



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:46 PM UTC

PDB ID : 8VRD / pdb_00008vrd
EMDB ID : EMD-43481
Title : Rigid body fitted model for free recombinant gamma tubulin ring complex.
Authors : Aher, A.; Urnavicius, L.; Kapoor, T.M.
Deposited on : 2024-01-21
Resolution : 7.00 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:

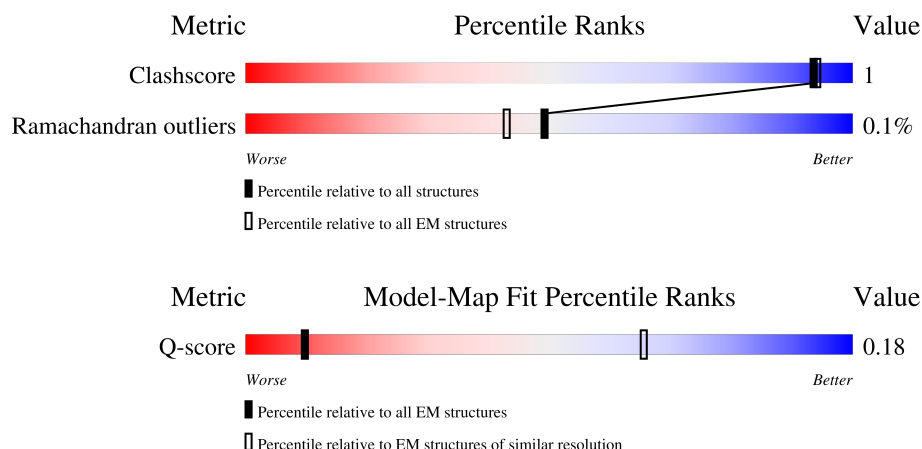
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 7.00 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.



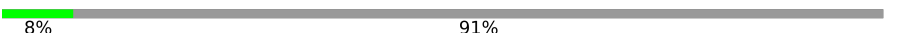
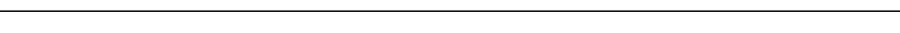
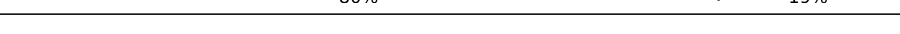
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	483 (6.50 - 7.50)

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	B	907	62% 37%
1	D	907	62% 37%
1	F	907	62% 37%
1	H	907	62% 37%
1	N	907	15% 62% 37%

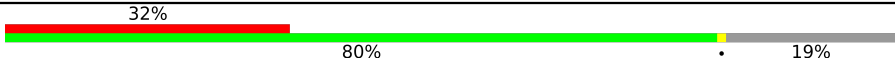
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Mol	Chain	Length	Quality of chain
1	O	907	
2	L	1811	
2	P	1811	
2	T	1811	
3	Q	82	
3	R	82	
4	S	375	
5	A	930	
5	C	930	
5	E	930	
5	G	930	
5	M	930	
6	a	457	
6	b	457	
6	c	457	
6	d	457	
6	e	457	
6	f	457	
6	g	457	
6	h	457	
6	i	457	
6	j	457	
6	k	457	
6	l	457	
6	m	457	

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Mol	Chain	Length	Quality of chain
6	n	457	
7	I	666	
7	K	666	
8	J	1024	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 67053 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 Gamma-tubulin complex component 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	O	116	Total	C	N	O	0	0
			577	345	116	116		
1	B	572	Total	C	N	O	0	0
			2840	1696	572	572		
1	D	572	Total	C	N	O	0	0
			2840	1696	572	572		
1	F	572	Total	C	N	O	0	0
			2840	1696	572	572		
1	H	572	Total	C	N	O	0	0
			2840	1696	572	572		
1	N	572	Total	C	N	O	0	0
			2840	1696	572	572		

- Molecule 2 is a protein called TUBGCP6 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	P	158	Total	C	N	O	0	0
			779	463	158	158		
2	L	198	Total	C	N	O	0	0
			978	582	198	198		
2	T	297	Total	C	N	O	0	0
			1476	882	297	297		

- Molecule 3 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	Q	65	Total	C	N	O	0	0
			323	193	65	65		
3	R	59	Total	C	N	O	0	0
			293	175	59	59		

- Molecule 4 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	S	354	Total	C	N	O	0	0
			1745	1037	354	354		

- Molecule 5 is a protein called Isoform 3 of Gamma-tubulin complex component 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	A	539	Total	C	N	O	0	0
			2676	1598	539	539		
5	C	539	Total	C	N	O	0	0
			2676	1598	539	539		
5	E	539	Total	C	N	O	0	0
			2676	1598	539	539		
5	G	539	Total	C	N	O	0	0
			2676	1598	539	539		
5	M	539	Total	C	N	O	0	0
			2676	1598	539	539		

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 6 is a protein called Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	a	368	Total	C	N	O	0	0
			1820	1084	368	368		
6	b	368	Total	C	N	O	0	0
			1820	1084	368	368		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	c	368	Total 1820	C 1084	N 368	O 368	0	0
6	d	368	Total 1820	C 1084	N 368	O 368	0	0
6	e	368	Total 1820	C 1084	N 368	O 368	0	0
6	f	368	Total 1820	C 1084	N 368	O 368	0	0
6	g	368	Total 1820	C 1084	N 368	O 368	0	0
6	h	368	Total 1820	C 1084	N 368	O 368	0	0
6	i	368	Total 1820	C 1084	N 368	O 368	0	0
6	j	368	Total 1820	C 1084	N 368	O 368	0	0
6	k	369	Total 1824	C 1086	N 369	O 369	0	0
6	l	369	Total 1824	C 1086	N 369	O 369	0	0
6	m	368	Total 1820	C 1084	N 368	O 368	0	0
6	n	368	Total 1820	C 1084	N 368	O 368	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

- Molecule 7 is a protein called Isoform 2 of Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	I	543	Total	C	N	O	2	0
			2703	1613	545	545		
7	K	543	Total	C	N	O	2	0
			2703	1613	545	545		

- Molecule 8 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	J	484	Total	C	N	O	0	0
			2408	1440	484	484		

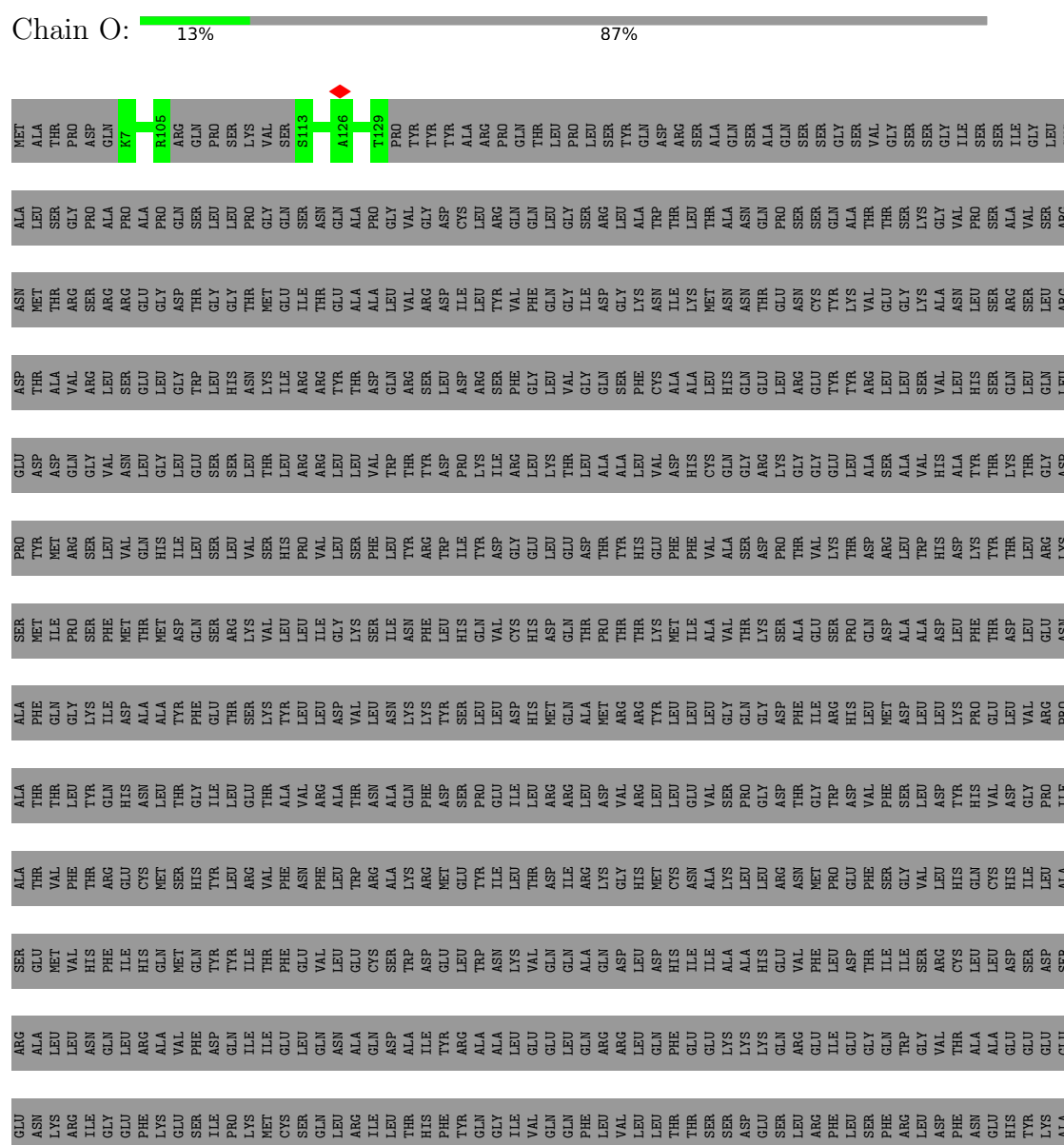
There is a discrepancy between the modelled and reference sequences:

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

3 Residue-property plots

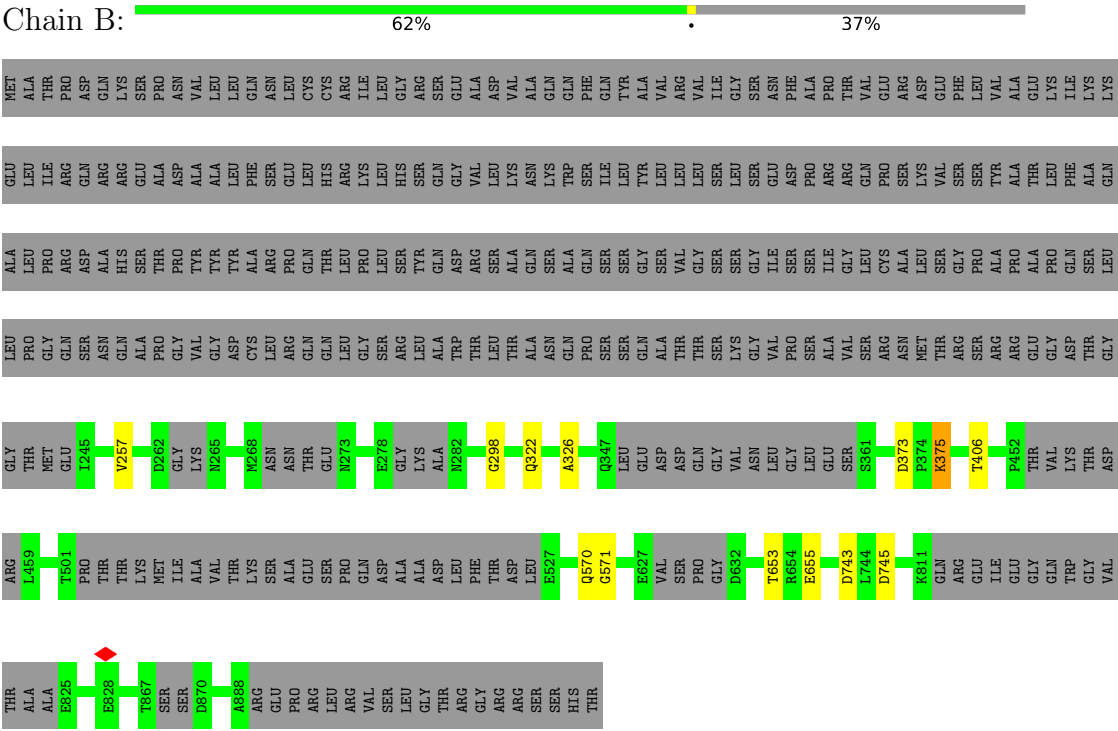
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Gamma-tubulin complex component 3

