



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:14 PM UTC

PDB ID : 8QV2 / pdb_00008qv2
EMDB ID : EMD-18665
Title : Structure of the native γ -Tubulin Ring Complex (γ TuRC) capping microtubule minus ends at the spindle pole body
Authors : Dendooven, T.; Yatskevich, S.; Burt, A.; Bellini, D.; Kilmartin, J.; Barford, D.
Deposited on : 2023-10-17
Resolution : 9.20 Å(reported)

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 : 2022.3.0, CSD as543be (2022)
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

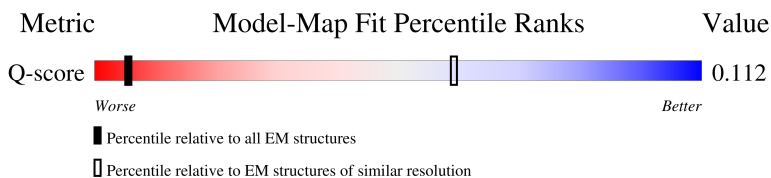
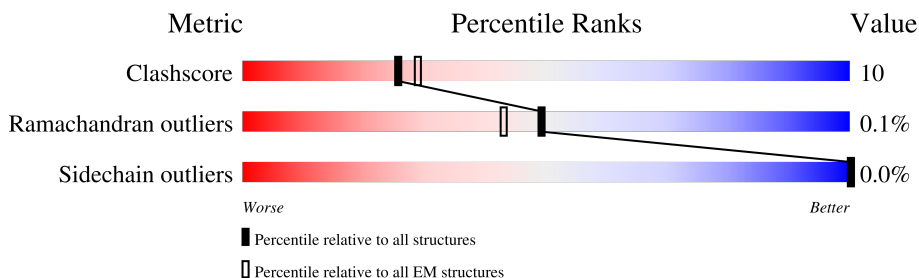
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.20 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.



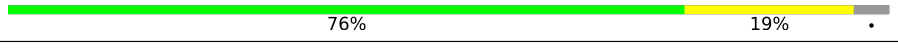
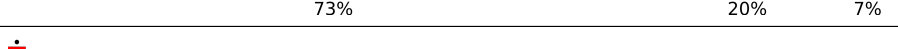
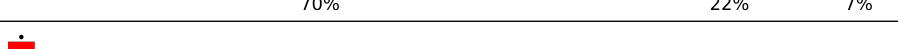
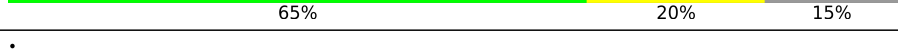
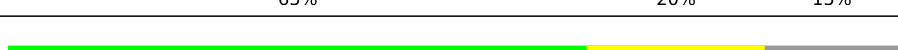
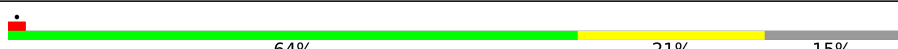
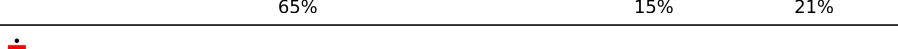
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	239 (8.70 - 9.70)

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	a	473	15% 74% 19% 7%
1	b	473	74% 21% .
1	c	473	69% 24% 7%
1	d	473	73% 23% .

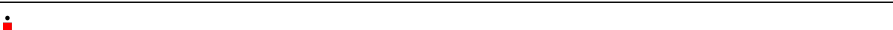
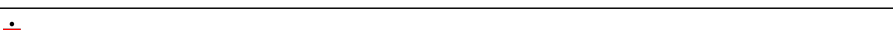
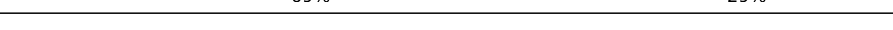
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	e	473	
1	f	473	
1	g	473	
1	h	473	
1	i	473	
1	j	473	
1	k	473	
1	l	473	
1	m	473	
1	n	473	
2	C	823	
2	E	823	
2	G	823	
2	I	823	
2	K	823	
2	M	823	
2	O	823	
3	D	846	
3	F	846	
3	H	846	
3	J	846	
3	L	846	
3	N	846	
3	P	846	
4	Ab	447	

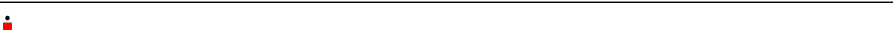
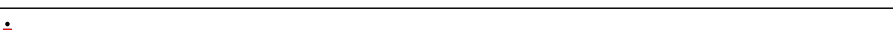
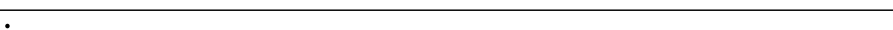
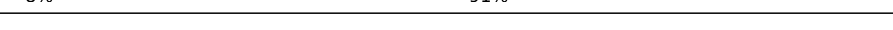
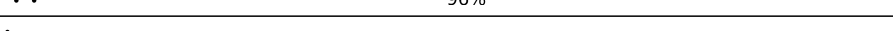
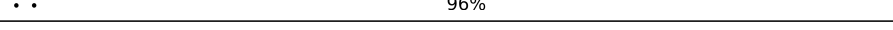
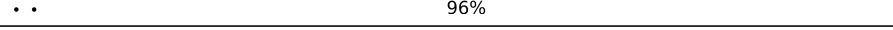
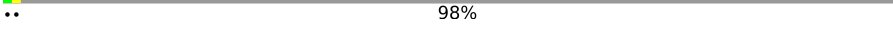
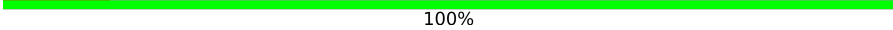
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	Ac	447	 69% 29% .
4	Ad	447	 67% 31% .
4	Ae	447	 68% 30% .
4	Af	447	 70% 28% .
4	Ag	447	 68% 30% .
4	Ah	447	 68% 30% .
4	Ai	447	 71% 27% .
4	Aj	447	 70% 28% .
4	Ak	447	 72% 26% .
4	Al	447	 70% 28% .
4	Am	447	 72% 27% .
4	An	447	 73% 26% .
4	Ao	447	 68% 30% .
4	Ap	447	 69% 29% .
4	Aq	447	 70% 28% ..
4	Ar	447	 72% 27% .
5	Bb	457	 60% 30% 9% .
5	Bc	457	 62% 31% 7%
5	Bd	457	 62% 32% 7%
5	Be	457	 64% 30% 7%
5	Bf	457	 65% 28% 7%
5	Bg	457	 65% 28% 7%
5	Bh	457	 64% 30% 7%
5	Bi	457	 71% 22% 7%
5	Bj	457	 67% 26% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	Bk	457	
5	Bl	457	
5	Bm	457	
5	Bn	457	
5	Bo	457	
5	Bp	457	
5	Bq	457	
5	Br	457	
6	Sa	944	
6	Sb	944	
6	Sc	944	
6	Sd	944	
6	Se	944	
6	Sf	944	
6	Sg	944	
6	Sh	944	
6	Si	944	
6	Sj	944	
6	Sk	944	
6	Sl	944	
6	Sm	944	
6	Sn	944	
7	Ua	67	
7	Ub	67	
7	Uc	67	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	Ud	67	
7	Ue	67	
7	Uf	67	
7	Ug	67	
7	Uh	67	
7	Ui	67	
7	Uj	67	
7	Uk	67	
7	Ul	67	
7	Um	67	
7	Un	67	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 255200 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Tubulin gamma chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	c	441	Total	C	N	O	S	0	0
			3448	2158	585	689	16		
1	d	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	e	439	Total	C	N	O	S	0	0
			3433	2149	581	687	16		
1	f	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	g	441	Total	C	N	O	S	0	0
			3448	2158	585	689	16		
1	h	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	i	439	Total	C	N	O	S	0	0
			3433	2149	581	687	16		
1	j	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	k	441	Total	C	N	O	S	0	0
			3448	2158	585	689	16		
1	l	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	m	439	Total	C	N	O	S	0	0
			3433	2149	581	687	16		
1	n	453	Total	C	N	O	S	0	0
			3545	2217	599	712	17		
1	a	440	Total	C	N	O	S	0	0
			3441	2153	584	688	16		

- Molecule 2 is a protein called Spindle pole body component.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	693	Total	C	N	O	S	0	0
			5778	3716	974	1059	29		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	G	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	I	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	K	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	M	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	O	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		

- Molecule 3 is a protein called Spindle pole body component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	651	Total	C	N	O	S	0	0
			5390	3494	886	994	16		
3	F	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	H	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	J	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	L	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	N	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	P	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		

- Molecule 4 is a protein called Tubulin alpha-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ad	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ac	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Af	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ae	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ah	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ag	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Aj	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ai	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Al	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ak	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	An	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Am	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ab	423	Total	C	N	O	S	0	0
			3312	2089	563	641	19		
4	Ap	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ao	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ar	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Aq	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		

- Molecule 5 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Bd	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bc	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bf	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Be	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bh	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bg	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Bj	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bi	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bl	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bk	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bn	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bm	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bb	414	Total	C	N	O	S	0	0
			3247	2038	554	634	21		
5	Bp	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bo	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Br	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bq	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		

- Molecule 6 is a protein called Spindle pole body component 110.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Sc	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sd	85	Total	C	N	O	S	0	0
			714	439	130	144	1		
6	Se	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sf	86	Total	C	N	O	S	0	0
			723	444	131	147	1		
6	Sg	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sh	85	Total	C	N	O	S	0	0
			714	439	130	144	1		
6	Si	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sj	86	Total	C	N	O	S	0	0
			723	444	131	147	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
6	Sk	42	Total	C	N	O	0	0
			352	215	61	76		
6	Sl	85	Total	C	N	O	S	0
			714	439	130	144	1	0
6	Sa	42	Total	C	N	O		0
			352	215	61	76		0
6	Sb	62	Total	C	N	O		0
			517	318	91	108		0
6	Sm	20	Total	C	N	O		0
			171	107	31	33		0
6	Sn	64	Total	C	N	O	S	0
			545	337	102	105	1	0

- Molecule 7 is a protein called Unkown protein.

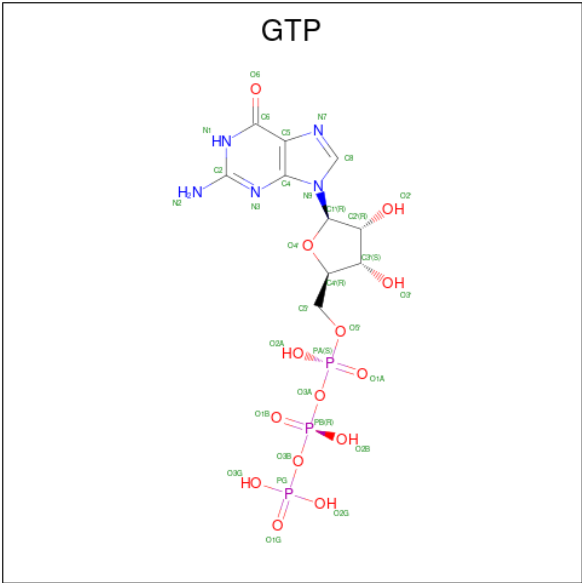
Mol	Chain	Residues	Atoms				AltConf	Trace
7	Ue	67	Total	C	N	O	0	0
			335	201	67	67		
7	Uf	55	Total	C	N	O	0	0
			275	165	55	55		
7	Ui	67	Total	C	N	O	0	0
			335	201	67	67		
7	Uj	55	Total	C	N	O	0	0
			275	165	55	55		
7	Um	67	Total	C	N	O	0	0
			335	201	67	67		
7	Un	55	Total	C	N	O	0	0
			275	165	55	55		
7	Ua	67	Total	C	N	O	0	0
			335	201	67	67		
7	Ub	55	Total	C	N	O	0	0
			275	165	55	55		
7	Ug	67	Total	C	N	O	0	0
			335	201	67	67		
7	Uh	55	Total	C	N	O	0	0
			275	165	55	55		
7	Uk	67	Total	C	N	O	0	0
			335	201	67	67		
7	Ul	55	Total	C	N	O	0	0
			275	165	55	55		
7	Uc	67	Total	C	N	O	0	0
			335	201	67	67		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	Ud	55	275	165	55	55	0	0

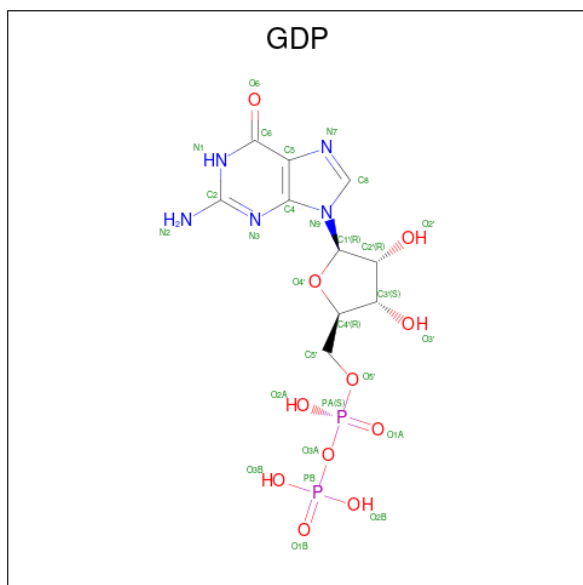
- Molecule 8 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
8	l	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	m	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	n	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
9	a	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		AltConf
10	Ue	1	Total	O	0
			1	1	
10	Ui	1	Total	O	0
			1	1	
10	Um	1	Total	O	0
			1	1	
10	Ua	1	Total	O	0
			1	1	
10	Ug	1	Total	O	0
			1	1	

Continued on next page...

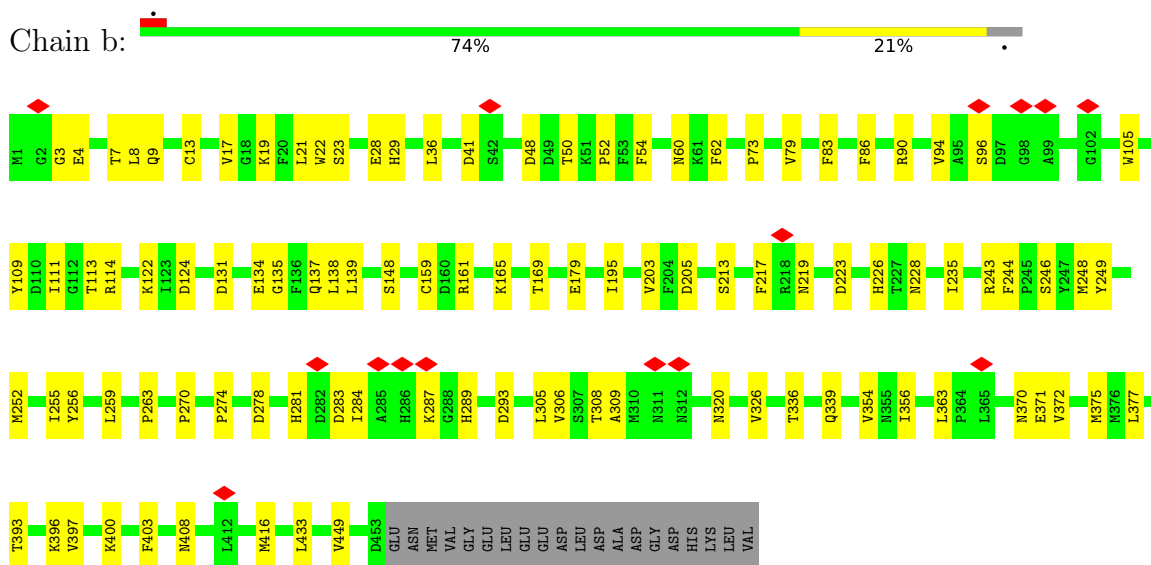
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
10	Uk	1	Total	O	0
			1	1	
10	Uc	1	Total	O	0
			1	1	

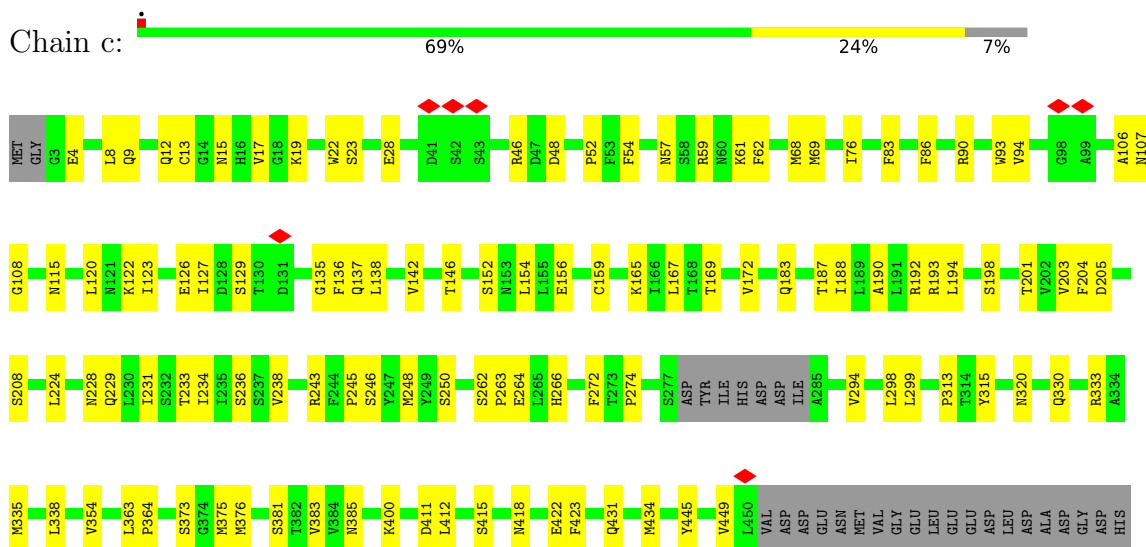
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Tubulin gamma chain



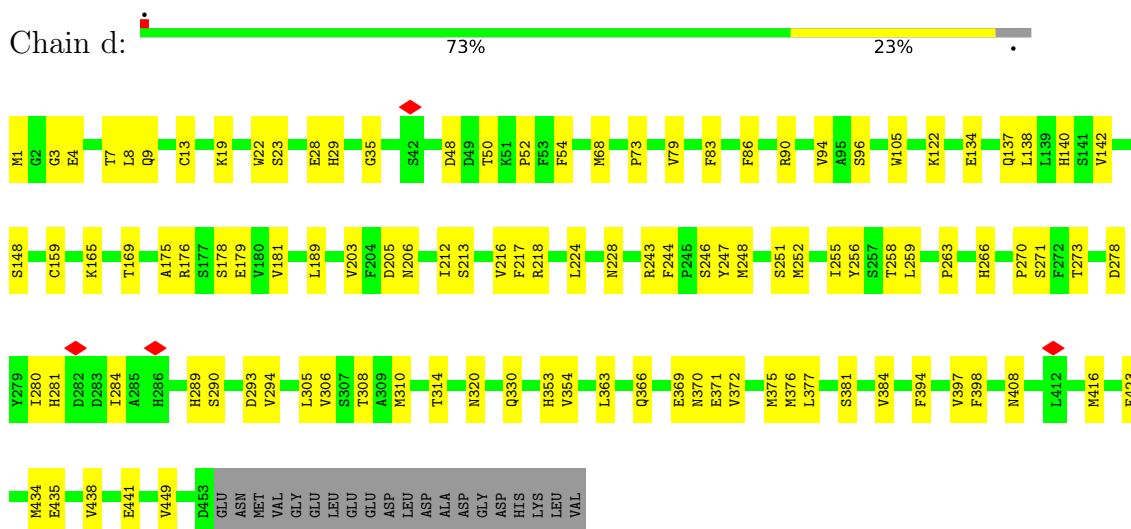
• Molecule 1: Tubulin gamma chain



LYS
LEU
VAL

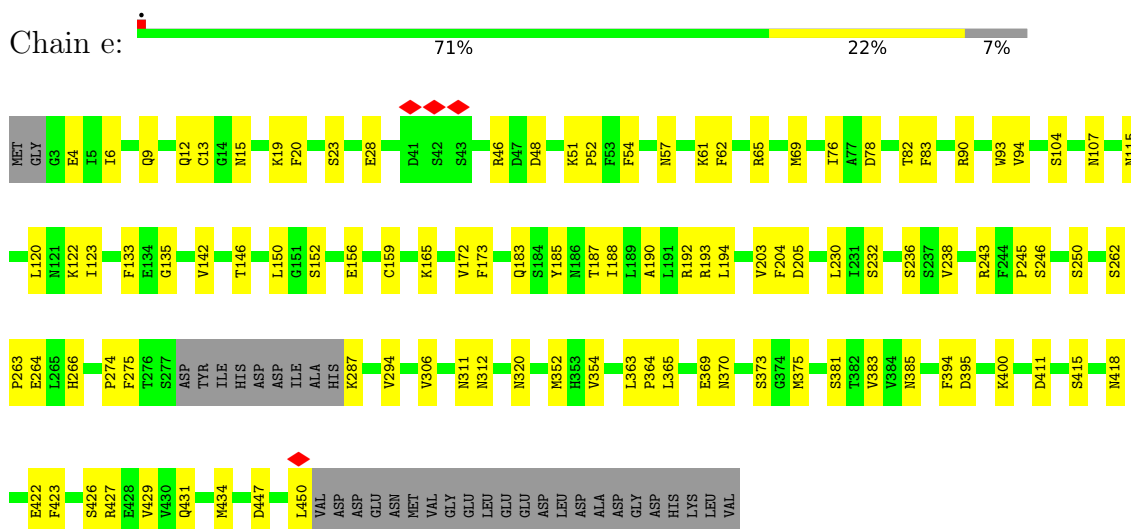
• Molecule 1: Tubulin gamma chain

Chain d:



