



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2024 – 04:01 PM EDT

PDB ID : 8VRK
EMDB ID : EMD-43483
Title : Rigid body fitted model for refined density map of gamma tubulin ring complex capped microtubule
Authors : Aher, A.; Urnavicius, L.; Kapoor, T.M.
Deposited on : 2024-01-22
Resolution : 8.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

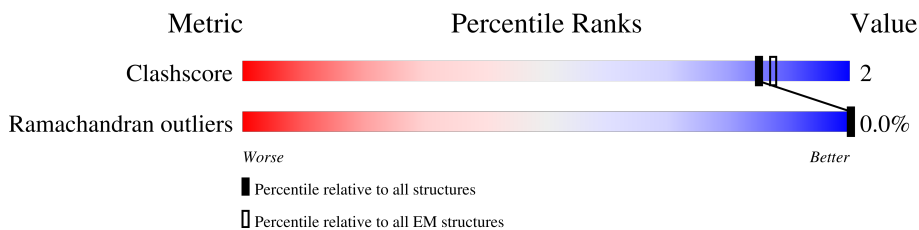
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.1

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 8.50 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.



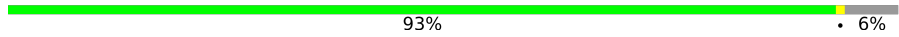
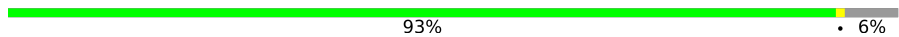

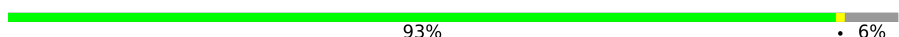

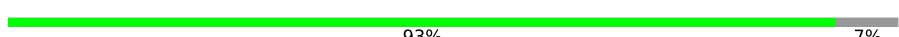




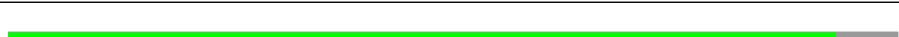


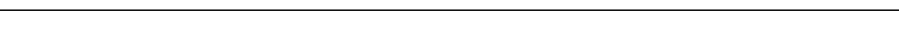
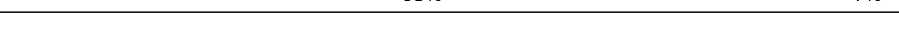
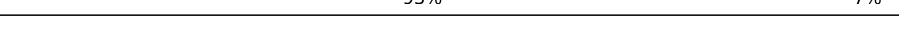
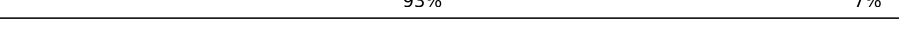
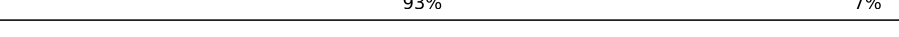

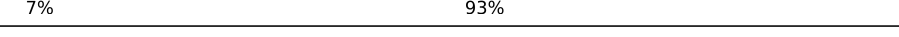





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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	1	457	93% • 6%
1	O	457	93% • 6%
1	P	457	93% • 6%
1	Q	457	93% • 6%
1	R	457	93% • 6%
1	S	457	93% • 6%
1	T	457	93% • 6%
1	U	457	93% • 6%
1	V	457	93% • 6%

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Mol	Chain	Length	Quality of chain
1	W	457	 93% • 6%
1	X	457	 93% • 6%
1	Y	457	 93% • 6%
1	Z	457	 93% • 6%
2	2	456	 91% • 7%
2	o	456	 93% 7%
2	p	456	 93% 7%
2	q	456	 93% 7%
2	r	456	 93% 7%
2	s	456	 93% 7%
2	t	456	 93% 7%
2	u	456	 93% 7%
2	v	456	 93% 7%
2	w	456	 93% 7%
2	x	456	 93% 7%
2	y	456	 93% 7%
2	z	456	 93% 7%
3	3	1811	 16% 84%
3	6	1811	 7% 93%
3	L	1811	 9% • 90%
4	5	907	 10% 90%
4	B	907	 61% • 39%
4	D	907	 61% 39%
4	F	907	 61% 39%
4	H	907	 61% 39%


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Mol	Chain	Length	Quality of chain
4	N	907	 5% 61% 39%
5	7	82	 77% 21%
5	8	82	 72% 28%
6	9	375	 10% 93% 6%
7	A	930	 7% 53% 46%
7	C	930	 53% 46%
7	E	930	 53% 46%
7	G	930	 53% 46%
7	M	930	 53% 46%
8	I	666	 73% 25%
8	K	666	 73% 25%
9	J	1024	 40% 59%
10	a	457	 9% 88% 12%
10	b	457	 88% 12%
10	c	457	 88% 12%
10	d	457	 88% 12%
10	e	457	 88% 12%
10	f	457	 88% 12%
10	g	457	 88% 12%
10	h	457	 88% 12%
10	i	457	 88% 12%
10	j	457	 88% 12%
10	k	457	 88% 12%
10	l	457	 88% 12%
10	m	457	 88% 12%

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Mol	Chain	Length	Quality of chain
10	n	457	 88% 12%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 121890 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 Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	1	431	2125	1263	431	431	0	0
1	O	431	2125	1263	431	431	0	0
1	P	431	2125	1263	431	431	0	0
1	Q	431	2125	1263	431	431	0	0
1	R	431	2125	1263	431	431	0	0
1	S	431	2125	1263	431	431	0	0
1	T	431	2125	1263	431	431	0	0
1	U	431	2125	1263	431	431	0	0
1	V	431	2125	1263	431	431	0	0
1	W	431	2125	1263	431	431	0	0
1	X	431	2125	1263	431	431	0	0
1	Y	431	2125	1263	431	431	0	0
1	Z	431	2125	1263	431	431	0	0

There are 91 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	37F	HIS	-	insertion	UNP P68363
1	37G	HIS	-	insertion	UNP P68363
1	37H	HIS	-	insertion	UNP P68363
1	37I	HIS	-	insertion	UNP P68363

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Chain	Residue	Modelled	Actual	Comment	Reference
1	37J	HIS	-	insertion	UNP P68363
1	37K	HIS	-	insertion	UNP P68363
1	254	ASP	GLU	conflict	UNP P68363
O	37F	HIS	-	insertion	UNP P68363
O	37G	HIS	-	insertion	UNP P68363
O	37H	HIS	-	insertion	UNP P68363
O	37I	HIS	-	insertion	UNP P68363
O	37J	HIS	-	insertion	UNP P68363
O	37K	HIS	-	insertion	UNP P68363
O	254	ASP	GLU	conflict	UNP P68363
P	37F	HIS	-	insertion	UNP P68363
P	37G	HIS	-	insertion	UNP P68363
P	37H	HIS	-	insertion	UNP P68363
P	37I	HIS	-	insertion	UNP P68363
P	37J	HIS	-	insertion	UNP P68363
P	37K	HIS	-	insertion	UNP P68363
P	254	ASP	GLU	conflict	UNP P68363
Q	37F	HIS	-	insertion	UNP P68363
Q	37G	HIS	-	insertion	UNP P68363
Q	37H	HIS	-	insertion	UNP P68363
Q	37I	HIS	-	insertion	UNP P68363
Q	37J	HIS	-	insertion	UNP P68363
Q	37K	HIS	-	insertion	UNP P68363
Q	254	ASP	GLU	conflict	UNP P68363
R	37F	HIS	-	insertion	UNP P68363
R	37G	HIS	-	insertion	UNP P68363
R	37H	HIS	-	insertion	UNP P68363
R	37I	HIS	-	insertion	UNP P68363
R	37J	HIS	-	insertion	UNP P68363
R	37K	HIS	-	insertion	UNP P68363
R	254	ASP	GLU	conflict	UNP P68363
S	37F	HIS	-	insertion	UNP P68363
S	37G	HIS	-	insertion	UNP P68363
S	37H	HIS	-	insertion	UNP P68363
S	37I	HIS	-	insertion	UNP P68363
S	37J	HIS	-	insertion	UNP P68363
S	37K	HIS	-	insertion	UNP P68363
S	254	ASP	GLU	conflict	UNP P68363
T	37F	HIS	-	insertion	UNP P68363
T	37G	HIS	-	insertion	UNP P68363
T	37H	HIS	-	insertion	UNP P68363
T	37I	HIS	-	insertion	UNP P68363

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Chain	Residue	Modelled	Actual	Comment	Reference
T	37J	HIS	-	insertion	UNP P68363
T	37K	HIS	-	insertion	UNP P68363
T	254	ASP	GLU	conflict	UNP P68363
U	37F	HIS	-	insertion	UNP P68363
U	37G	HIS	-	insertion	UNP P68363
U	37H	HIS	-	insertion	UNP P68363
U	37I	HIS	-	insertion	UNP P68363
U	37J	HIS	-	insertion	UNP P68363
U	37K	HIS	-	insertion	UNP P68363
U	254	ASP	GLU	conflict	UNP P68363
V	37F	HIS	-	insertion	UNP P68363
V	37G	HIS	-	insertion	UNP P68363
V	37H	HIS	-	insertion	UNP P68363
V	37I	HIS	-	insertion	UNP P68363
V	37J	HIS	-	insertion	UNP P68363
V	37K	HIS	-	insertion	UNP P68363
V	254	ASP	GLU	conflict	UNP P68363
W	37F	HIS	-	insertion	UNP P68363
W	37G	HIS	-	insertion	UNP P68363
W	37H	HIS	-	insertion	UNP P68363
W	37I	HIS	-	insertion	UNP P68363
W	37J	HIS	-	insertion	UNP P68363
W	37K	HIS	-	insertion	UNP P68363
W	254	ASP	GLU	conflict	UNP P68363
X	37F	HIS	-	insertion	UNP P68363
X	37G	HIS	-	insertion	UNP P68363
X	37H	HIS	-	insertion	UNP P68363
X	37I	HIS	-	insertion	UNP P68363
X	37J	HIS	-	insertion	UNP P68363
X	37K	HIS	-	insertion	UNP P68363
X	254	ASP	GLU	conflict	UNP P68363
Y	37F	HIS	-	insertion	UNP P68363
Y	37G	HIS	-	insertion	UNP P68363
Y	37H	HIS	-	insertion	UNP P68363
Y	37I	HIS	-	insertion	UNP P68363
Y	37J	HIS	-	insertion	UNP P68363
Y	37K	HIS	-	insertion	UNP P68363
Y	254	ASP	GLU	conflict	UNP P68363
Z	37F	HIS	-	insertion	UNP P68363
Z	37G	HIS	-	insertion	UNP P68363
Z	37H	HIS	-	insertion	UNP P68363
Z	37I	HIS	-	insertion	UNP P68363

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	37J	HIS	-	insertion	UNP P68363
Z	37K	HIS	-	insertion	UNP P68363
Z	254	ASP	GLU	conflict	UNP P68363

- Molecule 2 is a protein called Tubulin beta-3 chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	2	425	2093	1243	425	425	0	0
2	o	425	2093	1243	425	425	0	0
2	p	425	2093	1243	425	425	0	0
2	q	425	2093	1243	425	425	0	0
2	r	425	2093	1243	425	425	0	0
2	s	425	2093	1243	425	425	0	0
2	t	425	2093	1243	425	425	0	0
2	u	425	2093	1243	425	425	0	0
2	v	425	2093	1243	425	425	0	0
2	w	425	2093	1243	425	425	0	0
2	x	425	2093	1243	425	425	0	0
2	y	425	2093	1243	425	425	0	0
2	z	425	2093	1243	425	425	0	0

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	451	GLU	-	expression tag	UNP Q13509
2	452	ASN	-	expression tag	UNP Q13509
2	453	LEU	-	expression tag	UNP Q13509
2	454	TYR	-	expression tag	UNP Q13509
2	455	PHE	-	expression tag	UNP Q13509

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Chain	Residue	Modelled	Actual	Comment	Reference
2	456	GLN	-	expression tag	UNP Q13509
o	451	GLU	-	expression tag	UNP Q13509
o	452	ASN	-	expression tag	UNP Q13509
o	453	LEU	-	expression tag	UNP Q13509
o	454	TYR	-	expression tag	UNP Q13509
o	455	PHE	-	expression tag	UNP Q13509
o	456	GLN	-	expression tag	UNP Q13509
p	451	GLU	-	expression tag	UNP Q13509
p	452	ASN	-	expression tag	UNP Q13509
p	453	LEU	-	expression tag	UNP Q13509
p	454	TYR	-	expression tag	UNP Q13509
p	455	PHE	-	expression tag	UNP Q13509
p	456	GLN	-	expression tag	UNP Q13509
q	451	GLU	-	expression tag	UNP Q13509
q	452	ASN	-	expression tag	UNP Q13509
q	453	LEU	-	expression tag	UNP Q13509
q	454	TYR	-	expression tag	UNP Q13509
q	455	PHE	-	expression tag	UNP Q13509
q	456	GLN	-	expression tag	UNP Q13509
r	451	GLU	-	expression tag	UNP Q13509
r	452	ASN	-	expression tag	UNP Q13509
r	453	LEU	-	expression tag	UNP Q13509
r	454	TYR	-	expression tag	UNP Q13509
r	455	PHE	-	expression tag	UNP Q13509
r	456	GLN	-	expression tag	UNP Q13509
s	451	GLU	-	expression tag	UNP Q13509
s	452	ASN	-	expression tag	UNP Q13509
s	453	LEU	-	expression tag	UNP Q13509
s	454	TYR	-	expression tag	UNP Q13509
s	455	PHE	-	expression tag	UNP Q13509
s	456	GLN	-	expression tag	UNP Q13509
t	451	GLU	-	expression tag	UNP Q13509
t	452	ASN	-	expression tag	UNP Q13509
t	453	LEU	-	expression tag	UNP Q13509
t	454	TYR	-	expression tag	UNP Q13509
t	455	PHE	-	expression tag	UNP Q13509
t	456	GLN	-	expression tag	UNP Q13509
u	451	GLU	-	expression tag	UNP Q13509
u	452	ASN	-	expression tag	UNP Q13509
u	453	LEU	-	expression tag	UNP Q13509
u	454	TYR	-	expression tag	UNP Q13509
u	455	PHE	-	expression tag	UNP Q13509

