



wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 12:46 pm BST

PDB ID : 9SMX / pdb_00009smx
EMDB ID : EMD-55043
Title : CM1-activated gTuRC in complex with nascent alpha-E254D mutant microtubules
Authors : Llorca, O.; Serna, M.; Lopez-Perrote, A.
Deposited on : 2025-09-09
Resolution : 3.67 Å (reported)
Based on initial models : 6X0U, 7AS4

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

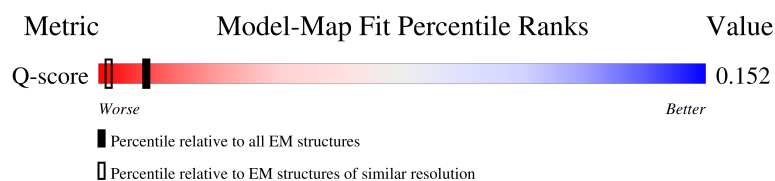
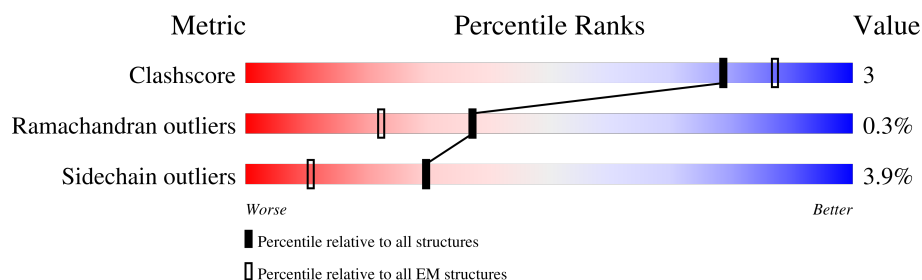
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.67 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	11424 (3.17 - 4.17)

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	3	907	 10% 89%
1	B	907	 8% 59% 10% 30%
1	D	907	 5% 58% 9% 33%
1	F	907	 5% 55% 9% 36%

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Mol	Chain	Length	Quality of chain
1	H	907	
1	N	907	
2	4	82	
2	6	82	
2	Y	82	
3	5	1819	
3	L	1819	
4	7	374	
5	A	902	
5	C	902	
5	CN	902	
5	E	902	
5	EN	902	
5	G	902	
5	GN	902	
5	M	902	
6	AC	229	
6	CC	229	
6	Cc	229	
6	EC	229	
6	Ec	229	
6	GC	229	
6	Gc	229	
6	MC	229	
6	Mc	229	

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Mol	Chain	Length	Quality of chain
7	BA	451	
7	CA	451	
7	DA	451	
7	EA	451	
7	FA	451	
7	GA	451	
7	HA	451	
7	IA	451	
7	JA	451	
7	KA	451	
7	LA	451	
8	BB	451	
8	CB	451	
8	DB	451	
8	EB	451	
8	FB	451	
8	GB	451	
8	HB	451	
8	IB	451	
8	JB	451	
8	KB	451	
8	LB	451	
9	CM	158	
9	EM	158	
9	GM	158	

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Mol	Chain	Length	Quality of chain
9	MM	158	
10	I	667	
10	K	667	
11	J	1024	
11	Z	1024	
12	a	451	
12	b	451	
12	c	451	
12	d	451	
12	e	451	
12	f	451	
12	g	451	
12	h	451	
12	i	451	
12	j	451	
12	k	451	
12	l	451	
12	m	451	
12	n	451	

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 405906 atoms, of which 200969 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	3	102	Total	C	H	N	O	S	0	0
			1693	525	861	156	149	2		
1	B	635	Total	C	H	N	O	S	0	0
			10402	3319	5183	917	957	26		
1	D	610	Total	C	H	N	O	S	0	0
			10017	3196	5000	885	911	25		
1	F	581	Total	C	H	N	O	S	0	0
			9576	3061	4780	842	868	25		
1	H	581	Total	C	H	N	O	S	0	0
			9576	3061	4780	842	868	25		
1	N	635	Total	C	H	N	O	S	0	0
			10368	3313	5161	911	957	26		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	4	60	Total	C	H	N	O	S	0	0
			926	278	474	79	91	4		
2	6	61	Total	C	H	N	O	S	0	0
			936	281	479	80	92	4		
2	Y	56	Total	C	H	N	O	S	0	0
			877	263	451	75	84	4		

- Molecule 3 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	5	46	Total	C	H	N	O	S	0	0
			737	229	382	58	67	1		
3	L	616	Total	C	H	N	O	S	0	0
			9873	3211	4954	826	856	26		

- Molecule 4 is a protein called Actin, cytoplasmic 2, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	7	364	Total	C	H	N	O	0	0
			2764	1103	932	364	365		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	ASP	GLU	conflict	UNP P63261
7	5	VAL	ILE	conflict	UNP P63261
7	10	VAL	ILE	conflict	UNP P63261
7	153	LEU	MET	conflict	UNP P63261
7	160	SER	THR	conflict	UNP P63261
7	204	GLU	ALA	conflict	UNP P63261
7	243	LYS	PRO	conflict	UNP P63261
7	271	ALA	SER	conflict	UNP P63261
7	279	TYR	PHE	conflict	UNP P63261

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	A	697	Total 11240	C 3604	H 5617	N 948	O 1036	S 35	0	0
5	C	697	Total 11258	C 3607	H 5629	N 951	O 1036	S 35	0	0
5	CN	111	Total 1803	C 565	H 907	N 156	O 174	S 1	0	0
5	E	654	Total 10667	C 3427	H 5347	N 894	O 966	S 33	0	0
5	EN	111	Total 1803	C 565	H 907	N 156	O 174	S 1	0	0
5	G	654	Total 10666	C 3427	H 5346	N 894	O 966	S 33	0	0
5	GN	111	Total 1803	C 565	H 907	N 156	O 174	S 1	0	0
5	M	846	Total 13534	C 4320	H 6768	N 1141	O 1268	S 37	0	0

- Molecule 6 is a protein called Ubiquitin-like protein SMT3,CDK5 regulatory subunit-associated protein 2, Microtubule-associated protein RP/EB family member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
6	AC	35	Total	C	H	N	O	S	0	0
			631	197	318	58	56	2		

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Mol	Chain	Residues	Atoms						AltConf	Trace
6	CC	35	Total 631	C 197	H 318	N 58	O 56	S 2	0	0
6	Cc	35	Total 632	C 202	H 315	N 55	O 58	S 2	0	0
6	EC	33	Total 597	C 188	H 300	N 53	O 54	S 2	0	0
6	Ec	29	Total 520	C 167	H 259	N 44	O 49	S 1	0	0
6	GC	34	Total 607	C 191	H 305	N 54	O 55	S 2	0	0
6	Gc	31	Total 556	C 178	H 277	N 47	O 53	S 1	0	0
6	MC	32	Total 573	C 182	H 287	N 49	O 53	S 2	0	0
6	Mc	32	Total 574	C 183	H 287	N 48	O 54	S 2	0	0

There are 189 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	-68	MET	-	initiating methionine	UNP Q12306
AC	-67	GLY	-	expression tag	UNP Q12306
AC	-66	SER	-	expression tag	UNP Q12306
AC	-65	SER	-	expression tag	UNP Q12306
AC	-64	HIS	-	expression tag	UNP Q12306
AC	-63	HIS	-	expression tag	UNP Q12306
AC	-62	HIS	-	expression tag	UNP Q12306
AC	-61	HIS	-	expression tag	UNP Q12306
AC	-60	HIS	-	expression tag	UNP Q12306
AC	-59	HIS	-	expression tag	UNP Q12306
AC	-58	GLY	-	expression tag	UNP Q12306
AC	41	TRP	-	linker	UNP Q12306
AC	42	SER	-	linker	UNP Q12306
AC	43	HIS	-	linker	UNP Q12306
AC	44	PRO	-	linker	UNP Q12306
AC	45	GLN	-	linker	UNP Q12306
AC	46	PHE	-	linker	UNP Q12306
AC	47	GLU	-	linker	UNP Q12306
AC	48	LYS	-	linker	UNP Q12306
AC	49	SER	-	linker	UNP Q12306
AC	50	ALA	-	linker	UNP Q12306
CC	-68	MET	-	initiating methionine	UNP Q12306
CC	-67	GLY	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
CC	-66	SER	-	expression tag	UNP Q12306
CC	-65	SER	-	expression tag	UNP Q12306
CC	-64	HIS	-	expression tag	UNP Q12306
CC	-63	HIS	-	expression tag	UNP Q12306
CC	-62	HIS	-	expression tag	UNP Q12306
CC	-61	HIS	-	expression tag	UNP Q12306
CC	-60	HIS	-	expression tag	UNP Q12306
CC	-59	HIS	-	expression tag	UNP Q12306
CC	-58	GLY	-	expression tag	UNP Q12306
CC	41	TRP	-	linker	UNP Q12306
CC	42	SER	-	linker	UNP Q12306
CC	43	HIS	-	linker	UNP Q12306
CC	44	PRO	-	linker	UNP Q12306
CC	45	GLN	-	linker	UNP Q12306
CC	46	PHE	-	linker	UNP Q12306
CC	47	GLU	-	linker	UNP Q12306
CC	48	LYS	-	linker	UNP Q12306
CC	49	SER	-	linker	UNP Q12306
CC	50	ALA	-	linker	UNP Q12306
Cc	-68	MET	-	initiating methionine	UNP Q12306
Cc	-67	GLY	-	expression tag	UNP Q12306
Cc	-66	SER	-	expression tag	UNP Q12306
Cc	-65	SER	-	expression tag	UNP Q12306
Cc	-64	HIS	-	expression tag	UNP Q12306
Cc	-63	HIS	-	expression tag	UNP Q12306
Cc	-62	HIS	-	expression tag	UNP Q12306
Cc	-61	HIS	-	expression tag	UNP Q12306
Cc	-60	HIS	-	expression tag	UNP Q12306
Cc	-59	HIS	-	expression tag	UNP Q12306
Cc	-58	GLY	-	expression tag	UNP Q12306
Cc	41	TRP	-	linker	UNP Q12306
Cc	42	SER	-	linker	UNP Q12306
Cc	43	HIS	-	linker	UNP Q12306
Cc	44	PRO	-	linker	UNP Q12306
Cc	45	GLN	-	linker	UNP Q12306
Cc	46	PHE	-	linker	UNP Q12306
Cc	47	GLU	-	linker	UNP Q12306
Cc	48	LYS	-	linker	UNP Q12306
Cc	49	SER	-	linker	UNP Q12306
Cc	50	ALA	-	linker	UNP Q12306
EC	-68	MET	-	initiating methionine	UNP Q12306
EC	-67	GLY	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
EC	-66	SER	-	expression tag	UNP Q12306
EC	-65	SER	-	expression tag	UNP Q12306
EC	-64	HIS	-	expression tag	UNP Q12306
EC	-63	HIS	-	expression tag	UNP Q12306
EC	-62	HIS	-	expression tag	UNP Q12306
EC	-61	HIS	-	expression tag	UNP Q12306
EC	-60	HIS	-	expression tag	UNP Q12306
EC	-59	HIS	-	expression tag	UNP Q12306
EC	-58	GLY	-	expression tag	UNP Q12306
EC	41	TRP	-	linker	UNP Q12306
EC	42	SER	-	linker	UNP Q12306
EC	43	HIS	-	linker	UNP Q12306
EC	44	PRO	-	linker	UNP Q12306
EC	45	GLN	-	linker	UNP Q12306
EC	46	PHE	-	linker	UNP Q12306
EC	47	GLU	-	linker	UNP Q12306
EC	48	LYS	-	linker	UNP Q12306
EC	49	SER	-	linker	UNP Q12306
EC	50	ALA	-	linker	UNP Q12306
Ec	-68	MET	-	initiating methionine	UNP Q12306
Ec	-67	GLY	-	expression tag	UNP Q12306
Ec	-66	SER	-	expression tag	UNP Q12306
Ec	-65	SER	-	expression tag	UNP Q12306
Ec	-64	HIS	-	expression tag	UNP Q12306
Ec	-63	HIS	-	expression tag	UNP Q12306
Ec	-62	HIS	-	expression tag	UNP Q12306
Ec	-61	HIS	-	expression tag	UNP Q12306
Ec	-60	HIS	-	expression tag	UNP Q12306
Ec	-59	HIS	-	expression tag	UNP Q12306
Ec	-58	GLY	-	expression tag	UNP Q12306
Ec	41	TRP	-	linker	UNP Q12306
Ec	42	SER	-	linker	UNP Q12306
Ec	43	HIS	-	linker	UNP Q12306
Ec	44	PRO	-	linker	UNP Q12306
Ec	45	GLN	-	linker	UNP Q12306
Ec	46	PHE	-	linker	UNP Q12306
Ec	47	GLU	-	linker	UNP Q12306
Ec	48	LYS	-	linker	UNP Q12306
Ec	49	SER	-	linker	UNP Q12306
Ec	50	ALA	-	linker	UNP Q12306
GC	-68	MET	-	initiating methionine	UNP Q12306
GC	-67	GLY	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
GC	-66	SER	-	expression tag	UNP Q12306
GC	-65	SER	-	expression tag	UNP Q12306
GC	-64	HIS	-	expression tag	UNP Q12306
GC	-63	HIS	-	expression tag	UNP Q12306
GC	-62	HIS	-	expression tag	UNP Q12306
GC	-61	HIS	-	expression tag	UNP Q12306
GC	-60	HIS	-	expression tag	UNP Q12306
GC	-59	HIS	-	expression tag	UNP Q12306
GC	-58	GLY	-	expression tag	UNP Q12306
GC	41	TRP	-	linker	UNP Q12306
GC	42	SER	-	linker	UNP Q12306
GC	43	HIS	-	linker	UNP Q12306
GC	44	PRO	-	linker	UNP Q12306
GC	45	GLN	-	linker	UNP Q12306
GC	46	PHE	-	linker	UNP Q12306
GC	47	GLU	-	linker	UNP Q12306
GC	48	LYS	-	linker	UNP Q12306
GC	49	SER	-	linker	UNP Q12306
GC	50	ALA	-	linker	UNP Q12306
Gc	-68	MET	-	initiating methionine	UNP Q12306
Gc	-67	GLY	-	expression tag	UNP Q12306
Gc	-66	SER	-	expression tag	UNP Q12306
Gc	-65	SER	-	expression tag	UNP Q12306
Gc	-64	HIS	-	expression tag	UNP Q12306
Gc	-63	HIS	-	expression tag	UNP Q12306
Gc	-62	HIS	-	expression tag	UNP Q12306
Gc	-61	HIS	-	expression tag	UNP Q12306
Gc	-60	HIS	-	expression tag	UNP Q12306
Gc	-59	HIS	-	expression tag	UNP Q12306
Gc	-58	GLY	-	expression tag	UNP Q12306
Gc	41	TRP	-	linker	UNP Q12306
Gc	42	SER	-	linker	UNP Q12306
Gc	43	HIS	-	linker	UNP Q12306
Gc	44	PRO	-	linker	UNP Q12306
Gc	45	GLN	-	linker	UNP Q12306
Gc	46	PHE	-	linker	UNP Q12306
Gc	47	GLU	-	linker	UNP Q12306
Gc	48	LYS	-	linker	UNP Q12306
Gc	49	SER	-	linker	UNP Q12306
Gc	50	ALA	-	linker	UNP Q12306
MC	-68	MET	-	initiating methionine	UNP Q12306
MC	-67	GLY	-	expression tag	UNP Q12306

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Chain	Residue	Modelled	Actual	Comment	Reference
MC	-66	SER	-	expression tag	UNP Q12306
MC	-65	SER	-	expression tag	UNP Q12306
MC	-64	HIS	-	expression tag	UNP Q12306
MC	-63	HIS	-	expression tag	UNP Q12306
MC	-62	HIS	-	expression tag	UNP Q12306
MC	-61	HIS	-	expression tag	UNP Q12306
MC	-60	HIS	-	expression tag	UNP Q12306
MC	-59	HIS	-	expression tag	UNP Q12306
MC	-58	GLY	-	expression tag	UNP Q12306
MC	41	TRP	-	linker	UNP Q12306
MC	42	SER	-	linker	UNP Q12306
MC	43	HIS	-	linker	UNP Q12306
MC	44	PRO	-	linker	UNP Q12306
MC	45	GLN	-	linker	UNP Q12306
MC	46	PHE	-	linker	UNP Q12306
MC	47	GLU	-	linker	UNP Q12306
MC	48	LYS	-	linker	UNP Q12306
MC	49	SER	-	linker	UNP Q12306
MC	50	ALA	-	linker	UNP Q12306
Mc	-68	MET	-	initiating methionine	UNP Q12306
Mc	-67	GLY	-	expression tag	UNP Q12306
Mc	-66	SER	-	expression tag	UNP Q12306
Mc	-65	SER	-	expression tag	UNP Q12306
Mc	-64	HIS	-	expression tag	UNP Q12306
Mc	-63	HIS	-	expression tag	UNP Q12306
Mc	-62	HIS	-	expression tag	UNP Q12306
Mc	-61	HIS	-	expression tag	UNP Q12306
Mc	-60	HIS	-	expression tag	UNP Q12306
Mc	-59	HIS	-	expression tag	UNP Q12306
Mc	-58	GLY	-	expression tag	UNP Q12306
Mc	41	TRP	-	linker	UNP Q12306
Mc	42	SER	-	linker	UNP Q12306
Mc	43	HIS	-	linker	UNP Q12306
Mc	44	PRO	-	linker	UNP Q12306
Mc	45	GLN	-	linker	UNP Q12306
Mc	46	PHE	-	linker	UNP Q12306
Mc	47	GLU	-	linker	UNP Q12306
Mc	48	LYS	-	linker	UNP Q12306
Mc	49	SER	-	linker	UNP Q12306
Mc	50	ALA	-	linker	UNP Q12306

- Molecule 7 is a protein called Isoform 1 of Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	BA	438	Total	C	H	N	O	S	0	0
			6675	2148	3275	577	654	21		
7	CA	428	Total	C	H	N	O	S	0	0
			6552	2104	3230	566	631	21		
7	DA	428	Total	C	H	N	O	S	0	0
			6552	2104	3230	566	631	21		
7	EA	428	Total	C	H	N	O	S	0	0
			6553	2104	3231	566	631	21		
7	FA	428	Total	C	H	N	O	S	0	0
			6552	2104	3230	566	631	21		
7	GA	428	Total	C	H	N	O	S	0	0
			6544	2104	3222	566	631	21		
7	HA	428	Total	C	H	N	O	S	0	0
			6552	2104	3230	566	631	21		
7	IA	428	Total	C	H	N	O	S	0	0
			6553	2104	3231	566	631	21		
7	JA	428	Total	C	H	N	O	S	0	0
			6551	2104	3229	566	631	21		
7	KA	428	Total	C	H	N	O	S	0	0
			6553	2104	3231	566	631	21		
7	LA	428	Total	C	H	N	O	S	0	0
			6552	2104	3230	566	631	21		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	254	ASP	GLU	engineered mutation	UNP P68363
CA	254	ASP	GLU	engineered mutation	UNP P68363
DA	254	ASP	GLU	engineered mutation	UNP P68363
EA	254	ASP	GLU	engineered mutation	UNP P68363
FA	254	ASP	GLU	engineered mutation	UNP P68363
GA	254	ASP	GLU	engineered mutation	UNP P68363
HA	254	ASP	GLU	engineered mutation	UNP P68363
IA	254	ASP	GLU	engineered mutation	UNP P68363
JA	254	ASP	GLU	engineered mutation	UNP P68363
KA	254	ASP	GLU	engineered mutation	UNP P68363
LA	254	ASP	GLU	engineered mutation	UNP P68363

- Molecule 8 is a protein called Tubulin beta-3 chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	BB	426	Total	C	H	N	O	P S	0	0
			6525	2094	3189	563	652	2 25		

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Mol	Chain	Residues	Atoms							AltConf	Trace
8	CB	426	Total	C	H	N	O	P	S	0	0
			6576	2103	3222	572	652	2	25		
8	DB	426	Total	C	H	N	O	P	S	0	0
			6559	2100	3211	569	652	2	25		
8	EB	426	Total	C	H	N	O	P	S	0	0
			6577	2103	3223	572	652	2	25		
8	FB	426	Total	C	H	N	O	P	S	0	0
			6576	2103	3222	572	652	2	25		
8	GB	426	Total	C	H	N	O	P	S	0	0
			6576	2103	3222	572	652	2	25		
8	HB	426	Total	C	H	N	O	P	S	0	0
			6577	2103	3223	572	652	2	25		
8	IB	426	Total	C	H	N	O	P	S	0	0
			6577	2103	3223	572	652	2	25		
8	JB	426	Total	C	H	N	O	P	S	0	0
			6577	2103	3223	572	652	2	25		
8	KB	426	Total	C	H	N	O	P	S	0	0
			6576	2103	3222	572	652	2	25		
8	LB	426	Total	C	H	N	O	P	S	0	0
			6576	2103	3222	572	652	2	25		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	501	GDP	-	expression tag	UNP Q13509
CB	501	GDP	-	expression tag	UNP Q13509
DB	501	GDP	-	expression tag	UNP Q13509
EB	501	GDP	-	expression tag	UNP Q13509
FB	501	GDP	-	expression tag	UNP Q13509
GB	501	GDP	-	expression tag	UNP Q13509
HB	501	GDP	-	expression tag	UNP Q13509
IB	501	GDP	-	expression tag	UNP Q13509
JB	501	GDP	-	expression tag	UNP Q13509
KB	501	GDP	-	expression tag	UNP Q13509
LB	501	GDP	-	expression tag	UNP Q13509

- Molecule 9 is a protein called Mitotic-spindle organizing protein 2A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	CM	54	Total	C	H	N	O	S	0	0
			837	263	429	65	76	4		
9	EM	54	Total	C	H	N	O	S	0	0
			837	263	429	65	76	4		

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Mol	Chain	Residues	Atoms						AltConf	Trace
9	GM	53	Total	C	H	N	O	S	0	0
			813	257	416	61	75	4		
9	MM	53	Total	C	H	N	O	S	0	0
			813	257	416	61	75	4		

- Molecule 10 is a protein called Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	I	521	Total	C	H	N	O	S	0	0
			8477	2734	4255	720	750	18		
10	K	553	Total	C	H	N	O	S	0	0
			9006	2915	4509	765	800	17		

- Molecule 11 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	J	594	Total	C	H	N	O	S	0	0
			9521	3086	4748	798	863	26		
11	Z	124	Total	C	H	N	O	S	0	0
			1988	642	982	175	188	1		

- Molecule 12 is a protein called Tubulin gamma-1 chain.

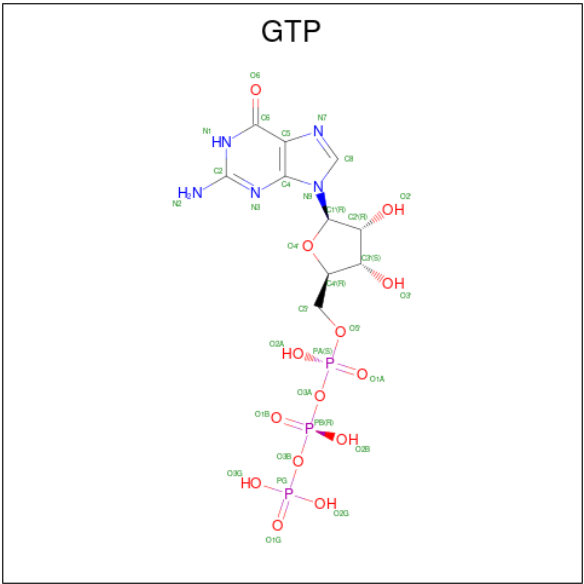
Mol	Chain	Residues	Atoms						AltConf	Trace
12	a	412	Total	C	H	N	O	S	0	0
			6595	2100	3282	576	622	15		
12	b	412	Total	C	H	N	O	S	0	0
			6595	2100	3282	576	622	15		
12	c	412	Total	C	H	N	O	S	0	0
			6596	2100	3283	576	622	15		
12	d	419	Total	C	H	N	O	S	0	0
			6697	2132	3328	585	637	15		
12	e	419	Total	C	H	N	O	S	0	0
			6680	2129	3317	582	637	15		
12	f	412	Total	C	H	N	O	S	0	0
			6595	2100	3282	576	622	15		
12	g	419	Total	C	H	N	O	S	0	0
			6646	2123	3295	576	637	15		
12	h	412	Total	C	H	N	O	S	0	0
			6578	2097	3271	573	622	15		
12	i	419	Total	C	H	N	O	S	0	0
			6697	2132	3328	585	637	15		

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Mol	Chain	Residues	Atoms						AltConf	Trace
12	j	419	Total	C	H	N	O	S	0	0
			6680	2129	3317	582	637	15		
12	k	412	Total	C	H	N	O	S	0	0
			6588	2099	3277	576	621	15		
12	l	419	Total	C	H	N	O	S	0	0
			6691	2131	3324	585	636	15		
12	m	412	Total	C	H	N	O	S	0	0
			6596	2100	3283	576	622	15		
12	n	412	Total	C	H	N	O	S	0	0
			6595	2100	3282	576	622	15		

- Molecule 13 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms						AltConf
13	BA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	CA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	DA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	EA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	FA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	GA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	

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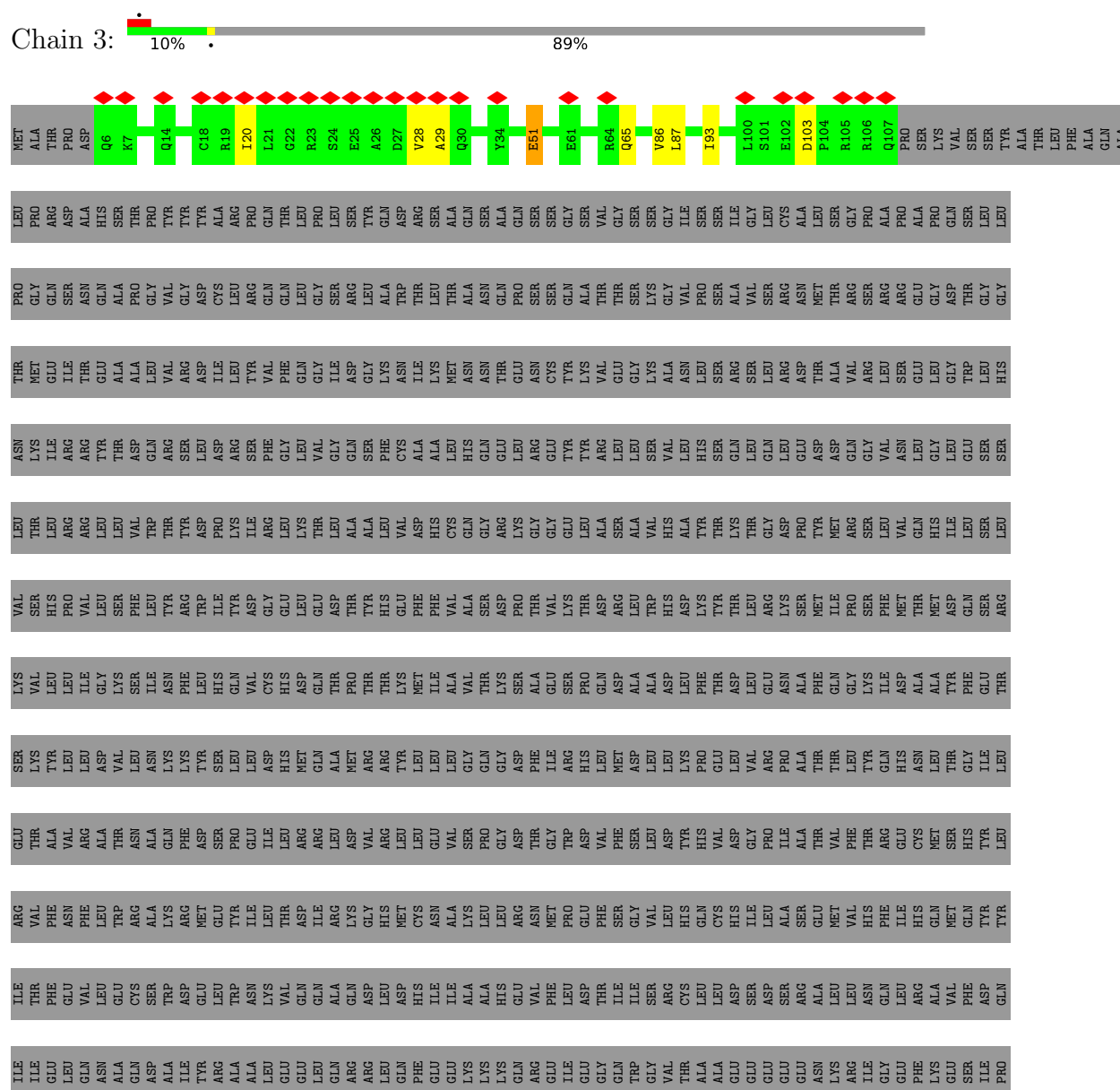
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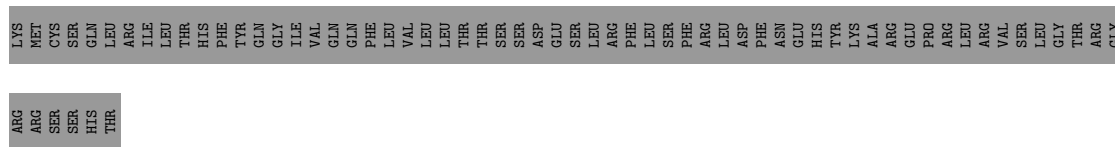
Mol	Chain	Residues	Atoms						AltConf
13	HA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	IA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	JA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	KA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
13	LA	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	

