



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 04:33 AM UTC

PDB ID : 9QVN / pdb_00009qvn
EMDB ID : EMD-53400
Title : Cryo-EM reconstruction of the NEDD1 anchor protein bound to the gamma-tubulin ring complex
Authors : Munoz-Hernandez, H.; Xu, Y.; Wieczorek, M.
Deposited on : 2025-04-11
Resolution : 4.70 Å(reported)
Based on initial model : .

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:

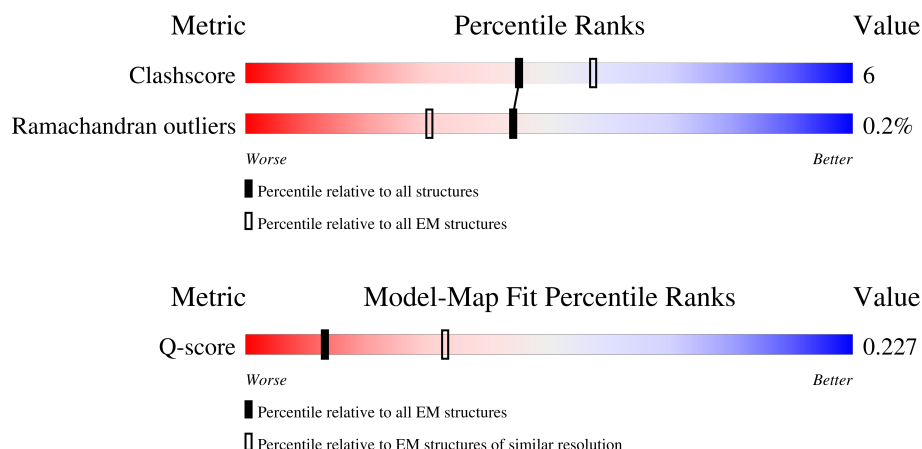
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (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 4.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	1989 (4.20 - 5.20)

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

Mol	Chain	Length	Quality of chain
1	B	907	
1	D	907	
1	F	907	
1	H	907	
1	N	907	

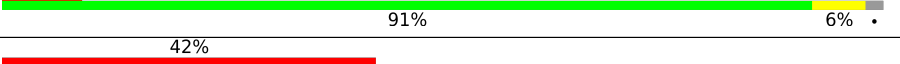
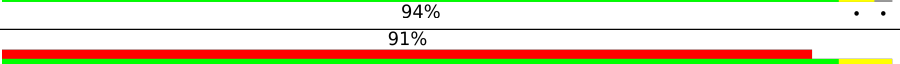
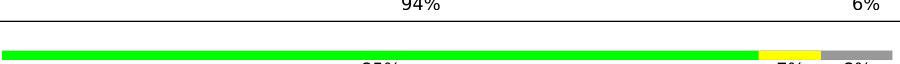
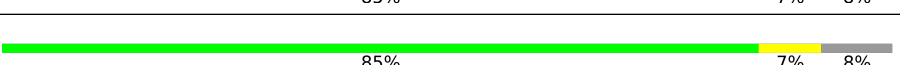
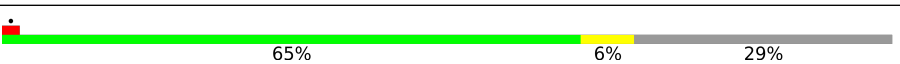
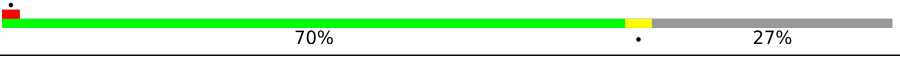
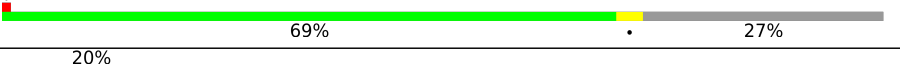
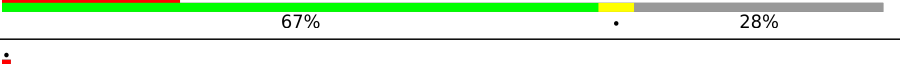
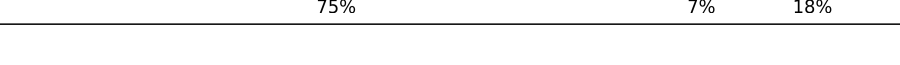
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	r	907	
1	s	907	
1	t	907	
1	u	907	
1	v	907	
2	O	82	
2	P	82	
2	Q	82	
2	R	82	
2	S	82	
2	T	82	
2	U	82	
3	V	660	
3	W	660	
3	X	660	
3	Y	660	
4	Z	375	
5	a	457	
5	b	457	
5	c	457	
5	d	457	
5	e	457	
5	f	457	
5	g	457	
5	h	457	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	i	457	
5	j	457	
5	k	457	
5	l	457	
5	m	457	
5	n	457	
6	I	667	
6	K	667	
7	A	930	
7	C	930	
7	E	930	
7	G	930	
7	M	930	
8	L	1811	
9	J	1024	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 87756 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Gamma-tubulin complex component 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	D	657	Total	C	N	O	0	0
			3256	1942	657	657		
1	F	657	Total	C	N	O	0	0
			3256	1942	657	657		
1	H	656	Total	C	N	O	0	0
			3252	1940	656	656		
1	r	113	Total	C	N	O	0	0
			562	336	113	113		
1	s	115	Total	C	N	O	0	0
			572	342	115	115		
1	t	120	Total	C	N	O	0	0
			597	357	120	120		
1	u	120	Total	C	N	O	0	0
			597	357	120	120		
1	v	129	Total	C	N	O	0	0
			642	384	129	129		
1	B	644	Total	C	N	O	0	0
			3192	1904	644	644		
1	N	630	Total	C	N	O	0	0
			3123	1863	630	630		

- Molecule 2 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	P	73	Total	C	N	O	0	0
			363	217	73	73		
2	R	66	Total	C	N	O	0	0
			328	196	66	66		
2	S	66	Total	C	N	O	0	0
			328	196	66	66		
2	T	82	Total	C	N	O	0	0
			406	242	82	82		
2	U	82	Total	C	N	O	0	0
			406	242	82	82		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
2	O	82	Total	C	N	O	0	0
			406	242	82	82		
2	Q	66	Total	C	N	O	0	0
			328	196	66	66		

- Molecule 3 is a protein called Protein NEDD1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	W	79	Total	C	N	O	0	0
			394	236	79	79		
3	X	78	Total	C	N	O	0	0
			389	233	78	78		
3	V	77	Total	C	N	O	0	0
			384	230	77	77		
3	Y	78	Total	C	N	O	0	0
			389	233	78	78		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	Z	375	Total	C	N	O	0	0
			1847	1097	375	375		

- Molecule 5 is a protein called Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	a	446	Total	C	N	O	0	0
			2204	1312	446	446		
5	b	452	Total	C	N	O	0	0
			2233	1329	452	452		
5	c	448	Total	C	N	O	0	0
			2213	1317	448	448		
5	e	448	Total	C	N	O	0	0
			2213	1317	448	448		
5	f	451	Total	C	N	O	0	0
			2228	1326	451	451		
5	g	450	Total	C	N	O	0	0
			2223	1323	450	450		
5	h	451	Total	C	N	O	0	0
			2228	1326	451	451		
5	i	448	Total	C	N	O	0	0
			2213	1317	448	448		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
5	j	449	Total	C	N	O	0	0
			2218	1320	449	449		
5	k	448	Total	C	N	O	0	0
			2213	1317	448	448		
5	l	447	Total	C	N	O	0	0
			2208	1314	447	447		
5	m	448	Total	C	N	O	0	0
			2213	1317	448	448		
5	n	457	Total	C	N	O	0	0
			2258	1344	457	457		
5	d	451	Total	C	N	O	0	0
			2228	1326	451	451		

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	452	GLU	-	expression tag	UNP P23258
a	453	ASN	-	expression tag	UNP P23258
a	454	LEU	-	expression tag	UNP P23258
a	455	TYR	-	expression tag	UNP P23258
a	456	PHE	-	expression tag	UNP P23258
a	457	GLN	-	expression tag	UNP P23258
b	452	GLU	-	expression tag	UNP P23258
b	453	ASN	-	expression tag	UNP P23258
b	454	LEU	-	expression tag	UNP P23258
b	455	TYR	-	expression tag	UNP P23258
b	456	PHE	-	expression tag	UNP P23258
b	457	GLN	-	expression tag	UNP P23258
c	452	GLU	-	expression tag	UNP P23258
c	453	ASN	-	expression tag	UNP P23258
c	454	LEU	-	expression tag	UNP P23258
c	455	TYR	-	expression tag	UNP P23258
c	456	PHE	-	expression tag	UNP P23258
c	457	GLN	-	expression tag	UNP P23258
e	452	GLU	-	expression tag	UNP P23258
e	453	ASN	-	expression tag	UNP P23258
e	454	LEU	-	expression tag	UNP P23258
e	455	TYR	-	expression tag	UNP P23258
e	456	PHE	-	expression tag	UNP P23258
e	457	GLN	-	expression tag	UNP P23258
f	452	GLU	-	expression tag	UNP P23258
f	453	ASN	-	expression tag	UNP P23258
f	454	LEU	-	expression tag	UNP P23258

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
f	455	TYR	-	expression tag	UNP P23258
f	456	PHE	-	expression tag	UNP P23258
f	457	GLN	-	expression tag	UNP P23258
g	452	GLU	-	expression tag	UNP P23258
g	453	ASN	-	expression tag	UNP P23258
g	454	LEU	-	expression tag	UNP P23258
g	455	TYR	-	expression tag	UNP P23258
g	456	PHE	-	expression tag	UNP P23258
g	457	GLN	-	expression tag	UNP P23258
h	452	GLU	-	expression tag	UNP P23258
h	453	ASN	-	expression tag	UNP P23258
h	454	LEU	-	expression tag	UNP P23258
h	455	TYR	-	expression tag	UNP P23258
h	456	PHE	-	expression tag	UNP P23258
h	457	GLN	-	expression tag	UNP P23258
i	452	GLU	-	expression tag	UNP P23258
i	453	ASN	-	expression tag	UNP P23258
i	454	LEU	-	expression tag	UNP P23258
i	455	TYR	-	expression tag	UNP P23258
i	456	PHE	-	expression tag	UNP P23258
i	457	GLN	-	expression tag	UNP P23258
j	452	GLU	-	expression tag	UNP P23258
j	453	ASN	-	expression tag	UNP P23258
j	454	LEU	-	expression tag	UNP P23258
j	455	TYR	-	expression tag	UNP P23258
j	456	PHE	-	expression tag	UNP P23258
j	457	GLN	-	expression tag	UNP P23258
k	452	GLU	-	expression tag	UNP P23258
k	453	ASN	-	expression tag	UNP P23258
k	454	LEU	-	expression tag	UNP P23258
k	455	TYR	-	expression tag	UNP P23258
k	456	PHE	-	expression tag	UNP P23258
k	457	GLN	-	expression tag	UNP P23258
l	452	GLU	-	expression tag	UNP P23258
l	453	ASN	-	expression tag	UNP P23258
l	454	LEU	-	expression tag	UNP P23258
l	455	TYR	-	expression tag	UNP P23258
l	456	PHE	-	expression tag	UNP P23258
l	457	GLN	-	expression tag	UNP P23258
m	452	GLU	-	expression tag	UNP P23258
m	453	ASN	-	expression tag	UNP P23258
m	454	LEU	-	expression tag	UNP P23258

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
m	455	TYR	-	expression tag	UNP P23258
m	456	PHE	-	expression tag	UNP P23258
m	457	GLN	-	expression tag	UNP P23258
n	452	GLU	-	expression tag	UNP P23258
n	453	ASN	-	expression tag	UNP P23258
n	454	LEU	-	expression tag	UNP P23258
n	455	TYR	-	expression tag	UNP P23258
n	456	PHE	-	expression tag	UNP P23258
n	457	GLN	-	expression tag	UNP P23258
d	452	GLU	-	expression tag	UNP P23258
d	453	ASN	-	expression tag	UNP P23258
d	454	LEU	-	expression tag	UNP P23258
d	455	TYR	-	expression tag	UNP P23258
d	456	PHE	-	expression tag	UNP P23258
d	457	GLN	-	expression tag	UNP P23258

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

Mol	Chain	Residues	Atoms				AltConf	Trace
6	K	614	Total	C	N	O	0	0
			3037	1809	614	614		
6	I	612	Total	C	N	O	0	0
			3027	1803	612	612		

- Molecule 7 is a protein called Isoform 3 of Gamma-tubulin complex component 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	678	Total	C	N	O	0	0
			3367	2011	678	678		
7	M	665	Total	C	N	O	0	0
			3303	1973	665	665		
7	C	653	Total	C	N	O	0	0
			3244	1938	653	653		
7	A	657	Total	C	N	O	0	0
			3264	1950	657	657		
7	E	678	Total	C	N	O	0	0
			3367	2011	678	678		

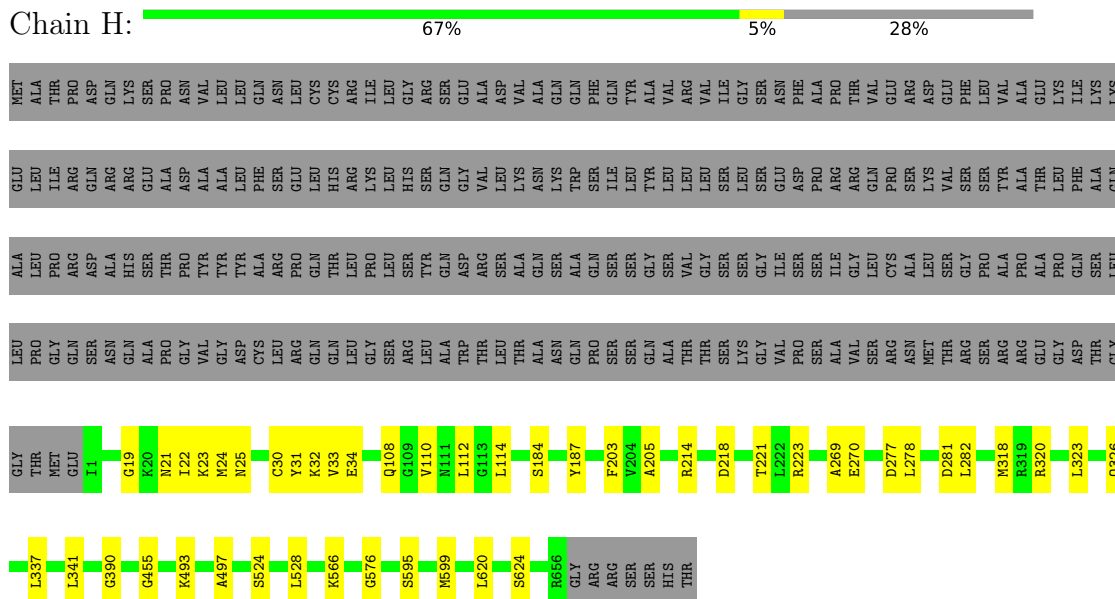
- Molecule 8 is a protein called TUBGCP6 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	L	982	Total 4851	C 2887	N 982	O 982	0	0

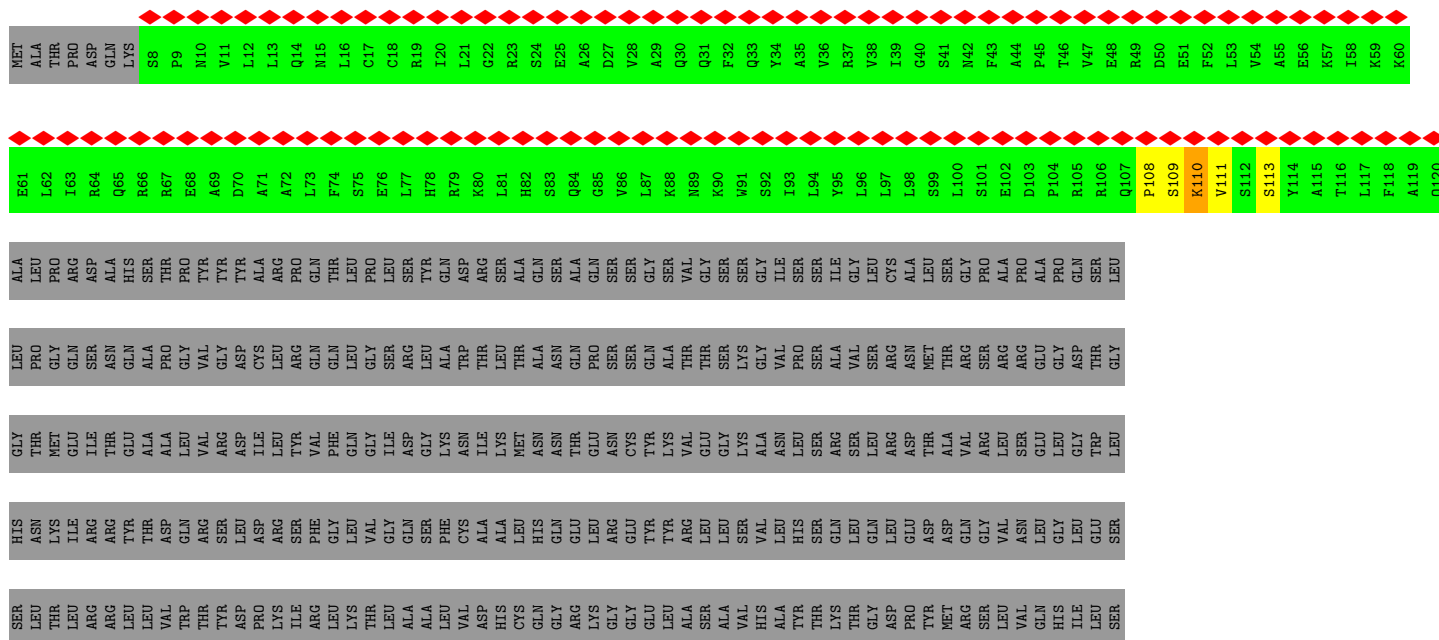
- Molecule 9 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	J	842	Total 4186	C 2502	N 842	O 842	0	0

