



wwPDB EM Validation Summary Report ⓘ

Jun 2, 2024 – 04:24 AM EDT

PDB ID : 8CVI
EMDB ID : EMD-27008
Title : Cryo-EM structure of the supercoiled EPEC H6 flagellar filament core Curly I waveform
Authors : Kreutzberger, M.A.; Chatterjee, S.; Frankel, G.; Egelman, E.H.
Deposited on : 2022-05-18
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

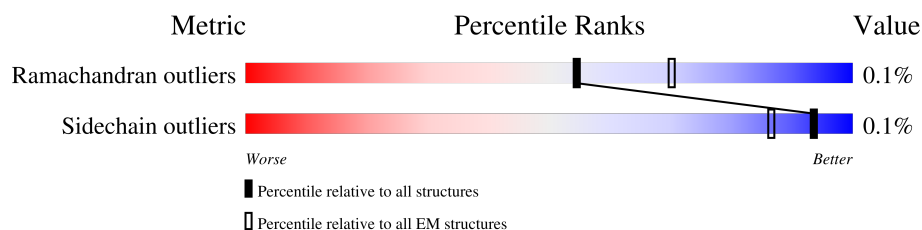
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY


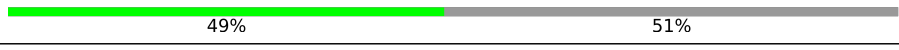
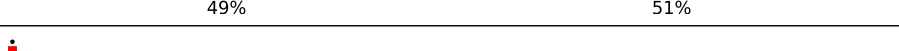
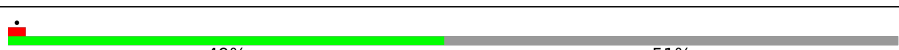





The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





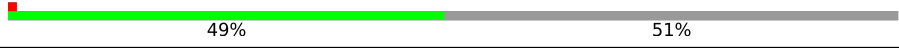

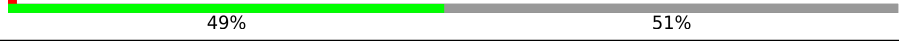



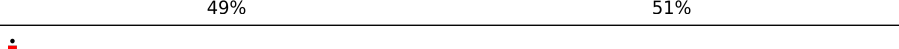
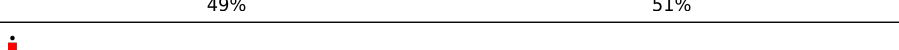

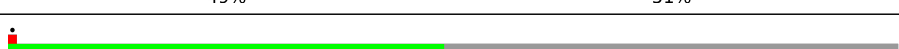
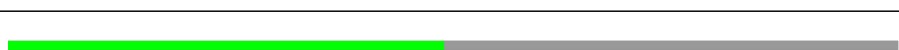
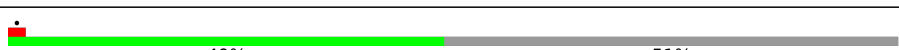
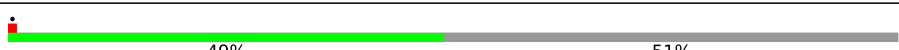






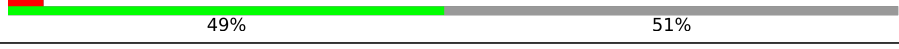
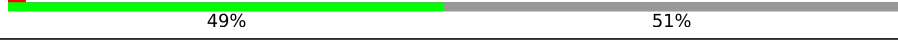

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	548	
1	B	548	
1	C	548	
1	D	548	
1	E	548	
1	F	548	
1	G	548	
1	H	548	
1	I	548	

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Mol	Chain	Length	Quality of chain	
1	J	548		
1	K	548		
1	L	548		
1	M	548		
1	N	548		
1	O	548		
1	P	548		
1	Q	548		
1	R	548		
1	S	548		
1	T	548		
1	U	548		
1	V	548		
1	W	548		
1	X	548		
1	Y	548		
1	Z	548		
1	a	548		
1	b	548		
1	c	548		
1	d	548		
1	e	548		
1	f	548		
1	g	548		

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 66030 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

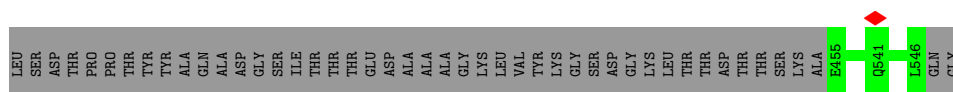
- Molecule 1 is a protein called Flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	267	Total 1985	C 1190	N 363	O 430	S 2	0	0
1	B	267	Total 1985	C 1190	N 363	O 430	S 2	0	0
1	C	267	Total 1985	C 1190	N 363	O 430	S 2	0	0
1	D	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	N	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	X	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	E	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	O	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	Y	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	F	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	P	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	Z	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	G	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	Q	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	a	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	H	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	R	268	Total 1996	C 1196	N 365	O 433	S 2	0	0

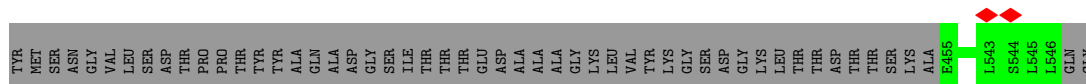
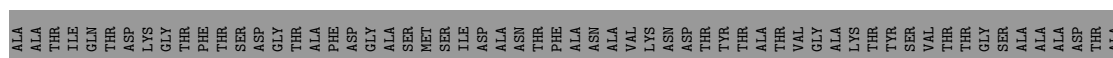
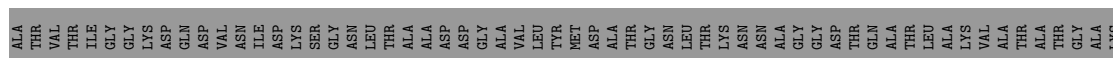
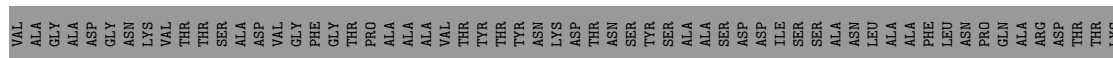
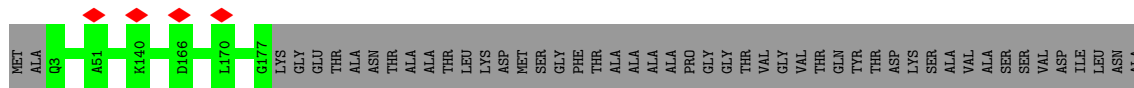
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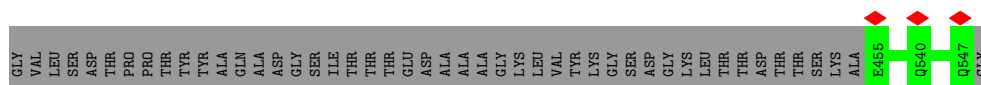
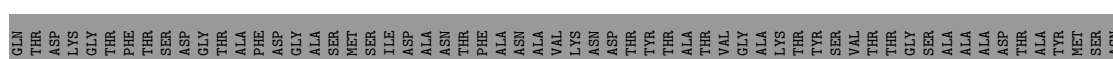
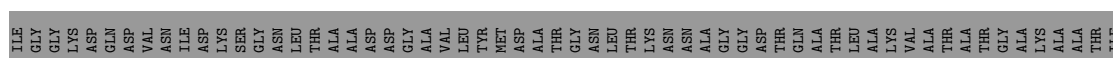
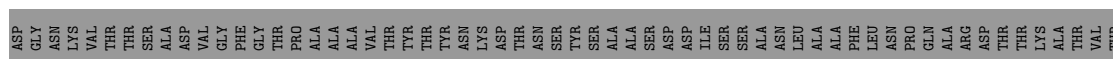
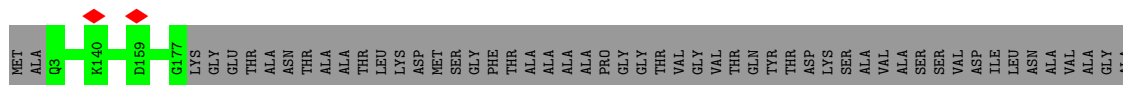
Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	268	Total 1996	C 1196	N 365	O 433	S 2	0	0
1	I	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	S	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	c	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	J	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	T	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	d	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	K	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	U	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	e	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	L	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	V	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	f	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	M	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	W	269	Total 2009	C 1205	N 367	O 435	S 2	1	0
1	g	269	Total 2009	C 1205	N 367	O 435	S 2	1	0



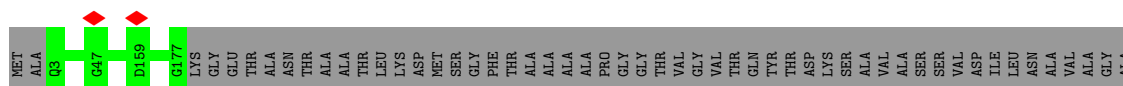
- Molecule 1: Flagellin



- Molecule 1: Flagellin



- Molecule 1: Flagellin



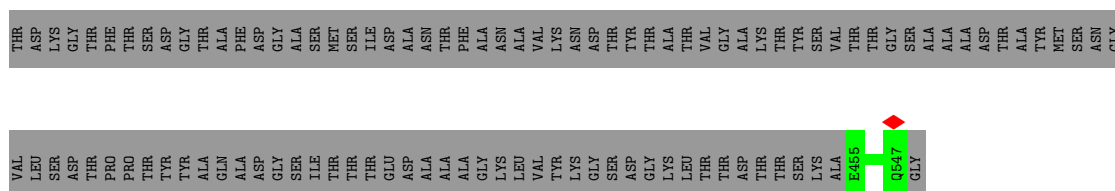
- Molecule 1: Flagellin

[illegible]