3 Residue-property plots

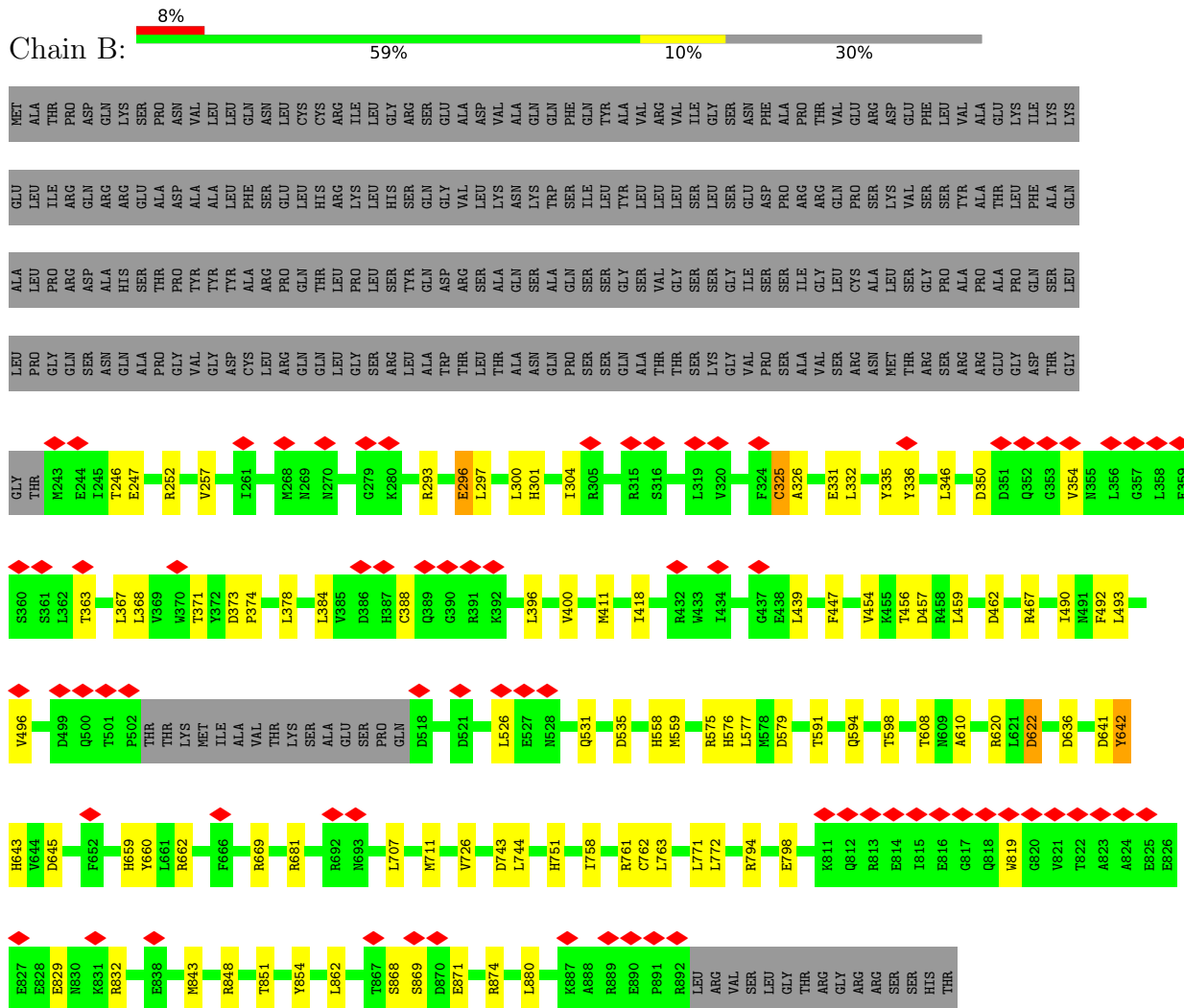
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Gamma-tubulin complex component 3



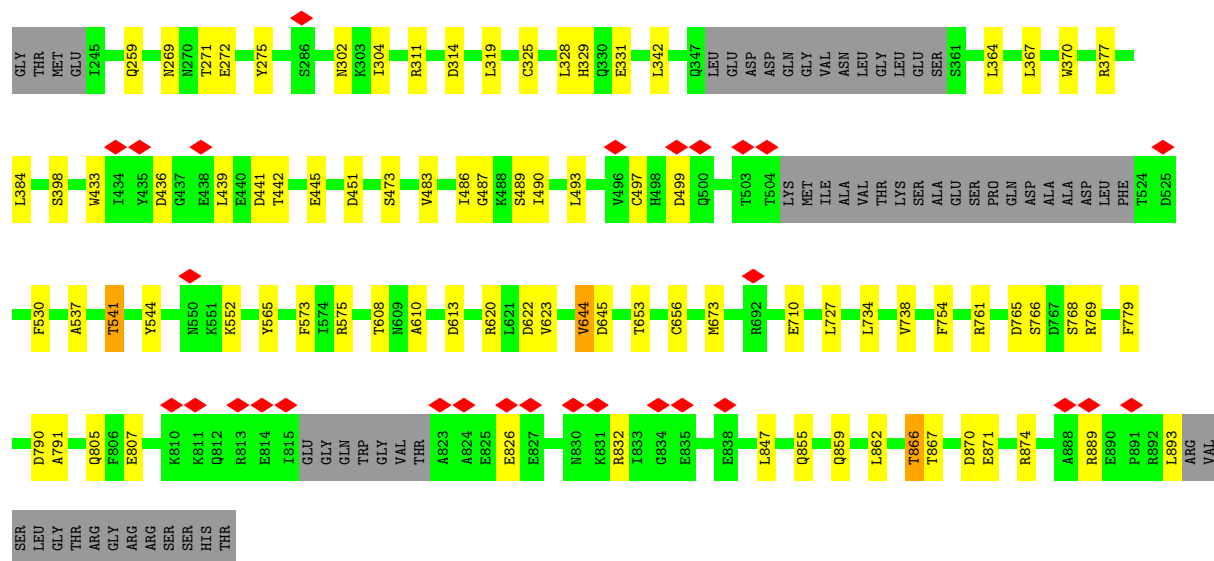


- Molecule 1: Gamma-tubulin complex component 3

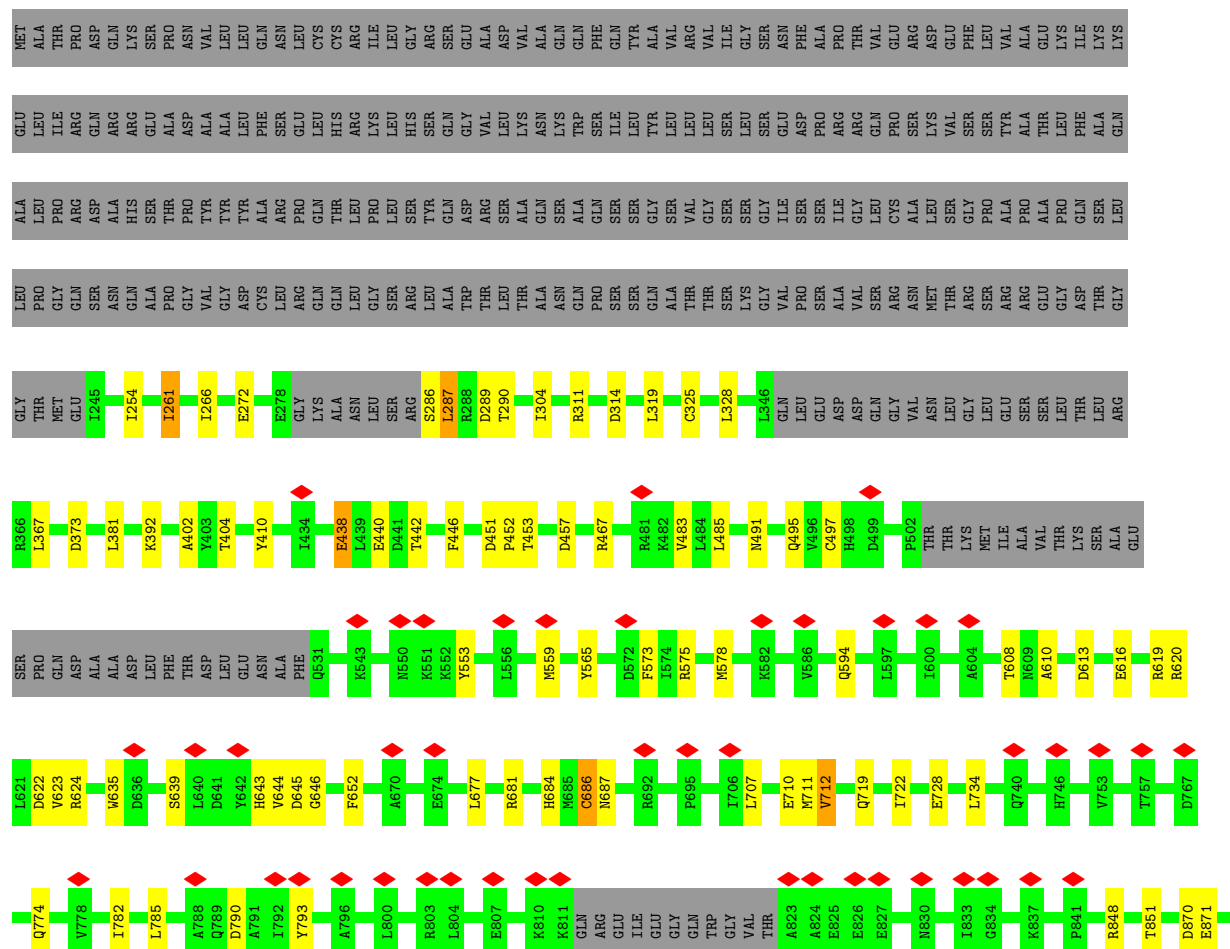


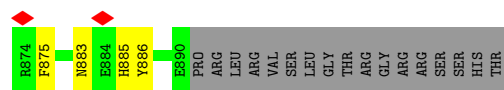
- Molecule 1: Gamma-tubulin complex component 3



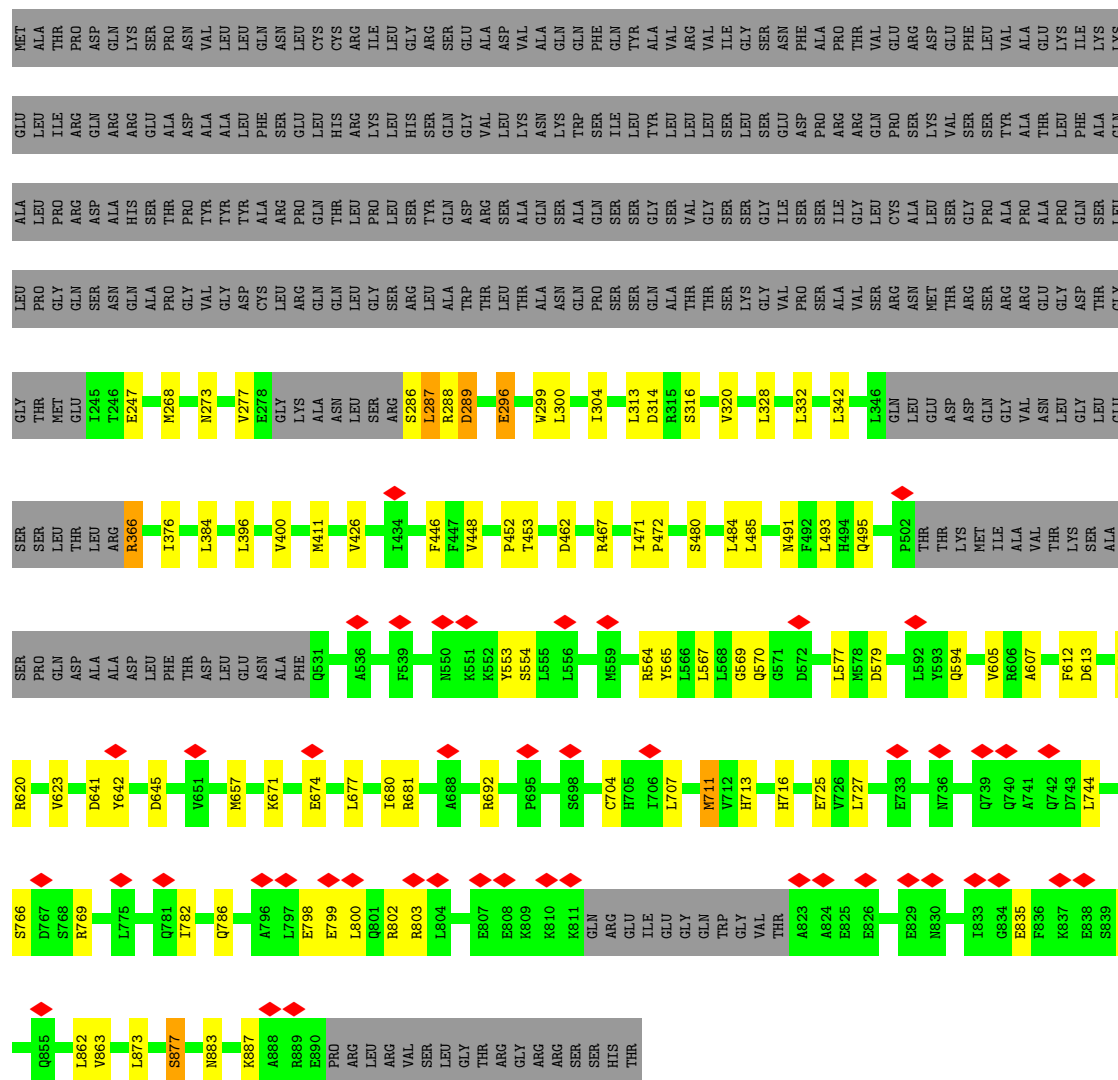


• Molecule 1: Gamma-tubulin complex component 3

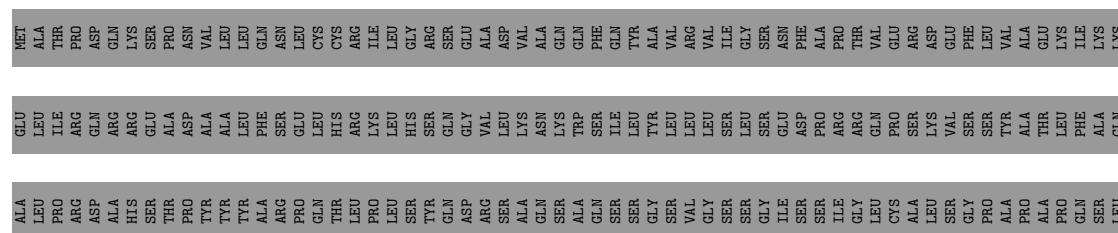




• Molecule 1: Gamma-tubulin complex component 3

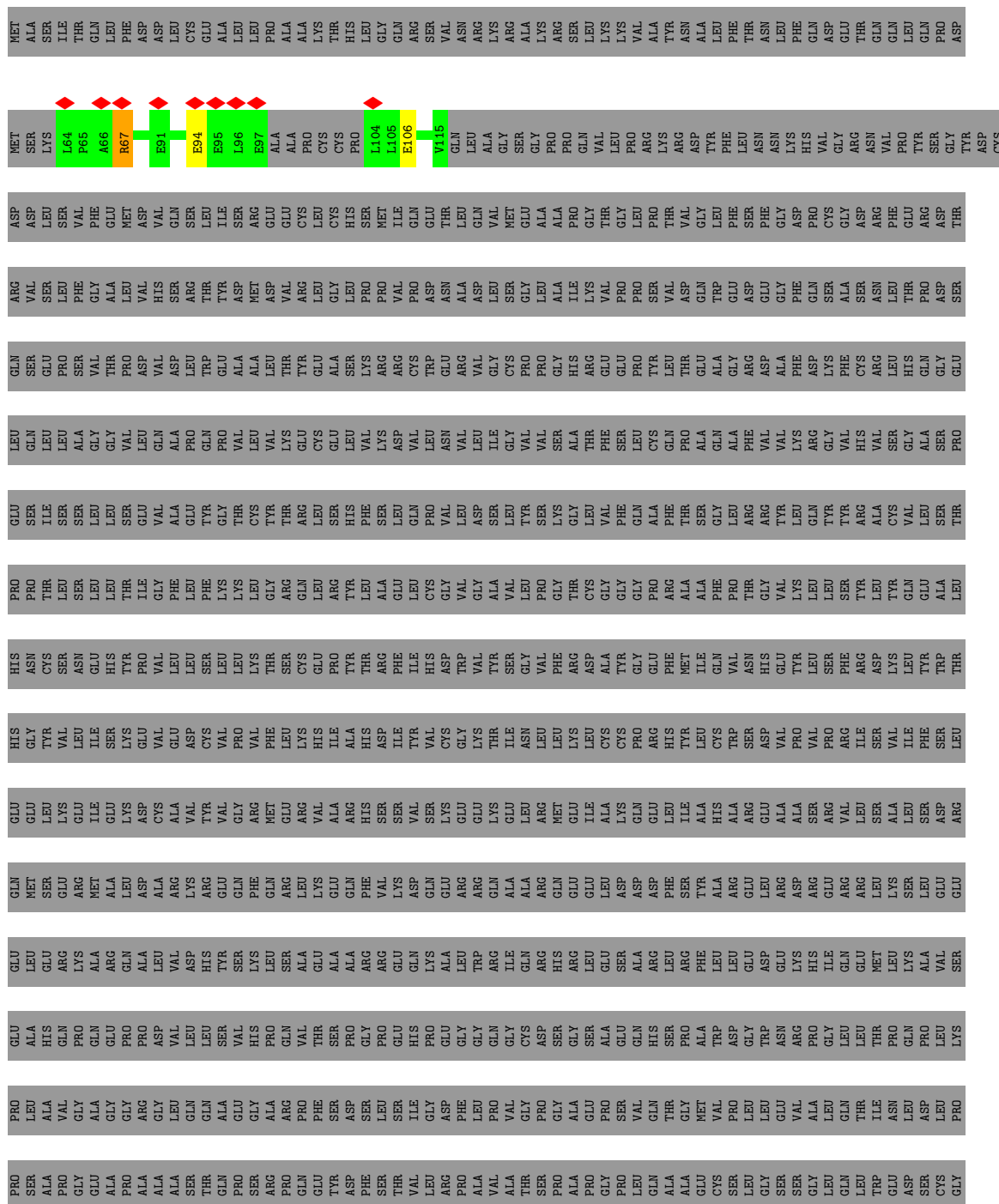


• Molecule 1: Gamma-tubulin complex component 3



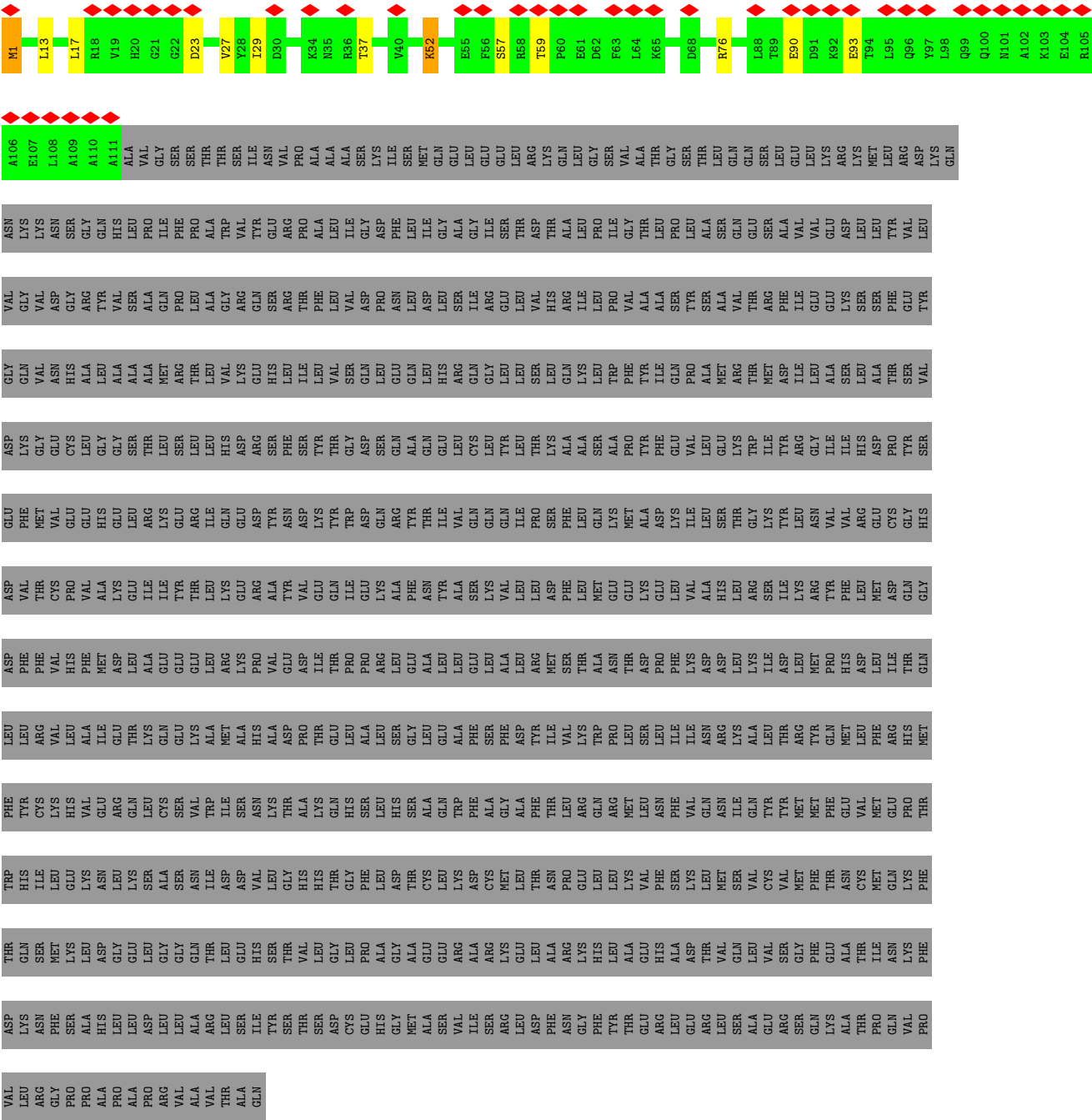
- Molecule 3: Gamma-tubulin complex component 6

Chain 5: 97%

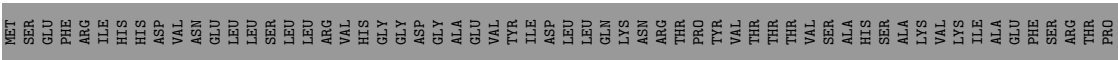




● Molecule 5: Gamma-tubulin complex component 2

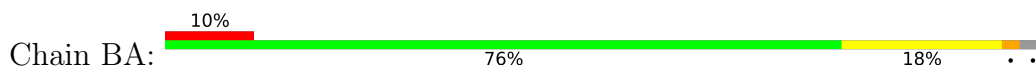


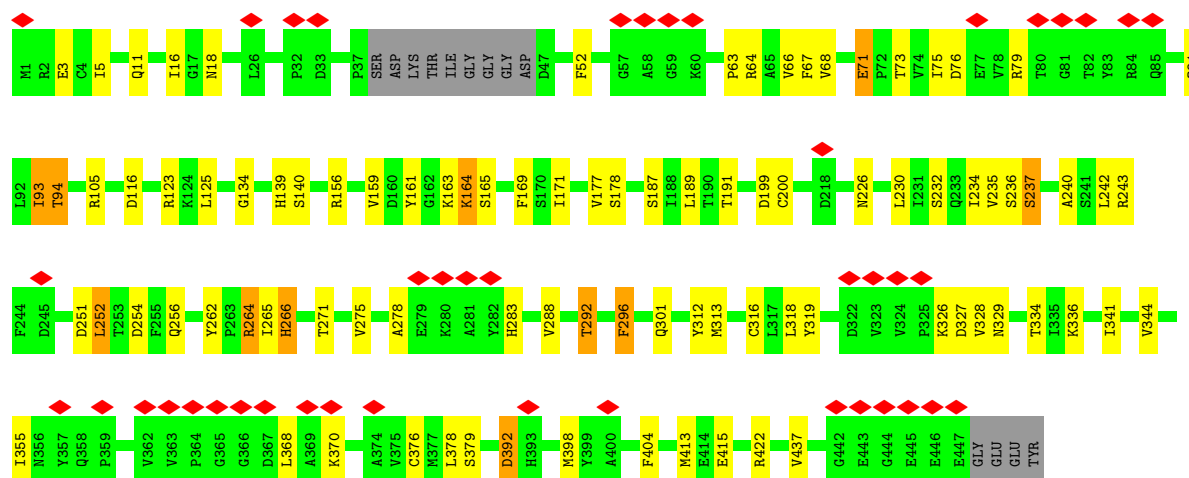
● Molecule 5: Gamma-tubulin complex component 2



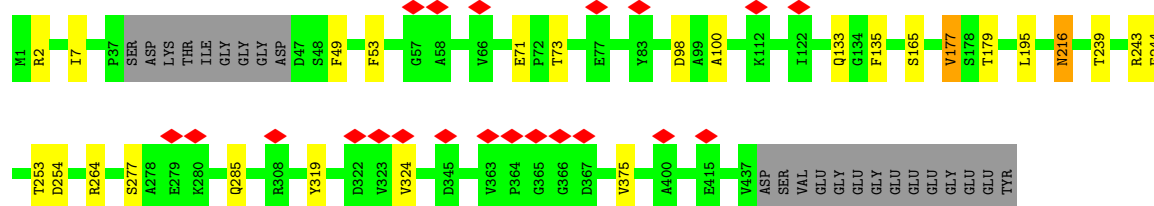
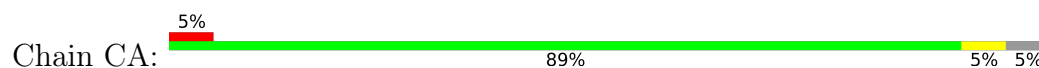




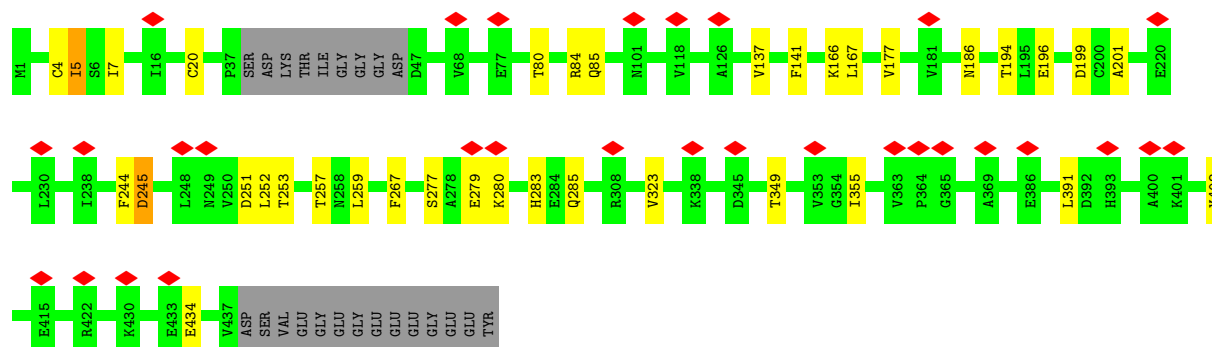
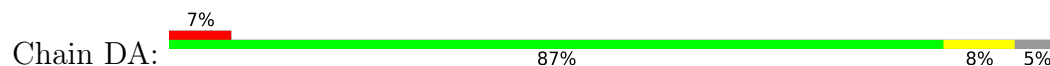




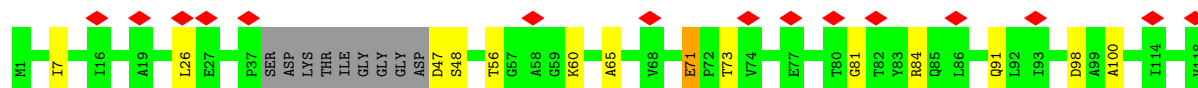
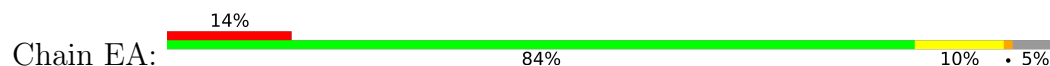
• Molecule 7: Isoform 1 of Tubulin alpha-1B chain