- Molecule 1: Gamma-tubulin complex component 3



- Molecule 1: Gamma-tubulin complex component 3



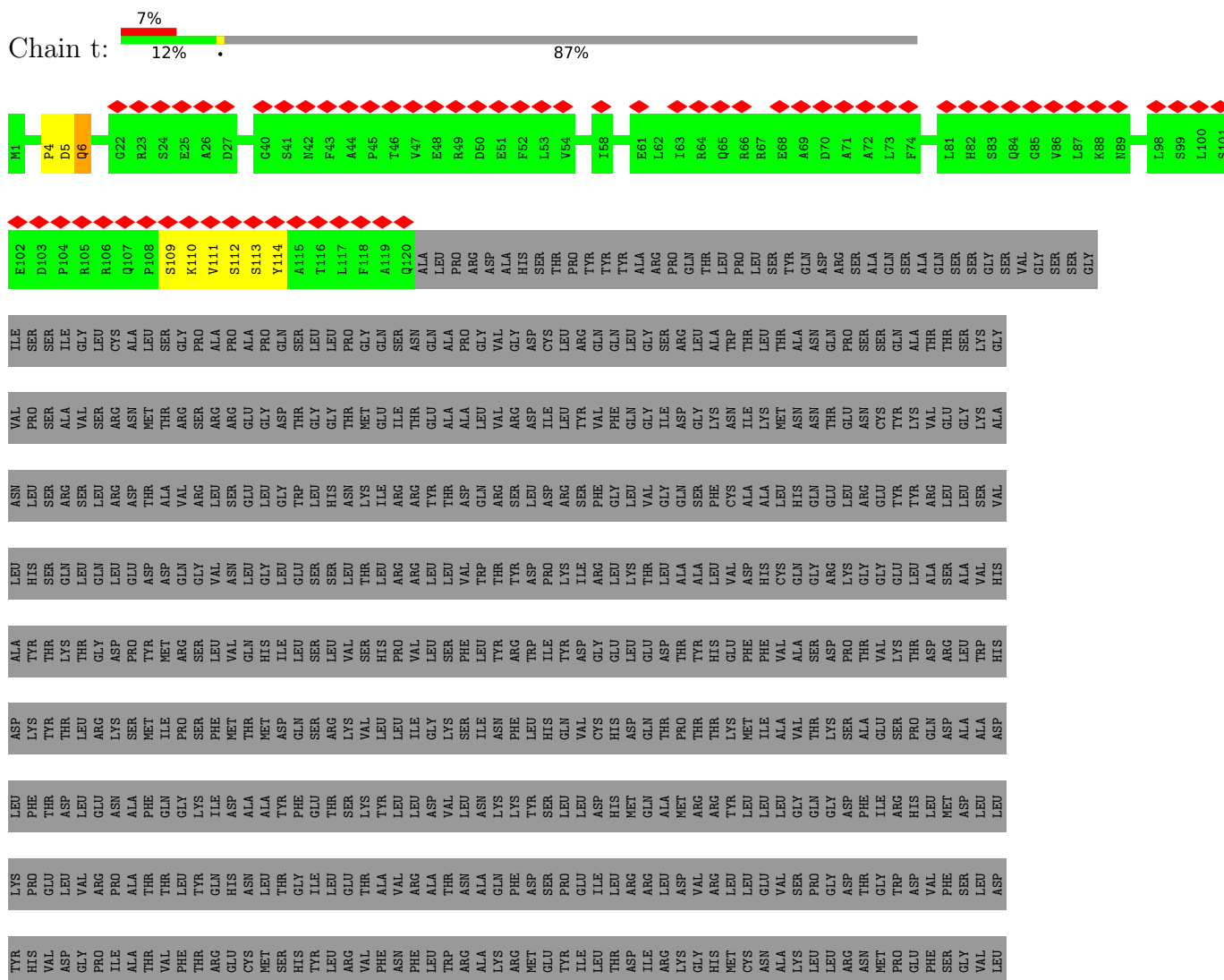
[illegible]

- Molecule 1: Gamma-tubulin complex component 3

[illegible]

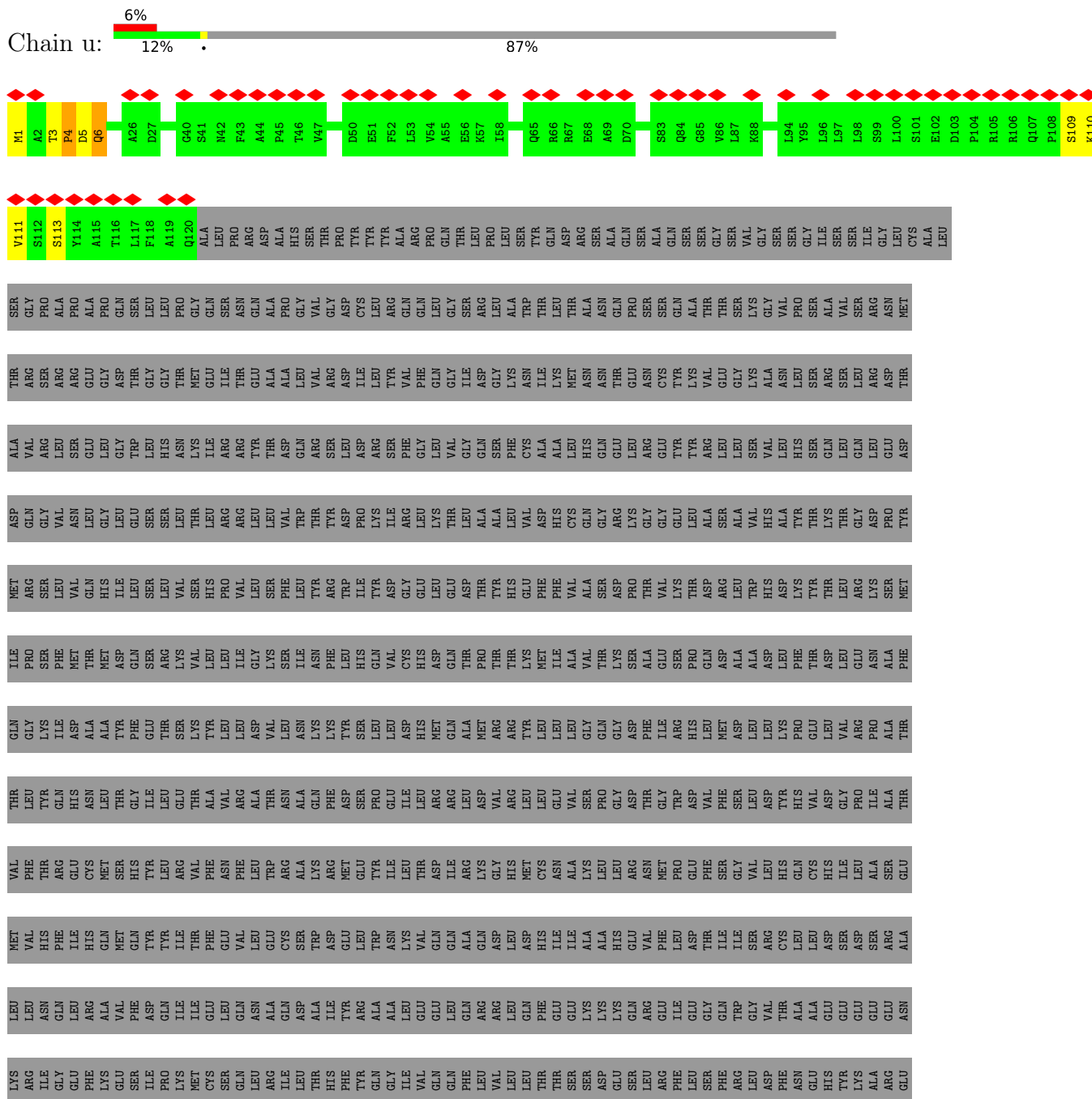
[illegible]

- Molecule 1: Gamma-tubulin complex component 3



[illegible]

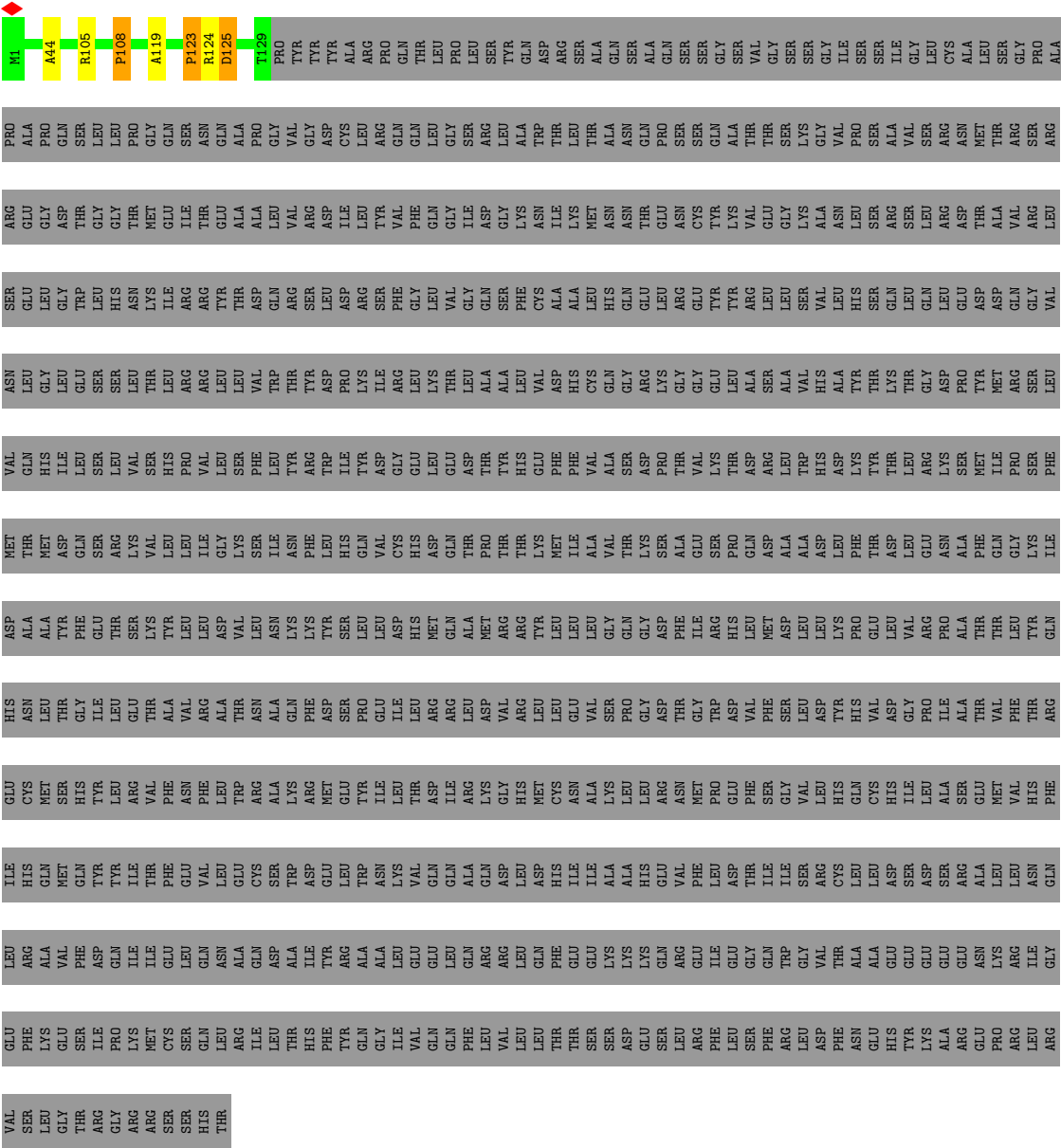
- Molecule 1: Gamma-tubulin complex component 3



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

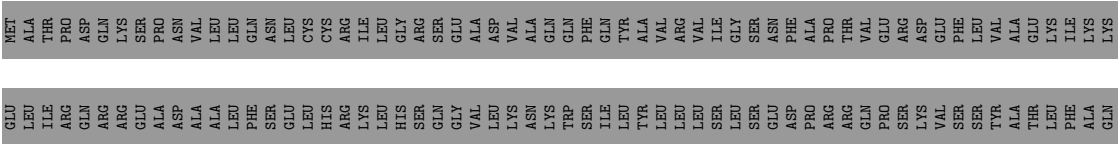
● Molecule 1: Gamma-tubulin complex component 3

Chain v: 13% 86%

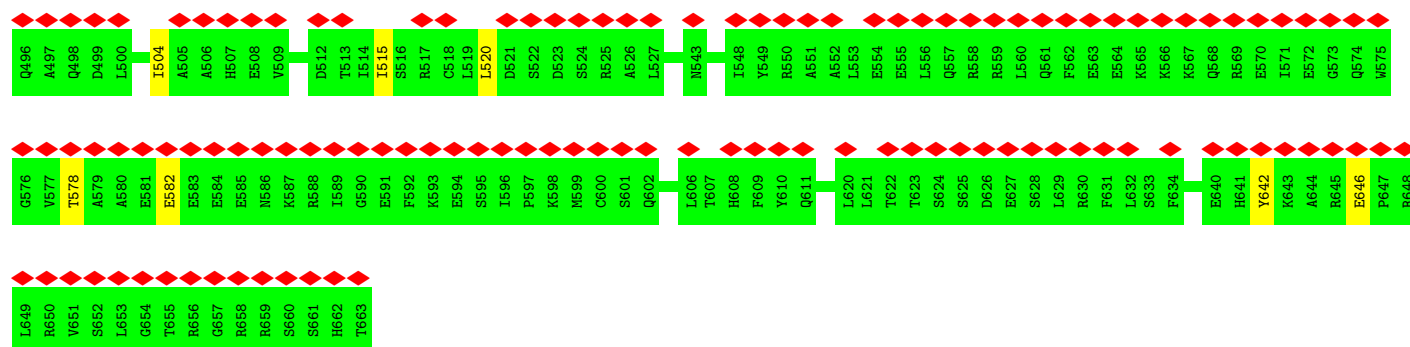


● Molecule 1: Gamma-tubulin complex component 3

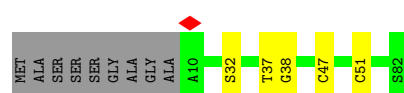
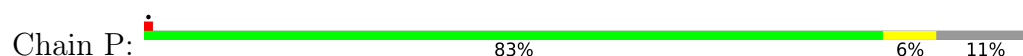
Chain B: 66% 5% 29%



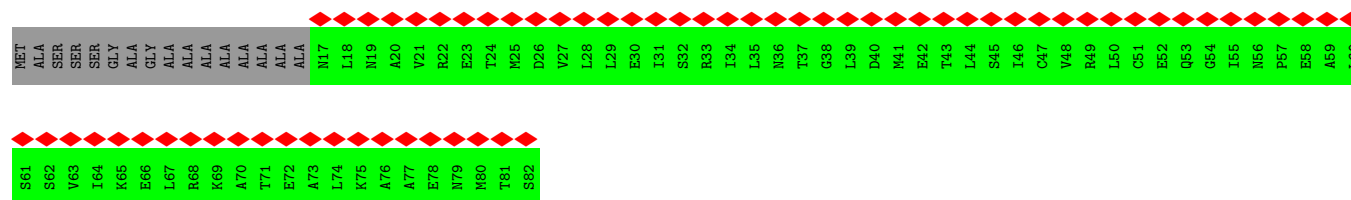
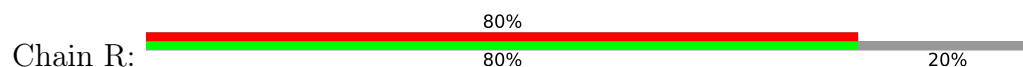




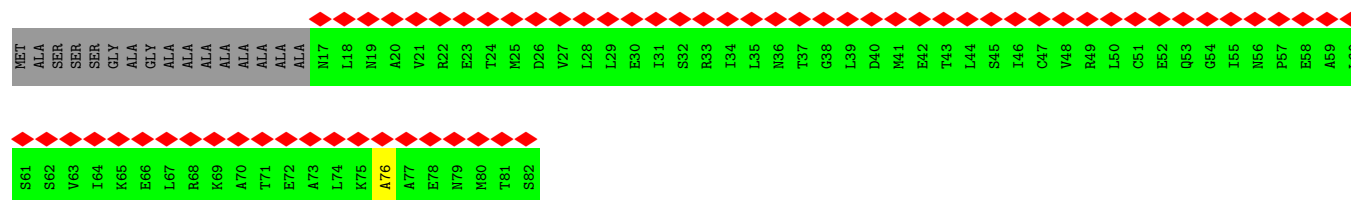
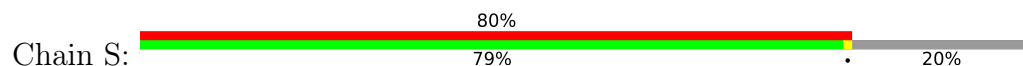
- Molecule 2: Mitotic-spindle organizing protein 1



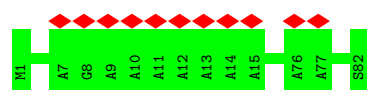
- Molecule 2: Mitotic-spindle organizing protein 1



