



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 08:02 PM UTC

PDB ID : 7QJ4 / pdb_00007qj4
EMDB ID : EMD-14009
Title : Structure of recombinant human gamma-Tubulin Ring Complex 10-spoked assembly intermediate (spokes 5-14)
Authors : Zupa, E.; Pfeffer, S.
Deposited on : 2021-12-16
Resolution : 9.00 Å (reported)
Based on initial models : 6V6S, 6L81, 6X0U, 7AS4

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:

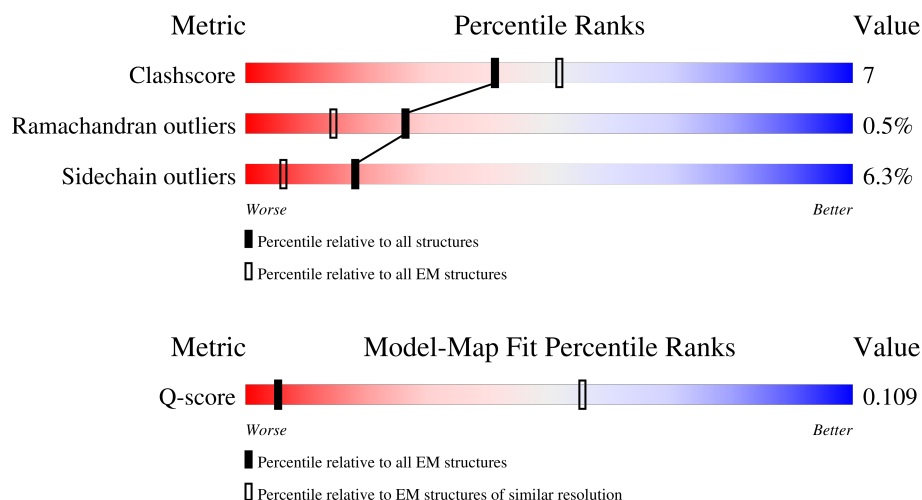
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.00 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	257 (8.50 - 9.50)

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	1	451	64% 64% 23% 6% 7%
1	2	451	80% 64% 23% 6% 7%
1	S	451	85% 64% 23% 6% 7%
1	T	451	53% 64% 23% 6% 7%

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Mol	Chain	Length	Quality of chain
1	U	451	
1	V	451	
1	W	451	
1	X	451	
1	Y	451	
1	Z	451	
2	J	1024	
2	l	1024	
3	F	907	
3	H	907	
3	N	907	
3	a	907	
3	j	907	
3	n	907	
4	b	82	
4	k	82	
4	m	82	
4	o	82	
5	E	902	
5	G	902	
5	M	902	
6	I	667	
6	K	667	
7	L	1819	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 87259 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	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 Gamma-tubulin complex component 5.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	n	99	Total	C	N	O	S	0	0
			803	509	148	144	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	599	Total	C	N	O	S	0	0
			4941	3151	871	894	25		
3	H	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
3	N	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
3	j	99	Total	C	N	O	S	0	0
			803	509	148	144	2		
3	a	116	Total	C	N	O	S	0	0
			933	591	171	169	2		

- Molecule 4 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	o	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
4	m	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
4	k	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
4	b	65	Total	C	N	O	S	0	0
			484	299	85	96	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	638	Total	C	N	O	S	0	0
			5202	3354	873	942	33		
5	G	640	Total	C	N	O	S	0	0
			5216	3359	878	946	33		
5	M	636	Total	C	N	O	S	0	0
			5186	3342	871	940	33		

- 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		

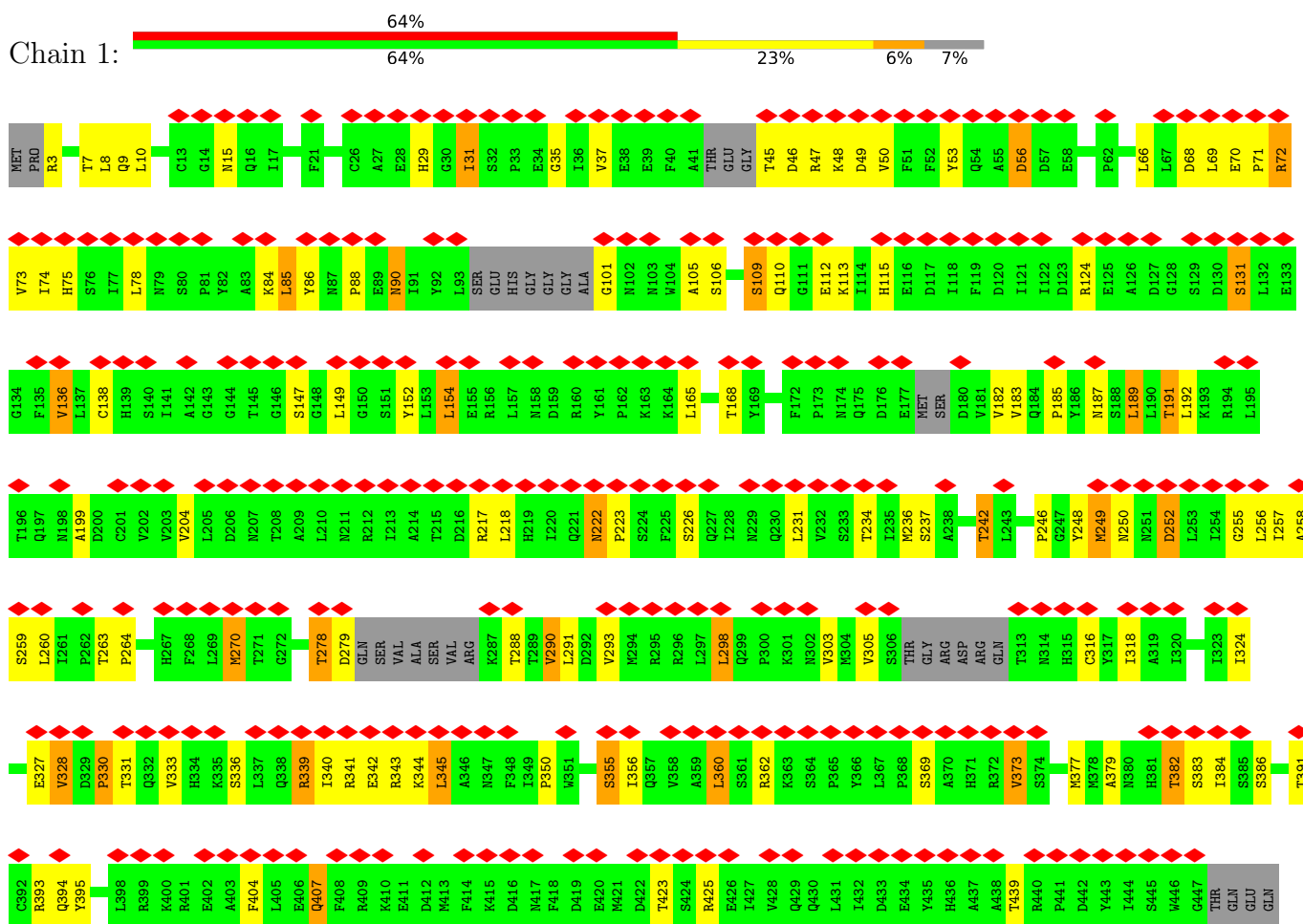
- Molecule 7 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	566	Total	C	N	O	S	0	0
			4587	3000	773	789	25		

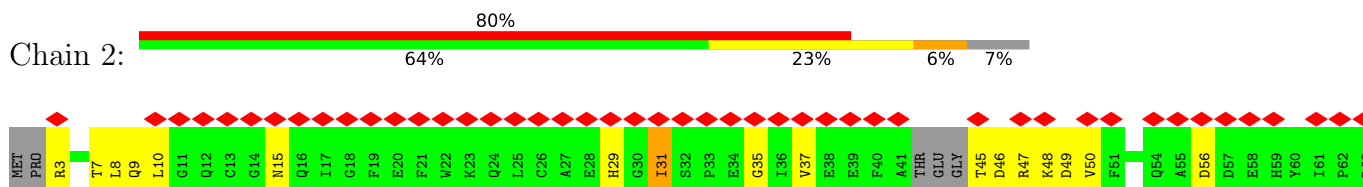
3 Residue-property plots

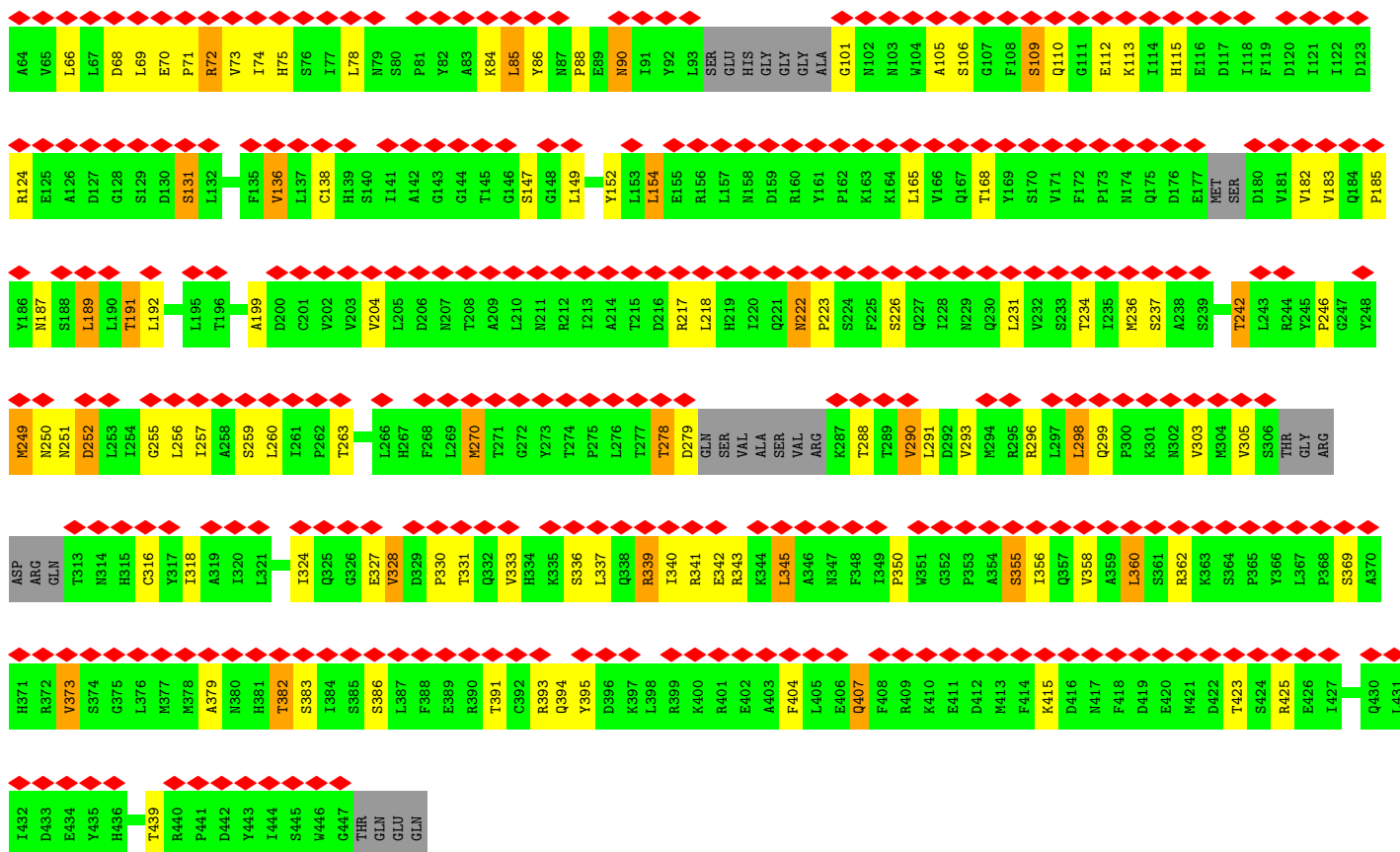
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

