



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:25 PM UTC

PDB ID : 7QJ5 / pdb_00007qj5
EMDB ID : EMD-14010
Title : Structure of recombinant human gamma-Tubulin Ring Complex (spokes 1-14)
Authors : Zupa, E.; Pfeffer, S.
Deposited on : 2021-12-16
Resolution : 8.70 Å(reported)
Based on initial models : 6X0U, 6L81, 7AS4, 6V6S

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:

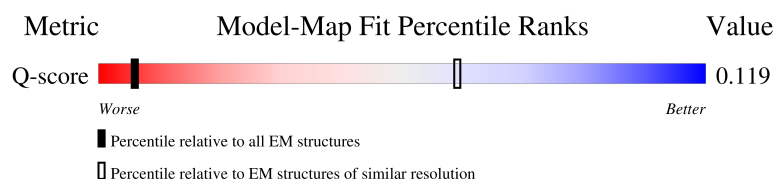
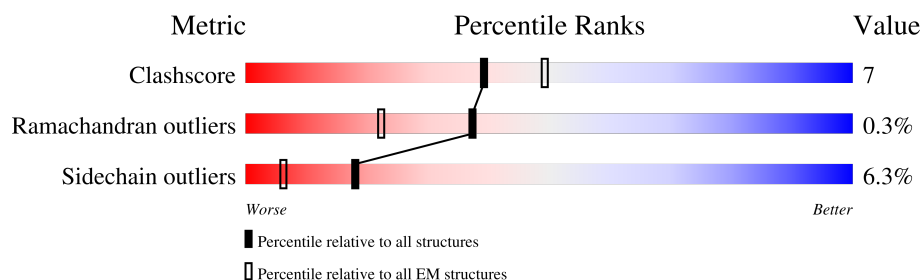
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.70 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	282 (8.20 - 9.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	451	
1	2	451	
1	O	451	
1	P	451	

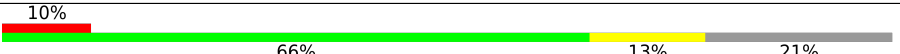
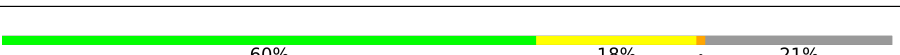
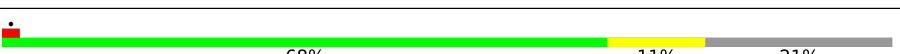
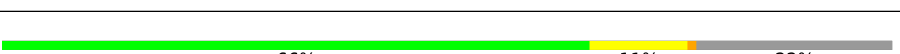
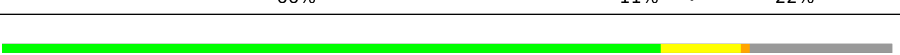
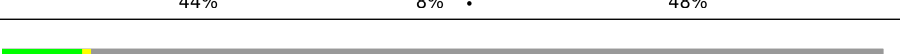
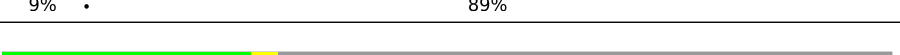
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Mol	Chain	Length	Quality of chain
1	Q	451	
1	R	451	
1	S	451	
1	T	451	
1	U	451	
1	V	451	
1	W	451	
1	X	451	
1	Y	451	
1	Z	451	
2	e	375	
3	A	902	
3	C	902	
3	E	902	
3	G	902	
3	M	902	
4	B	907	
4	D	907	
4	F	907	
4	H	907	
4	N	907	
4	a	907	
4	f	907	
4	h	907	
4	j	907	

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Mol	Chain	Length	Quality of chain
5	b	82	
5	d	82	
5	g	82	
5	i	82	
5	k	82	
5	m	82	
6	I	667	
6	K	667	
7	J	1024	
7	l	1024	
8	L	1819	
8	c	1819	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 126600 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 gamma-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	2	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	O	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	P	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	Q	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	R	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	S	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	T	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	U	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	V	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	W	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	X	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	Y	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	Z	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		

- Molecule 2 is a protein called actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	364	Total	C	N	O	S	0	0
			2847	1803	476	548	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	613	Total	C	N	O	S	0	0
			4978	3212	831	903	32		
3	C	620	Total	C	N	O	S	0	0
			5044	3257	845	910	32		
3	G	640	Total	C	N	O	S	0	0
			5216	3359	878	946	33		
3	M	636	Total	C	N	O	S	0	0
			5186	3342	871	940	33		
3	E	640	Total	C	N	O	S	0	0
			5216	3359	878	946	33		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	610	Total	C	N	O	S	0	0
			5029	3203	888	913	25		
4	D	581	Total	C	N	O	S	0	0
			4796	3061	842	868	25		
4	F	599	Total	C	N	O	S	0	0
			4941	3151	871	894	25		
4	H	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
4	N	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
4	a	116	Total	C	N	O	S	0	0
			933	591	171	169	2		
4	j	107	Total	C	N	O	S	0	0
			863	545	161	155	2		
4	h	107	Total	C	N	O	S	0	0
			863	545	161	155	2		
4	f	107	Total	C	N	O	S	0	0
			863	545	161	155	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	g	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	i	65	Total	C	N	O	S	0	0
			484	299	85	96	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	k	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	d	59	Total	C	N	O	S	0	0
			454	281	79	90	4		

- Molecule 6 is a protein called Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	521	Total	C	N	O	S	0	0
			4225	2737	720	750	18		
6	K	562	Total	C	N	O	S	0	0
			4579	2964	781	816	18		

- Molecule 7 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	534	Total	C	N	O	S	0	0
			4429	2893	737	776	23		
7	l	108	Total	C	N	O	S	0	0
			875	556	151	167	1		

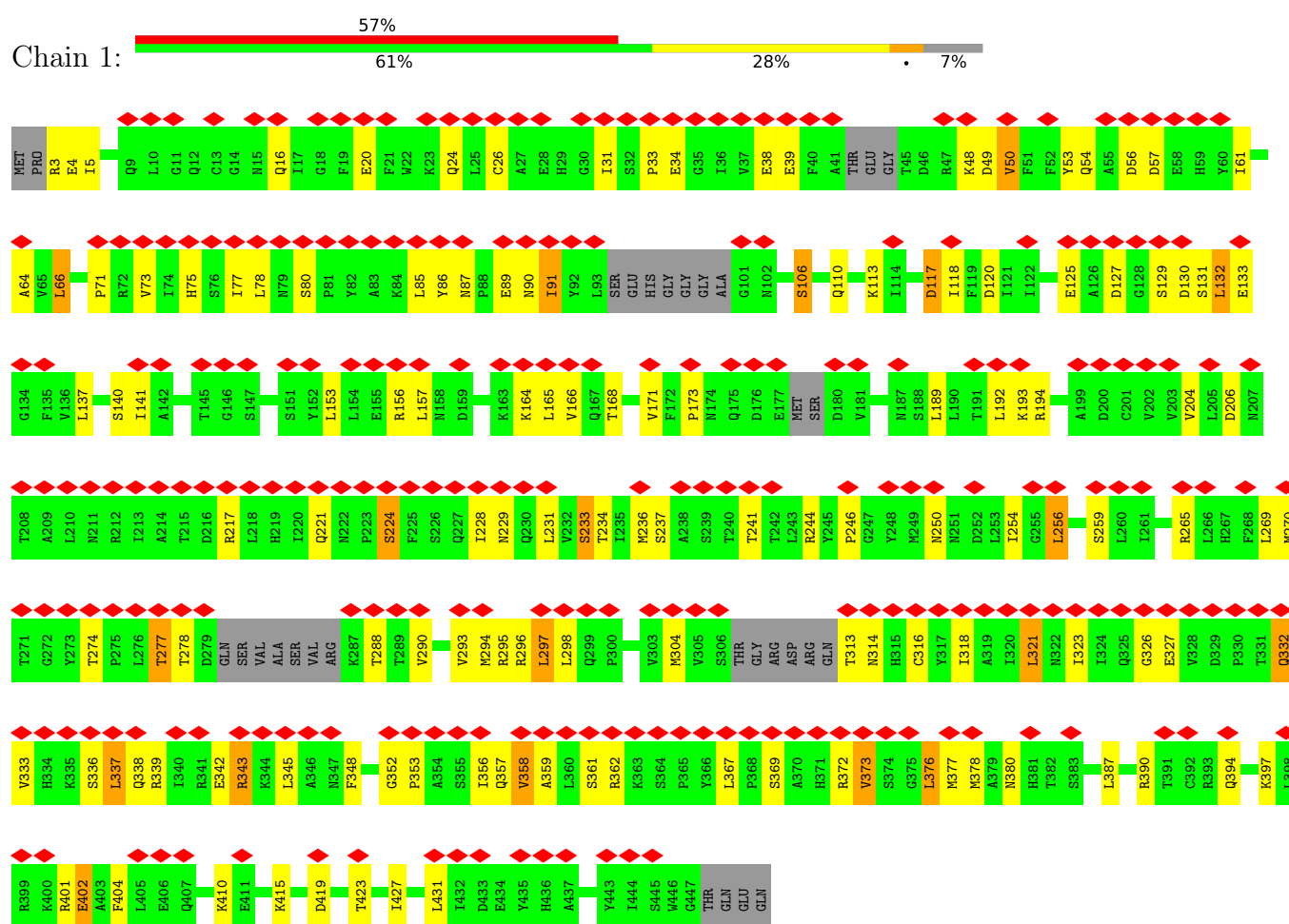
- Molecule 8 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	566	Total	C	N	O	S	0	0
			4587	3000	773	789	25		
8	c	158	Total	C	N	O	S	0	0
			1220	771	209	232	8		

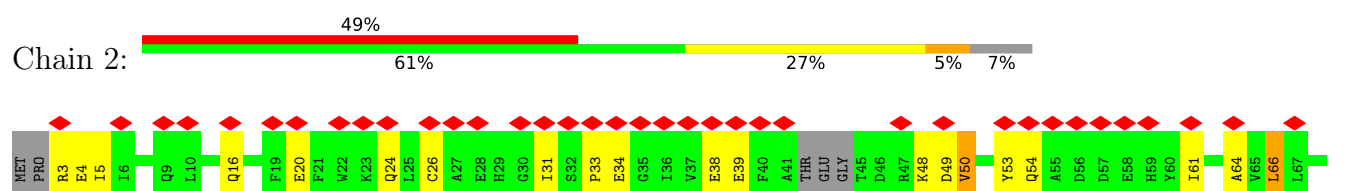
3 Residue-property plots [i](#)

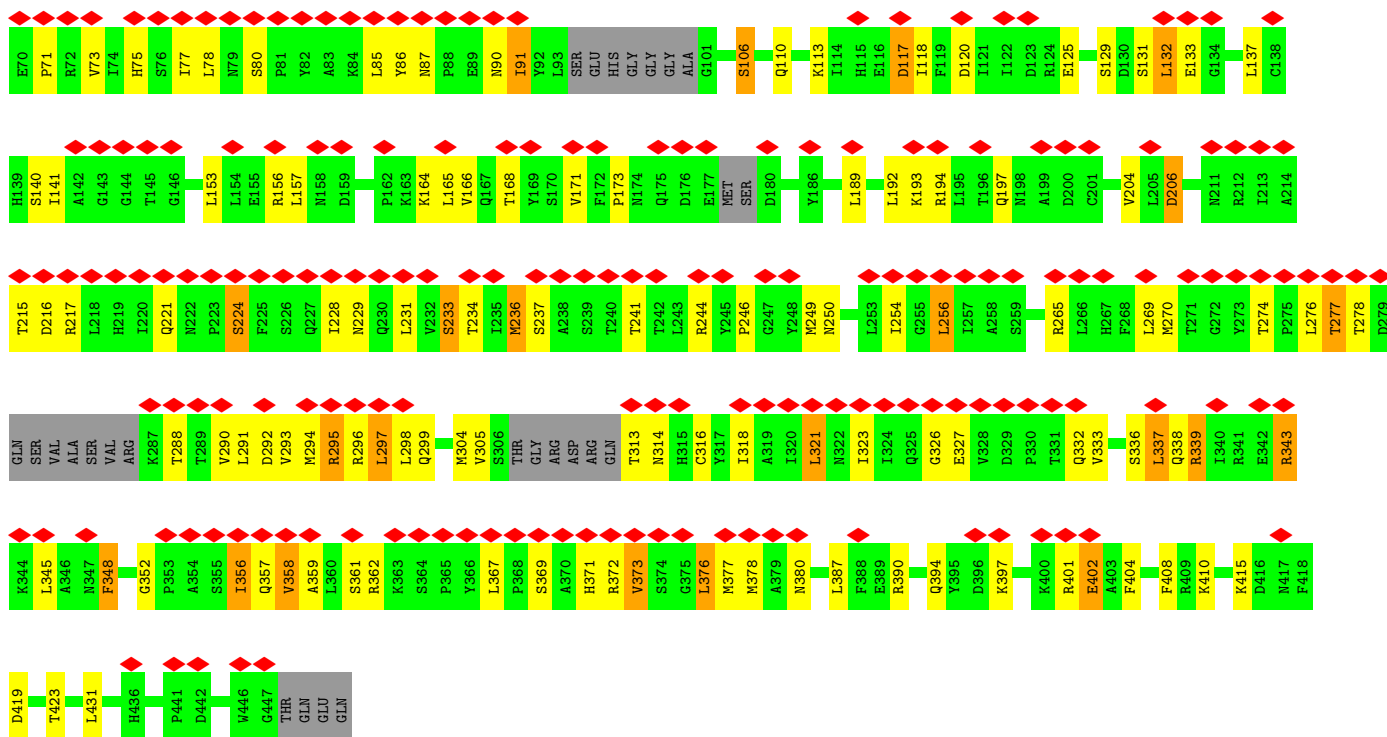
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 gamma-1 chain

