



wwPDB EM Validation Summary Report ⓘ

Jul 15, 2024 – 02:17 pm BST

PDB ID : 8B3P
EMDB ID : EMD-15832
Title : CryoEM structure of the round tip (proteins pVII/pVIII/pIX) from the filamentous bacteriophage
Authors : Conners, R.; McLaren, M.; Gold, V.A.M.
Deposited on : 2022-09-16
Resolution : 2.81 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:

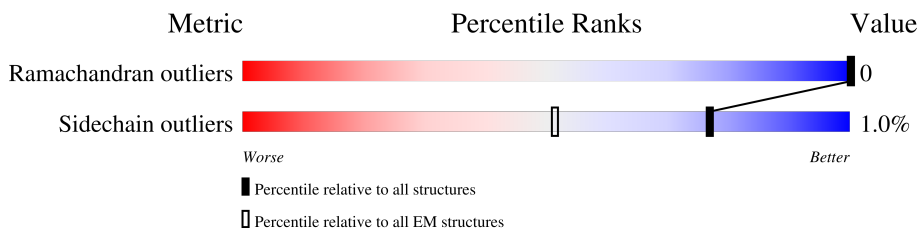
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.81 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.



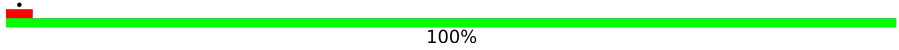

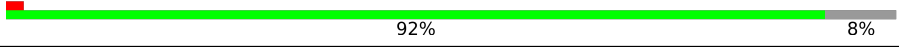
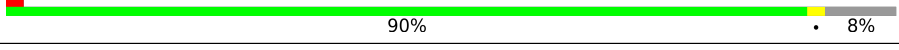
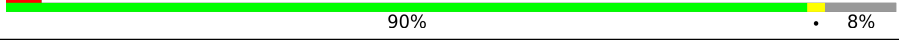

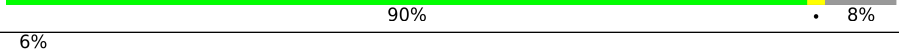
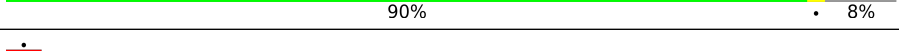
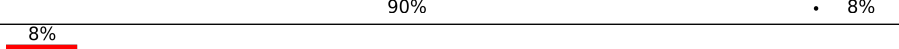
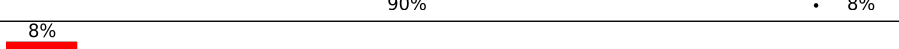
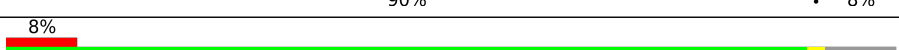

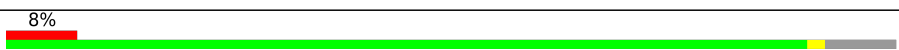
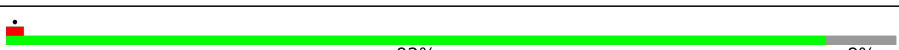
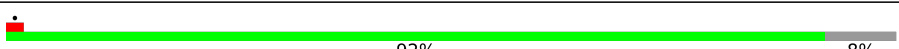



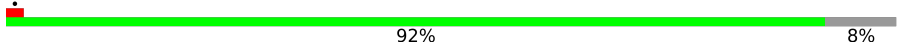
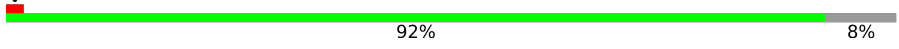
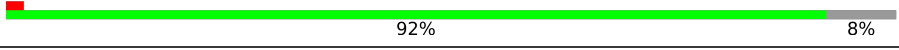
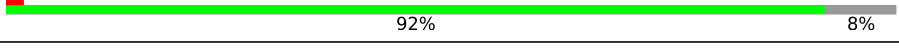
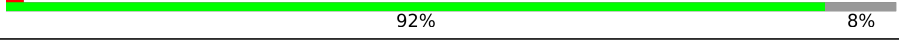
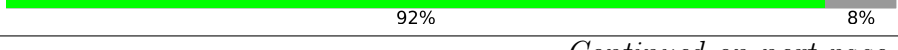

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	AAA	33	
1	BBB	33	
1	CCC	33	
1	DDD	33	
1	EEE	33	
2	FFF	32	
2	GGG	32	
2	HHH	32	
2	III	32	

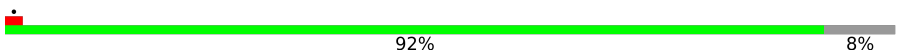
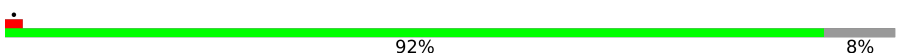

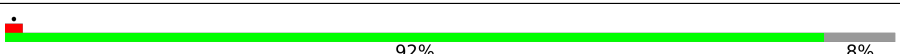
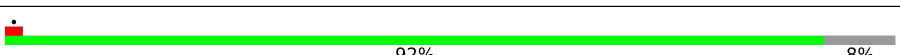
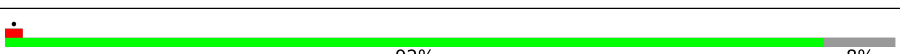
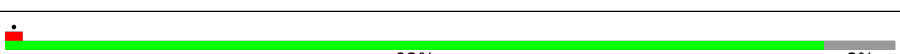
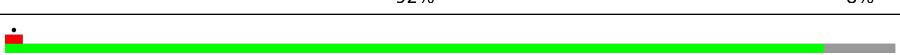
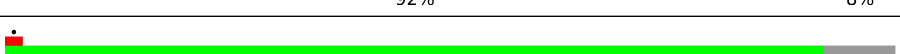
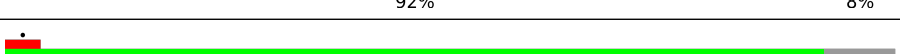
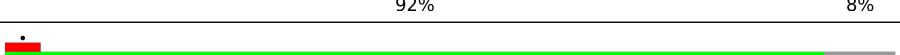
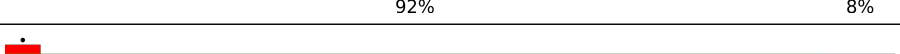
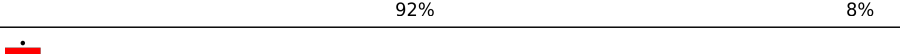
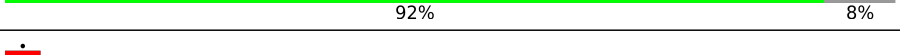
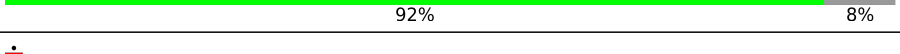
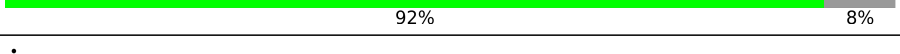
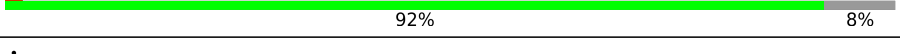
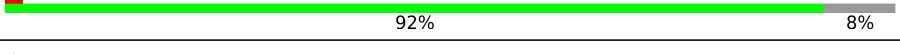
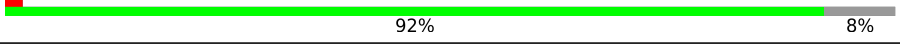
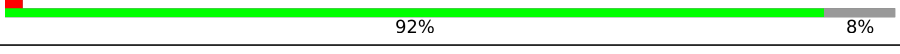
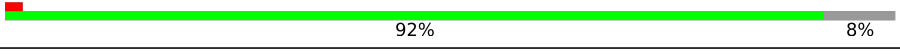
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Mol	Chain	Length	Quality of chain
2	JJJ	32	 100%
3	111	50	 90% 8%
3	222	50	 92% 8%
3	333	50	 90% 8%
3	KKK	50	 90% 8%
3	LLL	50	 90% 8%
3	MMM	50	 90% 8%
3	NNN	50	 90% 8%
3	OOO	50	 90% 8%
3	PPP	50	 90% 8%
3	QQQ	50	 90% 8%
3	RRR	50	 90% 8%
3	SSS	50	 90% 8%
3	TTT	50	 90% 8%
3	UUU	50	 92% 8%
3	VVV	50	 92% 8%
3	WWW	50	 92% 8%
3	XXX	50	 92% 8%
3	YYY	50	 92% 8%
3	ZZZ	50	 92% 8%
3	aaa	50	 92% 8%
3	bbb	50	 92% 8%
3	ccc	50	 92% 8%
3	ddd	50	 92% 8%
3	eee	50	 92% 8%

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Mol	Chain	Length	Quality of chain
3	fff	50	 92% 8%
3	ggg	50	 92% 8%
3	hhh	50	 92% 8%
3	iii	50	 92% 8%
3	jjj	50	 92% 8%
3	kkk	50	 92% 8%
3	lll	50	 92% 8%
3	mmm	50	 92% 8%
3	nnn	50	 92% 8%
3	ooo	50	 92% 8%
3	ppp	50	 92% 8%
3	qqq	50	 92% 8%
3	rrr	50	 92% 8%
3	sss	50	 92% 8%
3	ttt	50	 92% 8%
3	uuu	50	 92% 8%
3	vvv	50	 92% 8%
3	www	50	 92% 8%
3	xxx	50	 92% 8%
3	yyy	50	 92% 8%
3	zzz	50	 90% 8%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 17620 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 Tail virion protein G7P.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	AAA	28	212	138	34	38	2	0	0
1	BBB	28	212	138	34	38	2	0	0
1	CCC	28	212	138	34	38	2	0	0
1	DDD	28	212	138	34	38	2	0	0
1	EEE	28	212	138	34	38	2	0	0

