



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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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.













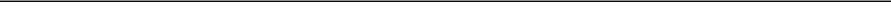

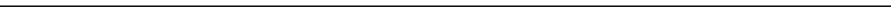











Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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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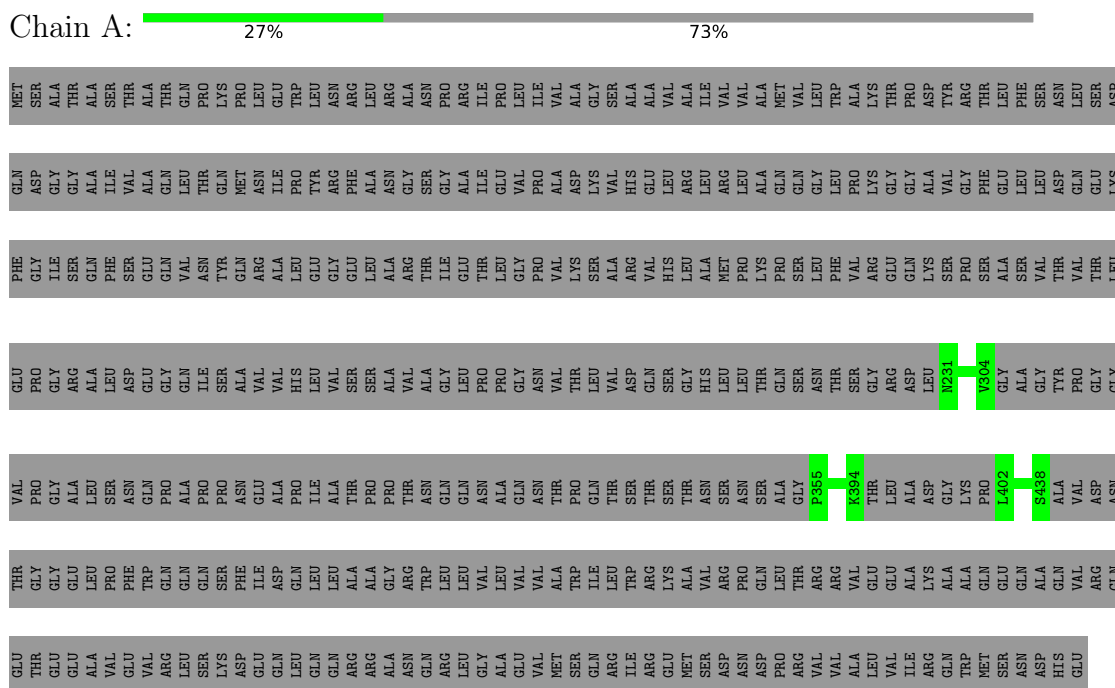
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	S	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	T	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	U	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	V	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	W	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	X	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	Y	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	Z	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
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		

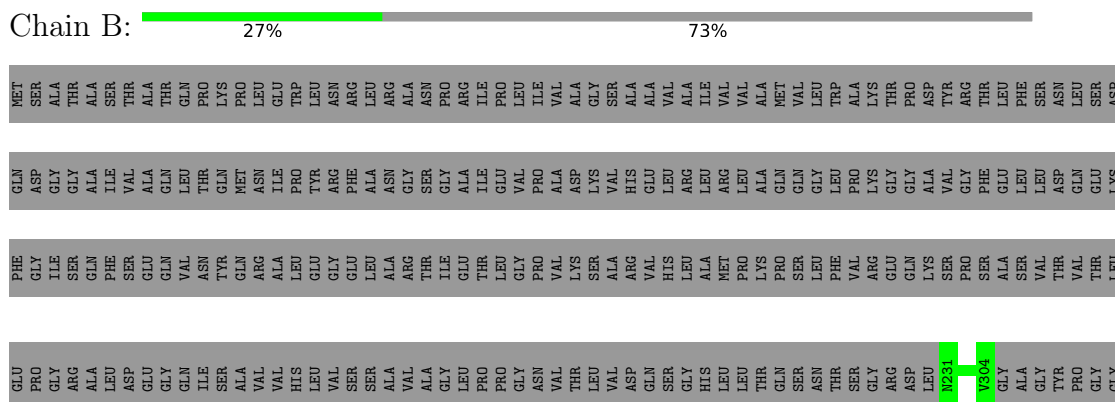
3 Residue-property plots

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



GLU THR	THR	VAL	GLU PRO	PHE
GLU	GLY	GLY	GLY	ILE
GLU	GLU	ALA	ARG	SER
ALA	LEU	LEU	ALA	GLN
VAL	PRO	SER	SER	PHE
GLU	PHE	ASN	ASP	SER
VAL	TRP	GLN	GLU	GLU
ARG	GLN	PRO	GLY	GLN
LEU	GLN	ALA	GLN	VAL
SER	GLN	PRO	ILE	ASN
LYS	SER	PRO	SER	TYR
ASP	PHE	ASN	SER	GLN
GLU	ILE	GLU	VAL	ARG
GLN	ASP	ALA	VAL	ALA
LEU	GLN	PRO	HIS	LEU
GLN	LEU	ILE	VAL	GLU
GLN	LEU	ALA	VAL	GLY
ARG	ALA	THR	SER	GLU
ARG	ALA	PRO	SER	LEU
ALA	GLY	PRO	ALA	ALA
ASN	ARG	THR	VAL	ARG
GLN	TRP	ASN	ALA	THR
ARG	LEU	GLN	GLY	ILE
LEU	LEU	GLN	LEU	GLU
GLY	VAL	ASN	PRO	THR
ALA	LEU	ALA	PRO	LEU
GLU	VAL	GLN	GLY	GLY
VAL	VAL	ASN	ASN	PRO
MET	ALA	THR	VAL	VAL
SER	TRP	PRO	THR	LYS
GLN	ILE	GLN	LEU	SER
ARG	LEU	THR	VAL	ALA
GLU	ARG	SER	GLN	ARG
MET	ALA	SER	SER	VAL
SER	VAL	THR	GLY	HIS
ASP	ARG	ASN	LEU	LEU
ASN	PRO	ASN	LEU	MET
PRO	GLN	SER	THR	PRO
ARG	LEU	ALA	GLN	LYS
VAL	THR	GLY	PRO	SER
VAL	ARG	P355	SER	LEU
ALA	VAL	K394	THR	PHE
LEU	GLU	THR	GLY	VAL
ILE	GLU	LEU	ARG	ARG
VAL	ALA	ALA	ASP	GLU
ARG	ALA	ALA	ASP	GLN
ARG	LYS	GLY	ASP	GLN
TRP	ALA	LYS	LEU	LYS
MET	GLN	PRO	GLY	SER
SER	GLU	P80	GLY	PRO
ASN	GLN	L402	ALA	ALA
ASP	ALA	S438	GLY	SER
HIS	GLN	ALA	TYR	VAL
GLU	VAL	VAL	PRO	THR
	ARG	ASP	GLY	VAL
	GLN	ASN	GLY	THR

- Molecule 1: Flagellar M-ring protein

Chain J:  27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain K:  27% 73%

[illegible]

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

Chain L:  27% 73%

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

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

Chain M:  27% 73%

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

- Molecule 1: Flagellar M-ring protein

Chain S: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain T:  27% 73%

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

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain U:  27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain V:  27% 73%