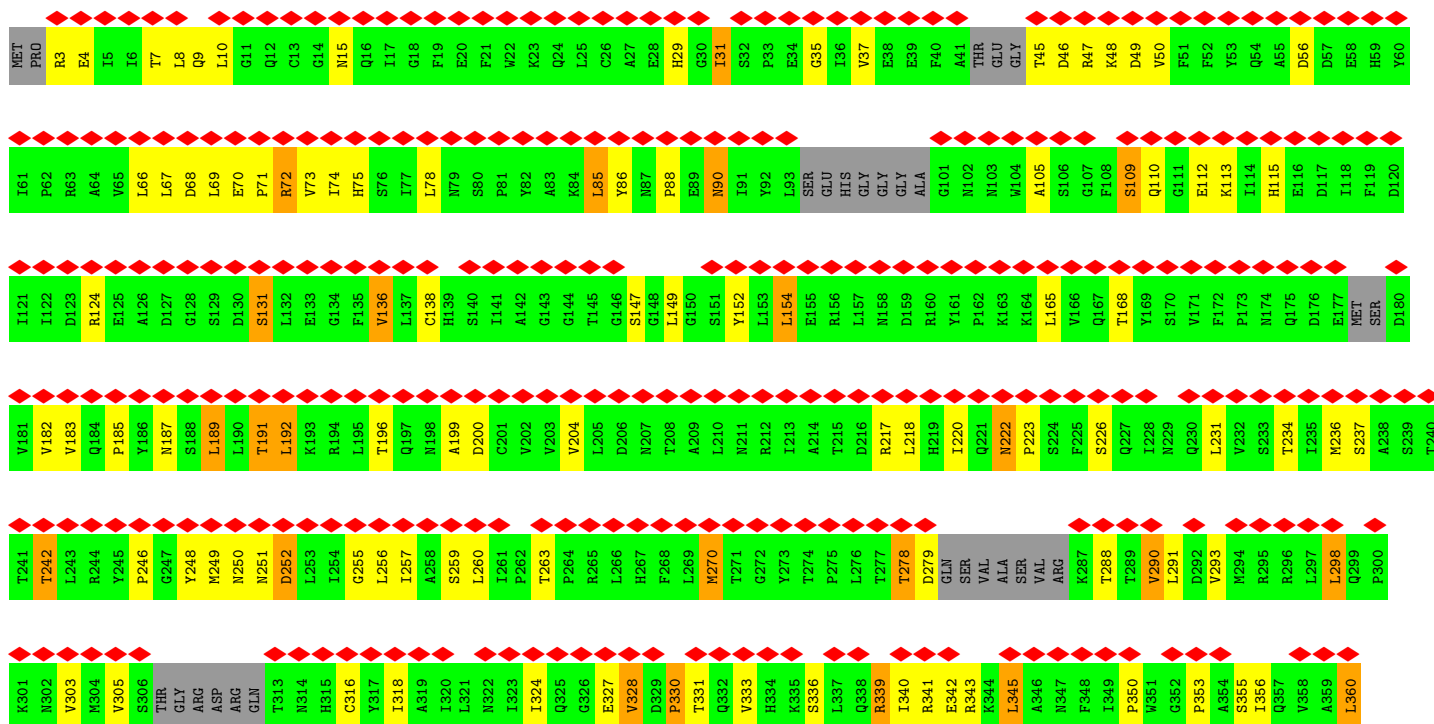
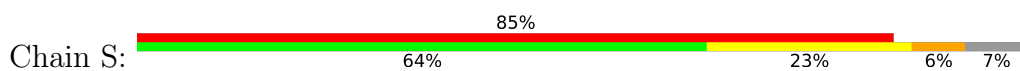