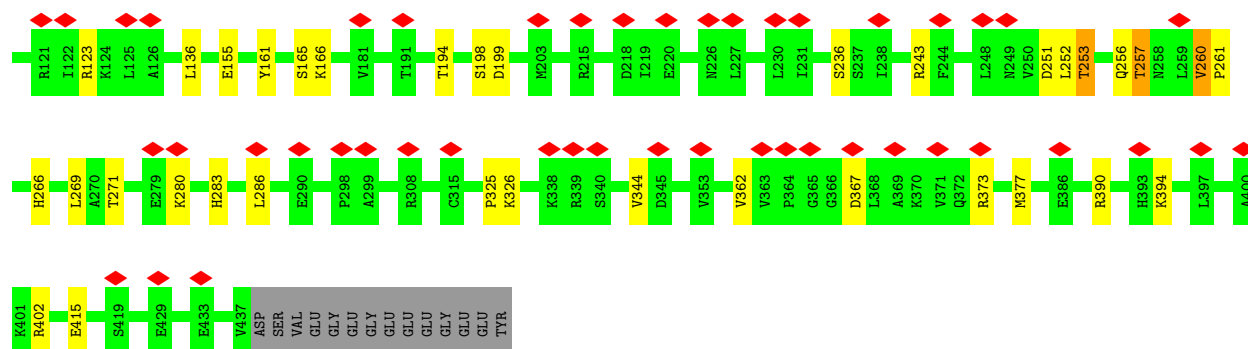


• Molecule 7: Isoform 1 of Tubulin alpha-1B chain

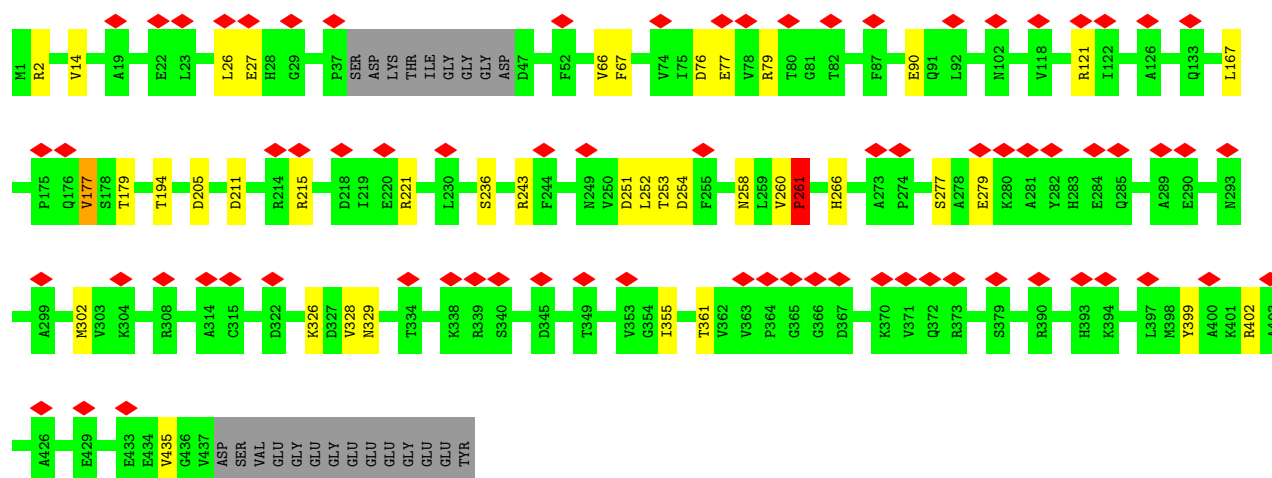


• Molecule 7: Isoform 1 of Tubulin alpha-1B chain

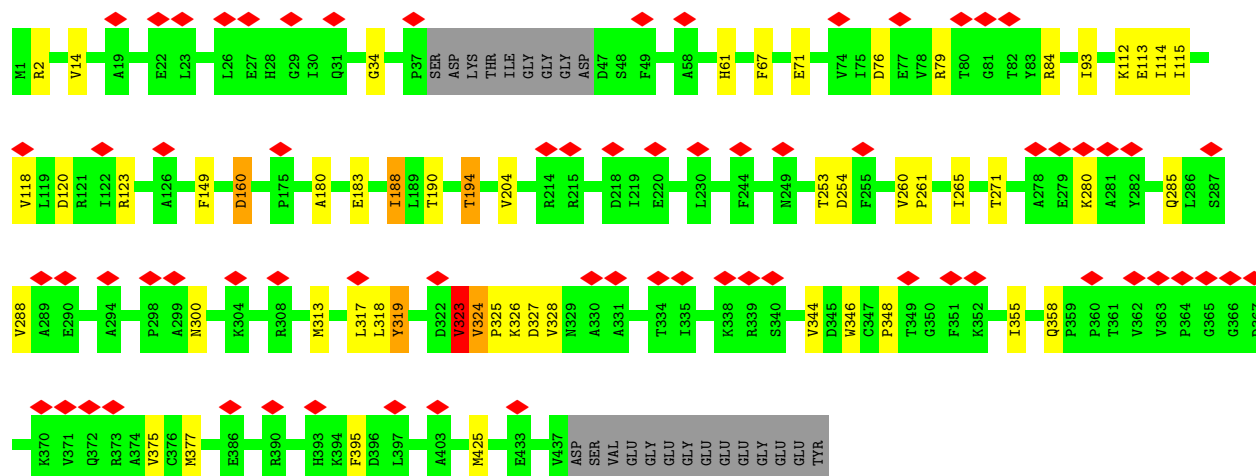
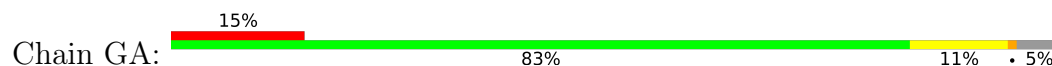




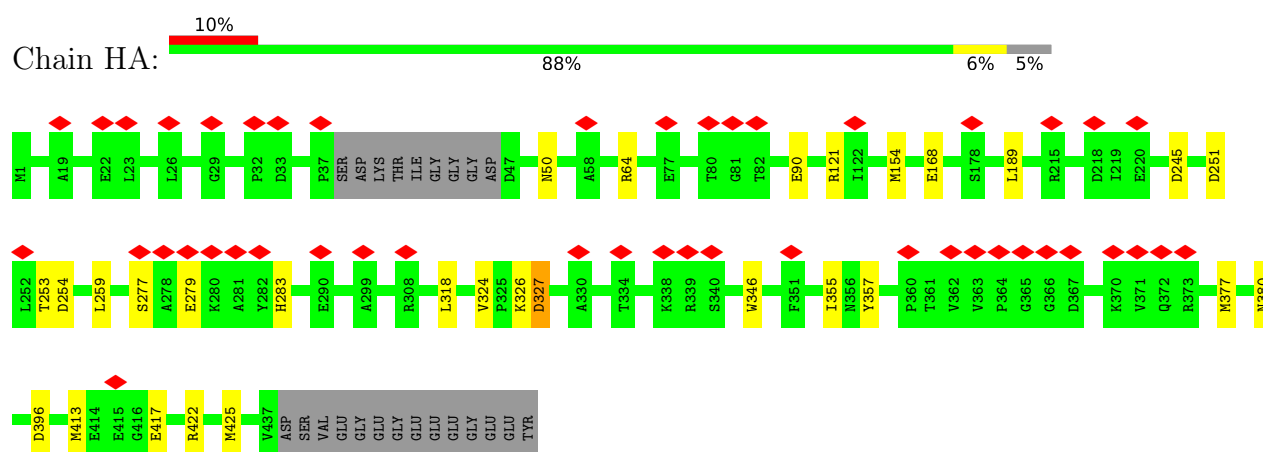
• Molecule 7: Isoform 1 of Tubulin alpha-1B chain



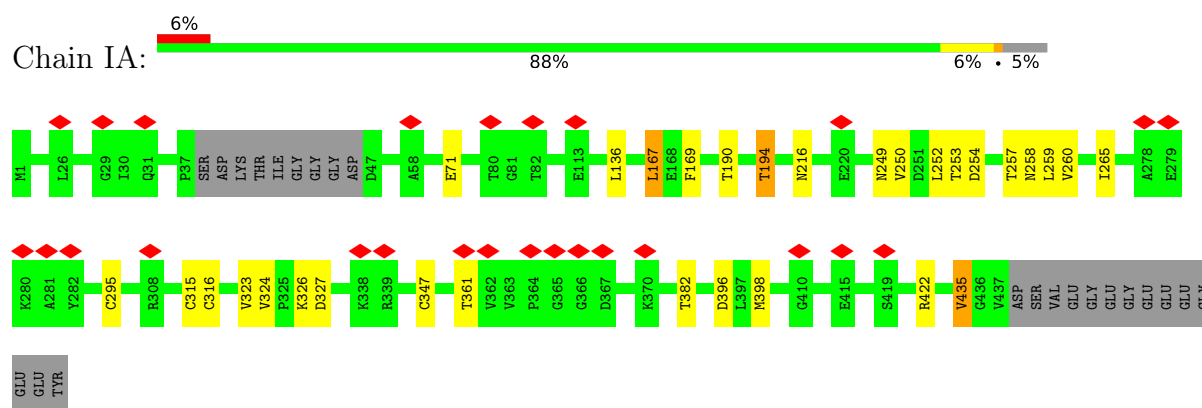
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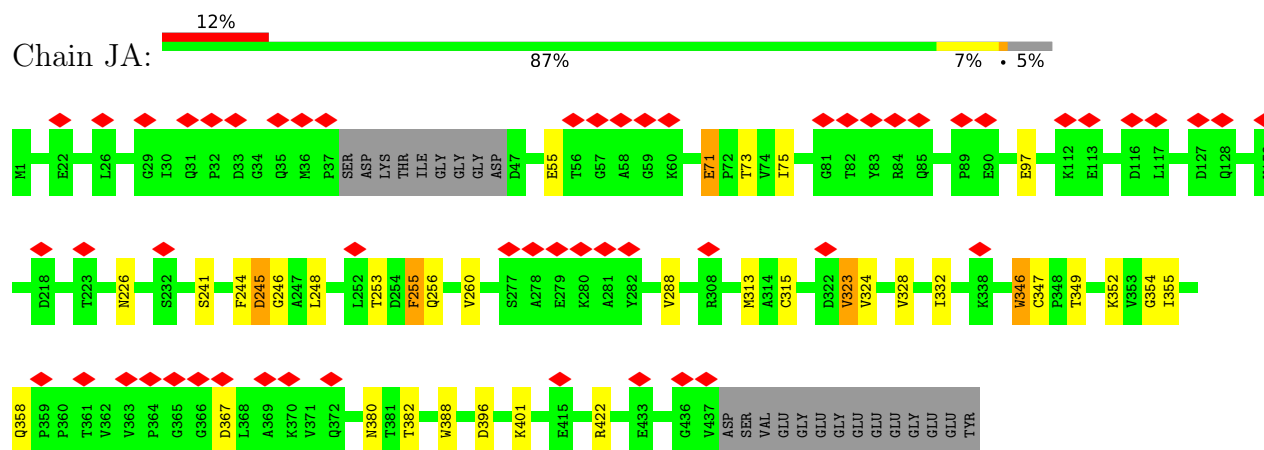
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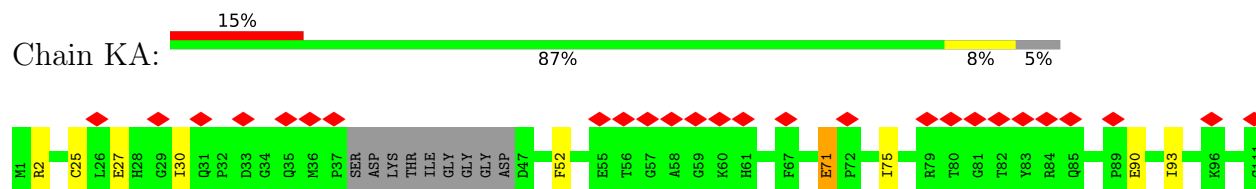
- Molecule 7: Isoform 1 of Tubulin alpha-1B chain

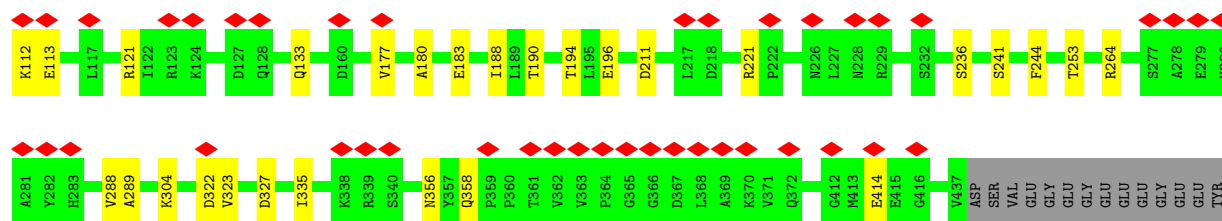


- Molecule 7: Isoform 1 of Tubulin alpha-1B chain

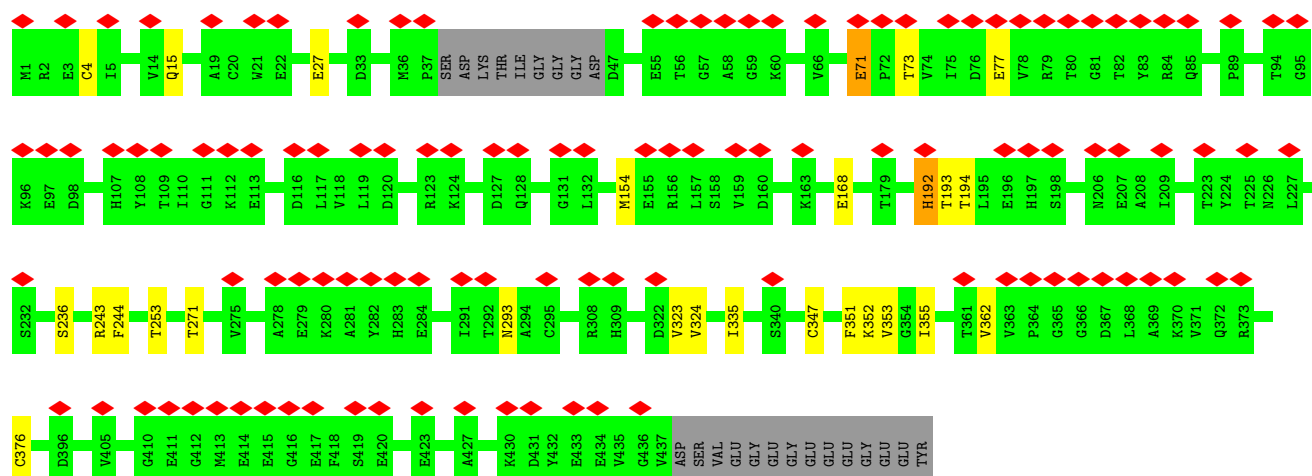
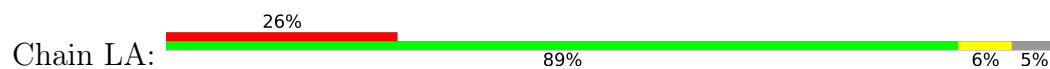


- Molecule 7: Isoform 1 of Tubulin alpha-1B chain

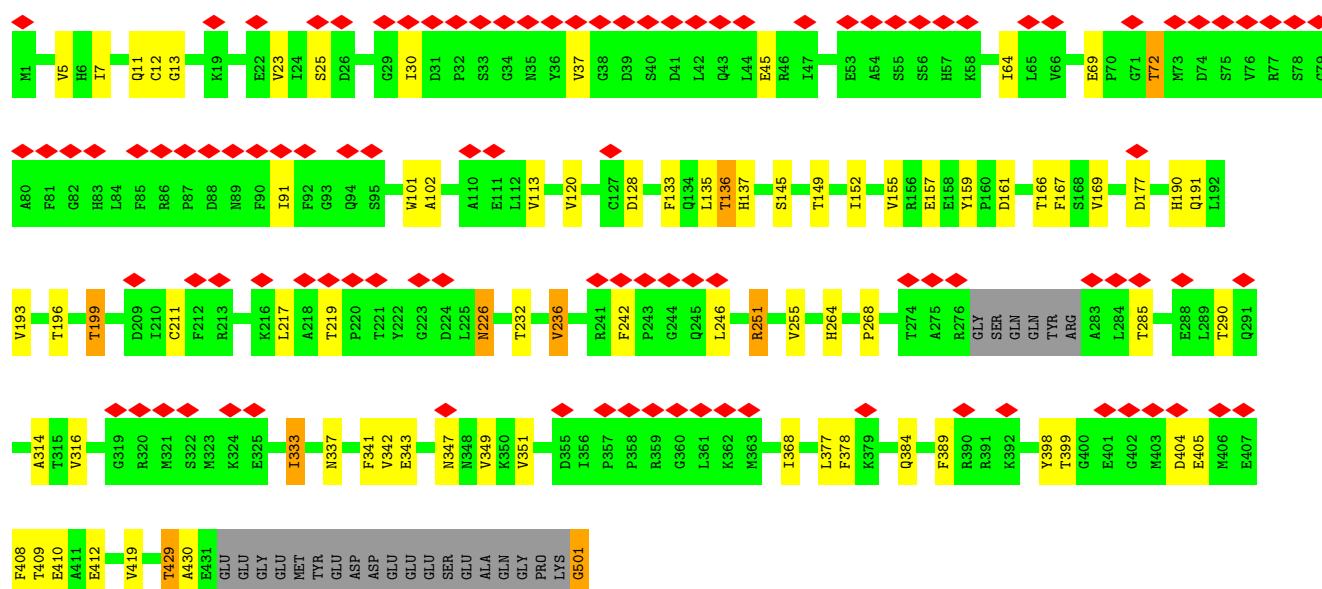
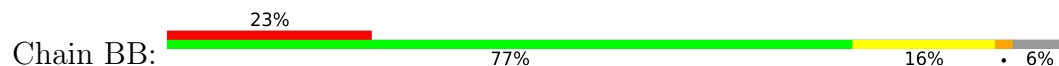




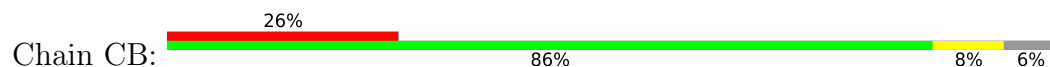
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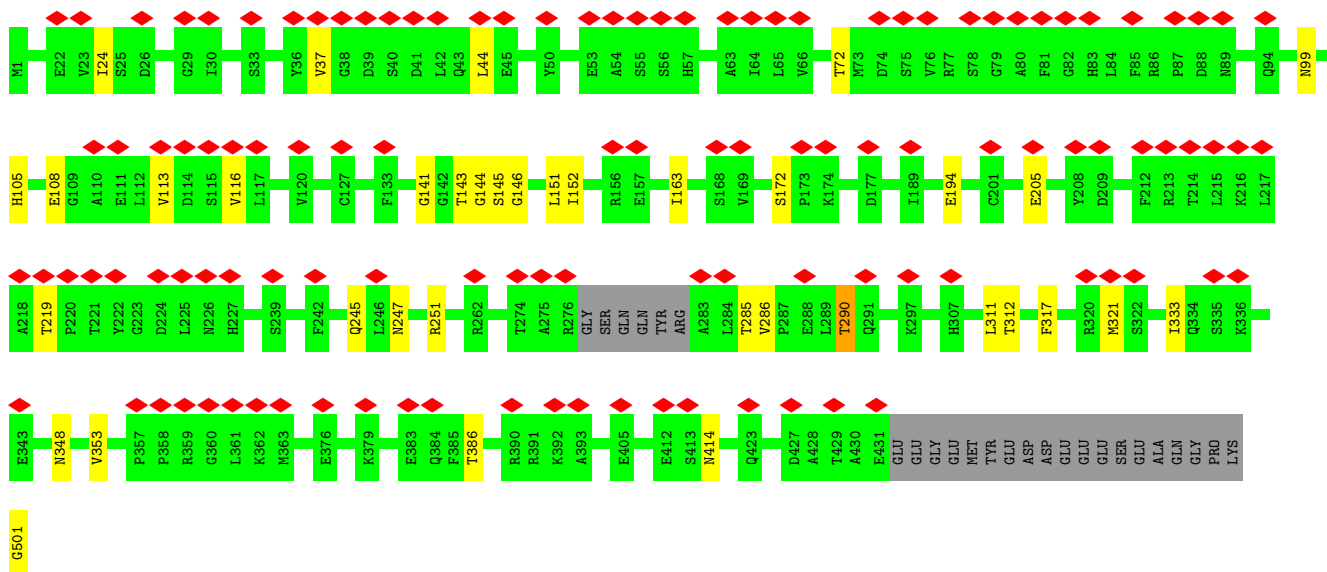


• Molecule 8: Tubulin beta-3 chain

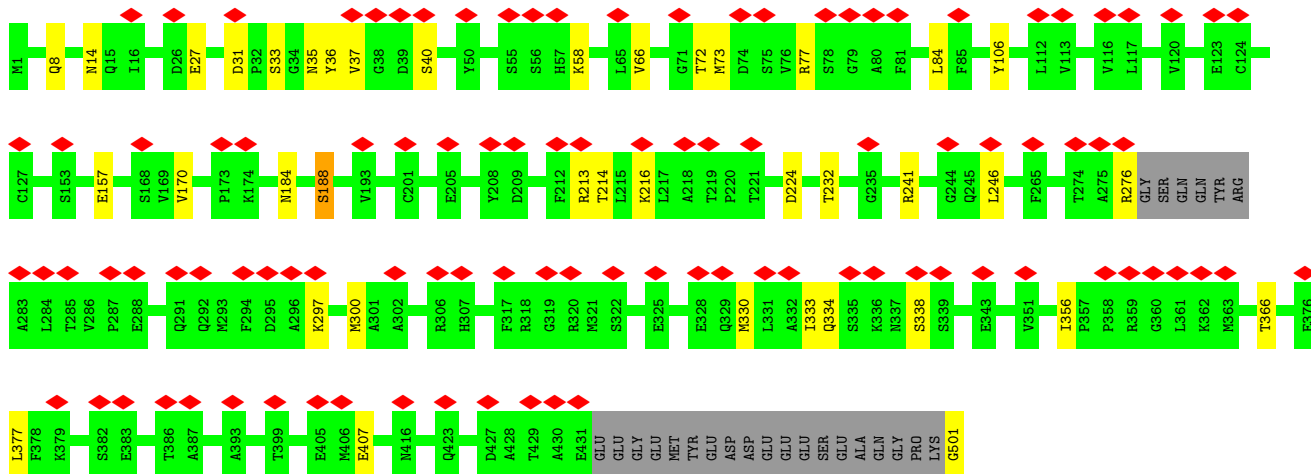


• Molecule 8: Tubulin beta-3 chain

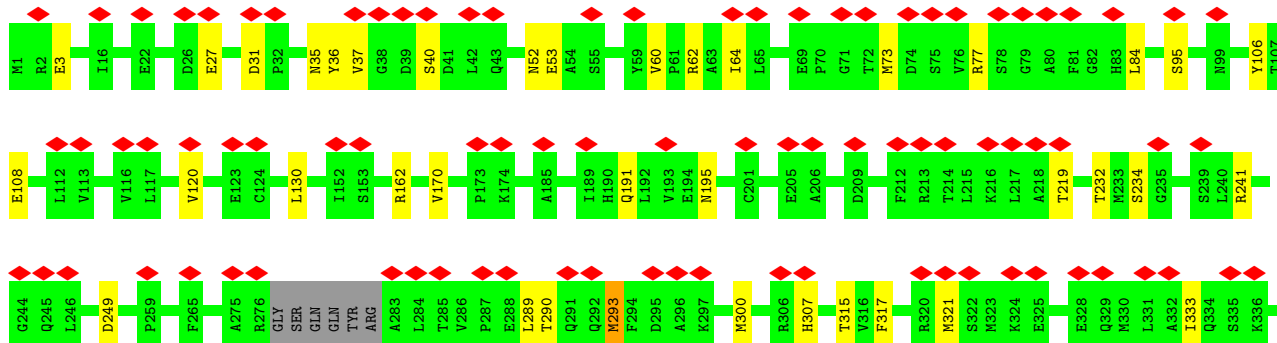
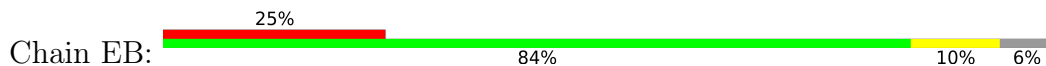


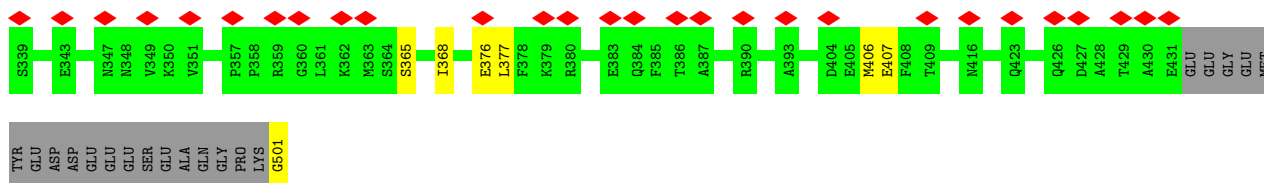


• Molecule 8: Tubulin beta-3 chain

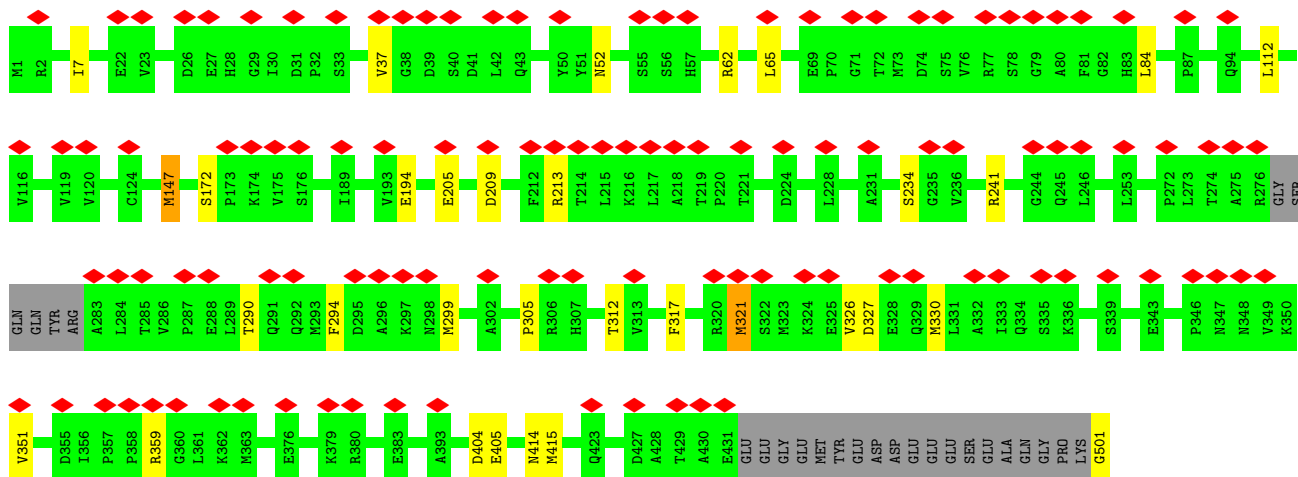
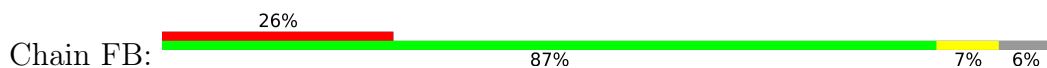


• Molecule 8: Tubulin beta-3 chain

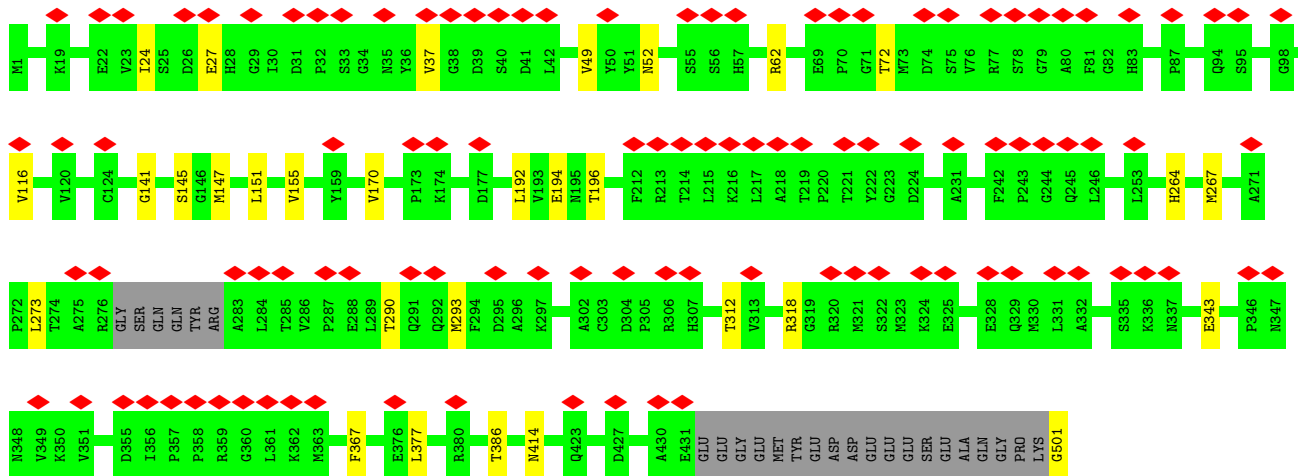
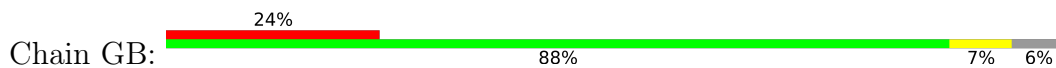




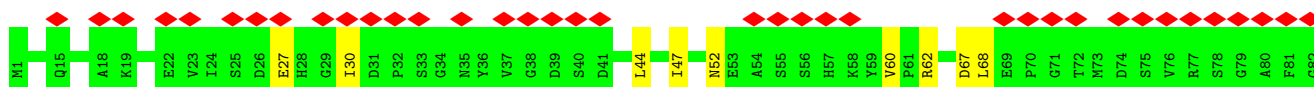
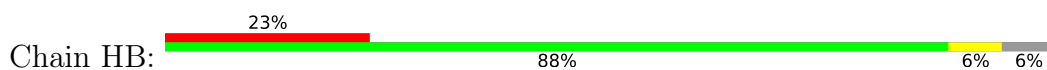
• Molecule 8: Tubulin beta-3 chain

