



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:54 AM UTC

PDB ID : 8RX1 / pdb_00008rx1
EMDB ID : EMD-19570
Title : CryoEM structure of the gTuRC-CM1dim complex
Authors : Llorca, O.; Serna, M.; Gonzalez-Rodriguez, N.
Deposited on : 2024-02-06
Resolution : 3.57 Å(reported)
Based on initial models : 6X0V, 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:

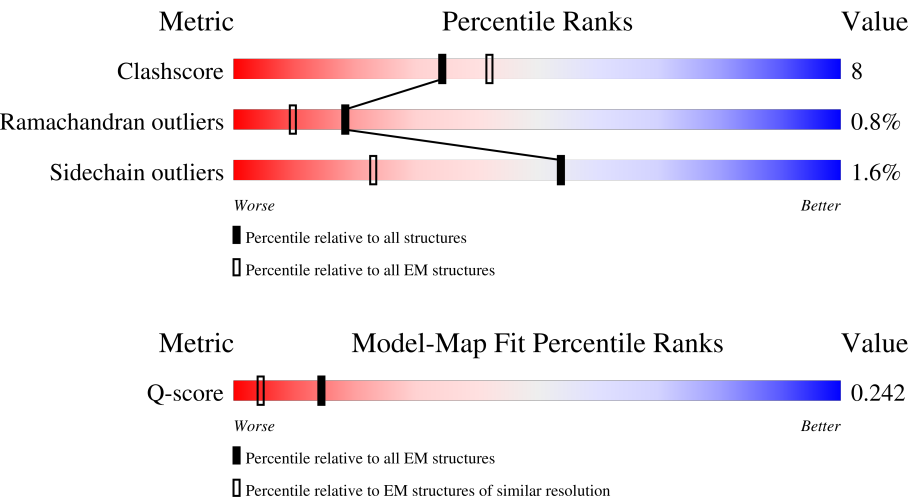
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.57 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.



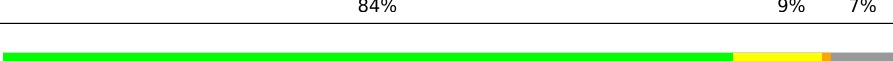
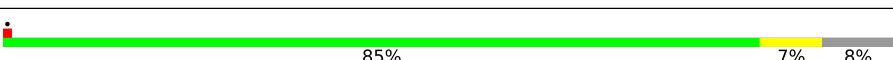
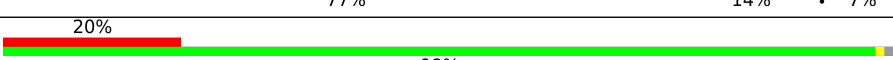
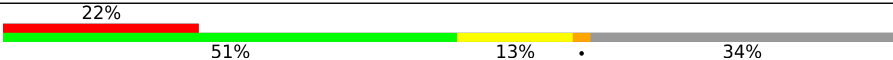
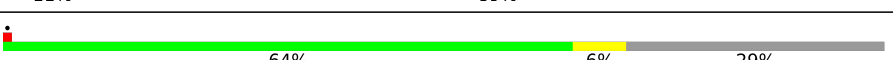
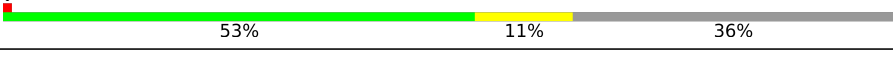
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12682 (3.07 - 4.07)

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	

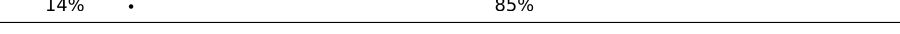
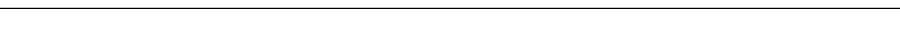
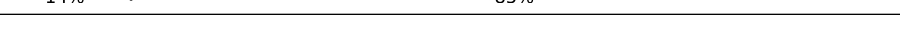
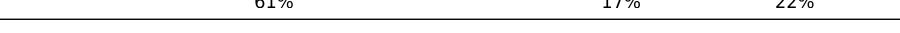
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Mol	Chain	Length	Quality of chain
1	Q	451	
1	R	451	
1	S	451	
1	T	451	
1	U	451	
1	V	451	
1	W	451	
1	X	451	
1	Y	451	
1	Z	451	
2	7	364	
3	A	902	
3	C	902	
3	E	902	
3	M	902	
3	f	902	
3	k	902	
4	B	907	
4	D	907	
4	F	907	
4	N	907	
4	b	907	
4	n	907	
5	G	229	
5	H	229	

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Mol	Chain	Length	Quality of chain
5	g	229	 13% 85%
5	h	229	 6% 14% 85%
5	i	229	 10% 86%
5	j	229	 7% 13% 86%
5	s	229	 14% 85%
5	t	229	 10% 5% 85%
5	u	229	 14% 85%
5	v	229	 14% 85%
6	I	667	 61% 17% 22%
6	K	667	 75% 9% 16%
7	J	1024	 48% 10% 41%
8	L	1819	 30% 66%
8	d	1819	 7% 92%
9	a	82	 62% 17% 21%
9	c	82	 5% 65% 7% 28%
10	e	158	 11% 29% 71%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 123860 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
			3365	2130	583	637	15		
1	2	415	Total	C	N	O	S	0	0
			3311	2095	574	627	15		
1	O	420	Total	C	N	O	S	0	0
			3365	2130	583	637	15		
1	P	420	Total	C	N	O	S	0	0
			3359	2127	580	637	15		
1	Q	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
1	R	420	Total	C	N	O	S	0	0
			3365	2130	583	637	15		
1	S	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
1	T	420	Total	C	N	O	S	0	0
			3359	2127	580	637	15		
1	U	420	Total	C	N	O	S	0	0
			3365	2130	583	637	15		
1	V	417	Total	C	N	O	S	0	0
			3325	2109	571	630	15		
1	W	417	Total	C	N	O	S	0	0
			3342	2114	579	634	15		
1	X	420	Total	C	N	O	S	0	0
			3371	2133	586	637	15		
1	Y	419	Total	C	N	O	S	0	0
			3363	2129	585	634	15		
1	Z	420	Total	C	N	O	S	0	0
			3365	2130	583	637	15		

- Molecule 2 is a protein called Actin b.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	7	360	Total	C	N	O	0	0
			1812	1091	360	361		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	599	Total	C	N	O	S	0	0
			4846	3135	802	877	32		
3	C	614	Total	C	N	O	S	0	0
			4973	3216	824	901	32		
3	E	638	Total	C	N	O	S	0	0
			5196	3351	870	942	33		
3	M	633	Total	C	N	O	S	0	0
			5158	3325	865	935	33		
3	f	95	Total	C	N	O		0	0
			481	291	95	95			
3	k	636	Total	C	N	O	S	0	0
			5180	3339	868	940	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
			5015	3195	885	910	25		
4	D	581	Total	C	N	O	S	0	0
			4790	3058	839	868	25		
4	F	599	Total	C	N	O	S	0	0
			4921	3140	865	891	25		
4	N	583	Total	C	N	O	S	0	0
			4810	3072	848	865	25		
4	b	116	Total	C	N	O	S	0	0
			933	591	171	169	2		
4	n	594	Total	C	N	O	S	0	0
			4875	3113	852	885	25		

- Molecule 5 is a protein called CM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	31	Total	C	N	O	S	0	0
			270	173	46	50	1		
5	H	35	Total	C	N	O	S	0	0
			317	202	55	58	2		
5	g	35	Total	C	N	O	S	0	0
			303	192	54	55	2		
5	h	35	Total	C	N	O	S	0	0
			317	202	55	58	2		
5	i	31	Total	C	N	O	S	0	0
			274	176	46	50	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	32	Total	C	N	O	S	0	0
			290	187	48	54	1		
5	s	35	Total	C	N	O	S	0	0
			303	192	54	55	2		
5	t	35	Total	C	N	O	S	0	0
			303	192	54	55	2		
5	u	35	Total	C	N	O	S	0	0
			317	202	55	58	2		
5	v	35	Total	C	N	O	S	0	0
			317	202	55	58	2		

- 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
			4203	2722	714	749	18		
6	K	562	Total	C	N	O	S	0	0
			4573	2961	778	816	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	601	Total	C	N	O	S	0	0
			4837	3127	811	872	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	617	Total	C	N	O	S	0	0
			4928	3217	830	855	26		
8	d	147	Total	C	N	O	S	0	0
			1152	727	198	219	8		

- Molecule 9 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
9	c	59	Total	C	N	O	S	0	0
			454	281	79	90	4		

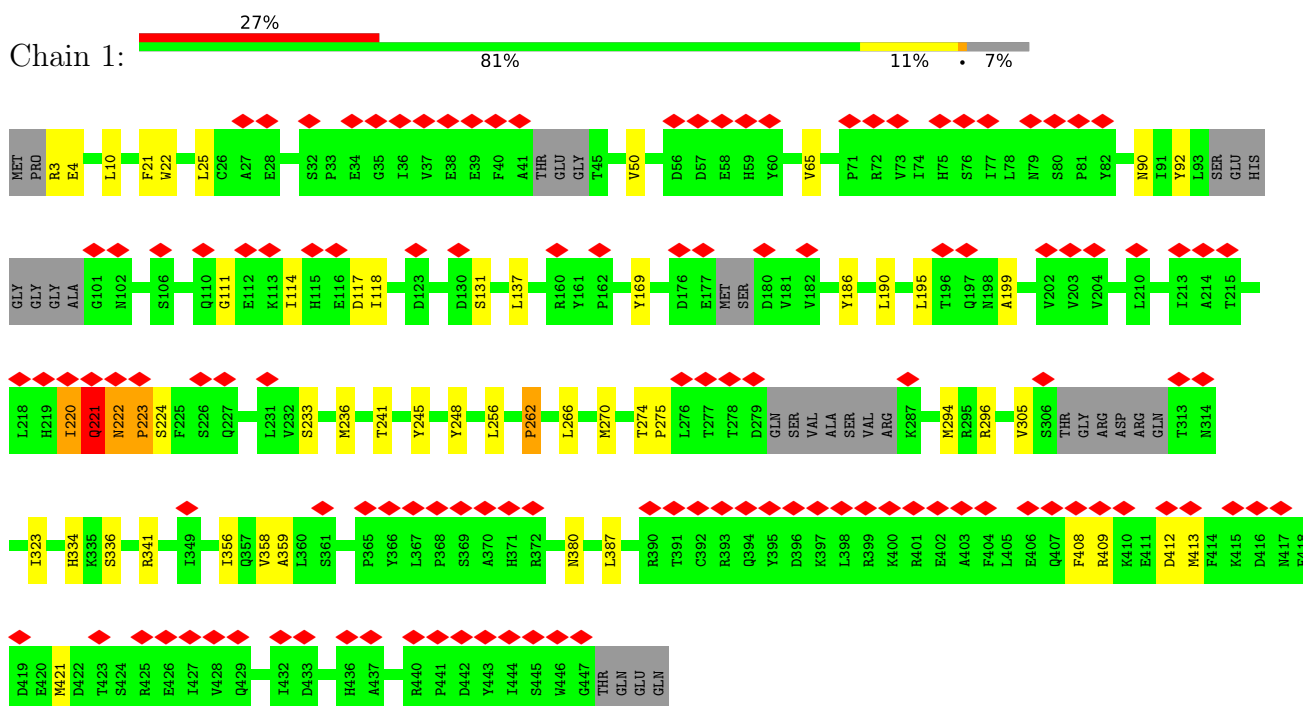
- Molecule 10 is a protein called Mitotic-spindle organizing protein 2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	e	46	Total	C	N	O	0	0
			231	139	46	46		

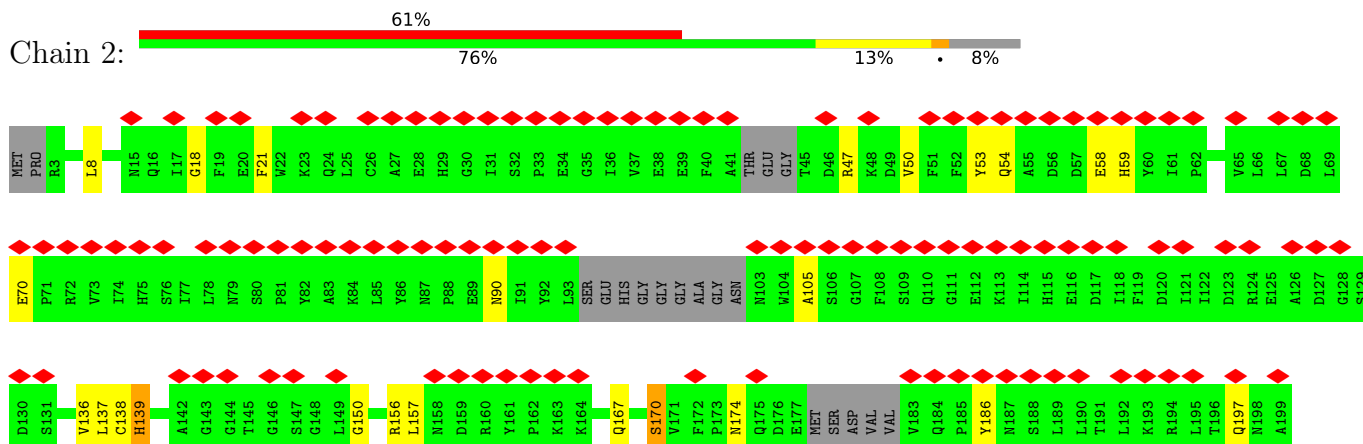
3 Residue-property plots

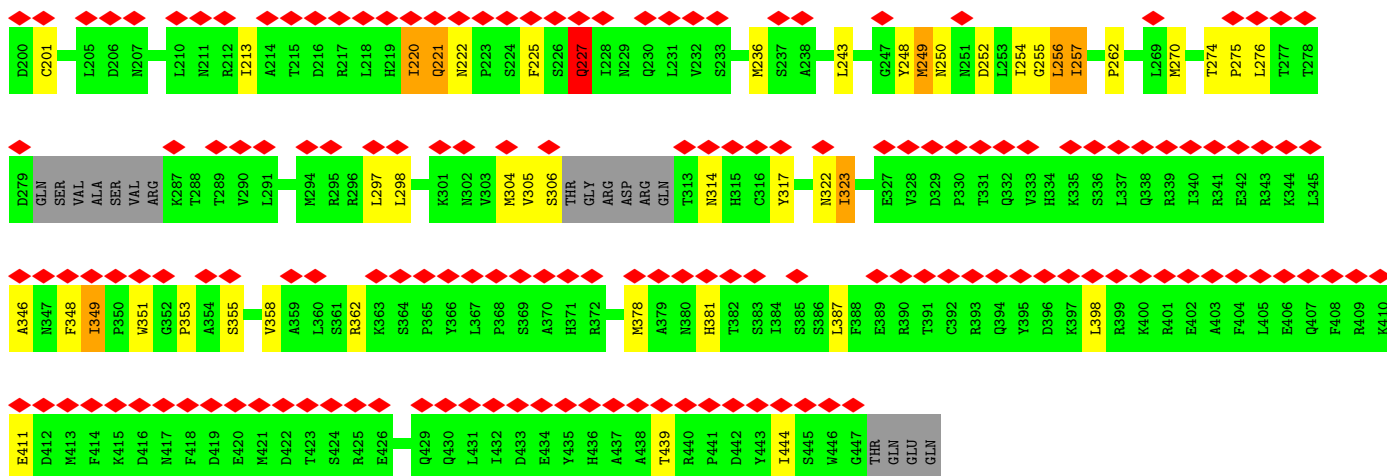
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