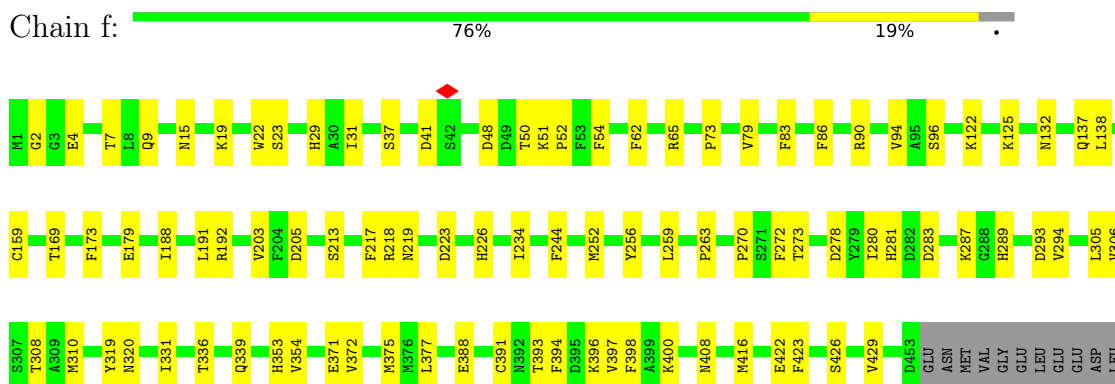
• Molecule 1: Tubulin gamma chain

Chain e:



• Molecule 1: Tubulin gamma chain

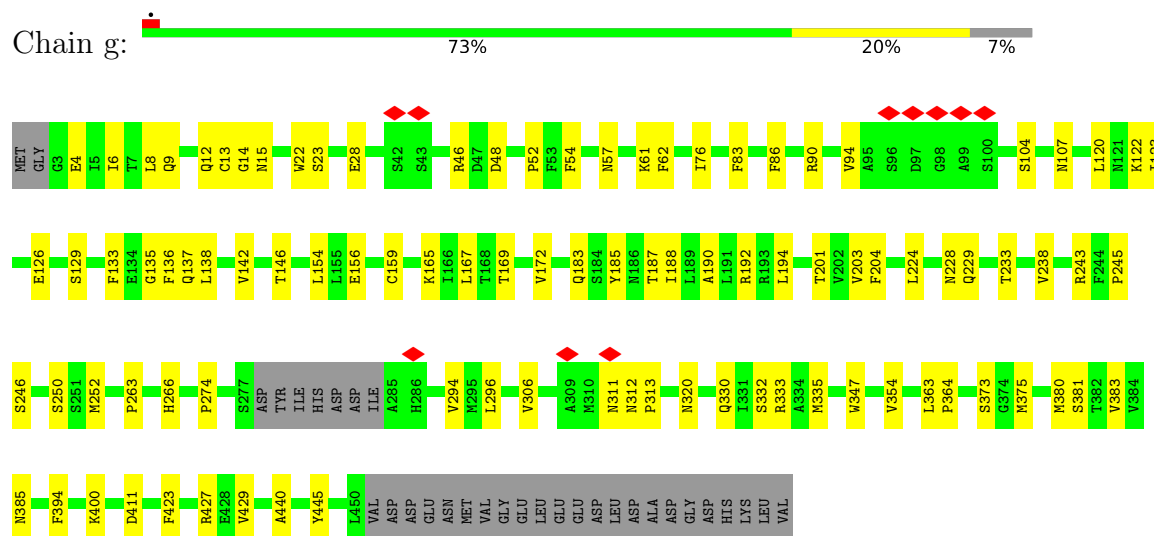
Chain f:



ASP
ALA
ASP
GLY
ASP
HIS
LYS
LEU
VAL

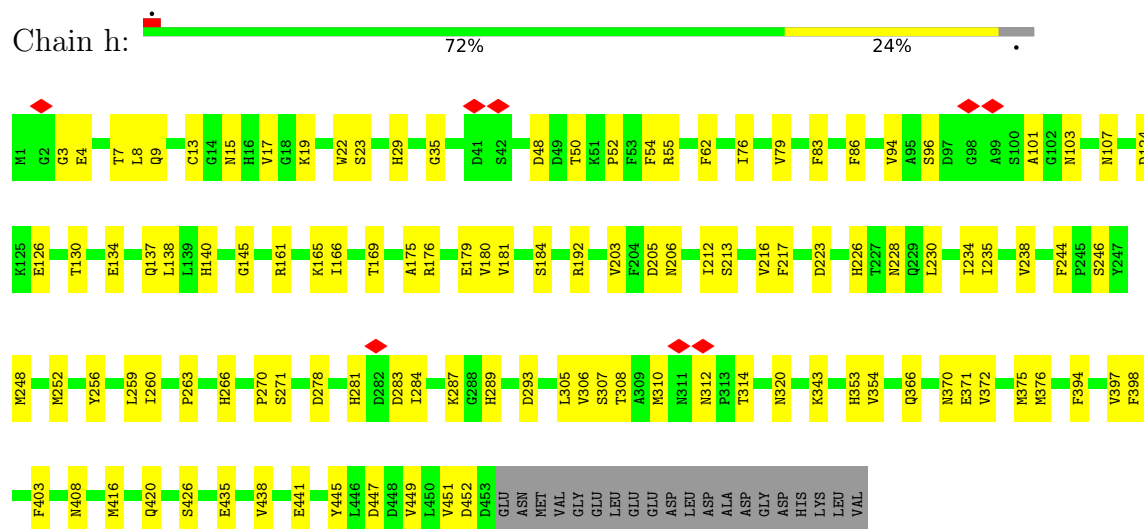
• Molecule 1: Tubulin gamma chain

Chain g:



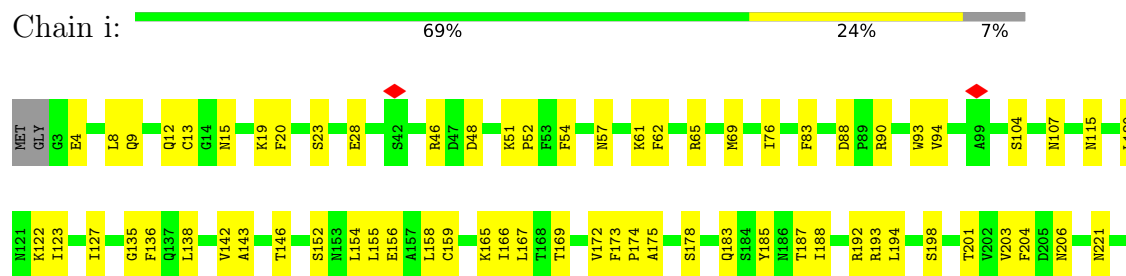
• Molecule 1: Tubulin gamma chain

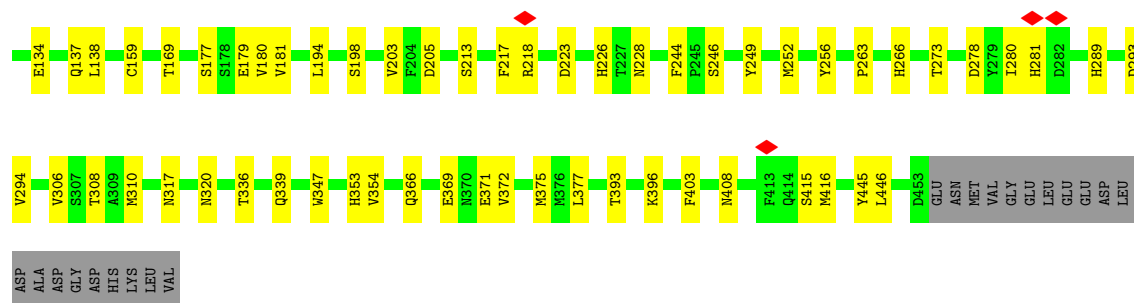
Chain h:



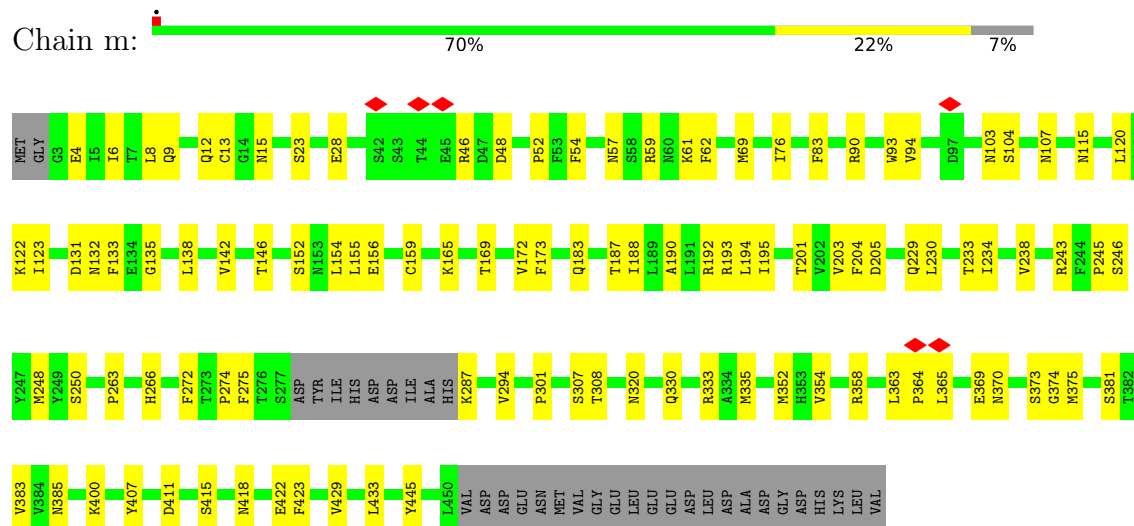
• Molecule 1: Tubulin gamma chain

Chain i:

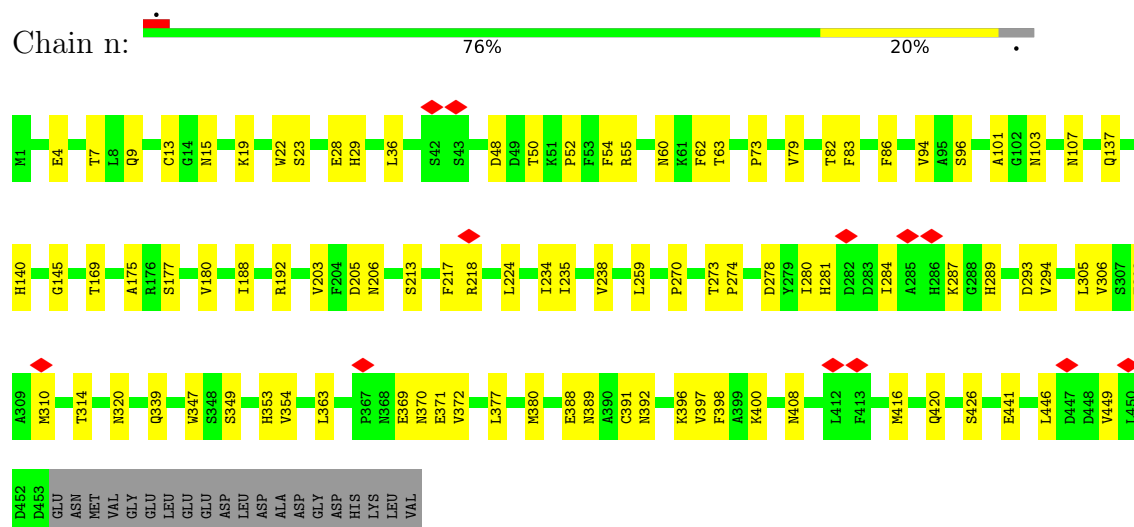




• Molecule 1: Tubulin gamma chain

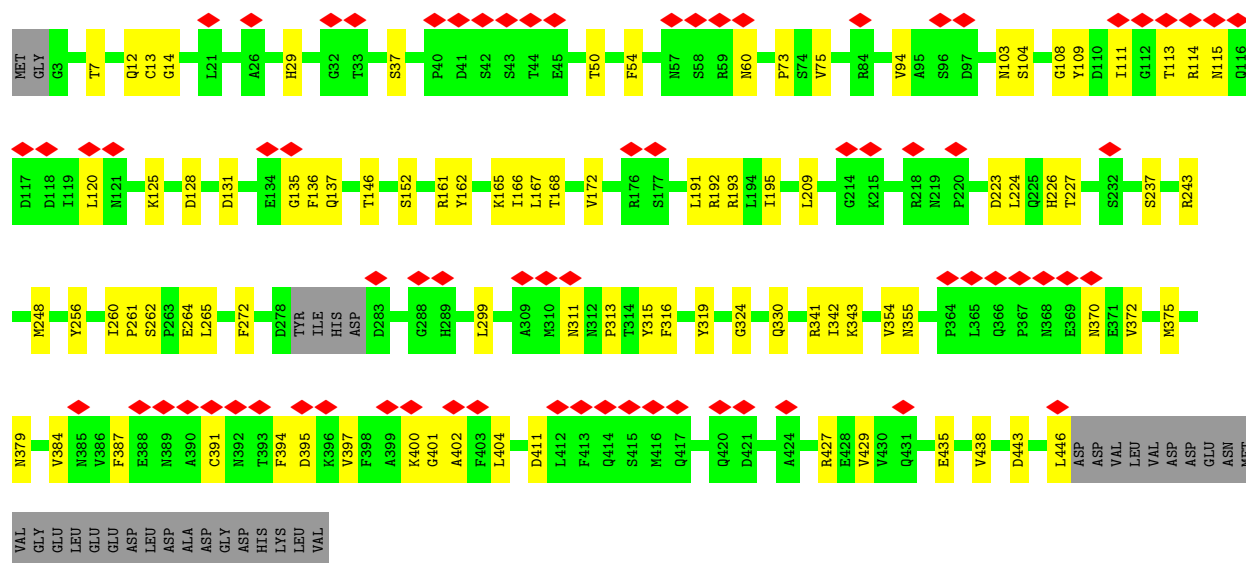


• Molecule 1: Tubulin gamma chain

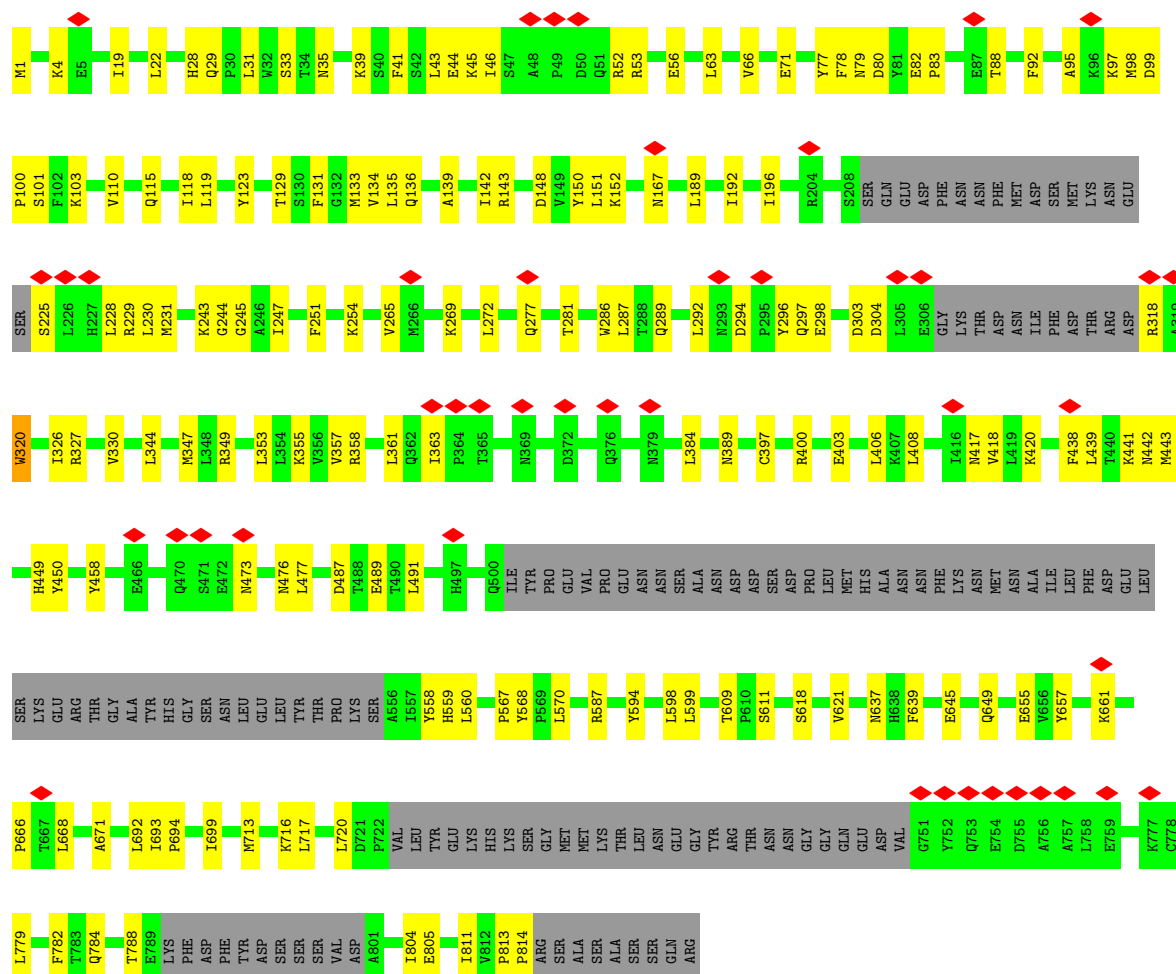


• Molecule 1: Tubulin gamma chain



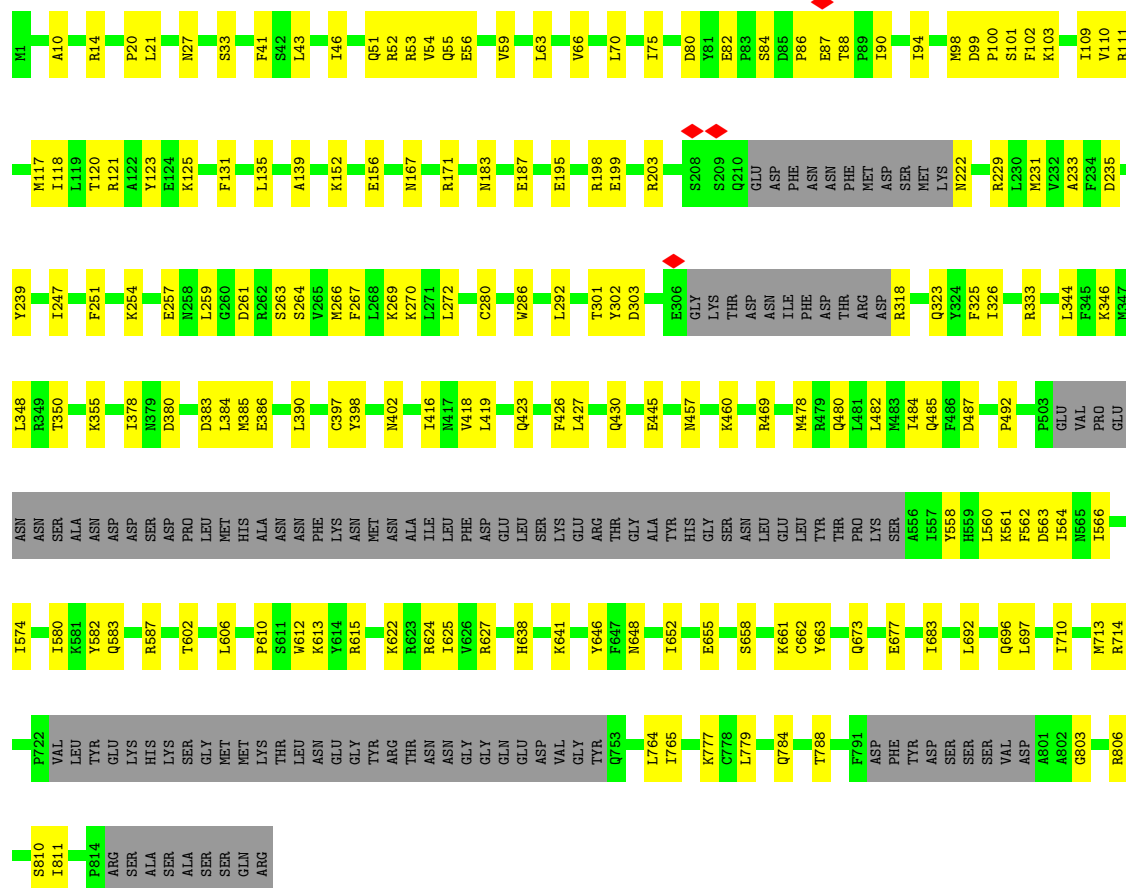


• Molecule 2: Spindle pole body component



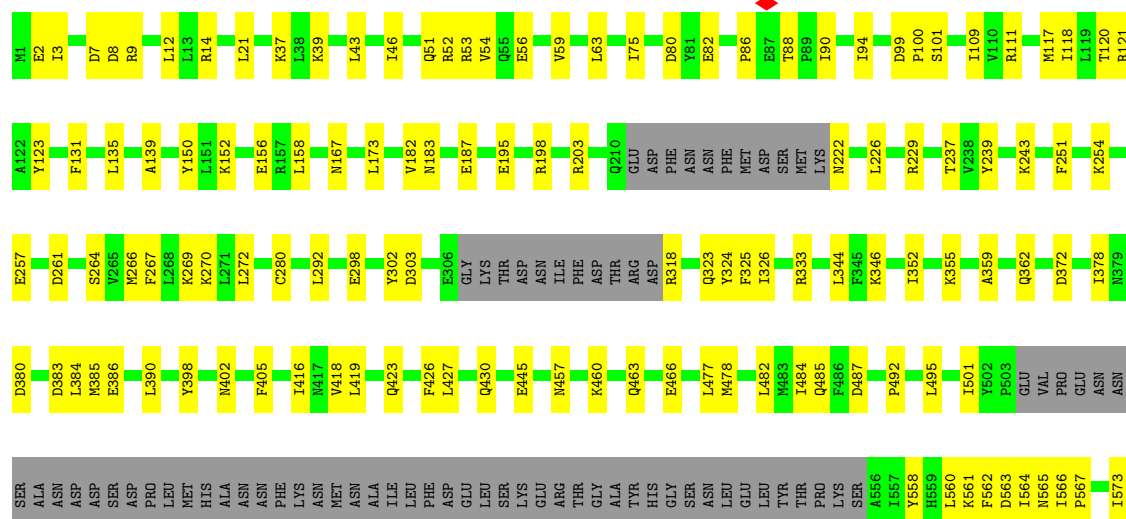
• Molecule 2: Spindle pole body component