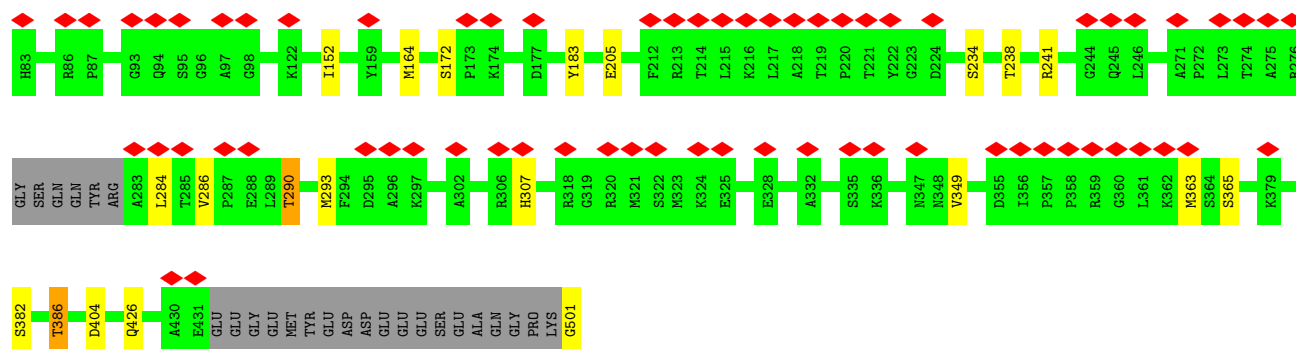


• Molecule 8: Tubulin beta-3 chain

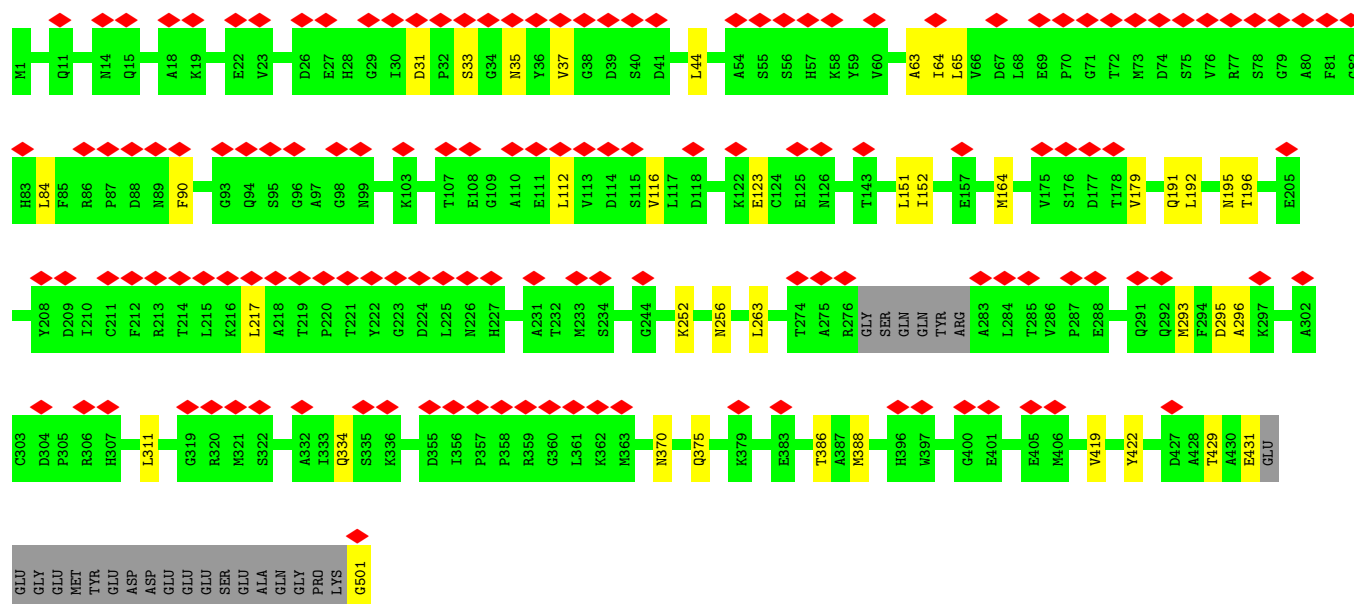
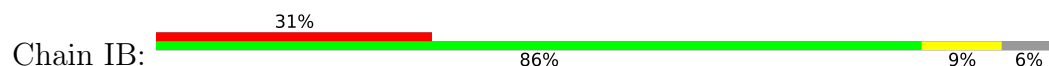


• Molecule 8: Tubulin beta-3 chain

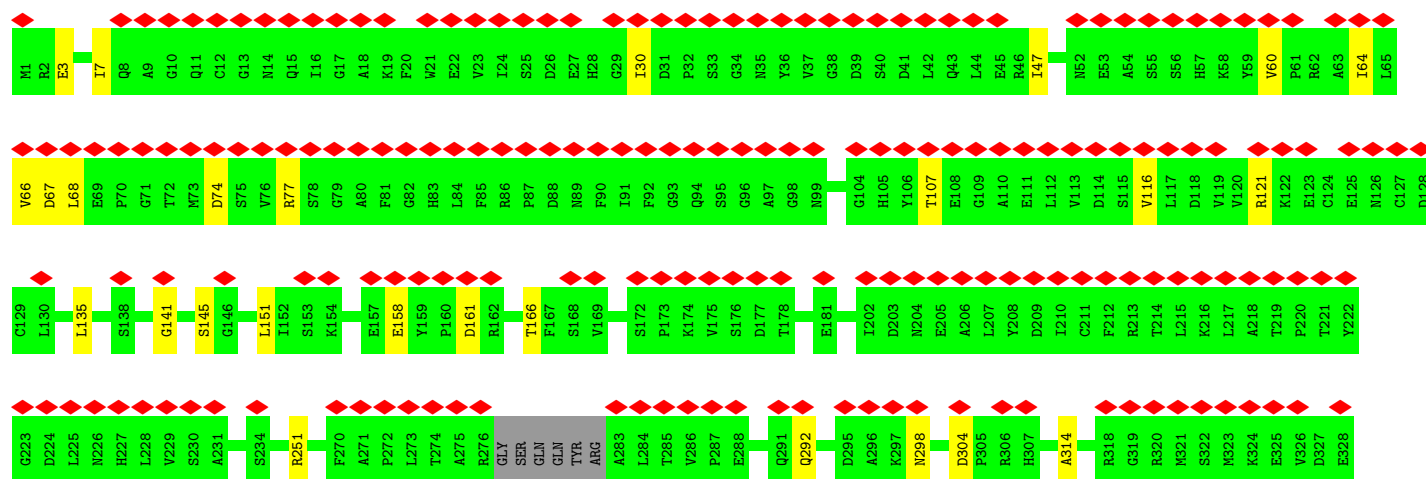
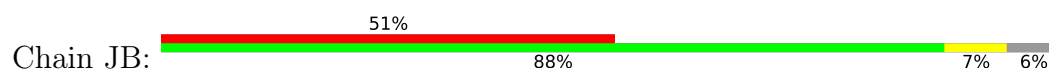


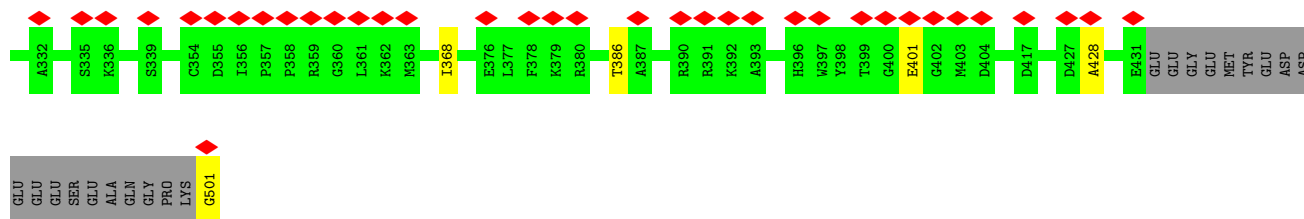


• Molecule 8: Tubulin beta-3 chain

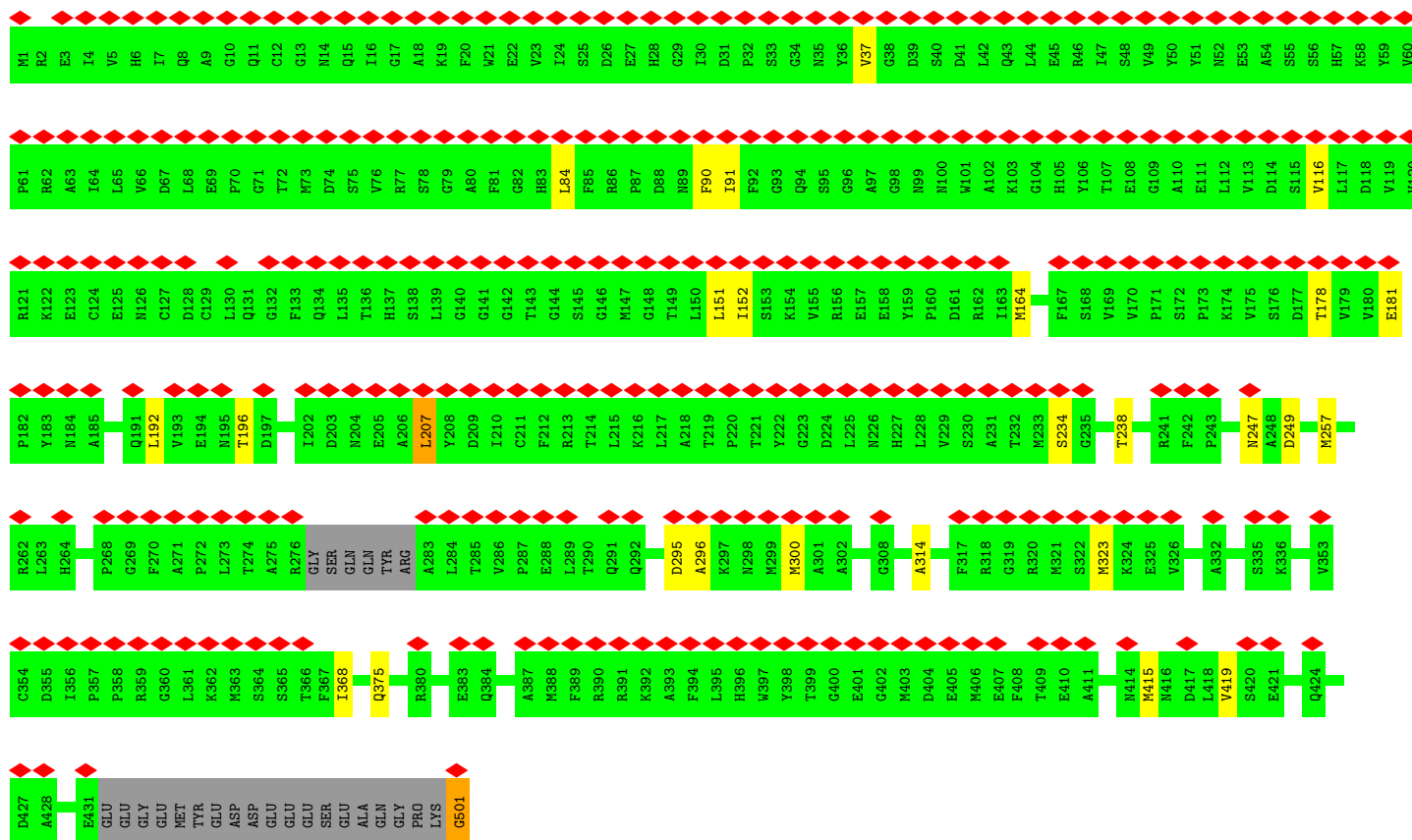
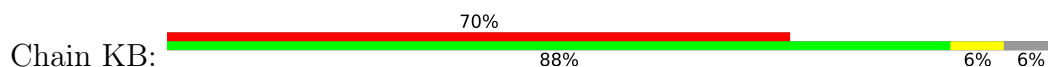


• Molecule 8: Tubulin beta-3 chain

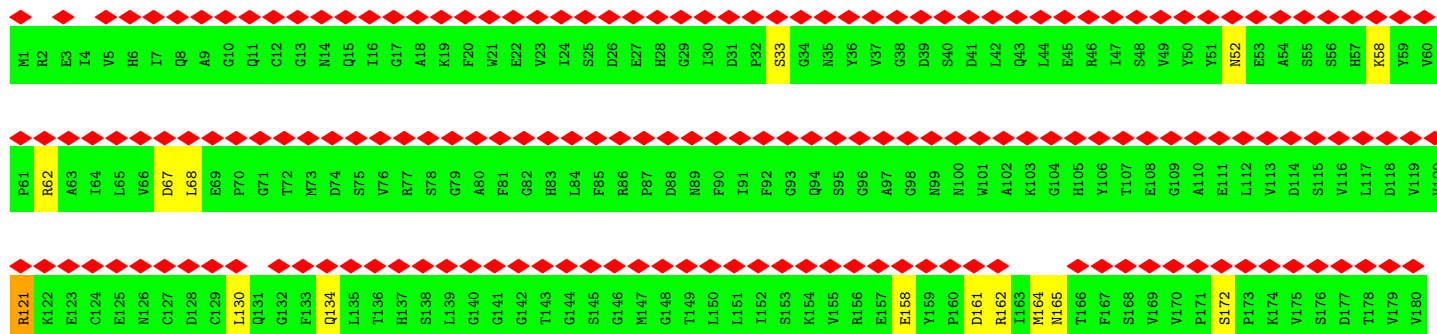
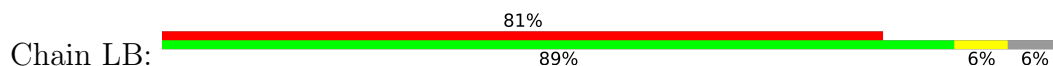


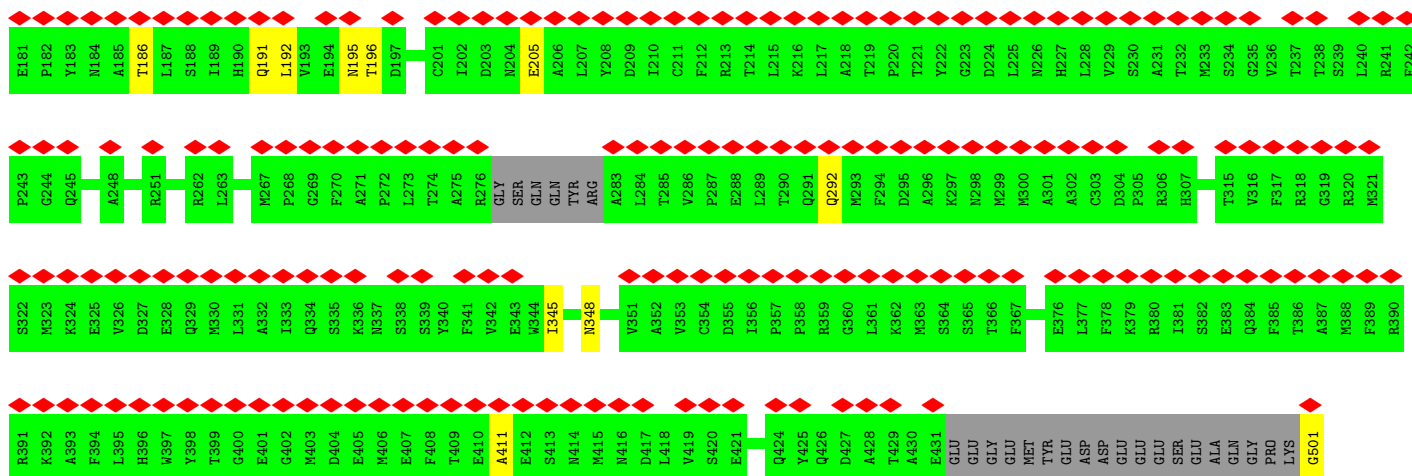


• Molecule 8: Tubulin beta-3 chain

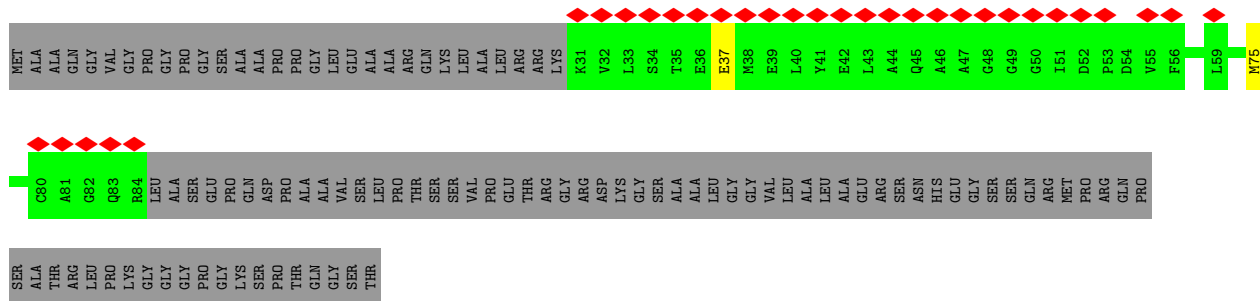


• Molecule 8: Tubulin beta-3 chain

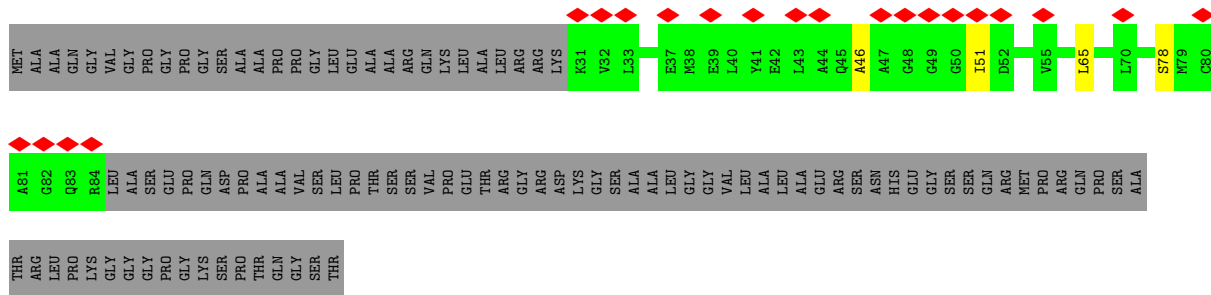




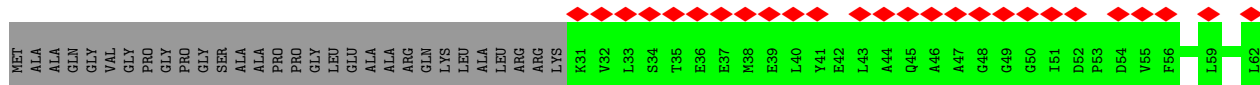
- Molecule 9: Mitotic-spindle organizing protein 2A



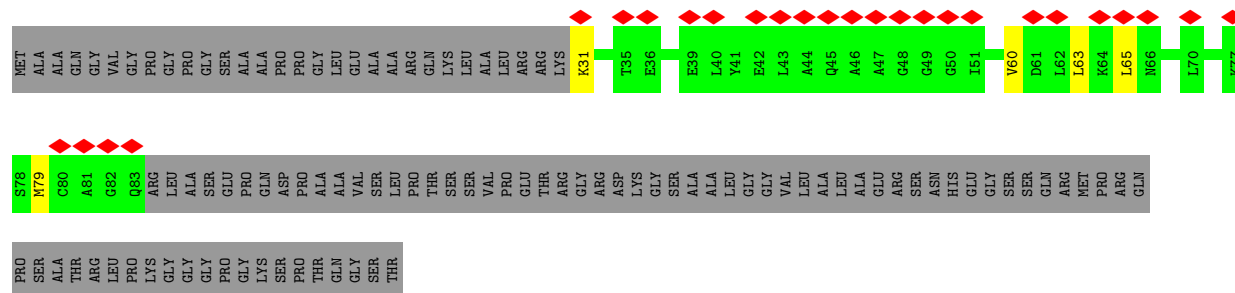
- Molecule 9: Mitotic-spindle organizing protein 2A



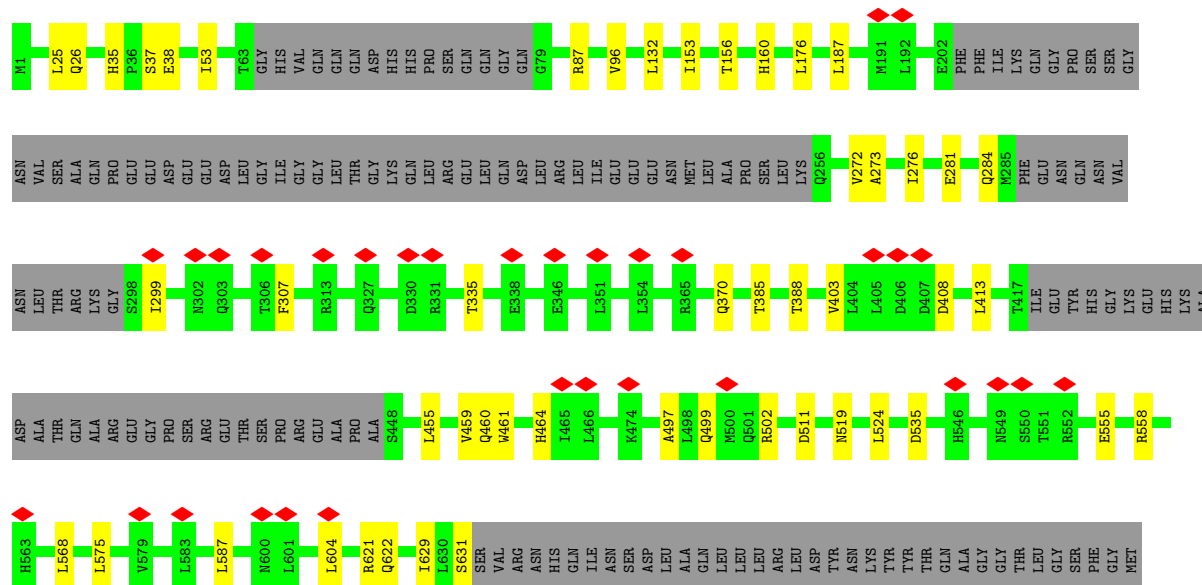
- Molecule 9: Mitotic-spindle organizing protein 2A



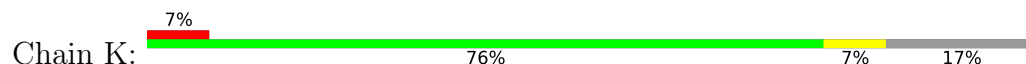
- Molecule 9: Mitotic-spindle organizing protein 2A

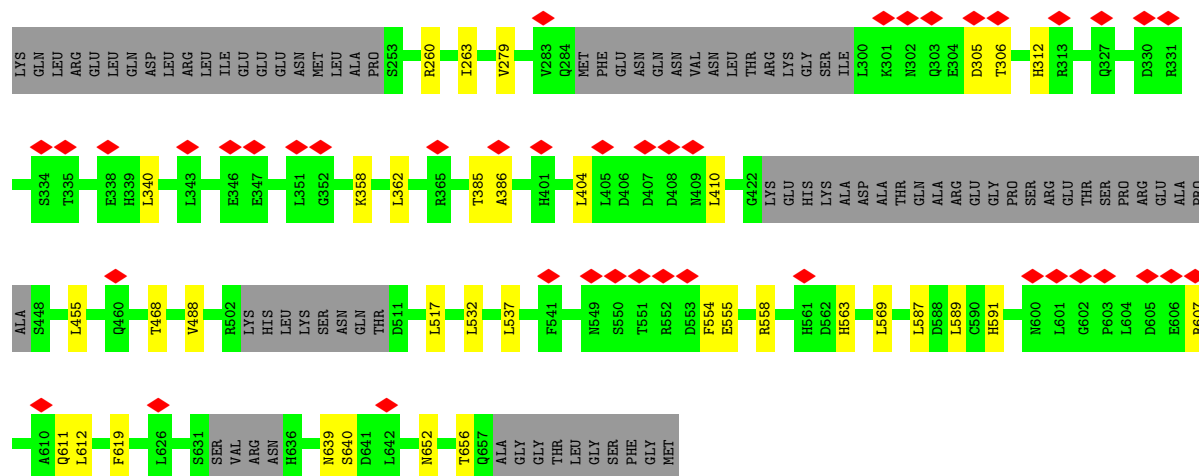


- Molecule 10: Gamma-tubulin complex component 4



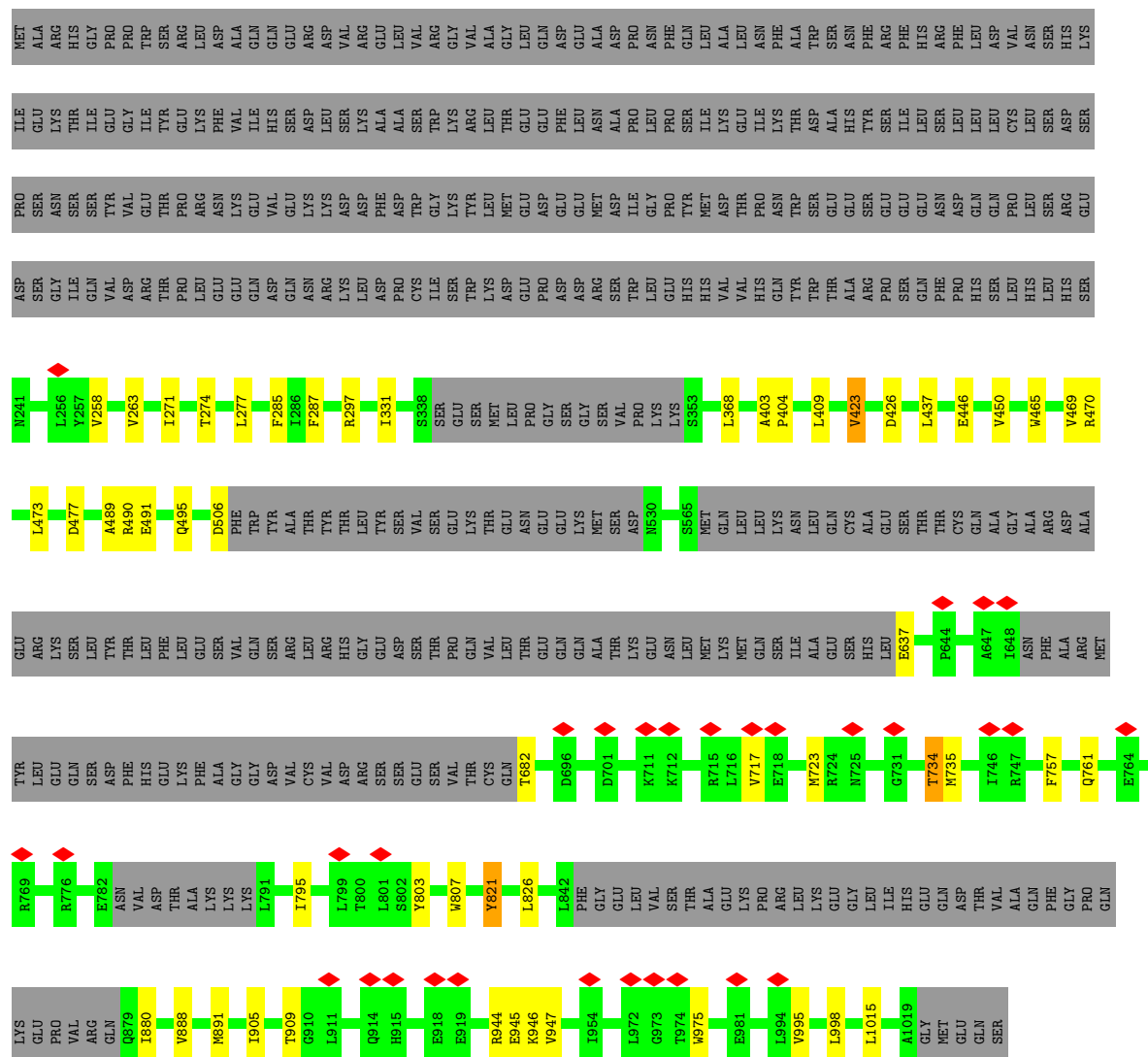
- Molecule 10: Gamma-tubulin complex component 4