- Molecule 1: Flagellin



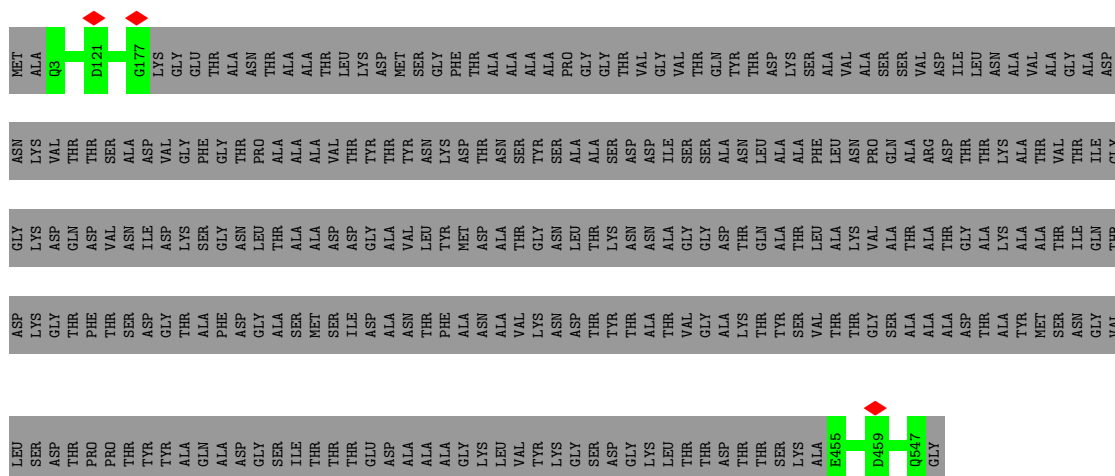
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GLY	GLN	GLN	ILE	ASP	ALA
VAL	THR	THR	GLY	GLY	Q3
LEU	ASP	ASP	GLY	ASN	D43
SER	LYS	LYS	LYS	VAL	D44
ASP	GLY	THR	GLN	THR	D70
PRO	PHE	THR	ASP	THR	G177
PRO	THR	THR	VAL	SER	LYS
THR	SER	ASN	ASN	ALA	GLY
TYR	ASP	ILE	ILE	ASP	GLY
TYR	GLY	THR	LYS	VAL	GLY
ALA	ALA	ALA	SER	PHE	GLY
GLN	PHE	ALA	GLY	GLY	THR
ALA	ASP	ASP	ASN	THR	ALA
ASP	ASP	GLY	LEU	PRO	ASN
GLY	GLY	THR	THR	ALA	THR
SER	SER	ALA	ALA	ALA	ALA
ILE	MET	SER	ALA	ALA	THR
THR	THR	SER	ASP	VAL	THR
THR	THR	ILE	ASP	THR	LEU
GLU	ASP	ASP	GLY	TYR	LYS
ALA	ASP	ALA	ALA	THR	ASP
ALA	ASN	THR	VAL	TYR	MET
ALA	THR	THR	LEU	ASN	SER
ALA	PHE	ALA	TYR	ASN	GLY
GLY	ALA	ALA	MET	ASP	PHE
LYS	ASN	ASN	ASP	THR	THR
LEU	ALA	ALA	ALA	ASN	ALA
VAL	VAL	VAL	THR	SER	ALA
TYR	LYS	LYS	GLY	TYR	ALA
LYS	ASN	ASN	THR	SER	ALA
GLY	THR	THR	ASN	ASP	ALA
ASP	THR	THR	LYS	SER	ALA
LEU	ALA	THR	ASN	ASP	VAL
THR	VAL	VAL	ALA	ILE	GLY
THR	VAL	GLY	GLY	SER	VAL
THR	GLY	GLY	THR	THR	THR
ASP	ALA	ALA	ASP	ALA	GLN
THR	LYS	LYS	THR	ASN	TYR
THR	THR	THR	GLN	LEU	THR
SER	TYR	THR	ALA	ALA	ASP
LYS	SER	SER	THR	PHE	LYS
VAL	VAL	THR	LEU	ALA	SER
E455	THR	THR	THR	ALA	VAL
D459	THR	THR	LYS	ASN	SER
Q37	THR	ALA	ALA	ARG	ALA
Q540	ALA	ASP	GLY	THR	ASP
L543	THR	THR	ALA	THR	ILE
S544	ALA	ALA	LYS	LYS	THR
L545	ALA	TYR	ALA	ALA	ASN
L546	THR	MET	ALA	THR	LEU
Q547	SER	SER	THR	VAL	ALA