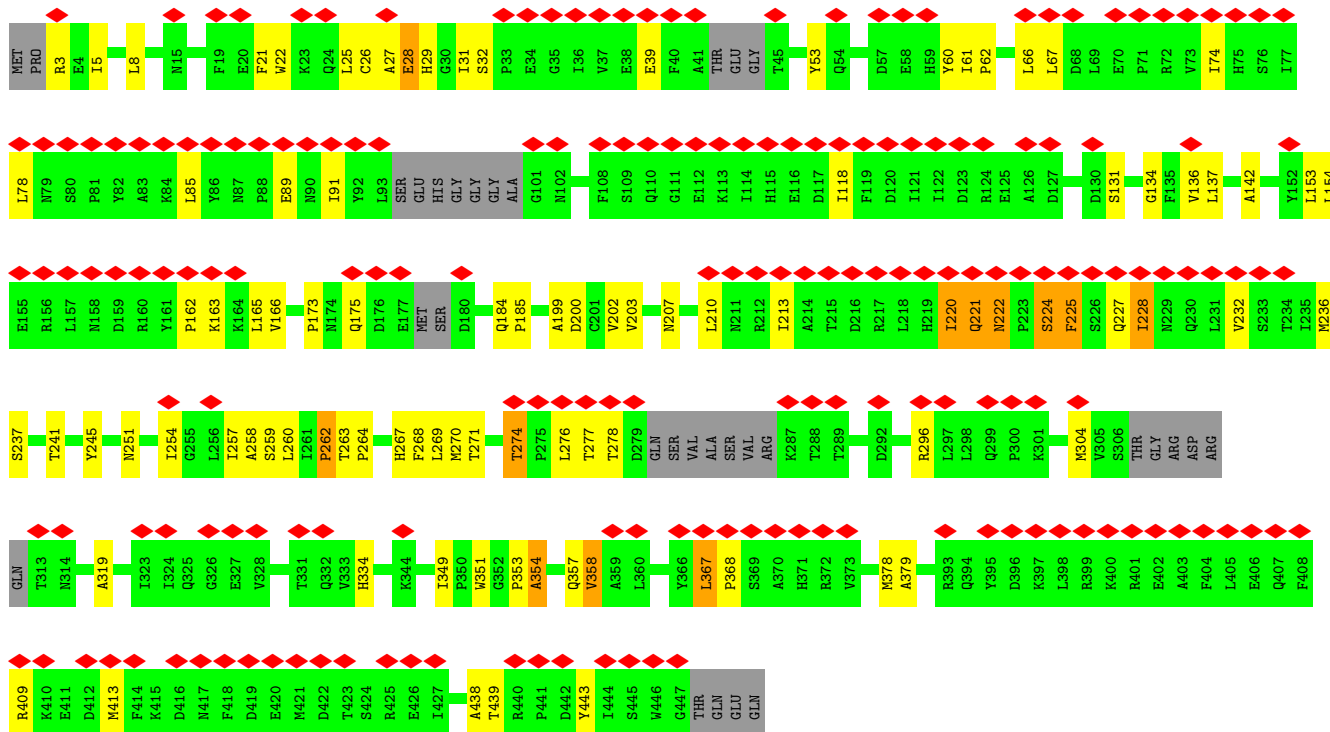
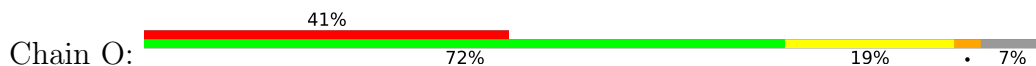


- Molecule 1: Tubulin gamma-1 chain

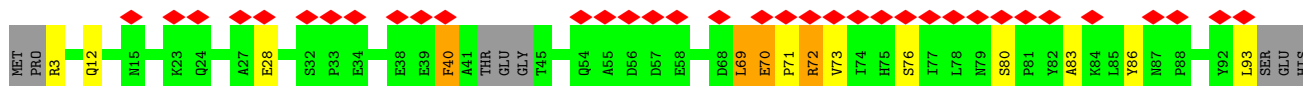
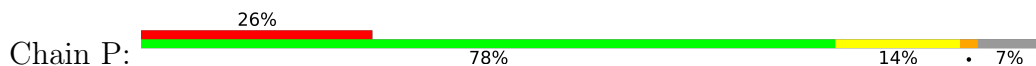