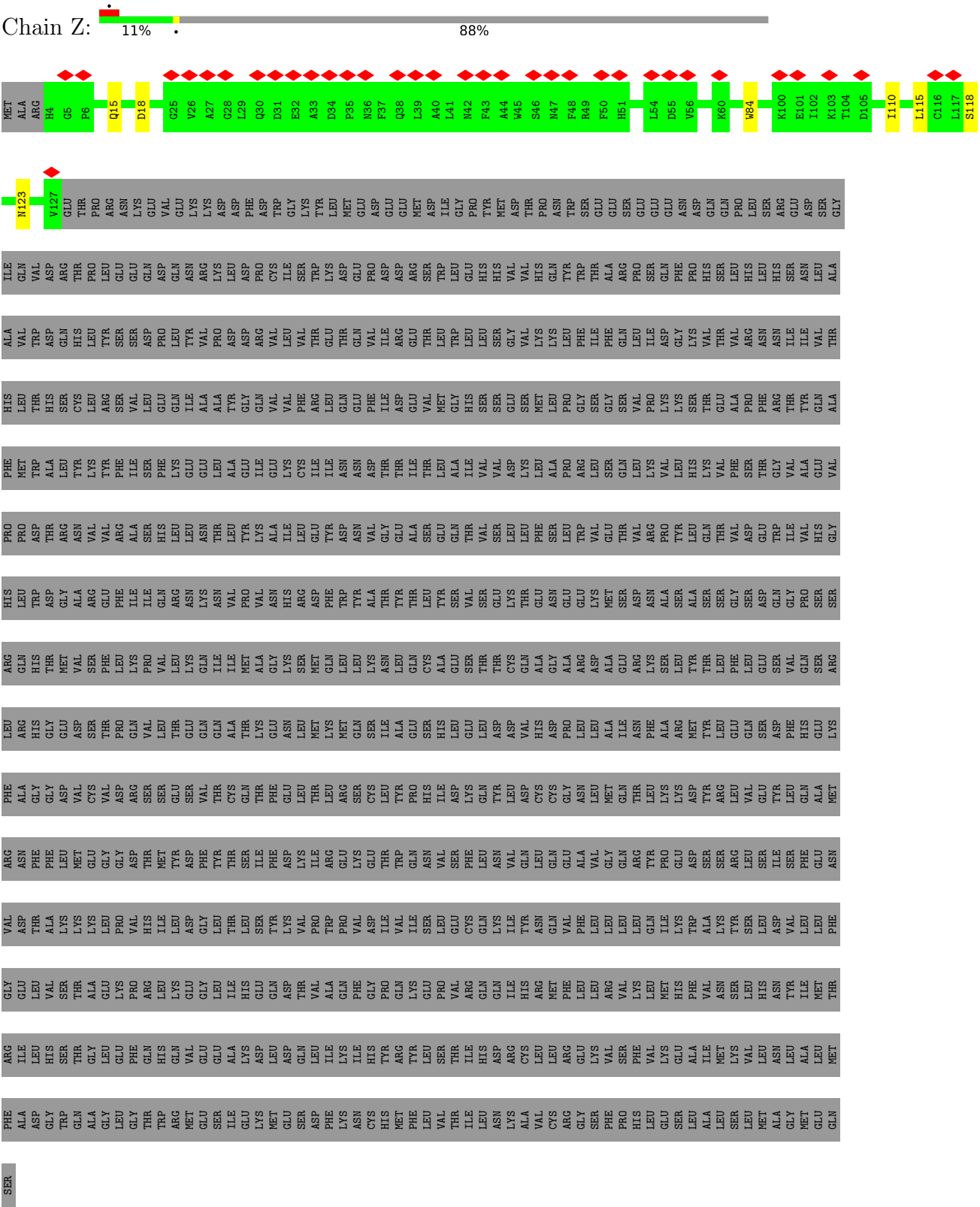


• Molecule 11: Gamma-tubulin complex component 5

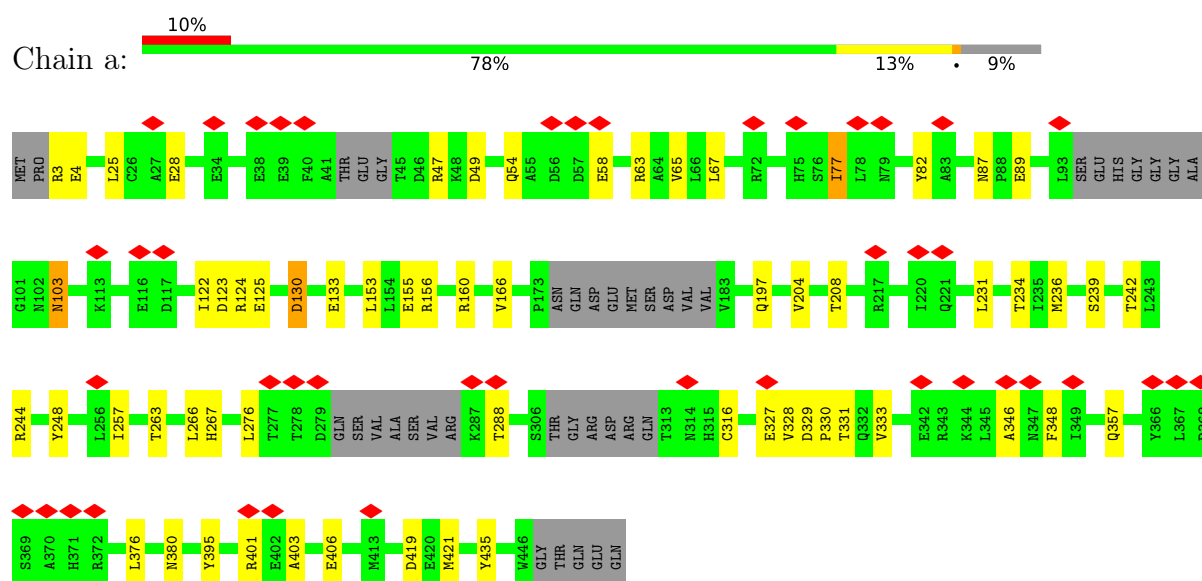
Chain J: 53% 5% 42%



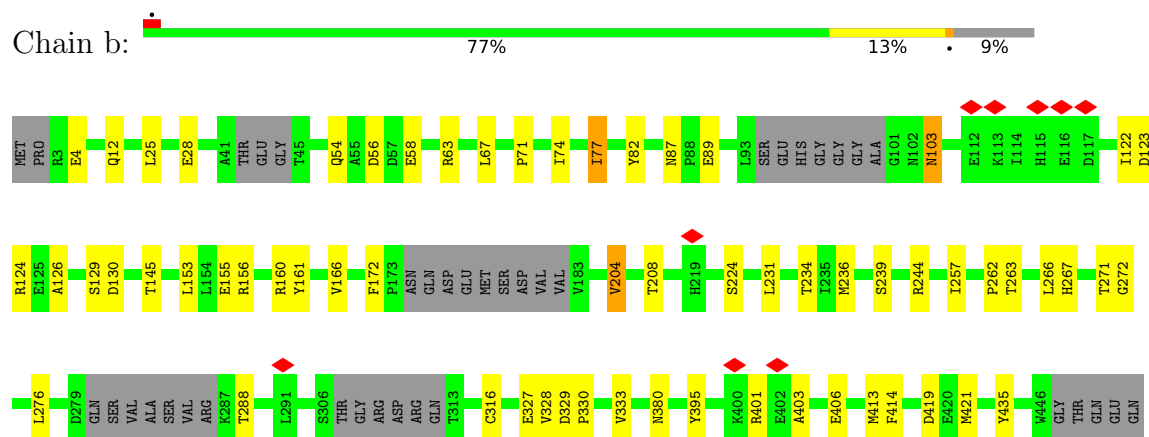
● Molecule 11: Gamma-tubulin complex component 5



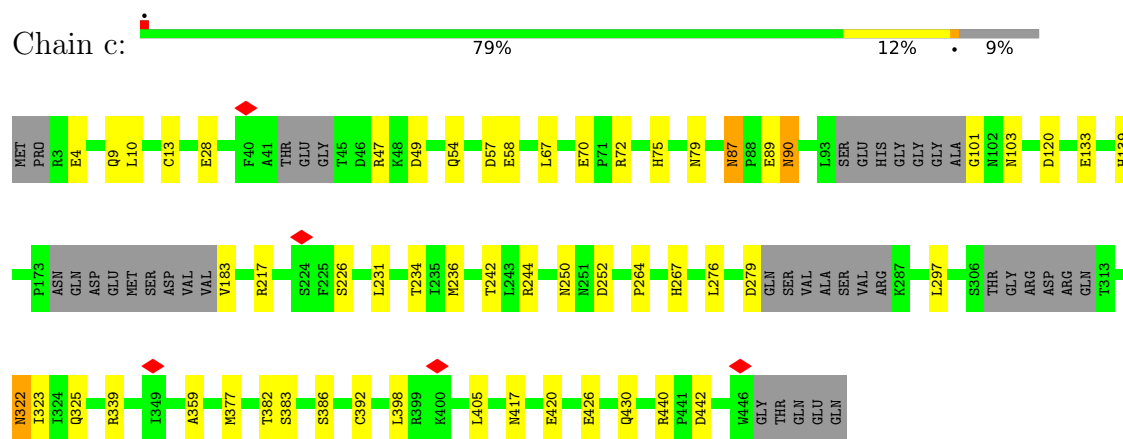
● Molecule 12: Tubulin gamma-1 chain



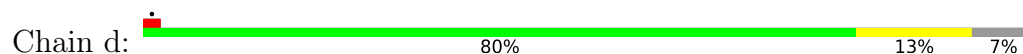
• Molecule 12: Tubulin gamma-1 chain

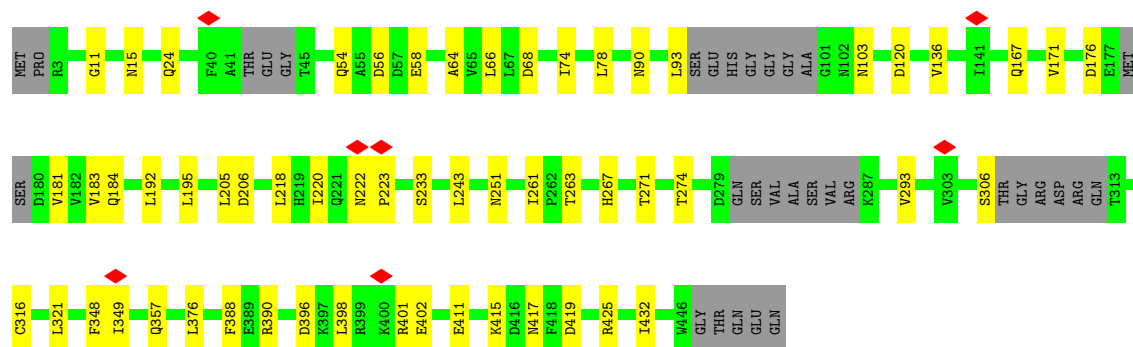


• Molecule 12: Tubulin gamma-1 chain



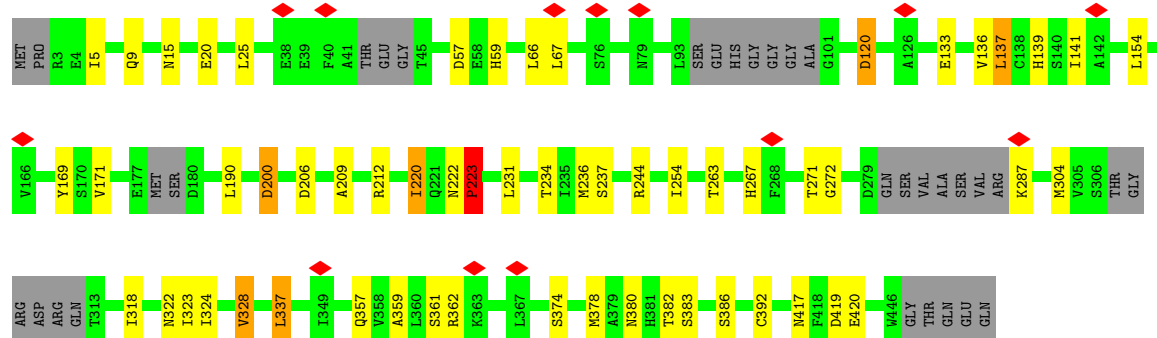
• Molecule 12: Tubulin gamma-1 chain





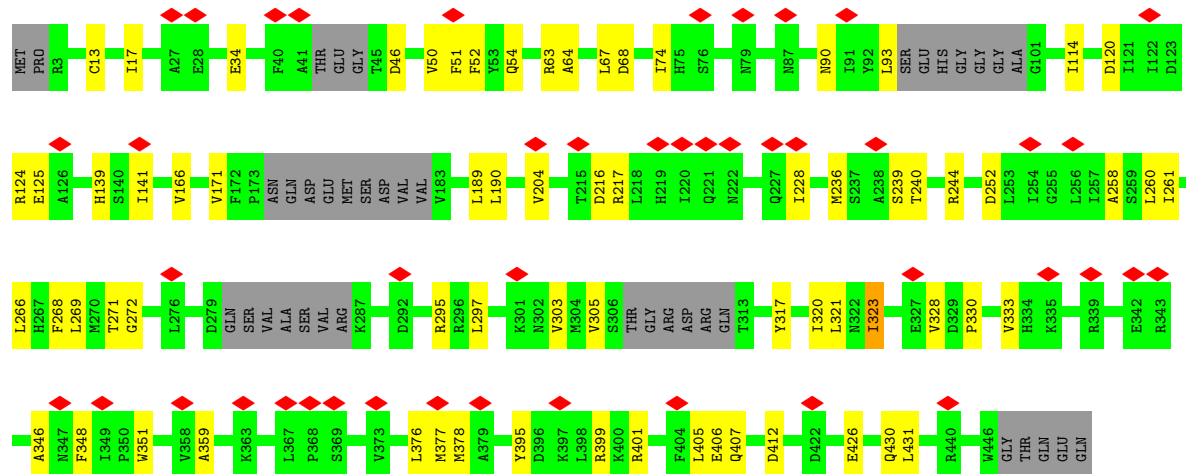
• Molecule 12: Tubulin gamma-1 chain

Chain e: 80% 11% 7%



• Molecule 12: Tubulin gamma-1 chain

Chain f: 10% 76% 15% 9%




• Molecule 12: Tubulin gamma-1 chain

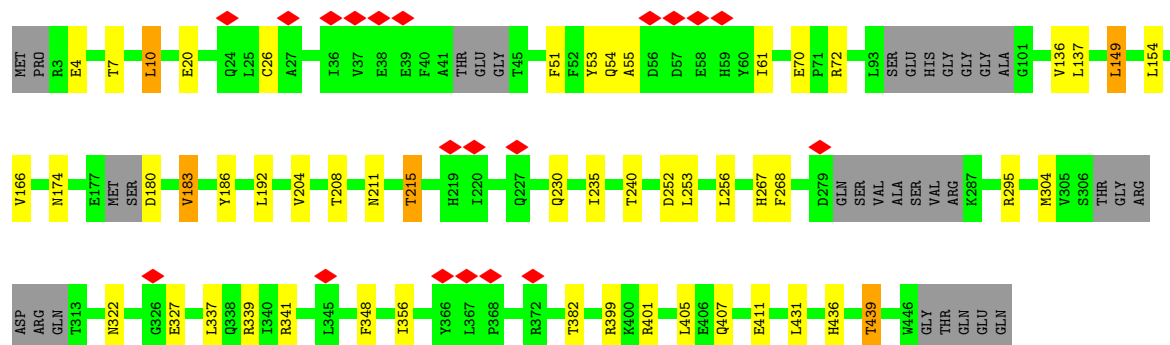
Chain g: 14% 77% 14% 7%






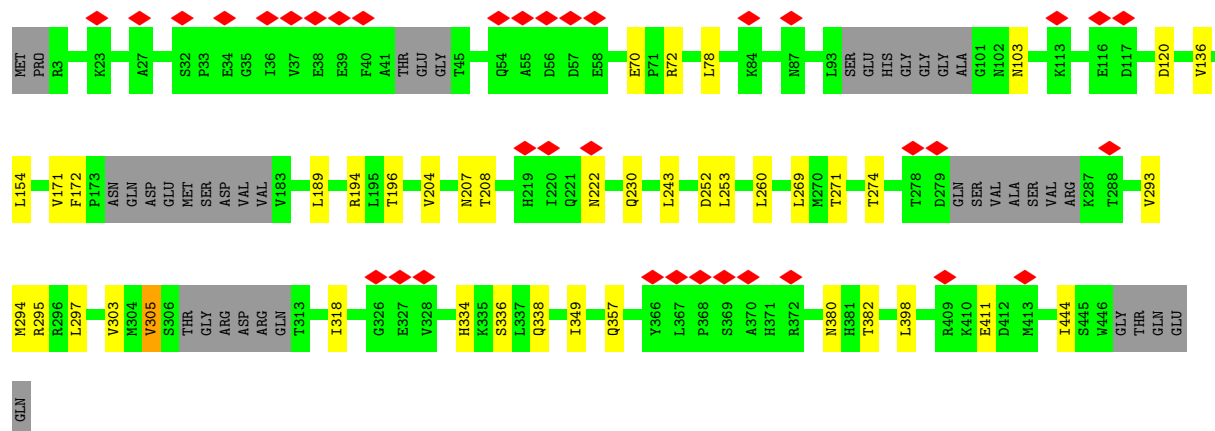
• Molecule 12: Tubulin gamma-1 chain

Chain j:  81% 10% 7%




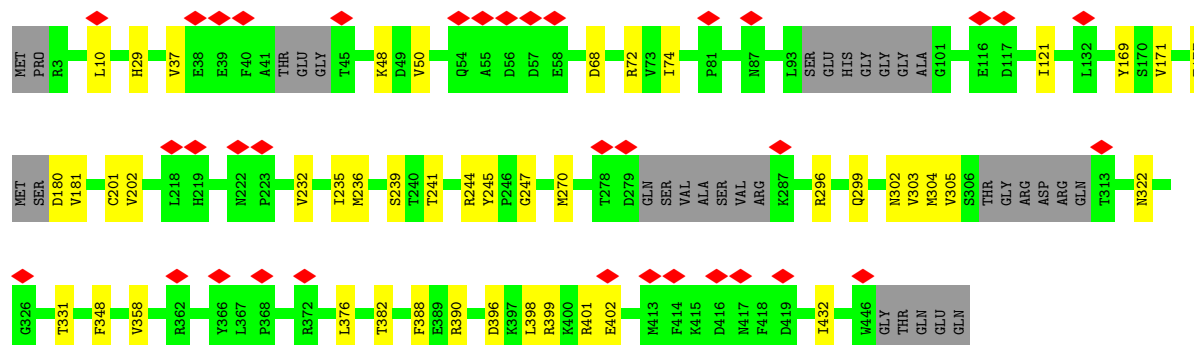
• Molecule 12: Tubulin gamma-1 chain

Chain k:  8% 82% 9% 9%

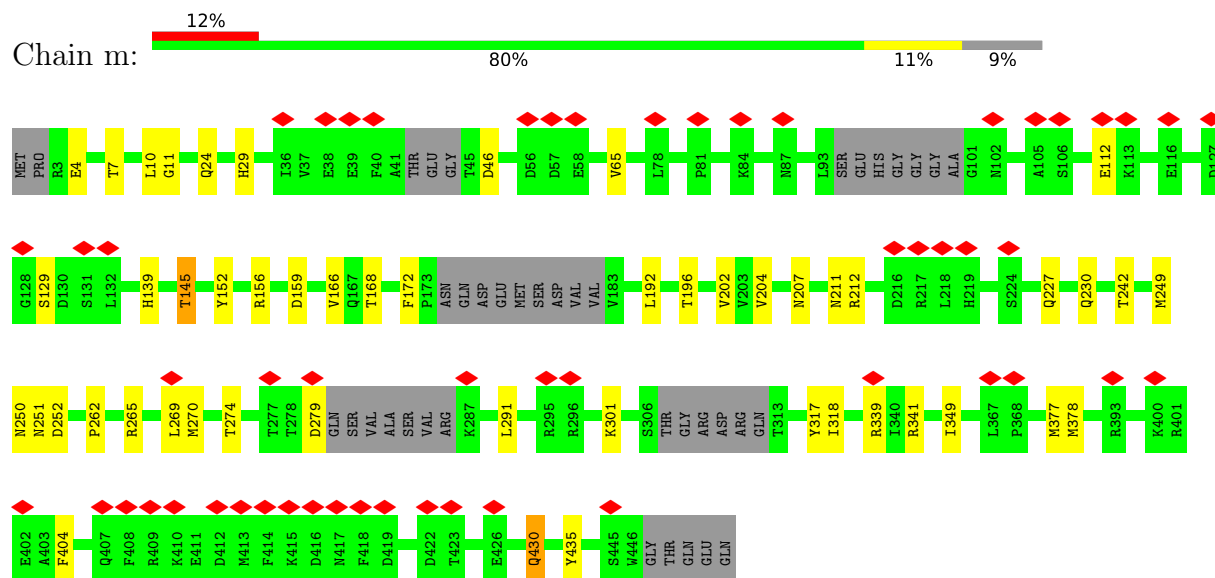


• Molecule 12: Tubulin gamma-1 chain

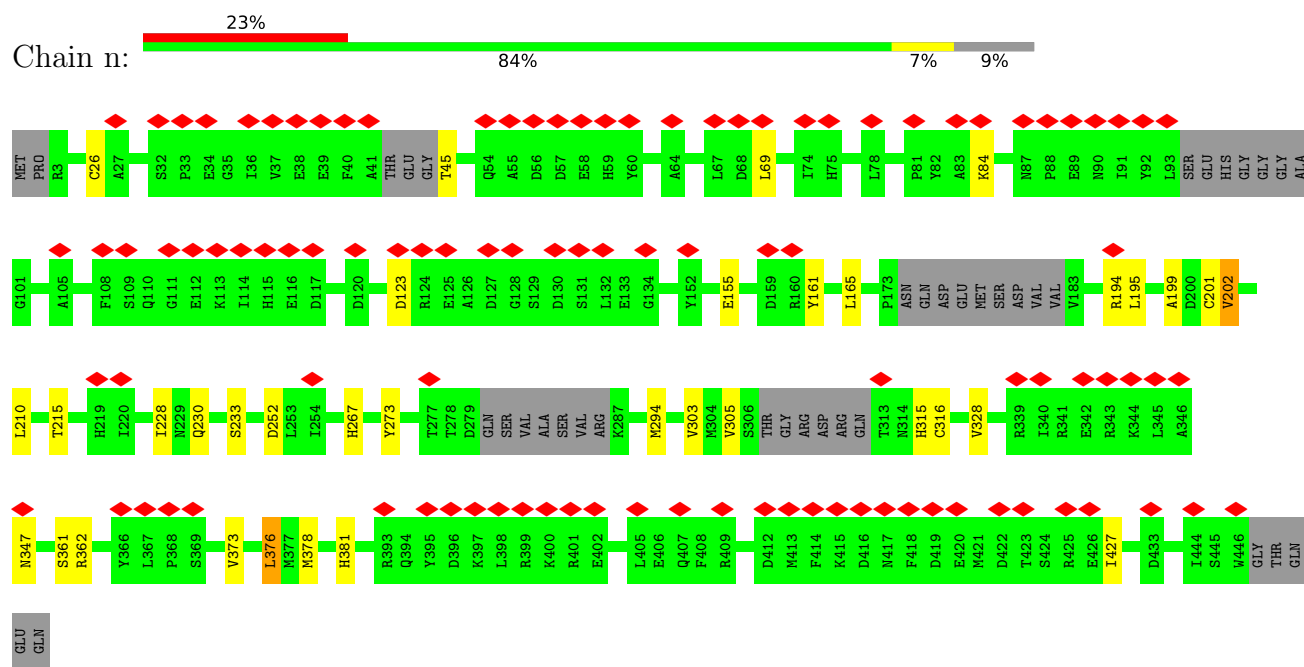
Chain l:  8% 83% 10% 7%



- Molecule 12: Tubulin gamma-1 chain



- Molecule 12: Tubulin gamma-1 chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	652699	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.01	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.018	Depositor
Minimum map value	-0.005	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0035	Depositor
Map size (Å)	576.63995, 576.63995, 576.63995	wwPDB
Map dimensions	544, 544, 544	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, GDP

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	3	0.29	0/844	0.55	0/1134
1	B	0.30	0/5328	0.56	0/7197
1	D	0.31	0/5121	0.53	0/6915
1	F	0.32	0/4897	0.55	0/6610
1	H	0.31	0/4897	0.52	0/6610
1	N	0.30	0/5316	0.49	0/7183
2	4	0.24	0/452	0.47	0/610
2	6	0.24	0/457	0.47	0/617
2	Y	0.31	0/426	0.58	0/574
3	5	0.25	0/356	0.46	0/478
3	L	0.37	1/5052 (0.0%)	0.55	0/6862
4	7	0.15	0/1848	0.33	0/2582
5	A	0.31	0/5742	0.55	0/7761
5	C	0.30	0/5748	0.53	0/7768
5	CN	0.23	0/910	0.48	0/1228
5	E	0.34	0/5432	0.56	0/7336
5	EN	0.26	0/910	0.55	0/1228
5	G	0.33	0/5432	0.56	0/7336
5	GN	0.24	0/910	0.49	0/1228
5	M	0.28	0/6901	0.54	0/9331
6	AC	0.28	0/316	0.48	0/417
6	CC	0.30	0/316	0.52	0/417
6	Cc	0.26	0/321	0.46	0/424
6	EC	0.29	0/300	0.50	0/396
6	Ec	0.27	0/264	0.46	0/350
6	GC	0.36	0/305	0.62	0/403
6	Gc	0.35	0/282	0.64	0/373
6	MC	0.31	0/289	0.48	0/382
6	Mc	0.34	0/290	0.53	0/383
7	BA	0.39	0/3473	0.71	0/4715
7	CA	0.28	1/3395 (0.0%)	0.48	0/4612
7	DA	0.28	0/3395	0.51	0/4612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	EA	0.29	0/3395	0.51	0/4612
7	FA	0.32	0/3395	0.55	0/4612
7	GA	0.33	0/3395	0.58	0/4612
7	HA	0.28	0/3395	0.52	0/4612
7	IA	0.29	1/3395 (0.0%)	0.55	0/4612
7	JA	0.28	0/3395	0.49	0/4612
7	KA	0.23	0/3395	0.44	0/4612
7	LA	0.24	0/3395	0.44	0/4612
8	BB	0.34	0/3381	0.64	0/4584
8	CB	0.23	0/3399	0.46	0/4605
8	DB	0.24	0/3393	0.45	0/4598
8	EB	0.26	0/3399	0.46	0/4605
8	FB	0.25	0/3399	0.45	0/4605
8	GB	0.24	0/3399	0.46	0/4605
8	HB	0.24	0/3399	0.46	0/4605
8	IB	0.23	0/3399	0.43	0/4605
8	JB	0.25	0/3399	0.44	0/4605
8	KB	0.25	0/3399	0.46	0/4605
8	LB	0.24	0/3399	0.44	0/4605
9	CM	0.23	0/412	0.44	0/554
9	EM	0.24	0/412	0.48	0/554
9	GM	0.25	0/401	0.43	0/540
9	MM	0.26	0/401	0.47	0/540
10	I	0.29	0/4319	0.52	0/5849
10	K	0.26	0/4600	0.49	0/6227
11	J	0.37	2/4875 (0.0%)	0.56	0/6609
11	Z	0.26	0/1032	0.45	0/1399
12	a	0.36	0/3381	0.60	0/4579
12	b	0.28	0/3381	0.55	0/4579
12	c	0.32	0/3381	0.55	0/4579
12	d	0.32	0/3437	0.56	0/4656
12	e	0.34	0/3431	0.62	0/4649
12	f	0.35	0/3381	0.58	0/4579
12	g	0.38	0/3419	0.63	0/4635
12	h	0.36	0/3375	0.60	0/4572
12	i	0.30	0/3437	0.56	0/4656
12	j	0.29	0/3431	0.54	0/4649
12	k	0.27	0/3379	0.50	0/4576
12	l	0.26	0/3435	0.52	0/4653
12	m	0.29	0/3381	0.54	0/4579
12	n	0.26	0/3381	0.50	0/4579
All	All	0.30	5/208532 (0.0%)	0.53	0/282387

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	1767	HIS	C-N	14.38	1.45	1.33
11	J	470	ARG	C-N	12.18	1.44	1.33
11	J	489	ALA	C-N	-7.00	1.23	1.33
7	IA	323	VAL	C-N	-5.64	1.28	1.33
7	CA	324	VAL	C-N	5.06	1.39	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3	832	861	860	5	0
1	B	5219	5183	5181	39	0
1	D	5017	5000	4996	38	0
1	F	4796	4780	4775	43	0
1	H	4796	4780	4775	46	0
1	N	5207	5161	5159	16	0
2	4	452	474	473	2	0
2	6	457	479	478	2	0
2	Y	426	451	450	2	0
3	5	355	382	380	2	0
3	L	4919	4954	4951	26	0
4	7	1832	932	928	2	0
5	A	5623	5617	5631	17	0
5	C	5629	5629	5642	32	0
5	CN	896	907	907	2	0
5	E	5320	5347	5357	37	0
5	EN	896	907	907	5	0
5	G	5320	5346	5357	39	0
5	GN	896	907	907	3	0
5	M	6766	6768	6780	40	0
6	AC	313	318	317	0	0
6	CC	313	318	317	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Cc	317	315	314	2	0
6	EC	297	300	299	2	0
6	Ec	261	259	258	0	0
6	GC	302	305	304	1	0
6	Gc	279	277	277	1	0
6	MC	286	287	286	2	0
6	Mc	287	287	286	1	0
7	BA	3400	3275	3294	44	0
7	CA	3322	3230	3229	11	0
7	DA	3322	3230	3229	15	0
7	EA	3322	3231	3229	25	0
7	FA	3322	3230	3229	21	0
7	GA	3322	3222	3229	34	0
7	HA	3322	3230	3229	16	0
7	IA	3322	3231	3229	12	0
7	JA	3322	3229	3229	18	0
7	KA	3322	3231	3229	19	0
7	LA	3322	3230	3229	11	0
8	BB	3336	3189	3187	31	0
8	CB	3354	3222	3220	15	0
8	DB	3348	3211	3209	14	0
8	EB	3354	3223	3220	21	0
8	FB	3354	3222	3220	12	0
8	GB	3354	3222	3220	13	0
8	HB	3354	3223	3220	14	0
8	IB	3354	3223	3220	16	0
8	JB	3354	3223	3220	14	0
8	KB	3354	3222	3220	13	0
8	LB	3354	3222	3220	13	0
9	CM	408	429	428	0	0
9	EM	408	429	428	3	0
9	GM	397	416	415	0	0
9	MM	397	416	415	4	0
10	I	4222	4255	4250	15	0
10	K	4497	4509	4507	18	0
11	J	4773	4748	4742	19	0
11	Z	1006	982	981	4	0
12	a	3313	3282	3276	27	0
12	b	3313	3282	3276	28	0
12	c	3313	3283	3276	27	0
12	d	3369	3328	3322	23	0
12	e	3363	3317	3311	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	f	3313	3282	3276	36	0
12	g	3351	3295	3289	43	0
12	h	3307	3271	3265	37	0
12	i	3369	3328	3322	30	0
12	j	3363	3317	3311	22	0
12	k	3311	3277	3271	21	0
12	l	3367	3324	3317	24	0
12	m	3313	3283	3276	21	0
12	n	3313	3282	3276	12	0
13	BA	32	12	12	0	0
13	CA	32	12	12	0	0
13	DA	32	12	12	0	0
13	EA	32	12	12	0	0
13	FA	32	12	12	0	0
13	GA	32	12	12	0	0
13	HA	32	12	12	0	0
13	IA	32	12	12	0	0
13	JA	32	12	12	0	0
13	KA	32	12	12	0	0
13	LA	32	12	12	0	0
All	All	204937	200969	200874	1132	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 3.