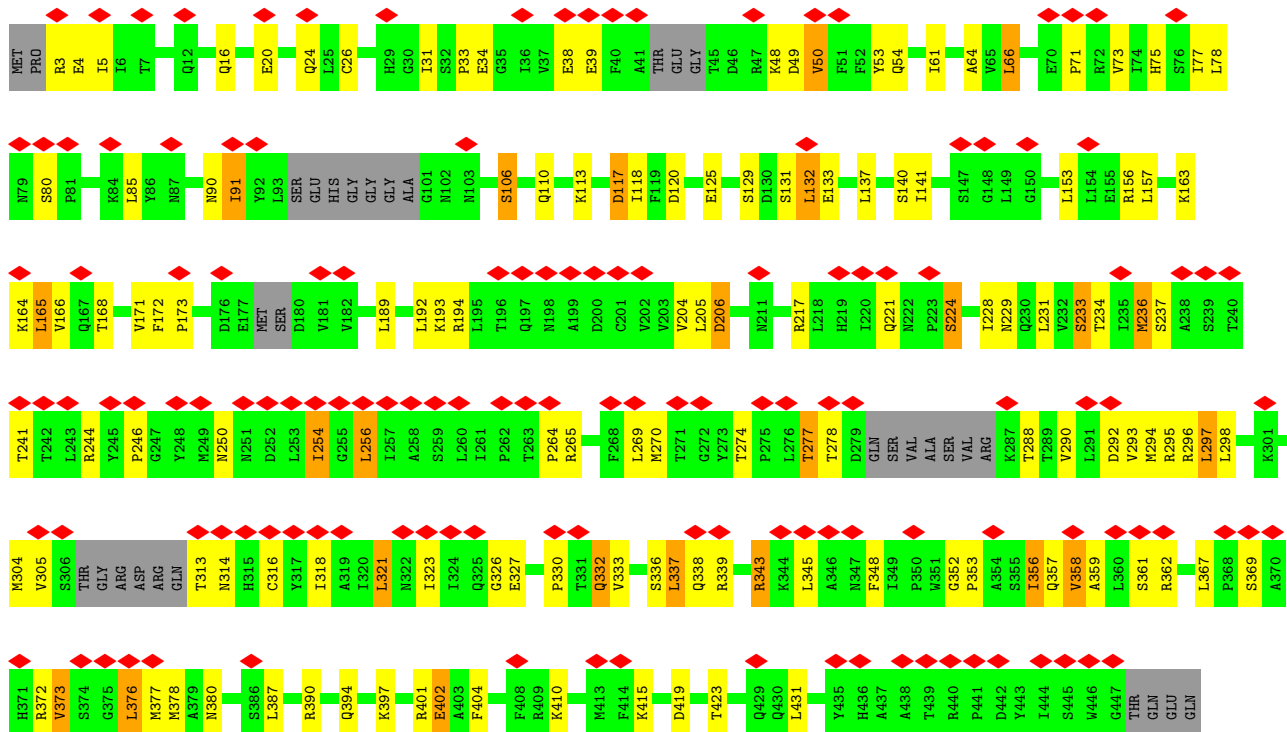


- Molecule 1: Tubulin gamma-1 chain

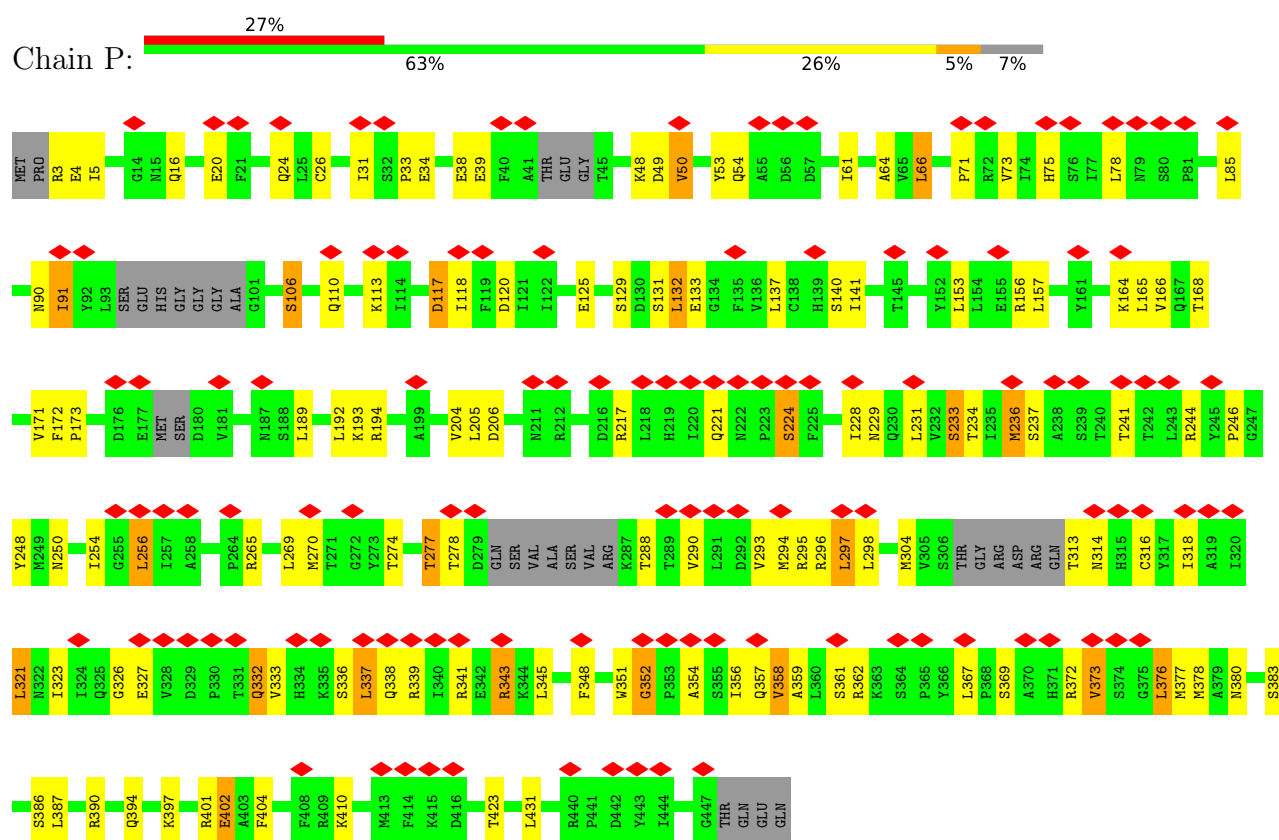




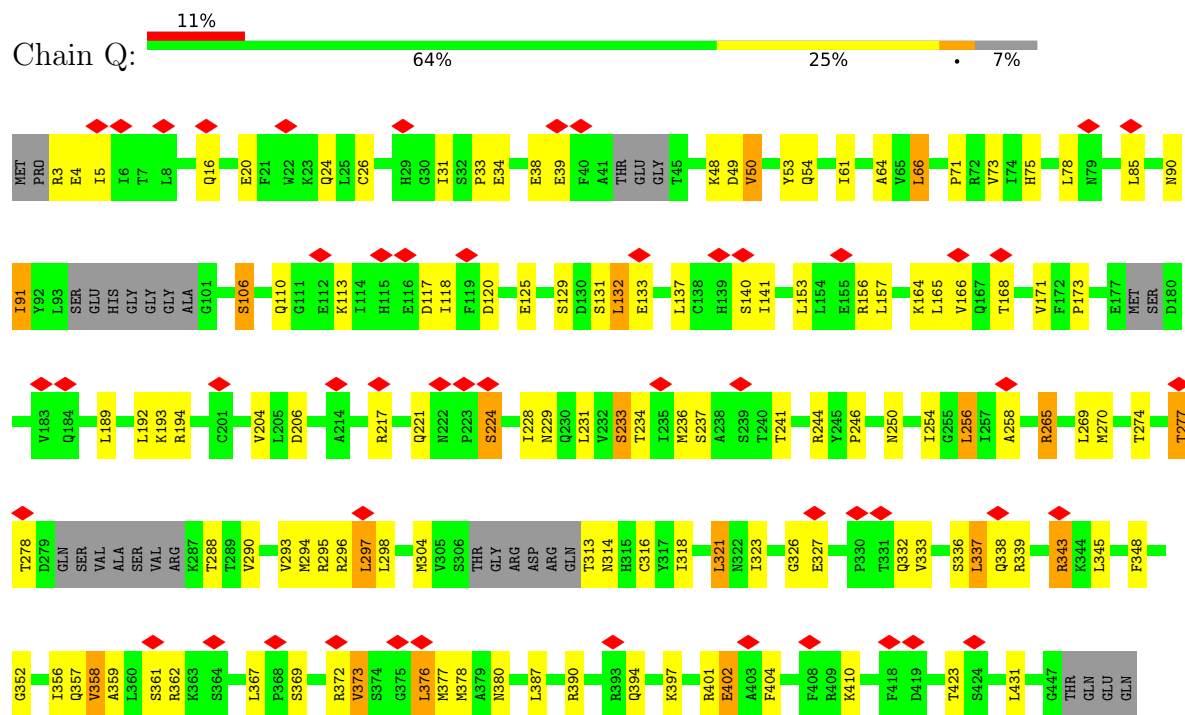
• Molecule 1: Tubulin gamma-1 chain



• Molecule 1: Tubulin gamma-1 chain

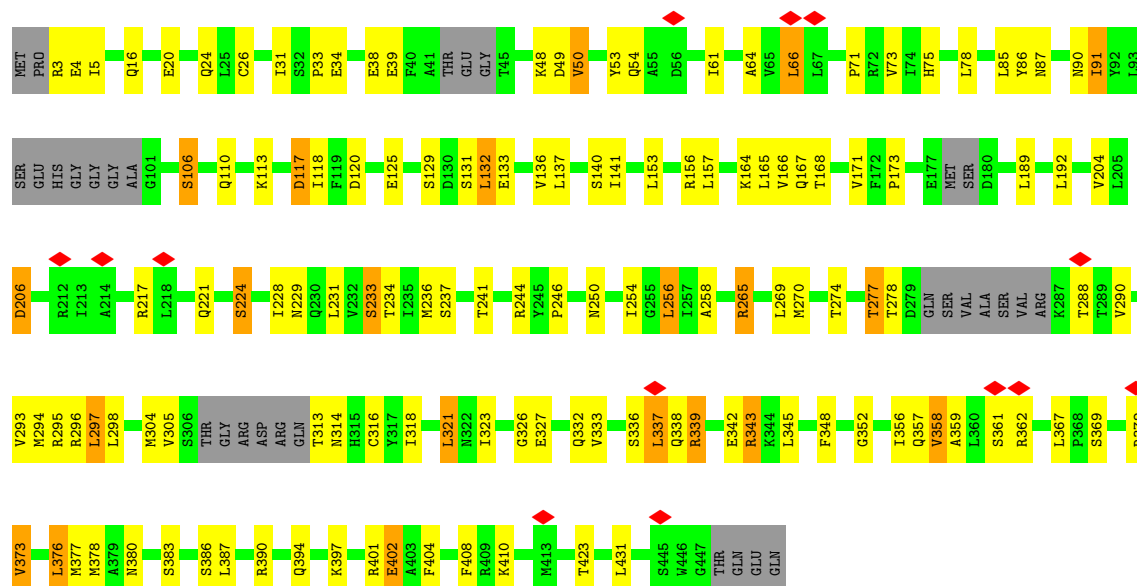


• Molecule 1: Tubulin gamma-1 chain



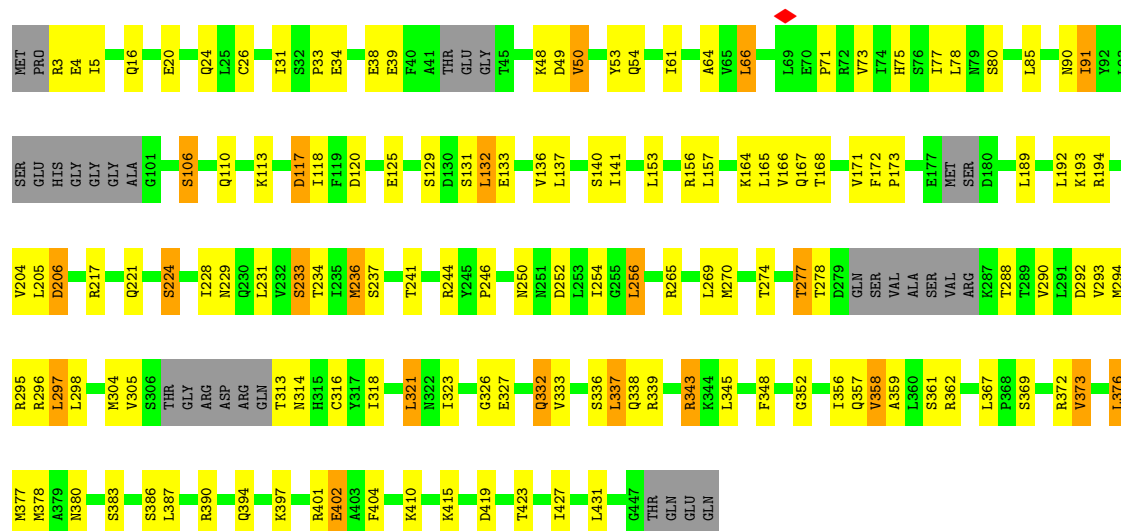
• Molecule 1: Tubulin gamma-1 chain





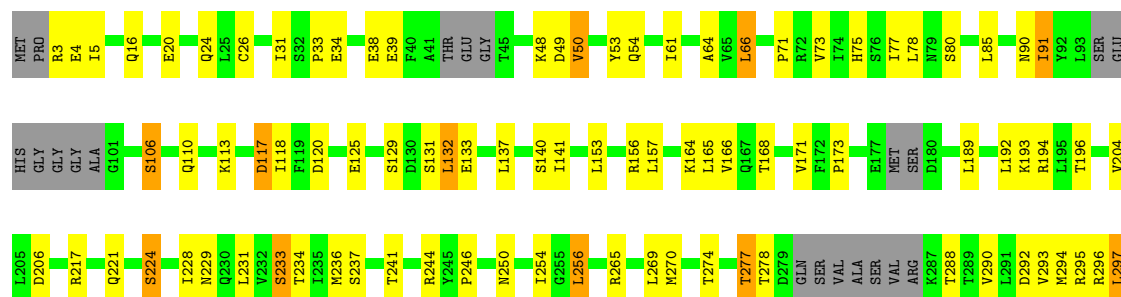
• Molecule 1: Tubulin gamma-1 chain

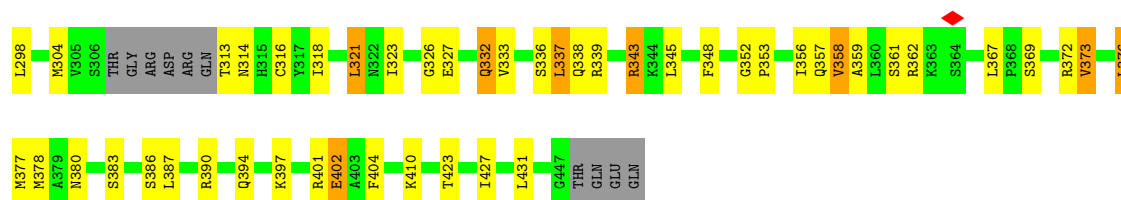
Chain S: 61% 27% 5% 7%



• Molecule 1: Tubulin gamma-1 chain

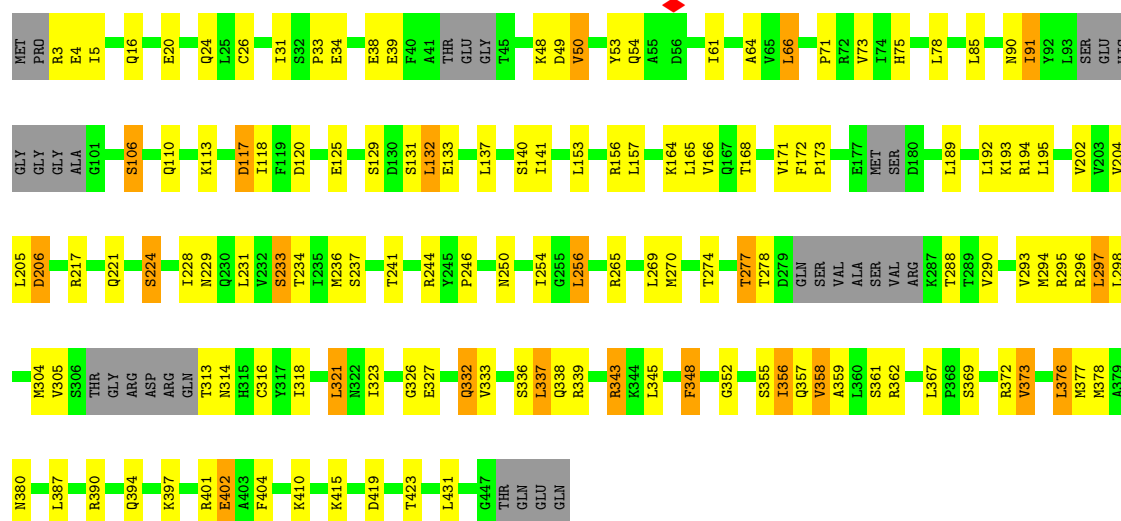
Chain T: 63% 26% 7%





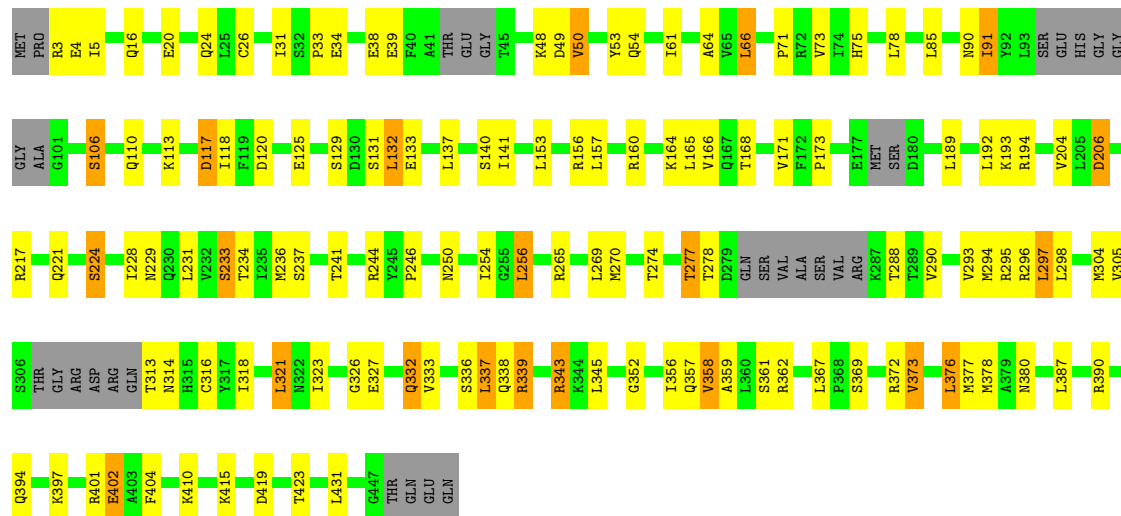
