Full wwPDB EM Validation 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 Full wwPDB EM Validation 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:

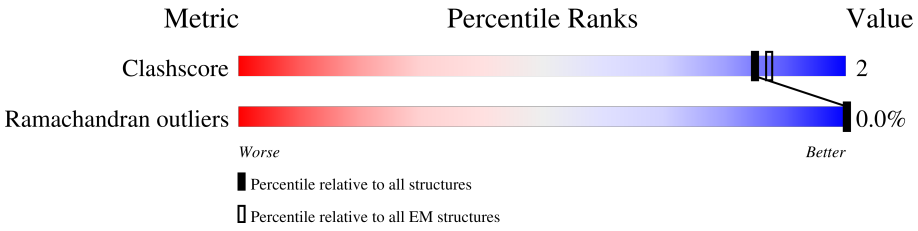
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.1

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 <=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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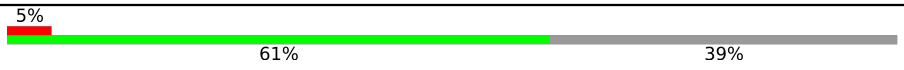
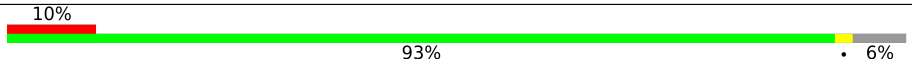
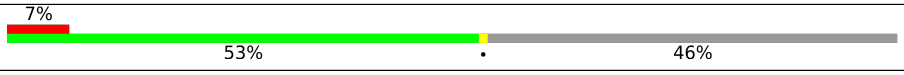
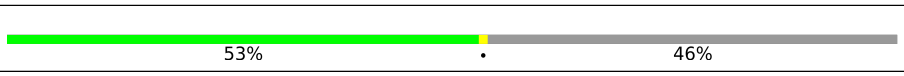
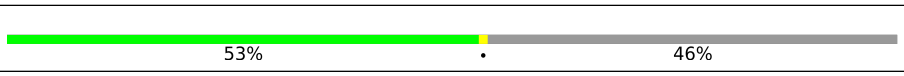
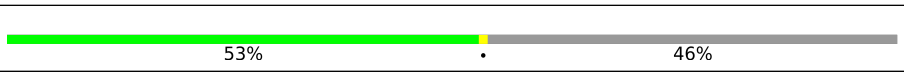
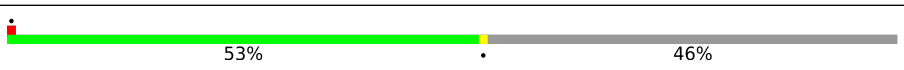
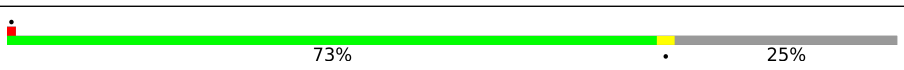
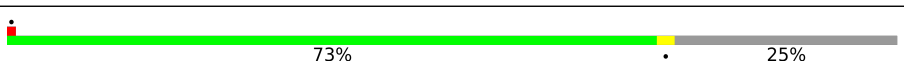
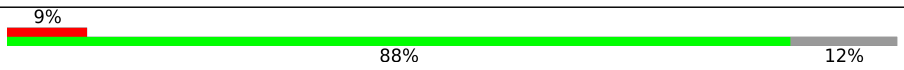
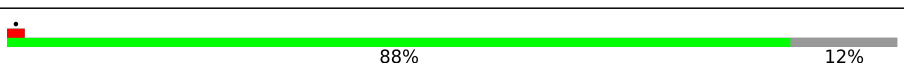
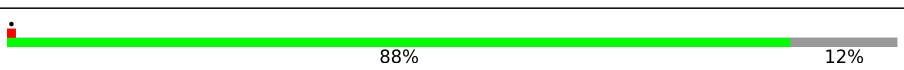
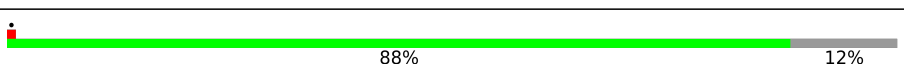
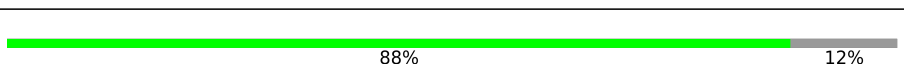
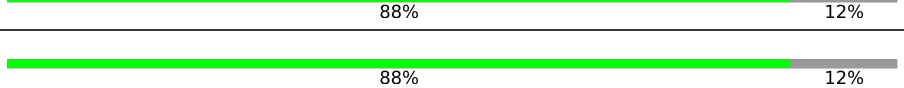
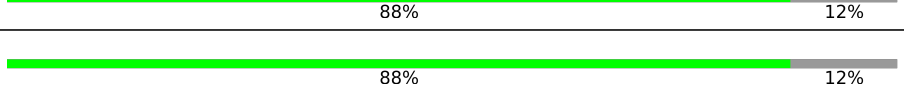
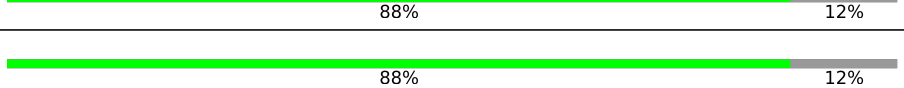
Mol	Chain	Length	Quality of chain
4	N	907	
5	7	82	
5	8	82	
6	9	375	
7	A	930	
7	C	930	
7	E	930	
7	G	930	
7	M	930	
8	I	666	
8	K	666	
9	J	1024	
10	a	457	
10	b	457	
10	c	457	
10	d	457	
10	e	457	
10	f	457	
10	g	457	
10	h	457	
10	i	457	
10	j	457	
10	k	457	
10	l	457	
10	m	457	

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Mol	Chain	Length	Quality of chain
10	n	457	

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
1	1	431	Total 2125	C 1263	N 431	O 431	0	0
1	O	431	Total 2125	C 1263	N 431	O 431	0	0
1	P	431	Total 2125	C 1263	N 431	O 431	0	0
1	Q	431	Total 2125	C 1263	N 431	O 431	0	0
1	R	431	Total 2125	C 1263	N 431	O 431	0	0
1	S	431	Total 2125	C 1263	N 431	O 431	0	0
1	T	431	Total 2125	C 1263	N 431	O 431	0	0
1	U	431	Total 2125	C 1263	N 431	O 431	0	0
1	V	431	Total 2125	C 1263	N 431	O 431	0	0
1	W	431	Total 2125	C 1263	N 431	O 431	0	0
1	X	431	Total 2125	C 1263	N 431	O 431	0	0
1	Y	431	Total 2125	C 1263	N 431	O 431	0	0
1	Z	431	Total 2125	C 1263	N 431	O 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
2	2	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	o	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	p	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	q	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	r	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	s	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	t	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	u	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	v	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	w	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	x	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	y	425	Total	C	N	O	0	0
			2093	1243	425	425		
2	z	425	Total	C	N	O	0	0
			2093	1243	425	425		

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 447 267 90 90	0	0
4	B	557	Total C N O 2766 1652 557 557	0	0
4	D	557	Total C N O 2766 1652 557 557	0	0
4	F	557	Total C N O 2766 1652 557 557	0	0
4	H	557	Total C N O 2766 1652 557 557	0	0
4	N	557	Total C N O 2766 1652 557 557	0	0

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

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

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

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

- 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 2504 1496 504 504	0	0
7	C	504	Total C N O 2504 1496 504 504	0	0
7	E	504	Total C N O 2504 1496 504 504	0	0
7	G	504	Total C N O 2504 1496 504 504	0	0
7	M	504	Total C N O 2504 1496 504 504	0	0

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 2475	C 1477	N 499	O 499	2	0
8	K	497	Total 2475	C 1477	N 499	O 499	2	0

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

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

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 1999	C 1191	N 404	O 404	0	0
10	b	403	Total 1994	C 1188	N 403	O 403	0	0

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

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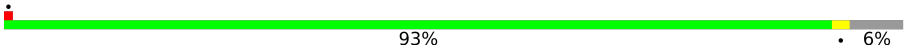
Chain	Residue	Modelled	Actual	Comment	Reference
j	455	TYR	-	expression tag	UNP P23258
j	456	PHE	-	expression tag	UNP P23258
j	457	GLN	-	expression tag	UNP P23258
k	452	GLU	-	expression tag	UNP P23258
k	453	ASN	-	expression tag	UNP P23258
k	454	LEU	-	expression tag	UNP P23258
k	455	TYR	-	expression tag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

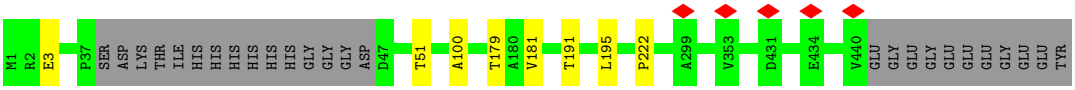
3 Residue-property plots (i)

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

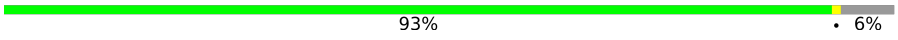
Chain 1:

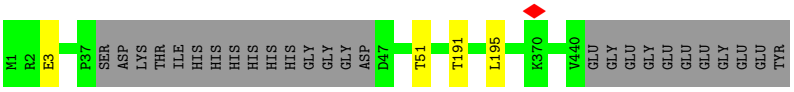




• Molecule 1: Tubulin alpha-1B chain

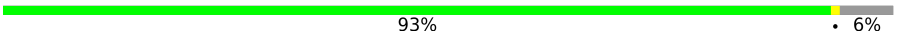
Chain O:

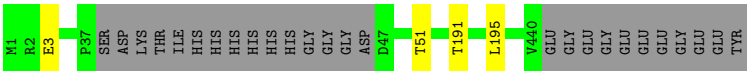




• Molecule 1: Tubulin alpha-1B chain

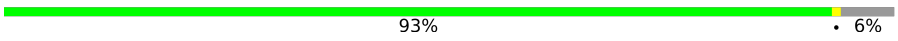
Chain P:





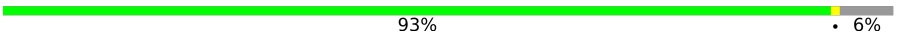
• Molecule 1: Tubulin alpha-1B chain

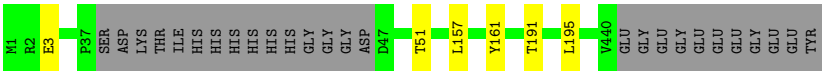
Chain Q:



• Molecule 1: Tubulin alpha-1B chain

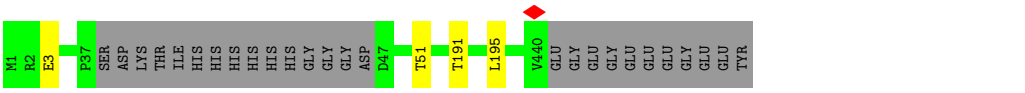
Chain R:





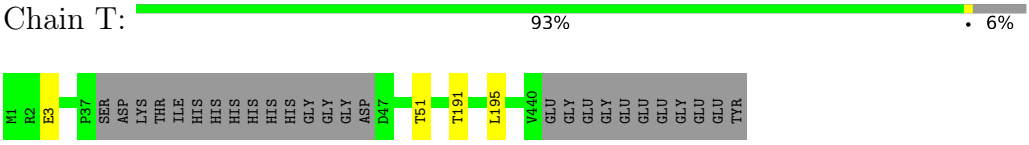
• Molecule 1: Tubulin alpha-1B chain

Chain S:



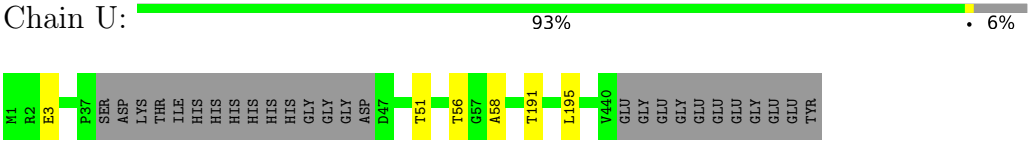
• Molecule 1: Tubulin alpha-1B chain

Chain T:



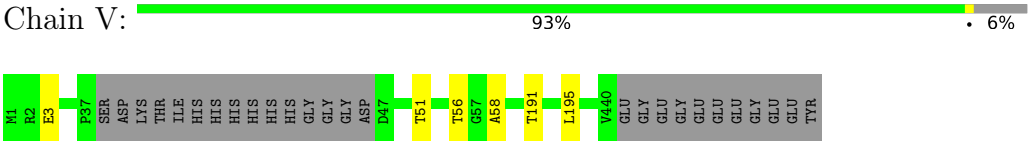
• Molecule 1: Tubulin alpha-1B chain

Chain U:



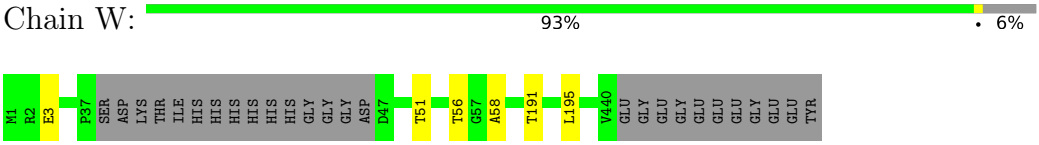
• Molecule 1: Tubulin alpha-1B chain

Chain V:



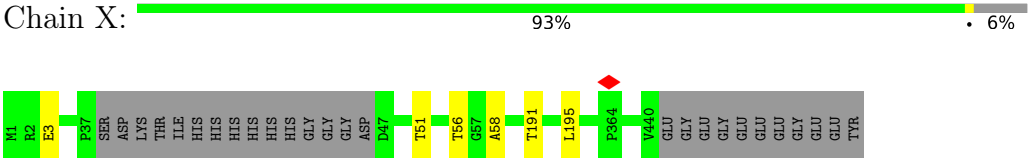
• Molecule 1: Tubulin alpha-1B chain

Chain W:



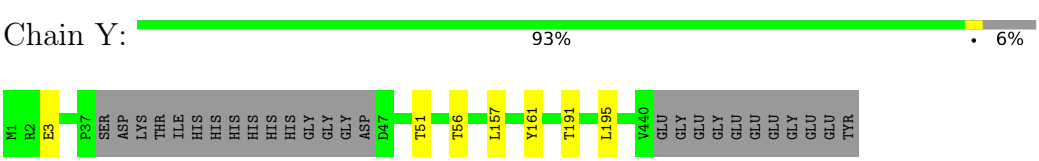
• Molecule 1: Tubulin alpha-1B chain

Chain X:



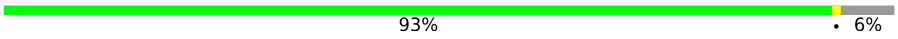
• Molecule 1: Tubulin alpha-1B chain

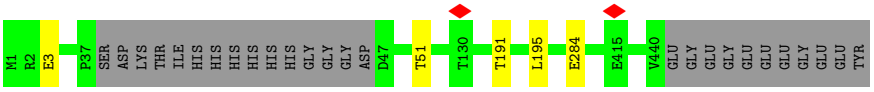
Chain Y:



• Molecule 1: Tubulin alpha-1B chain

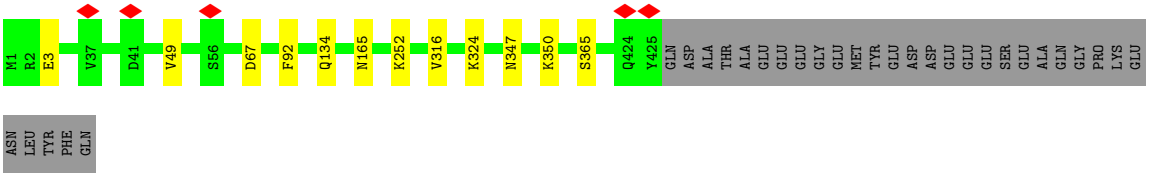
Chain Z:





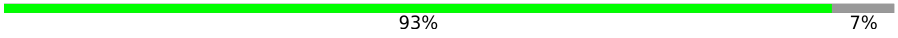
• Molecule 2: Tubulin beta-3 chain

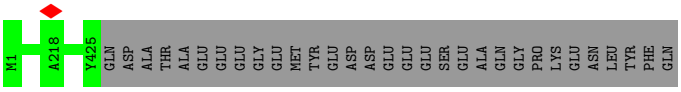
Chain 2:



• Molecule 2: Tubulin beta-3 chain

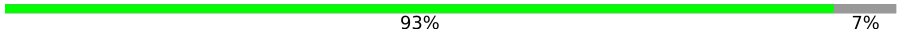
Chain o:





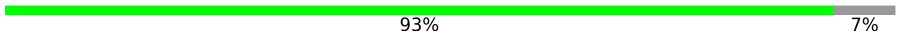
• Molecule 2: Tubulin beta-3 chain

Chain p:



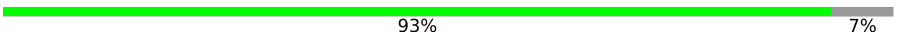
• Molecule 2: Tubulin beta-3 chain

Chain q:



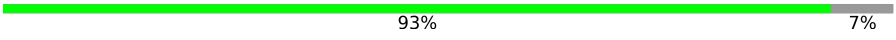
• Molecule 2: Tubulin beta-3 chain

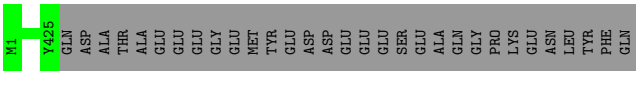
Chain r:



• Molecule 2: Tubulin beta-3 chain

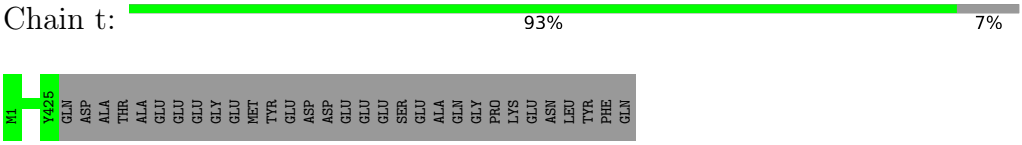
Chain s:





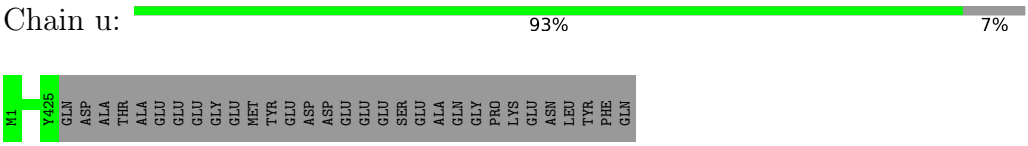
• Molecule 2: Tubulin beta-3 chain

Chain t:



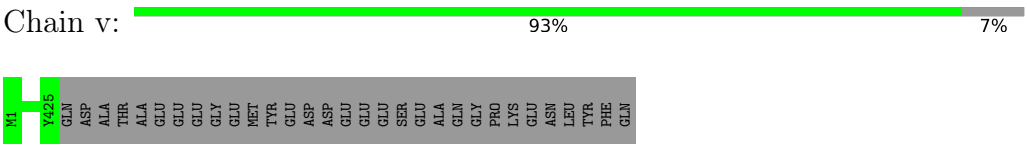
• Molecule 2: Tubulin beta-3 chain

Chain u:



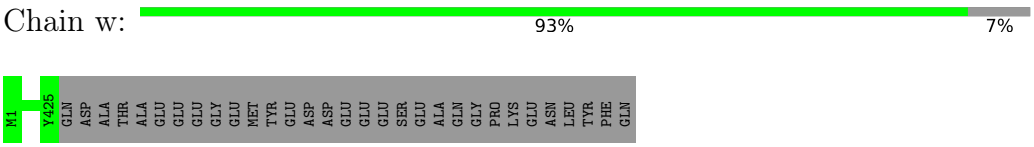
• Molecule 2: Tubulin beta-3 chain

Chain v:



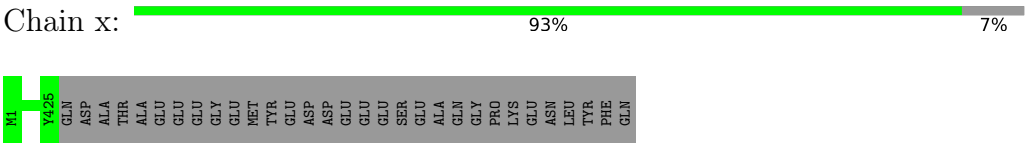
• Molecule 2: Tubulin beta-3 chain

Chain w:



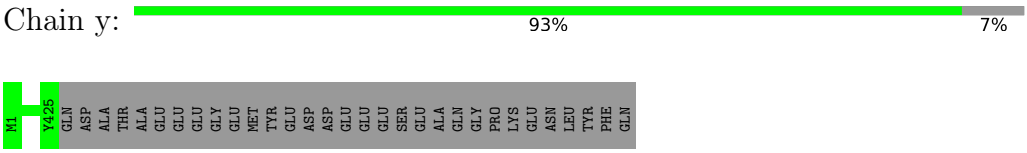
• Molecule 2: Tubulin beta-3 chain

Chain x:



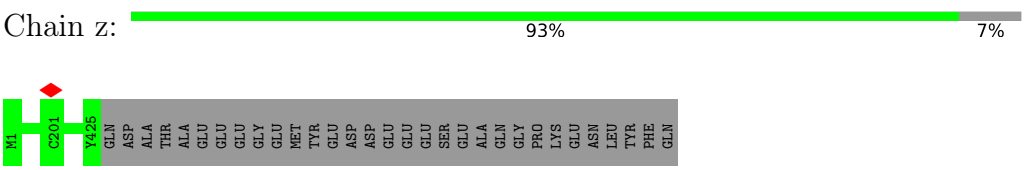
• Molecule 2: Tubulin beta-3 chain

Chain y:



• Molecule 2: Tubulin beta-3 chain

Chain z:



• Molecule 3: TUBGCP6 protein

Chain 3: 16% 84%

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

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

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

VAL MET GLU ALA ALA PRO GLY THR GLY LEU PRO THR VAL GLY LEU PHE SER PHE GLY ASP PRO CYS GLY ASP ARG PHE GLU ARG ASP THR ARG VAL SER LEU PHE GLY ALA LEU VAL HIS SER ARG THR TYR ASP MET ASP VAL ARG LEU GLY LEU PRO PRO VAL PRO ASP ASN ALA ASP

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

GLY CYS PRO PRO GLY HIS ARG GLU GLU PRO TYR LEU THR GLU ALA GLY ARG ASP ALA PHE ASP LYS PHE CYS ARG LEU HIS GLN GLY GLU LEU GLN LEU LEU ALA GLY GLY VAL LEU GLN ALA PRO GLN PRO VAL LEU VAL LYS GLU CYS GLU LEU VAL LYS ASP VAL LEU ASN VAL LEU

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

SER LEU TYR SER LYS GLY LEU VAL PHE GLN ALA PHE THR SER GLY LEU ARG ARG TYR LEU GLN TYR TYR ARG ALA CYS VAL LEU SER THR PRO PRO THR LEU SER LEU LEU THR ILE GLY PHE LEU PHE LYS LYS LEU GLY ARG GLN LEU ARG TYR LEU ALA GLU LEU CYS GLY VAL GLY

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

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

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

LYS GLU LEU ARG MET GLU ILE ALA LYS GLN GLU LEU ILE ALA HIS ALA ARG GLU ALA ALA SER ARG VAL LEU SER ALA LEU SER ASP ARG GLN MET SER GLU ARG MET ALA LEU ASP ALA ARG LYS ARG GLU GLN PHE GLN ARG LEU LYS GLU GLN PHE VAL LYS ASP GLN GLU ARG ARG

GLN ALA ALA ARG GLN GLU GLU LEU ASP ASP ASP PHE SER TYR ALA ARG GLU LEU ARG ASP ARG GLU ARG ARG LEU LYS SER LEU GLU GLU GLU LEU GLU ARG LYS ALA SER LYS LEU SER ALA GLU ALA ALA ARG ARG GLU GLN LYS ALA LEU TRP ARG ILE GLN ARG HIS ARG LEU GLU

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

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

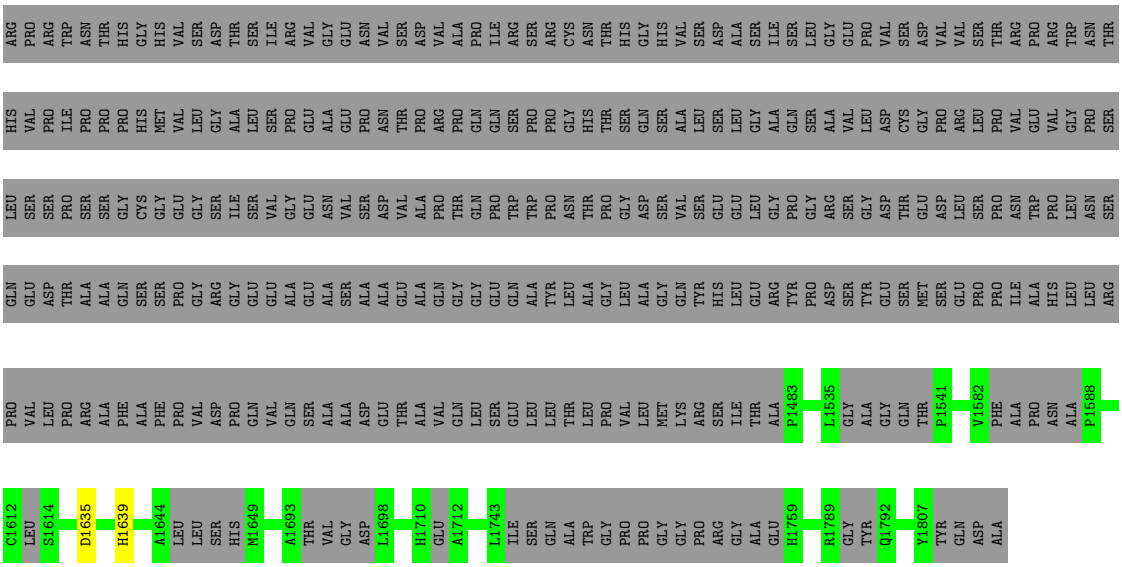
SER VAL GLN THR GLY MET VAL PRO LEU LEU GLU VAL ALA LEU GLN THR ILE ASN LEU ASP LEU PRO PRO SER ALA PRO GLY GLU ALA PRO ALA ALA ALA SER THR GLN PRO SER ARG PRO GLN GLU TYR ASP PHE SER THR VAL LEU ARG PRO ALA VAL ALA THR SER PRO ALA PRO GLY

PRO LEU GLN ALA ALA GLU CYS SER LEU GLY SER SER GLY LEU GLN LEU TRP GLU ASP SER CYS GLY LYS MET ASP ALA CYS GLY SER ALA SER ARG GLU THR LEU LEU PRO SER HIS PRO PRO ARG ARG ALA ALA LEU GLU GLU GLY SER SER GLN PRO THR GLU ARG LEU PHE GLY GLN

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

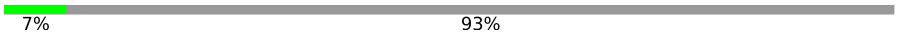
SER LEU GLY GLU SER VAL SER ASP VAL ALA PRO THR ARG PRO ARG TRP ASN ILE HIS GLY HIS VAL SER ASN ALA SER ILE ARG VAL GLY GLU ASN VAL SER ASP VAL ALA PRO THR ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASN ALA SER ILE ARG VAL GLY GLU ASN VAL

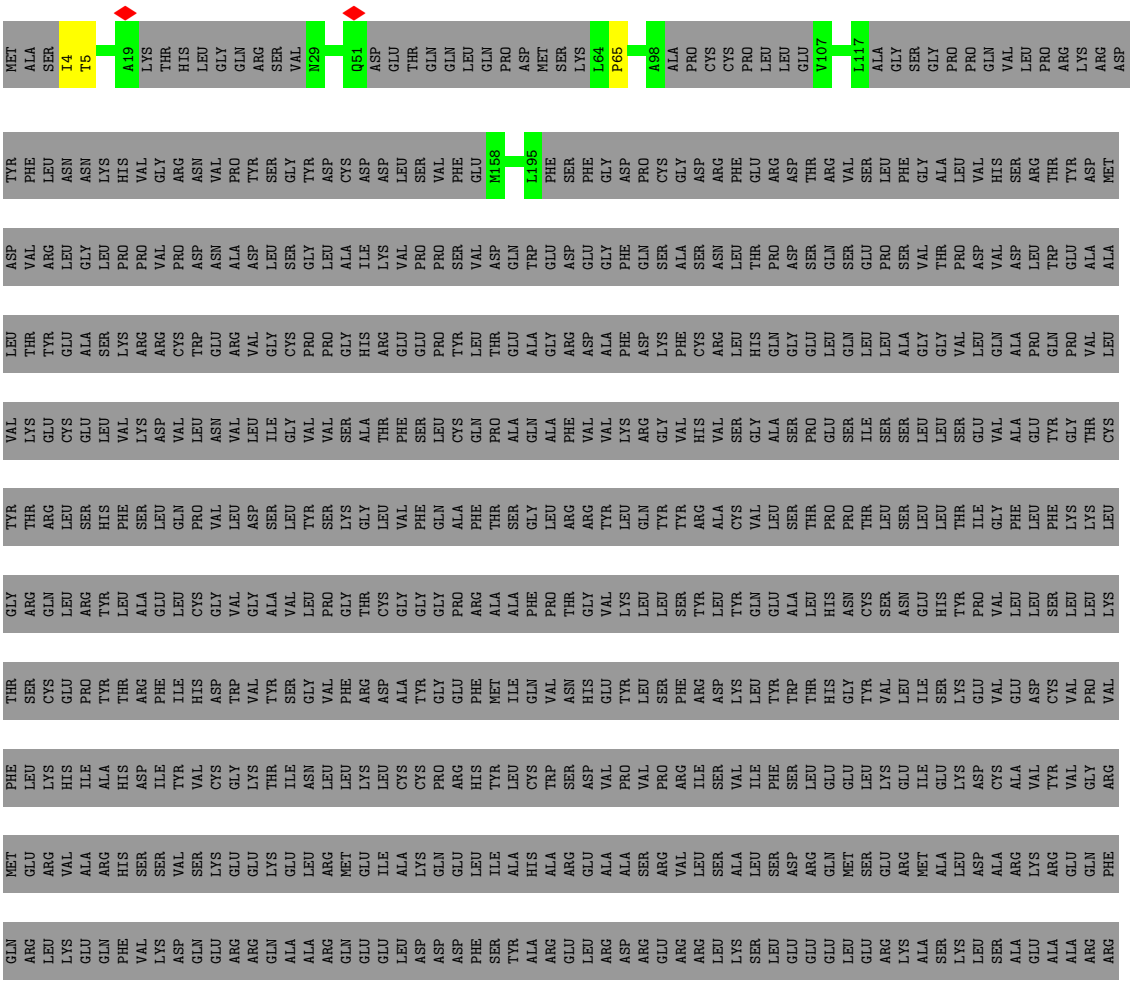
SER ASP VAL ALA PRO THR ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASP ALA SER ILE SER LEU GLY GLU SER VAL SER ASP MET ALA PRO ALA ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASP ALA SER ILE SER LEU GLY GLU SER VAL SER ASP MET ALA PRO THR

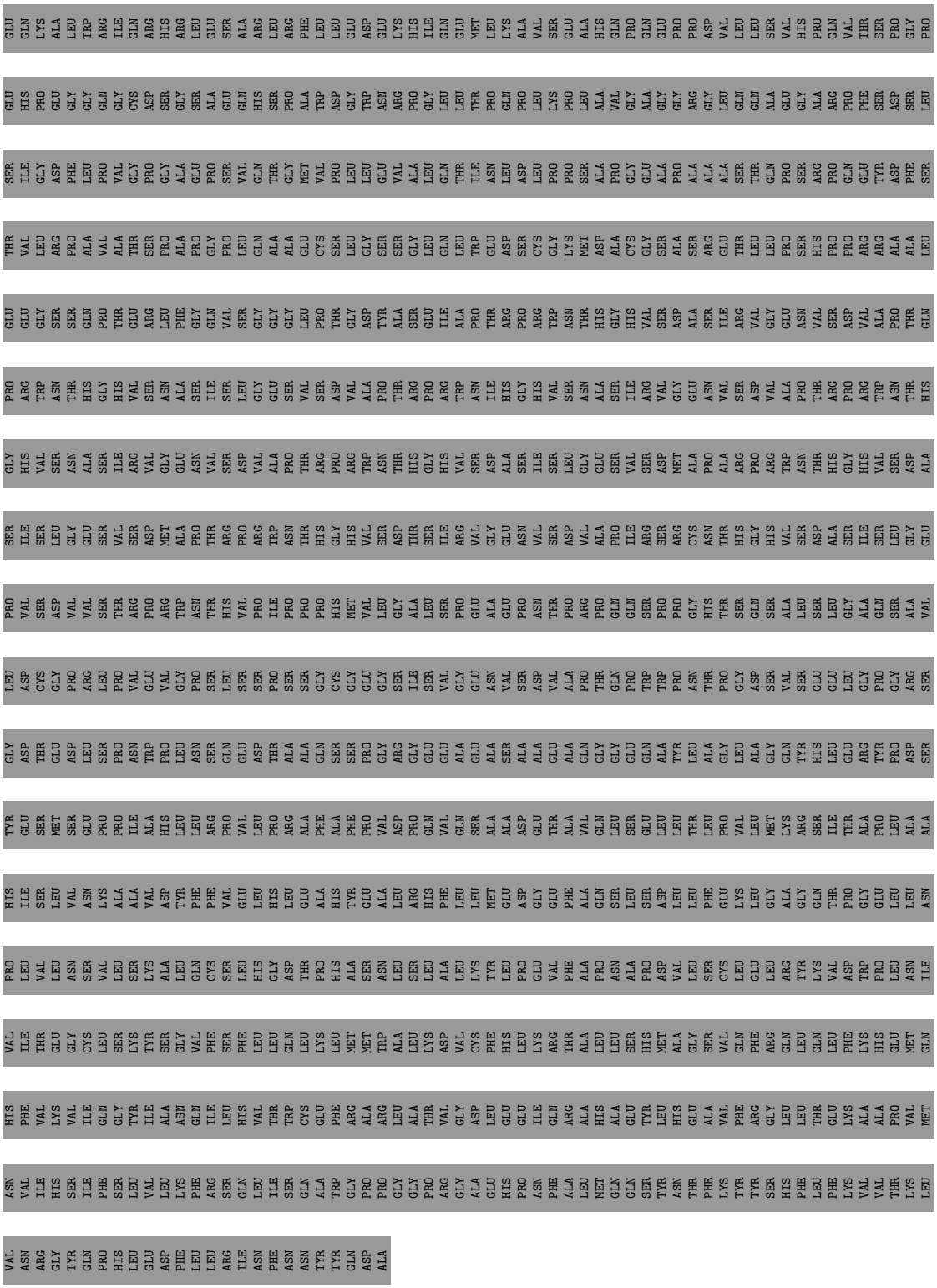


• Molecule 3: TUBGCP6 protein

Chain 6:

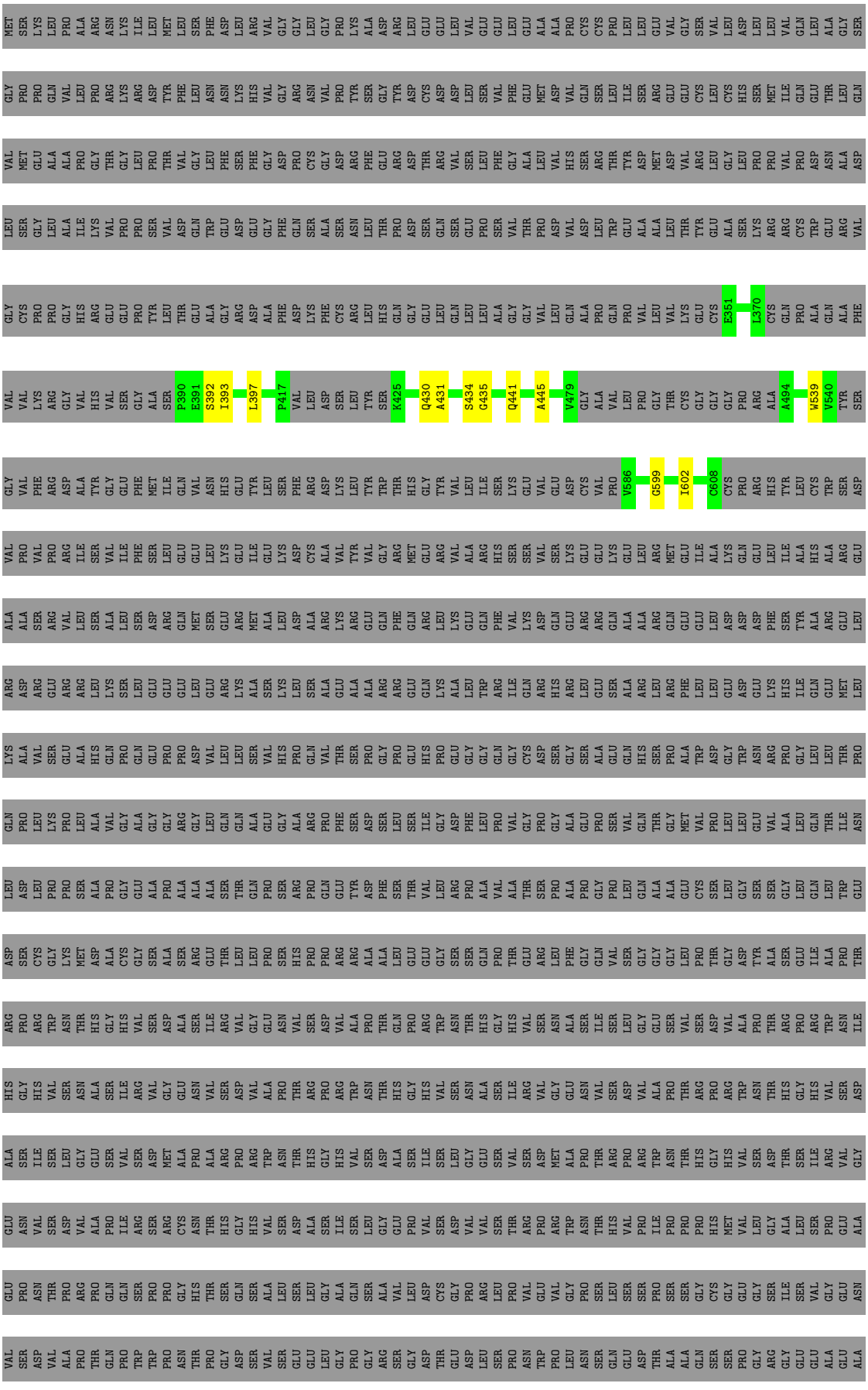






• Molecule 3: TUBGCP6 protein

Chain L: 9% 90%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L397
P417
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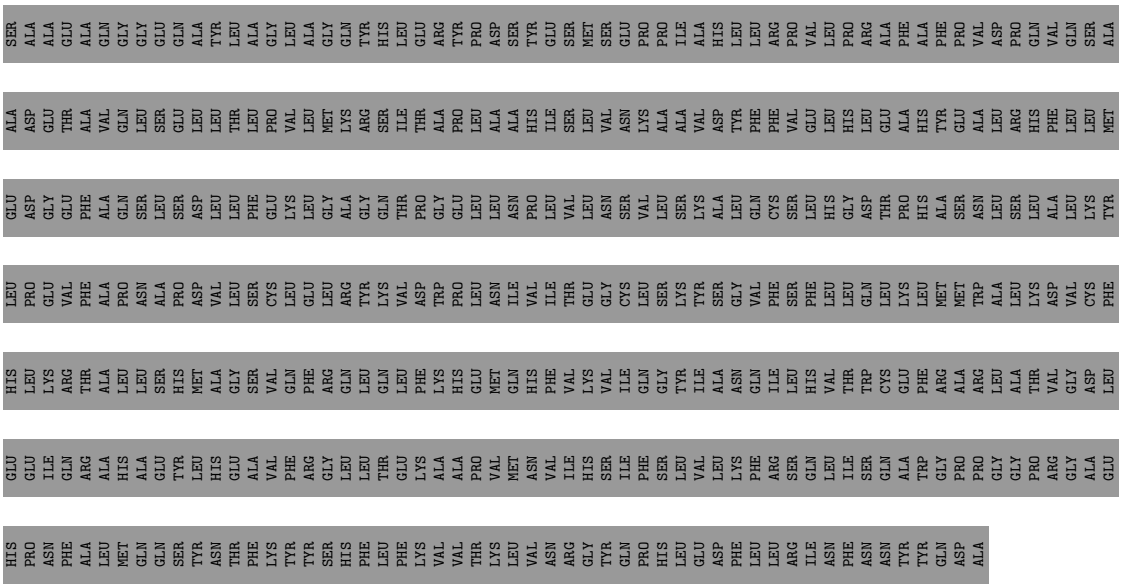
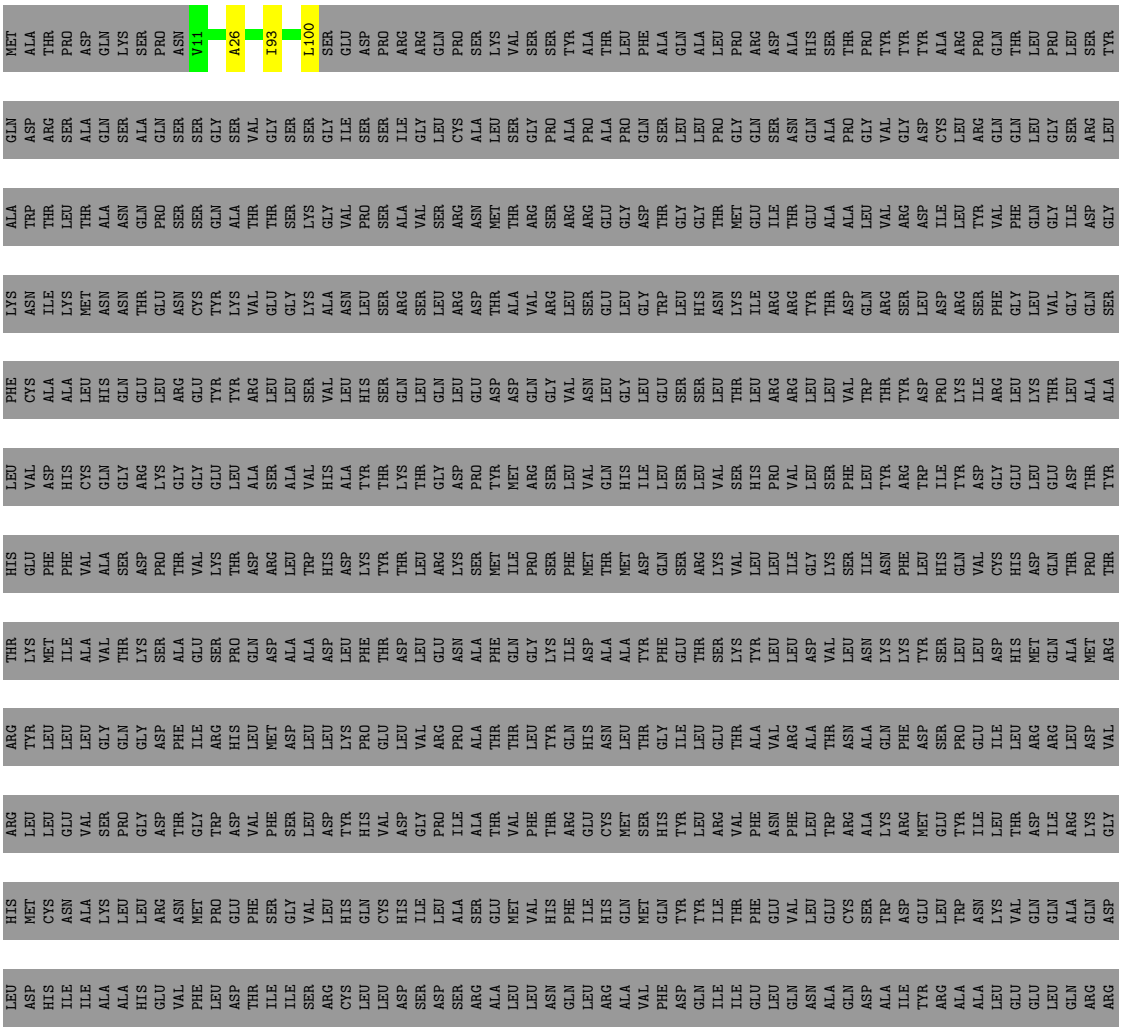
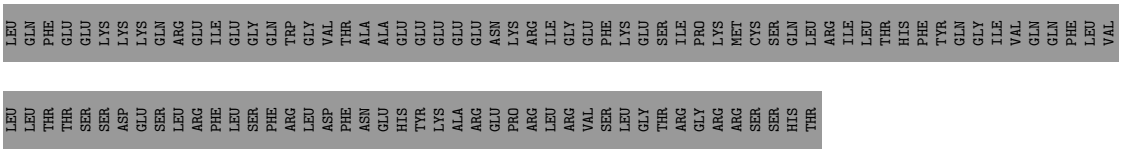


• Molecule 4: Gamma-tubulin complex component 3

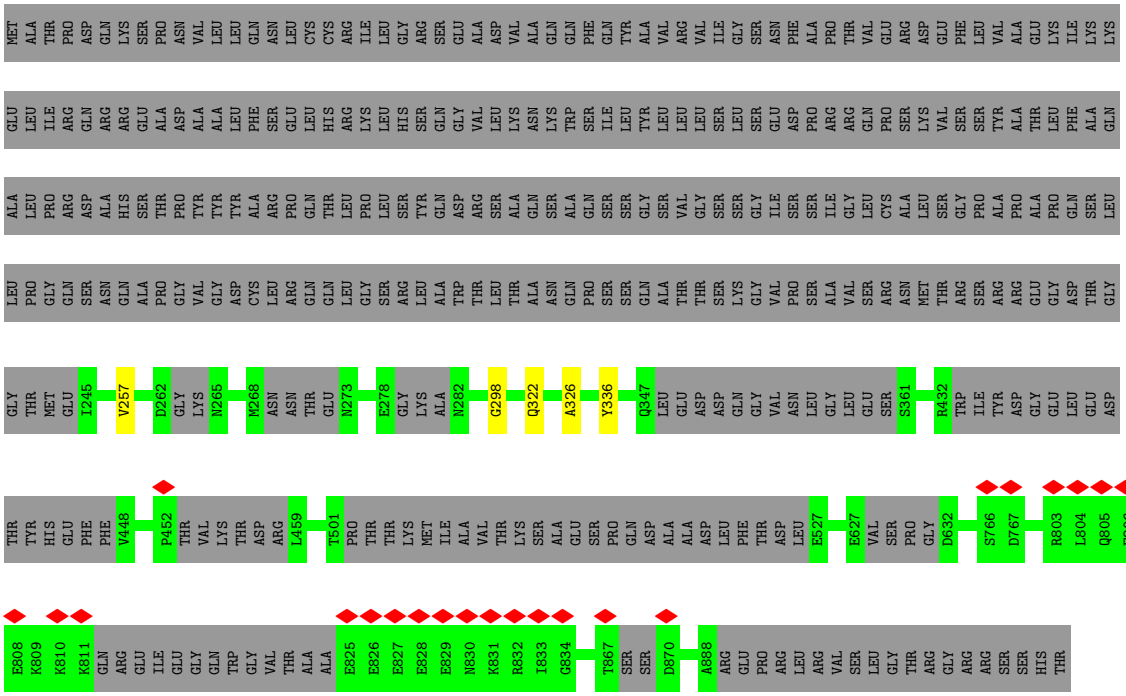
Chain 5:





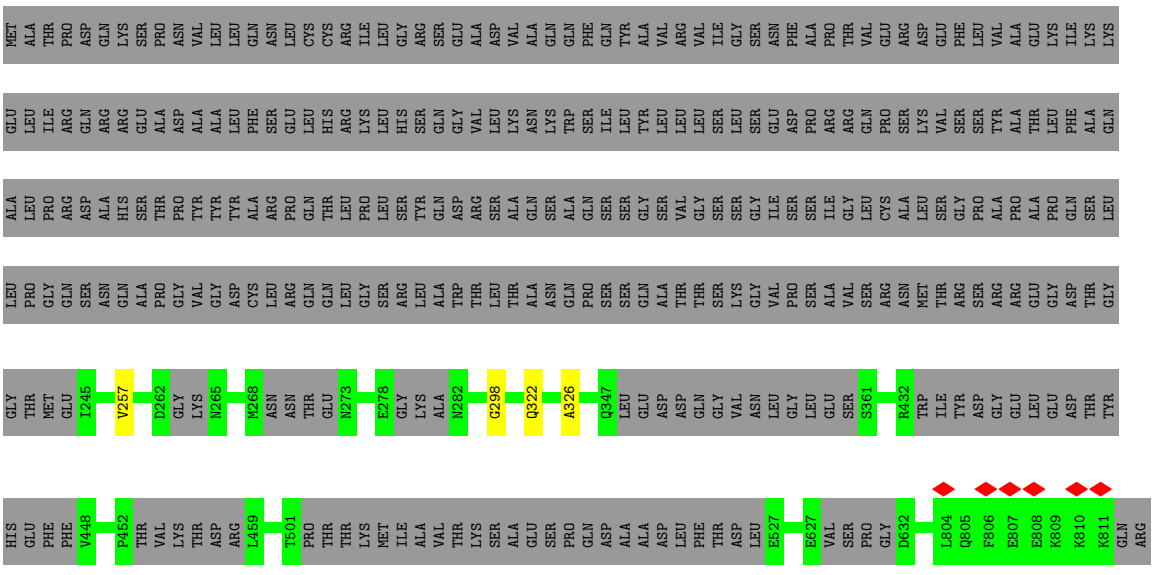
• Molecule 4: Gamma-tubulin complex component 3

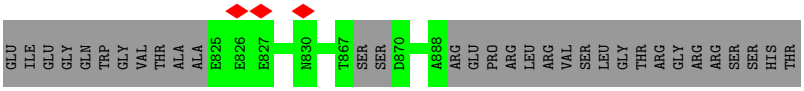
Chain B:



• Molecule 4: Gamma-tubulin complex component 3

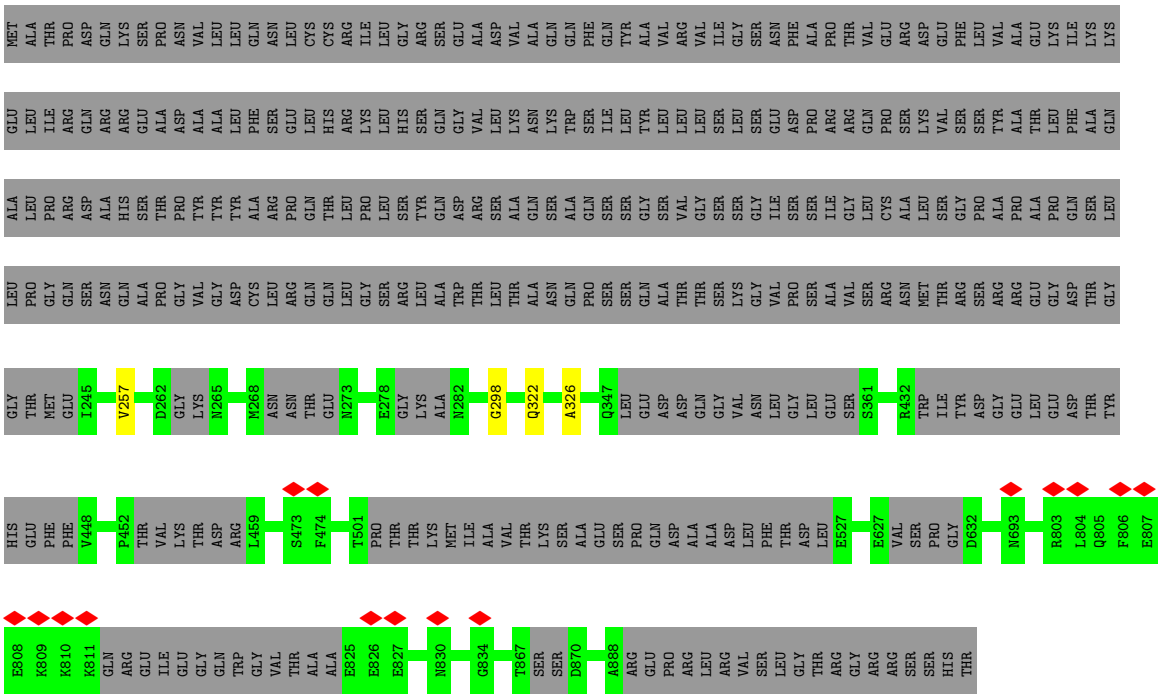
Chain D:





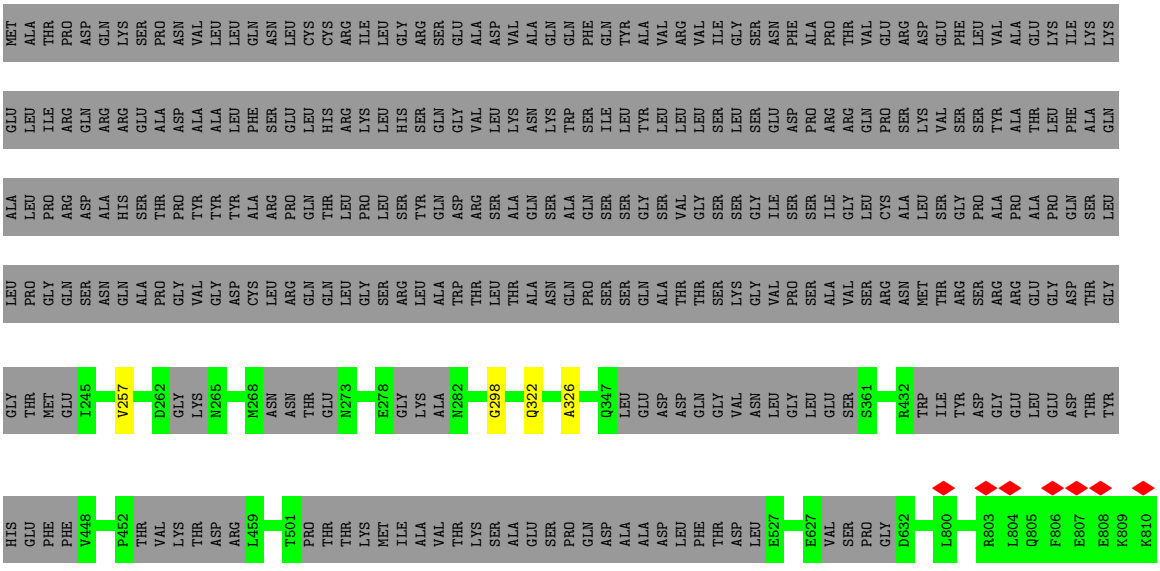
• Molecule 4: Gamma-tubulin complex component 3

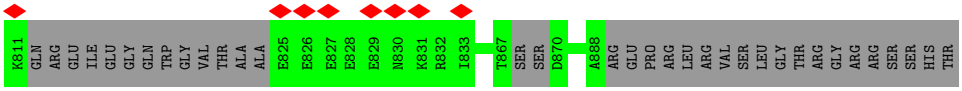
Chain F:



