	277	GLN
1	C	365	ASN
1	C	434	ASN
1	D	261	ASN
1	D	263	HIS
1	D	365	ASN
1	D	434	ASN
1	E	263	HIS
1	E	365	ASN
1	E	434	ASN
1	F	261	ASN
1	F	263	HIS
1	F	365	ASN
1	F	434	ASN
1	G	261	ASN
1	G	263	HIS
1	G	365	ASN
1	G	434	ASN
1	H	261	ASN
1	H	434	ASN
1	I	231	ASN
1	I	261	ASN
1	I	263	HIS
1	I	431	ASN
1	I	434	ASN
1	J	261	ASN
1	J	434	ASN
1	K	263	HIS
1	K	277	GLN
1	K	365	ASN
1	K	434	ASN
1	L	261	ASN
1	L	263	HIS

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Mol	Chain	Res	Type
1	L	365	ASN
1	L	434	ASN
1	M	261	ASN
1	M	263	HIS
1	M	365	ASN
1	M	434	ASN
1	N	261	ASN
1	N	263	HIS
1	N	365	ASN
1	N	434	ASN
1	O	261	ASN
1	O	263	HIS
1	O	365	ASN
1	O	434	ASN
1	P	261	ASN
1	P	263	HIS
1	P	365	ASN
1	P	434	ASN
1	Q	261	ASN
1	Q	263	HIS
1	Q	365	ASN
1	Q	434	ASN
1	R	261	ASN
1	R	263	HIS
1	R	365	ASN
1	R	431	ASN
1	R	434	ASN
1	S	261	ASN
1	S	263	HIS
1	S	274	ASN
1	S	365	ASN
1	S	434	ASN
1	T	261	ASN
1	T	263	HIS
1	T	277	GLN
1	T	365	ASN
1	T	434	ASN
1	U	261	ASN
1	U	263	HIS
1	U	434	ASN
1	V	261	ASN
1	V	263	HIS

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Mol	Chain	Res	Type
1	V	365	ASN
1	V	434	ASN
1	W	261	ASN
1	W	263	HIS
1	W	277	GLN
1	W	365	ASN
1	W	434	ASN
1	X	261	ASN
1	X	263	HIS
1	X	277	GLN
1	X	365	ASN
1	X	434	ASN
1	Y	261	ASN
1	Y	263	HIS
1	Y	434	ASN
1	Z	365	ASN
1	Z	434	ASN
1	a	261	ASN
1	a	263	HIS
1	a	365	ASN
1	a	434	ASN
1	b	261	ASN
1	b	263	HIS
1	b	365	ASN
1	b	434	ASN
1	c	261	ASN
1	c	365	ASN
1	c	434	ASN
1	d	261	ASN
1	d	263	HIS
1	d	434	ASN
1	e	261	ASN
1	e	263	HIS
1	e	434	ASN
1	f	231	ASN
1	f	261	ASN
1	f	263	HIS
1	f	434	ASN
1	g	231	ASN
1	g	261	ASN
1	g	263	HIS
1	g	365	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	g	434	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

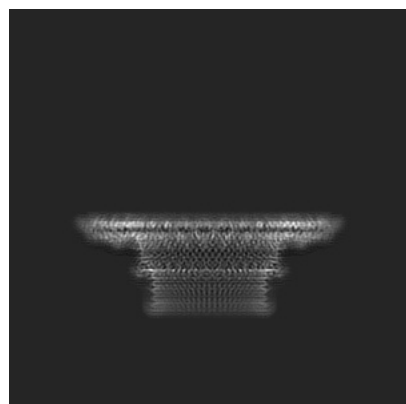
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10145. These allow visual inspection of the internal detail of the map and identification of artifacts.

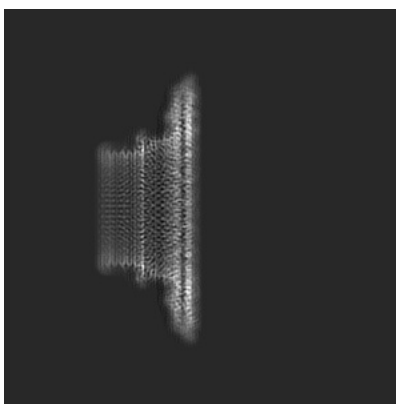
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