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Chain	Residue	Modelled	Actual	Comment	Reference
u	456	GLN	-	expression tag	UNP Q13509
v	451	GLU	-	expression tag	UNP Q13509
v	452	ASN	-	expression tag	UNP Q13509
v	453	LEU	-	expression tag	UNP Q13509
v	454	TYR	-	expression tag	UNP Q13509
v	455	PHE	-	expression tag	UNP Q13509
v	456	GLN	-	expression tag	UNP Q13509
w	451	GLU	-	expression tag	UNP Q13509
w	452	ASN	-	expression tag	UNP Q13509
w	453	LEU	-	expression tag	UNP Q13509
w	454	TYR	-	expression tag	UNP Q13509
w	455	PHE	-	expression tag	UNP Q13509
w	456	GLN	-	expression tag	UNP Q13509
x	451	GLU	-	expression tag	UNP Q13509
x	452	ASN	-	expression tag	UNP Q13509
x	453	LEU	-	expression tag	UNP Q13509
x	454	TYR	-	expression tag	UNP Q13509
x	455	PHE	-	expression tag	UNP Q13509
x	456	GLN	-	expression tag	UNP Q13509
y	451	GLU	-	expression tag	UNP Q13509
y	452	ASN	-	expression tag	UNP Q13509
y	453	LEU	-	expression tag	UNP Q13509
y	454	TYR	-	expression tag	UNP Q13509
y	455	PHE	-	expression tag	UNP Q13509
y	456	GLN	-	expression tag	UNP Q13509
z	451	GLU	-	expression tag	UNP Q13509
z	452	ASN	-	expression tag	UNP Q13509
z	453	LEU	-	expression tag	UNP Q13509
z	454	TYR	-	expression tag	UNP Q13509
z	455	PHE	-	expression tag	UNP Q13509
z	456	GLN	-	expression tag	UNP Q13509

- Molecule 3 is a protein called TUBGCP6 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	3	288	Total	C	N	O	0	0
			1431	855	288	288		
3	6	123	Total	C	N	O	0	0
			608	362	123	123		
3	L	173	Total	C	N	O	0	0
			856	510	173	173		

- Molecule 4 is a protein called Gamma-tubulin complex component 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	5	90	Total	C	N	O	0	0
			447	267	90	90		
4	B	557	Total	C	N	O	0	0
			2766	1652	557	557		
4	D	557	Total	C	N	O	0	0
			2766	1652	557	557		
4	F	557	Total	C	N	O	0	0
			2766	1652	557	557		
4	H	557	Total	C	N	O	0	0
			2766	1652	557	557		
4	N	557	Total	C	N	O	0	0
			2766	1652	557	557		

- Molecule 5 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	7	65	Total	C	N	O	0	0
			323	193	65	65		
5	8	59	Total	C	N	O	0	0
			293	175	59	59		

- Molecule 6 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	9	354	Total	C	N	O	0	0
			1745	1037	354	354		

- Molecule 7 is a protein called Isoform 3 of Gamma-tubulin complex component 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	A	504	Total	C	N	O	0	0
			2504	1496	504	504		
7	C	504	Total	C	N	O	0	0
			2504	1496	504	504		
7	E	504	Total	C	N	O	0	0
			2504	1496	504	504		
7	G	504	Total	C	N	O	0	0
			2504	1496	504	504		
7	M	504	Total	C	N	O	0	0
			2504	1496	504	504		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	209	GLY	ARG	conflict	UNP Q9BSJ2
A	211	SER	ASN	conflict	UNP Q9BSJ2
A	229	GLY	ASN	conflict	UNP Q9BSJ2
C	209	GLY	ARG	conflict	UNP Q9BSJ2
C	211	SER	ASN	conflict	UNP Q9BSJ2
C	229	GLY	ASN	conflict	UNP Q9BSJ2
E	209	GLY	ARG	conflict	UNP Q9BSJ2
E	211	SER	ASN	conflict	UNP Q9BSJ2
E	229	GLY	ASN	conflict	UNP Q9BSJ2
G	209	GLY	ARG	conflict	UNP Q9BSJ2
G	211	SER	ASN	conflict	UNP Q9BSJ2
G	229	GLY	ASN	conflict	UNP Q9BSJ2
M	209	GLY	ARG	conflict	UNP Q9BSJ2
M	211	SER	ASN	conflict	UNP Q9BSJ2
M	229	GLY	ASN	conflict	UNP Q9BSJ2

- Molecule 8 is a protein called Isoform 2 of Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	I	497	Total	C	N	O	2	0
			2475	1477	499	499		
8	K	497	Total	C	N	O	2	0
			2475	1477	499	499		

- Molecule 9 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	J	417	Total	C	N	O	0	0
			2077	1243	417	417		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	198	GLY	ARG	conflict	UNP Q96RT8

- Molecule 10 is a protein called Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	a	404	Total	C	N	O	0	0
			1999	1191	404	404		
10	b	403	Total	C	N	O	0	0
			1994	1188	403	403		

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Mol	Chain	Residues	Atoms				AltConf	Trace
10	c	403	Total 1994	C 1188	N 403	O 403	0	0
10	d	404	Total 1999	C 1191	N 404	O 404	0	0
10	e	404	Total 1999	C 1191	N 404	O 404	0	0
10	f	404	Total 1999	C 1191	N 404	O 404	0	0
10	g	404	Total 1999	C 1191	N 404	O 404	0	0
10	h	404	Total 1999	C 1191	N 404	O 404	0	0
10	i	404	Total 1999	C 1191	N 404	O 404	0	0
10	j	404	Total 1999	C 1191	N 404	O 404	0	0
10	k	404	Total 1999	C 1191	N 404	O 404	0	0
10	l	404	Total 1999	C 1191	N 404	O 404	0	0
10	m	404	Total 1999	C 1191	N 404	O 404	0	0
10	n	404	Total 1999	C 1191	N 404	O 404	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	452	GLU	-	expression tag	UNP P23258
a	453	ASN	-	expression tag	UNP P23258
a	454	LEU	-	expression tag	UNP P23258
a	455	TYR	-	expression tag	UNP P23258
a	456	PHE	-	expression tag	UNP P23258
a	457	GLN	-	expression tag	UNP P23258
b	452	GLU	-	expression tag	UNP P23258
b	453	ASN	-	expression tag	UNP P23258
b	454	LEU	-	expression tag	UNP P23258
b	455	TYR	-	expression tag	UNP P23258
b	456	PHE	-	expression tag	UNP P23258
b	457	GLN	-	expression tag	UNP P23258
c	452	GLU	-	expression tag	UNP P23258
c	453	ASN	-	expression tag	UNP P23258
c	454	LEU	-	expression tag	UNP P23258

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Chain	Residue	Modelled	Actual	Comment	Reference
c	455	TYR	-	expression tag	UNP P23258
c	456	PHE	-	expression tag	UNP P23258
c	457	GLN	-	expression tag	UNP P23258
d	452	GLU	-	expression tag	UNP P23258
d	453	ASN	-	expression tag	UNP P23258
d	454	LEU	-	expression tag	UNP P23258
d	455	TYR	-	expression tag	UNP P23258
d	456	PHE	-	expression tag	UNP P23258
d	457	GLN	-	expression tag	UNP P23258
e	452	GLU	-	expression tag	UNP P23258
e	453	ASN	-	expression tag	UNP P23258
e	454	LEU	-	expression tag	UNP P23258
e	455	TYR	-	expression tag	UNP P23258
e	456	PHE	-	expression tag	UNP P23258
e	457	GLN	-	expression tag	UNP P23258
f	452	GLU	-	expression tag	UNP P23258
f	453	ASN	-	expression tag	UNP P23258
f	454	LEU	-	expression tag	UNP P23258
f	455	TYR	-	expression tag	UNP P23258
f	456	PHE	-	expression tag	UNP P23258
f	457	GLN	-	expression tag	UNP P23258
g	452	GLU	-	expression tag	UNP P23258
g	453	ASN	-	expression tag	UNP P23258
g	454	LEU	-	expression tag	UNP P23258
g	455	TYR	-	expression tag	UNP P23258
g	456	PHE	-	expression tag	UNP P23258
g	457	GLN	-	expression tag	UNP P23258
h	452	GLU	-	expression tag	UNP P23258
h	453	ASN	-	expression tag	UNP P23258
h	454	LEU	-	expression tag	UNP P23258
h	455	TYR	-	expression tag	UNP P23258
h	456	PHE	-	expression tag	UNP P23258
h	457	GLN	-	expression tag	UNP P23258
i	452	GLU	-	expression tag	UNP P23258
i	453	ASN	-	expression tag	UNP P23258
i	454	LEU	-	expression tag	UNP P23258
i	455	TYR	-	expression tag	UNP P23258
i	456	PHE	-	expression tag	UNP P23258
i	457	GLN	-	expression tag	UNP P23258
j	452	GLU	-	expression tag	UNP P23258
j	453	ASN	-	expression tag	UNP P23258
j	454	LEU	-	expression tag	UNP P23258

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Chain	Residue	Modelled	Actual	Comment	Reference
j	455	TYR	-	expression tag	UNP P23258
j	456	PHE	-	expression tag	UNP P23258
j	457	GLN	-	expression tag	UNP P23258
k	452	GLU	-	expression tag	UNP P23258
k	453	ASN	-	expression tag	UNP P23258
k	454	LEU	-	expression tag	UNP P23258
k	455	TYR	-	expression tag	UNP P23258
k	456	PHE	-	expression tag	UNP P23258
k	457	GLN	-	expression tag	UNP P23258
l	452	GLU	-	expression tag	UNP P23258
l	453	ASN	-	expression tag	UNP P23258
l	454	LEU	-	expression tag	UNP P23258
l	455	TYR	-	expression tag	UNP P23258
l	456	PHE	-	expression tag	UNP P23258
l	457	GLN	-	expression tag	UNP P23258
m	452	GLU	-	expression tag	UNP P23258
m	453	ASN	-	expression tag	UNP P23258
m	454	LEU	-	expression tag	UNP P23258
m	455	TYR	-	expression tag	UNP P23258
m	456	PHE	-	expression tag	UNP P23258
m	457	GLN	-	expression tag	UNP P23258
n	452	GLU	-	expression tag	UNP P23258
n	453	ASN	-	expression tag	UNP P23258
n	454	LEU	-	expression tag	UNP P23258
n	455	TYR	-	expression tag	UNP P23258
n	456	PHE	-	expression tag	UNP P23258
n	457	GLN	-	expression tag	UNP P23258

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.

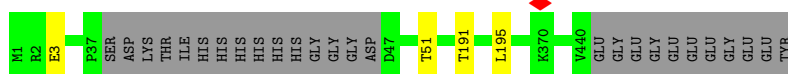
- Molecule 1: Tubulin alpha-1B chain

Chain 1:  93% 6%



- Molecule 1: Tubulin alpha-1B chain

Chain O:  93% 6%



- Molecule 1: Tubulin alpha-1B chain

Chain P:  93% 6%



- Molecule 1: Tubulin alpha-1B chain

Chain Q:  93% 6%



- Molecule 1: Tubulin alpha-1B chain

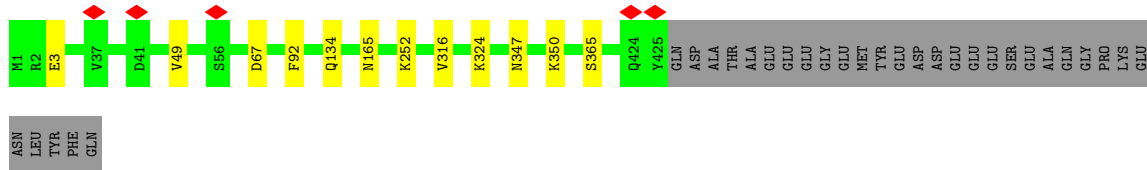
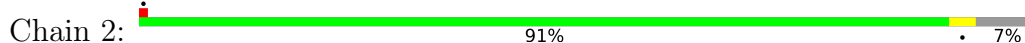
Chain R:  93% 6%



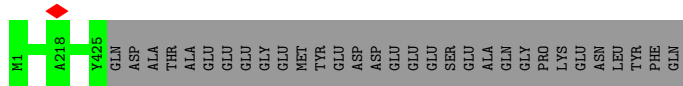
- Molecule 1: Tubulin alpha-1B chain



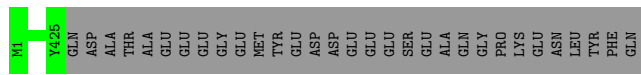
• Molecule 2: Tubulin beta-3 chain



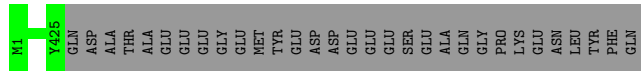
• Molecule 2: Tubulin beta-3 chain



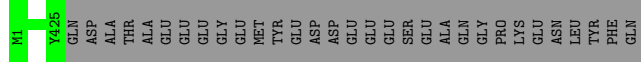
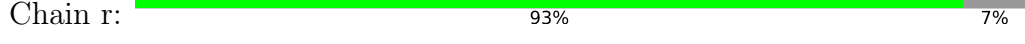
• Molecule 2: Tubulin beta-3 chain



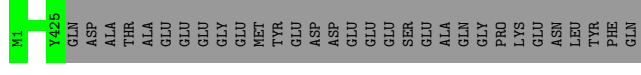
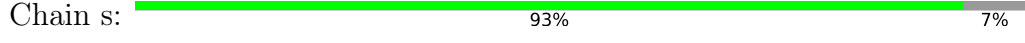
• Molecule 2: Tubulin beta-3 chain