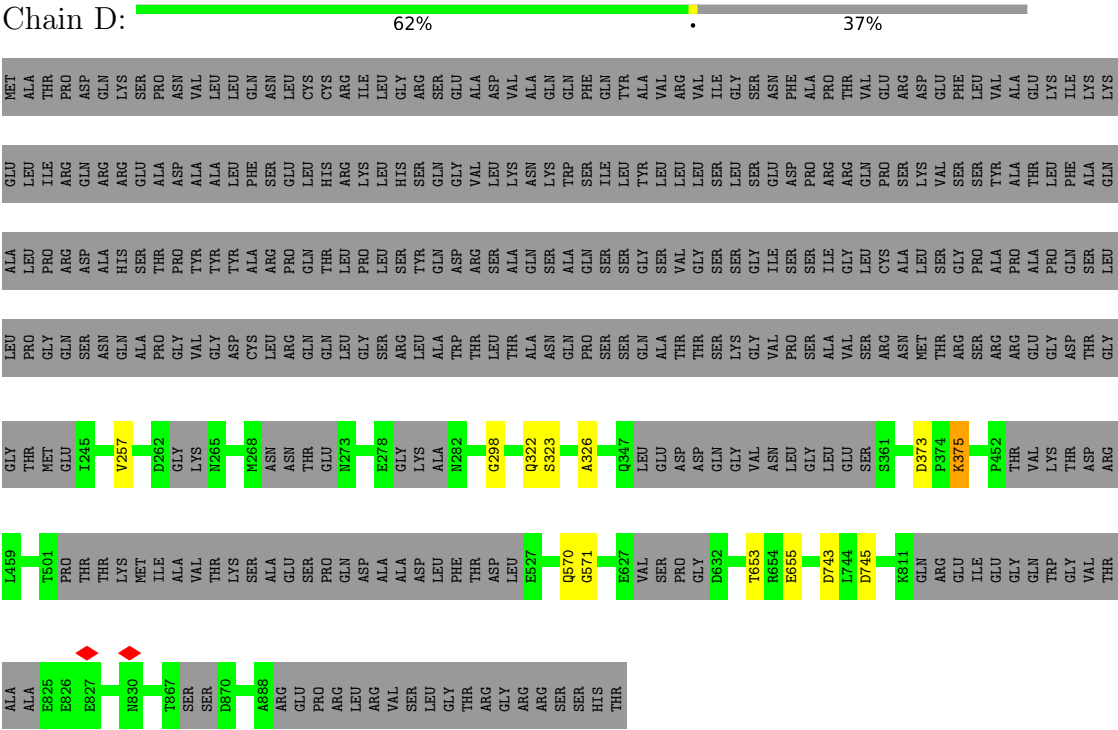


ARG	GLU
PRO	PRO
ARG	ARG
LEU	LEU
VAL	VAL
SER	SER
LEU	LEU
GLY	GLY
THR	THR
ARG	ARG
GLY	GLY
ARG	ARG
SER	SER
SER	SER
HIS	HIS
THR	THR

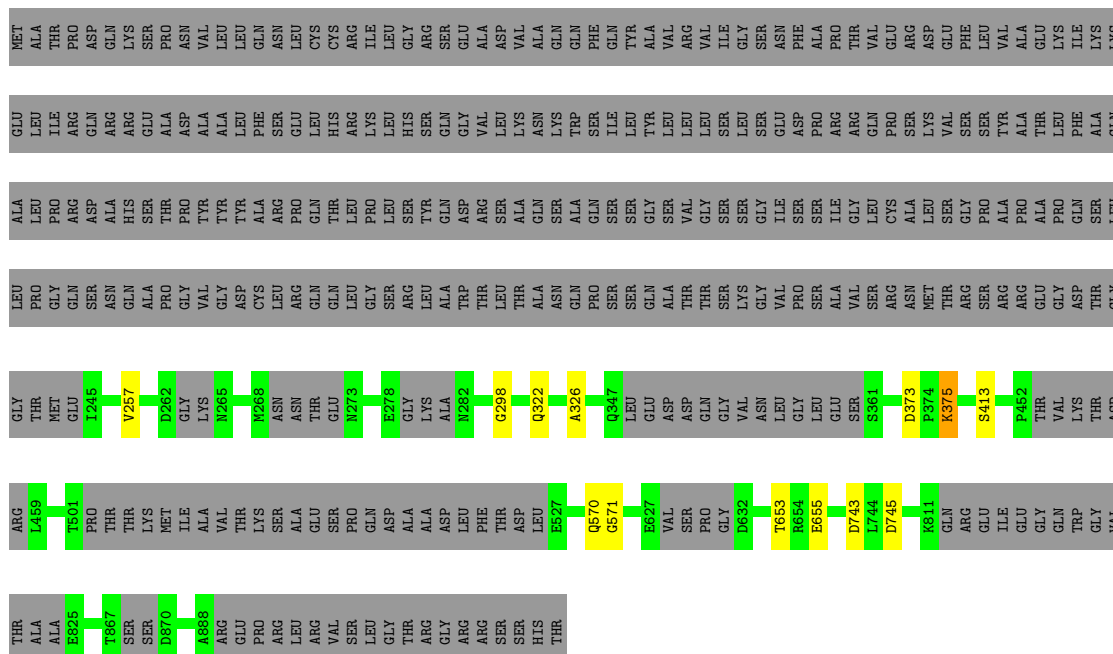
● Molecule 1: Gamma-tubulin complex component 3



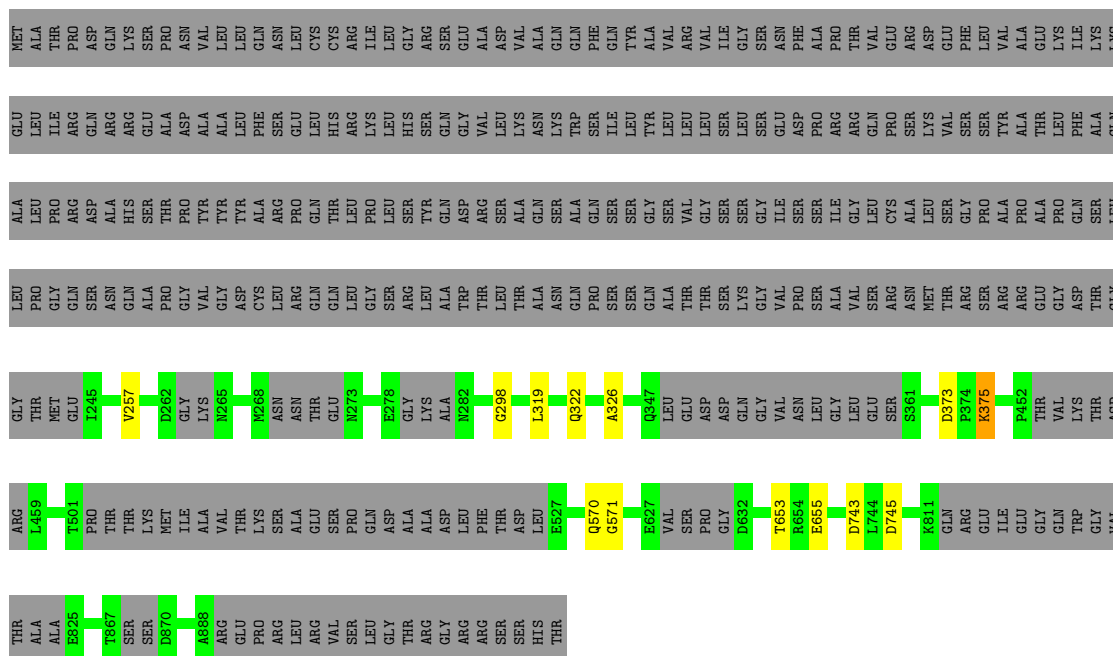
● Molecule 1: Gamma-tubulin complex component 3



Chain F: 62% . 37%



Chain H: 62% . 37%



Chain N: 15% 62% 37%



Chain P: 8% 91%





GLY	PRO	ARG	GLY	ALA	GLU	HIS	PRO	ASN	PHE	ALA	LEU	MET	GLN	GLN	SER	TYR	THR	ASN	PHE	LYS	TYR	TYR	SER	HIS	PHE	LEU	PHE	LYS	VAL	VAL	THR	THR	LYS	VAL	ASN	ARG	GLY	GLN	PRO	HIS	LEU	GLU	ASP	PHE	LEU	LEU	LEU	ARG	ILE	ILE	ASN	PHE	ASN	ASN	TYR	TYR	GLN	ASP	ALA
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- Molecule 2: TUBGCP6 protein

Chain L: 10% . 89%

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

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	HIS	LEU	GLN	GLY	GLU	LEU	GLN	LEU	LEU	ALA	GLY	GLY	VAL	LEU	LEU	GLN	ALA	PRO	GLN	PRO	PRO	VAL	VAL	VAL	LYS	GLU	CYS	E351	V363	L370	CYS	GLN	PRO	PRO	ALA	GLN
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ALA
PHE
VAL
LYS
ARG
GLY
VAL
HIS
VAL
SER
GLY
ALA
SER
P390
I393
L397
P417
VAL
LEU
ASP
SER
LEU
TYR
SER
K425
Q430
A431
S434
G435
Q441
A445
V479
GLY
ALA
VAL
LEU
PRO
PRO
GLY
THR
CYS
GLY
GLY
PRO
ARG
ALA
A494
T533
E537

V556	ASN	HIS	GLU	TYR	LEU	SER	PHE	ARG	ASP	V566	V574	ILE	SER	LYS	GLU	VAL	GLU	ASP	CYS	VAL	PRO	V586	C608	PRO	ARG	HIS	TYR	LEU	CYS	TRP	SER	ASP	VAL	PRO	VAL	PRO	ARG	ILE	SER	VAL	ILE	PHE	SER	LEU	GLU	GLU	LYS	ASP	CYS
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ALA	VAL	TYR	VAL	GLY	ARG	MET	GLU	ARG	VAL	ALA	ALA	ARG	HIS	SER	SER	VAL	SER	LYS	GLU	GLU	LYS	GLU	LEU	ARG	MET	GLU	ILE	ALA	LYS	LYS	GLN	GLU	LEU	ILE	ALA	ALA	HIS	ALA	ARG	GLU	ALA	ALA	SER	SER	ASP	VAL	LEU	SER	ALA	ALA	LEU	SER	SER	GLU	ARG	MET	ALA	ALA	LEU	ASP	ALA
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ARG LYS ARG ARG GLU GLN PHE GLN LYS LYS ASP GLN GLU ARG ARG ARG GLN ALA ALA ARG ARG GLN GLU ASP ASP ASP PHE SER SER TYR TYR ALA ALA ARG ARG GLU ARG ARG ARG ARG GLU GLU GLU GLU LEU LEU LEU LEU LEU LEU LEU LEU LYS LYS SER SER LEU LEU GLU GLU LYS LYS ARG ARG LYS LYS SER SER LYS LYS LEU LEU SER

ALA	GLU	ALA	ALA	ALA	ARG	ARG	GLU	GLN	LYS	ALA	ALA	LEU	TRP	ARG	ARG	ILE	GLN	ARG	HIS	ARG	LEU	GLU	GLU	SER	ALA	ALA	ARG	ARG	ARG	PHE	LEU	LEU	LEU	LEU	GLU	ASP	GLU	GLY	LYS	HIS	ILE	ILE	GLN	GLU	GLU	MET	LEU	LEU	LYS	ALA	ALA	VAL	SER	GLU	ALA	HIS	GLN	PRO	PRO	GLN	GLU	GLN	ASP	VAL	LEU	LEU	SER	VAL	HIS	PRO	GLN	ALA
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VAL	THR	SER	PRO	GLY	PRO	GLU	HIS	GLU	PRO	GLY	GLN	GLY	CYS	ASP	SER	SER	GLY	GLY	ALA	ALA	GLN	GLN	HIS	SER	SER	PRO	TRP	TRP	GLY	GLY	ASN	ARG	PRO	PRO	GLY	LEU	LEU	LEU	LYS	PRO	PRO	LEU	ALA	VAL	VAL	GLY	ALA	GLY	GLY	ARG	GLY	GLY	GLY	ALA	ALA	PRO
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PRO	PHE	SER	ASP	SER	LEU	SER	ILE	GLY	ASP	PHE	LEU	PRO	VAL	GLY	GLY	ALA	GLU	PRO	SER	VAL	GLN	THR	GLY	MET	VAL	PRO	LEU	LEU	GLU	VAL	ALA	GLN	THR	ILE	ASN	LEU	ASP	LEU	PRO	SER	ALA	ALA	ALA	ALA	ALA	SER	THR	GLN	PRO	SER	ARG	PRO
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GLN	GLU	TYR	ASP	PHE	SER	THR	VAL	LEU	ARG	PRO	ALA	VAL	ALA	THR	SER	PRO	ALA	GLY	GLU	PRO	PRO	GLN	ALA	ALA	CYS	SER	GLY	SER	GLY	LEU	GLN	LEU	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
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PRO	ARG	ARG	ALA	ALA	LEU	GLU	GLU	GLY	SER	SER	GLN	PRO	THR	THR	GLU	ARG	LEU	LEU	PHE	GLY	GLN	VAL	SER	SER	GLY	GLY	GLY	LEU	PRO	THR	THR	GLY	ASP	TYR	ALA	ALA	THR	ARG	PRO	PRO	ARG	ARG	TRP	ASN	THR	HIS	GLY	HIS	VAL	SER	ASP	ALA	SER	SER	ILE	ARG	VAL	GLY	GLU	ASN	VAL	SER
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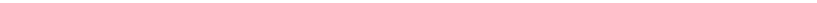
ASP	VAL	ALA	PRO	THR	GLN	PRO	ARG	TRP	ASN	THR	HIS	GLY	HIS	VAL	SER	ASN	ALA	SER	ILE	LEU	LEU	GLY	GLU	SER	VAL	SER	ASP	ALA	ALA	PRO	THR	ARG	PRO	PRO	ARG	ARG	TRP	ASN	ILE	ILE	HIS	HIS	GLY	HIS	VAL	SER	ASN	ALA	ALA	VAL	SER	ASP	VAL	GLY	GLU	ASN	ASN	VAL	VAL	SER	ASP	ALA	ALA	PRO	PRO	THR	THR
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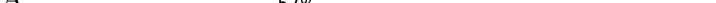
MET
 ALA
 SER
 SER
 SER
 GLY
 ALA
 GLY
 ALA
 ALA
 A11
 K75
 ALA
 ALA
 GLU
 ASN
 MET
 THR
 SER