- Molecule 2 is a protein called Tail virion protein G9P.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	FFF	32	255	168	39	45	3	0	0
2	GGG	32	255	168	39	45	3	0	0
2	HHH	32	255	168	39	45	3	0	0
2	III	32	255	168	39	45	3	0	0
2	JJJ	32	255	168	39	45	3	0	0

- Molecule 3 is a protein called Capsid protein G8P.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	KKK	46	339	223	53	61	2	0	0
3	PPP	46	339	223	53	61	2	0	0
3	UUU	46	339	223	53	61	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	ZZZ	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	eee	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	jjj	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	ooo	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	ttt	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	yyy	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	LLL	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	QQQ	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	VVV	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	aaa	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	fff	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	kkk	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	ppp	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	uuu	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	222	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	MMM	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	RRR	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	WWW	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	bbb	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	ggg	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	lll	46	Total	C	N	O	S	0	0
			340	223	53	62	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	qqq	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	vvv	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	111	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	NNN	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	SSS	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	XXX	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	ccc	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	hhh	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	mmm	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	rrr	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	www	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	zzz	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	OOO	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	TTT	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	YYY	46	Total	C	N	O	S	0	0
			339	223	53	61	2		
3	ddd	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	iii	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	nnn	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	sss	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	xxx	46	Total	C	N	O	S	0	0
			340	223	53	62	2		
3	333	46	Total	C	N	O	S	0	0
			340	223	53	62	2		

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
KKK	21	MET	TYR	engineered mutation	UNP P69540
PPP	21	MET	TYR	engineered mutation	UNP P69540
UUU	21	MET	TYR	engineered mutation	UNP P69540
ZZZ	21	MET	TYR	engineered mutation	UNP P69540
eee	21	MET	TYR	engineered mutation	UNP P69540
jjj	21	MET	TYR	engineered mutation	UNP P69540
ooo	21	MET	TYR	engineered mutation	UNP P69540
ttt	21	MET	TYR	engineered mutation	UNP P69540
yyy	21	MET	TYR	engineered mutation	UNP P69540
LLL	21	MET	TYR	engineered mutation	UNP P69540
QQQ	21	MET	TYR	engineered mutation	UNP P69540
VVV	21	MET	TYR	engineered mutation	UNP P69540
aaa	21	MET	TYR	engineered mutation	UNP P69540
fff	21	MET	TYR	engineered mutation	UNP P69540
kkk	21	MET	TYR	engineered mutation	UNP P69540
ppp	21	MET	TYR	engineered mutation	UNP P69540
uuu	21	MET	TYR	engineered mutation	UNP P69540
222	21	MET	TYR	engineered mutation	UNP P69540
MMM	21	MET	TYR	engineered mutation	UNP P69540
RRR	21	MET	TYR	engineered mutation	UNP P69540
WWW	21	MET	TYR	engineered mutation	UNP P69540
bbb	21	MET	TYR	engineered mutation	UNP P69540
ggg	21	MET	TYR	engineered mutation	UNP P69540
lll	21	MET	TYR	engineered mutation	UNP P69540
qqq	21	MET	TYR	engineered mutation	UNP P69540
vvv	21	MET	TYR	engineered mutation	UNP P69540
111	21	MET	TYR	engineered mutation	UNP P69540
NNN	21	MET	TYR	engineered mutation	UNP P69540
SSS	21	MET	TYR	engineered mutation	UNP P69540
XXX	21	MET	TYR	engineered mutation	UNP P69540
ccc	21	MET	TYR	engineered mutation	UNP P69540
hhh	21	MET	TYR	engineered mutation	UNP P69540
mmm	21	MET	TYR	engineered mutation	UNP P69540
rrr	21	MET	TYR	engineered mutation	UNP P69540
www	21	MET	TYR	engineered mutation	UNP P69540
zzz	21	MET	TYR	engineered mutation	UNP P69540
OOO	21	MET	TYR	engineered mutation	UNP P69540
TTT	21	MET	TYR	engineered mutation	UNP P69540
YYY	21	MET	TYR	engineered mutation	UNP P69540
ddd	21	MET	TYR	engineered mutation	UNP P69540
iii	21	MET	TYR	engineered mutation	UNP P69540
nnn	21	MET	TYR	engineered mutation	UNP P69540

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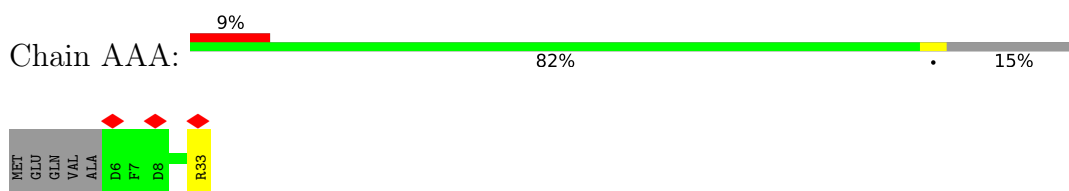
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Chain	Residue	Modelled	Actual	Comment	Reference
sss	21	MET	TYR	engineered mutation	UNP P69540
xxx	21	MET	TYR	engineered mutation	UNP P69540
333	21	MET	TYR	engineered mutation	UNP P69540

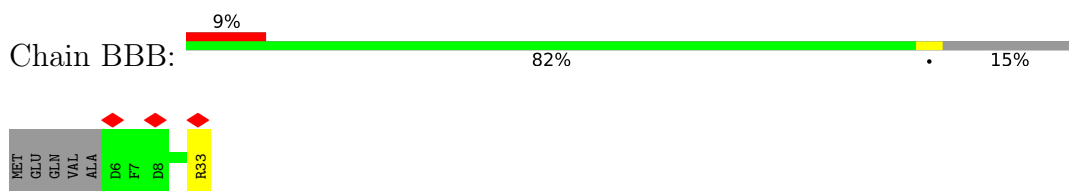
3 Residue-property plots [i](#)

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.

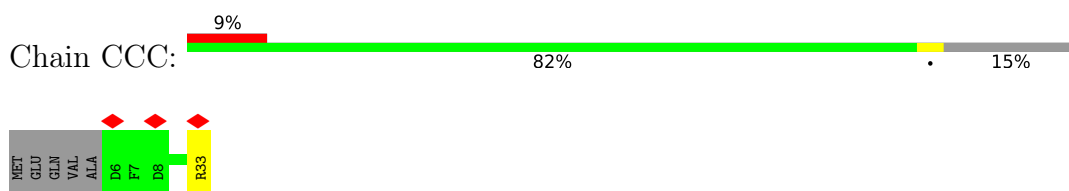
- Molecule 1: Tail virion protein G7P



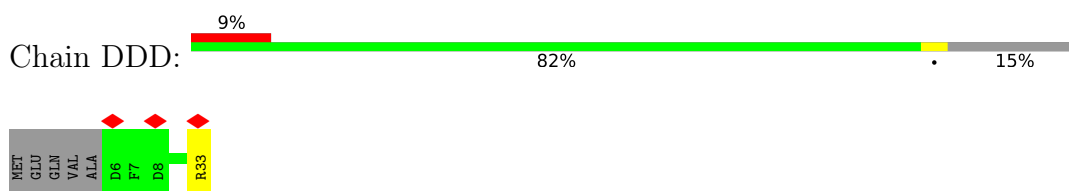
- Molecule 1: Tail virion protein G7P



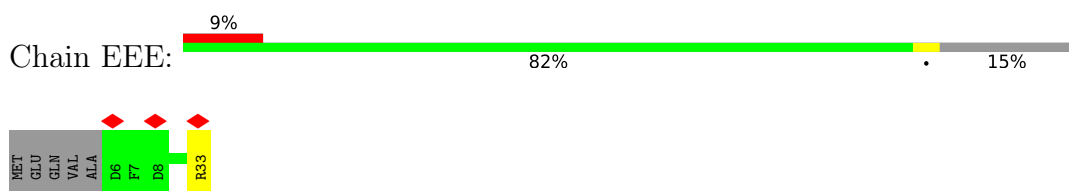
- Molecule 1: Tail virion protein G7P



- Molecule 1: Tail virion protein G7P



- Molecule 1: Tail virion protein G7P



- Molecule 2: Tail virion protein G9P



- Molecule 2: Tail virion protein G9P



- Molecule 2: Tail virion protein G9P



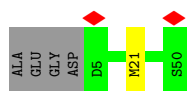
- Molecule 2: Tail virion protein G9P



- Molecule 2: Tail virion protein G9P

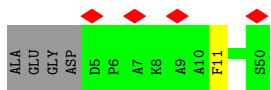


- Molecule 3: Capsid protein G8P

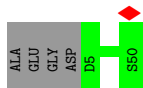


- Molecule 3: Capsid protein G8P

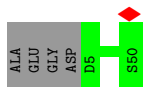




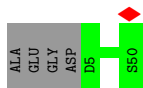
• Molecule 3: Capsid protein G8P



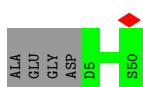
• Molecule 3: Capsid protein G8P



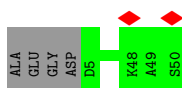
• Molecule 3: Capsid protein G8P



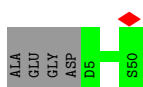
• Molecule 3: Capsid protein G8P



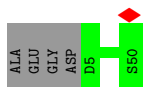
• Molecule 3: Capsid protein G8P



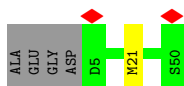
• Molecule 3: Capsid protein G8P



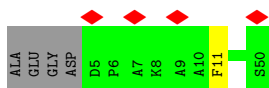
• Molecule 3: Capsid protein G8P



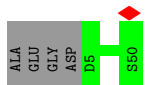
• Molecule 3: Capsid protein G8P



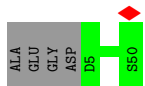
• Molecule 3: Capsid protein G8P



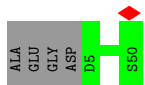
• Molecule 3: Capsid protein G8P



• Molecule 3: Capsid protein G8P

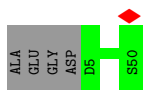


• Molecule 3: Capsid protein G8P

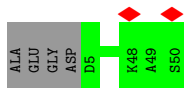


• Molecule 3: Capsid protein G8P

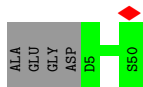




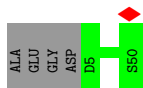
- Molecule 3: Capsid protein G8P



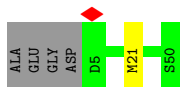
- Molecule 3: Capsid protein G8P



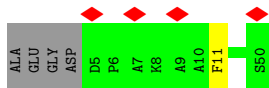
- Molecule 3: Capsid protein G8P



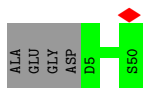
- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P



