



wwPDB EM Validation Summary Report ⓘ

Apr 24, 2023 – 01:22 PM EDT

PDB ID : 8HC1
EMDB ID : EMD-34648
Title : CryoEM structure of Helicobacter pylori UreFD/urease complex
Authors : Nim, Y.S.; Fong, I.Y.H.; Deme, J.; Tsang, K.L.; Caesar, J.; Johnson, S.; Wong, K.B.; Lea, S.M.
Deposited on : 2022-11-01
Resolution : 2.30 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:

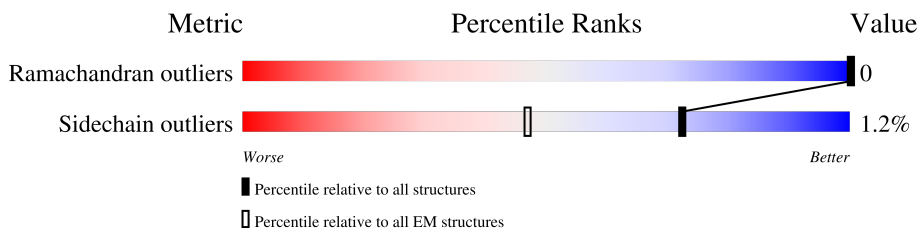
EMDB validation analysis : 0.0.1.dev50
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.2

1 Overall quality at a glance

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

The reported resolution of this entry is 2.30 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.


















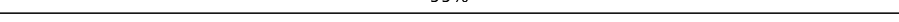
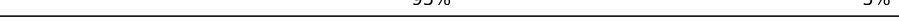
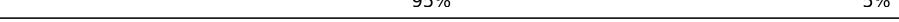
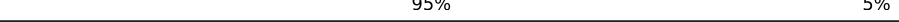
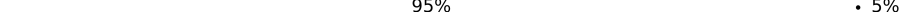
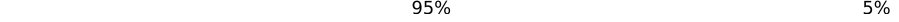
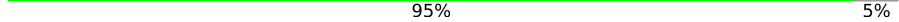
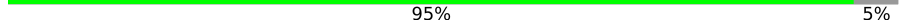
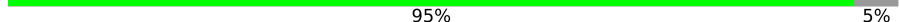
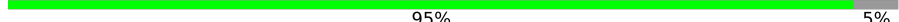
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	238	100%
1	E	238	100%
1	I	238	100%
1	M	238	100%
1	Q	238	100%
1	U	238	100%
1	Y	238	100%
1	c	238	100%
1	g	238	100%

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Mol	Chain	Length	Quality of chain
1	k	238	 100%
1	o	238	 100%
1	s	238	 100%
2	B	569	 99%
2	F	569	 99%
2	J	569	 99%
2	N	569	 99%
2	R	569	 99%
2	V	569	 99%
2	Z	569	 99%
2	d	569	 99%
2	h	569	 99%
2	l	569	 99%
2	p	569	 99%
2	t	569	 99%
3	C	273	 95%
3	G	273	 95%
3	K	273	 95%
3	O	273	 95%
3	S	273	 95%
3	W	273	 95%
3	a	273	 95%
3	e	273	 95%
3	i	273	 95%
3	m	273	 95%

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Mol	Chain	Length	Quality of chain
3	q	273	 95% 5%
3	u	273	 95% 5%
4	D	254	 29% 86% 13%
4	H	254	 28% 86% 13%
4	L	254	 26% 86% 13%
4	P	254	 28% 86% 13%
4	T	254	 26% 86% 13%
4	X	254	 26% 86% 13%
4	b	254	 28% 86% 13%
4	f	254	 27% 86% 13%
4	j	254	 25% 86% 13%
4	n	254	 26% 86% 13%
4	r	254	 28% 86% 13%
4	v	254	 27% 86% 13%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 120048 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 Urease subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	E	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	I	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	M	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	Q	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	U	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	Y	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	c	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	g	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	k	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	o	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		
1	s	238	Total	C	N	O	S	1	0
			1872	1180	335	349	8		

- Molecule 2 is a protein called Urease subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	F	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	J	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	R	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	V	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	Z	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	d	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	h	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	l	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	p	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		
2	t	569	Total	C	N	O	S	1	0
			4345	2725	749	850	21		

- Molecule 3 is a protein called Urease accessory protein UreH.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	G	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	K	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	O	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	S	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	W	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	a	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	e	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	i	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	m	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	q	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		
3	u	260	Total	C	N	O	S	0	0
			2041	1295	347	385	14		

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	140	ALA	GLU	engineered mutation	UNP Q09067
C	266	TRP	-	expression tag	UNP Q09067
C	267	SER	-	expression tag	UNP Q09067
C	268	HIS	-	expression tag	UNP Q09067
C	269	PRO	-	expression tag	UNP Q09067
C	270	GLN	-	expression tag	UNP Q09067
C	271	PHE	-	expression tag	UNP Q09067
C	272	GLU	-	expression tag	UNP Q09067
C	273	LYS	-	expression tag	UNP Q09067
G	140	ALA	GLU	engineered mutation	UNP Q09067
G	266	TRP	-	expression tag	UNP Q09067
G	267	SER	-	expression tag	UNP Q09067
G	268	HIS	-	expression tag	UNP Q09067
G	269	PRO	-	expression tag	UNP Q09067
G	270	GLN	-	expression tag	UNP Q09067
G	271	PHE	-	expression tag	UNP Q09067
G	272	GLU	-	expression tag	UNP Q09067
G	273	LYS	-	expression tag	UNP Q09067
K	140	ALA	GLU	engineered mutation	UNP Q09067
K	266	TRP	-	expression tag	UNP Q09067
K	267	SER	-	expression tag	UNP Q09067
K	268	HIS	-	expression tag	UNP Q09067
K	269	PRO	-	expression tag	UNP Q09067
K	270	GLN	-	expression tag	UNP Q09067
K	271	PHE	-	expression tag	UNP Q09067
K	272	GLU	-	expression tag	UNP Q09067
K	273	LYS	-	expression tag	UNP Q09067
O	140	ALA	GLU	engineered mutation	UNP Q09067
O	266	TRP	-	expression tag	UNP Q09067
O	267	SER	-	expression tag	UNP Q09067
O	268	HIS	-	expression tag	UNP Q09067
O	269	PRO	-	expression tag	UNP Q09067
O	270	GLN	-	expression tag	UNP Q09067
O	271	PHE	-	expression tag	UNP Q09067

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Chain	Residue	Modelled	Actual	Comment	Reference
O	272	GLU	-	expression tag	UNP Q09067
O	273	LYS	-	expression tag	UNP Q09067
S	140	ALA	GLU	engineered mutation	UNP Q09067
S	266	TRP	-	expression tag	UNP Q09067
S	267	SER	-	expression tag	UNP Q09067
S	268	HIS	-	expression tag	UNP Q09067
S	269	PRO	-	expression tag	UNP Q09067
S	270	GLN	-	expression tag	UNP Q09067
S	271	PHE	-	expression tag	UNP Q09067
S	272	GLU	-	expression tag	UNP Q09067
S	273	LYS	-	expression tag	UNP Q09067
W	140	ALA	GLU	engineered mutation	UNP Q09067
W	266	TRP	-	expression tag	UNP Q09067
W	267	SER	-	expression tag	UNP Q09067
W	268	HIS	-	expression tag	UNP Q09067
W	269	PRO	-	expression tag	UNP Q09067
W	270	GLN	-	expression tag	UNP Q09067
W	271	PHE	-	expression tag	UNP Q09067
W	272	GLU	-	expression tag	UNP Q09067
W	273	LYS	-	expression tag	UNP Q09067
a	140	ALA	GLU	engineered mutation	UNP Q09067
a	266	TRP	-	expression tag	UNP Q09067
a	267	SER	-	expression tag	UNP Q09067
a	268	HIS	-	expression tag	UNP Q09067
a	269	PRO	-	expression tag	UNP Q09067
a	270	GLN	-	expression tag	UNP Q09067
a	271	PHE	-	expression tag	UNP Q09067
a	272	GLU	-	expression tag	UNP Q09067
a	273	LYS	-	expression tag	UNP Q09067
e	140	ALA	GLU	engineered mutation	UNP Q09067
e	266	TRP	-	expression tag	UNP Q09067
e	267	SER	-	expression tag	UNP Q09067
e	268	HIS	-	expression tag	UNP Q09067
e	269	PRO	-	expression tag	UNP Q09067
e	270	GLN	-	expression tag	UNP Q09067
e	271	PHE	-	expression tag	UNP Q09067
e	272	GLU	-	expression tag	UNP Q09067
e	273	LYS	-	expression tag	UNP Q09067
i	140	ALA	GLU	engineered mutation	UNP Q09067
i	266	TRP	-	expression tag	UNP Q09067
i	267	SER	-	expression tag	UNP Q09067
i	268	HIS	-	expression tag	UNP Q09067

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Chain	Residue	Modelled	Actual	Comment	Reference
i	269	PRO	-	expression tag	UNP Q09067
i	270	GLN	-	expression tag	UNP Q09067
i	271	PHE	-	expression tag	UNP Q09067
i	272	GLU	-	expression tag	UNP Q09067
i	273	LYS	-	expression tag	UNP Q09067
m	140	ALA	GLU	engineered mutation	UNP Q09067
m	266	TRP	-	expression tag	UNP Q09067
m	267	SER	-	expression tag	UNP Q09067
m	268	HIS	-	expression tag	UNP Q09067
m	269	PRO	-	expression tag	UNP Q09067
m	270	GLN	-	expression tag	UNP Q09067
m	271	PHE	-	expression tag	UNP Q09067
m	272	GLU	-	expression tag	UNP Q09067
m	273	LYS	-	expression tag	UNP Q09067
q	140	ALA	GLU	engineered mutation	UNP Q09067
q	266	TRP	-	expression tag	UNP Q09067
q	267	SER	-	expression tag	UNP Q09067
q	268	HIS	-	expression tag	UNP Q09067
q	269	PRO	-	expression tag	UNP Q09067
q	270	GLN	-	expression tag	UNP Q09067
q	271	PHE	-	expression tag	UNP Q09067
q	272	GLU	-	expression tag	UNP Q09067
q	273	LYS	-	expression tag	UNP Q09067
u	140	ALA	GLU	engineered mutation	UNP Q09067
u	266	TRP	-	expression tag	UNP Q09067
u	267	SER	-	expression tag	UNP Q09067
u	268	HIS	-	expression tag	UNP Q09067
u	269	PRO	-	expression tag	UNP Q09067
u	270	GLN	-	expression tag	UNP Q09067
u	271	PHE	-	expression tag	UNP Q09067
u	272	GLU	-	expression tag	UNP Q09067
u	273	LYS	-	expression tag	UNP Q09067