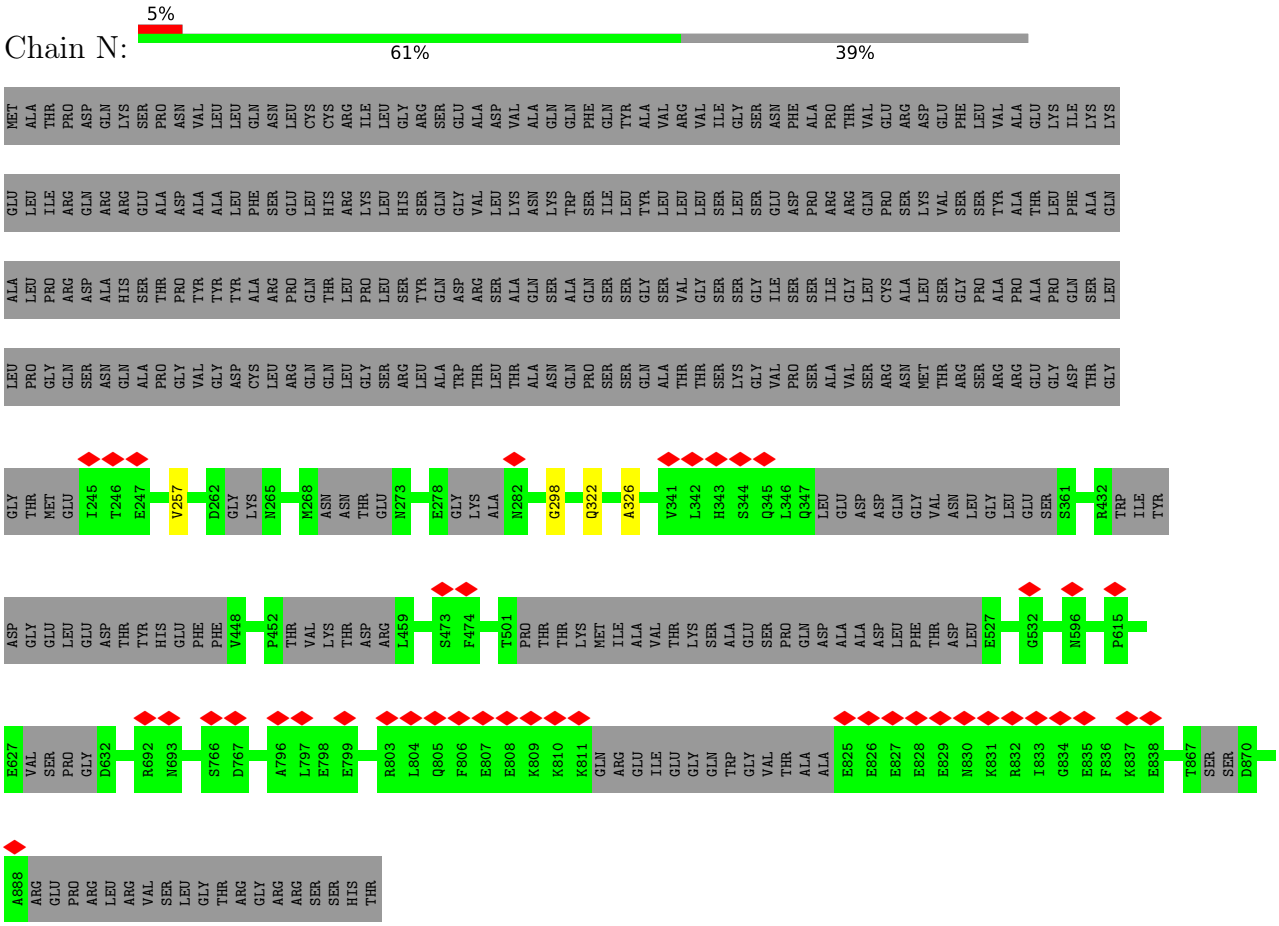
• Molecule 4: Gamma-tubulin complex component 3

Chain H:

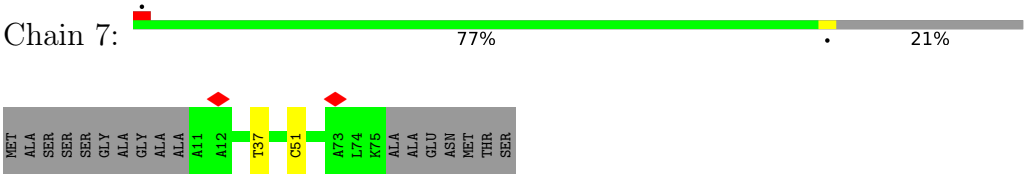




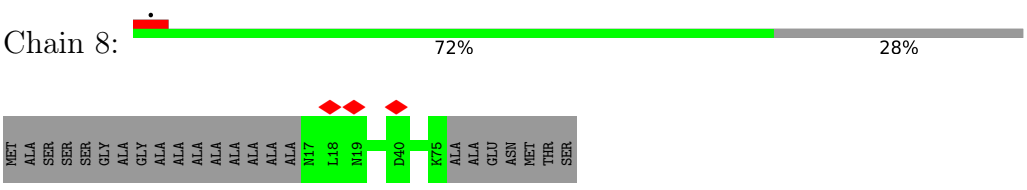
• Molecule 4: Gamma-tubulin complex component 3



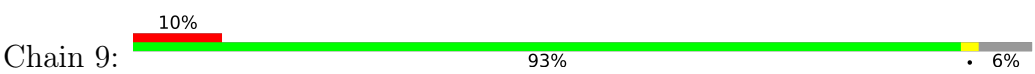
• Molecule 5: Mitotic-spindle organizing protein 1

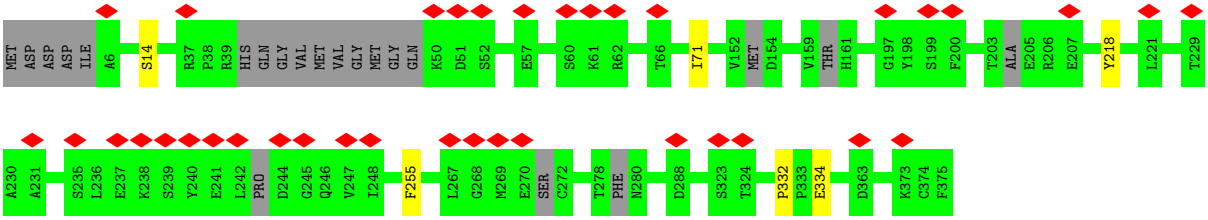


• Molecule 5: Mitotic-spindle organizing protein 1

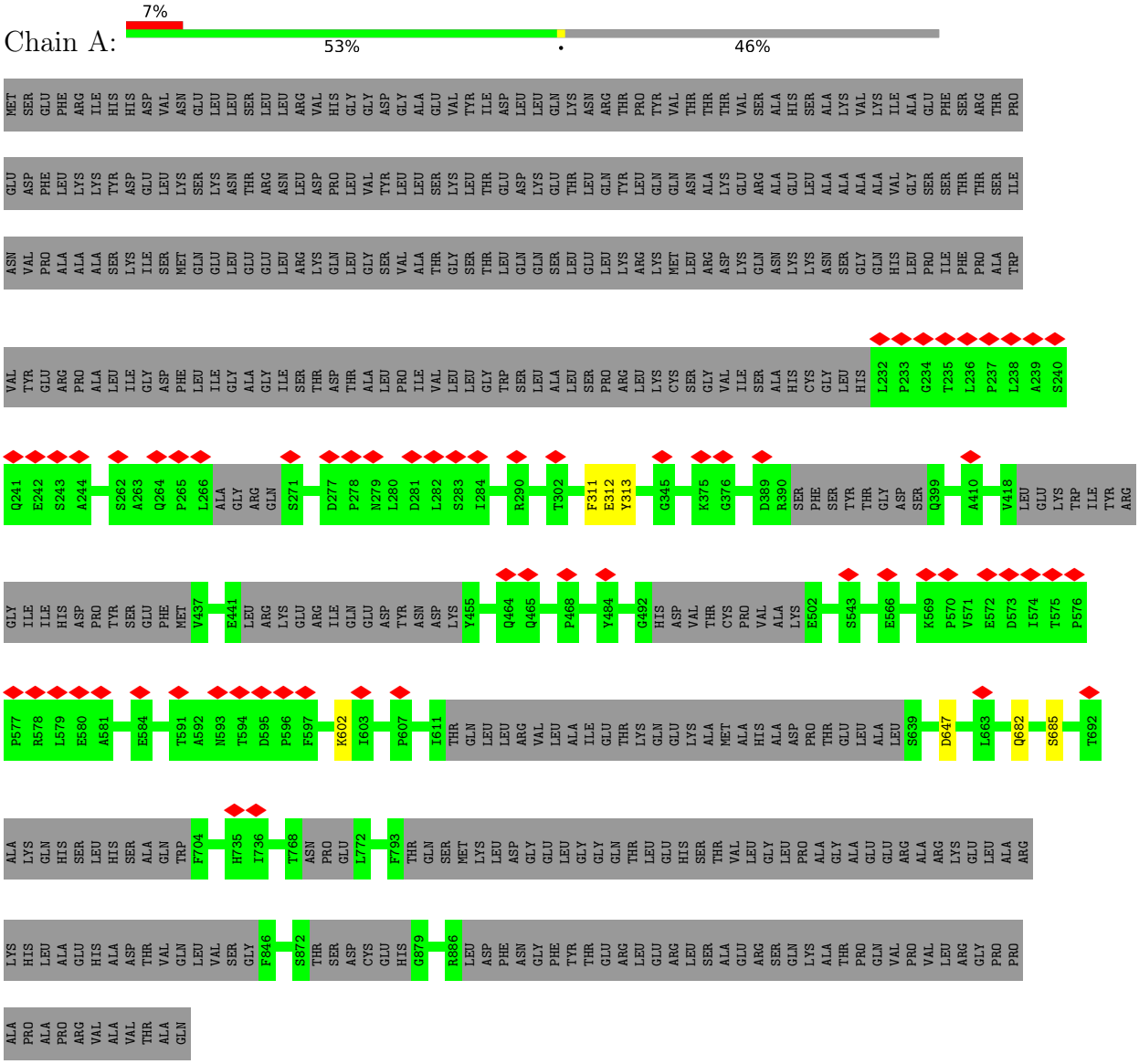


• Molecule 6: Actin, cytoplasmic 1

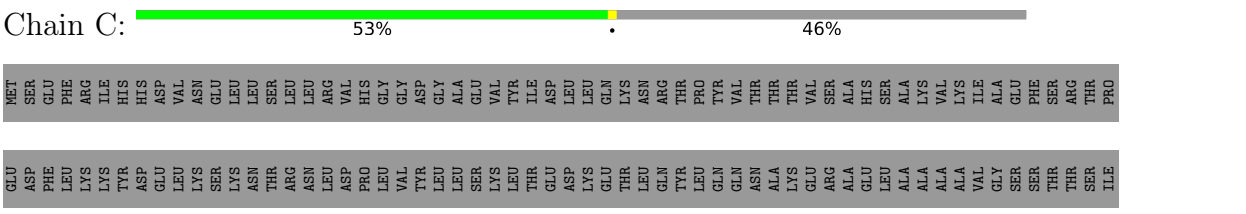


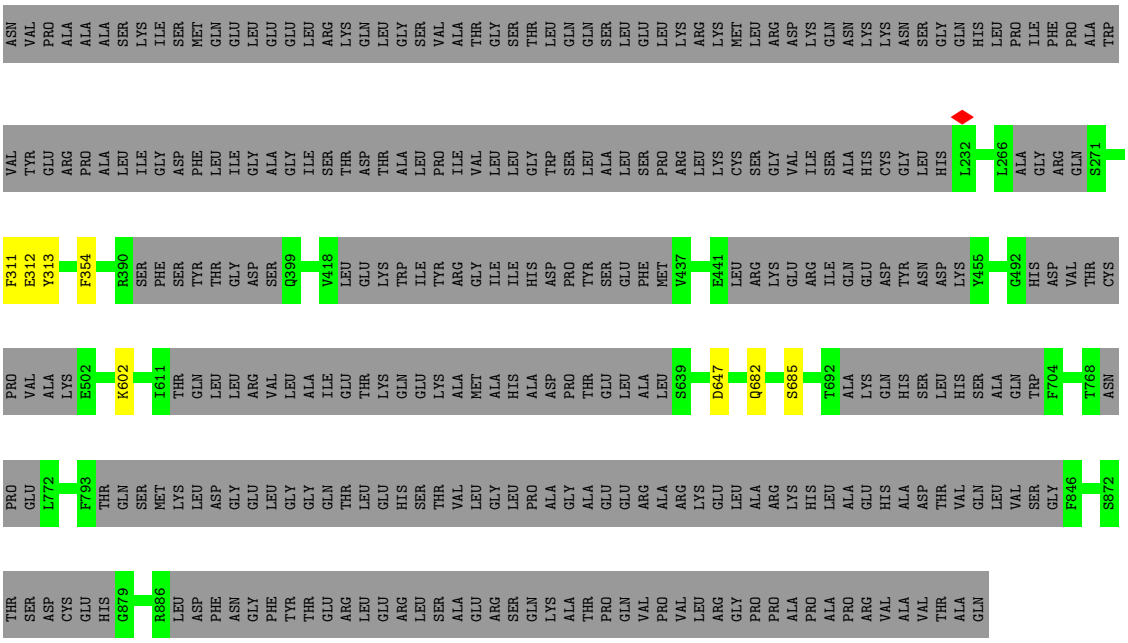


• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2



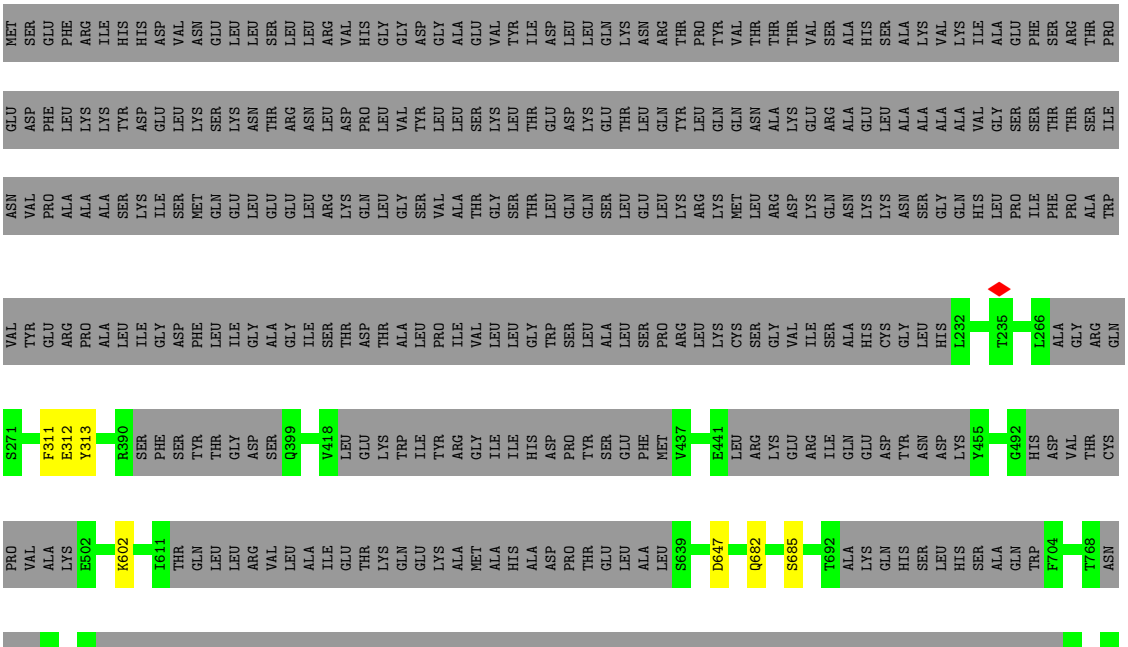
• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2





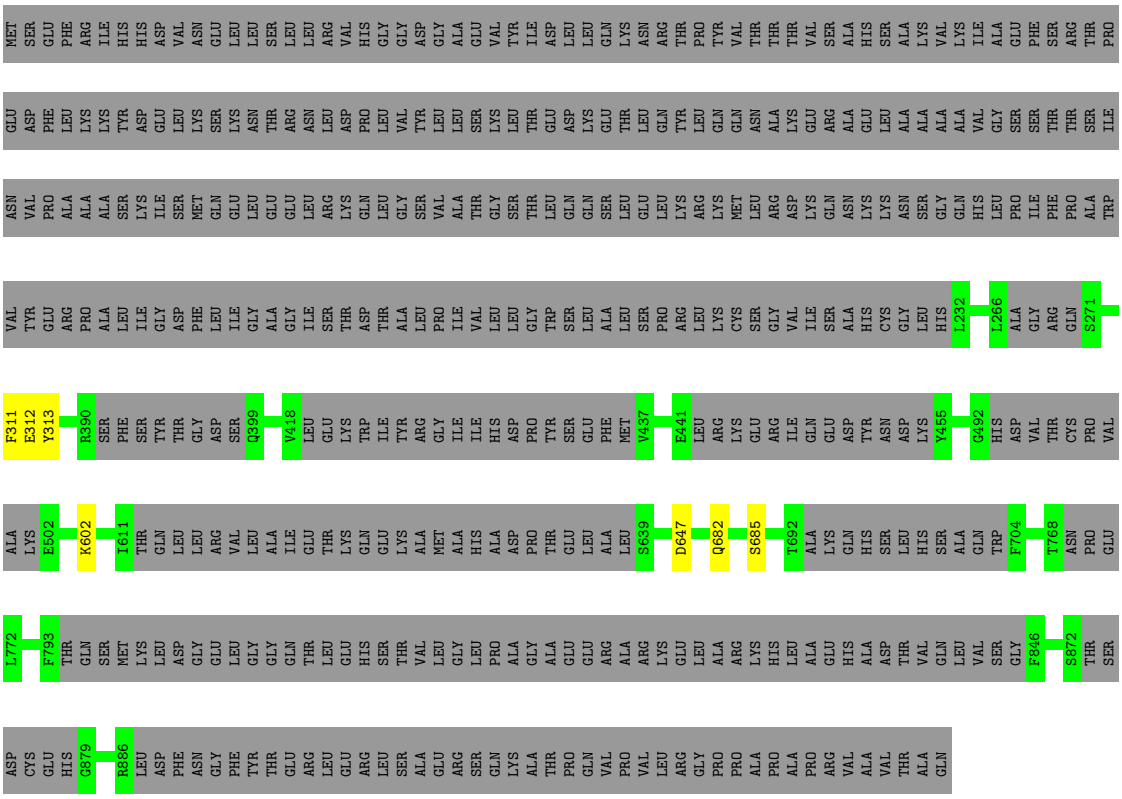
• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