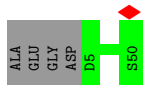
- Molecule 3: Capsid protein G8P



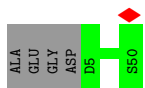
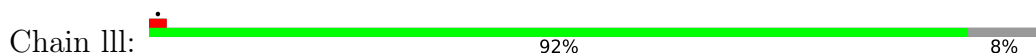
- Molecule 3: Capsid protein G8P



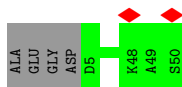
- Molecule 3: Capsid protein G8P



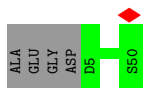
- Molecule 3: Capsid protein G8P



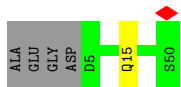
- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P

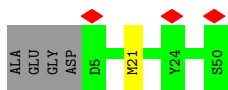


- Molecule 3: Capsid protein G8P

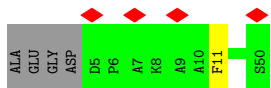
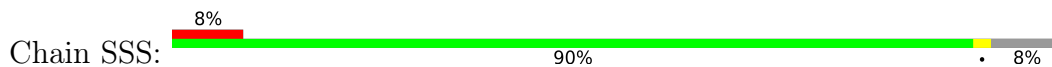


- Molecule 3: Capsid protein G8P

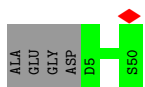




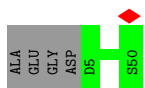
- Molecule 3: Capsid protein G8P



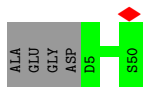
- Molecule 3: Capsid protein G8P



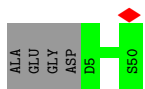
- Molecule 3: Capsid protein G8P



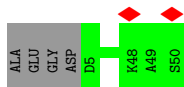
- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P

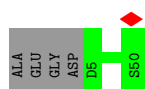


- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P

Chain www:  92% 8%



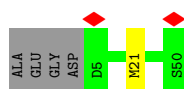
- Molecule 3: Capsid protein G8P

Chain zzz:  90% 8%



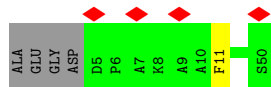
- Molecule 3: Capsid protein G8P

Chain OOO:  90% 8%



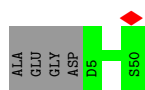
- Molecule 3: Capsid protein G8P

Chain TTT:  90% 8%



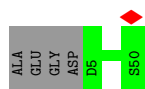
- Molecule 3: Capsid protein G8P

Chain YYY:  92% 8%



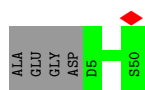
- Molecule 3: Capsid protein G8P

Chain ddd:  92% 8%

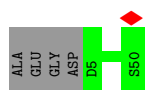


- Molecule 3: Capsid protein G8P

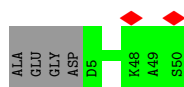
Chain iii:  92% 8%



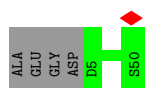
- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P



- Molecule 3: Capsid protein G8P



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	255372	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.838	Depositor
Minimum map value	-0.236	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	422.86078, 422.86078, 422.86078	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1012, 1.1012, 1.1012	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	AAA	0.31	0/214	0.56	0/288
1	BBB	0.31	0/214	0.56	0/288
1	CCC	0.31	0/214	0.56	0/288
1	DDD	0.31	0/214	0.57	0/288
1	EEE	0.31	0/214	0.56	0/288
2	FFF	0.36	0/261	0.58	0/352
2	GGG	0.36	0/261	0.58	0/352
2	HHH	0.36	0/261	0.58	0/352
2	III	0.36	0/261	0.58	0/352
2	JJJ	0.36	0/261	0.58	0/352
3	111	0.30	0/346	0.64	0/465
3	222	0.31	0/346	0.64	0/465
3	333	0.31	0/346	0.64	0/465
3	KKK	0.33	0/345	0.64	0/465
3	LLL	0.33	0/345	0.64	0/465
3	MMM	0.32	0/345	0.64	0/465
3	NNN	0.32	0/345	0.63	0/465
3	OOO	0.33	0/345	0.63	0/465
3	PPP	0.32	0/345	0.64	0/465
3	QQQ	0.32	0/345	0.64	0/465
3	RRR	0.32	0/345	0.64	0/465
3	SSS	0.32	0/345	0.64	0/465
3	TTT	0.32	0/345	0.64	0/465
3	UUU	0.32	0/345	0.64	0/465
3	VVV	0.32	0/345	0.64	0/465
3	WWW	0.32	0/345	0.64	0/465
3	XXX	0.32	0/345	0.64	0/465
3	YYY	0.32	0/345	0.64	0/465
3	ZZZ	0.32	0/346	0.63	0/465
3	aaa	0.32	0/346	0.63	0/465
3	bbb	0.32	0/346	0.63	0/465
3	ccc	0.32	0/346	0.63	0/465
3	ddd	0.32	0/346	0.64	0/465
3	eee	0.33	0/346	0.63	0/465

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	fff	0.32	0/346	0.63	0/465
3	ggg	0.33	0/346	0.62	0/465
3	hhh	0.32	0/346	0.62	0/465
3	iii	0.32	0/346	0.63	0/465
3	jjj	0.32	0/346	0.61	0/465
3	kkk	0.32	0/346	0.61	0/465
3	lll	0.32	0/346	0.61	0/465
3	mmm	0.32	0/346	0.61	0/465
3	nnn	0.32	0/346	0.61	0/465
3	ooo	0.31	0/346	0.60	0/465
3	ppp	0.31	0/346	0.59	0/465
3	qqq	0.31	0/346	0.59	0/465
3	rrr	0.31	0/346	0.59	0/465
3	sss	0.31	0/346	0.59	0/465
3	ttt	0.31	0/346	0.62	0/465
3	uuu	0.31	0/346	0.62	0/465
3	vvv	0.31	0/346	0.62	0/465
3	www	0.31	0/346	0.62	0/465
3	xxx	0.31	0/346	0.62	0/465
3	yyy	0.31	0/346	0.64	0/465
3	zzz	0.31	0/346	0.64	0/465
All	All	0.32	0/17930	0.62	0/24125