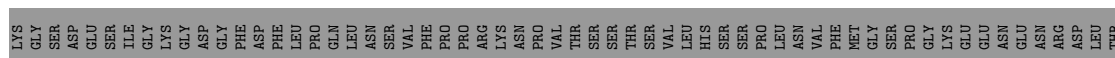
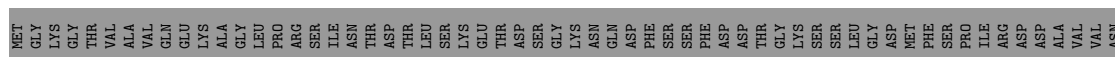
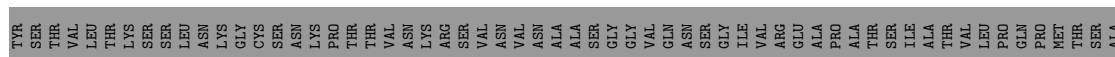
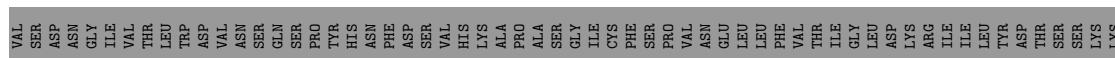
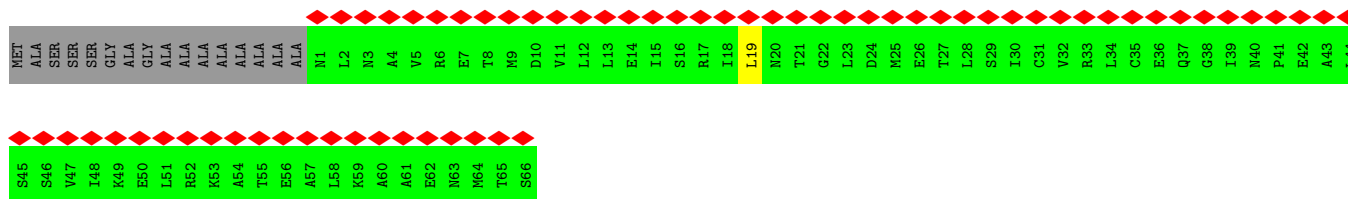
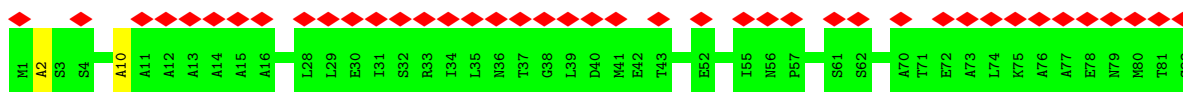
- Molecule 2: Mitotic-spindle organizing protein 1

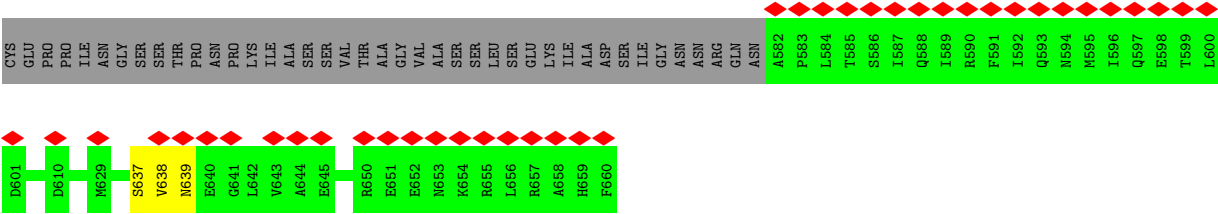


- Molecule 2: Mitotic-spindle organizing protein 1

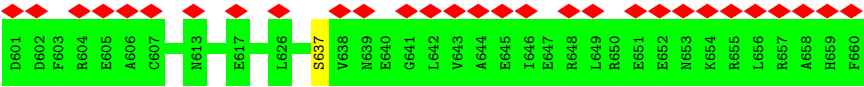
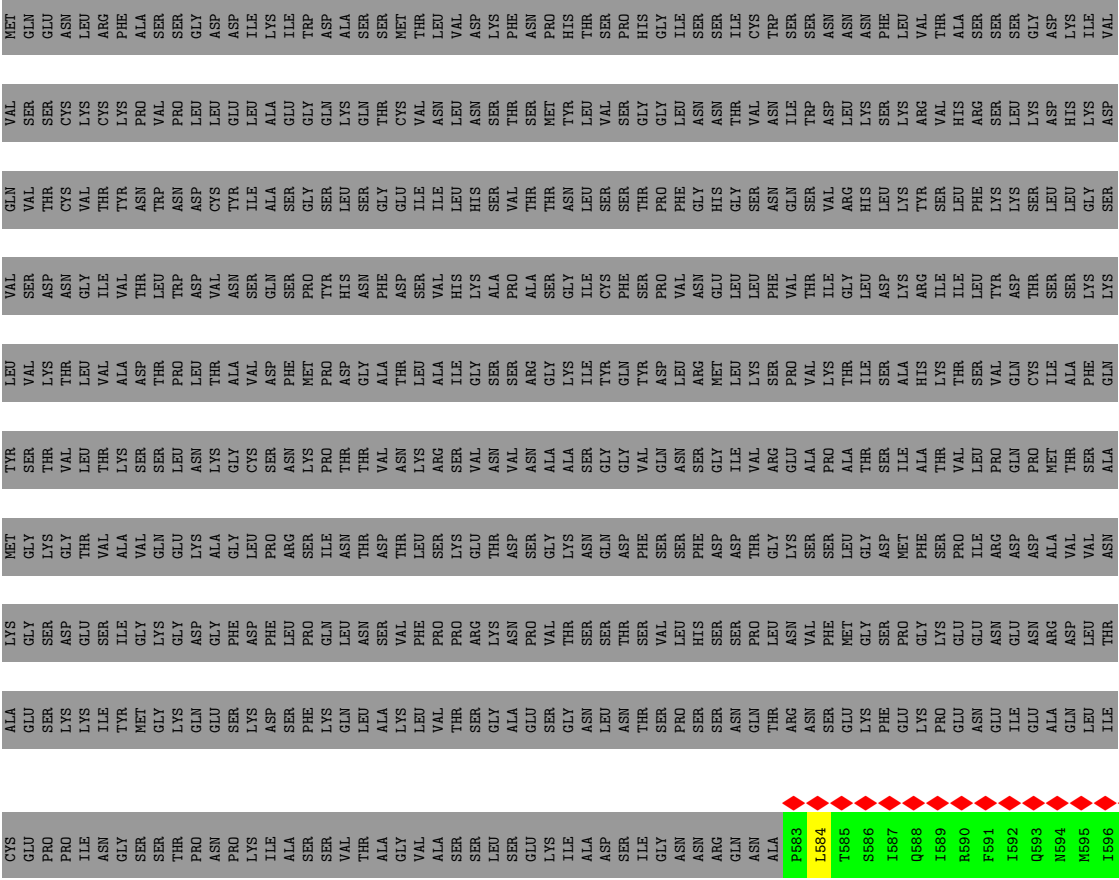


- Molecule 2: Mitotic-spindle organizing protein 1

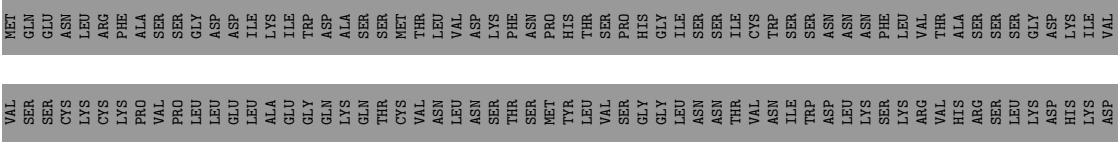




• Molecule 3: Protein NEDD1

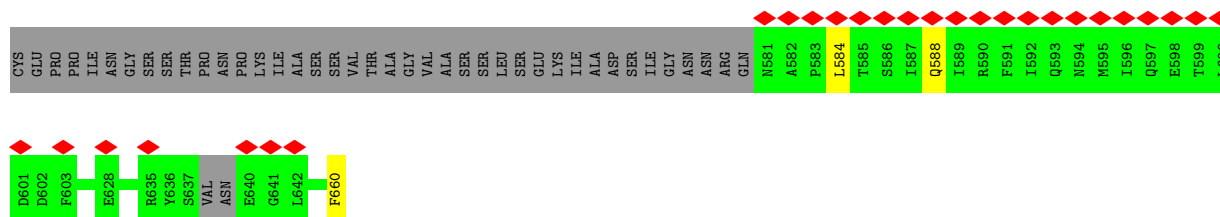


• Molecule 3: Protein NEDD1

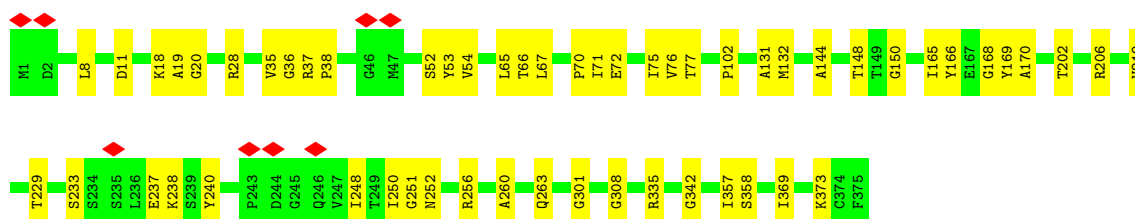
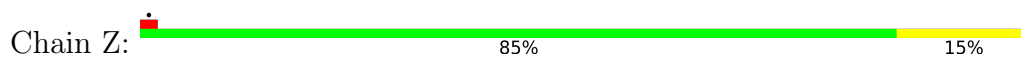


- Molecule 3: Protein NEDD1

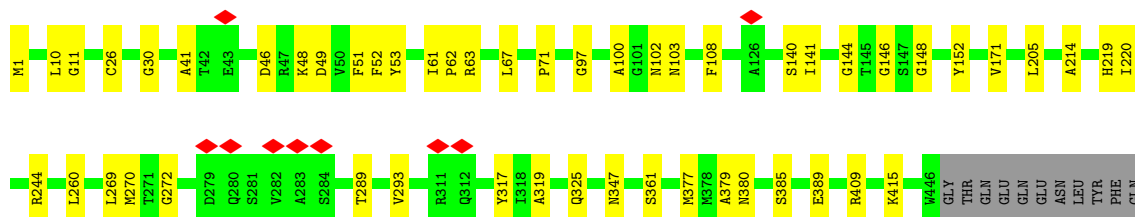
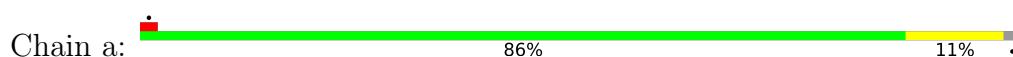
[illegible]



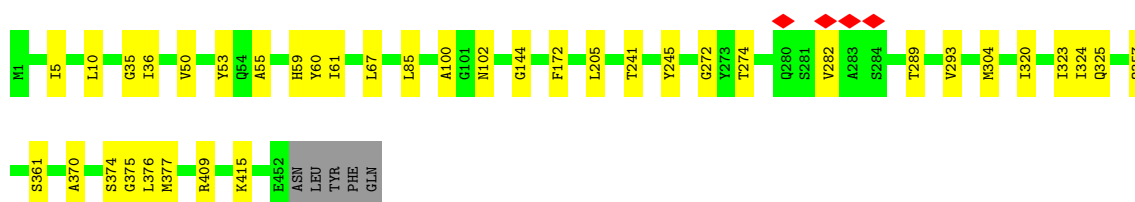
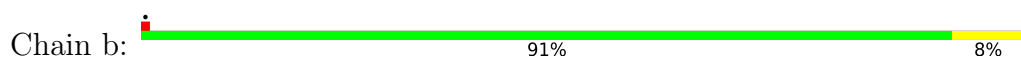
- Molecule 4: Actin, cytoplasmic 1, N-terminally processed



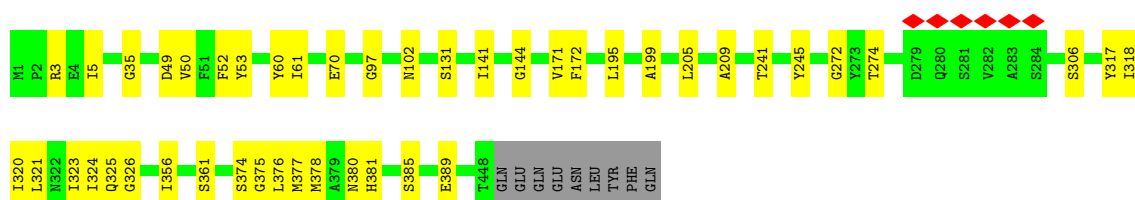
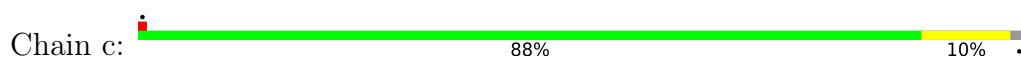
- Molecule 5: Tubulin gamma-1 chain



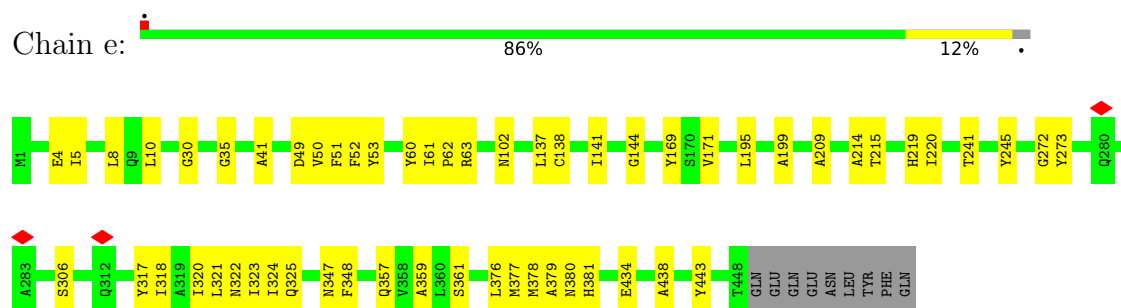
- Molecule 5: Tubulin gamma-1 chain



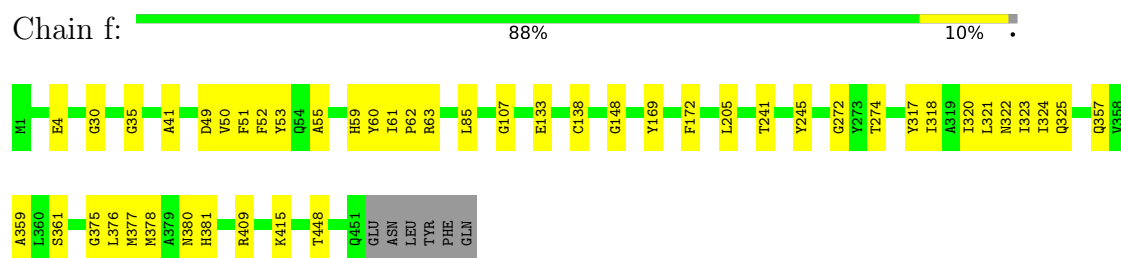
- Molecule 5: Tubulin gamma-1 chain



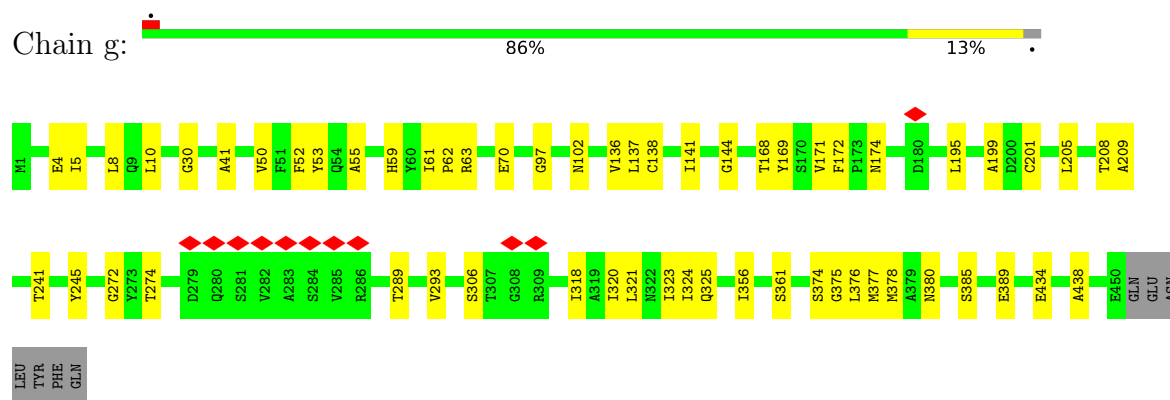
- Molecule 5: Tubulin gamma-1 chain



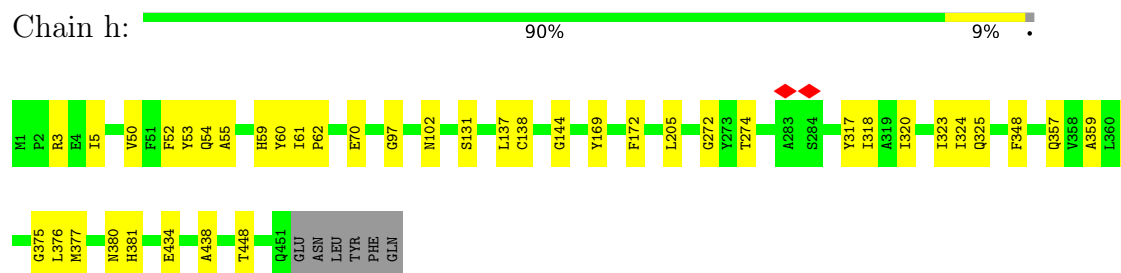
- Molecule 5: Tubulin gamma-1 chain



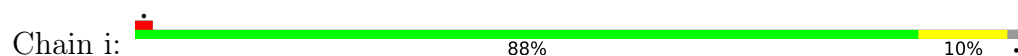
- Molecule 5: Tubulin gamma-1 chain

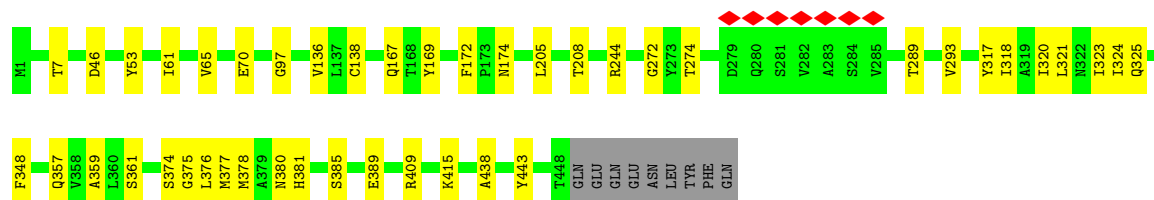


- Molecule 5: Tubulin gamma-1 chain

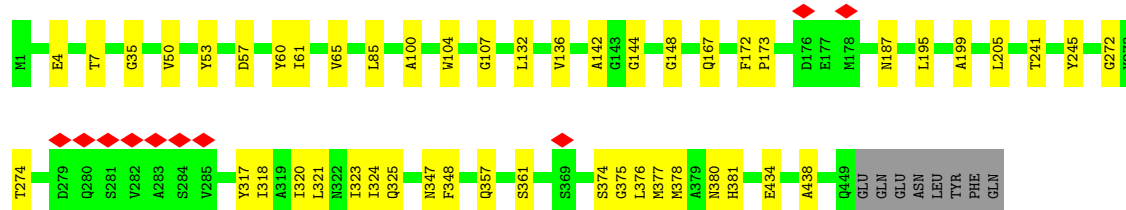
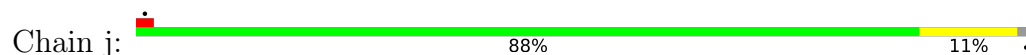