• Molecule 1: Tubulin gamma-1 chain

Chain U: 63% 25% 5% 7%



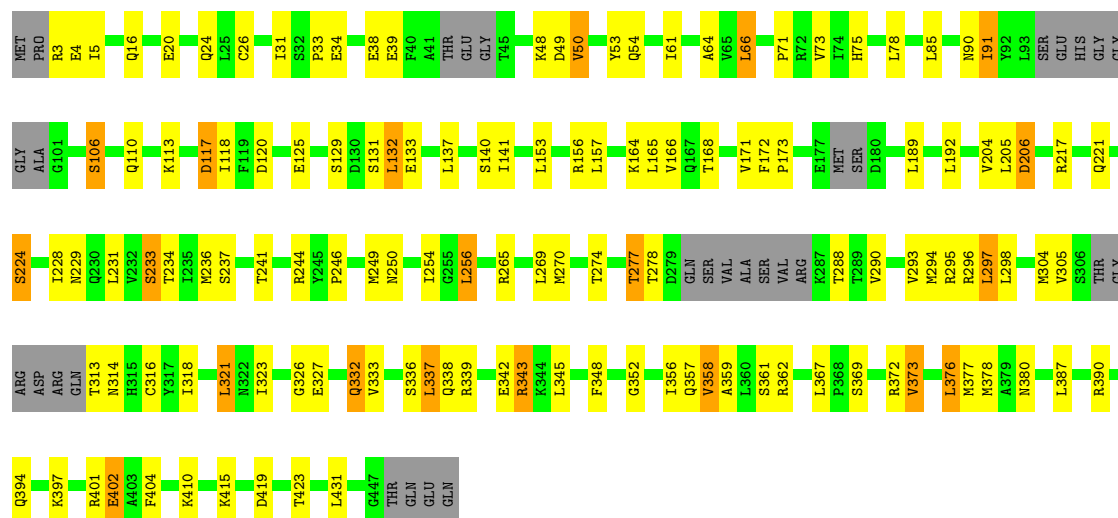
• Molecule 1: Tubulin gamma-1 chain

Chain V: 64% 25% 5% 7%



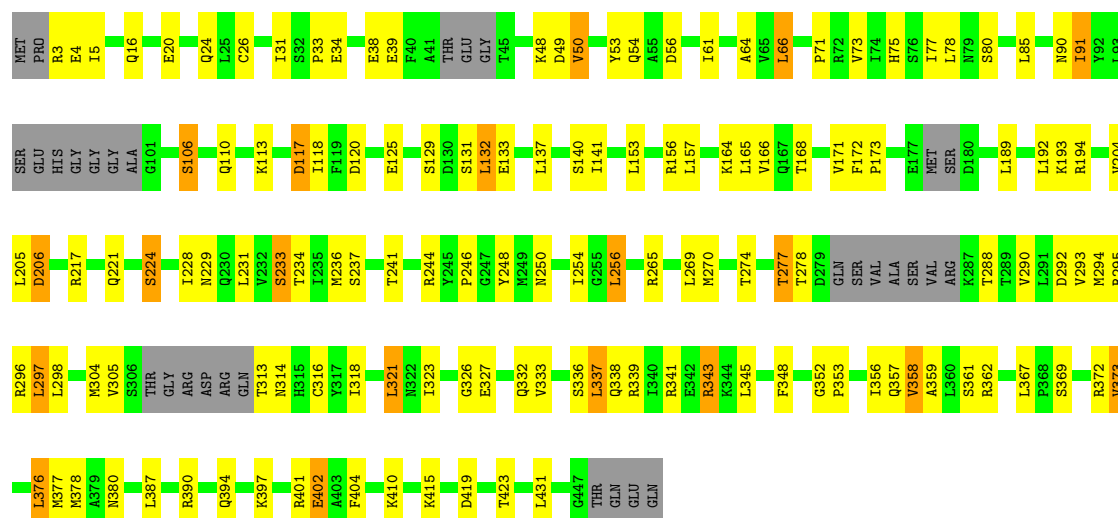
• Molecule 1: Tubulin gamma-1 chain

Chain W: 63% 25% 7%



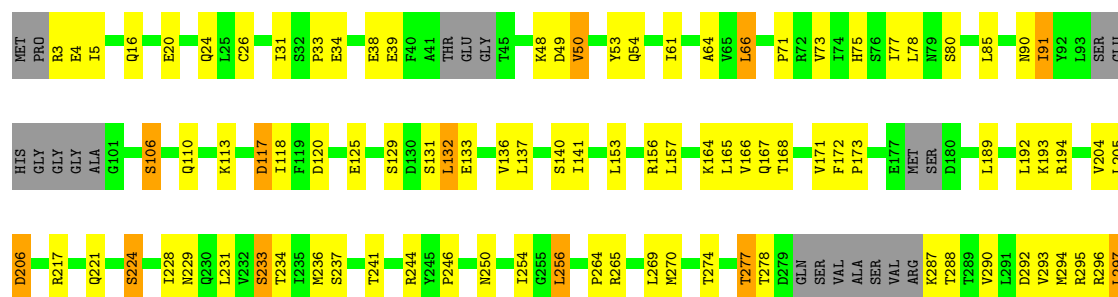
• Molecule 1: Tubulin gamma-1 chain

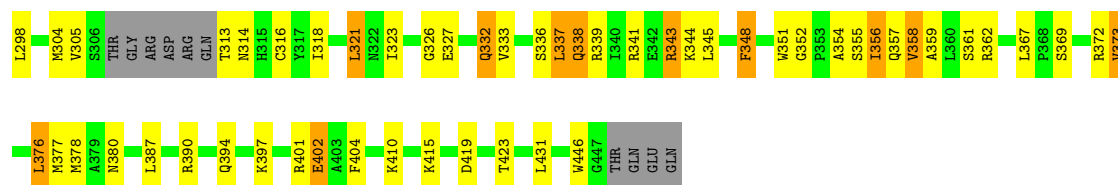
Chain X: 62% 27% 7%



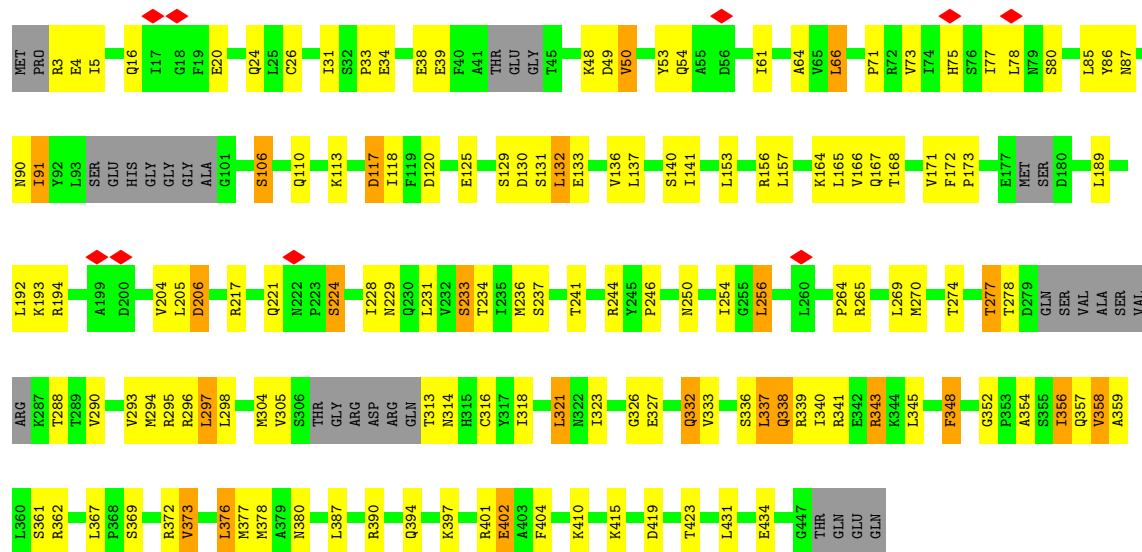
• Molecule 1: Tubulin gamma-1 chain

Chain Y: 61% 27% 5% 7%

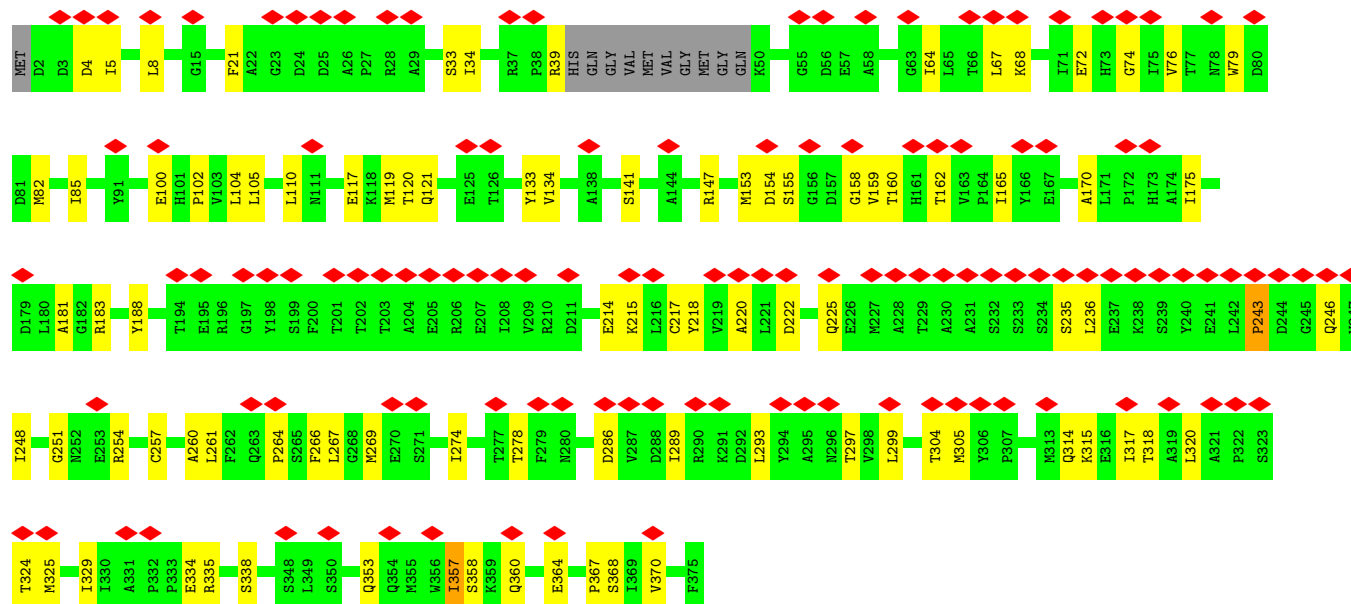




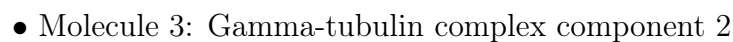
• Molecule 1: Tubulin gamma-1 chain



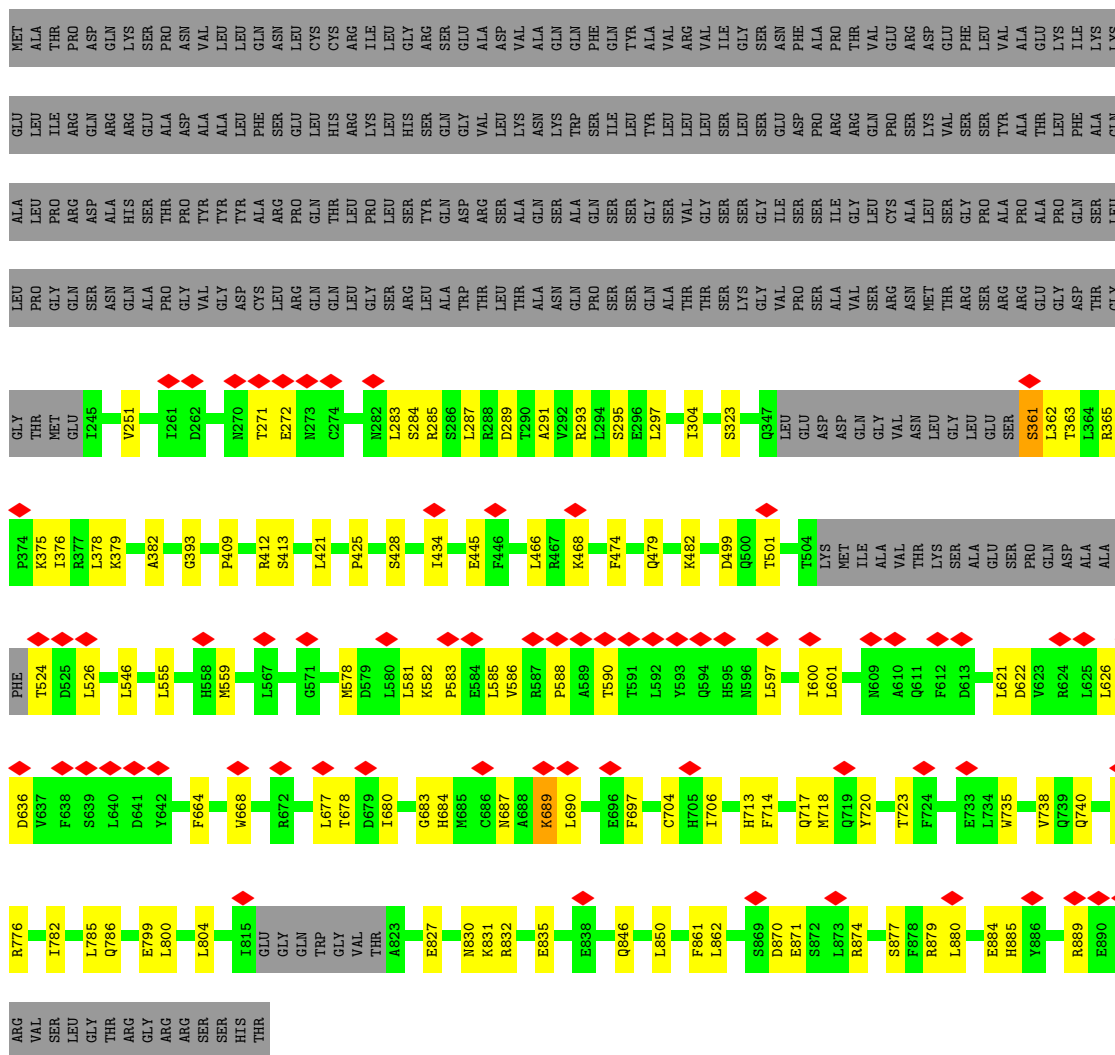
• Molecule 2: actin, cytoplasmic 1



