



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:30 AM UTC

PDB ID : 7QJC / pdb_00007qjc
EMDB ID : EMD-14017
Title : Structure of recombinant human gamma-Tubulin Ring Complex (spokes 1-14, homogeneous dataset)
Authors : Zupa, E.; Pfeffer, S.
Deposited on : 2021-12-16
Resolution : 16.10 Å (reported)
Based on initial models : 6L81, 7AS4, 6V6S, 6X0U

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:

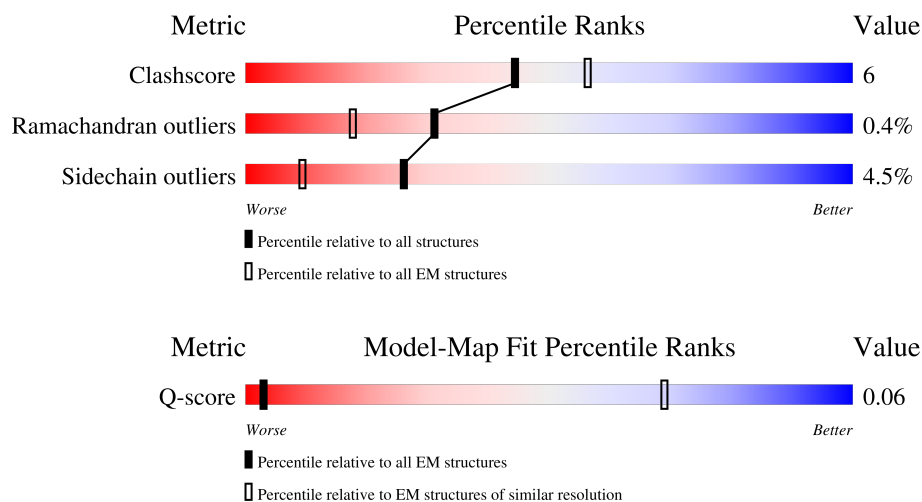
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 16.10 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.



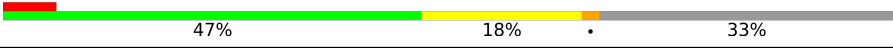
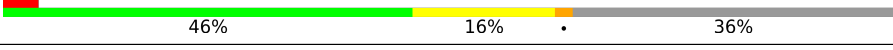
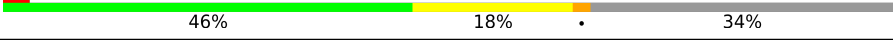
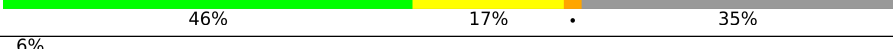
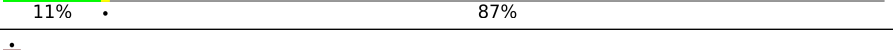
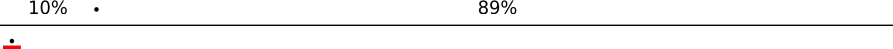
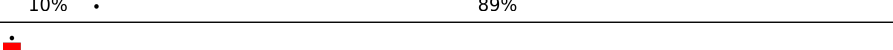
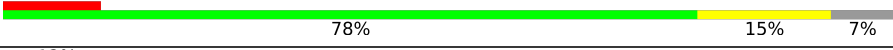
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	32 (15.90 - 16.50)

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	e	375	48% 94%
2	A	902	49% 17% 32%
2	C	902	6% 49% 18% 31%
2	E	902	52% 17% 29%

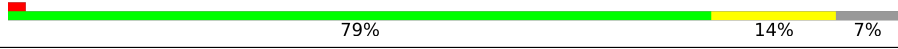
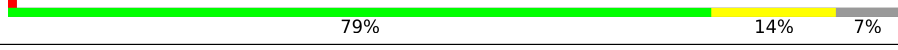
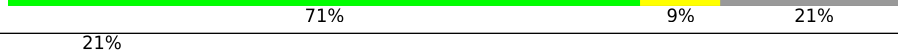
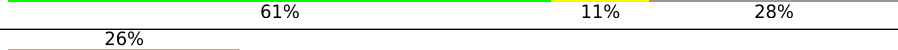
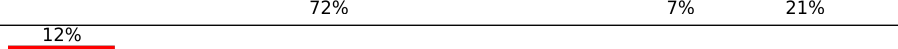
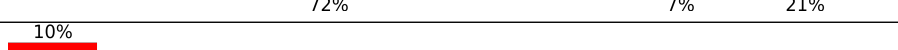
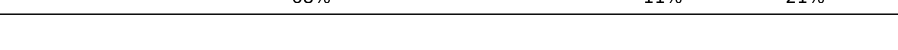
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Mol	Chain	Length	Quality of chain
2	G	902	
2	M	902	
3	B	907	
3	D	907	
3	F	907	
3	H	907	
3	N	907	
3	a	907	
3	f	907	
3	h	907	
3	j	907	
4	I	667	
4	K	667	
5	J	1024	
5	l	1024	
6	L	1819	
6	c	1819	
7	1	451	
7	2	451	
7	O	451	
7	P	451	
7	Q	451	
7	R	451	
7	S	451	
7	T	451	

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Mol	Chain	Length	Quality of chain
7	U	451	
7	V	451	
7	W	451	
7	X	451	
7	Y	451	
7	Z	451	
8	b	82	
8	d	82	
8	g	82	
8	i	82	
8	k	82	
8	m	82	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 125323 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 actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	e	364	Total	C	N	O	S	0	0
			1818	1083	364	370	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	613	Total	C	N	O	S	0	0
			4978	3212	831	903	32		
2	C	620	Total	C	N	O	S	0	0
			5044	3257	845	910	32		
2	E	638	Total	C	N	O	S	0	0
			5202	3354	873	942	33		
2	G	640	Total	C	N	O	S	0	0
			5217	3359	878	947	33		
2	M	636	Total	C	N	O	S	0	0
			5186	3342	871	940	33		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	610	Total	C	N	O	S	0	0
			5021	3198	888	910	25		
3	D	581	Total	C	N	O	S	0	0
			4796	3061	842	868	25		
3	F	599	Total	C	N	O	S	0	0
			4933	3146	871	891	25		
3	H	594	Total	C	N	O	S	0	0
			4899	3125	864	885	25		
3	a	116	Total	C	N	O	S	0	0
			933	591	171	169	2		
3	f	99	Total	C	N	O	S	0	0
			803	509	148	144	2		
3	h	99	Total	C	N	O	S	0	0
			803	509	148	144	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	j	107	Total	C	N	O	S	0	0
			864	545	161	156	2		
3	N	594	Total	C	N	O	S	0	0
			4899	3125	864	885	25		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	521	Total	C	N	O	S	0	0
			4222	2734	720	750	18		
4	K	562	Total	C	N	O	S	0	0
			4579	2964	781	816	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	534	Total	C	N	O	S	0	0
			4406	2879	733	771	23		
5	l	108	Total	C	N	O	S	0	0
			876	556	151	168	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	566	Total	C	N	O	S	0	0
			4556	2977	767	788	24		
6	c	158	Total	C	N	O	S	0	0
			1220	771	209	232	8		

- Molecule 7 is a protein called Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
7	P	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
7	Q	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
7	R	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
7	S	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		

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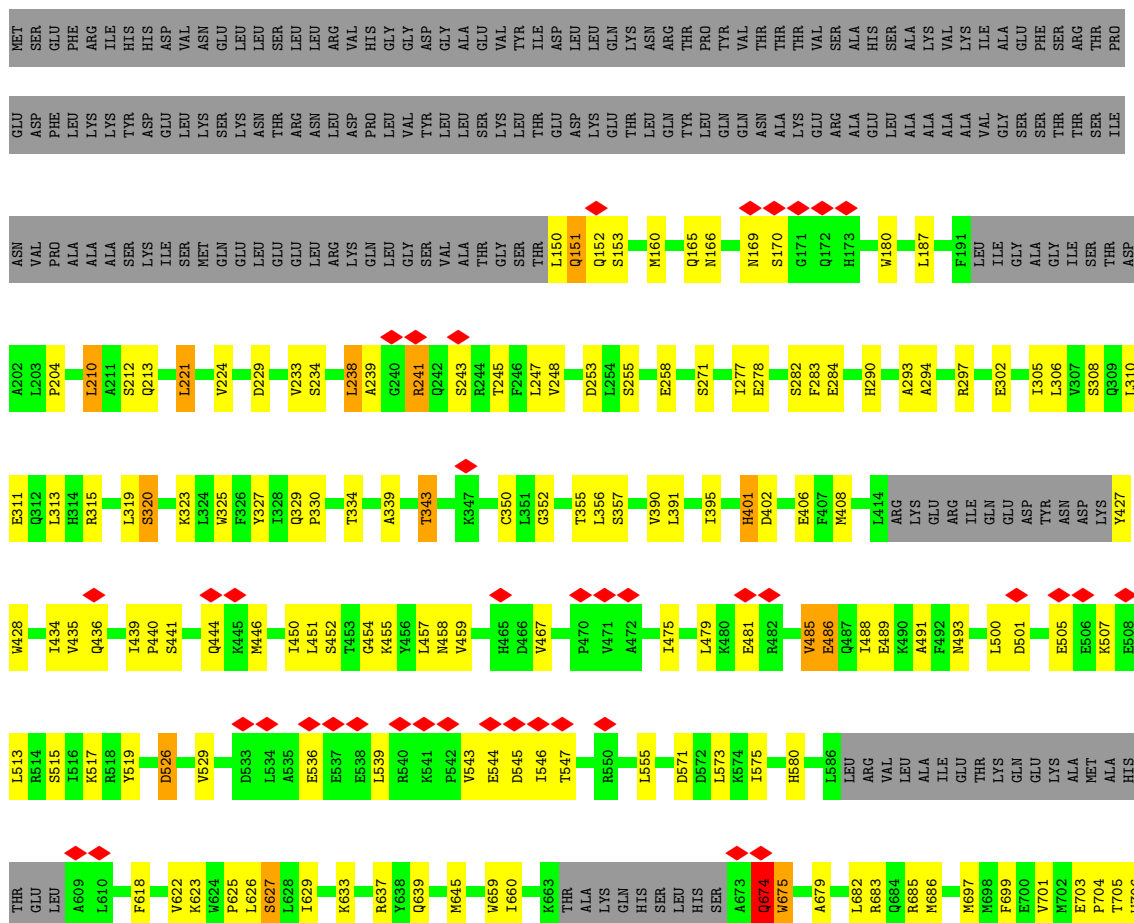
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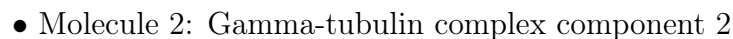
Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	U	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	V	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	W	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	X	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	Y	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	Z	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	1	420	Total 3371	C 2133	N 586	O 637	S 15	0	0
7	2	420	Total 3371	C 2133	N 586	O 637	S 15	0	0

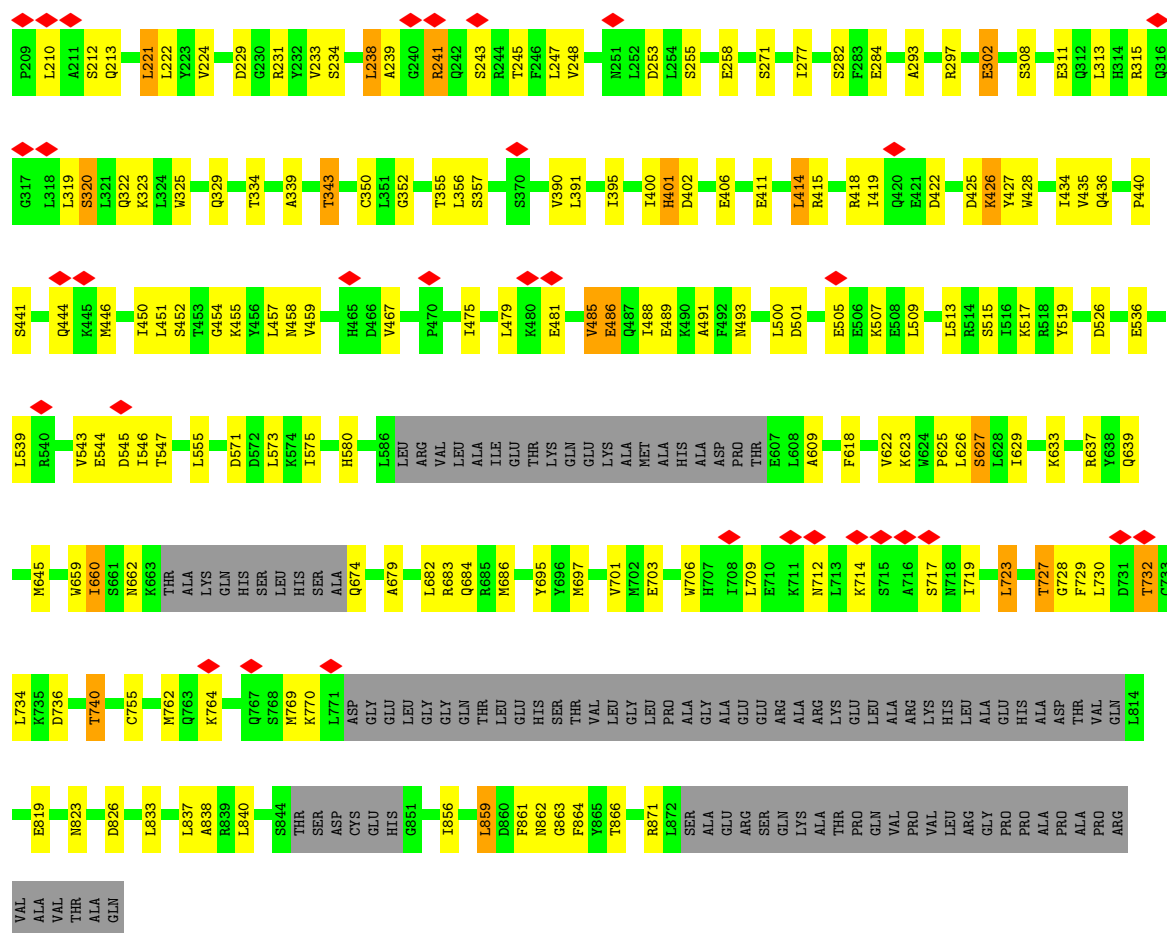
- Molecule 8 is a protein called Mitotic-spindle organizing protein 1.