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	AAA	26/33 (79%)	26 (100%)	0	0	100	100
1	BBB	26/33 (79%)	26 (100%)	0	0	100	100
1	CCC	26/33 (79%)	26 (100%)	0	0	100	100
1	DDD	26/33 (79%)	26 (100%)	0	0	100	100
1	EEE	26/33 (79%)	26 (100%)	0	0	100	100
2	FFF	30/32 (94%)	30 (100%)	0	0	100	100
2	GGG	30/32 (94%)	30 (100%)	0	0	100	100
2	HHH	30/32 (94%)	30 (100%)	0	0	100	100
2	III	30/32 (94%)	30 (100%)	0	0	100	100
2	JJJ	30/32 (94%)	30 (100%)	0	0	100	100
3	111	44/50 (88%)	44 (100%)	0	0	100	100
3	222	44/50 (88%)	44 (100%)	0	0	100	100
3	333	44/50 (88%)	44 (100%)	0	0	100	100
3	KKK	44/50 (88%)	44 (100%)	0	0	100	100
3	LLL	44/50 (88%)	44 (100%)	0	0	100	100
3	MMM	44/50 (88%)	44 (100%)	0	0	100	100
3	NNN	44/50 (88%)	44 (100%)	0	0	100	100
3	OOO	44/50 (88%)	44 (100%)	0	0	100	100
3	PPP	44/50 (88%)	44 (100%)	0	0	100	100
3	QQQ	44/50 (88%)	44 (100%)	0	0	100	100
3	RRR	44/50 (88%)	44 (100%)	0	0	100	100
3	SSS	44/50 (88%)	44 (100%)	0	0	100	100
3	TTT	44/50 (88%)	44 (100%)	0	0	100	100
3	UUU	44/50 (88%)	44 (100%)	0	0	100	100
3	VVV	44/50 (88%)	44 (100%)	0	0	100	100
3	WWW	44/50 (88%)	44 (100%)	0	0	100	100
3	XXX	44/50 (88%)	44 (100%)	0	0	100	100
3	YYY	44/50 (88%)	44 (100%)	0	0	100	100
3	ZZZ	44/50 (88%)	44 (100%)	0	0	100	100
3	aaa	44/50 (88%)	44 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	bbb	44/50 (88%)	44 (100%)	0	0	100	100
3	ccc	44/50 (88%)	44 (100%)	0	0	100	100
3	ddd	44/50 (88%)	44 (100%)	0	0	100	100
3	eee	44/50 (88%)	44 (100%)	0	0	100	100
3	fff	44/50 (88%)	44 (100%)	0	0	100	100
3	ggg	44/50 (88%)	44 (100%)	0	0	100	100
3	hhh	44/50 (88%)	44 (100%)	0	0	100	100
3	iii	44/50 (88%)	44 (100%)	0	0	100	100
3	jjj	44/50 (88%)	44 (100%)	0	0	100	100
3	kkk	44/50 (88%)	44 (100%)	0	0	100	100
3	lll	44/50 (88%)	44 (100%)	0	0	100	100
3	mmm	44/50 (88%)	44 (100%)	0	0	100	100
3	nnn	44/50 (88%)	44 (100%)	0	0	100	100
3	ooo	44/50 (88%)	44 (100%)	0	0	100	100
3	ppp	44/50 (88%)	44 (100%)	0	0	100	100
3	qqq	44/50 (88%)	44 (100%)	0	0	100	100
3	rrr	44/50 (88%)	44 (100%)	0	0	100	100
3	sss	44/50 (88%)	44 (100%)	0	0	100	100
3	ttt	44/50 (88%)	44 (100%)	0	0	100	100
3	uuu	44/50 (88%)	44 (100%)	0	0	100	100
3	vvv	44/50 (88%)	44 (100%)	0	0	100	100
3	www	44/50 (88%)	44 (100%)	0	0	100	100
3	xxx	44/50 (88%)	44 (100%)	0	0	100	100
3	yyy	44/50 (88%)	44 (100%)	0	0	100	100
3	zzz	44/50 (88%)	44 (100%)	0	0	100	100
All	All	2260/2575 (88%)	2260 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	AAA	22/26 (85%)	21 (96%)	1 (4%)	27	59
1	BBB	22/26 (85%)	21 (96%)	1 (4%)	27	59
1	CCC	22/26 (85%)	21 (96%)	1 (4%)	27	59
1	DDD	22/26 (85%)	21 (96%)	1 (4%)	27	59
1	EEE	22/26 (85%)	21 (96%)	1 (4%)	27	59
2	FFF	29/29 (100%)	29 (100%)	0	100	100
2	GGG	29/29 (100%)	29 (100%)	0	100	100
2	HHH	29/29 (100%)	29 (100%)	0	100	100
2	III	29/29 (100%)	29 (100%)	0	100	100
2	JJJ	29/29 (100%)	29 (100%)	0	100	100
3	111	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	222	34/36 (94%)	34 (100%)	0	100	100
3	333	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	KKK	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	LLL	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	MMM	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	NNN	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	OOO	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	PPP	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	QQQ	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	RRR	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	SSS	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	TTT	34/36 (94%)	33 (97%)	1 (3%)	42	74
3	UUU	34/36 (94%)	34 (100%)	0	100	100
3	VVV	34/36 (94%)	34 (100%)	0	100	100
3	WWW	34/36 (94%)	34 (100%)	0	100	100
3	XXX	34/36 (94%)	34 (100%)	0	100	100
3	YYY	34/36 (94%)	34 (100%)	0	100	100
3	ZZZ	34/36 (94%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	aaa	34/36 (94%)	34 (100%)	0	100	100
3	bbb	34/36 (94%)	34 (100%)	0	100	100
3	ccc	34/36 (94%)	34 (100%)	0	100	100
3	ddd	34/36 (94%)	34 (100%)	0	100	100
3	eee	34/36 (94%)	34 (100%)	0	100	100
3	fff	34/36 (94%)	34 (100%)	0	100	100
3	ggg	34/36 (94%)	34 (100%)	0	100	100
3	hhh	34/36 (94%)	34 (100%)	0	100	100
3	iii	34/36 (94%)	34 (100%)	0	100	100
3	jjj	34/36 (94%)	34 (100%)	0	100	100
3	kkk	34/36 (94%)	34 (100%)	0	100	100
3	lll	34/36 (94%)	34 (100%)	0	100	100
3	mmm	34/36 (94%)	34 (100%)	0	100	100
3	nnn	34/36 (94%)	34 (100%)	0	100	100
3	ooo	34/36 (94%)	34 (100%)	0	100	100
3	ppp	34/36 (94%)	34 (100%)	0	100	100
3	qqq	34/36 (94%)	34 (100%)	0	100	100
3	rrr	34/36 (94%)	34 (100%)	0	100	100
3	sss	34/36 (94%)	34 (100%)	0	100	100
3	ttt	34/36 (94%)	34 (100%)	0	100	100
3	uuu	34/36 (94%)	34 (100%)	0	100	100
3	vvv	34/36 (94%)	34 (100%)	0	100	100
3	www	34/36 (94%)	34 (100%)	0	100	100
3	xxx	34/36 (94%)	34 (100%)	0	100	100
3	yyy	34/36 (94%)	34 (100%)	0	100	100
3	zzz	34/36 (94%)	33 (97%)	1 (3%)	42	74
All	All	1785/1895 (94%)	1767 (99%)	18 (1%)	77	92

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	EEE	33	ARG
3	333	15	GLN

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Mol	Chain	Res	Type
3	TTT	11	PHE
3	RRR	11	PHE
3	zzz	15	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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.

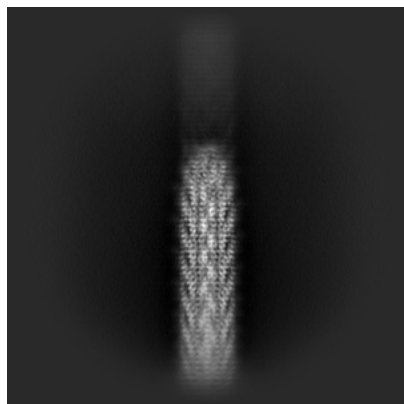
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15832. These allow visual inspection of the internal detail of the map and identification of artifacts.

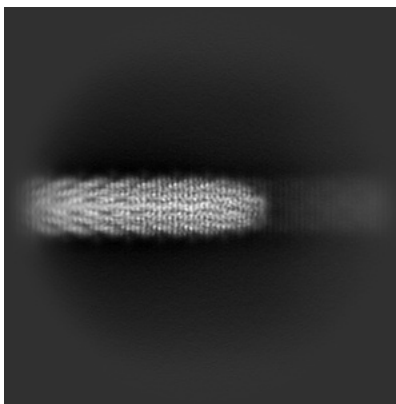
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

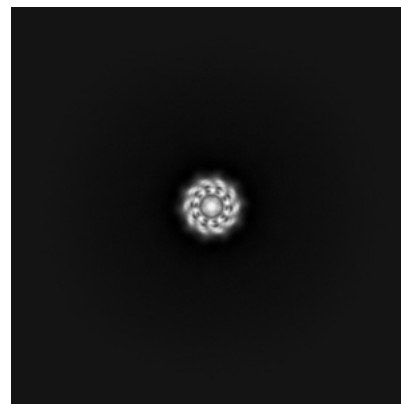
6.1.1 Primary map



X

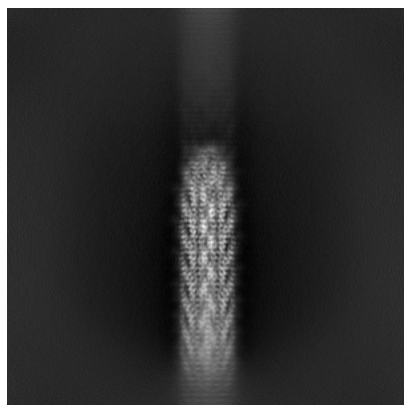


Y

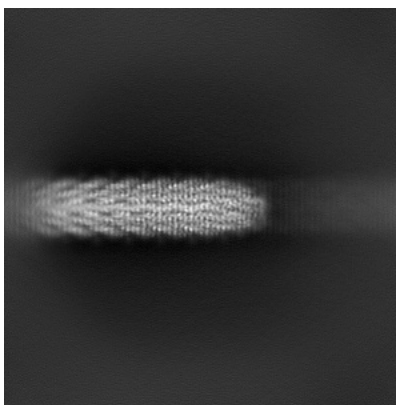


Z

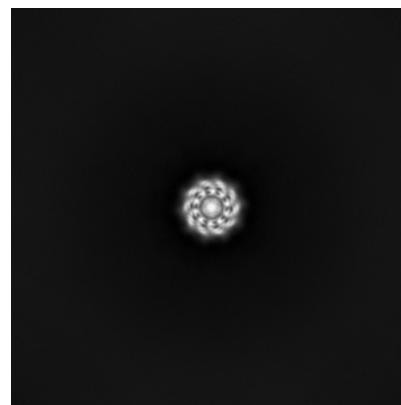
6.1.2 Raw map



X



Y

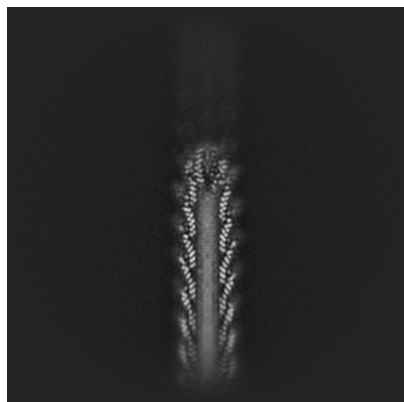


Z

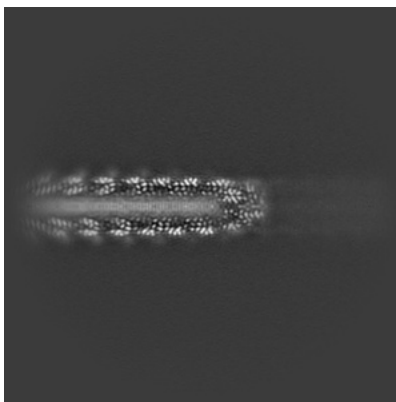
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