• Molecule 3: Gamma-tubulin complex component 2



- Molecule 4: Gamma-tubulin complex component 3

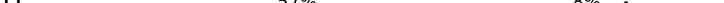


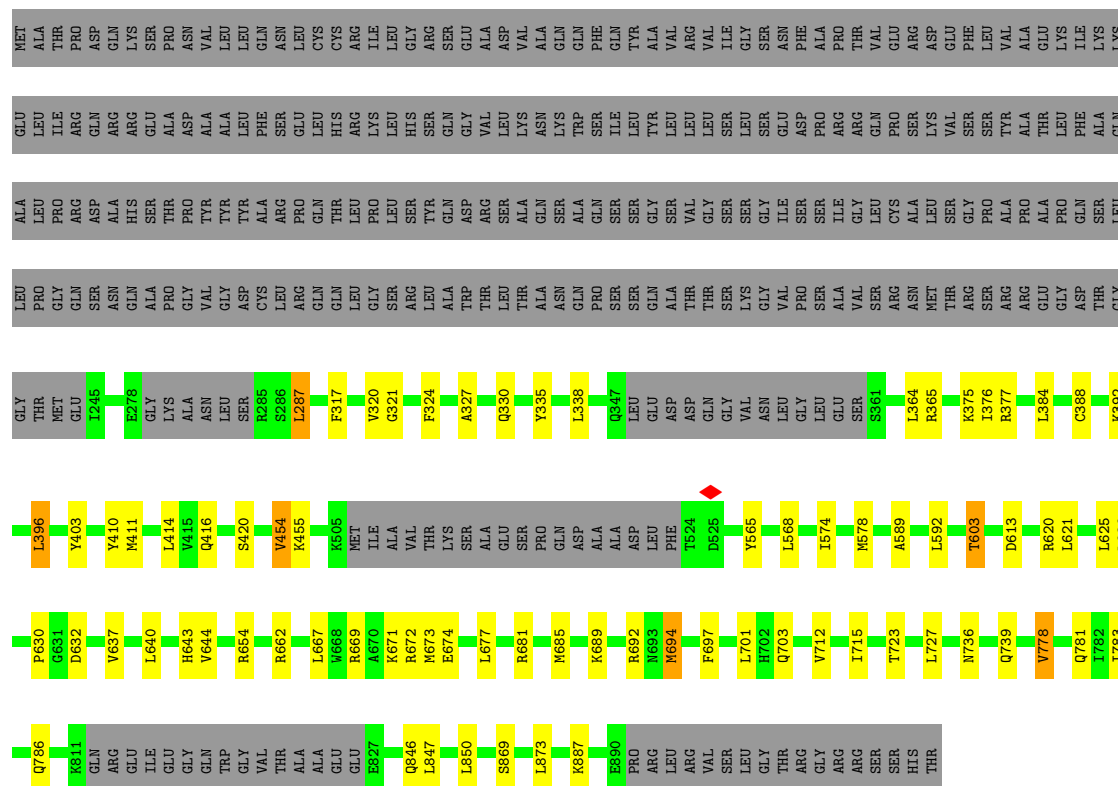
- Molecule 4: Gamma-tubulin complex component 3



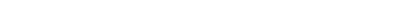


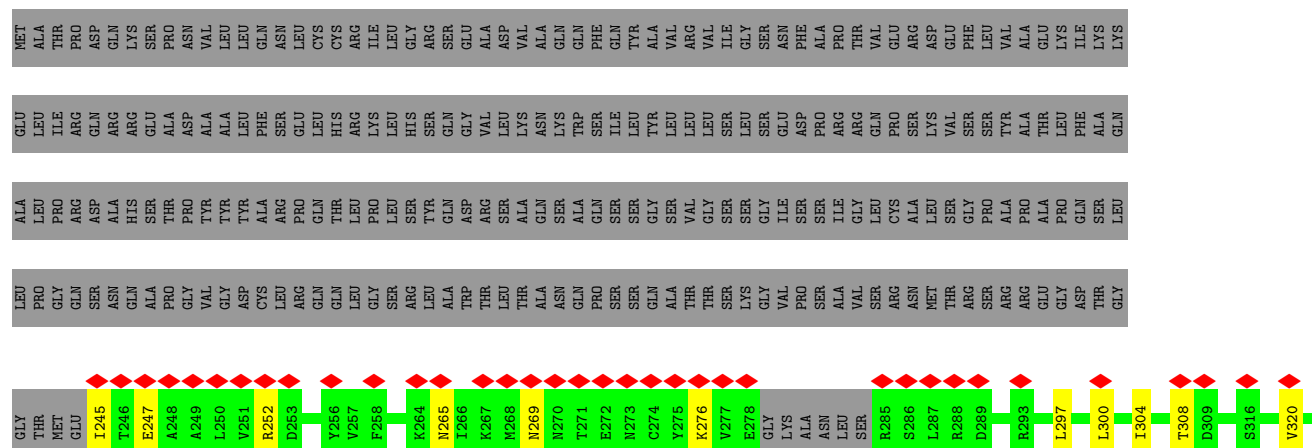
- Molecule 4: Gamma-tubulin complex component 3

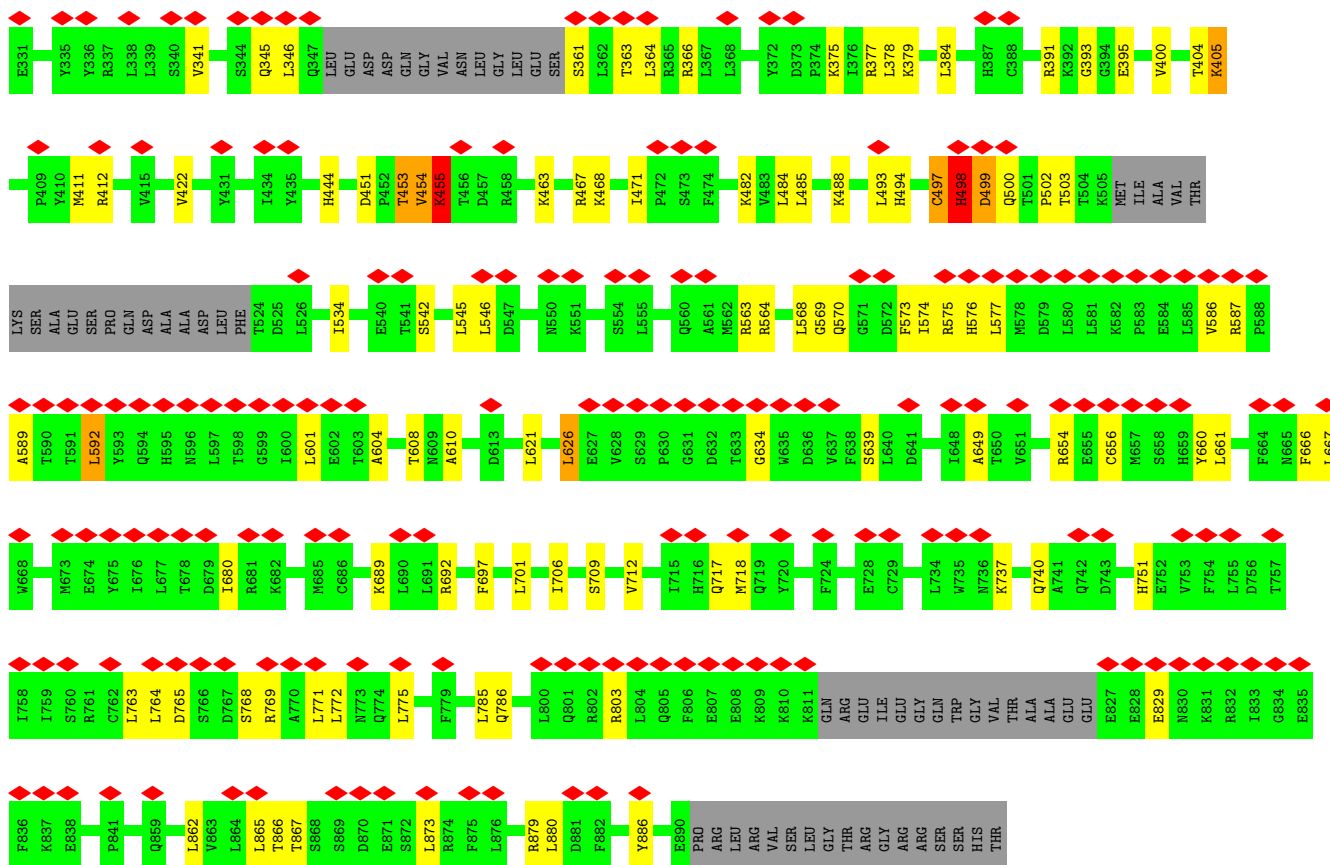
Chain H:  57% 8% 35%



- Molecule 4: Gamma-tubulin complex component 3

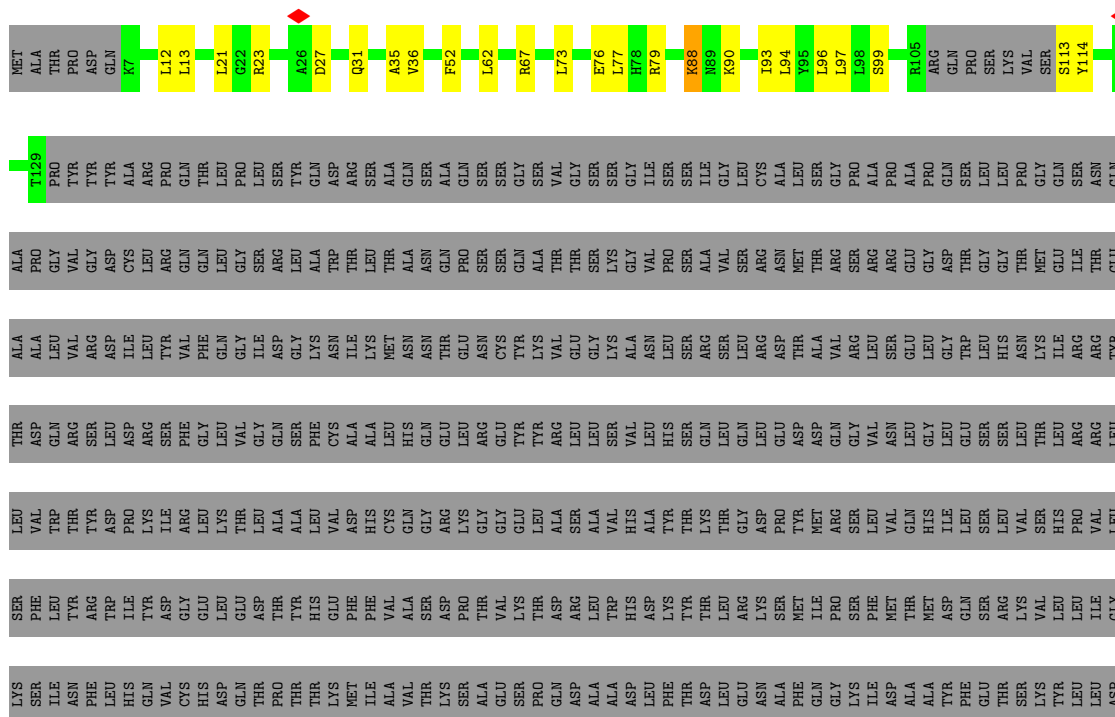
Chain N:  24% 52% 12% 35%





• Molecule 4: Gamma-tubulin complex component 3

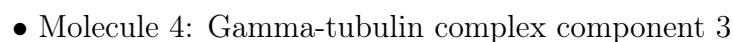
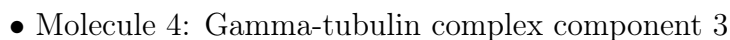
Chain a: 10% 87%