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

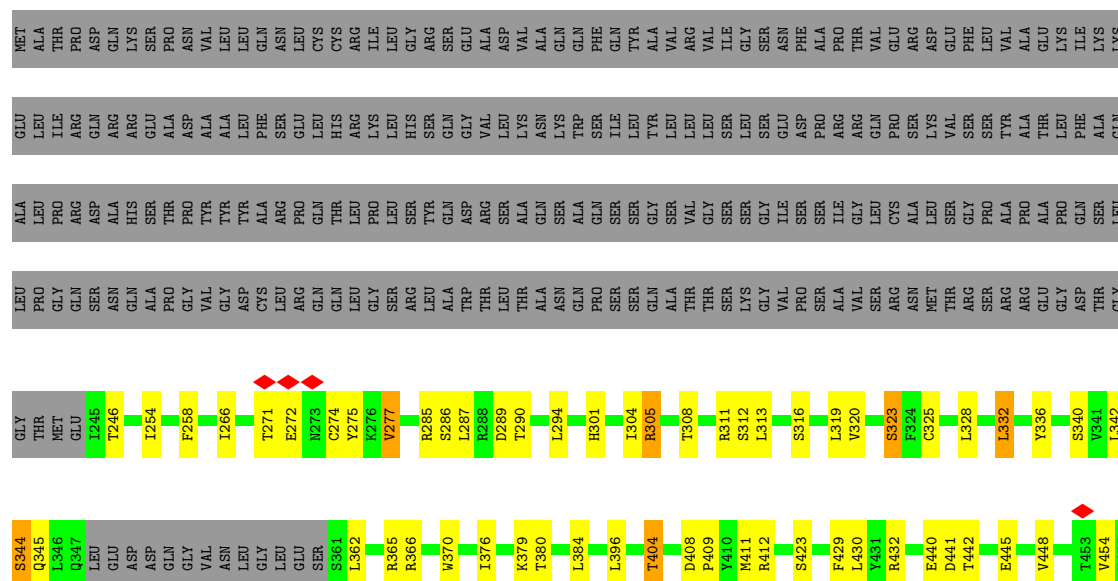
- Molecule 2: Gamma-tubulin complex component 2

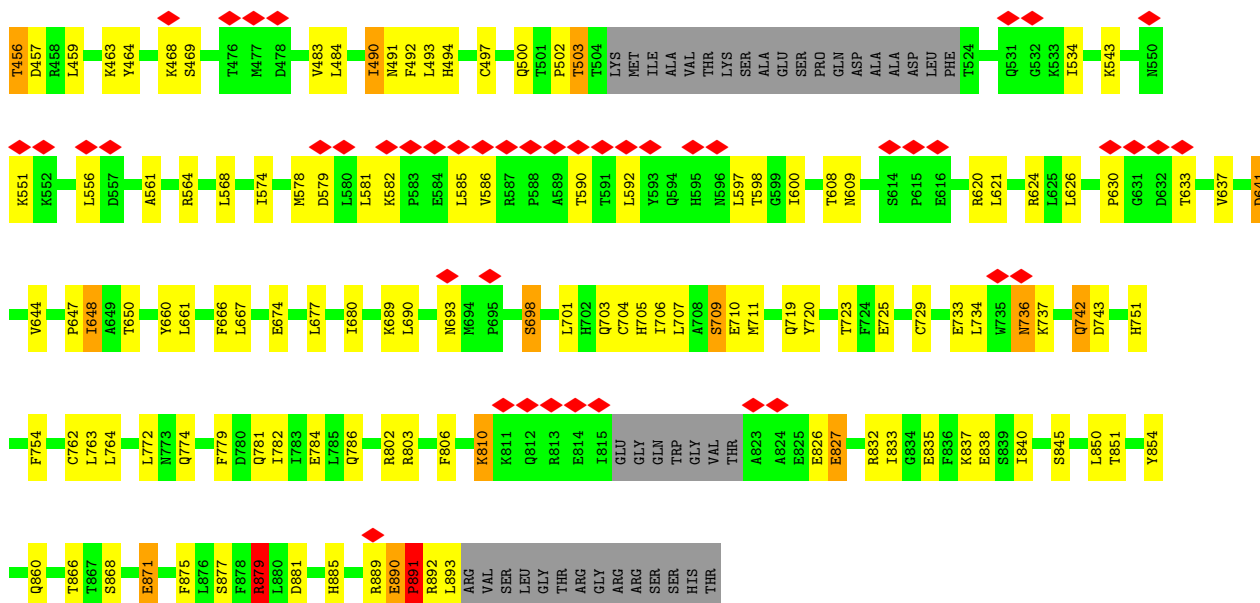




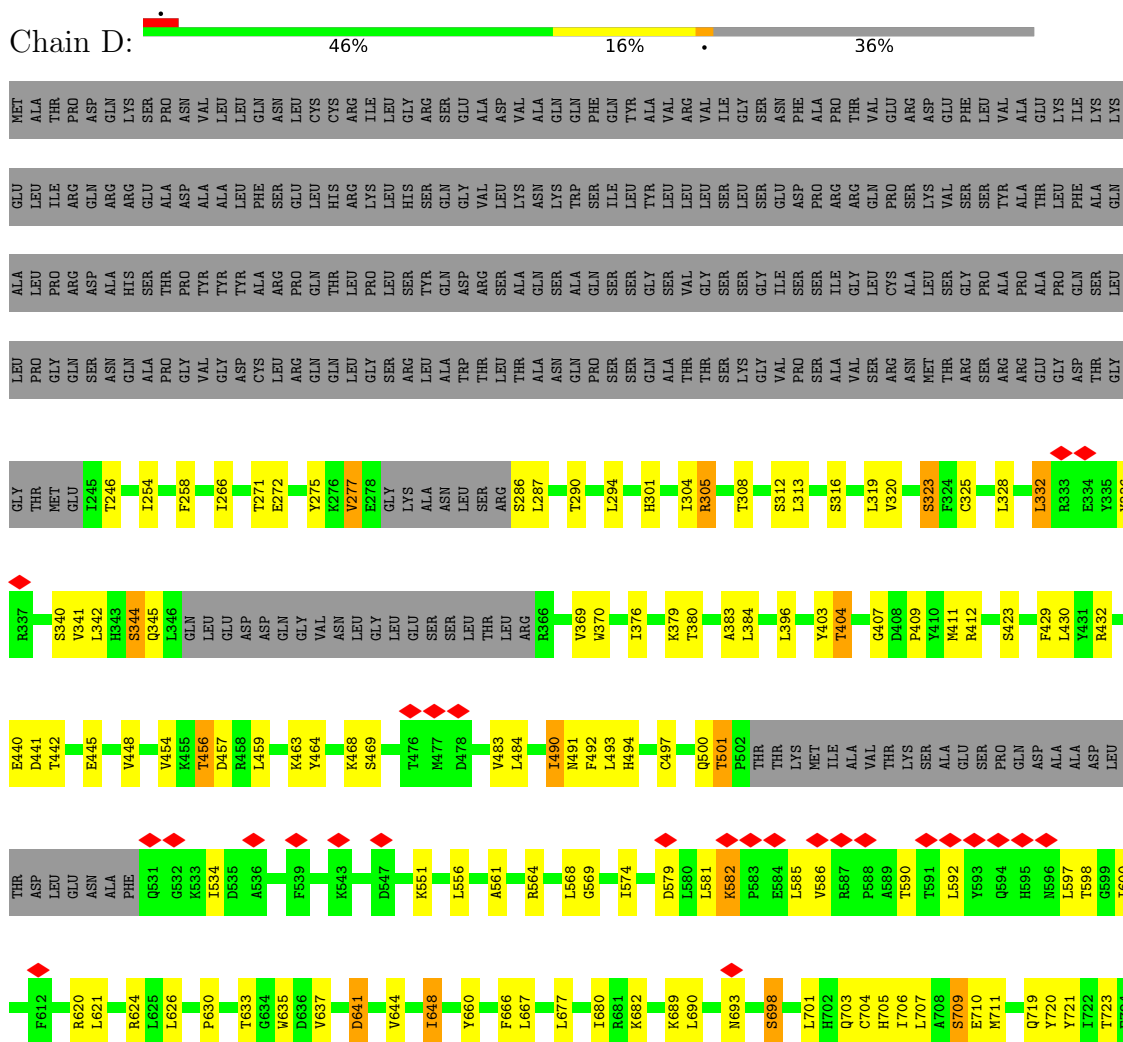


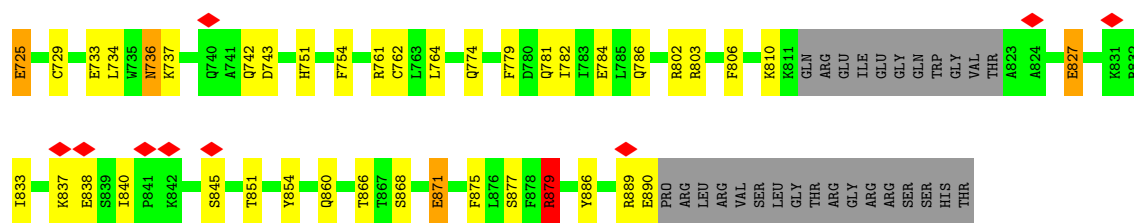
• Molecule 3: Gamma-tubulin complex component 3





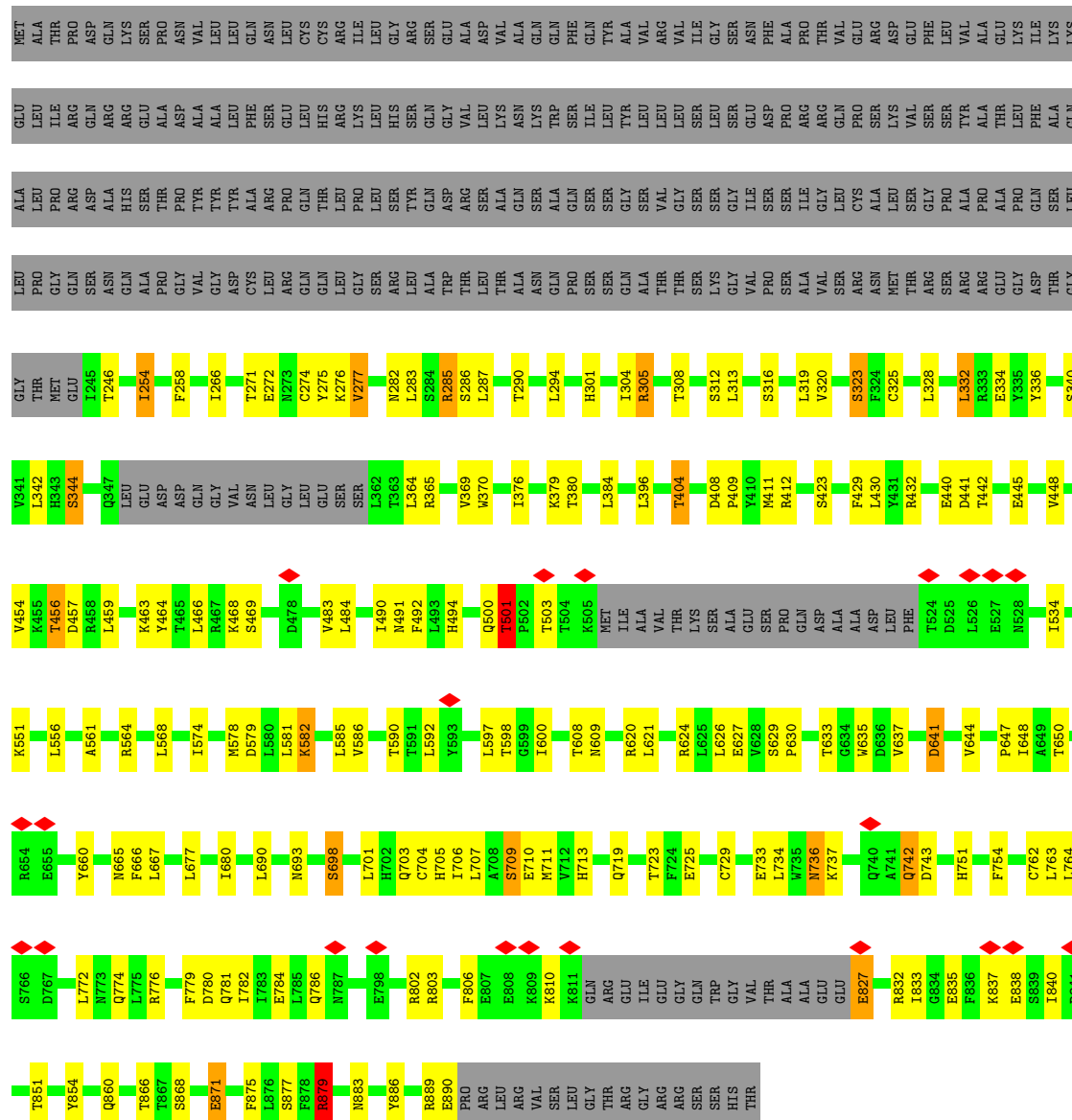
- Molecule 3: Gamma-tubulin complex component 3





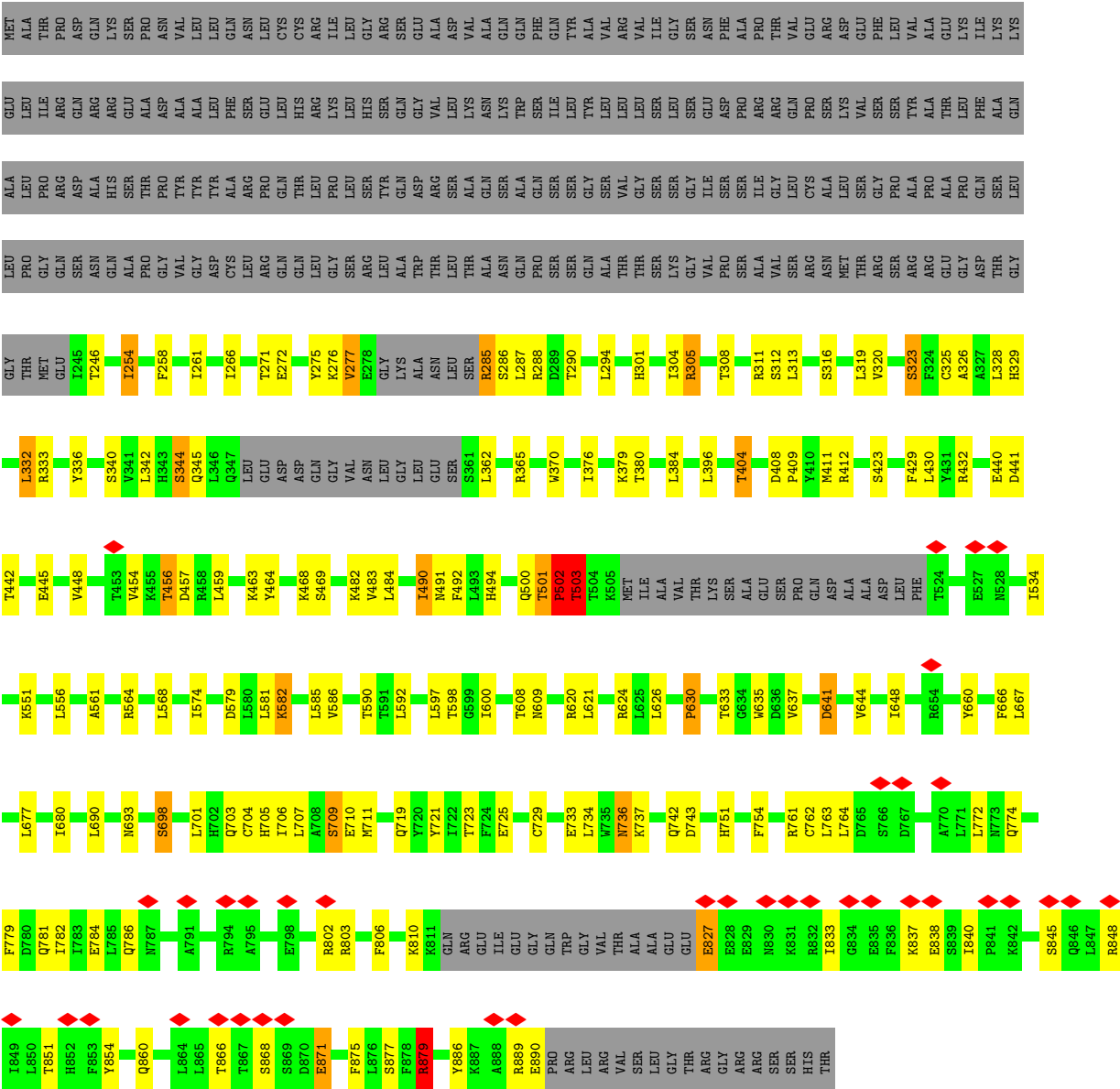
• Molecule 3: Gamma-tubulin complex component 3