- Chain R: 72% 28%

MET	ALA	SER	SER	SER	GLY	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	N17	K75	ALA	ALA	GLU	ASN	MET	THR	SER
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- Chain S:  93% • 6%

MET	ASP	ASP	ASP	IIE	A6	S14	R39	HIS	GLN	GLY	VAL	MET	VAL	GLY	MET	GLN	K50	I71	V152	MET	D154	V159	THR	H161	T162	V163	T203	E205	Z218	L242	PRO	D244	P255	E270	SER	C272	T278	PHE	N280	G366
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- Chain A:  57% 42%

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

ASN	VAL	PRO	ALA	ALA	ALA	SER	LYS	ILE	SER	MET	GLN	GLU	LEU	GLU	GLY	LEU	ARG	LYS	GLN	LEU	GLY	SER	VAL	ALA	THR	GLY	SER	THR	THR	LEU	GLN	GLN	SER	LEU	GLU	LEU	LYS	ARG	LYS	MET	ARG	ASP	LYS	GLN	GLN	ASN	LYS	LYS	ASN	GLY	GLN	HIS	LEU	PRO	ILE	PHE	PRO	ALA	THR
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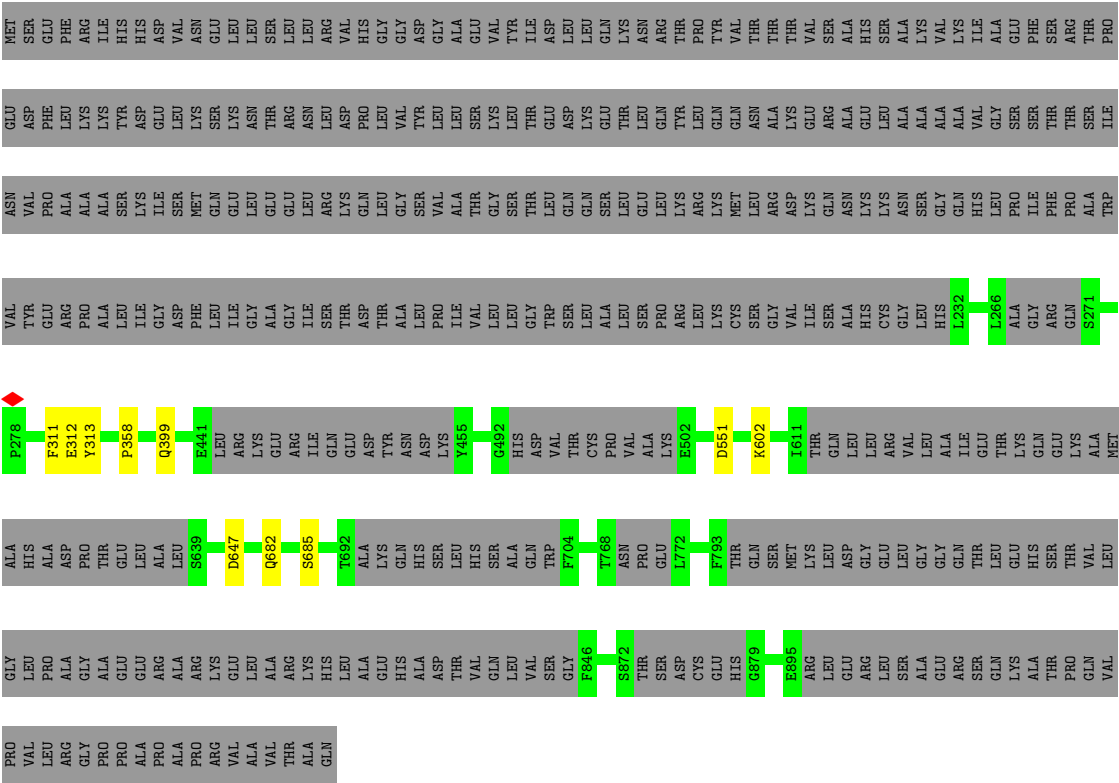
[illegible][illegible]

GLU	LYS	ALA	MET	ALA	HIS	ASP	PRO	THR	GLY	LEU	ALA	LEU	S639	D647	Q682	S695	T692	ALA	LYS	GLN	HIS	SER	SEU	HIS	SER	ALA	ALA	GLN	TRP	F704	T768	ASN	PRO	GLY	L772	P793	THR	GLN	GLN	SER	MET	LYS	LEU	ASP	GLY	GLY	GLY	THR	GLN	THR	GLY
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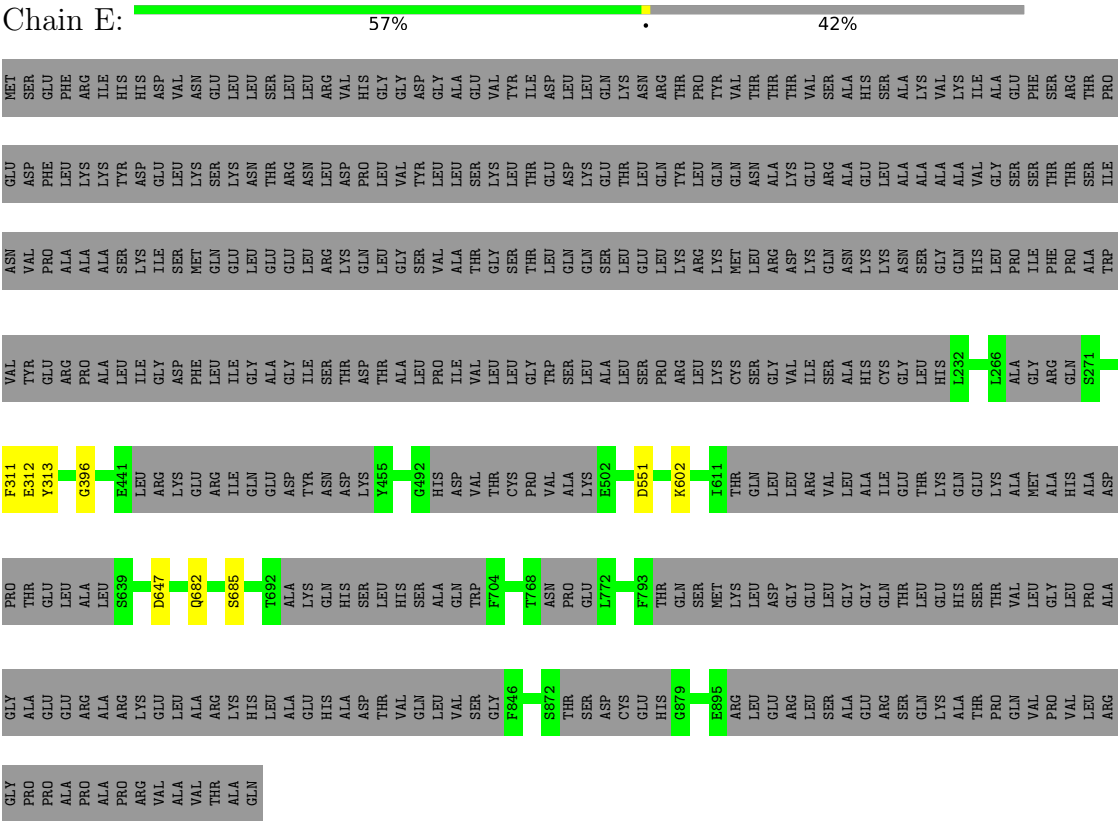
SER	THR	VAL	LEU	GLY	PRO	ALA	GLY	GLU	GILU	ARG	ALA	ARG	LYS	HIS	LEU	ALA	GLU	ALA	ASP	THR	VAL	GLN	VAL	SER	SER	GLY	F846		S872	THR	SER	ASP	CYS	GLI	HIS	G879		F805	ARG	LEU	GLU	ARG	ARG	SER	SER	ALA	GLU	LYS	ALA	VAL
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THR	PRO	GLN	VAL	PRO	VAL	LEU	ARG	GLY	PRO	PRO	ALA	PRO	ALA	PRO	ARG	VAL	ALA	VAL	THR	ALA	GLN
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- Chain C: 57% . 42%

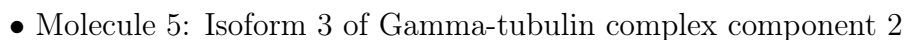


● Molecule 5: Isoform 3 of Gamma-tubulin complex component 2



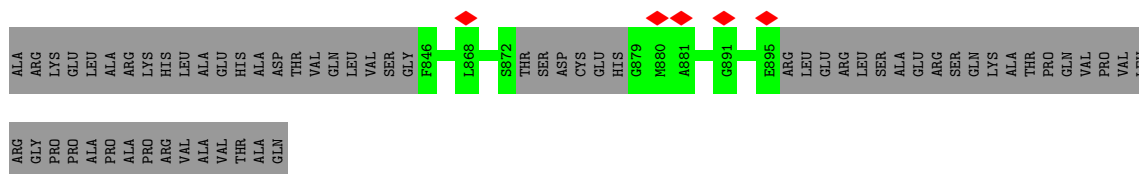
● Molecule 5: Isoform 3 of Gamma-tubulin complex component 2

Response	Percentage
U.S. is a democracy	57%
U.S. is not a democracy	42%



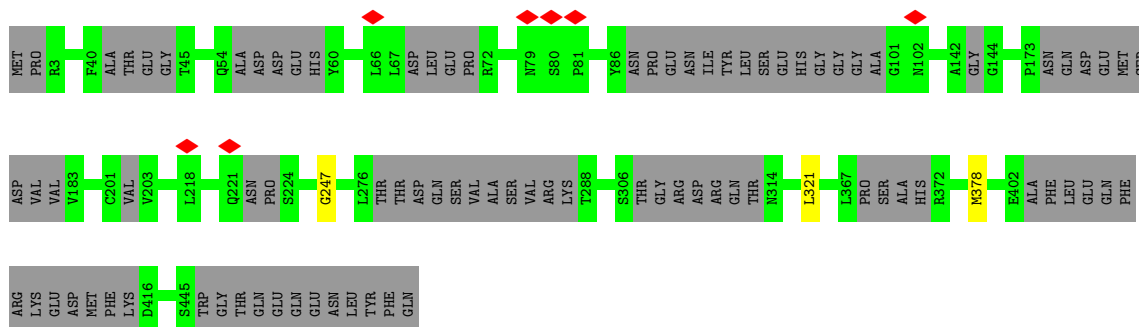
Frequency	Percentage
5%	5%
57%	57%
42%	42%