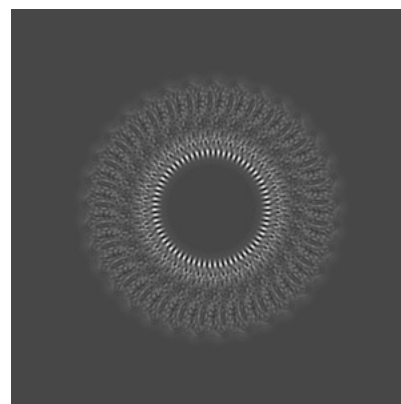
6.1.1 Primary map



X

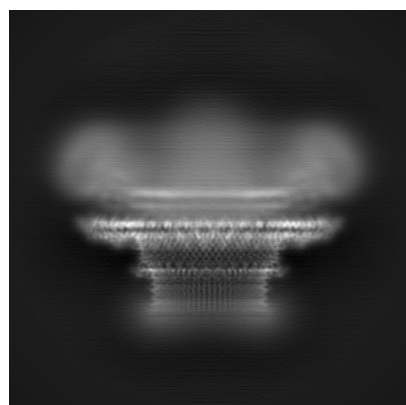


Y

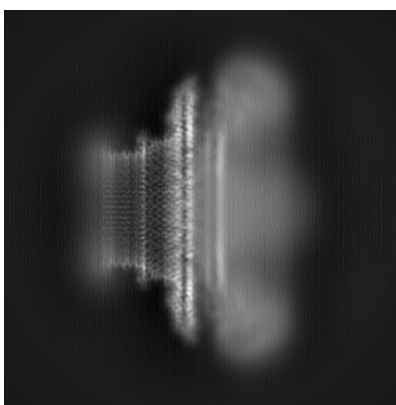


Z

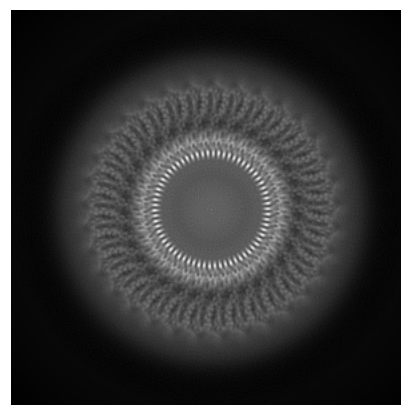
6.1.2 Raw map



X



Y

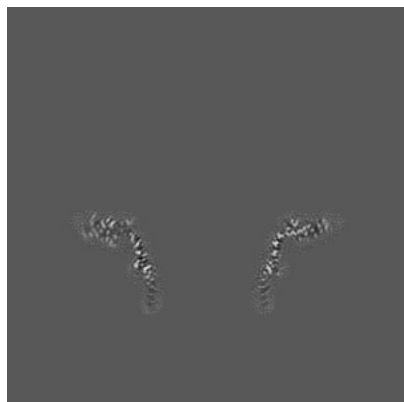


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 216

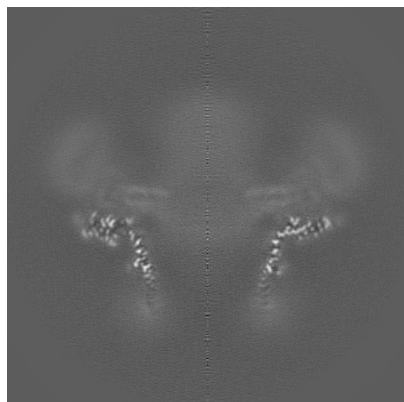


Y Index: 216



Z Index: 216

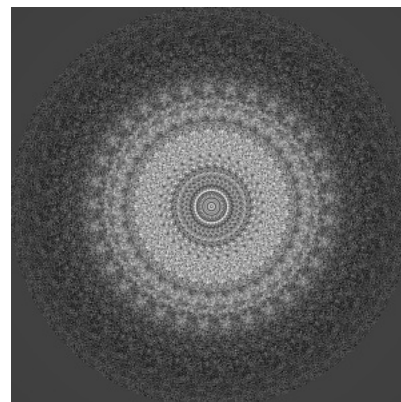
6.2.2 Raw map



X Index: 216



Y Index: 216

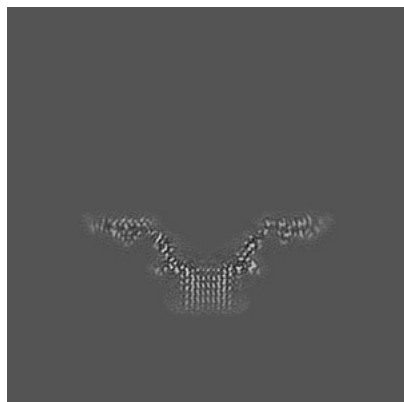


Z Index: 216

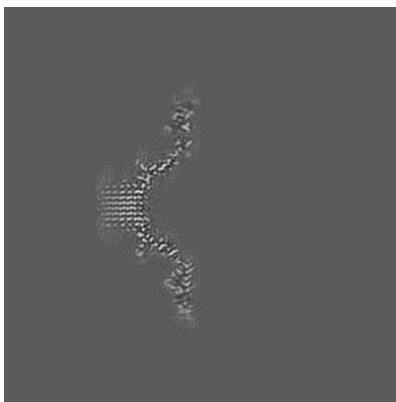
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