Chain F: 46% 18% 34%

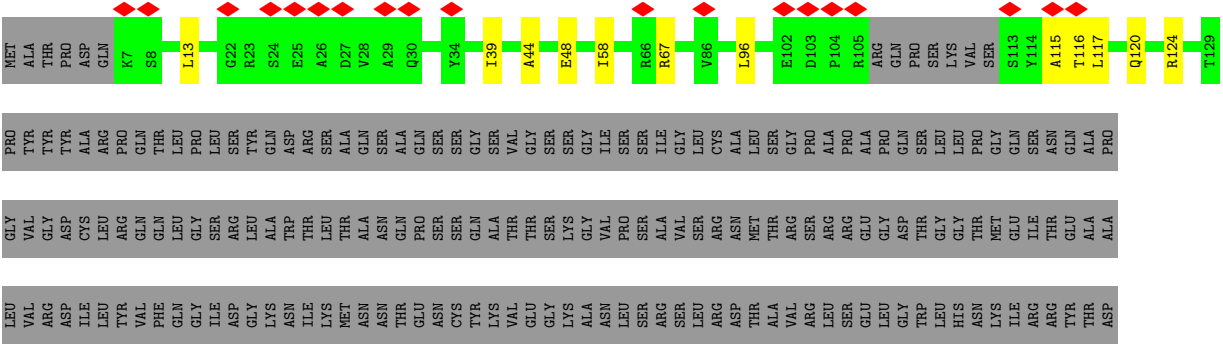


• Molecule 3: Gamma-tubulin complex component 3

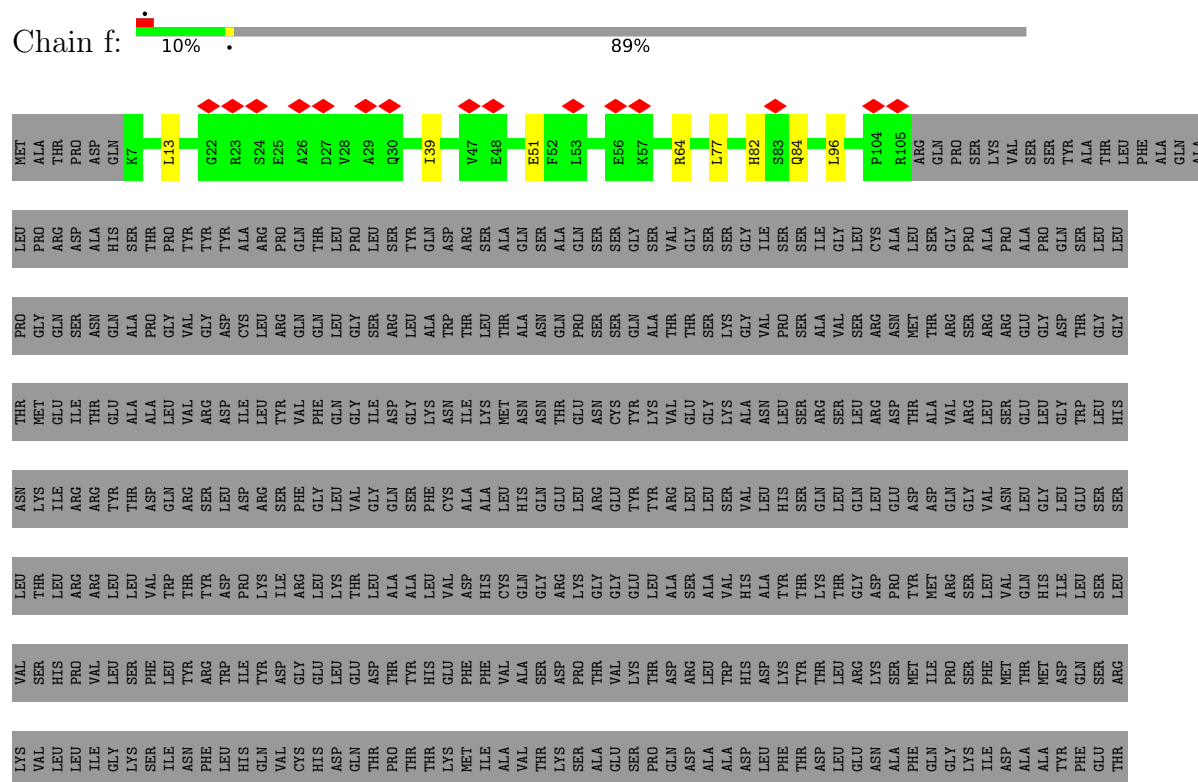
Chain H: 46% 17% 35%



• Molecule 3: Gamma-tubulin complex component 3

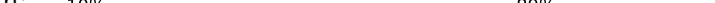


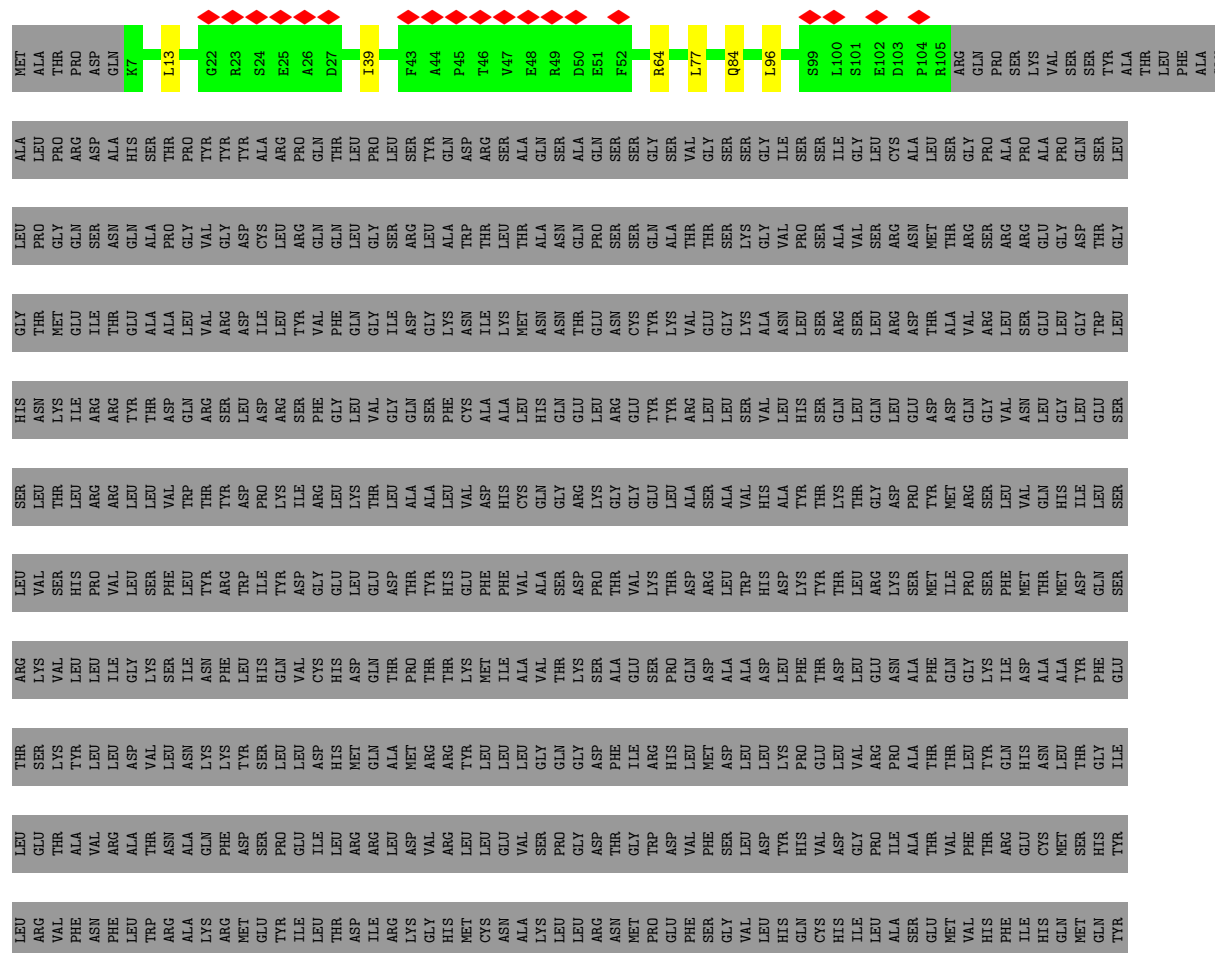
- Molecule 3: Gamma-tubulin complex component 3



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

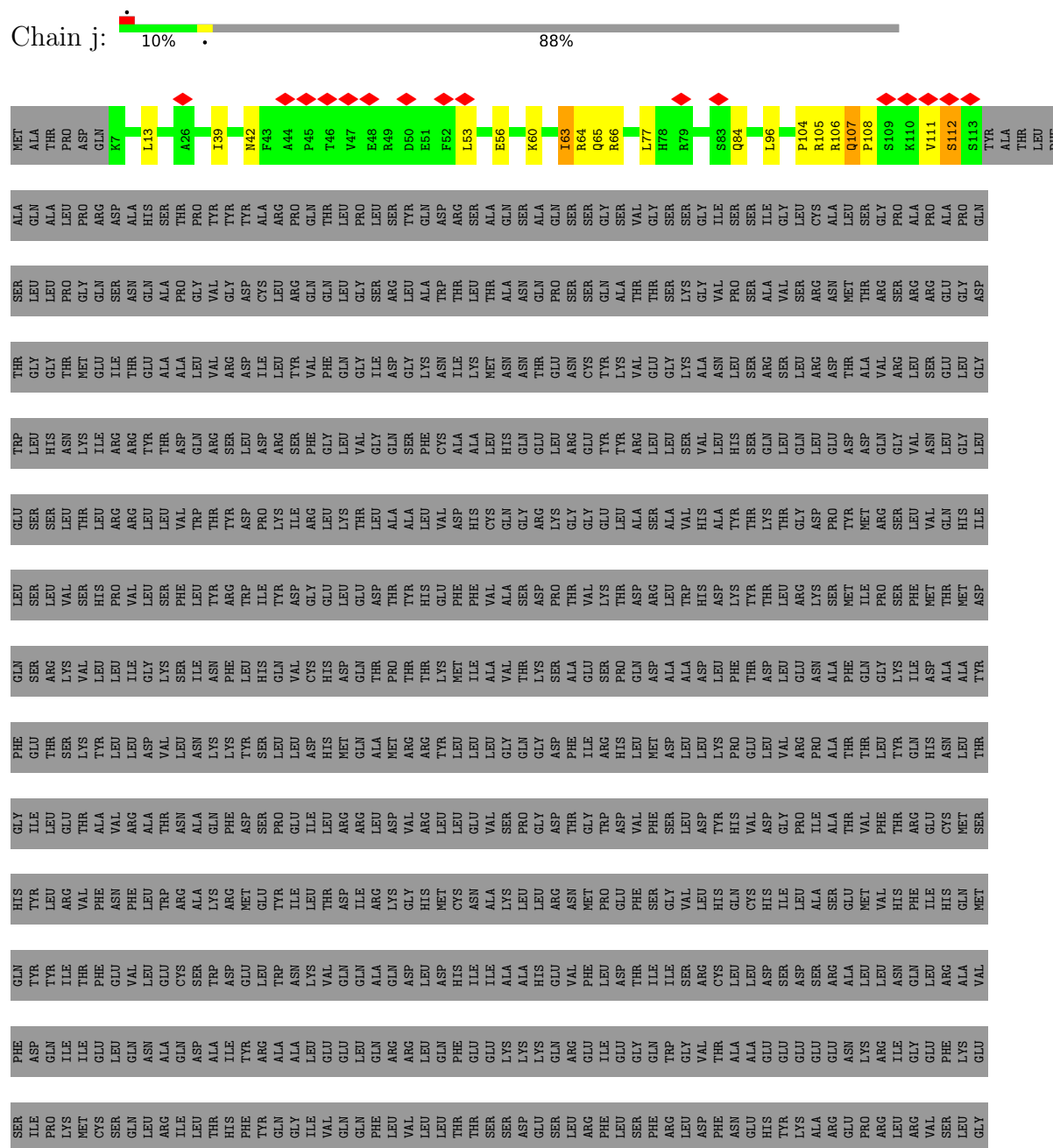
- Molecule 3: Gamma-tubulin complex component 3