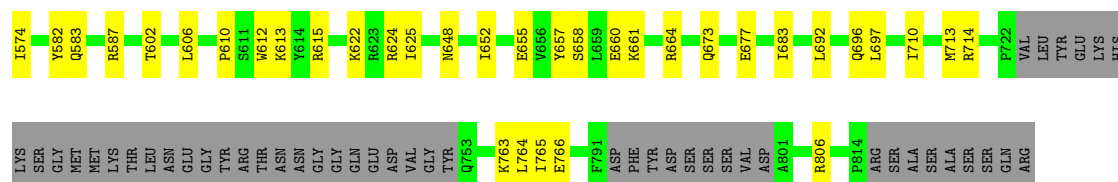
Chain E:  65% 21% 15%



• Molecule 2: Spindle pole body component

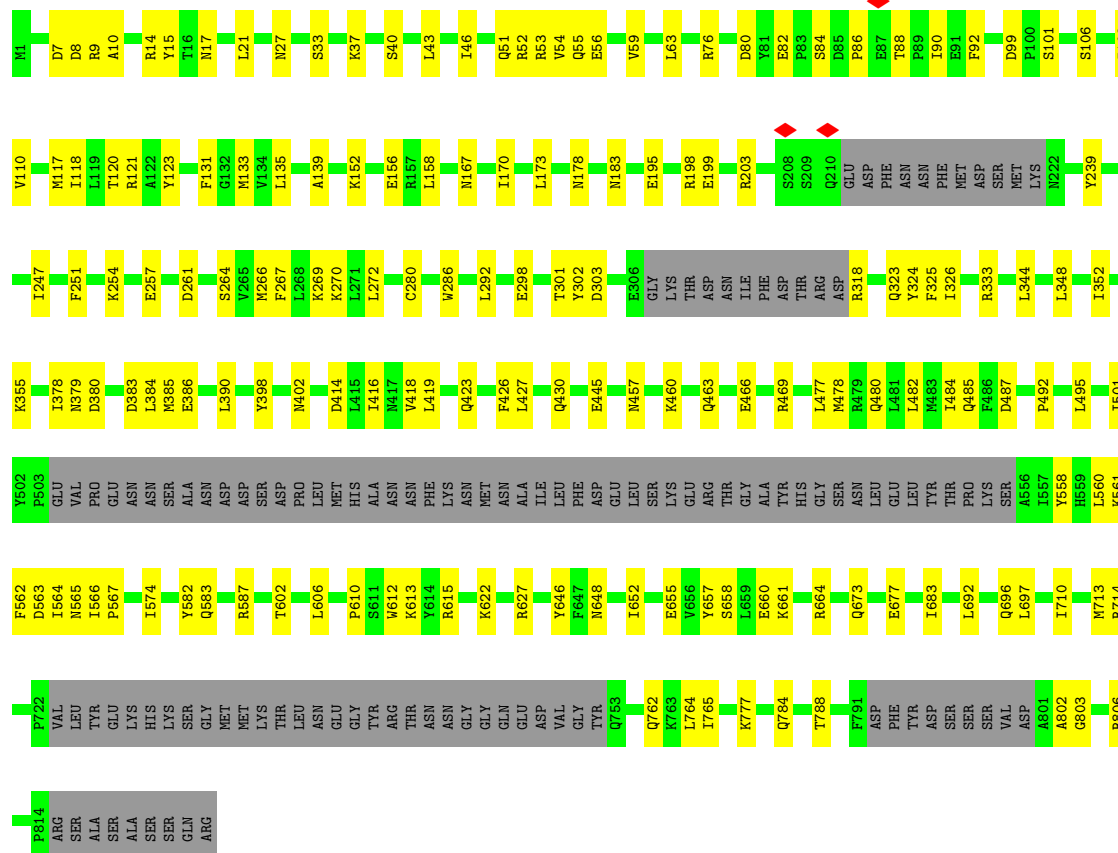
Chain G:  66% 20% 15%





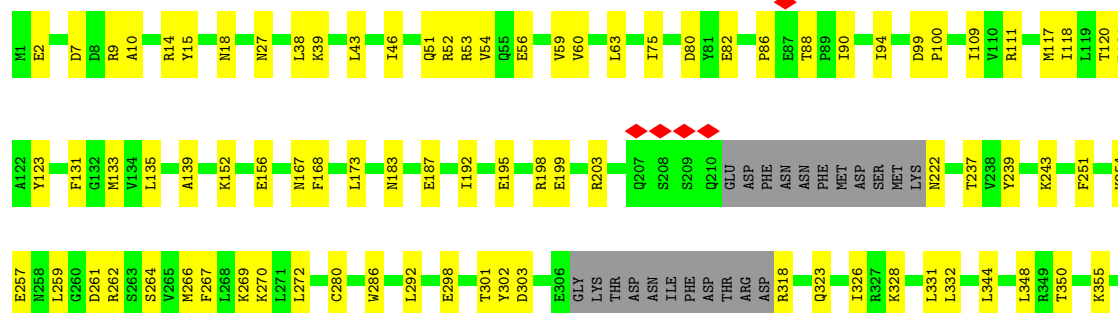
• Molecule 2: Spindle pole body component

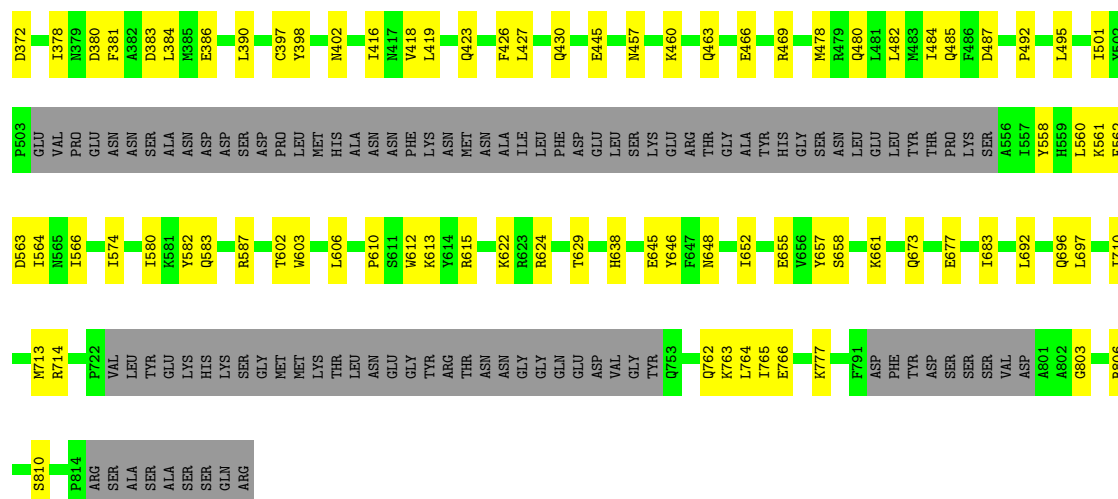
Chain I: 65% 20% 15%



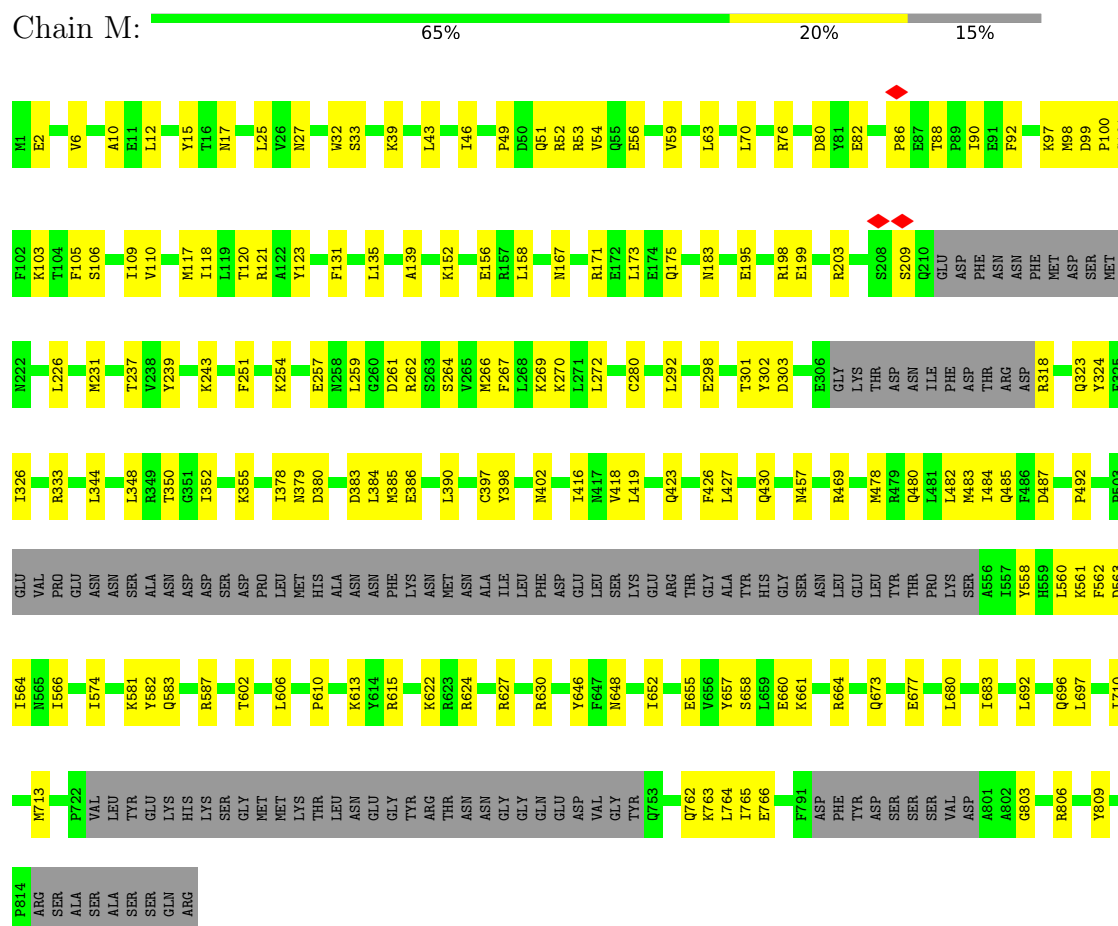
• Molecule 2: Spindle pole body component

Chain K: 65% 20% 15%



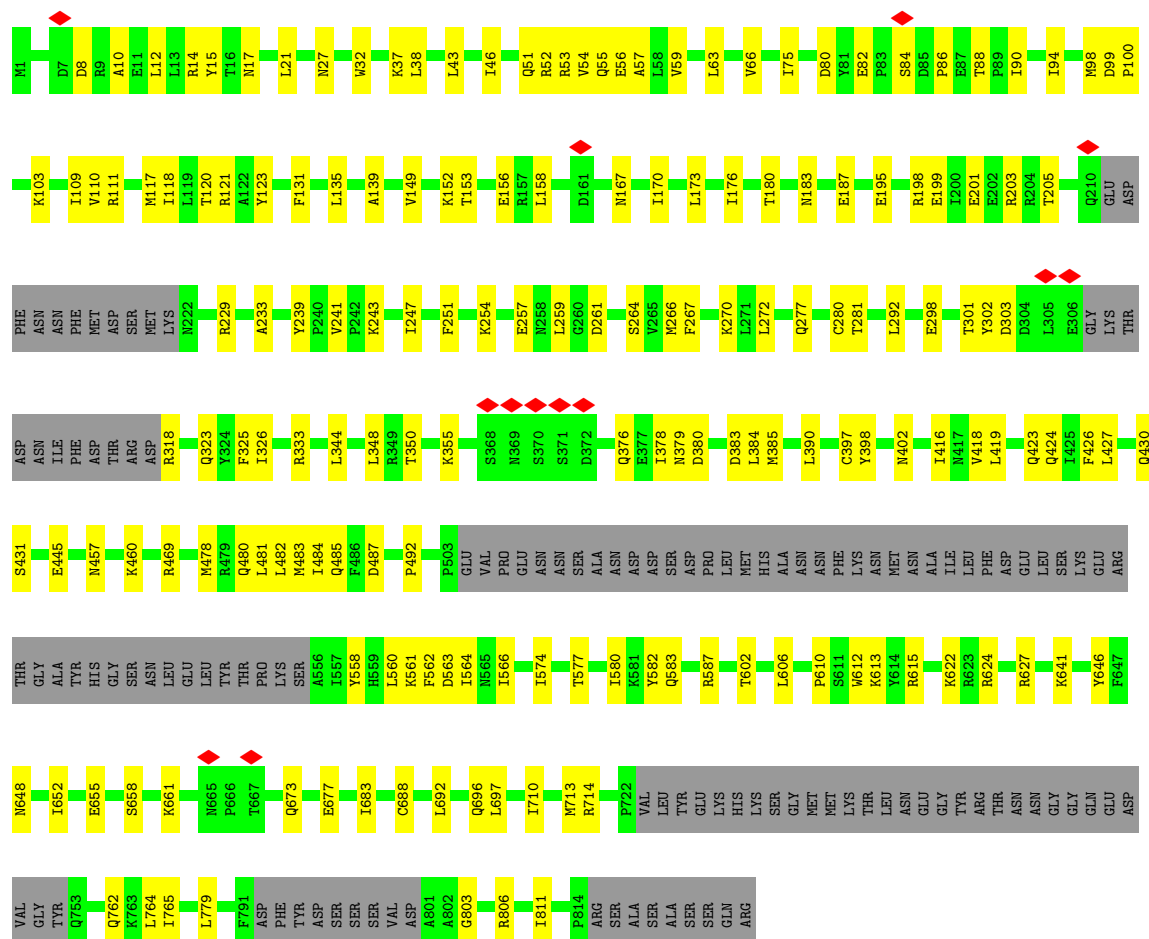


• Molecule 2: Spindle pole body component



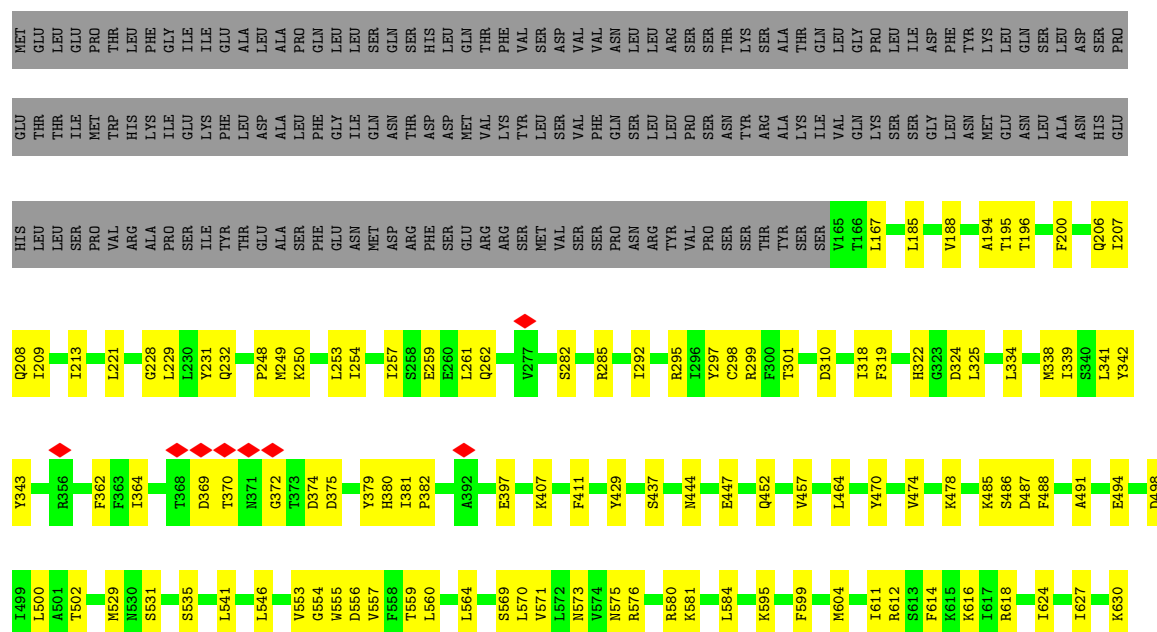
• Molecule 2: Spindle pole body component