- Molecule 4 is a protein called Urease accessory protein UreF.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	222	1746	1111	286	339	10	0	0
4	H	222	1746	1111	286	339	10	0	0
4	L	222	1746	1111	286	339	10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	P	222	1746	1111	286	339	10	0	0
4	T	222	1746	1111	286	339	10	0	0
4	X	222	1746	1111	286	339	10	0	0
4	b	222	1746	1111	286	339	10	0	0
4	f	222	1746	1111	286	339	10	0	0
4	j	222	1746	1111	286	339	10	0	0
4	n	222	1746	1111	286	339	10	0	0
4	r	222	1746	1111	286	339	10	0	0
4	v	222	1746	1111	286	339	10	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	179	ALA	ARG	engineered mutation	UNP Q09065
D	183	ASP	TYR	engineered mutation	UNP Q09065
H	179	ALA	ARG	engineered mutation	UNP Q09065
H	183	ASP	TYR	engineered mutation	UNP Q09065
L	179	ALA	ARG	engineered mutation	UNP Q09065
L	183	ASP	TYR	engineered mutation	UNP Q09065
P	179	ALA	ARG	engineered mutation	UNP Q09065
P	183	ASP	TYR	engineered mutation	UNP Q09065
T	179	ALA	ARG	engineered mutation	UNP Q09065
T	183	ASP	TYR	engineered mutation	UNP Q09065
X	179	ALA	ARG	engineered mutation	UNP Q09065
X	183	ASP	TYR	engineered mutation	UNP Q09065
b	179	ALA	ARG	engineered mutation	UNP Q09065
b	183	ASP	TYR	engineered mutation	UNP Q09065
f	179	ALA	ARG	engineered mutation	UNP Q09065
f	183	ASP	TYR	engineered mutation	UNP Q09065
j	179	ALA	ARG	engineered mutation	UNP Q09065
j	183	ASP	TYR	engineered mutation	UNP Q09065
n	179	ALA	ARG	engineered mutation	UNP Q09065
n	183	ASP	TYR	engineered mutation	UNP Q09065
r	179	ALA	ARG	engineered mutation	UNP Q09065

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Chain	Residue	Modelled	Actual	Comment	Reference
r	183	ASP	TYR	engineered mutation	UNP Q09065
v	179	ALA	ARG	engineered mutation	UNP Q09065
v	183	ASP	TYR	engineered mutation	UNP Q09065

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Urease subunit alpha

Chain A:  100%



- Molecule 1: Urease subunit alpha

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Urease subunit alpha

Chain I:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Urease subunit alpha

Chain M:  100%



- Molecule 1: Urease subunit alpha

Chain Q:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Urease subunit alpha

Chain U:  100%



- Molecule 1: Urease subunit alpha

Chain Y:  100%



- Molecule 1: Urease subunit alpha

Chain c:  100%

There are no outlier residues recorded for this chain.

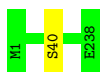
- Molecule 1: Urease subunit alpha

Chain g:  100%

There are no outlier residues recorded for this chain.

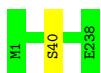
- Molecule 1: Urease subunit alpha

Chain k:  100%



- Molecule 1: Urease subunit alpha

Chain o:  100%



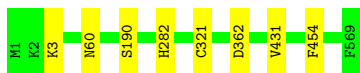
- Molecule 1: Urease subunit alpha

Chain s:  100%



- Molecule 2: Urease subunit beta

Chain B:  99%



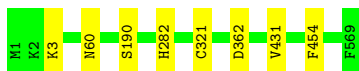
- Molecule 2: Urease subunit beta

Chain F:  99%



- Molecule 2: Urease subunit beta

Chain J: 99%



- Molecule 2: Urease subunit beta

Chain N: 99%



- Molecule 2: Urease subunit beta

Chain R: 99%



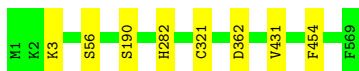
- Molecule 2: Urease subunit beta

Chain V: 99%



- Molecule 2: Urease subunit beta

Chain Z: 99%



- Molecule 2: Urease subunit beta

Chain d: 99%



- Molecule 2: Urease subunit beta

Chain h: 99%



- Molecule 2: Urease subunit beta



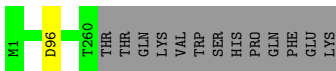
- Molecule 2: Urease subunit beta



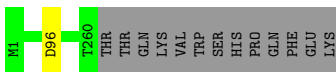
- Molecule 2: Urease subunit beta



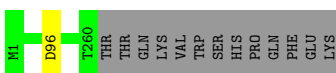
- Molecule 3: Urease accessory protein UreH



- Molecule 3: Urease accessory protein UreH

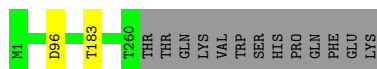


- Molecule 3: Urease accessory protein UreH

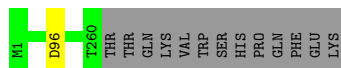


- Molecule 3: Urease accessory protein UreH

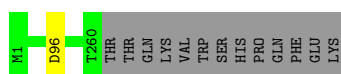




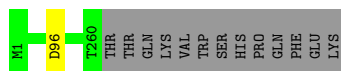
- Molecule 3: Urease accessory protein UreH



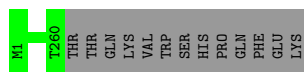
- Molecule 3: Urease accessory protein UreH



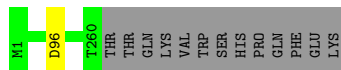
- Molecule 3: Urease accessory protein UreH



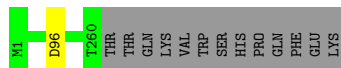
- Molecule 3: Urease accessory protein UreH



- Molecule 3: Urease accessory protein UreH

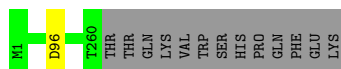


- Molecule 3: Urease accessory protein UreH

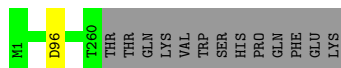


- Molecule 3: Urease accessory protein UreH

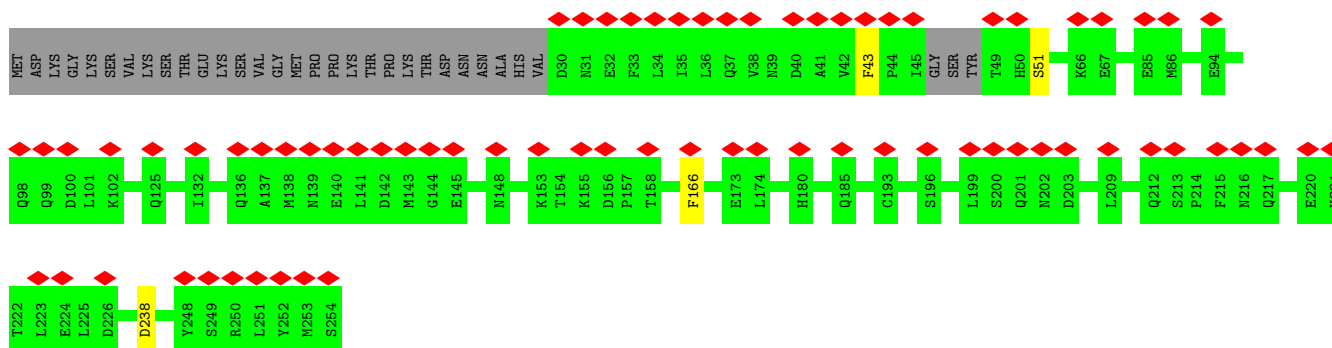
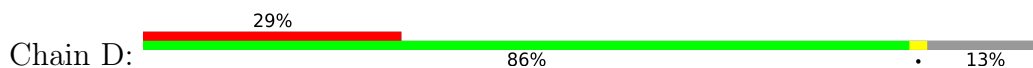




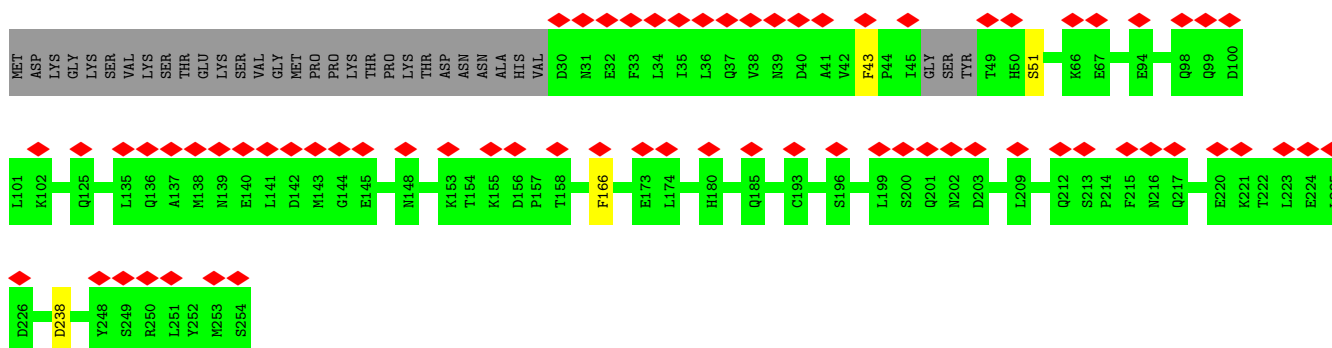
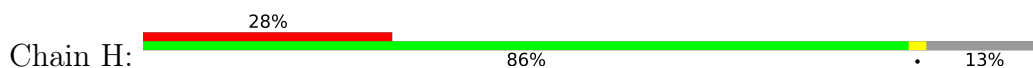
• Molecule 3: Urease accessory protein UreH



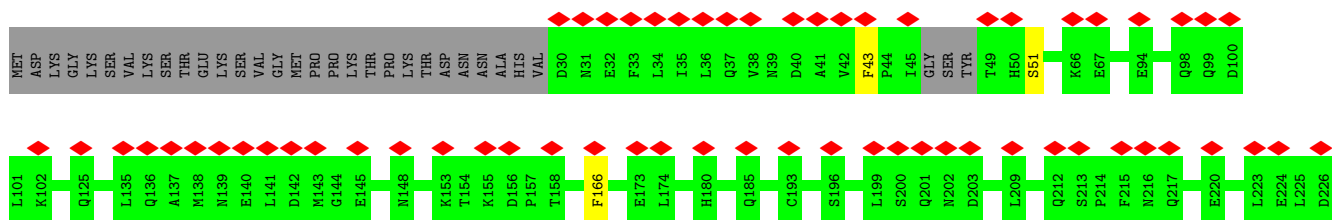
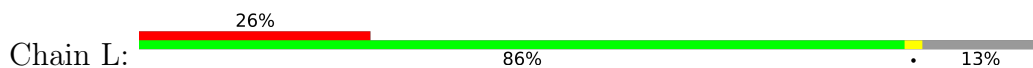
• Molecule 4: Urease accessory protein UreF

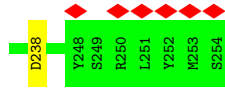


• Molecule 4: Urease accessory protein UreF

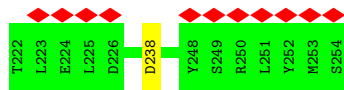
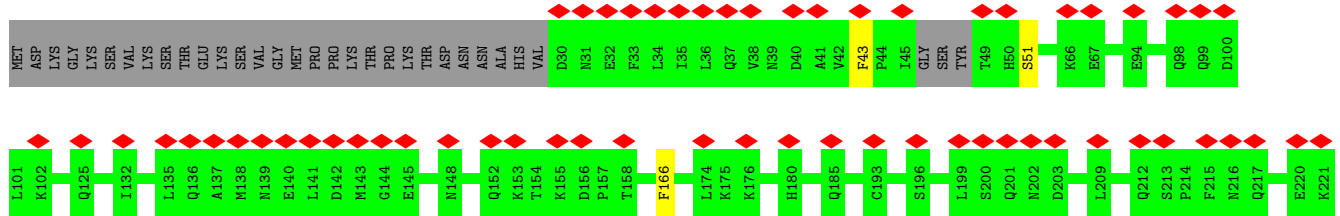
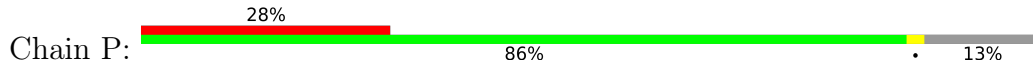