Chain E:



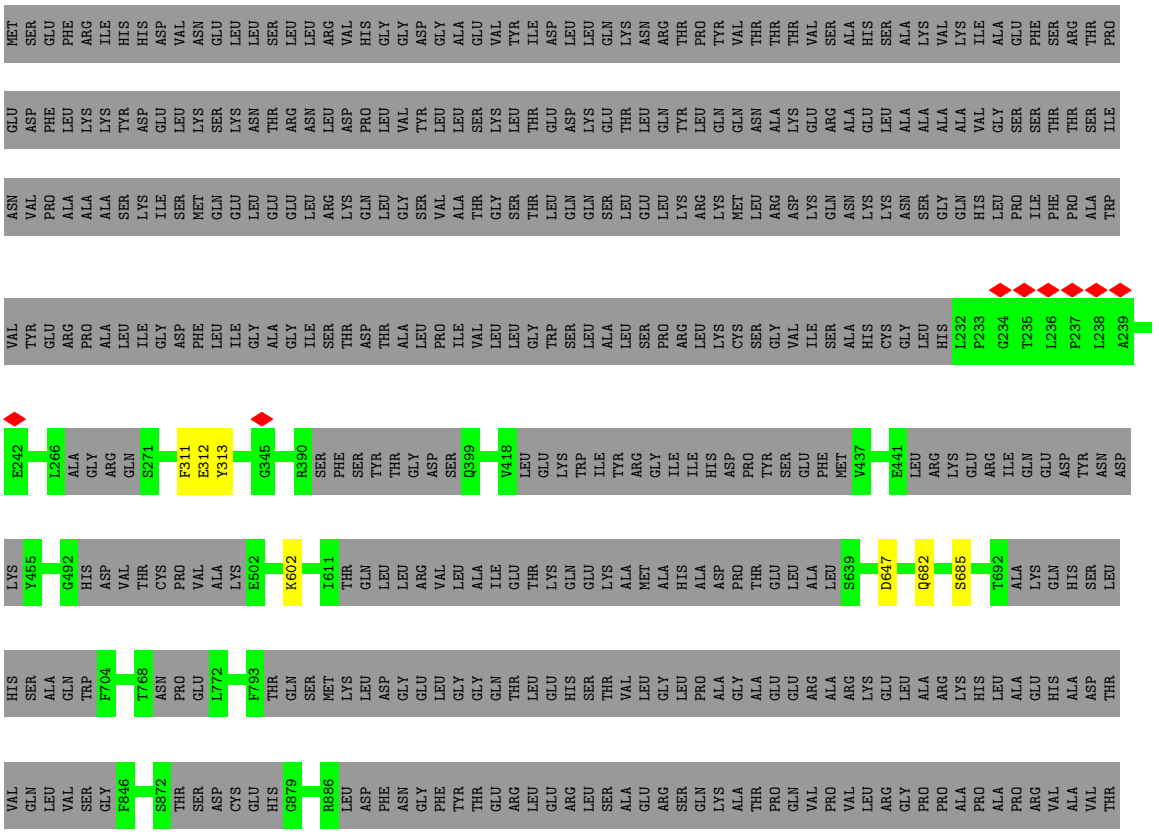
• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

Chain G:



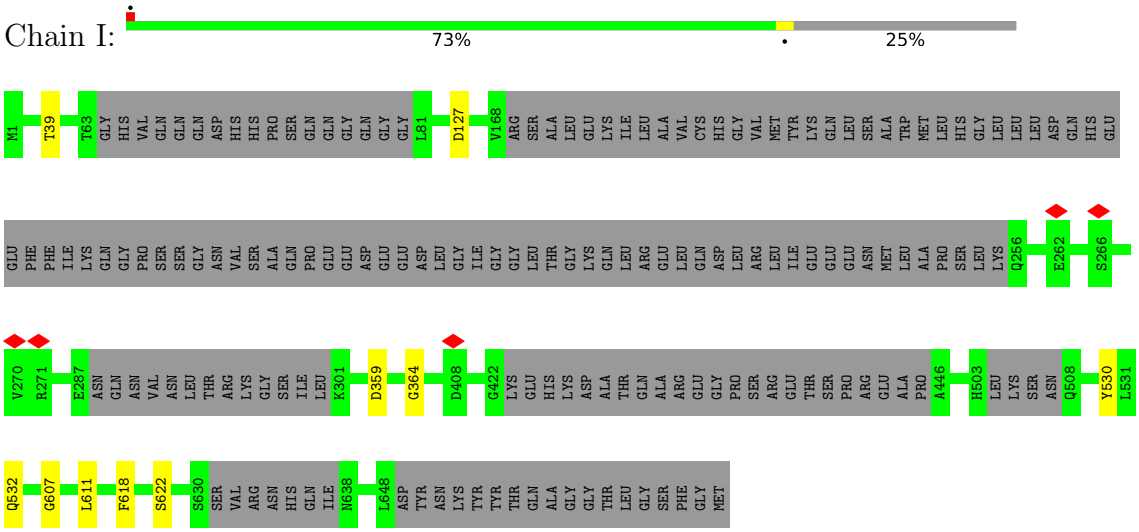
• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

Chain M:



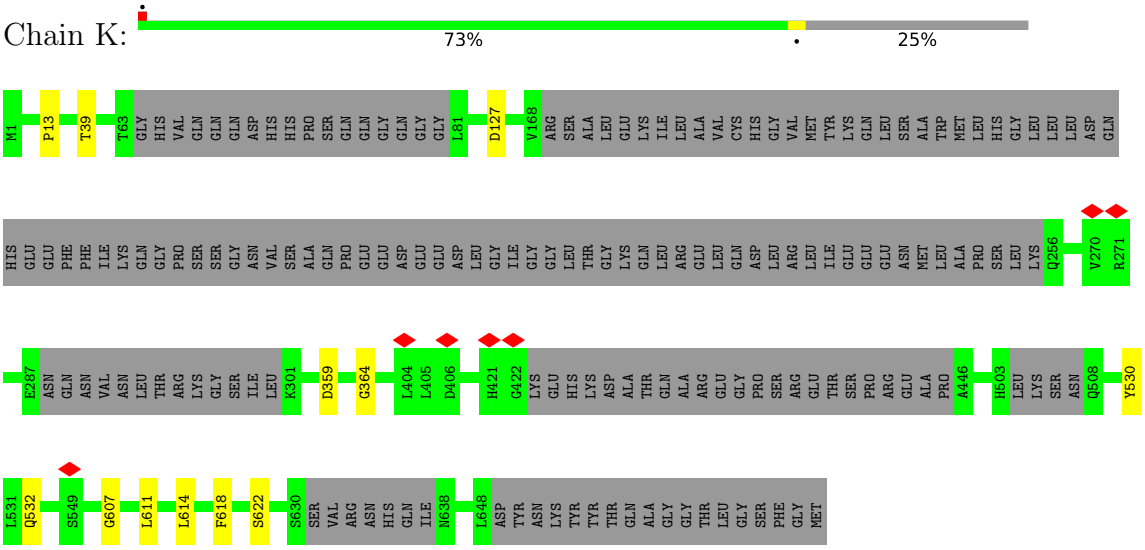
• Molecule 8: Isoform 2 of Gamma-tubulin complex component 4

Chain I:



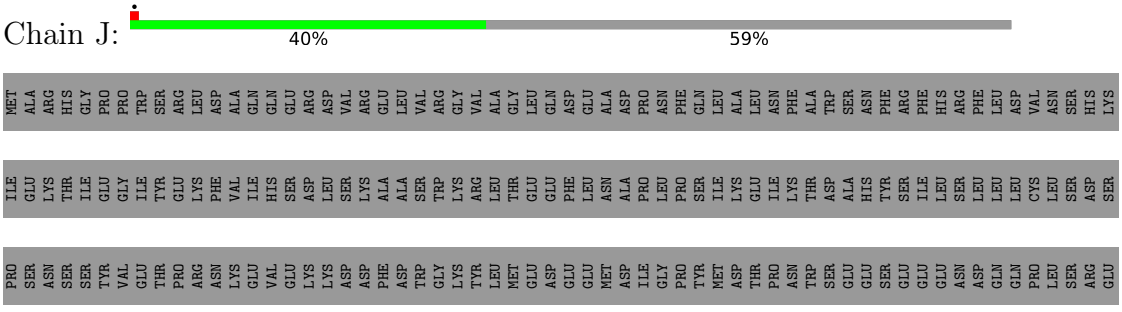
• Molecule 8: Isoform 2 of Gamma-tubulin complex component 4

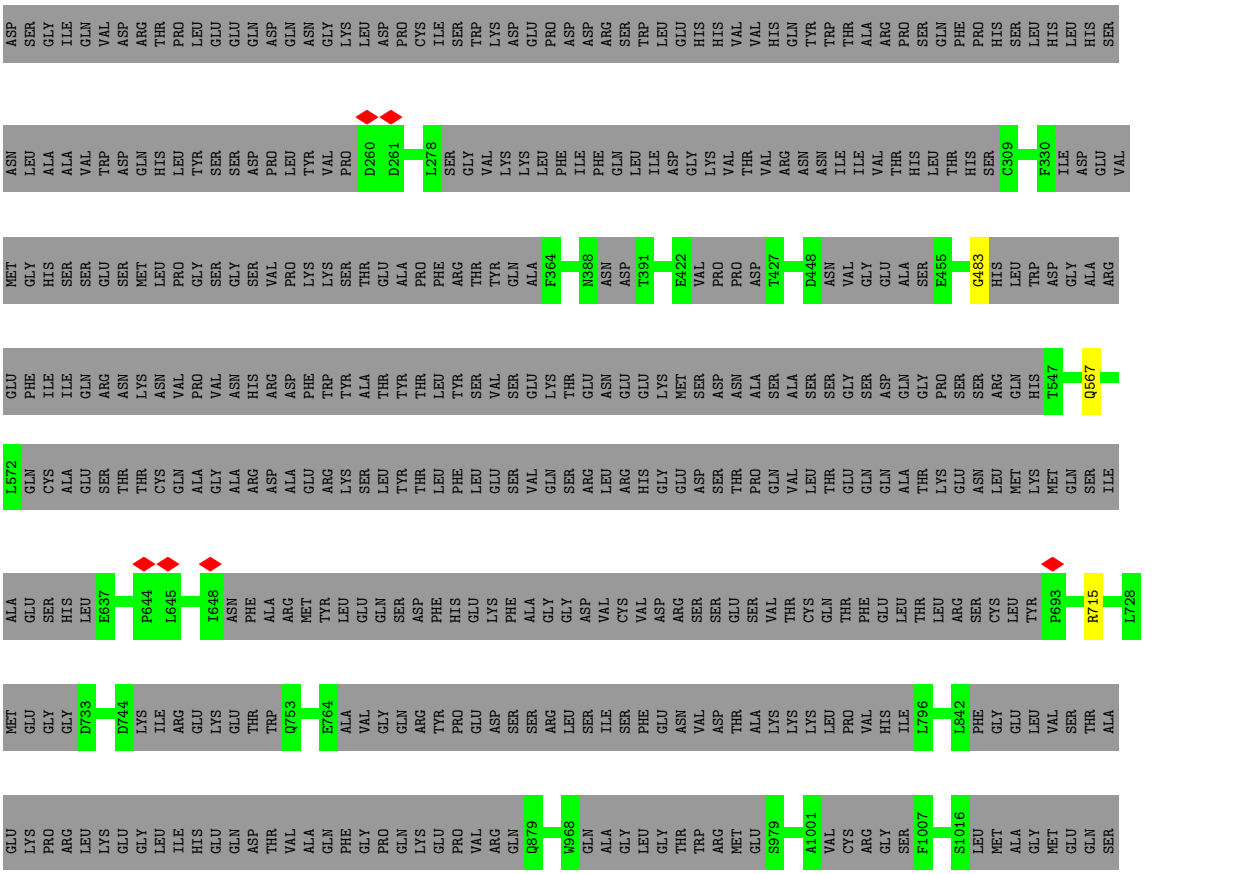
Chain K:



• Molecule 9: Gamma-tubulin complex component 5

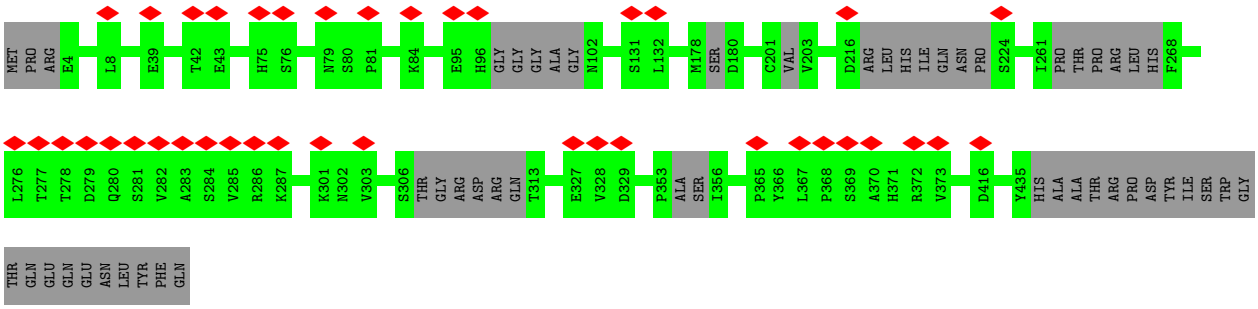
Chain J:





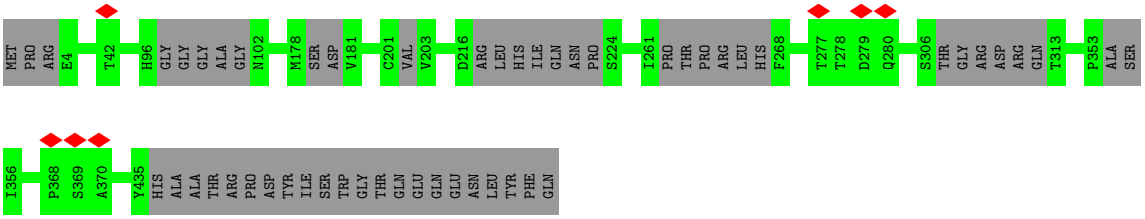
• Molecule 10: Tubulin gamma-1 chain

Chain a:



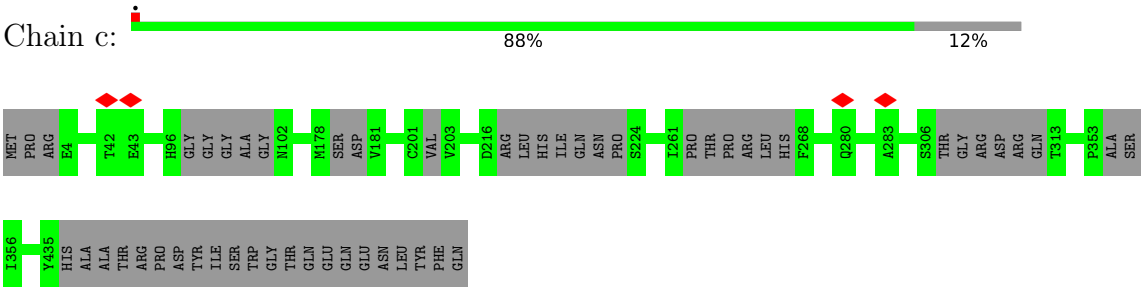
• Molecule 10: Tubulin gamma-1 chain

Chain b:



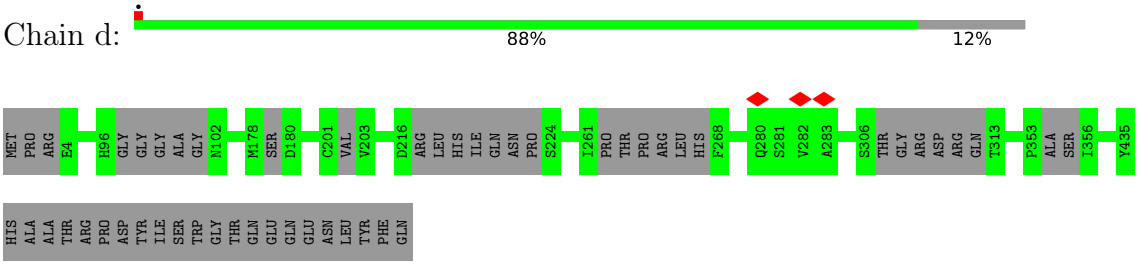
• Molecule 10: Tubulin gamma-1 chain

Chain c:



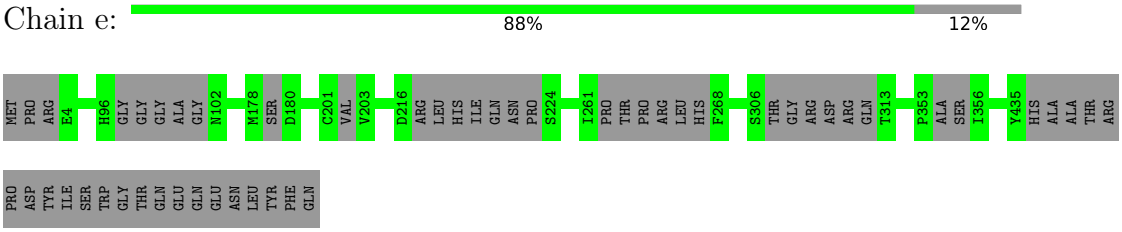
• Molecule 10: Tubulin gamma-1 chain

Chain d:



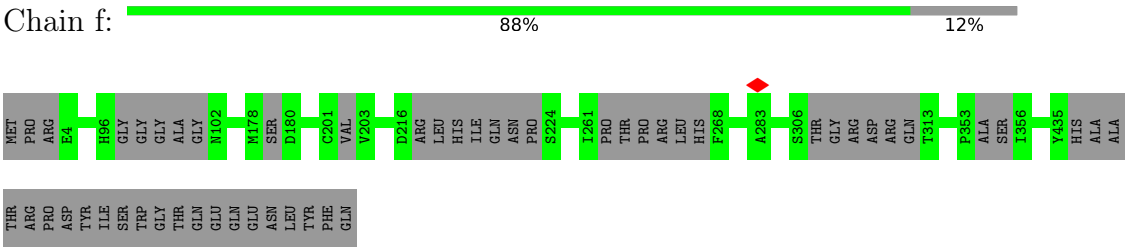
• Molecule 10: Tubulin gamma-1 chain

Chain e:



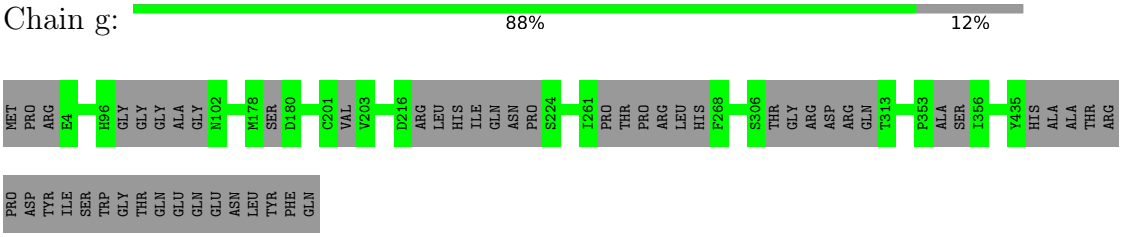
• Molecule 10: Tubulin gamma-1 chain

Chain f:



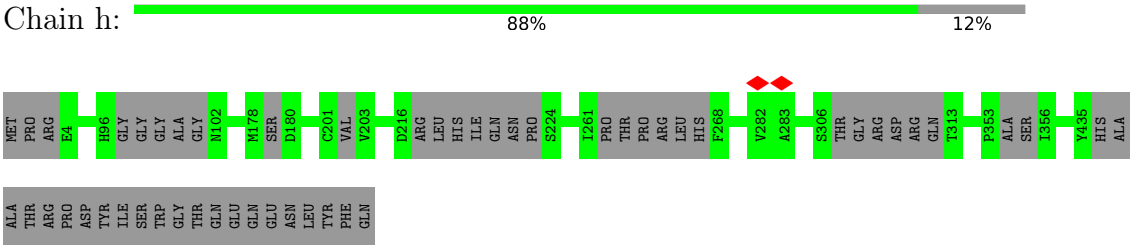
• Molecule 10: Tubulin gamma-1 chain

Chain g:



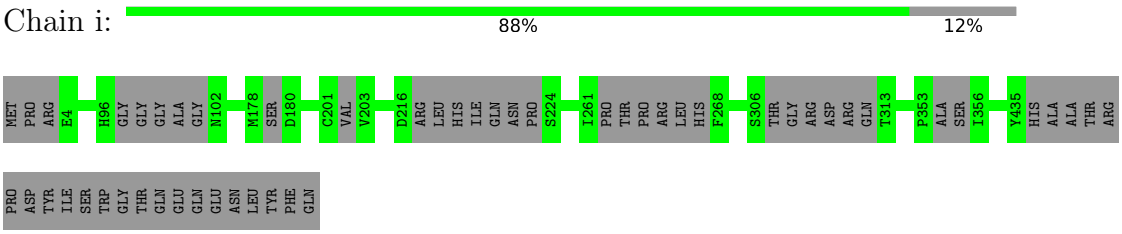
• Molecule 10: Tubulin gamma-1 chain

Chain h:



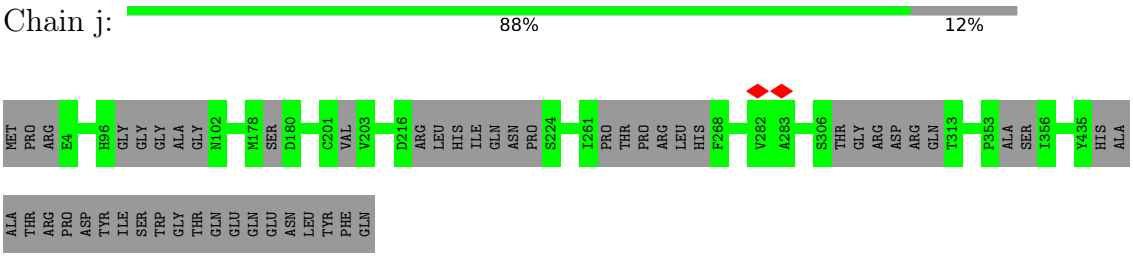
• Molecule 10: Tubulin gamma-1 chain

Chain i:



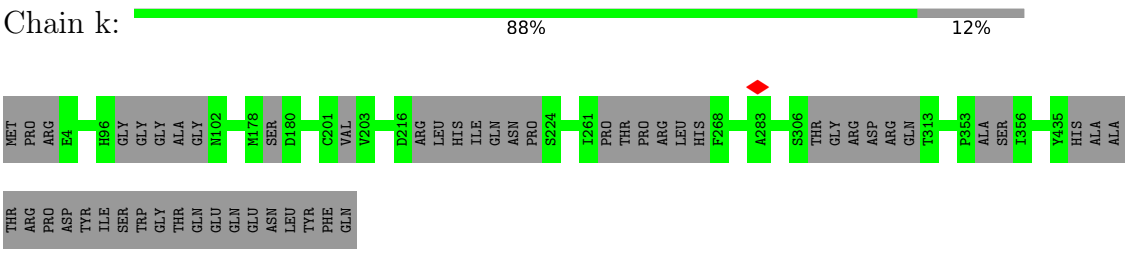
• Molecule 10: Tubulin gamma-1 chain

Chain j:



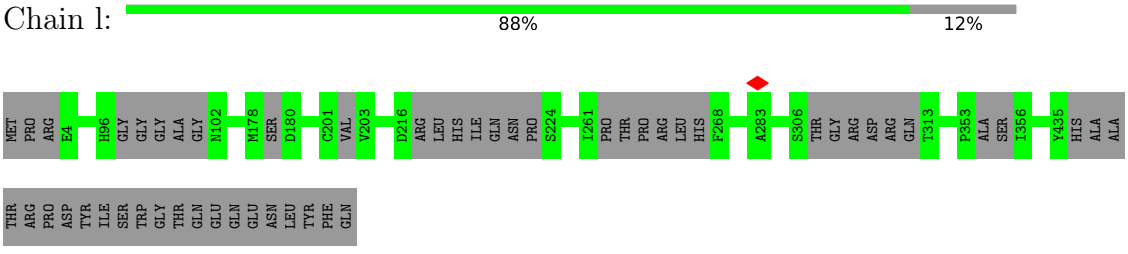
• Molecule 10: Tubulin gamma-1 chain

Chain k:



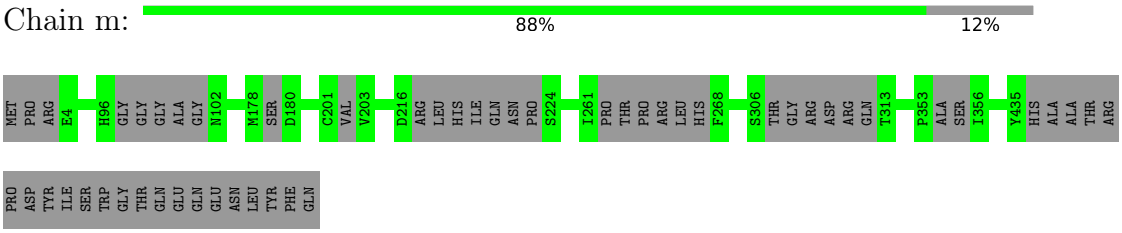
• Molecule 10: Tubulin gamma-1 chain

Chain l:



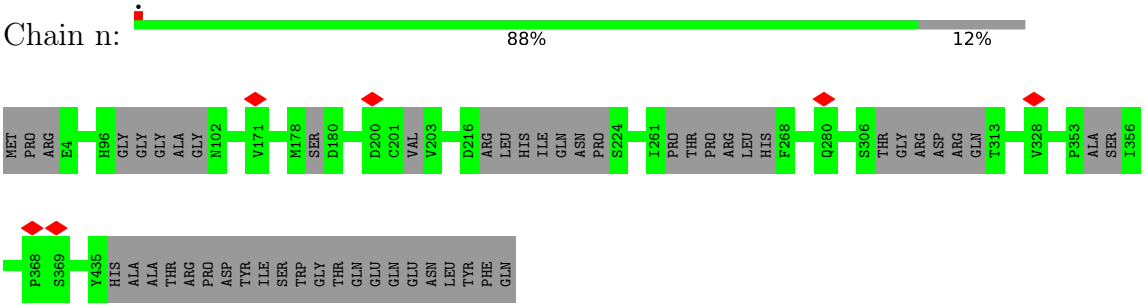
• Molecule 10: Tubulin gamma-1 chain

Chain m:



• Molecule 10: Tubulin gamma-1 chain

Chain n:



4 Experimental information (i)

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 ($e^-/Å^2$)	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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	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.

All (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
9:J:483:GLY:O	9:J:567:GLN:HA	1.78	0.82
3:6:4:ILE:N	6:9:332:PRO:CA	2.48	0.73
3:L:539:TRP:CB	3:L:599:GLY:CA	2.65	0.73
1:1:181:VAL:HA	2:2:347:ASN:O	1.89	0.73
8:K:13:PRO:O	3:L:392:SER:CB	2.38	0.71
4:5:100:LEU:O	5:7:37:THR:CB	2.40	0.69
3:L:539:TRP:O	3:L:602:ILE:CB	2.44	0.66
4:B:257:VAL:O	4:B:298:GLY:HA3	1.99	0.63
4:D:257:VAL:O	4:D:298:GLY:HA3	1.99	0.63
4:F:257:VAL:O	4:F:298:GLY:HA3	1.99	0.63
7:E:311:PHE:O	7:E:313:TYR:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:257:VAL:O	4:N:298:GLY:HA3	1.99	0.63
4:H:257:VAL:O	4:H:298:GLY:HA3	1.99	0.62
7:A:311:PHE:O	7:A:313:TYR:N	2.32	0.62
1:1:222:PRO:O	2:2:324:LYS:CB	2.48	0.61
7:G:311:PHE:O	7:G:313:TYR:N	2.32	0.61
7:M:311:PHE:O	7:M:313:TYR:N	2.32	0.60
7:C:311:PHE:O	7:C:313:TYR:N	2.32	0.58
1:Y:56:THR:CB	1:Z:284:GLU:O	2.52	0.58
3:L:539:TRP:HA	3:L:602:ILE:CB	2.34	0.58
4:5:26:ALA:CB	3:6:65:PRO:CB	2.84	0.55
2:2:3:GLU:HA	2:2:49:VAL:HA	1.88	0.55
3:3:1635:ASP:O	3:3:1639:HIS:N	2.30	0.54
7:A:682:GLN:O	7:A:685:SER:N	2.40	0.54
7:M:682:GLN:O	7:M:685:SER:N	2.40	0.53
7:G:682:GLN:O	7:G:685:SER:N	2.40	0.53
4:B:336:TYR:CB	7:C:354:PHE:CB	2.87	0.52
8:K:618:PHE:O	8:K:622:SER:N	2.40	0.52
7:C:682:GLN:O	7:C:685:SER:N	2.40	0.52
7:M:311:PHE:C	7:M:313:TYR:H	2.14	0.51
7:A:311:PHE:C	7:A:313:TYR:H	2.14	0.51
8:I:618:PHE:O	8:I:622:SER:N	2.40	0.51
7:E:682:GLN:O	7:E:685:SER:N	2.40	0.50
2:2:134:GLN:HA	2:2:165:ASN:O	2.10	0.50
7:C:311:PHE:C	7:C:313:TYR:H	2.14	0.50
7:G:311:PHE:C	7:G:313:TYR:H	2.14	0.49
7:E:311:PHE:C	7:E:313:TYR:H	2.14	0.49
3:L:393:ILE:O	3:L:397:LEU:N	2.41	0.48
8:I:607:GLY:O	8:I:611:LEU:N	2.47	0.47
8:K:607:GLY:O	8:K:611:LEU:N	2.47	0.47
4:B:336:TYR:O	7:C:354:PHE:CB	2.62	0.47
2:2:67:ASP:O	2:2:92:PHE:HA	2.14	0.47
4:5:93:ILE:HA	5:7:51:CYS:CB	2.45	0.46
6:9:14:SER:HA	6:9:71:ILE:O	2.15	0.46
7:E:602:LYS:O	7:E:647:ASP:N	2.49	0.46
7:G:602:LYS:O	7:G:647:ASP:N	2.49	0.46
4:B:322:GLN:O	4:B:326:ALA:N	2.47	0.45
4:N:322:GLN:O	4:N:326:ALA:N	2.47	0.45
7:A:602:LYS:O	7:A:647:ASP:N	2.49	0.45
7:C:602:LYS:O	7:C:647:ASP:N	2.49	0.45
3:L:430:GLN:O	3:L:434:SER:N	2.46	0.45
4:D:322:GLN:O	4:D:326:ALA:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:602:LYS:O	7:M:647:ASP:N	2.49	0.44
4:H:322:GLN:O	4:H:326:ALA:N	2.47	0.44
3:6:5:THR:H	6:9:332:PRO:CB	2.30	0.44
3:6:5:THR:CB	6:9:334:GLU:CB	2.96	0.44
1:O:191:THR:O	1:O:195:LEU:CB	2.67	0.43
3:L:441:GLN:O	3:L:445:ALA:N	2.51	0.43
1:V:191:THR:O	1:V:195:LEU:CB	2.67	0.43
6:9:218:TYR:O	6:9:255:PHE:HA	2.19	0.43
1:Q:191:THR:O	1:Q:195:LEU:CB	2.67	0.43
4:F:322:GLN:O	4:F:326:ALA:N	2.47	0.43
1:S:191:THR:O	1:S:195:LEU:CB	2.67	0.43
1:W:191:THR:O	1:W:195:LEU:CB	2.67	0.43
8:K:359:ASP:HA	8:K:364:GLY:HA3	2.01	0.43
1:Z:191:THR:O	1:Z:195:LEU:CB	2.67	0.43
1:1:191:THR:O	1:1:195:LEU:CB	2.67	0.43
1:R:191:THR:O	1:R:195:LEU:CB	2.67	0.42
1:T:191:THR:O	1:T:195:LEU:CB	2.67	0.42
1:U:191:THR:O	1:U:195:LEU:CB	2.67	0.42
1:X:191:THR:O	1:X:195:LEU:CB	2.67	0.42
1:Q:3:GLU:HA	1:Q:51:THR:HA	2.02	0.42
1:Y:191:THR:O	1:Y:195:LEU:CB	2.67	0.42
1:1:179:THR:O	2:2:350:LYS:HA	2.19	0.42
1:X:3:GLU:HA	1:X:51:THR:HA	2.02	0.42
1:P:191:THR:O	1:P:195:LEU:CB	2.67	0.42
1:R:3:GLU:HA	1:R:51:THR:HA	2.02	0.42
1:S:3:GLU:HA	1:S:51:THR:HA	2.02	0.42
1:W:3:GLU:HA	1:W:51:THR:HA	2.02	0.42
8:I:359:ASP:HA	8:I:364:GLY:HA3	2.01	0.42
8:K:614:LEU:O	8:K:618:PHE:N	2.30	0.41
1:Z:3:GLU:HA	1:Z:51:THR:HA	2.02	0.41
8:K:530:TYR:C	8:K:532:GLN:H	2.23	0.41
1:P:3:GLU:HA	1:P:51:THR:HA	2.02	0.41
1:T:3:GLU:HA	1:T:51:THR:HA	2.02	0.41
1:V:3:GLU:HA	1:V:51:THR:HA	2.02	0.41
1:Y:3:GLU:HA	1:Y:51:THR:HA	2.02	0.41
8:I:530:TYR:C	8:I:532:GLN:H	2.23	0.41
1:U:3:GLU:HA	1:U:51:THR:HA	2.02	0.41
3:L:431:ALA:O	3:L:435:GLY:N	2.50	0.41
1:O:3:GLU:HA	1:O:51:THR:HA	2.02	0.41
1:1:3:GLU:HA	1:1:51:THR:HA	2.02	0.41
2:2:316:VAL:O	2:2:365:SER:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:56:THR:O	1:V:58:ALA:N	2.54	0.41
1:W:56:THR:O	1:W:58:ALA:N	2.54	0.41
1:X:56:THR:O	1:X:58:ALA:N	2.54	0.41
1:1:100:ALA:CB	2:2:252:LYS:HA	2.40	0.40
1:U:56:THR:O	1:U:58:ALA:N	2.54	0.40
1:Q:157:LEU:O	1:Q:161:TYR:N	2.54	0.40
1:R:157:LEU:O	1:R:161:TYR:N	2.54	0.40
1:Y:157:LEU:O	1:Y:161:TYR:N	2.54	0.40

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

All (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
7	E	312	GLU
7	G	312	GLU
7	M	312	GLU
8	I	39	THR
8	K	39	THR

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

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

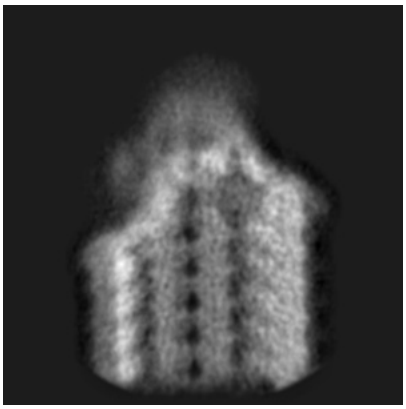
6 Map visualisation

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.