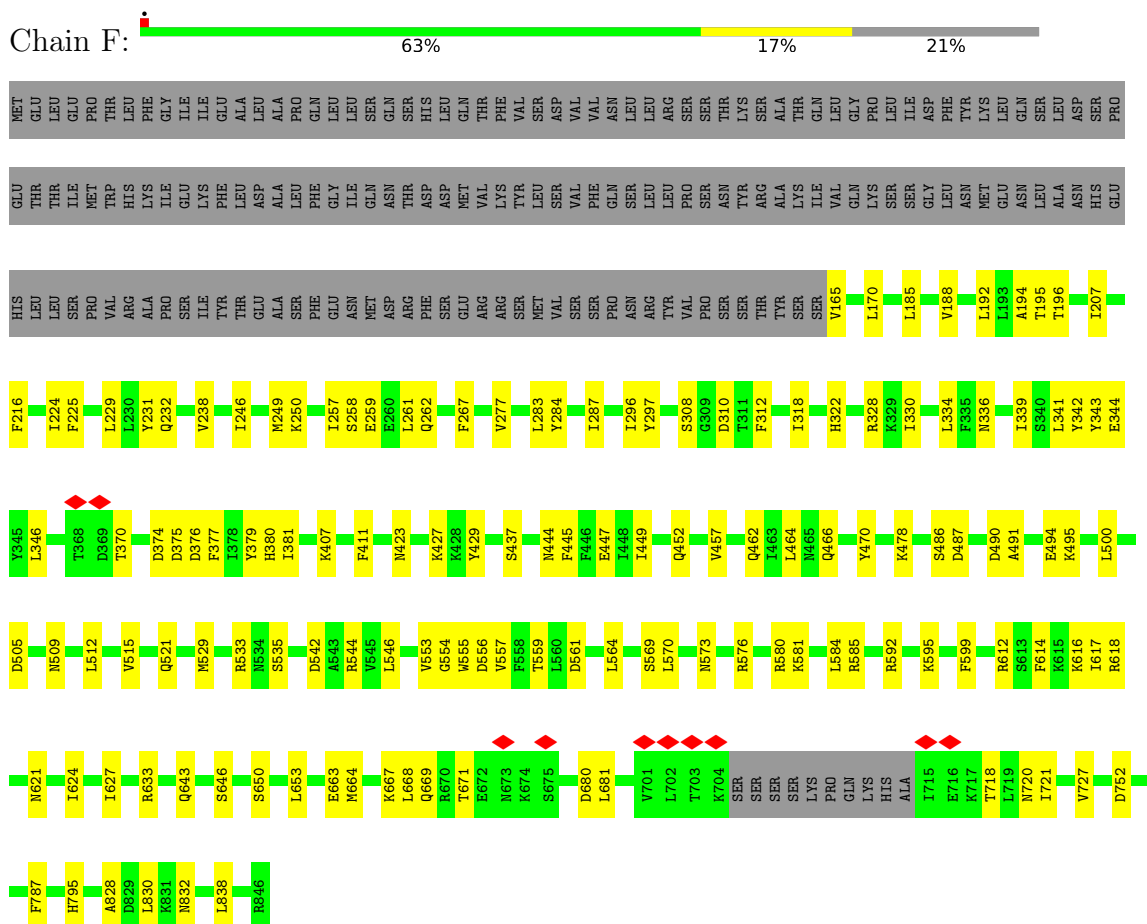


• Molecule 3: Spindle pole body component

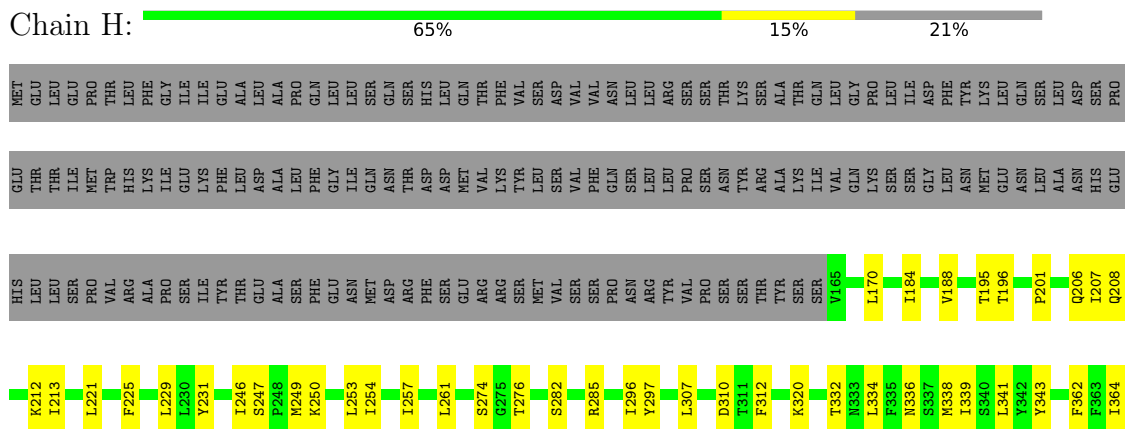
Chain D: 60% 16% 23%

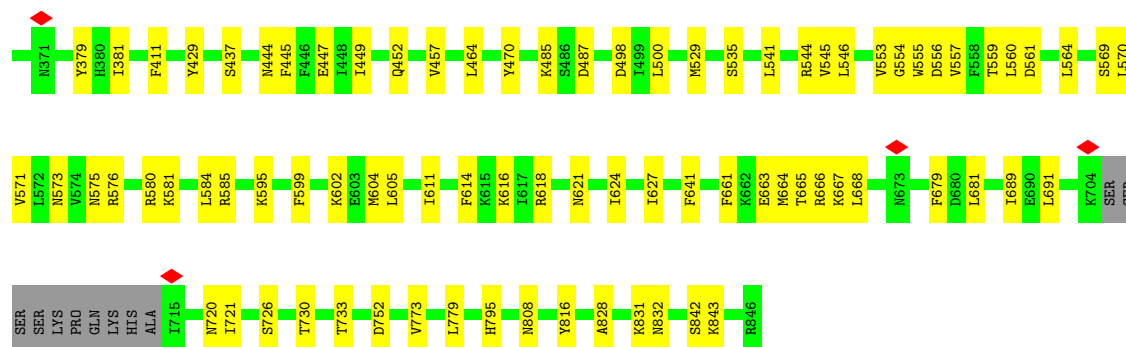


- Molecule 3: Spindle pole body component

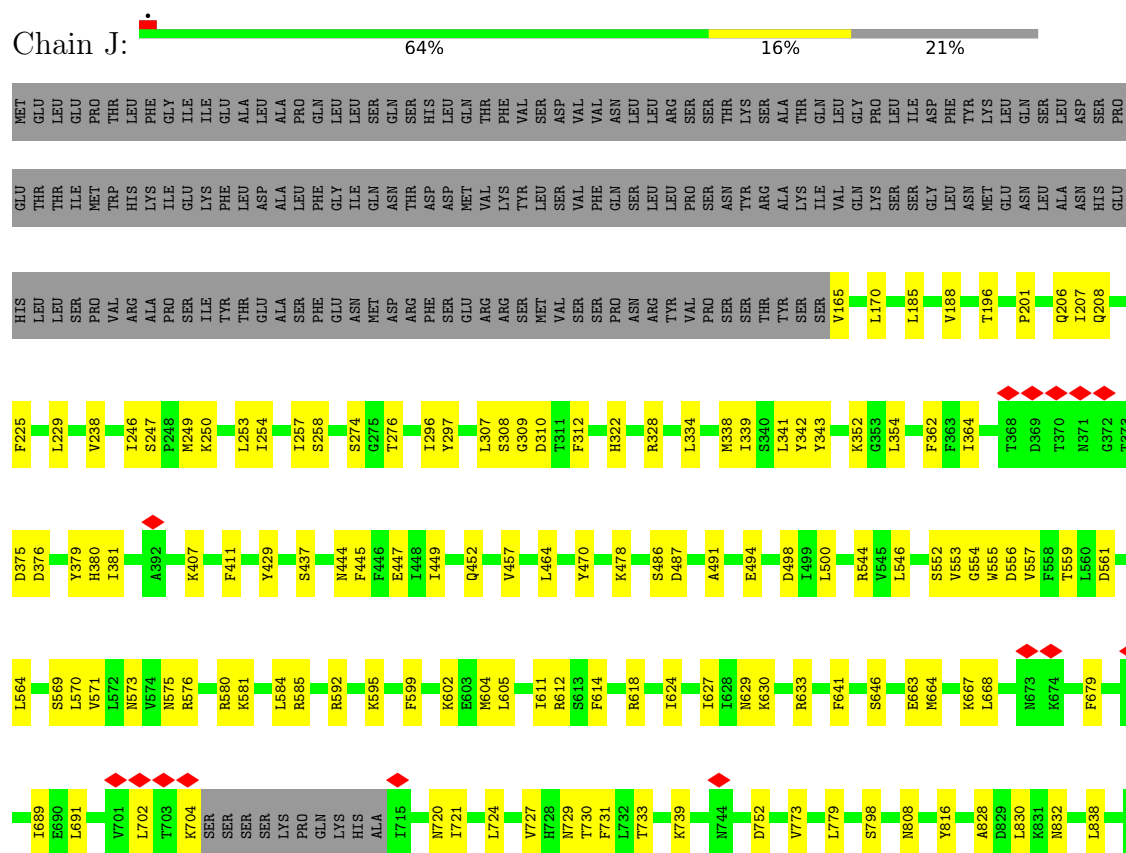


- Molecule 3: Spindle pole body component

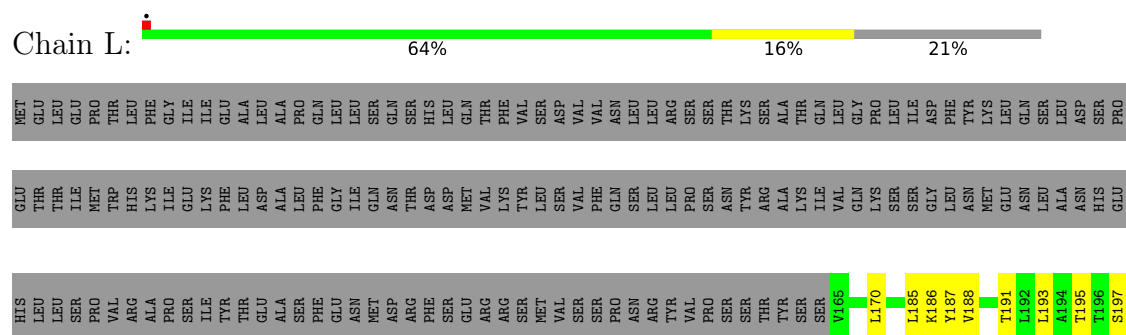


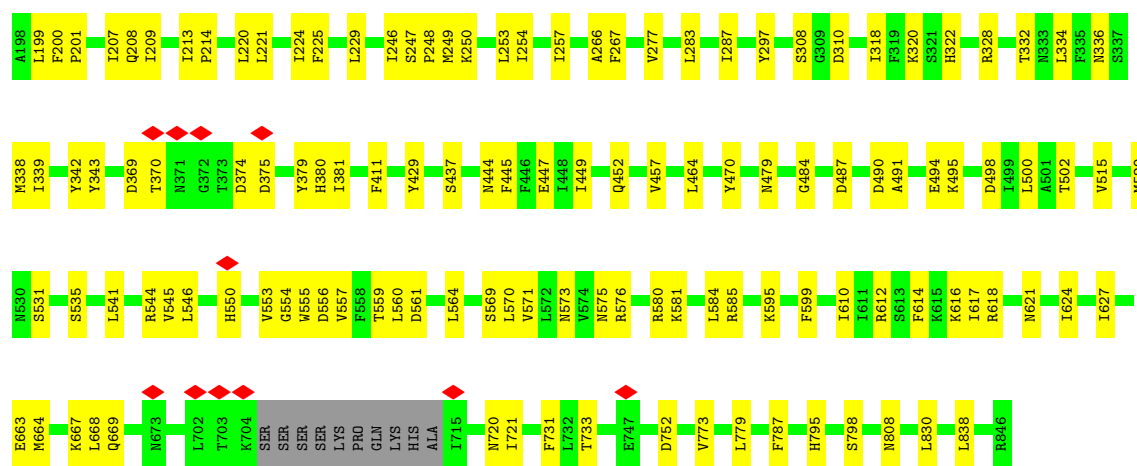


• Molecule 3: Spindle pole body component



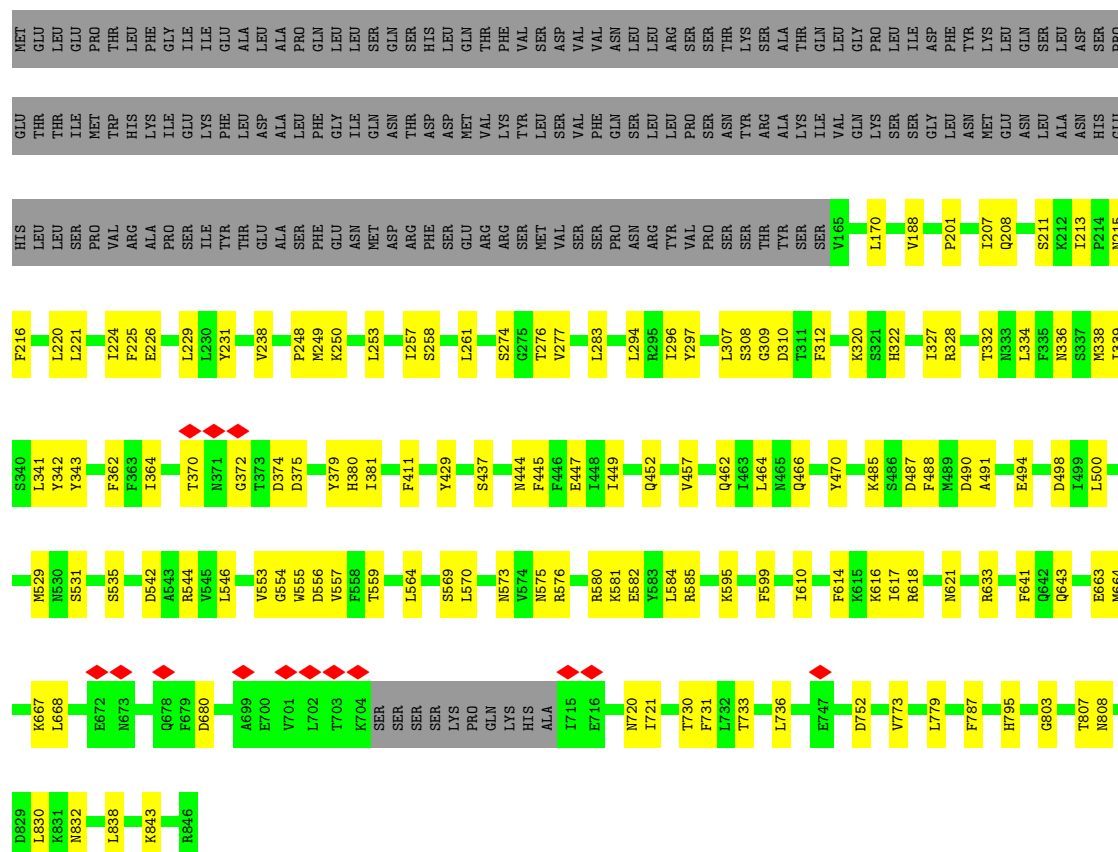
• Molecule 3: Spindle pole body component





• Molecule 3: Spindle pole body component

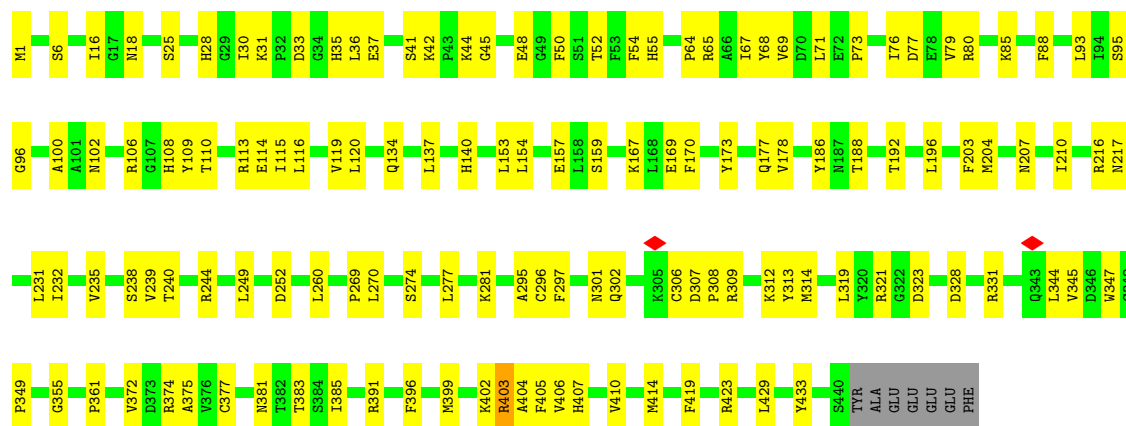
Chain N: 63% 16% 21%



• Molecule 3: Spindle pole body component

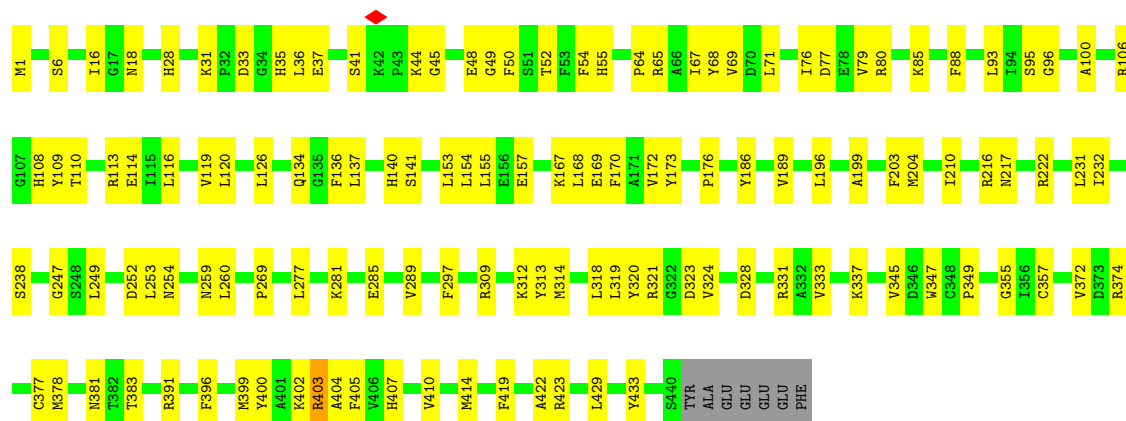
Chain P: 6% 61% 18% 21%





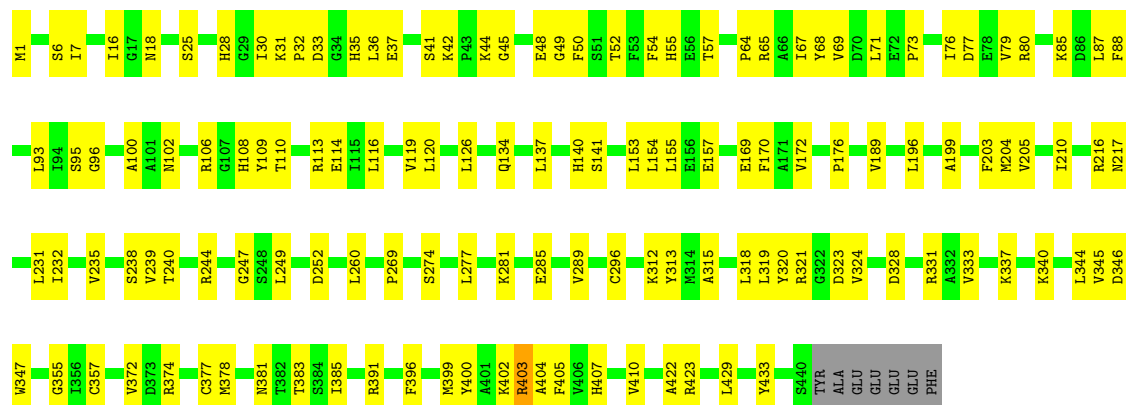
• Molecule 4: Tubulin alpha-1 chain

Chain Af: 70% 28% .



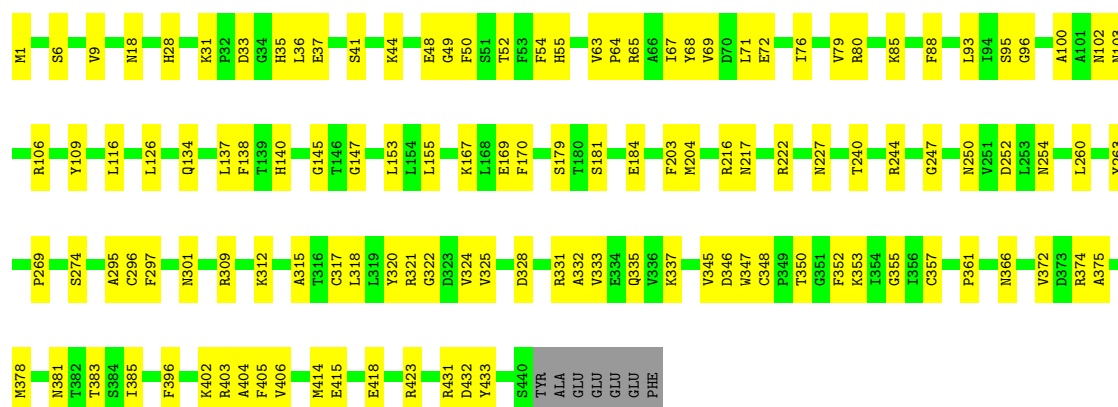
• Molecule 4: Tubulin alpha-1 chain

Chain Ae: 68% 30% .



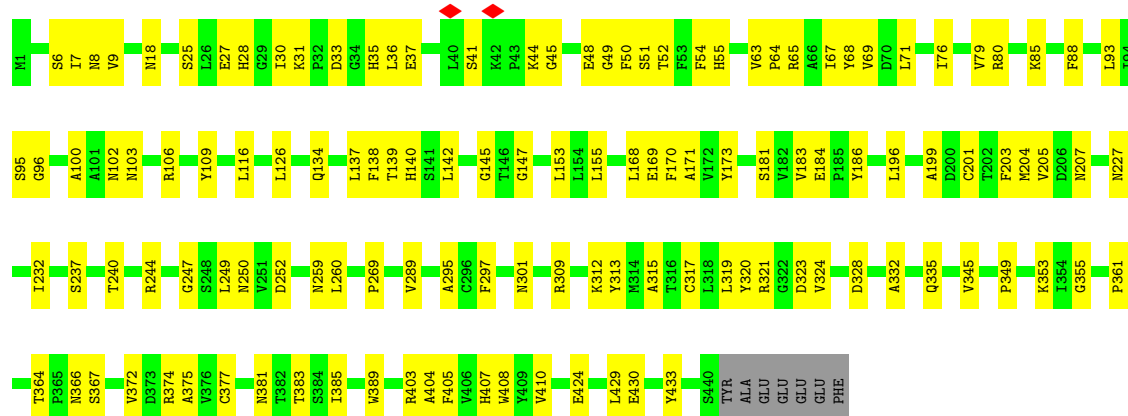
• Molecule 4: Tubulin alpha-1 chain

Chain Ah: 68% 30% .



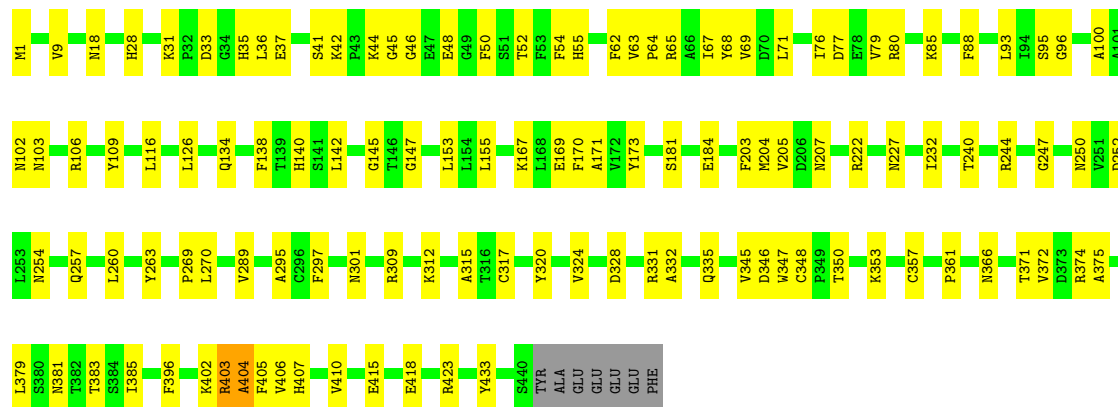
• Molecule 4: Tubulin alpha-1 chain

Chain Al: 70% 28% .



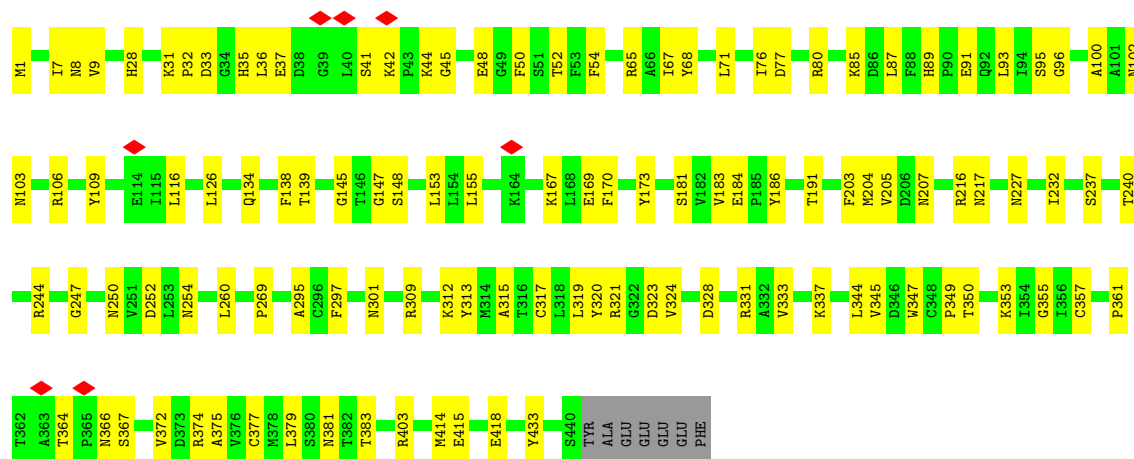
• Molecule 4: Tubulin alpha-1 chain

Chain Ak: 72% 26% .