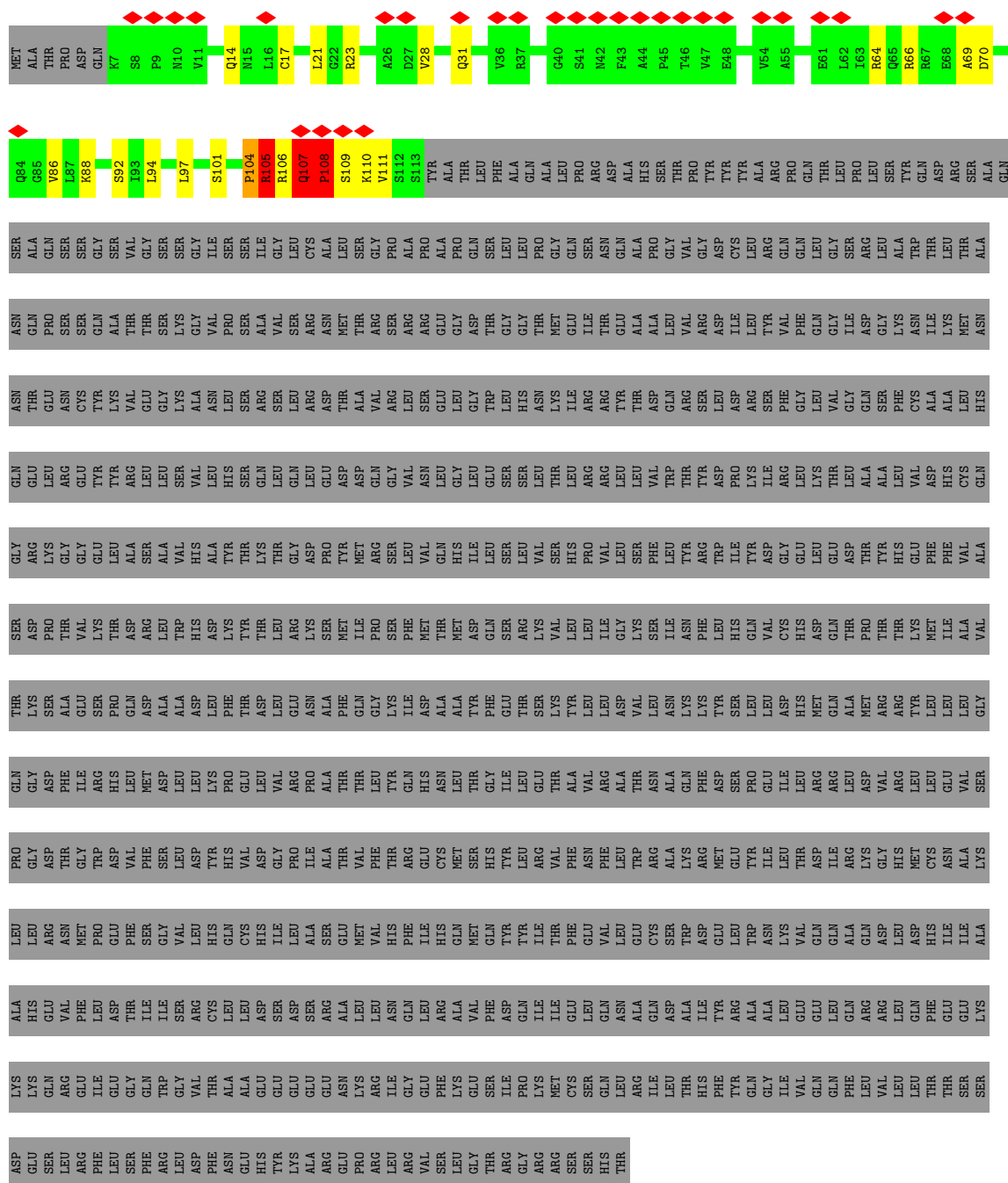


- Molecule 4: Gamma-tubulin complex component 3



GLN	ASP	GLY	LYS	ASP	MET	PRO	THR	ALA	GLN	ASP	GLY	LEU	ARG	SER	MET
LEU	LEU	HIS	HIS	ARG	ARG	THR	THR	ALA	LEU	ALA	THR	GLN	ALA	TYR	ALA
ASP	ASP	MET	LEU	TYR	LEU	LYS	GLU	VAL	ASP	VAL	GLU	TRP	THR	ASP	THR
HIS	HIS	CYS	LEU	LEU	LEU	ILE	PHE	HIS	ALA	LEU	ALA	LEU	ALA	SER	GLN
ILE	ILE	ASN	GLU	LEU	LEU	VAL	VAL	CYS	GLN	LEU	ASP	THR	THR	ALA	K7
ILE	ILE	ALA	VAL	SER	GLY	VAL	ALA	GLN	GLN	HIS	ASN	ASP	ALA	GLN	
LYS	SER	LEU	ASP	GLY	GLY	VAL	ALA	GLN	GLY	GLN	ASN	THR	GLN	SER	R37
PRO	PRO	LEU	PRO	GLY	GLN	THR	SER	ASP	ARG	ALA	THR	ASP	GLN	ALA	V38
HIS	HIS	LEU	GLY	GLY	GLY	LYS	THR	ASP	GLY	LEU	GLU	GLU	PRO	GLN	I39
GLU	GLU	ASP	ASP	ASP	ASP	SER	PRO	GLY	ARG	CYS	ASN	SER	SER	SER	G40
VAL	VAL	ASN	THR	PHE	PHE	ALA	THR	GLY	GLY	GLU	GLY	SER	SER	SER	S41
PHE	PHE	MET	GLY	ILE	ILE	GLU	VAL	GLY	GLU	TYR	TYR	GLY	GLN	GLY	M42
LEU	LEU	TRP	TRP	ARG	ARG	SER	LYS	GLU	TYR	TYR	LYS	SER	ALA	SER	F43
THR	THR	PHE	VAL	VAL	VAL	GLN	ASP	ALA	ARG	ARG	VAL	VAL	THR	VAL	A44
ILE	ILE	PHE	PHE	MET	MET	ASP	ASP	SER	LEU	LEU	GLU	GLY	THR	GLY	
ILE	ILE	SER	ASP	ASP	ASP	ALA	LEU	ALA	LEU	SER	GLY	SER	SER	SER	E61
SER	SER	VAL	LEU	LEU	LEU	ASP	TRP	VAL	HIS	VAL	LYS	GLY	GLY	SER	
ARG	ARG	LEU	ASP	LEU	LEU	ASP	HIS	VAL	GLN	VAL	ALA	GLY	GLY	GLY	R64
LEU	LEU	TYR	TYR	LYS	LYS	LEU	ASP	ALA	LEU	LEU	ASN	VAL	ILE	ILE	
HIS	HIS	HIS	PRO	PRO	PRO	PHE	LYS	THR	HIS	HIS	LEU	PRO	PRO	SER	S92
VAL	VAL	VAL	VAL	GLU	GLU	THR	THR	THR	THR	GLN	SER	SER	SER	SER	
HIS	ASP	ASP	ASP	LEU	VAL	ASP	THR	LYS	LYS	LEU	ARG	ALA	ILE	ILE	Y96
SER	GLY	ILE	GLY	VAL	VAL	LEU	LEU	THR	THR	GLN	SER	VAL	VAL	GLY	
ASP	ASP	PRO	PRO	ARG	ARG	GLU	ARG	GLY	GLN	LEU	LEU	SER	ARG	LEU	R106
LEU	ILE	ILE	ILE	PRO	PRO	ASN	ASN	ASP	LYS	LYS	ARG	ARG	ARG	CYS	G107
ALA	ALA	SER	ALA	ALA	ALA	ALA	SER	PRO	GLU	GLU	ASP	ASN	ALA	ALA	P108
ALA	ALA	THR	PHE	THR	THR	PHE	MET	THR	THR	ASP	THR	MET	THR	LEU	
LEU	LEU	VAL	GLN	GLN	THR	GLY	ILE	MET	THR	ASP	ALA	THR	THR	SER	V111
LEU	LEU	VAL	VAL	LYS	LYS	GLY	PRO	ARG	GLN	GLN	VAL	ARG	ARG	GLY	S12
ASN	ASN	HIS	LYS	THR	THR	LYS	THR	SER	SER	GLY	VAL	SER	SER	PRO	S13
GLN	GLN	PHE	ILE	PHE	GLN	ILE	PHE	LEU	VAL	VAL	LEU	ARG	ARG	ALA	TYR
LEU	LEU	ILE	ALA	HIS	HIS	ALA	THR	GLN	LEU	LEU	GLU	GLU	GLU	ALA	ALA
ALA	ALA	GLN	ALA	LEU	LEU	ALA	MET	HIS	LEU	GLY	GLU	GLY	GLY	LEU	THR
VAL	VAL	MET	THR	THR	THR	LYS	VAL	VAL	SER	THR	ASN	THR	THR	PRO	LEU
THR	THR	ARG	ARG	ARG	ARG	LYS	VAL	SER	THR	THR	LYS	MET	MET	GLY	PRO
PHE	PHE	PHE	VAL	VAL	VAL	TYR	ASP	HIS	LEU	LEU	ILE	GLU	GLU	GLN	ARG
GLU	GLU	ASN	ASN	ASN	ALA	TYR	LEU	PRO	GLN	LEU	ILE	ILE	ILE	SER	ASP
LEU	LEU	VAL	LEU	LEU	ALA	LEU	ILE	VAL	ARG	THR	ARG	THR	THR	ASN	ALA
ALA	ALA	GLU	GLY	THR	THR	VAL	LYS	SER	LEU	LEU	LEU	ALA	ALA	ALA	HIS
GLN	GLN	CYS	CYS	ALA	ALA	ASN	ILE	PHE	THR	THR	LYS	PRO	PRO	PRO	SER
ASP	ASP	SER	SER	ALA	ALA	ASN	ILE	ILE	HIS	LEU	ILE	GLY	GLY	GLY	THR
THR	THR	TRP	TRP	LYS	LYS	LYS	PHE	THR	THR	THR	THR	ASP	ARG	VAL	TYR
ALA	ALA	TRP	TRP	THR	THR	THR	ILE	THR	THR	THR	THR	VAL	VAL	VAL	TYR
ALA	ALA	ASN	ASN	LEU	LEU	LEU	VAL	VAL	GLY	GLN	GLN	LEU	LEU	LEU	ARG
PRO	PRO	LYS	LYS	GLU	GLU	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLN
GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR					





- Molecule 5: Mitotic-spindle organizing protein 1

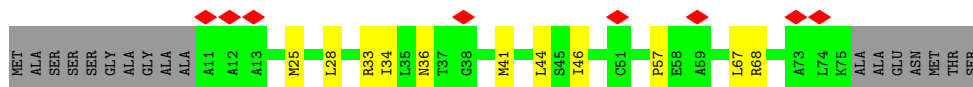
Chain b: 57% 21% 21%



- Molecule 5: Mitotic-spindle organizing protein 1

Chain g: 29% 61% 18% 21%

- Molecule 5: Mitotic-spindle organizing protein 1



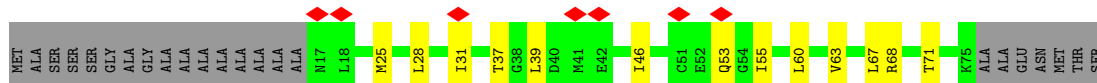
- Molecule 5: Mitotic-spindle organizing protein 1



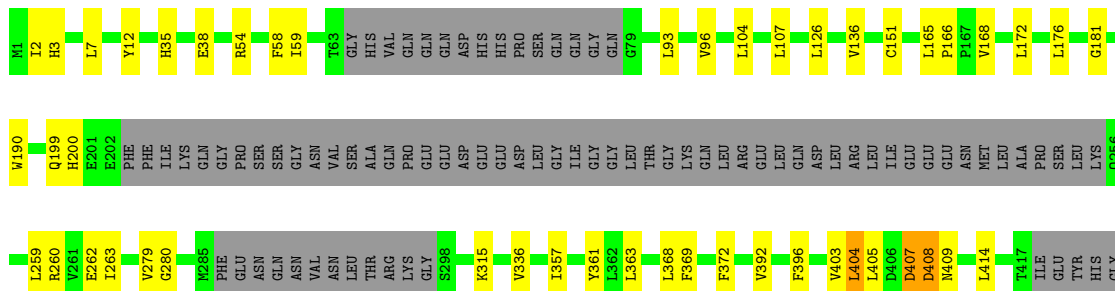
- Molecule 5: Mitotic-spindle organizing protein 1