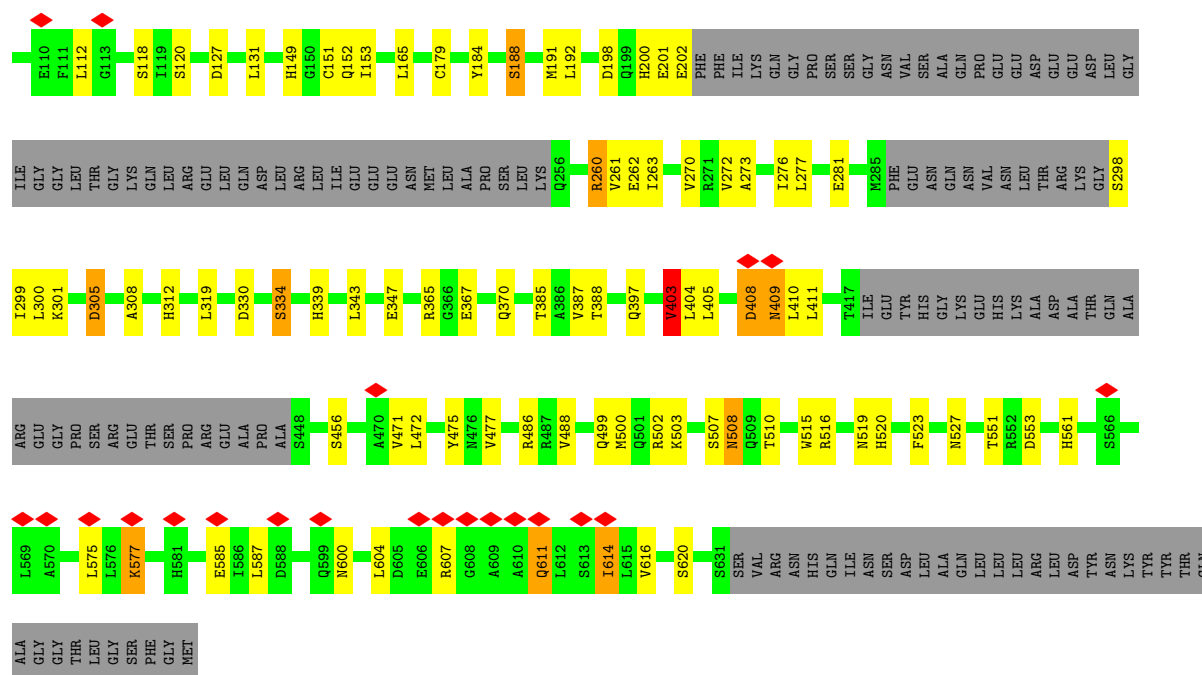
Chain h:  10% 89%



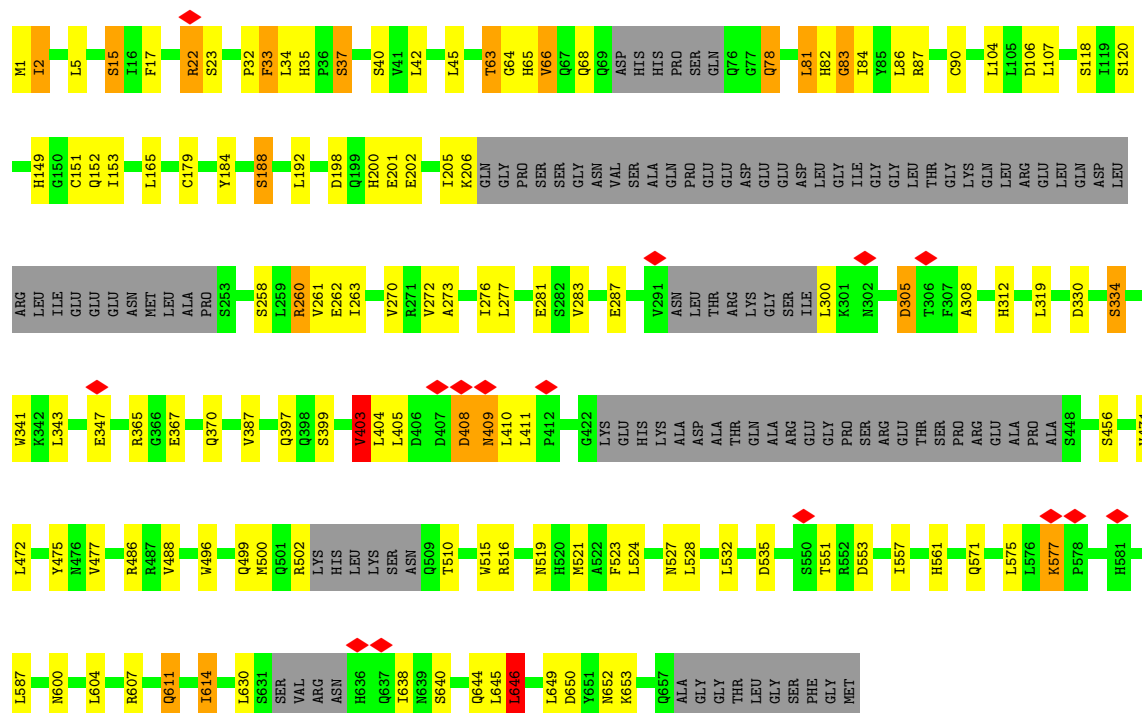
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- Molecule 3: Gamma-tubulin complex component 3



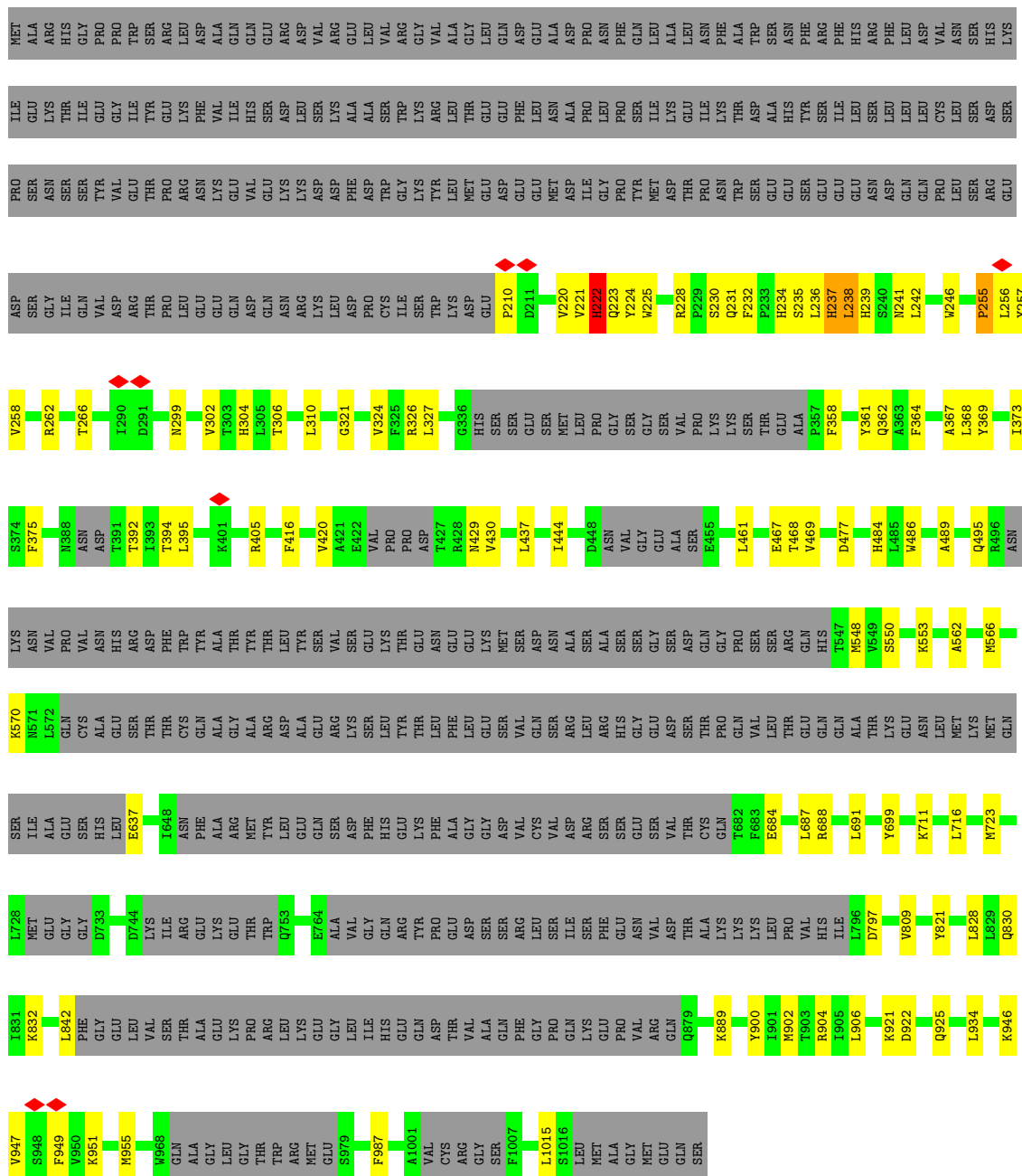


• Molecule 4: Gamma-tubulin complex component 4

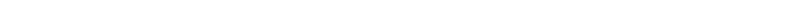


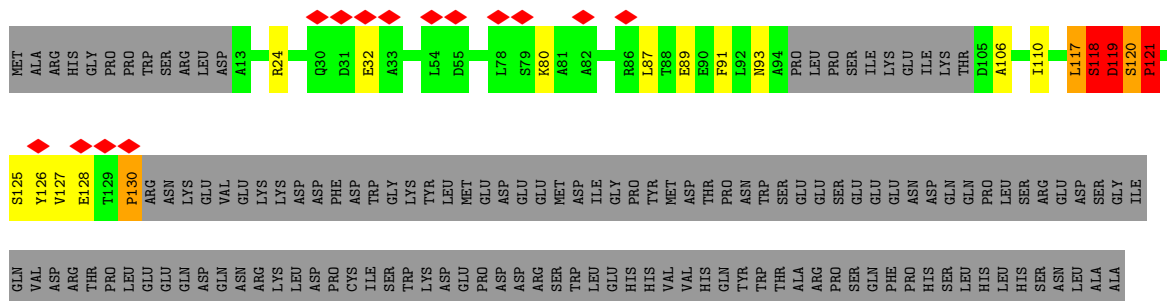
• Molecule 5: Gamma-tubulin complex component 5





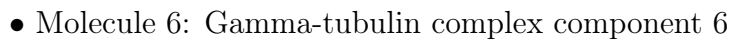
- Molecule 5: Gamma-tubulin complex component 5

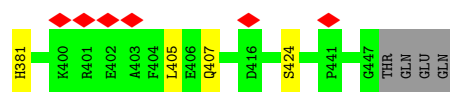
Chain 1:  9% 89%



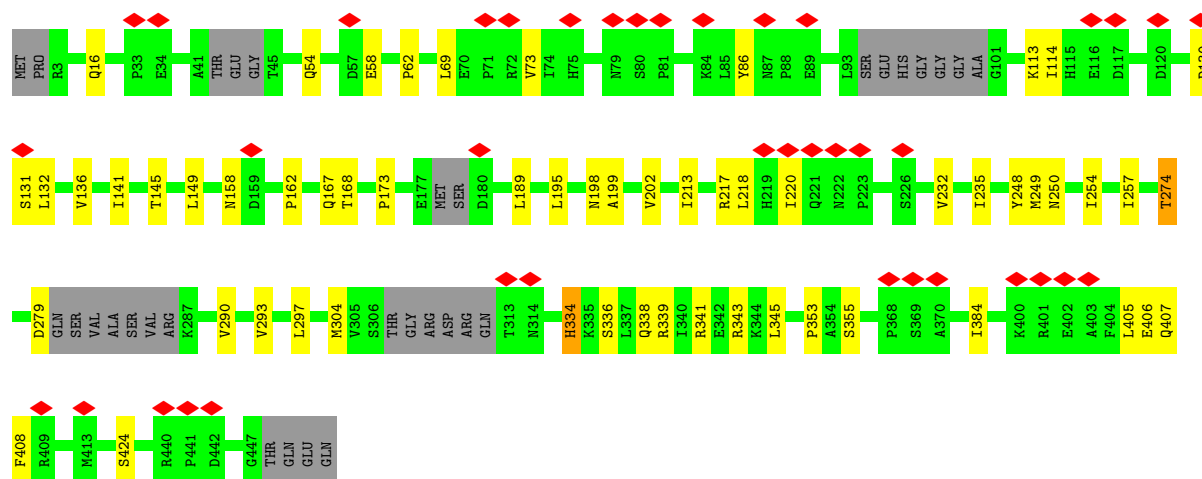
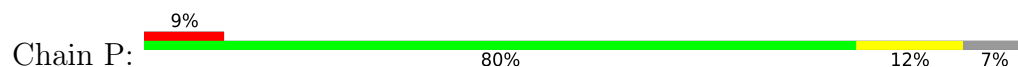




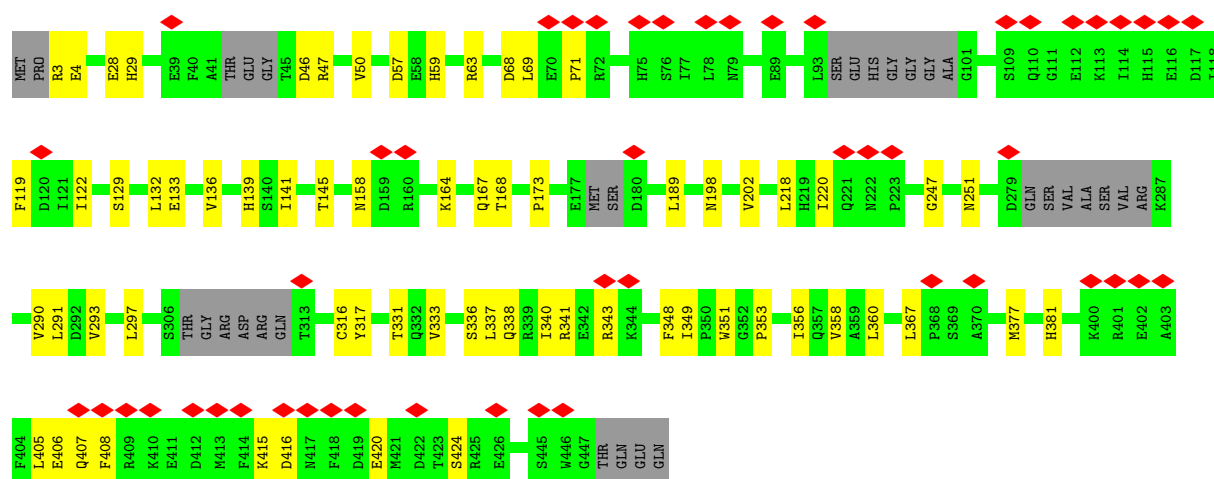
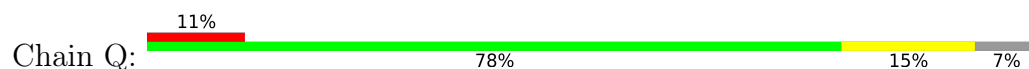




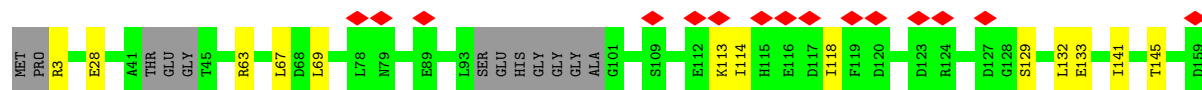
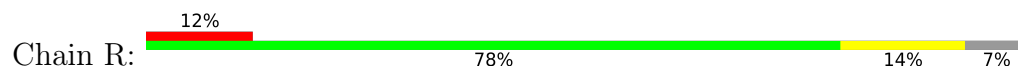
• Molecule 7: Tubulin gamma-1 chain