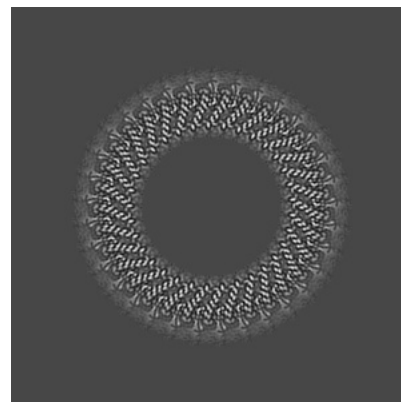
6.3.1 Primary map



X Index: 274

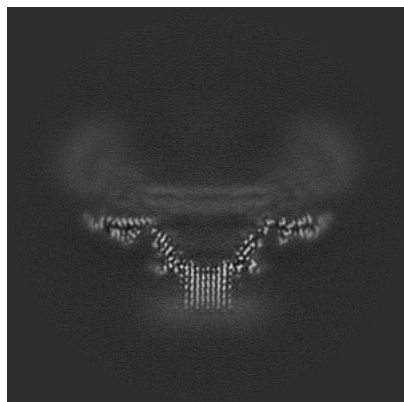


Y Index: 156

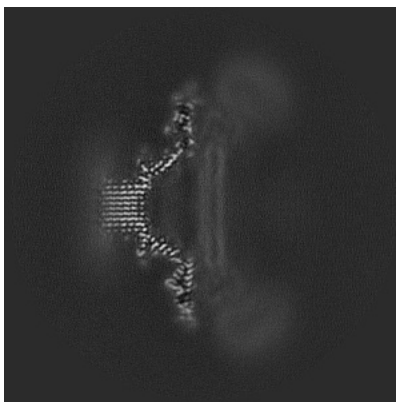


Z Index: 197

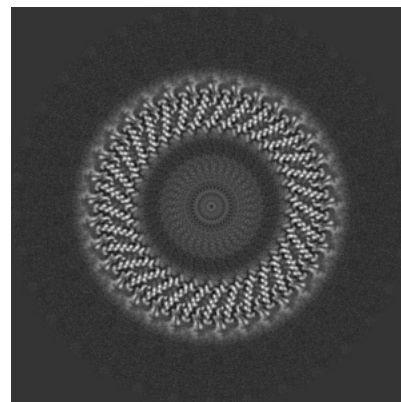
6.3.2 Raw map



X Index: 275



Y Index: 157

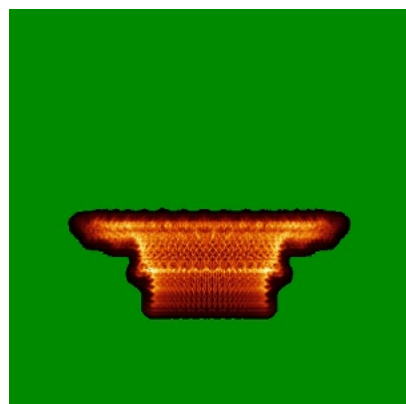


Z Index: 199

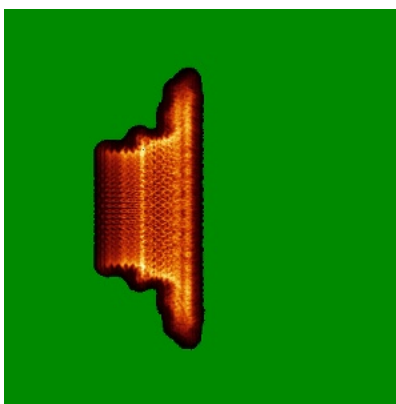
The images above show the largest variance slices of the map in three orthogonal directions.

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

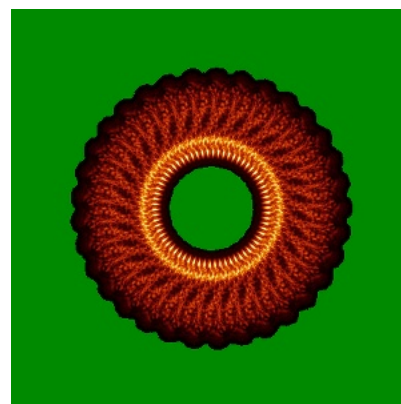
6.4.1 Primary map



X

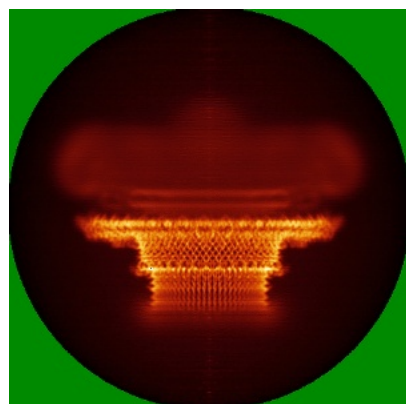


Y

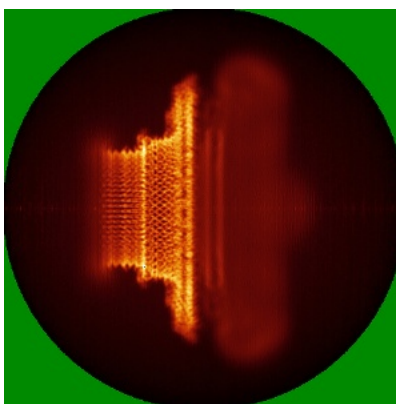


Z

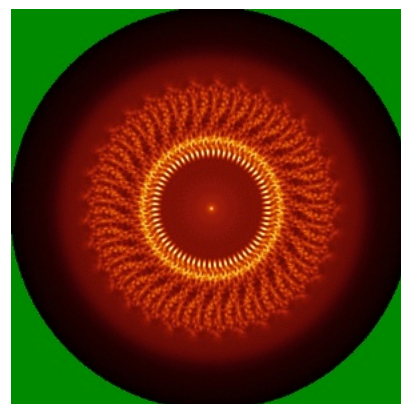
6.4.2 Raw map



X



Y

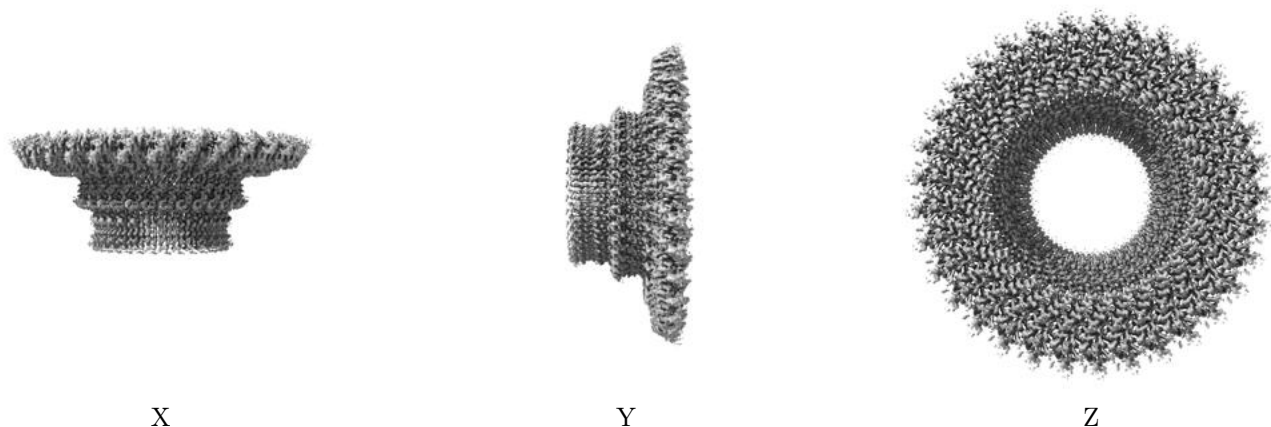


Z

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.