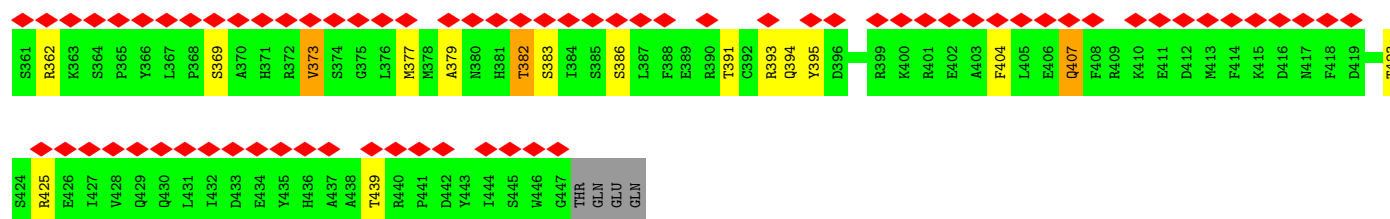
- Molecule 1: Tubulin gamma-1 chain



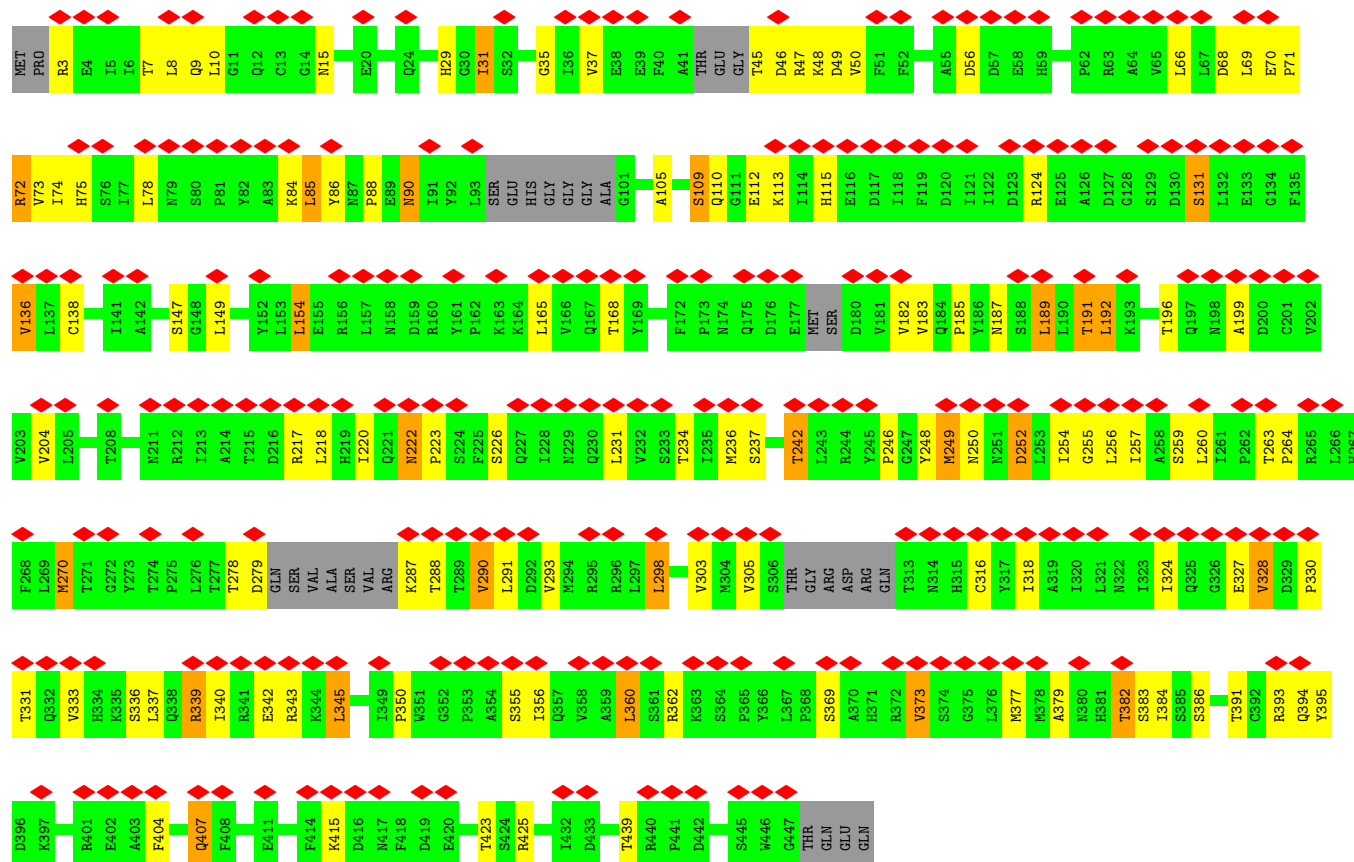


• Molecule 1: Tubulin gamma-1 chain

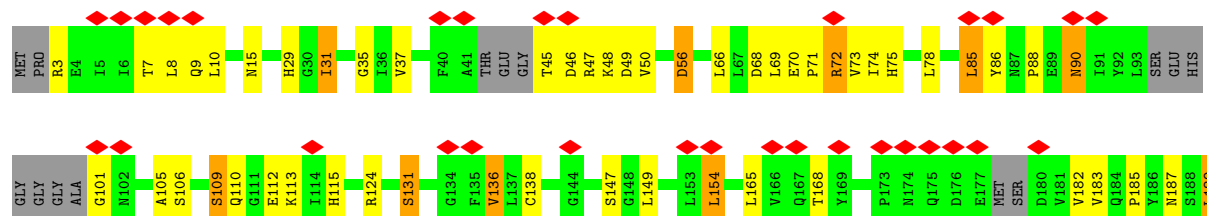


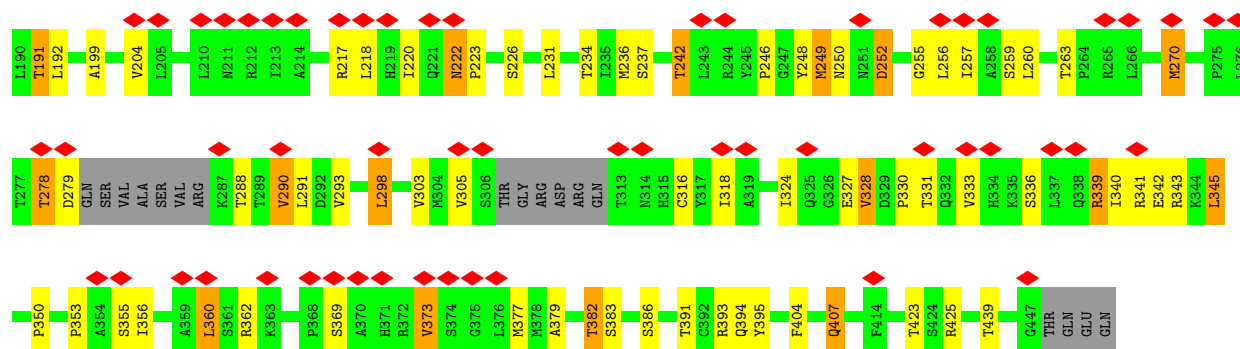


• Molecule 1: Tubulin gamma-1 chain

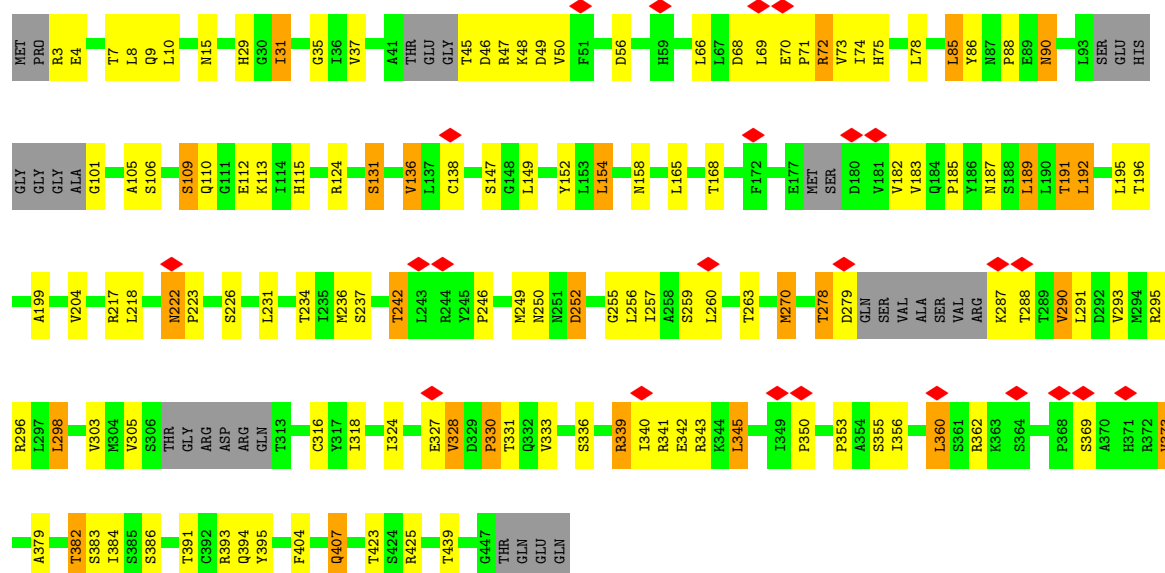


• Molecule 1: Tubulin gamma-1 chain

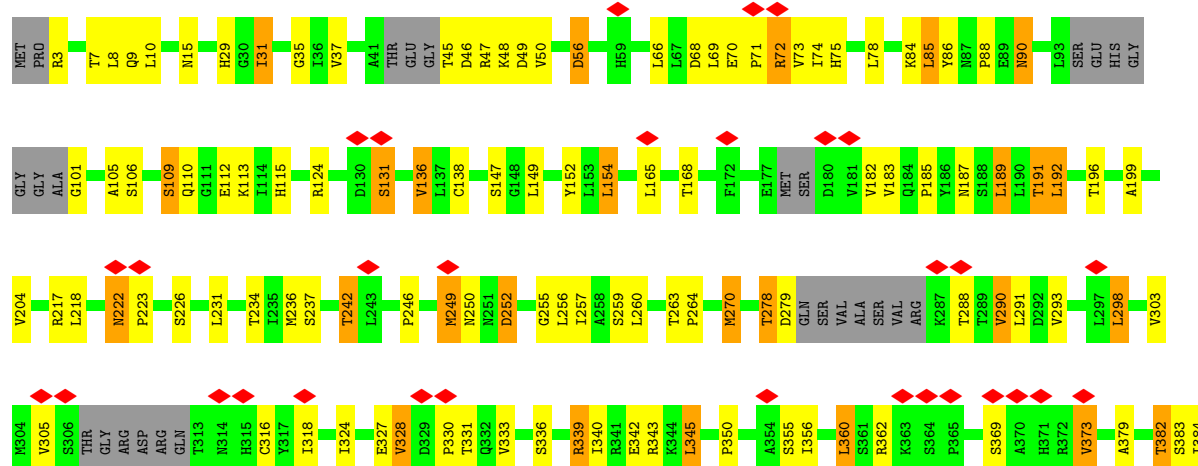


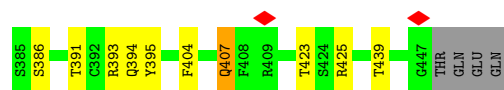


• Molecule 1: Tubulin gamma-1 chain



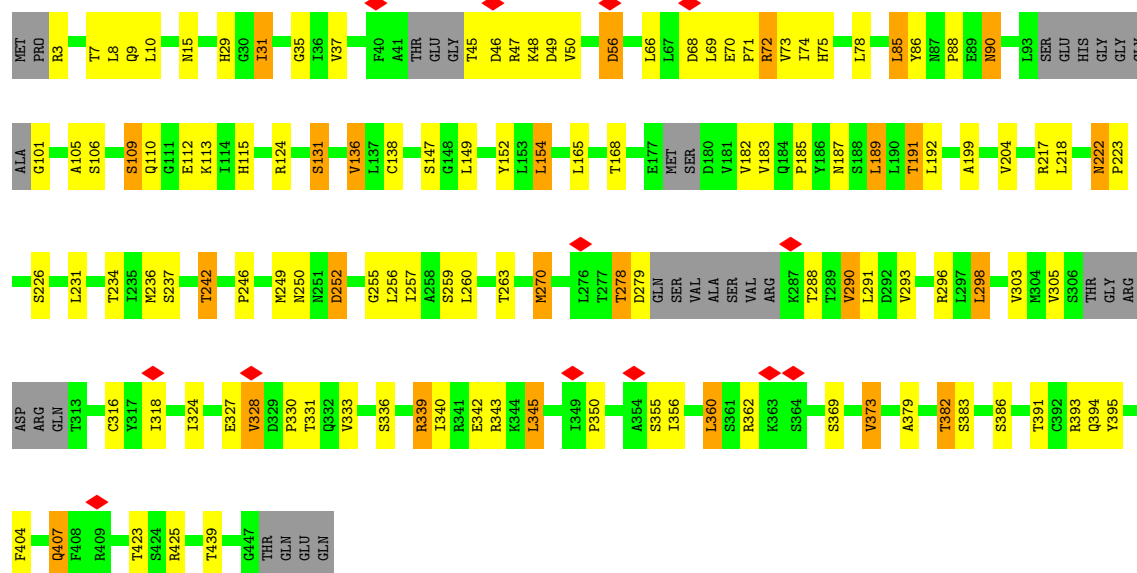
• Molecule 1: Tubulin gamma-1 chain





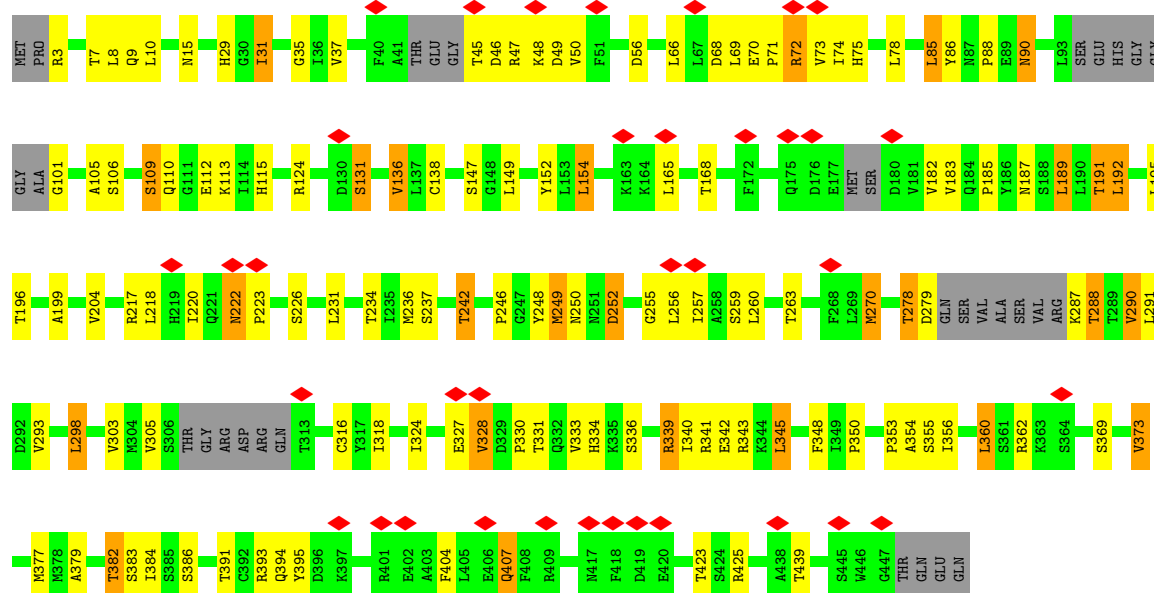
• Molecule 1: Tubulin gamma-1 chain

Chain X: 66% 22% 6% 7%



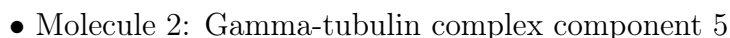
• Molecule 1: Tubulin gamma-1 chain

Chain Y: 8% 63% 24% 6% 7%

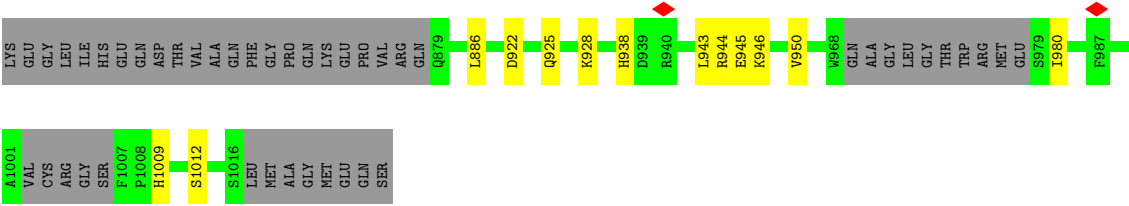


• Molecule 1: Tubulin gamma-1 chain

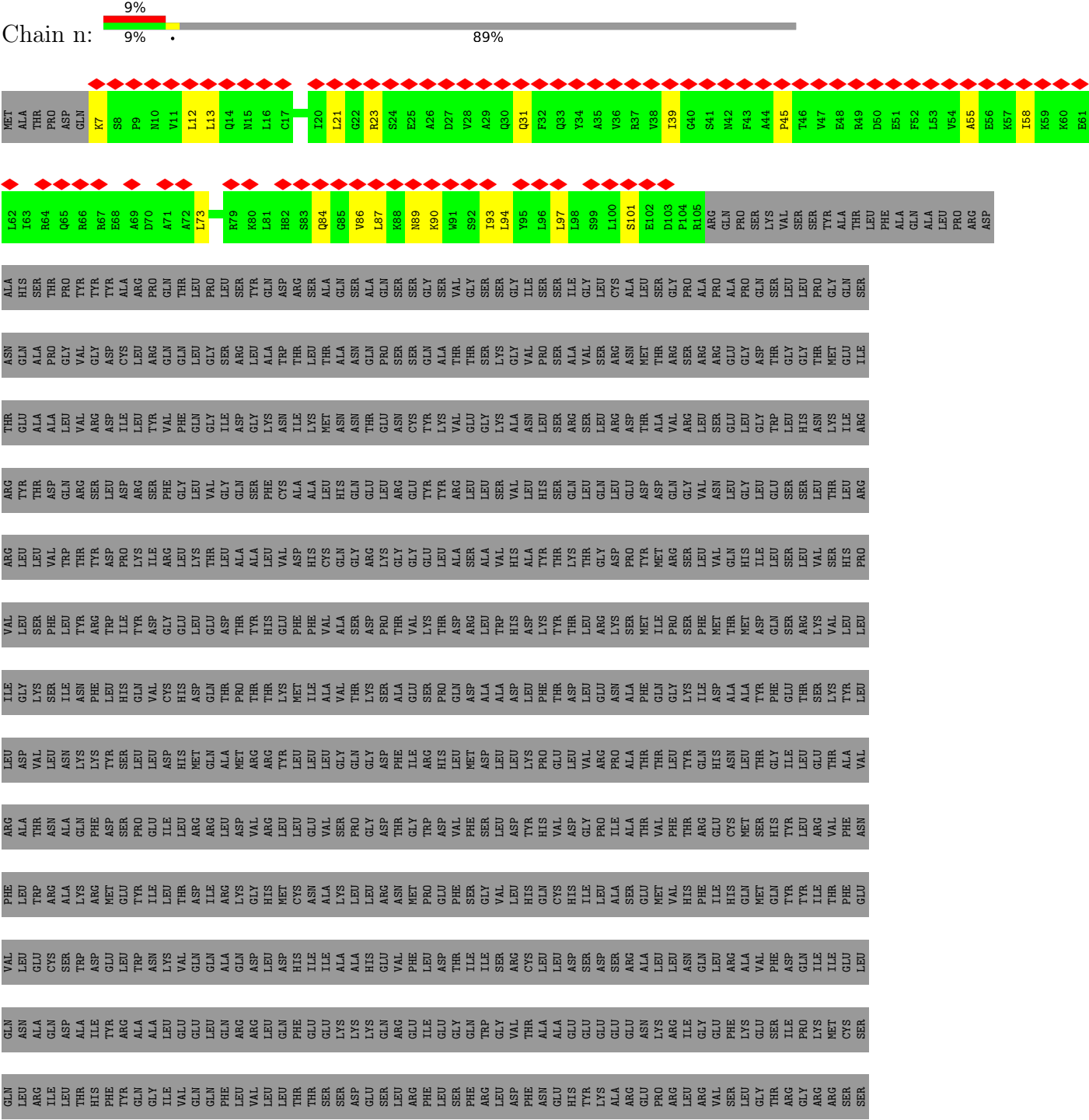
Chain Z: 15% 64% 23% 6% 7%

[illegible]





• Molecule 3: Gamma-tubulin complex component 3



- Molecule 3: Gamma-tubulin complex component 3

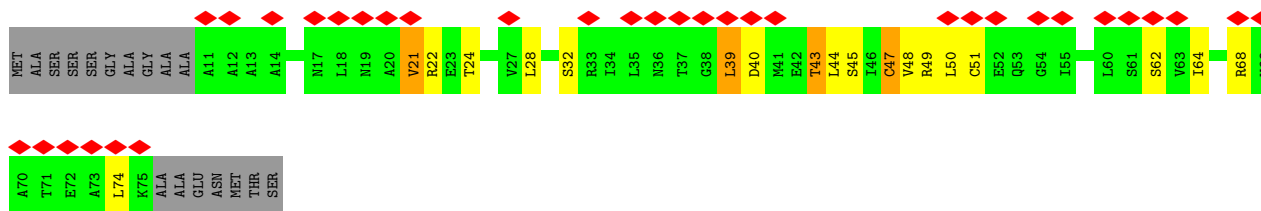


GLU	E827	T833	F836	K837	T857	L862	S868	F878	R879	F882	N883	E884	H885	Y886	K887	A888	H889	PRO	ARG	LEU	ARG	VAL	SER	LEU	GLY	THR	ARG	GLY	ARG	ARG	SER	SER	HIS	THR	VAL	THR	GLY	GLY	TRP	GLY	GLY	GLY	ARG	GLU	ARG	GLN	GLN	ARG	GLU	GLY	THR	PRO	GLY	LEU	PRO	ALA	LEU	GLU	MET																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