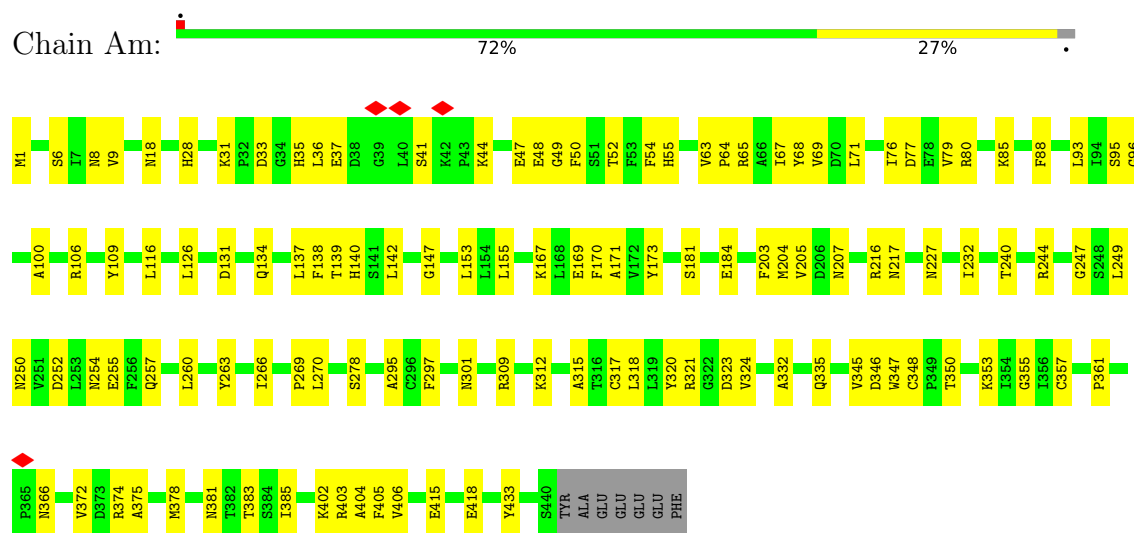


• Molecule 4: Tubulin alpha-1 chain

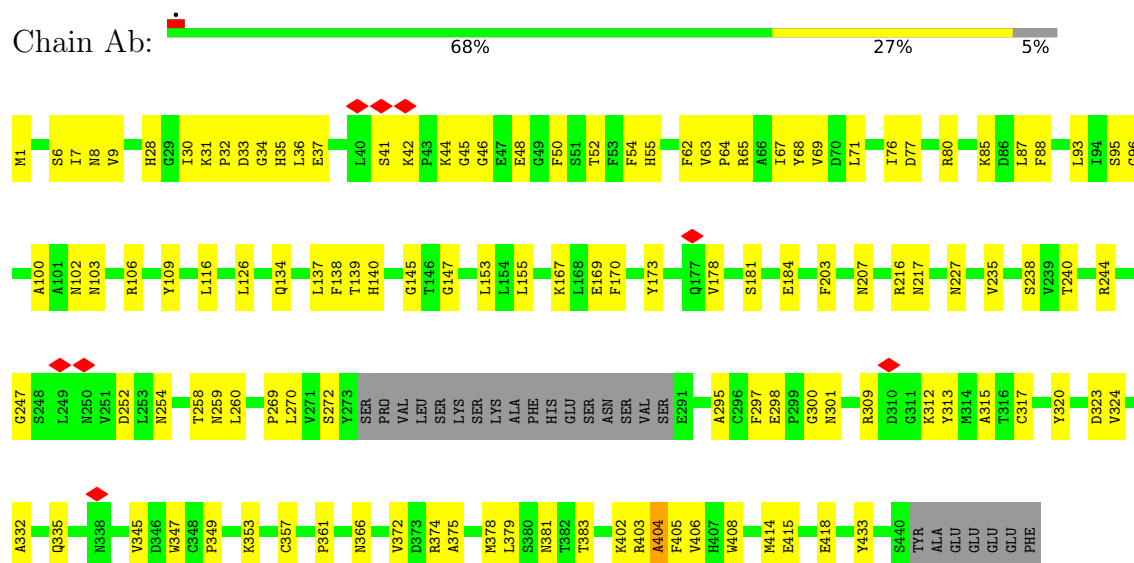
Chain An: 73% 26% .



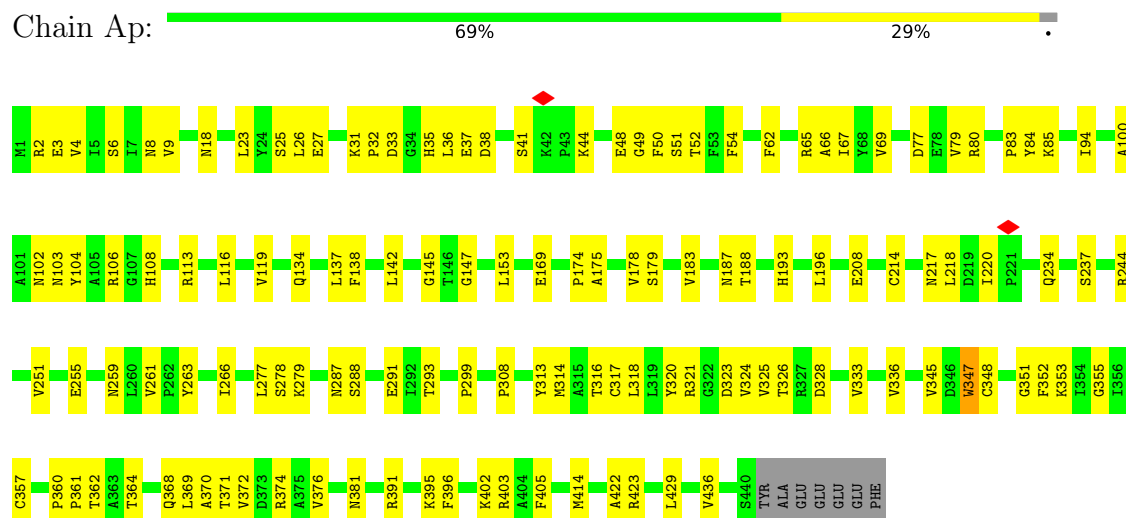
• Molecule 4: Tubulin alpha-1 chain



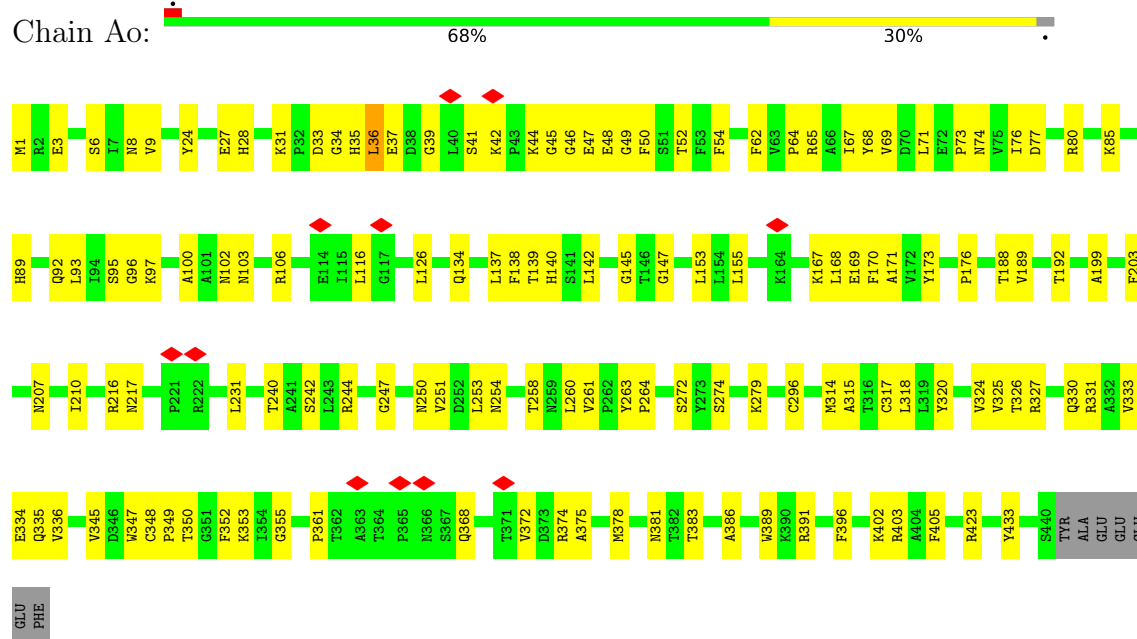
• Molecule 4: Tubulin alpha-1 chain



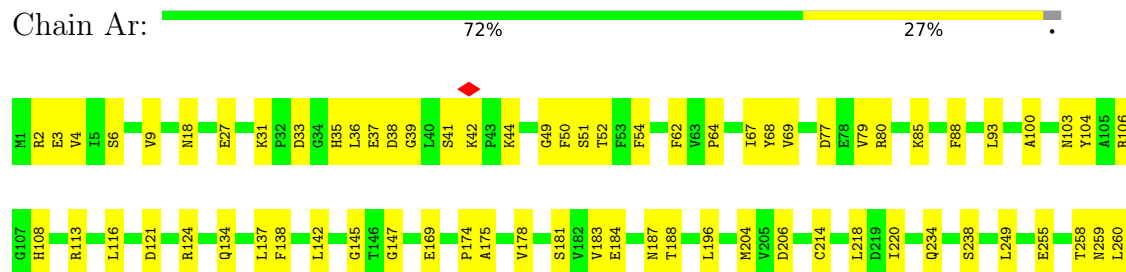
- Molecule 4: Tubulin alpha-1 chain

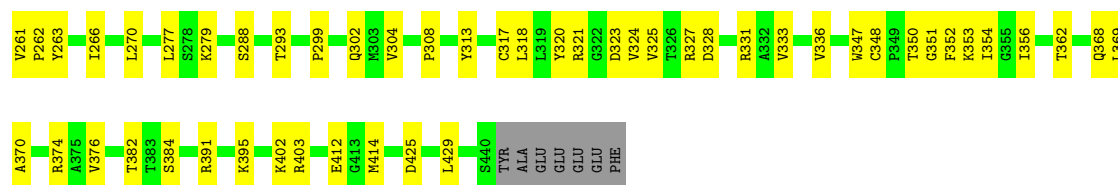


- Molecule 4: Tubulin alpha-1 chain



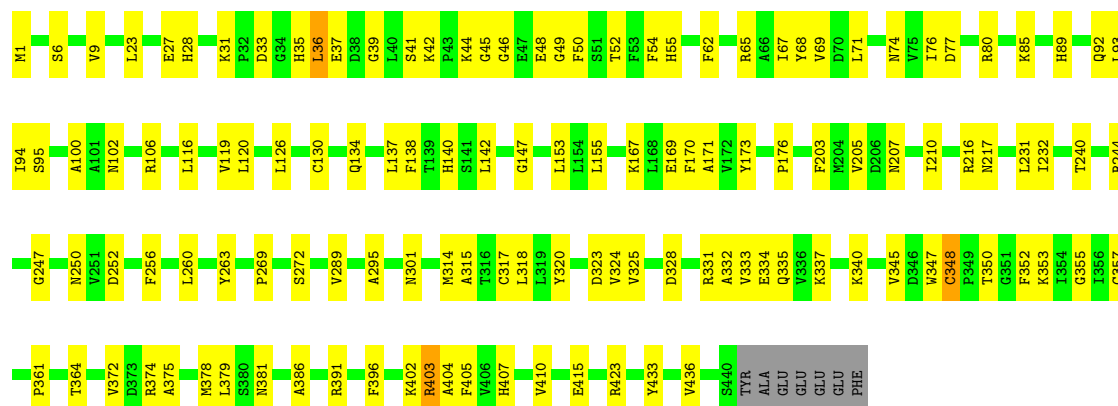
- Molecule 4: Tubulin alpha-1 chain





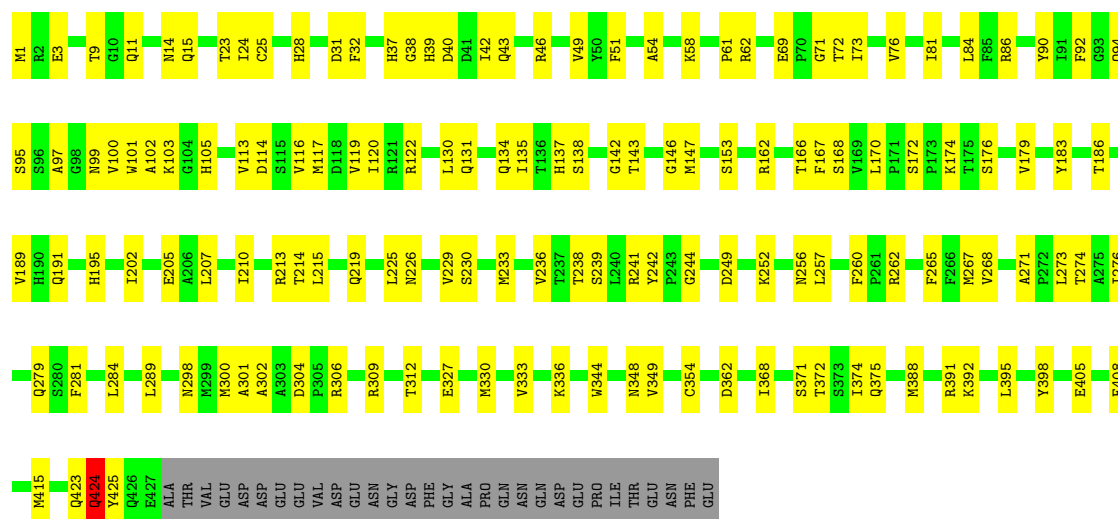
• Molecule 4: Tubulin alpha-1 chain

Chain Aq: 70% 28% ..



• Molecule 5: Tubulin beta chain

Chain Bd: 62% 32% 7%

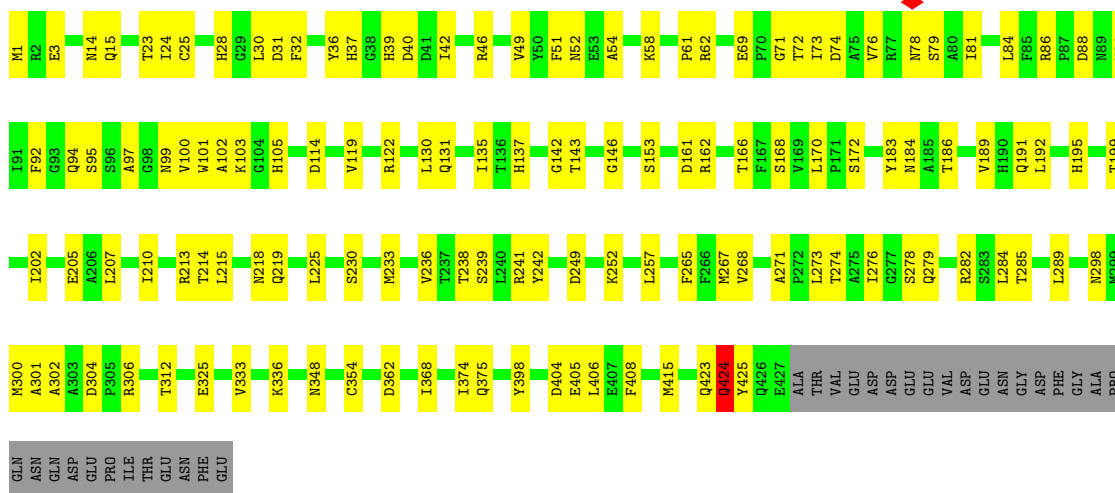


• Molecule 5: Tubulin beta chain

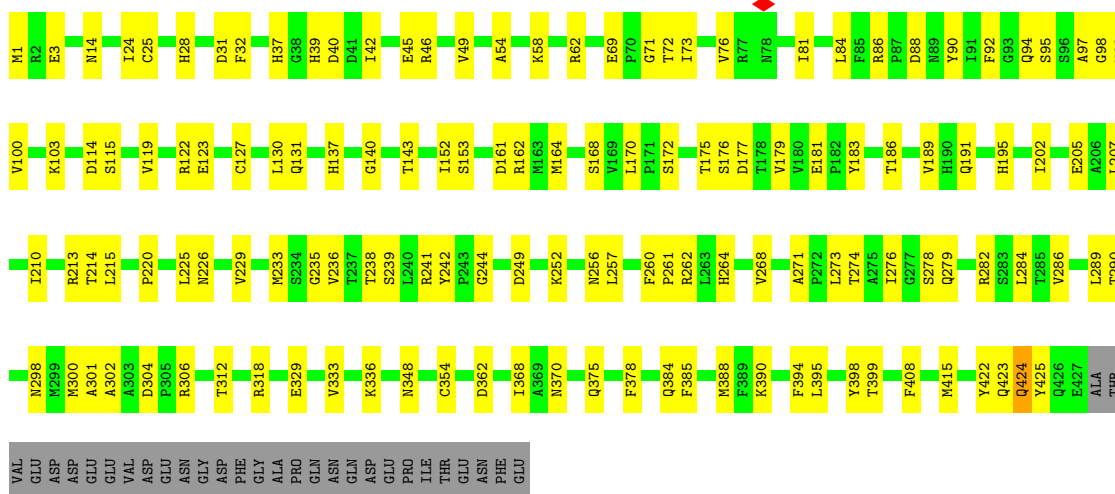
Chain Bc: 62% 31% 7%



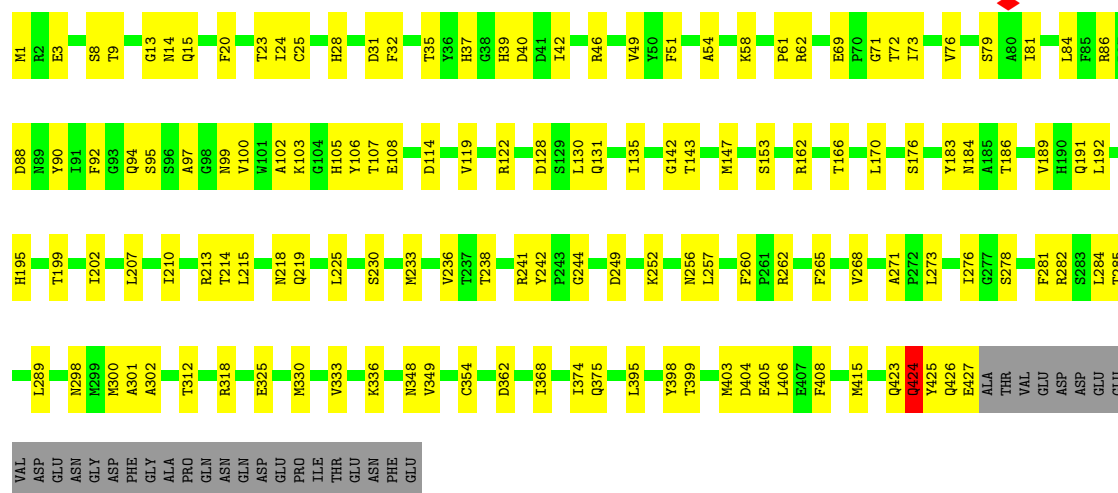
- Molecule 5: Tubulin beta chain



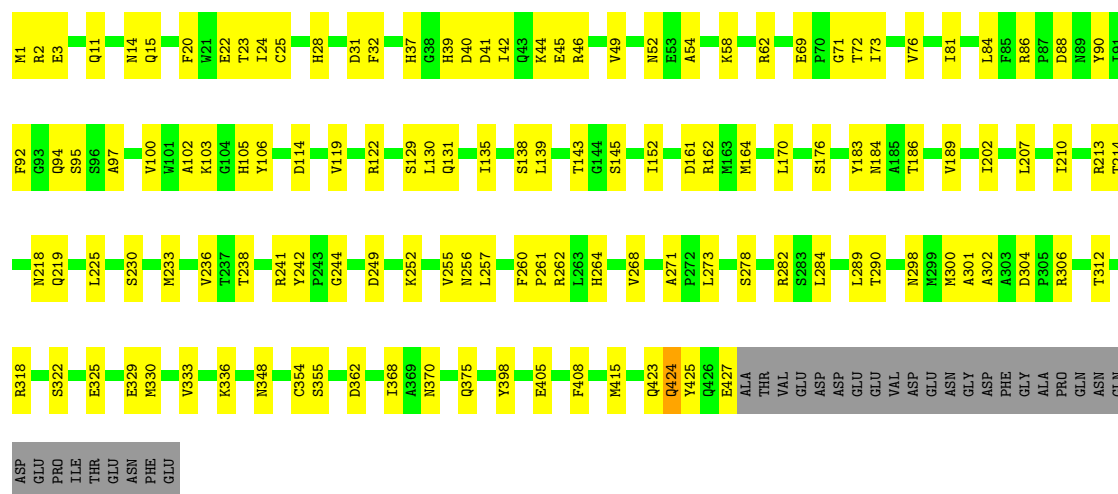
- Molecule 5: Tubulin beta chain



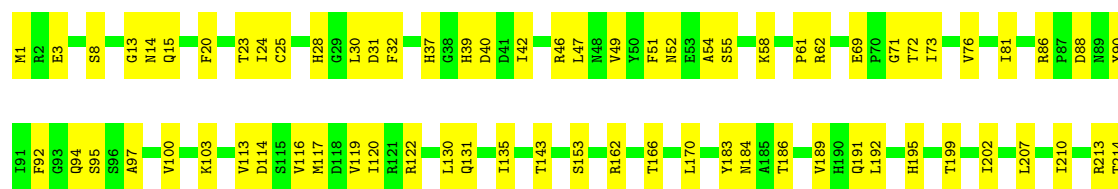
- Molecule 5: Tubulin beta chain

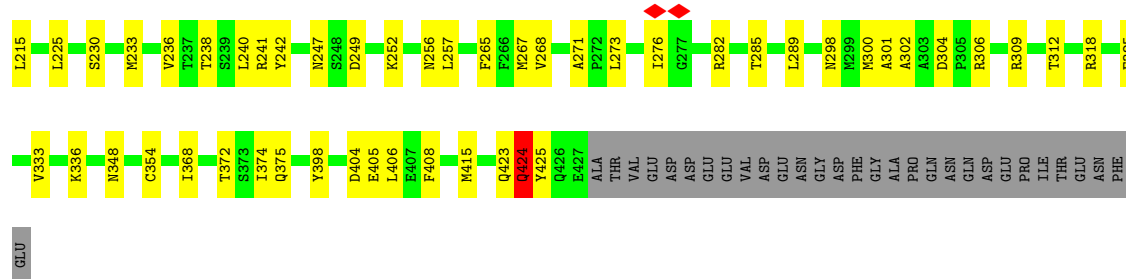
Chain Bh: 