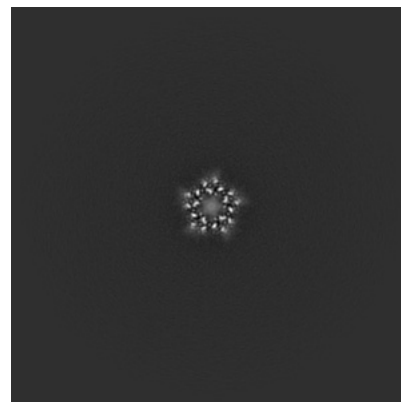
6.2.1 Primary map



X Index: 192

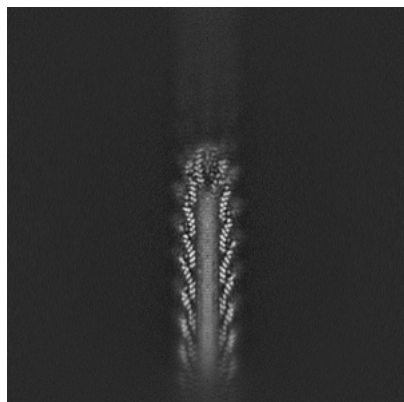


Y Index: 192

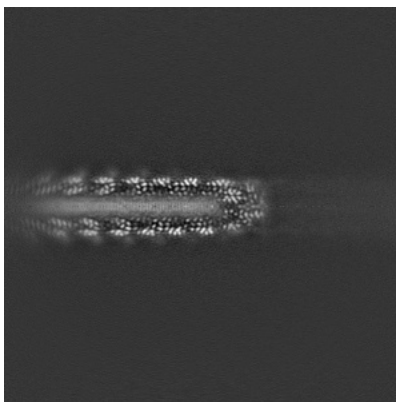


Z Index: 192

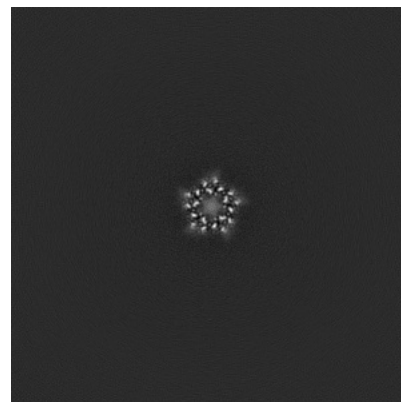
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

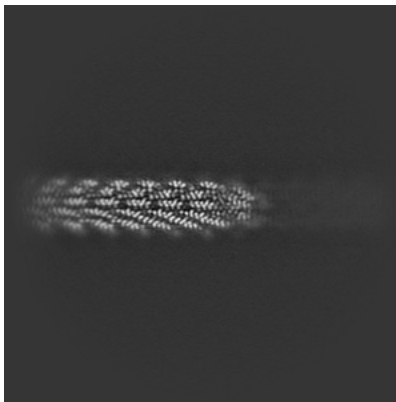
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

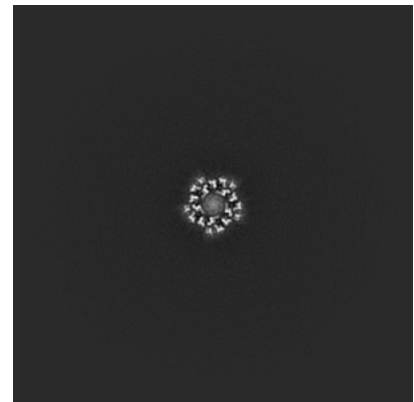
6.3.1 Primary map



X Index: 192

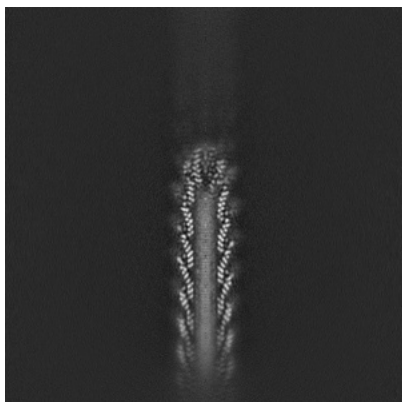


Y Index: 207

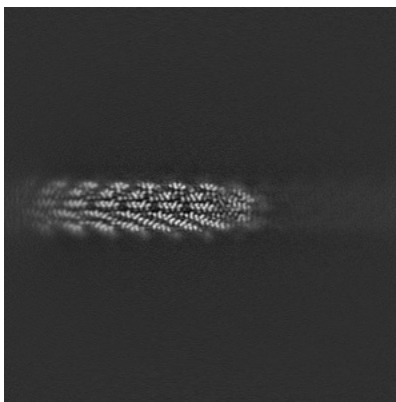


Z Index: 174

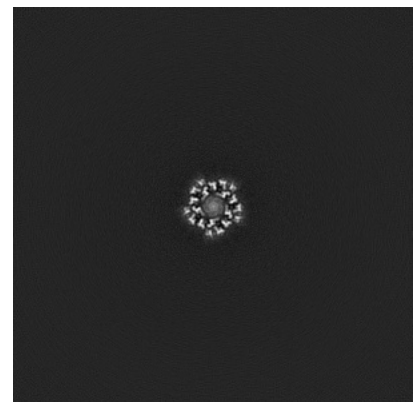
6.3.2 Raw map



X Index: 192



Y Index: 207

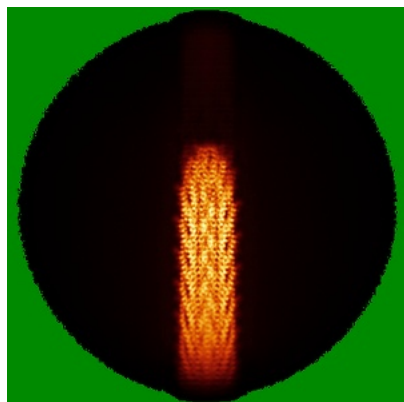


Z Index: 174

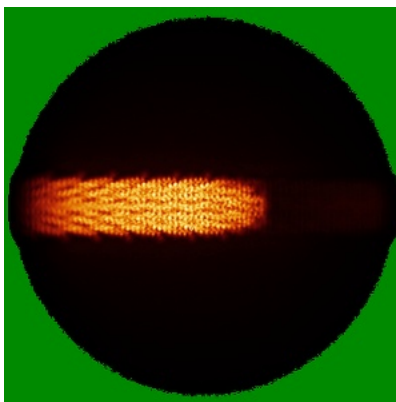
The images above show the largest variance slices of the map in three orthogonal directions.

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

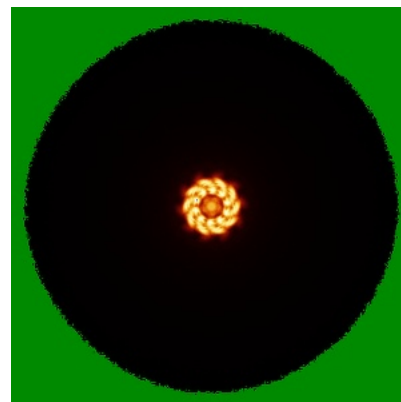
6.4.1 Primary map



X

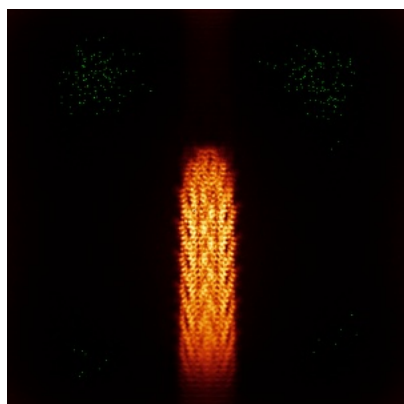


Y

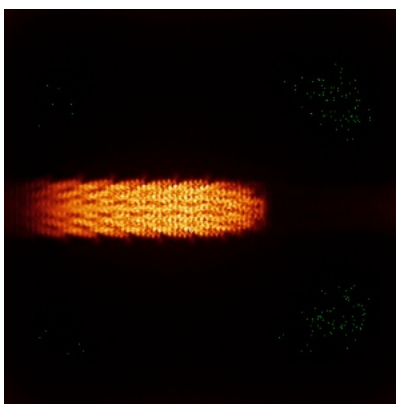


Z

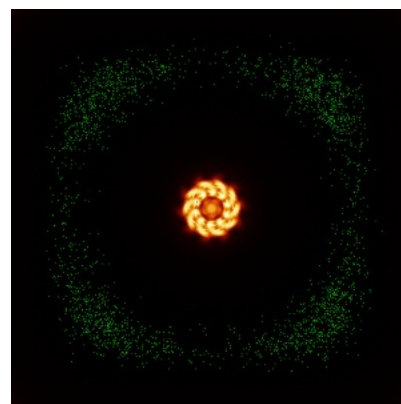
6.4.2 Raw map



X



Y

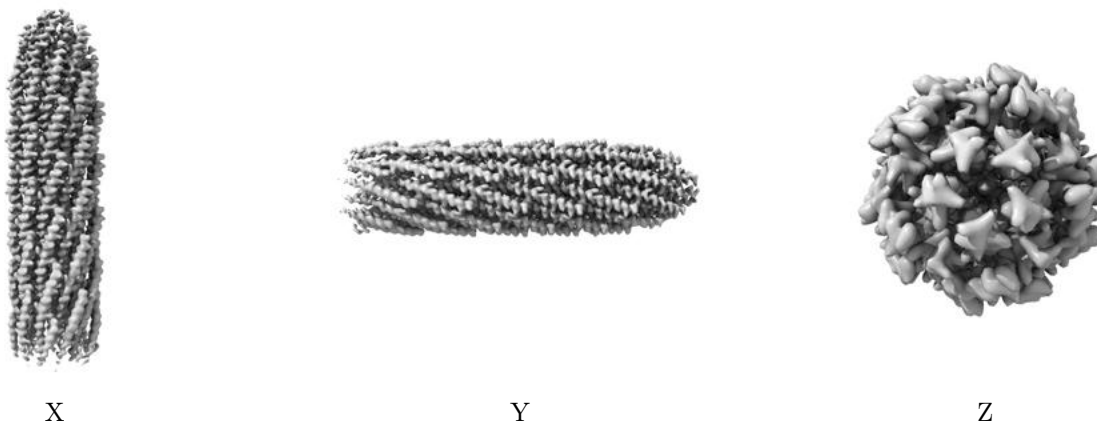


Z

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.