R365	R366	L367	L368	T380	H387	C388	Q389	R391	A397	S398	A399	V400	P409	V410	H411	R412	L419	V422	R432	W433	L439	V448	T456	L466	R467	R468	I471	P472	S473	F474	L484	G487	L493	T501	V505	MET	ILE	ALA	VAL	THR	LYS	PHE	LEU	THR	ALA	TYR	PRO	GLY	SER	VAL	LEU	LYS	ASP	GLN	PRO	ARG	GLN	THR	ARG	GLY	PRO	ASP	GLN	THR	PRO	GLY	LEU	ALA	LEU	GLU	MET																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
GLY	THR	MET	GLU	T245	D253	T266	N269	N270	C274	Y275	K276	V277	E278	GLY	LYS	ALA	ASN	LEU	SER	R285	R288	A291	L294	K303	S312	F324	L332	Y335	Y336	Q347	LEU	GLU	ASP	GLN	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

• Molecule 3: Gamma-tubulin complex component 3



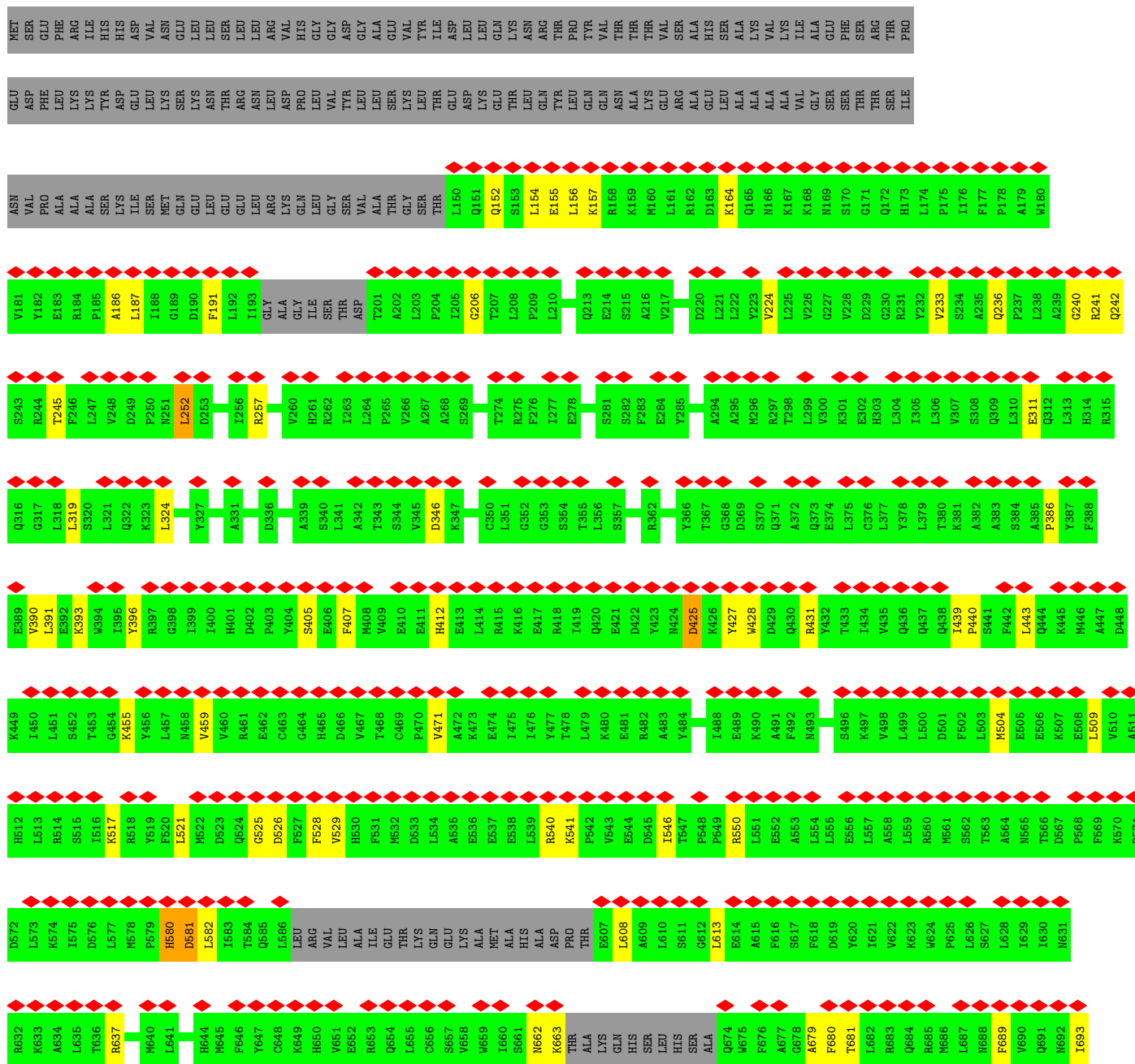
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GLY	THR	MET	GLU	T245	T246	E247	A248	A249	L250	I254	G260	I261	D262	G263	K264	N265	I266	K267	M268	N269	N270	T271	C274	Y275	K276	V277	E278	GLY	LYS	ALA	ASN	LEU	SER	R285	S286	L287	R288	V292	R293	L294	L297	G298	W299	L300	H301	N302	K303	I304	R305	R306	T307	T308	D309	Q310
PRO	GLY	GLN	SER	ASN	GLN	ALA	PRO	GLY	VAL	GLY	ARG	GLN	GLN	GLY	SER	ARG	LEU	THR	TRP	THR	THR	ASN	GLN	PRO	SER	GLY	THR	SER	LYS	GLY	VAL	PRO	SER	SER	ALA	VAL	SER	ARG	ASN	MET	THR	ARG	SER	ARG	ARG	ARG	GLU	GLY	ASP	THR	GLY			
ALA	LEU	PRO	ARG	ASP	HIS	THR	THR	PRO	TYR	TYR	PRO	THR	GLN	THR	ASP	GLN	LEU	PRO	ARG	SER	TYR	GLN	ALA	GLN	SER	VAL	GLY	SER	SER	ILE	GLY	CYS	ALA	PRO	ALA	VAL	LEU	LYS	VAL	SER	GLY	THR	ALA	GLU	LEU	ALA	GLN	LEU						
MET	ALA	THR	PRO	GLN	LYS	SER	PRO	ALA	ASN	VAL	LEU	CYS	GLN	CYS	GLY	ARG	LEU	GLY	THR	THR	THR	ASN	GLN	ALA	GLN	VAL	LEU	LEU	ILE	SER	GLY	GLN	VAL	ARG	ASP	GLU	ASP	GLY	THR	VAL	LEU	GLY	THR	ALA	GLN	LYS	LYS							