• Molecule 4: Urease accessory protein UreF

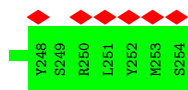
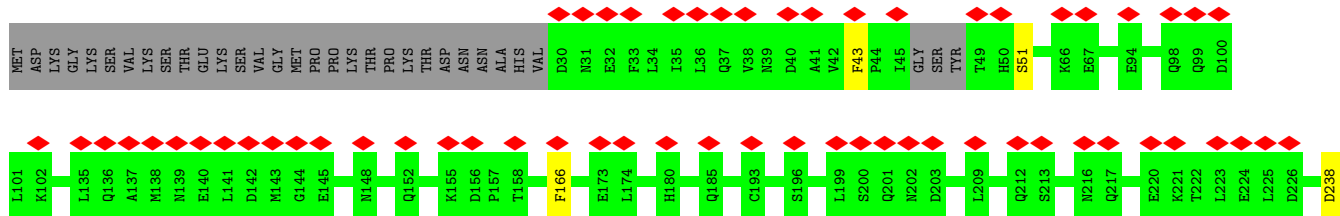
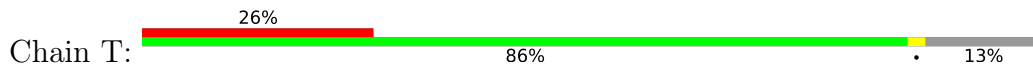




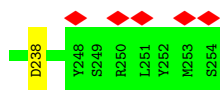
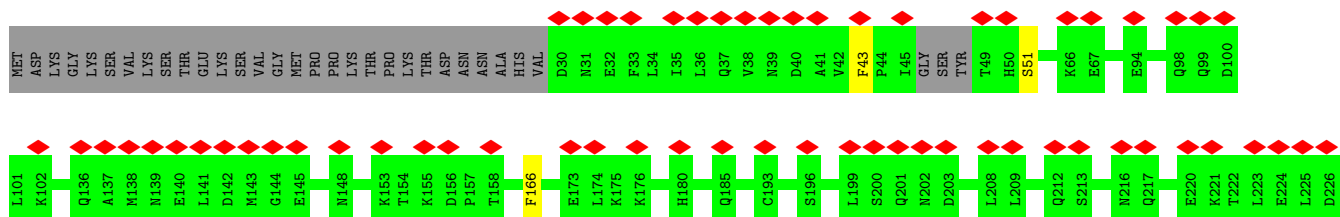
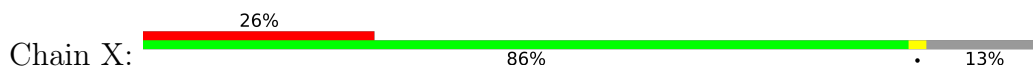
• Molecule 4: Urease accessory protein UreF



• Molecule 4: Urease accessory protein UreF

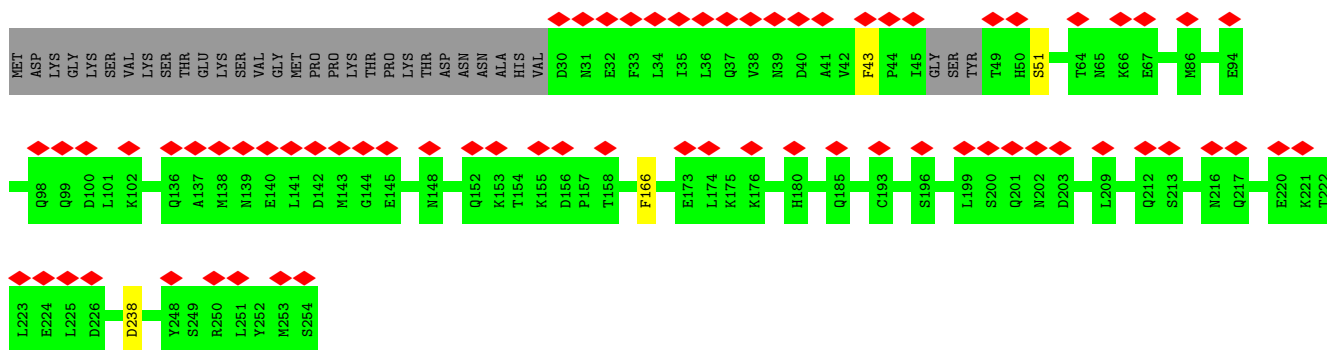


• Molecule 4: Urease accessory protein UreF



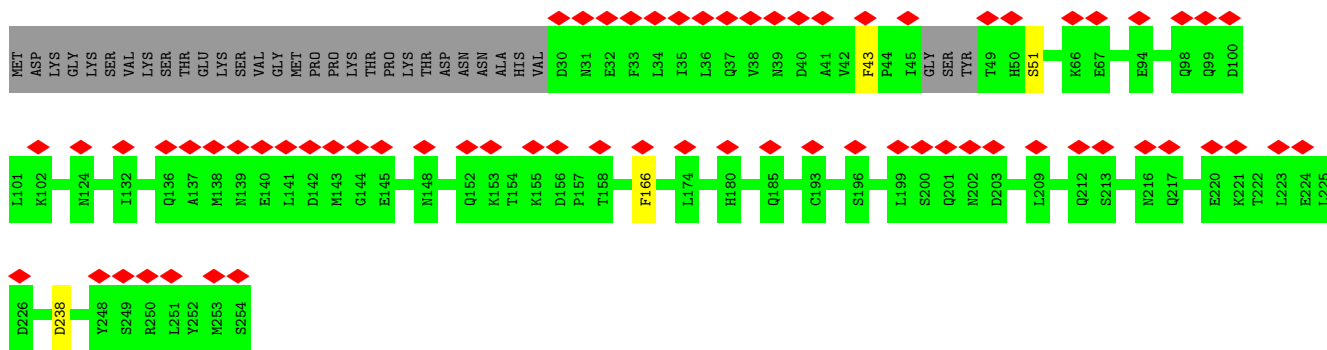
• Molecule 4: Urease accessory protein UreF

Chain b: 28% 86% 13%



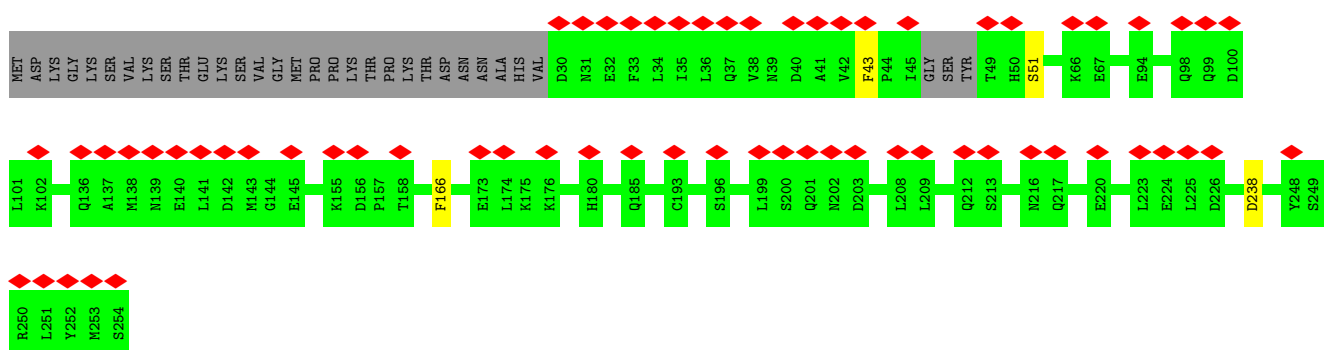
- Molecule 4: Urease accessory protein UreF

Chain f: 27% 86% 13%



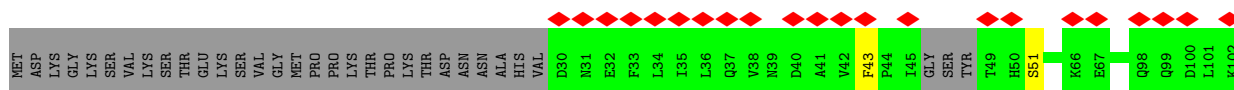
- Molecule 4: Urease accessory protein UreF

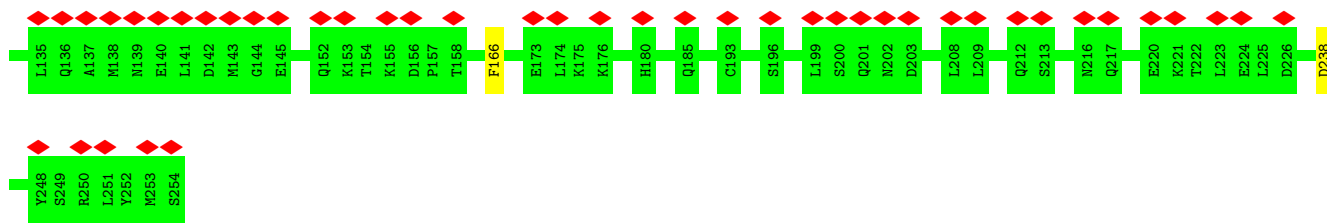
Chain j: 25% 86% 13%



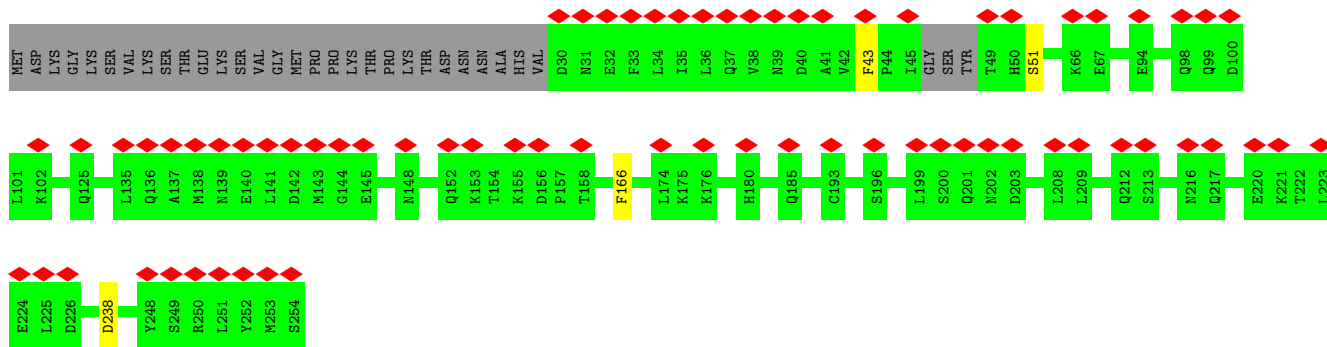
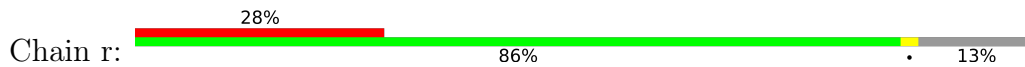
- Molecule 4: Urease accessory protein UreF