THR	VAL	GLU	PHE	GLN	MET
PRO	PRO	PRO	GLY	GLY	ASP
GLY	GLY	GLY	ILE	GLY	GLY
GLU	ALA	ARG	SER	GLY	ALA
LEU	SER	LEU	PHE	ILE	SER
PRO	ASP	ASP	SER	VAL	THR
PHE	ASN	GLU	GLU	ALA	THR
TRP	GLN	GLY	GLN	GLN	THR
GLN	ALA	GLN	VAL	LEU	GLN
GLN	PRO	ILE	ASN	THR	PRO
SER	PRO	SER	TYR	GLN	LYS
PHE	ASN	ALA	GLN	MET	PRO
ILE	GLU	VAL	ALA	ASN	LEU
ASP	ALA	VAL	ALA	ILE	GLU
GLN	PRO	HIS	LEU	PRO	TRP
LEU	ILE	VAL	GLU	TYR	LEU
LEU	ALA	VAL	GLY	ARG	ASN
ALA	THR	SER	GLU	PHE	ARG
ALA	PRO	ALA	LEU	ALA	LEU
GLY	PRO	VAL	ALA	ASN	ARG
ARG	THR	VAL	ARG	GLY	ALA
ASN	ASN	ALA	THR	SER	ASN
GLN	GLN	GLY	ILE	GLY	PRO
LEU	ASN	LEU	ILE	ALA	ARG
VAL	ASN	PRO	THR	ILE	ILE
LEU	ALA	PRO	LEU	GLU	PRO
VAL	GLN	GLY	GLY	VAL	LEU
ASN	ASN	ASN	PRO	PRO	ILE
ALA	THR	VAL	VAL	ALA	VAL
PRO	PRO	THR	LYS	ASP	GLY
ILE	GLN	LEU	SER	LYS	ALA
THR	THR	VAL	ALA	VAL	SER
TRP	SER	ASP	ARG	HIS	ALA
ARG	THR	GLN	VAL	GLU	ALA
LYS	SER	SER	HIS	LEU	VAL
ALA	THR	GLY	ALA	ARG	ILE
VAL	ASN	HIS	ASN	ALA	ILE
ARG	SER	LEU	MET	ARG	VAL
PRO	ASN	LEU	PRO	LEU	VAL
GLN	SER	THR	LYS	ALA	ALA
LEU	ALA	GLN	PRO	GLN	MET
THR	GLY	SER	LEU	GLY	VAL
ARG	P355	THR	PHE	PRO	TRP
VAL	K394	SER	VAL	LEU	ALA
GLU	THR	GLY	ARG	LYS	LYS
GLU	LEU	ASP	GLU	GLY	THR
ALA	ALA	ARG	GLN	GLY	PRO
LYS	ASP	LYS	LYS	ALA	ASP
ALA	GLY	W231	SER	VAL	TYR
ALA	LYS	PRO	PRO	GLY	ARG
GLN	PRO	I402	SER	PHE	THR
GLU	GLU	GLY	ALA	GLU	LEU
GLN	GLN	ALA	SER	LEU	PHE
ALA	ALA	GLY	VAL	LEU	SER
GLN	GLN	VAL	THR	ASP	ASN
VAL	VAL	PRO	VAL	GLN	LEU
ARG	ASP	GLY	THR	GLU	SER

- Molecule 1: Flagellar M-ring protein

Chain W: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain X:  27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain Y: 27% 73%

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

- Molecule 1: Flagellar M-ring protein

Chain Z: 27% 73%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain a:  27% 73%

[illegible]

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain d: 27% 73%

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

- Molecule 1: Flagellar M-ring protein

Chain e: 27% 73%

THR	VAL	GLU	PHE	GLN	MET
PRO	PRO	PRO	GLY	GLY	ASP
GLY	GLY	GLY	ILE	ILE	GLY
GLU	ALA	ARG	SER	SER	GLY
LEU	LEU	ALA	GLN	ALA	ALA
PRO	SER	LEU	PHE	ILE	SER
PHE	ASN	ASP	SER	VAL	THR
TRP	GLN	GLU	GLU	ALA	ALA
GLN	PRO	GLY	GLN	GLN	THR
GLN	ALA	ILE	VAL	LEU	GLN
GLN	PRO	ILE	ASN	THR	PRO
SER	PRO	SER	TYR	GLN	LYS
PHE	ASN	ALA	GLN	MET	PRO
ILE	GLU	VAL	ALA	ASN	LEU
ASP	ALA	VAL	ARG	ILE	GLU
GLN	PRO	HIS	LEU	PRO	TRP
LEU	ILE	VAL	GLU	TYR	LEU
LEU	ALA	VAL	GLY	ARG	ASN
ALA	THR	SER	GLU	PHE	ARG
ALA	PRO	ALA	LEU	ALA	LEU
GLY	PRO	VAL	ALA	ASN	ARG
ARG	THR	VAL	ARG	GLY	ALA
ASN	ASN	ALA	THR	SER	ASN
GLN	GLN	GLY	ILE	GLY	PRO
LEU	ASN	LEU	ILE	ALA	ARG
VAL	ASN	PRO	THR	ILE	ILE
LEU	ALA	PRO	LEU	GLU	PRO
VAL	GLN	GLY	GLY	VAL	LEU
ASN	ASN	ASN	PRO	PRO	ILE
THR	THR	VAL	VAL	ALA	VAL
PRO	PRO	THR	LYS	ASP	GLY
ILE	GLN	LEU	SER	LYS	ALA
THR	THR	VAL	ALA	VAL	SER
TRP	SER	ASP	ARG	HIS	ALA
ARG	THR	GLN	VAL	GLU	ALA
LYS	SER	SER	HIS	LEU	VAL
ALA	THR	GLY	ALA	ARG	VAL
VAL	ASN	HIS	ASN	ALA	ILE
ARG	SER	LEU	MET	ARG	VAL
PRO	ASN	LEU	PRO	LEU	VAL
GLN	SER	THR	LYS	ALA	ALA
LEU	ALA	GLN	PRO	GLN	MET
THR	GLY	SER	LEU	GLY	VAL
ARG	P355	THR	PHE	PRO	TRP
VAL	K394	SER	VAL	LEU	ALA
GLU	THR	GLY	ARG	LYS	LYS
GLU	LEU	ASP	GLU	GLY	THR
ALA	ALA	ASP	GLN	ALA	PRO
LYS	ASP	LYS	LYS	ALA	TYR
ALA	GLY	W231	SER	VAL	ASP
ALA	LYS	PRO	PRO	GLY	ARG
GLN	PRO	L402	SER	PHE	THR
GLU	GLY	GLY	ALA	GLU	LEU
GLN	ALA	ALA	SER	LEU	PHE
ALA	ALA	GLY	VAL	LEU	SER
GLN	GLN	VAL	THR	ASP	ASN
VAL	VAL	PRO	VAL	GLN	LEU
ARG	ASP	GLY	THR	GLU	SER