The worst 5 of 1132 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:696:TYR:HH	5:G:853:ALA:N	1.78	0.80
12:e:383:SER:O	12:e:386:SER:OG	2.01	0.78
1:F:681:ARG:NH1	12:f:261:ILE:O	2.17	0.78
12:h:56:ASP:OD1	12:i:287:LYS:N	2.17	0.77
12:d:415:LYS:NZ	12:d:419:ASP:OD1	2.15	0.77

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	3	100/907 (11%)	94 (94%)	6 (6%)	0	100	100
1	B	631/907 (70%)	585 (93%)	46 (7%)	0	100	100
1	D	602/907 (66%)	572 (95%)	29 (5%)	1 (0%)	43	71
1	F	571/907 (63%)	544 (95%)	25 (4%)	2 (0%)	30	60
1	H	571/907 (63%)	550 (96%)	20 (4%)	1 (0%)	43	71
1	N	631/907 (70%)	604 (96%)	26 (4%)	1 (0%)	43	71
2	4	58/82 (71%)	57 (98%)	1 (2%)	0	100	100
2	6	59/82 (72%)	59 (100%)	0	0	100	100
2	Y	54/82 (66%)	52 (96%)	2 (4%)	0	100	100
3	5	42/1819 (2%)	42 (100%)	0	0	100	100
3	L	610/1819 (34%)	567 (93%)	43 (7%)	0	100	100
4	7	360/374 (96%)	357 (99%)	3 (1%)	0	100	100
5	A	693/902 (77%)	645 (93%)	42 (6%)	6 (1%)	14	45
5	C	693/902 (77%)	646 (93%)	44 (6%)	3 (0%)	30	60
5	CN	109/902 (12%)	103 (94%)	6 (6%)	0	100	100
5	E	644/902 (71%)	591 (92%)	52 (8%)	1 (0%)	43	71
5	EN	109/902 (12%)	104 (95%)	5 (5%)	0	100	100
5	G	644/902 (71%)	598 (93%)	44 (7%)	2 (0%)	36	65
5	GN	109/902 (12%)	103 (94%)	5 (5%)	1 (1%)	14	45
5	M	842/902 (93%)	793 (94%)	46 (6%)	3 (0%)	30	60
6	AC	33/229 (14%)	33 (100%)	0	0	100	100
6	CC	33/229 (14%)	33 (100%)	0	0	100	100
6	Cc	33/229 (14%)	32 (97%)	1 (3%)	0	100	100
6	EC	31/229 (14%)	30 (97%)	1 (3%)	0	100	100
6	Ec	27/229 (12%)	27 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	GC	32/229 (14%)	32 (100%)	0	0	100	100
6	Gc	29/229 (13%)	29 (100%)	0	0	100	100
6	MC	30/229 (13%)	29 (97%)	0	1 (3%)	3	24
6	Mc	30/229 (13%)	30 (100%)	0	0	100	100
7	BA	434/451 (96%)	375 (86%)	54 (12%)	5 (1%)	10	39
7	CA	424/451 (94%)	408 (96%)	14 (3%)	2 (0%)	24	56
7	DA	424/451 (94%)	405 (96%)	18 (4%)	1 (0%)	43	71
7	EA	424/451 (94%)	408 (96%)	15 (4%)	1 (0%)	43	71
7	FA	424/451 (94%)	398 (94%)	23 (5%)	3 (1%)	18	50
7	GA	424/451 (94%)	401 (95%)	18 (4%)	5 (1%)	10	39
7	HA	424/451 (94%)	404 (95%)	19 (4%)	1 (0%)	43	71
7	IA	424/451 (94%)	408 (96%)	15 (4%)	1 (0%)	43	71
7	JA	424/451 (94%)	396 (93%)	25 (6%)	3 (1%)	18	50
7	KA	424/451 (94%)	412 (97%)	10 (2%)	2 (0%)	24	56
7	LA	424/451 (94%)	412 (97%)	12 (3%)	0	100	100
8	BB	421/451 (93%)	382 (91%)	36 (9%)	3 (1%)	18	50
8	CB	421/451 (93%)	410 (97%)	11 (3%)	0	100	100
8	DB	421/451 (93%)	412 (98%)	9 (2%)	0	100	100
8	EB	421/451 (93%)	407 (97%)	14 (3%)	0	100	100
8	FB	421/451 (93%)	413 (98%)	8 (2%)	0	100	100
8	GB	421/451 (93%)	416 (99%)	5 (1%)	0	100	100
8	HB	421/451 (93%)	408 (97%)	13 (3%)	0	100	100
8	IB	421/451 (93%)	415 (99%)	6 (1%)	0	100	100
8	JB	421/451 (93%)	410 (97%)	11 (3%)	0	100	100
8	KB	421/451 (93%)	409 (97%)	12 (3%)	0	100	100
8	LB	421/451 (93%)	414 (98%)	7 (2%)	0	100	100
9	CM	52/158 (33%)	51 (98%)	1 (2%)	0	100	100
9	EM	52/158 (33%)	50 (96%)	2 (4%)	0	100	100
9	GM	51/158 (32%)	50 (98%)	1 (2%)	0	100	100
9	MM	51/158 (32%)	49 (96%)	2 (4%)	0	100	100
10	I	511/667 (77%)	480 (94%)	29 (6%)	2 (0%)	30	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	K	539/667 (81%)	518 (96%)	19 (4%)	2 (0%)	30	60
11	J	580/1024 (57%)	546 (94%)	30 (5%)	4 (1%)	18	50
11	Z	122/1024 (12%)	119 (98%)	3 (2%)	0	100	100
12	a	400/451 (89%)	359 (90%)	41 (10%)	0	100	100
12	b	400/451 (89%)	354 (88%)	46 (12%)	0	100	100
12	c	400/451 (89%)	380 (95%)	18 (4%)	2 (0%)	24	56
12	d	407/451 (90%)	380 (93%)	26 (6%)	1 (0%)	43	71
12	e	407/451 (90%)	376 (92%)	29 (7%)	2 (0%)	24	56
12	f	400/451 (89%)	380 (95%)	19 (5%)	1 (0%)	36	65
12	g	407/451 (90%)	374 (92%)	30 (7%)	3 (1%)	18	50
12	h	400/451 (89%)	374 (94%)	26 (6%)	0	100	100
12	i	407/451 (90%)	380 (93%)	25 (6%)	2 (0%)	24	56
12	j	407/451 (90%)	370 (91%)	36 (9%)	1 (0%)	43	71
12	k	400/451 (89%)	372 (93%)	27 (7%)	1 (0%)	36	65
12	l	407/451 (90%)	377 (93%)	29 (7%)	1 (0%)	43	71
12	m	400/451 (89%)	368 (92%)	30 (8%)	2 (0%)	24	56
12	n	400/451 (89%)	381 (95%)	19 (5%)	0	100	100
All	All	25315/39227 (64%)	23952 (95%)	1290 (5%)	73 (0%)	37	65

5 of 73 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	604	ASP
5	A	858	ARG
7	BA	52	PHE
7	BA	164	LYS
7	BA	177	VAL

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	3	91/798 (11%)	87 (96%)	4 (4%)	25	49
1	B	570/798 (71%)	539 (95%)	31 (5%)	20	46
1	D	548/798 (69%)	527 (96%)	21 (4%)	29	52
1	F	525/798 (66%)	502 (96%)	23 (4%)	25	49
1	H	525/798 (66%)	493 (94%)	32 (6%)	17	43
1	N	568/798 (71%)	545 (96%)	23 (4%)	28	52
2	4	51/62 (82%)	49 (96%)	2 (4%)	28	52
2	6	51/62 (82%)	50 (98%)	1 (2%)	48	64
2	Y	49/62 (79%)	38 (78%)	11 (22%)	1	6
3	5	40/1546 (3%)	38 (95%)	2 (5%)	22	47
3	L	539/1546 (35%)	521 (97%)	18 (3%)	33	55
4	7	18/317 (6%)	18 (100%)	0	100	100
5	A	618/791 (78%)	600 (97%)	18 (3%)	37	57
5	C	619/791 (78%)	598 (97%)	21 (3%)	32	54
5	CN	99/791 (12%)	95 (96%)	4 (4%)	28	52
5	E	585/791 (74%)	559 (96%)	26 (4%)	25	49
5	EN	99/791 (12%)	90 (91%)	9 (9%)	9	32
5	G	585/791 (74%)	564 (96%)	21 (4%)	31	54
5	GN	99/791 (12%)	95 (96%)	4 (4%)	28	52
5	M	744/791 (94%)	713 (96%)	31 (4%)	26	50
6	AC	34/207 (16%)	33 (97%)	1 (3%)	37	57
6	CC	34/207 (16%)	33 (97%)	1 (3%)	37	57
6	Cc	35/207 (17%)	35 (100%)	0	100	100
6	EC	33/207 (16%)	30 (91%)	3 (9%)	9	32
6	Ec	29/207 (14%)	27 (93%)	2 (7%)	14	41
6	GC	33/207 (16%)	31 (94%)	2 (6%)	17	43
6	Gc	31/207 (15%)	30 (97%)	1 (3%)	34	55
6	MC	32/207 (16%)	30 (94%)	2 (6%)	16	43
6	Mc	32/207 (16%)	30 (94%)	2 (6%)	16	43
7	BA	364/379 (96%)	328 (90%)	36 (10%)	7	30
7	CA	355/379 (94%)	347 (98%)	8 (2%)	44	62
7	DA	355/379 (94%)	342 (96%)	13 (4%)	30	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	EA	355/379 (94%)	346 (98%)	9 (2%)	42	60
7	FA	355/379 (94%)	346 (98%)	9 (2%)	42	60
7	GA	355/379 (94%)	339 (96%)	16 (4%)	24	49
7	HA	355/379 (94%)	350 (99%)	5 (1%)	59	70
7	IA	355/379 (94%)	342 (96%)	13 (4%)	30	53
7	JA	355/379 (94%)	344 (97%)	11 (3%)	35	56
7	KA	355/379 (94%)	349 (98%)	6 (2%)	53	67
7	LA	355/379 (94%)	344 (97%)	11 (3%)	35	56
8	BB	360/386 (93%)	325 (90%)	35 (10%)	8	30
8	CB	363/386 (94%)	352 (97%)	11 (3%)	36	57
8	DB	362/386 (94%)	350 (97%)	12 (3%)	33	55
8	EB	363/386 (94%)	355 (98%)	8 (2%)	45	62
8	FB	363/386 (94%)	353 (97%)	10 (3%)	38	58
8	GB	363/386 (94%)	353 (97%)	10 (3%)	38	58
8	HB	363/386 (94%)	356 (98%)	7 (2%)	50	65
8	IB	363/386 (94%)	354 (98%)	9 (2%)	42	60
8	JB	363/386 (94%)	359 (99%)	4 (1%)	65	72
8	KB	363/386 (94%)	357 (98%)	6 (2%)	53	67
8	LB	363/386 (94%)	361 (99%)	2 (1%)	78	79
9	CM	44/118 (37%)	42 (96%)	2 (4%)	24	49
9	EM	44/118 (37%)	43 (98%)	1 (2%)	44	62
9	GM	43/118 (36%)	42 (98%)	1 (2%)	44	62
9	MM	43/118 (36%)	41 (95%)	2 (5%)	23	48
10	I	471/594 (79%)	449 (95%)	22 (5%)	23	48
10	K	499/594 (84%)	485 (97%)	14 (3%)	38	58
11	J	523/933 (56%)	507 (97%)	16 (3%)	35	56
11	Z	111/933 (12%)	109 (98%)	2 (2%)	51	66
12	a	369/400 (92%)	348 (94%)	21 (6%)	18	45
12	b	369/400 (92%)	350 (95%)	19 (5%)	21	47
12	c	369/400 (92%)	353 (96%)	16 (4%)	26	50
12	d	376/400 (94%)	360 (96%)	16 (4%)	26	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	e	375/400 (94%)	352 (94%)	23 (6%)	17	43
12	f	369/400 (92%)	354 (96%)	15 (4%)	27	51
12	g	373/400 (93%)	347 (93%)	26 (7%)	14	41
12	h	368/400 (92%)	347 (94%)	21 (6%)	18	45
12	i	376/400 (94%)	364 (97%)	12 (3%)	34	55
12	j	375/400 (94%)	352 (94%)	23 (6%)	17	43
12	k	368/400 (92%)	357 (97%)	11 (3%)	36	57
12	l	375/400 (94%)	367 (98%)	8 (2%)	47	63
12	m	369/400 (92%)	355 (96%)	14 (4%)	29	52
12	n	369/400 (92%)	354 (96%)	15 (4%)	27	51
All	All	22197/34115 (65%)	21330 (96%)	867 (4%)	30	52

5 of 867 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	IB	293	MET
5	M	442	PHE
12	j	70	GLU
11	J	803	TYR
8	IB	217	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 190 such sidechains are listed below:

Mol	Chain	Res	Type
8	KB	43	GLN
12	b	222	ASN
3	L	1547	GLN
5	M	152	GLN
12	c	207	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

11 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GDP	DB	501	-	28,30,30	3.36	13 (46%)	44,47,47	1.75	10 (22%)
8	GDP	FB	501	-	28,30,30	3.37	13 (46%)	44,47,47	1.81	11 (25%)
8	GDP	JB	501	-	28,30,30	3.35	13 (46%)	44,47,47	1.77	11 (25%)
8	GDP	CB	501	-	28,30,30	3.34	13 (46%)	44,47,47	1.74	10 (22%)
8	GDP	HB	501	-	28,30,30	3.37	13 (46%)	44,47,47	1.76	10 (22%)
8	GDP	IB	501	-	28,30,30	3.36	13 (46%)	44,47,47	1.80	11 (25%)
8	GDP	LB	501	-	28,30,30	3.36	13 (46%)	44,47,47	1.78	11 (25%)
8	GDP	EB	501	-	28,30,30	3.36	13 (46%)	44,47,47	1.79	11 (25%)
8	GDP	BB	501	-	28,30,30	3.30	14 (50%)	44,47,47	1.63	10 (22%)
8	GDP	GB	501	-	28,30,30	3.37	13 (46%)	44,47,47	1.86	12 (27%)
8	GDP	KB	501	-	28,30,30	3.35	13 (46%)	44,47,47	1.79	11 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GDP	DB	501	-	-	2/16/32/32	0/3/3/3
8	GDP	FB	501	-	-	0/16/32/32	0/3/3/3
8	GDP	JB	501	-	-	4/16/32/32	0/3/3/3
8	GDP	CB	501	-	-	4/16/32/32	0/3/3/3
8	GDP	HB	501	-	-	5/16/32/32	0/3/3/3
8	GDP	IB	501	-	-	2/16/32/32	0/3/3/3
8	GDP	LB	501	-	-	3/16/32/32	0/3/3/3
8	GDP	EB	501	-	-	1/16/32/32	0/3/3/3
8	GDP	BB	501	-	-	5/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GDP	GB	501	-	-	3/16/32/32	0/3/3/3
8	GDP	KB	501	-	-	2/16/32/32	0/3/3/3

The worst 5 of 144 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	LB	501	GDP	C3'-C4'	-8.87	1.30	1.53
8	HB	501	GDP	C3'-C4'	-8.85	1.30	1.53
8	GB	501	GDP	C3'-C4'	-8.82	1.30	1.53
8	IB	501	GDP	C3'-C4'	-8.79	1.30	1.53
8	FB	501	GDP	C3'-C4'	-8.78	1.30	1.53

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	HB	501	GDP	C5-C4-N3	-5.37	119.75	128.46
8	GB	501	GDP	C5-C4-N3	-5.20	120.03	128.46
8	EB	501	GDP	C5-C4-N3	-5.11	120.16	128.46
8	IB	501	GDP	C5-C4-N3	-5.11	120.17	128.46
8	KB	501	GDP	C5-C4-N3	-5.10	120.19	128.46

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	BB	501	GDP	PA-O3A-PB-O3B
8	BB	501	GDP	C5'-O5'-PA-O3A
8	BB	501	GDP	C5'-O5'-PA-O1A
8	BB	501	GDP	C5'-O5'-PA-O2A
8	CB	501	GDP	C5'-O5'-PA-O3A

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	BB	501	GDP	1	0
8	KB	501	GDP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
13	GTP	BA	501	-	30,34,34	0.55	0	46,54,54	0.54	0
13	GTP	IA	501	-	30,34,34	0.55	0	46,54,54	0.58	0
13	GTP	FA	501	-	30,34,34	0.54	0	46,54,54	0.55	0
13	GTP	JA	501	-	30,34,34	0.54	0	46,54,54	0.58	0
13	GTP	CA	501	-	30,34,34	0.55	0	46,54,54	0.64	0
13	GTP	EA	501	-	30,34,34	0.58	0	46,54,54	0.59	0
13	GTP	DA	501	-	30,34,34	0.57	0	46,54,54	0.64	0
13	GTP	HA	501	-	30,34,34	0.55	0	46,54,54	0.61	0
13	GTP	GA	501	-	30,34,34	0.54	0	46,54,54	0.49	0
13	GTP	KA	501	-	30,34,34	0.54	0	46,54,54	0.54	0
13	GTP	LA	501	-	30,34,34	0.54	0	46,54,54	0.54	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	GTP	BA	501	-	-	0/22/38/38	0/3/3/3
13	GTP	IA	501	-	-	3/22/38/38	0/3/3/3
13	GTP	FA	501	-	-	2/22/38/38	0/3/3/3
13	GTP	JA	501	-	-	4/22/38/38	0/3/3/3
13	GTP	CA	501	-	-	1/22/38/38	0/3/3/3
13	GTP	EA	501	-	-	3/22/38/38	0/3/3/3
13	GTP	DA	501	-	-	0/22/38/38	0/3/3/3
13	GTP	HA	501	-	-	4/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	GTP	GA	501	-	-	2/22/38/38	0/3/3/3
13	GTP	KA	501	-	-	2/22/38/38	0/3/3/3
13	GTP	LA	501	-	-	2/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

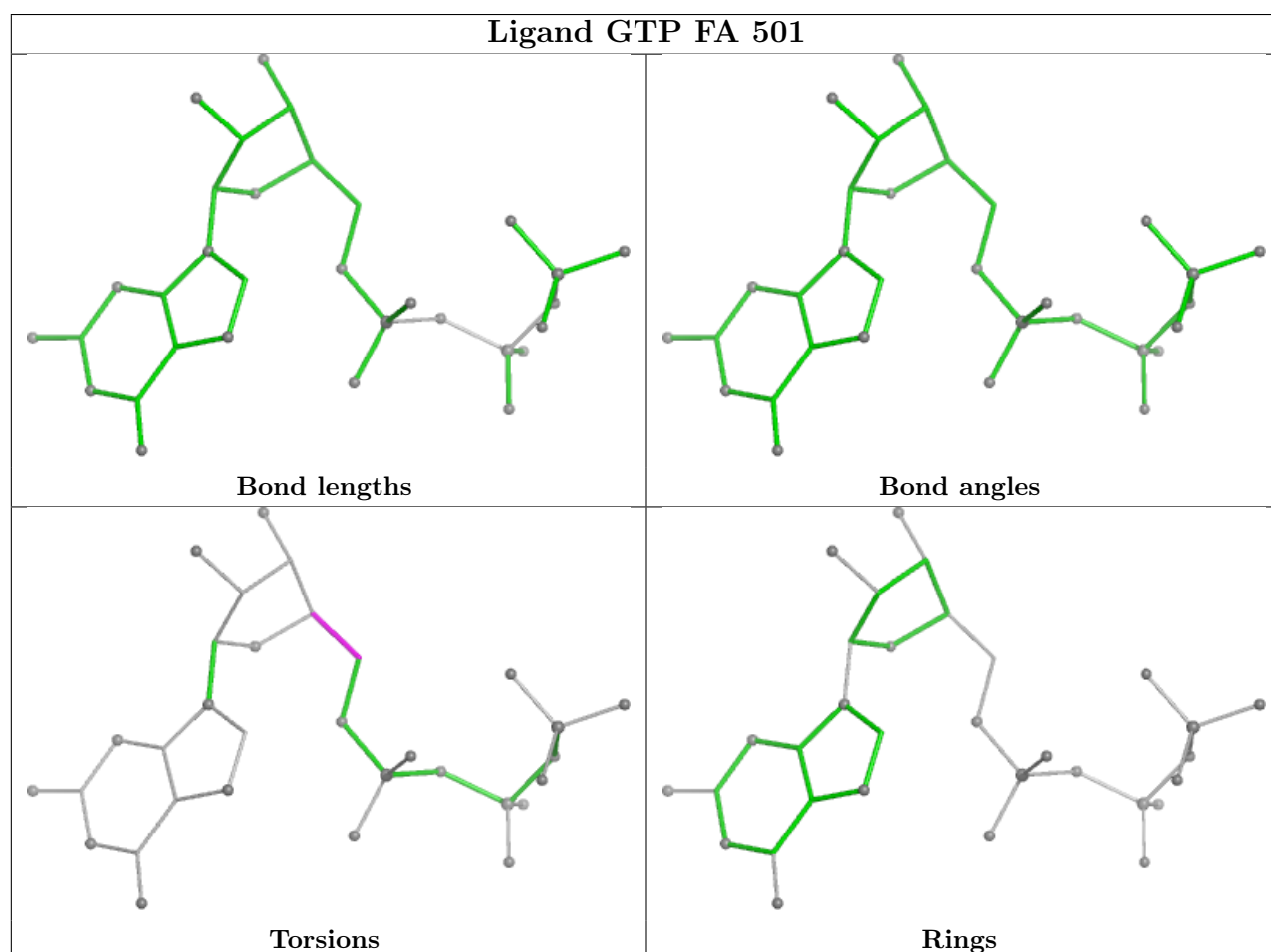
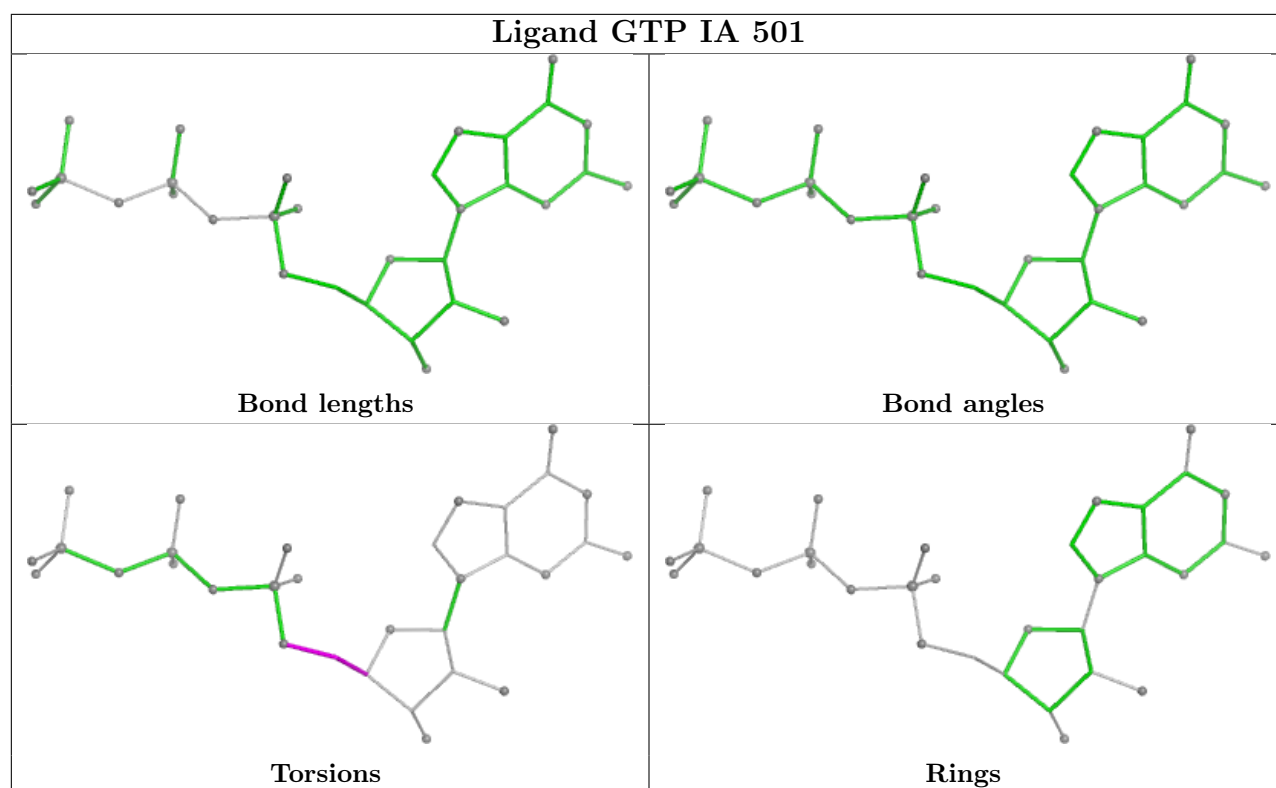
5 of 23 torsion outliers are listed below:

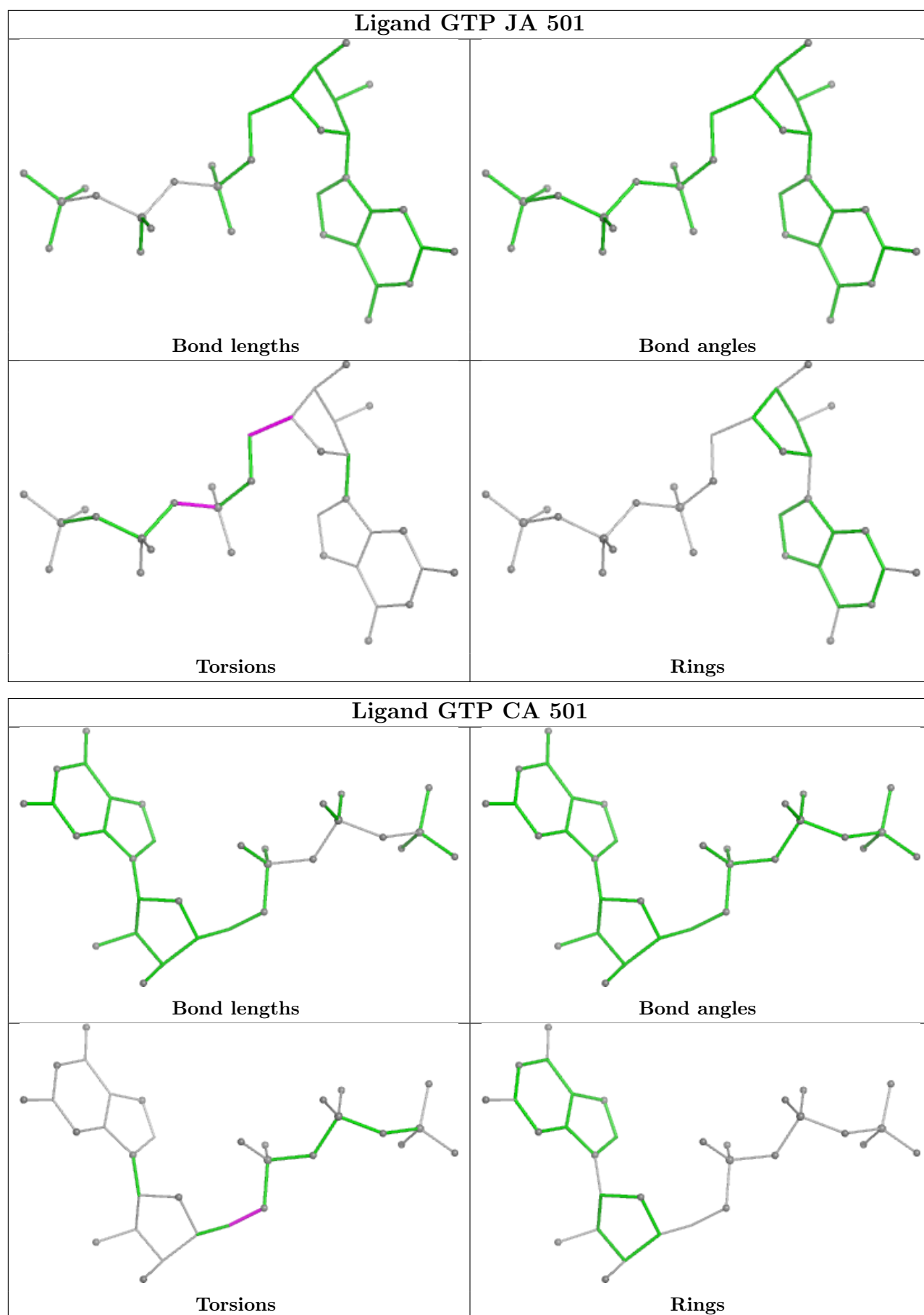
Mol	Chain	Res	Type	Atoms
13	FA	501	GTP	O4'-C4'-C5'-O5'
13	FA	501	GTP	C3'-C4'-C5'-O5'
13	GA	501	GTP	O4'-C4'-C5'-O5'
13	GA	501	GTP	C3'-C4'-C5'-O5'
13	HA	501	GTP	C5'-O5'-PA-O1A

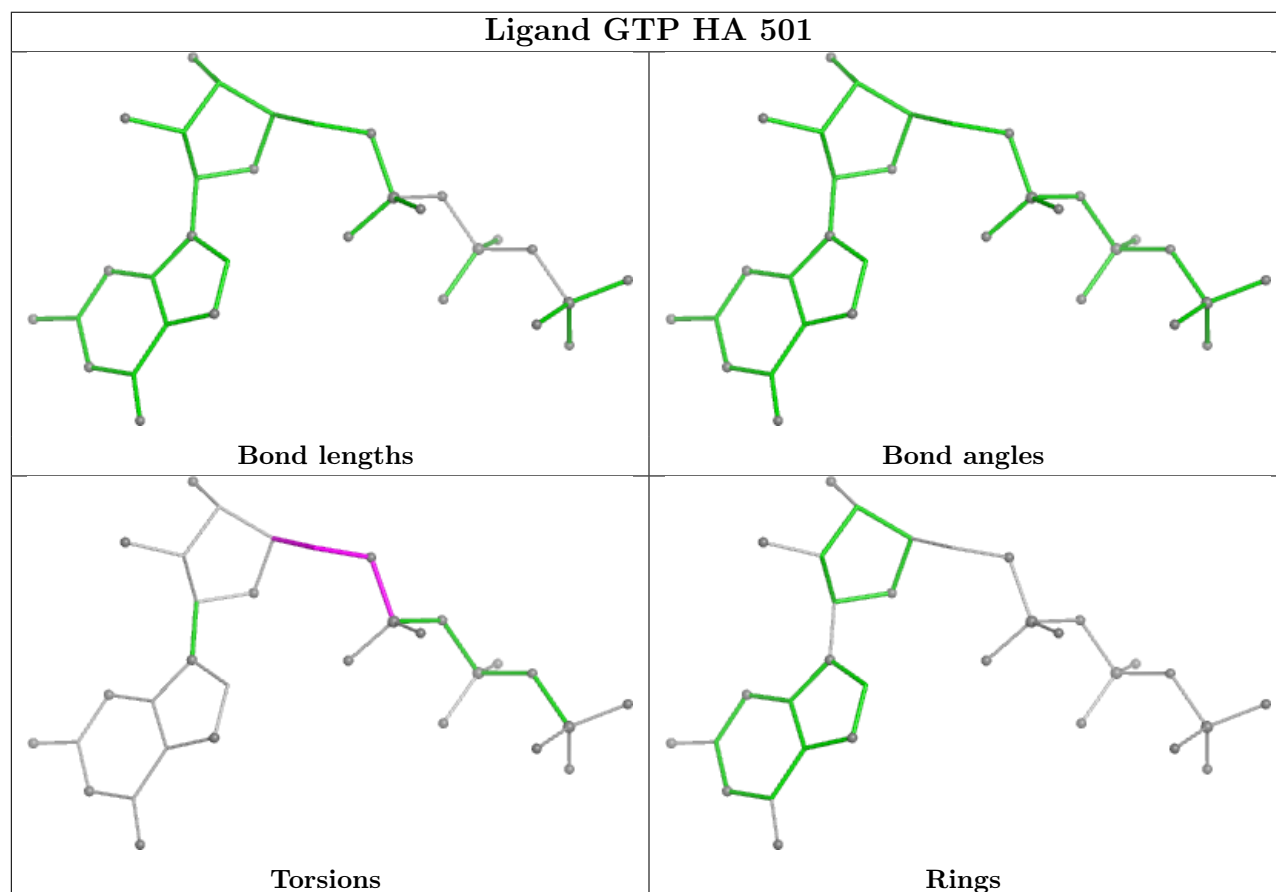
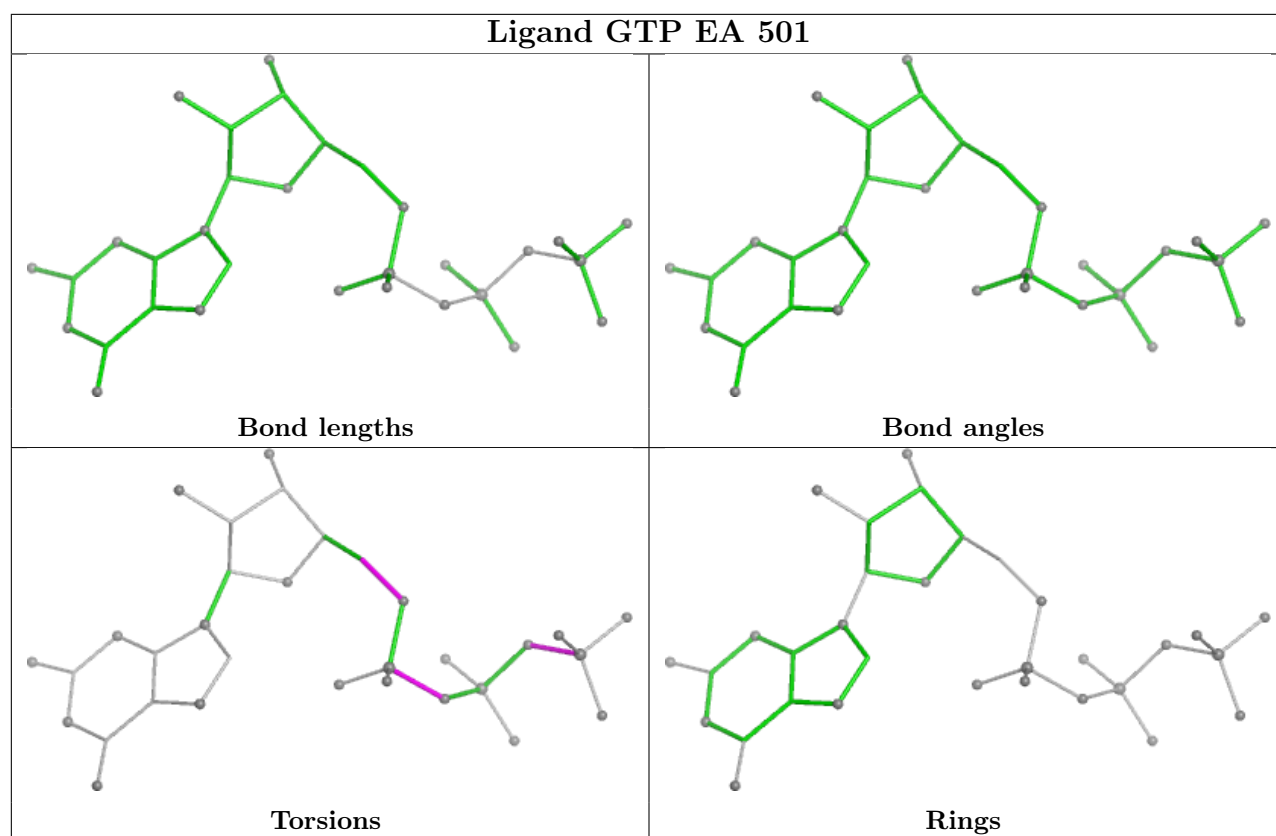
There are no ring outliers.