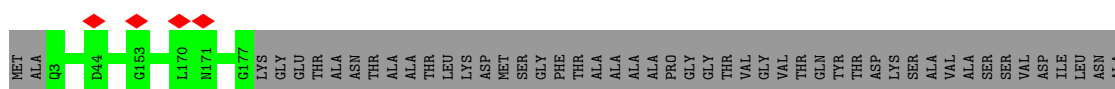
- Molecule 1: Flagellin

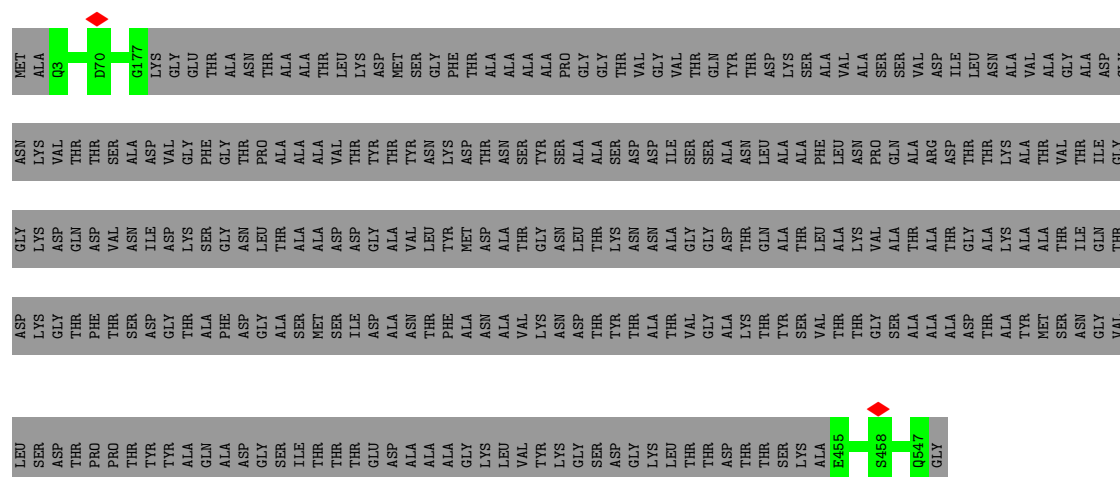


- Molecule 1: Flagellin

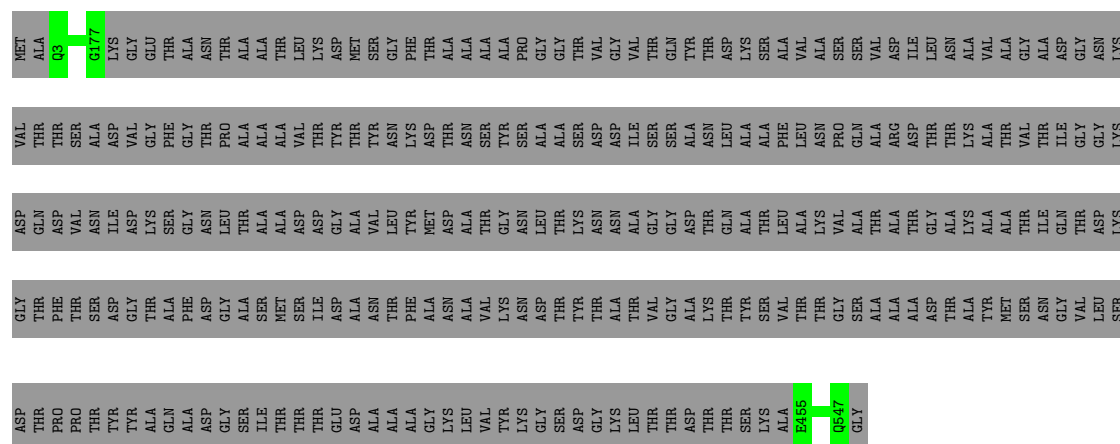


- Molecule 1: Flagellin

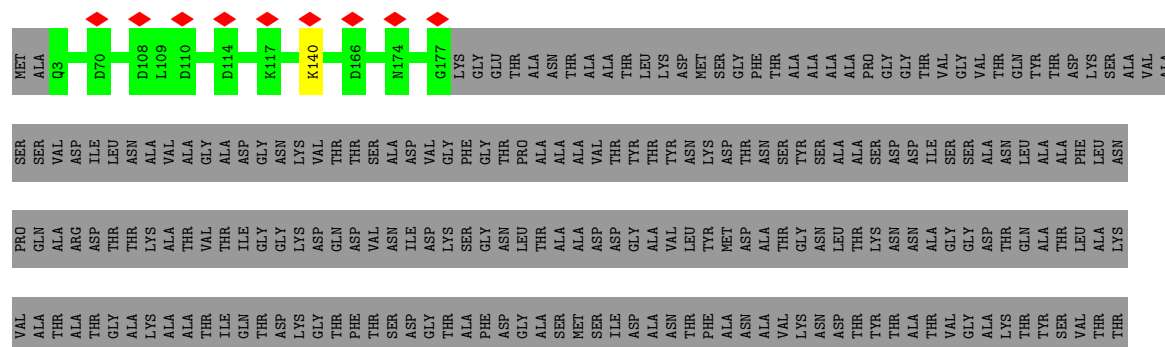


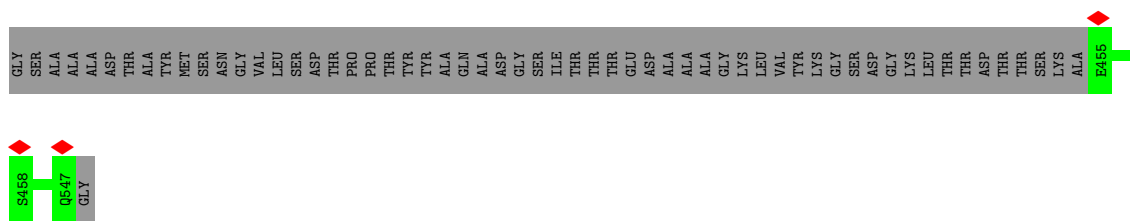


- Molecule 1: Flagellin

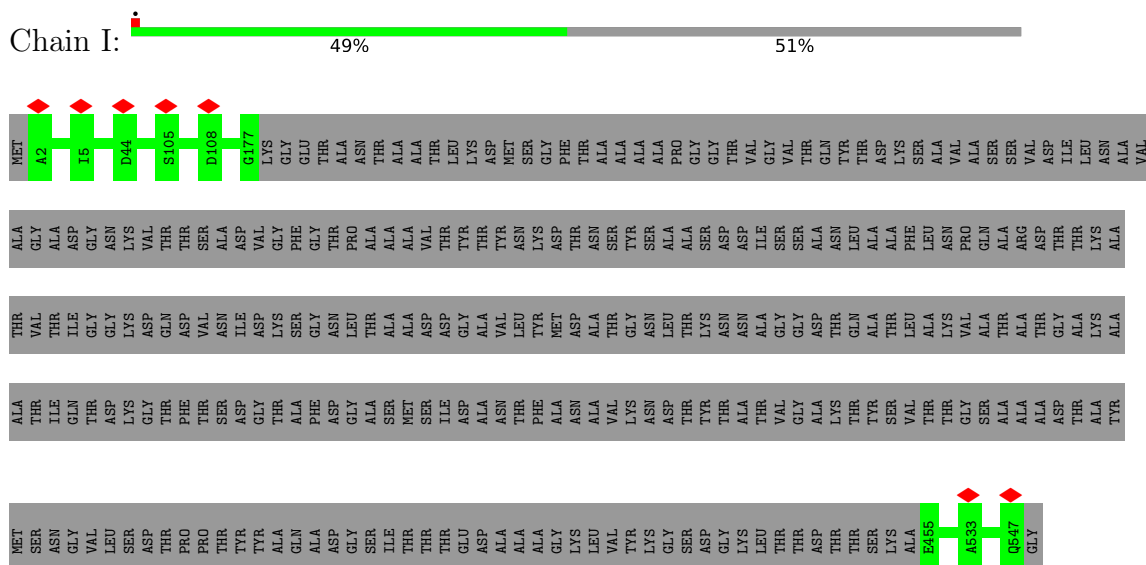


- Molecule 1: Flagellin

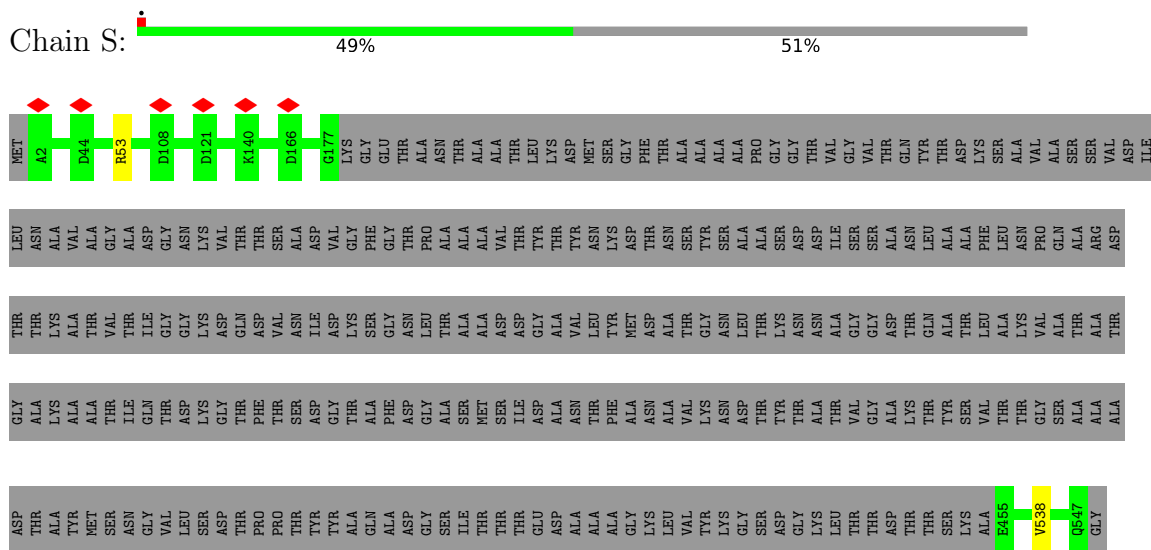




- Molecule 1: Flagellin

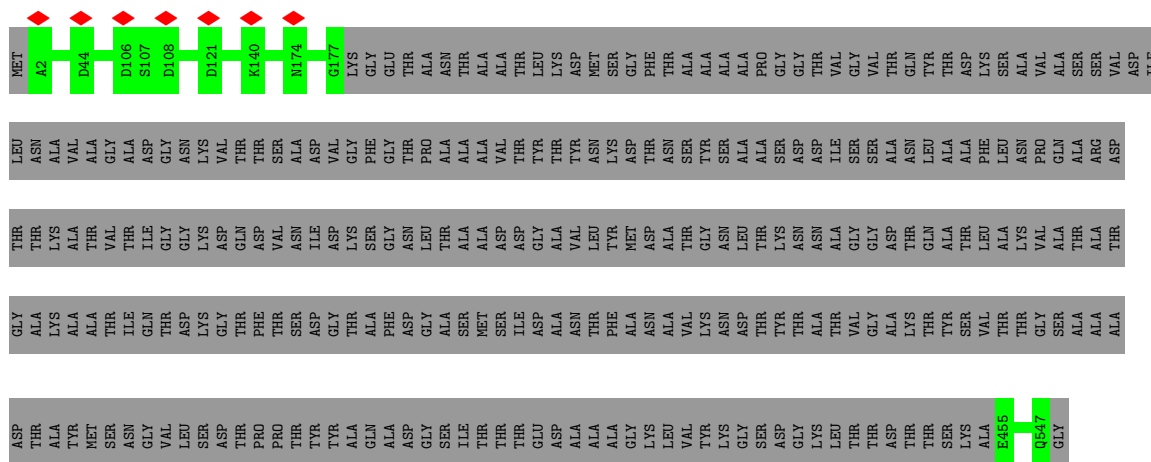


- Molecule 1: Flagellin



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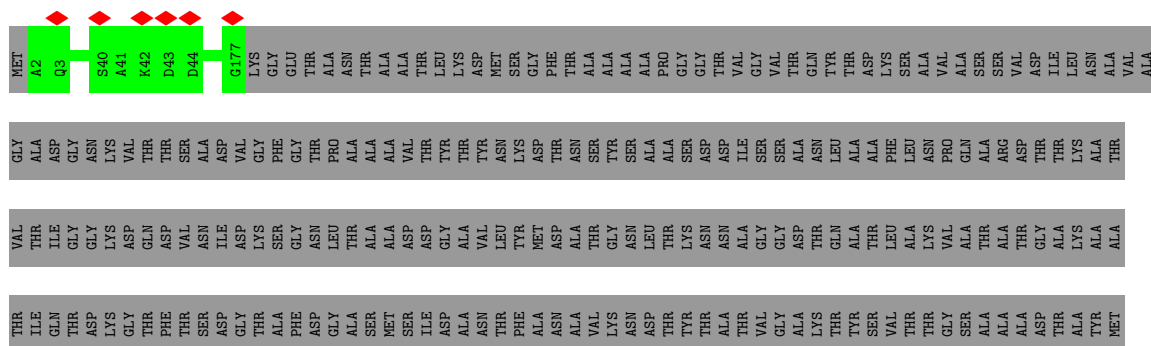


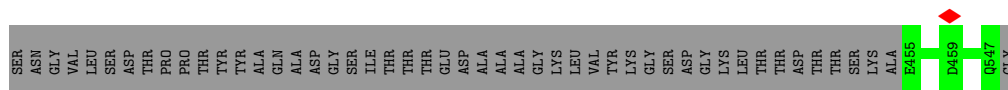


- Molecule 1: Flagellin

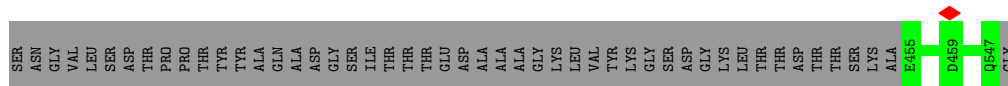
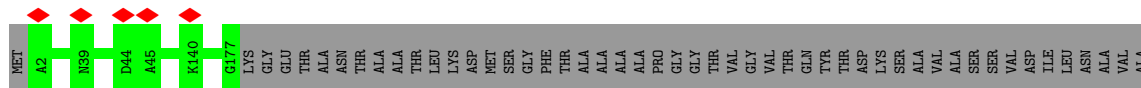


- Molecule 1: Flagellin

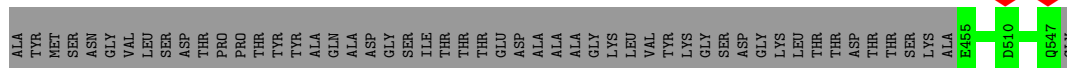
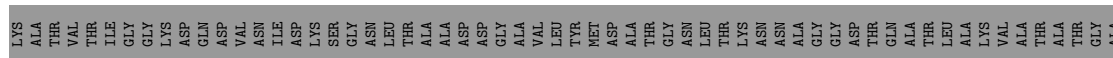
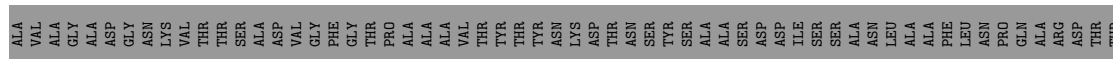
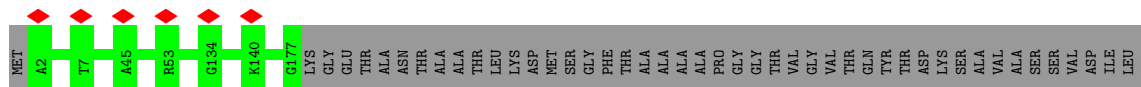




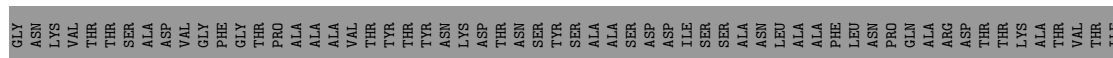
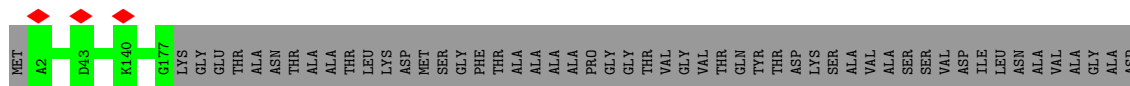
- Molecule 1: Flagellin