- Molecule 1: Flagellar M-ring protein

Chain f:  27% 73%

GLU	THR	GLU	THR	VAL	GLU	PHE	GLN	GLN	MET
THR	GLY	PRO	GLY	PRO	GLY	GLY	ASP	ASP	SER
GLU	GLY	ALA	GLY	ALA	ARG	SER	GLY	GLY	ALA
ALA	LEU	LEU	ALA	LEU	SER	LEU	ALA	ALA	ALA
VAL	PRO	ASN	PHE	ASN	ASP	SER	VAL	VAL	SER
GLU	THR	GLN	THR	GLN	VAL	GLU	ALA	ALA	THR
VAL	GLN	PRO	GLN	PRO	GLN	VAL	LEU	LEU	GLN
ARG	GLN	ALA	GLN	ALA	GLN	ASN	THR	PRO	PRO
LEU	GLN	LEU	LEU	LEU	ILE	HIS	LEU	TRP	GLN
SER	GLN	ILE	LEU	ILE	VAL	VAL	GLY	TYR	LYS
LYS	SER	PRO	SER	PRO	ALA	ALA	GLN	GLN	PRO
ASP	PHE	ASN	GLU	ASN	VAL	ARG	MET	MET	LEU
GLU	ILE	GLU	ASP	ALA	VAL	ALA	ASN	ASN	GLU
GLN	GLN	ALA	GLN	ALA	VAL	VAL	ILE	ILE	LEU
ARG	ALA	PRO	ALA	PRO	THR	SER	GLY	ARG	ASN
ARG	ALA	THR	ALA	THR	ALA	GLY	PHE	PHE	ARG
ALA	GLY	PRO	GLY	PRO	VAL	ALA	ASN	ALA	ARG
ASN	ASN	THR	ARG	THR	VAL	ARG	GLY	GLY	ALA
GLN	GLN	ASN	TRP	ASN	ALA	THR	SER	SER	ASN
ARG	LEU	GLN	LEU	GLN	GLY	ILE	GLY	GLY	PRO
LEU	LEU	GLN	VAL	GLN	LEU	GLU	ALA	ALA	ARG
GLY	VAL	ASN	VAL	ASN	PRO	THR	ILE	ILE	ILE
ALA	LEU	ALA	LEU	ALA	PRO	LEU	VAL	VAL	LEU
GLU	VAL	GLU	VAL	GLN	GLY	GLY	VAL	VAL	LEU
VAL	VAL	ASN	VAL	ASN	ASN	PRO	PRO	PRO	ILE
MET	MET	THR	ALA	THR	VAL	VAL	ALA	ALA	VAL
SER	TRP	PRO	TRP	PRO	THR	LYS	ASP	ASP	ALA
GLN	ILE	GLN	ILE	GLN	LEU	SER	LYS	LYS	ALA
ARG	LEU	THR	LEU	THR	THR	ALA	GLY	GLY	SER
ARG	TRP	SER	TRP	SER	ASP	ARG	HIS	ALA	ALA
ARG	ARG	THR	ARG	THR	GLN	VAL	GLU	LEU	VAL
GLU	LYS	SER	LYS	SER	SER	HIS	LEU	ARG	ALA
MET	ALA	THR	ALA	THR	GLY	LEU	ARG	ARG	ALA
SER	VAL	ASN	VAL	ASN	HIS	ALA	LEU	ILE	ALA
ASP	ARG	SER	ARG	SER	LEU	LEU	MET	ARG	VAL
ASN	PRO	ASN	PRO	ASN	LEU	THR	LEU	VAL	ALA
ASP	ASP	SER	GLN	SER	THR	LYS	GLN	ALA	ALA
PRO	PRO	ALA	LEU	ALA	PRO	PRO	GLN	MET	MET
ARG	THR	GLY	THR	GLY	SER	SER	GLN	VAL	VAL
VAL	ARG	P355	ARG	P355	THR	SER	GLN	GLN	GLN
VAL	VAL	K394	VAL	K394	THR	VAL	LEU	LEU	TRP
LEU	LEU	THR	GLU	THR	GLY	ARG	GLY	LYS	LYS
VAL	ILE	ALA	ALA	ALA	ASP	GLU	GLY	GLY	THR
ARG	ARG	LYS	LYS	ASP	ASP	GLN	ALA	ALA	PRO
GLN	GLN	ALA	ALA	GLY	GLY	SER	VAL	VAL	TYR
TRP	TRP	ALA	ALA	LYS	H231	PRO	GLY	GLY	ARG
MET	MET	PRO	GLN	PRO	K304	SER	PHE	PHE	THR
SER	SER	GLU	GLU	GLY	GLY	ALA	GLU	GLU	LEU
ASN	ASN	GLN	GLN	ALA	ALA	SER	LEU	LEU	PHE
ASP	ASP	ALA	ALA	GLY	GLY	VAL	LEU	LEU	ASN
HIS	HIS	GLN	GLN	TYR	TYR	THR	ASP	ASP	ASN
GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLU
		ASN	ARG	ASN	GLY	THR	TYR	THR	SER

- Molecule 1: Flagellar M-ring protein

Chain g:  27% 73%

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

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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.26	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. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	365	ASN
1	c	434	ASN
1	S	365	ASN
1	c	365	ASN
1	f	261	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.

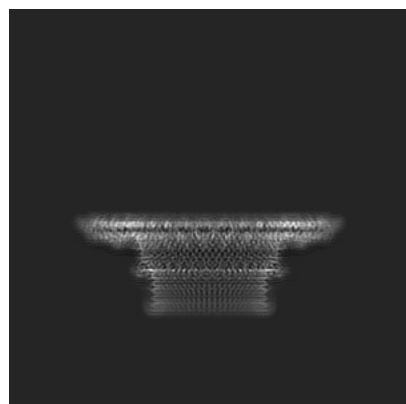
6 Map visualisation [i](#)

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.

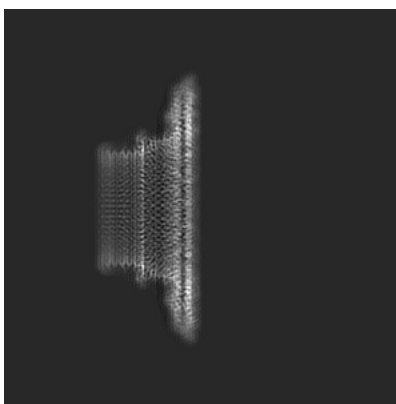
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