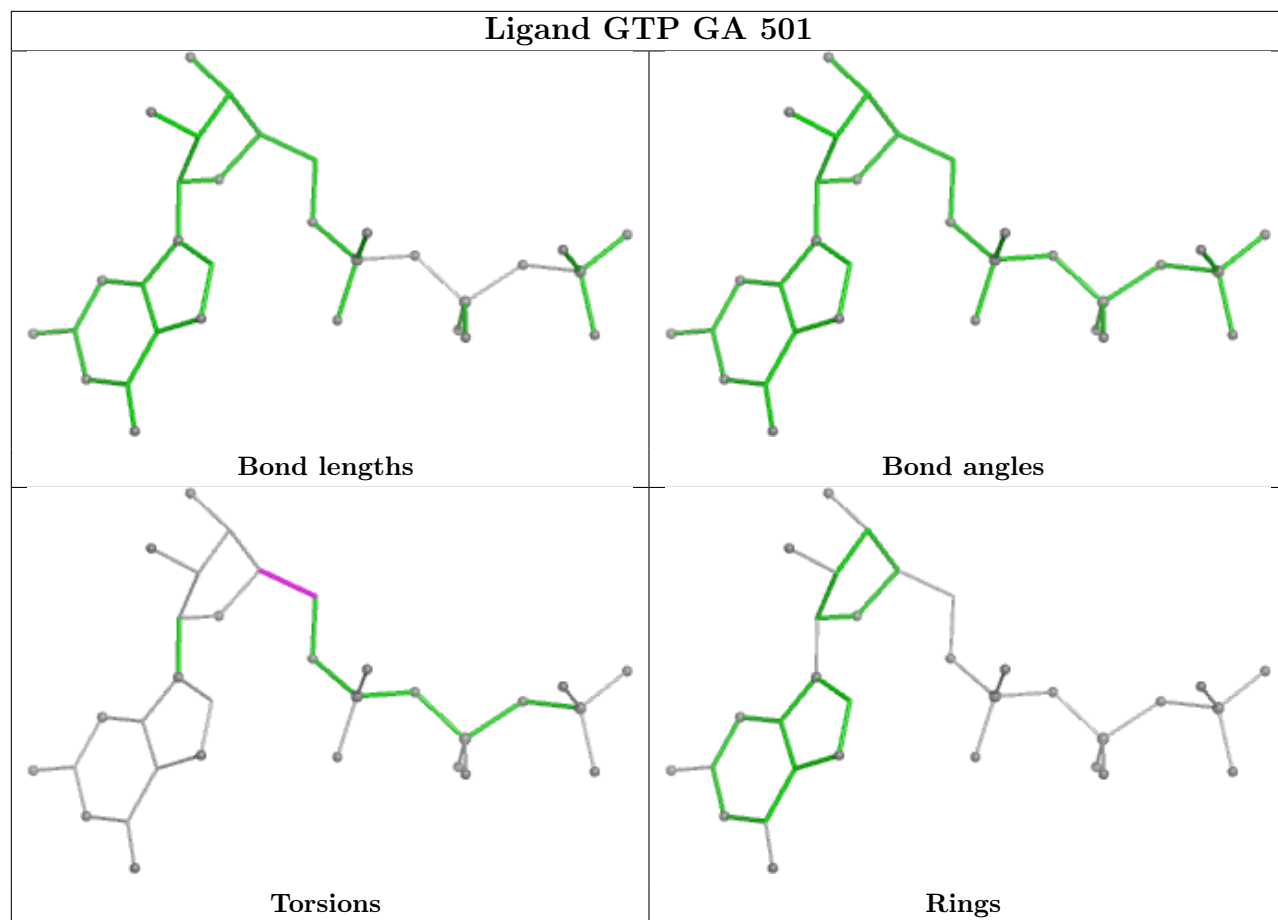
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

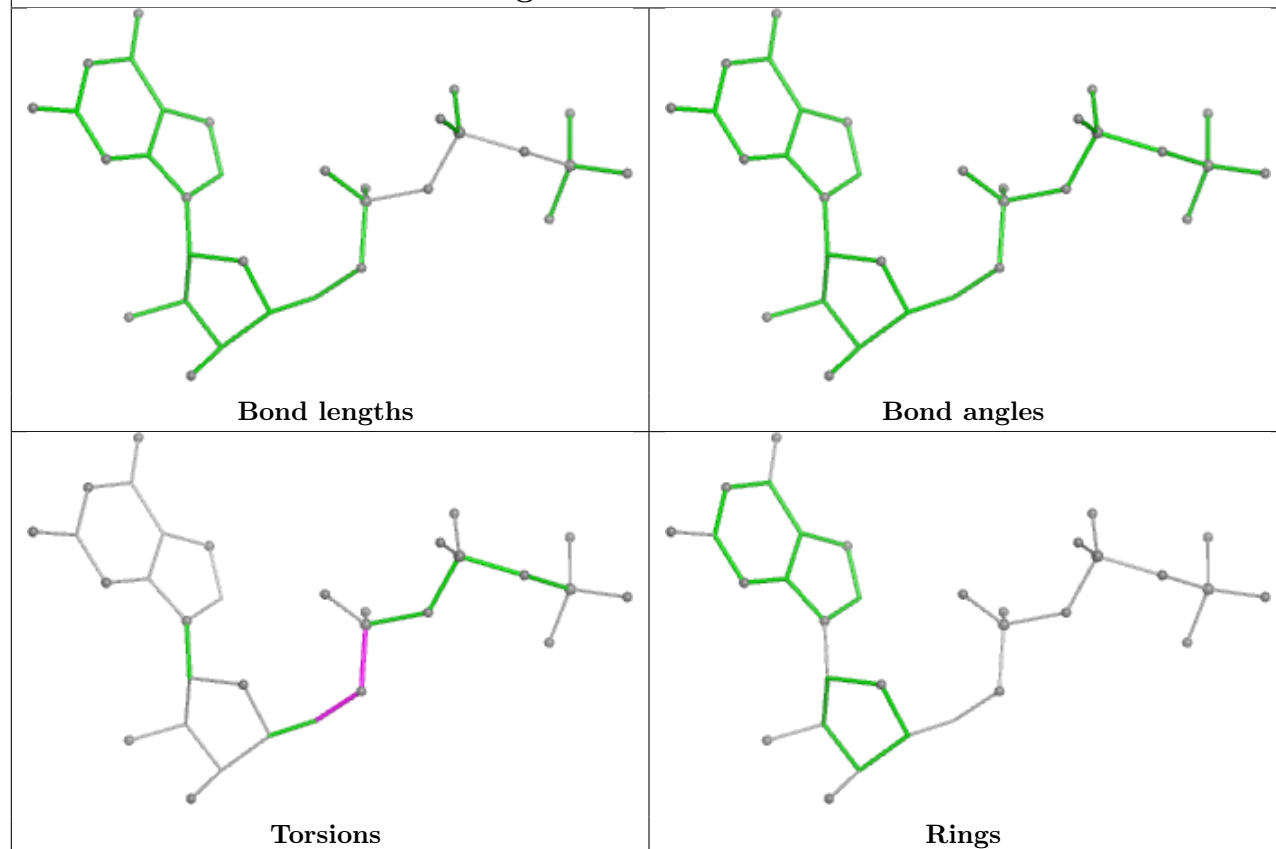




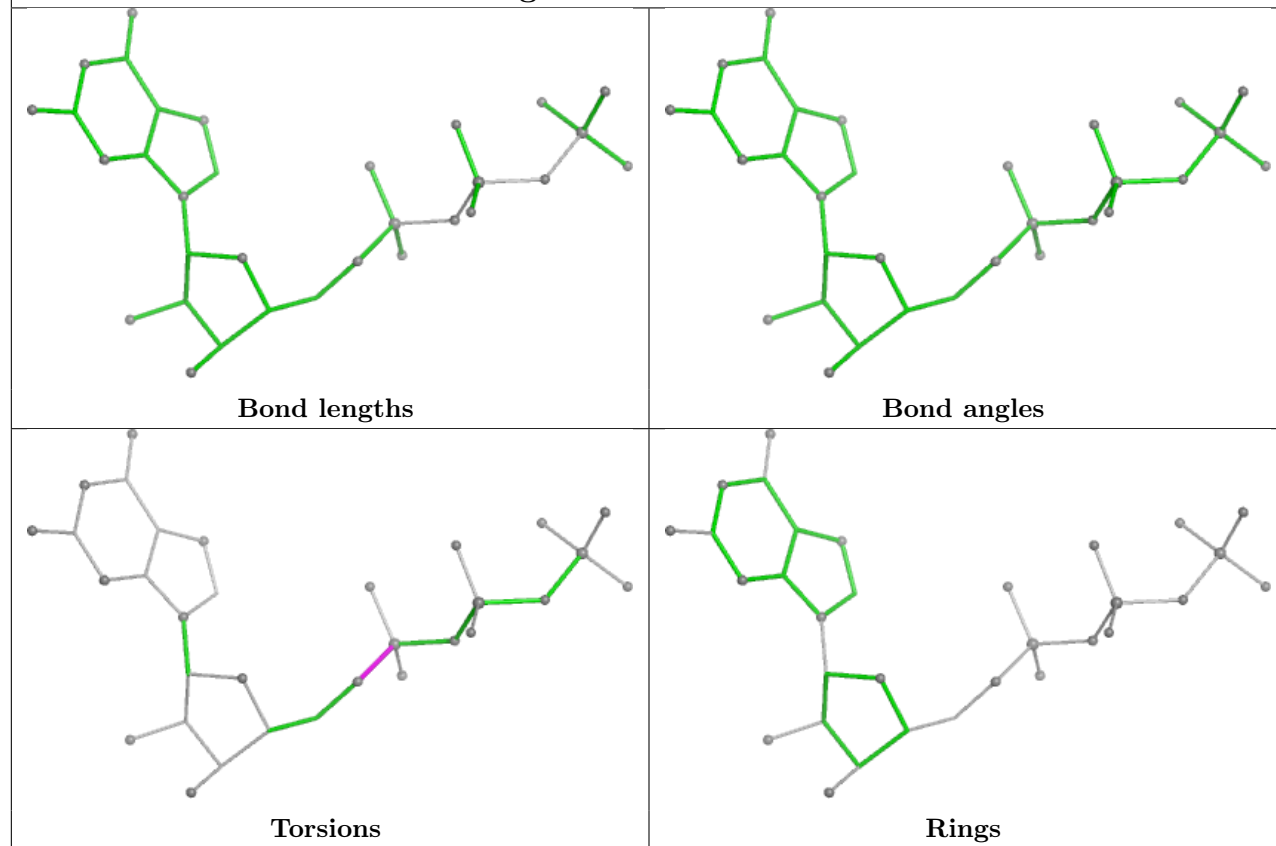




Ligand GTP KA 501



Ligand GTP LA 501



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.

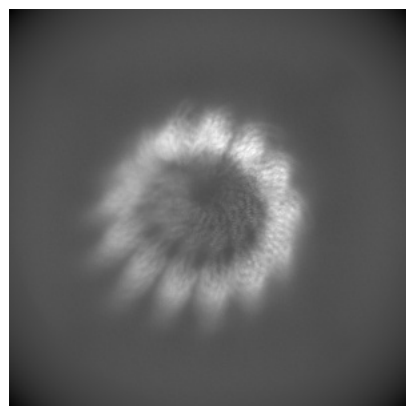
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55043. These allow visual inspection of the internal detail of the map and identification of artifacts.

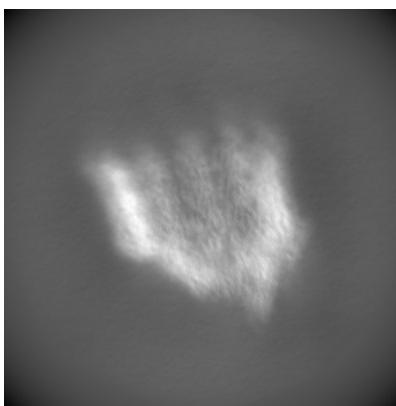
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

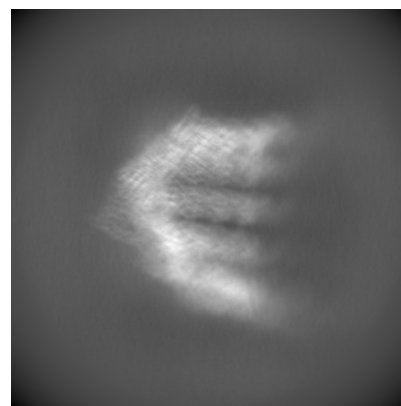
6.1.1 Primary map



X

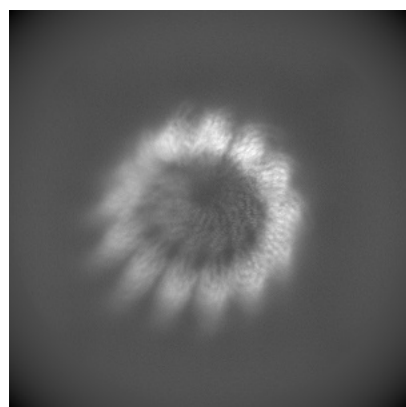


Y

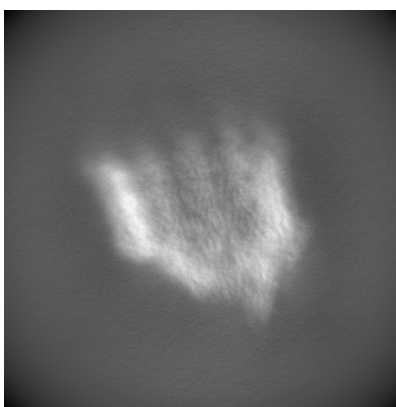


Z

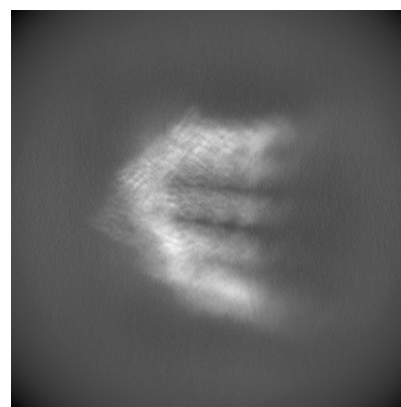
6.1.2 Raw map



X



Y

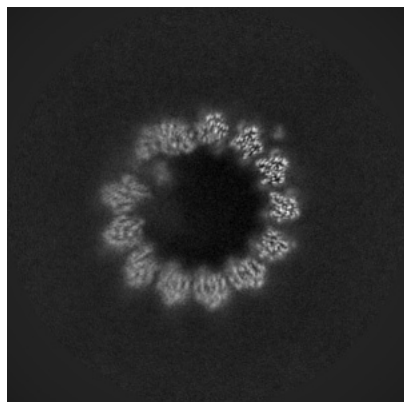


Z

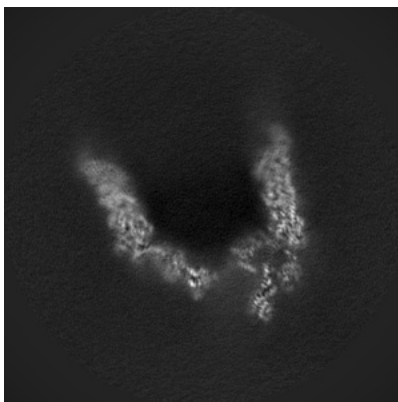
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

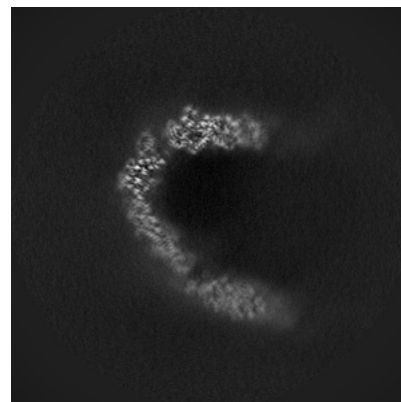
6.2.1 Primary map



X Index: 272

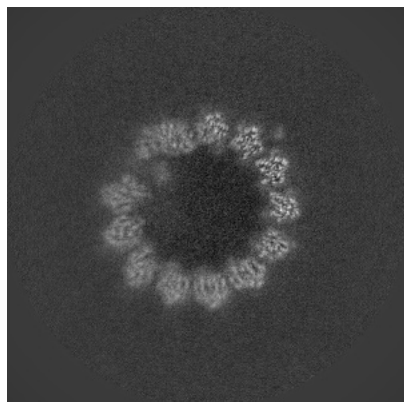


Y Index: 272

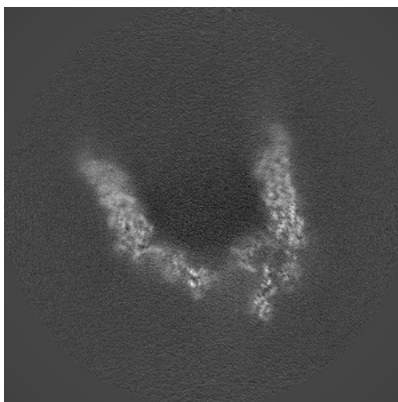


Z Index: 272

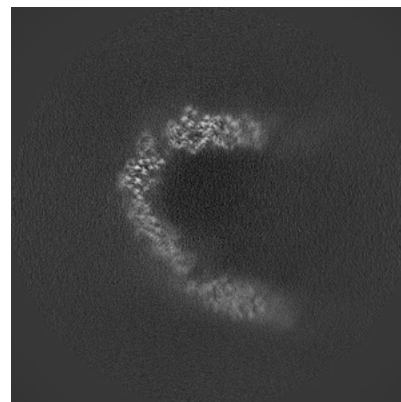
6.2.2 Raw map



X Index: 272



Y Index: 272

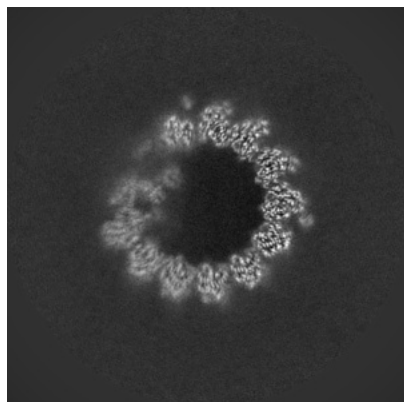


Z Index: 272

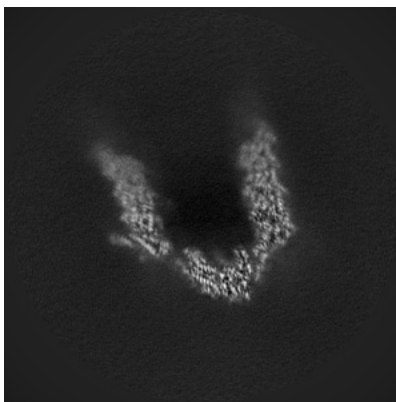
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

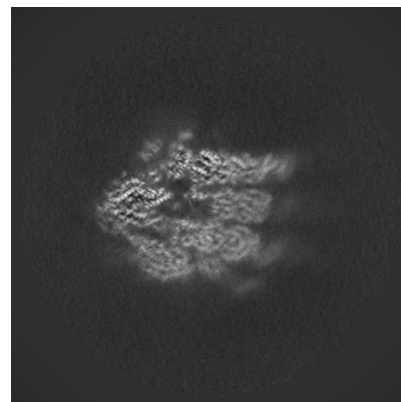
6.3.1 Primary map



X Index: 251

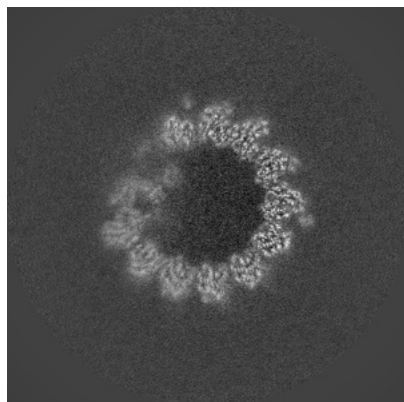


Y Index: 326

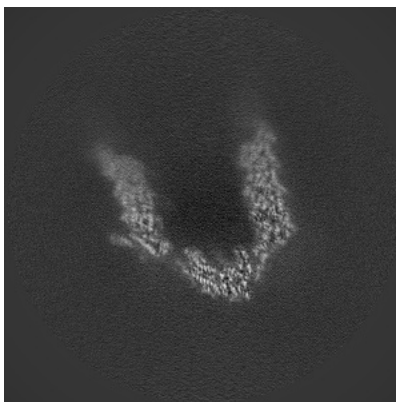


Z Index: 358

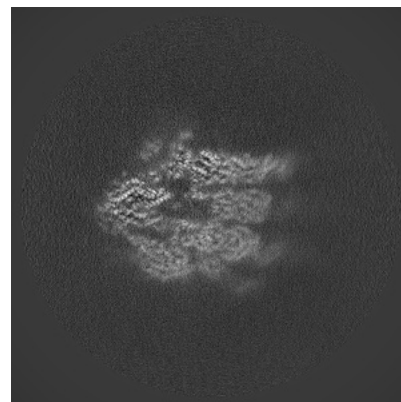
6.3.2 Raw map



X Index: 251



Y Index: 326

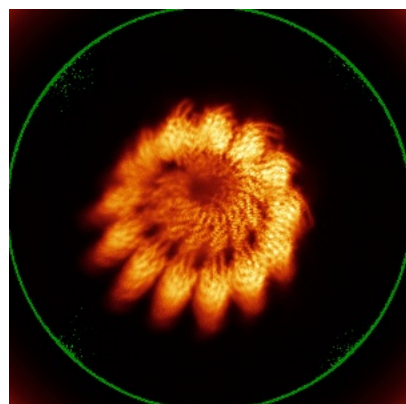


Z Index: 358

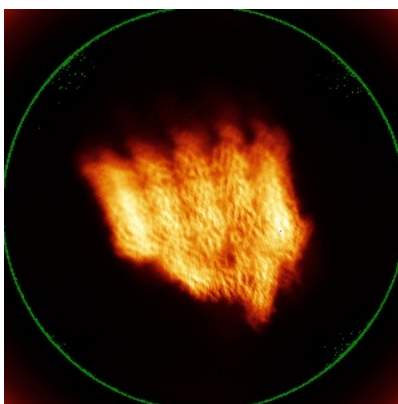
The images above show the largest variance slices of the map in three orthogonal directions.

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

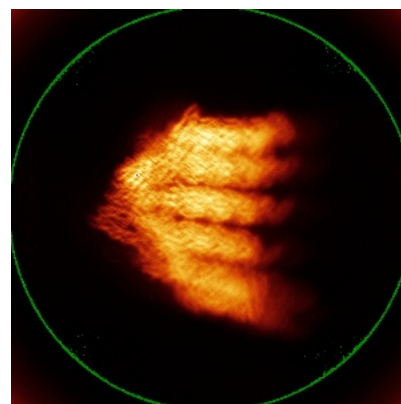
6.4.1 Primary map



X

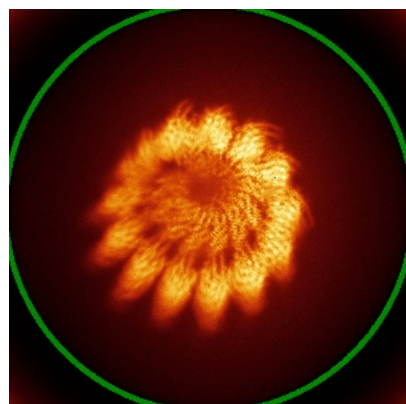


Y

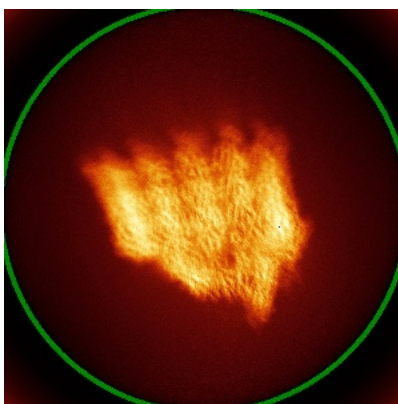


Z

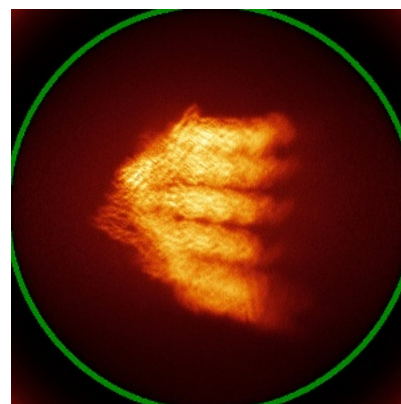
6.4.2 Raw map



X



Y

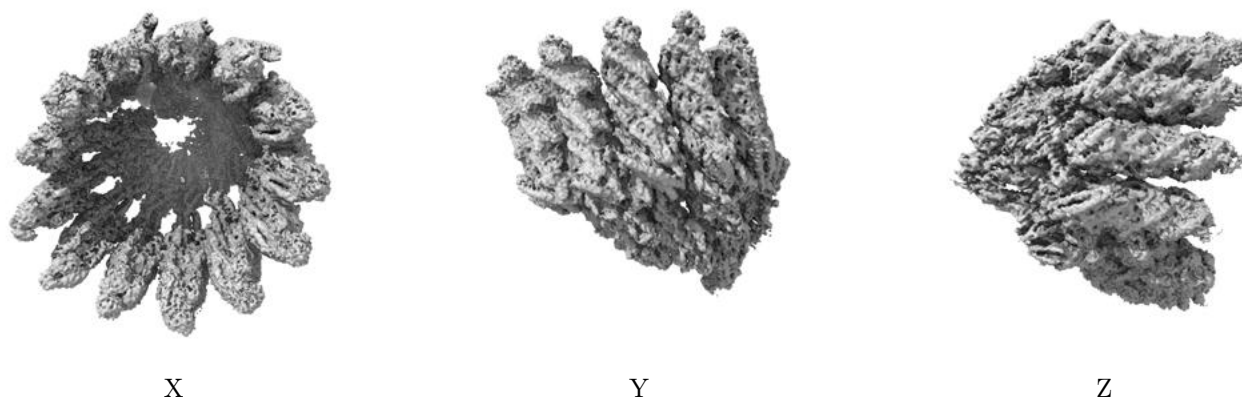


Z

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.