- Molecule 5: Tubulin gamma-1 chain

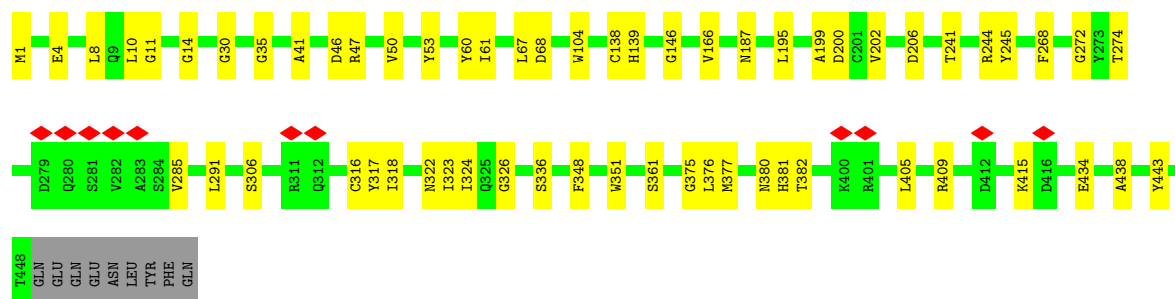
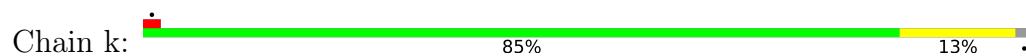




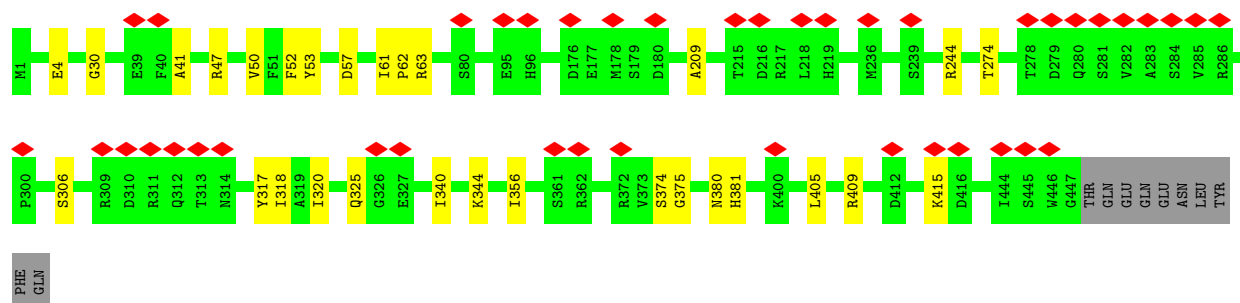
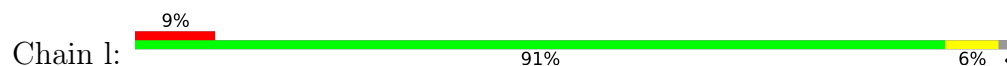
- Molecule 5: Tubulin gamma-1 chain



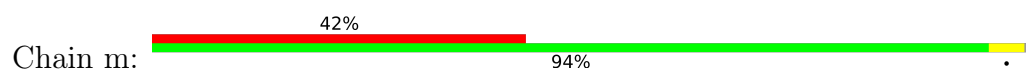
- Molecule 5: Tubulin gamma-1 chain

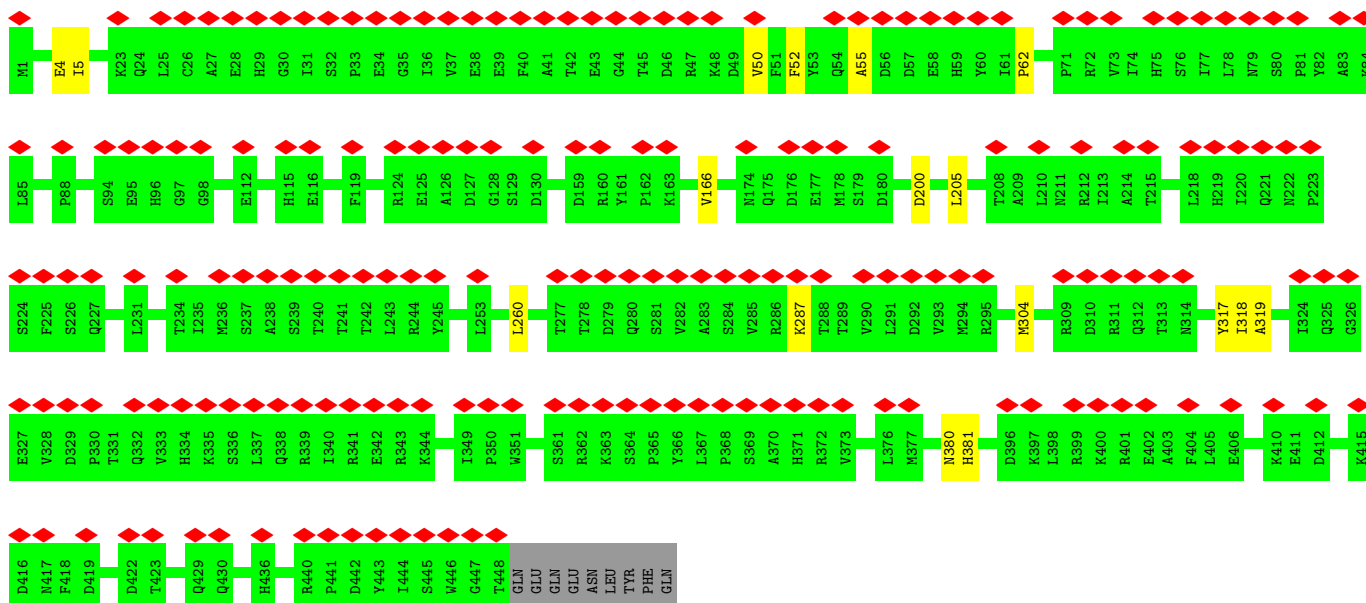


- Molecule 5: Tubulin gamma-1 chain

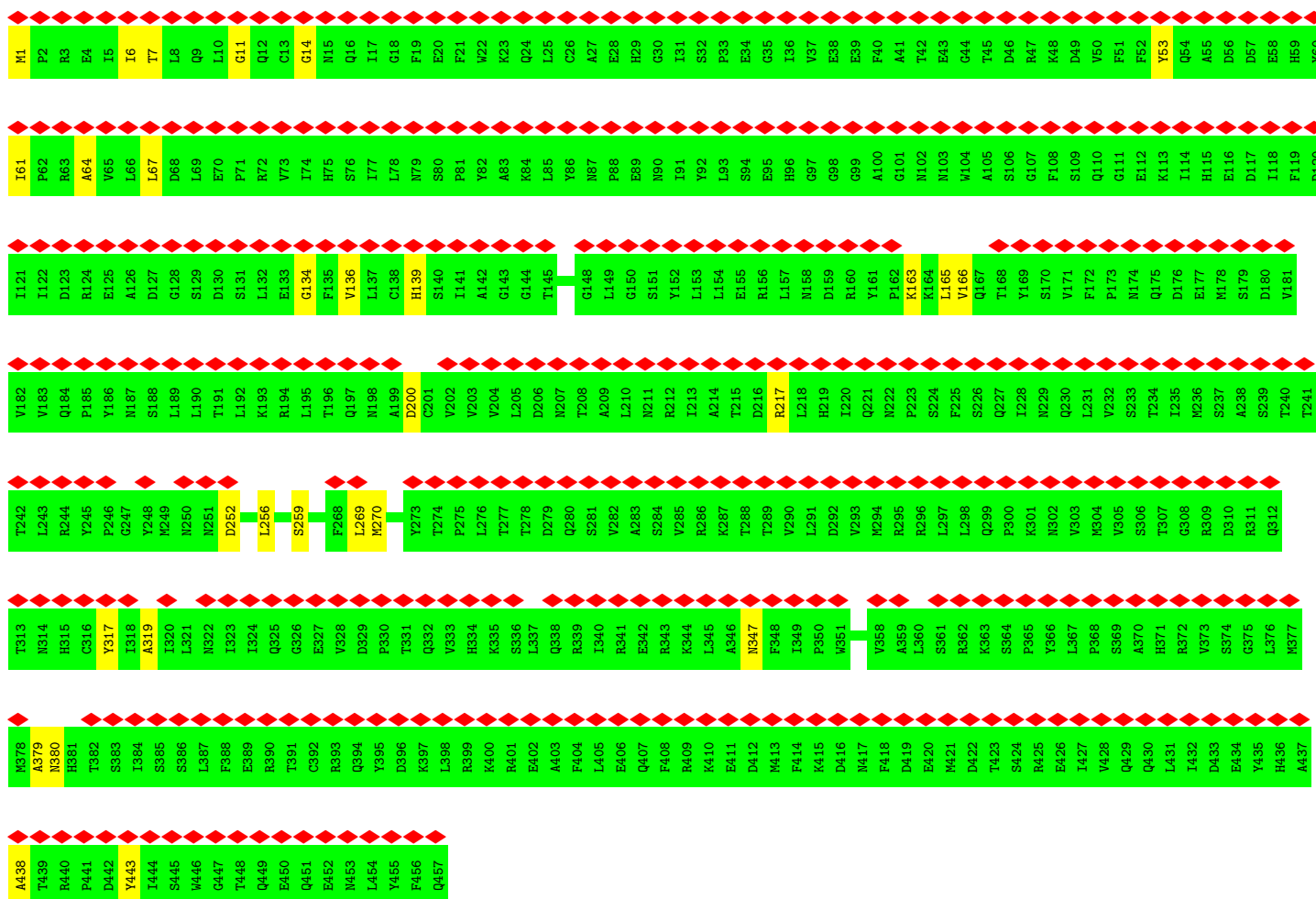
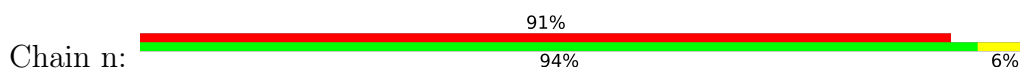


- Molecule 5: Tubulin gamma-1 chain

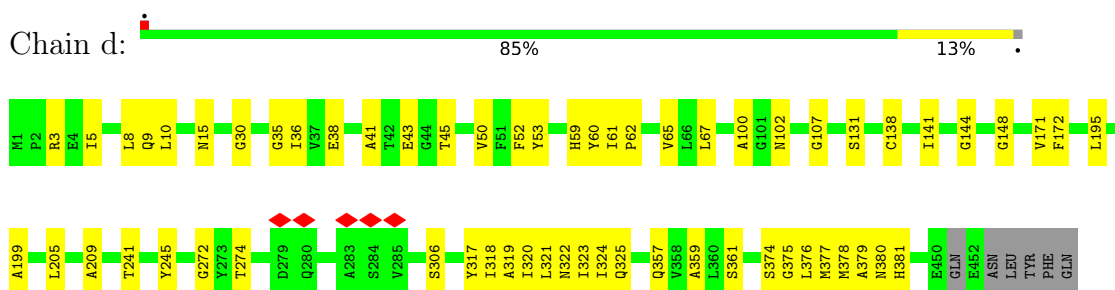




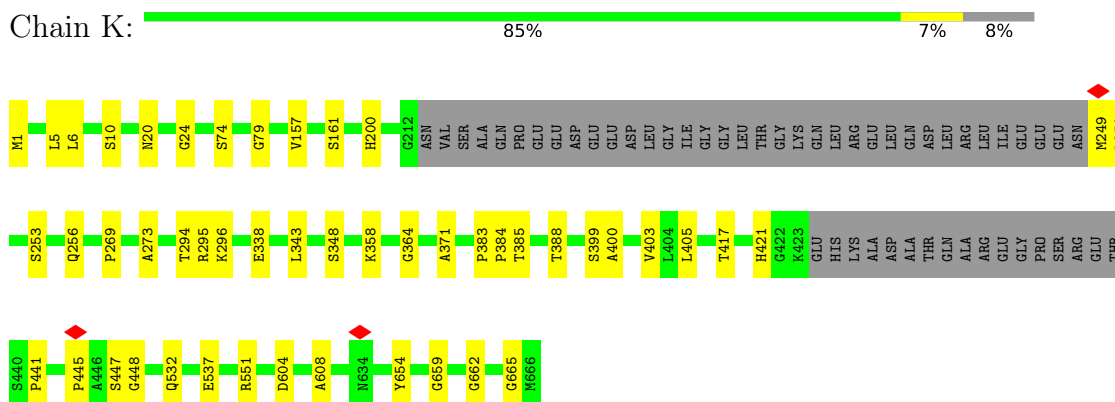
• Molecule 5: Tubulin gamma-1 chain



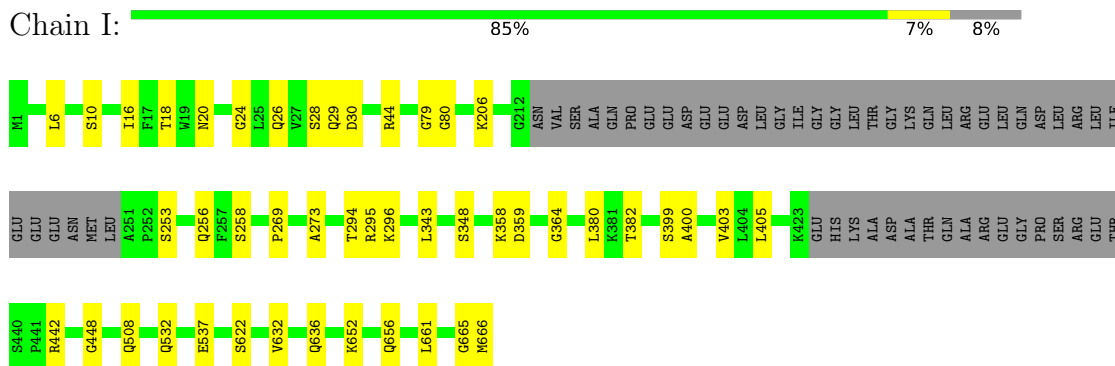
- Molecule 5: Tubulin gamma-1 chain



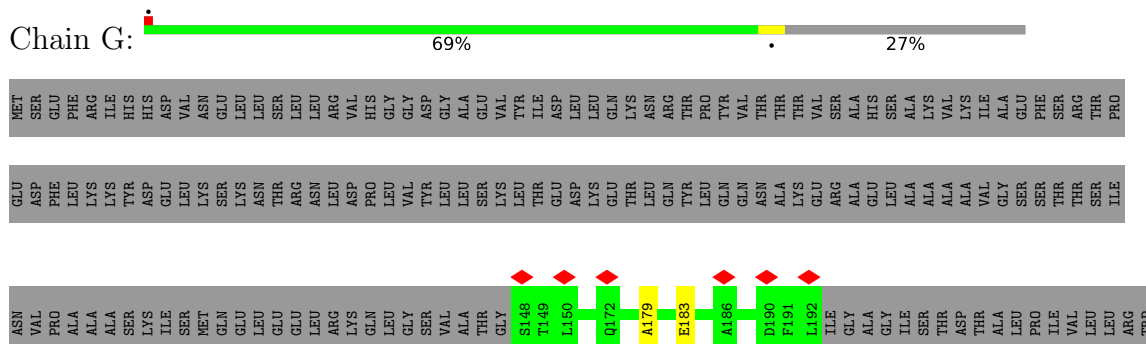
- Molecule 6: Gamma-tubulin complex component 4