Chain n: 26% 86% 13%

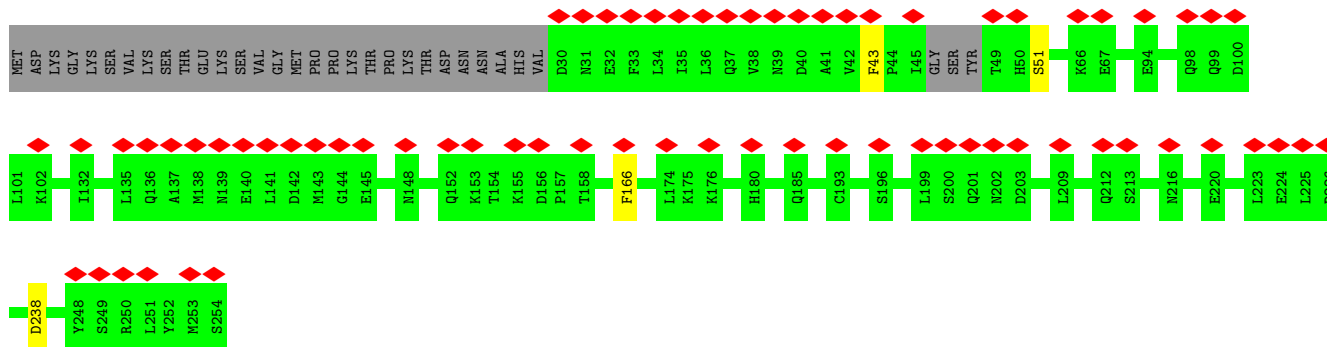
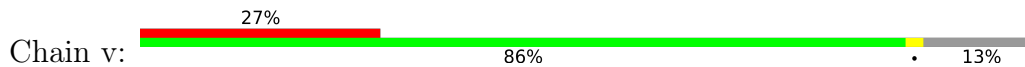




• Molecule 4: Urease accessory protein UreF



• Molecule 4: Urease accessory protein UreF



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68516	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	-500	Depositor
Maximum defocus (nm)	-1500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.054	Depositor
Minimum map value	-0.018	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0026525	Depositor
Map size (\AA)	327.156, 327.156, 327.156	wwPDB
Map dimensions	398, 398, 398	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.822, 0.822, 0.822	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.33	0/1904	0.48	0/2548
1	E	0.33	0/1904	0.48	0/2548
1	I	0.33	0/1904	0.48	0/2548
1	M	0.33	0/1904	0.48	0/2548
1	Q	0.33	0/1904	0.48	0/2548
1	U	0.33	0/1904	0.48	0/2548
1	Y	0.33	0/1904	0.48	0/2548
1	c	0.33	0/1904	0.48	0/2548
1	g	0.33	0/1904	0.48	0/2548
1	k	0.33	0/1904	0.48	0/2548
1	o	0.33	0/1904	0.48	0/2548
1	s	0.33	0/1904	0.48	0/2548
2	B	0.36	0/4430	0.49	0/5992
2	F	0.36	0/4430	0.49	0/5992
2	J	0.36	0/4430	0.49	0/5992
2	N	0.36	0/4430	0.49	0/5992
2	R	0.36	0/4430	0.49	0/5992
2	V	0.36	0/4430	0.49	0/5992
2	Z	0.36	0/4430	0.49	0/5992
2	d	0.36	0/4430	0.49	0/5992
2	h	0.36	0/4430	0.49	0/5992
2	l	0.36	0/4430	0.49	0/5992
2	p	0.36	0/4430	0.49	0/5992
2	t	0.36	0/4430	0.49	0/5992
3	C	0.27	0/2081	0.48	0/2815
3	G	0.27	0/2081	0.48	0/2815
3	K	0.27	0/2081	0.48	0/2815
3	O	0.27	0/2081	0.49	0/2815
3	S	0.27	0/2081	0.48	0/2815
3	W	0.27	0/2081	0.49	0/2815
3	a	0.27	0/2081	0.48	0/2815
3	e	0.27	0/2081	0.48	0/2815
3	i	0.27	0/2081	0.48	0/2815
3	m	0.27	0/2081	0.49	0/2815

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	q	0.27	0/2081	0.49	0/2815
3	u	0.27	0/2081	0.49	0/2815
4	D	0.24	0/1772	0.40	0/2389
4	H	0.24	0/1772	0.40	0/2389
4	L	0.24	0/1772	0.40	0/2389
4	P	0.24	0/1772	0.40	0/2389
4	T	0.24	0/1772	0.40	0/2389
4	X	0.24	0/1772	0.41	0/2389
4	b	0.24	0/1772	0.40	0/2389
4	f	0.24	0/1772	0.40	0/2389
4	j	0.24	0/1772	0.40	0/2389
4	n	0.24	0/1772	0.40	0/2389
4	r	0.24	0/1772	0.40	0/2389
4	v	0.24	0/1772	0.40	0/2389
All	All	0.32	0/122244	0.47	0/164928

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/238 (100%)	228 (96%)	9 (4%)	0	100	100
1	E	237/238 (100%)	229 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	237/238 (100%)	229 (97%)	8 (3%)	0	100	100
1	M	237/238 (100%)	230 (97%)	7 (3%)	0	100	100
1	Q	237/238 (100%)	229 (97%)	8 (3%)	0	100	100
1	U	237/238 (100%)	230 (97%)	7 (3%)	0	100	100
1	Y	237/238 (100%)	228 (96%)	9 (4%)	0	100	100
1	c	237/238 (100%)	229 (97%)	8 (3%)	0	100	100
1	g	237/238 (100%)	229 (97%)	8 (3%)	0	100	100
1	k	237/238 (100%)	229 (97%)	8 (3%)	0	100	100
1	o	237/238 (100%)	228 (96%)	9 (4%)	0	100	100
1	s	237/238 (100%)	230 (97%)	7 (3%)	0	100	100
2	B	568/569 (100%)	550 (97%)	18 (3%)	0	100	100
2	F	568/569 (100%)	548 (96%)	20 (4%)	0	100	100
2	J	568/569 (100%)	548 (96%)	20 (4%)	0	100	100
2	N	568/569 (100%)	551 (97%)	17 (3%)	0	100	100
2	R	568/569 (100%)	545 (96%)	23 (4%)	0	100	100
2	V	568/569 (100%)	547 (96%)	21 (4%)	0	100	100
2	Z	568/569 (100%)	549 (97%)	19 (3%)	0	100	100
2	d	568/569 (100%)	548 (96%)	20 (4%)	0	100	100
2	h	568/569 (100%)	548 (96%)	20 (4%)	0	100	100
2	l	568/569 (100%)	547 (96%)	21 (4%)	0	100	100
2	p	568/569 (100%)	550 (97%)	18 (3%)	0	100	100
2	t	568/569 (100%)	549 (97%)	19 (3%)	0	100	100
3	C	258/273 (94%)	253 (98%)	5 (2%)	0	100	100
3	G	258/273 (94%)	253 (98%)	5 (2%)	0	100	100
3	K	258/273 (94%)	254 (98%)	4 (2%)	0	100	100
3	O	258/273 (94%)	252 (98%)	6 (2%)	0	100	100
3	S	258/273 (94%)	253 (98%)	5 (2%)	0	100	100
3	W	258/273 (94%)	252 (98%)	6 (2%)	0	100	100
3	a	258/273 (94%)	253 (98%)	5 (2%)	0	100	100
3	e	258/273 (94%)	253 (98%)	5 (2%)	0	100	100
3	i	258/273 (94%)	253 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	m	258/273 (94%)	254 (98%)	4 (2%)	0	100	100
3	q	258/273 (94%)	253 (98%)	5 (2%)	0	100	100
3	u	258/273 (94%)	252 (98%)	6 (2%)	0	100	100
4	D	218/254 (86%)	211 (97%)	7 (3%)	0	100	100
4	H	218/254 (86%)	210 (96%)	8 (4%)	0	100	100
4	L	218/254 (86%)	211 (97%)	7 (3%)	0	100	100
4	P	218/254 (86%)	210 (96%)	8 (4%)	0	100	100
4	T	218/254 (86%)	209 (96%)	9 (4%)	0	100	100
4	X	218/254 (86%)	210 (96%)	8 (4%)	0	100	100
4	b	218/254 (86%)	211 (97%)	7 (3%)	0	100	100
4	f	218/254 (86%)	212 (97%)	6 (3%)	0	100	100
4	j	218/254 (86%)	212 (97%)	6 (3%)	0	100	100
4	n	218/254 (86%)	212 (97%)	6 (3%)	0	100	100
4	r	218/254 (86%)	209 (96%)	9 (4%)	0	100	100
4	v	218/254 (86%)	212 (97%)	6 (3%)	0	100	100
All	All	15372/16008 (96%)	14892 (97%)	480 (3%)	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	A	199/198 (100%)	198 (100%)	1 (0%)	88	95
1	E	199/198 (100%)	199 (100%)	0	100	100
1	I	199/198 (100%)	199 (100%)	0	100	100
1	M	199/198 (100%)	198 (100%)	1 (0%)	88	95
1	Q	199/198 (100%)	199 (100%)	0	100	100
1	U	199/198 (100%)	198 (100%)	1 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	199/198 (100%)	198 (100%)	1 (0%)	88	95
1	c	199/198 (100%)	199 (100%)	0	100	100
1	g	199/198 (100%)	199 (100%)	0	100	100
1	k	199/198 (100%)	198 (100%)	1 (0%)	88	95
1	o	199/198 (100%)	198 (100%)	1 (0%)	88	95
1	s	199/198 (100%)	198 (100%)	1 (0%)	88	95
2	B	461/460 (100%)	453 (98%)	8 (2%)	60	76
2	F	461/460 (100%)	454 (98%)	7 (2%)	65	79
2	J	461/460 (100%)	453 (98%)	8 (2%)	60	76
2	N	461/460 (100%)	454 (98%)	7 (2%)	65	79
2	R	461/460 (100%)	456 (99%)	5 (1%)	73	86
2	V	461/460 (100%)	454 (98%)	7 (2%)	65	79
2	Z	461/460 (100%)	453 (98%)	8 (2%)	60	76
2	d	461/460 (100%)	454 (98%)	7 (2%)	65	79
2	h	461/460 (100%)	454 (98%)	7 (2%)	65	79
2	l	461/460 (100%)	456 (99%)	5 (1%)	73	86
2	p	461/460 (100%)	453 (98%)	8 (2%)	60	76
2	t	461/460 (100%)	454 (98%)	7 (2%)	65	79
3	C	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	G	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	K	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	O	228/241 (95%)	226 (99%)	2 (1%)	78	89
3	S	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	W	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	a	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	e	228/241 (95%)	228 (100%)	0	100	100
3	i	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	m	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	q	228/241 (95%)	227 (100%)	1 (0%)	91	96
3	u	228/241 (95%)	227 (100%)	1 (0%)	91	96
4	D	195/227 (86%)	191 (98%)	4 (2%)	53	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	L	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	P	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	T	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	X	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	b	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	f	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	j	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	n	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	r	195/227 (86%)	191 (98%)	4 (2%)	53	70
4	v	195/227 (86%)	191 (98%)	4 (2%)	53	70
All	All	12996/13512 (96%)	12845 (99%)	151 (1%)	72	84

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	l	190	SER
2	t	362	ASP
3	m	96	ASP
2	p	321	CYS
4	v	238	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
4	j	76	ASN
4	r	237	ASN
4	j	237	ASN
4	n	237	ASN
4	v	76	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.