• Molecule 2: Tubulin beta-3 chain



• Molecule 2: Tubulin beta-3 chain



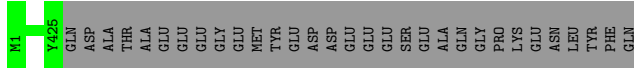
- Molecule 2: Tubulin beta-3 chain

Chain t:  93% 7%



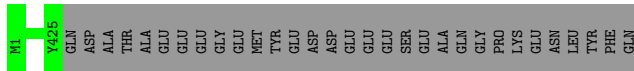
- Molecule 2: Tubulin beta-3 chain

Chain u:  93% 7%



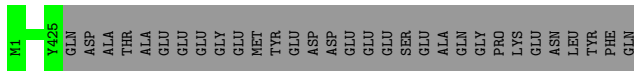
- Molecule 2: Tubulin beta-3 chain

Chain v:  93% 7%



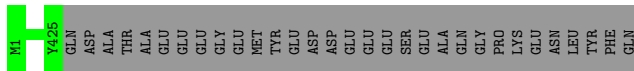
- Molecule 2: Tubulin beta-3 chain

Chain w:  93% 7%



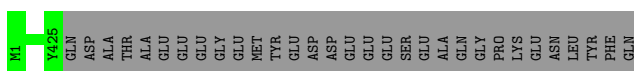
- Molecule 2: Tubulin beta-3 chain

Chain x:  93% 7%



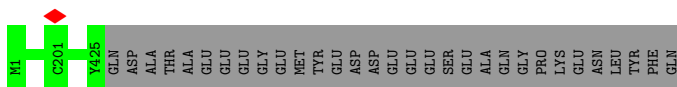
- Molecule 2: Tubulin beta-3 chain

Chain y:  93% 7%

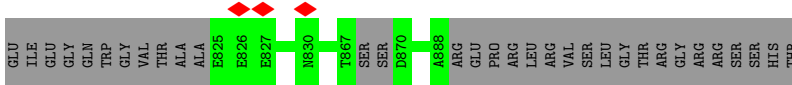


- Molecule 2: Tubulin beta-3 chain

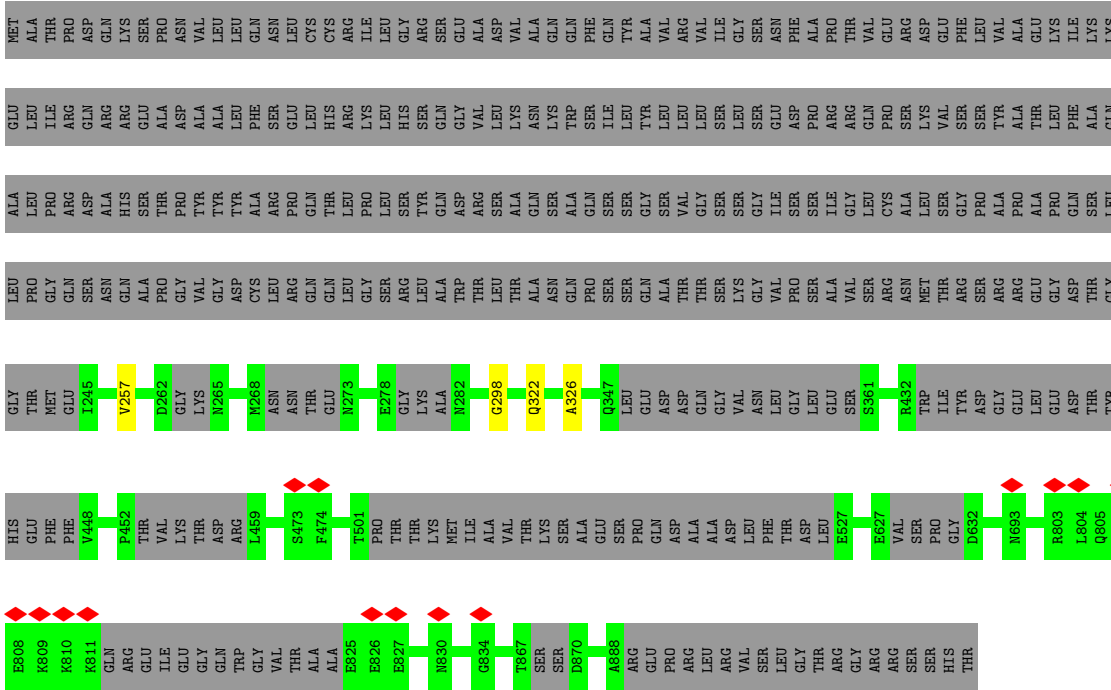
Chain z:  93% 7%



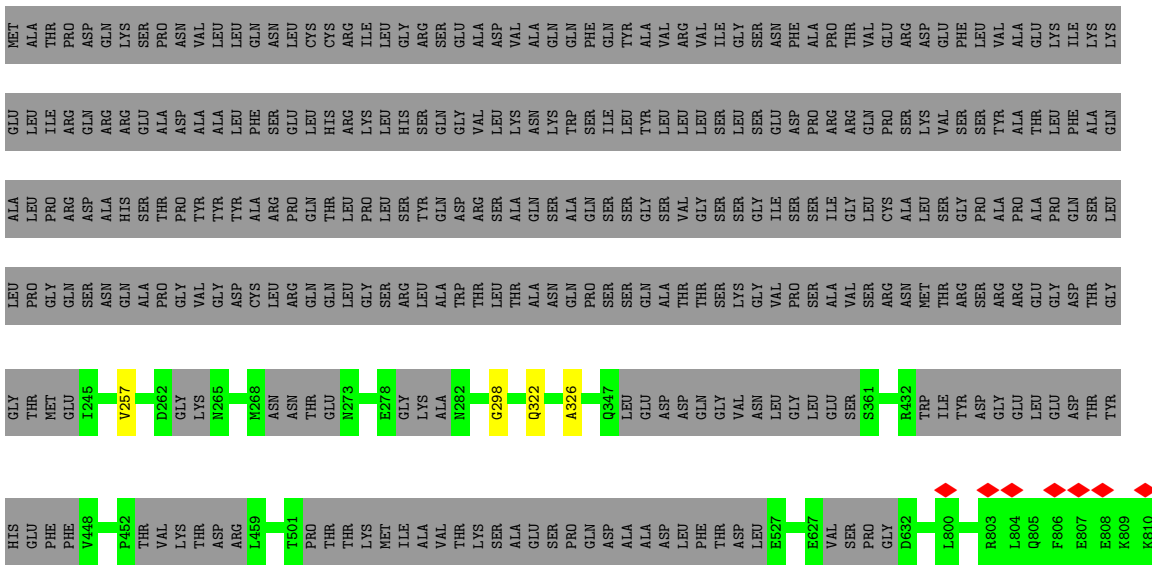
- Molecule 3: TUBGCP6 protein

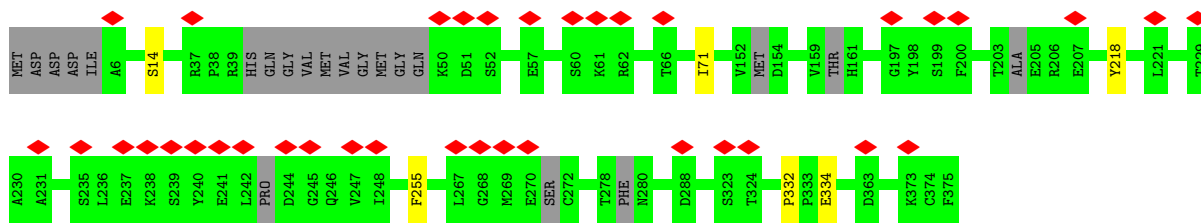


• Molecule 4: Gamma-tubulin complex component 3

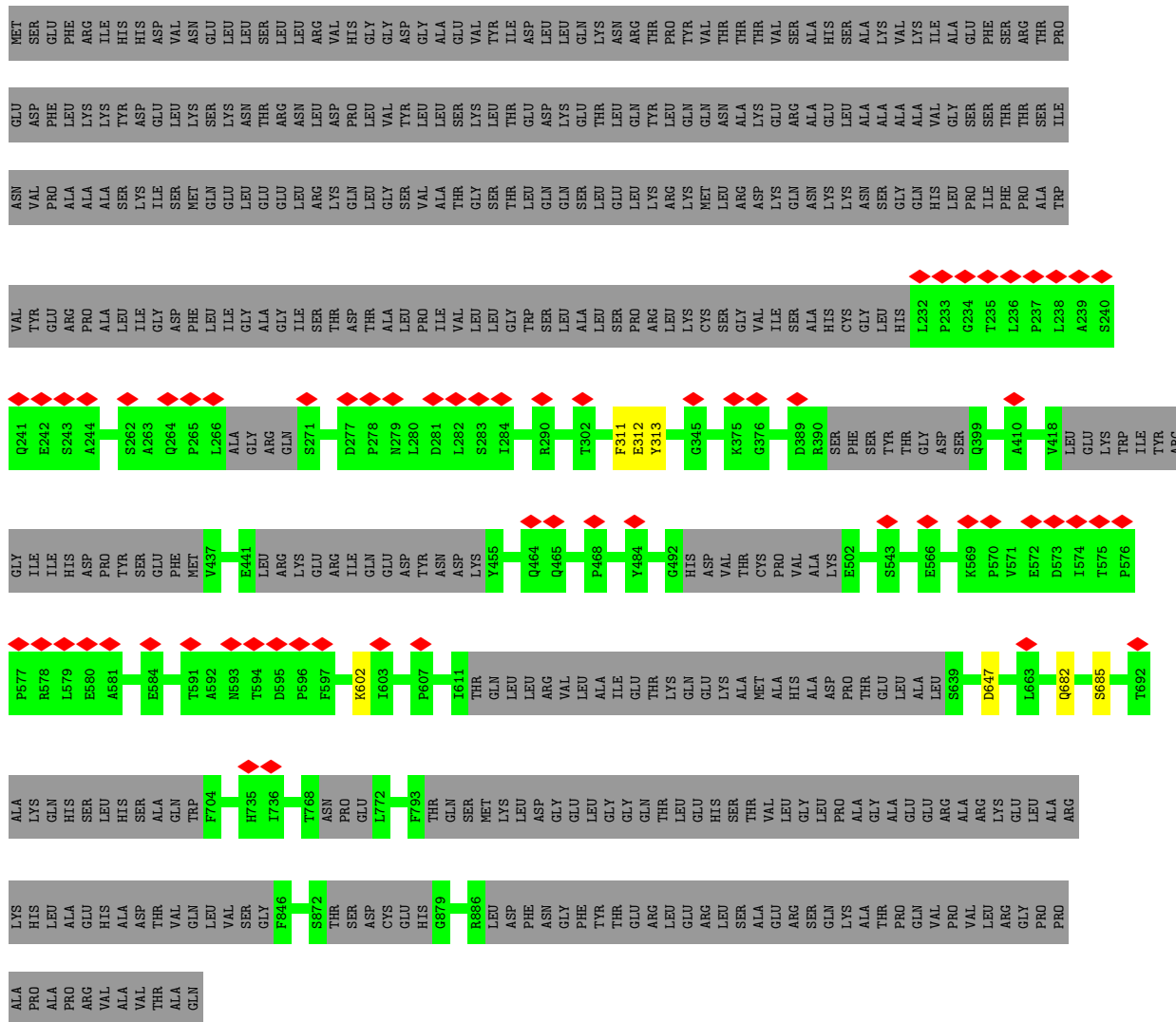


• Molecule 4: Gamma-tubulin complex component 3

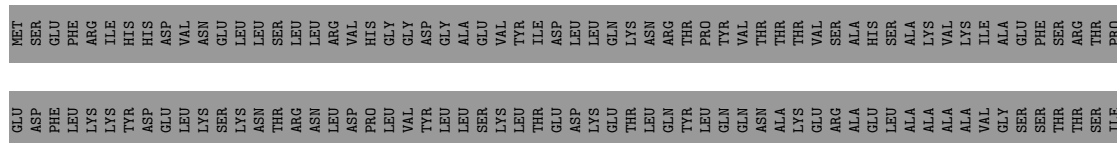