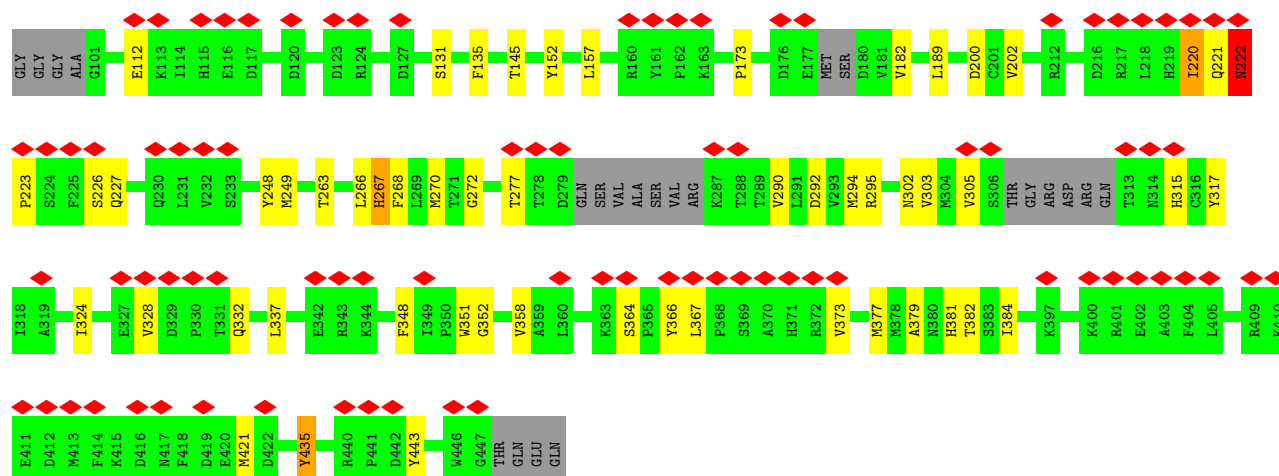


• Molecule 1: Tubulin gamma-1 chain



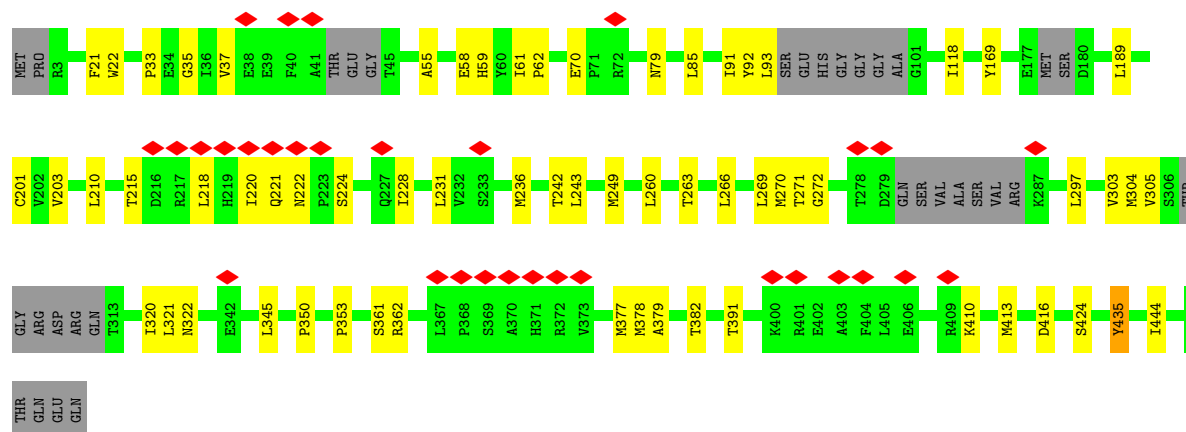
• Molecule 1: Tubulin gamma-1 chain





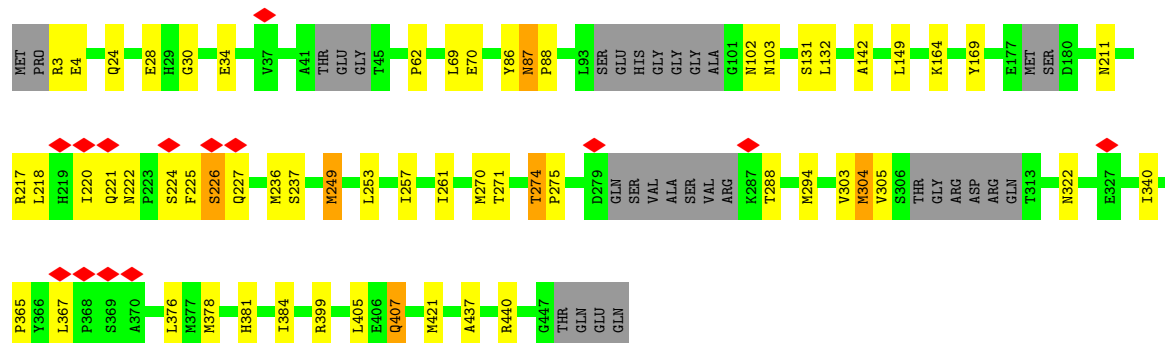
• Molecule 1: Tubulin gamma-1 chain

Chain Q: 79% 14% 7%



• Molecule 1: Tubulin gamma-1 chain

Chain R: 80% 12% 7%



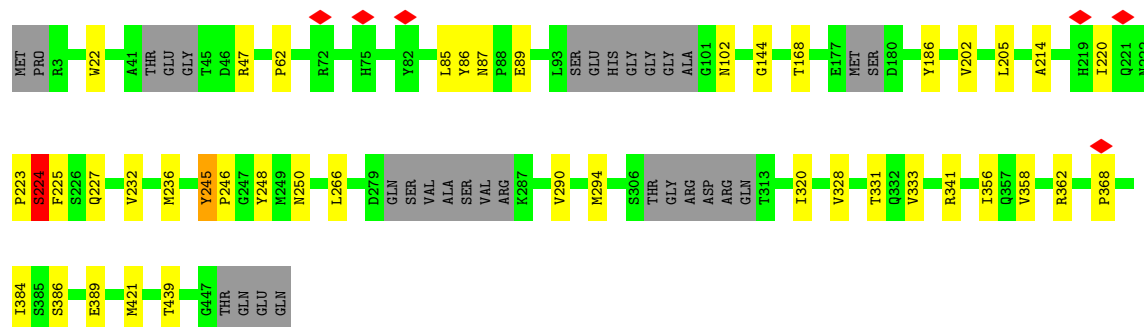
• Molecule 1: Tubulin gamma-1 chain

Chain S: 82% 11% 7%



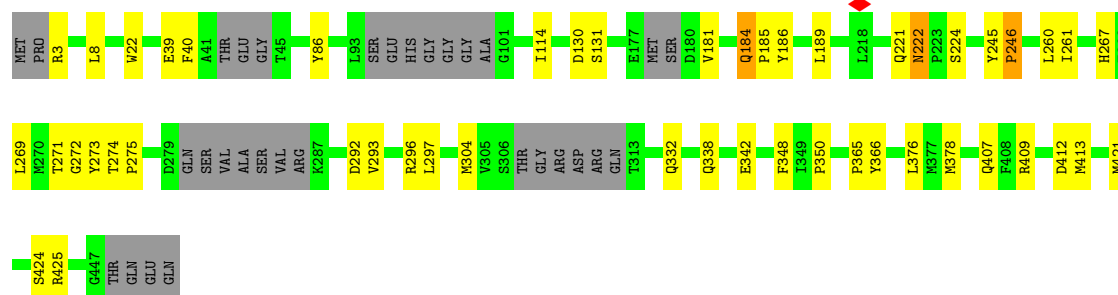
- Molecule 1: Tubulin gamma-1 chain

Chain T: 84% 9% 7%



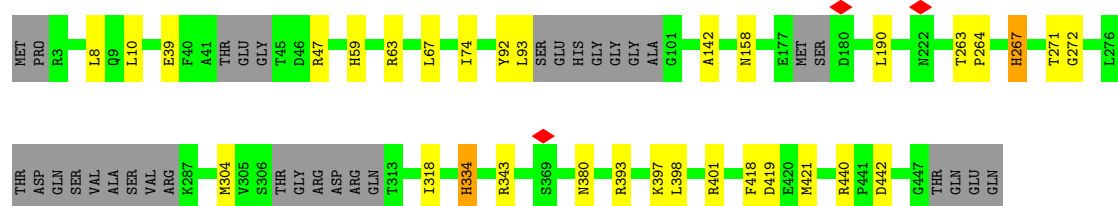
- Molecule 1: Tubulin gamma-1 chain

Chain U: 82% 10% 7%



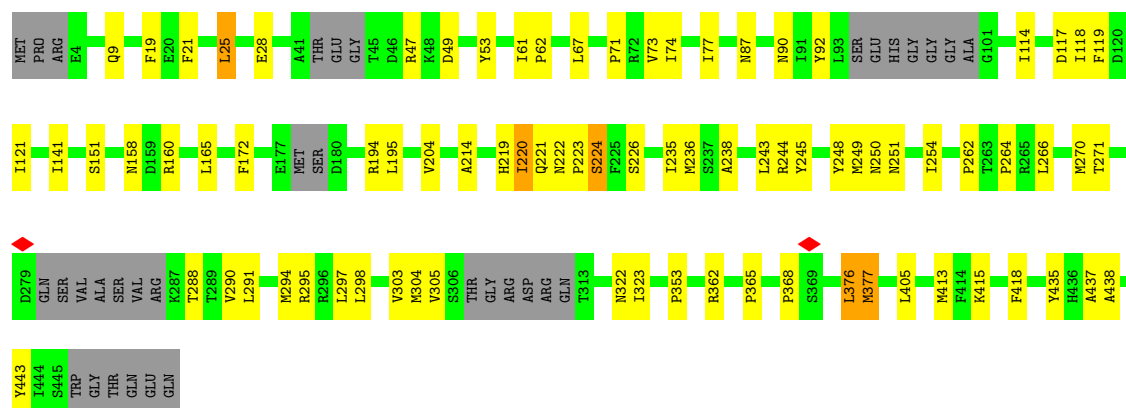
- Molecule 1: Tubulin gamma-1 chain

Chain V: 85% 7% 8%



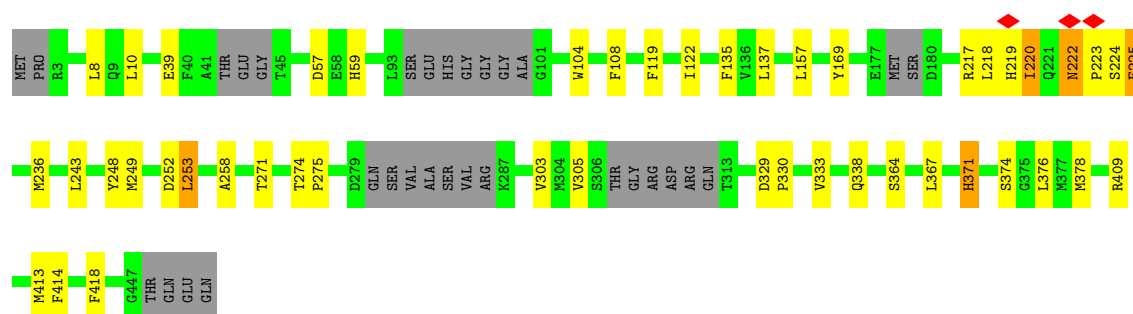
- Molecule 1: Tubulin gamma-1 chain

Chain W:  74% 17% 8%



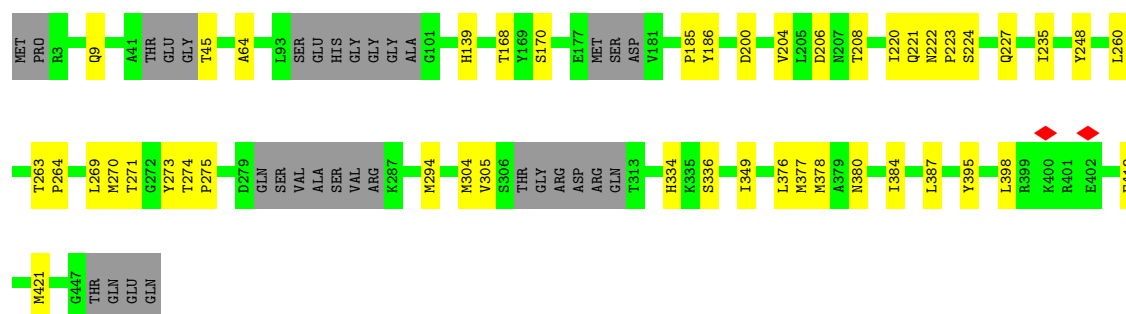
- Molecule 1: Tubulin gamma-1 chain

Chain X:  83% 9% 7%



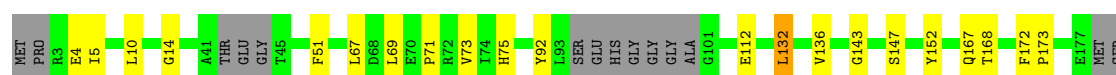
- Molecule 1: Tubulin gamma-1 chain

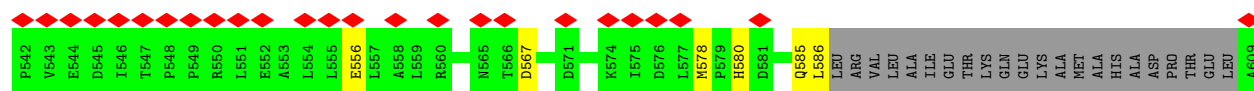
Chain Y:  83% 10% 7%

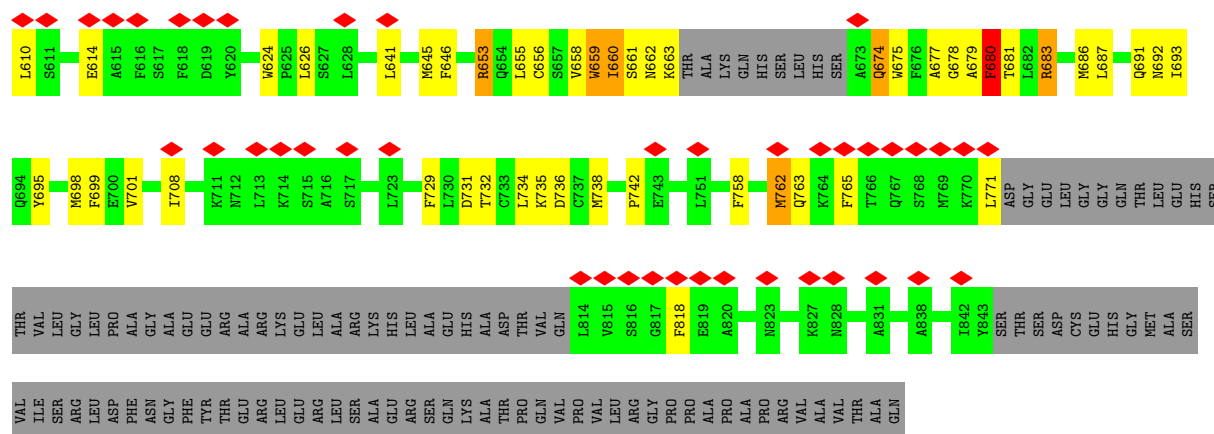


- Molecule 1: Tubulin gamma-1 chain

Chain Z:  77% 14% 7%

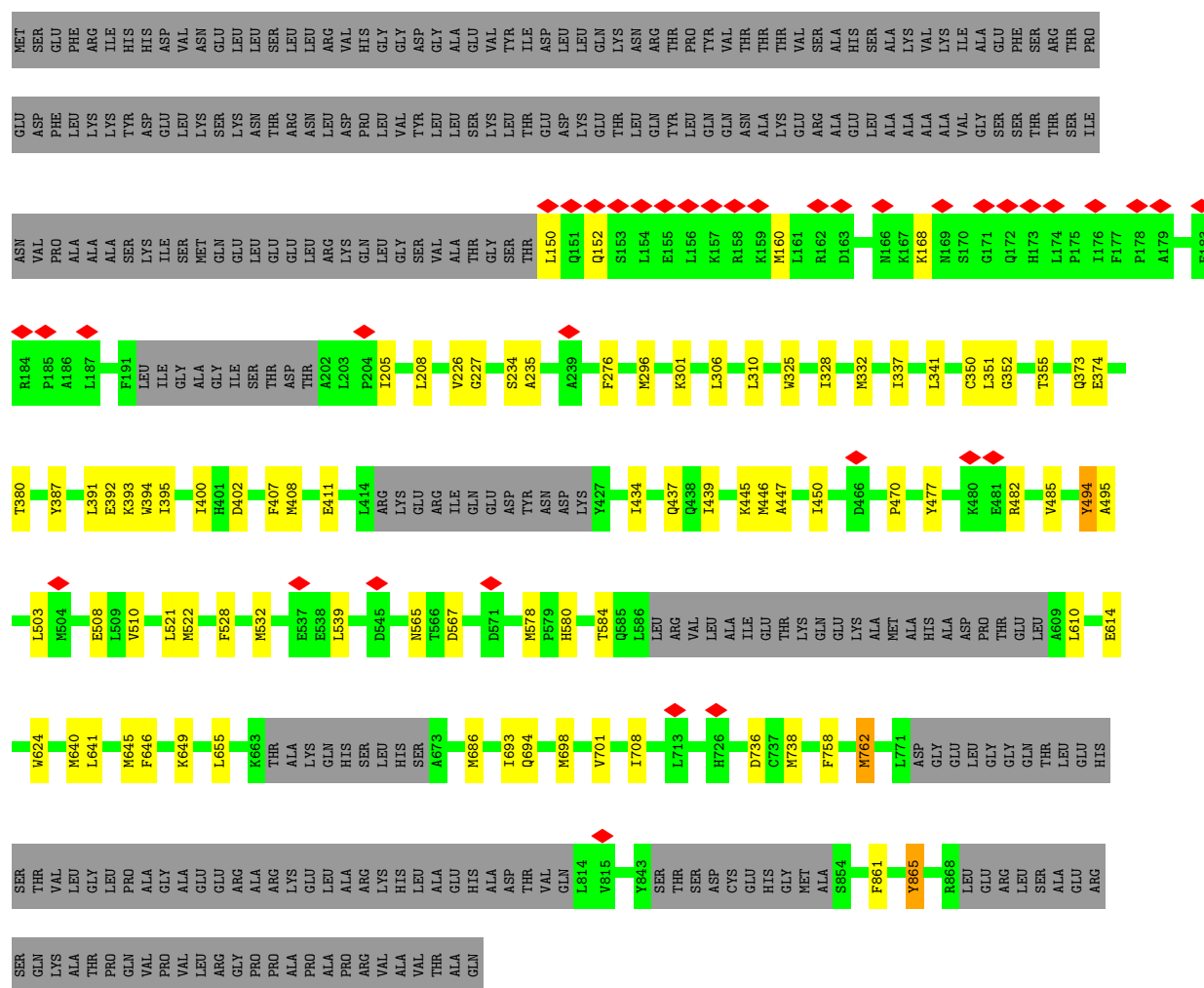






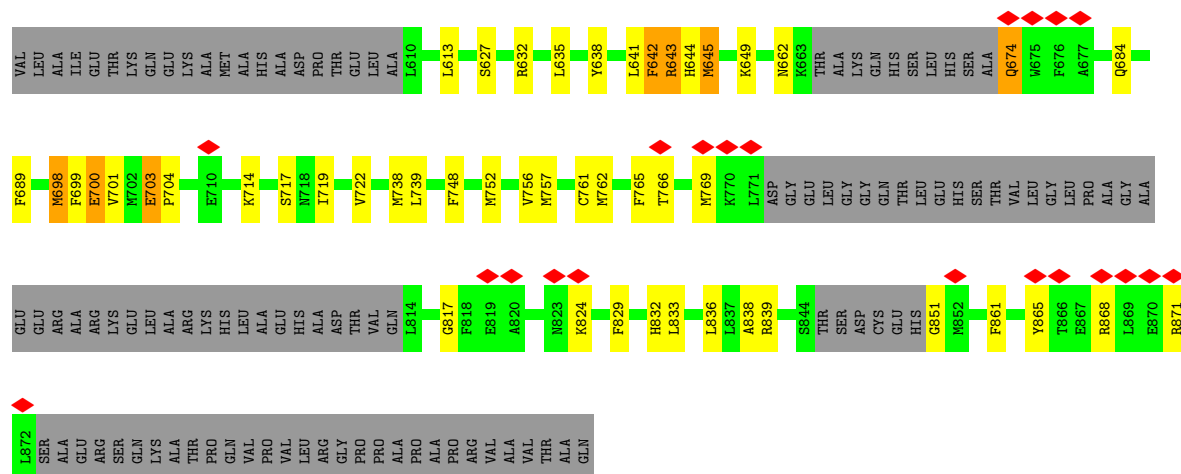
• Molecule 3: Gamma-tubulin complex component 2

Chain C:

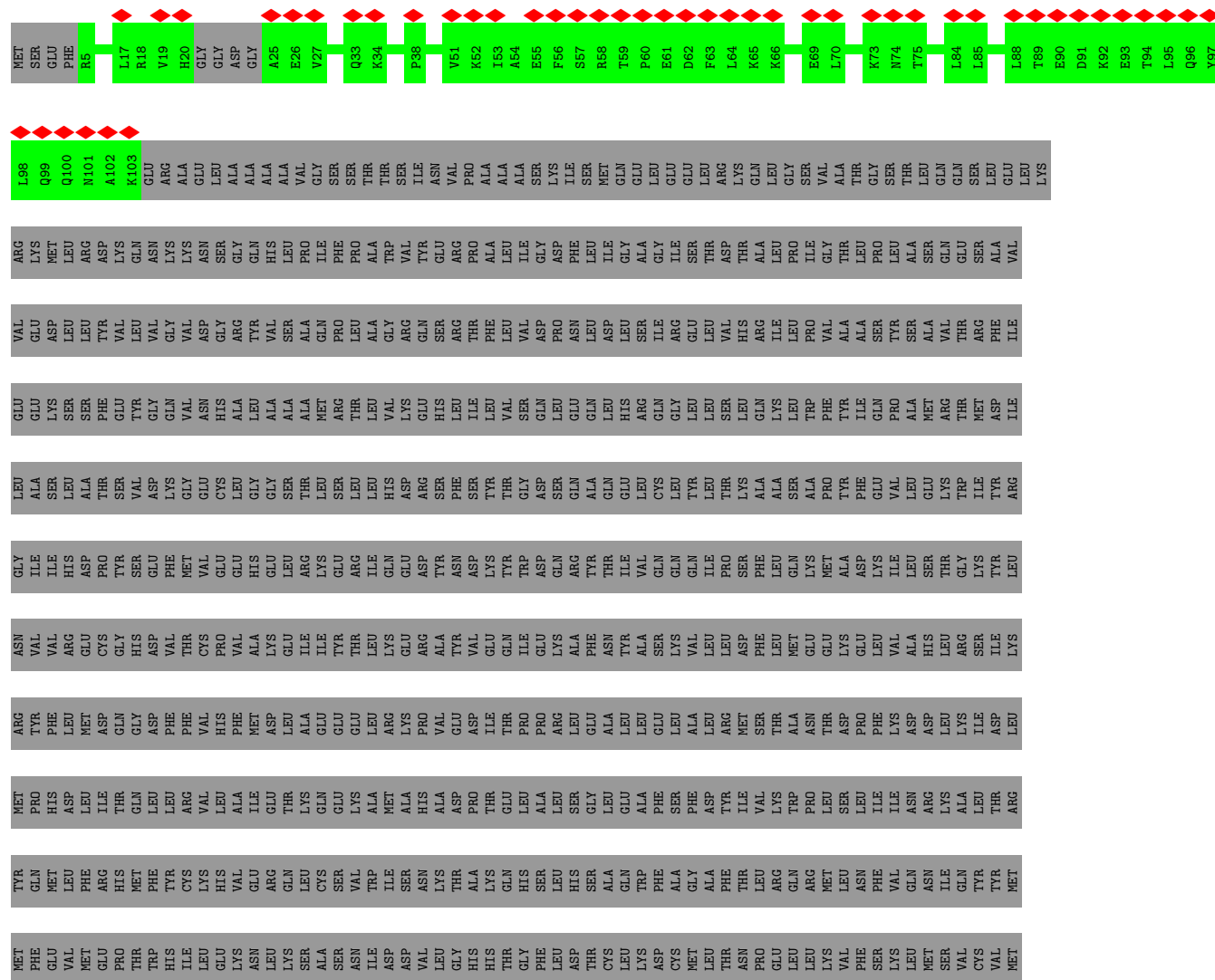


• Molecule 3: Gamma-tubulin complex component 2

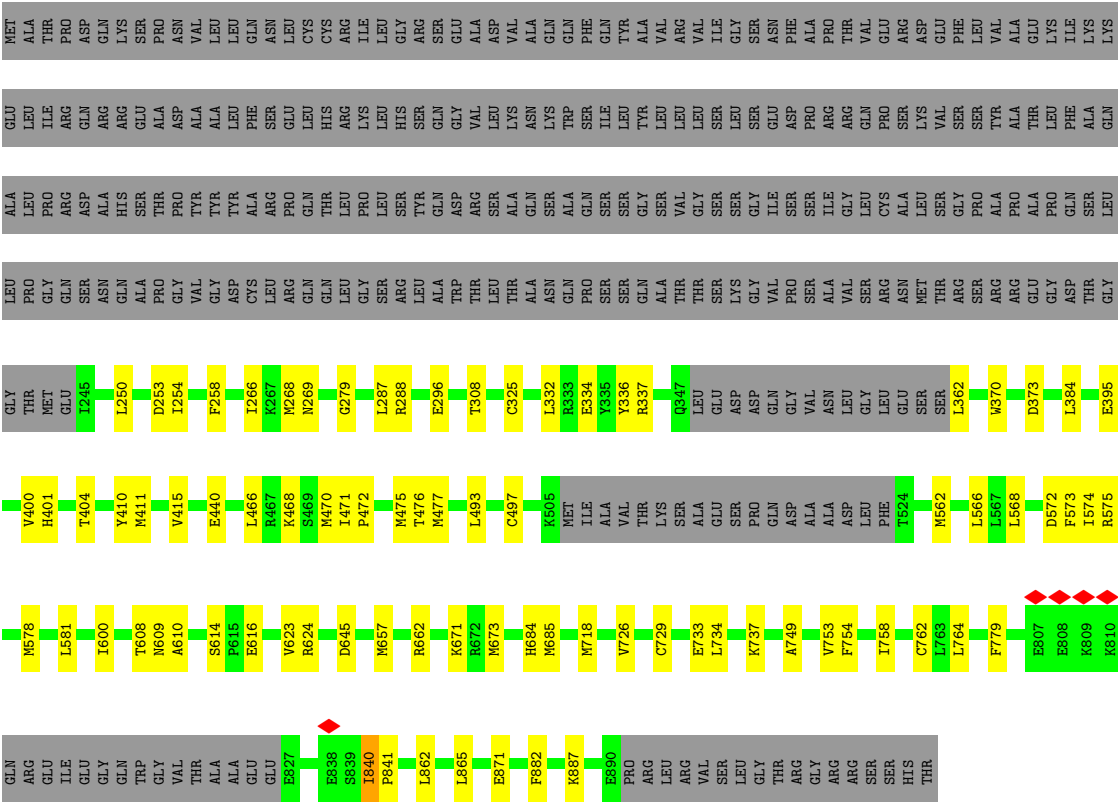
Chain E:



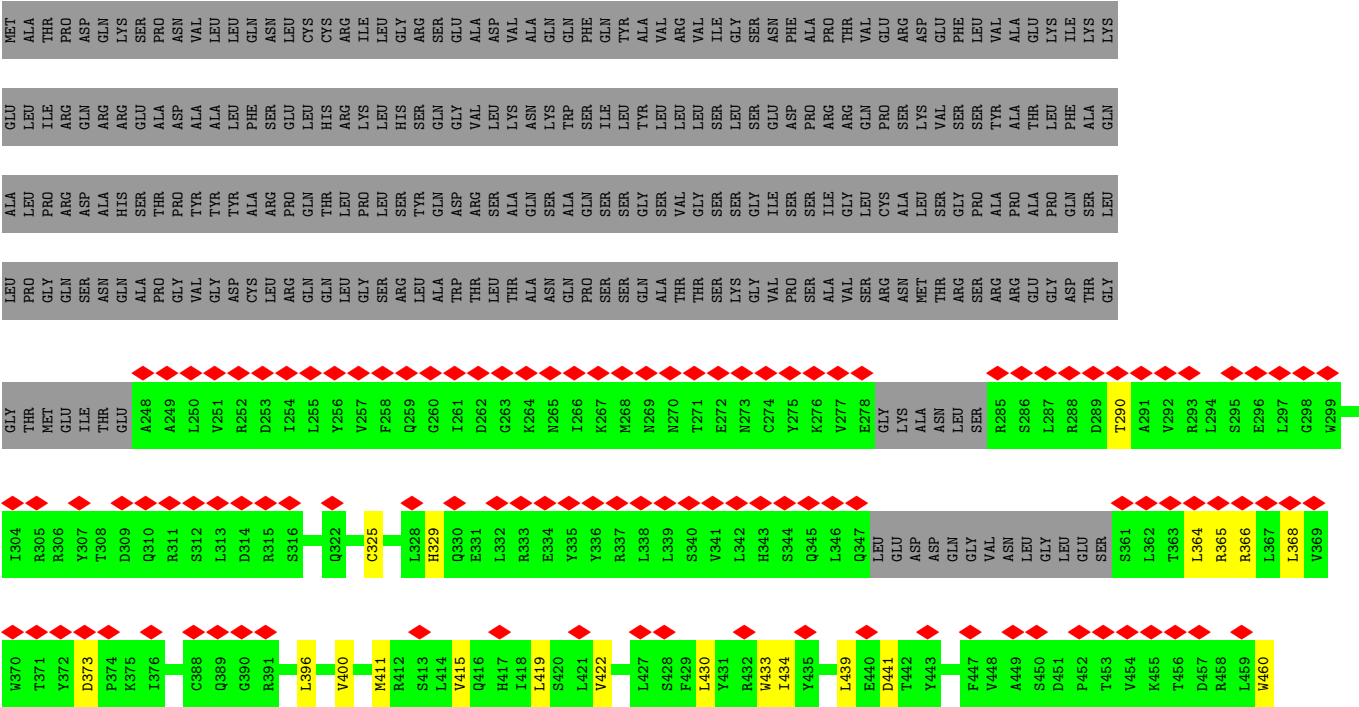
• Molecule 3: Gamma-tubulin complex component 2

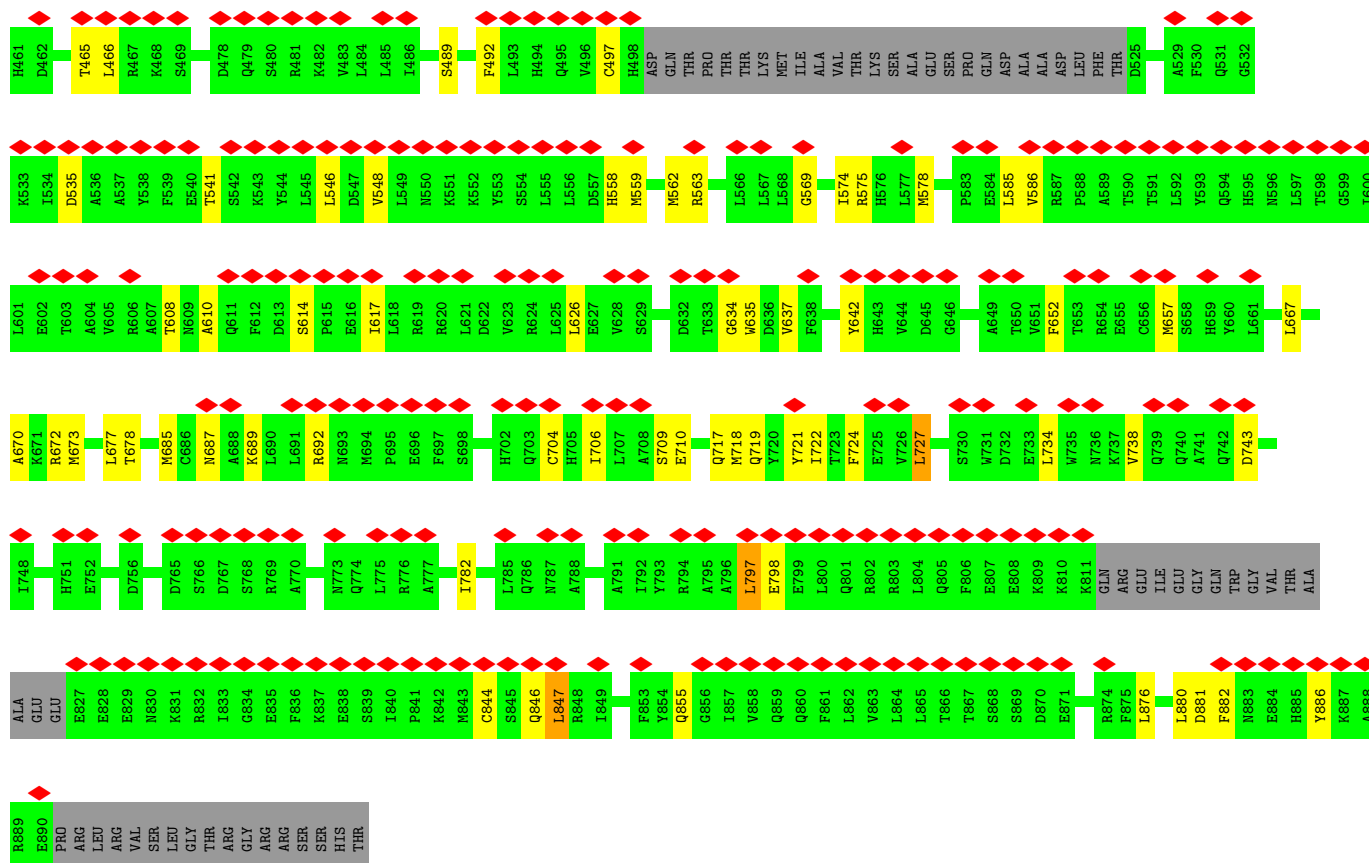






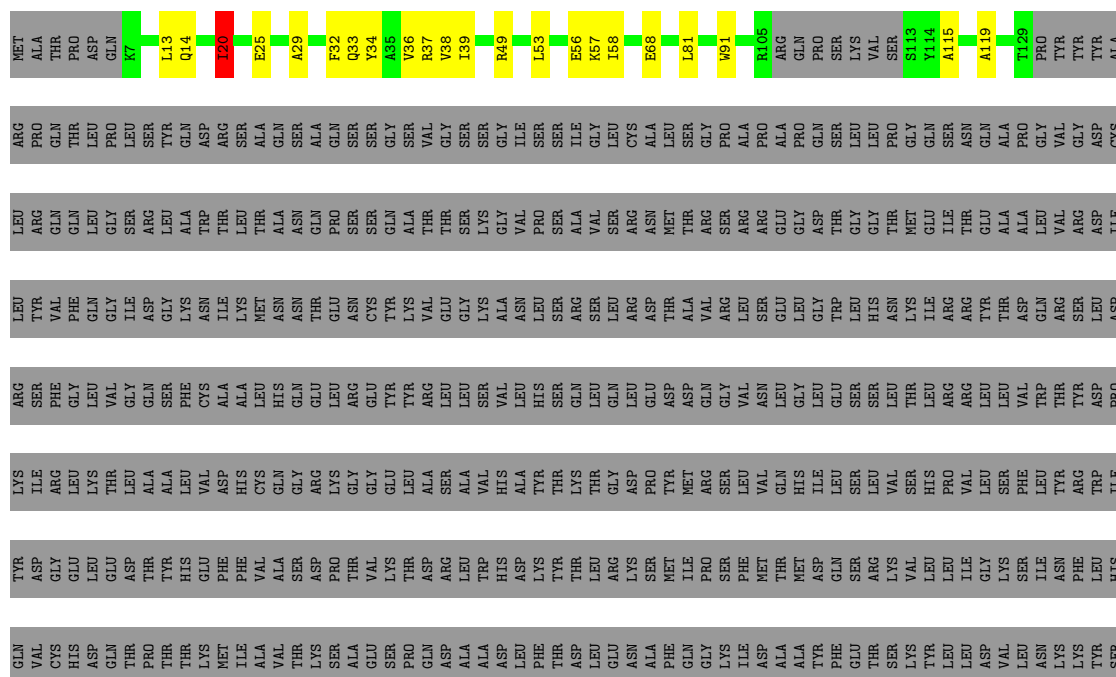
● Molecule 4: Gamma-tubulin complex component 3



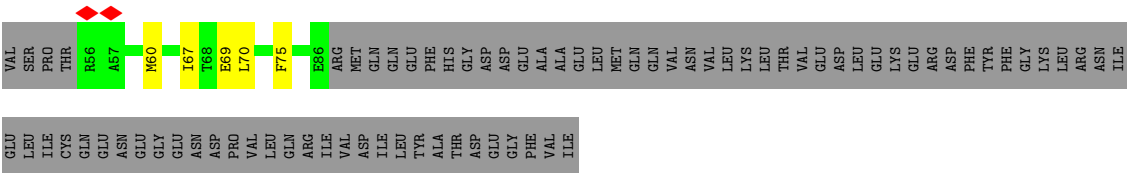


● Molecule 4: Gamma-tubulin complex component 3

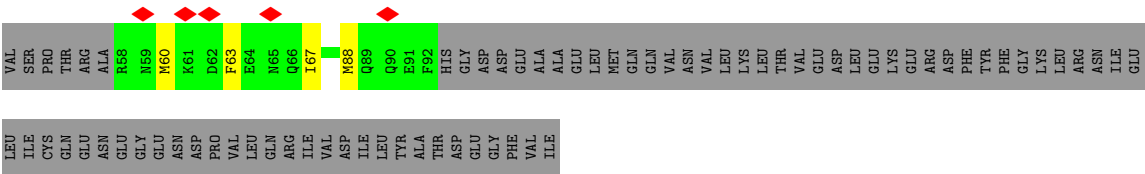
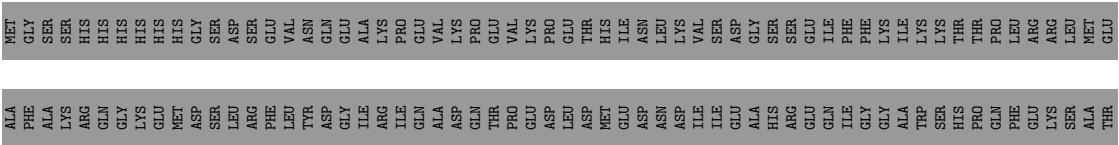
Chain b: 10% . 87%



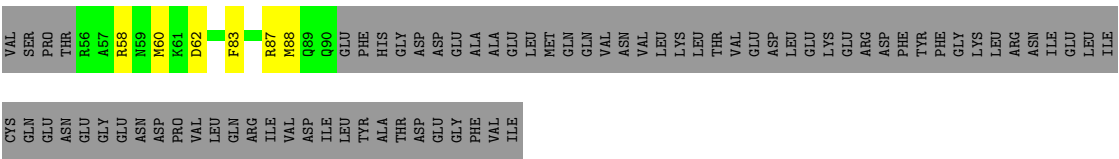
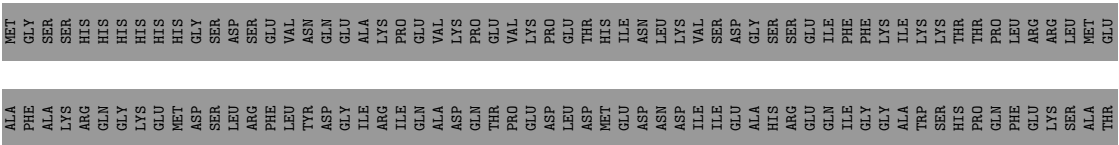




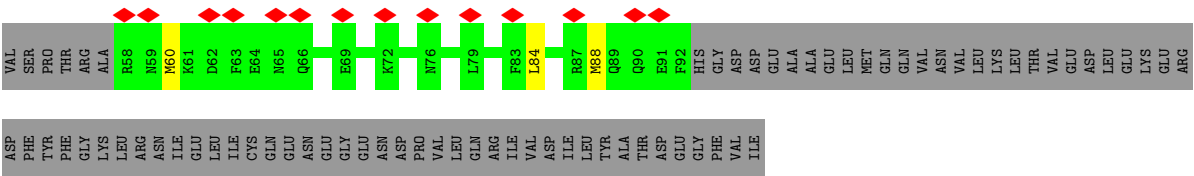
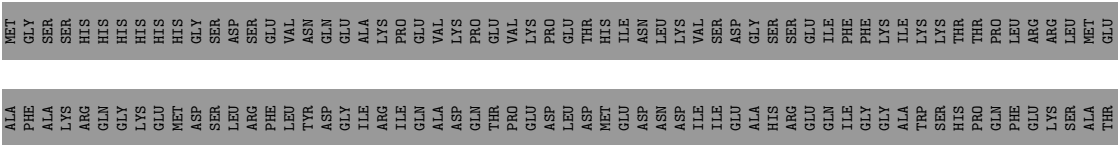
• Molecule 5: CM1