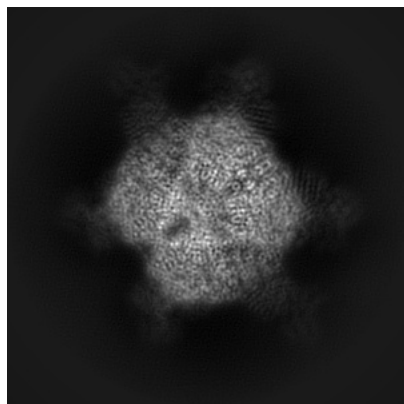
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34648. These allow visual inspection of the internal detail of the map and identification of artifacts.

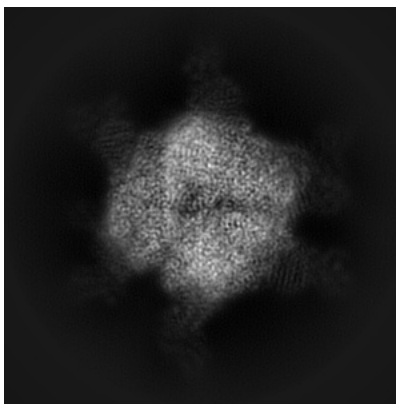
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

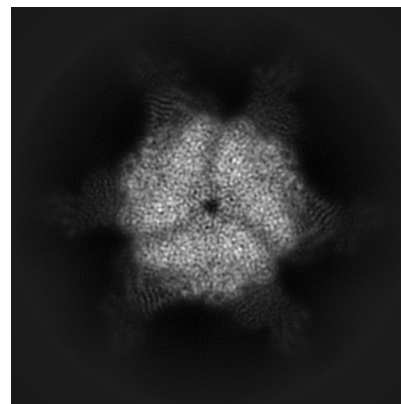
6.1.1 Primary map



X

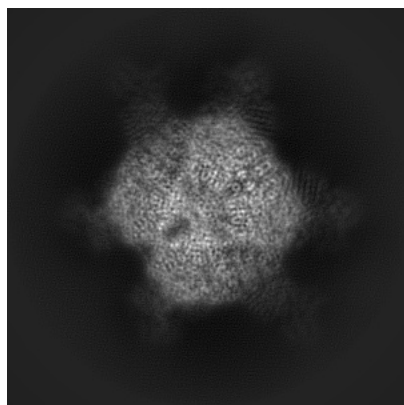


Y

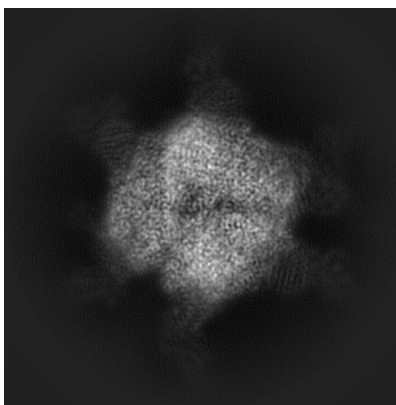


Z

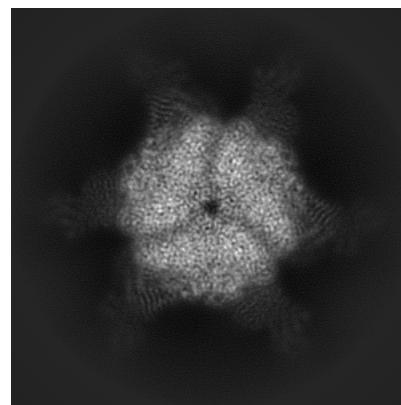
6.1.2 Raw map



X



Y

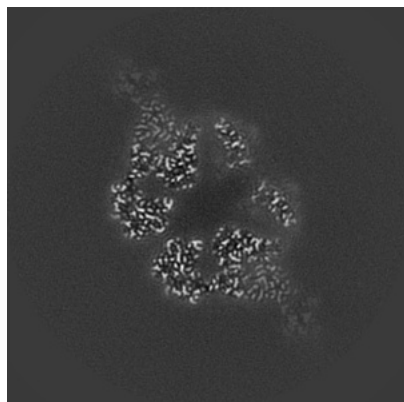


Z

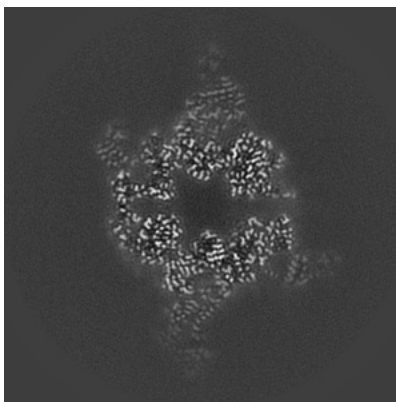
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

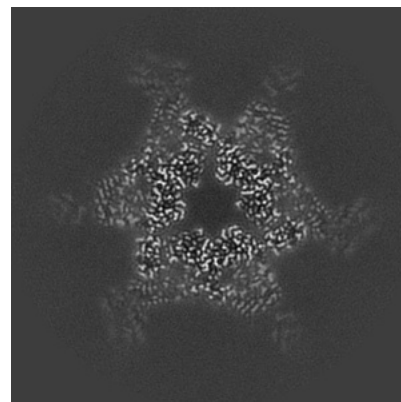
6.2.1 Primary map



X Index: 199

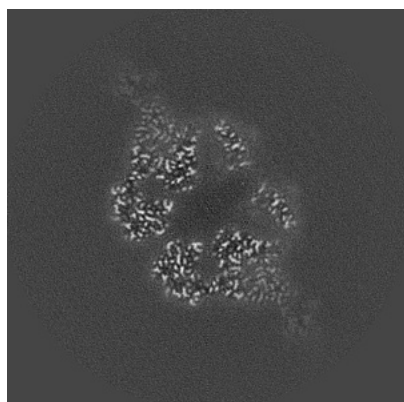


Y Index: 199

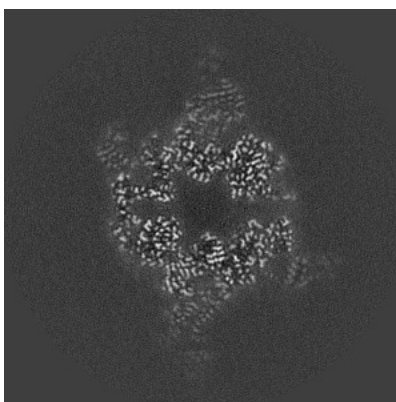


Z Index: 199

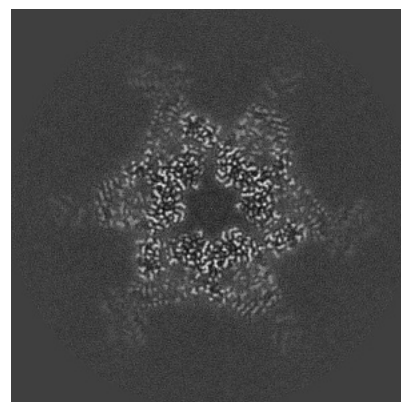
6.2.2 Raw map



X Index: 199



Y Index: 199

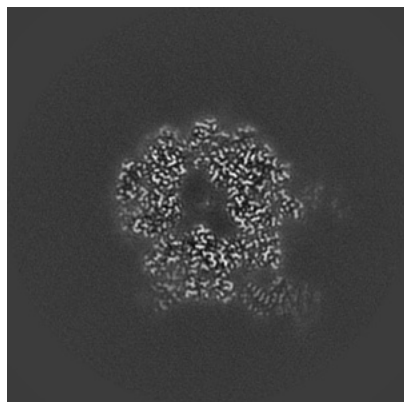


Z Index: 199

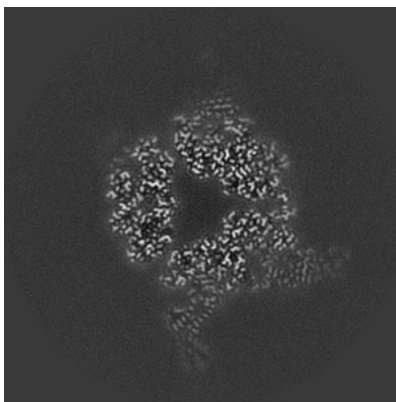
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

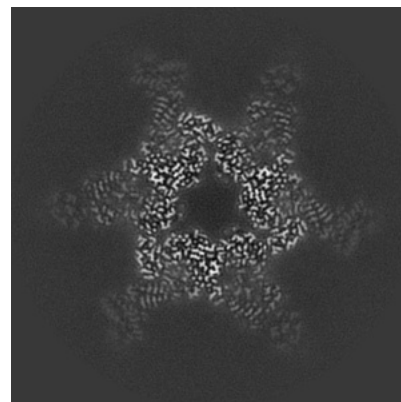
6.3.1 Primary map



X Index: 175

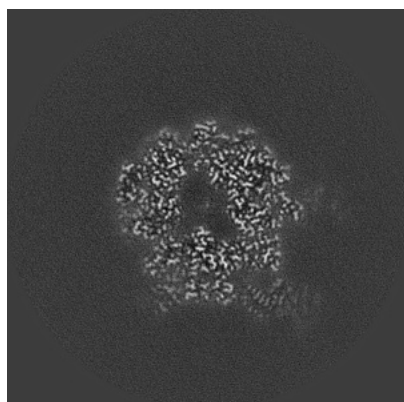


Y Index: 208

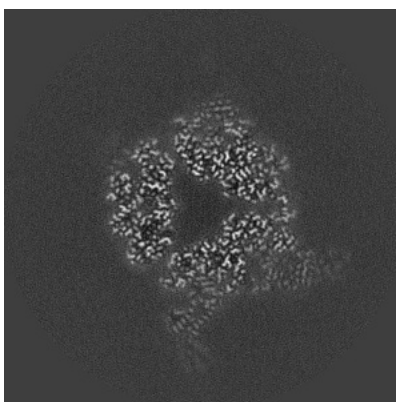


Z Index: 195

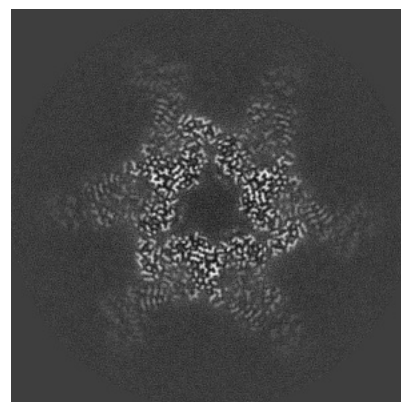
6.3.2 Raw map



X Index: 175



Y Index: 208

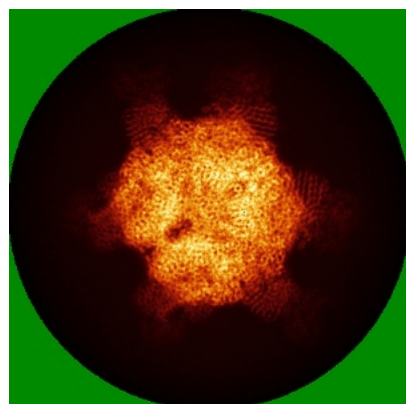


Z Index: 195

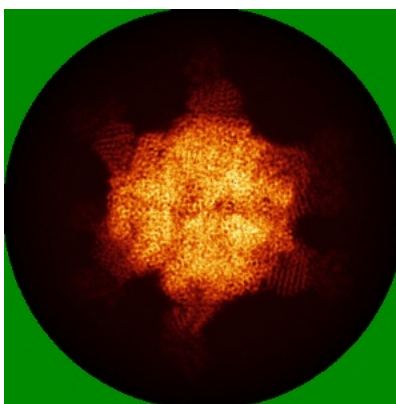
The images above show the largest variance slices of the map in three orthogonal directions.