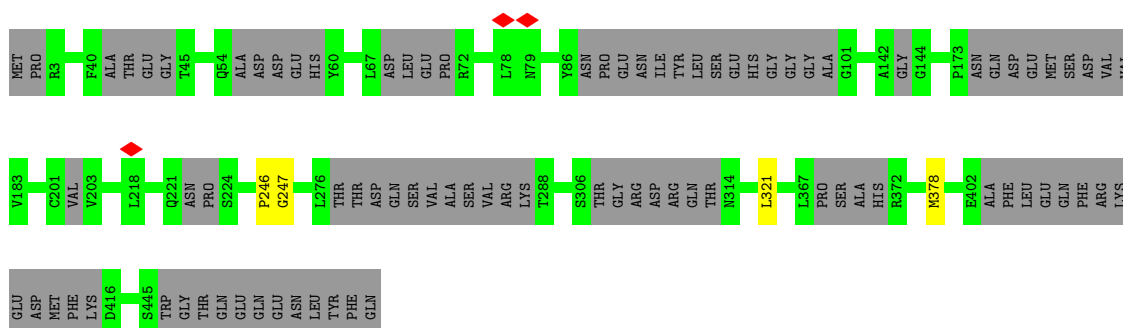
• Molecule 6: Tubulin gamma-1 chain

Chain a: 80% 19%



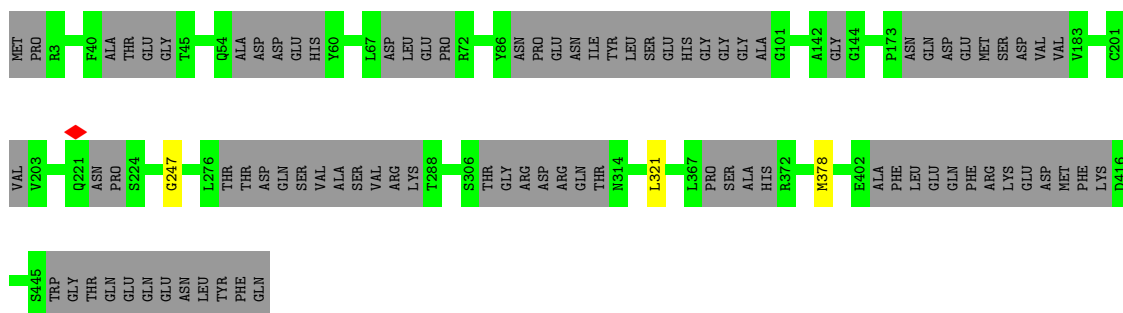
• Molecule 6: Tubulin gamma-1 chain

Chain b: 80% 19%



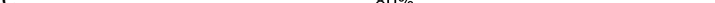
• Molecule 6: Tubulin gamma-1 chain

Chain c: 80% 19%

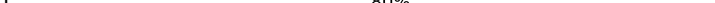


• Molecule 6: Tubulin gamma-1 chain

[illegible]

- Chain e:  80% 19%

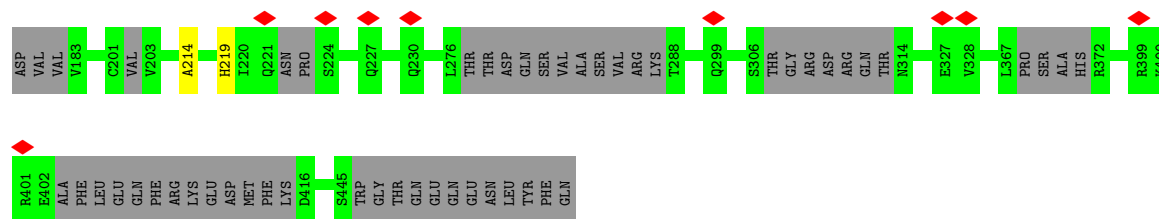
[illegible]

- Chain f:  80% 19%

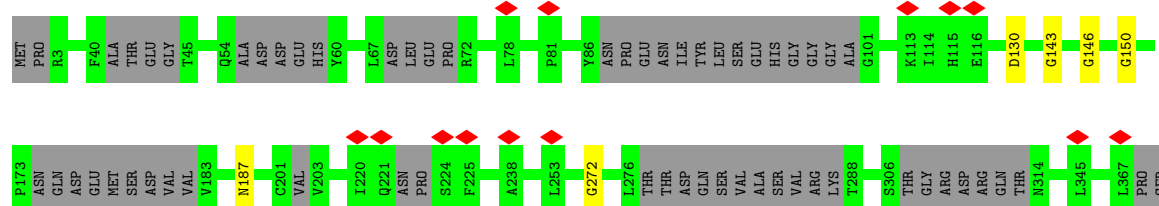
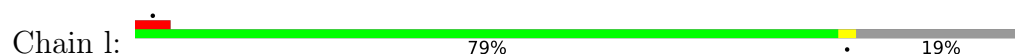
[illegible]

- Chain g: 80% 19%

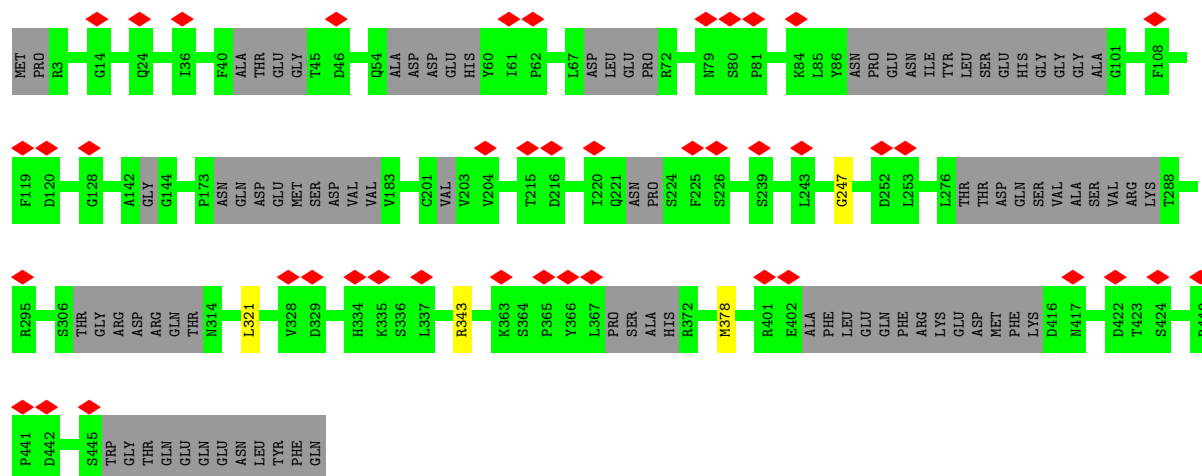
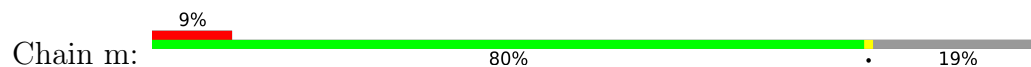
VAL	V203	Q221	ASN	PRO	S224	Q247	L276	THR	THR	ASP	GLN	ASP	SER	VAL	ALA	ALA	Y60	HIS	GLU	ASP	ASP	ASP	GLN	ASP	LEU	GLU	PRO	R72	Y86	ASN	PRO	PRO	GLU	ASN	ILE	TYR	LEU	SER	GLU	HIS	GLY	GLY	ALA	G101	A142	GLY	G144	P173	ASN	GLN	ASP	ASP	GLU	GLU	THR	SER	ASP	THR	VAL	VAL	V183	C201
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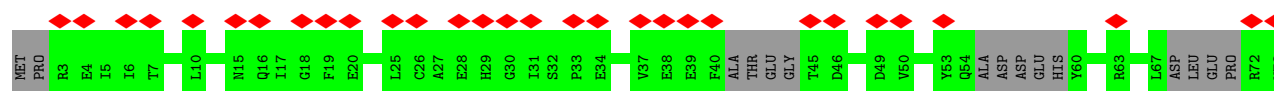
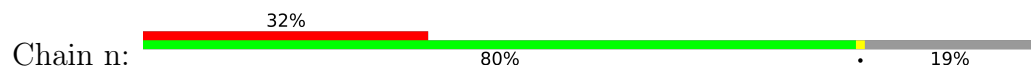
• Molecule 6: Tubulin gamma-1 chain

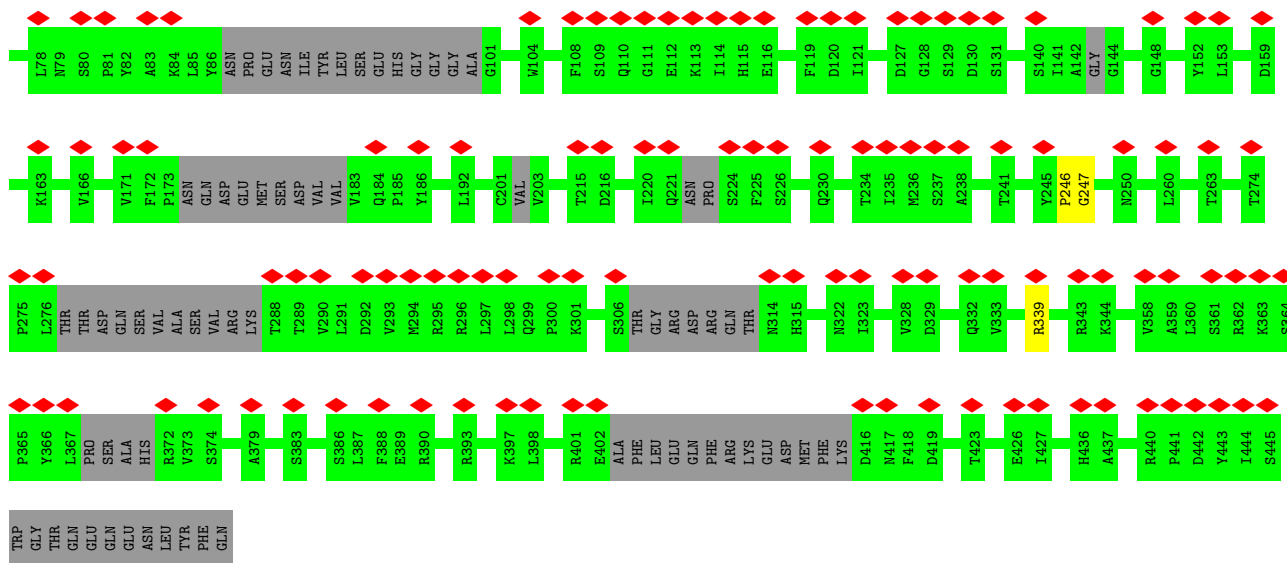


• Molecule 6: Tubulin gamma-1 chain

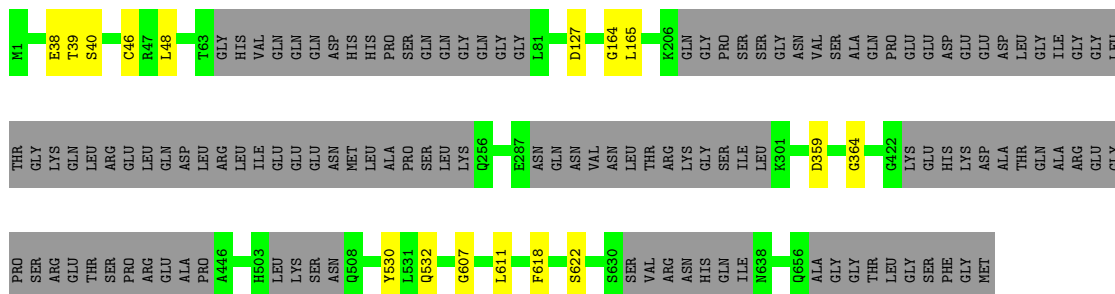
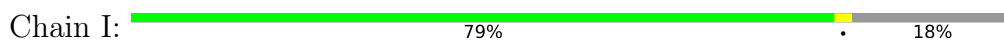


• Molecule 6: Tubulin gamma-1 chain

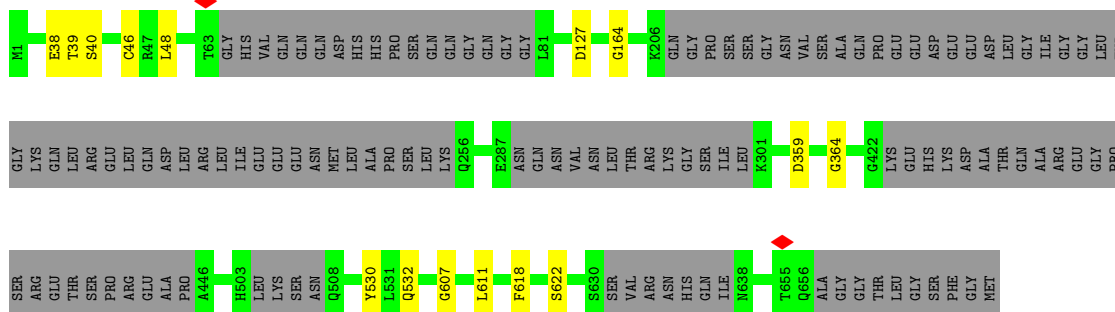
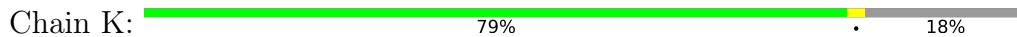