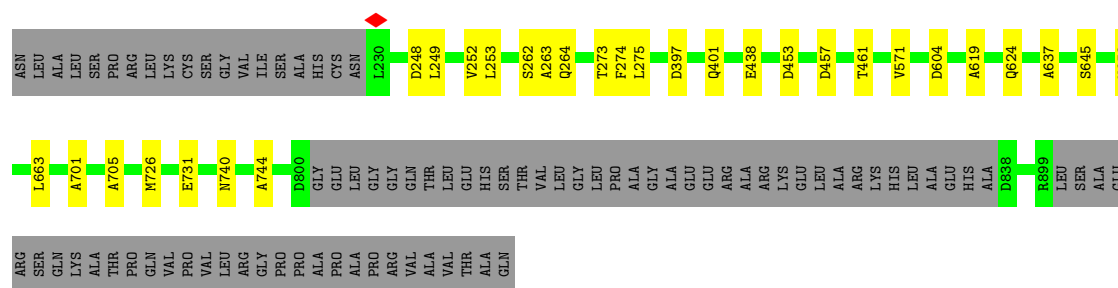


- Molecule 6: Gamma-tubulin complex component 4

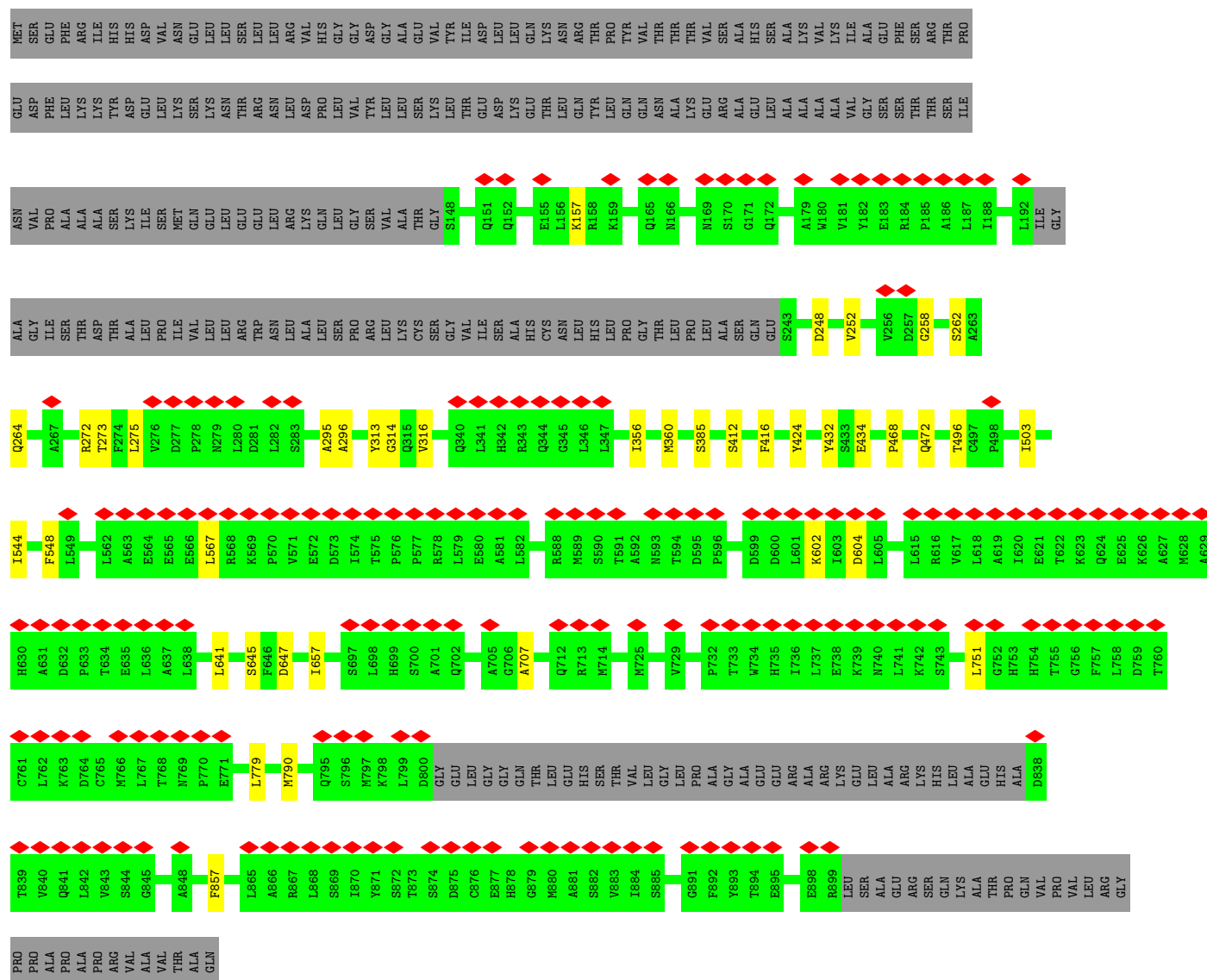


- Molecule 7: Isoform 3 of Gamma-tubulin complex component 2



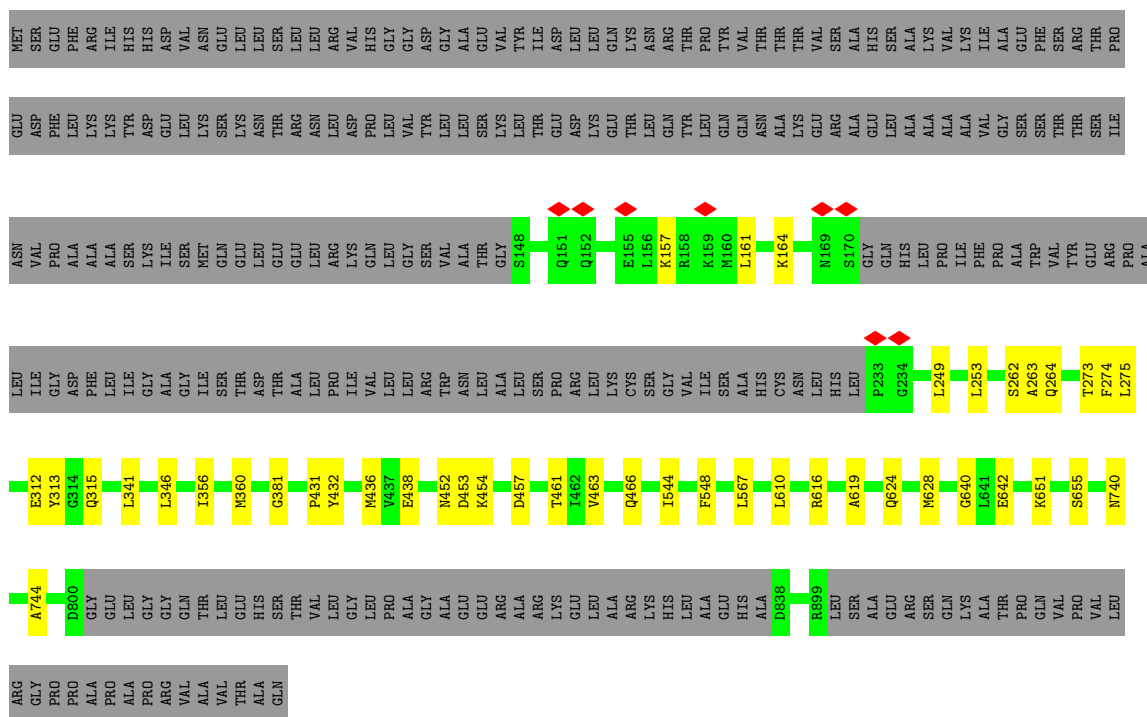


• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

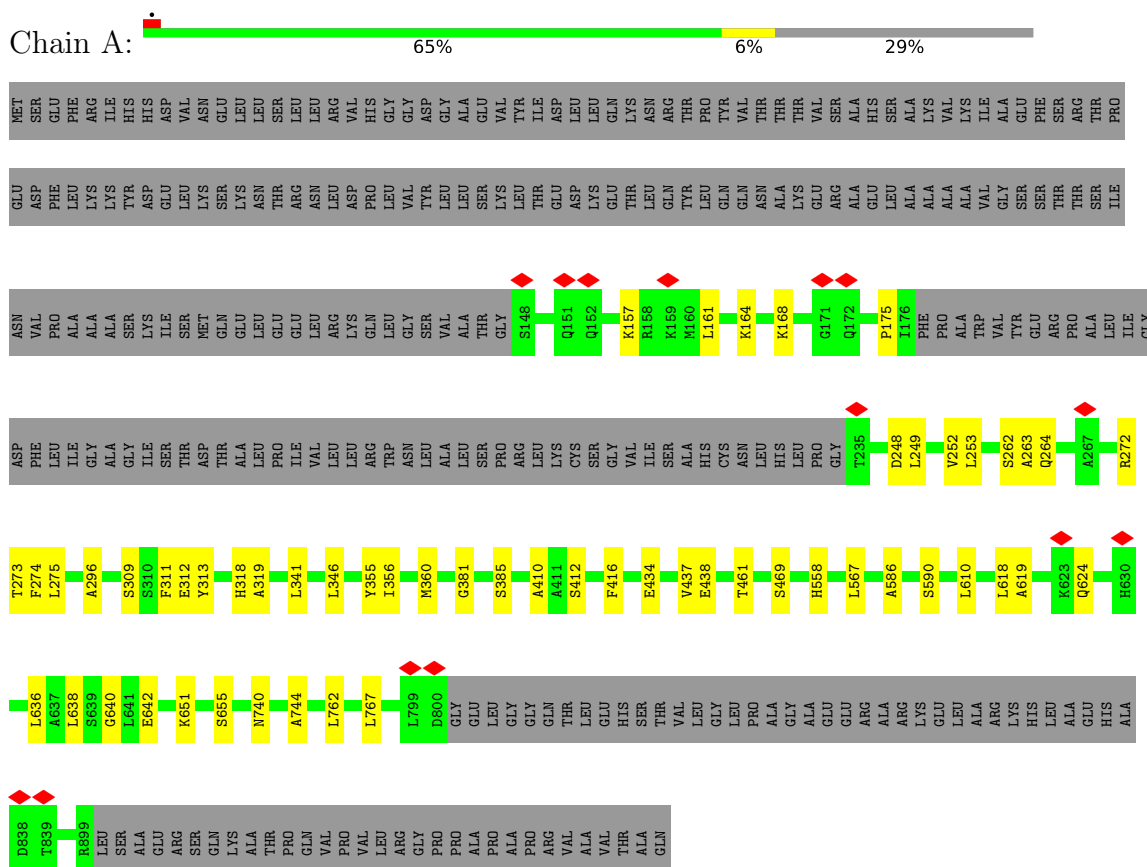


• Molecule 7: Isoform 3 of Gamma-tubulin complex component 2





- Molecule 7: Isoform 3 of Gamma-tubulin complex component 2



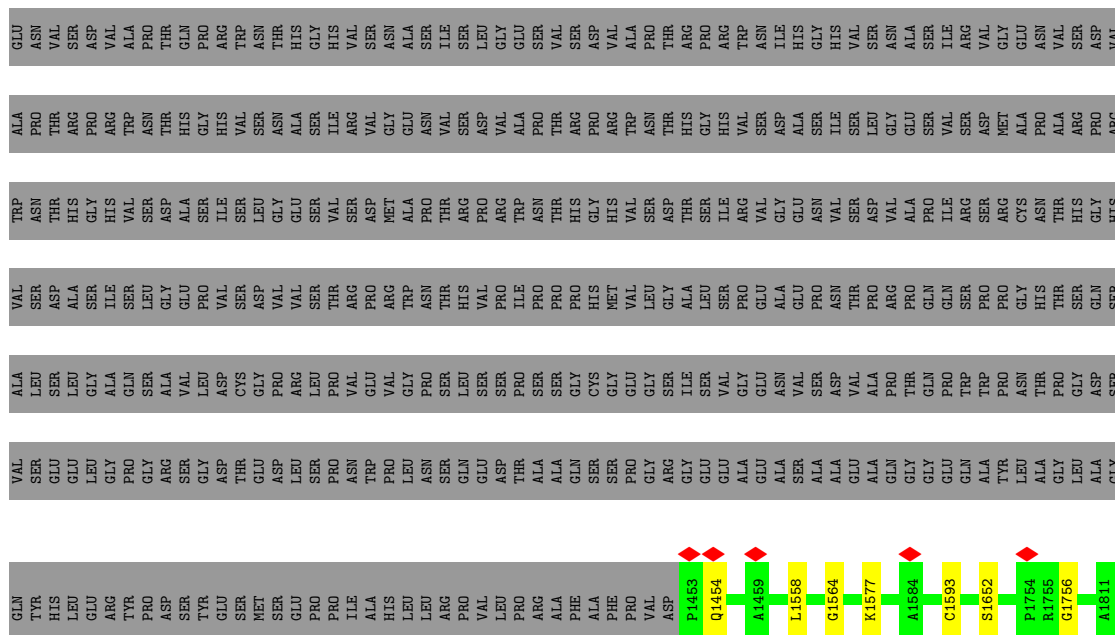
- Molecule 7: Isoform 3 of Gamma-tubulin complex component 2

Response	Percentage
Doing a good job	70%
Not doing a good job	27%

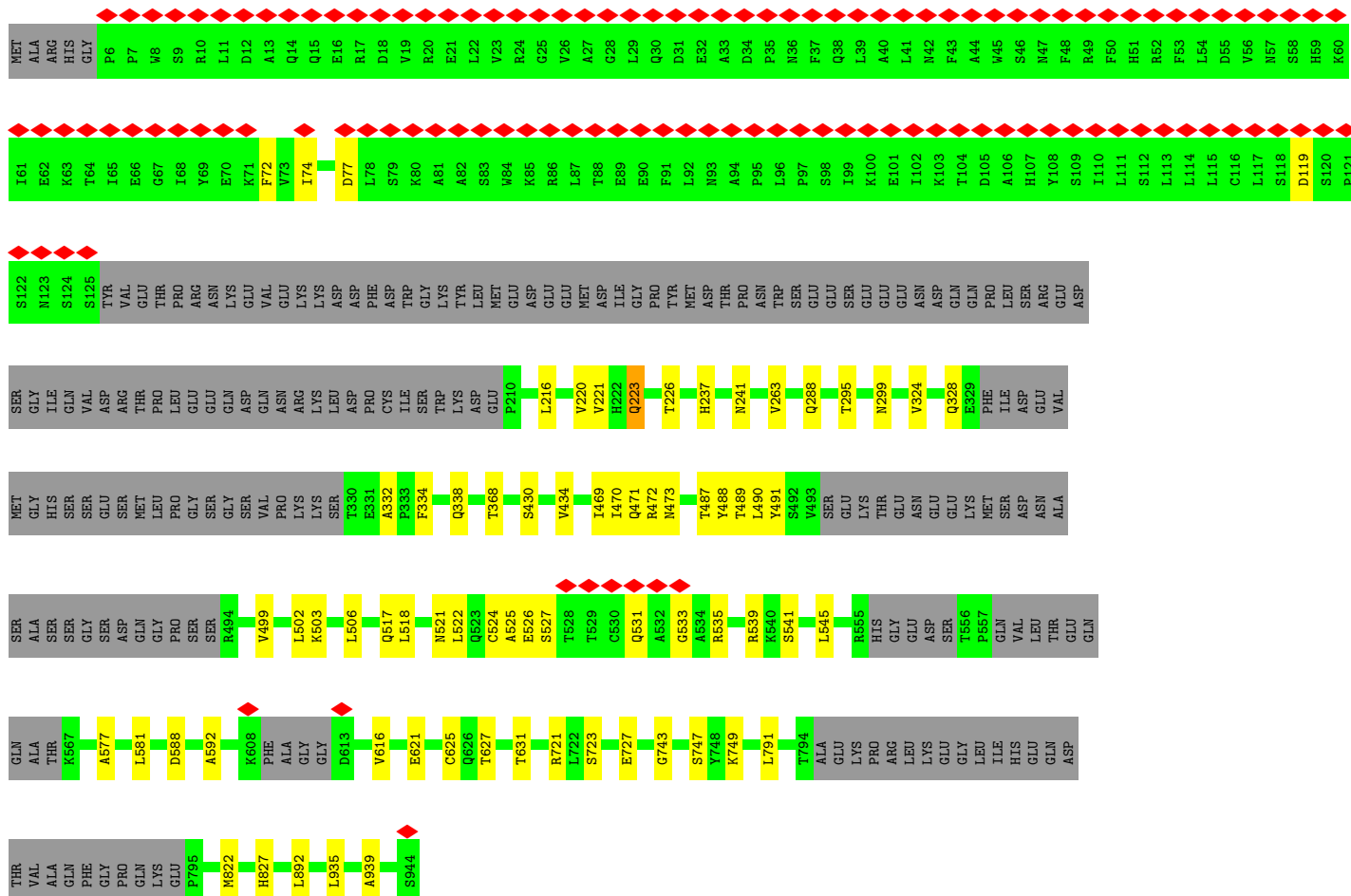
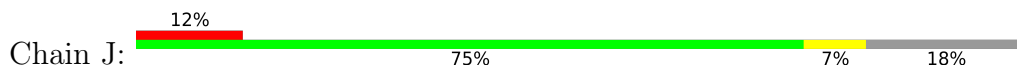