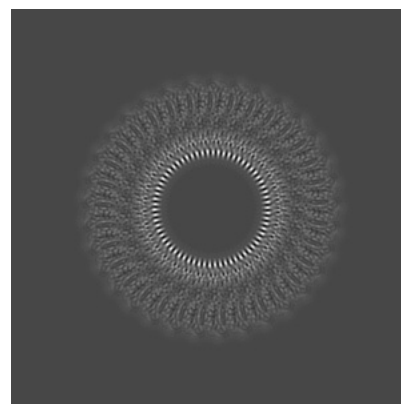
6.1.1 Primary map



X

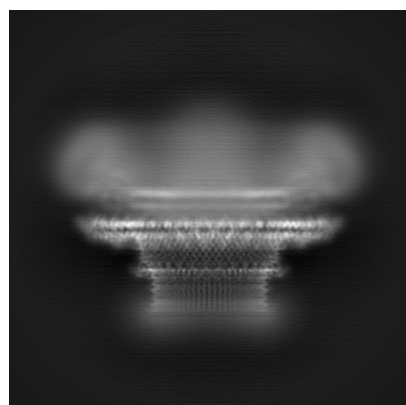


Y

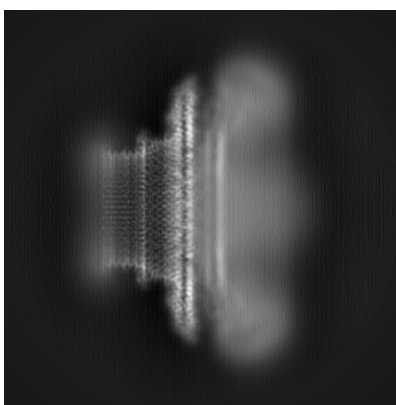


Z

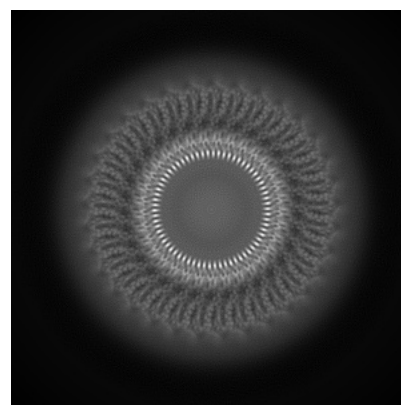
6.1.2 Raw map



X



Y

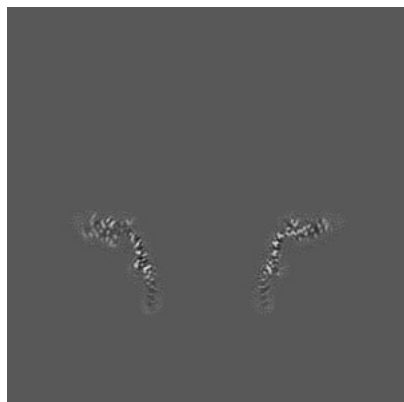


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 216

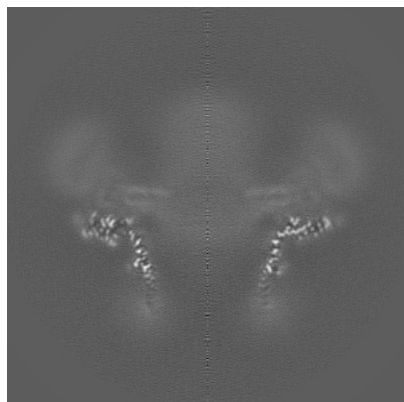


Y Index: 216



Z Index: 216

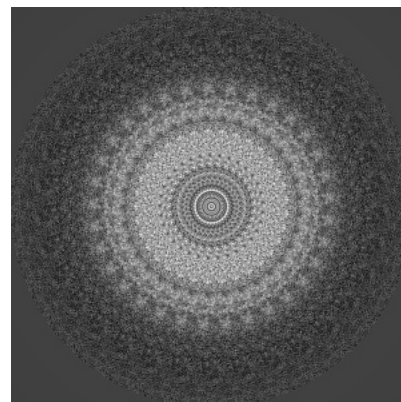
6.2.2 Raw map



X Index: 216



Y Index: 216

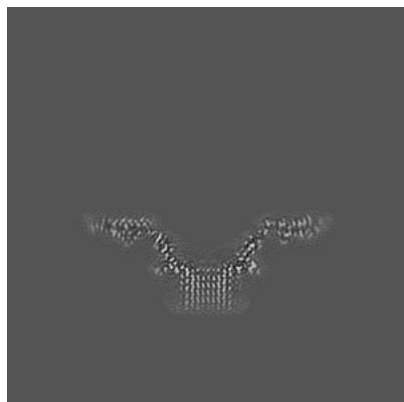


Z Index: 216

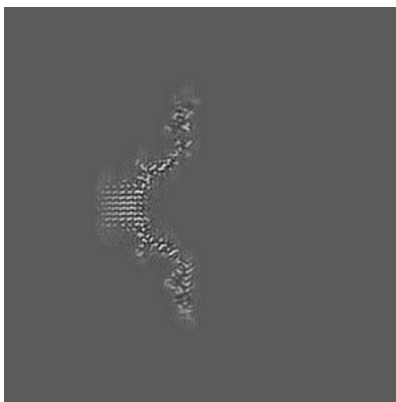
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

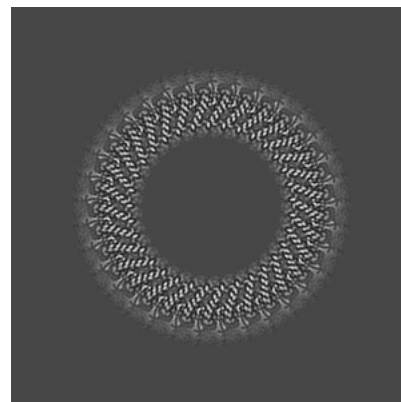
6.3.1 Primary map



X Index: 274

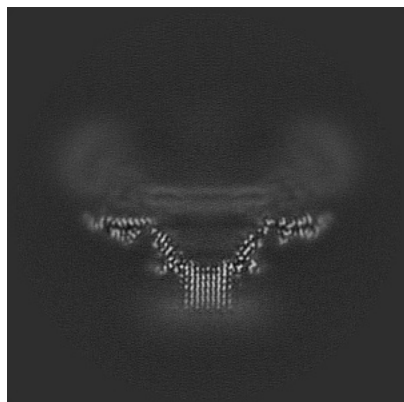


Y Index: 156

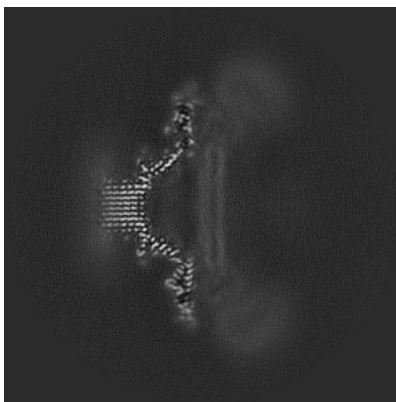


Z Index: 197

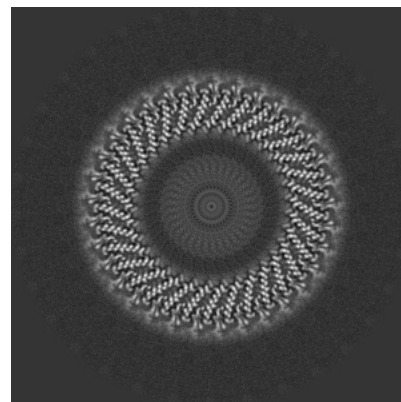
6.3.2 Raw map



X Index: 275



Y Index: 157

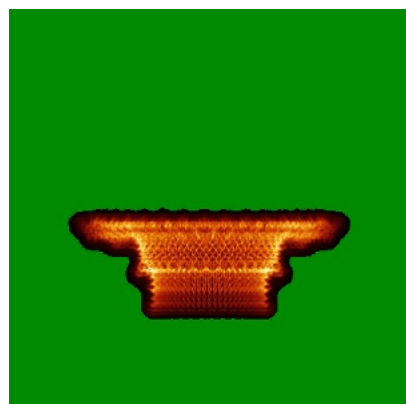


Z Index: 199

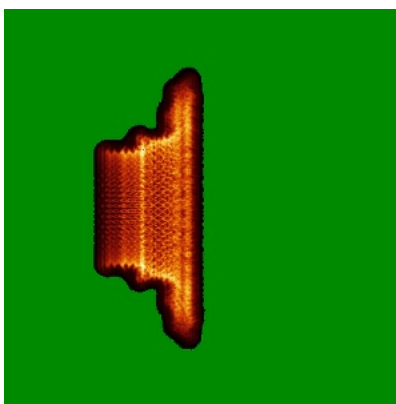
The images above show the largest variance slices of the map in three orthogonal directions.