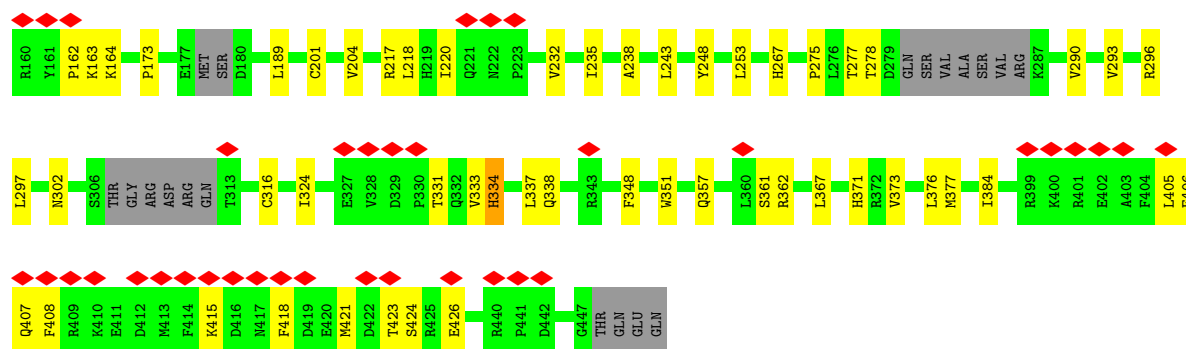


• Molecule 7: Tubulin gamma-1 chain

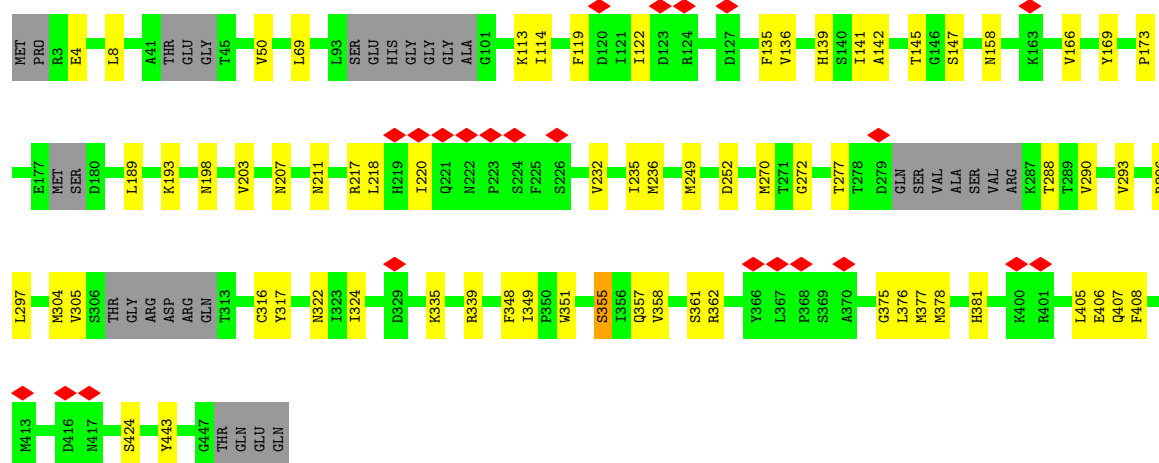
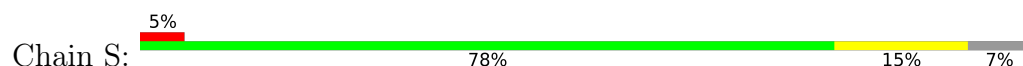


• Molecule 7: Tubulin gamma-1 chain

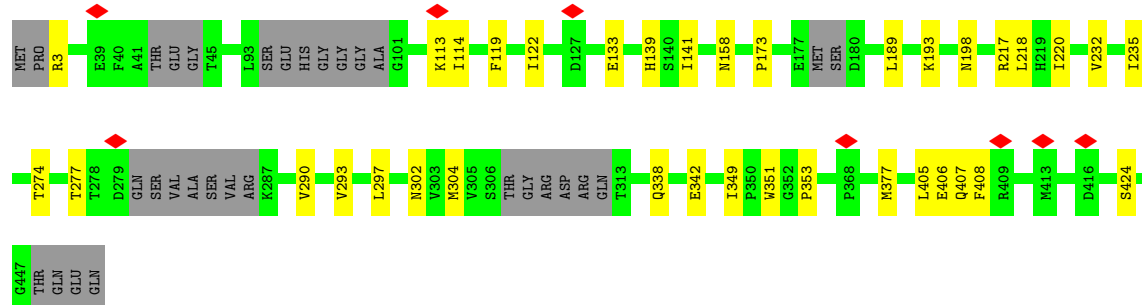
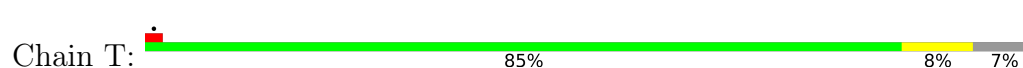




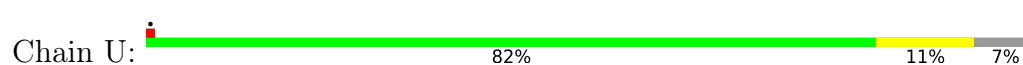
• Molecule 7: Tubulin gamma-1 chain

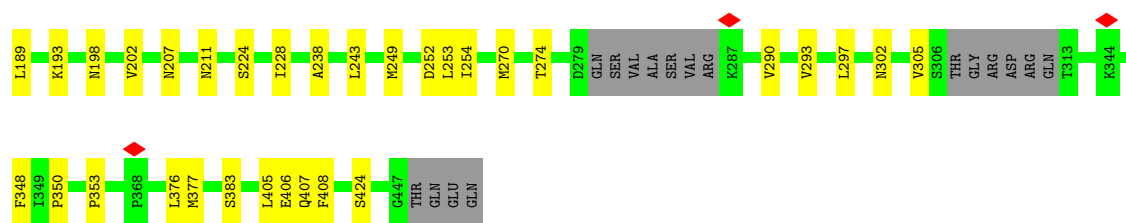


• Molecule 7: Tubulin gamma-1 chain

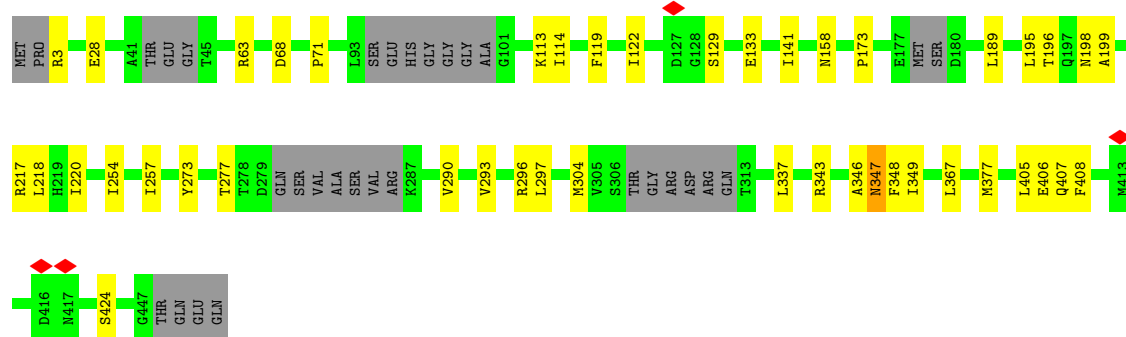
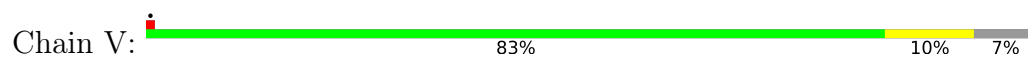


• Molecule 7: Tubulin gamma-1 chain

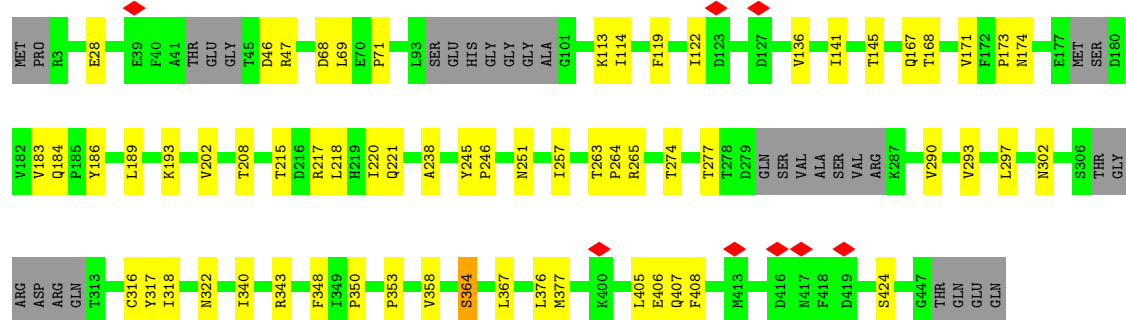
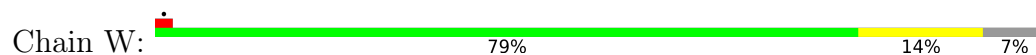




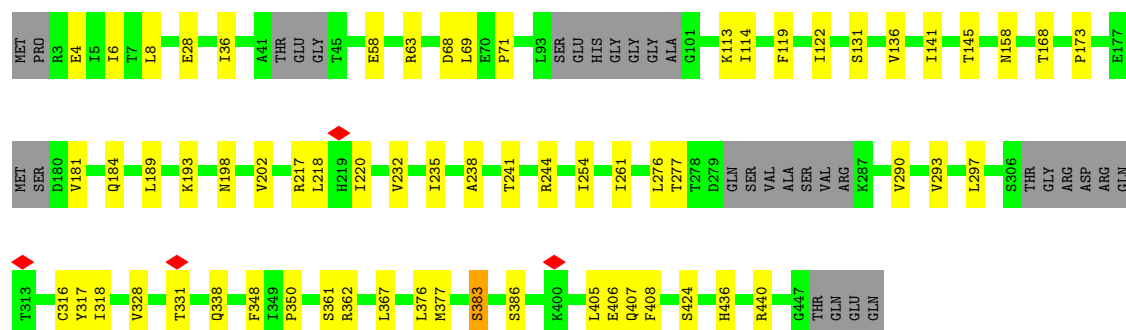
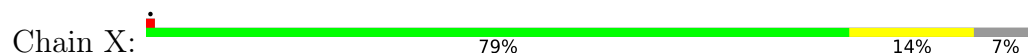
• Molecule 7: Tubulin gamma-1 chain