• Molecule 5: CM1

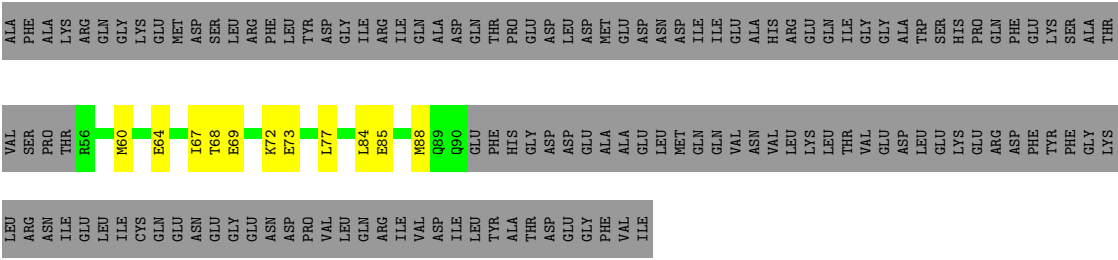


• Molecule 5: CM1

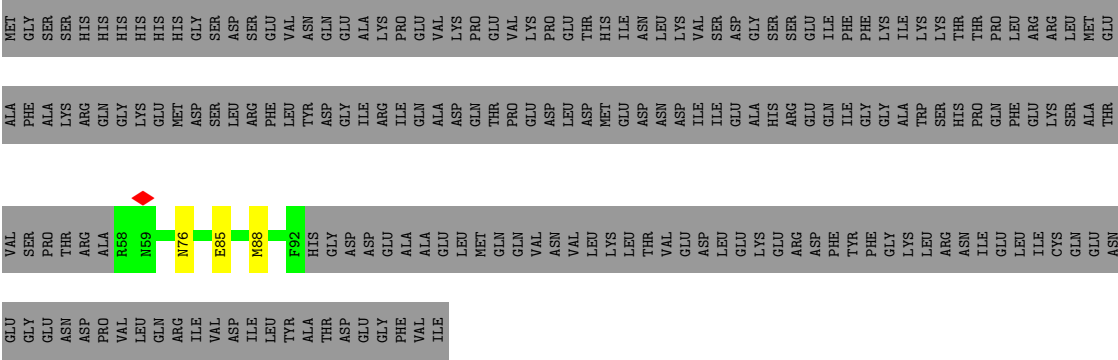


Chain i: 10% 86%

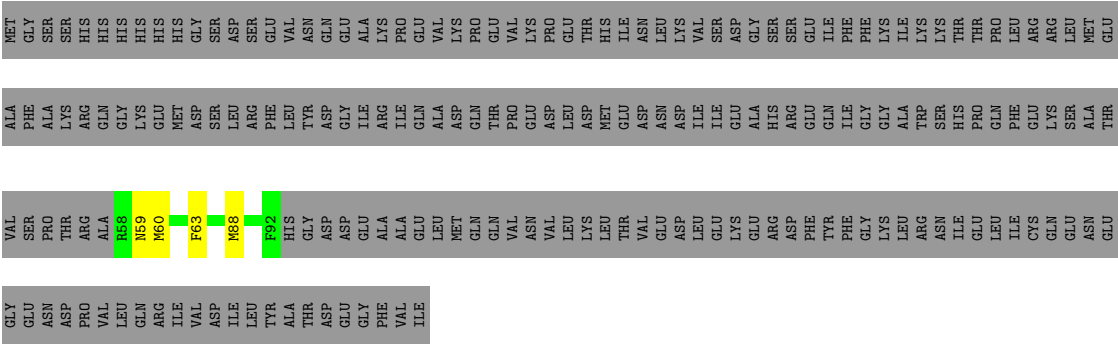




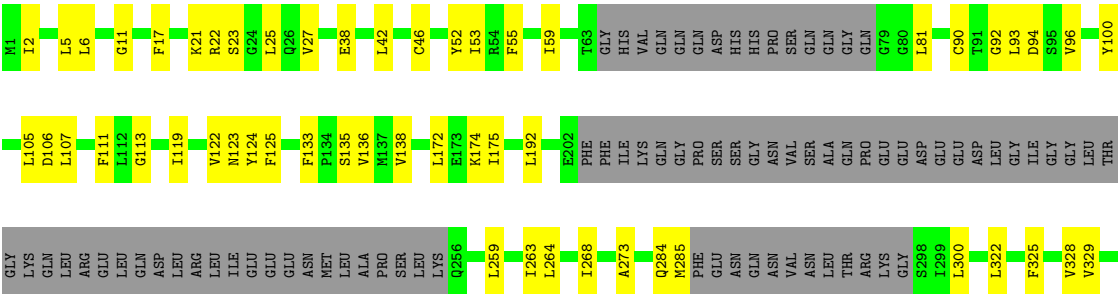
• Molecule 5: CM1



• Molecule 5: CM1

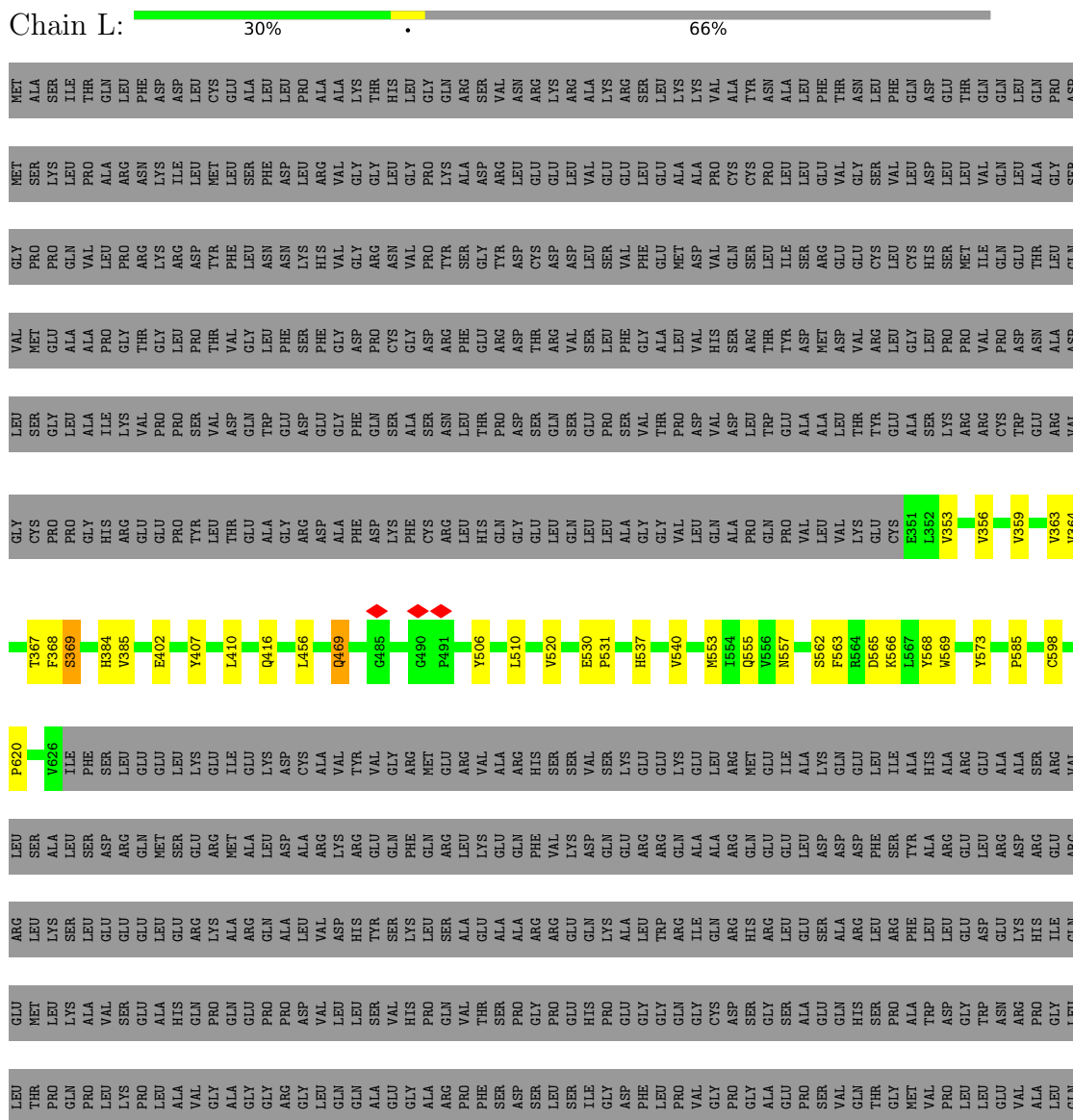


• Molecule 6: Gamma-tubulin complex component 4

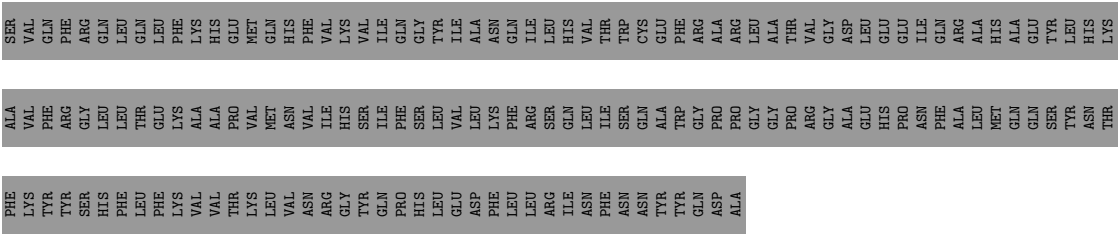




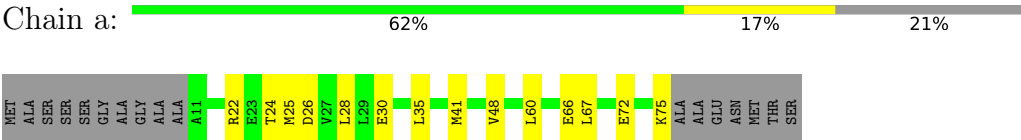
- Molecule 8: Gamma-tubulin complex component 6



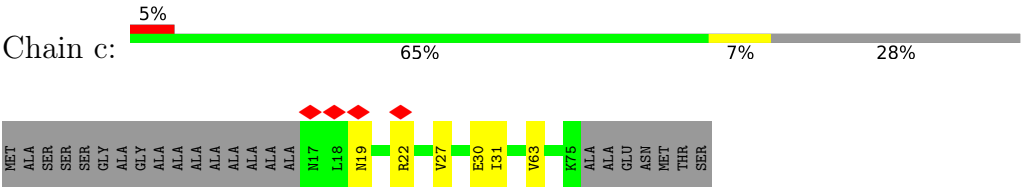




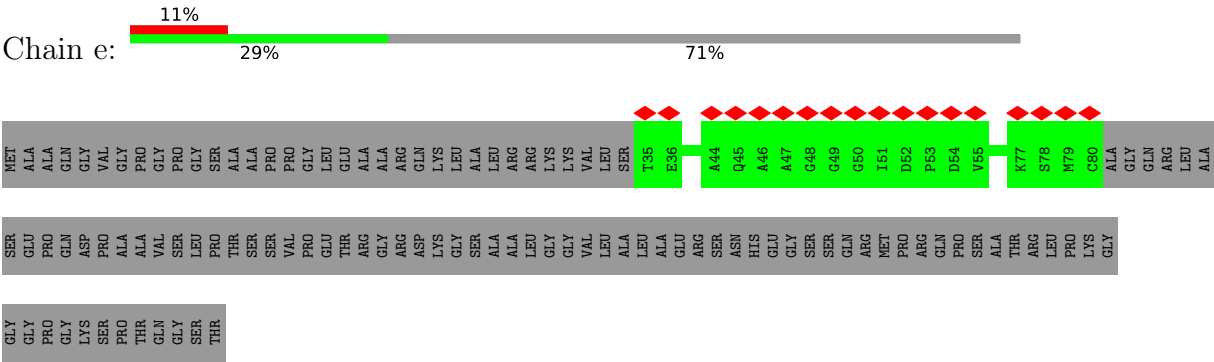
● Molecule 9: Mitotic-spindle organizing protein 1



● Molecule 9: Mitotic-spindle organizing protein 1



● Molecule 10: Mitotic-spindle organizing protein 2A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	579078	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 ($e^-/\text{\AA}^2$)	55.4	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	601.2, 601.2, 601.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6700001, 1.6700001, 1.6700001	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	0.50	0/3433	0.86	0/4651
1	2	0.64	2/3377 (0.1%)	1.02	6/4575 (0.1%)
1	O	0.63	0/3433	0.95	1/4651 (0.0%)
1	P	0.57	0/3427	0.89	0/4644
1	Q	0.48	0/3439	0.85	0/4658
1	R	0.53	2/3433 (0.1%)	0.86	0/4651
1	S	0.49	0/3439	0.88	0/4658
1	T	0.53	0/3427	0.92	0/4644
1	U	0.51	0/3433	0.96	1/4651 (0.0%)
1	V	0.51	0/3393	0.91	1/4599 (0.0%)
1	W	0.51	0/3408	0.95	2/4616 (0.0%)
1	X	0.46	0/3439	0.86	0/4658
1	Y	0.52	0/3431	0.90	2/4647 (0.0%)
1	Z	0.57	0/3433	0.99	2/4651 (0.0%)
2	7	0.34	0/1828	0.68	0/2554
3	A	0.54	0/4951	0.92	2/6692 (0.0%)
3	C	0.46	0/5080	0.87	0/6864
3	E	0.41	0/5305	0.83	0/7162
3	M	0.55	1/5267 (0.0%)	0.90	3/7110 (0.0%)
3	f	0.17	0/482	0.52	0/674
3	k	0.50	0/5289	0.94	4/7140 (0.1%)
4	B	0.45	0/5119	0.82	2/6912 (0.0%)
4	D	0.41	0/4891	0.81	4/6603 (0.1%)
4	F	0.47	1/5024 (0.0%)	0.88	1/6784 (0.0%)
4	N	0.51	0/4911	0.88	0/6627
4	b	0.44	1/948 (0.1%)	0.89	0/1277
4	n	0.46	0/4977	0.89	7/6722 (0.1%)
5	G	0.56	0/273	0.98	1/362 (0.3%)
5	H	0.44	0/321	0.80	0/424
5	g	0.40	0/306	0.82	0/405
5	h	0.36	0/321	0.65	0/424
5	i	0.55	0/277	0.83	0/366
5	j	0.39	0/294	0.68	0/389
5	s	0.43	0/306	0.87	0/405

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	t	0.44	0/306	0.80	0/405
5	u	0.43	0/321	0.84	0/424
5	v	0.44	0/321	0.85	0/424
6	I	0.54	1/4299 (0.0%)	1.00	4/5824 (0.1%)
6	K	0.39	0/4677	0.81	5/6331 (0.1%)
7	J	0.52	0/4939	0.98	3/6693 (0.0%)
8	L	0.42	0/5062	0.84	0/6877
8	d	0.47	0/1165	0.93	0/1566
9	a	0.37	0/484	0.81	0/653
9	c	0.61	0/454	1.04	0/611
10	e	0.22	0/232	0.42	0/323
All	All	0.50	8/126375 (0.0%)	0.89	51/170981 (0.0%)

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
3	A	0	4
4	B	0	2
All	All	0	6

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	840	ILE	CA-CB	-11.46	1.48	1.54
1	2	70	GLU	C-O	6.73	1.27	1.23
1	2	323	ILE	CG1-CD1	-6.29	1.27	1.51
1	R	70	GLU	C-O	-5.97	1.21	1.23
6	I	529	GLN	C-N	-5.50	1.26	1.34

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	496	TRP	N-CA-C	-11.10	98.71	112.47
3	k	567	ASP	CA-CB-CG	7.38	119.98	112.60
4	D	719	GLN	CA-C-O	-7.27	113.37	121.00
1	2	139	HIS	CA-CB-CG	7.01	120.81	113.80
4	n	378	LEU	N-CA-C	-6.76	103.71	112.23

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	244	ARG	Sidechain
3	A	540	ARG	Sidechain
3	A	653	ARG	Sidechain
3	A	683	ARG	Sidechain
4	B	285	ARG	Sidechain

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	3365	0	3309	50	0
1	2	3311	0	3253	66	0
1	O	3365	0	3309	155	0
1	P	3359	0	3298	57	0
1	Q	3371	0	3320	62	0
1	R	3365	0	3309	44	0
1	S	3371	0	3320	45	0
1	T	3359	0	3298	43	0
1	U	3365	0	3309	40	0
1	V	3325	0	3258	26	0
1	W	3342	0	3294	77	0
1	X	3371	0	3320	43	0
1	Y	3363	0	3316	46	0
1	Z	3365	0	3309	54	0
2	7	1812	0	920	1	0
3	A	4846	0	4867	227	0
3	C	4973	0	4986	79	0
3	E	5196	0	5230	87	0
3	M	5158	0	5186	92	0
3	f	481	0	218	0	0
3	k	5180	0	5208	49	0
4	B	5015	0	4991	100	0
4	D	4790	0	4764	101	0
4	F	4921	0	4897	69	0
4	N	4810	0	4790	80	0
4	b	933	0	953	36	0
4	n	4875	0	4836	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	270	0	268	4	0
5	H	317	0	314	5	0
5	g	303	0	300	5	0
5	h	317	0	314	5	0
5	i	274	0	274	30	0
5	j	290	0	286	2	0
5	s	303	0	300	11	0
5	t	303	0	300	20	0
5	u	317	0	314	5	0
5	v	317	0	314	8	0
6	I	4203	0	4221	123	0
6	K	4573	0	4575	63	0
7	J	4837	0	4822	118	0
8	L	4928	0	4971	71	0
8	d	1152	0	1158	26	0
9	a	484	0	512	22	0
9	c	454	0	482	5	0
10	e	231	0	119	0	0
All	All	123860	0	121912	1996	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 8.