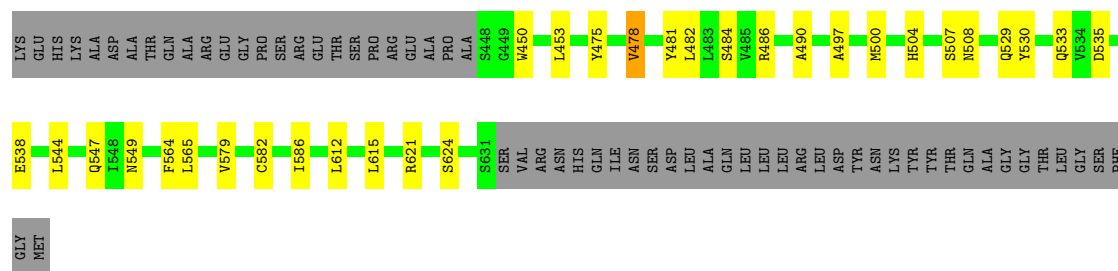


- Molecule 5: Mitotic-spindle organizing protein 1



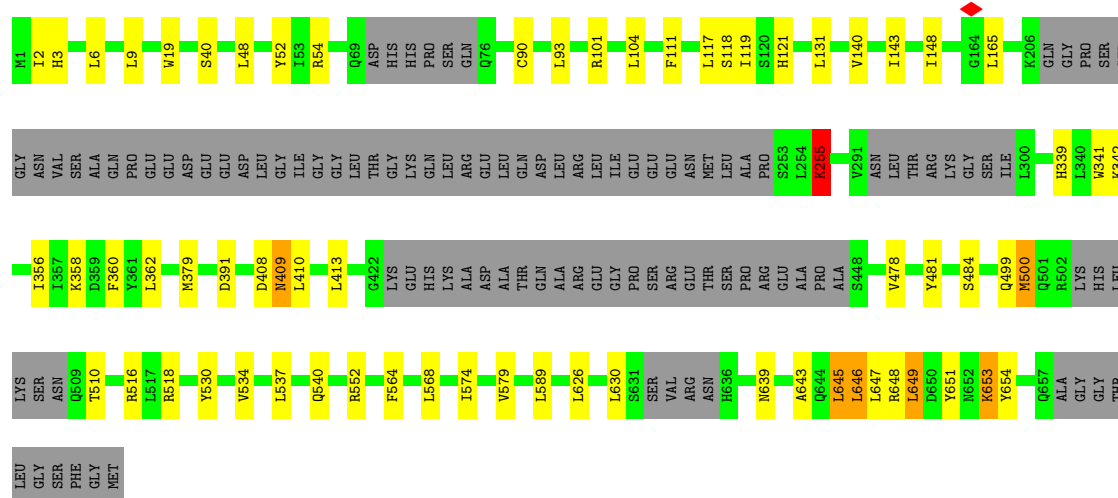
- Molecule 6: Gamma-tubulin complex component 4





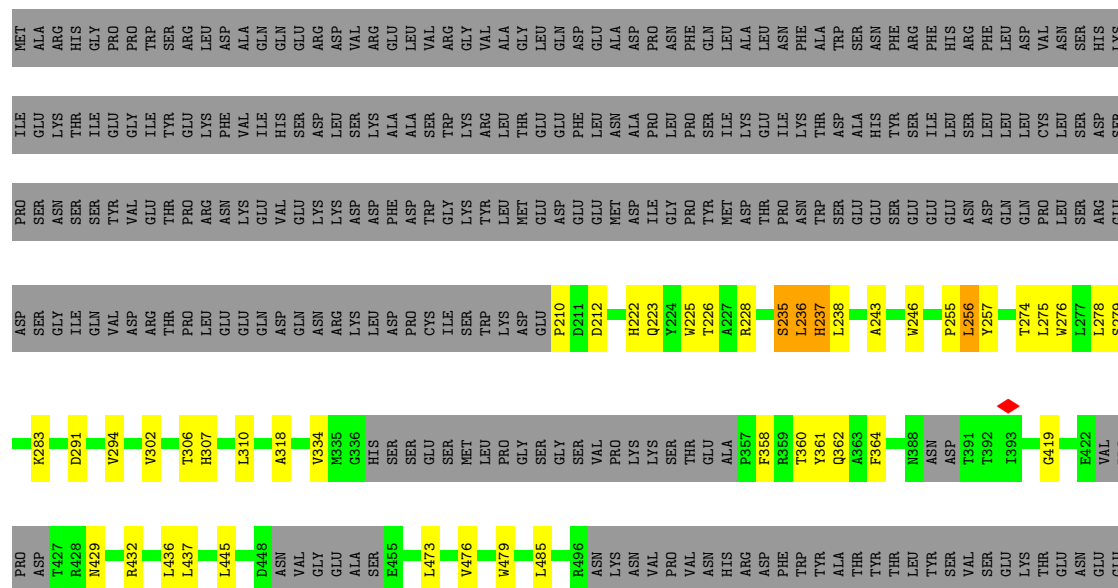
• Molecule 6: Gamma-tubulin complex component 4

Chain K: 74% 9% 16%



• Molecule 7: Gamma-tubulin complex component 5

Chain J: 44% 8% 48%









[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36881	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.292	Depositor
Minimum map value	-0.125	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0224	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.66, 2.66, 2.66	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	0.30	0/3441	0.71	2/4661 (0.0%)
1	2	0.31	0/3441	0.72	2/4661 (0.0%)
1	O	0.31	0/3441	0.71	2/4661 (0.0%)
1	P	0.31	0/3441	0.72	2/4661 (0.0%)
1	Q	0.31	0/3441	0.72	2/4661 (0.0%)
1	R	0.30	0/3441	0.72	2/4661 (0.0%)
1	S	0.30	0/3441	0.72	2/4661 (0.0%)
1	T	0.30	0/3441	0.72	2/4661 (0.0%)
1	U	0.30	0/3441	0.71	2/4661 (0.0%)
1	V	0.30	0/3441	0.71	2/4661 (0.0%)
1	W	0.30	0/3441	0.72	2/4661 (0.0%)
1	X	0.30	0/3441	0.72	2/4661 (0.0%)
1	Y	0.30	0/3441	0.72	2/4661 (0.0%)
1	Z	0.30	0/3441	0.72	2/4661 (0.0%)
2	e	0.51	2/2908 (0.1%)	0.80	1/3938 (0.0%)
3	A	0.43	0/5085	0.82	4/6866 (0.1%)
3	C	0.36	0/5151	0.81	10/6955 (0.1%)
3	E	0.35	0/5325	0.75	10/7187 (0.1%)
3	G	0.38	0/5325	0.79	4/7187 (0.1%)
3	M	0.48	2/5295 (0.0%)	0.86	5/7147 (0.1%)
4	B	0.40	0/5133	0.81	4/6930 (0.1%)
4	D	0.34	0/4897	0.74	3/6610 (0.0%)
4	F	0.39	0/5044	0.81	15/6809 (0.2%)
4	H	0.40	0/5009	0.77	2/6761 (0.0%)
4	N	0.42	1/5009 (0.0%)	0.82	7/6761 (0.1%)
4	a	0.31	0/948	0.71	1/1277 (0.1%)
4	f	0.33	0/876	0.90	8/1178 (0.7%)
4	h	0.34	0/876	0.89	2/1178 (0.2%)
4	j	0.32	0/876	0.76	2/1178 (0.2%)
5	b	0.40	0/484	0.85	0/653
5	d	0.33	0/454	0.68	0/611
5	g	0.32	0/484	0.73	1/653 (0.2%)
5	i	0.30	0/484	0.61	0/653
5	k	0.30	0/484	0.62	0/653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	m	0.29	0/484	0.60	0/653
6	I	0.41	0/4322	0.76	5/5853 (0.1%)
6	K	0.40	0/4683	0.80	5/6338 (0.1%)
7	J	0.41	0/4525	0.88	13/6119 (0.2%)
7	l	0.37	0/894	0.82	2/1209 (0.2%)
8	L	0.36	0/4697	0.74	2/6348 (0.0%)
8	c	0.34	0/1235	0.72	0/1664
All	All	0.36	5/129161 (0.0%)	0.77	134/174623 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
1	2	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
1	Y	0	1
1	Z	0	1
3	C	0	1
3	E	0	2
3	G	0	2
3	M	0	5
4	B	0	1
4	N	0	4
4	f	0	3
4	h	0	1
6	I	0	2
6	K	0	3
7	J	0	5
8	L	0	1
All	All	0	44

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	e	243	PRO	N-CD	16.99	1.71	1.47
3	M	404	TYR	CD1-CE1	9.59	1.67	1.38
2	e	257	CYS	C-N	7.31	1.39	1.33
3	M	404	TYR	CD2-CE2	5.61	1.55	1.38
4	N	405	LYS	CG-CD	5.23	1.68	1.52

The worst 5 of 134 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	108	PRO	CA-N-CD	-9.93	98.10	112.00
4	D	418	ILE	N-CA-C	-9.68	104.06	111.90
4	j	108	PRO	CA-N-CD	-9.41	98.82	112.00
7	l	121	PRO	CA-N-CD	-8.99	99.41	112.00
4	h	108	PRO	CA-N-CD	-8.66	99.87	112.00

There are no chirality outliers.

5 of 44 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	352	GLY	Peptide
1	2	352	GLY	Peptide
4	B	740	GLN	Peptide
3	C	238	LEU	Peptide
3	G	240	GLY	Peptide

5.2 Too-close contacts ⓘ

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	3373	0	3325	74	0
1	2	3373	0	3325	78	0
1	O	3373	0	3325	69	0
1	P	3373	0	3325	67	0
1	Q	3373	0	3325	53	0
1	R	3373	0	3325	61	0
1	S	3373	0	3325	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	3373	0	3325	60	0
1	U	3373	0	3325	60	0
1	V	3373	0	3325	57	0
1	W	3373	0	3325	58	0
1	X	3373	0	3325	63	0
1	Y	3373	0	3325	73	0
1	Z	3373	0	3325	69	0
2	e	2847	0	2810	68	0
3	A	4978	0	4996	61	0
3	C	5044	0	5081	40	0
3	E	5216	0	5248	48	0
3	G	5216	0	5246	81	0
3	M	5186	0	5219	65	0
4	B	5029	0	5018	74	0
4	D	4796	0	4775	50	0
4	F	4941	0	4935	64	0
4	H	4907	0	4896	50	0
4	N	4907	0	4896	74	0
4	a	933	0	953	16	0
4	f	863	0	896	53	0
4	h	863	0	896	32	0
4	j	863	0	896	27	0
5	b	484	0	512	13	0
5	d	454	0	482	10	0
5	g	484	0	512	13	0
5	i	484	0	512	25	0
5	k	484	0	512	20	0
5	m	484	0	512	18	0
6	I	4225	0	4259	41	0
6	K	4579	0	4586	48	0
7	J	4429	0	4482	46	0
7	l	875	0	842	36	0
8	L	4587	0	4636	36	0
8	c	1220	0	1231	13	0
All	All	126600	0	126389	1819	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 7.

The worst 5 of 1819 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)
5:i:34:ILE:CG2	4:h:110:LYS:HE2	1.31	1.58
4:f:66:ARG:CD	4:f:106:ARG:HE	1.25	1.45
3:G:876:ARG:HH22	4:j:39:ILE:CA	1.30	1.42
3:G:876:ARG:NH2	4:j:39:ILE:HA	1.36	1.40
5:i:34:ILE:HG21	4:h:110:LYS:CE	1.56	1.32

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	408/451 (90%)	382 (94%)	26 (6%)	0	100	100
1	2	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	O	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	P	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	Q	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	R	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	S	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	T	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	U	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	V	408/451 (90%)	383 (94%)	25 (6%)	0	100	100
1	W	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	X	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	Y	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	Z	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
2	e	360/375 (96%)	340 (94%)	20 (6%)	0	100	100
3	A	599/902 (66%)	567 (95%)	32 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	606/902 (67%)	563 (93%)	42 (7%)	1 (0%)	43	78
3	E	628/902 (70%)	594 (95%)	32 (5%)	2 (0%)	36	72
3	G	628/902 (70%)	591 (94%)	33 (5%)	4 (1%)	21	59
3	M	624/902 (69%)	590 (95%)	32 (5%)	2 (0%)	36	72
4	B	602/907 (66%)	581 (96%)	19 (3%)	2 (0%)	36	72
4	D	571/907 (63%)	554 (97%)	17 (3%)	0	100	100
4	F	591/907 (65%)	566 (96%)	25 (4%)	0	100	100
4	H	584/907 (64%)	563 (96%)	20 (3%)	1 (0%)	43	78
4	N	584/907 (64%)	553 (95%)	28 (5%)	3 (0%)	24	63
4	a	112/907 (12%)	107 (96%)	5 (4%)	0	100	100
4	f	105/907 (12%)	97 (92%)	5 (5%)	3 (3%)	3	23
4	h	105/907 (12%)	97 (92%)	6 (6%)	2 (2%)	6	32
4	j	105/907 (12%)	98 (93%)	6 (6%)	1 (1%)	12	49
5	b	63/82 (77%)	60 (95%)	3 (5%)	0	100	100
5	d	57/82 (70%)	56 (98%)	1 (2%)	0	100	100
5	g	63/82 (77%)	61 (97%)	2 (3%)	0	100	100
5	i	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
5	k	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
5	m	63/82 (77%)	63 (100%)	0	0	100	100
6	I	511/667 (77%)	487 (95%)	20 (4%)	4 (1%)	16	54
6	K	548/667 (82%)	534 (97%)	12 (2%)	2 (0%)	30	67
7	J	506/1024 (49%)	473 (94%)	30 (6%)	3 (1%)	21	59
7	l	104/1024 (10%)	100 (96%)	2 (2%)	2 (2%)	6	32
8	L	540/1819 (30%)	504 (93%)	33 (6%)	3 (1%)	21	59
8	c	148/1819 (8%)	140 (95%)	8 (5%)	0	100	100
All	All	15245/26874 (57%)	14424 (95%)	774 (5%)	47 (0%)	37	72

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	871	GLU
3	G	241	ARG
6	I	408	ASP

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Mol	Chain	Res	Type
6	I	508	ASN
7	J	236	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	376/400 (94%)	317 (84%)	59 (16%)	2	12
1	2	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	O	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	P	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	Q	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	R	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	S	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	T	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	U	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	V	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	W	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	X	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	Y	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	Z	376/400 (94%)	319 (85%)	57 (15%)	3	12
2	e	310/318 (98%)	304 (98%)	6 (2%)	50	67
3	A	549/791 (69%)	543 (99%)	6 (1%)	65	76
3	C	556/791 (70%)	555 (100%)	1 (0%)	87	87
3	E	575/791 (73%)	570 (99%)	5 (1%)	70	79
3	G	575/791 (73%)	575 (100%)	0	100	100
3	M	572/791 (72%)	566 (99%)	6 (1%)	68	78
4	B	551/798 (69%)	546 (99%)	5 (1%)	70	79
4	D	525/798 (66%)	522 (99%)	3 (1%)	78	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	F	542/798 (68%)	538 (99%)	4 (1%)	76	81
4	H	539/798 (68%)	531 (98%)	8 (2%)	57	72
4	N	539/798 (68%)	531 (98%)	8 (2%)	57	72
4	a	101/798 (13%)	100 (99%)	1 (1%)	68	78
4	f	96/798 (12%)	96 (100%)	0	100	100
4	h	96/798 (12%)	96 (100%)	0	100	100
4	j	96/798 (12%)	96 (100%)	0	100	100
5	b	53/62 (86%)	52 (98%)	1 (2%)	50	67
5	d	53/62 (86%)	53 (100%)	0	100	100
5	g	53/62 (86%)	53 (100%)	0	100	100
5	i	53/62 (86%)	53 (100%)	0	100	100
5	k	53/62 (86%)	52 (98%)	1 (2%)	50	67
5	m	53/62 (86%)	53 (100%)	0	100	100
6	I	472/594 (80%)	467 (99%)	5 (1%)	65	76
6	K	509/594 (86%)	504 (99%)	5 (1%)	68	78
7	J	498/933 (53%)	493 (99%)	5 (1%)	68	78
7	l	96/933 (10%)	96 (100%)	0	100	100
8	L	501/1546 (32%)	496 (99%)	5 (1%)	68	78
8	c	135/1546 (9%)	134 (99%)	1 (1%)	76	81
All	All	14015/23573 (60%)	13139 (94%)	876 (6%)	18	37

5 of 876 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	367	LEU
1	U	343	ARG
1	Y	337	LEU
1	T	66	LEU
1	S	361	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 379 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	207	ASN

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Mol	Chain	Res	Type
1	U	198	ASN
1	Q	16	GLN
1	R	394	GLN
1	V	227	GLN

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.