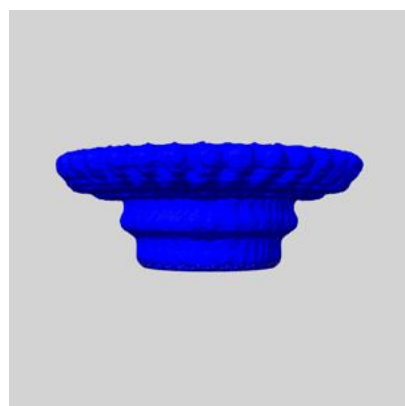
6.6 Mask visualisation [i](#)

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

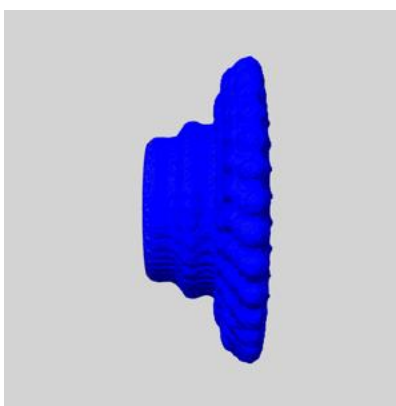
A mask typically either:

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

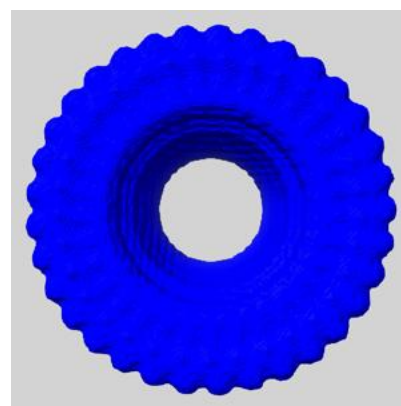
6.6.1 emd_10145_msk_1.map [i](#)