Response	Percentage
Yes, the U.S. is a threat to my country's security	51%
No, the U.S. is not a threat to my country's security	46%





- Molecule 9: Gamma-tubulin complex component 5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	266675	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.796	Depositor
Minimum map value	-0.165	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	485.76, 485.76, 485.76	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.18	0/3190	0.34	0/4446
1	D	0.23	0/3255	0.37	0/4538
1	F	0.24	0/3255	0.36	0/4538
1	H	0.25	0/3251	0.36	0/4533
1	N	0.11	0/3120	0.33	0/4347
1	r	0.08	0/561	0.32	0/782
1	s	0.09	0/571	0.34	0/796
1	t	0.12	0/596	0.42	0/831
1	u	0.13	0/596	0.42	0/831
1	v	0.29	0/640	0.51	0/891
2	O	0.33	0/405	0.39	0/563
2	P	0.30	0/362	0.49	0/504
2	Q	0.12	0/327	0.40	0/455
2	R	0.09	0/327	0.28	0/455
2	S	0.07	0/327	0.20	0/455
2	T	0.15	0/405	0.33	0/563
2	U	0.11	0/405	0.34	0/563
3	V	0.11	0/382	0.28	0/531
3	W	0.11	0/393	0.32	0/548
3	X	0.10	0/388	0.25	0/541
3	Y	0.11	0/387	0.24	0/538
4	Z	0.16	0/1846	0.35	0/2566
5	a	0.12	0/2203	0.40	0/3067
5	b	0.14	0/2232	0.36	0/3107
5	c	0.15	0/2212	0.37	0/3079
5	d	0.15	0/2226	0.37	0/3097
5	e	0.15	0/2212	0.42	0/3079
5	f	0.16	0/2227	0.37	0/3100
5	g	0.15	0/2222	0.37	0/3093
5	h	0.16	0/2227	0.37	0/3100
5	i	0.14	0/2212	0.36	0/3079
5	j	0.13	0/2217	0.34	0/3086
5	k	0.12	0/2212	0.38	0/3079
5	l	0.11	0/2207	0.35	0/3072

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	m	0.10	0/2212	0.37	0/3079
5	n	0.10	0/2257	0.38	0/3142
6	I	0.23	0/3024	0.42	2/4209 (0.0%)
6	K	0.19	0/3034	0.40	1/4223 (0.0%)
7	A	0.17	0/3261	0.39	0/4548
7	C	0.23	0/3241	0.37	0/4520
7	E	0.23	0/3364	0.36	0/4691
7	G	0.23	0/3364	0.36	0/4691
7	M	0.11	0/3300	0.34	0/4602
8	L	0.18	0/4846	0.40	0/6741
9	J	0.21	0/4182	0.42	0/5834
All	All	0.18	0/87683	0.37	3/122133 (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	X	0	1
6	I	0	2
6	K	0	3
8	L	0	1
All	All	0	7

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	79	GLY	N-CA-C	-6.40	98.02	113.18
6	I	80	GLY	N-CA-C	-5.44	101.06	112.04
6	K	79	GLY	N-CA-C	-5.17	100.92	113.18

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	K	249	MET	Peptide
6	K	417	THR	Peptide
6	K	665	GLY	Peptide
8	L	313	THR	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	X	637	SER	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3192	0	1417	25	0
1	D	3256	0	1450	19	0
1	F	3256	0	1450	33	0
1	H	3252	0	1447	26	0
1	N	3123	0	1382	19	0
1	r	562	0	254	1	0
1	s	572	0	258	2	0
1	t	597	0	273	2	0
1	u	597	0	273	3	0
1	v	642	0	295	4	0
2	O	406	0	217	3	0
2	P	363	0	185	7	0
2	Q	328	0	153	1	0
2	R	328	0	150	0	0
2	S	328	0	150	1	0
2	T	406	0	217	0	0
2	U	406	0	217	4	0
3	V	384	0	164	1	0
3	W	394	0	169	1	0
3	X	389	0	165	1	0
3	Y	389	0	166	3	0
4	Z	1847	0	848	33	0
5	a	2204	0	971	34	0
5	b	2233	0	984	26	0
5	c	2213	0	976	26	0
5	d	2228	0	981	43	0
5	e	2213	0	976	40	0
5	f	2228	0	982	31	0
5	g	2223	0	980	36	0
5	h	2228	0	982	27	0
5	i	2213	0	976	31	0
5	j	2218	0	978	30	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	k	2213	0	976	39	0
5	l	2208	0	974	16	0
5	m	2213	0	976	10	0
5	n	2258	0	994	16	0
6	I	3027	0	1327	24	0
6	K	3037	0	1331	22	0
7	A	3264	0	1445	34	0
7	C	3244	0	1438	26	0
7	E	3367	0	1492	15	0
7	G	3367	0	1492	18	0
7	M	3303	0	1464	22	0
8	L	4851	0	2185	35	0
9	J	4186	0	1817	41	0
All	All	87756	0	38997	796	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 796 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:H:24:MET:HA	1:H:31:TYR:HA	1.56	0.86
4:Z:237:GLU:HA	4:Z:251:GLY:HA2	1.58	0.84
4:Z:36:GLY:HA2	4:Z:67:LEU:HA	1.58	0.83
1:F:24:MET:HA	1:F:31:TYR:HA	1.59	0.83
1:D:24:MET:HA	1:D:31:TYR:HA	1.60	0.83

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	B	640/907 (71%)	628 (98%)	12 (2%)	0	100	100
1	D	655/907 (72%)	644 (98%)	11 (2%)	0	100	100
1	F	655/907 (72%)	644 (98%)	11 (2%)	0	100	100
1	H	654/907 (72%)	642 (98%)	12 (2%)	0	100	100
1	N	624/907 (69%)	617 (99%)	7 (1%)	0	100	100
1	r	111/907 (12%)	102 (92%)	5 (4%)	4 (4%)	2	20
1	s	113/907 (12%)	104 (92%)	5 (4%)	4 (4%)	3	20
1	t	118/907 (13%)	103 (87%)	9 (8%)	6 (5%)	1	15
1	u	118/907 (13%)	103 (87%)	8 (7%)	7 (6%)	1	14
1	v	125/907 (14%)	111 (89%)	9 (7%)	5 (4%)	2	18
2	O	80/82 (98%)	80 (100%)	0	0	100	100
2	P	71/82 (87%)	71 (100%)	0	0	100	100
2	Q	64/82 (78%)	64 (100%)	0	0	100	100
2	R	64/82 (78%)	64 (100%)	0	0	100	100
2	S	64/82 (78%)	64 (100%)	0	0	100	100
2	T	80/82 (98%)	80 (100%)	0	0	100	100
2	U	80/82 (98%)	80 (100%)	0	0	100	100
3	V	73/660 (11%)	73 (100%)	0	0	100	100
3	W	77/660 (12%)	76 (99%)	0	1 (1%)	9	41
3	X	76/660 (12%)	75 (99%)	1 (1%)	0	100	100
3	Y	74/660 (11%)	73 (99%)	1 (1%)	0	100	100
4	Z	373/375 (100%)	365 (98%)	8 (2%)	0	100	100
5	a	444/457 (97%)	437 (98%)	7 (2%)	0	100	100
5	b	450/457 (98%)	442 (98%)	8 (2%)	0	100	100
5	c	446/457 (98%)	439 (98%)	7 (2%)	0	100	100
5	d	448/457 (98%)	440 (98%)	8 (2%)	0	100	100
5	e	446/457 (98%)	438 (98%)	8 (2%)	0	100	100
5	f	449/457 (98%)	441 (98%)	8 (2%)	0	100	100
5	g	448/457 (98%)	440 (98%)	8 (2%)	0	100	100
5	h	449/457 (98%)	441 (98%)	8 (2%)	0	100	100
5	i	446/457 (98%)	438 (98%)	8 (2%)	0	100	100
5	j	447/457 (98%)	439 (98%)	8 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	k	446/457 (98%)	438 (98%)	8 (2%)	0	100	100
5	l	445/457 (97%)	438 (98%)	7 (2%)	0	100	100
5	m	446/457 (98%)	438 (98%)	8 (2%)	0	100	100
5	n	455/457 (100%)	448 (98%)	7 (2%)	0	100	100
6	I	606/667 (91%)	586 (97%)	19 (3%)	1 (0%)	43	78
6	K	608/667 (91%)	589 (97%)	15 (2%)	4 (1%)	18	55
7	A	651/930 (70%)	640 (98%)	11 (2%)	0	100	100
7	C	647/930 (70%)	637 (98%)	10 (2%)	0	100	100
7	E	672/930 (72%)	661 (98%)	11 (2%)	0	100	100
7	G	672/930 (72%)	661 (98%)	11 (2%)	0	100	100
7	M	659/930 (71%)	650 (99%)	9 (1%)	0	100	100
8	L	972/1811 (54%)	923 (95%)	45 (5%)	4 (0%)	30	67
9	J	834/1024 (81%)	807 (97%)	23 (3%)	4 (0%)	24	63
All	All	17575/27876 (63%)	17174 (98%)	361 (2%)	40 (0%)	44	78

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	W	638	VAL
1	r	109	SER
1	s	109	SER
1	s	111	VAL
1	t	5	ASP

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	L	2
1	v	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	106:ARG	C	107:GLN	N	8.98
1	L	123:PRO	C	124:GLN	N	5.52
1	L	311:TYR	C	312:LEU	N	3.84

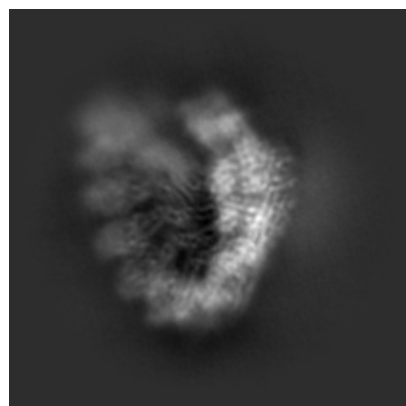
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53400. These allow visual inspection of the internal detail of the map and identification of artifacts.

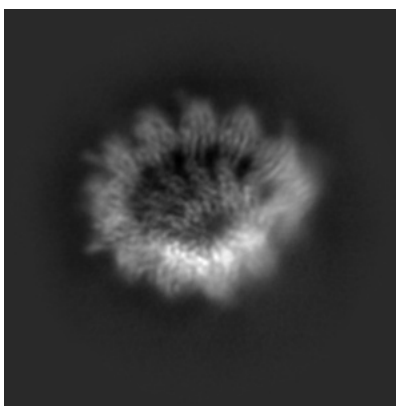
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

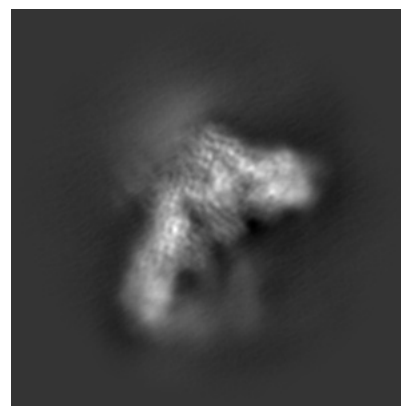
6.1.1 Primary map



X

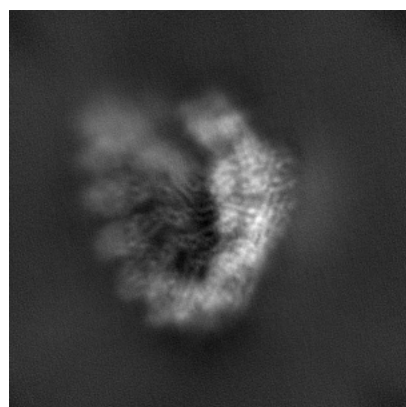


Y

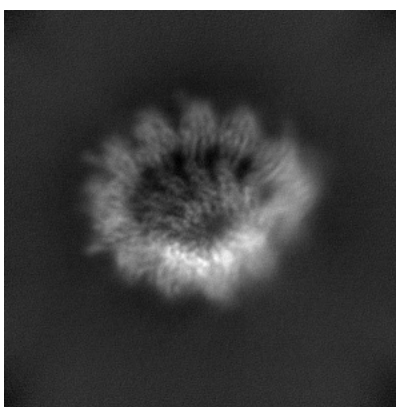


Z

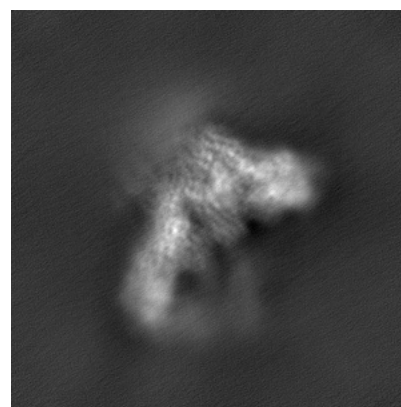
6.1.2 Raw map



X



Y

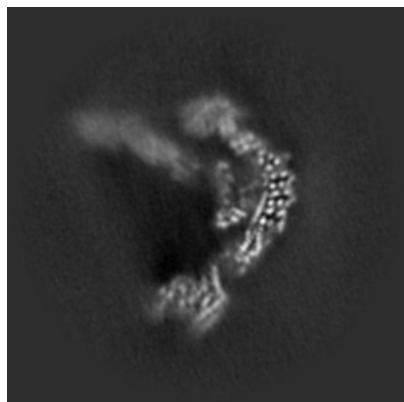


Z

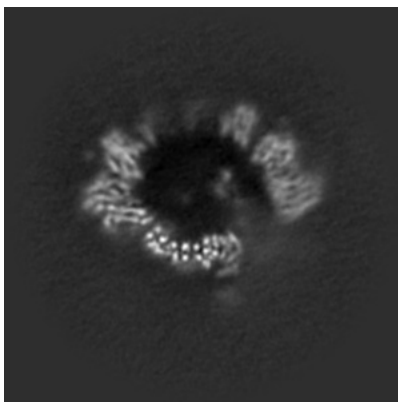
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

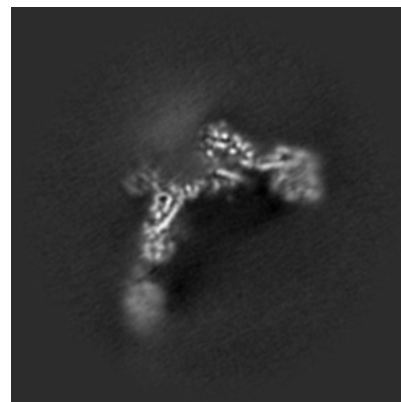
6.2.1 Primary map



X Index: 184

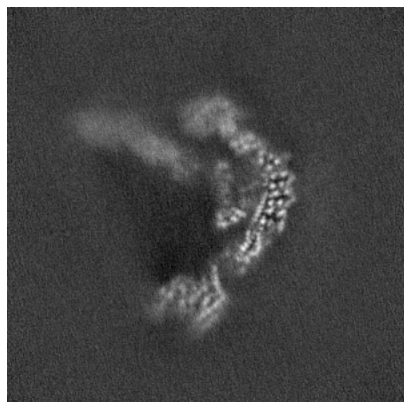


Y Index: 184

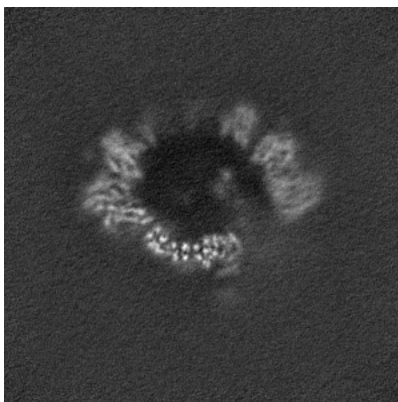


Z Index: 184

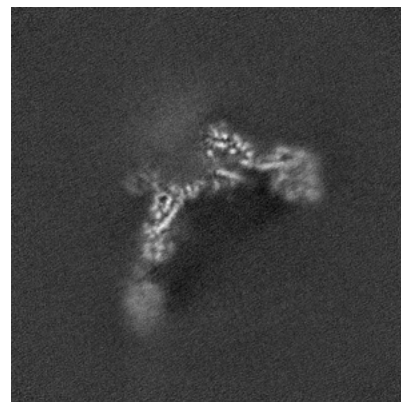
6.2.2 Raw map



X Index: 184



Y Index: 184

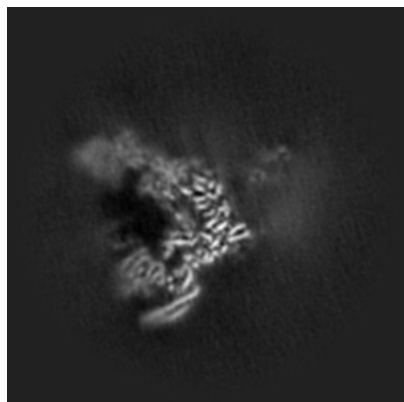


Z Index: 184

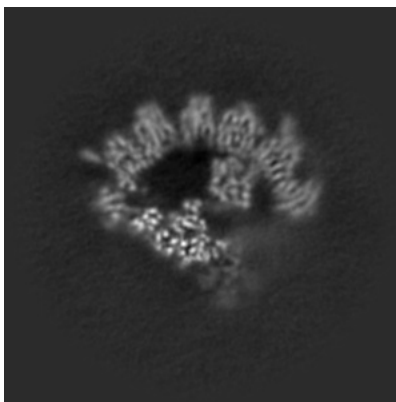
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