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

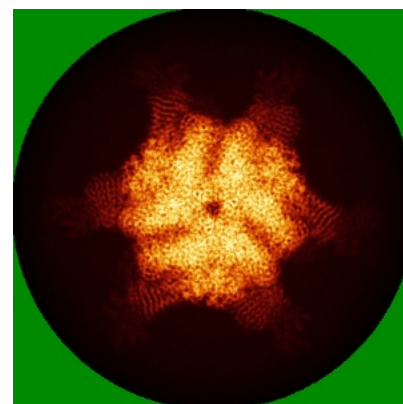
6.4.1 Primary map



X

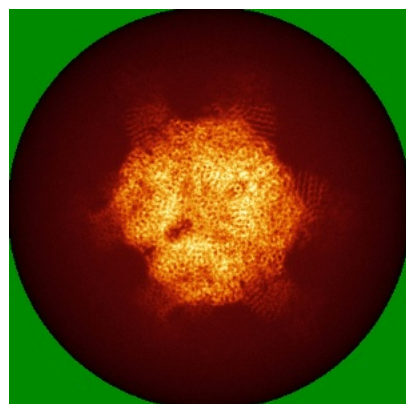


Y

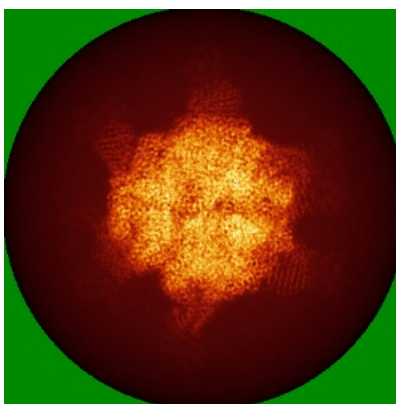


Z

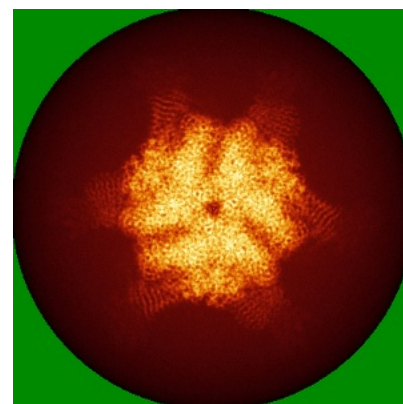
6.4.2 Raw map



X



Y

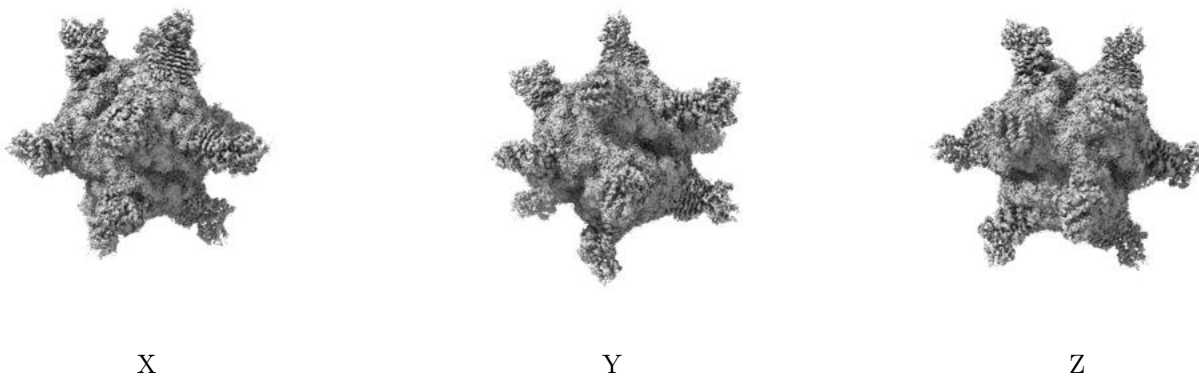


Z

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.

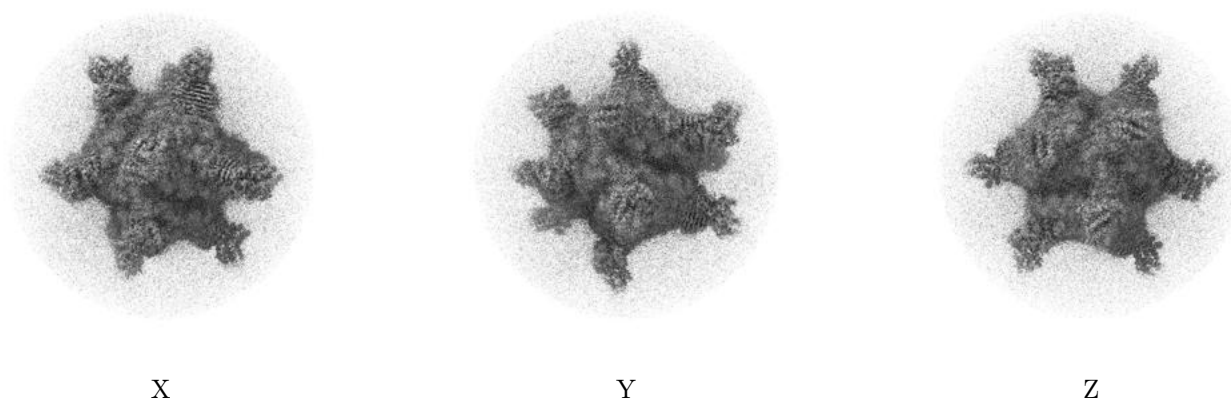
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0026525. 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.

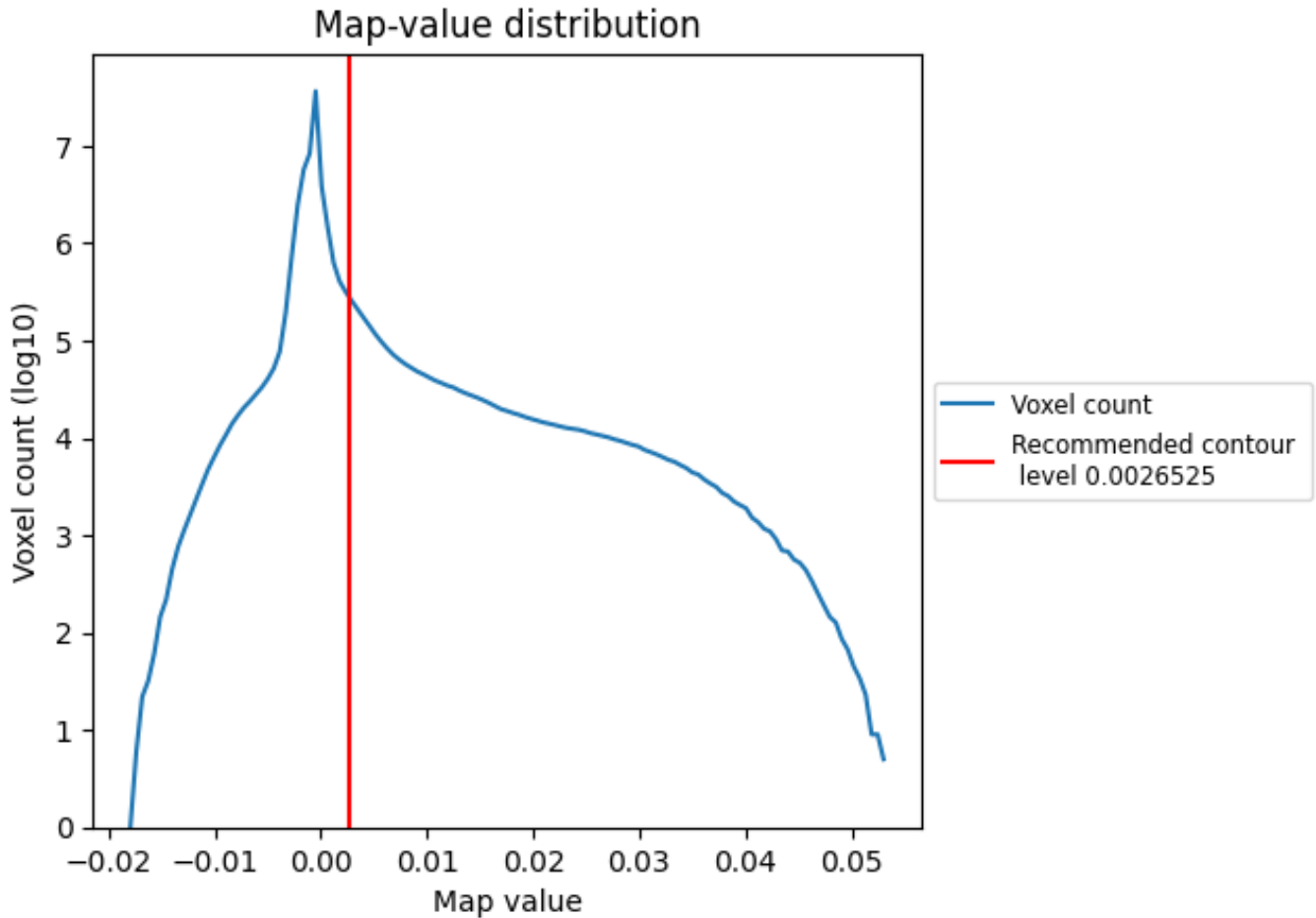
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