- Molecule 7: Isoform 2 of Gamma-tubulin complex component 4



- Molecule 7: Isoform 2 of Gamma-tubulin complex component 4



- Molecule 8: Gamma-tubulin complex component 5



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98558	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	0.052	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	485.76, 485.76, 485.76	wwPDB
Map dimensions	368, 368, 368	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	B	0.36	0/2830	0.52	1/3934 (0.0%)
1	D	0.36	0/2830	0.52	1/3934 (0.0%)
1	F	0.36	0/2830	0.52	1/3934 (0.0%)
1	H	0.36	0/2830	0.52	1/3934 (0.0%)
1	N	0.36	0/2830	0.52	1/3934 (0.0%)
1	O	0.19	0/575	0.37	0/800
2	L	0.28	0/972	0.44	0/1344
2	P	0.16	0/774	0.37	0/1069
2	T	0.26	0/1467	0.39	0/2034
3	Q	0.16	0/322	0.40	0/448
3	R	0.12	0/292	0.25	0/406
4	S	0.41	0/1737	1.02	4/2404 (0.2%)
5	A	0.33	0/2667	0.49	0/3708
5	C	0.33	0/2667	0.49	0/3708
5	E	0.33	0/2667	0.49	0/3708
5	G	0.33	0/2667	0.49	0/3708
5	M	0.33	0/2667	0.50	0/3708
6	a	0.44	0/1807	0.58	0/2497
6	b	0.44	0/1807	0.58	0/2497
6	c	0.44	0/1807	0.58	0/2497
6	d	0.44	0/1807	0.58	0/2497
6	e	0.44	0/1807	0.58	0/2497
6	f	0.43	0/1807	0.58	0/2497
6	g	0.44	0/1807	0.58	0/2497
6	h	0.44	0/1807	0.58	0/2497
6	i	0.32	0/1807	0.52	0/2497
6	j	0.16	0/1807	0.38	0/2497
6	k	0.38	0/1812	0.54	0/2505
6	l	0.26	0/1812	0.47	0/2505
6	m	0.44	0/1807	0.58	0/2497
6	n	0.44	0/1807	0.58	0/2497
7	I	0.42	0/2696	0.56	0/3750
7	K	0.42	0/2696	0.56	0/3750
8	J	0.39	0/2394	0.54	0/3322

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.37	0/66718	0.54	9/92511 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	163	VAL	N-CA-C	7.55	115.63	108.15
4	S	366	GLY	CA-C-N	6.03	126.19	119.32
4	S	366	GLY	C-N-CA	6.03	126.19	119.32
1	F	375	LYS	N-CA-C	-5.96	106.06	113.38
1	H	375	LYS	N-CA-C	-5.94	106.08	113.38

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	B	2840	0	1242	8	0
1	D	2840	0	1242	8	0
1	F	2840	0	1242	8	0
1	H	2840	0	1242	12	0
1	N	2840	0	1242	7	0
1	O	577	0	265	0	0
2	L	978	0	423	8	0
2	P	779	0	350	6	0
2	T	1476	0	653	1	0
3	Q	323	0	160	0	0
3	R	293	0	130	0	0
4	S	1745	0	791	2	0
5	A	2676	0	1177	7	0
5	C	2676	0	1177	9	0
5	E	2676	0	1177	7	0
5	G	2676	0	1177	7	0
5	M	2676	0	1177	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	a	1820	0	781	2	0
6	b	1820	0	781	3	0
6	c	1820	0	781	2	0
6	d	1820	0	781	3	0
6	e	1820	0	781	2	0
6	f	1820	0	781	3	0
6	g	1820	0	781	1	0
6	h	1820	0	781	4	0
6	i	1820	0	781	3	0
6	j	1820	0	781	3	0
6	k	1824	0	785	2	0
6	l	1824	0	785	5	0
6	m	1820	0	781	3	0
6	n	1820	0	781	3	0
7	I	2703	0	1172	12	0
7	K	2703	0	1172	8	0
8	J	2408	0	1021	2	0
All	All	67053	0	29174	127	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 1.

The worst 5 of 127 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)
2:L:363:VAL:CB	5:M:283:SER:HA	1.68	1.22
2:L:363:VAL:CB	5:M:283:SER:CA	2.52	0.86
5:A:318:HIS:CB	1:B:406:THR:O	2.34	0.76
1:H:319:LEU:O	7:I:164:GLY:HA3	1.88	0.74
2:P:193:VAL:CB	5:C:358:PRO:CB	2.66	0.73

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	B	552/907 (61%)	531 (96%)	21 (4%)	0	100	100
1	D	552/907 (61%)	530 (96%)	22 (4%)	0	100	100
1	F	552/907 (61%)	530 (96%)	22 (4%)	0	100	100
1	H	552/907 (61%)	530 (96%)	22 (4%)	0	100	100
1	N	552/907 (61%)	530 (96%)	22 (4%)	0	100	100
1	O	112/907 (12%)	109 (97%)	3 (3%)	0	100	100
2	L	186/1811 (10%)	170 (91%)	16 (9%)	0	100	100
2	P	148/1811 (8%)	138 (93%)	9 (6%)	1 (1%)	18	56
2	T	279/1811 (15%)	262 (94%)	17 (6%)	0	100	100
3	Q	63/82 (77%)	63 (100%)	0	0	100	100
3	R	57/82 (70%)	55 (96%)	2 (4%)	0	100	100
4	S	338/375 (90%)	331 (98%)	7 (2%)	0	100	100
5	A	521/930 (56%)	483 (93%)	37 (7%)	1 (0%)	43	78
5	C	521/930 (56%)	482 (92%)	38 (7%)	1 (0%)	43	78
5	E	521/930 (56%)	483 (93%)	37 (7%)	1 (0%)	43	78
5	G	521/930 (56%)	483 (93%)	37 (7%)	1 (0%)	43	78
5	M	521/930 (56%)	483 (93%)	37 (7%)	1 (0%)	43	78
6	a	342/457 (75%)	326 (95%)	16 (5%)	0	100	100
6	b	342/457 (75%)	325 (95%)	17 (5%)	0	100	100
6	c	342/457 (75%)	325 (95%)	17 (5%)	0	100	100
6	d	342/457 (75%)	325 (95%)	17 (5%)	0	100	100
6	e	342/457 (75%)	326 (95%)	16 (5%)	0	100	100
6	f	342/457 (75%)	325 (95%)	17 (5%)	0	100	100
6	g	342/457 (75%)	326 (95%)	16 (5%)	0	100	100
6	h	342/457 (75%)	325 (95%)	17 (5%)	0	100	100
6	i	342/457 (75%)	327 (96%)	15 (4%)	0	100	100
6	j	342/457 (75%)	327 (96%)	15 (4%)	0	100	100
6	k	345/457 (76%)	325 (94%)	20 (6%)	0	100	100
6	l	345/457 (76%)	326 (94%)	19 (6%)	0	100	100
6	m	342/457 (75%)	326 (95%)	16 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	n	342/457 (75%)	325 (95%)	17 (5%)	0	100	100
7	I	531/666 (80%)	498 (94%)	31 (6%)	2 (0%)	30	67
7	K	531/666 (80%)	498 (94%)	31 (6%)	2 (0%)	30	67
8	J	456/1024 (44%)	435 (95%)	20 (4%)	1 (0%)	43	78
All	All	12860/24818 (52%)	12183 (95%)	666 (5%)	11 (0%)	49	83

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	I	127	ASP
8	J	715	ARG
7	K	127	ASP
2	P	134	LEU
5	A	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 oligosaccharides 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.

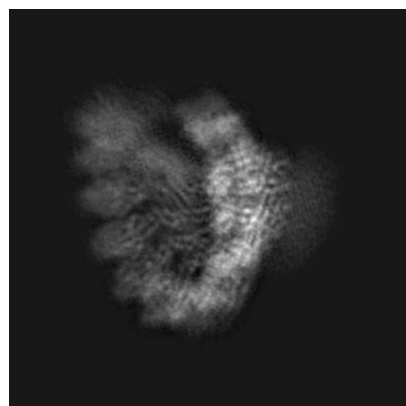
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43481. These allow visual inspection of the internal detail of the map and identification of artifacts.

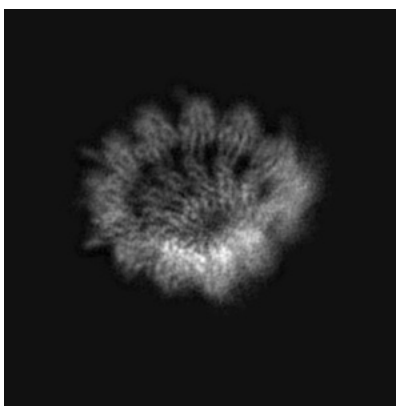
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

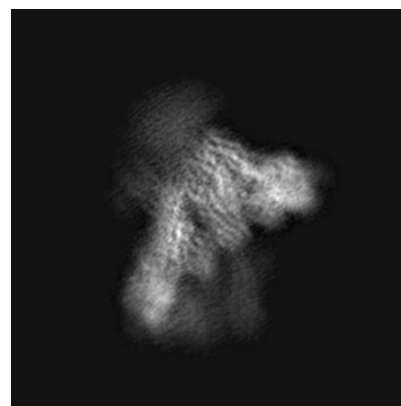
6.1.1 Primary map



X

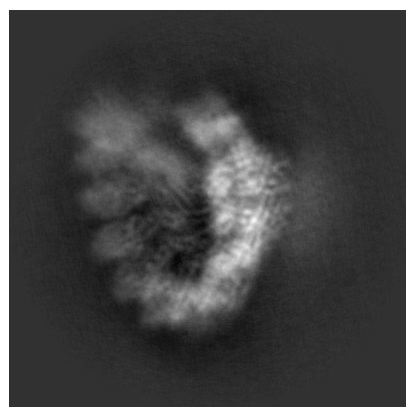


Y

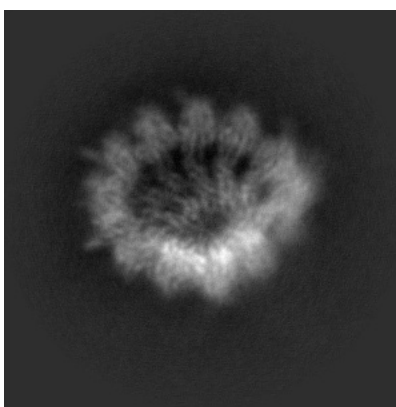


Z

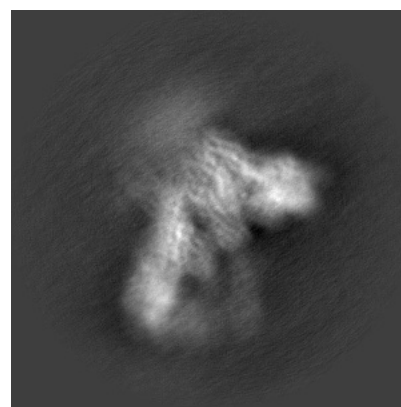
6.1.2 Raw map



X



Y

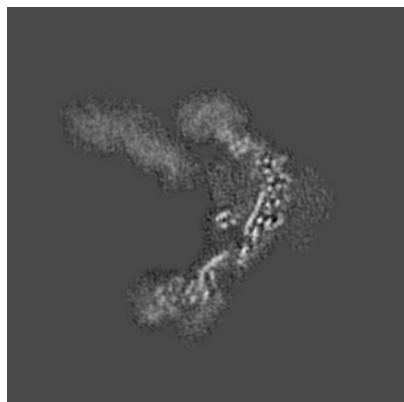


Z

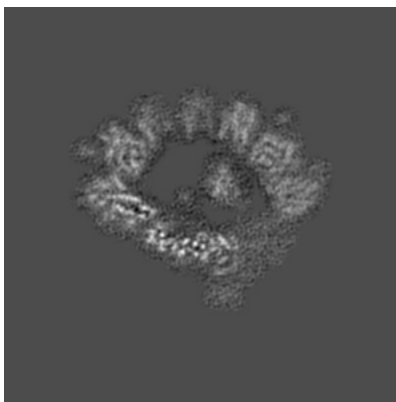
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