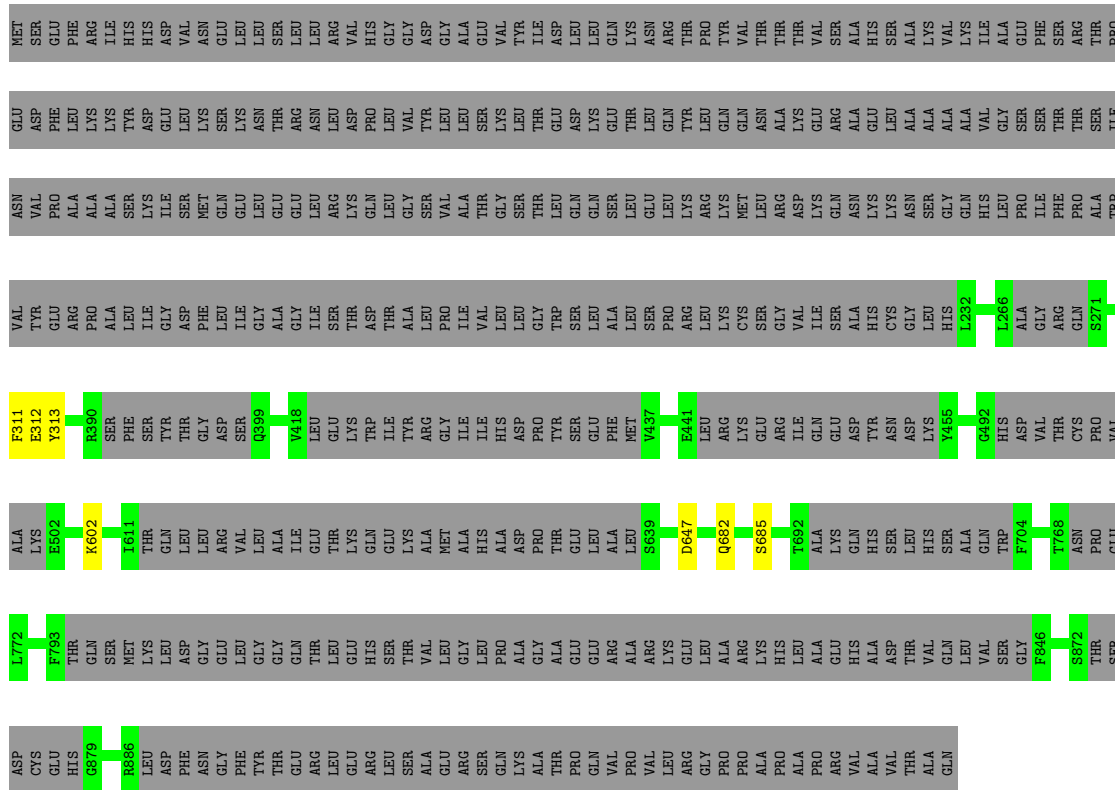


• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

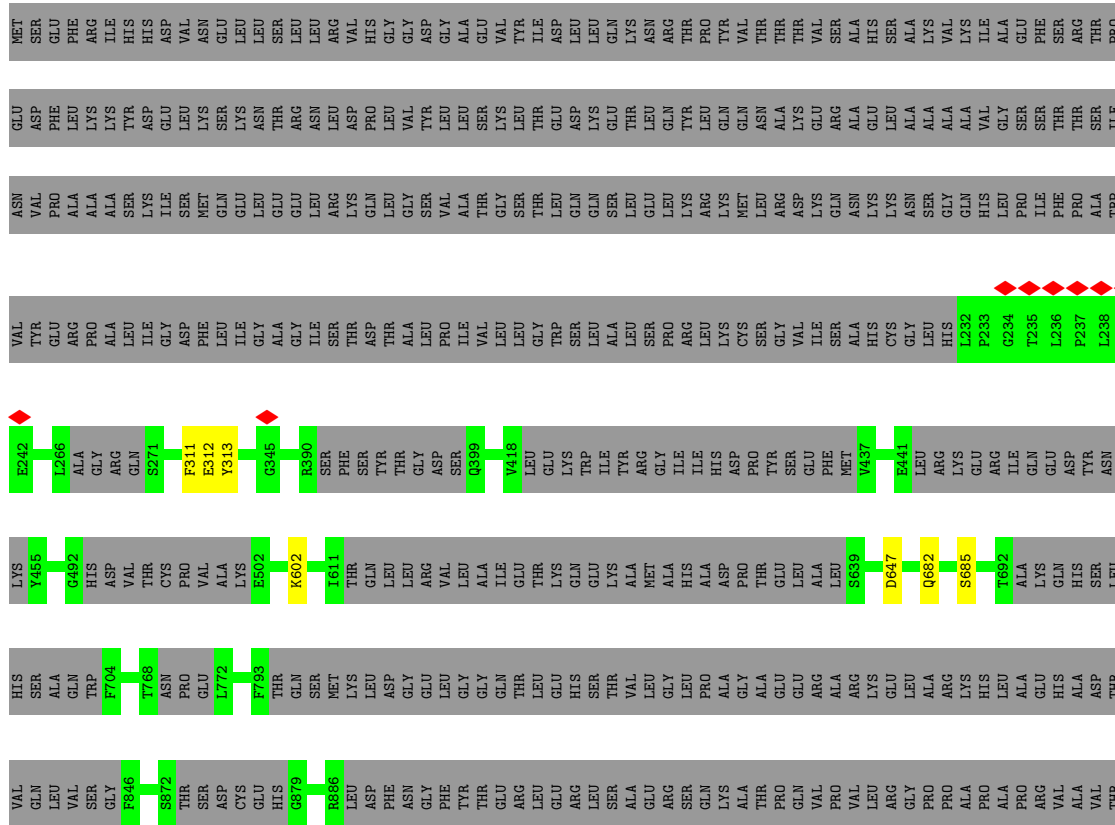


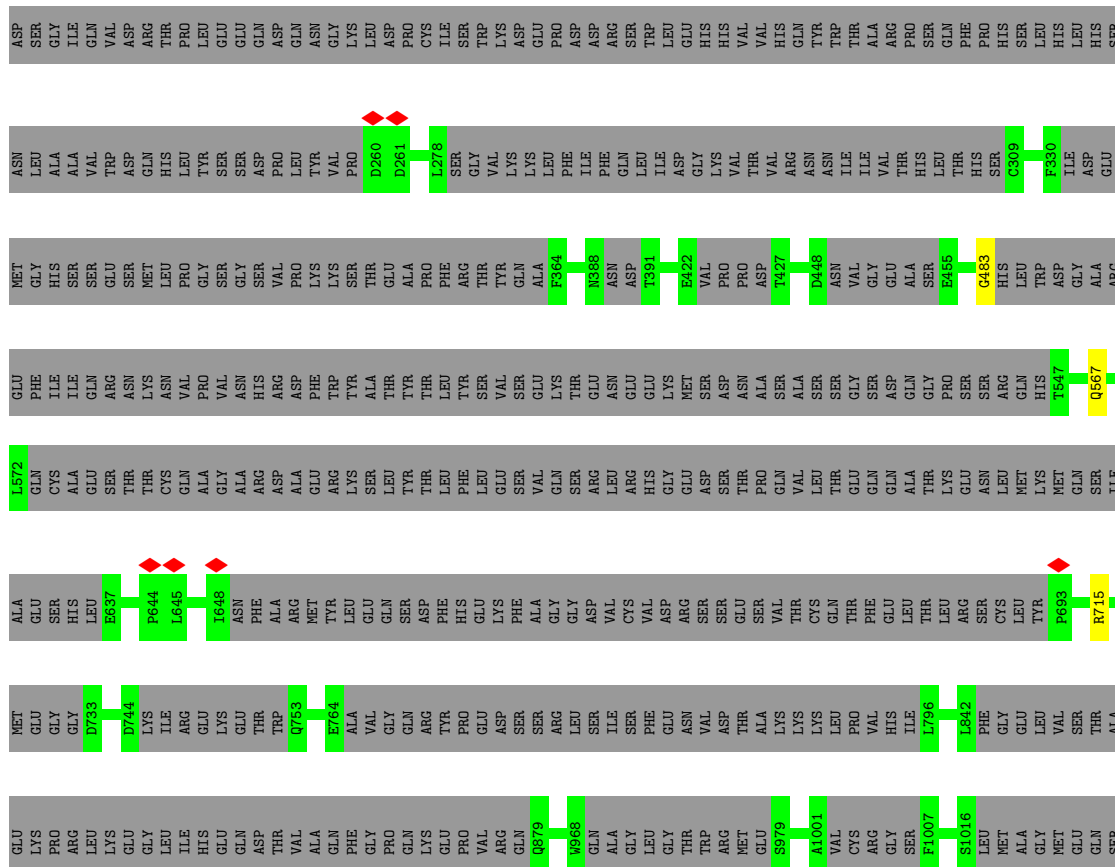
• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2



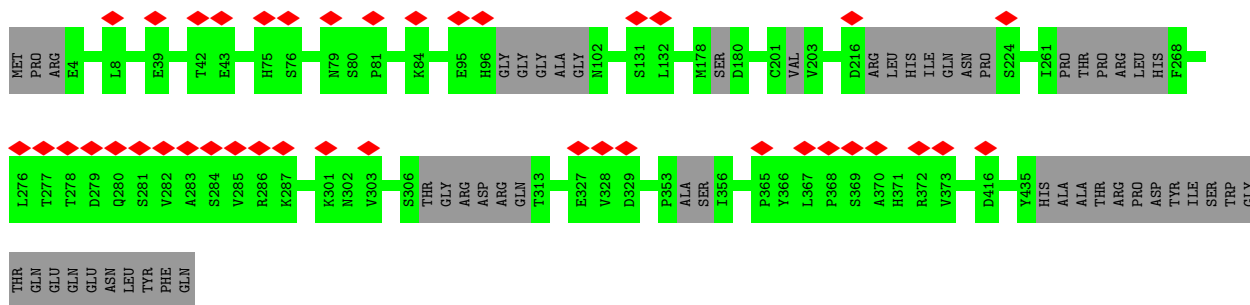
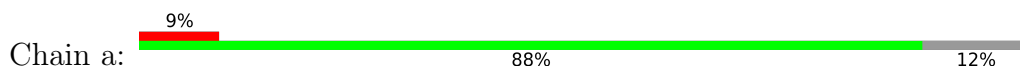


- Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

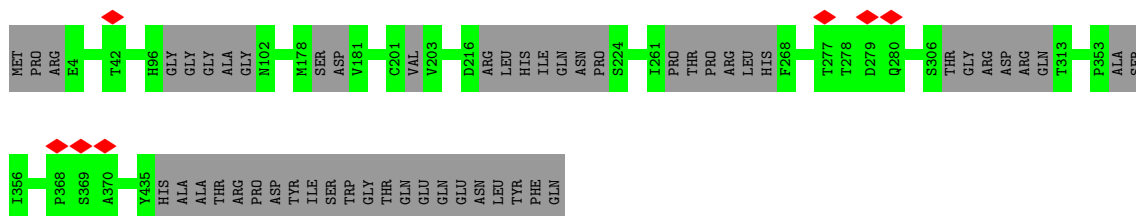
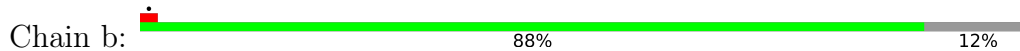





• Molecule 10: Tubulin gamma-1 chain

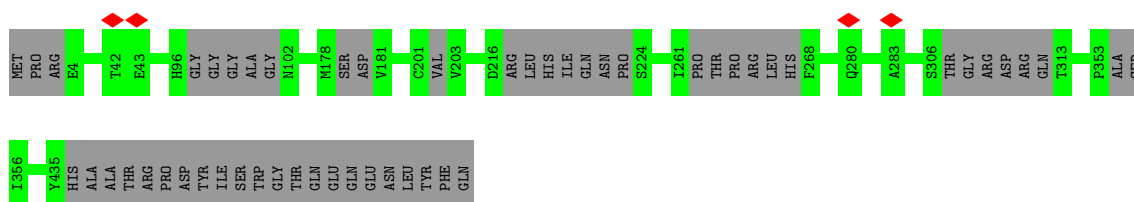


• Molecule 10: Tubulin gamma-1 chain




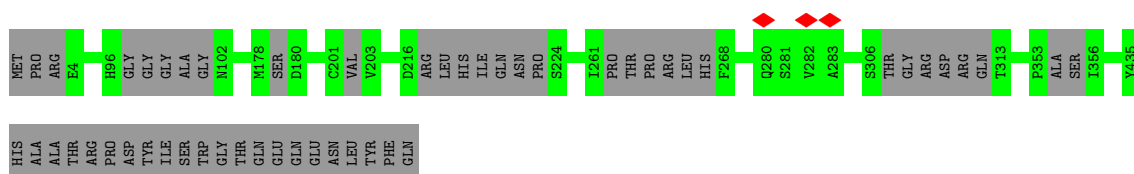
- Molecule 10: Tubulin gamma-1 chain

Chain c:  88% 12%




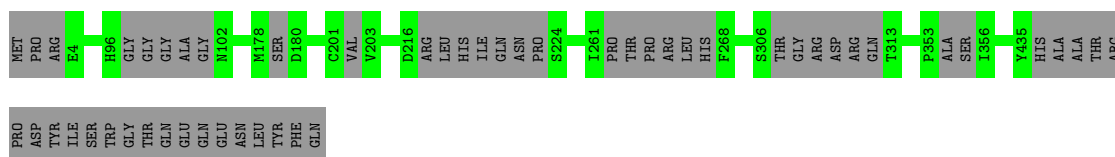
- Molecule 10: Tubulin gamma-1 chain

Chain d:  88% 12%




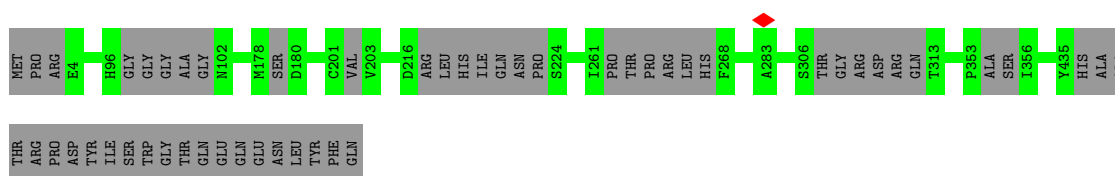
- Molecule 10: Tubulin gamma-1 chain

Chain e:  88% 12%




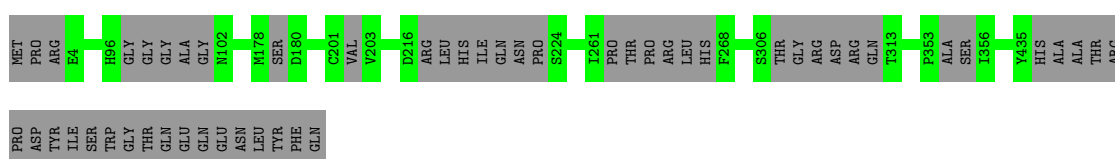
- Molecule 10: Tubulin gamma-1 chain

Chain f:  88% 12%

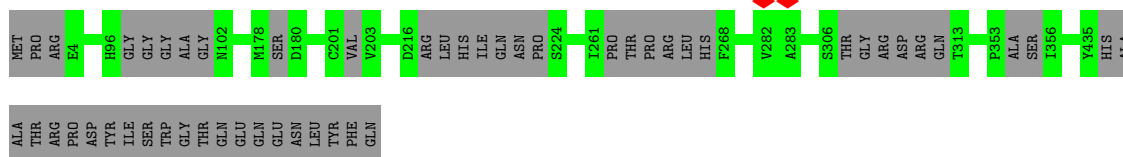
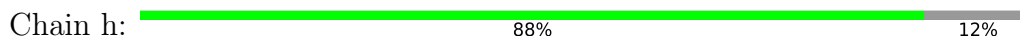