- Molecule 1: Flagellin

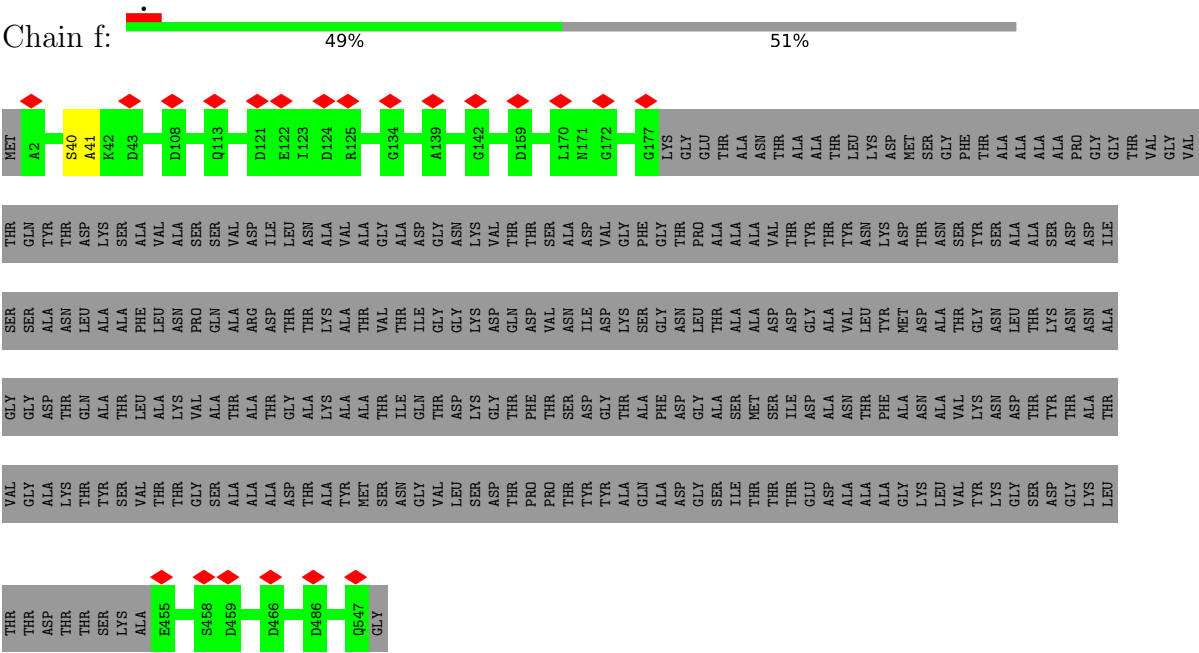


- Molecule 1: Flagellin

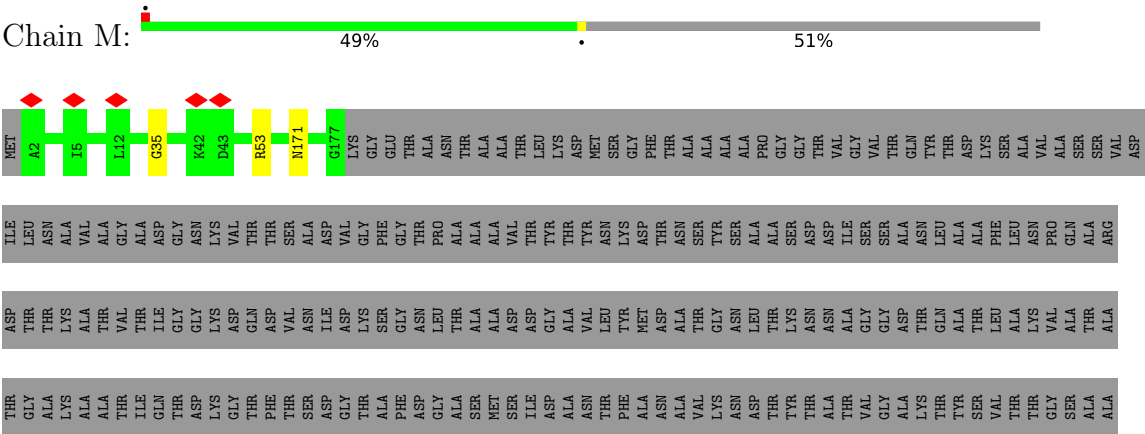




• Molecule 1: Flagellin



• Molecule 1: Flagellin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97477	Depositor
Resolution determination method	FSC 0.33 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.755	Depositor
Minimum map value	-0.525	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.136	Depositor
Map size (Å)	414.72003, 414.72003, 414.72003	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0.24	0/1990	0.40	0/2691
1	B	0.24	0/1990	0.41	0/2691
1	C	0.25	0/1990	0.41	0/2691
1	D	0.24	0/2001	0.41	0/2706
1	E	0.24	0/2001	0.40	0/2706
1	F	0.25	0/2001	0.40	0/2706
1	G	0.24	0/2001	0.40	0/2706
1	H	0.24	0/2001	0.40	0/2706
1	I	0.24	0/2014	0.43	0/2724
1	J	0.24	0/2014	0.43	0/2724
1	K	0.24	0/2014	0.42	0/2724
1	L	0.24	0/2014	0.39	0/2724
1	M	0.25	0/2014	0.43	0/2724
1	N	0.24	0/2001	0.40	0/2706
1	O	0.24	0/2001	0.40	0/2706
1	P	0.24	0/2001	0.40	0/2706
1	Q	0.24	0/2001	0.39	0/2706
1	R	0.25	0/2001	0.40	0/2706
1	S	0.25	0/2014	0.42	0/2724
1	T	0.24	0/2014	0.44	0/2724
1	U	0.25	0/2014	0.43	0/2724
1	V	0.24	0/2014	0.42	0/2724
1	W	0.25	0/2014	0.42	0/2724
1	X	0.24	0/2001	0.41	0/2706
1	Y	0.24	0/2001	0.39	0/2706
1	Z	0.24	0/2001	0.40	0/2706
1	a	0.24	0/2001	0.39	0/2706
1	b	0.24	0/2001	0.39	0/2706
1	c	0.24	0/2014	0.41	0/2724
1	d	0.24	0/2014	0.41	0/2724
1	e	0.24	0/2014	0.43	0/2724
1	f	0.24	0/2014	0.42	0/2724
1	g	0.24	0/2014	0.42	0/2724
All	All	0.24	0/66195	0.41	0/89523

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	S	0	1
1	V	0	2
1	f	0	2
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	S	538	VAL	Peptide
1	V	40	SER	Peptide
1	V	41	ALA	Peptide
1	f	40	SER	Peptide
1	f	41	ALA	Peptide

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	263/548 (48%)	248 (94%)	15 (6%)	0	100	100
1	B	263/548 (48%)	253 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	263/548 (48%)	253 (96%)	10 (4%)	0	100	100
1	D	264/548 (48%)	257 (97%)	7 (3%)	0	100	100
1	E	264/548 (48%)	259 (98%)	5 (2%)	0	100	100
1	F	264/548 (48%)	253 (96%)	11 (4%)	0	100	100
1	G	264/548 (48%)	255 (97%)	9 (3%)	0	100	100
1	H	264/548 (48%)	257 (97%)	7 (3%)	0	100	100
1	I	266/548 (48%)	248 (93%)	18 (7%)	0	100	100
1	J	266/548 (48%)	251 (94%)	15 (6%)	0	100	100
1	K	266/548 (48%)	252 (95%)	14 (5%)	0	100	100
1	L	266/548 (48%)	259 (97%)	7 (3%)	0	100	100
1	M	266/548 (48%)	254 (96%)	10 (4%)	2 (1%)	19	51
1	N	264/548 (48%)	254 (96%)	10 (4%)	0	100	100
1	O	264/548 (48%)	259 (98%)	5 (2%)	0	100	100
1	P	264/548 (48%)	252 (96%)	12 (4%)	0	100	100
1	Q	264/548 (48%)	253 (96%)	11 (4%)	0	100	100
1	R	264/548 (48%)	254 (96%)	10 (4%)	0	100	100
1	S	266/548 (48%)	250 (94%)	16 (6%)	0	100	100
1	T	266/548 (48%)	253 (95%)	13 (5%)	0	100	100
1	U	266/548 (48%)	248 (93%)	18 (7%)	0	100	100
1	V	266/548 (48%)	257 (97%)	8 (3%)	1 (0%)	34	67
1	W	266/548 (48%)	255 (96%)	10 (4%)	1 (0%)	34	67
1	X	264/548 (48%)	255 (97%)	9 (3%)	0	100	100
1	Y	264/548 (48%)	260 (98%)	4 (2%)	0	100	100
1	Z	264/548 (48%)	254 (96%)	10 (4%)	0	100	100
1	a	264/548 (48%)	252 (96%)	12 (4%)	0	100	100
1	b	264/548 (48%)	258 (98%)	6 (2%)	0	100	100
1	c	266/548 (48%)	248 (93%)	18 (7%)	0	100	100
1	d	266/548 (48%)	255 (96%)	11 (4%)	0	100	100
1	e	266/548 (48%)	249 (94%)	17 (6%)	0	100	100
1	f	266/548 (48%)	255 (96%)	11 (4%)	0	100	100
1	g	266/548 (48%)	250 (94%)	15 (6%)	1 (0%)	34	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	8739/18084 (48%)	8370 (96%)	364 (4%)	5 (0%)	54	82

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	41	ALA
1	W	171	ASN
1	M	35	GLY
1	M	171	ASN
1	g	35	GLY

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	224/425 (53%)	223 (100%)	1 (0%)	91	95
1	B	224/425 (53%)	224 (100%)	0	100	100
1	C	224/425 (53%)	224 (100%)	0	100	100
1	D	226/425 (53%)	226 (100%)	0	100	100
1	E	226/425 (53%)	226 (100%)	0	100	100
1	F	226/425 (53%)	226 (100%)	0	100	100
1	G	226/425 (53%)	226 (100%)	0	100	100
1	H	226/425 (53%)	226 (100%)	0	100	100
1	I	227/425 (53%)	227 (100%)	0	100	100
1	J	227/425 (53%)	227 (100%)	0	100	100
1	K	227/425 (53%)	227 (100%)	0	100	100
1	L	227/425 (53%)	227 (100%)	0	100	100
1	M	227/425 (53%)	226 (100%)	1 (0%)	91	95
1	N	226/425 (53%)	226 (100%)	0	100	100
1	O	226/425 (53%)	226 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	226/425 (53%)	226 (100%)	0	100	100
1	Q	226/425 (53%)	226 (100%)	0	100	100
1	R	226/425 (53%)	226 (100%)	0	100	100
1	S	227/425 (53%)	226 (100%)	1 (0%)	91	95
1	T	227/425 (53%)	227 (100%)	0	100	100
1	U	227/425 (53%)	227 (100%)	0	100	100
1	V	227/425 (53%)	226 (100%)	1 (0%)	91	95
1	W	227/425 (53%)	226 (100%)	1 (0%)	91	95
1	X	226/425 (53%)	226 (100%)	0	100	100
1	Y	226/425 (53%)	226 (100%)	0	100	100
1	Z	226/425 (53%)	226 (100%)	0	100	100
1	a	226/425 (53%)	226 (100%)	0	100	100
1	b	226/425 (53%)	225 (100%)	1 (0%)	91	95
1	c	227/425 (53%)	227 (100%)	0	100	100
1	d	227/425 (53%)	227 (100%)	0	100	100
1	e	227/425 (53%)	227 (100%)	0	100	100
1	f	227/425 (53%)	227 (100%)	0	100	100
1	g	227/425 (53%)	226 (100%)	1 (0%)	91	95
All	All	7467/14025 (53%)	7460 (100%)	7 (0%)	93	98

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	V	93	ARG
1	M	53	ARG
1	g	53	ARG
1	W	53	ARG
1	S	53	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
1	b	537	GLN
1	V	526	GLN
1	J	22	GLN

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Mol	Chain	Res	Type
1	V	507	GLN
1	W	136	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.