X



Y

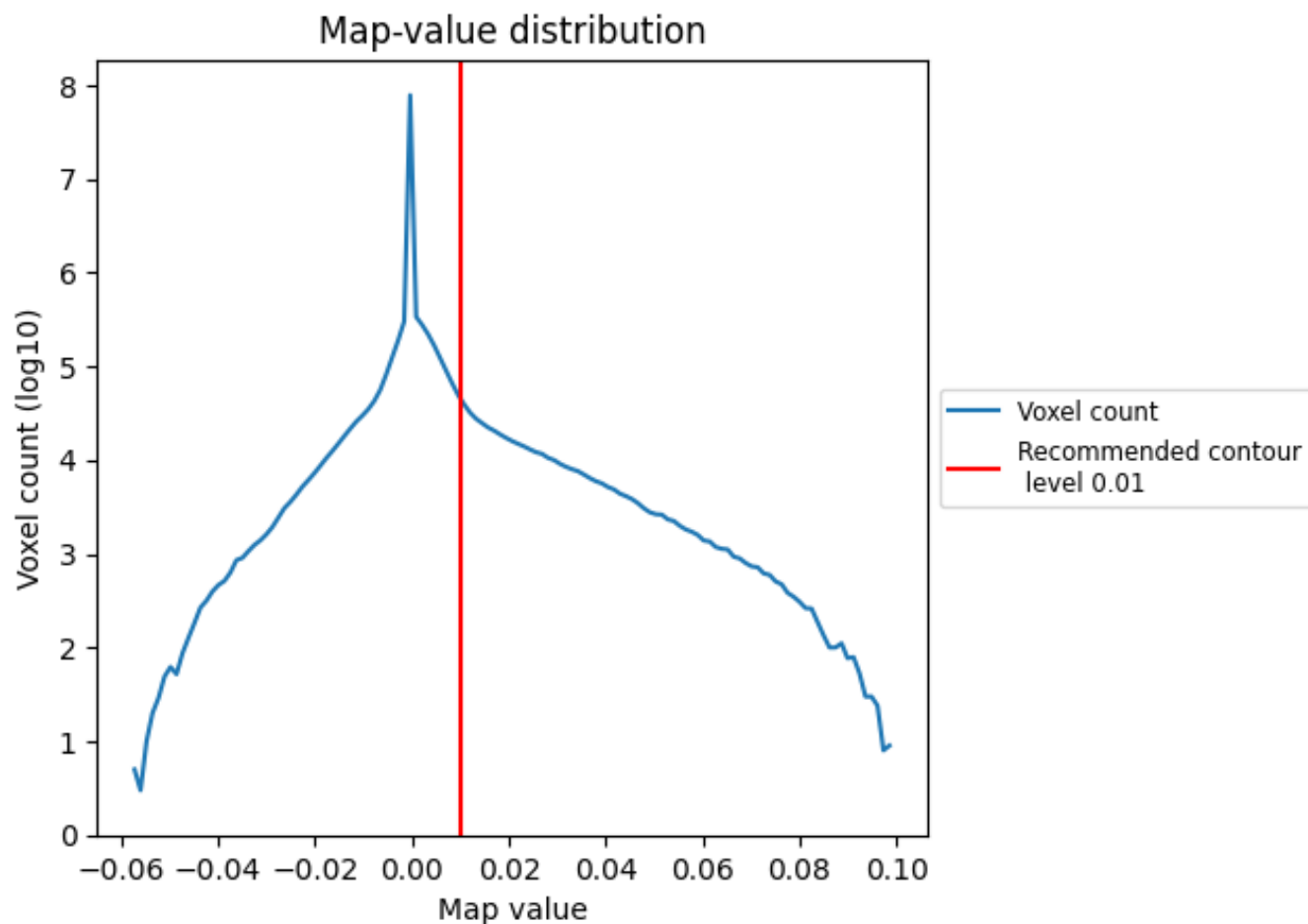


Z

7 Map analysis [i](#)

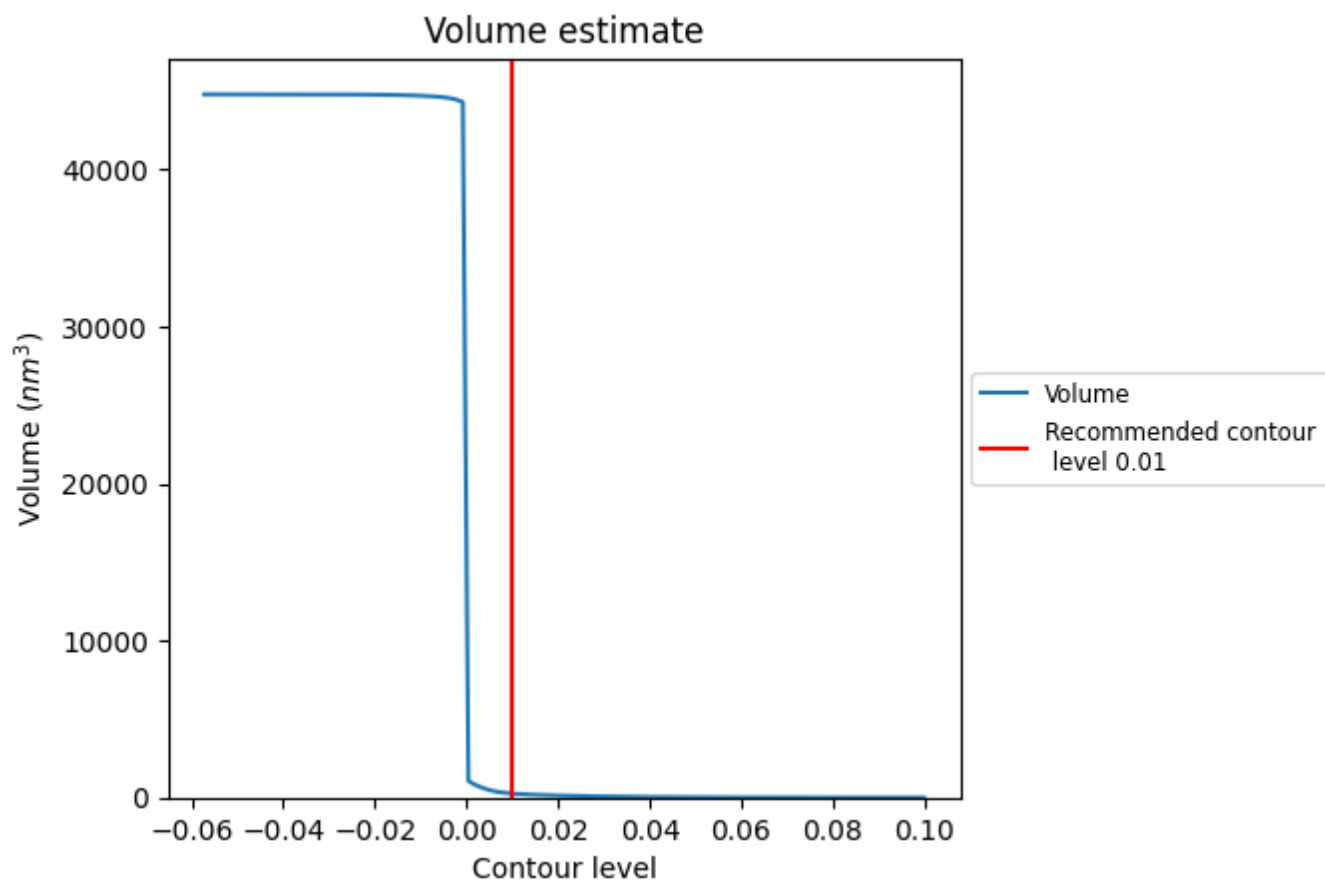
This section contains the results of statistical analysis of the map.

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.