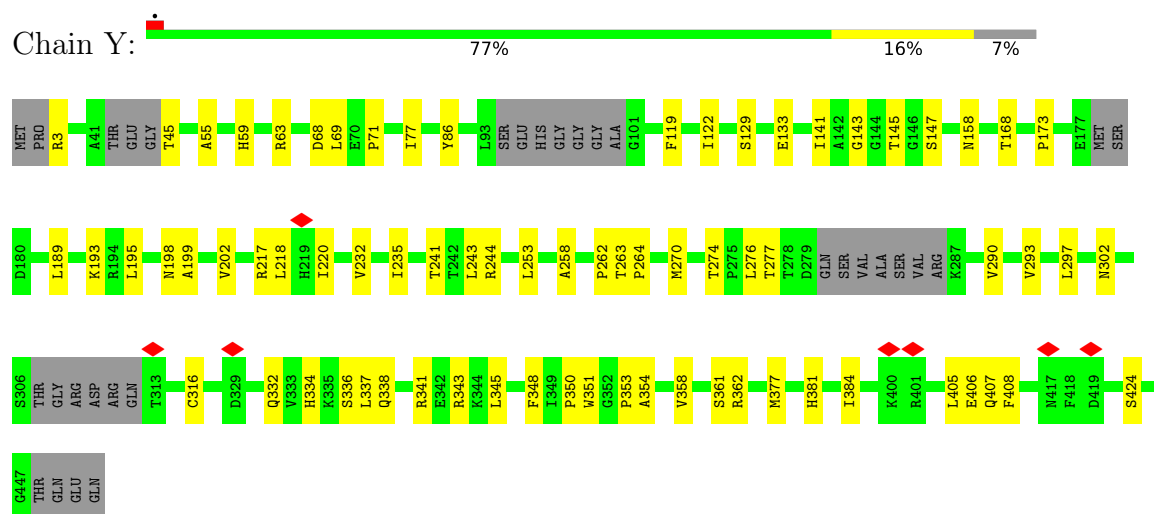
• Molecule 7: Tubulin gamma-1 chain



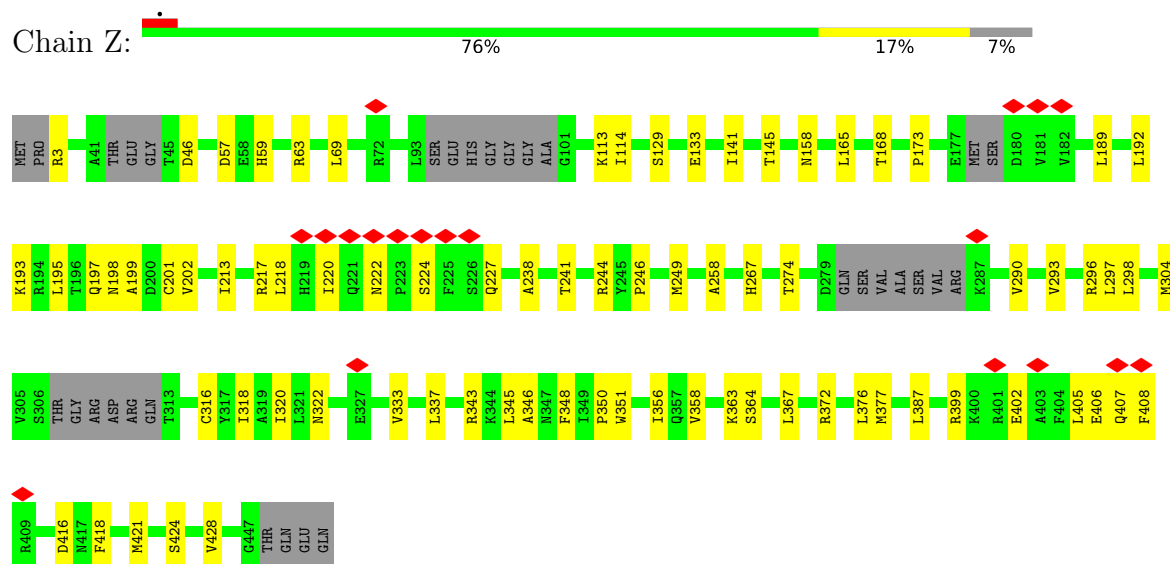
• Molecule 7: Tubulin gamma-1 chain



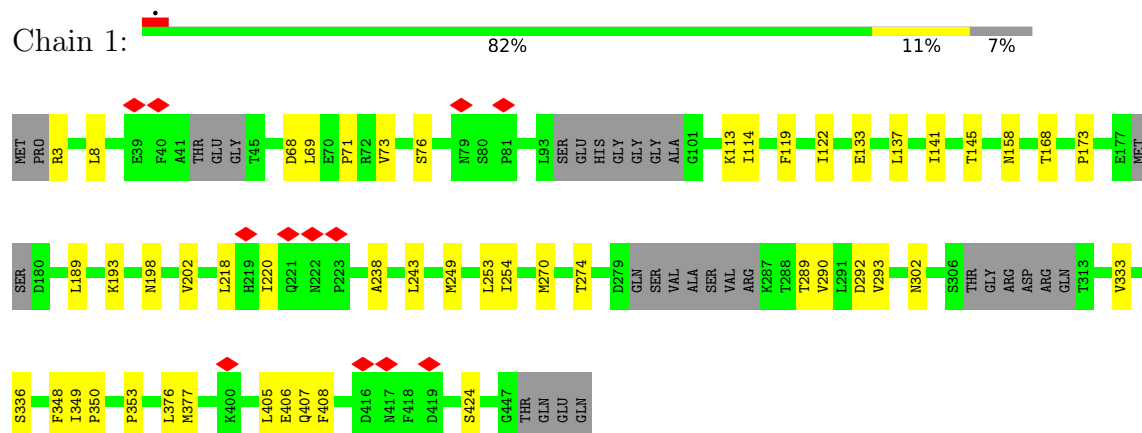
- Molecule 7: Tubulin gamma-1 chain



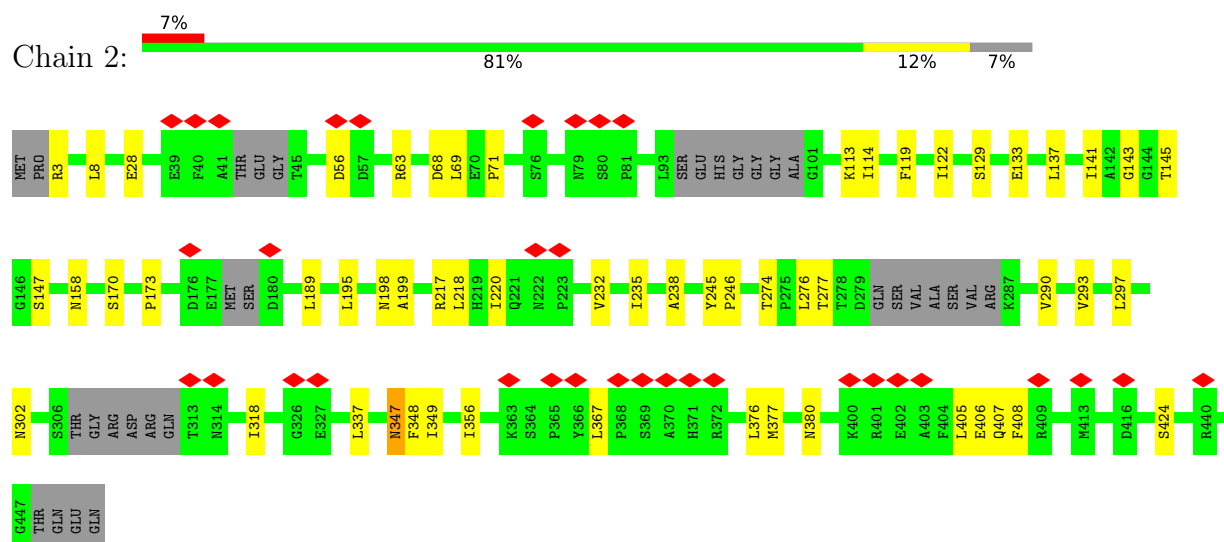
- Molecule 7: Tubulin gamma-1 chain



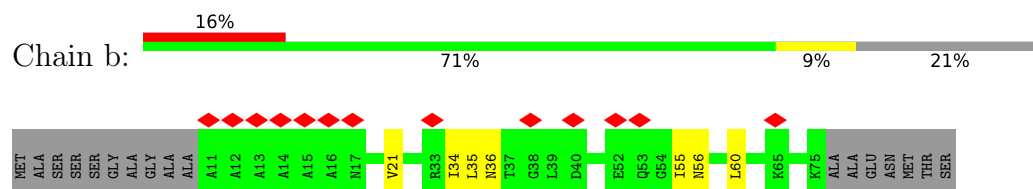
- Molecule 7: Tubulin gamma-1 chain



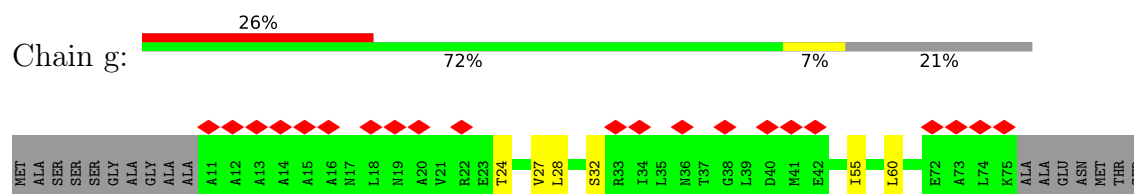
- Molecule 7: Tubulin gamma-1 chain



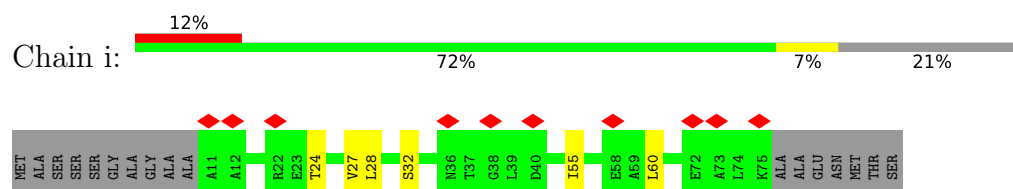
- Molecule 8: Mitotic-spindle organizing protein 1



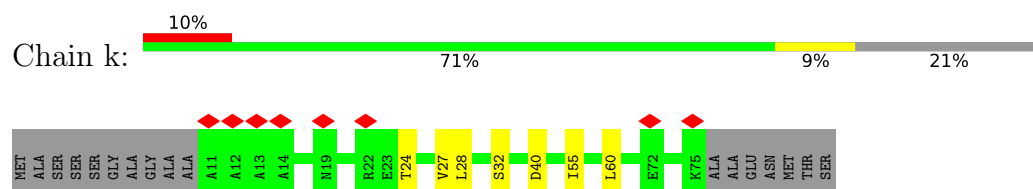
- Molecule 8: Mitotic-spindle organizing protein 1



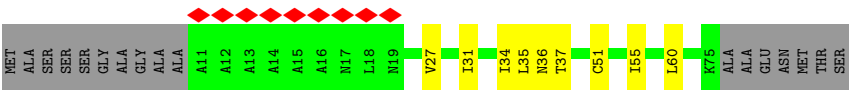
- Molecule 8: Mitotic-spindle organizing protein 1



- Molecule 8: Mitotic-spindle organizing protein 1



- Molecule 8: Mitotic-spindle organizing protein 1



● Molecule 8: Mitotic-spindle organizing protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2645	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	0.091	Depositor
Minimum map value	-0.035	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0319	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	e	0.45	1/1818 (0.1%)	0.43	1/2525 (0.0%)
2	A	0.29	0/5085	0.69	6/6866 (0.1%)
2	C	0.29	0/5151	0.68	4/6955 (0.1%)
2	E	0.29	0/5311	0.69	4/7169 (0.1%)
2	G	0.30	0/5326	0.69	5/7188 (0.1%)
2	M	0.29	0/5295	0.68	3/7147 (0.0%)
3	B	0.30	1/5125 (0.0%)	0.69	6/6919 (0.1%)
3	D	0.28	1/4897 (0.0%)	0.65	3/6610 (0.0%)
3	F	0.29	1/5036 (0.0%)	0.66	4/6798 (0.1%)
3	H	0.30	2/5001 (0.0%)	0.68	4/6750 (0.1%)
3	N	0.31	2/5001 (0.0%)	0.68	8/6750 (0.1%)
3	a	0.23	0/948	0.56	0/1277
3	f	0.23	0/815	0.57	0/1096
3	h	0.22	0/815	0.55	0/1096
3	j	0.42	0/877	0.82	3/1179 (0.3%)
4	I	0.32	0/4319	0.74	8/5849 (0.1%)
4	K	0.34	0/4683	0.76	8/6338 (0.1%)
5	J	0.35	0/4501	0.73	11/6089 (0.2%)
5	l	0.31	0/895	0.85	6/1210 (0.5%)
6	L	0.37	0/4666	0.72	9/6310 (0.1%)
6	c	0.33	0/1235	0.71	1/1664 (0.1%)
7	1	0.31	0/3439	0.69	2/4658 (0.0%)
7	2	0.31	0/3439	0.68	4/4658 (0.1%)
7	O	0.34	0/3439	0.72	2/4658 (0.0%)
7	P	0.36	0/3439	0.75	3/4658 (0.1%)
7	Q	0.35	0/3439	0.73	3/4658 (0.1%)
7	R	0.34	0/3439	0.72	2/4658 (0.0%)
7	S	0.34	0/3439	0.74	3/4658 (0.1%)
7	T	0.31	0/3439	0.67	2/4658 (0.0%)
7	U	0.32	0/3439	0.68	2/4658 (0.0%)
7	V	0.31	0/3439	0.68	5/4658 (0.1%)
7	W	0.30	0/3439	0.66	2/4658 (0.0%)
7	X	0.30	0/3439	0.66	2/4658 (0.0%)
7	Y	0.32	0/3439	0.71	2/4658 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	Z	0.32	0/3439	0.65	2/4658 (0.0%)
8	b	0.31	0/484	0.64	0/653
8	d	0.28	0/454	0.57	0/611
8	g	0.25	0/484	0.58	0/653
8	i	0.25	0/484	0.54	0/653
8	k	0.25	0/484	0.57	0/653
8	m	0.33	0/484	0.76	0/653
All	All	0.32	8/127820 (0.0%)	0.69	130/172873 (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
2	A	0	9
2	C	0	7
2	E	0	7
2	G	0	10
2	M	0	8
3	B	0	3
3	D	0	3
3	F	0	5
3	H	0	7
3	N	0	6
3	j	0	1
4	I	0	7
4	K	0	7
5	J	0	1
5	l	0	3
6	L	0	1
7	2	0	1
7	P	0	2
7	V	0	2
All	All	0	90

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	e	243	PRO	N-CD	17.82	1.72	1.47
3	N	503	THR	N-CA	5.68	1.53	1.46
3	B	840	ILE	CA-CB	5.38	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	840	ILE	CA-CB	5.37	1.57	1.53
3	H	840	ILE	CA-CB	5.37	1.57	1.53

The worst 5 of 130 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	577	LYS	CB-CG-CD	8.81	131.56	111.30
4	I	577	LYS	CB-CG-CD	8.78	131.48	111.30
5	l	121	PRO	CA-N-CD	-8.69	99.83	112.00
5	l	130	PRO	CA-N-CD	-8.69	99.83	112.00
3	H	871	GLU	CA-CB-CG	8.64	131.38	114.10

There are no chirality outliers.

5 of 90 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	238	LEU	Peptide
2	A	239	ALA	Peptide
2	A	426	LYS	Peptide
2	A	467	VAL	Peptide
2	A	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	e	1818	0	860	7	0
2	A	4978	0	4996	83	0
2	C	5044	0	5081	99	0
2	E	5202	0	5241	82	0
2	G	5217	0	5248	91	0
2	M	5186	0	5219	86	0
3	B	5021	0	5002	90	0
3	D	4796	0	4775	98	0
3	F	4933	0	4919	104	0
3	H	4899	0	4880	84	0
3	N	4899	0	4880	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	a	933	0	953	10	0
3	f	803	0	831	8	0
3	h	803	0	831	5	0
3	j	864	0	894	34	0
4	I	4222	0	4250	59	0
4	K	4579	0	4586	60	0
5	J	4406	0	4452	58	0
5	l	876	0	842	39	0
6	L	4556	0	4559	43	0
6	c	1220	0	1231	27	0
7	1	3371	0	3320	27	0
7	2	3371	0	3320	28	0
7	O	3371	0	3320	42	0
7	P	3371	0	3320	34	0
7	Q	3371	0	3320	41	0
7	R	3371	0	3320	44	0
7	S	3371	0	3320	36	0
7	T	3371	0	3320	21	0
7	U	3371	0	3320	29	0
7	V	3371	0	3320	20	0
7	W	3371	0	3320	35	0
7	X	3371	0	3320	34	0
7	Y	3371	0	3320	44	0
7	Z	3371	0	3320	42	0
8	b	484	0	512	8	0
8	d	454	0	482	7	0
8	g	484	0	512	5	0
8	i	484	0	512	5	0
8	k	484	0	512	6	0
8	m	484	0	512	26	0
All	All	125323	0	124052	1591	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 6.

The worst 5 of 1591 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)
8:m:36:ASN:HB2	5:l:121:PRO:CG	1.44	1.43
8:m:36:ASN:CB	5:l:121:PRO:CG	2.00	1.39
1:e:243:PRO:CD	1:e:243:PRO:N	1.72	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:776:ARG:NH2	3:j:106:ARG:HE	1.52	1.08
8:m:36:ASN:CB	5:l:121:PRO:HG3	1.76	1.06

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	e	360/375 (96%)	345 (96%)	15 (4%)	0	100	100
2	A	599/902 (66%)	567 (95%)	31 (5%)	1 (0%)	43	78
2	C	606/902 (67%)	573 (95%)	30 (5%)	3 (0%)	24	63
2	E	626/902 (69%)	587 (94%)	36 (6%)	3 (0%)	24	63
2	G	628/902 (70%)	594 (95%)	33 (5%)	1 (0%)	43	78
2	M	624/902 (69%)	592 (95%)	31 (5%)	1 (0%)	43	78
3	B	602/907 (66%)	568 (94%)	31 (5%)	3 (0%)	24	63
3	D	571/907 (63%)	546 (96%)	25 (4%)	0	100	100
3	F	591/907 (65%)	561 (95%)	29 (5%)	1 (0%)	43	78
3	H	584/907 (64%)	550 (94%)	32 (6%)	2 (0%)	36	72
3	N	584/907 (64%)	551 (94%)	31 (5%)	2 (0%)	36	72
3	a	112/907 (12%)	106 (95%)	6 (5%)	0	100	100
3	f	97/907 (11%)	92 (95%)	5 (5%)	0	100	100
3	h	97/907 (11%)	92 (95%)	5 (5%)	0	100	100
3	j	105/907 (12%)	94 (90%)	11 (10%)	0	100	100
4	I	511/667 (77%)	483 (94%)	23 (4%)	5 (1%)	12	49
4	K	548/667 (82%)	515 (94%)	27 (5%)	6 (1%)	11	46
5	J	506/1024 (49%)	476 (94%)	25 (5%)	5 (1%)	12	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	l	104/1024 (10%)	95 (91%)	6 (6%)	3 (3%)	3	23
6	L	540/1819 (30%)	506 (94%)	29 (5%)	5 (1%)	14	51
6	c	148/1819 (8%)	141 (95%)	7 (5%)	0	100	100
7	1	408/451 (90%)	389 (95%)	18 (4%)	1 (0%)	43	78
7	2	408/451 (90%)	388 (95%)	18 (4%)	2 (0%)	24	63
7	O	408/451 (90%)	392 (96%)	14 (3%)	2 (0%)	24	63
7	P	408/451 (90%)	396 (97%)	11 (3%)	1 (0%)	43	78
7	Q	408/451 (90%)	391 (96%)	16 (4%)	1 (0%)	43	78
7	R	408/451 (90%)	390 (96%)	17 (4%)	1 (0%)	43	78
7	S	408/451 (90%)	391 (96%)	15 (4%)	2 (0%)	24	63
7	T	408/451 (90%)	393 (96%)	14 (3%)	1 (0%)	43	78
7	U	408/451 (90%)	390 (96%)	17 (4%)	1 (0%)	43	78
7	V	408/451 (90%)	389 (95%)	17 (4%)	2 (0%)	24	63
7	W	408/451 (90%)	386 (95%)	21 (5%)	1 (0%)	43	78
7	X	408/451 (90%)	393 (96%)	14 (3%)	1 (0%)	43	78
7	Y	408/451 (90%)	391 (96%)	16 (4%)	1 (0%)	43	78
7	Z	408/451 (90%)	396 (97%)	11 (3%)	1 (0%)	43	78
8	b	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
8	d	57/82 (70%)	56 (98%)	1 (2%)	0	100	100
8	g	63/82 (77%)	63 (100%)	0	0	100	100
8	i	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
8	k	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
8	m	63/82 (77%)	61 (97%)	2 (3%)	0	100	100
All	All	15227/26874 (57%)	14475 (95%)	693 (5%)	59 (0%)	31	67