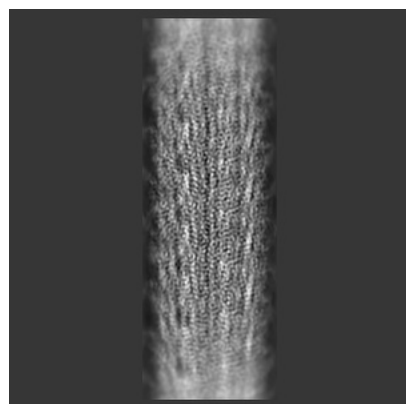
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27008. These allow visual inspection of the internal detail of the map and identification of artifacts.

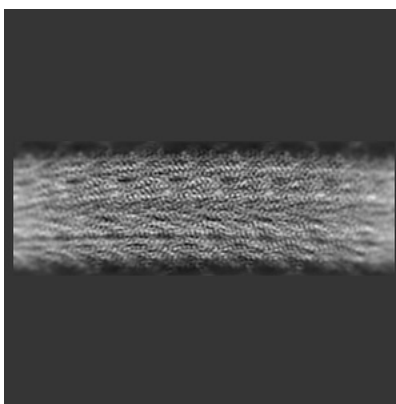
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

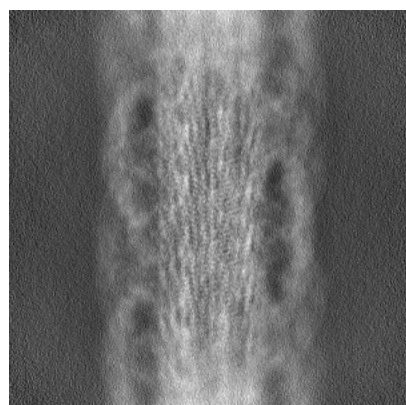


Y

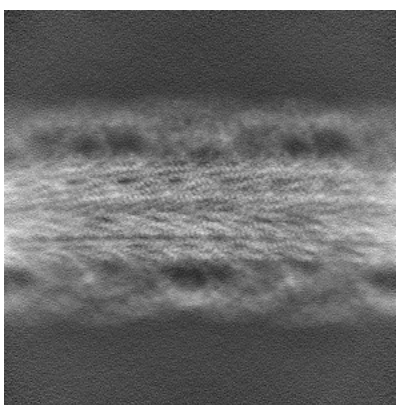


Z

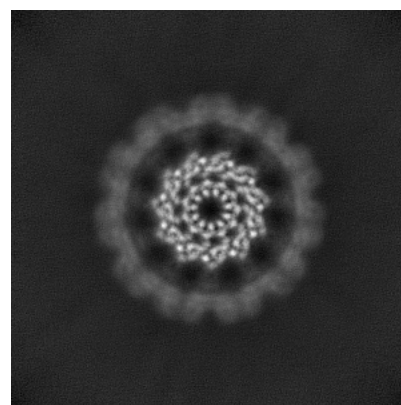
6.1.2 Raw map



X



Y

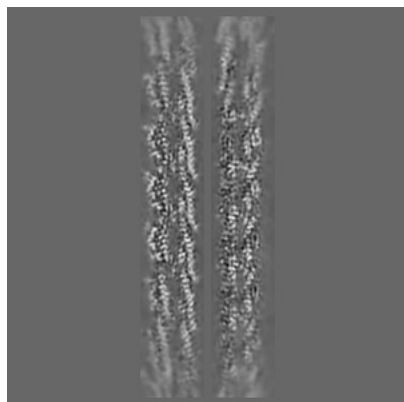


Z

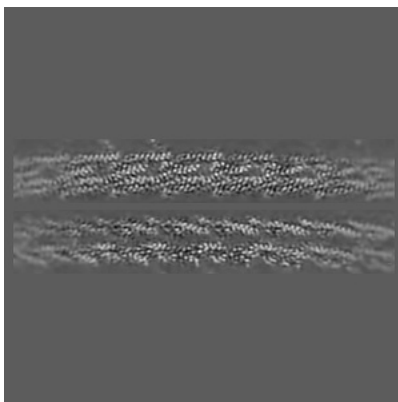
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

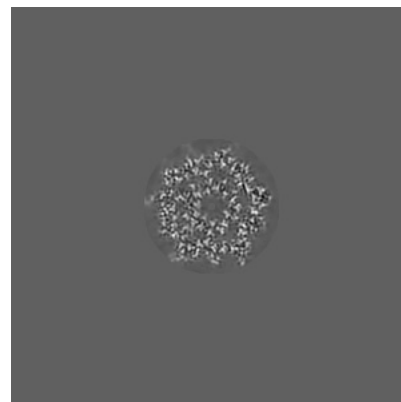
6.2.1 Primary map



X Index: 192

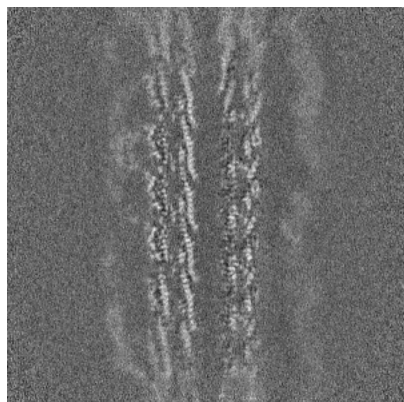


Y Index: 192

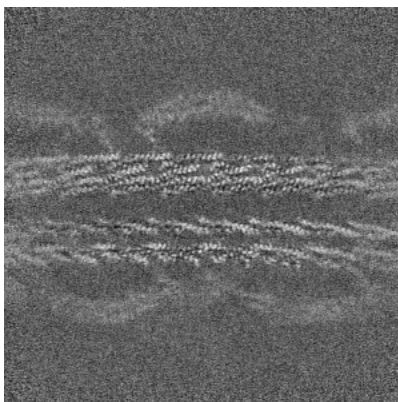


Z Index: 192

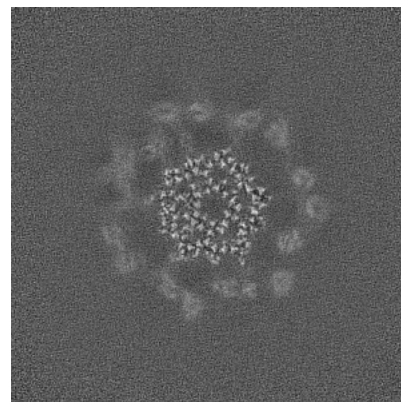
6.2.2 Raw map



X Index: 192



Y Index: 192

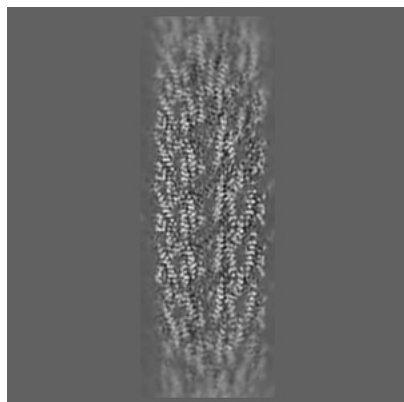


Z Index: 192

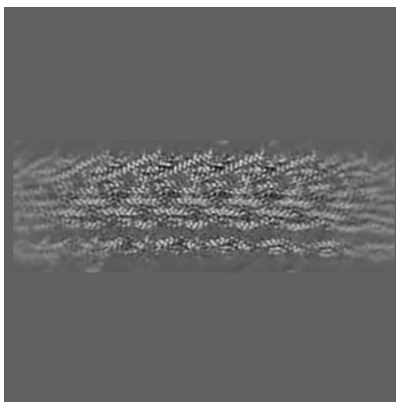
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