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

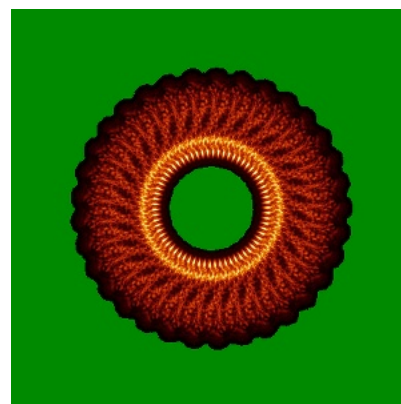
6.4.1 Primary map



X

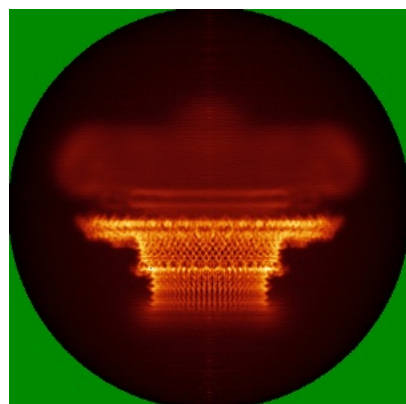


Y

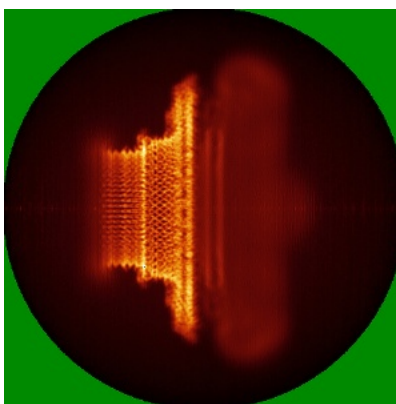


Z

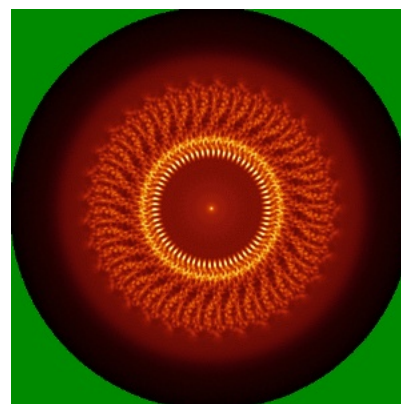
6.4.2 Raw map



X



Y

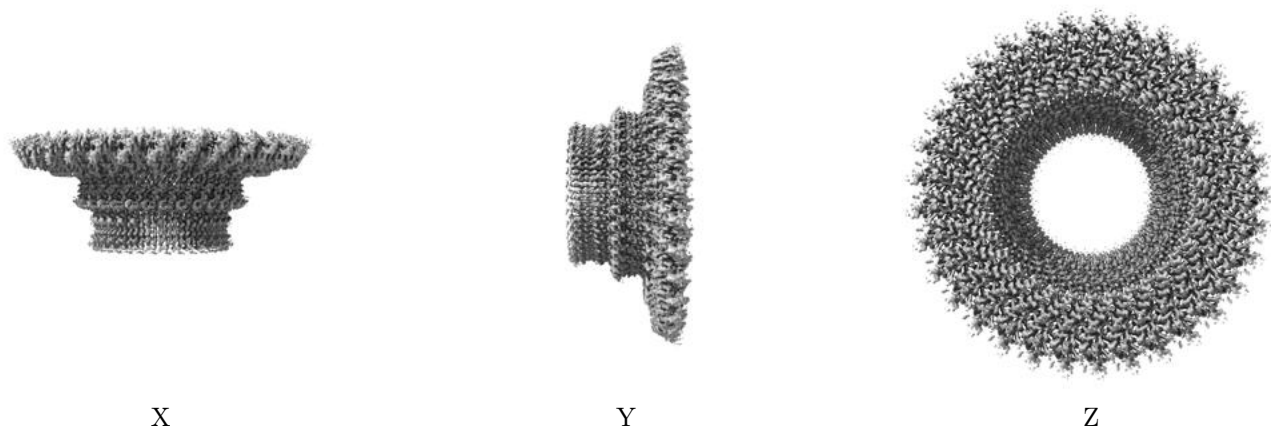


Z

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.

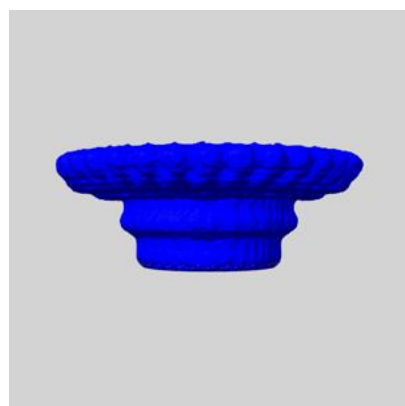
6.6 Mask visualisation [i](#)

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

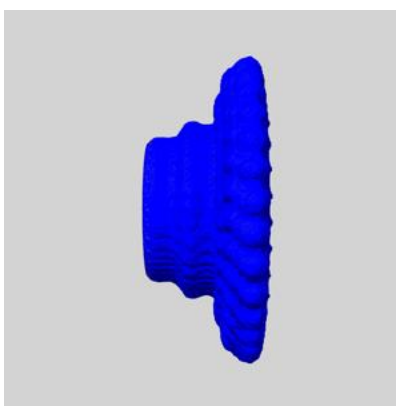
A mask typically either:

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

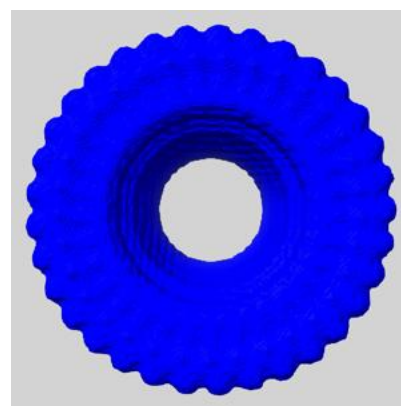
6.6.1 emd_10145_msk_1.map [i](#)