- Molecule 5: Tubulin beta chain

Chain Bg: 

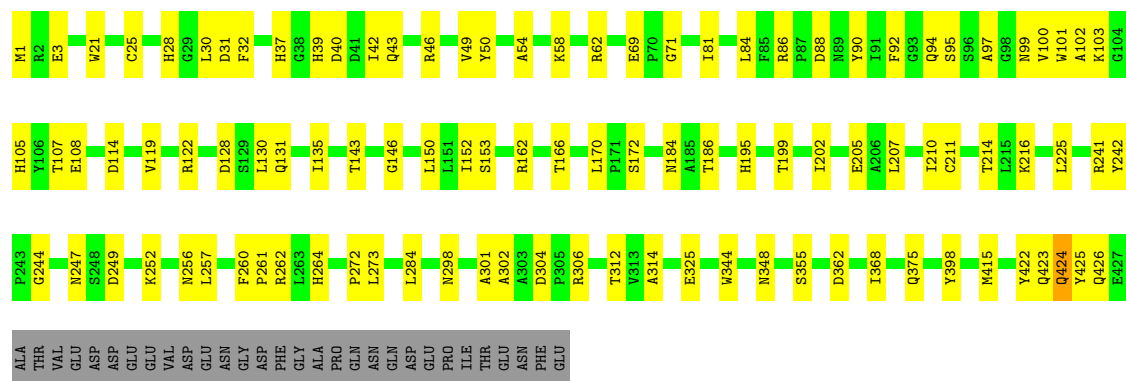
- Molecule 5: Tubulin beta chain

Chain Bj: 



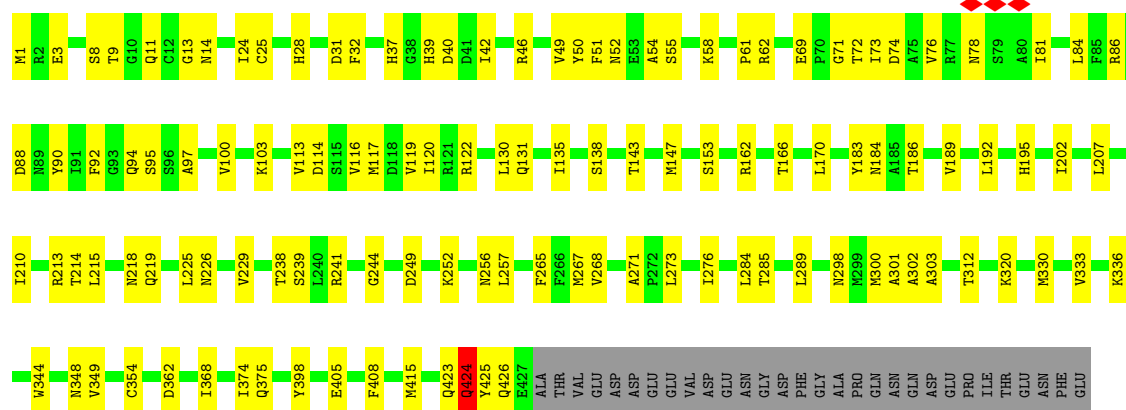
• Molecule 5: Tubulin beta chain

Chain Bi: 71% 22% 7%



• Molecule 5: Tubulin beta chain

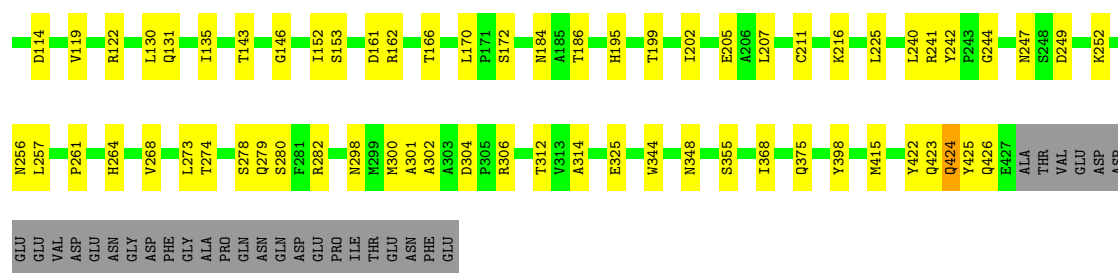
Chain Bl: 67% 26% 7%



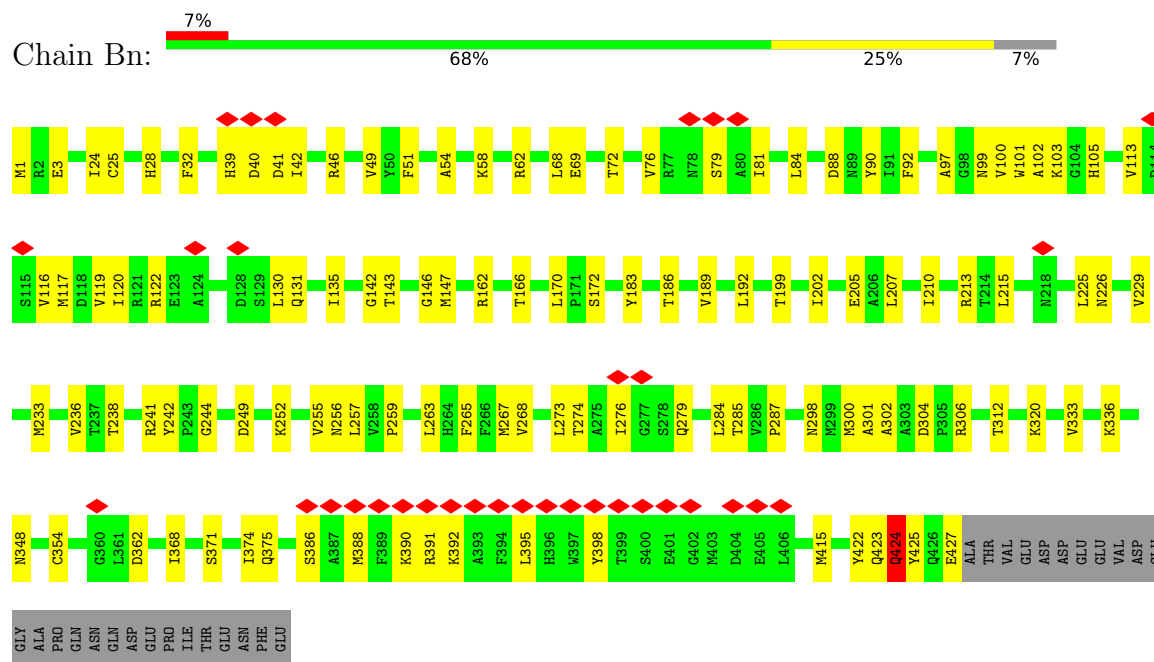
• Molecule 5: Tubulin beta chain

Chain Bk: 72% 21% 7%

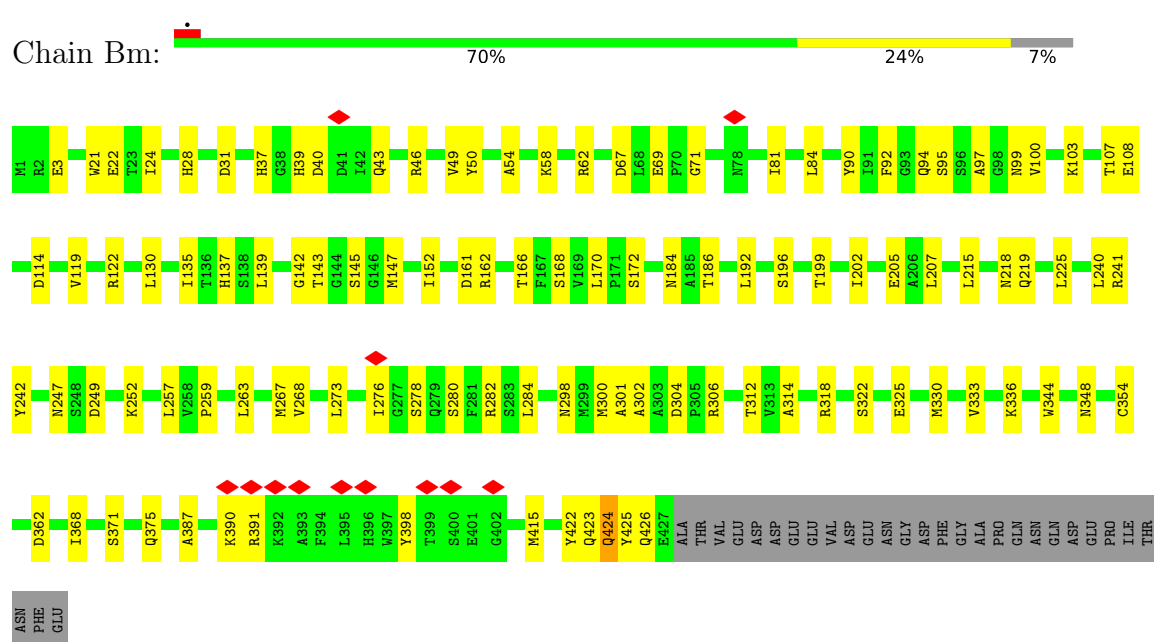




• Molecule 5: Tubulin beta chain



• Molecule 5: Tubulin beta chain



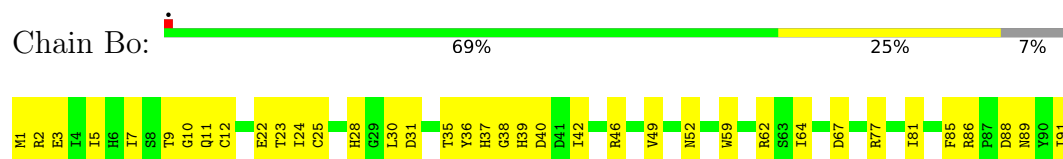
Chain Bb:

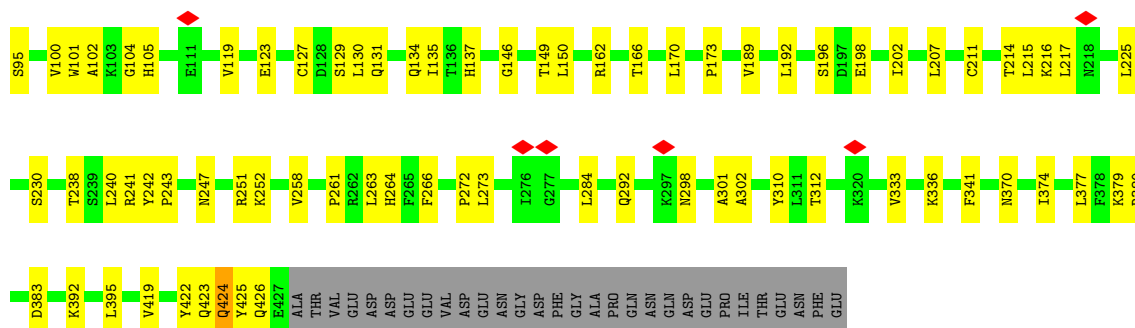


Chain Bp:

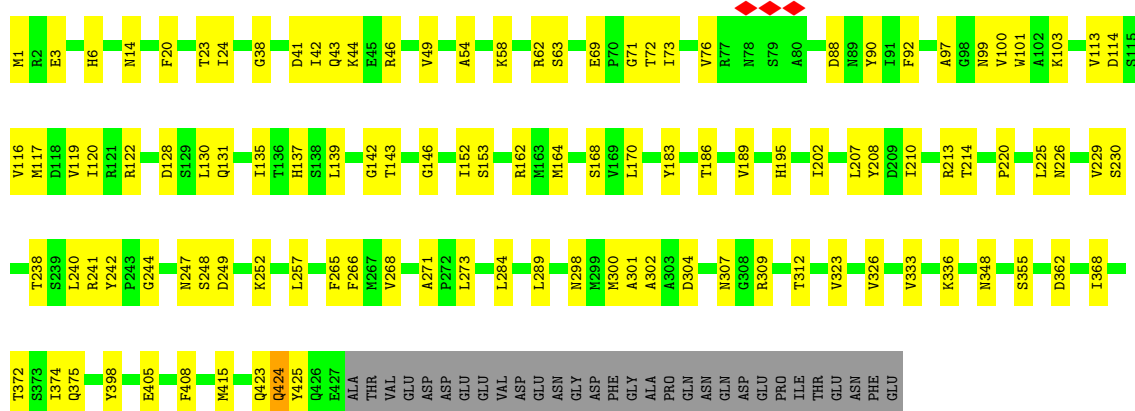


Chain Bo:

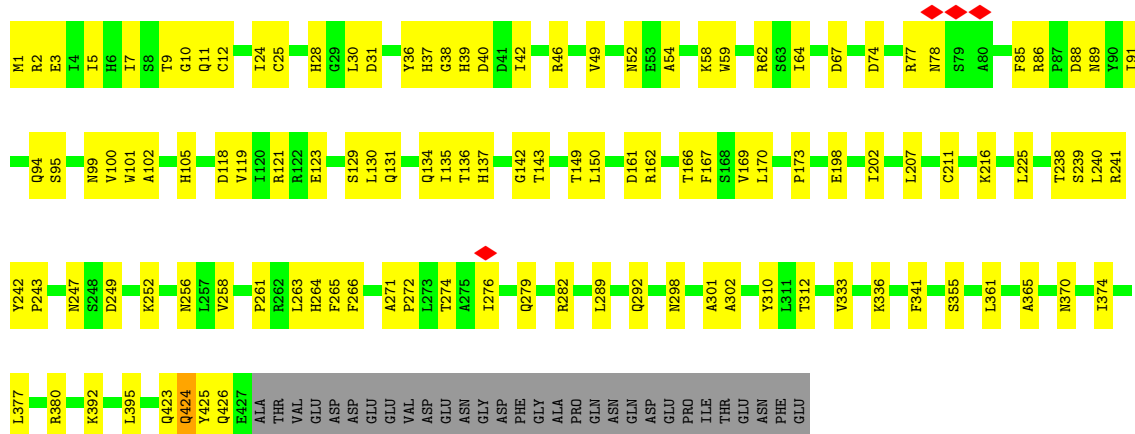




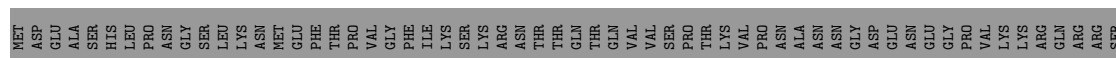
• Molecule 5: Tubulin beta chain



• Molecule 5: Tubulin beta chain



• Molecule 6: Spindle pole body component 110



[illegible]

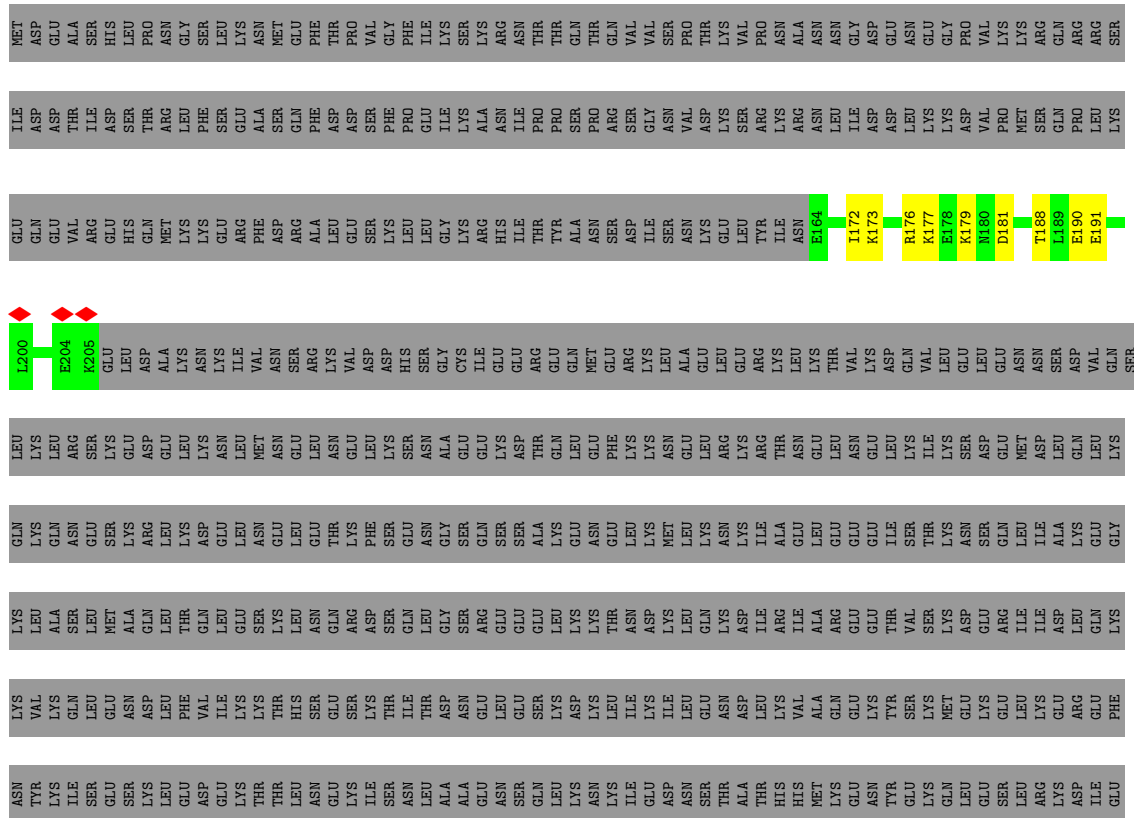
- Molecule 6: Spindle pole body component 110

[illegible]

[illegible]

- Molecule 6: Spindle pole body component 110

Chain Sg: .. 96%



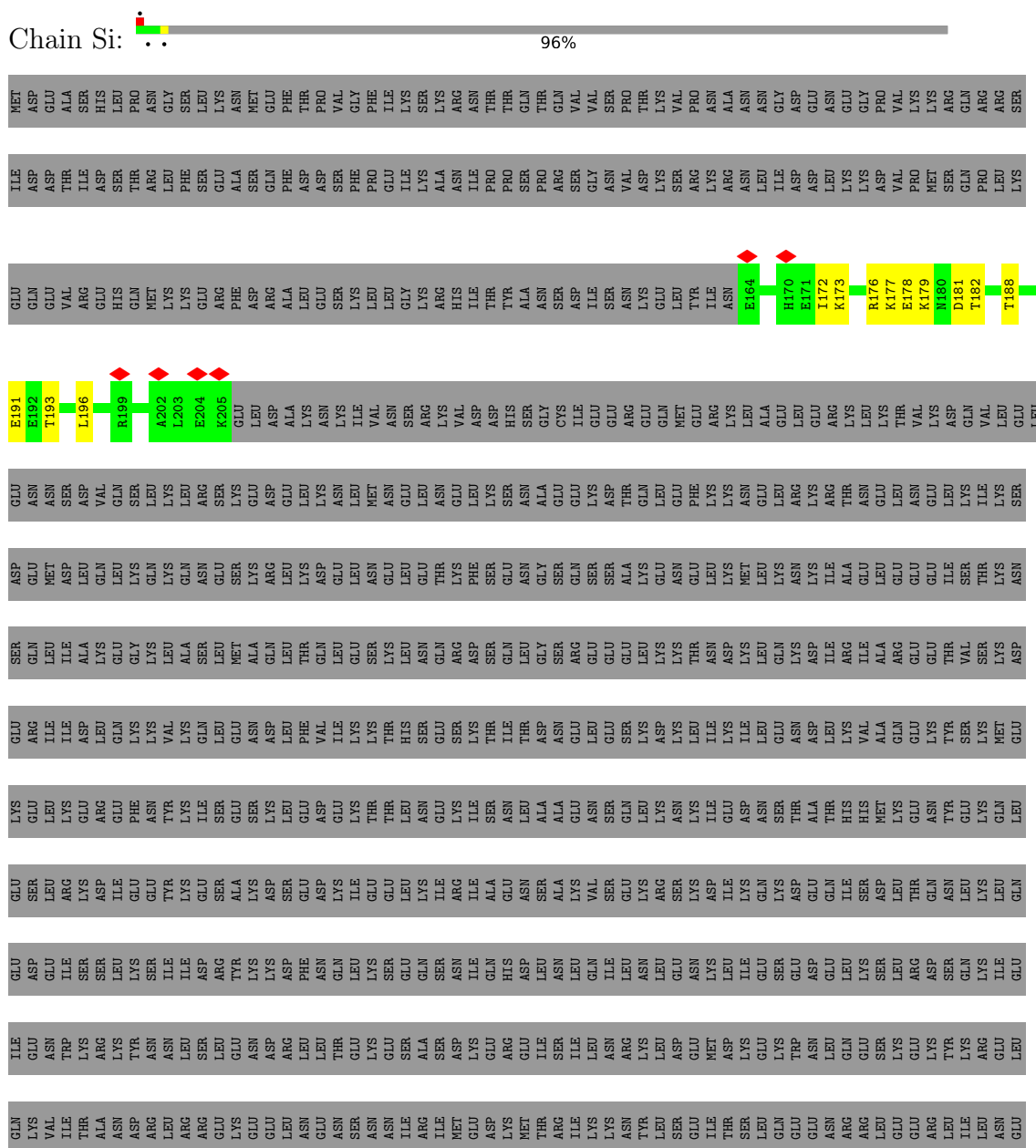
ARG	ARG	ASP	MET	ARG	ASN	SER	GLU
SER	SER	GLU	GLN	LEU	LEU	ILE	TYR
ASP	ASP	LEU	LEU	ARG	ASN	ILE	TYR
ASP	ASN	ASP	ASN	GLU	SER	ASP	GLU
ARG	ARG	ASP	ILE	LYS	GLU	TYR	ALA
LEU	LEU	TYR	ILE	GLU	ASN	LYS	LYS
ARG	ARG	TYR	SER	GLU	ASP	ASP	ASP
ARG	ARG	TYR	SER	GLU	ARG	ASP	GLU
ILE	ILE	ASN	TYR	LEU	ASN	PHE	GLU
LEU	LEU	SER	TYR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