- Molecule 10: Tubulin gamma-1 chain

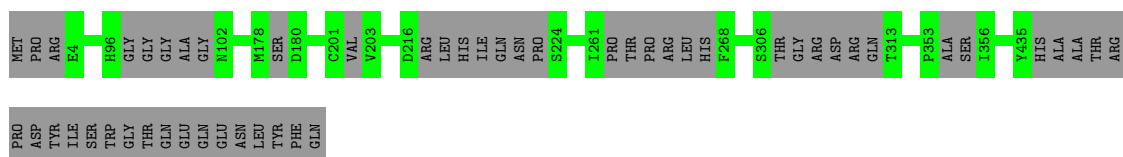
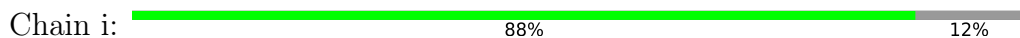
Chain g:  88% 12%



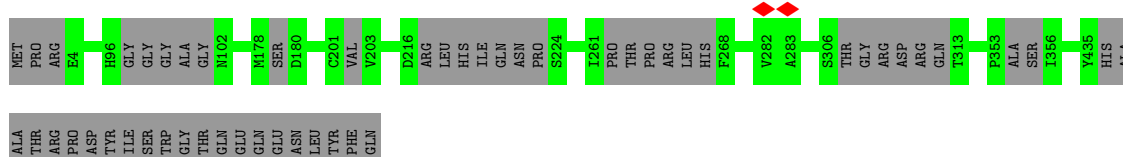
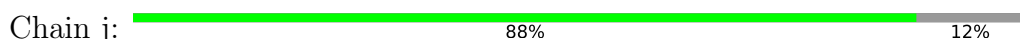
• Molecule 10: Tubulin gamma-1 chain



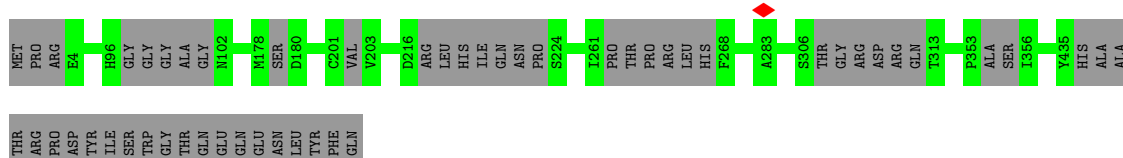
• Molecule 10: Tubulin gamma-1 chain



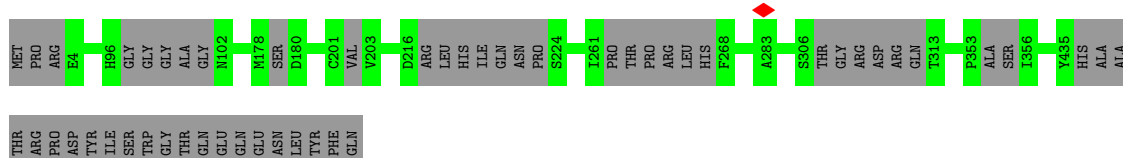
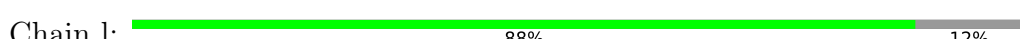
• Molecule 10: Tubulin gamma-1 chain




• Molecule 10: Tubulin gamma-1 chain

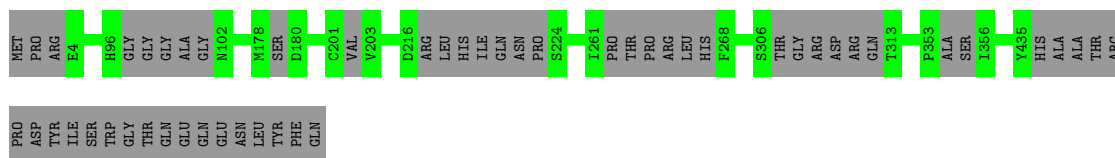


• Molecule 10: Tubulin gamma-1 chain




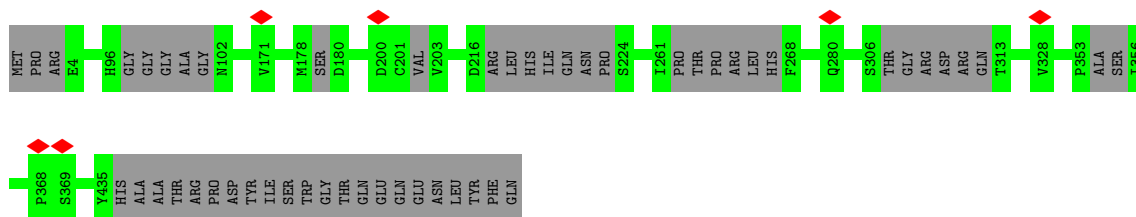
• Molecule 10: Tubulin gamma-1 chain

Chain m:  88% 12%



• Molecule 10: Tubulin gamma-1 chain

Chain n:  88% 12%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9856	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	475.2, 475.2, 475.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	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	1	0.26	0/2123	0.44	0/2951
1	O	0.26	0/2123	0.44	0/2951
1	P	0.26	0/2123	0.44	0/2951
1	Q	0.26	0/2123	0.44	0/2951
1	R	0.26	0/2123	0.44	0/2951
1	S	0.26	0/2123	0.44	0/2951
1	T	0.26	0/2123	0.44	0/2951
1	U	0.26	0/2123	0.44	0/2951
1	V	0.26	0/2123	0.44	0/2951
1	W	0.26	0/2123	0.44	0/2951
1	X	0.26	0/2123	0.44	0/2951
1	Y	0.26	0/2123	0.44	0/2951
1	Z	0.26	0/2123	0.44	0/2951
2	2	0.26	0/2092	0.47	0/2908
2	o	0.26	0/2092	0.47	0/2908
2	p	0.26	0/2092	0.47	0/2908
2	q	0.26	0/2092	0.47	0/2908
2	r	0.26	0/2092	0.47	0/2908
2	s	0.26	0/2092	0.47	0/2908
2	t	0.26	0/2092	0.47	0/2908
2	u	0.26	0/2092	0.47	0/2908
2	v	0.26	0/2092	0.47	0/2908
2	w	0.26	0/2092	0.47	0/2908
2	x	0.26	0/2092	0.47	0/2908
2	y	0.26	0/2092	0.47	0/2908
2	z	0.26	0/2092	0.47	0/2908
3	3	0.27	0/1422	0.41	0/1971
3	6	0.23	0/603	0.39	0/832
3	L	0.25	0/851	0.41	0/1178
4	5	0.24	0/446	0.39	0/621
4	B	0.32	0/2755	0.45	0/3828
4	D	0.32	0/2755	0.45	0/3828
4	F	0.32	0/2755	0.45	0/3828
4	H	0.32	0/2755	0.45	0/3828

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	N	0.32	0/2755	0.45	0/3828
5	7	0.23	0/322	0.36	0/448
5	8	0.22	0/292	0.35	0/406
6	9	0.24	0/1737	0.59	0/2404
7	A	0.30	0/2493	0.44	0/3463
7	C	0.30	0/2493	0.44	0/3463
7	E	0.30	0/2493	0.44	0/3463
7	G	0.30	0/2493	0.44	0/3463
7	M	0.30	0/2493	0.44	0/3463
8	I	0.35	0/2468	0.44	0/3432
8	K	0.35	0/2468	0.44	0/3432
9	J	0.32	0/2062	0.41	0/2858
10	a	0.24	0/1991	0.45	0/2762
10	b	0.24	0/1986	0.45	0/2755
10	c	0.24	0/1986	0.45	0/2755
10	d	0.24	0/1991	0.45	0/2762
10	e	0.24	0/1991	0.45	0/2762
10	f	0.25	0/1991	0.45	0/2762
10	g	0.25	0/1991	0.45	0/2762
10	h	0.24	0/1991	0.45	0/2762
10	i	0.24	0/1991	0.45	0/2762
10	j	0.24	0/1991	0.45	0/2762
10	k	0.24	0/1991	0.45	0/2762
10	l	0.24	0/1991	0.45	0/2762
10	m	0.24	0/1991	0.45	0/2762
10	n	0.25	0/1991	0.45	0/2762
All	All	0.27	0/121570	0.45	0/168858

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](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	2125	0	981	7	0
1	O	2125	0	981	2	0
1	P	2125	0	981	2	0
1	Q	2125	0	981	3	0
1	R	2125	0	981	3	0
1	S	2125	0	981	2	0
1	T	2125	0	981	2	0
1	U	2125	0	981	3	0
1	V	2125	0	981	3	0
1	W	2125	0	981	3	0
1	X	2125	0	981	3	0
1	Y	2125	0	981	4	0
1	Z	2125	0	981	3	0
2	2	2093	0	946	9	0
2	o	2093	0	946	0	0
2	p	2093	0	946	0	0
2	q	2093	0	946	0	0
2	r	2093	0	946	0	0
2	s	2093	0	946	0	0
2	t	2093	0	946	0	0
2	u	2093	0	946	0	0
2	v	2093	0	946	0	0
2	w	2093	0	946	0	0
2	x	2093	0	946	0	0
2	y	2093	0	946	0	0
2	z	2093	0	946	0	0
3	3	1431	0	633	1	0
3	6	608	0	276	7	0
3	L	856	0	368	9	0
4	5	447	0	205	5	0
4	B	2766	0	1210	4	0
4	D	2766	0	1210	2	0
4	F	2766	0	1210	2	0
4	H	2766	0	1210	2	0
4	N	2766	0	1210	2	0
5	7	323	0	160	2	0
5	8	293	0	130	0	0
6	9	1745	0	791	6	0
7	A	2504	0	1103	4	0
7	C	2504	0	1103	6	0
7	E	2504	0	1103	4	0
7	G	2504	0	1103	4	0
7	M	2504	0	1103	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	I	2475	0	1069	4	0
8	K	2475	0	1069	6	0
9	J	2077	0	877	1	0
10	a	1999	0	865	0	0
10	b	1994	0	863	0	0
10	c	1994	0	863	0	0
10	d	1999	0	865	0	0
10	e	1999	0	865	0	0
10	f	1999	0	865	0	0
10	g	1999	0	865	0	0
10	h	1999	0	865	0	0
10	i	1999	0	865	0	0
10	j	1999	0	865	0	0
10	k	1999	0	865	0	0
10	l	1999	0	865	0	0
10	m	1999	0	865	0	0
10	n	1999	0	865	0	0
All	All	121890	0	54300	106	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 106 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:26:ALA:HA	3:6:65:PRO:CB	1.61	1.27
3:L:539:TRP:CB	3:L:599:GLY:HA2	1.82	1.10
3:6:4:ILE:N	6:9:332:PRO:HA	1.67	1.08
4:5:26:ALA:CA	3:6:65:PRO:CB	2.38	1.02
1:1:100:ALA:HB1	2:2:252:LYS:HA	1.58	0.85

There are no symmetry-related clashes.

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	1	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	O	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	P	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	Q	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	R	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	S	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	T	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	U	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	V	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	W	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	X	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	Y	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
1	Z	427/457 (93%)	410 (96%)	17 (4%)	0	100	100
2	2	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	o	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	p	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	q	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	r	423/456 (93%)	409 (97%)	14 (3%)	0	100	100
2	s	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	t	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	u	423/456 (93%)	409 (97%)	14 (3%)	0	100	100
2	v	423/456 (93%)	409 (97%)	14 (3%)	0	100	100
2	w	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	x	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
2	y	423/456 (93%)	409 (97%)	14 (3%)	0	100	100
2	z	423/456 (93%)	410 (97%)	13 (3%)	0	100	100
3	3	270/1811 (15%)	253 (94%)	17 (6%)	0	100	100
3	6	113/1811 (6%)	111 (98%)	2 (2%)	0	100	100
3	L	163/1811 (9%)	151 (93%)	12 (7%)	0	100	100
4	5	88/907 (10%)	85 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	535/907 (59%)	513 (96%)	22 (4%)	0	100	100
4	D	535/907 (59%)	513 (96%)	22 (4%)	0	100	100
4	F	535/907 (59%)	513 (96%)	22 (4%)	0	100	100
4	H	535/907 (59%)	513 (96%)	22 (4%)	0	100	100
4	N	535/907 (59%)	512 (96%)	23 (4%)	0	100	100
5	7	63/82 (77%)	63 (100%)	0	0	100	100
5	8	57/82 (70%)	55 (96%)	2 (4%)	0	100	100
6	9	338/375 (90%)	331 (98%)	7 (2%)	0	100	100
7	A	482/930 (52%)	446 (92%)	35 (7%)	1 (0%)	47	81
7	C	482/930 (52%)	445 (92%)	36 (8%)	1 (0%)	47	81
7	E	482/930 (52%)	445 (92%)	36 (8%)	1 (0%)	47	81
7	G	482/930 (52%)	446 (92%)	35 (7%)	1 (0%)	47	81
7	M	482/930 (52%)	446 (92%)	35 (7%)	1 (0%)	47	81
8	I	485/666 (73%)	457 (94%)	26 (5%)	2 (0%)	34	72
8	K	485/666 (73%)	456 (94%)	27 (6%)	2 (0%)	34	72
9	J	387/1024 (38%)	375 (97%)	11 (3%)	1 (0%)	41	77
10	a	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	b	387/457 (85%)	366 (95%)	21 (5%)	0	100	100
10	c	387/457 (85%)	366 (95%)	21 (5%)	0	100	100
10	d	388/457 (85%)	367 (95%)	21 (5%)	0	100	100
10	e	388/457 (85%)	367 (95%)	21 (5%)	0	100	100
10	f	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	g	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	h	388/457 (85%)	367 (95%)	21 (5%)	0	100	100
10	i	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	j	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	k	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	l	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
10	m	388/457 (85%)	367 (95%)	21 (5%)	0	100	100
10	n	388/457 (85%)	366 (94%)	22 (6%)	0	100	100
All	All	24014/36687 (66%)	22913 (95%)	1091 (4%)	10 (0%)	100	100

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	127	ASP
9	J	715	ARG
8	K	127	ASP
7	A	312	GLU
7	C	312	GLU

5.3.2 Protein sidechains [i](#)

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

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.