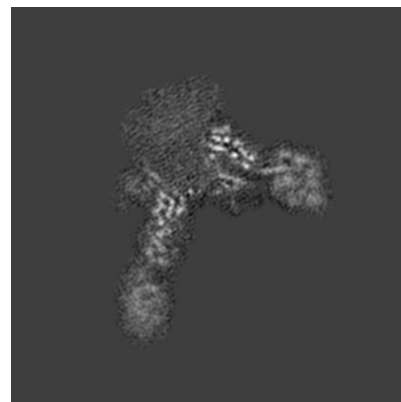
6.2.1 Primary map



X Index: 184

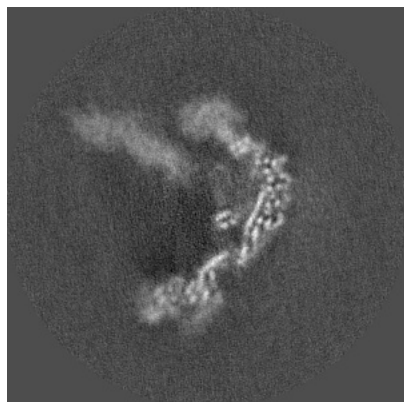


Y Index: 184

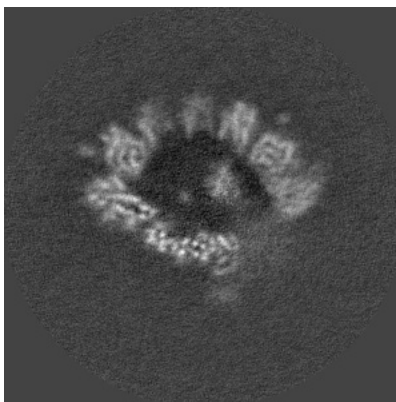


Z Index: 184

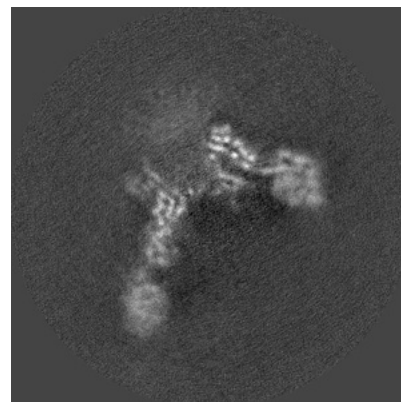
6.2.2 Raw map



X Index: 184



Y Index: 184

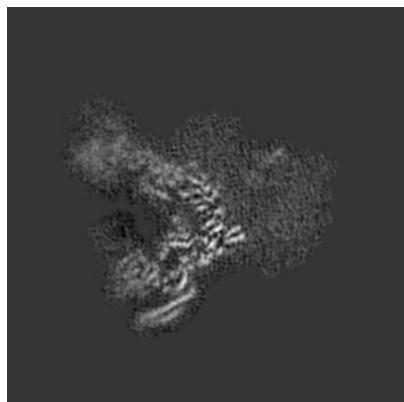


Z Index: 184

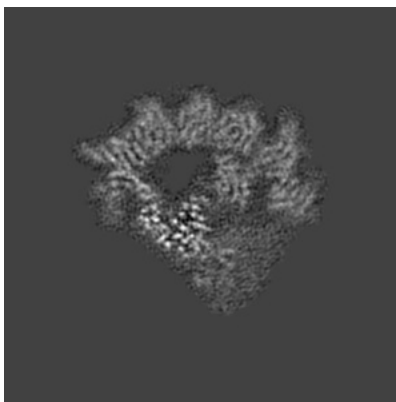
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

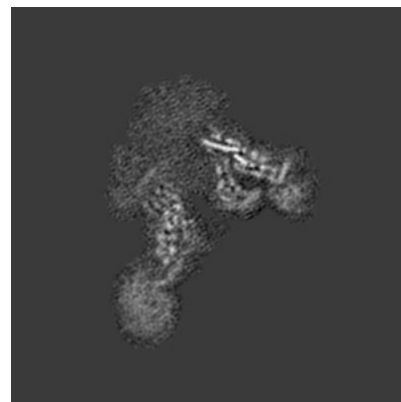
6.3.1 Primary map



X Index: 153

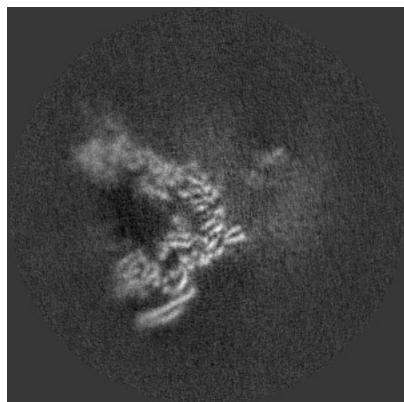


Y Index: 197

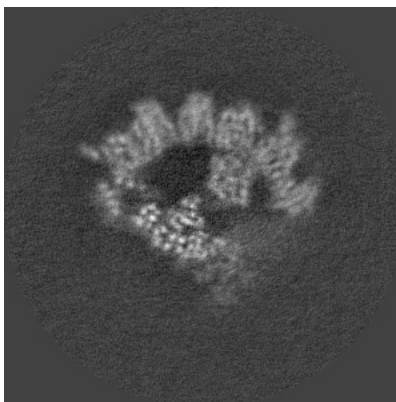


Z Index: 200

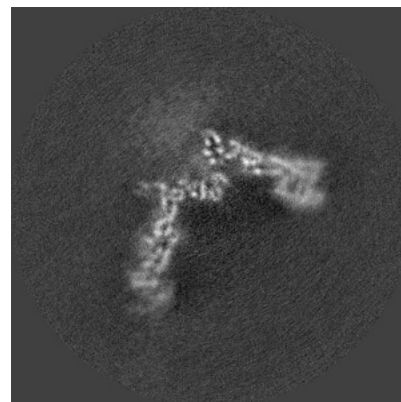
6.3.2 Raw map



X Index: 153



Y Index: 193

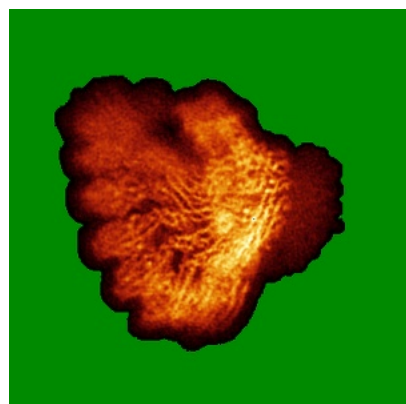


Z Index: 174

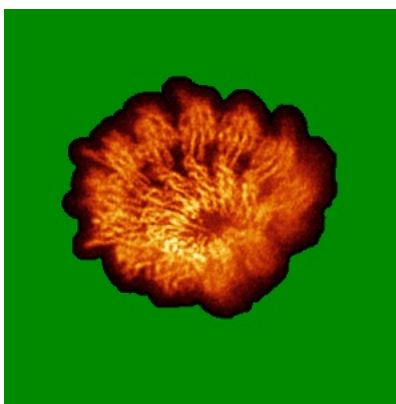
The images above show the largest variance slices of the map in three orthogonal directions.

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

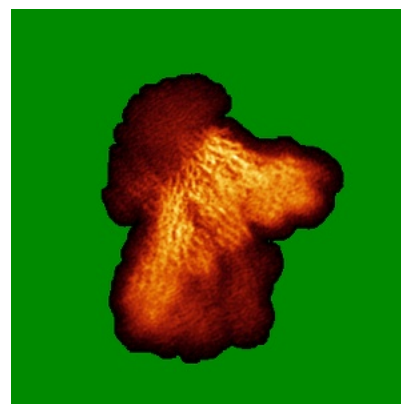
6.4.1 Primary map



X

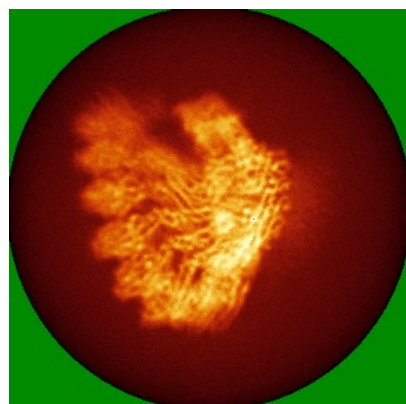


Y

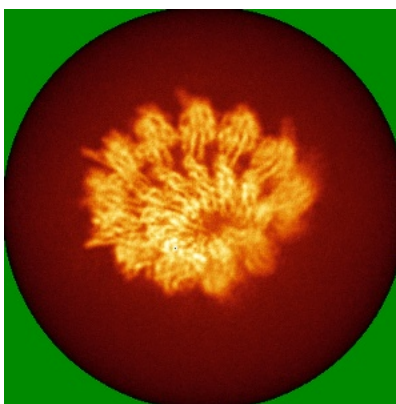


Z

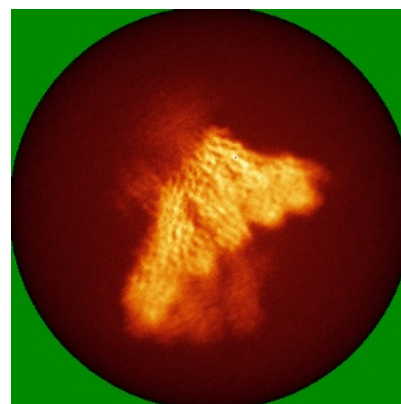
6.4.2 Raw map



X



Y

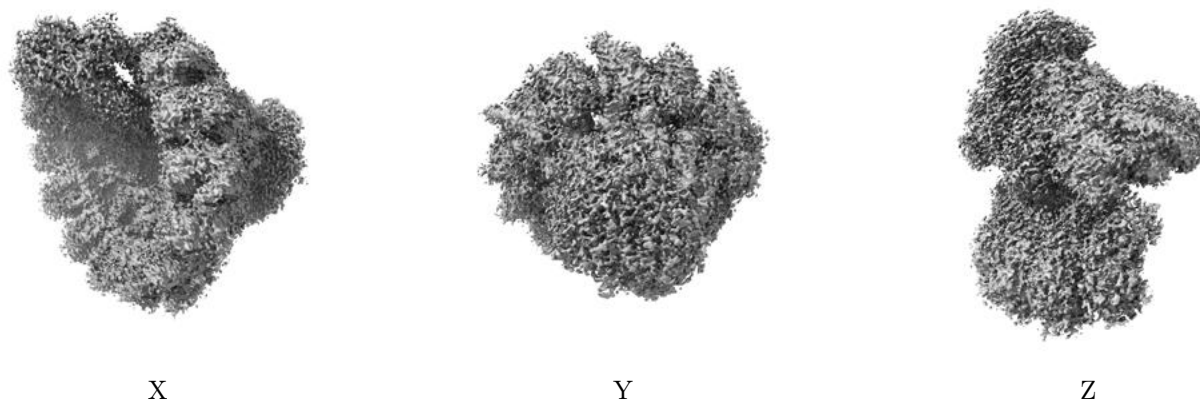


Z

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

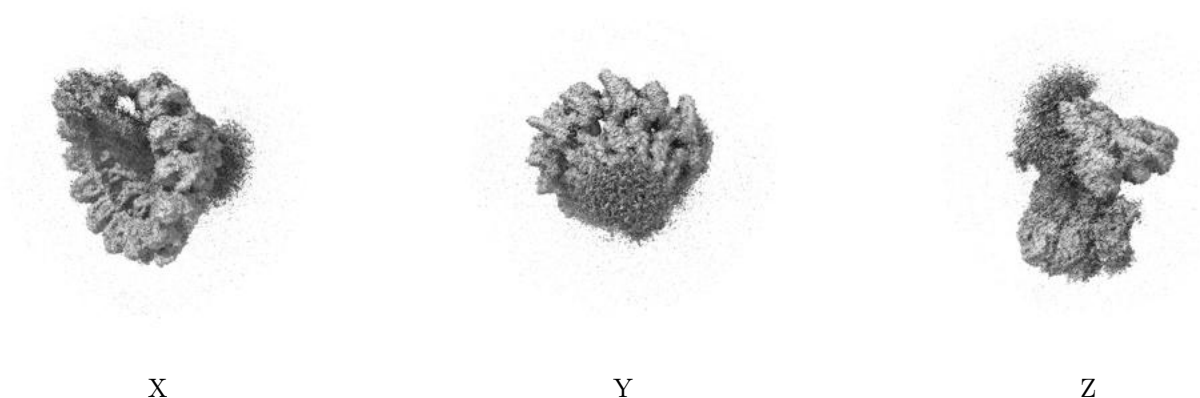
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. 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



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.

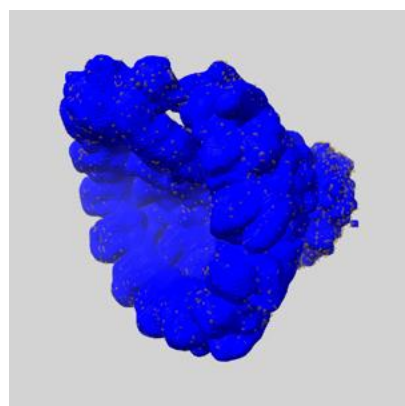
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

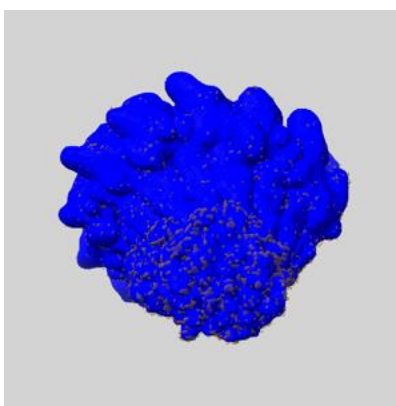
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

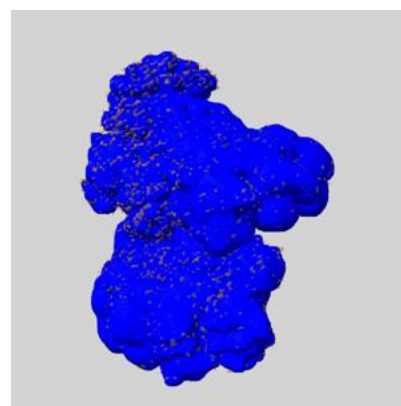
6.6.1 emd_43481_msk_1.map [i](#)