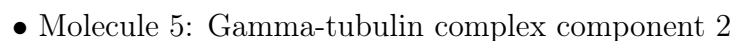


• Molecule 5: Gamma-tubulin complex component 2



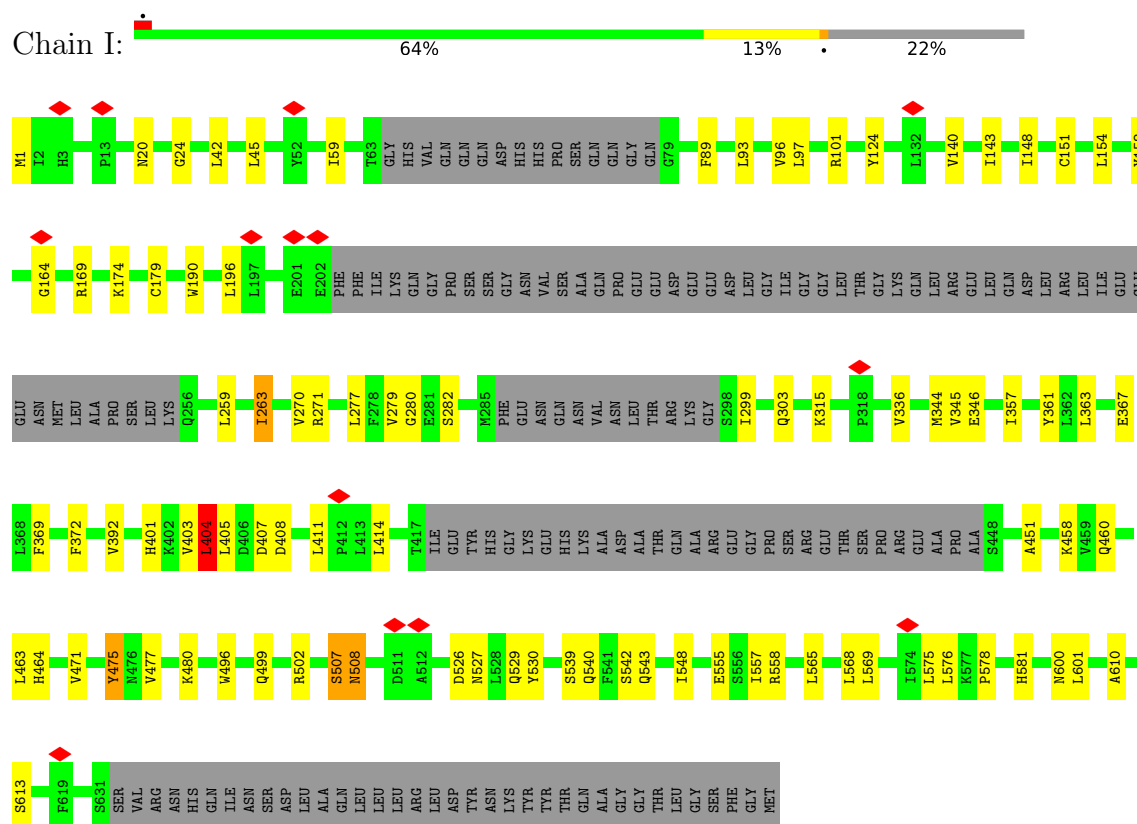
Chain E:



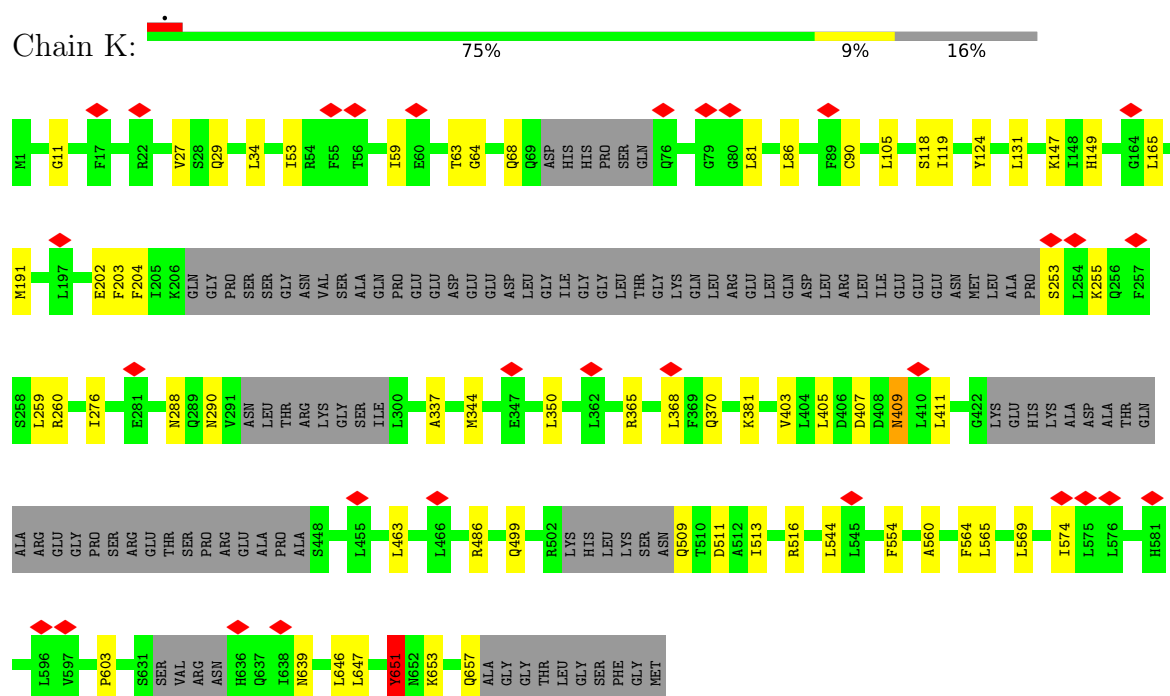




- Molecule 6: Gamma-tubulin complex component 4



- Molecule 6: Gamma-tubulin complex component 4



- Molecule 7: Gamma-tubulin complex component 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6097	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	0.272	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0514	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	0.33	0/3441	0.70	1/4661 (0.0%)
1	2	0.33	0/3441	0.70	1/4661 (0.0%)
1	S	0.33	0/3441	0.70	1/4661 (0.0%)
1	T	0.33	0/3441	0.70	1/4661 (0.0%)
1	U	0.33	0/3441	0.70	1/4661 (0.0%)
1	V	0.33	0/3441	0.70	1/4661 (0.0%)
1	W	0.33	0/3441	0.70	1/4661 (0.0%)
1	X	0.33	0/3441	0.70	1/4661 (0.0%)
1	Y	0.33	0/3441	0.70	1/4661 (0.0%)
1	Z	0.33	0/3441	0.70	1/4661 (0.0%)
2	J	0.41	1/4525 (0.0%)	0.82	10/6119 (0.2%)
2	l	0.39	0/894	0.82	2/1209 (0.2%)
3	F	0.34	0/5044	0.75	7/6809 (0.1%)
3	H	0.45	1/5009 (0.0%)	0.80	10/6761 (0.1%)
3	N	0.39	0/5009	0.75	2/6761 (0.0%)
3	a	0.37	0/948	0.78	1/1277 (0.1%)
3	j	0.36	0/815	0.74	0/1096
3	n	0.37	0/815	0.76	0/1096
4	b	0.32	0/484	0.77	0/653
4	k	0.32	0/484	0.77	0/653
4	m	0.32	0/484	0.77	0/653
4	o	0.32	0/484	0.77	0/653
5	E	0.39	1/5311 (0.0%)	0.75	7/7169 (0.1%)
5	G	0.37	0/5325	0.75	2/7187 (0.0%)
5	M	0.41	0/5295	0.87	20/7147 (0.3%)
6	I	0.41	0/4322	0.81	5/5853 (0.1%)
6	K	0.37	0/4683	0.77	12/6338 (0.2%)
7	L	0.34	0/4697	0.74	3/6348 (0.0%)
All	All	0.37	3/89038 (0.0%)	0.75	91/120392 (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	2
1	2	0	2
1	S	0	2
1	T	0	2
1	U	0	2
1	V	0	2
1	W	0	2
1	X	0	2
1	Y	0	2
1	Z	0	2
2	J	0	2
3	H	0	5
3	N	0	2
5	E	0	2
5	G	0	2
5	M	0	5
6	I	0	4
7	L	0	3
All	All	0	45

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	703	GLU	C-N	7.40	1.43	1.34
3	H	603	THR	CB-CG2	6.69	1.74	1.52
2	J	403	ALA	C-N	5.40	1.39	1.34

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	705	THR	N-CA-C	-13.99	95.54	112.89
6	K	651	TYR	CA-CB-CG	9.28	130.61	113.90
2	J	235	SER	N-CA-C	-8.81	103.65	114.75
2	l	121	PRO	CA-N-CD	-8.43	100.20	112.00
2	l	130	PRO	CA-N-CD	-8.41	100.22	112.00

There are no chirality outliers.