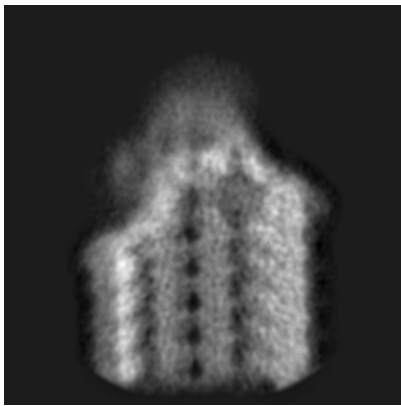
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43483. These allow visual inspection of the internal detail of the map and identification of artifacts.

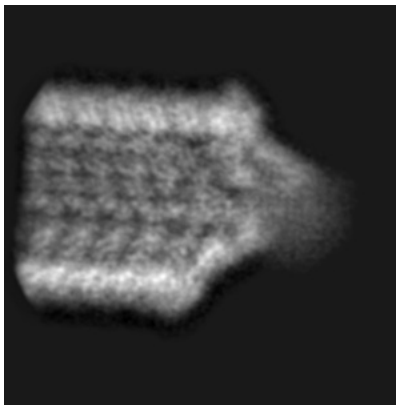
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

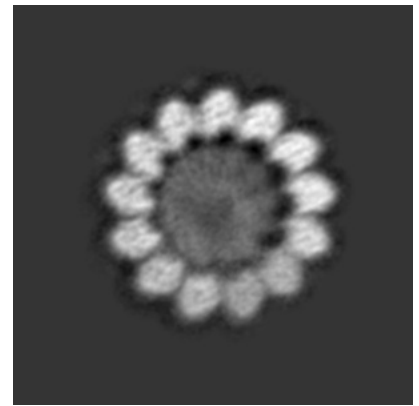
6.1.1 Primary map



X

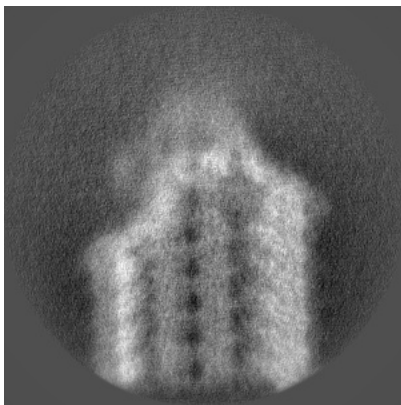


Y

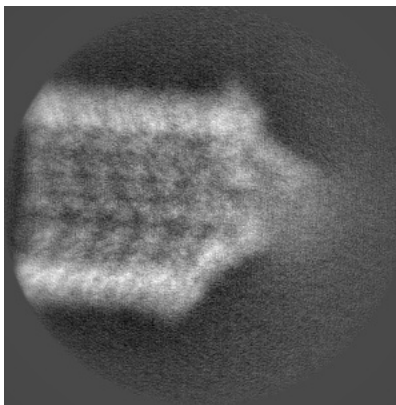


Z

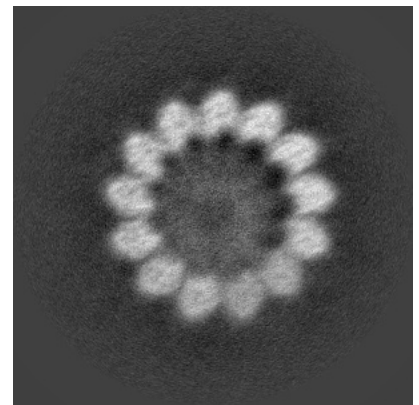
6.1.2 Raw map



X



Y

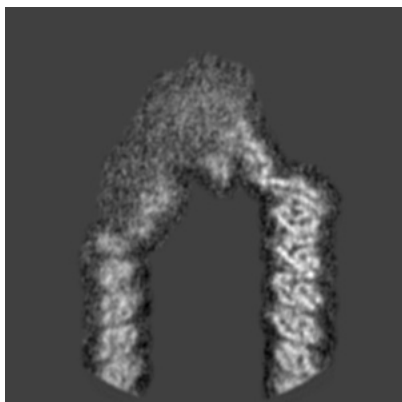


Z

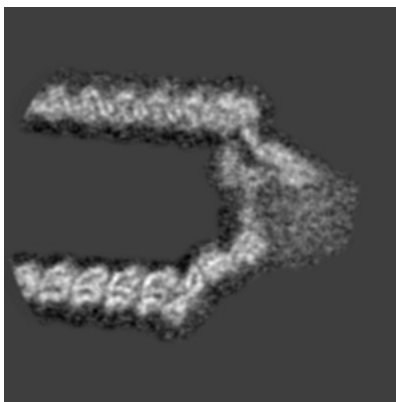
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

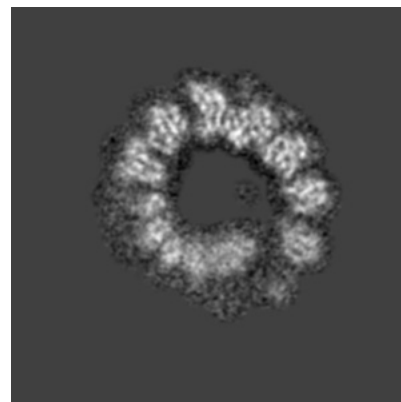
6.2.1 Primary map



X Index: 180

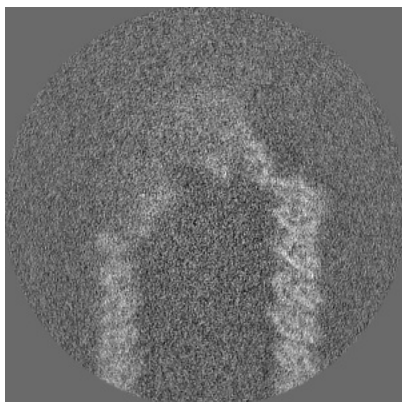


Y Index: 180

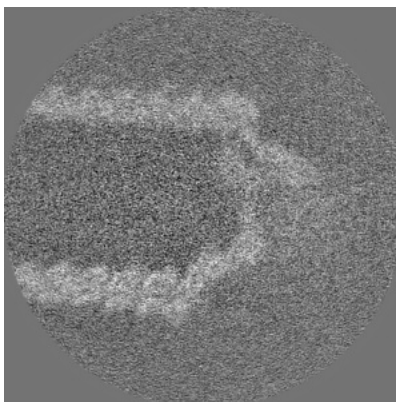


Z Index: 180

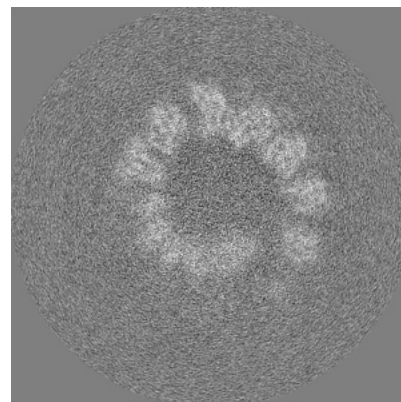
6.2.2 Raw map



X Index: 180



Y Index: 180

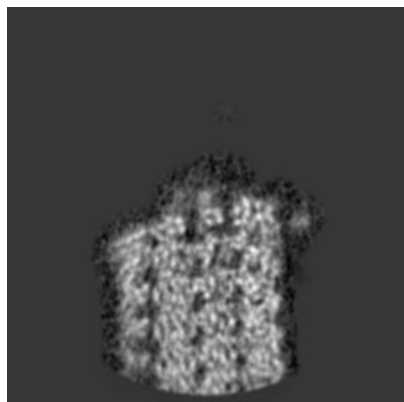


Z Index: 180

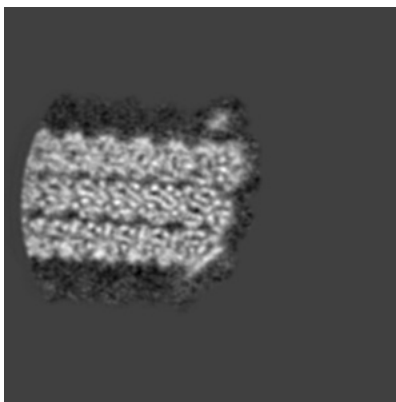
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

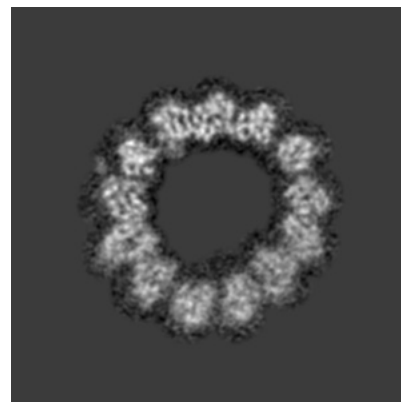
6.3.1 Primary map



X Index: 116

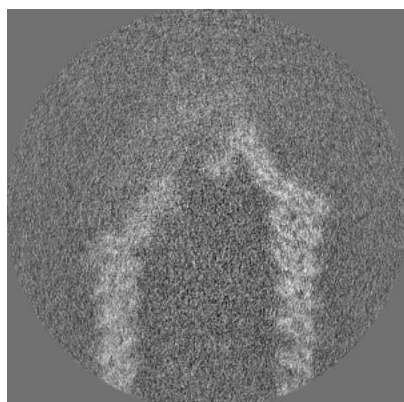


Y Index: 256

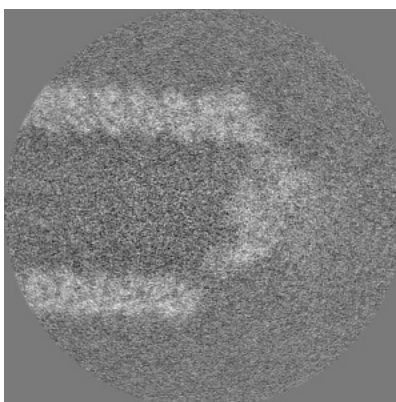


Z Index: 140

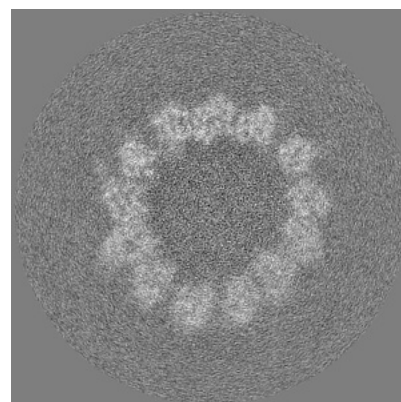
6.3.2 Raw map



X Index: 175



Y Index: 197

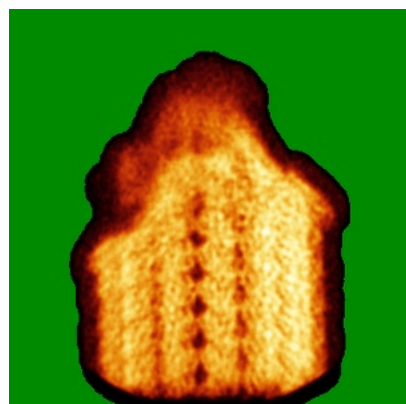


Z Index: 140

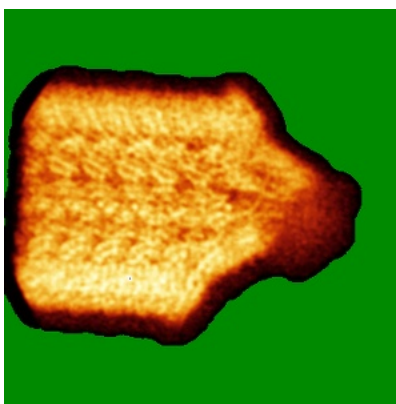
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

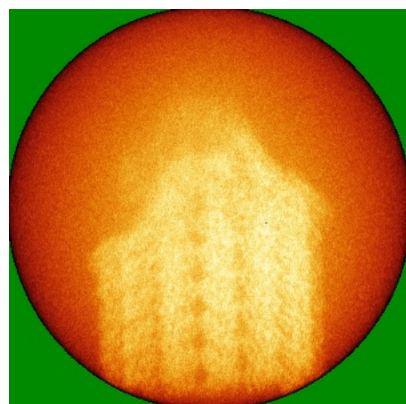


Y

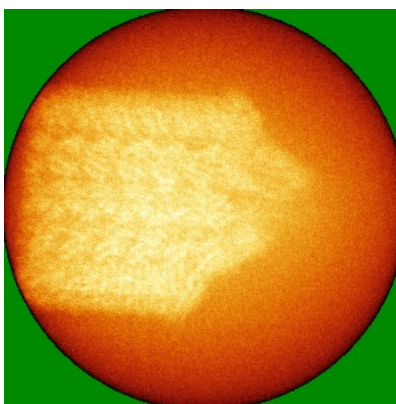


Z

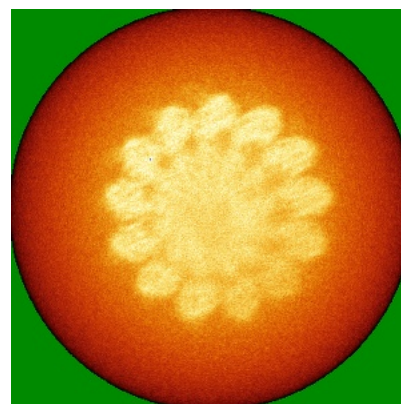
6.4.2 Raw map



X



Y

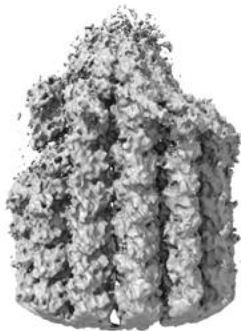


Z

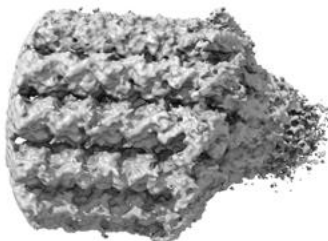
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

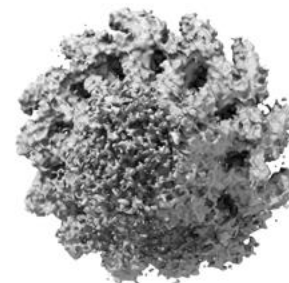
6.5.1 Primary map



X



Y



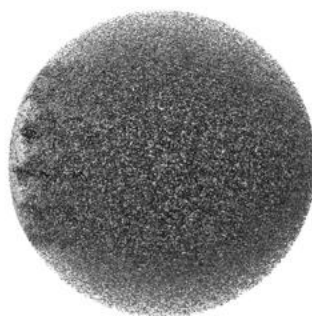
Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

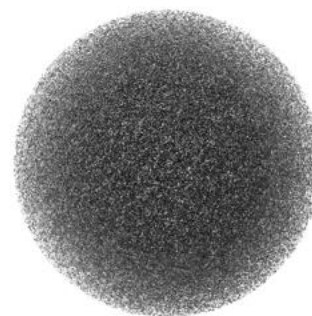
6.5.2 Raw map



X



Y



Z

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.