X



Y

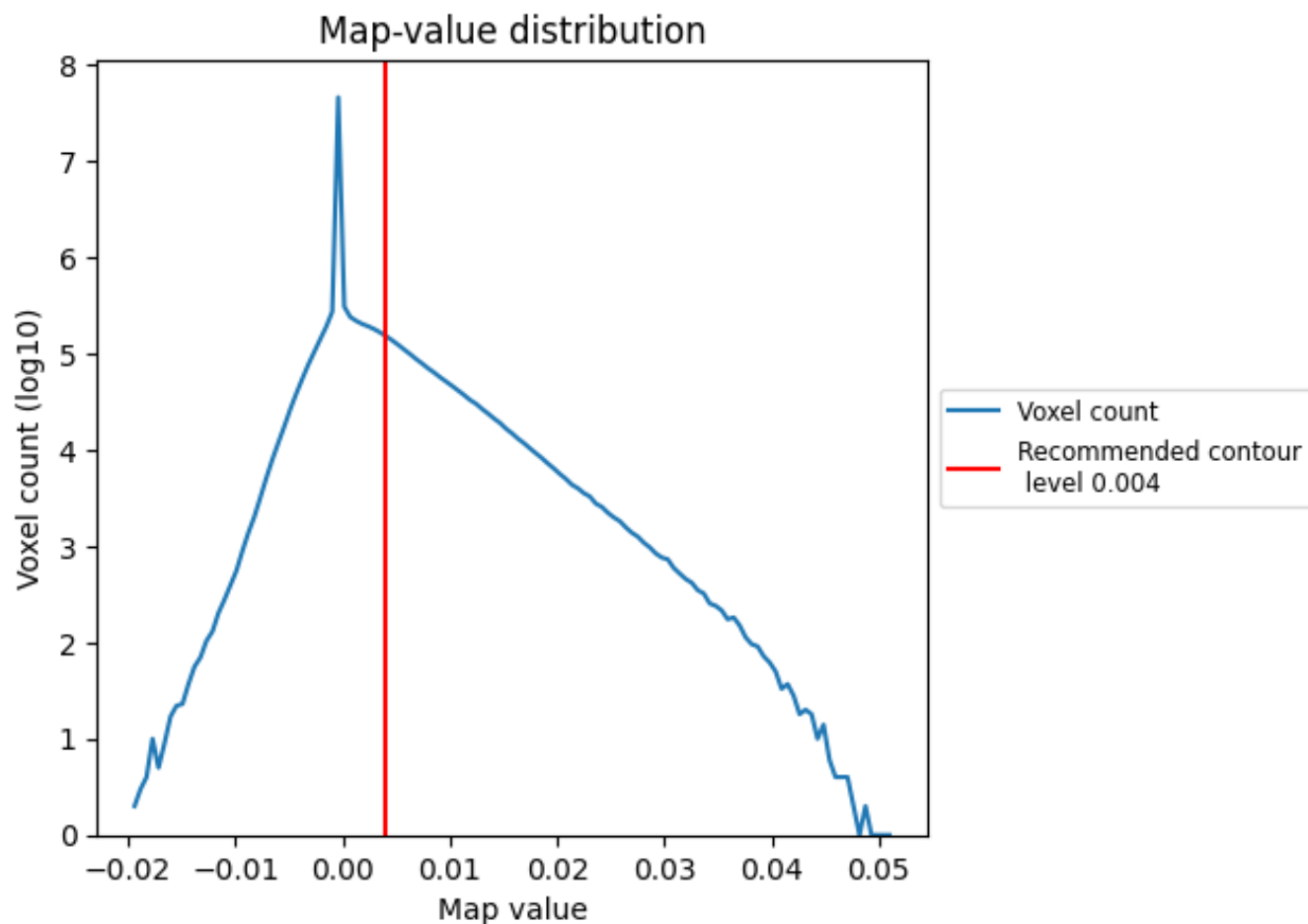


Z

7 Map analysis [i](#)

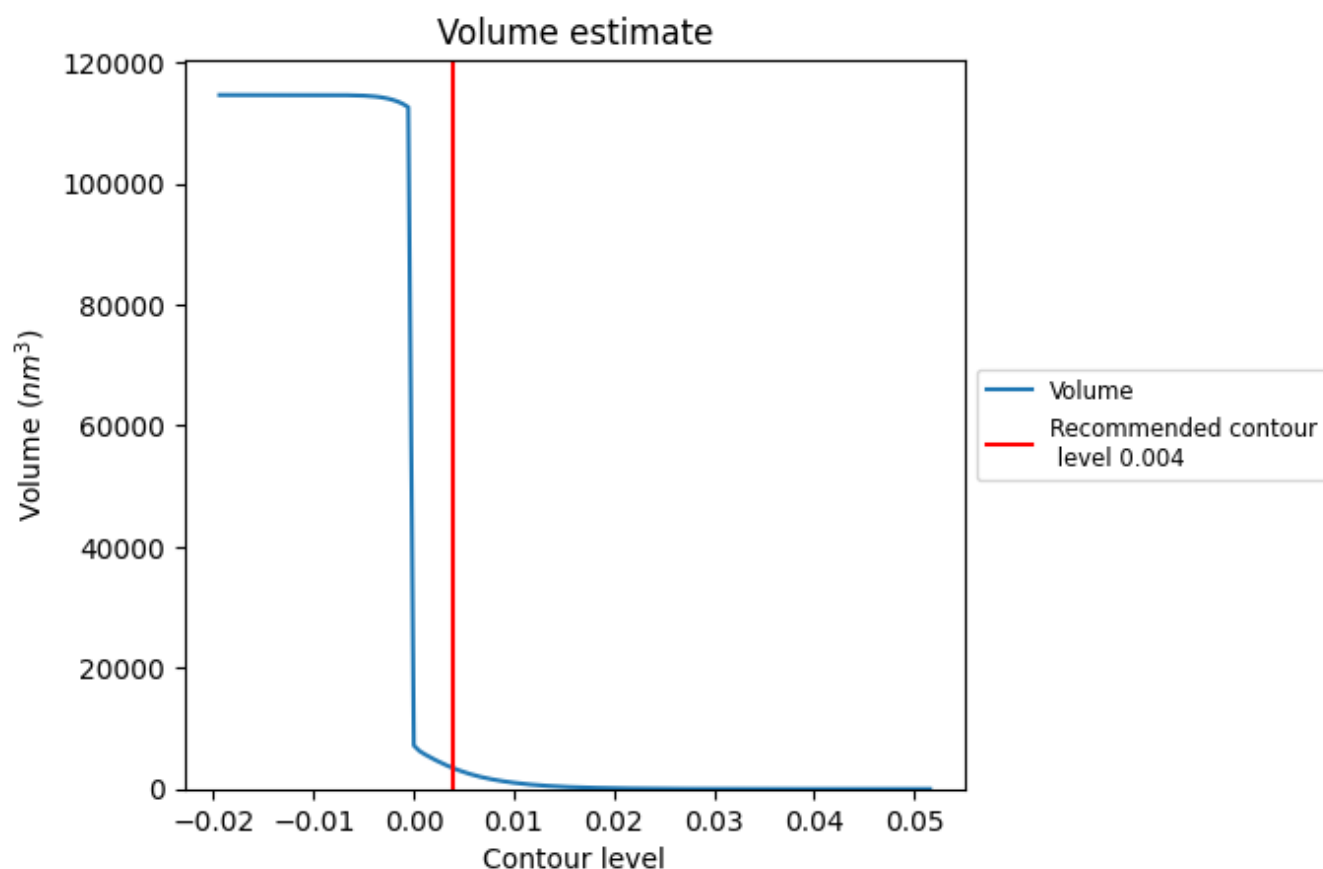
This section contains the results of statistical analysis of the map.

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.

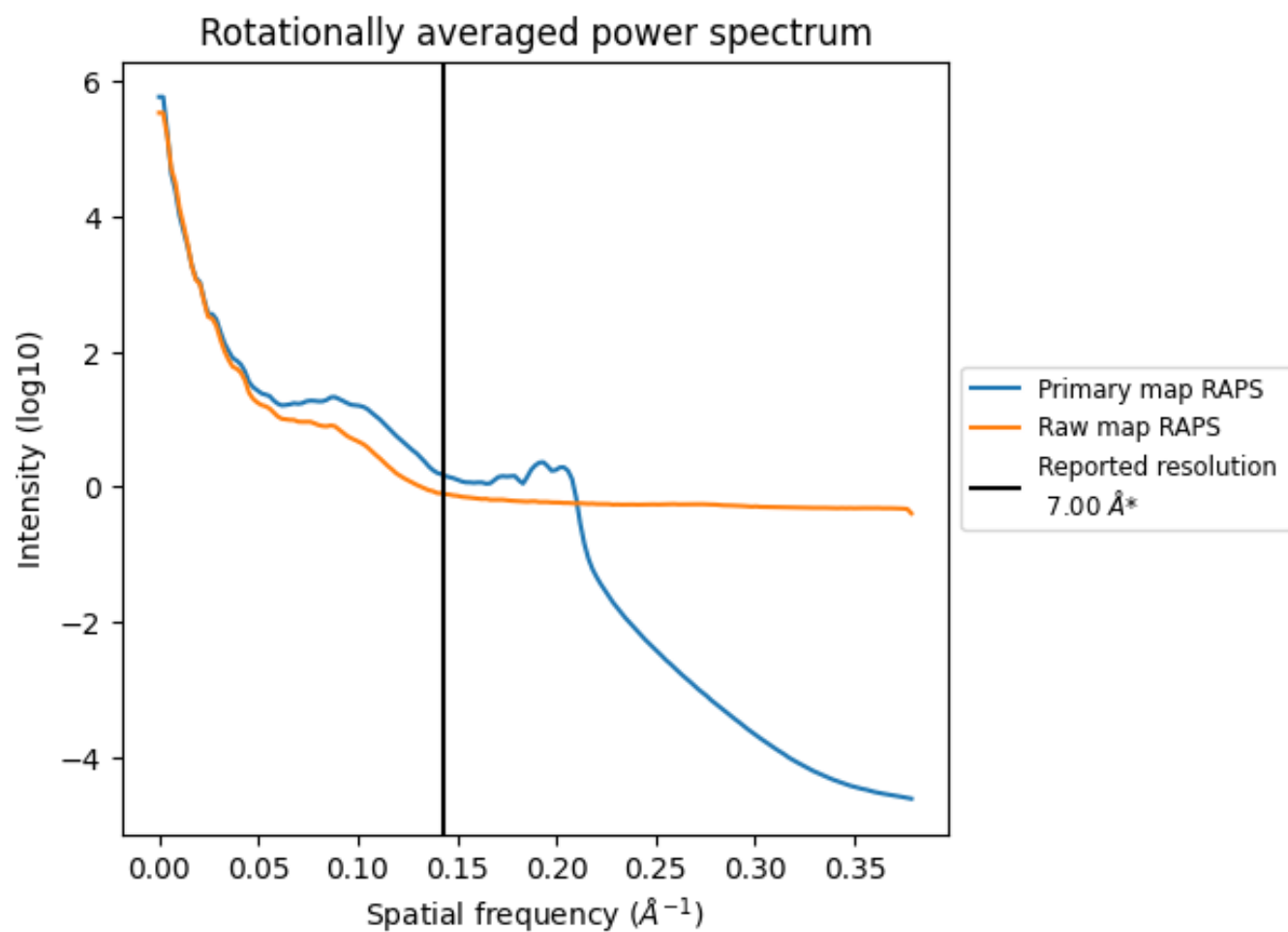
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3402 nm³; this corresponds to an approximate mass of 3073 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