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	891	PRO
2	E	425	ASP
3	H	503	THR
4	I	404	LEU
5	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	e	8/318 (2%)	8 (100%)	0	100	100
2	A	549/791 (69%)	496 (90%)	53 (10%)	8	24
2	C	556/791 (70%)	504 (91%)	52 (9%)	8	26
2	E	574/791 (73%)	523 (91%)	51 (9%)	9	28
2	G	575/791 (73%)	521 (91%)	54 (9%)	8	26
2	M	572/791 (72%)	520 (91%)	52 (9%)	9	27
3	B	548/798 (69%)	493 (90%)	55 (10%)	7	24
3	D	525/798 (66%)	474 (90%)	51 (10%)	8	24
3	F	539/798 (68%)	487 (90%)	52 (10%)	8	25
3	H	536/798 (67%)	485 (90%)	51 (10%)	8	25
3	N	536/798 (67%)	485 (90%)	51 (10%)	8	25
3	a	101/798 (13%)	101 (100%)	0	100	100
3	f	88/798 (11%)	88 (100%)	0	100	100
3	h	88/798 (11%)	88 (100%)	0	100	100
3	j	96/798 (12%)	95 (99%)	1 (1%)	68	78
4	I	471/594 (79%)	441 (94%)	30 (6%)	16	37
4	K	509/594 (86%)	473 (93%)	36 (7%)	13	35
5	J	493/933 (53%)	491 (100%)	2 (0%)	84	84
5	l	96/933 (10%)	96 (100%)	0	100	100
6	L	492/1546 (32%)	486 (99%)	6 (1%)	63	75
6	c	135/1546 (9%)	135 (100%)	0	100	100
7	1	375/400 (94%)	375 (100%)	0	100	100
7	2	375/400 (94%)	375 (100%)	0	100	100
7	O	375/400 (94%)	375 (100%)	0	100	100
7	P	375/400 (94%)	374 (100%)	1 (0%)	86	86
7	Q	375/400 (94%)	375 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	R	375/400 (94%)	374 (100%)	1 (0%)	86	86
7	S	375/400 (94%)	374 (100%)	1 (0%)	86	86
7	T	375/400 (94%)	375 (100%)	0	100	100
7	U	375/400 (94%)	375 (100%)	0	100	100
7	V	375/400 (94%)	374 (100%)	1 (0%)	86	86
7	W	375/400 (94%)	373 (100%)	2 (0%)	81	83
7	X	375/400 (94%)	373 (100%)	2 (0%)	81	83
7	Y	375/400 (94%)	374 (100%)	1 (0%)	86	86
7	Z	375/400 (94%)	371 (99%)	4 (1%)	65	76
8	b	53/62 (86%)	53 (100%)	0	100	100
8	d	53/62 (86%)	53 (100%)	0	100	100
8	g	53/62 (86%)	53 (100%)	0	100	100
8	i	53/62 (86%)	53 (100%)	0	100	100
8	k	53/62 (86%)	53 (100%)	0	100	100
8	m	53/62 (86%)	53 (100%)	0	100	100
All	All	13655/23573 (58%)	13045 (96%)	610 (4%)	26	46

5 of 610 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	K	120	SER
3	N	423	SER
4	K	399	SER
4	K	118	SER
2	M	271	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 329 such sidechains are listed below:

Mol	Chain	Res	Type
7	W	54	GLN
8	d	53	GLN
7	W	338	GLN
7	Z	302	ASN
7	2	54	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.

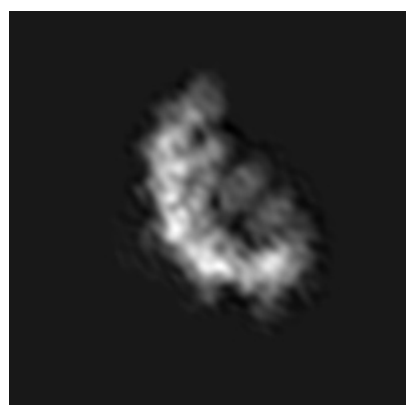
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14017. 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

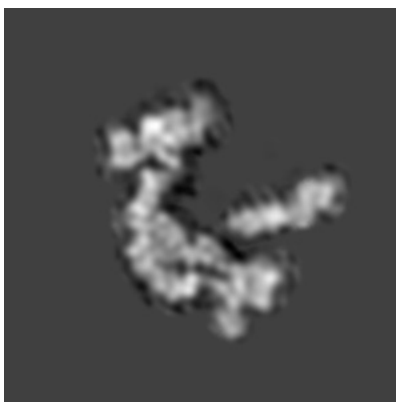
The images above show the map projected in three orthogonal directions.

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: 63



Y Index: 81

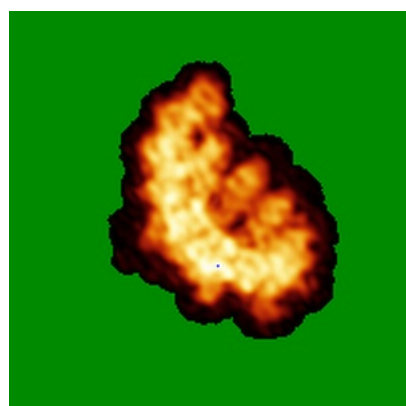


Z Index: 71

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

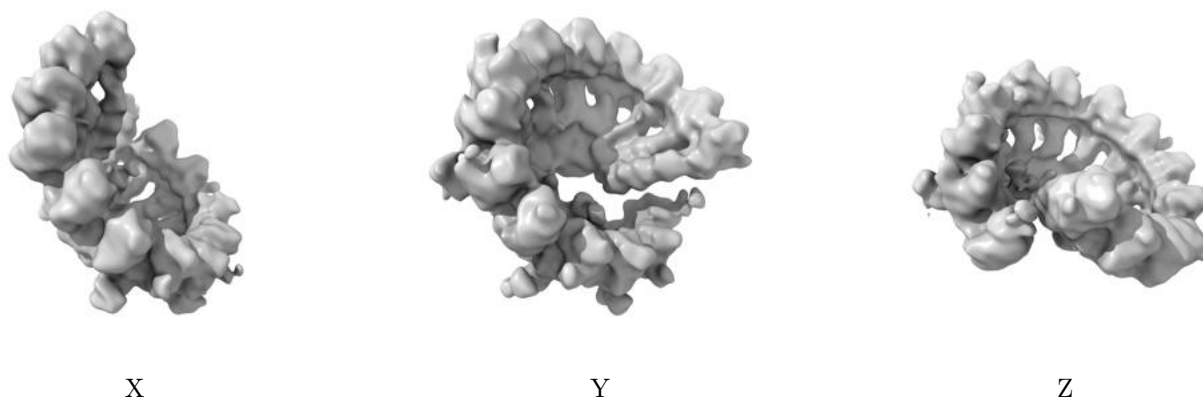


Z

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 0.0319. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

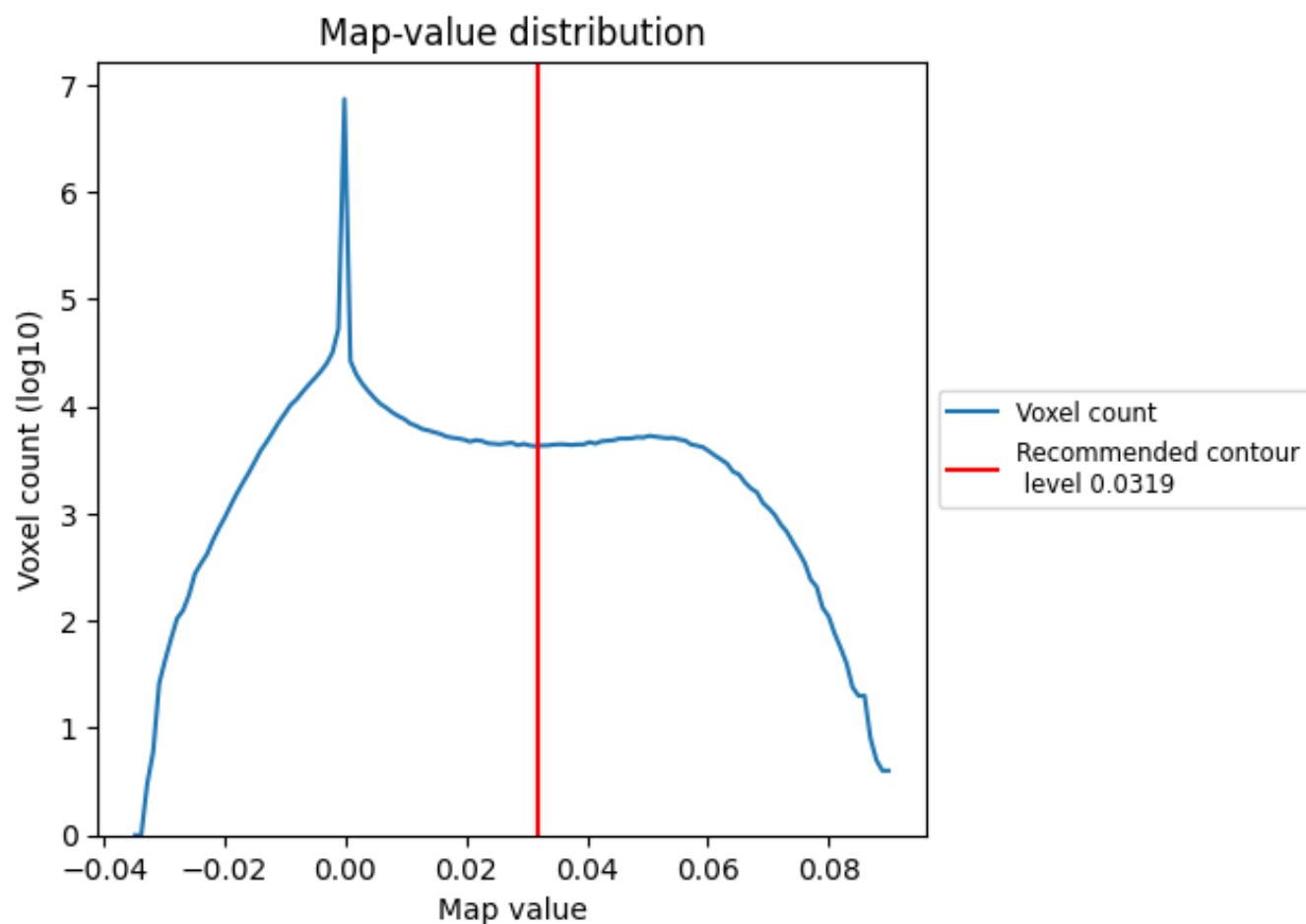
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

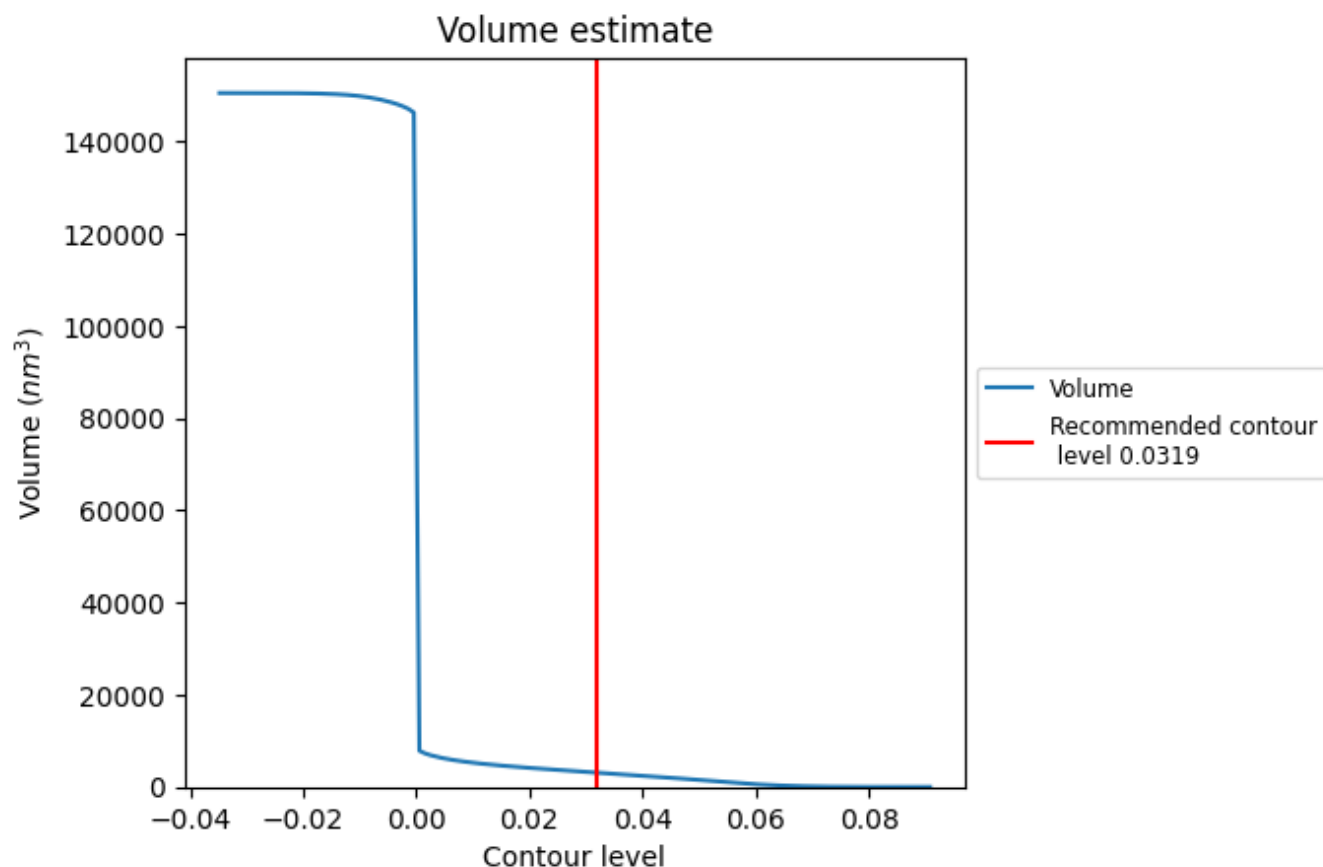
This section contains the results of statistical analysis of the map.