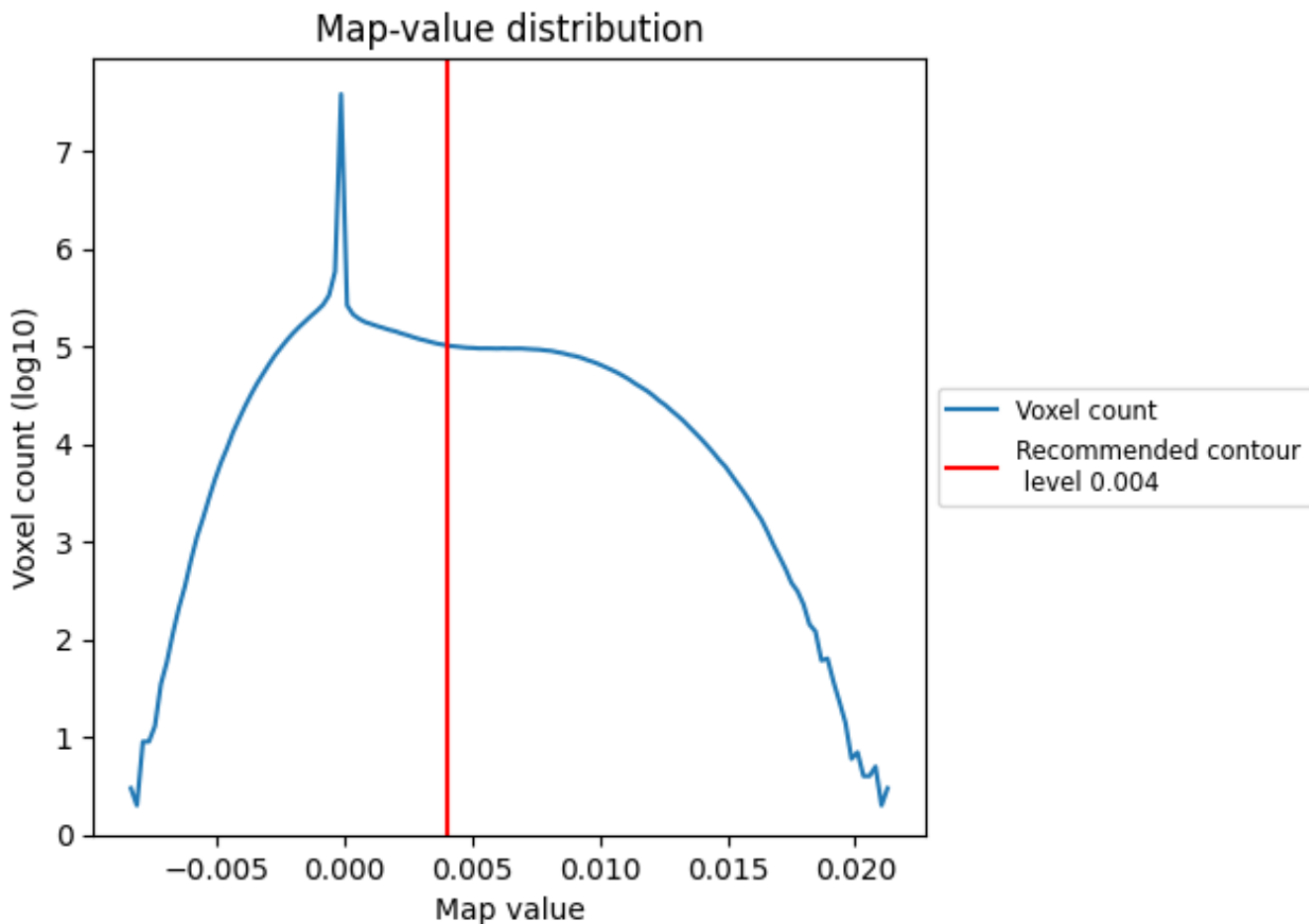
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

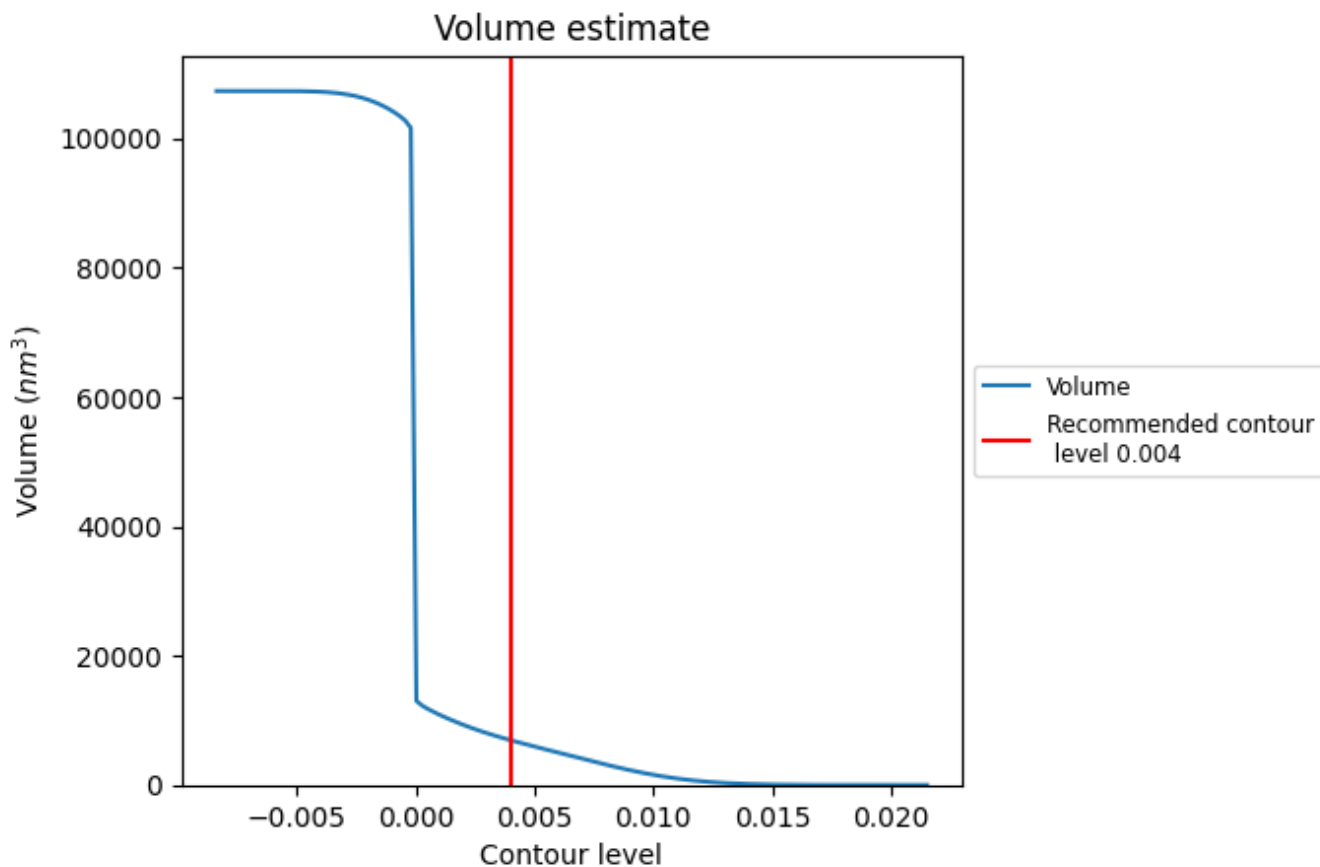
This section contains the results of statistical analysis of the map.

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.

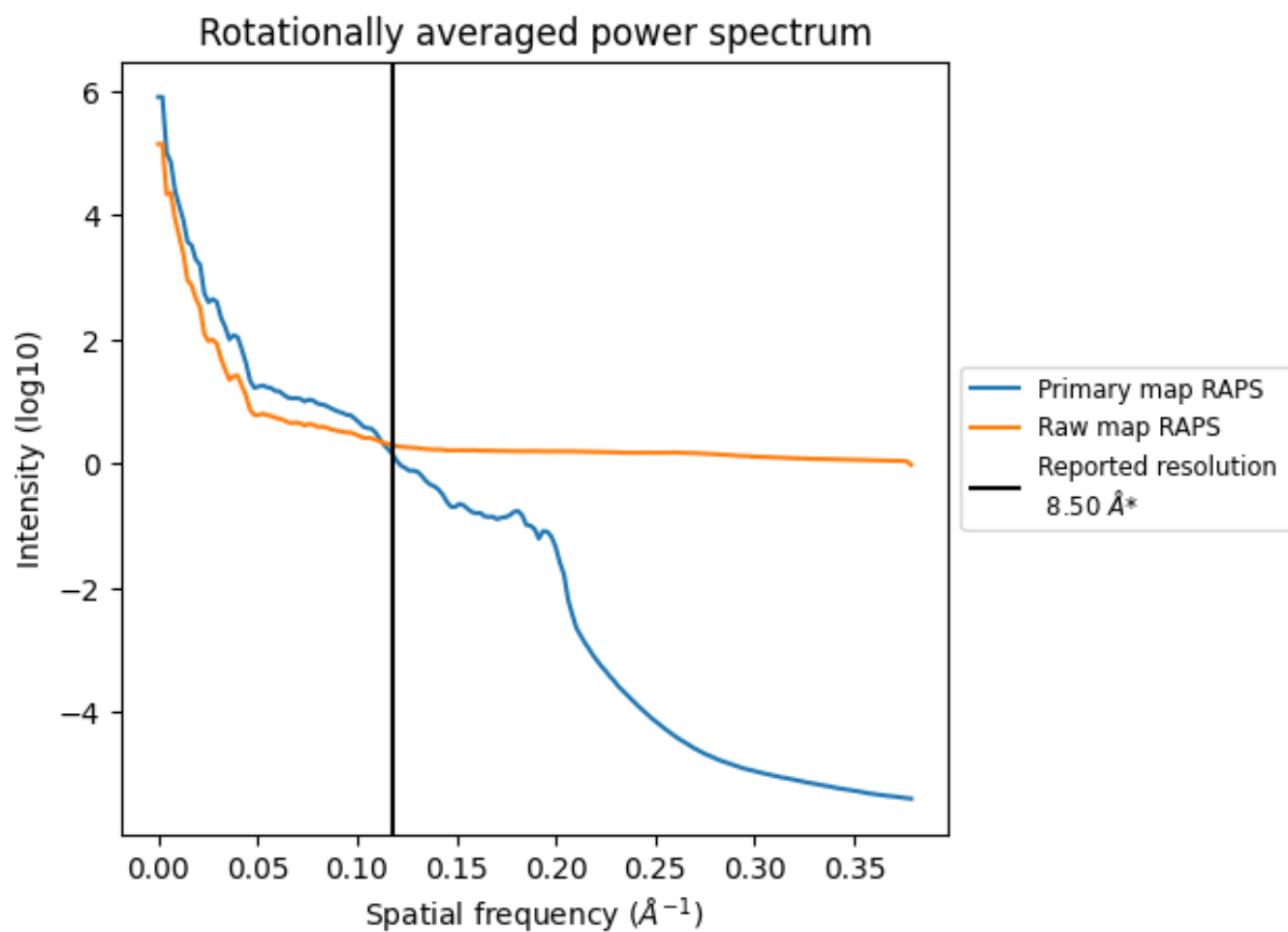
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 6913 nm^3 ; this corresponds to an approximate mass of 6244 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