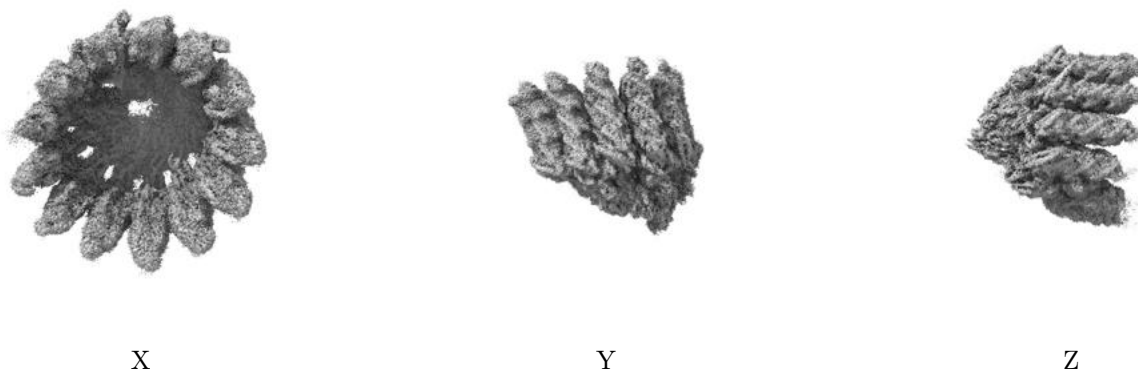
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0035. 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.

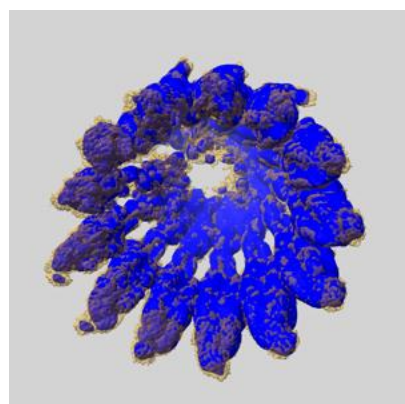
6.6 Mask visualisation [i](#)

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

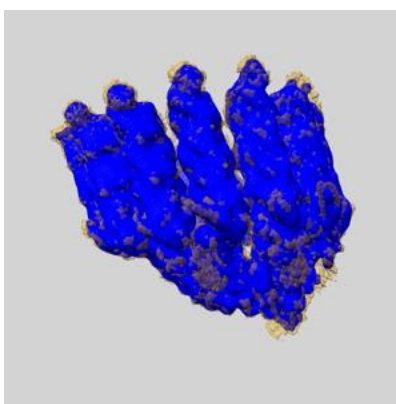
A mask typically either:

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

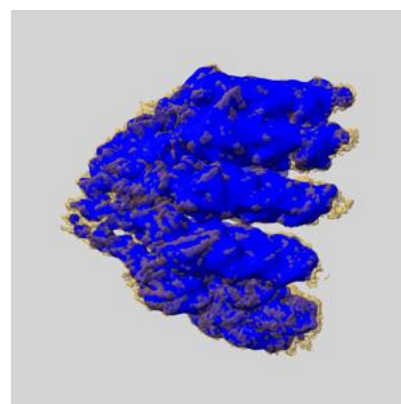
6.6.1 emd_55043_msk_1.map [i](#)



X



Y

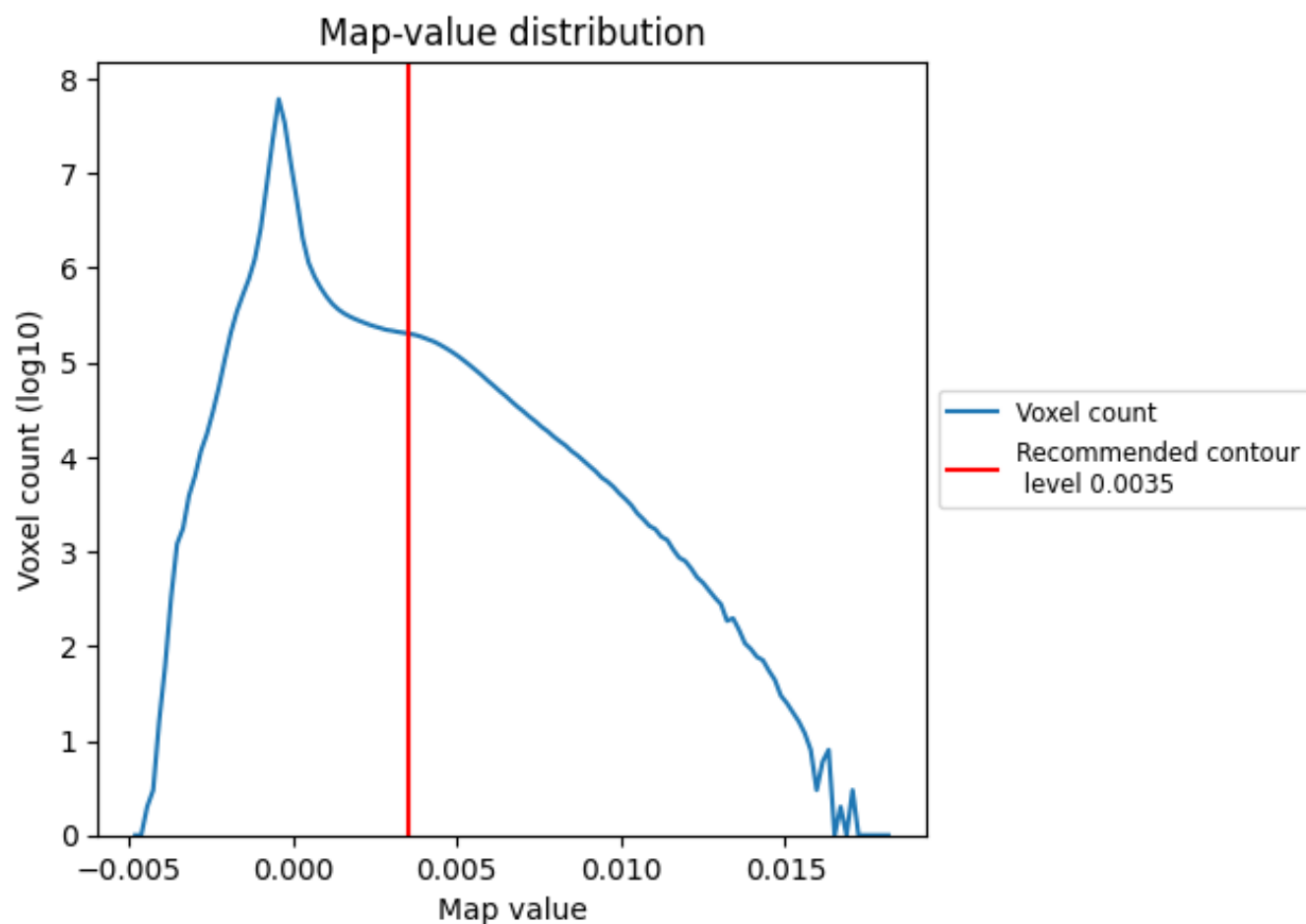


Z

7 Map analysis [i](#)

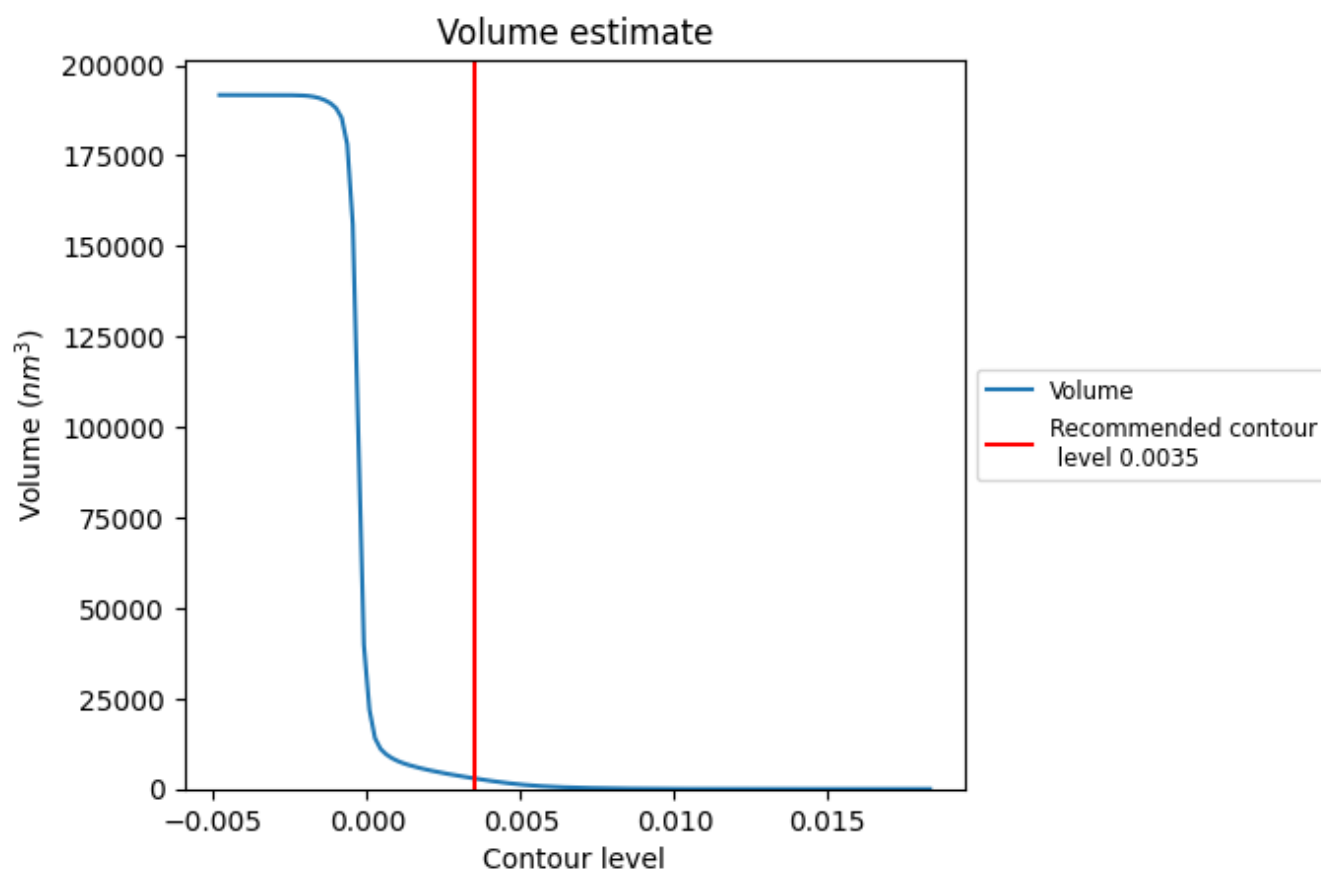
This section contains the results of statistical analysis of the map.

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.

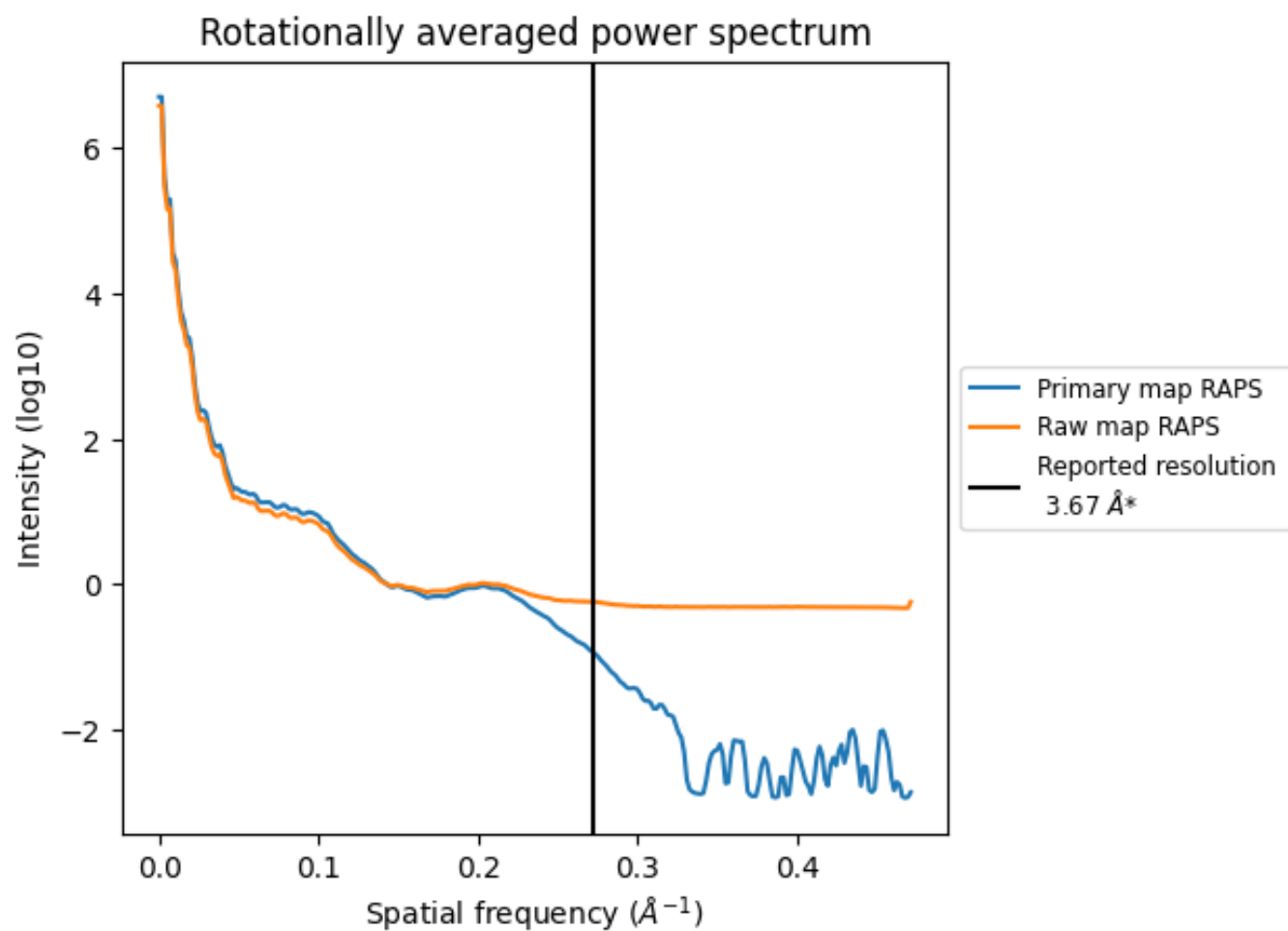
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2908 nm^3 ; this corresponds to an approximate mass of 2627 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 ⓘ

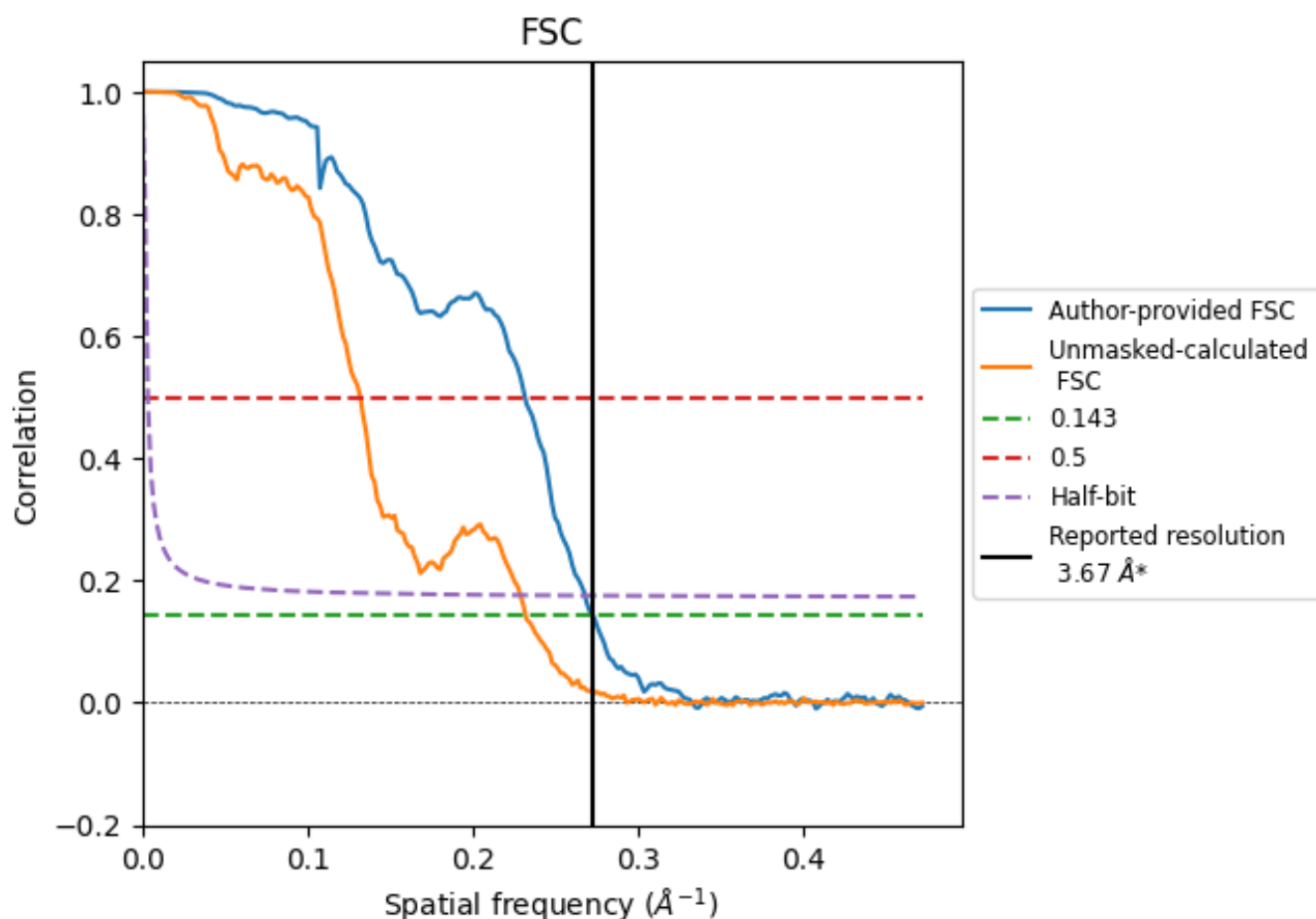


*Reported resolution corresponds to spatial frequency of 0.272 Å⁻¹

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 0.272 \AA^{-1}

8.2 Resolution estimates [i](#)

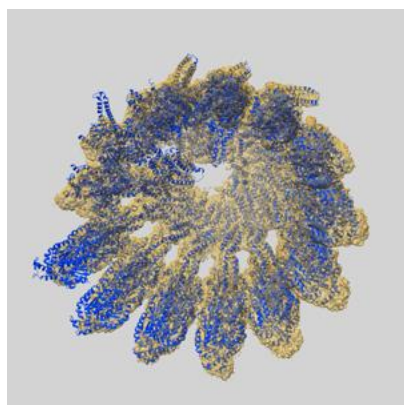
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.67	-	-
Author-provided FSC curve	3.67	4.32	3.74
Unmasked-calculated*	4.31	7.58	4.37

*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 4.31 differs from the reported value 3.67 by more than 10 %

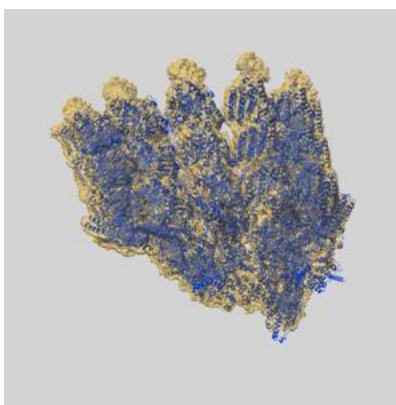
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55043 and PDB model 9SMX. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

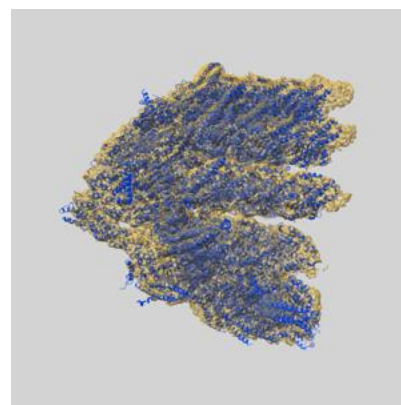
9.1 Map-model overlay [i](#)



X



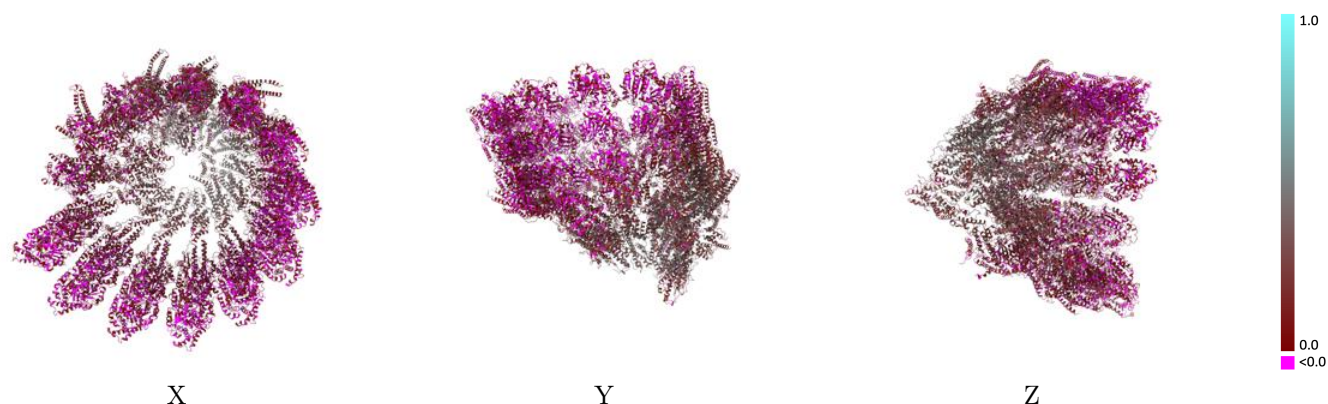
Y



Z

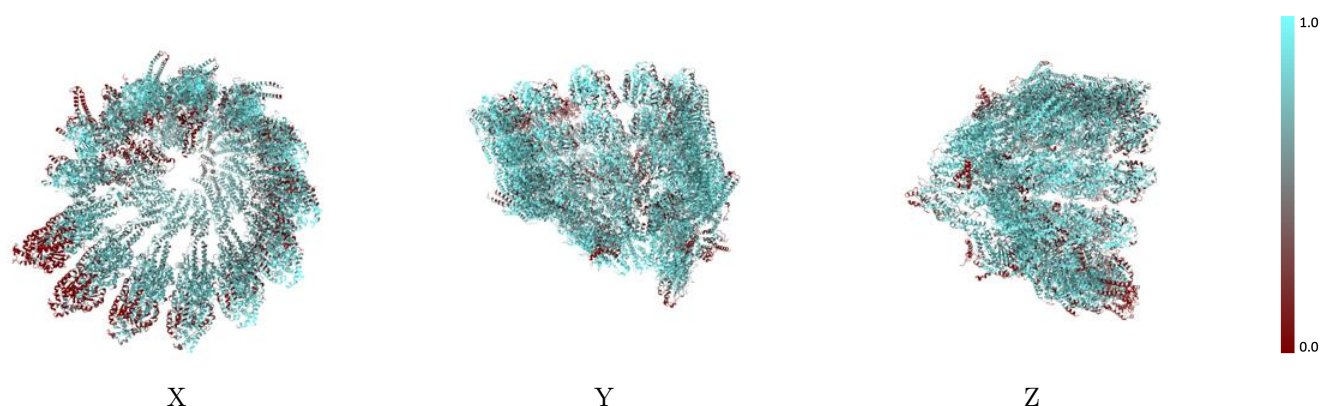
The images above show the 3D surface view of the map at the recommended contour level 0.0035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



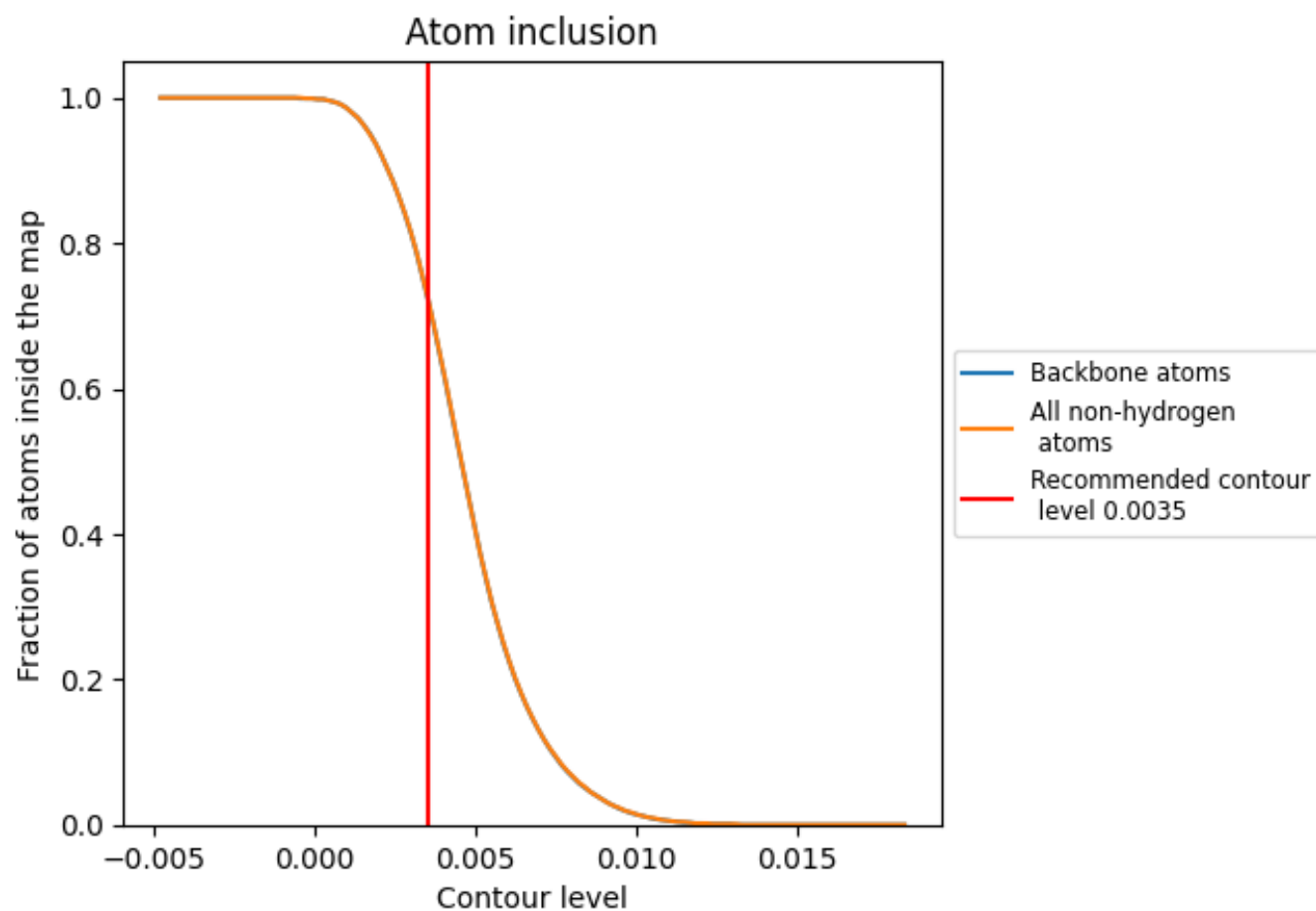
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0035).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 73% 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 (0.0035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7260	 0.1520
3	 0.6120	 0.2970
4	 0.6010	 0.3120
5	 0.6360	 0.3160
6	 0.5880	 0.2700
7	 0.5500	 0.3170
A	 0.6130	 0.2200
AC	 0.1350	 0.1170
B	 0.7470	 0.2800
BA	 0.8240	 0.1520
BB	 0.6900	 0.0940
C	 0.8470	 0.3500
CA	 0.8520	 0.1770
CB	 0.6320	 0.0890
CC	 0.7860	 0.3540
CM	 0.3140	 0.2820
CN	 0.3770	 0.2960
Cc	 0.6580	 0.2840
D	 0.8530	 0.3070
DA	 0.8090	 0.1050
DB	 0.6730	 0.0540
E	 0.8440	 0.3060
EA	 0.7400	 0.0250
EB	 0.6760	 0.0280
EC	 0.7970	 0.2830
EM	 0.5040	 0.2450
EN	 0.5150	 0.2460
Ec	 0.7190	 0.2440
F	 0.8050	 0.2250
FA	 0.7370	 0.0080
FB	 0.6850	 0.0250
G	 0.7990	 0.2080
GA	 0.7680	 0.0220
GB	 0.6920	 0.0550
GC	 0.5760	 -0.0220



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Chain	Atom inclusion	Q-score
GM	 0.3330	 0.1790
GN	 0.4490	 0.1740
Gc	 0.6530	 0.0270
H	 0.8090	 0.1930
HA	 0.8500	 0.0560
HB	 0.7060	 0.0320
I	 0.8350	 0.1960
IA	 0.9030	 0.0890
IB	 0.6010	 0.0440
J	 0.8710	 0.1980
JA	 0.8360	 0.0790
JB	 0.4190	 0.0430
K	 0.8450	 0.2030
KA	 0.7770	 0.0820
KB	 0.2310	 0.0460
L	 0.8150	 0.1690
LA	 0.6590	 0.0870
LB	 0.1320	 0.0520
M	 0.6680	 0.1690
MC	 0.7900	 0.1880
MM	 0.4600	 0.1280
Mc	 0.4860	 0.1430
N	 0.4480	 0.1520
Y	 0.6870	 0.1490
Z	 0.6420	 0.1230
a	 0.8050	 0.1550
b	 0.9140	 0.2940
c	 0.9030	 0.3170
d	 0.8570	 0.2520
e	 0.8100	 0.1670
f	 0.7440	 0.0590
g	 0.7410	 0.0580
h	 0.7920	 0.0810
i	 0.8250	 0.1060
j	 0.8860	 0.1370
k	 0.8430	 0.1400
l	 0.8340	 0.1560
m	 0.7720	 0.1230
n	 0.6630	 0.0980