5 of 45 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	327	GLU	Peptide
1	1	56	ASP	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	2	327	GLU	Peptide
1	2	56	ASP	Peptide
5	E	580	HIS	Peptide

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	3373	0	3325	81	0
1	2	3373	0	3325	73	0
1	S	3373	0	3325	66	0
1	T	3373	0	3325	68	0
1	U	3373	0	3325	61	0
1	V	3373	0	3325	75	0
1	W	3373	0	3325	62	0
1	X	3373	0	3325	58	0
1	Y	3373	0	3325	74	0
1	Z	3373	0	3325	68	0
2	J	4429	0	4482	39	0
2	l	875	0	842	28	0
3	F	4941	0	4935	43	0
3	H	4907	0	4896	64	0
3	N	4907	0	4896	63	0
3	a	933	0	953	10	0
3	j	803	0	831	23	0
3	n	803	0	831	16	0
4	b	484	0	512	9	0
4	k	484	0	512	8	0
4	m	484	0	512	15	0
4	o	484	0	512	12	0
5	E	5202	0	5241	45	0
5	G	5216	0	5246	82	0
5	M	5186	0	5219	72	0
6	I	4225	0	4259	52	0
6	K	4579	0	4586	44	0
7	L	4587	0	4636	41	0
All	All	87259	0	87151	1210	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 1210 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)
3:H:603:THR:CB	3:H:603:THR:CG2	1.74	1.62
5:G:876:ARG:HH22	3:j:37:ARG:CA	1.39	1.35
5:G:876:ARG:NH2	3:j:37:ARG:CB	1.95	1.29
5:G:876:ARG:HH22	3:j:37:ARG:CB	1.49	1.25
5:G:876:ARG:NH2	3:j:37:ARG:HB3	1.47	1.24

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%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	2	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	S	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	T	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	U	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	V	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	W	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	X	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	Y	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
1	Z	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
2	J	506/1024 (49%)	470 (93%)	33 (6%)	3 (1%)	21	59
2	l	104/1024 (10%)	94 (90%)	7 (7%)	3 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	591/907 (65%)	559 (95%)	32 (5%)	0	100	100
3	H	584/907 (64%)	560 (96%)	22 (4%)	2 (0%)	36	72
3	N	584/907 (64%)	556 (95%)	26 (4%)	2 (0%)	36	72
3	a	112/907 (12%)	106 (95%)	6 (5%)	0	100	100
3	j	97/907 (11%)	96 (99%)	1 (1%)	0	100	100
3	n	97/907 (11%)	91 (94%)	6 (6%)	0	100	100
4	b	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
4	k	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
4	m	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
4	o	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
5	E	626/902 (69%)	590 (94%)	33 (5%)	3 (0%)	24	63
5	G	628/902 (70%)	590 (94%)	35 (6%)	3 (0%)	24	63
5	M	624/902 (69%)	581 (93%)	38 (6%)	5 (1%)	16	54
6	I	511/667 (77%)	477 (93%)	30 (6%)	4 (1%)	16	54
6	K	548/667 (82%)	528 (96%)	19 (4%)	1 (0%)	43	78
7	L	540/1819 (30%)	505 (94%)	30 (6%)	5 (1%)	14	51
All	All	10484/18187 (58%)	9961 (95%)	472 (4%)	51 (0%)	26	63

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	l	117	LEU
5	E	581	ASP
5	G	241	ARG
3	H	270	ASN
6	I	408	ASP

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%)	324 (86%)	52 (14%)	3	14
1	2	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	S	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	T	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	U	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	V	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	W	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	X	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	Y	376/400 (94%)	324 (86%)	52 (14%)	3	14
1	Z	376/400 (94%)	324 (86%)	52 (14%)	3	14
2	J	498/933 (53%)	494 (99%)	4 (1%)	73	80
2	l	96/933 (10%)	94 (98%)	2 (2%)	47	65
3	F	542/798 (68%)	539 (99%)	3 (1%)	78	83
3	H	539/798 (68%)	537 (100%)	2 (0%)	84	84
3	N	539/798 (68%)	536 (99%)	3 (1%)	78	83
3	a	101/798 (13%)	99 (98%)	2 (2%)	48	66
3	j	88/798 (11%)	88 (100%)	0	100	100
3	n	88/798 (11%)	88 (100%)	0	100	100
4	b	53/62 (86%)	41 (77%)	12 (23%)	1	6
4	k	53/62 (86%)	41 (77%)	12 (23%)	1	6
4	m	53/62 (86%)	41 (77%)	12 (23%)	1	6
4	o	53/62 (86%)	41 (77%)	12 (23%)	1	6
5	E	574/791 (73%)	571 (100%)	3 (0%)	81	83
5	G	575/791 (73%)	570 (99%)	5 (1%)	70	79
5	M	572/791 (72%)	563 (98%)	9 (2%)	55	70
6	I	472/594 (80%)	467 (99%)	5 (1%)	65	76
6	K	509/594 (86%)	506 (99%)	3 (1%)	78	83
7	L	501/1546 (32%)	497 (99%)	4 (1%)	73	80
All	All	9666/16009 (60%)	9053 (94%)	613 (6%)	18	37

5 of 613 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	73	VAL
1	Z	136	VAL
1	X	192	LEU
1	X	72	ARG
1	Y	131	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 263 such sidechains are listed below:

Mol	Chain	Res	Type
1	X	103	ASN
1	X	394	GLN
1	Z	334	HIS
2	J	642	HIS
2	J	269	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.

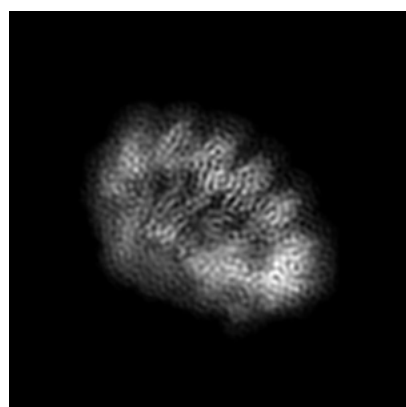
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14009. These allow visual inspection of the internal detail of the map and identification of artifacts.

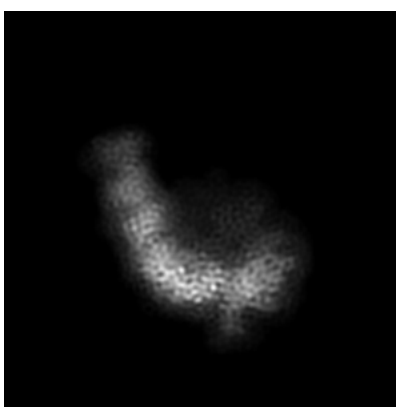
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

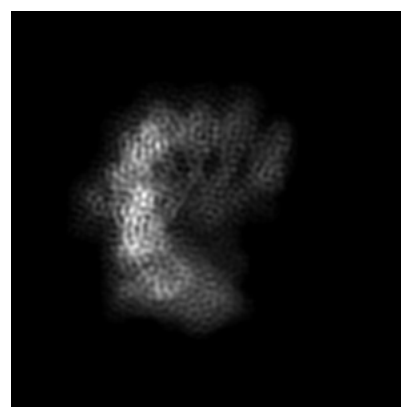
6.1.1 Primary map



X



Y



Z

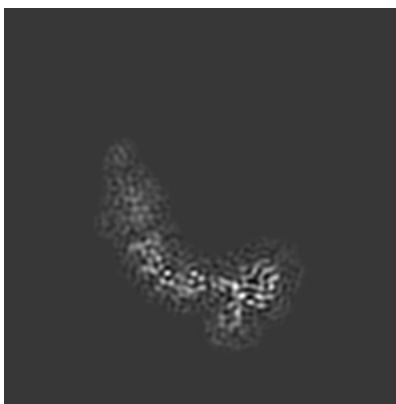
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 100



Y Index: 100

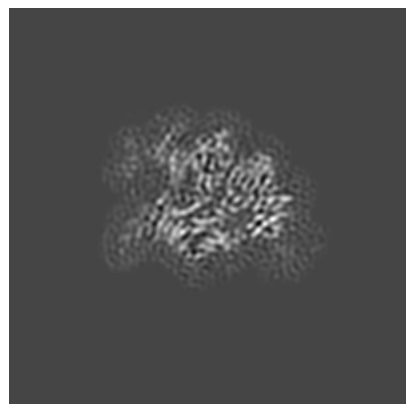


Z Index: 100

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

6.3 Largest variance slices [i](#)

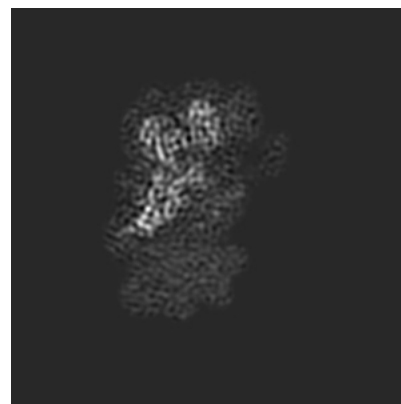
6.3.1 Primary map



X Index: 62



Y Index: 98



Z Index: 74

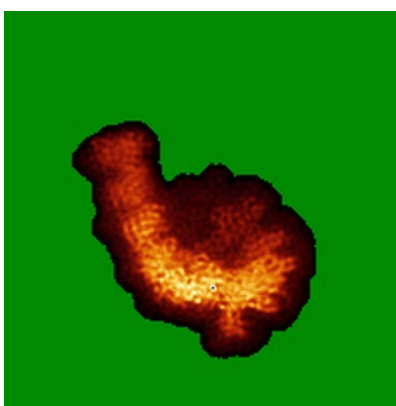
The images above show the largest variance slices of the map in three orthogonal directions.