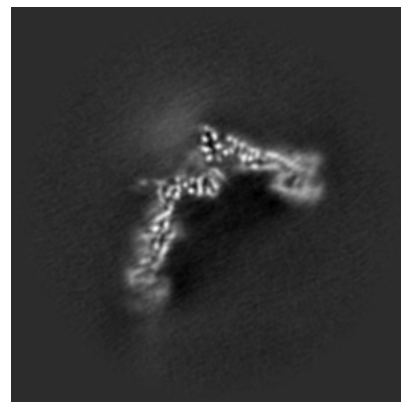
6.3.1 Primary map



X Index: 149

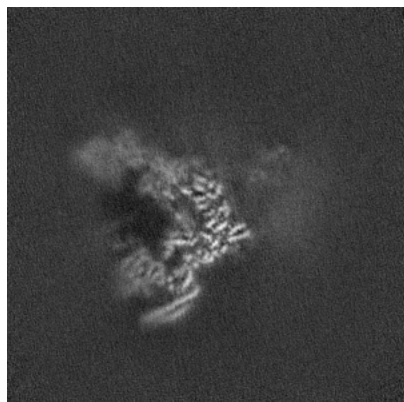


Y Index: 196

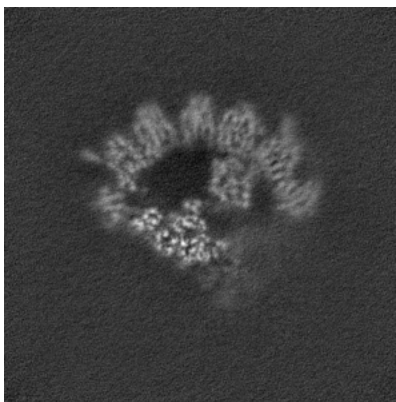


Z Index: 175

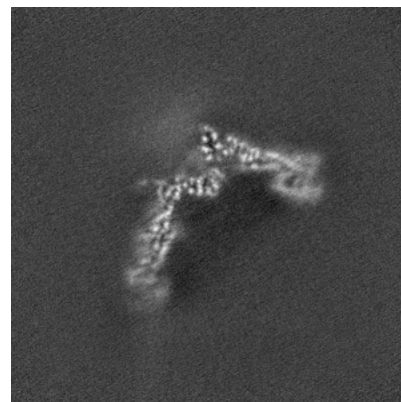
6.3.2 Raw map



X Index: 149



Y Index: 196

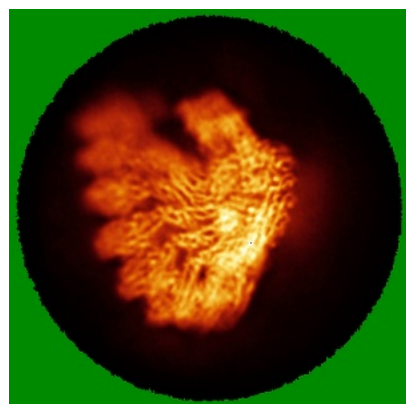


Z Index: 175

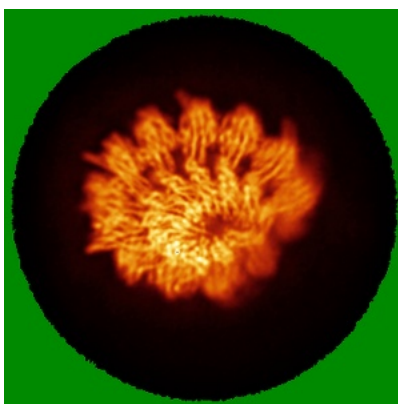
The images above show the largest variance slices of the map in three orthogonal directions.

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

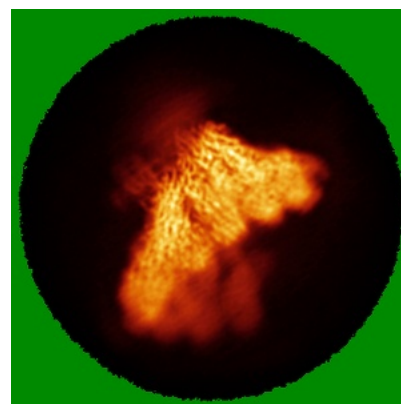
6.4.1 Primary map



X

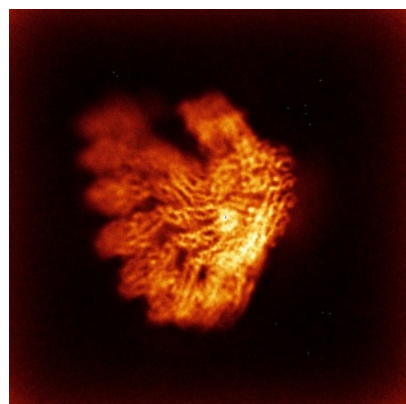


Y

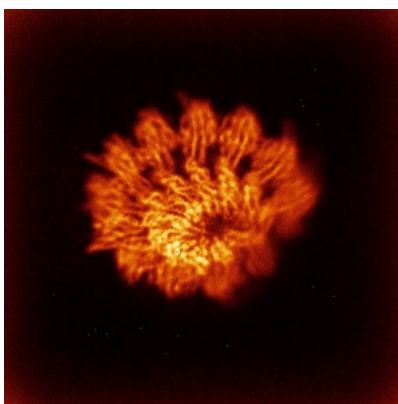


Z

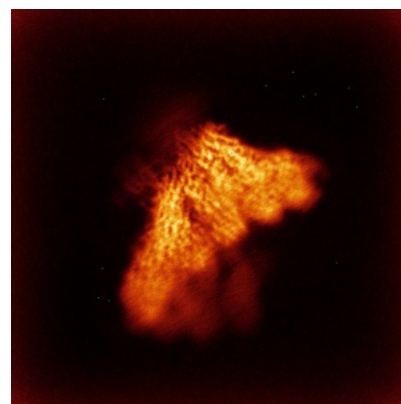
6.4.2 Raw map



X



Y



Z

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

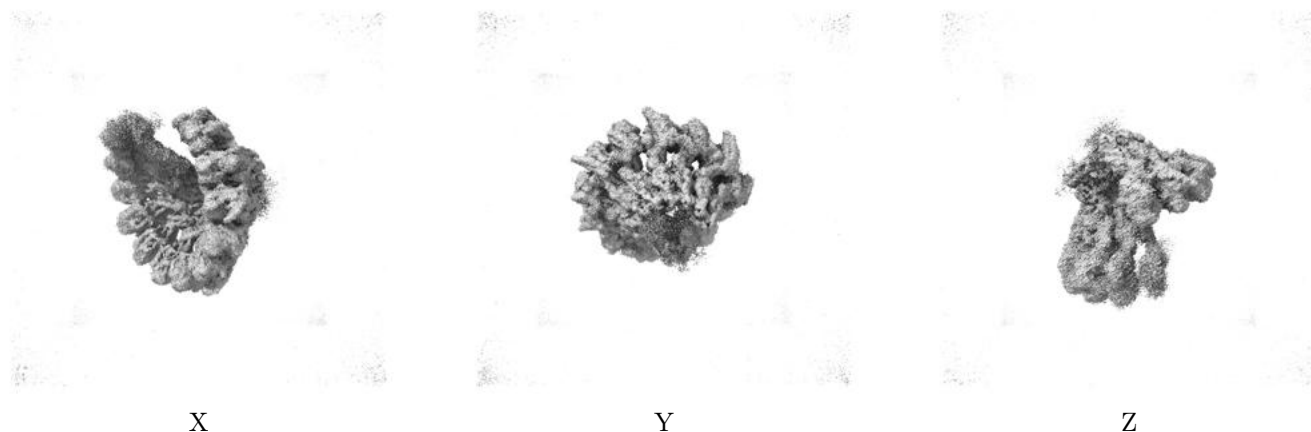
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

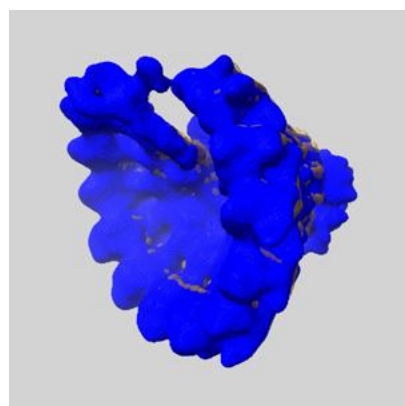
6.6 Mask visualisation [i](#)

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

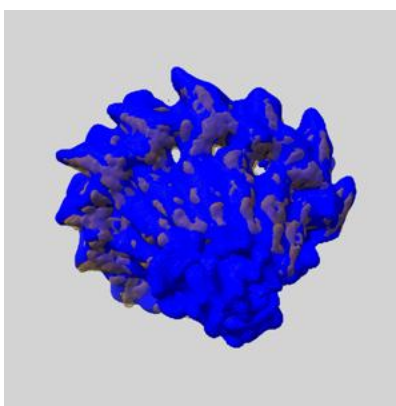
A mask typically either:

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

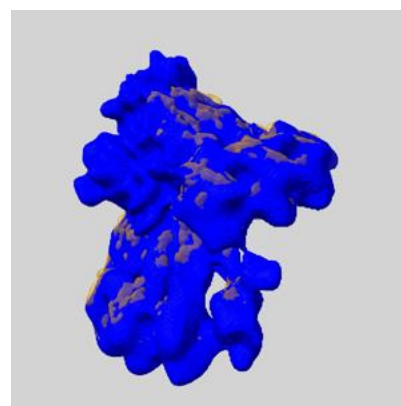
6.6.1 emd_53400_msk_1.map [i](#)



X



Y

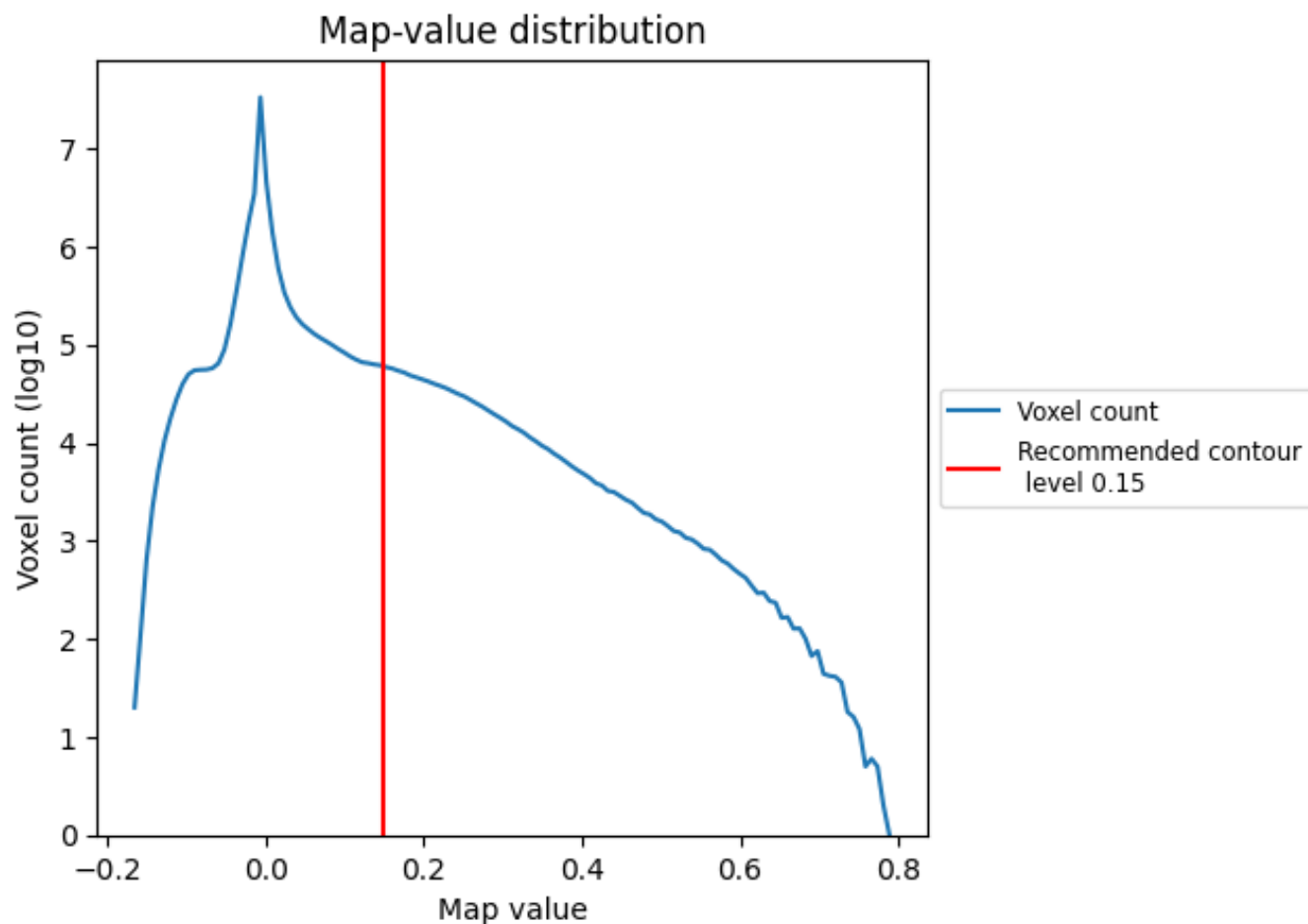


Z

7 Map analysis [i](#)

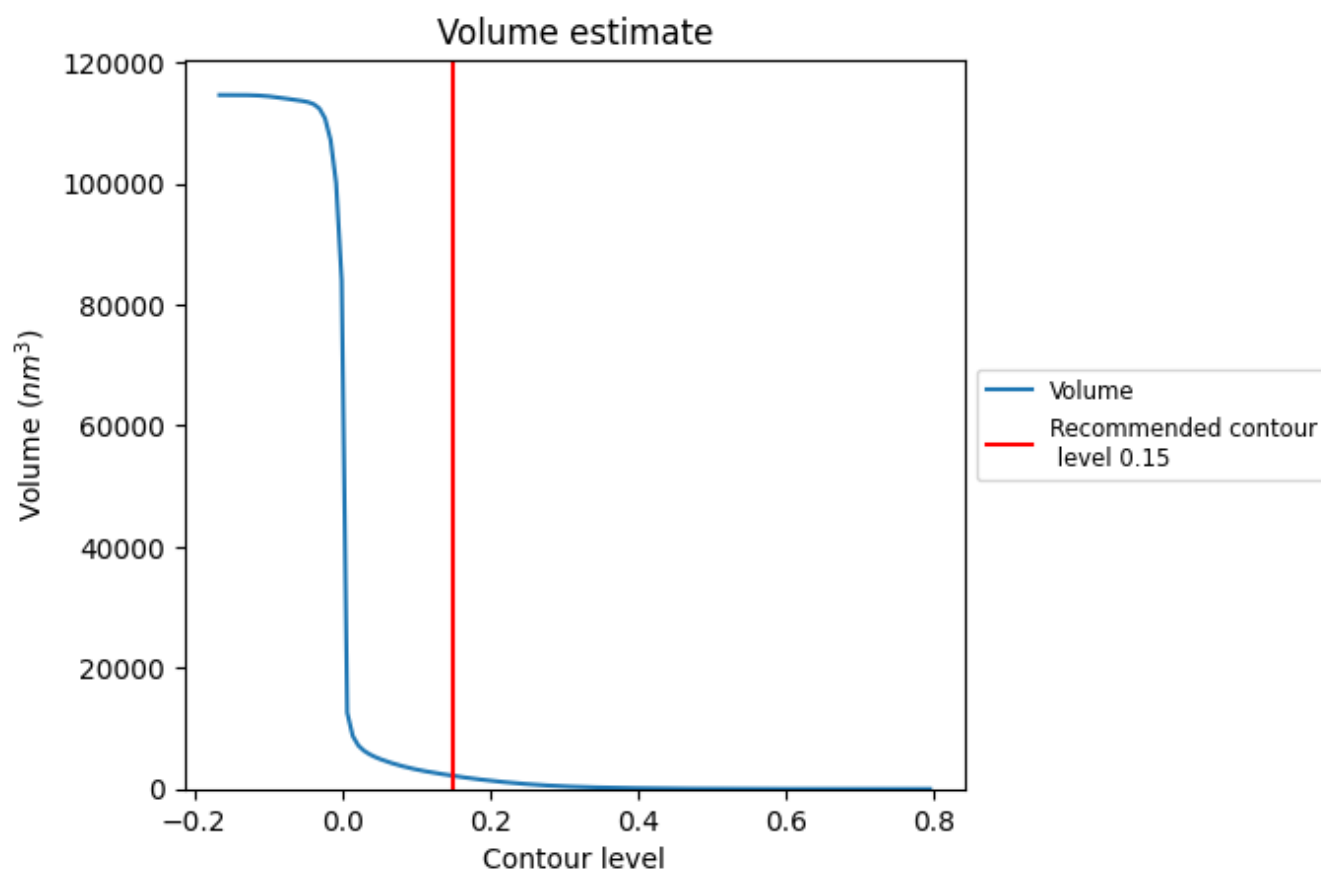
This section contains the results of statistical analysis of the map.

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.