- Molecule 6: Spindle pole body component 110

[illegible]

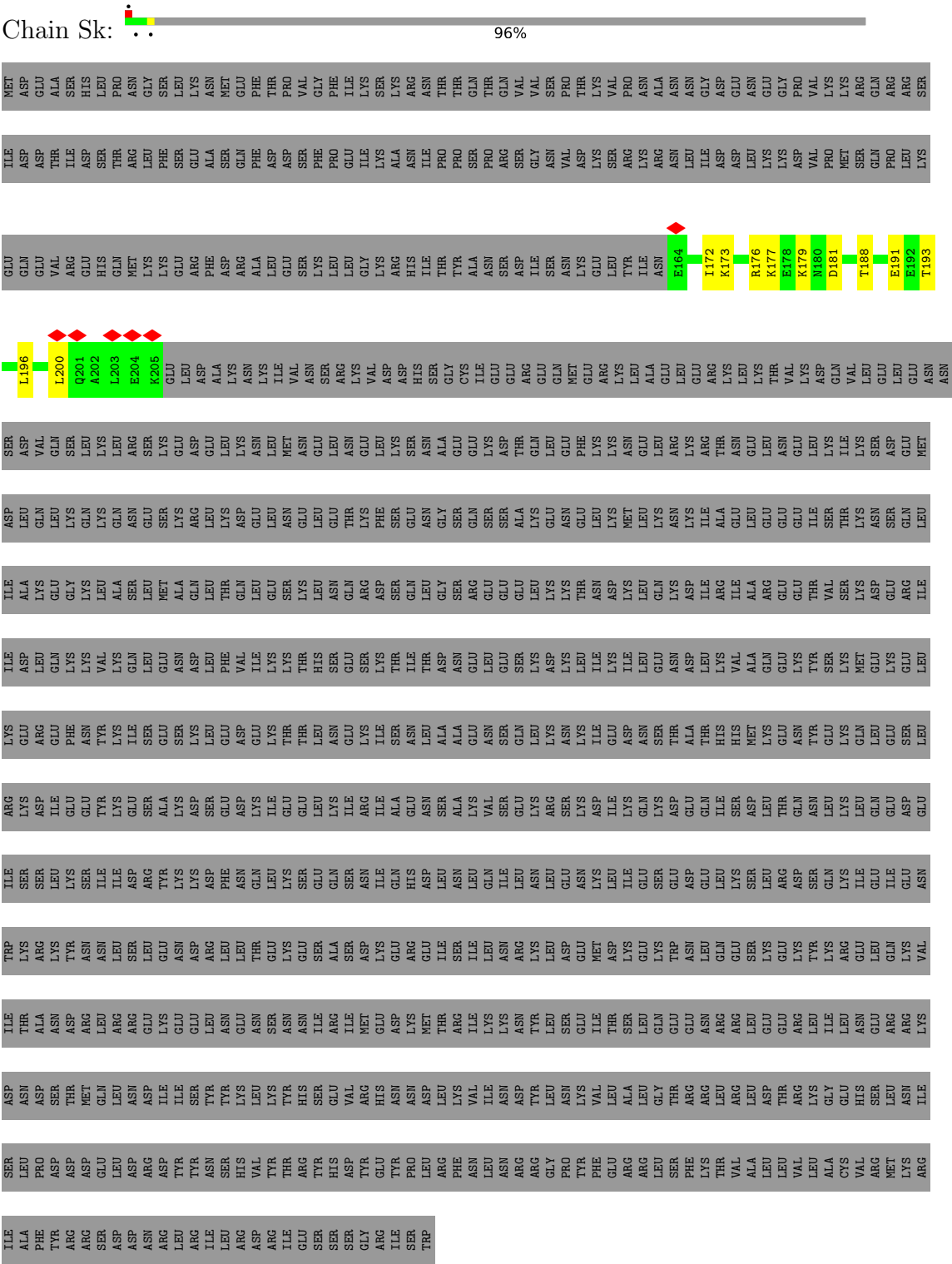
[illegible]

● Molecule 6: Spindle pole body component 110



SER
GLY
ARG
ILE
SER
TRP

• Molecule 6: Spindle pole body component 110

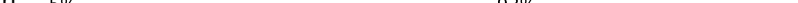


• Molecule 6: Spindle pole body component 110



[illegible]

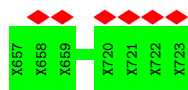
● Molecule 6: Spindle pole body component 110

Chain Sn:  5% 93%

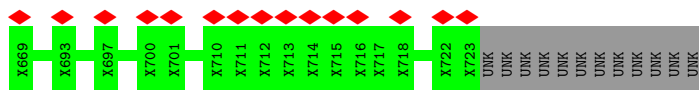
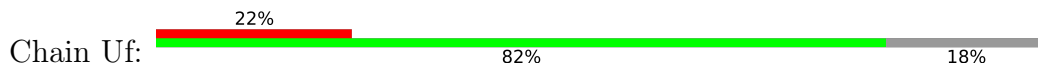
[illegible]

[illegible]

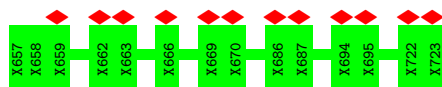
- Molecule 7: Unknown protein



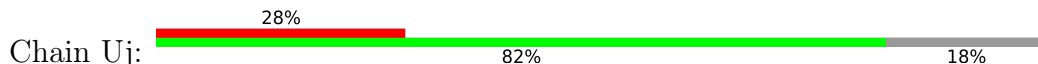
- Molecule 7: Unknown protein

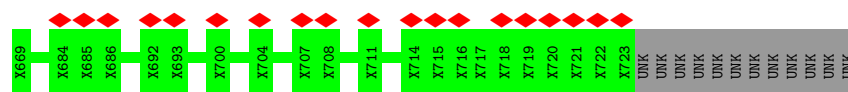


- Molecule 7: Unknown protein

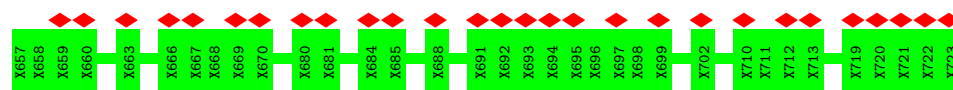


- Molecule 7: Unknown protein

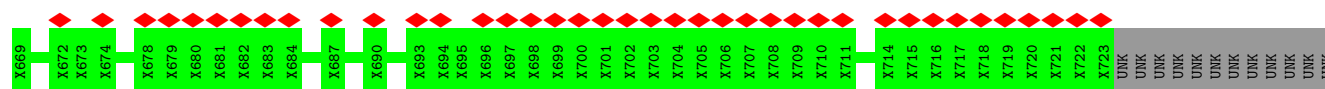
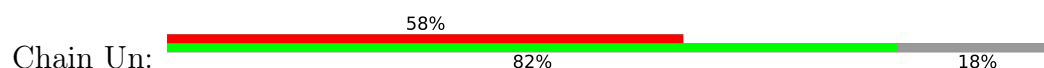




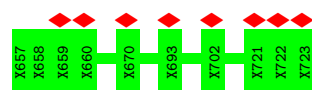
- Molecule 7: Unkown protein



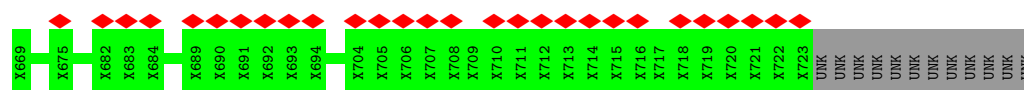
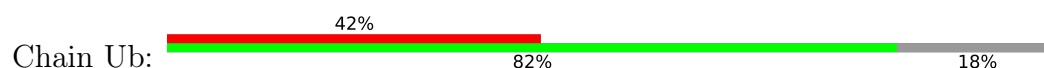
- Molecule 7: Unkown protein



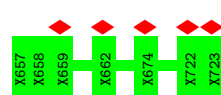
- Molecule 7: Unkown protein



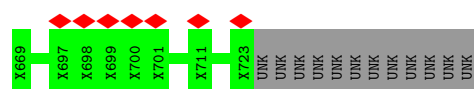
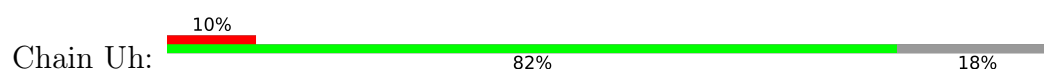
- Molecule 7: Unkown protein



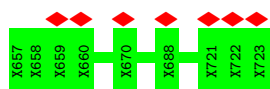
- Molecule 7: Unkown protein



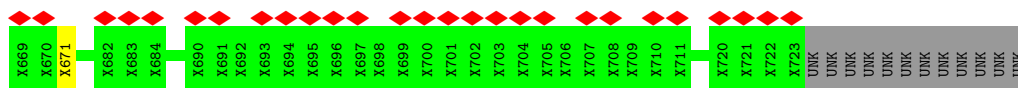
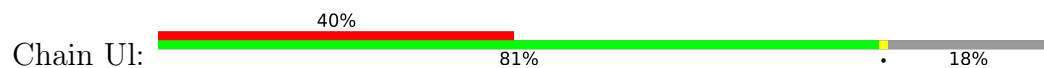
- Molecule 7: Unkown protein



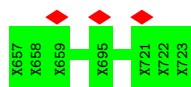
- Molecule 7: Unkown protein



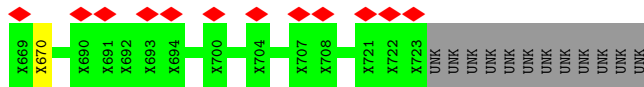
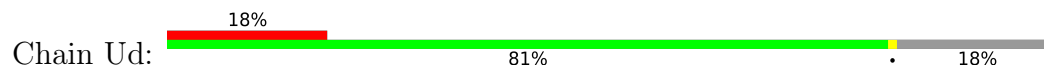
- Molecule 7: Unkown protein



- Molecule 7: Unkown protein



- Molecule 7: Unkown protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	7910	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	123	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.814	Depositor
Minimum map value	-0.437	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.243	Depositor
Map size (Å)	554.39996, 554.39996, 554.39996	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.2999997, 3.2999997, 3.2999997	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	a	0.13	0/3513	0.35	0/4769
1	b	0.10	0/3620	0.25	0/4917
1	c	0.10	0/3520	0.25	0/4779
1	d	0.10	0/3620	0.26	0/4917
1	e	0.10	0/3504	0.25	0/4757
1	f	0.10	0/3620	0.25	0/4917
1	g	0.10	0/3520	0.25	0/4779
1	h	0.10	0/3620	0.24	0/4917
1	i	0.10	0/3504	0.25	0/4757
1	j	0.10	0/3620	0.25	0/4917
1	k	0.10	0/3520	0.25	0/4779
1	l	0.10	0/3620	0.24	0/4917
1	m	0.10	0/3504	0.25	0/4757
1	n	0.10	0/3620	0.24	0/4917
2	C	0.63	6/5890 (0.1%)	0.36	1/7949 (0.0%)
2	E	0.10	0/5961	0.26	0/8045
2	G	0.10	0/5961	0.26	0/8045
2	I	0.10	0/5961	0.26	0/8045
2	K	0.10	0/5961	0.26	0/8045
2	M	0.10	0/5961	0.26	0/8045
2	O	0.10	0/5961	0.26	0/8045
3	D	0.16	0/5507	0.29	0/7443
3	F	0.11	0/5676	0.26	0/7672
3	H	0.10	0/5676	0.23	0/7672
3	J	0.10	0/5676	0.23	0/7672
3	L	0.10	0/5676	0.23	0/7672
3	N	0.10	0/5676	0.24	0/7672
3	P	0.10	0/5676	0.25	0/7672
4	Ab	0.10	0/3384	0.31	0/4589
4	Ac	0.12	0/3514	0.33	0/4766
4	Ad	0.12	0/3514	0.33	0/4766
4	Ae	0.12	0/3514	0.33	0/4766

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	Af	0.12	0/3514	0.32	0/4766
4	Ag	0.12	0/3514	0.34	0/4766
4	Ah	0.12	0/3514	0.32	0/4766
4	Ai	0.10	0/3514	0.30	0/4766
4	Aj	0.11	0/3514	0.29	0/4766
4	Ak	0.10	0/3514	0.30	0/4766
4	Al	0.11	0/3514	0.29	0/4766
4	Am	0.10	0/3514	0.31	0/4766
4	An	0.11	0/3514	0.30	0/4766
4	Ao	0.12	0/3514	0.33	0/4766
4	Ap	0.58	6/3514 (0.2%)	0.33	0/4766
4	Aq	0.12	0/3514	0.34	0/4766
4	Ar	0.13	0/3514	0.31	0/4766
5	Bb	0.12	0/3318	0.33	2/4493 (0.0%)
5	Bc	1.09	1/3416 (0.0%)	0.36	4/4627 (0.1%)
5	Bd	0.12	0/3416	0.32	2/4627 (0.0%)
5	Be	0.11	0/3416	0.32	2/4627 (0.0%)
5	Bf	0.11	0/3416	0.32	2/4627 (0.0%)
5	Bg	0.10	0/3416	0.30	2/4627 (0.0%)
5	Bh	0.11	0/3416	0.32	2/4627 (0.0%)
5	Bi	0.10	0/3416	0.28	2/4627 (0.0%)
5	Bj	0.11	0/3416	0.32	2/4627 (0.0%)
5	Bk	0.10	0/3416	0.28	2/4627 (0.0%)
5	Bl	0.11	0/3416	0.31	2/4627 (0.0%)
5	Bm	0.10	0/3416	0.28	2/4627 (0.0%)
5	Bn	0.12	0/3416	0.34	2/4627 (0.0%)
5	Bo	0.10	0/3416	0.30	2/4627 (0.0%)
5	Bp	0.11	0/3416	0.32	2/4627 (0.0%)
5	Bq	0.10	0/3416	0.31	2/4627 (0.0%)
5	Br	0.12	0/3416	0.32	2/4627 (0.0%)
6	Sa	0.14	0/353	0.33	0/471
6	Sb	0.12	0/521	0.32	0/698
6	Sc	0.11	0/353	0.27	0/471
6	Sd	0.10	0/720	0.25	0/960
6	Se	0.11	0/353	0.25	0/471
6	Sf	0.11	0/729	0.24	0/972
6	Sg	0.10	0/353	0.24	0/471
6	Sh	0.10	0/720	0.25	0/960
6	Si	0.11	0/353	0.24	0/471
6	Sj	0.10	0/729	0.24	0/972
6	Sk	0.11	0/353	0.27	0/471
6	Sl	0.10	0/720	0.24	0/960
6	Sm	0.12	0/171	0.28	0/224

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	Sn	0.10	0/550	0.30	0/729
All	All	0.20	13/255704 (0.0%)	0.29	37/346161 (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
4	Ab	0	2
4	Ac	0	2
4	Ad	0	2
4	Ae	0	2
4	Af	0	2
4	Ag	0	2
4	Ah	0	2
4	Ai	0	2
4	Aj	0	2
4	Ak	0	2
4	Al	0	2
4	Am	0	2
4	An	0	2
4	Ao	0	2
4	Ap	0	1
4	Aq	0	3
4	Ar	0	1
5	Bb	0	1
5	Bd	0	1
5	Bf	0	1
5	Bh	0	1
5	Bj	0	1
5	Bl	0	1
5	Bn	0	1
All	All	0	40

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Bc	391	ARG	CB-CG	63.13	3.41	1.52
2	C	320	TRP	CE3-CZ3	29.17	2.26	1.38
2	C	320	TRP	CE2-CZ2	21.01	1.83	1.39
4	Ap	347	TRP	CE3-CZ3	18.64	1.94	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	320	TRP	CZ3-CH2	17.87	1.85	1.40

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Bc	391	ARG	CA-CB-CG	9.49	133.09	114.10
5	Bc	391	ARG	CB-CG-CD	8.09	129.91	111.30
5	Bn	424	GLN	CA-C-N	6.93	134.18	121.70
5	Bn	424	GLN	C-N-CA	6.93	134.18	121.70
5	Bf	424	GLN	CA-C-N	6.89	134.10	121.70

There are no chirality outliers.

5 of 40 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	Ac	35	HIS	Peptide
4	Ac	36	LEU	Peptide
4	Ad	35	HIS	Peptide
4	Ad	36	LEU	Peptide
5	Bd	424	GLN	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	a	3441	0	3304	54	0
1	b	3545	0	3396	68	0
1	c	3448	0	3313	73	0
1	d	3545	0	3396	74	0
1	e	3433	0	3301	63	0
1	f	3545	0	3396	59	0
1	g	3448	0	3313	61	0
1	h	3545	0	3396	76	0
1	i	3433	0	3301	73	0
1	j	3545	0	3396	61	0
1	k	3448	0	3313	65	0
1	l	3545	0	3396	60	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	m	3433	0	3301	69	0
1	n	3545	0	3396	59	0
2	C	5778	0	5841	121	0
2	E	5847	0	5908	114	0
2	G	5847	0	5908	103	0
2	I	5847	0	5908	115	0
2	K	5847	0	5908	107	0
2	M	5847	0	5908	113	0
2	O	5847	0	5908	117	0
3	D	5390	0	5413	105	0
3	F	5557	0	5578	99	0
3	H	5557	0	5578	85	0
3	J	5557	0	5578	92	0
3	L	5557	0	5578	94	0
3	N	5557	0	5578	95	0
3	P	5557	0	5578	100	0
4	Ab	3312	0	3213	81	0
4	Ac	3438	0	3339	90	0
4	Ad	3438	0	3339	98	0
4	Ae	3438	0	3339	89	0
4	Af	3438	0	3339	82	0
4	Ag	3438	0	3339	86	0
4	Ah	3438	0	3339	90	0
4	Ai	3438	0	3339	80	0
4	Aj	3438	0	3339	82	0
4	Ak	3438	0	3339	80	0
4	Al	3438	0	3339	81	0
4	Am	3438	0	3339	83	0
4	An	3438	0	3339	77	0
4	Ao	3438	0	3339	104	0
4	Ap	3438	0	3339	117	0
4	Aq	3438	0	3339	90	0
4	Ar	3438	0	3339	88	0
5	Bb	3247	0	3107	105	0
5	Bc	3343	0	3208	123	0
5	Bd	3343	0	3208	99	0
5	Be	3343	0	3208	91	0
5	Bf	3343	0	3208	87	0
5	Bg	3343	0	3208	89	0
5	Bh	3343	0	3208	95	0
5	Bi	3343	0	3208	67	0
5	Bj	3343	0	3208	85	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	Bk	3343	0	3208	63	0
5	Bl	3343	0	3208	83	0
5	Bm	3343	0	3208	66	0
5	Bn	3343	0	3208	80	0
5	Bo	3343	0	3208	71	0
5	Bp	3343	0	3208	87	0
5	Bq	3343	0	3208	75	0
5	Br	3343	0	3208	75	0
6	Sa	352	0	347	18	0
6	Sb	517	0	507	19	0
6	Sc	352	0	347	13	0
6	Sd	714	0	709	25	0
6	Se	352	0	347	8	0
6	Sf	723	0	715	12	0
6	Sg	352	0	347	8	0
6	Sh	714	0	709	17	0
6	Si	352	0	347	10	0
6	Sj	723	0	715	16	0
6	Sk	352	0	347	10	0
6	Sl	714	0	709	15	0
6	Sm	171	0	185	7	0
6	Sn	545	0	557	19	0
7	Ua	335	0	69	0	0
7	Ub	275	0	57	0	0
7	Uc	335	0	69	0	0
7	Ud	275	0	57	1	0
7	Ue	335	0	69	0	0
7	Uf	275	0	57	0	0
7	Ug	335	0	69	0	0
7	Uh	275	0	57	0	0
7	Ui	335	0	69	0	0
7	Uj	275	0	57	0	0
7	Uk	335	0	69	0	0
7	Ul	275	0	57	1	0
7	Um	335	0	69	0	0
7	Un	275	0	57	0	0
8	b	32	0	12	0	0
8	c	32	0	12	3	0
8	d	32	0	12	3	0
8	e	32	0	12	3	0
8	f	32	0	12	0	0
8	g	32	0	12	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	h	32	0	12	0	0
8	i	32	0	12	3	0
8	j	32	0	12	1	0
8	k	32	0	12	3	0
8	l	32	0	12	1	0
8	m	32	0	12	3	0
8	n	32	0	12	2	0
9	a	28	0	12	3	0
10	Ua	1	0	0	0	0
10	Uc	1	0	0	0	0
10	Ue	1	0	0	0	0
10	Ug	1	0	0	0	0
10	Ui	1	0	0	0	0
10	Uk	1	0	0	0	0
10	Um	1	0	0	0	0
All	All	255200	0	246098	5147	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 10.