X



Y

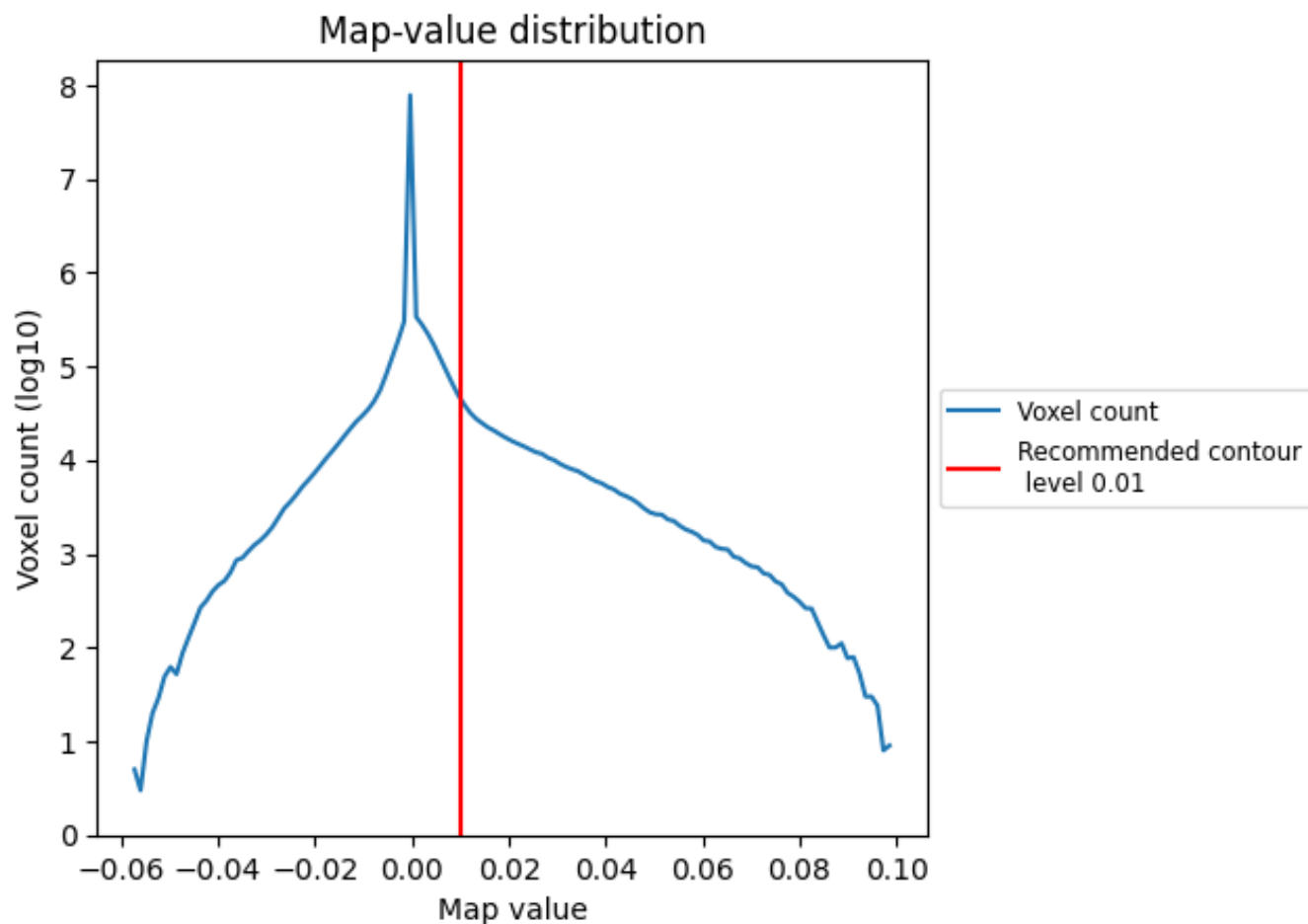


Z

7 Map analysis [i](#)

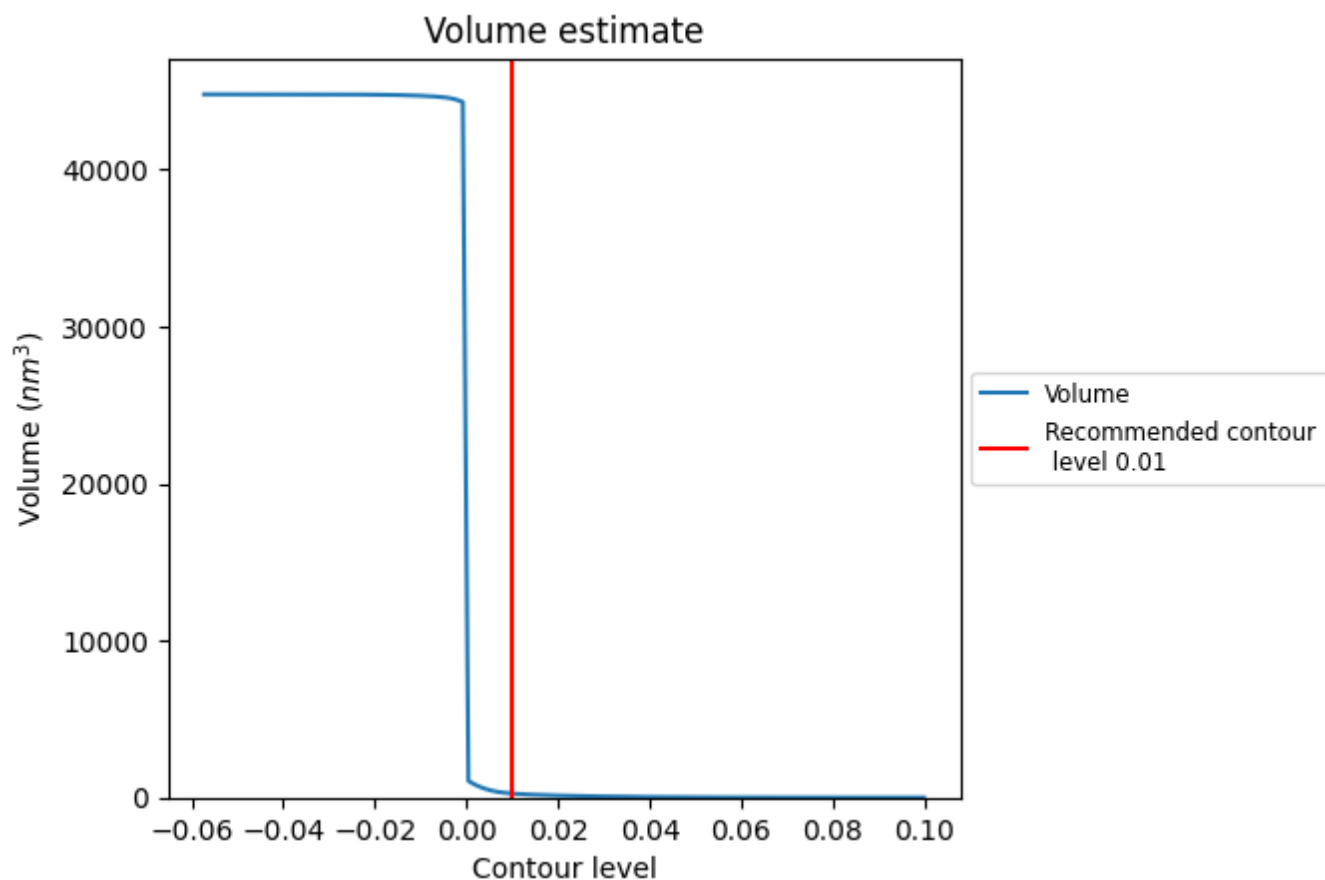
This section contains the results of statistical analysis of the map.

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.

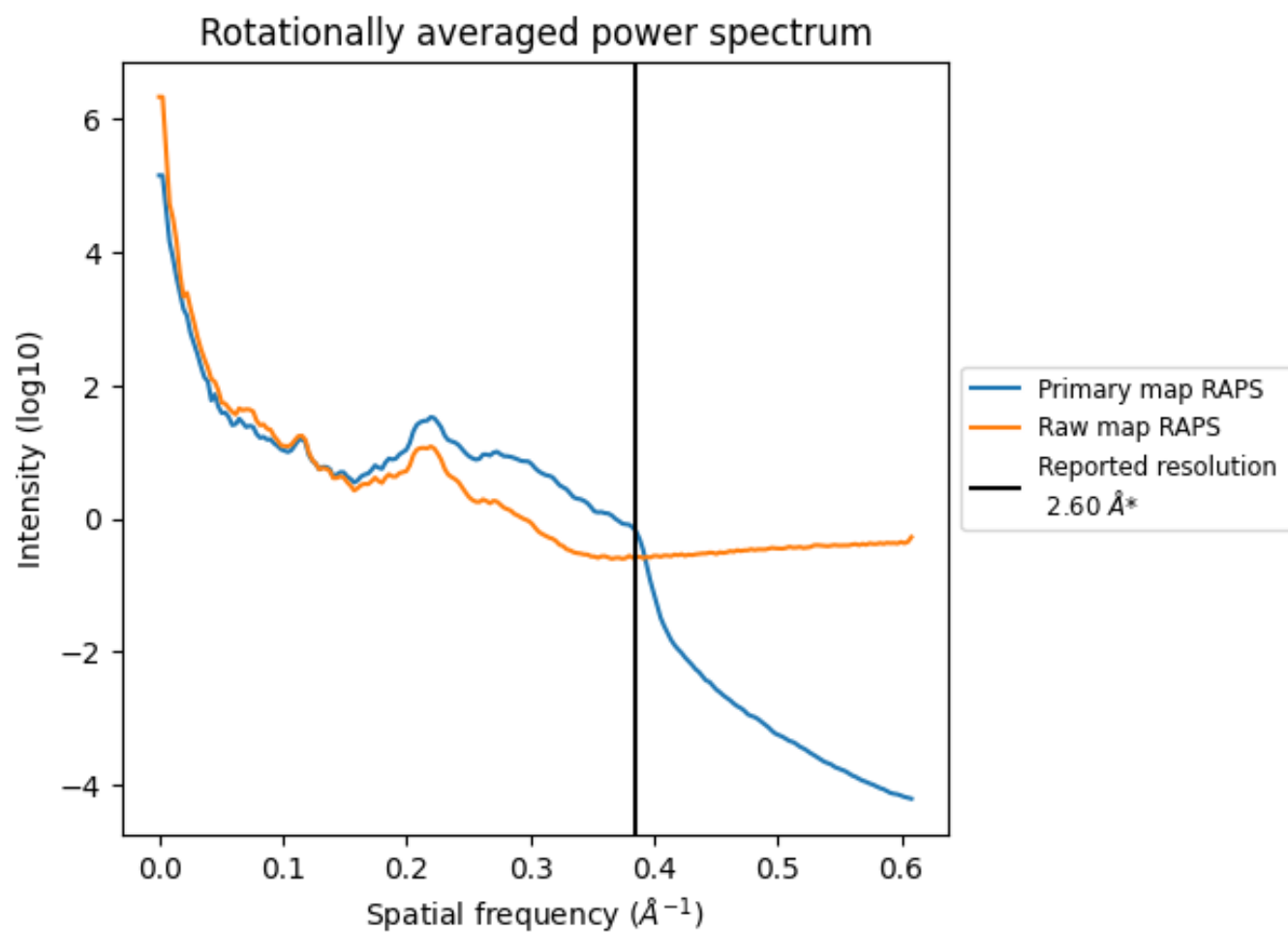
7.2 Volume estimate [i](#)