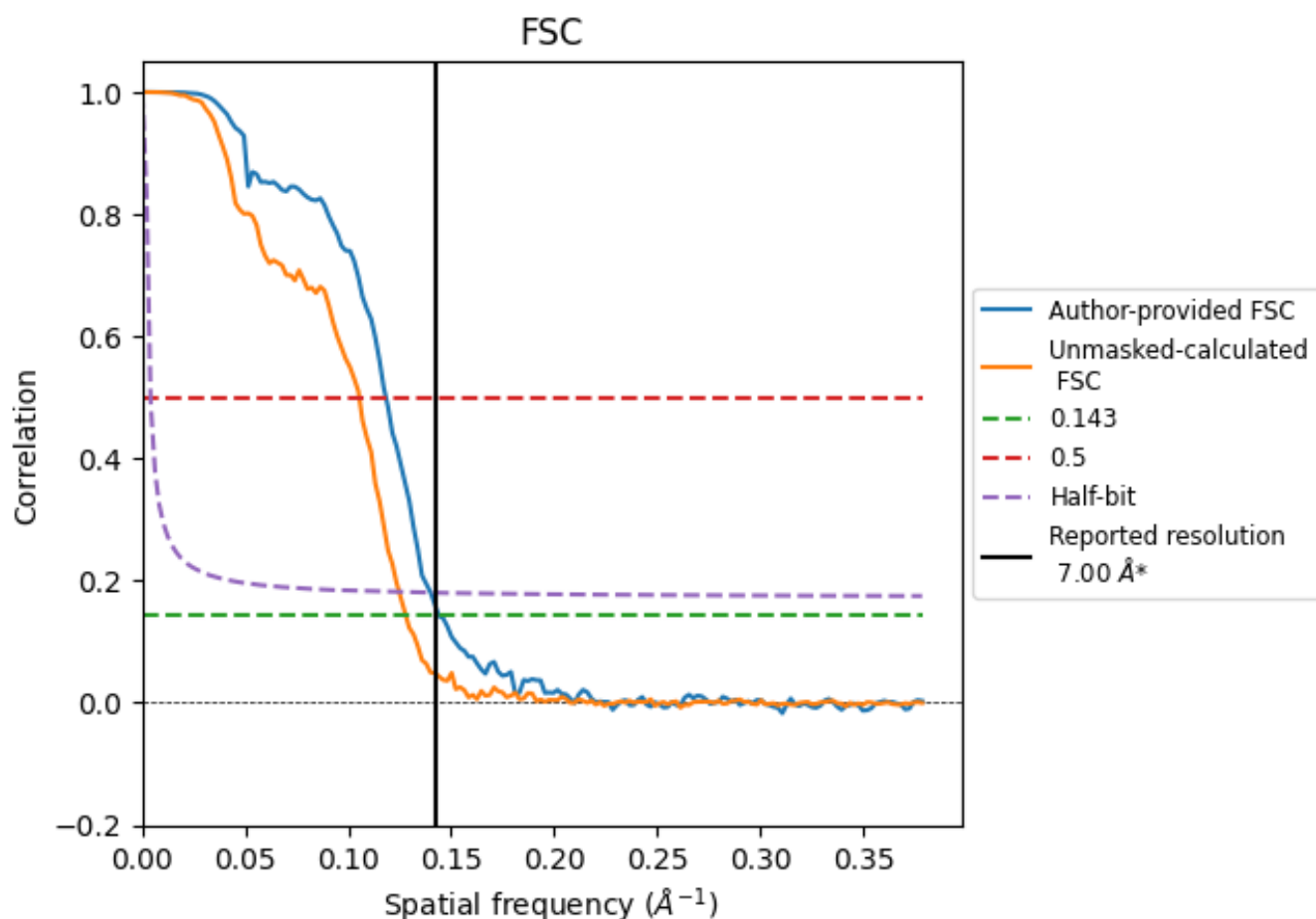


*Reported resolution corresponds to spatial frequency of 0.143 Å⁻¹

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 0.143 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

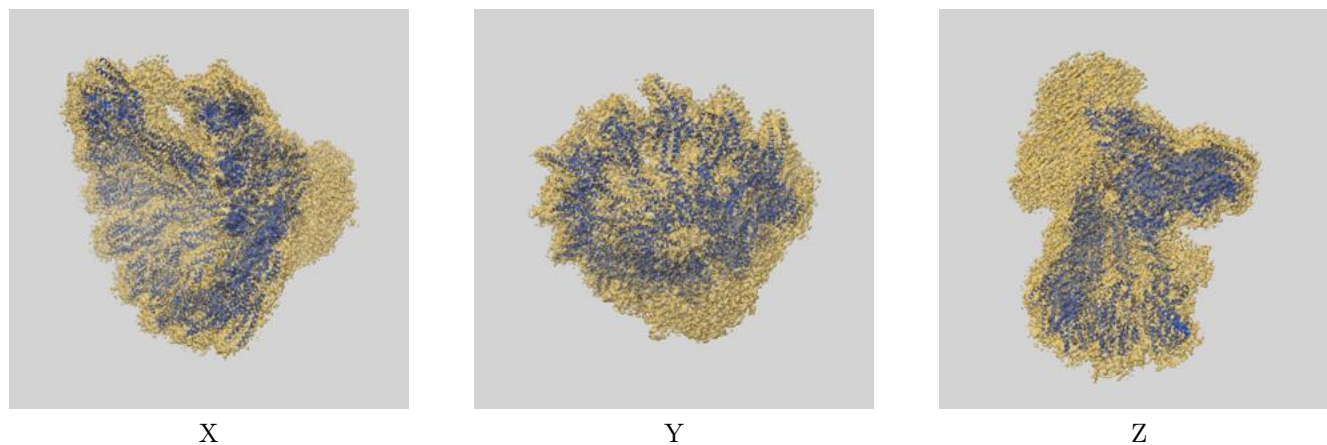
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.00	-	-
Author-provided FSC curve	6.94	8.45	7.14
Unmasked-calculated*	7.81	9.49	8.01

*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 7.81 differs from the reported value 7.0 by more than 10 %

9 Map-model fit [i](#)

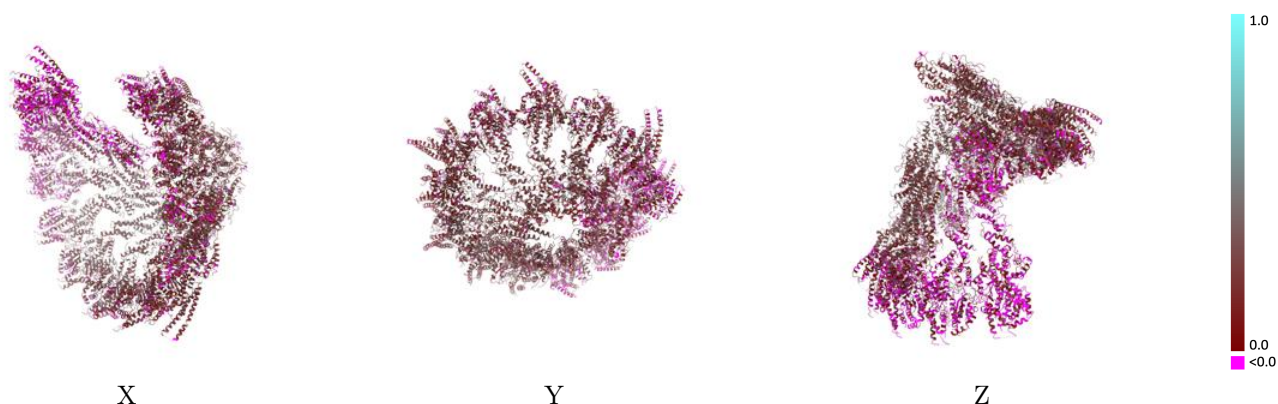
This section contains information regarding the fit between EMDB map EMD-43481 and PDB model 8VRD. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



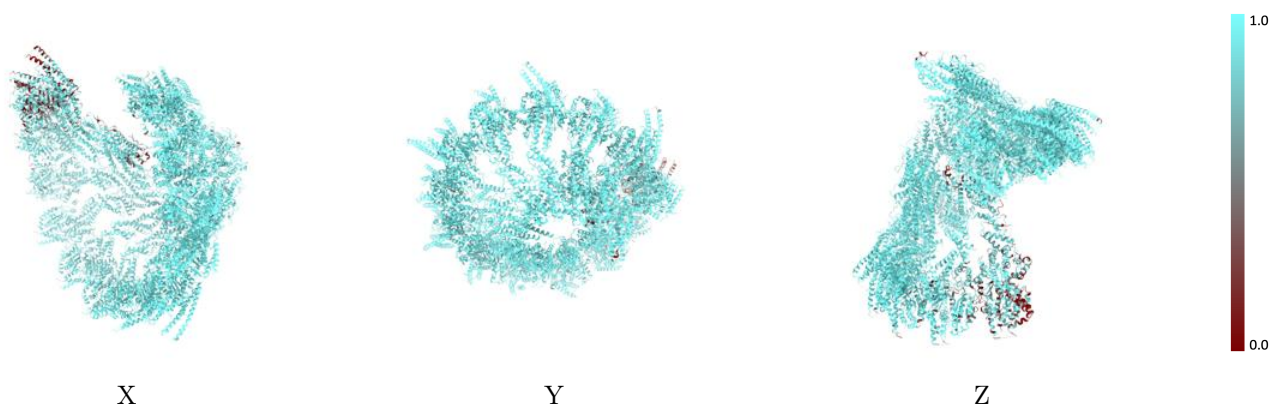
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



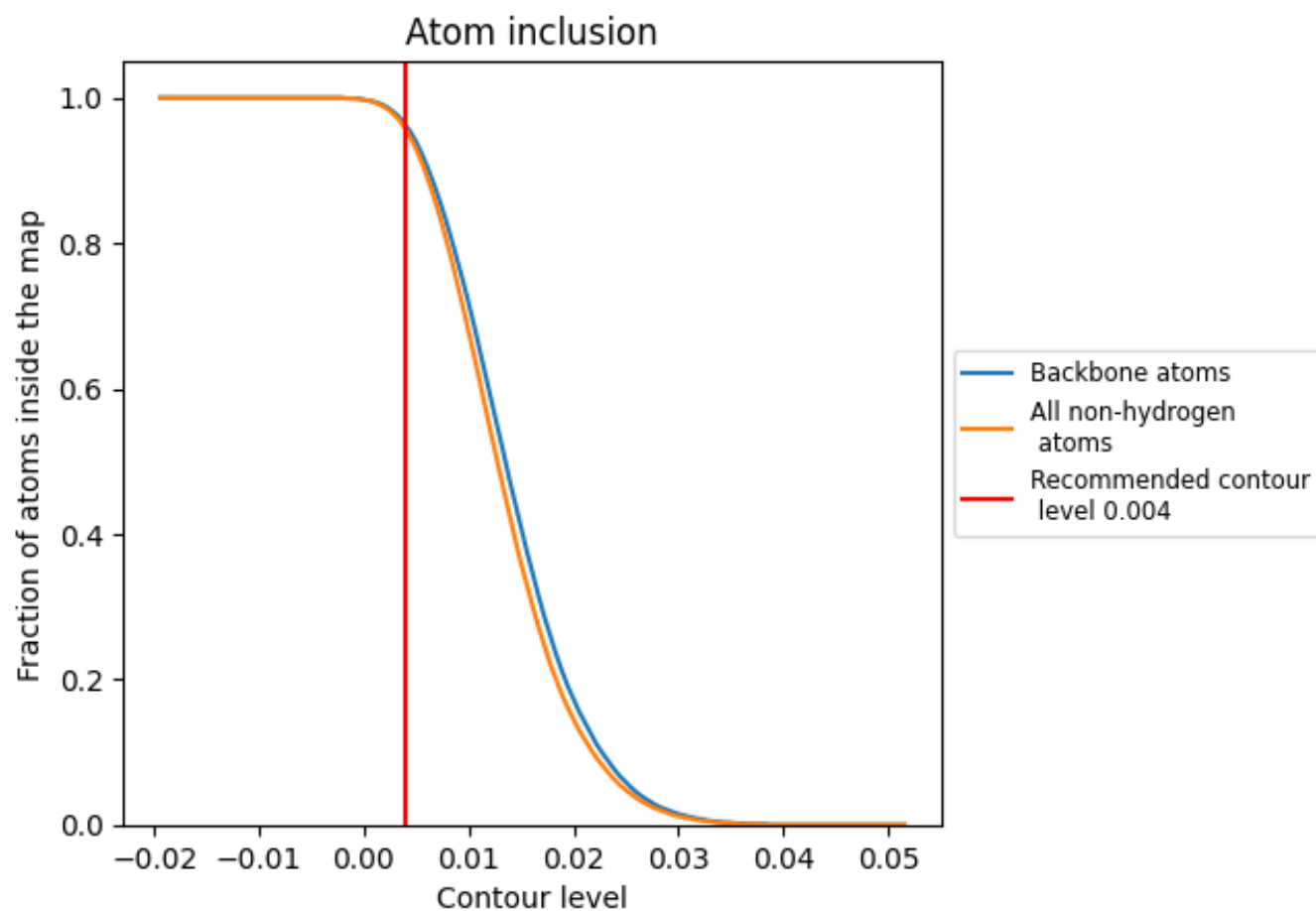
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 96% of all backbone atoms, 96% 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	 0.9560	 0.1800
A	 0.9770	 0.1740
B	 0.9870	 0.2250
C	 0.9820	 0.2300
D	 0.9880	 0.2320
E	 0.9910	 0.2430
F	 0.9940	 0.2470
G	 0.9900	 0.2520
H	 0.9950	 0.2580
I	 0.9940	 0.2710
J	 0.9950	 0.2540
K	 0.9860	 0.2000
L	 0.9980	 0.2110
M	 0.8860	 0.0570
N	 0.7240	 0.0210
O	 0.9790	 0.3080
P	 0.9880	 0.2790
Q	 0.9880	 0.2820
R	 1.0000	 0.2730
S	 0.9780	 0.2150
T	 0.9750	 0.1440
a	 0.9660	 0.0860
b	 0.9840	 0.1590
c	 0.9870	 0.1950
d	 0.9850	 0.1620
e	 0.9890	 0.1580
f	 0.9920	 0.2010
g	 0.9890	 0.2000
h	 0.9950	 0.2430
i	 0.9960	 0.1990
j	 0.9900	 0.1570
k	 0.9530	 0.0530
l	 0.9360	 0.0550
m	 0.8590	 0.0300
n	 0.5860	 -0.0020