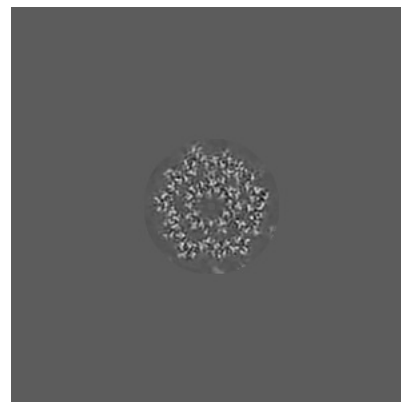
6.3.1 Primary map



X Index: 204

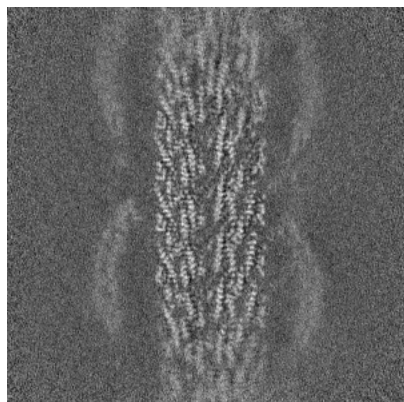


Y Index: 209

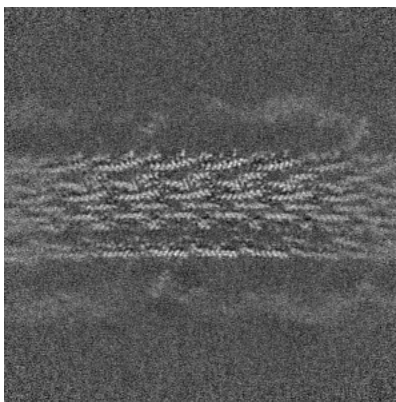


Z Index: 182

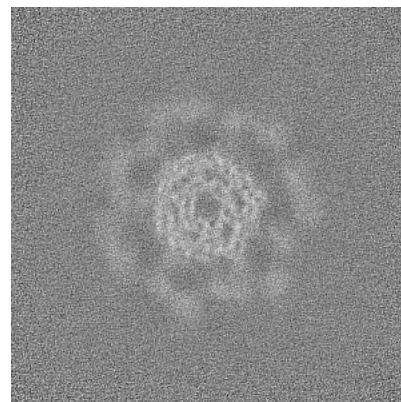
6.3.2 Raw map



X Index: 204



Y Index: 177

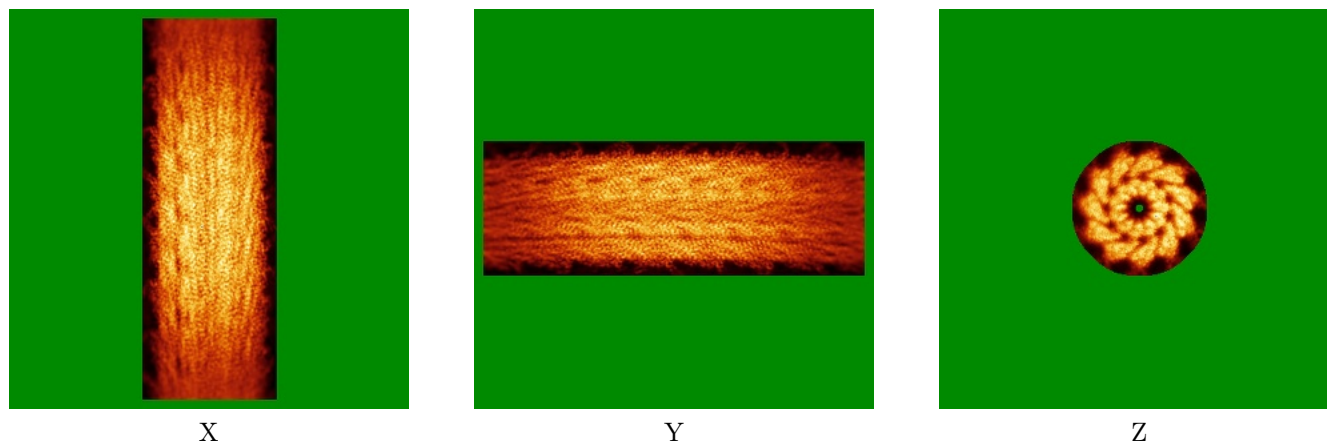


Z Index: 0

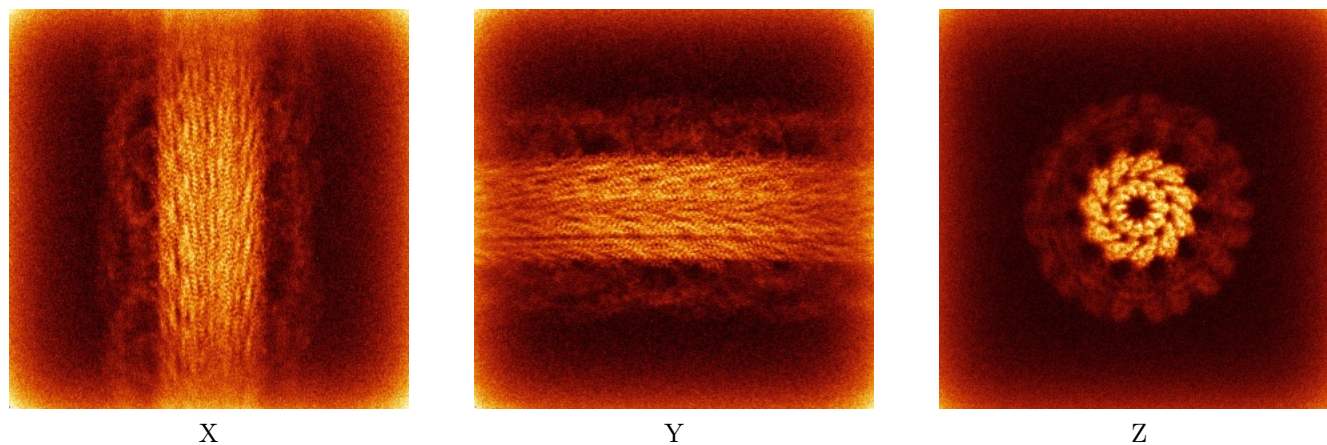
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



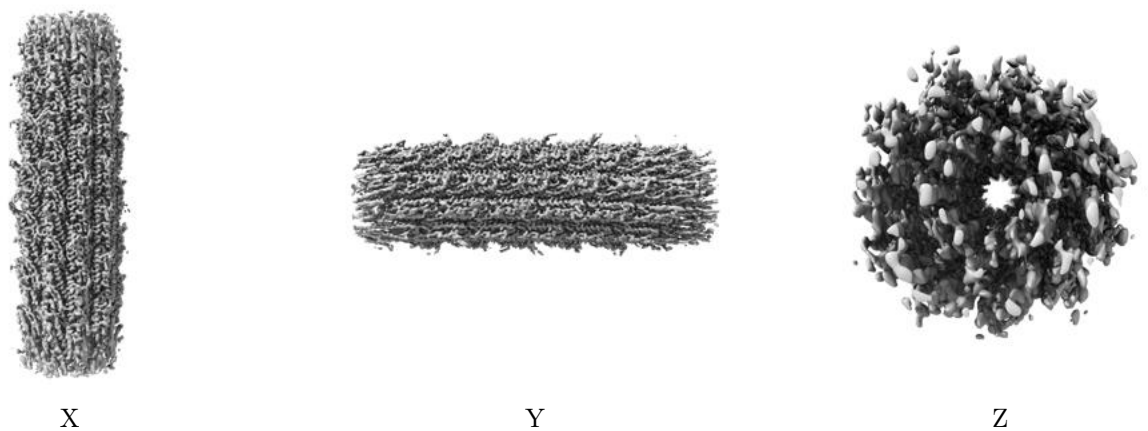
6.4.2 Raw map



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.

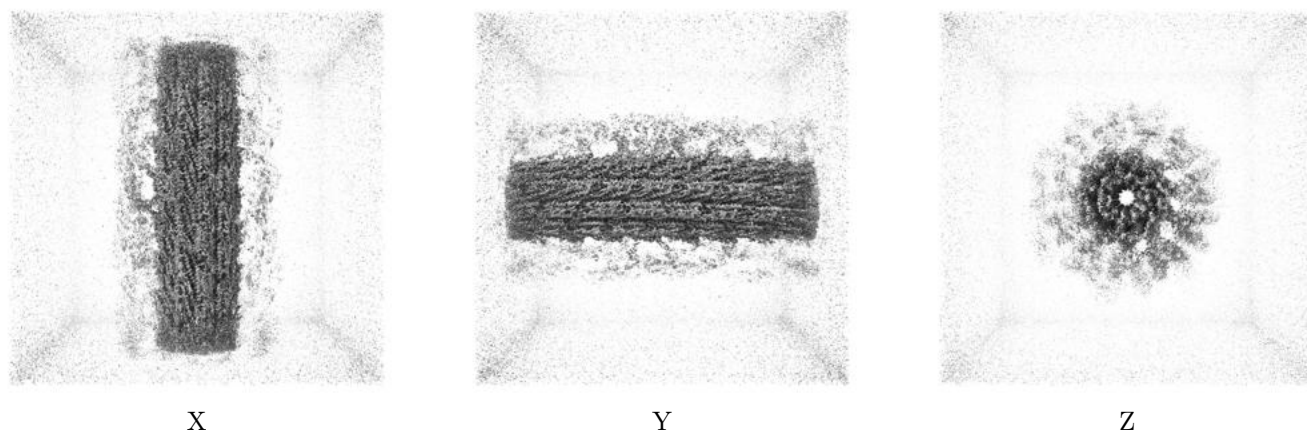
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.136. 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.

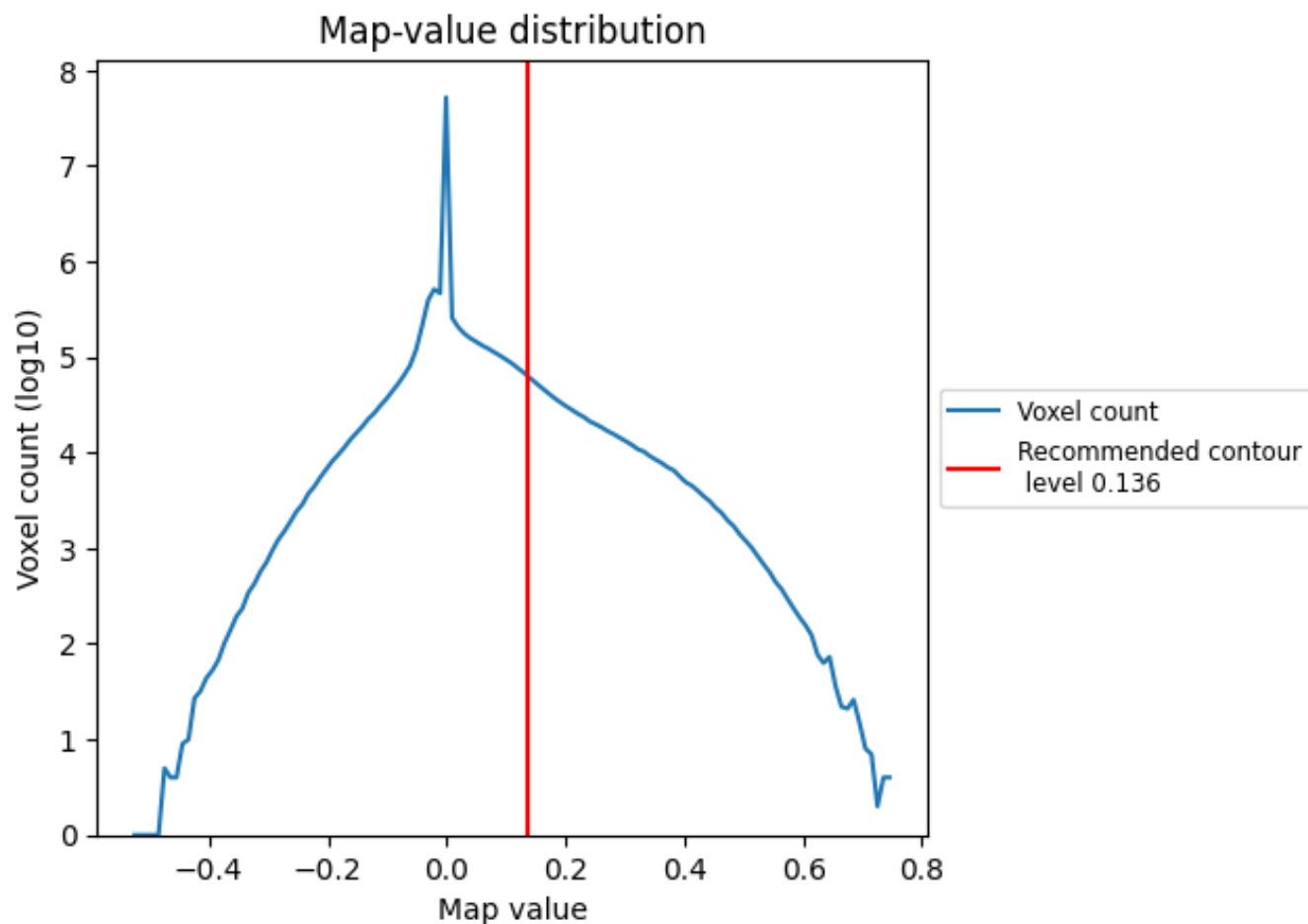
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