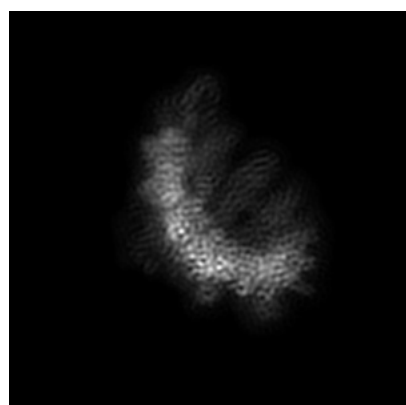
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14010. These allow visual inspection of the internal detail of the map and identification of artifacts.

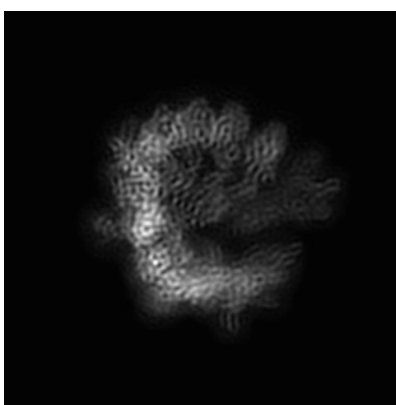
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

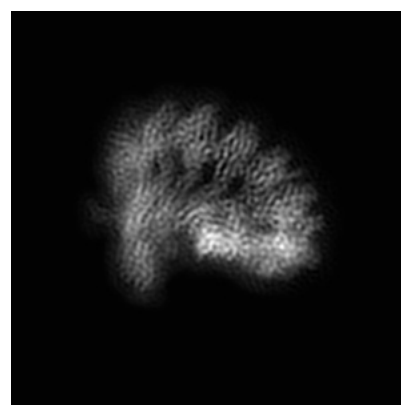
6.1.1 Primary map



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: 100



Y Index: 100



Z Index: 100

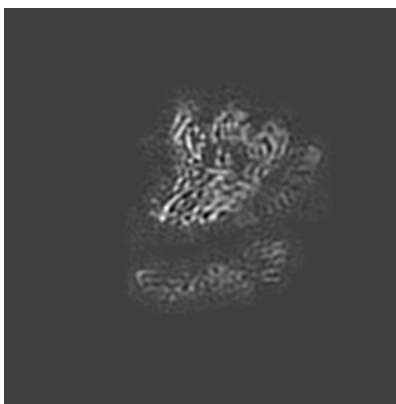
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

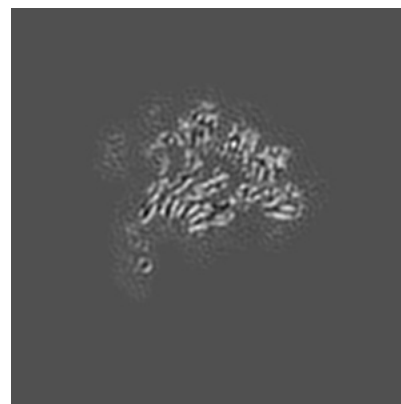
6.3.1 Primary map



X Index: 134



Y Index: 82

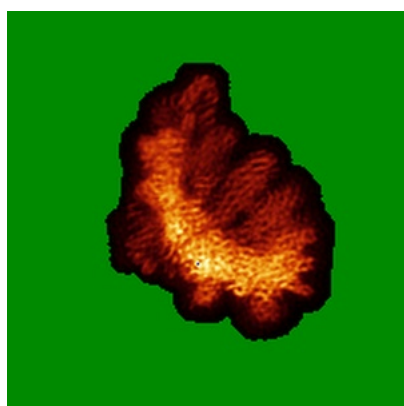


Z Index: 72

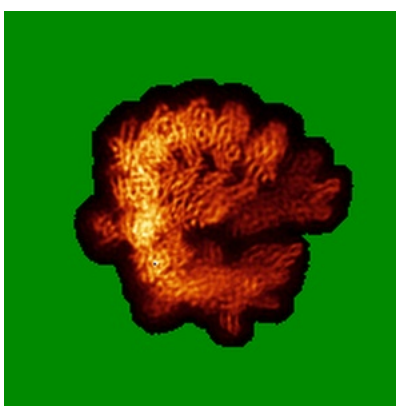
The images above show the largest variance slices of the map in three orthogonal directions.

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

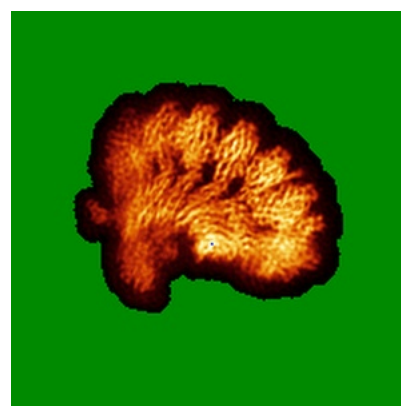
6.4.1 Primary map



X



Y

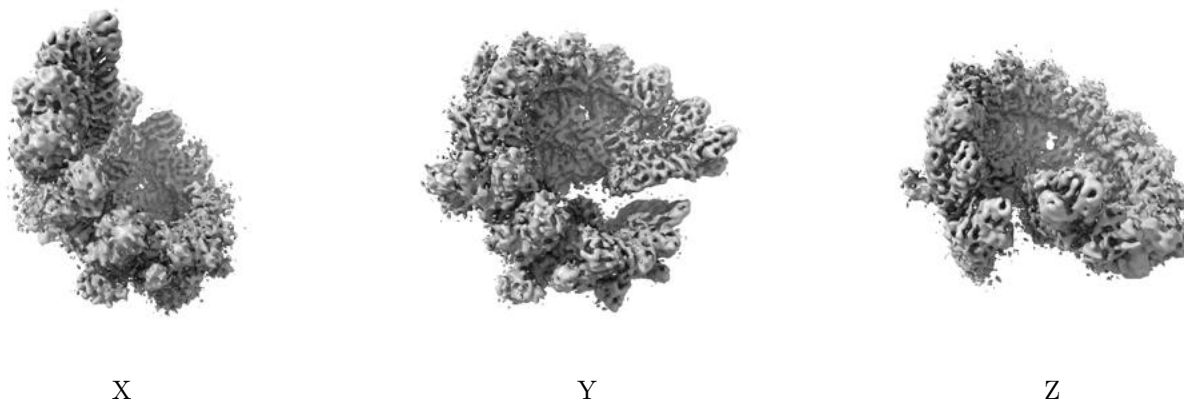


Z

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 0.0224. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

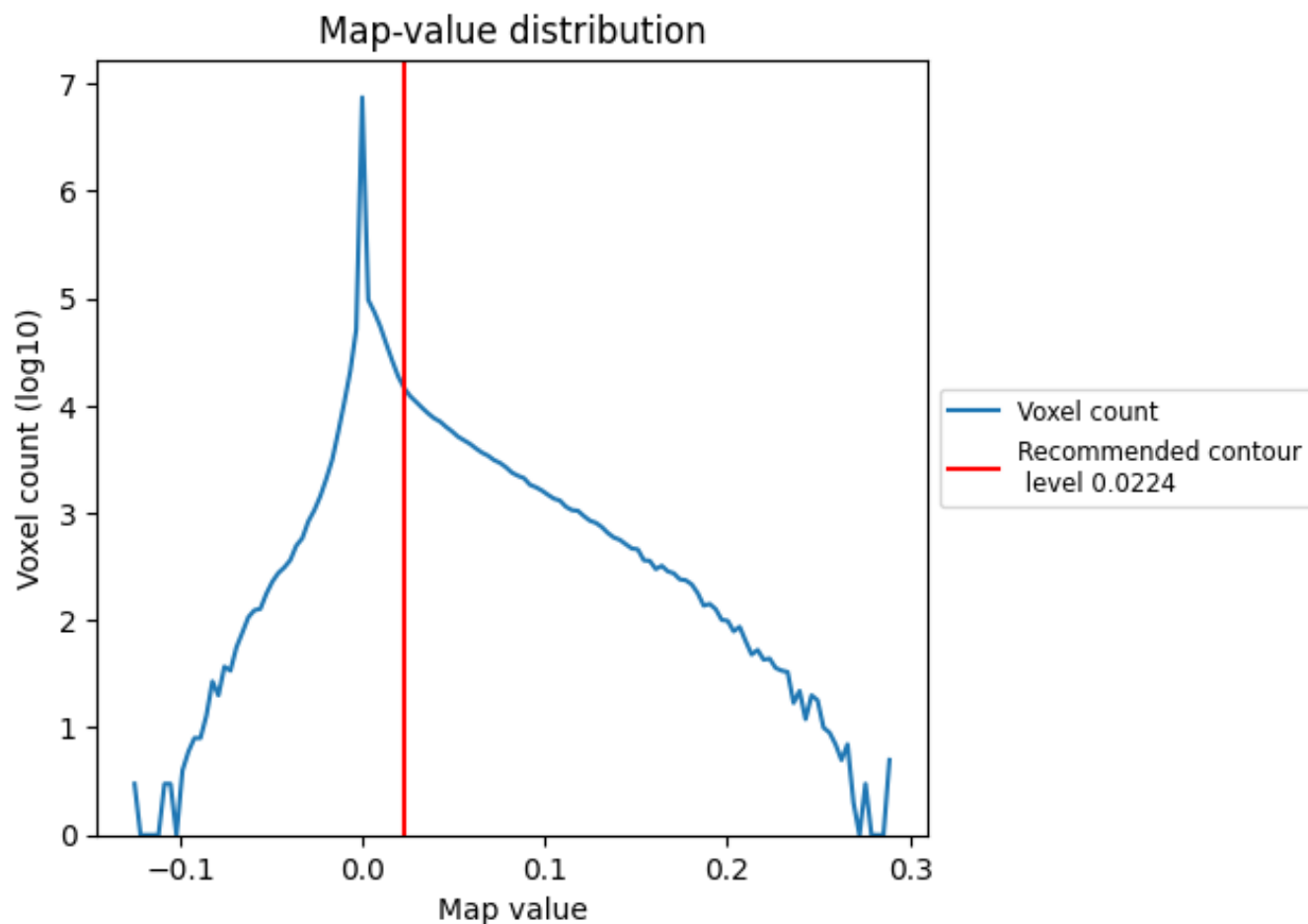
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

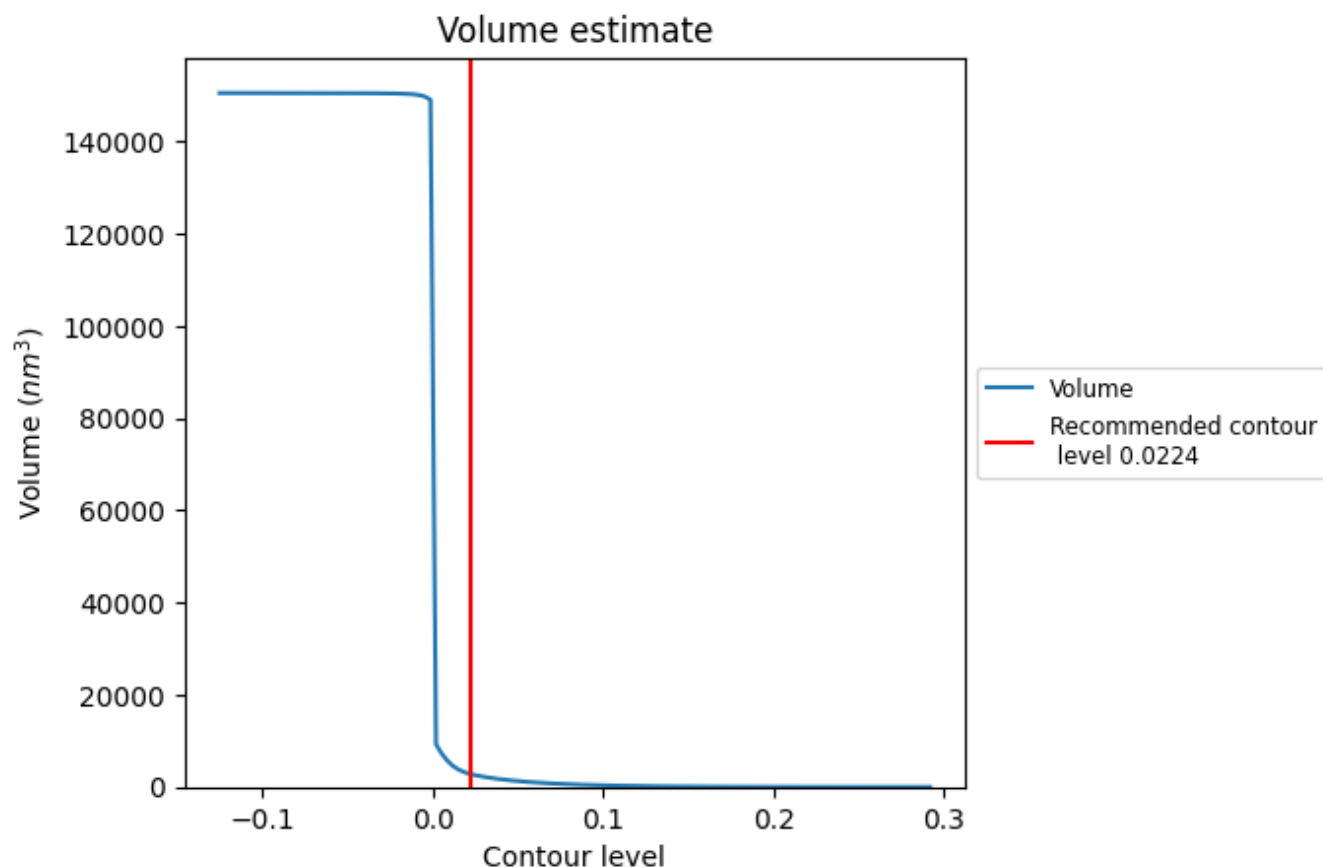
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