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 ⓘ

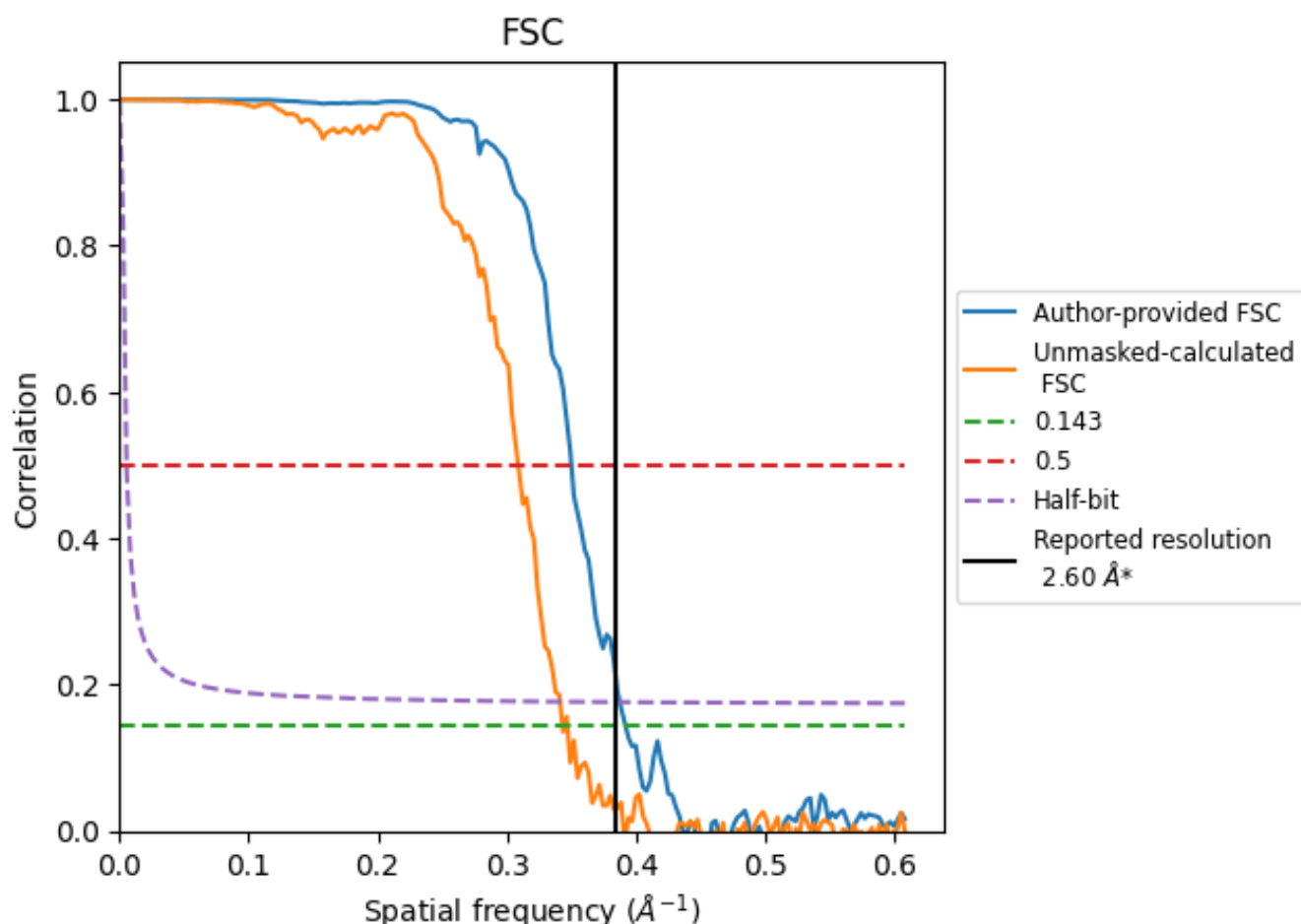


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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](#)

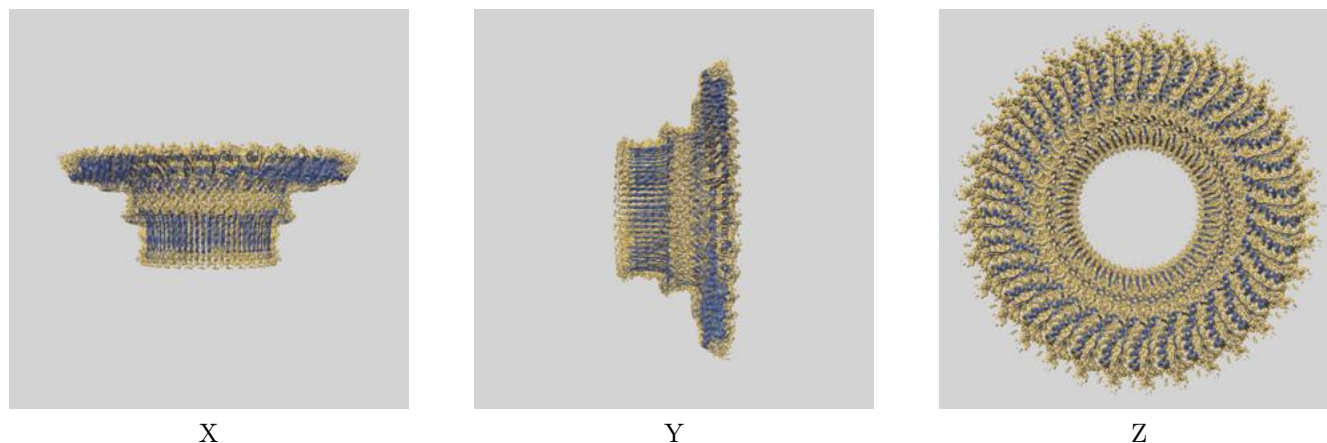
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.55	2.86	2.58
Unmasked-calculated*	2.91	3.24	2.93