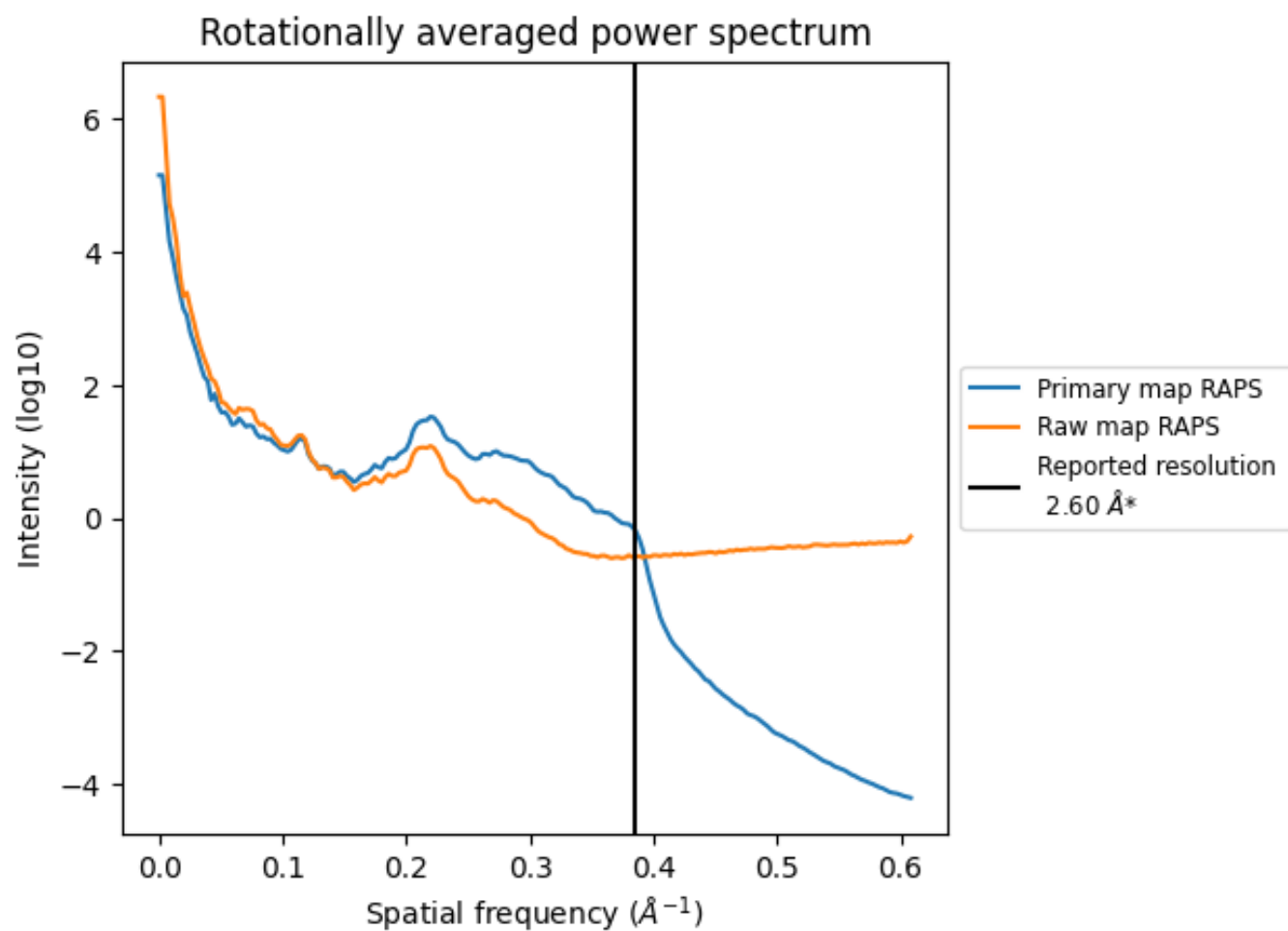
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 254 nm^3 ; this corresponds to an approximate mass of 229 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 ⓘ