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

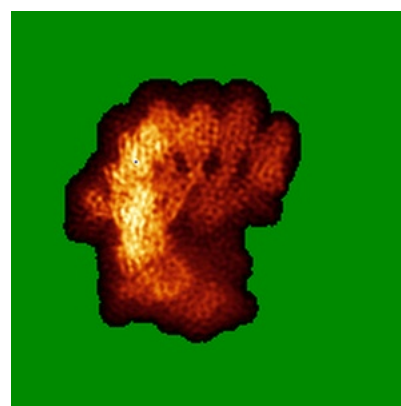
6.4.1 Primary map



X



Y

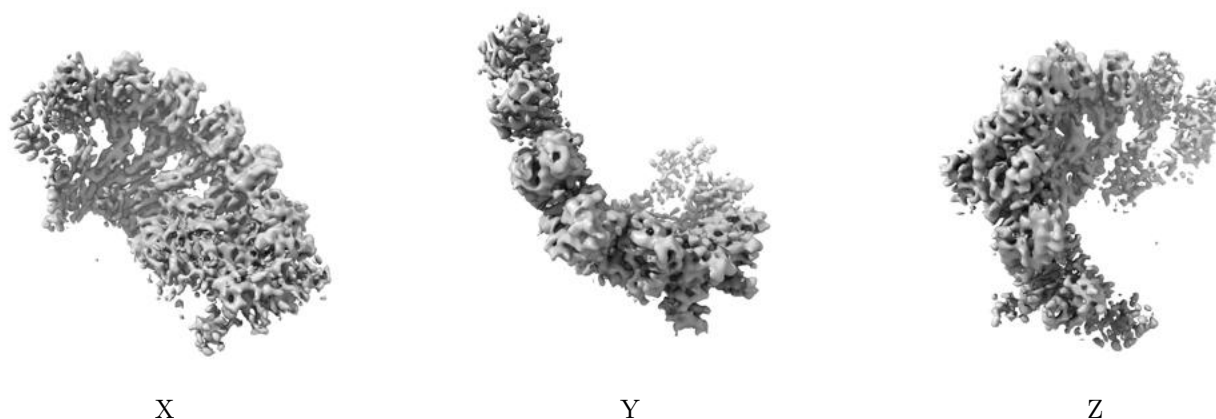


Z

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 0.0514. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

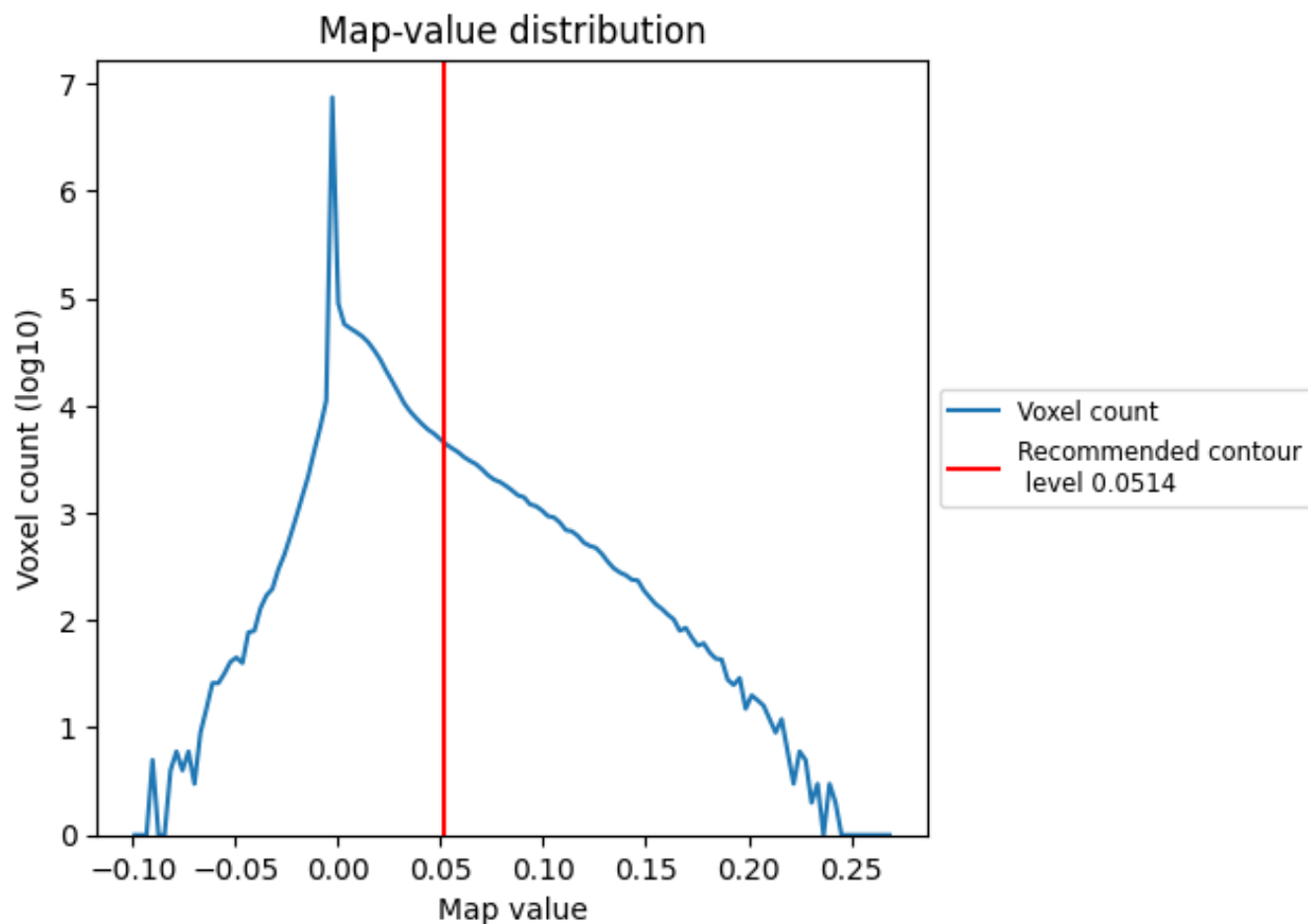
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

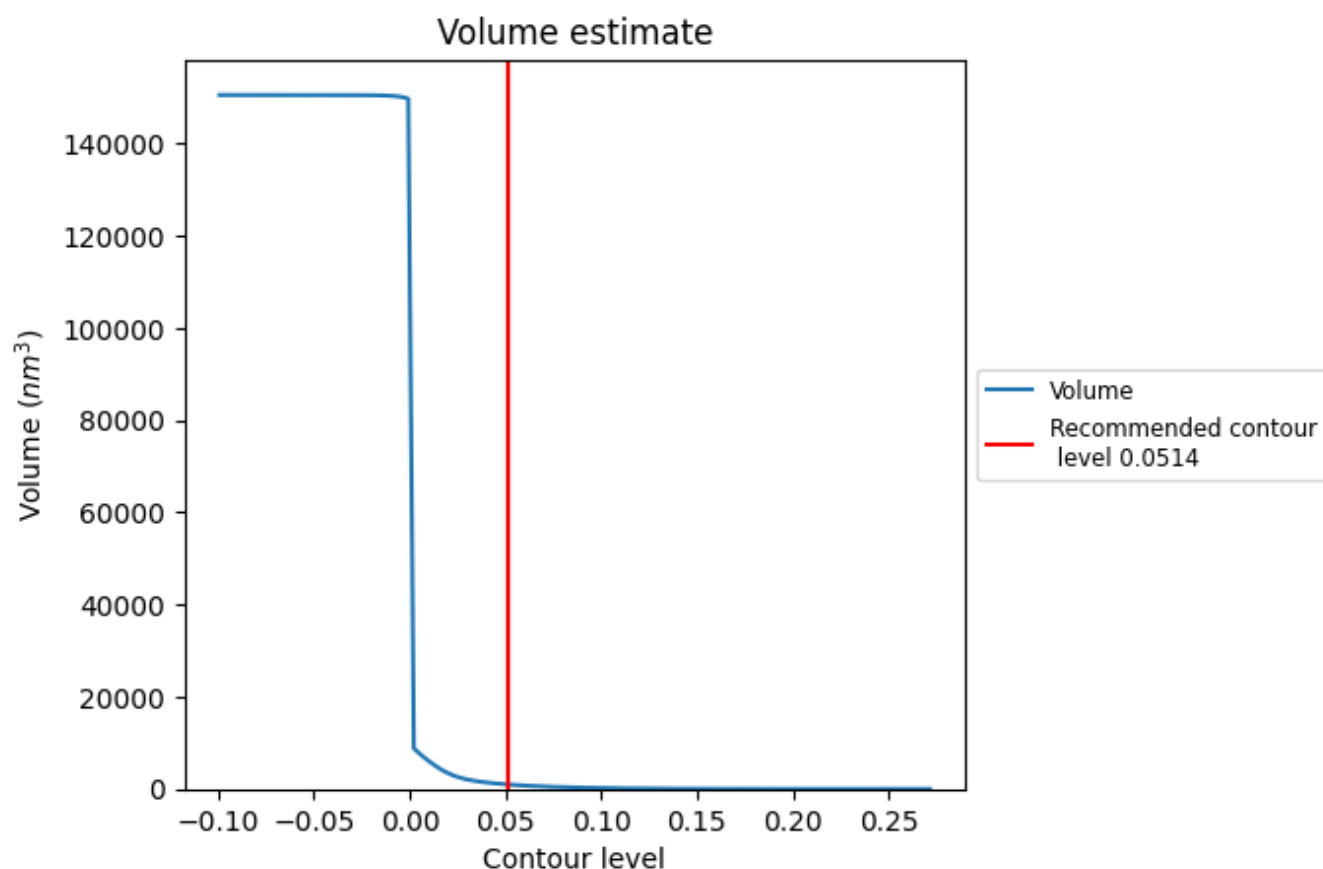
This section contains the results of statistical analysis of the map.

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.