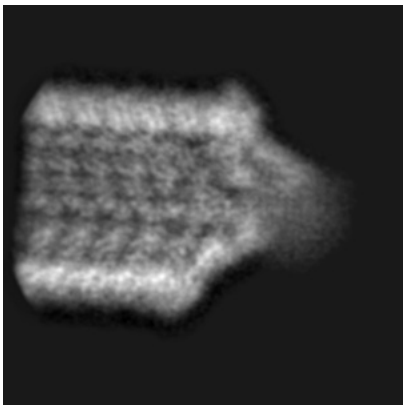
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

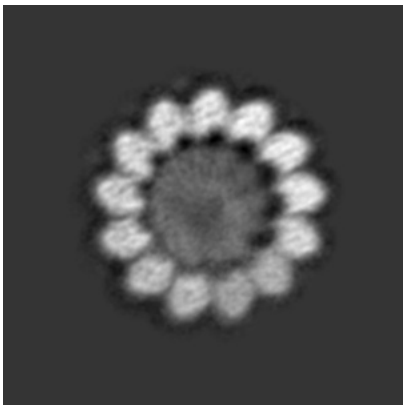
6.1.1 Primary map



X

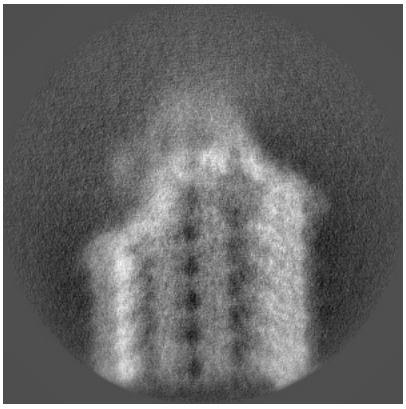


Y

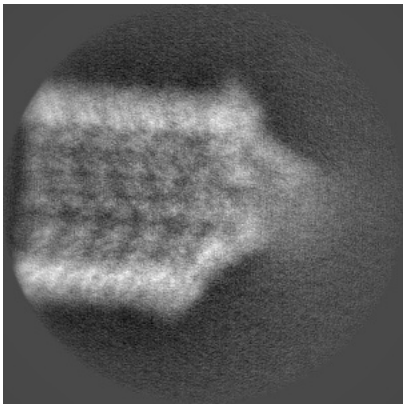


Z

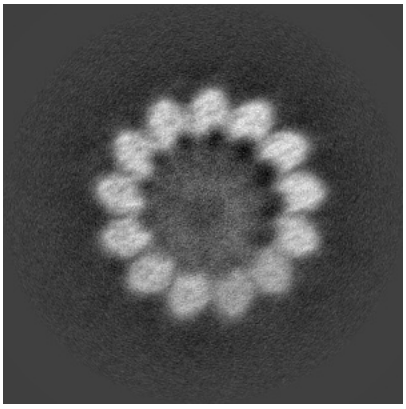
6.1.2 Raw map



X



Y

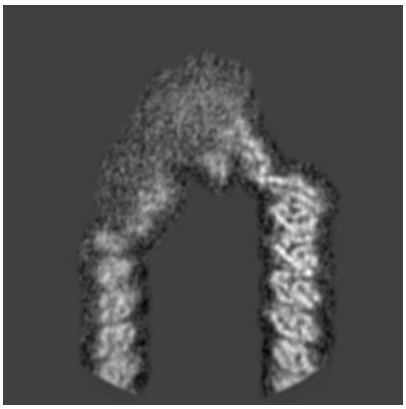


Z

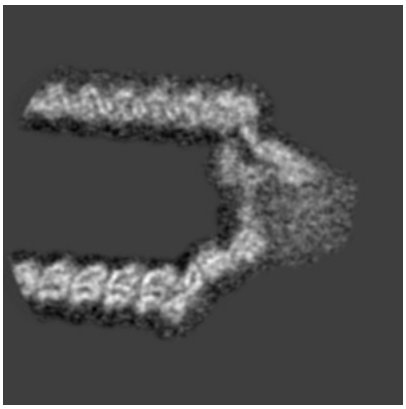
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

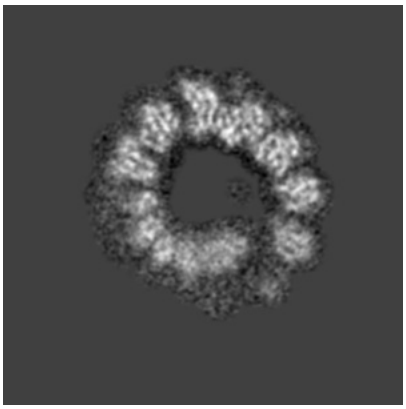
6.2.1 Primary map



X Index: 180

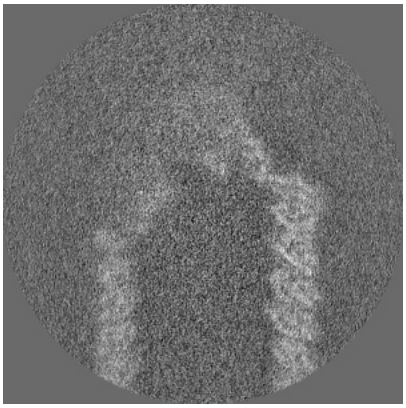


Y Index: 180

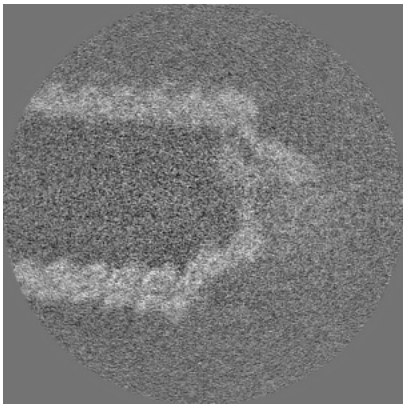


Z Index: 180

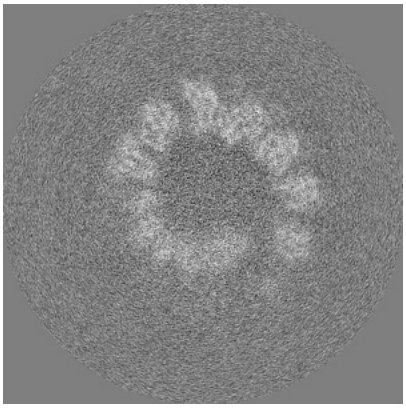
6.2.2 Raw map



X Index: 180



Y Index: 180

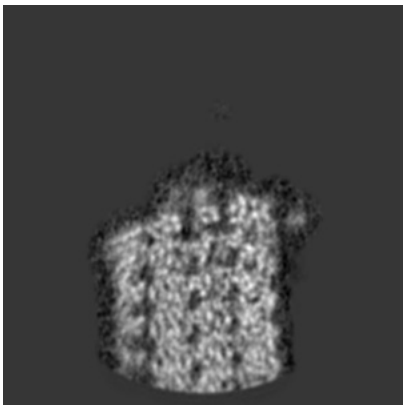


Z Index: 180

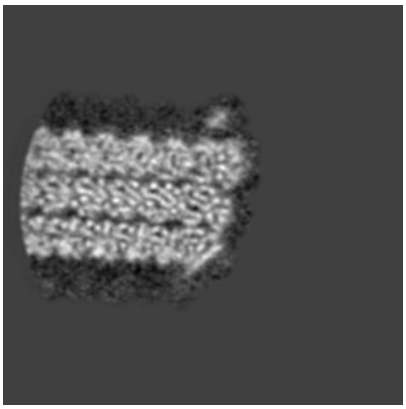
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

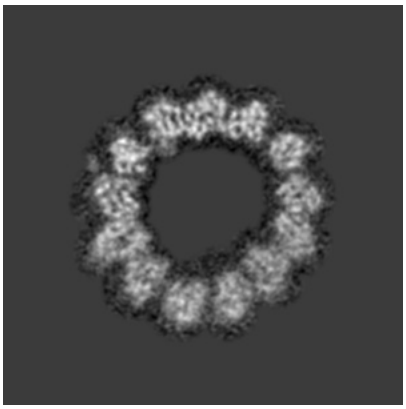
6.3.1 Primary map



X Index: 116

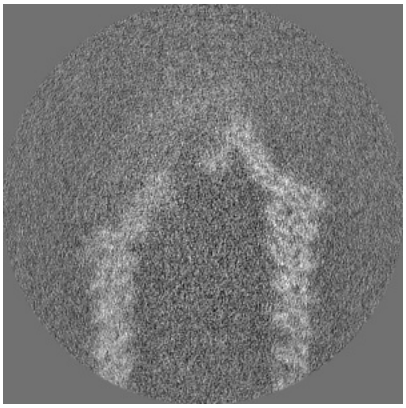


Y Index: 256

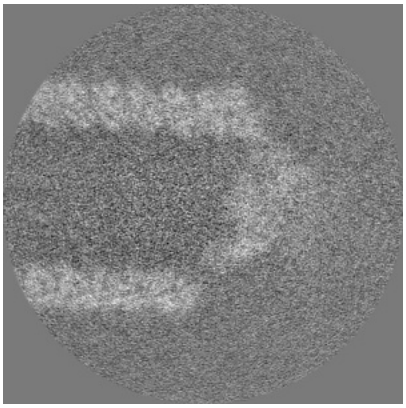


Z Index: 140

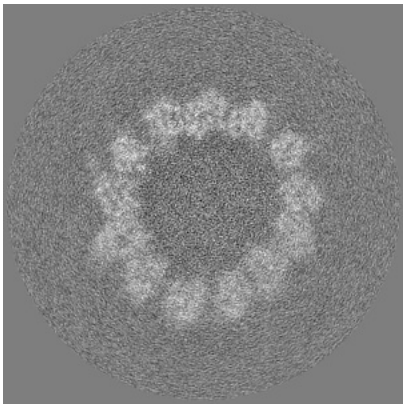
6.3.2 Raw map



X Index: 175



Y Index: 197

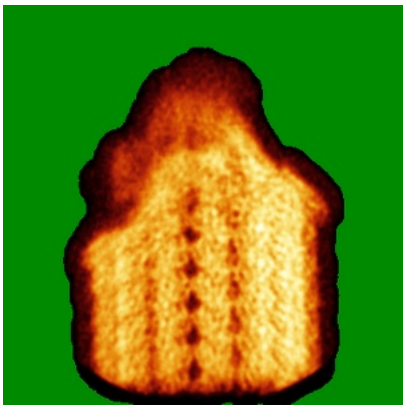


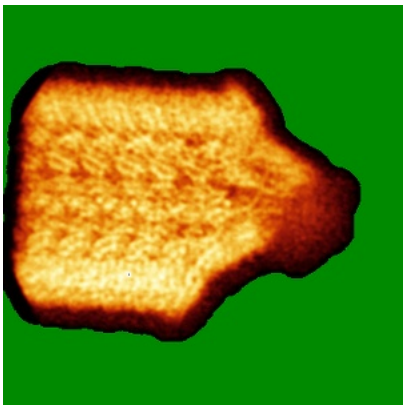
Z Index: 140

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

6.4 Orthogonal standard-deviation projections (False-color) (i)

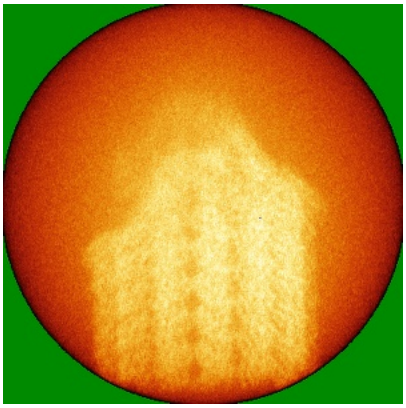
6.4.1 Primary map

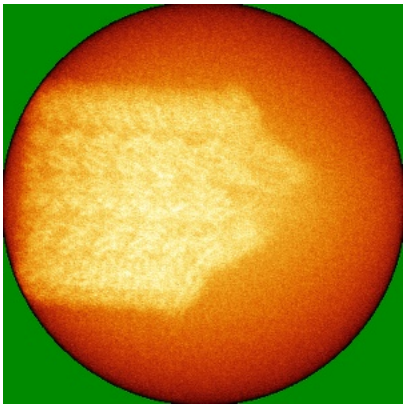

X

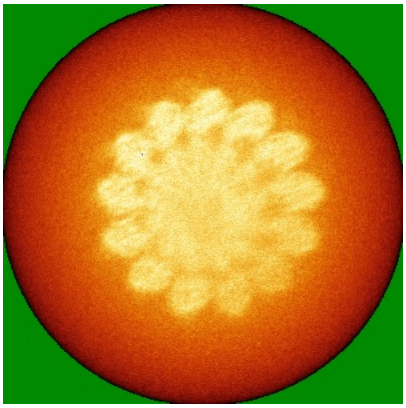

Y


Z

6.4.2 Raw map


X

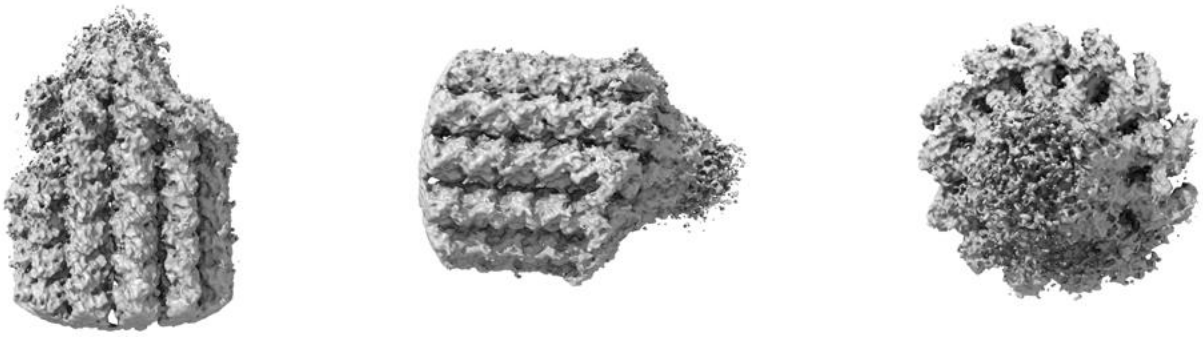

Y


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)

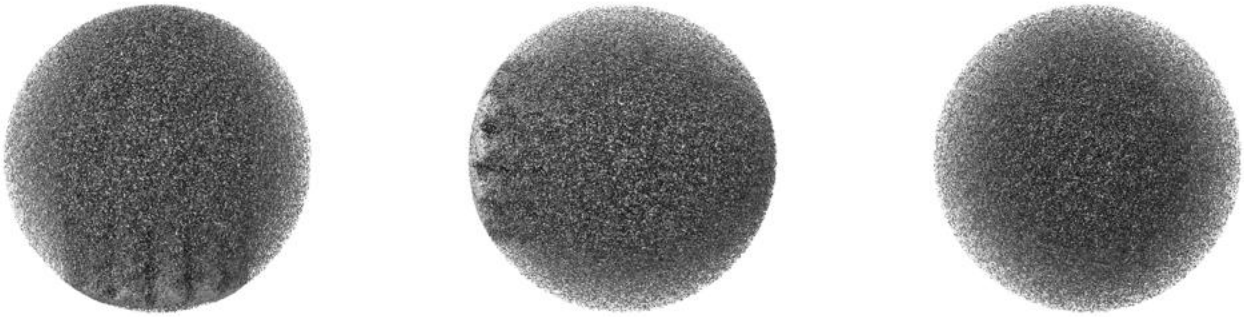
6.5.1 Primary map



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.

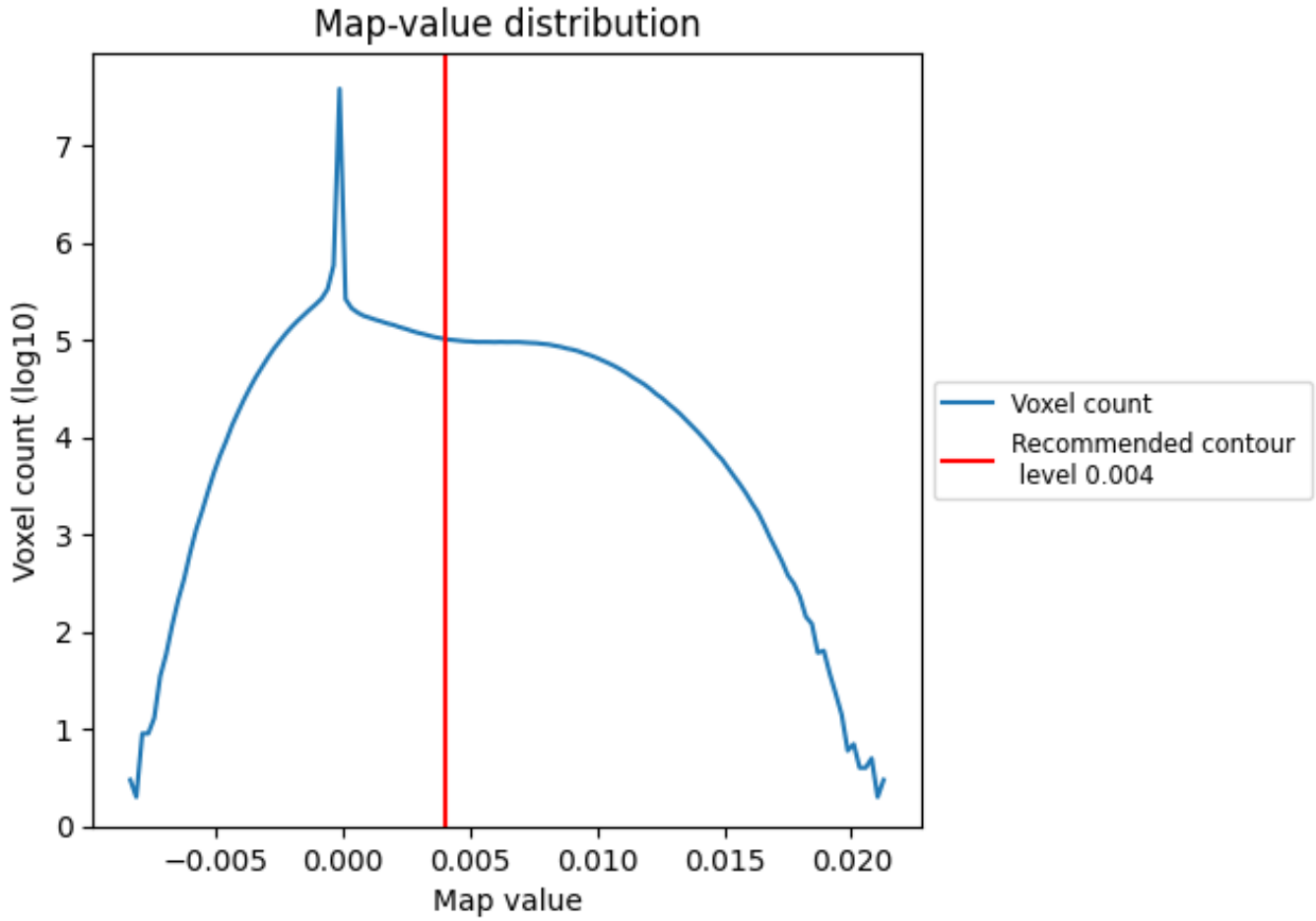
6.6 Mask visualisation (i)