The worst 5 of 1996 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)
1:O:220:ILE:CG2	1:O:224:SER:HB2	1.52	1.40
3:A:771:LEU:CD2	1:O:162:PRO:HG3	1.54	1.35
3:A:677:ALA:HB1	1:O:263:THR:CG2	1.73	1.17
3:A:765:PHE:CZ	1:O:163:LYS:HD3	1.78	1.16
3:M:505:GLU:CA	3:M:508:GLU:HG2	1.75	1.16

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	408/451 (90%)	373 (91%)	32 (8%)	3 (1%)	18	51
1	2	403/451 (89%)	363 (90%)	40 (10%)	0	100	100
1	O	408/451 (90%)	357 (88%)	43 (10%)	8 (2%)	6	32
1	P	408/451 (90%)	359 (88%)	43 (10%)	6 (2%)	8	37
1	Q	408/451 (90%)	370 (91%)	32 (8%)	6 (2%)	8	37
1	R	408/451 (90%)	363 (89%)	40 (10%)	5 (1%)	10	41
1	S	408/451 (90%)	356 (87%)	49 (12%)	3 (1%)	18	51
1	T	408/451 (90%)	362 (89%)	42 (10%)	4 (1%)	12	44
1	U	408/451 (90%)	365 (90%)	39 (10%)	4 (1%)	12	44
1	V	405/451 (90%)	356 (88%)	46 (11%)	3 (1%)	18	51
1	W	405/451 (90%)	363 (90%)	35 (9%)	7 (2%)	7	35
1	X	408/451 (90%)	360 (88%)	47 (12%)	1 (0%)	43	72
1	Y	407/451 (90%)	353 (87%)	53 (13%)	1 (0%)	43	72
1	Z	408/451 (90%)	355 (87%)	44 (11%)	9 (2%)	5	30
2	7	356/364 (98%)	305 (86%)	48 (14%)	3 (1%)	16	49
3	A	587/902 (65%)	542 (92%)	43 (7%)	2 (0%)	36	65
3	C	600/902 (66%)	549 (92%)	45 (8%)	6 (1%)	12	44
3	E	626/902 (69%)	558 (89%)	64 (10%)	4 (1%)	21	54
3	M	621/902 (69%)	555 (89%)	65 (10%)	1 (0%)	43	72
3	f	91/902 (10%)	81 (89%)	10 (11%)	0	100	100
3	k	624/902 (69%)	564 (90%)	55 (9%)	5 (1%)	16	49
4	B	602/907 (66%)	544 (90%)	57 (10%)	1 (0%)	43	72
4	D	571/907 (63%)	529 (93%)	40 (7%)	2 (0%)	30	60
4	F	591/907 (65%)	535 (90%)	55 (9%)	1 (0%)	43	72
4	N	573/907 (63%)	521 (91%)	51 (9%)	1 (0%)	43	72
4	b	112/907 (12%)	104 (93%)	7 (6%)	1 (1%)	14	46
4	n	584/907 (64%)	526 (90%)	54 (9%)	4 (1%)	18	51
5	G	29/229 (13%)	25 (86%)	4 (14%)	0	100	100
5	H	33/229 (14%)	32 (97%)	1 (3%)	0	100	100
5	g	33/229 (14%)	31 (94%)	2 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	h	33/229 (14%)	30 (91%)	3 (9%)	0	100	100
5	i	29/229 (13%)	26 (90%)	3 (10%)	0	100	100
5	j	30/229 (13%)	30 (100%)	0	0	100	100
5	s	33/229 (14%)	31 (94%)	2 (6%)	0	100	100
5	t	33/229 (14%)	30 (91%)	3 (9%)	0	100	100
5	u	33/229 (14%)	33 (100%)	0	0	100	100
5	v	33/229 (14%)	31 (94%)	2 (6%)	0	100	100
6	I	511/667 (77%)	436 (85%)	69 (14%)	6 (1%)	10	41
6	K	548/667 (82%)	504 (92%)	41 (8%)	3 (0%)	24	57
7	J	587/1024 (57%)	499 (85%)	82 (14%)	6 (1%)	12	44
8	L	613/1819 (34%)	537 (88%)	69 (11%)	7 (1%)	11	43
8	d	137/1819 (8%)	128 (93%)	8 (6%)	1 (1%)	18	51
9	a	63/82 (77%)	60 (95%)	3 (5%)	0	100	100
9	c	57/82 (70%)	54 (95%)	3 (5%)	0	100	100
10	e	44/158 (28%)	40 (91%)	4 (9%)	0	100	100
All	All	15117/26140 (58%)	13525 (90%)	1478 (10%)	114 (1%)	18	49

5 of 114 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	589	ALA
4	D	314	ASP
3	E	370	SER
4	F	287	LEU
6	I	470	ALA

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	374/400 (94%)	369 (99%)	5 (1%)	61	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	367/400 (92%)	355 (97%)	12 (3%)	33	58
1	O	374/400 (94%)	362 (97%)	12 (3%)	34	58
1	P	373/400 (93%)	362 (97%)	11 (3%)	37	60
1	Q	375/400 (94%)	371 (99%)	4 (1%)	65	74
1	R	374/400 (94%)	365 (98%)	9 (2%)	43	63
1	S	375/400 (94%)	371 (99%)	4 (1%)	65	74
1	T	373/400 (93%)	368 (99%)	5 (1%)	61	72
1	U	374/400 (94%)	369 (99%)	5 (1%)	61	72
1	V	368/400 (92%)	364 (99%)	4 (1%)	65	74
1	W	373/400 (93%)	363 (97%)	10 (3%)	39	61
1	X	375/400 (94%)	367 (98%)	8 (2%)	47	65
1	Y	374/400 (94%)	373 (100%)	1 (0%)	86	83
1	Z	374/400 (94%)	362 (97%)	12 (3%)	34	58
2	7	18/310 (6%)	18 (100%)	0	100	100
3	A	533/791 (67%)	503 (94%)	30 (6%)	19	46
3	C	547/791 (69%)	538 (98%)	9 (2%)	55	69
3	E	573/791 (72%)	565 (99%)	8 (1%)	59	71
3	M	569/791 (72%)	555 (98%)	14 (2%)	42	63
3	f	3/791 (0%)	3 (100%)	0	100	100
3	k	571/791 (72%)	565 (99%)	6 (1%)	65	74
4	B	547/798 (68%)	538 (98%)	9 (2%)	55	69
4	D	524/798 (66%)	519 (99%)	5 (1%)	68	75
4	F	537/798 (67%)	533 (99%)	4 (1%)	76	78
4	N	525/798 (66%)	518 (99%)	7 (1%)	61	72
4	b	101/798 (13%)	100 (99%)	1 (1%)	68	75
4	n	532/798 (67%)	527 (99%)	5 (1%)	70	76
5	G	29/207 (14%)	29 (100%)	0	100	100
5	H	35/207 (17%)	35 (100%)	0	100	100
5	g	32/207 (16%)	32 (100%)	0	100	100
5	h	35/207 (17%)	34 (97%)	1 (3%)	37	60
5	i	30/207 (14%)	28 (93%)	2 (7%)	15	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	j	32/207 (16%)	32 (100%)	0	100	100
5	s	32/207 (16%)	32 (100%)	0	100	100
5	t	32/207 (16%)	32 (100%)	0	100	100
5	u	35/207 (17%)	35 (100%)	0	100	100
5	v	35/207 (17%)	35 (100%)	0	100	100
6	I	468/594 (79%)	466 (100%)	2 (0%)	84	81
6	K	508/594 (86%)	507 (100%)	1 (0%)	87	85
7	J	531/933 (57%)	526 (99%)	5 (1%)	70	76
8	L	540/1546 (35%)	537 (99%)	3 (1%)	78	79
8	d	128/1546 (8%)	128 (100%)	0	100	100
9	a	53/62 (86%)	53 (100%)	0	100	100
9	c	53/62 (86%)	52 (98%)	1 (2%)	50	67
10	e	2/118 (2%)	2 (100%)	0	100	100
All	All	13413/22969 (58%)	13198 (98%)	215 (2%)	54	69

5 of 215 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	220	ILE
1	R	164	LYS
4	b	20	ILE
1	O	225	PHE
1	P	73	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 188 such sidechains are listed below:

Mol	Chain	Res	Type
1	R	222	ASN
1	V	167	GLN
1	S	24	GLN
1	T	429	GLN
1	W	207	ASN

5.3.3 RNA ⓘ

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.

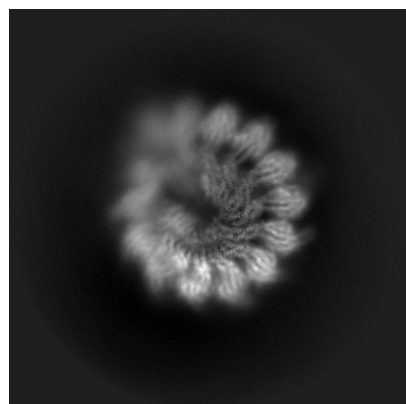
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19570. These allow visual inspection of the internal detail of the map and identification of artifacts.

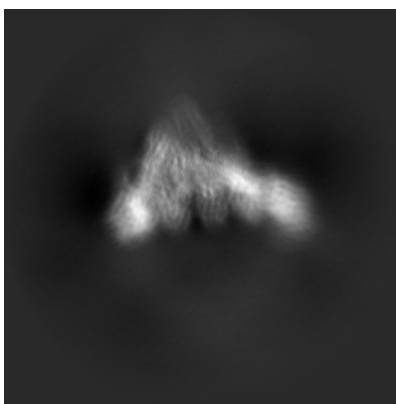
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

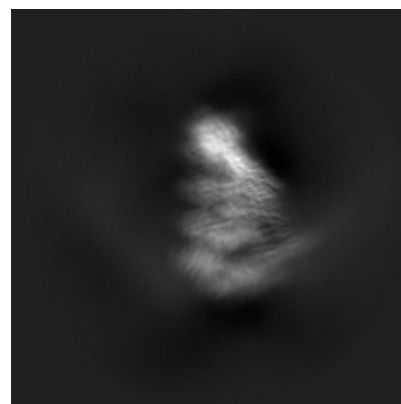
6.1.1 Primary map



X

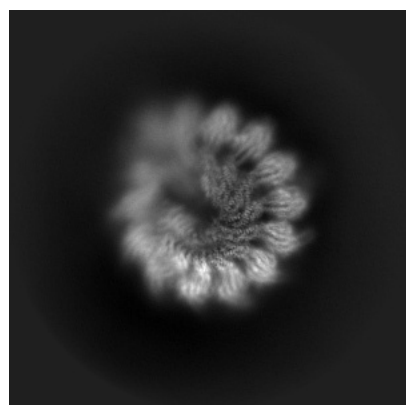


Y

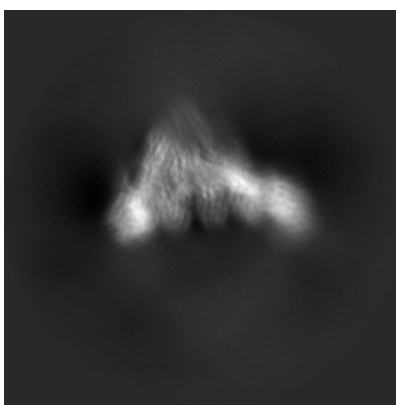


Z

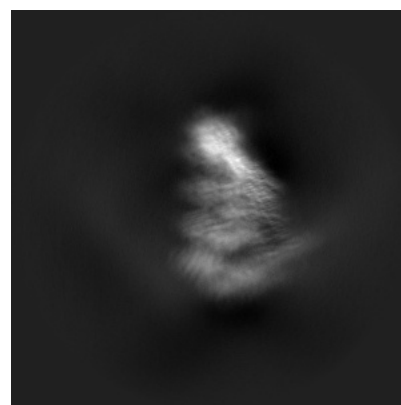
6.1.2 Raw map



X



Y

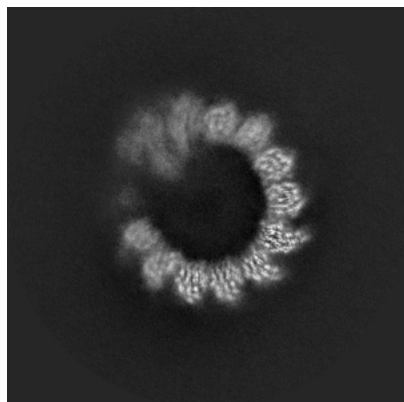


Z

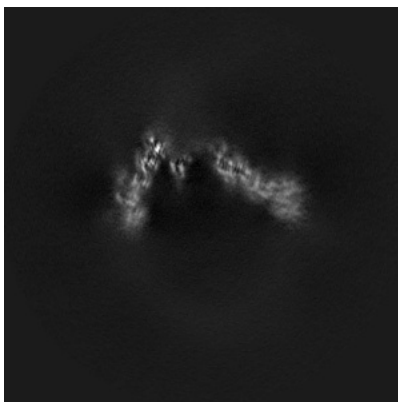
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

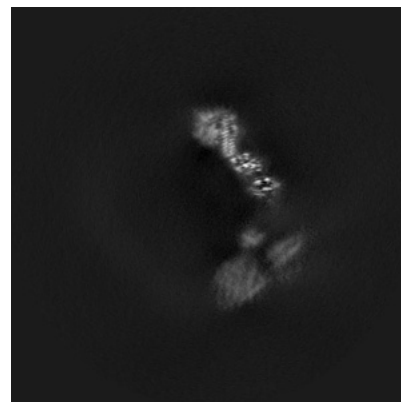
6.2.1 Primary map



X Index: 180

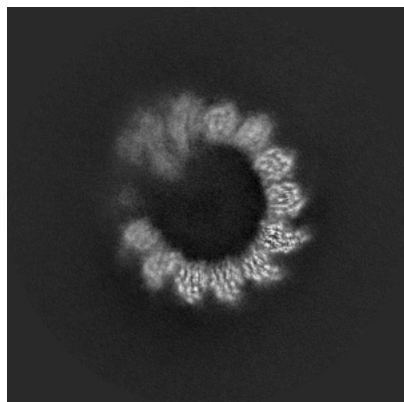


Y Index: 180

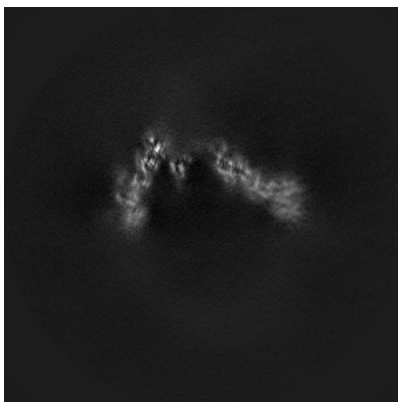


Z Index: 180

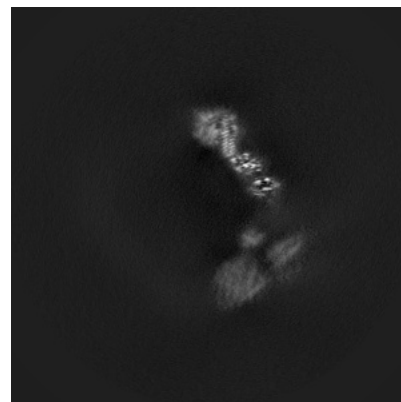
6.2.2 Raw map



X Index: 180



Y Index: 180

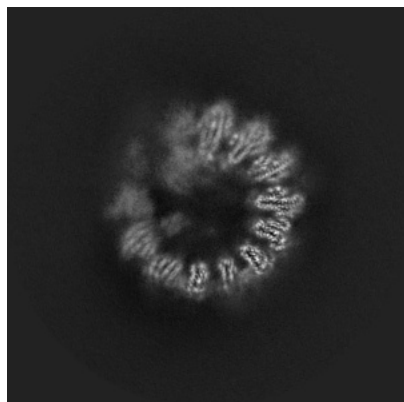


Z Index: 180

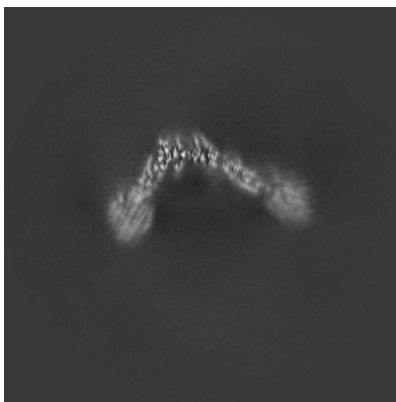
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