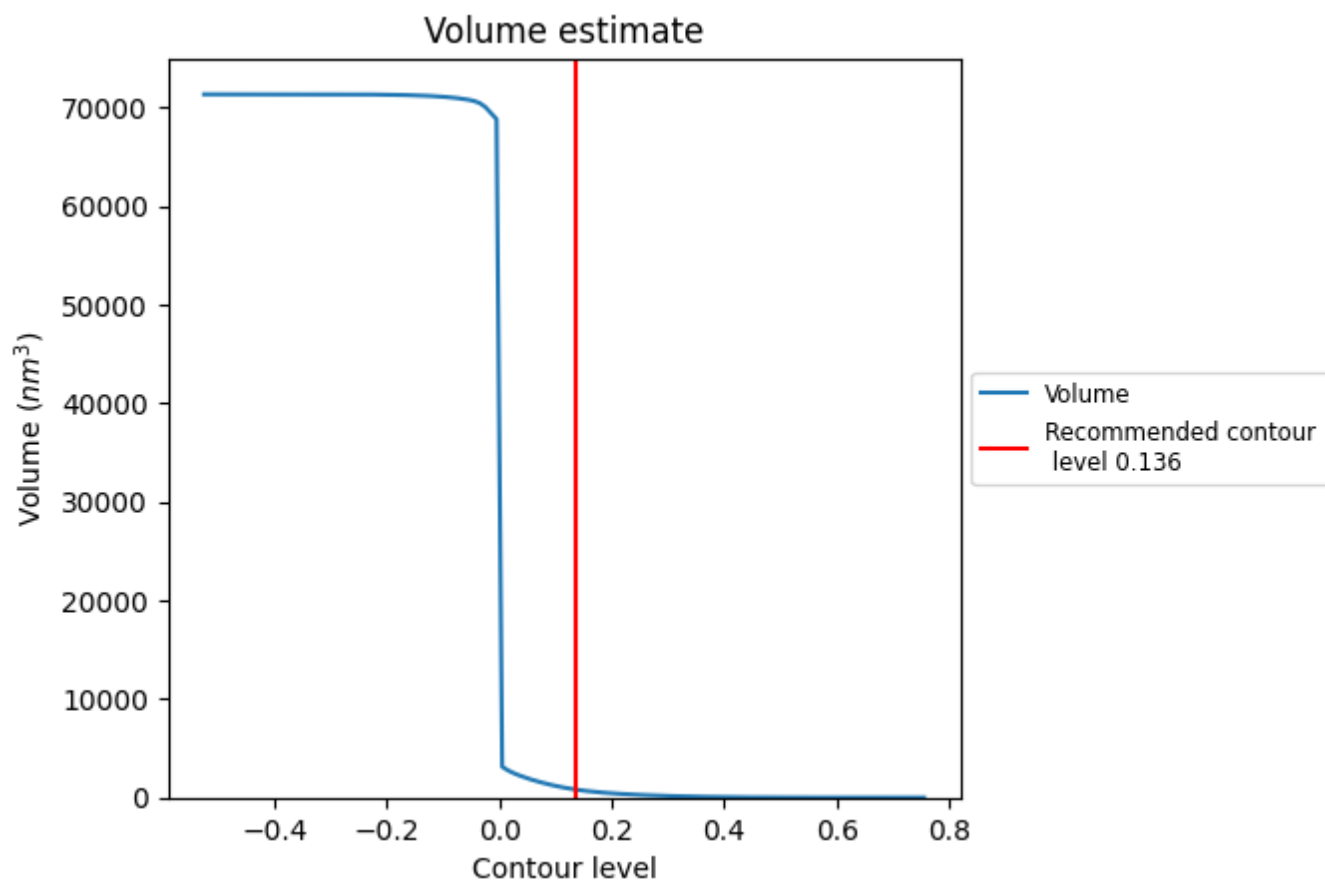
This section contains the results of statistical analysis of the map.

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.

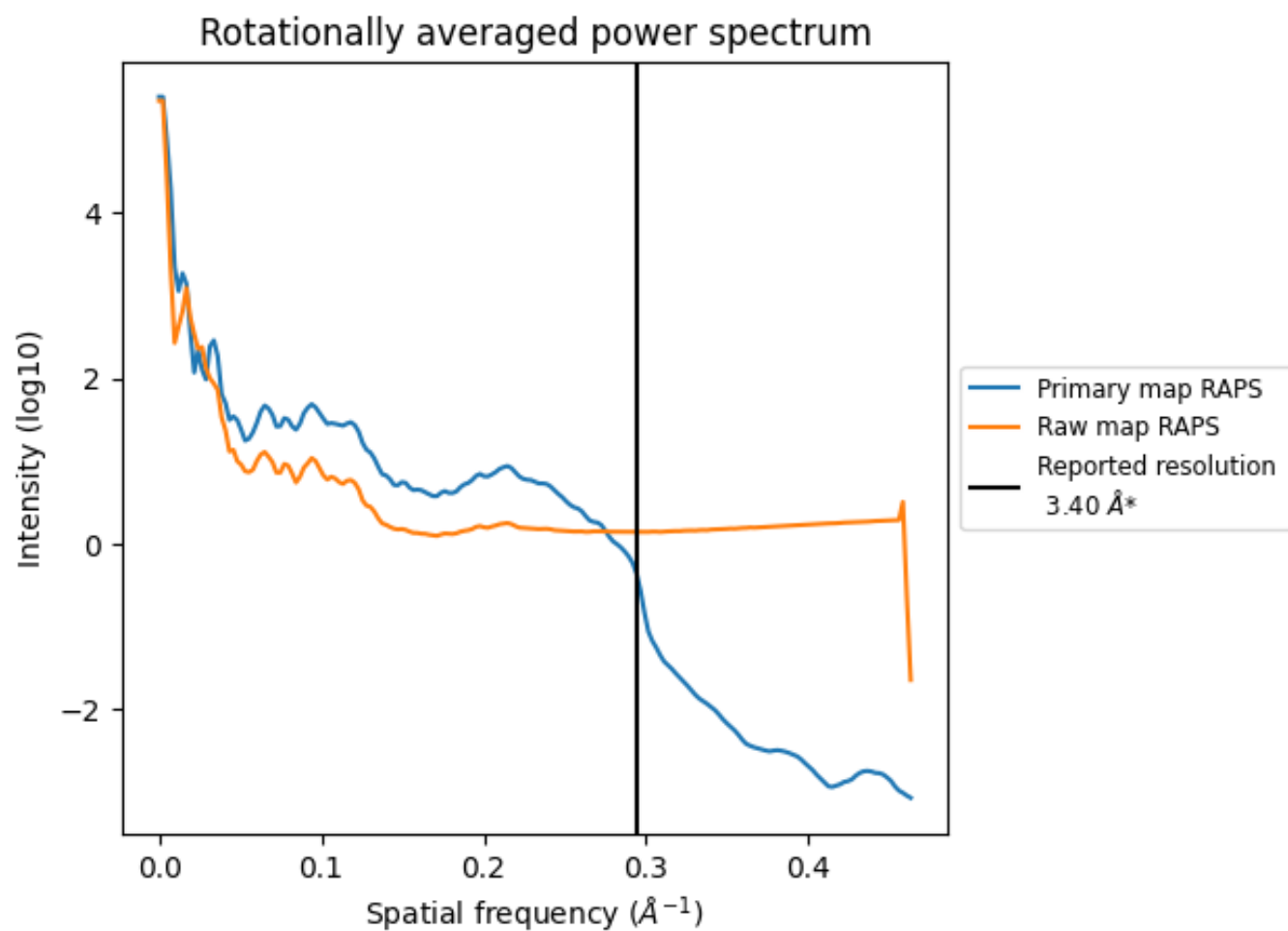
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 811 nm³; this corresponds to an approximate mass of 733 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 ⓘ