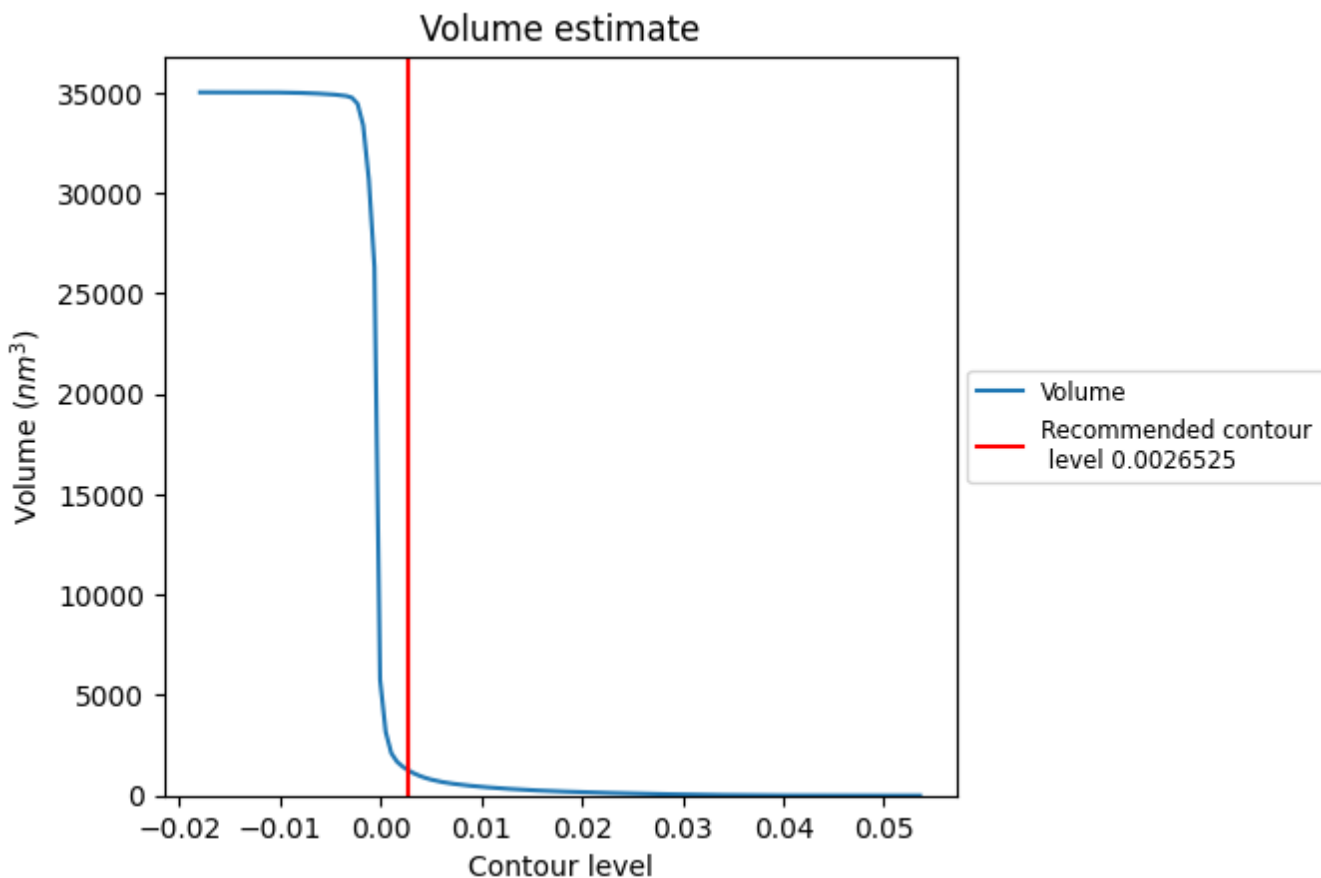
This section contains the results of statistical analysis of the map.

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.

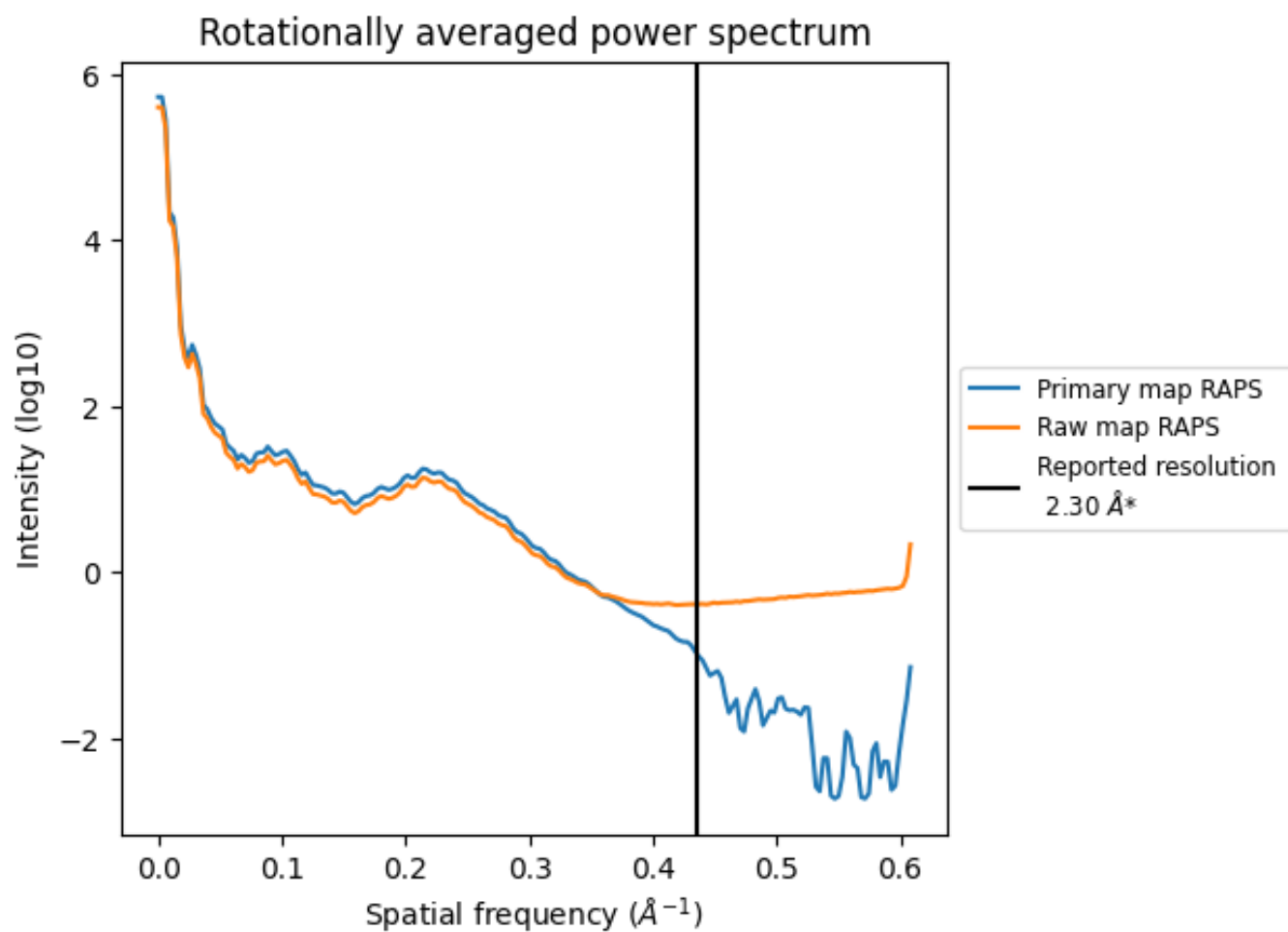
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1287 nm³; this corresponds to an approximate mass of 1162 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](#)