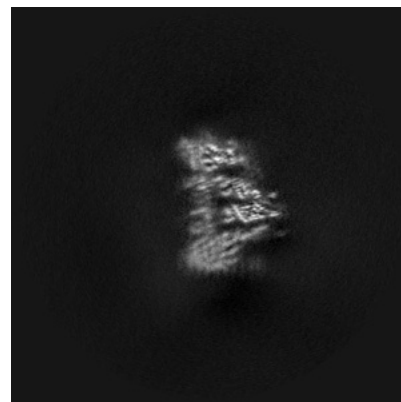
6.3.1 Primary map



X Index: 195

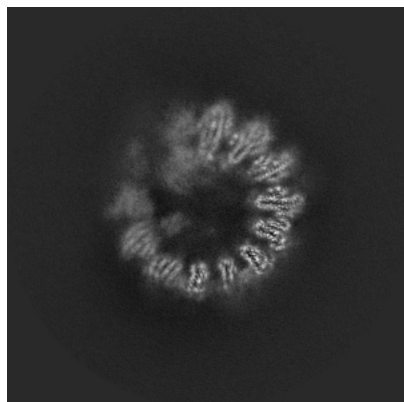


Y Index: 200

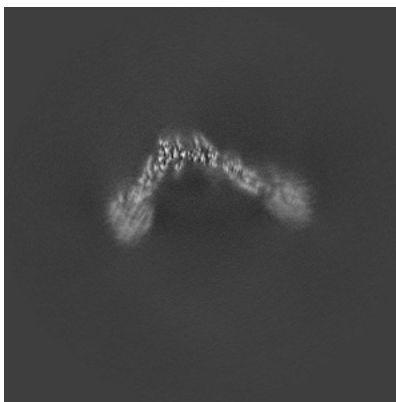


Z Index: 126

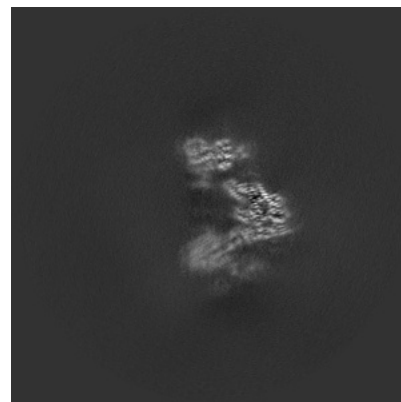
6.3.2 Raw map



X Index: 195



Y Index: 200



Z Index: 132

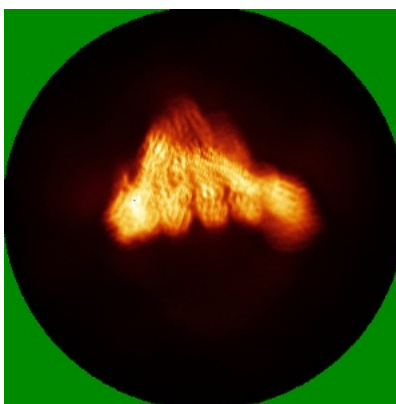
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

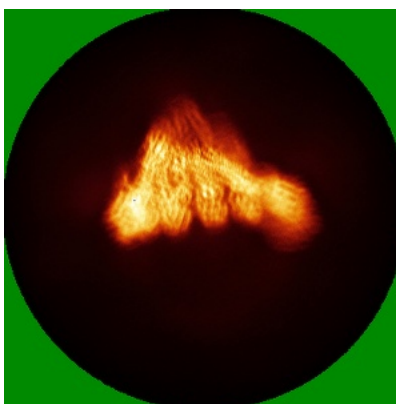


Z

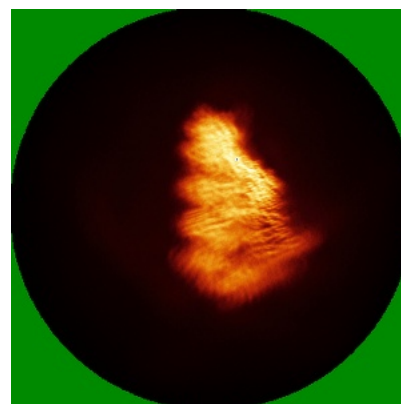
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

This section was not generated.

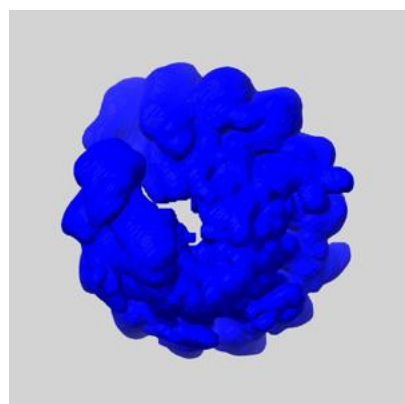
6.6 Mask visualisation [i](#)

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

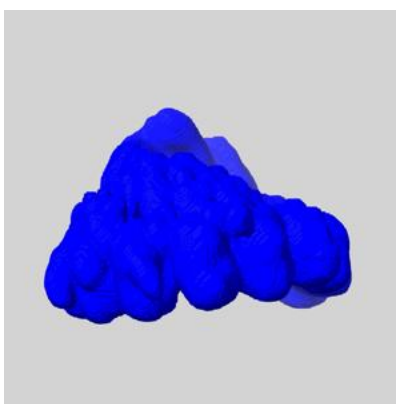
A mask typically either:

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

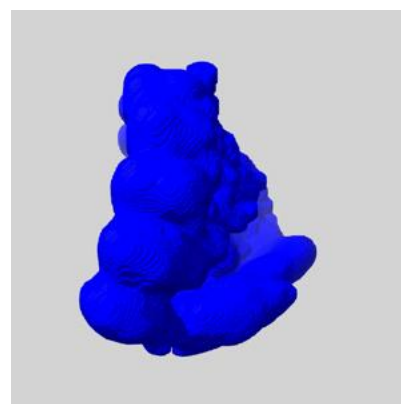
6.6.1 emd_19570_msk_1.map [i](#)



X



Y

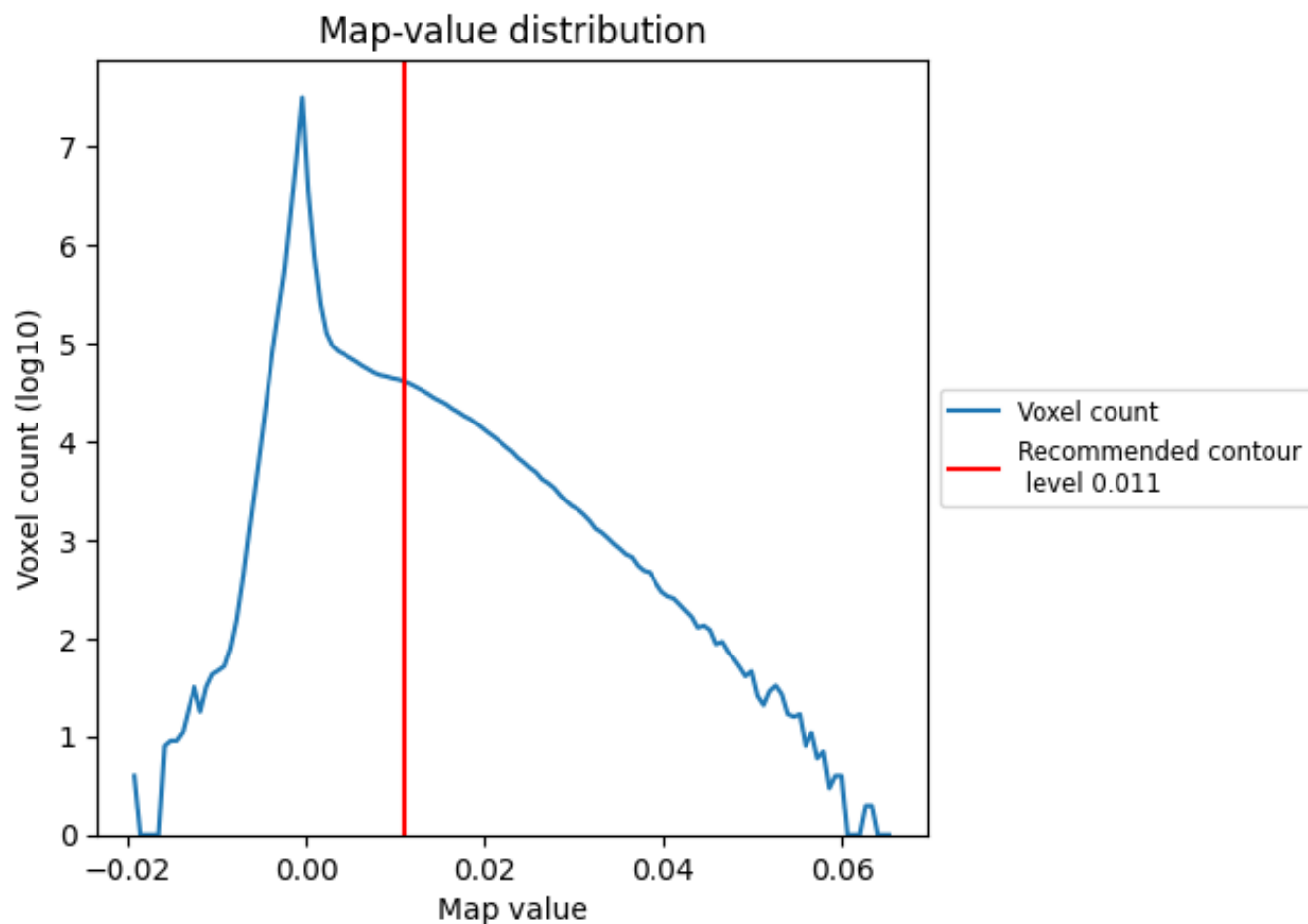


Z

7 Map analysis [i](#)

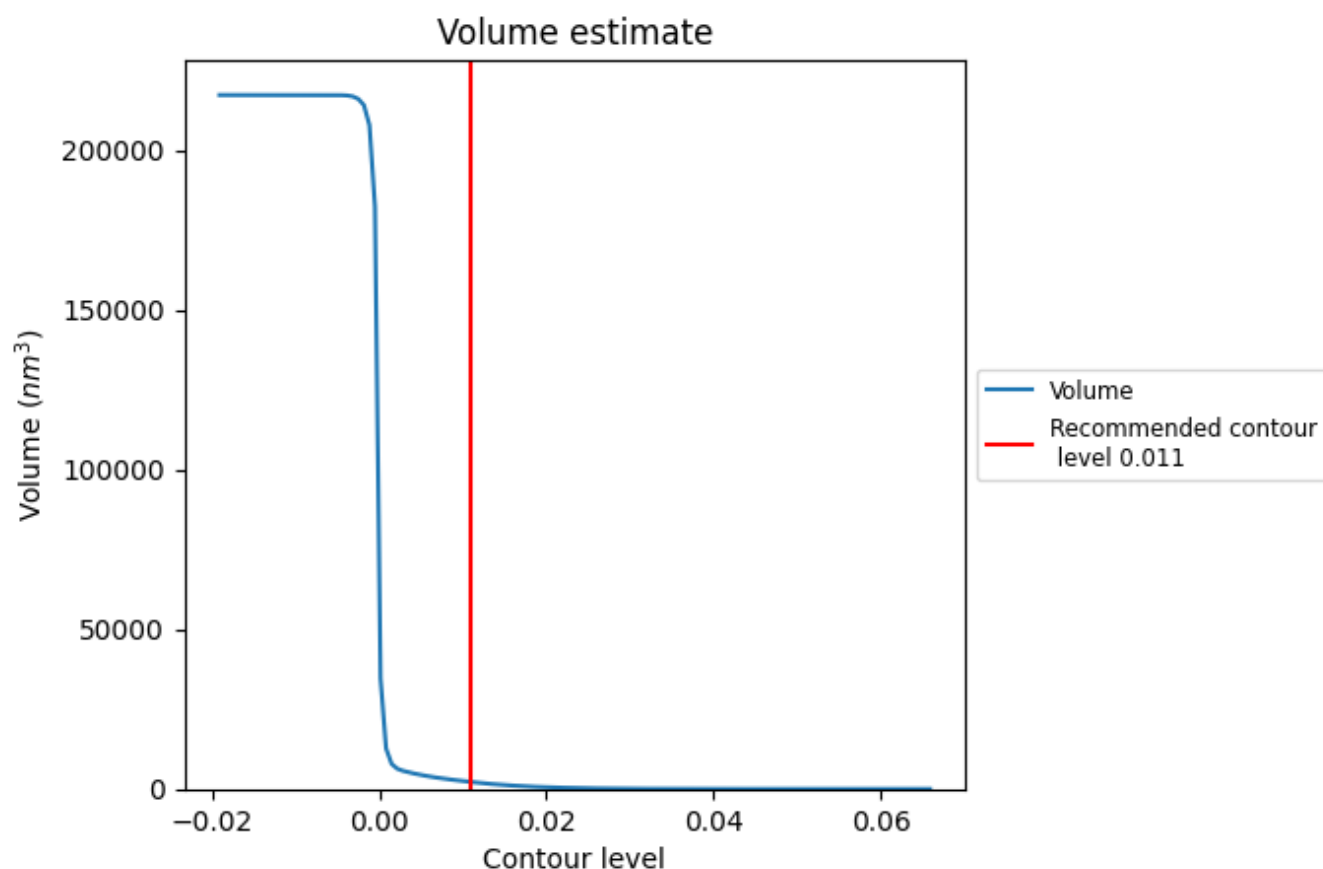
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