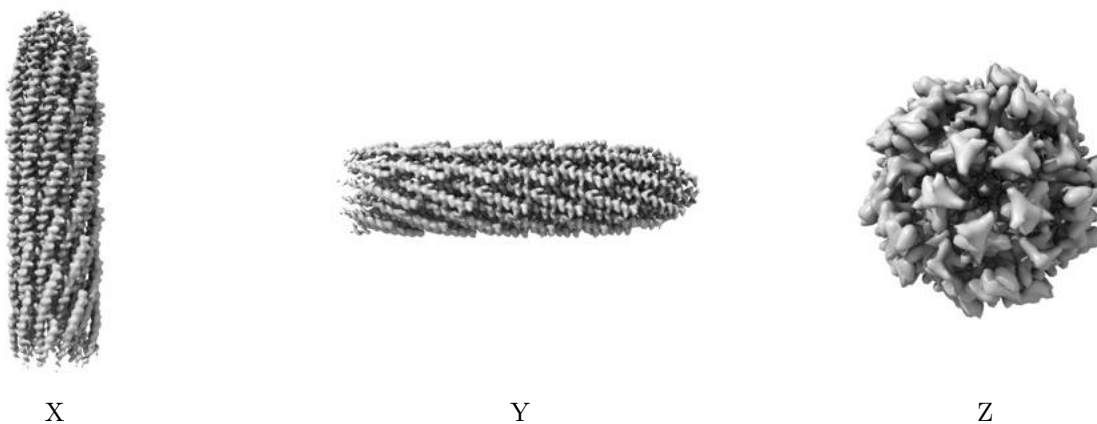
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

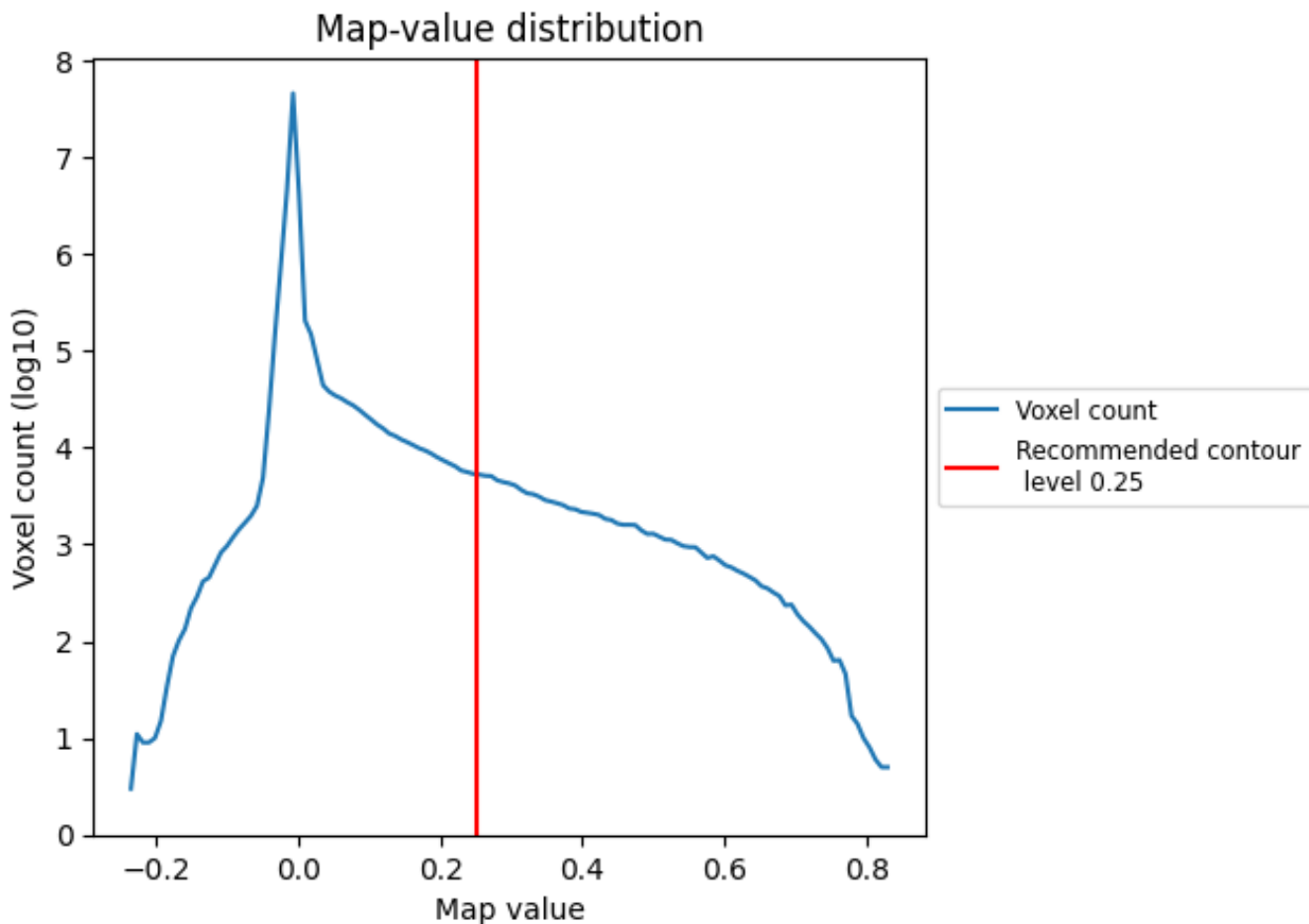
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

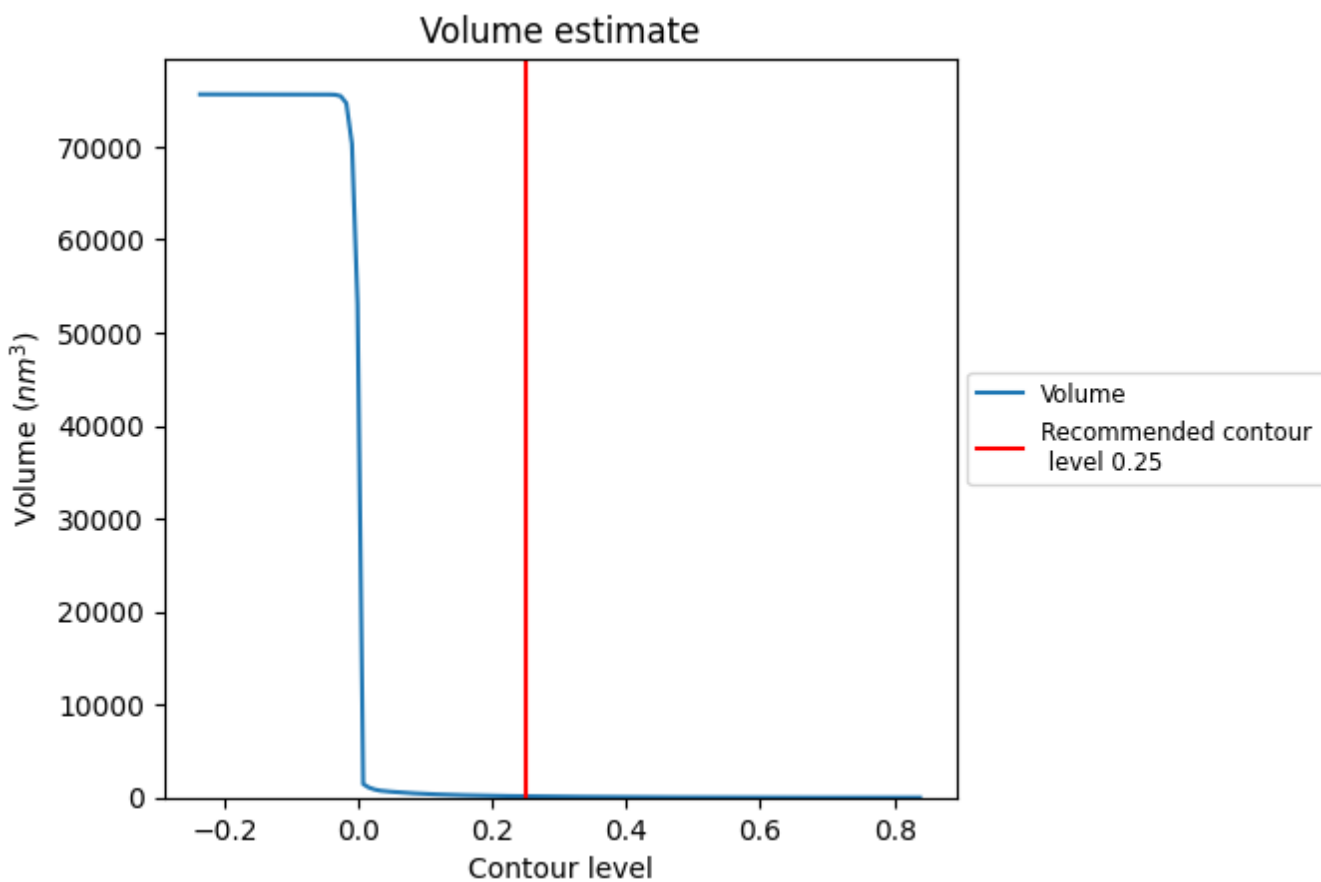
This section contains the results of statistical analysis of the map.