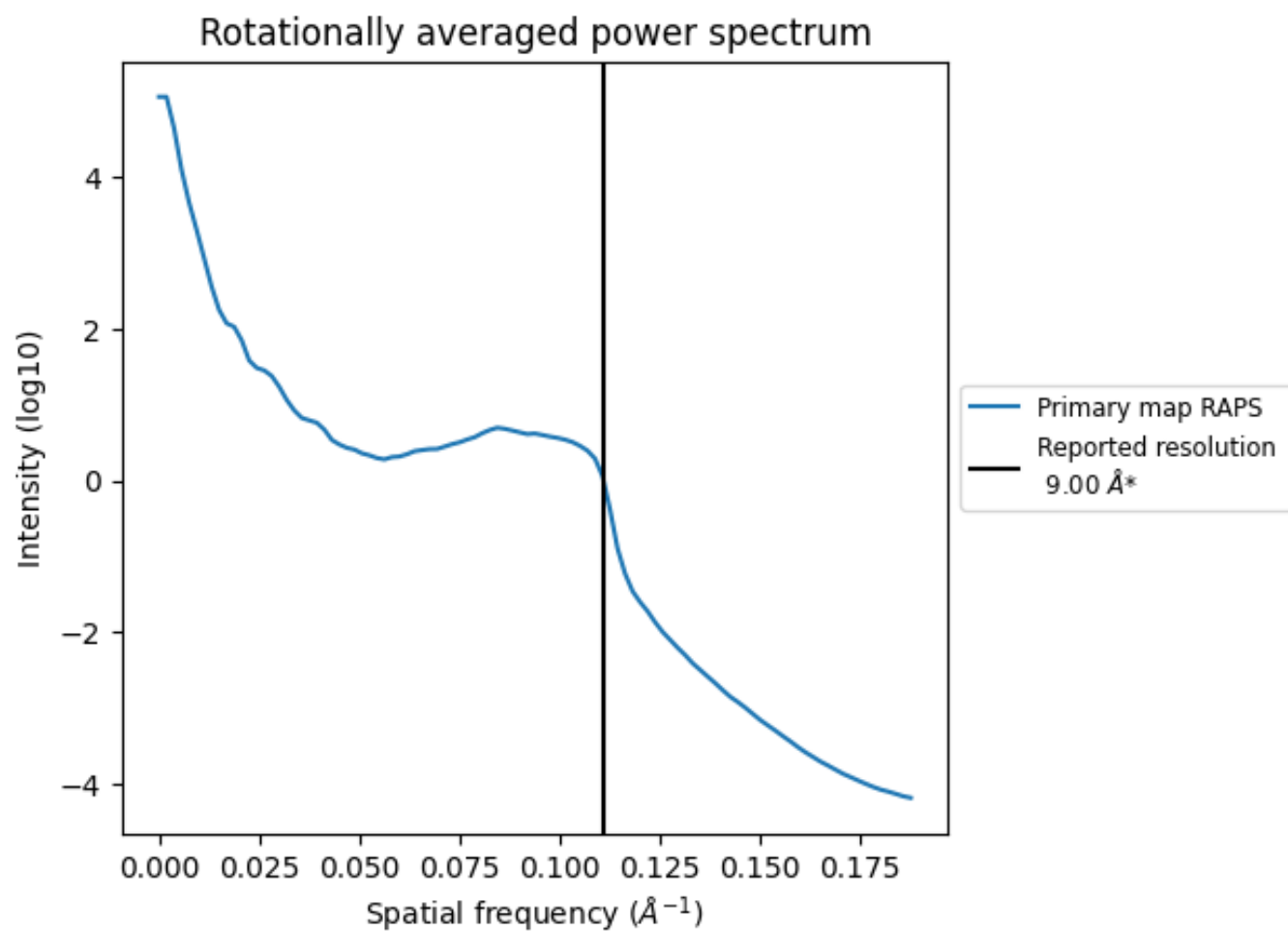
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 970 nm^3 ; this corresponds to an approximate mass of 876 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 0.111 Å⁻¹

8 Fourier-Shell correlation

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

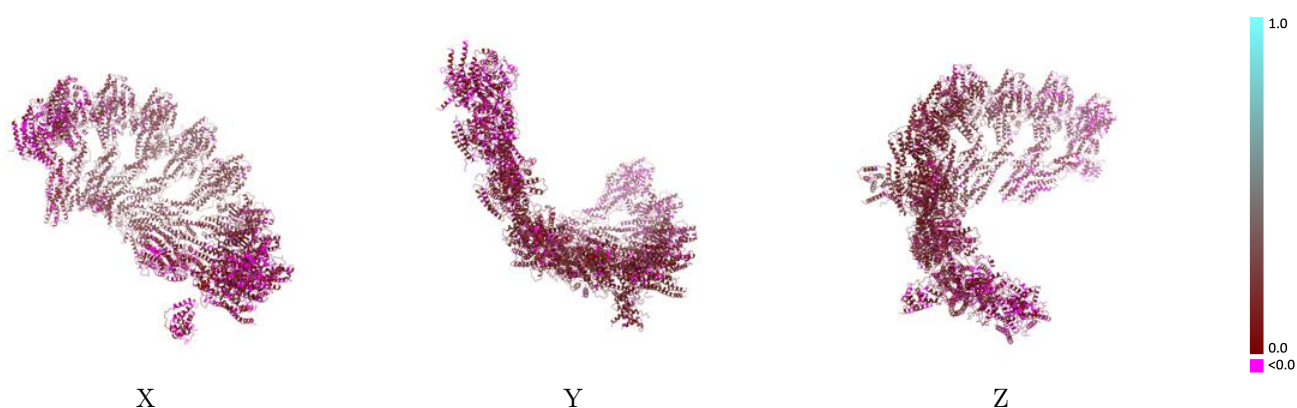
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-14009 and PDB model 7QJ4. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

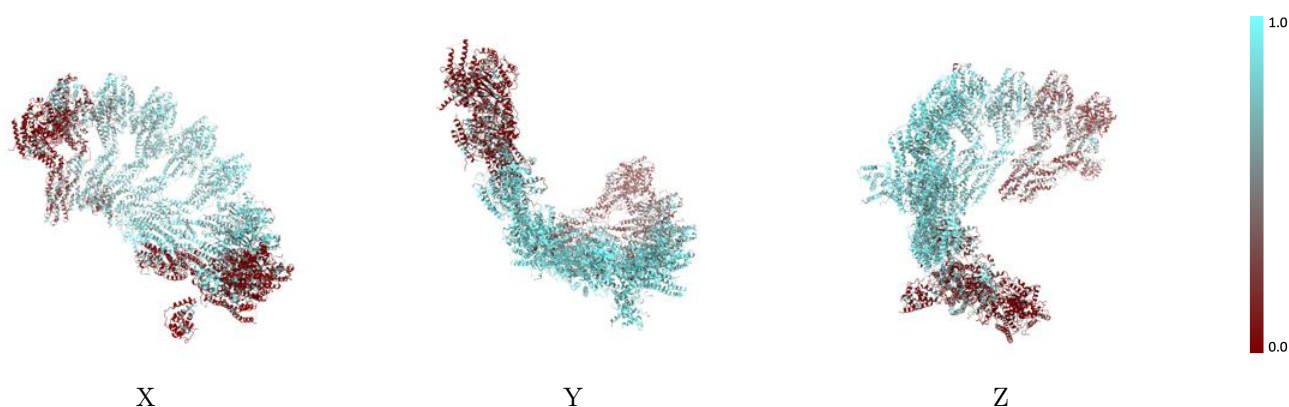
This section was not generated.

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



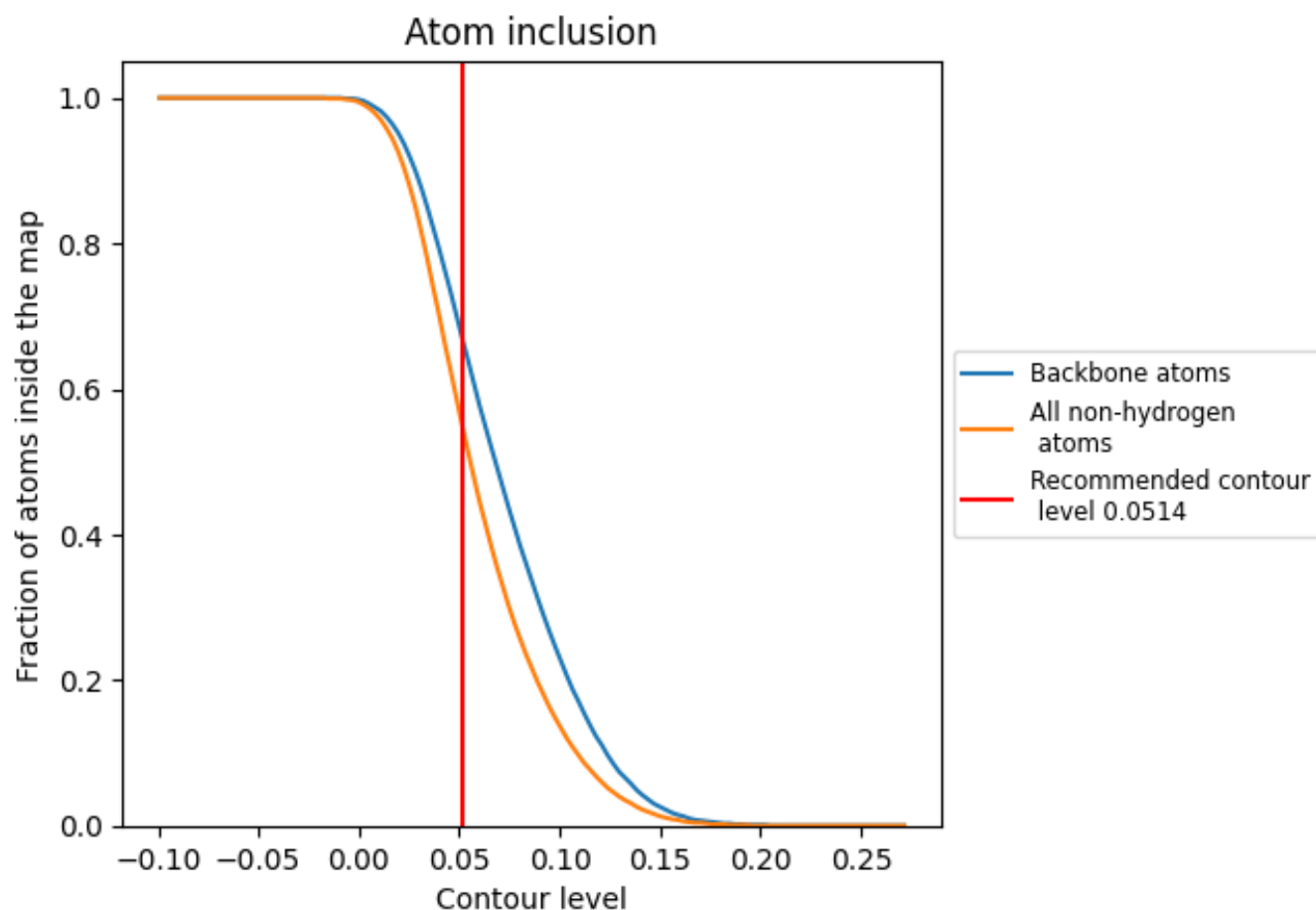
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0514).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 55% 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 (0.0514) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5510	 0.1090
1	 0.2640	 0.0620
2	 0.1360	 0.0390
E	 0.1810	 0.0680
F	 0.4140	 0.1160
G	 0.7340	 0.1390
H	 0.7970	 0.1480
I	 0.7980	 0.1570
J	 0.8170	 0.1580
K	 0.7930	 0.1380
L	 0.7720	 0.1310
M	 0.2980	 0.0810
N	 0.2730	 0.0760
S	 0.0880	 0.0420
T	 0.3620	 0.0720
U	 0.6790	 0.1040
V	 0.7740	 0.1270
W	 0.7930	 0.1320
X	 0.8320	 0.1400
Y	 0.7740	 0.1070
Z	 0.6950	 0.1160
a	 0.3940	 0.1220
b	 0.3970	 0.1150
j	 0.2400	 0.1020
k	 0.1680	 0.0770
l	 0.7840	 0.1480
m	 0.7650	 0.1600
n	 0.1470	 0.0420
o	 0.1850	 0.0310