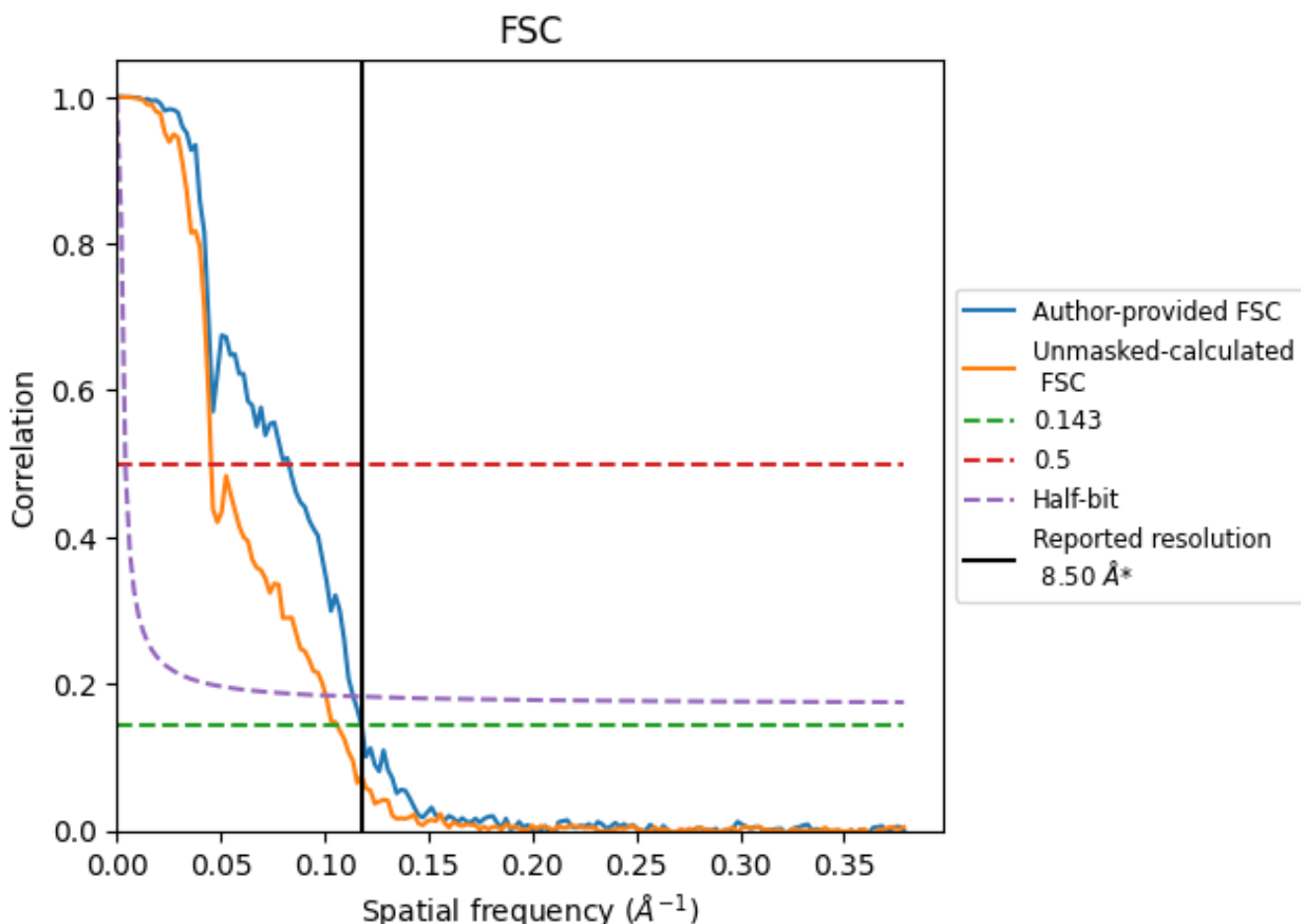


*Reported resolution corresponds to spatial frequency of 0.118 Å⁻¹

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 0.118 Å⁻¹

8.2 Resolution estimates [i](#)

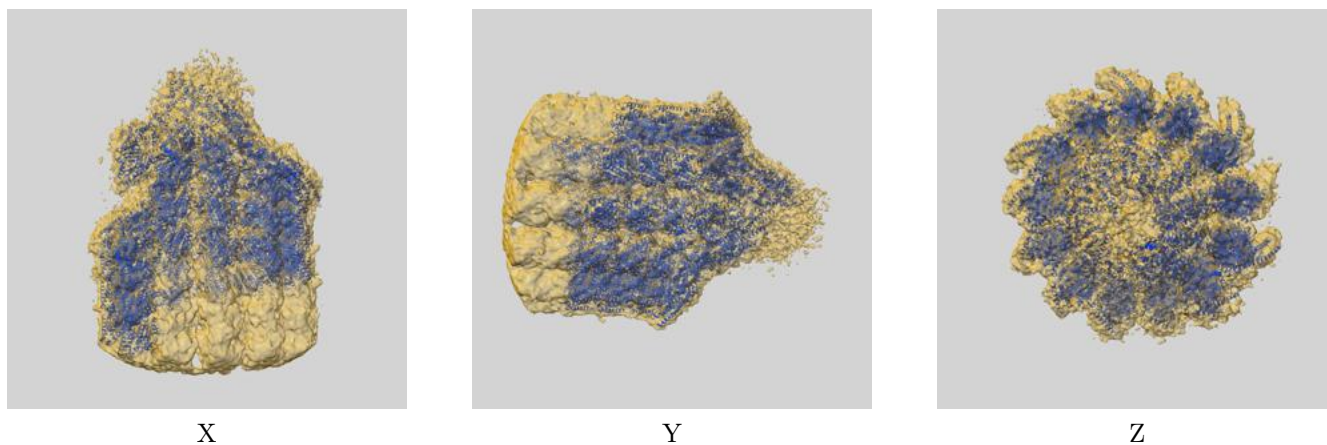
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.50	-	-
Author-provided FSC curve	8.48	12.09	8.78
Unmasked-calculated*	9.43	21.98	9.94

*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 9.43 differs from the reported value 8.5 by more than 10 %

9 Map-model fit [i](#)

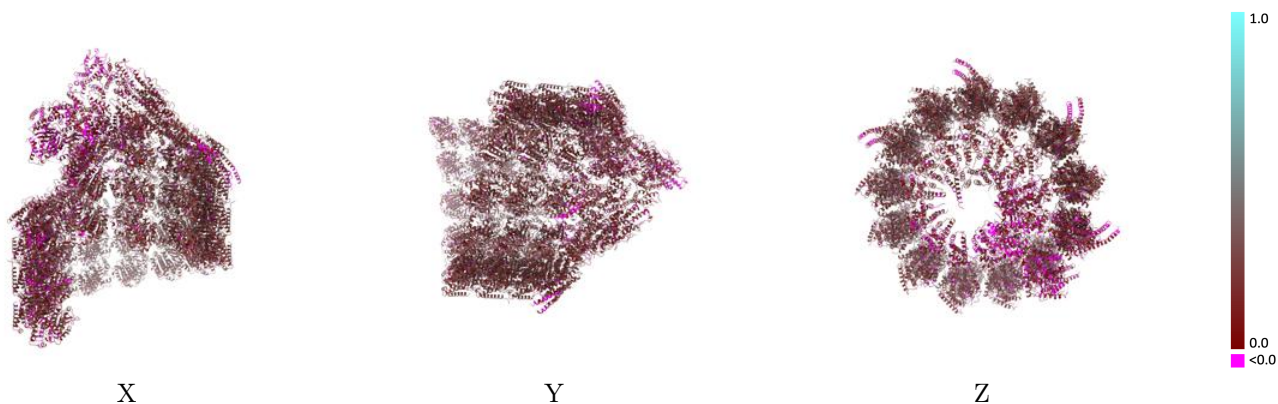
This section contains information regarding the fit between EMDB map EMD-43483 and PDB model 8VRK. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



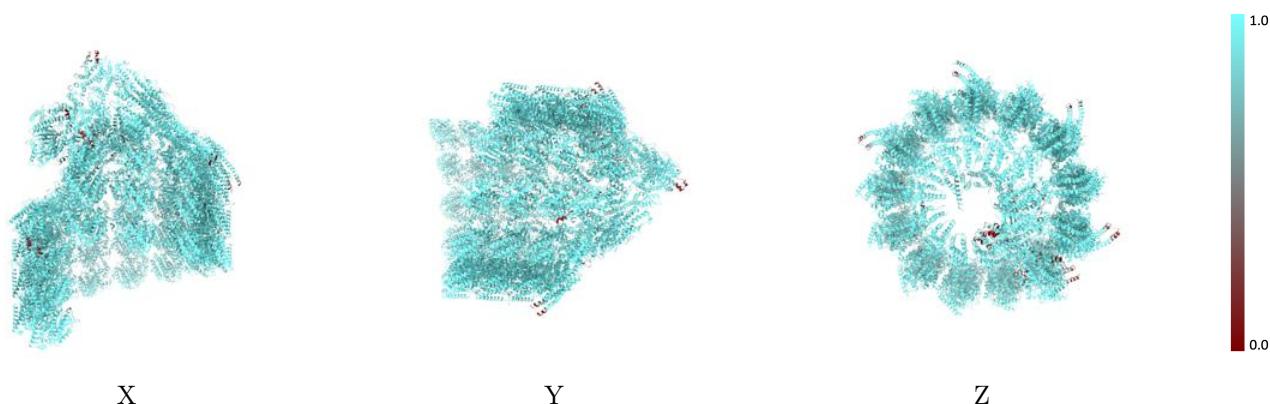
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



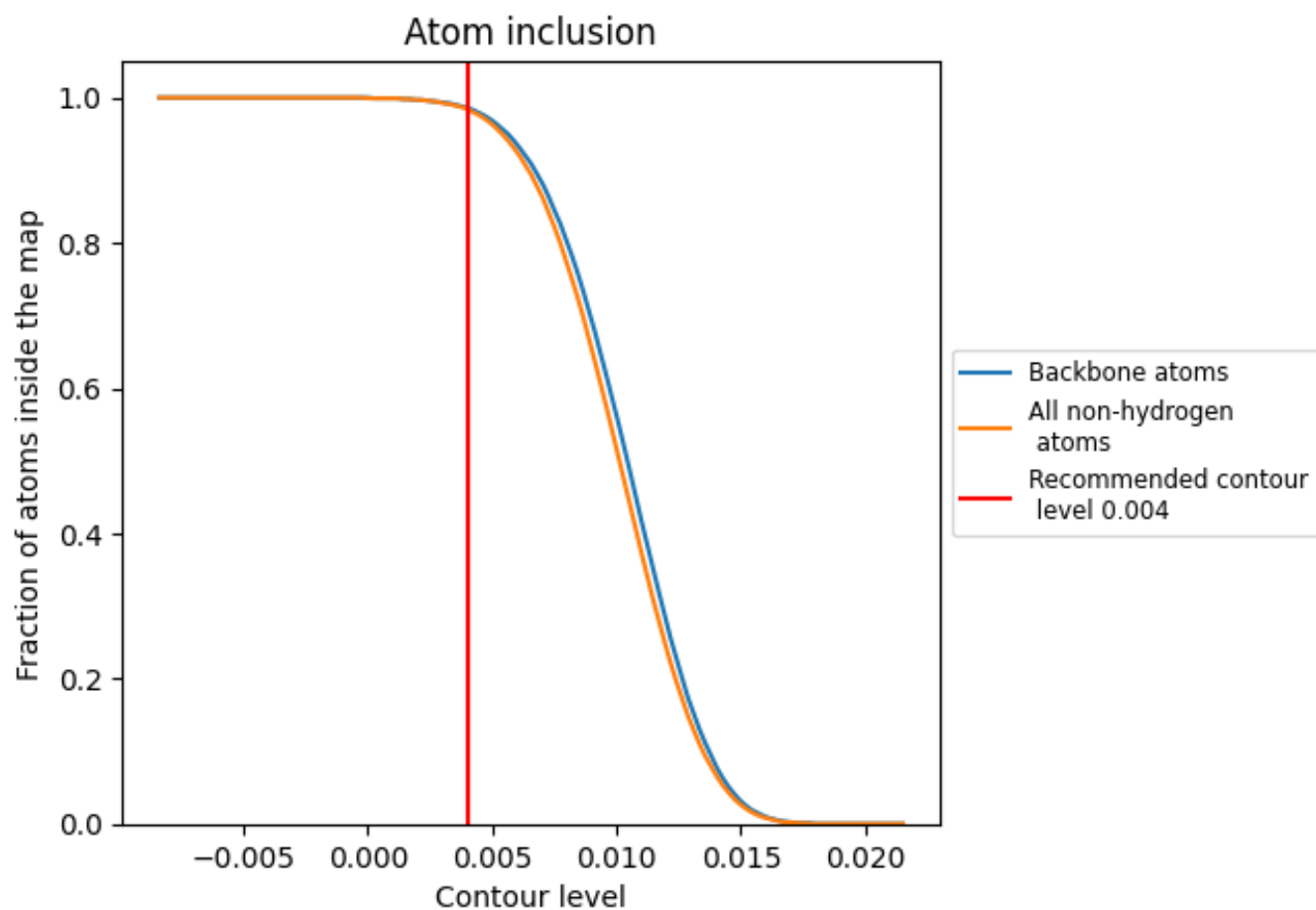
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9840	 0.1980
1	 0.9800	 0.1730
2	 0.9790	 0.1770
3	 0.9990	 0.1810
5	 0.9960	 0.1740
6	 0.9660	 0.1460
7	 0.9660	 0.2100
8	 0.9350	 0.1000
9	 0.8880	 0.0940
A	 0.8440	 0.0650
B	 0.9560	 0.1050
C	 0.9960	 0.1800
D	 0.9820	 0.1840
E	 0.9980	 0.2110
F	 0.9740	 0.1880
G	 0.9970	 0.2090
H	 0.9720	 0.1950
I	 0.9840	 0.1920
J	 0.9840	 0.1860
K	 0.9840	 0.1570
L	 0.9990	 0.1300
M	 0.9810	 0.1550
N	 0.9140	 0.1410
O	 0.9920	 0.1900
P	 0.9980	 0.2230
Q	 1.0000	 0.2370
R	 1.0000	 0.2460
S	 0.9980	 0.2510
T	 1.0000	 0.2520
U	 1.0000	 0.2490
V	 1.0000	 0.2390
W	 0.9990	 0.2230
X	 0.9980	 0.1870
Y	 0.9990	 0.1860
Z	 0.9930	 0.1730



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Chain	Atom inclusion	Q-score
a	 0.8900	 0.0830
b	 0.9810	 0.1750
c	 0.9910	 0.2100
d	 0.9930	 0.2310
e	 0.9960	 0.2410
f	 0.9970	 0.2500
g	 0.9980	 0.2540
h	 0.9960	 0.2460
i	 0.9980	 0.2450
j	 0.9950	 0.2340
k	 0.9960	 0.2070
l	 0.9950	 0.1940
m	 0.9900	 0.1860
n	 0.9760	 0.1850
o	 0.9950	 0.1880
p	 0.9980	 0.2220
q	 0.9990	 0.2330
r	 1.0000	 0.2440
s	 1.0000	 0.2390
t	 0.9990	 0.2440
u	 1.0000	 0.2430
v	 1.0000	 0.2320
w	 1.0000	 0.2230
x	 0.9980	 0.2090
y	 0.9970	 0.1680
z	 0.9960	 0.1830