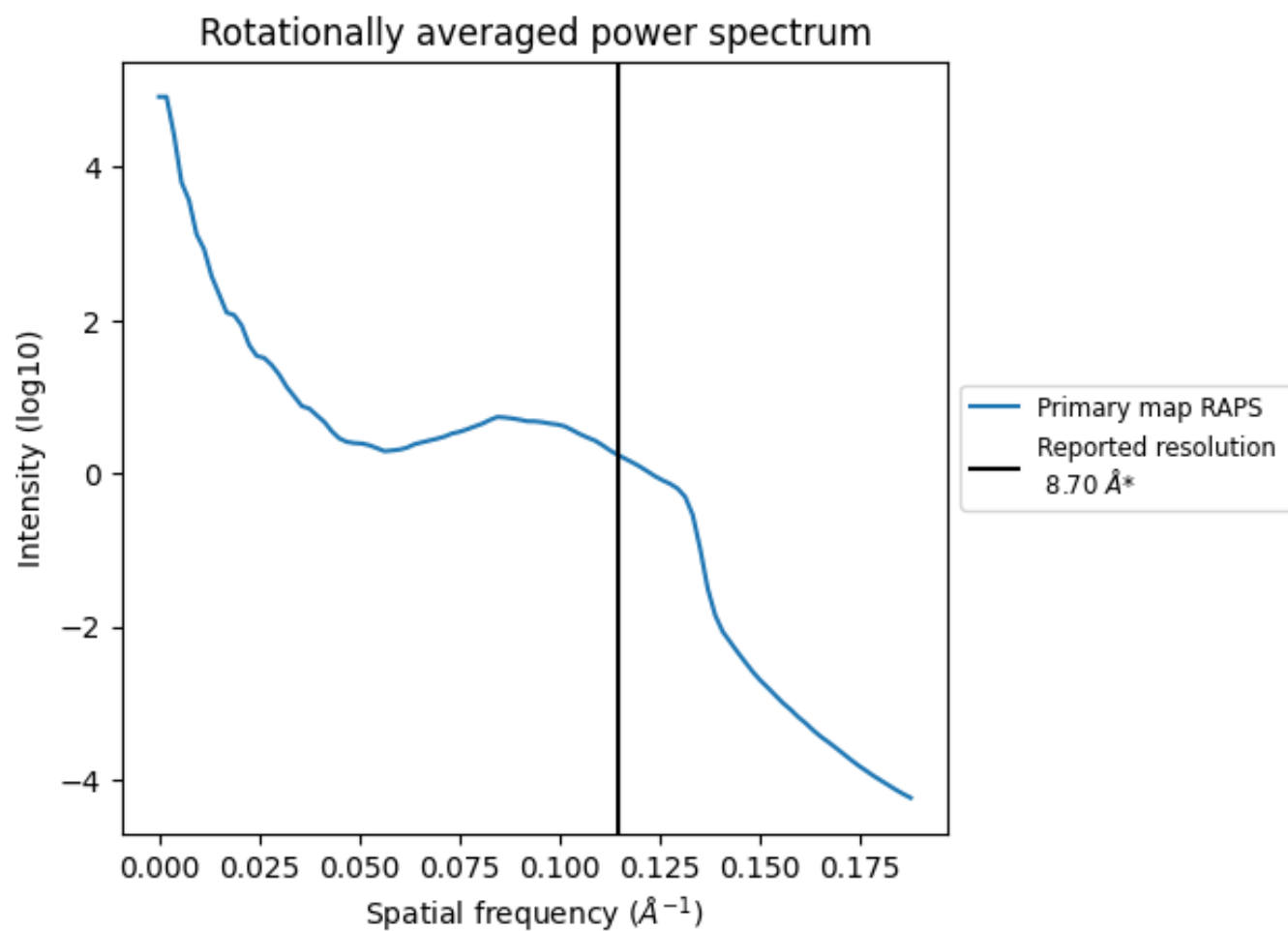
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2805 nm³; this corresponds to an approximate mass of 2533 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 0.115 Å⁻¹

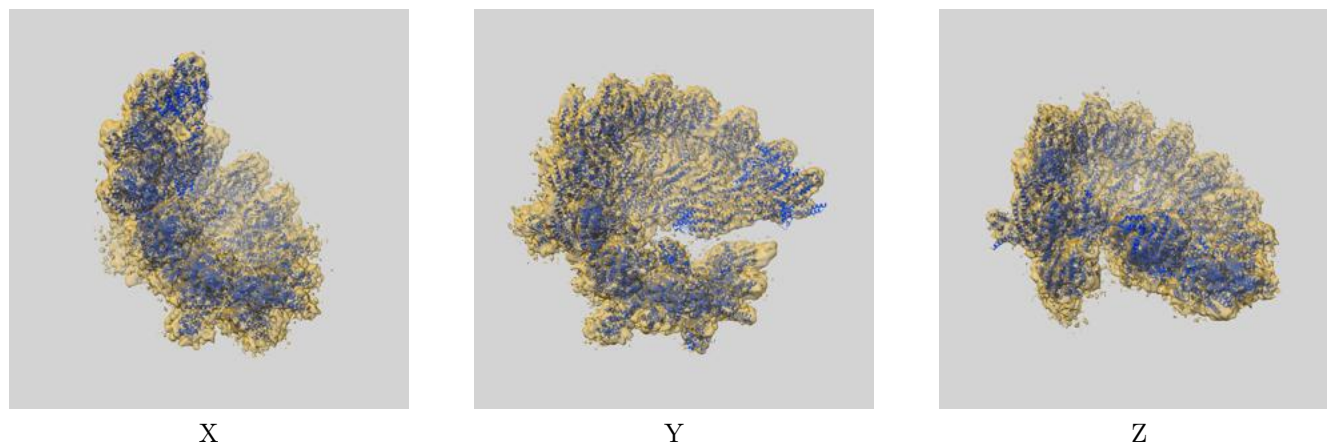
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

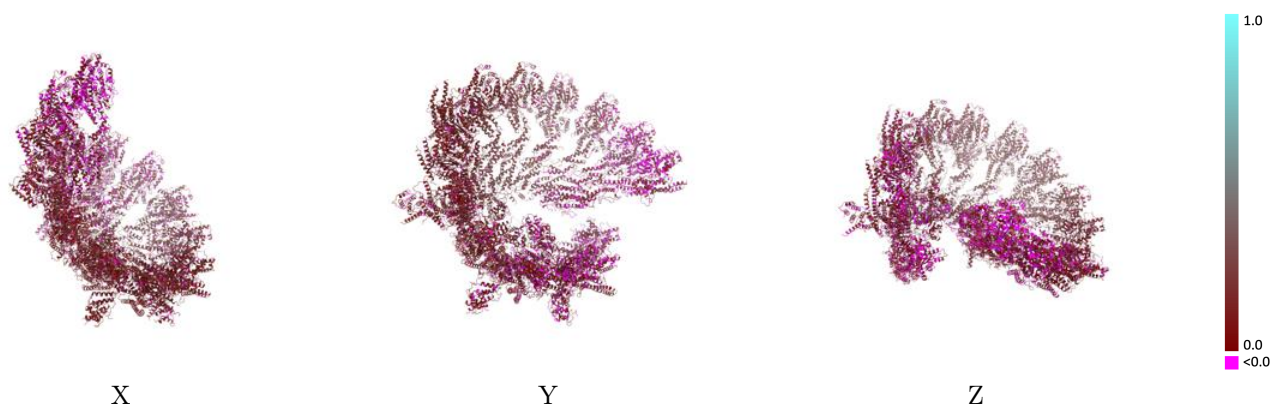
This section contains information regarding the fit between EMDB map EMD-14010 and PDB model 7QJ5. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



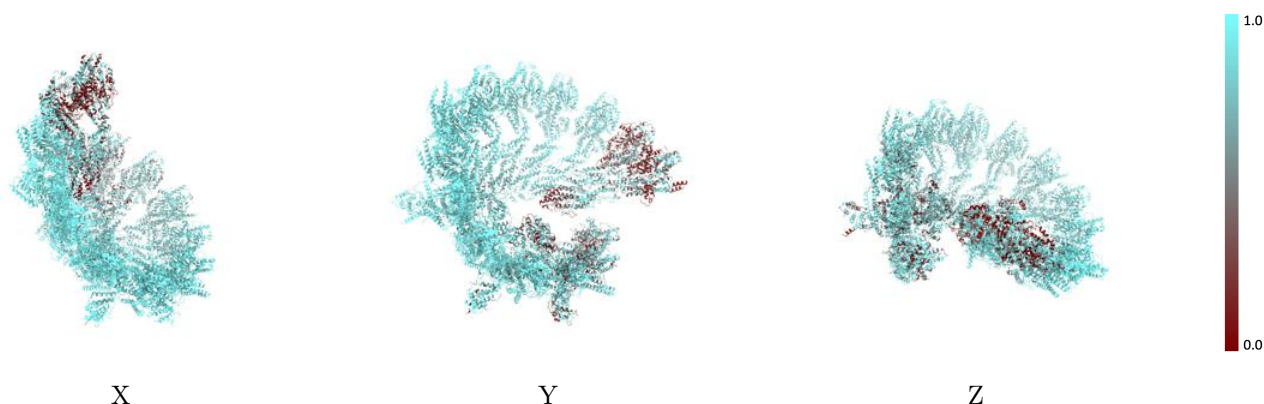
The images above show the 3D surface view of the map at the recommended contour level 0.0224 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



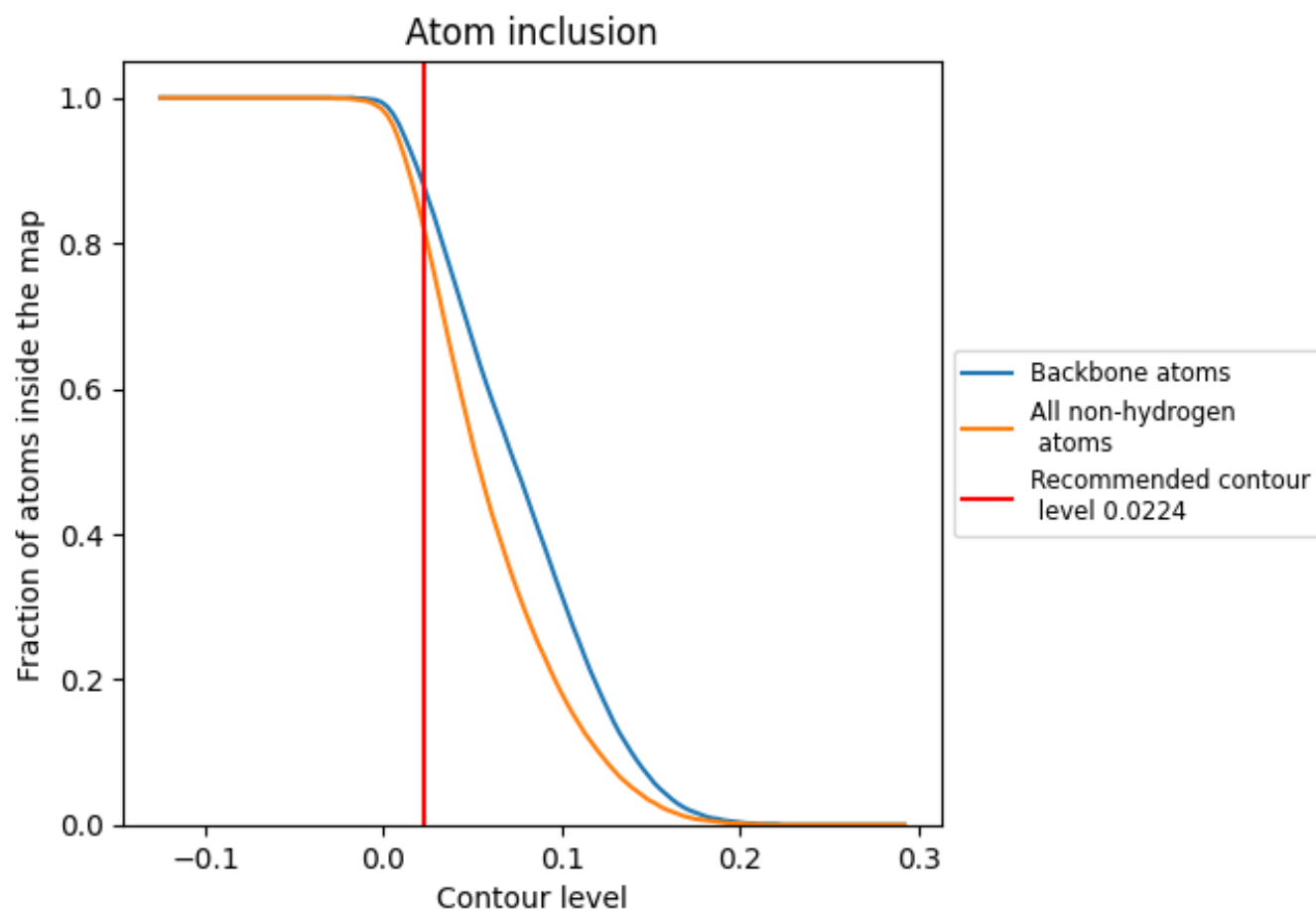
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0224).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0224) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8230	 0.1190
1	 0.3540	 0.0160
2	 0.4000	 -0.0000
A	 0.7820	 0.0960
B	 0.7620	 0.1100
C	 0.9150	 0.1170
D	 0.9000	 0.1300
E	 0.9260	 0.1530
F	 0.9330	 0.1510
G	 0.9410	 0.1620
H	 0.9340	 0.1600
I	 0.9380	 0.1660
J	 0.9370	 0.1670
K	 0.9470	 0.1550
L	 0.9560	 0.1360
M	 0.5690	 0.0680
N	 0.5640	 0.0650
O	 0.5910	 0.0360
P	 0.6120	 0.0570
Q	 0.7610	 0.0590
R	 0.8860	 0.1090
S	 0.9230	 0.1450
T	 0.9310	 0.1460
U	 0.9270	 0.1470
V	 0.9360	 0.1650
W	 0.9420	 0.1550
X	 0.9420	 0.1510
Y	 0.9580	 0.1350
Z	 0.9220	 0.1080
a	 0.8720	 0.1550
b	 0.9080	 0.1770
c	 0.8290	 0.1480
d	 0.8050	 0.1460
e	 0.5710	 0.0840
f	 0.6160	 0.0880



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Chain	Atom inclusion	Q-score
g	 0.5860	 0.0680
h	 0.8390	 0.1160
i	 0.7980	 0.0960
j	 0.9310	 0.1400
k	 0.9540	 0.1570
l	 0.9240	 0.1630
m	 0.9410	 0.1620