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

7 Map analysis

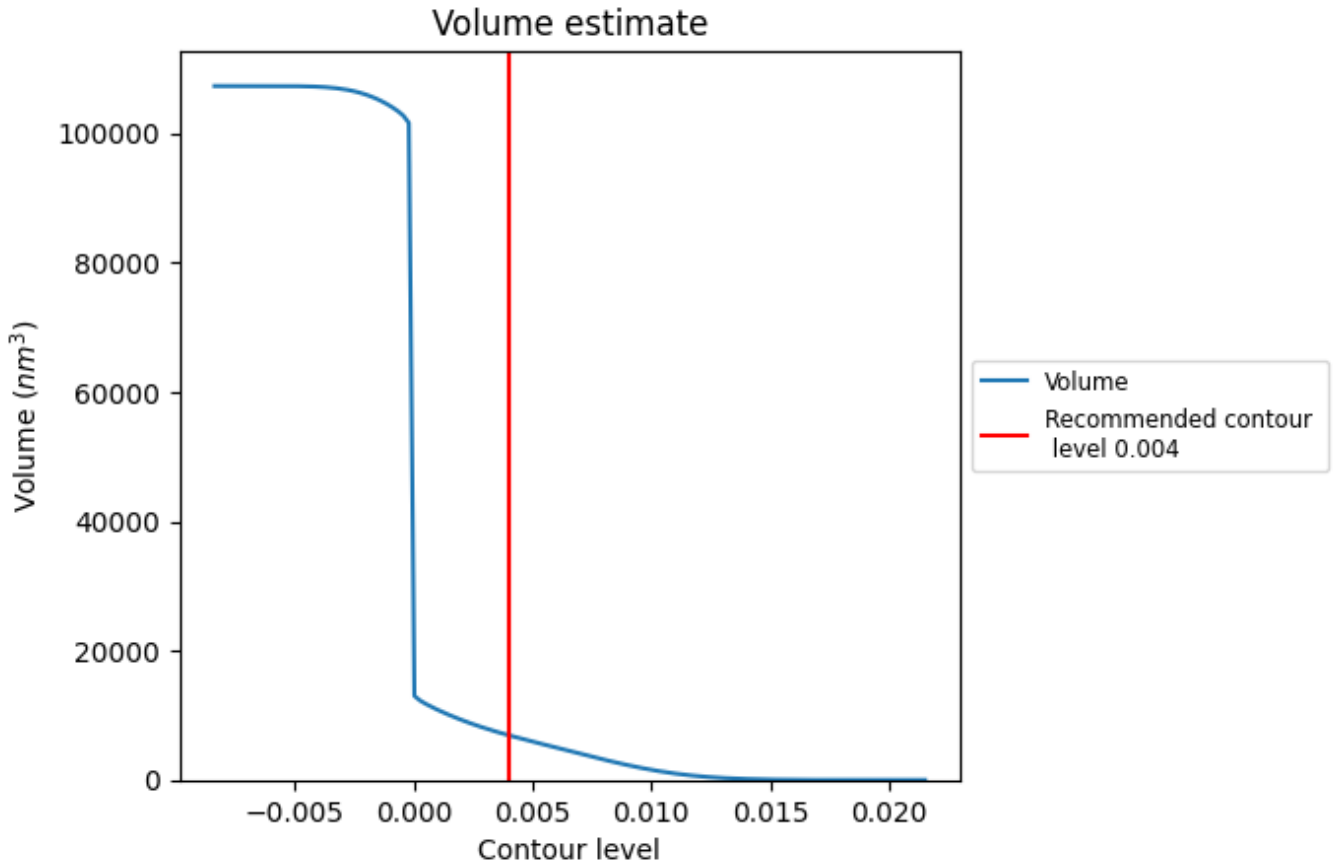
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

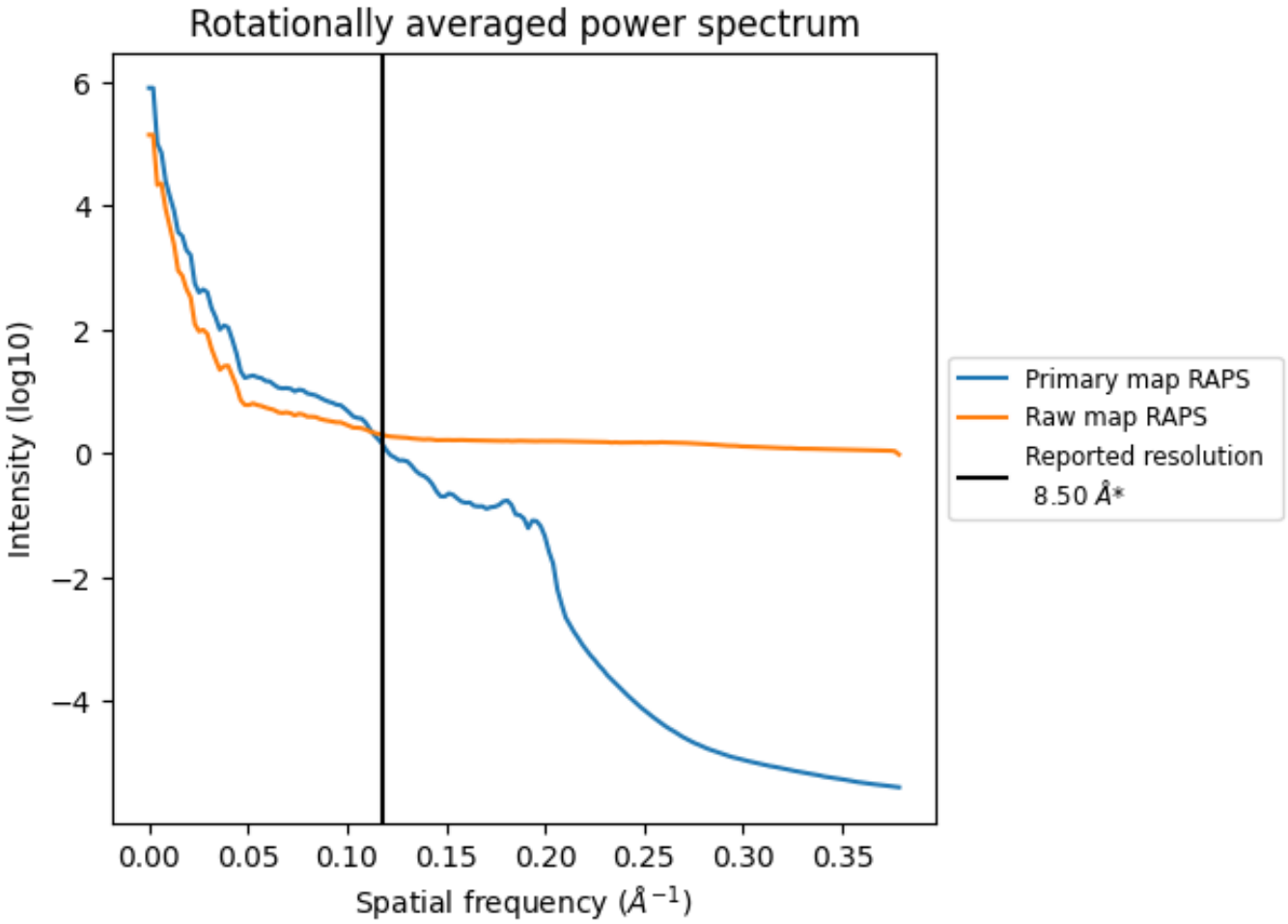
7.2 Volume estimate (i)



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)

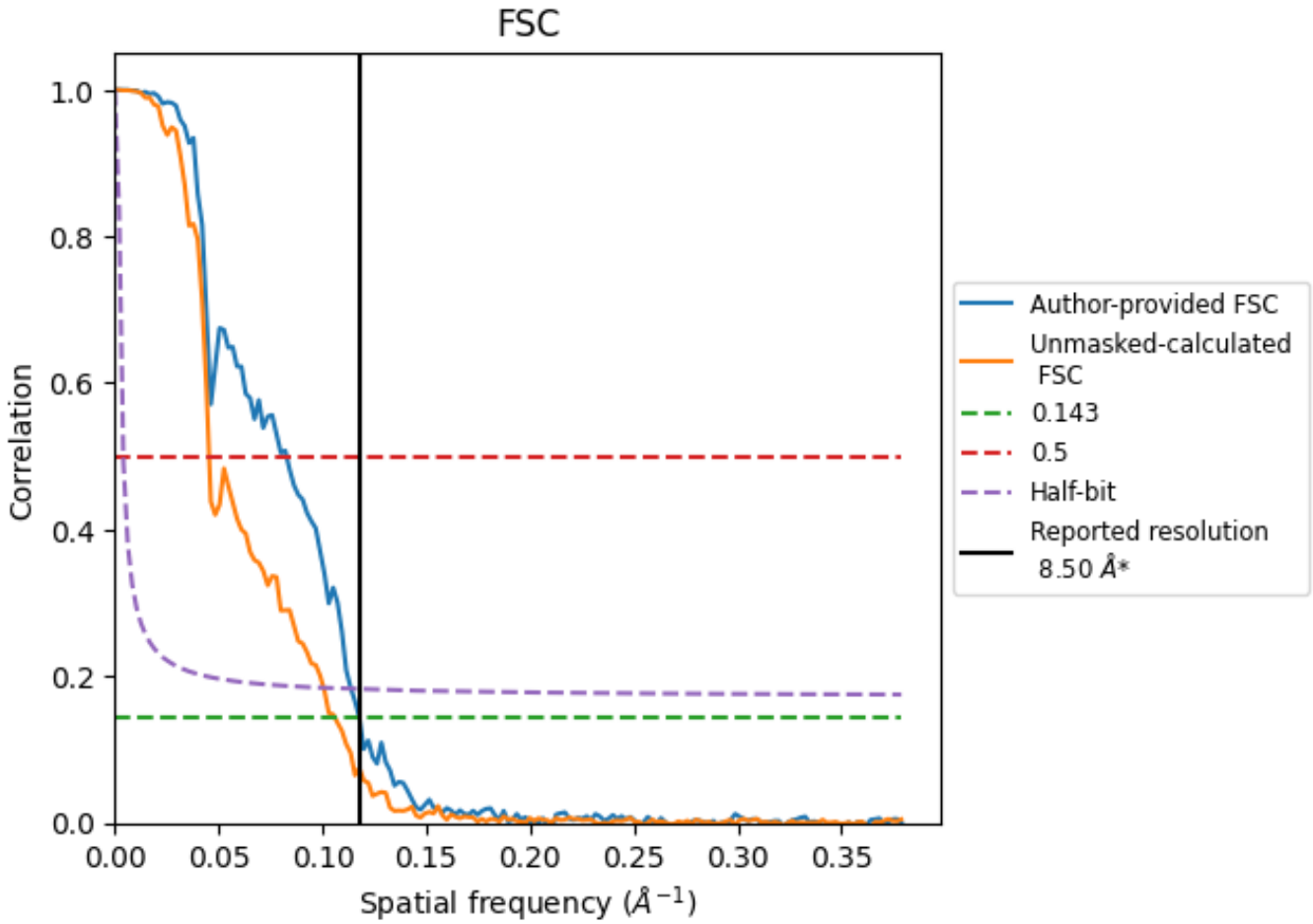


*Reported resolution corresponds to spatial frequency of 0.118 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.118 Å^{-1}

8.2 Resolution estimates (i)

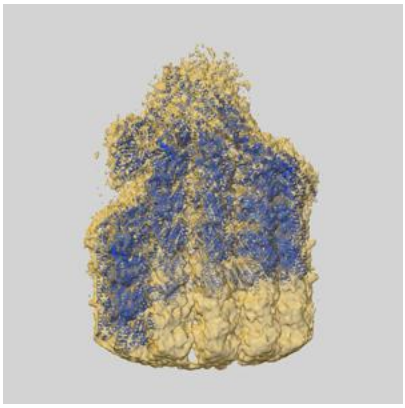
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.50	-	-
Author-provided FSC curve	8.48	12.09	8.78
Unmasked-calculated*	9.43	21.98	9.94

*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 %

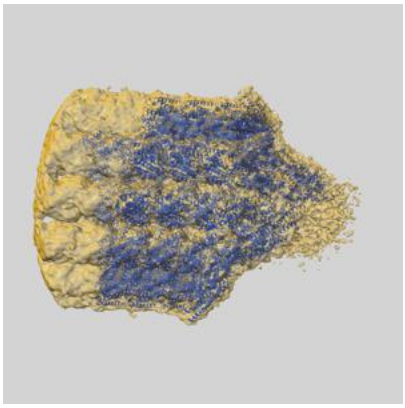
9 Map-model fit

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.

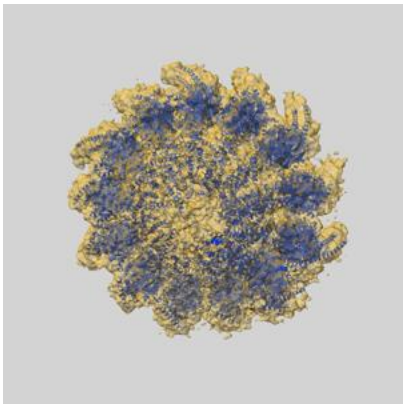
9.1 Map-model overlay



X



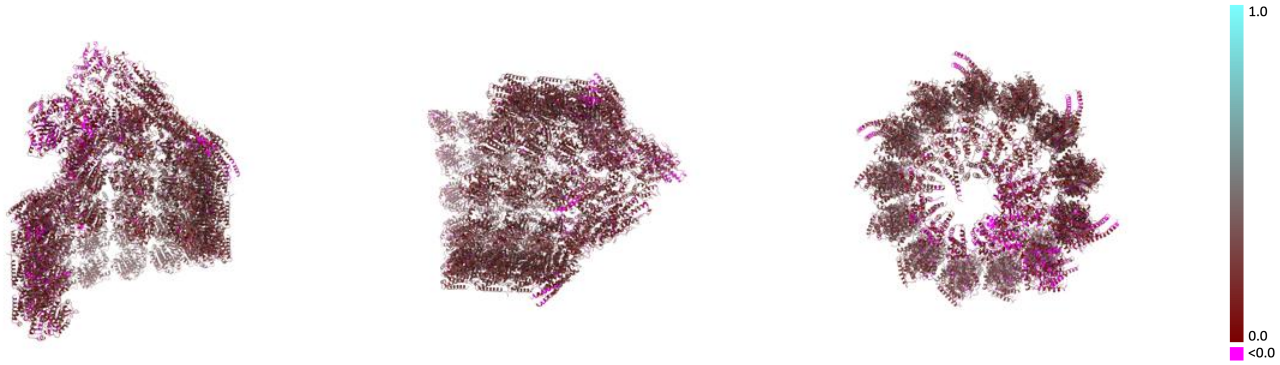
Y



Z

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.

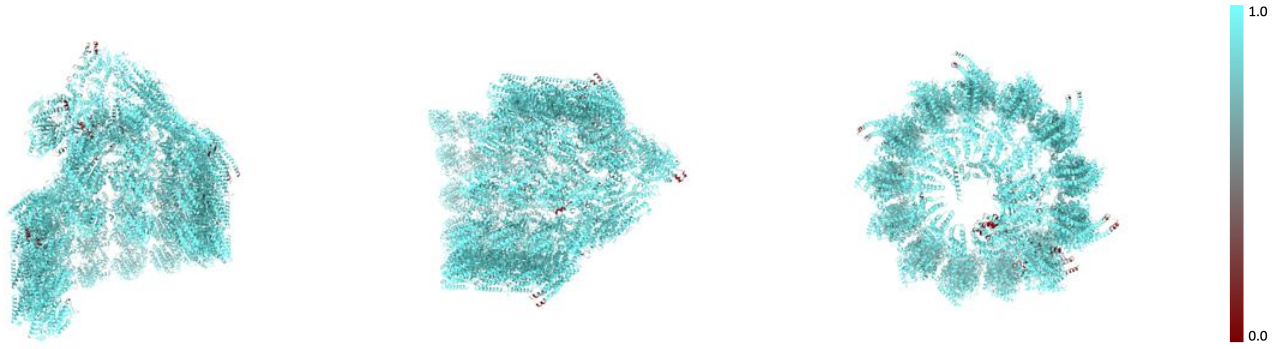
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

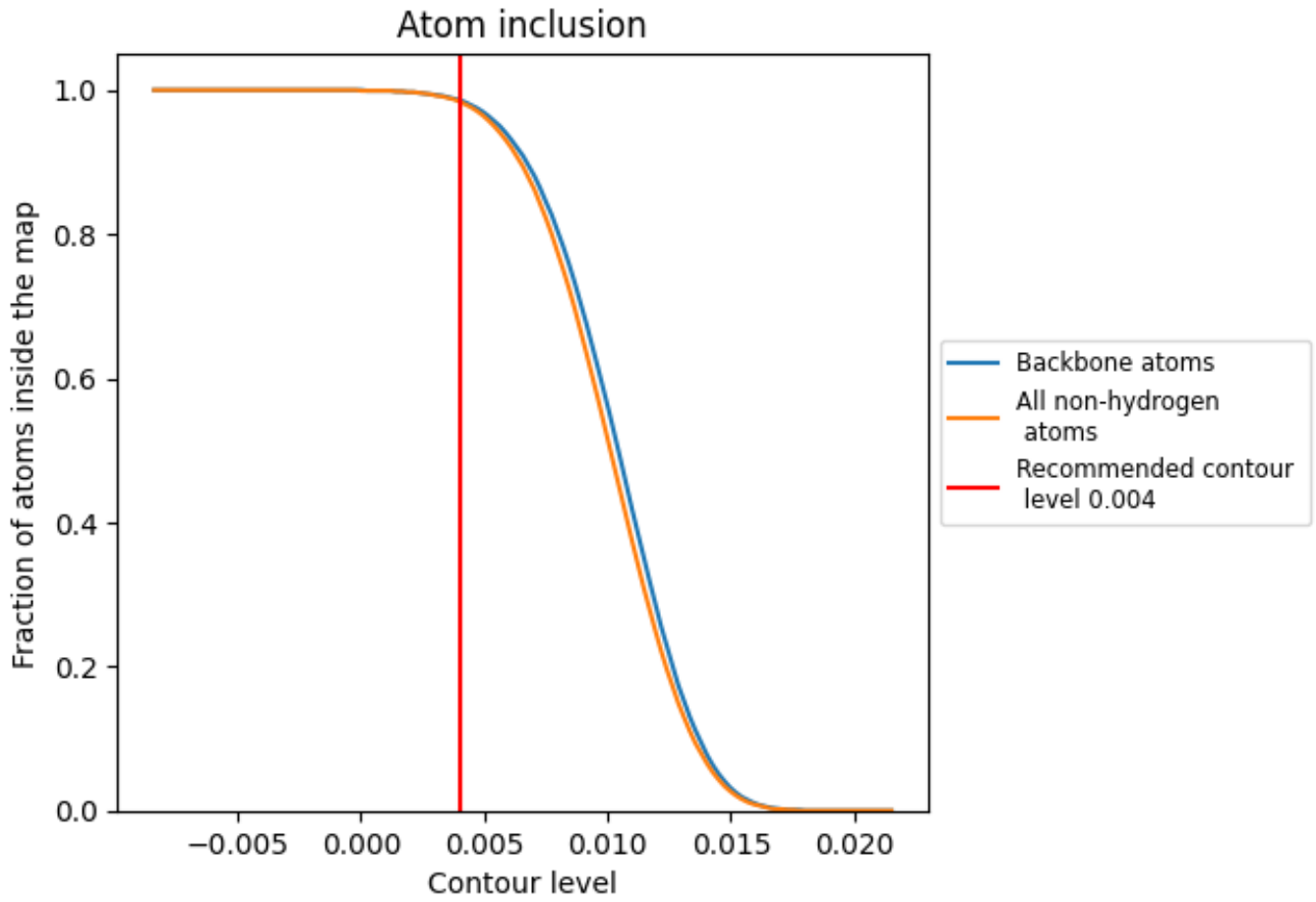
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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

Continued on next page...

Continued from previous page...

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