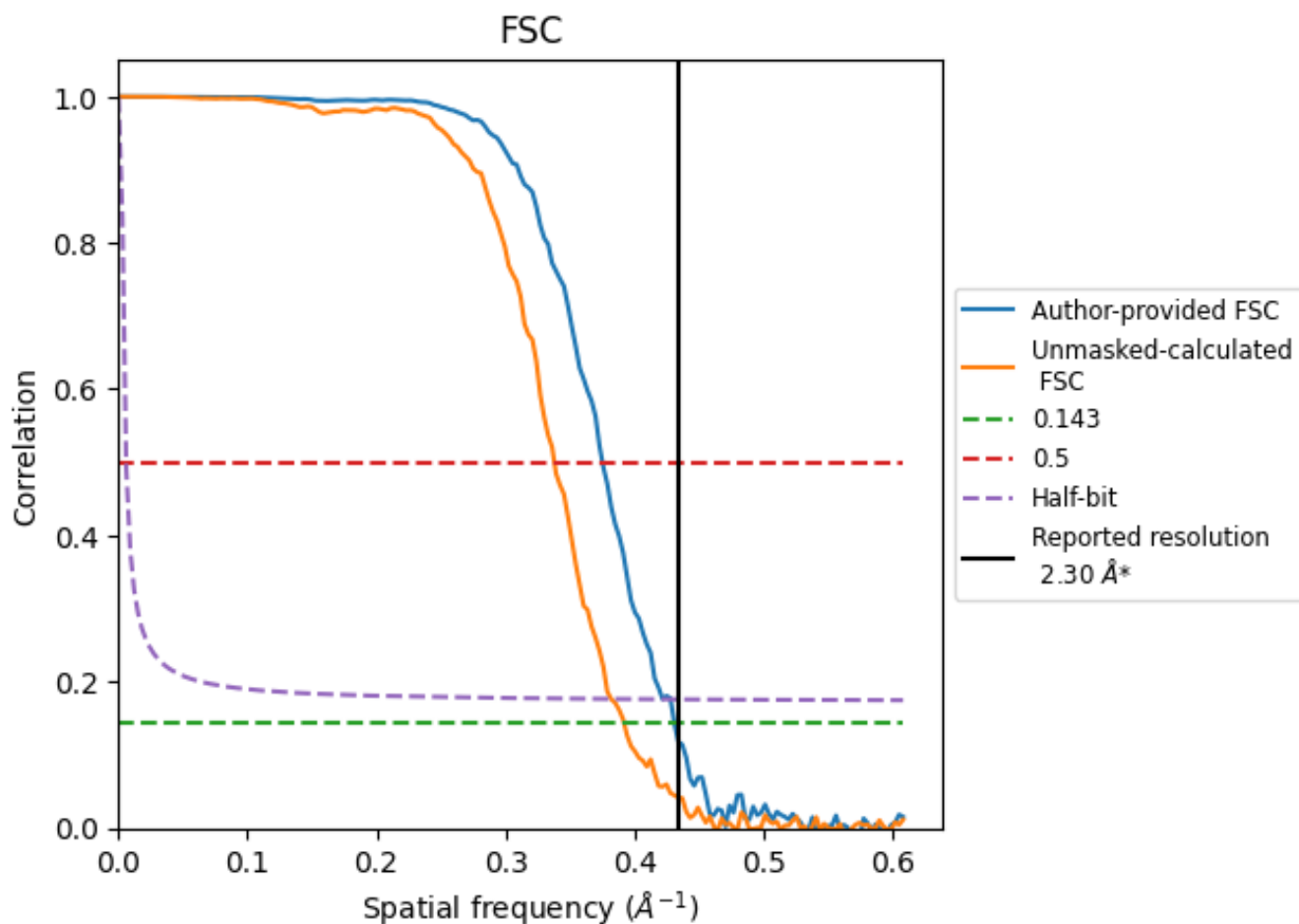


*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

8.2 Resolution estimates

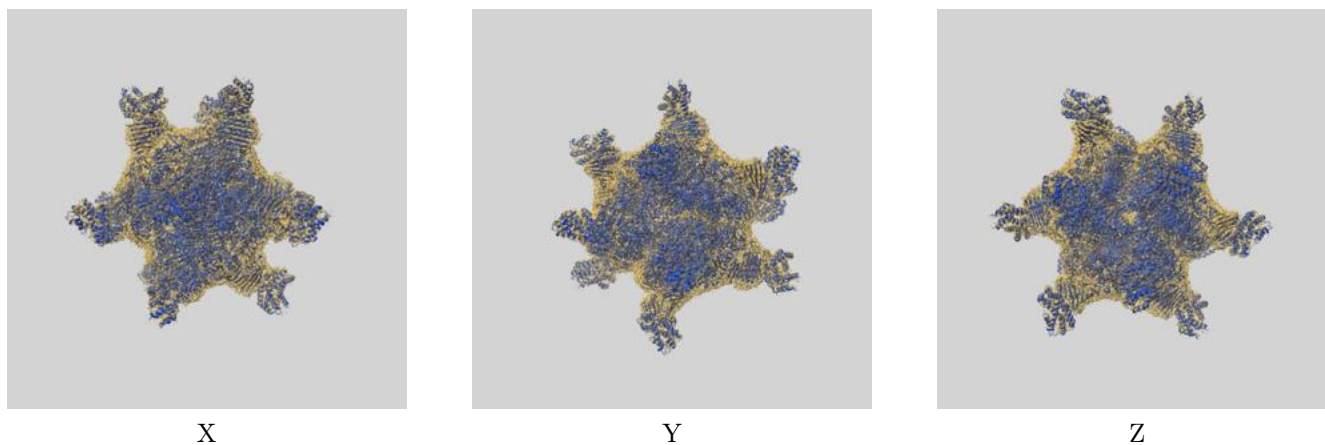
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	2.32	2.67	2.34
Unmasked-calculated*	2.55	2.96	2.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.55 differs from the reported value 2.3 by more than 10 %

9 Map-model fit [i](#)

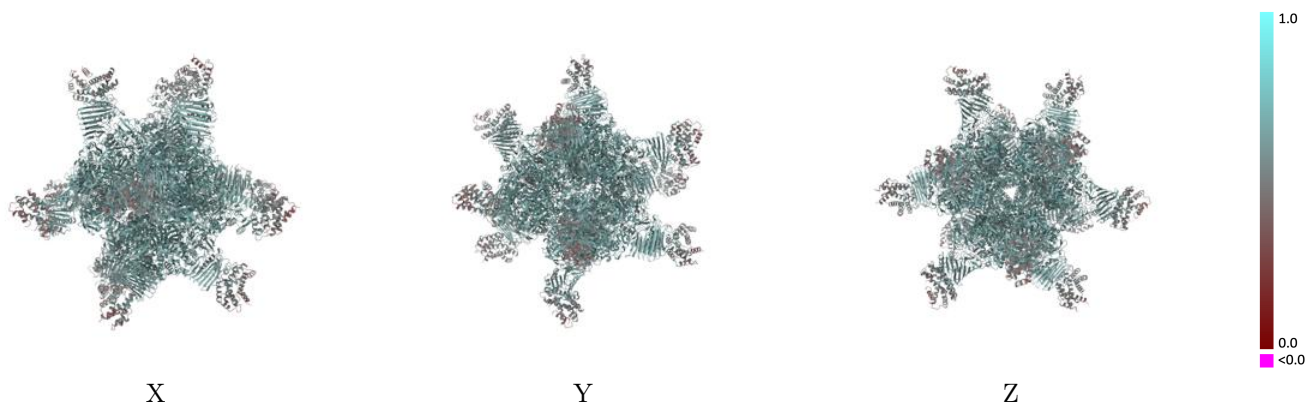
This section contains information regarding the fit between EMDB map EMD-34648 and PDB model 8HC1. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



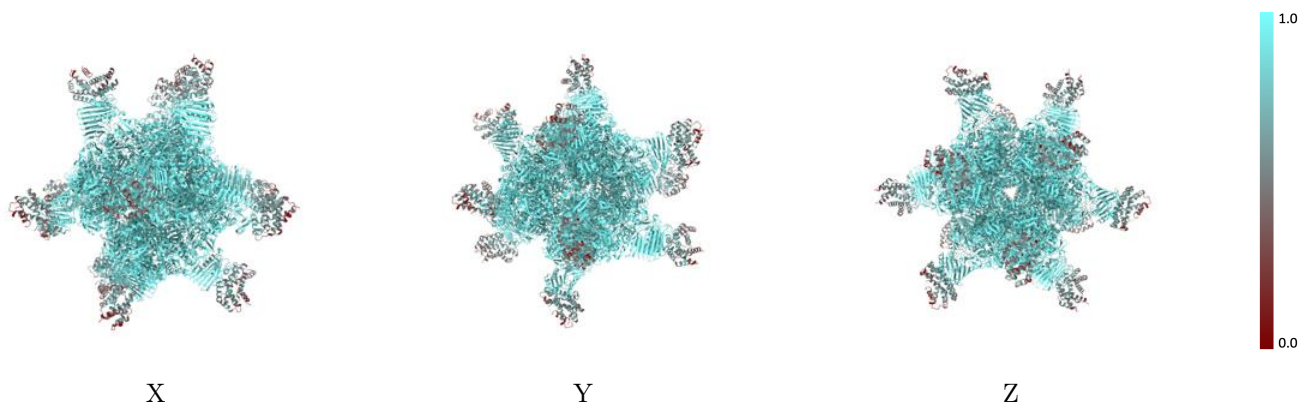
The images above show the 3D surface view of the map at the recommended contour level 0.0026525 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



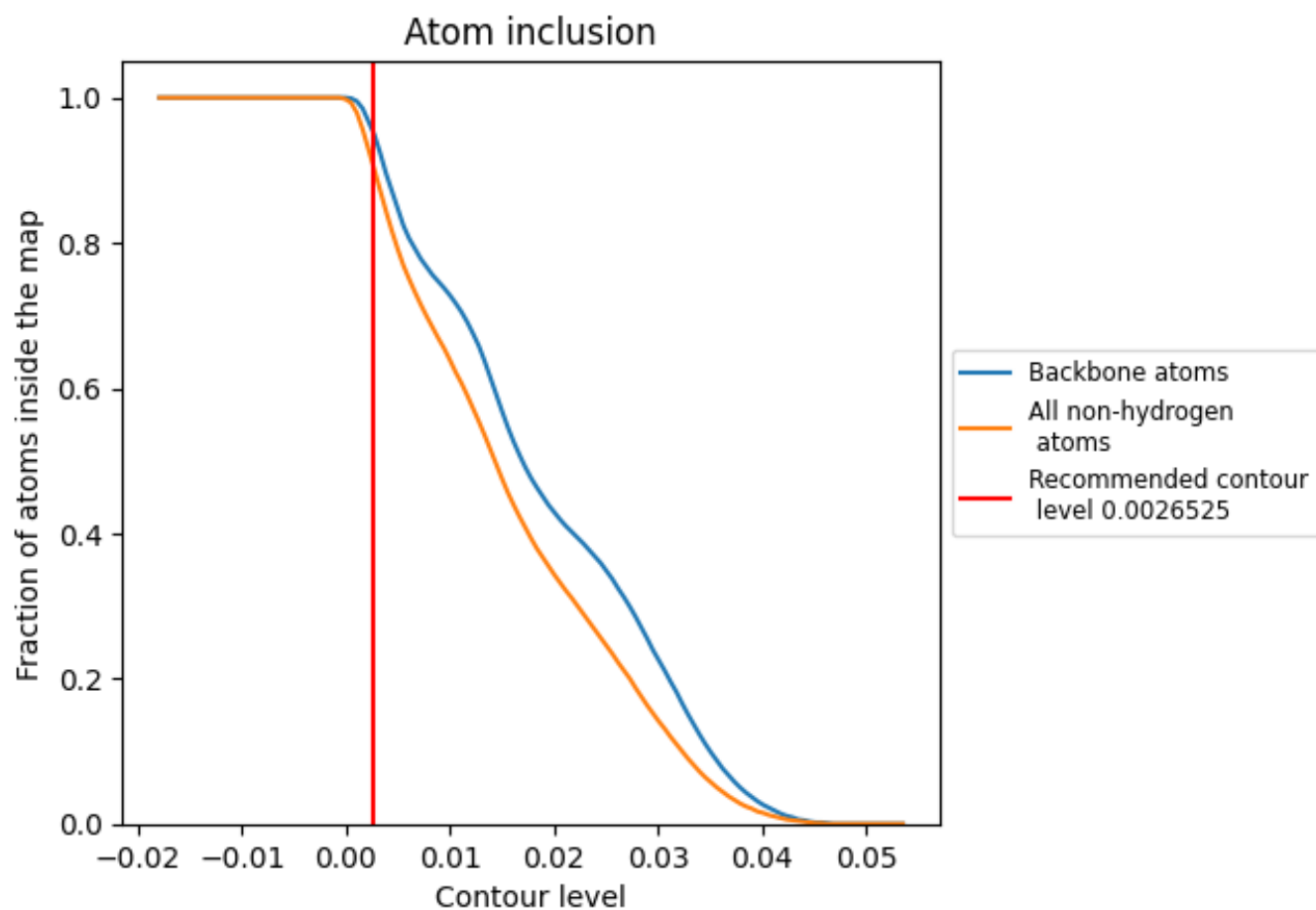
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0026525).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 90% 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 (0.0026525) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.6070
A	 0.9950	 0.6380
B	 0.9950	 0.6450
C	 0.9520	 0.6050
D	 0.5270	 0.4820
E	 0.9950	 0.6360
F	 0.9950	 0.6450
G	 0.9500	 0.6030
H	 0.5240	 0.4830
I	 0.9950	 0.6370
J	 0.9950	 0.6440
K	 0.9510	 0.6040
L	 0.5290	 0.4840
M	 0.9950	 0.6380
N	 0.9950	 0.6450
O	 0.9550	 0.6040
P	 0.5240	 0.4820
Q	 0.9950	 0.6360
R	 0.9950	 0.6450
S	 0.9550	 0.6050
T	 0.5340	 0.4870
U	 0.9960	 0.6350
V	 0.9950	 0.6450
W	 0.9530	 0.6060
X	 0.5260	 0.4830
Y	 0.9960	 0.6360
Z	 0.9950	 0.6450
a	 0.9540	 0.6040
b	 0.5200	 0.4820
c	 0.9950	 0.6360
d	 0.9950	 0.6450
e	 0.9550	 0.6040
f	 0.5190	 0.4830
g	 0.9950	 0.6370
h	 0.9950	 0.6440



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.9560	 0.6070
j	 0.5370	 0.4860
k	 0.9960	 0.6370
l	 0.9960	 0.6450
m	 0.9560	 0.6080
n	 0.5350	 0.4870
o	 0.9950	 0.6380
p	 0.9950	 0.6450
q	 0.9520	 0.6040
r	 0.5240	 0.4850
s	 0.9950	 0.6360
t	 0.9950	 0.6440
u	 0.9570	 0.6050
v	 0.5310	 0.4840