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.

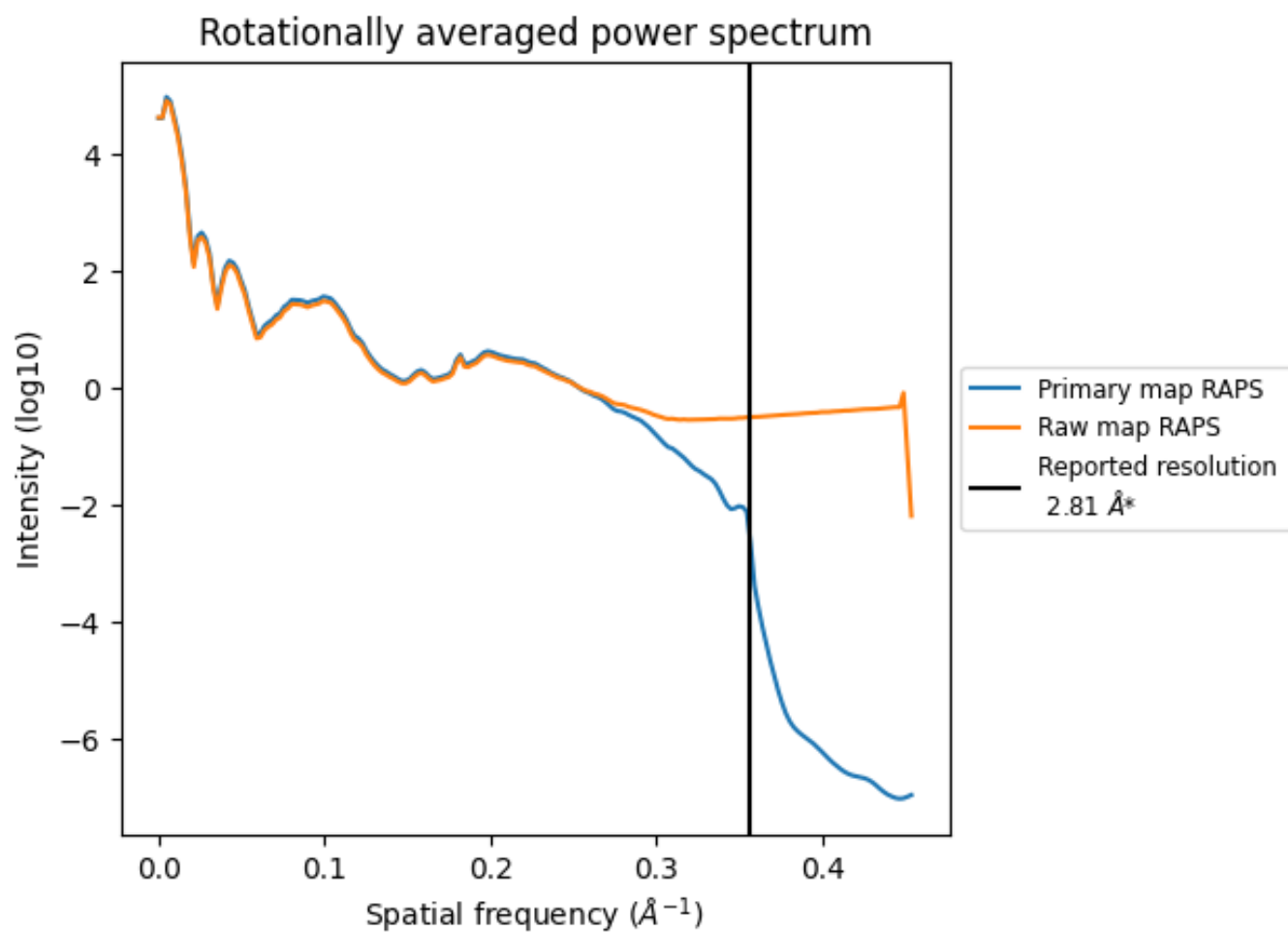
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 138 nm³; this corresponds to an approximate mass of 125 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 i

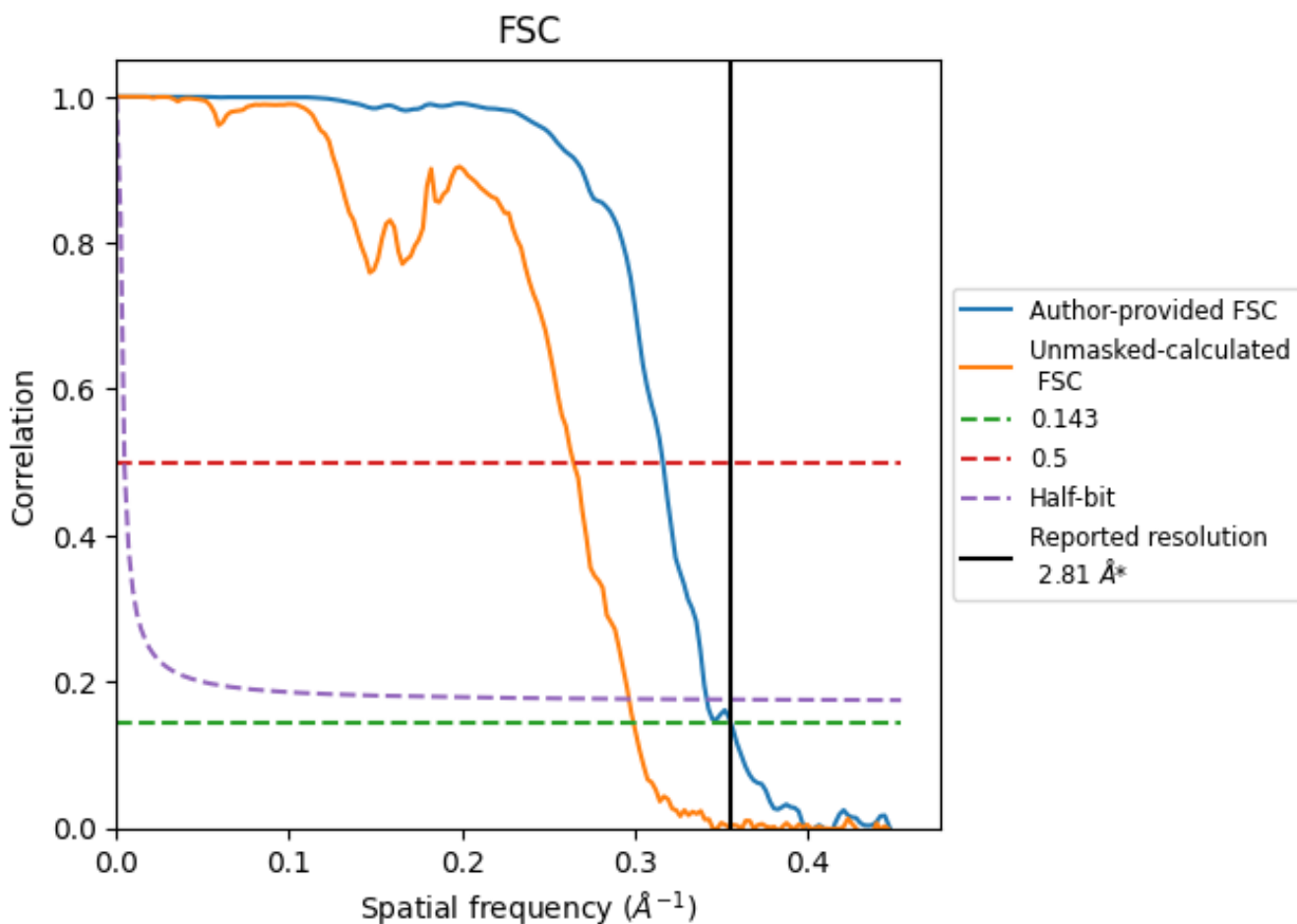


*Reported resolution corresponds to spatial frequency of 0.356 \AA^{-1}

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 0.356 Å⁻¹

8.2 Resolution estimates [i](#)

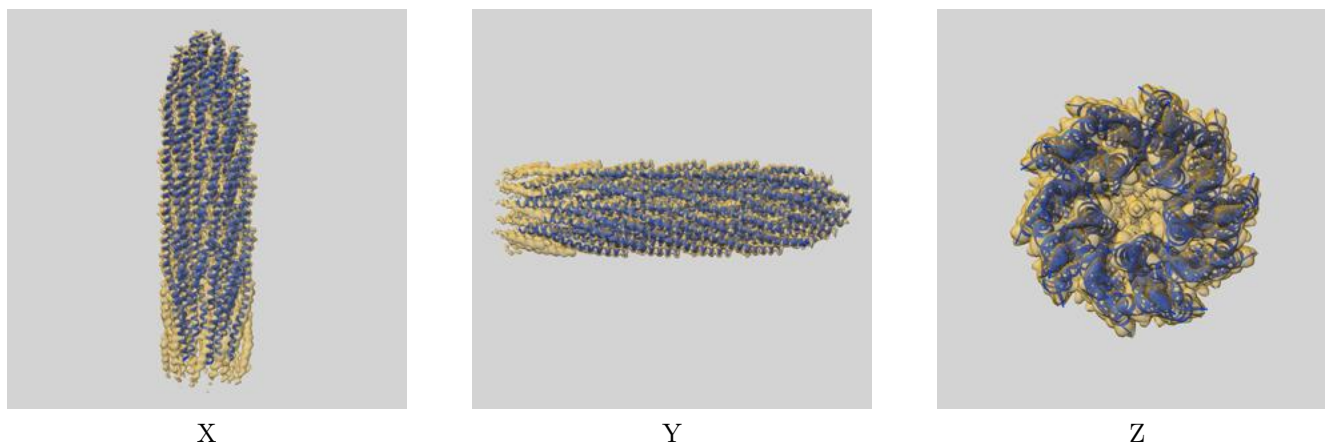
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.81	-	-
Author-provided FSC curve	2.81	3.16	2.93
Unmasked-calculated*	3.34	3.78	3.37