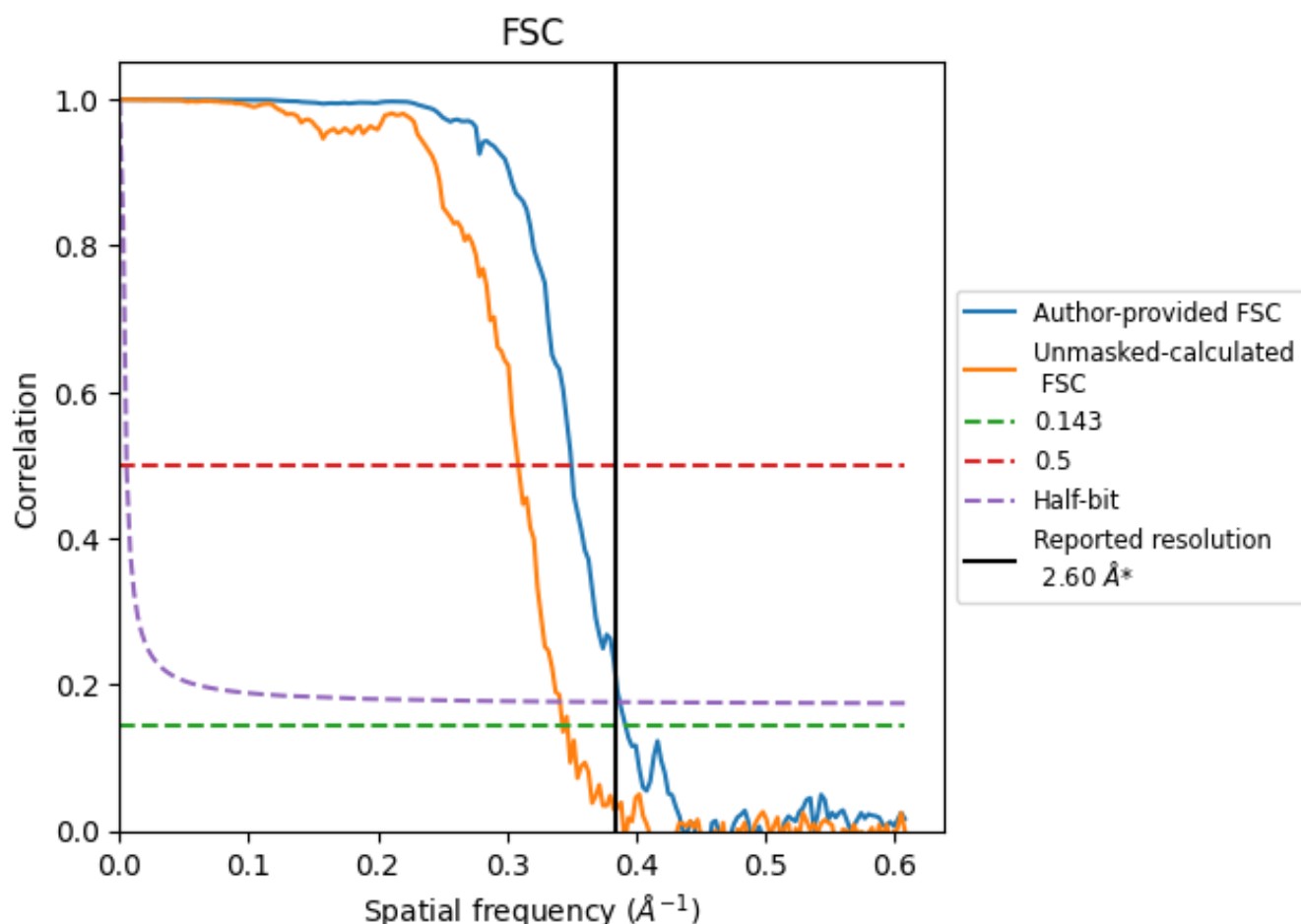


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

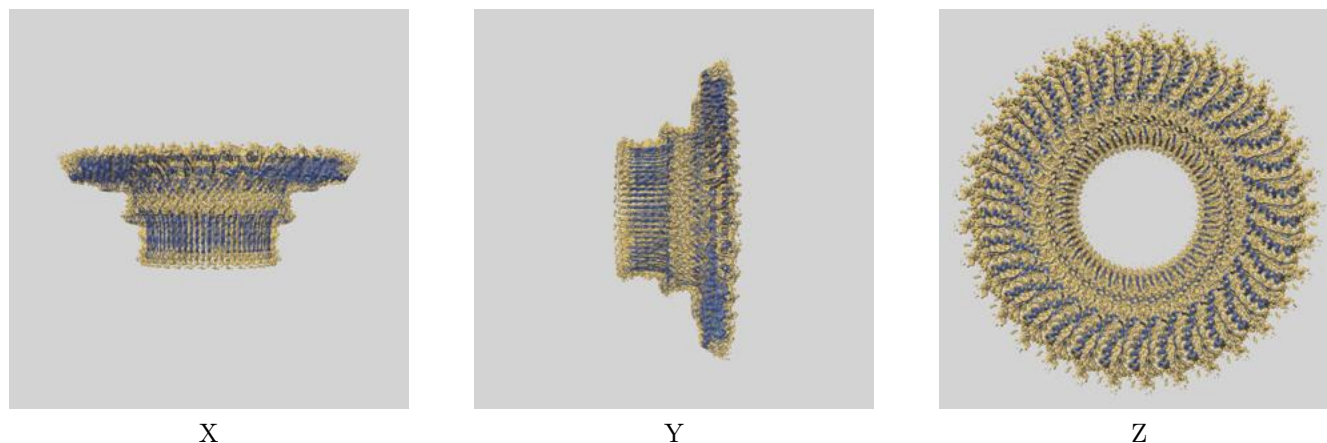
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.55	2.86	2.58
Unmasked-calculated*	2.91	3.24	2.93

*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 2.91 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

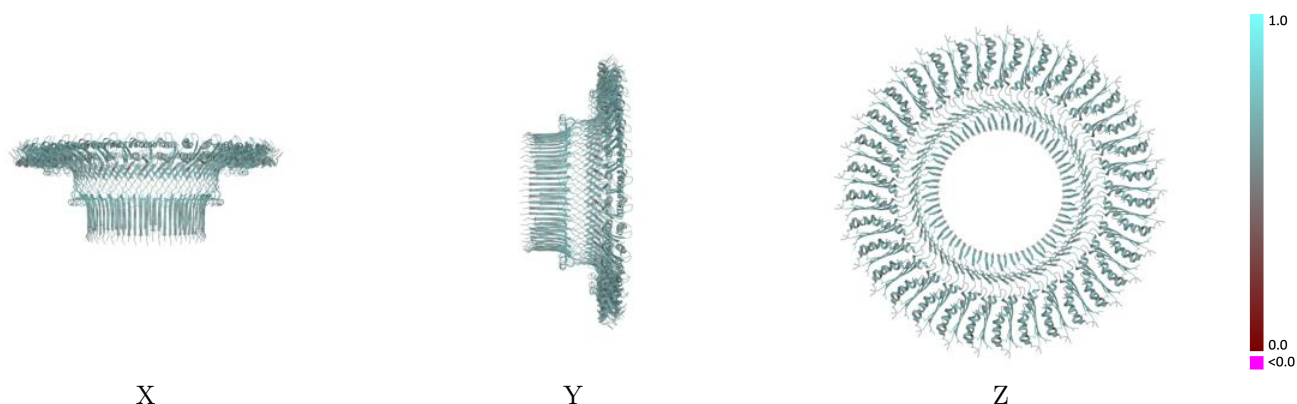
This section contains information regarding the fit between EMDB map EMD-10145 and PDB model 6SD1. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



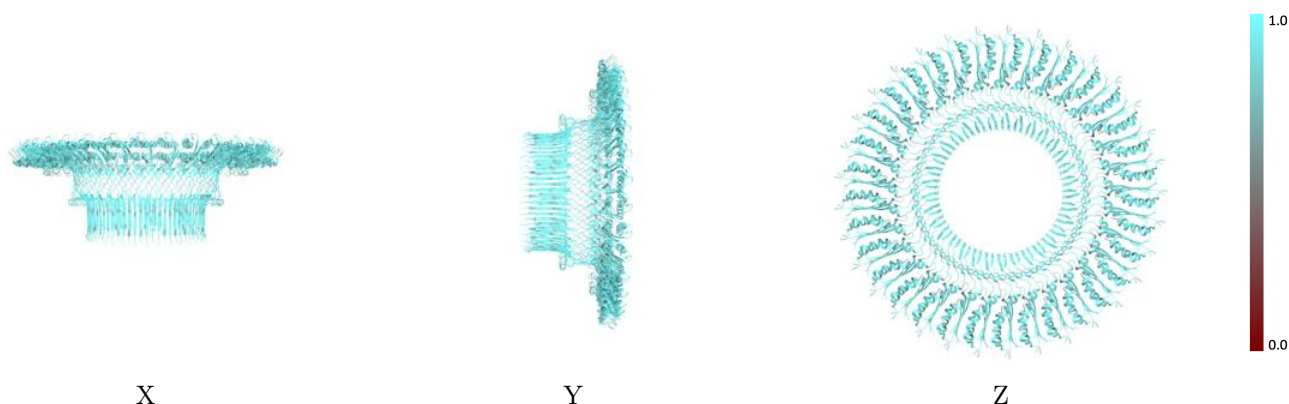
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