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.

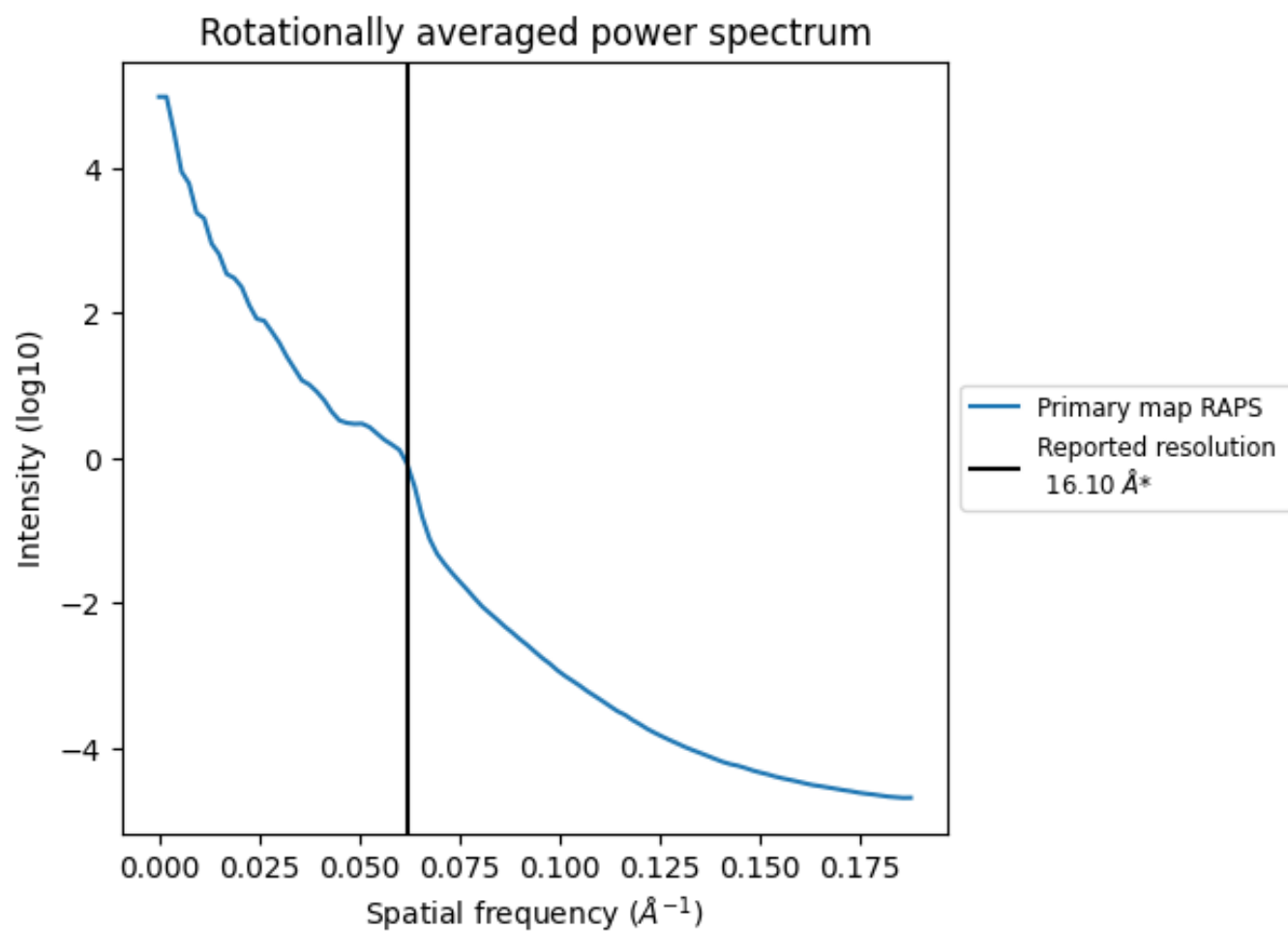
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3109 nm^3 ; this corresponds to an approximate mass of 2809 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 0.062 Å⁻¹

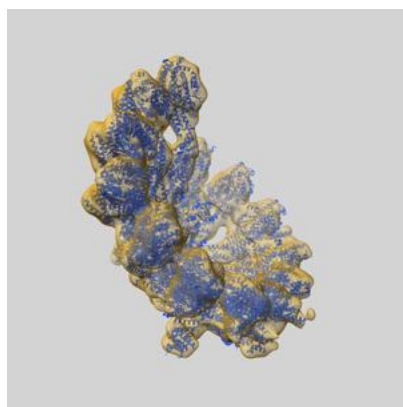
8 Fourier-Shell correlation

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

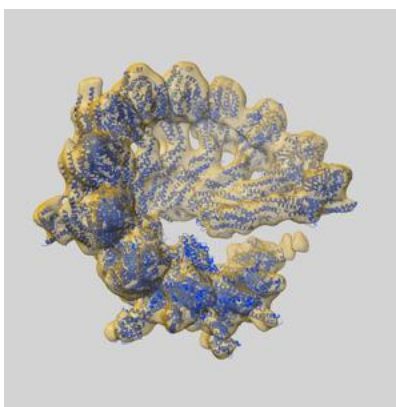
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14017 and PDB model 7QJC. Per-residue inclusion information can be found in section [3](#) on page [8](#).

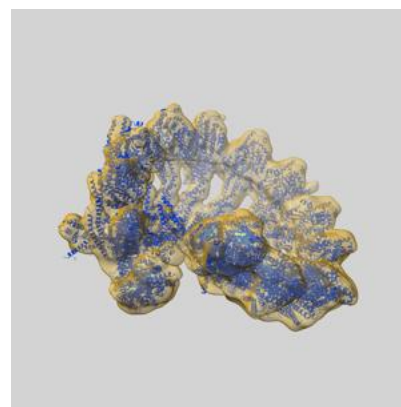
9.1 Map-model overlay [i](#)



X



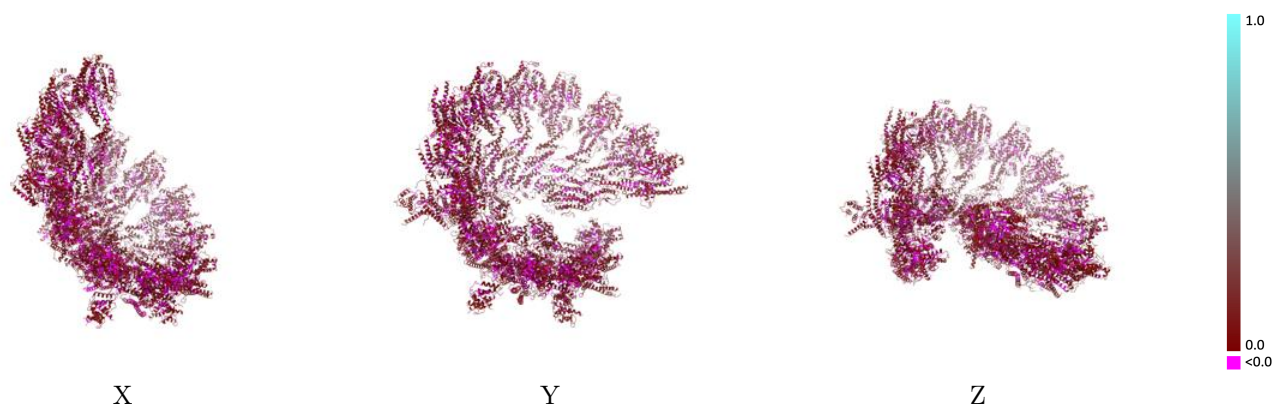
Y



Z

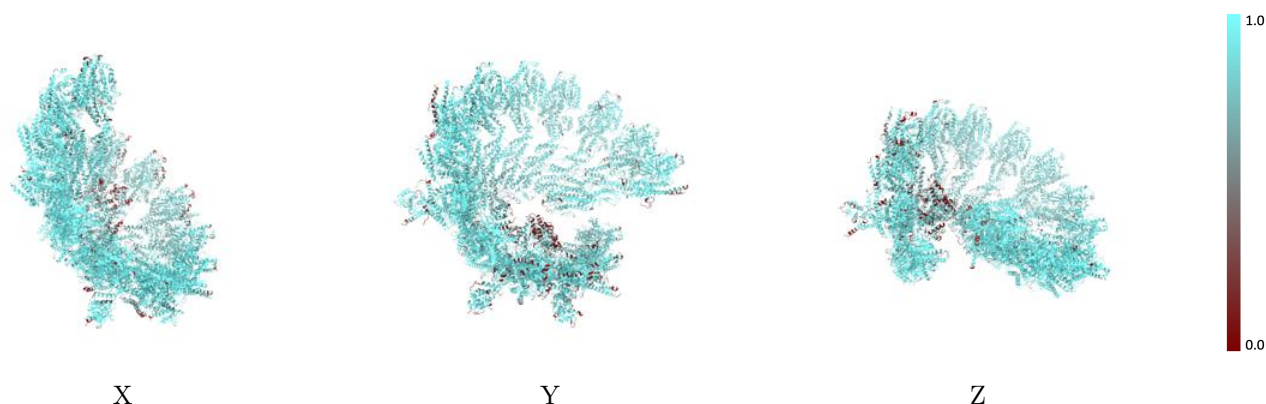
The images above show the 3D surface view of the map at the recommended contour level 0.0319 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



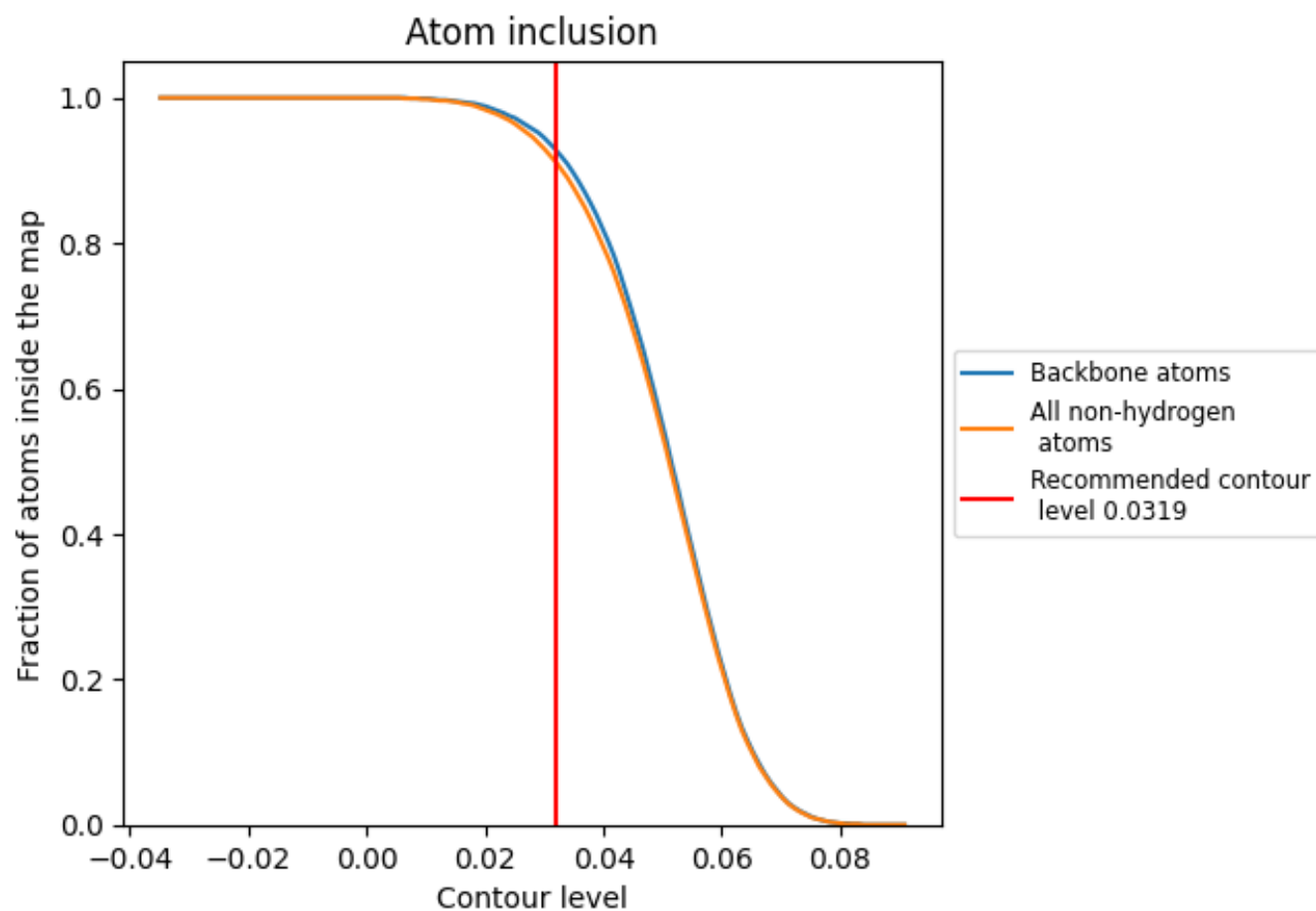
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0319).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (0.0319) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.0600
1	 0.9560	 0.0550
2	 0.9120	 0.0460
A	 0.9530	 0.0720
B	 0.9060	 0.0580
C	 0.8960	 0.0590
D	 0.9160	 0.0600
E	 0.9370	 0.0600
F	 0.9370	 0.0650
G	 0.9230	 0.0630
H	 0.9160	 0.0650
I	 0.9330	 0.0620
J	 0.9640	 0.0680
K	 0.9490	 0.0730
L	 0.9440	 0.0630
M	 0.9160	 0.0630
N	 0.8850	 0.0630
O	 0.9230	 0.0440
P	 0.8770	 0.0430
Q	 0.8460	 0.0540
R	 0.8550	 0.0500
S	 0.9260	 0.0570
T	 0.9640	 0.0520
U	 0.9760	 0.0510
V	 0.9770	 0.0550
W	 0.9650	 0.0510
X	 0.9780	 0.0590
Y	 0.9660	 0.0550
Z	 0.9400	 0.0550
a	 0.8090	 0.0610
b	 0.7480	 0.0860
c	 0.6540	 0.0660
d	 0.6260	 0.0820
e	 0.4940	 0.0720
f	 0.8260	 0.0770



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Chain	Atom inclusion	Q-score
g	 0.6680	 0.0710
h	 0.7740	 0.0630
i	 0.7750	 0.0790
j	 0.8360	 0.0650
k	 0.8760	 0.0850
l	 0.8380	 0.0790
m	 0.8510	 0.0660