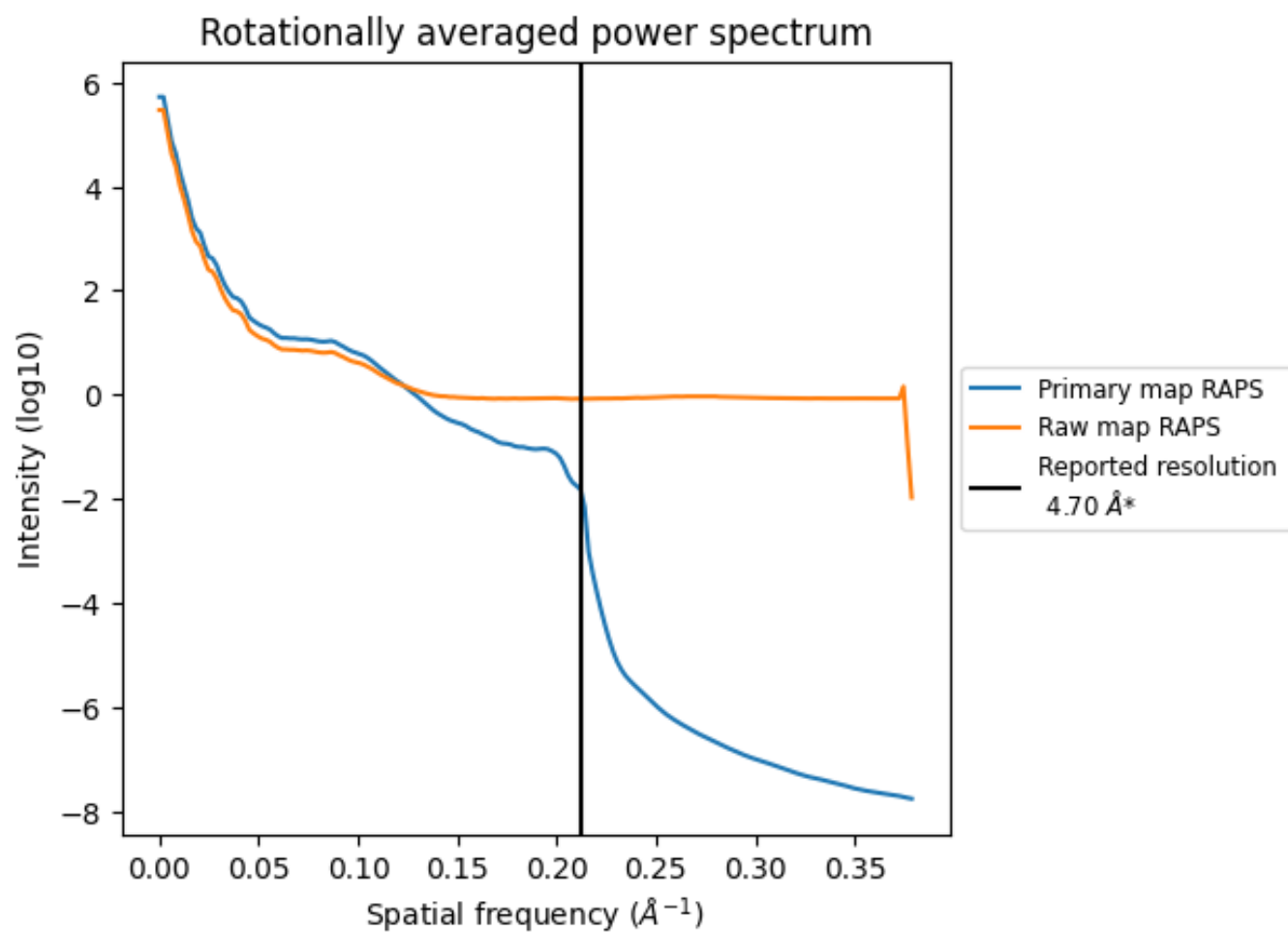
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2190 nm³; this corresponds to an approximate mass of 1978 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 ⓘ

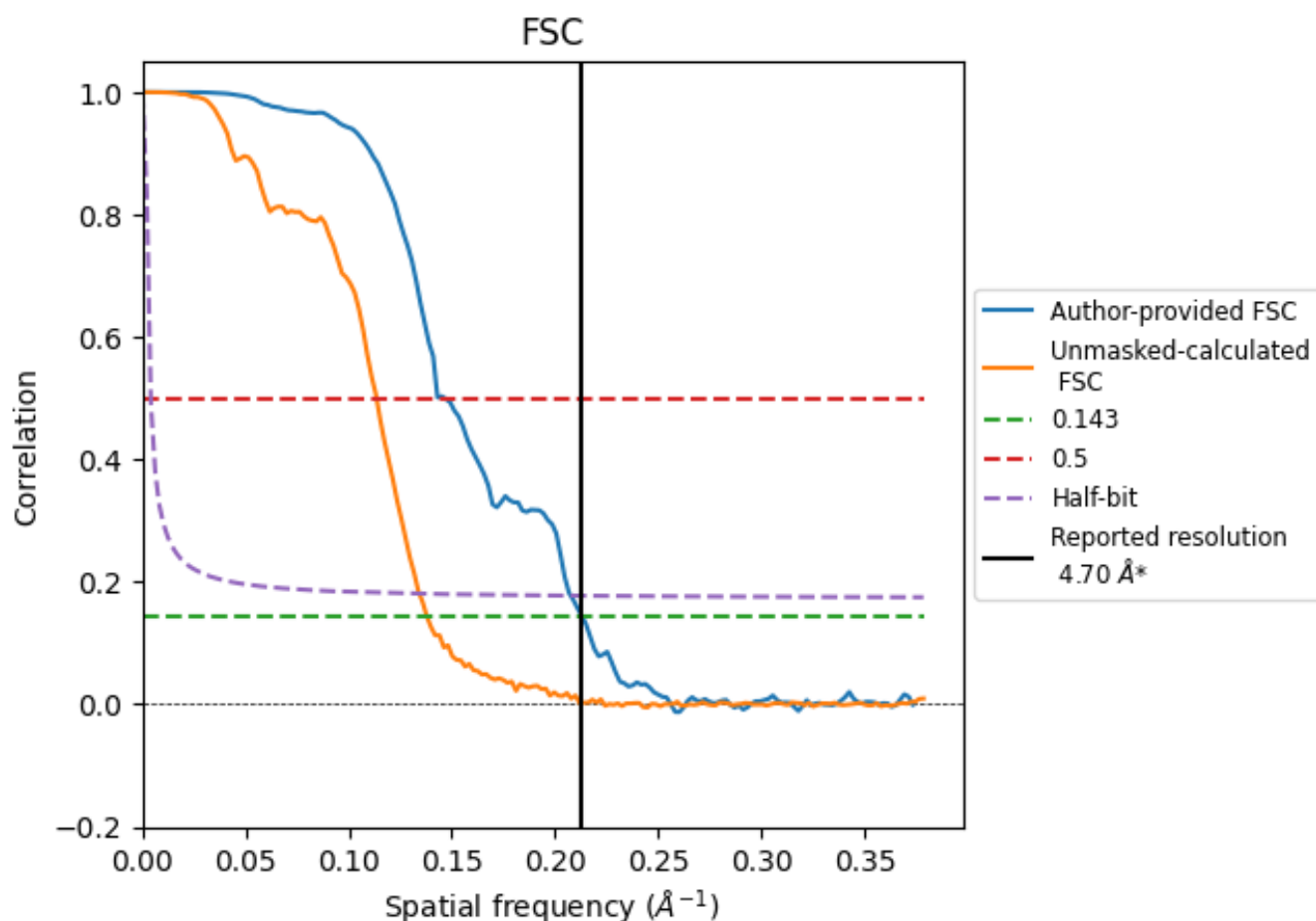


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

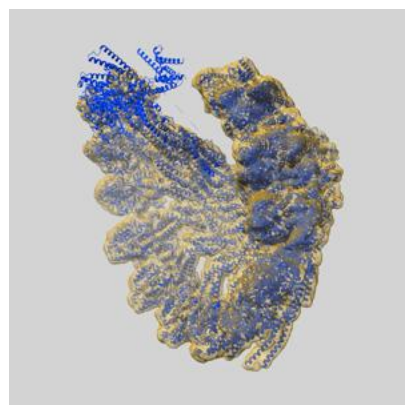
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.69	6.82	4.81
Unmasked-calculated*	7.25	8.80	7.45

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.25 differs from the reported value 4.7 by more than 10 %

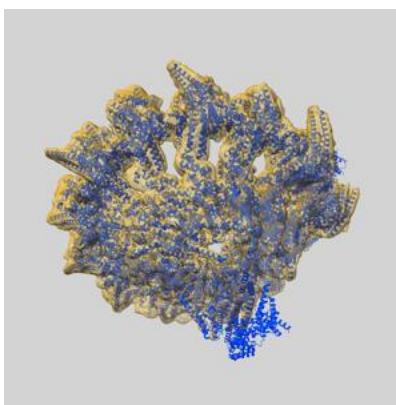
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53400 and PDB model 9QVN. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

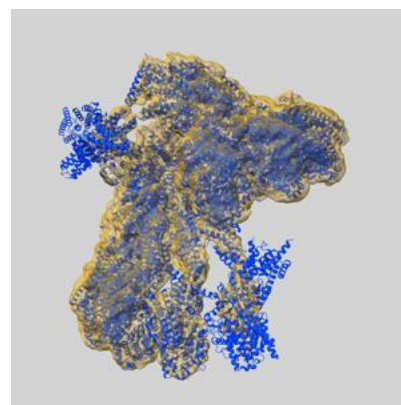
9.1 Map-model overlay [i](#)



X



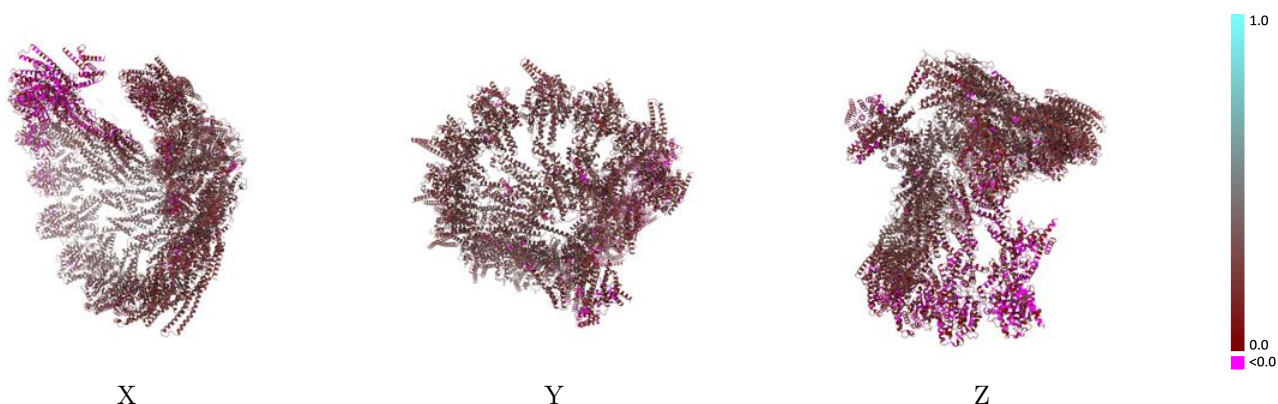
Y



Z

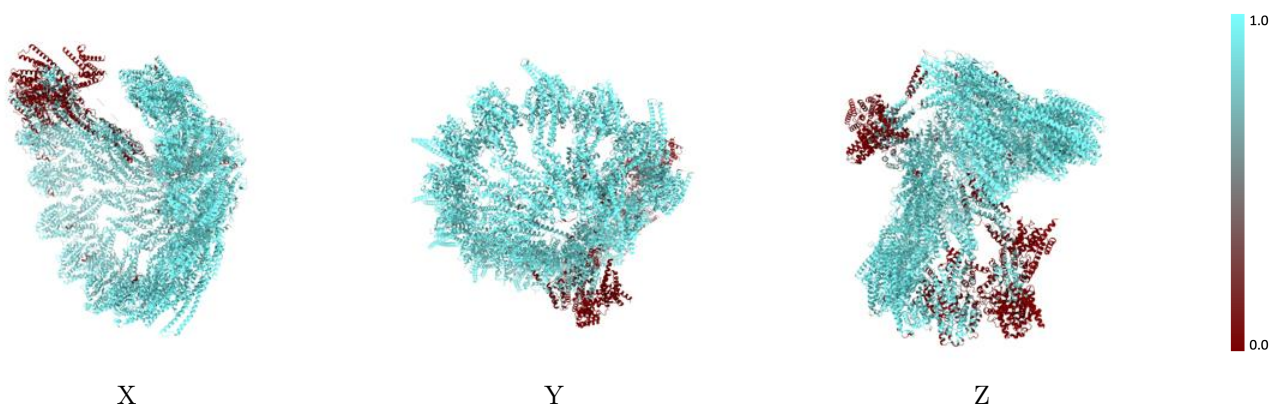
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



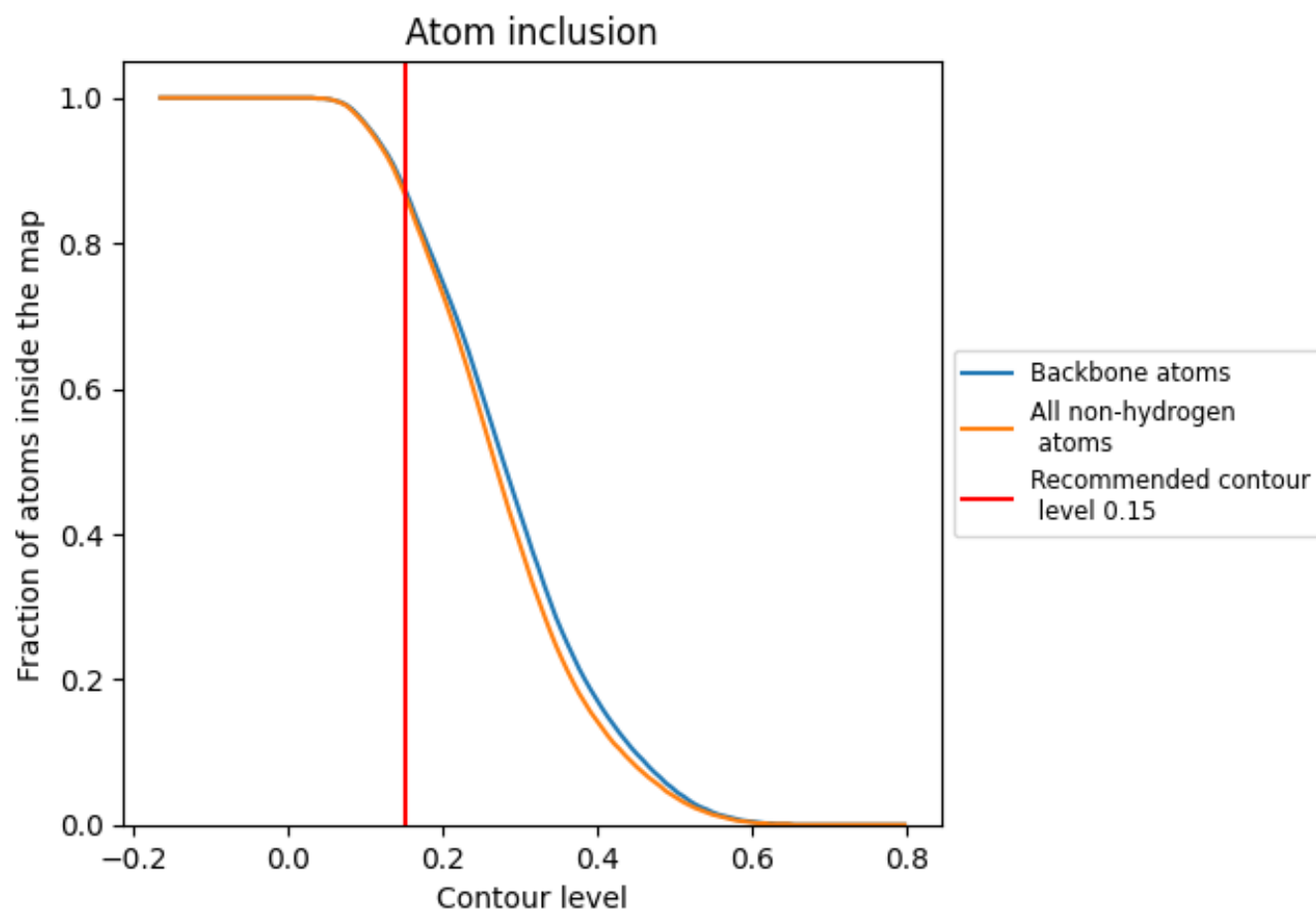
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 87% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8680	 0.2270
A	 0.9740	 0.2350
B	 0.9840	 0.2660
C	 0.9860	 0.2760
D	 0.9860	 0.2780
E	 0.9780	 0.2830
F	 0.9920	 0.2860
G	 0.9860	 0.2790
H	 0.9970	 0.2950
I	 0.9990	 0.2850
J	 0.8500	 0.2510
K	 0.9940	 0.2540
L	 0.9690	 0.2470
M	 0.7240	 0.1350
N	 0.4040	 0.0870
O	 0.8990	 0.2870
P	 0.9810	 0.2800
Q	 0.0000	 0.0710
R	 0.0000	 0.1830
S	 0.0000	 0.1520
T	 0.7780	 0.2340
U	 0.4700	 0.2380
V	 0.5650	 0.2420
W	 0.4310	 0.2260
X	 0.3910	 0.2160
Y	 0.5730	 0.2340
Z	 0.9720	 0.2750
a	 0.9740	 0.1620
b	 0.9840	 0.2180
c	 0.9820	 0.2450
d	 0.9860	 0.2350
e	 0.9890	 0.2280
f	 0.9970	 0.2640
g	 0.9730	 0.2480
h	 0.9920	 0.2820



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.9830	 0.2480
j	 0.9770	 0.2270
k	 0.9720	 0.1480
l	 0.8940	 0.1090
m	 0.5730	 0.0610
n	 0.0860	 0.0490
r	 0.0000	 0.1660
s	 0.0090	 0.1350
t	 0.4120	 0.2310
u	 0.5490	 0.2660
v	 0.9910	 0.3160