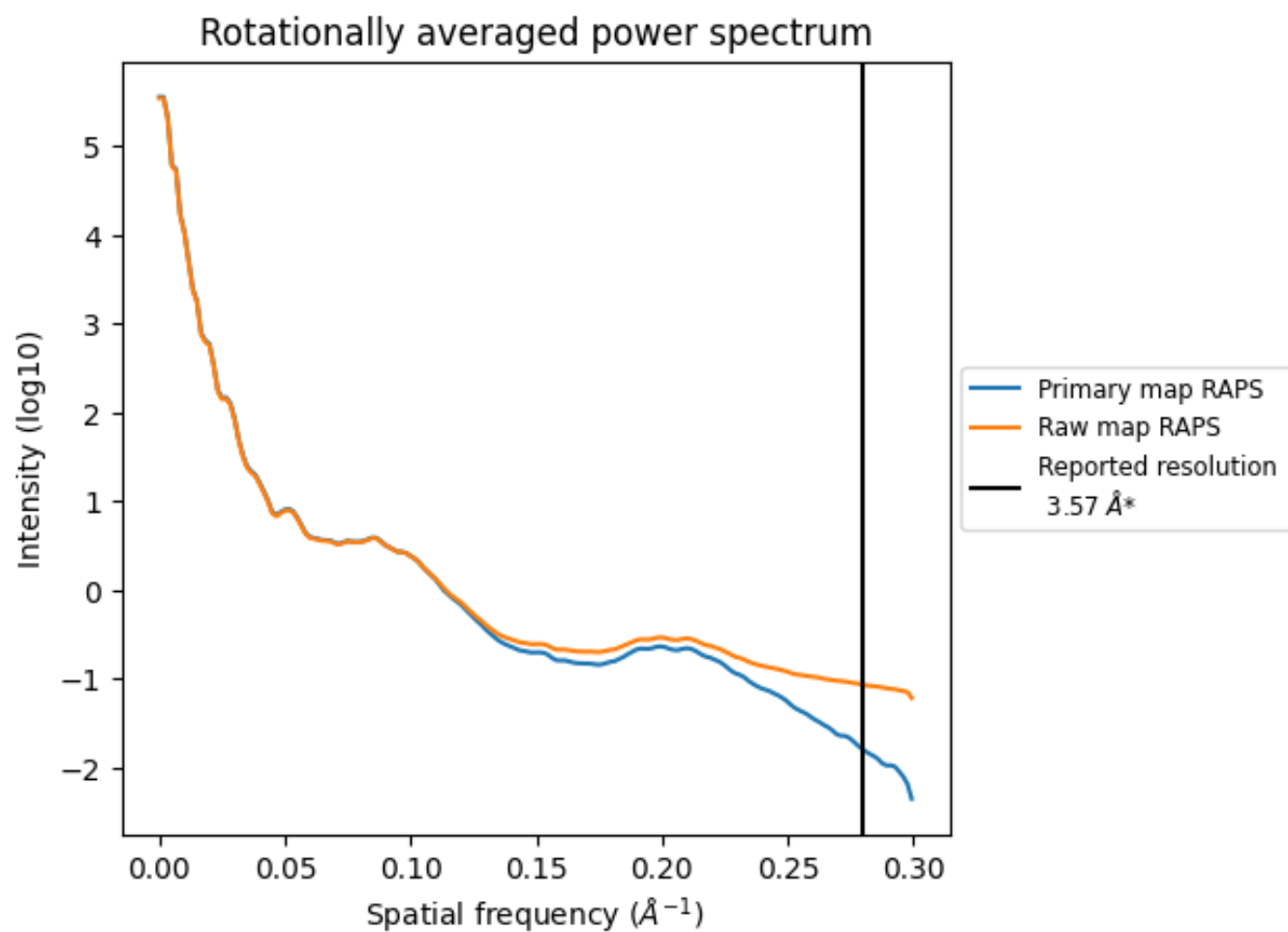
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2186 nm^3 ; this corresponds to an approximate mass of 1974 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 ⓘ

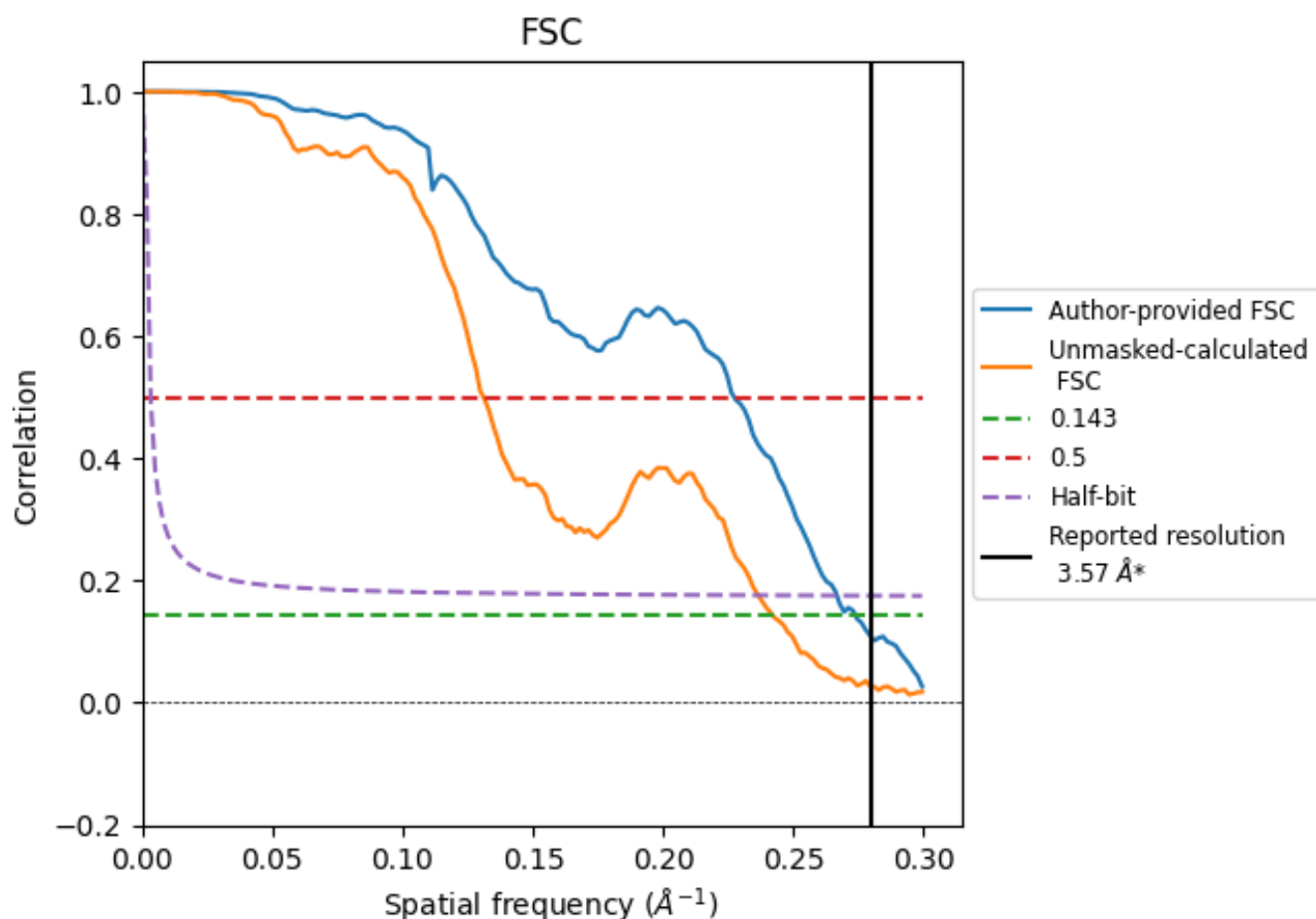


*Reported resolution corresponds to spatial frequency of 0.280 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.280 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.57	-	-
Author-provided FSC curve	3.65	4.40	3.75
Unmasked-calculated*	4.13	7.63	4.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.13 differs from the reported value 3.57 by more than 10 %

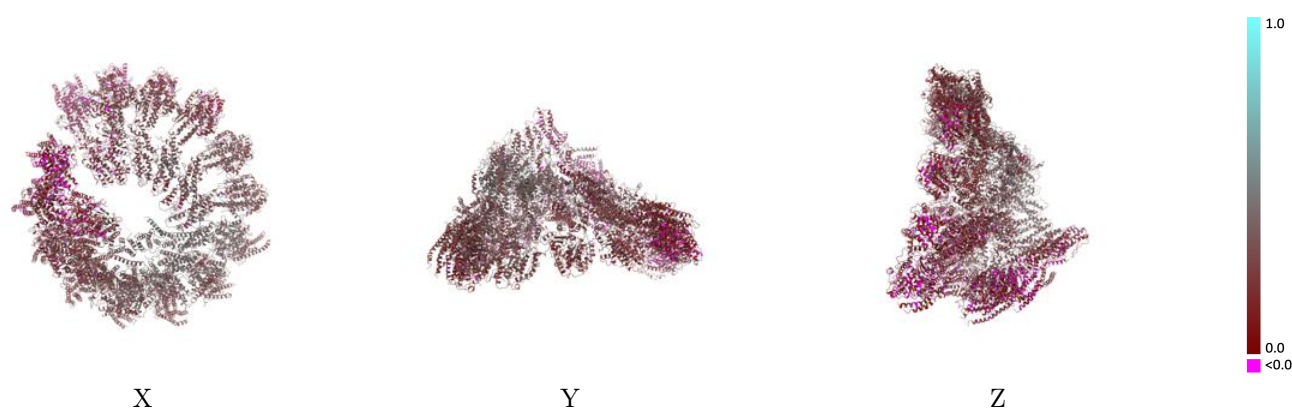
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19570 and PDB model 8RX1. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

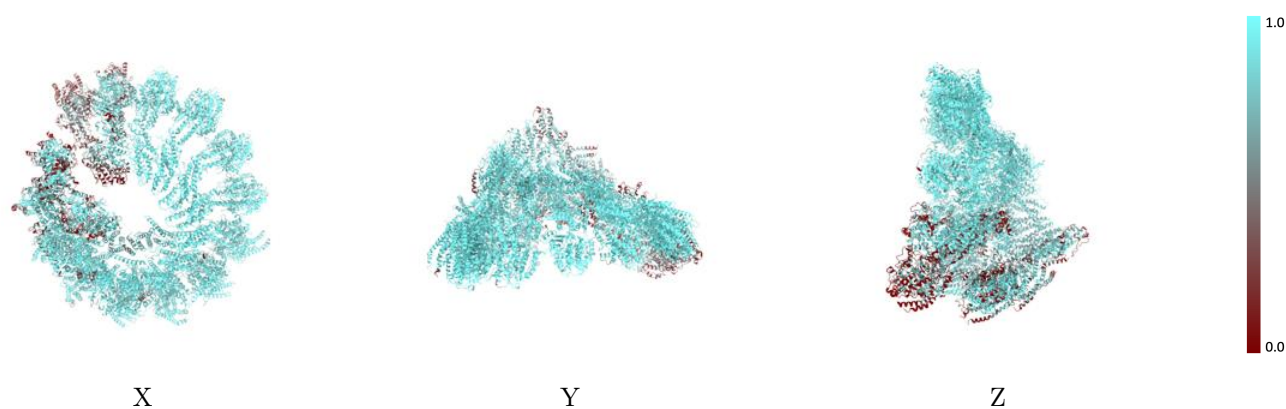
This section was not generated.

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



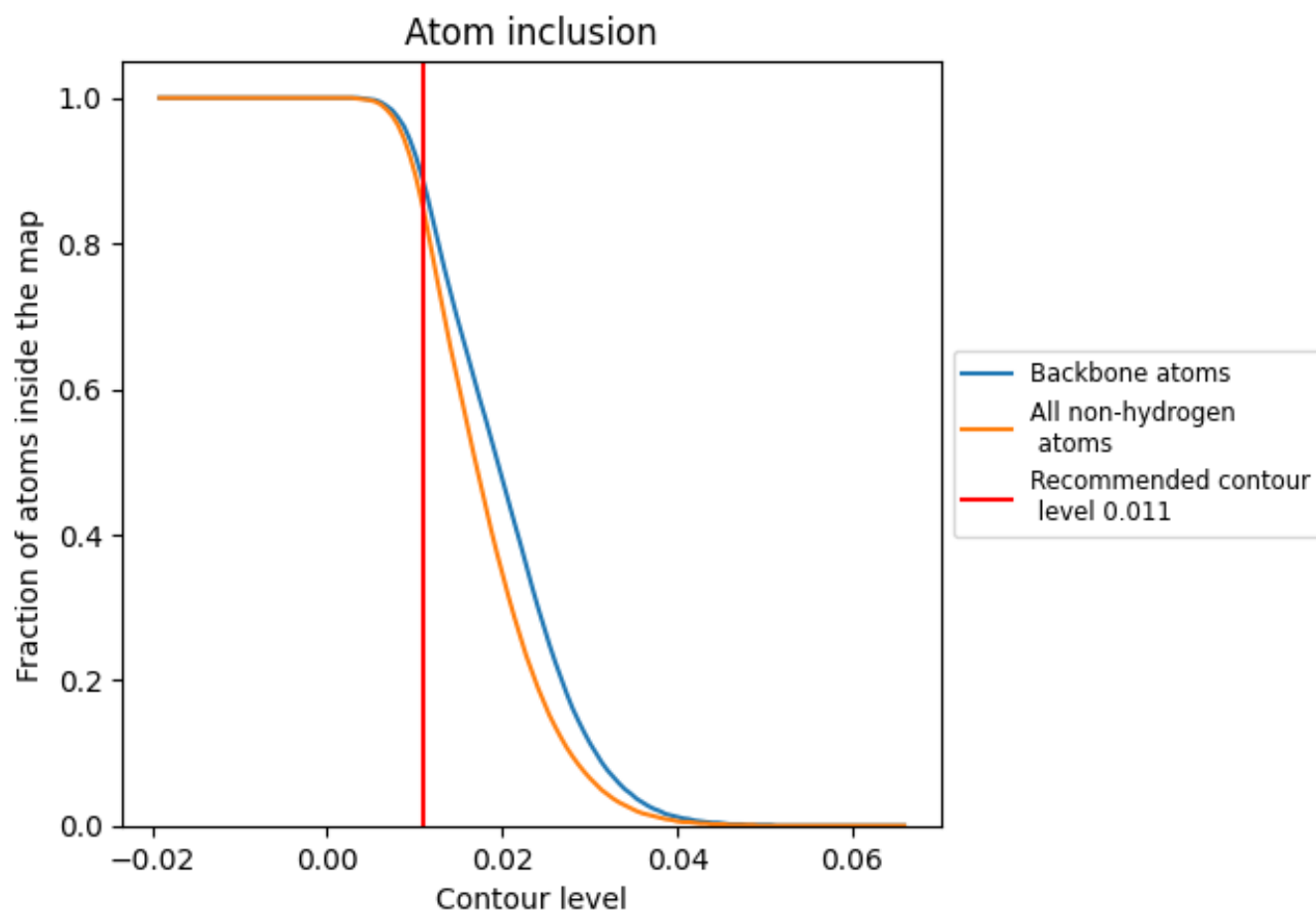
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8470	 0.2420
1	 0.6500	 0.1390
2	 0.2930	 0.1280
7	 0.7740	 0.2890
A	 0.5960	 0.0970
B	 0.7720	 0.2080
C	 0.8890	 0.2370
D	 0.9390	 0.2560
E	 0.9270	 0.3150
F	 0.9630	 0.3150
G	 0.8450	 0.2400
H	 0.7190	 0.2450
I	 0.9670	 0.3310
J	 0.9680	 0.3030
K	 0.9860	 0.2860
L	 0.9870	 0.2510
M	 0.7860	 0.1870
N	 0.3640	 0.1570
O	 0.5060	 0.1430
P	 0.6560	 0.1500
Q	 0.8800	 0.1800
R	 0.9380	 0.1760
S	 0.9840	 0.2480
T	 0.9640	 0.2310
U	 0.9760	 0.2810
V	 0.9640	 0.3260
W	 0.9760	 0.2510
X	 0.9800	 0.2330
Y	 0.9780	 0.1470
Z	 0.9680	 0.1580
a	 0.8470	 0.3880
b	 0.8690	 0.4020
c	 0.7440	 0.2880
d	 0.8240	 0.3470
e	 0.5630	 0.3180



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Chain	Atom inclusion	Q-score
f	 0.5280	 0.2940
g	 0.9560	 0.2570
h	 0.5900	 0.2510
i	 0.5990	 0.2530
j	 0.4390	 0.2430
k	 0.9510	 0.3560
n	 0.9730	 0.3800
s	 0.9260	 0.2890
t	 0.9830	 0.3430
u	 0.8680	 0.2570
v	 0.9520	 0.2860