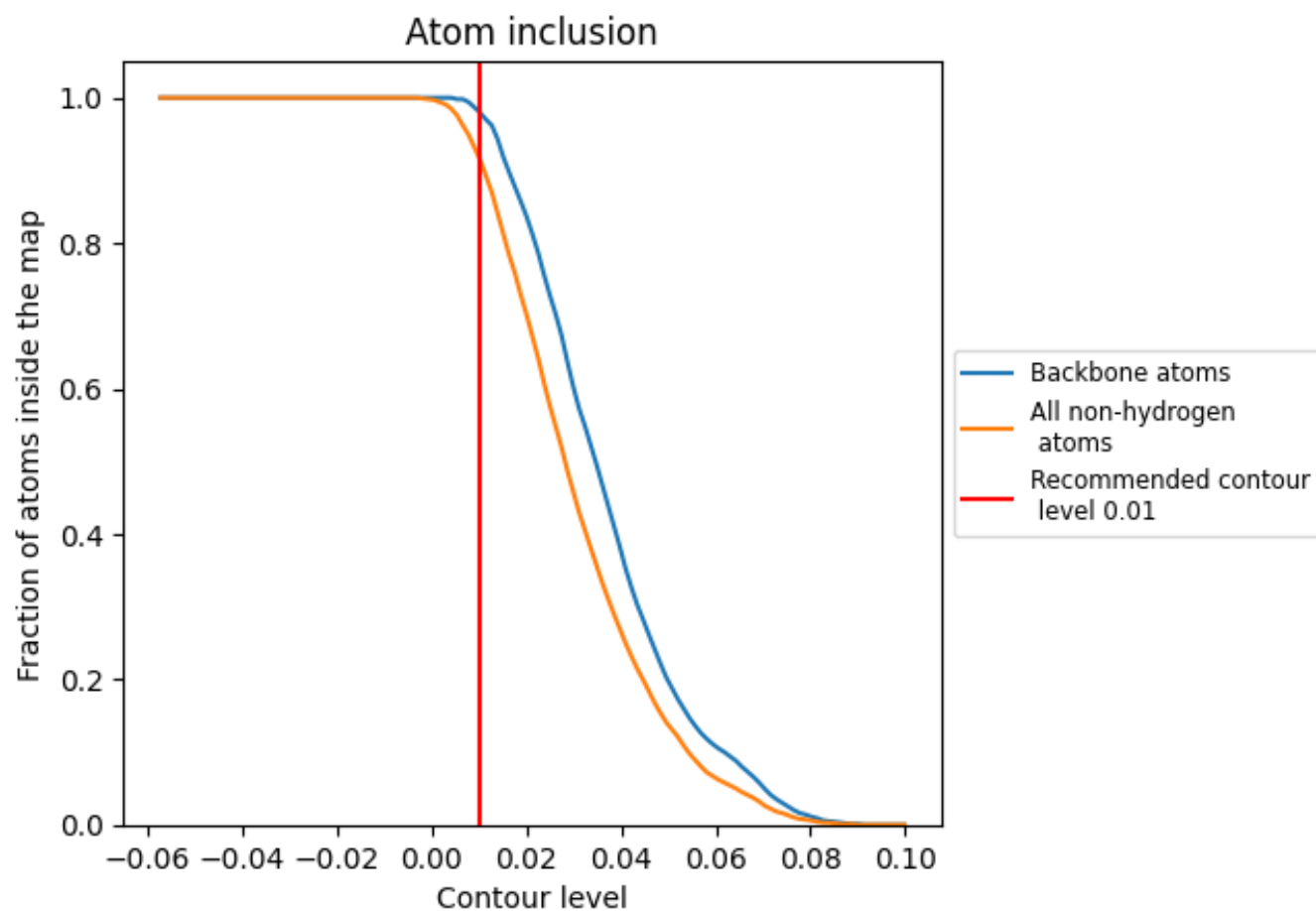
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 98% of all backbone atoms, 92% 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	 0.9180	 0.6230
A	 0.9170	 0.6230
B	 0.9200	 0.6220
C	 0.9150	 0.6210
D	 0.9190	 0.6220
E	 0.9170	 0.6210
F	 0.9190	 0.6230
G	 0.9190	 0.6260
H	 0.9190	 0.6240
I	 0.9180	 0.6220
J	 0.9180	 0.6240
K	 0.9140	 0.6230
L	 0.9230	 0.6230
M	 0.9190	 0.6210
N	 0.9180	 0.6230
O	 0.9150	 0.6230
P	 0.9180	 0.6240
Q	 0.9150	 0.6240
R	 0.9160	 0.6240
S	 0.9150	 0.6230
T	 0.9190	 0.6220
U	 0.9180	 0.6220
V	 0.9130	 0.6230
W	 0.9180	 0.6240
X	 0.9180	 0.6220
Y	 0.9200	 0.6260
Z	 0.9170	 0.6250
a	 0.9170	 0.6220
b	 0.9220	 0.6250
c	 0.9150	 0.6220
d	 0.9190	 0.6180
e	 0.9170	 0.6250
f	 0.9160	 0.6250
g	 0.9160	 0.6240