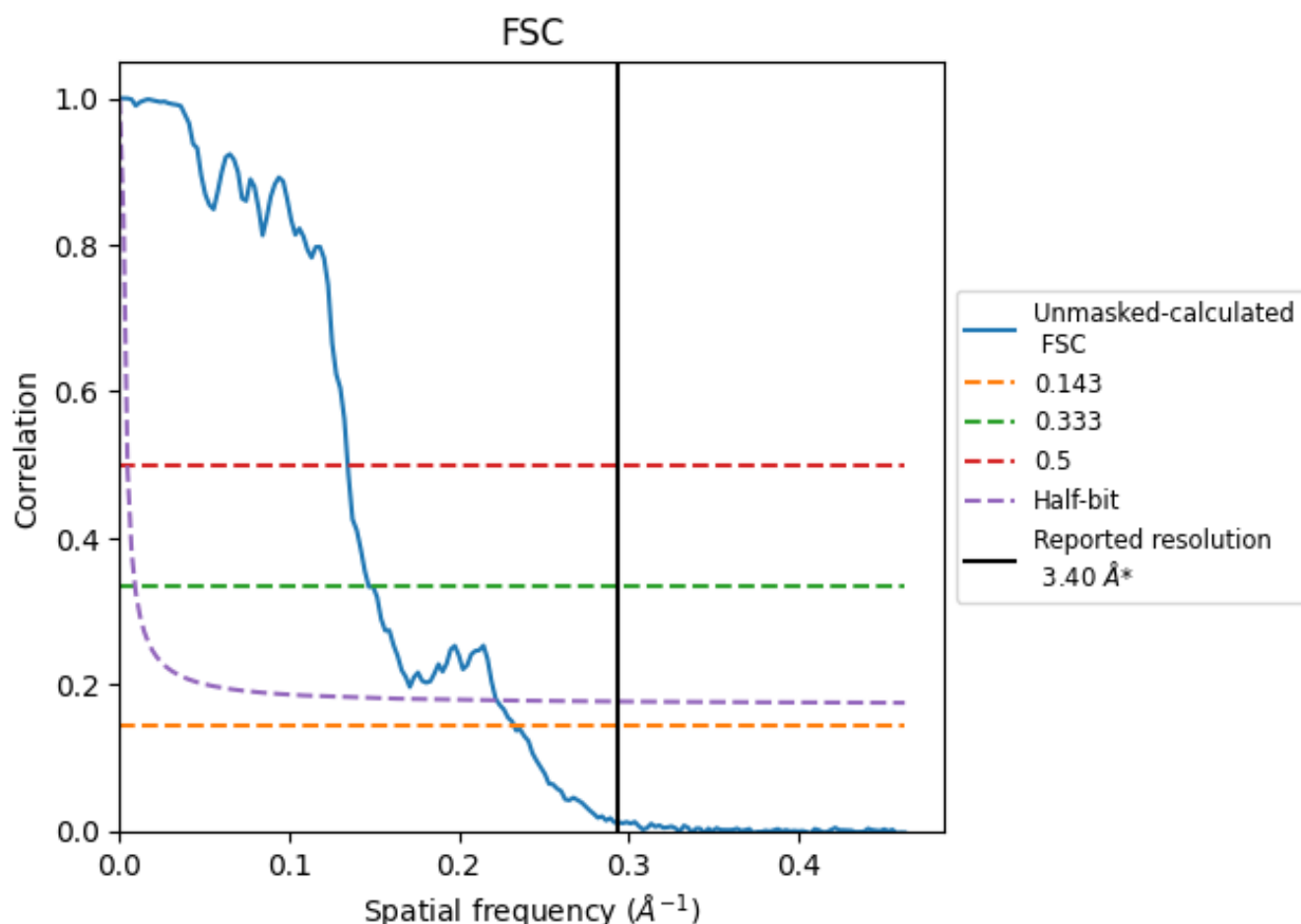


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

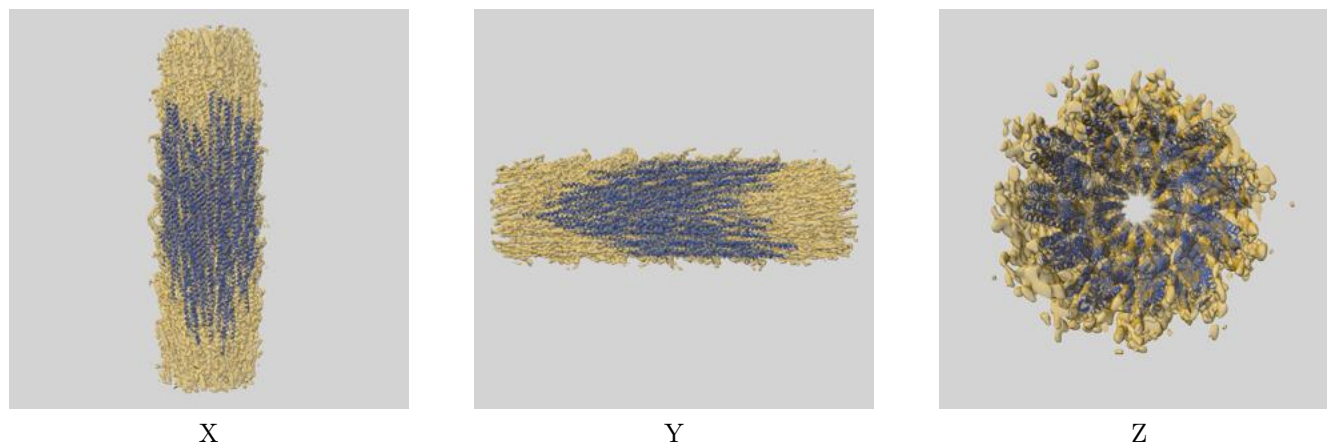
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	0.333
Reported by author	-	-	-	3.40
Author-provided FSC curve	-	-	-	-
Unmasked-calculated*	4.30	7.43	4.49	6.80

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.33 CUT-OFF 6.80 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

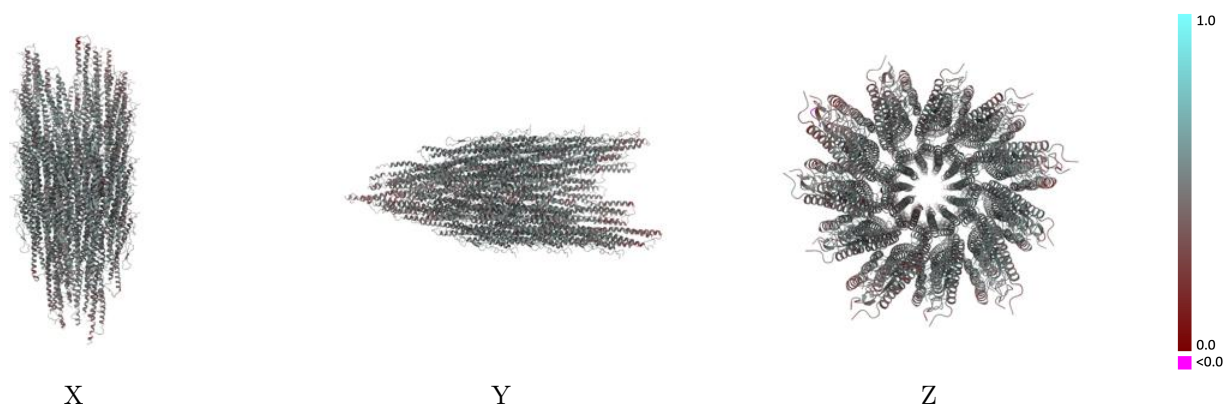
This section contains information regarding the fit between EMDB map EMD-27008 and PDB model 8CVI. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



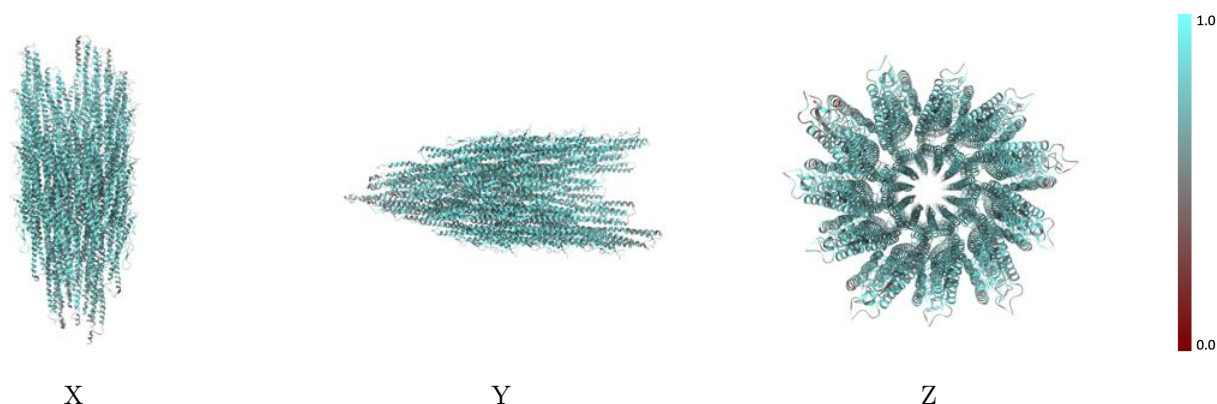
The images above show the 3D surface view of the map at the recommended contour level 0.136 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



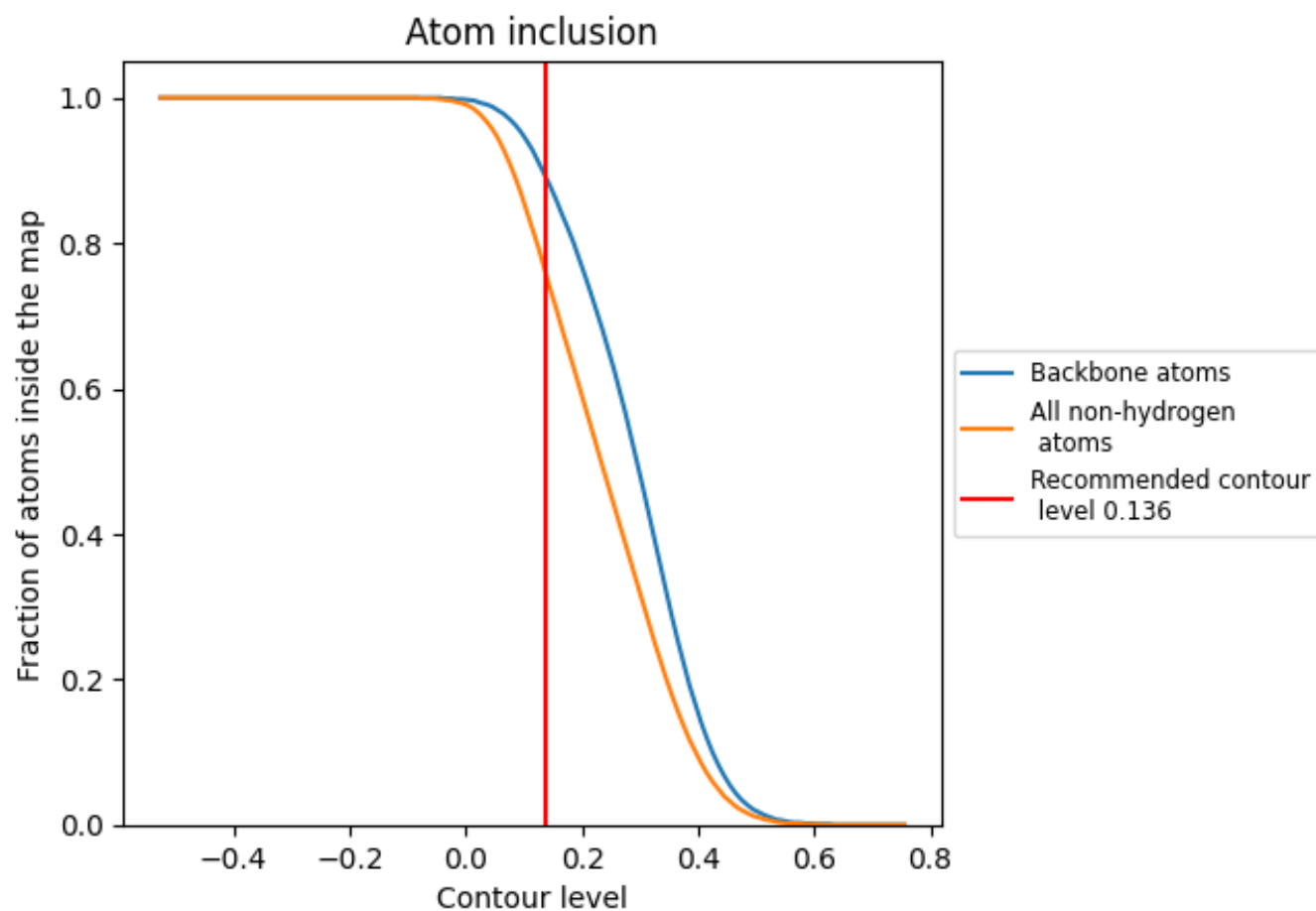
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.136).





































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 76% 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 (0.136) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7630	 0.4860
A	 0.7460	 0.4760
B	 0.7770	 0.4910
C	 0.7480	 0.4610
D	 0.7640	 0.4870
E	 0.7530	 0.4740
F	 0.7890	 0.5000
G	 0.7680	 0.4920
H	 0.7930	 0.5050
I	 0.7580	 0.4930
J	 0.6880	 0.4420
K	 0.7430	 0.4760
L	 0.7720	 0.4910
M	 0.7500	 0.4900
N	 0.7700	 0.4860
O	 0.7950	 0.5110
P	 0.8040	 0.5140
Q	 0.7930	 0.5110
R	 0.7910	 0.5070
S	 0.7790	 0.4960
T	 0.7720	 0.4940
U	 0.7830	 0.4970
V	 0.7540	 0.4850
W	 0.7720	 0.4920
X	 0.7230	 0.4520
Y	 0.7940	 0.5010
Z	 0.7620	 0.4980
a	 0.7910	 0.5050
b	 0.7490	 0.4740
c	 0.7520	 0.4690
d	 0.7690	 0.4760
e	 0.7430	 0.4700
f	 0.6950	 0.4500
g	 0.7390	 0.4630