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.34 differs from the reported value 2.81 by more than 10 %

9 Map-model fit [i](#)

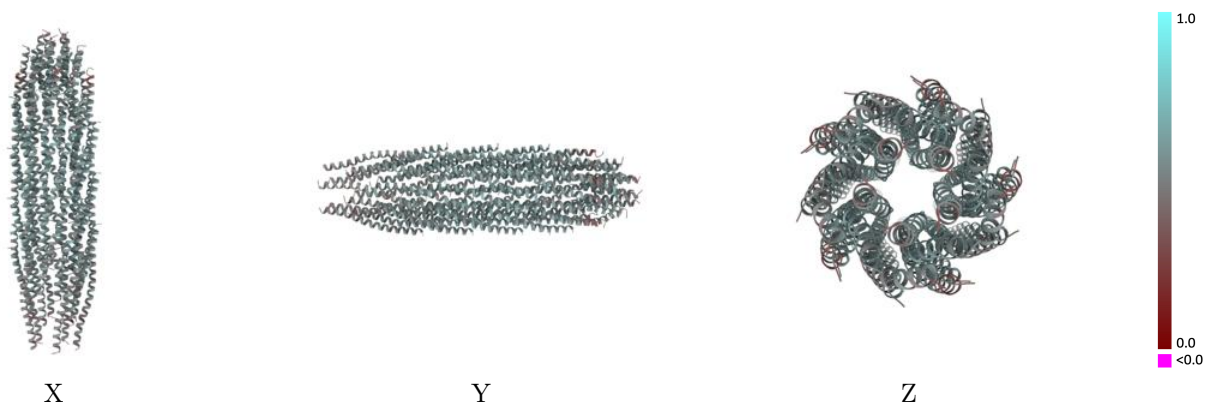
This section contains information regarding the fit between EMDB map EMD-15832 and PDB model 8B3P. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



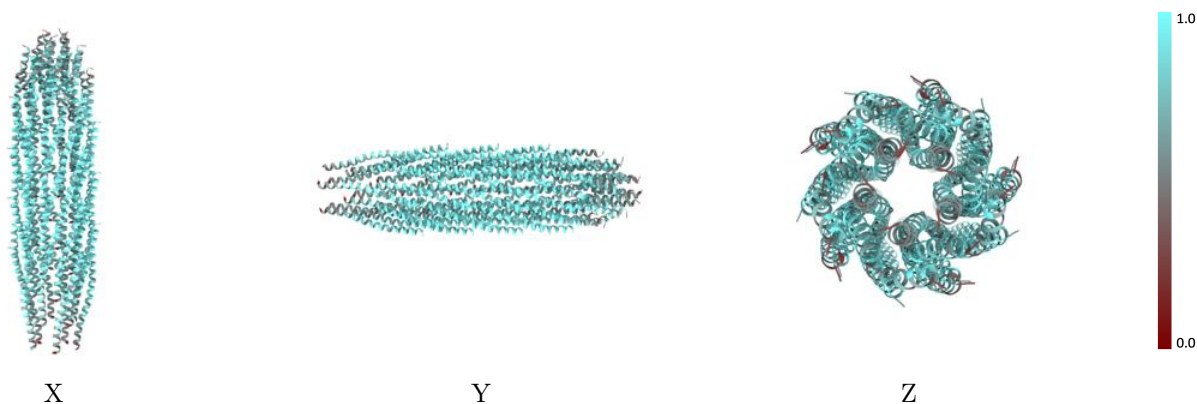
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



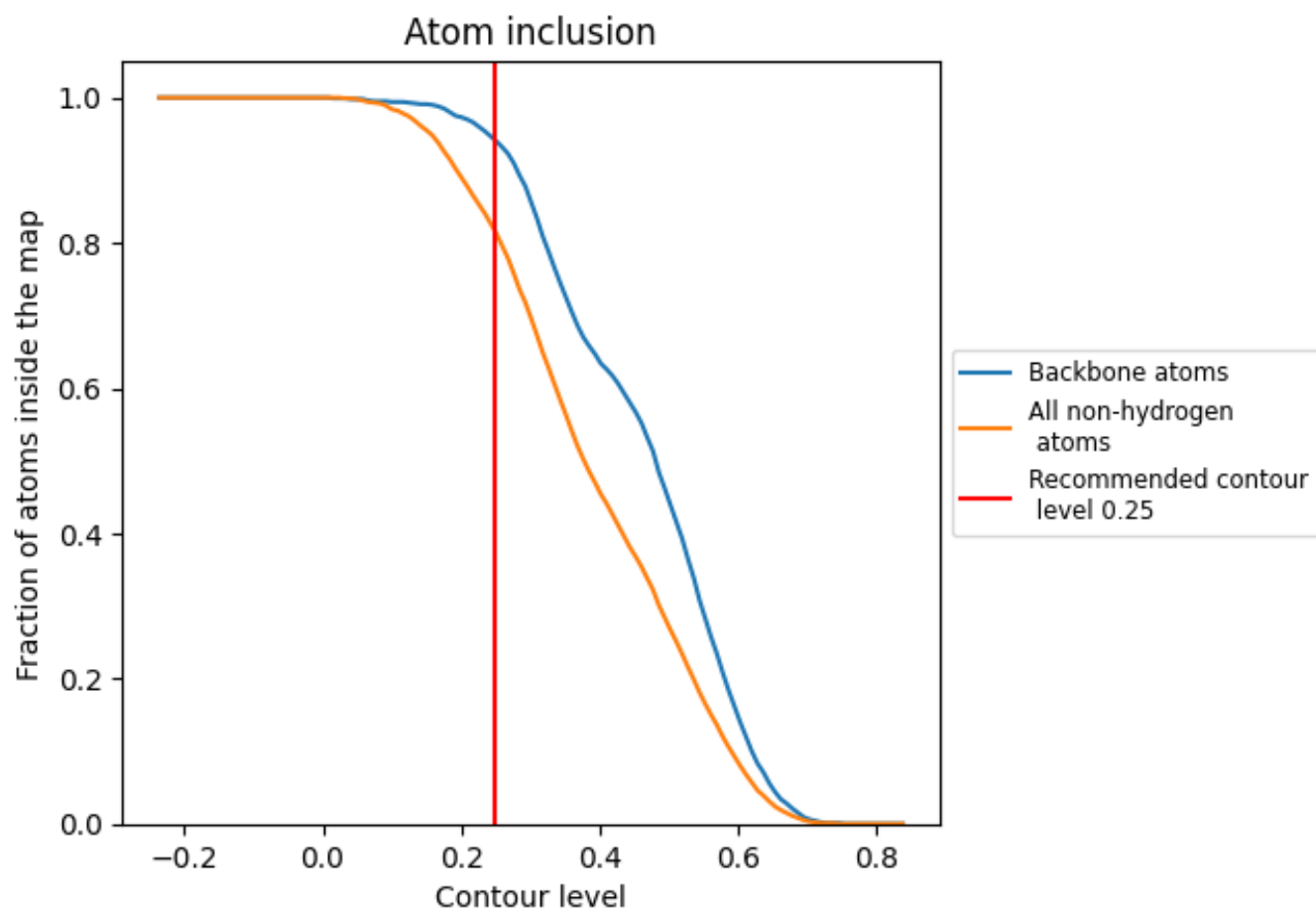
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 82% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8150	 0.5340
111	 0.7720	 0.5080
222	 0.7690	 0.5090
333	 0.7750	 0.5100
AAA	 0.6790	 0.5250
BBB	 0.6840	 0.5300
CCC	 0.6700	 0.5250
DDD	 0.6700	 0.5220
EEE	 0.6650	 0.5230
FFF	 0.8150	 0.5540
GGG	 0.8190	 0.5510
HHH	 0.8060	 0.5570
III	 0.8230	 0.5600
JJJ	 0.8150	 0.5590
KKK	 0.7480	 0.5200
LLL	 0.7450	 0.5160
MMM	 0.7480	 0.5140
NNN	 0.7360	 0.5210
OOO	 0.7480	 0.5210
PPP	 0.8100	 0.5240
QQQ	 0.8010	 0.5220
RRR	 0.8130	 0.5240
SSS	 0.8130	 0.5240
TTT	 0.8070	 0.5250
UUU	 0.8840	 0.5520
VVV	 0.8840	 0.5540
WWW	 0.8840	 0.5520
XXX	 0.8690	 0.5520
YYY	 0.8810	 0.5530
ZZZ	 0.8900	 0.5610
aaa	 0.8930	 0.5610
bbb	 0.8820	 0.5590
ccc	 0.8930	 0.5610
ddd	 0.8900	 0.5620
eee	 0.8820	 0.5580



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Chain	Atom inclusion	Q-score
fff	 0.8790	 0.5560
ggg	 0.8790	 0.5560
hhh	 0.8850	 0.5570
iii	 0.8850	 0.5570
jjj	 0.8400	 0.5380
kkk	 0.8370	 0.5370
lll	 0.8400	 0.5350
mmm	 0.8310	 0.5360
nnn	 0.8400	 0.5380
ooo	 0.7400	 0.4890
ppp	 0.7370	 0.4850
qqq	 0.7310	 0.4820
rrr	 0.7250	 0.4850
sss	 0.7310	 0.4860
ttt	 0.8670	 0.5540
uuu	 0.8730	 0.5490
vvv	 0.8640	 0.5510
www	 0.8640	 0.5520
xxx	 0.8670	 0.5530
yyy	 0.7780	 0.5070
zzz	 0.7750	 0.5070