*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](#)

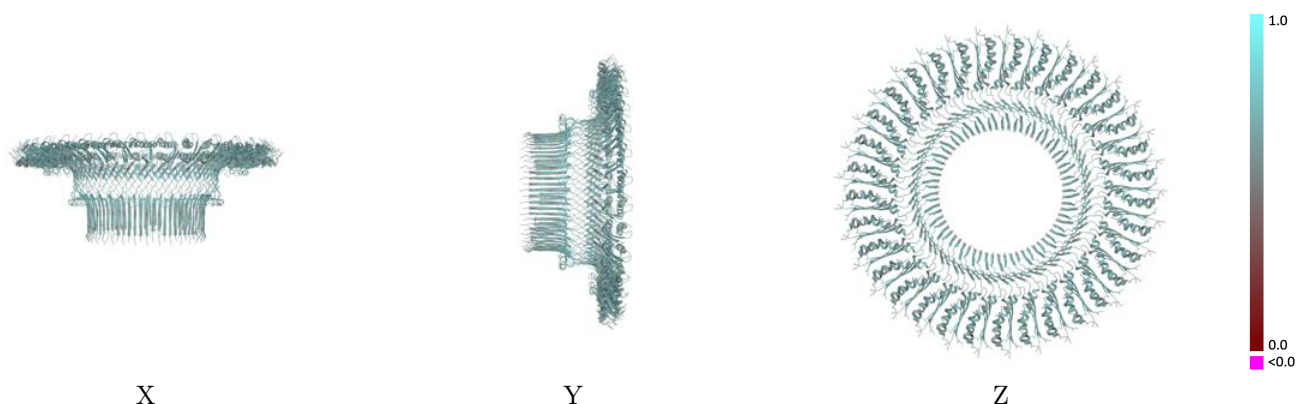
This section contains information regarding the fit between EMDB map EMD-10145 and PDB model 6SD1. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



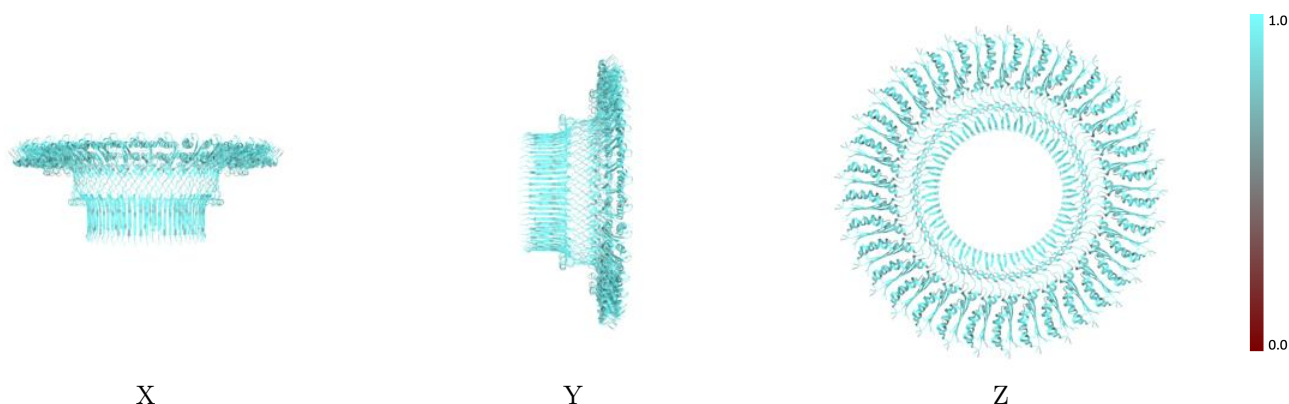
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



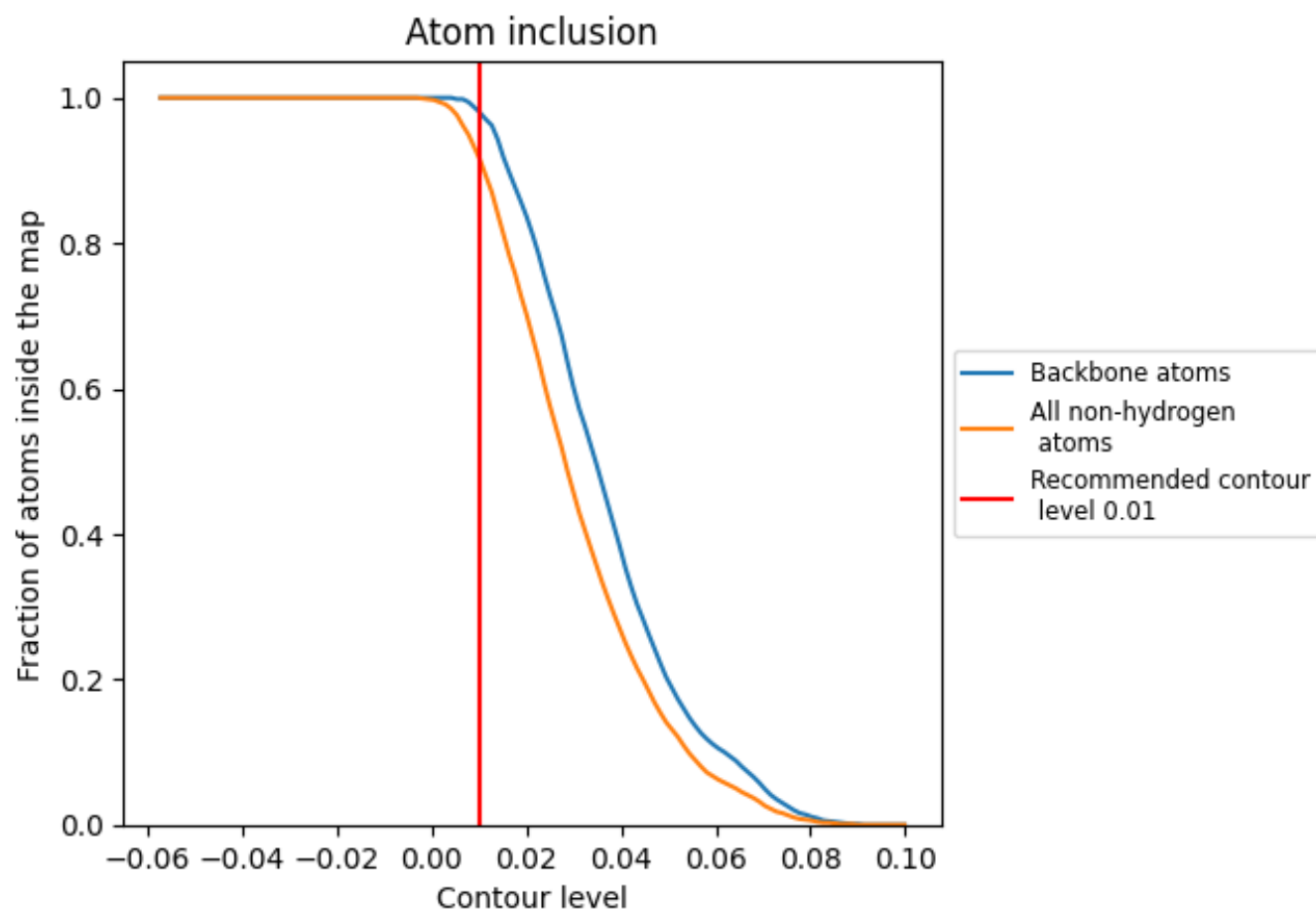
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