The worst 5 of 5147 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)
2:C:320:TRP:CE2	2:C:320:TRP:CZ2	1.84	1.66
2:C:320:TRP:CZ3	2:C:320:TRP:CH2	1.85	1.59
4:Ap:347:TRP:CE3	4:Ap:347:TRP:CZ3	1.94	1.52
2:C:320:TRP:CZ3	2:C:320:TRP:CE3	2.26	1.23
5:Bc:391:ARG:CB	4:Ap:347:TRP:CE3	2.30	1.13

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	a	436/473 (92%)	419 (96%)	17 (4%)	0	100	100
1	b	451/473 (95%)	444 (98%)	7 (2%)	0	100	100
1	c	437/473 (92%)	431 (99%)	6 (1%)	0	100	100
1	d	451/473 (95%)	444 (98%)	7 (2%)	0	100	100
1	e	435/473 (92%)	428 (98%)	7 (2%)	0	100	100
1	f	451/473 (95%)	441 (98%)	10 (2%)	0	100	100
1	g	437/473 (92%)	428 (98%)	9 (2%)	0	100	100
1	h	451/473 (95%)	443 (98%)	8 (2%)	0	100	100
1	i	435/473 (92%)	428 (98%)	7 (2%)	0	100	100
1	j	451/473 (95%)	443 (98%)	8 (2%)	0	100	100
1	k	437/473 (92%)	428 (98%)	9 (2%)	0	100	100
1	l	451/473 (95%)	444 (98%)	7 (2%)	0	100	100
1	m	435/473 (92%)	428 (98%)	7 (2%)	0	100	100
1	n	451/473 (95%)	445 (99%)	6 (1%)	0	100	100
2	C	681/823 (83%)	648 (95%)	33 (5%)	0	100	100
2	E	689/823 (84%)	675 (98%)	14 (2%)	0	100	100
2	G	689/823 (84%)	674 (98%)	15 (2%)	0	100	100
2	I	689/823 (84%)	674 (98%)	15 (2%)	0	100	100
2	K	689/823 (84%)	676 (98%)	13 (2%)	0	100	100
2	M	689/823 (84%)	672 (98%)	17 (2%)	0	100	100
2	O	689/823 (84%)	678 (98%)	11 (2%)	0	100	100
3	D	645/846 (76%)	623 (97%)	22 (3%)	0	100	100
3	F	668/846 (79%)	651 (98%)	17 (2%)	0	100	100
3	H	668/846 (79%)	646 (97%)	22 (3%)	0	100	100
3	J	668/846 (79%)	649 (97%)	19 (3%)	0	100	100
3	L	668/846 (79%)	646 (97%)	22 (3%)	0	100	100
3	N	668/846 (79%)	646 (97%)	22 (3%)	0	100	100
3	P	668/846 (79%)	650 (97%)	18 (3%)	0	100	100
4	Ab	419/447 (94%)	396 (94%)	22 (5%)	1 (0%)	43	78
4	Ac	438/447 (98%)	408 (93%)	28 (6%)	2 (0%)	24	63
4	Ad	438/447 (98%)	408 (93%)	28 (6%)	2 (0%)	24	63
4	Ae	438/447 (98%)	410 (94%)	26 (6%)	2 (0%)	24	63

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Af	438/447 (98%)	410 (94%)	26 (6%)	2 (0%)	24	63
4	Ag	438/447 (98%)	410 (94%)	27 (6%)	1 (0%)	43	78
4	Ah	438/447 (98%)	412 (94%)	24 (6%)	2 (0%)	24	63
4	Ai	438/447 (98%)	410 (94%)	28 (6%)	0	100	100
4	Aj	438/447 (98%)	413 (94%)	25 (6%)	0	100	100
4	Ak	438/447 (98%)	411 (94%)	25 (6%)	2 (0%)	24	63
4	Al	438/447 (98%)	414 (94%)	24 (6%)	0	100	100
4	Am	438/447 (98%)	412 (94%)	26 (6%)	0	100	100
4	An	438/447 (98%)	415 (95%)	23 (5%)	0	100	100
4	Ao	438/447 (98%)	413 (94%)	25 (6%)	0	100	100
4	Ap	438/447 (98%)	421 (96%)	17 (4%)	0	100	100
4	Aq	438/447 (98%)	414 (94%)	22 (5%)	2 (0%)	24	63
4	Ar	438/447 (98%)	423 (97%)	15 (3%)	0	100	100
5	Bb	410/457 (90%)	398 (97%)	12 (3%)	0	100	100
5	Bc	425/457 (93%)	415 (98%)	10 (2%)	0	100	100
5	Bd	425/457 (93%)	410 (96%)	15 (4%)	0	100	100
5	Be	425/457 (93%)	411 (97%)	14 (3%)	0	100	100
5	Bf	425/457 (93%)	414 (97%)	11 (3%)	0	100	100
5	Bg	425/457 (93%)	416 (98%)	9 (2%)	0	100	100
5	Bh	425/457 (93%)	413 (97%)	12 (3%)	0	100	100
5	Bi	425/457 (93%)	416 (98%)	9 (2%)	0	100	100
5	Bj	425/457 (93%)	411 (97%)	14 (3%)	0	100	100
5	Bk	425/457 (93%)	417 (98%)	8 (2%)	0	100	100
5	Bl	425/457 (93%)	412 (97%)	13 (3%)	0	100	100
5	Bm	425/457 (93%)	416 (98%)	9 (2%)	0	100	100
5	Bn	425/457 (93%)	412 (97%)	13 (3%)	0	100	100
5	Bo	425/457 (93%)	419 (99%)	6 (1%)	0	100	100
5	Bp	425/457 (93%)	418 (98%)	7 (2%)	0	100	100
5	Bq	425/457 (93%)	420 (99%)	5 (1%)	0	100	100
5	Br	425/457 (93%)	418 (98%)	7 (2%)	0	100	100
6	Sa	40/944 (4%)	40 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Sb	60/944 (6%)	60 (100%)	0	0	100	100
6	Sc	40/944 (4%)	40 (100%)	0	0	100	100
6	Sd	83/944 (9%)	81 (98%)	2 (2%)	0	100	100
6	Se	40/944 (4%)	40 (100%)	0	0	100	100
6	Sf	84/944 (9%)	82 (98%)	2 (2%)	0	100	100
6	Sg	40/944 (4%)	40 (100%)	0	0	100	100
6	Sh	83/944 (9%)	81 (98%)	2 (2%)	0	100	100
6	Si	40/944 (4%)	40 (100%)	0	0	100	100
6	Sj	84/944 (9%)	82 (98%)	2 (2%)	0	100	100
6	Sk	40/944 (4%)	40 (100%)	0	0	100	100
6	Sl	83/944 (9%)	81 (98%)	2 (2%)	0	100	100
6	Sm	18/944 (2%)	18 (100%)	0	0	100	100
6	Sn	62/944 (7%)	60 (97%)	2 (3%)	0	100	100
All	All	31111/46889 (66%)	30123 (97%)	972 (3%)	16 (0%)	49	83

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	Af	404	ALA
4	Ae	404	ALA
4	Ad	404	ALA
4	Ac	404	ALA
4	Ah	404	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	391/420 (93%)	391 (100%)	0	100	100
1	b	403/420 (96%)	403 (100%)	0	100	100
1	c	392/420 (93%)	392 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	d	403/420 (96%)	403 (100%)	0	100	100
1	e	391/420 (93%)	391 (100%)	0	100	100
1	f	403/420 (96%)	403 (100%)	0	100	100
1	g	392/420 (93%)	392 (100%)	0	100	100
1	h	403/420 (96%)	403 (100%)	0	100	100
1	i	391/420 (93%)	391 (100%)	0	100	100
1	j	403/420 (96%)	403 (100%)	0	100	100
1	k	392/420 (93%)	392 (100%)	0	100	100
1	l	403/420 (96%)	403 (100%)	0	100	100
1	m	391/420 (93%)	391 (100%)	0	100	100
1	n	403/420 (96%)	403 (100%)	0	100	100
2	C	649/766 (85%)	649 (100%)	0	100	100
2	E	658/766 (86%)	658 (100%)	0	100	100
2	G	658/766 (86%)	658 (100%)	0	100	100
2	I	658/766 (86%)	658 (100%)	0	100	100
2	K	658/766 (86%)	658 (100%)	0	100	100
2	M	658/766 (86%)	658 (100%)	0	100	100
2	O	658/766 (86%)	658 (100%)	0	100	100
3	D	607/787 (77%)	604 (100%)	3 (0%)	81	83
3	F	626/787 (80%)	626 (100%)	0	100	100
3	H	626/787 (80%)	626 (100%)	0	100	100
3	J	626/787 (80%)	626 (100%)	0	100	100
3	L	626/787 (80%)	626 (100%)	0	100	100
3	N	626/787 (80%)	626 (100%)	0	100	100
3	P	626/787 (80%)	626 (100%)	0	100	100
4	Ab	359/381 (94%)	359 (100%)	0	100	100
4	Ac	375/381 (98%)	375 (100%)	0	100	100
4	Ad	375/381 (98%)	375 (100%)	0	100	100
4	Ae	375/381 (98%)	375 (100%)	0	100	100
4	Af	375/381 (98%)	375 (100%)	0	100	100
4	Ag	375/381 (98%)	375 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Ah	375/381 (98%)	375 (100%)	0	100	100
4	Ai	375/381 (98%)	375 (100%)	0	100	100
4	Aj	375/381 (98%)	375 (100%)	0	100	100
4	Ak	375/381 (98%)	375 (100%)	0	100	100
4	Al	375/381 (98%)	375 (100%)	0	100	100
4	Am	375/381 (98%)	375 (100%)	0	100	100
4	An	375/381 (98%)	375 (100%)	0	100	100
4	Ao	375/381 (98%)	375 (100%)	0	100	100
4	Ap	375/381 (98%)	375 (100%)	0	100	100
4	Aq	375/381 (98%)	375 (100%)	0	100	100
4	Ar	375/381 (98%)	375 (100%)	0	100	100
5	Bb	355/392 (91%)	355 (100%)	0	100	100
5	Bc	366/392 (93%)	366 (100%)	0	100	100
5	Bd	366/392 (93%)	366 (100%)	0	100	100
5	Be	366/392 (93%)	366 (100%)	0	100	100
5	Bf	366/392 (93%)	366 (100%)	0	100	100
5	Bg	366/392 (93%)	366 (100%)	0	100	100
5	Bh	366/392 (93%)	366 (100%)	0	100	100
5	Bi	366/392 (93%)	366 (100%)	0	100	100
5	Bj	366/392 (93%)	366 (100%)	0	100	100
5	Bk	366/392 (93%)	366 (100%)	0	100	100
5	Bl	366/392 (93%)	366 (100%)	0	100	100
5	Bm	366/392 (93%)	366 (100%)	0	100	100
5	Bn	366/392 (93%)	366 (100%)	0	100	100
5	Bo	366/392 (93%)	366 (100%)	0	100	100
5	Bp	366/392 (93%)	366 (100%)	0	100	100
5	Bq	366/392 (93%)	366 (100%)	0	100	100
5	Br	366/392 (93%)	366 (100%)	0	100	100
6	Sa	40/901 (4%)	40 (100%)	0	100	100
6	Sb	58/901 (6%)	58 (100%)	0	100	100
6	Sc	40/901 (4%)	40 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Sd	79/901 (9%)	79 (100%)	0	100	100
6	Se	40/901 (4%)	40 (100%)	0	100	100
6	Sf	80/901 (9%)	80 (100%)	0	100	100
6	Sg	40/901 (4%)	40 (100%)	0	100	100
6	Sh	79/901 (9%)	79 (100%)	0	100	100
6	Si	40/901 (4%)	40 (100%)	0	100	100
6	Sj	80/901 (9%)	80 (100%)	0	100	100
6	Sk	40/901 (4%)	40 (100%)	0	100	100
6	Sl	79/901 (9%)	79 (100%)	0	100	100
6	Sm	20/901 (2%)	20 (100%)	0	100	100
6	Sn	61/901 (7%)	61 (100%)	0	100	100
All	All	27867/42506 (66%)	27864 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	694	ILE
3	D	696	THR
3	D	702	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 624 such sidechains are listed below:

Mol	Chain	Res	Type
5	Bl	298	ASN
5	Bp	191	GLN
4	An	229	ASN
5	Bl	291	GLN
4	Ab	254	ASN

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](#)

14 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
8	GTP	m	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.65	9 (18%)
8	GTP	n	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.64	9 (18%)
8	GTP	d	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.64	9 (18%)
8	GTP	f	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.64	9 (18%)
8	GTP	c	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.64	9 (18%)
8	GTP	j	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.64	9 (18%)
8	GTP	e	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.63	9 (18%)
8	GTP	k	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.63	9 (18%)
8	GTP	h	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.65	9 (18%)
8	GTP	i	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.64	9 (18%)
9	GDP	a	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.76	6 (13%)
8	GTP	g	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.63	9 (18%)
8	GTP	b	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.64	9 (18%)
8	GTP	l	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.60	9 (18%)

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	GTP	m	501	-	-	4/22/38/38	0/3/3/3
8	GTP	n	501	-	-	5/22/38/38	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GTP	d	501	-	-	4/22/38/38	0/3/3/3
8	GTP	f	501	-	-	4/22/38/38	0/3/3/3
8	GTP	c	501	-	-	4/22/38/38	0/3/3/3
8	GTP	j	501	-	-	4/22/38/38	0/3/3/3
8	GTP	e	501	-	-	5/22/38/38	0/3/3/3
8	GTP	k	501	-	-	5/22/38/38	0/3/3/3
8	GTP	h	501	-	-	5/22/38/38	0/3/3/3
8	GTP	i	501	-	-	4/22/38/38	0/3/3/3
9	GDP	a	501	-	-	3/16/32/32	0/3/3/3
8	GTP	g	501	-	-	5/22/38/38	0/3/3/3
8	GTP	b	501	-	-	4/22/38/38	0/3/3/3
8	GTP	l	501	-	-	4/22/38/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	a	501	GDP	C5-C4	3.18	1.47	1.38
9	a	501	GDP	C6-N1	-2.57	1.34	1.38
8	f	501	GTP	C2-N3	2.27	1.38	1.33
8	c	501	GTP	C2-N3	2.26	1.38	1.33
8	h	501	GTP	C2-N3	2.24	1.38	1.33

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	a	501	GDP	C5-C4-N3	-6.23	118.47	128.39
8	m	501	GTP	C5-C4-N3	-5.57	119.53	128.39
8	c	501	GTP	C5-C4-N3	-5.54	119.57	128.39
8	i	501	GTP	C5-C4-N3	-5.54	119.58	128.39
8	e	501	GTP	C5-C4-N3	-5.50	119.64	128.39

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	b	501	GTP	C5'-O5'-PA-O3A
8	b	501	GTP	C5'-O5'-PA-O2A
8	c	501	GTP	C5'-O5'-PA-O3A
8	c	501	GTP	C5'-O5'-PA-O1A

Continued on next page...

Continued from previous page...

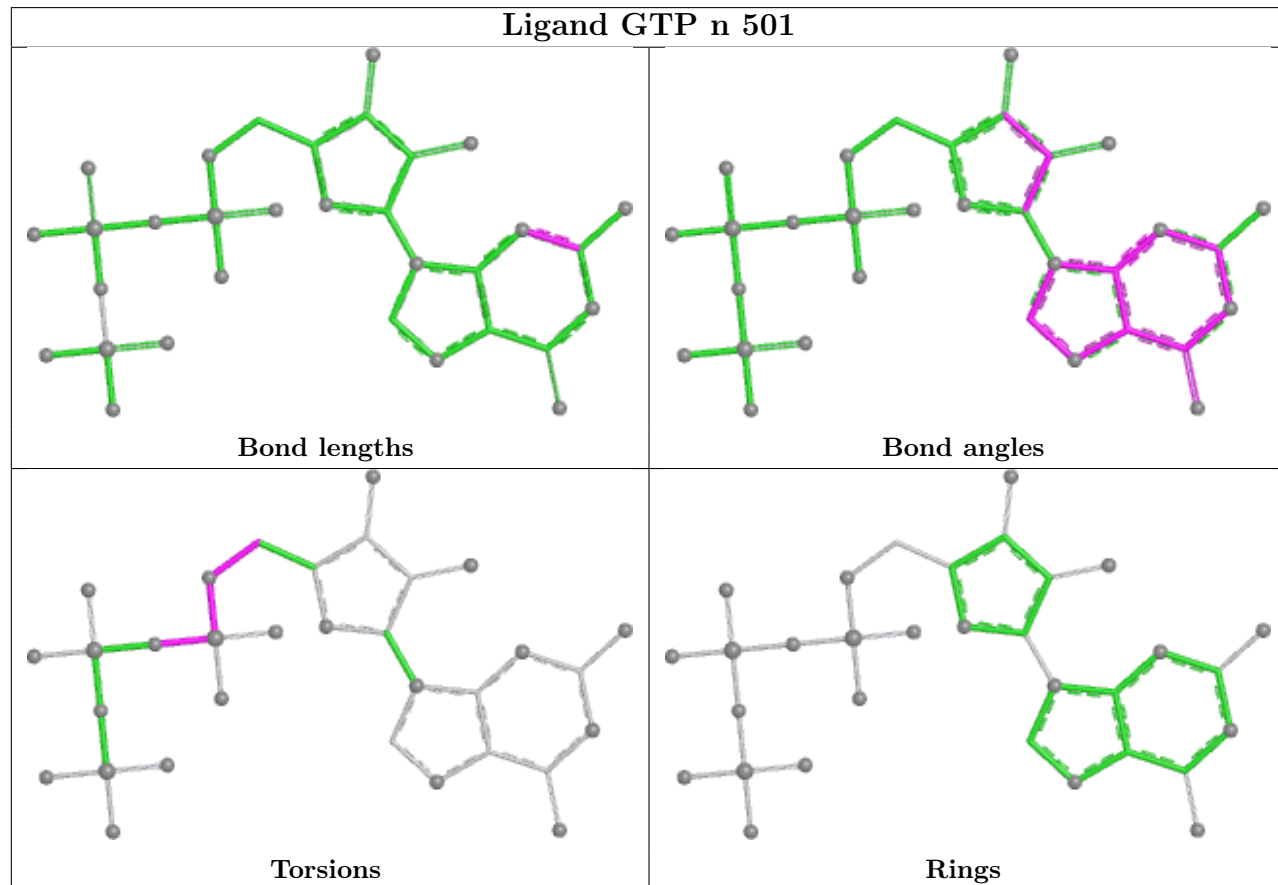
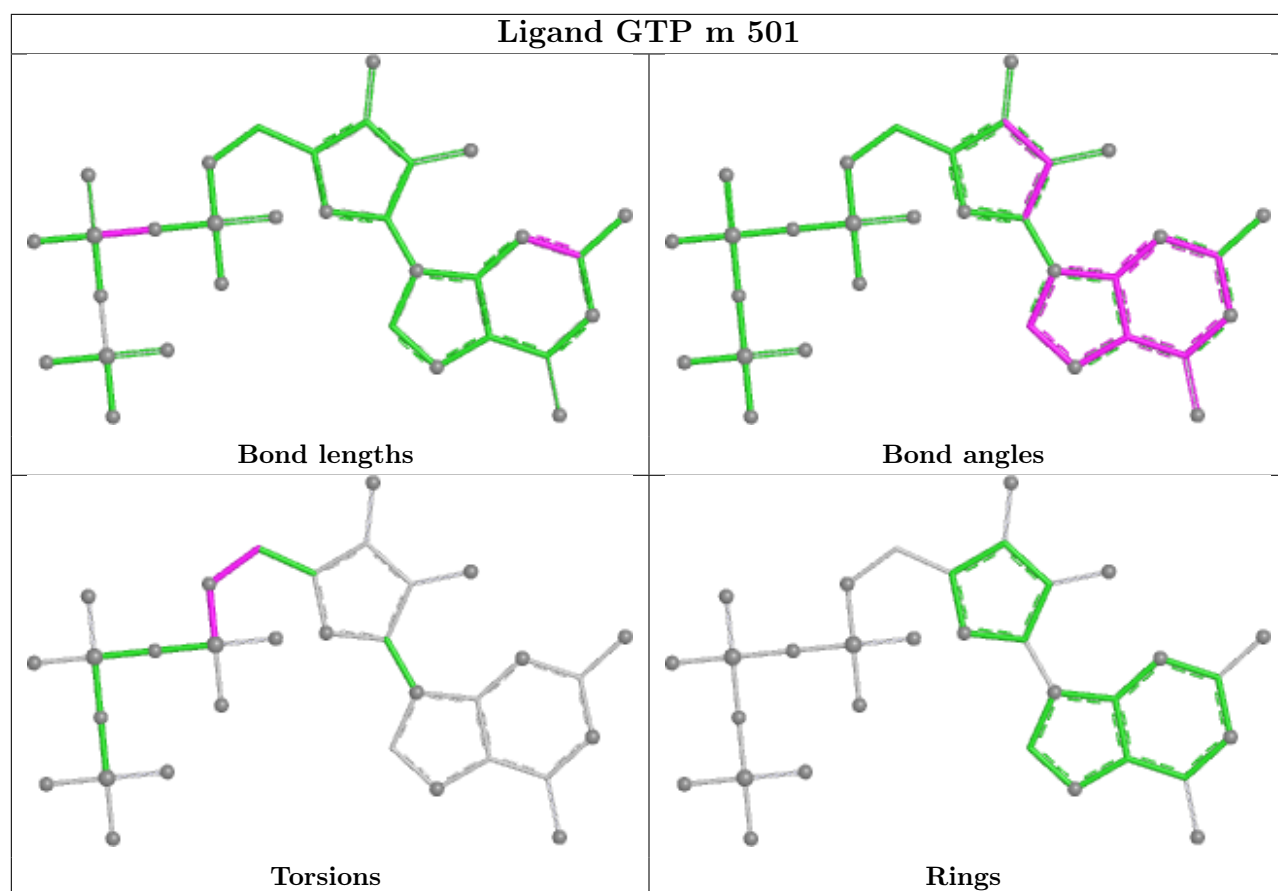
Mol	Chain	Res	Type	Atoms
8	c	501	GTP	C5'-O5'-PA-O2A

There are no ring outliers.

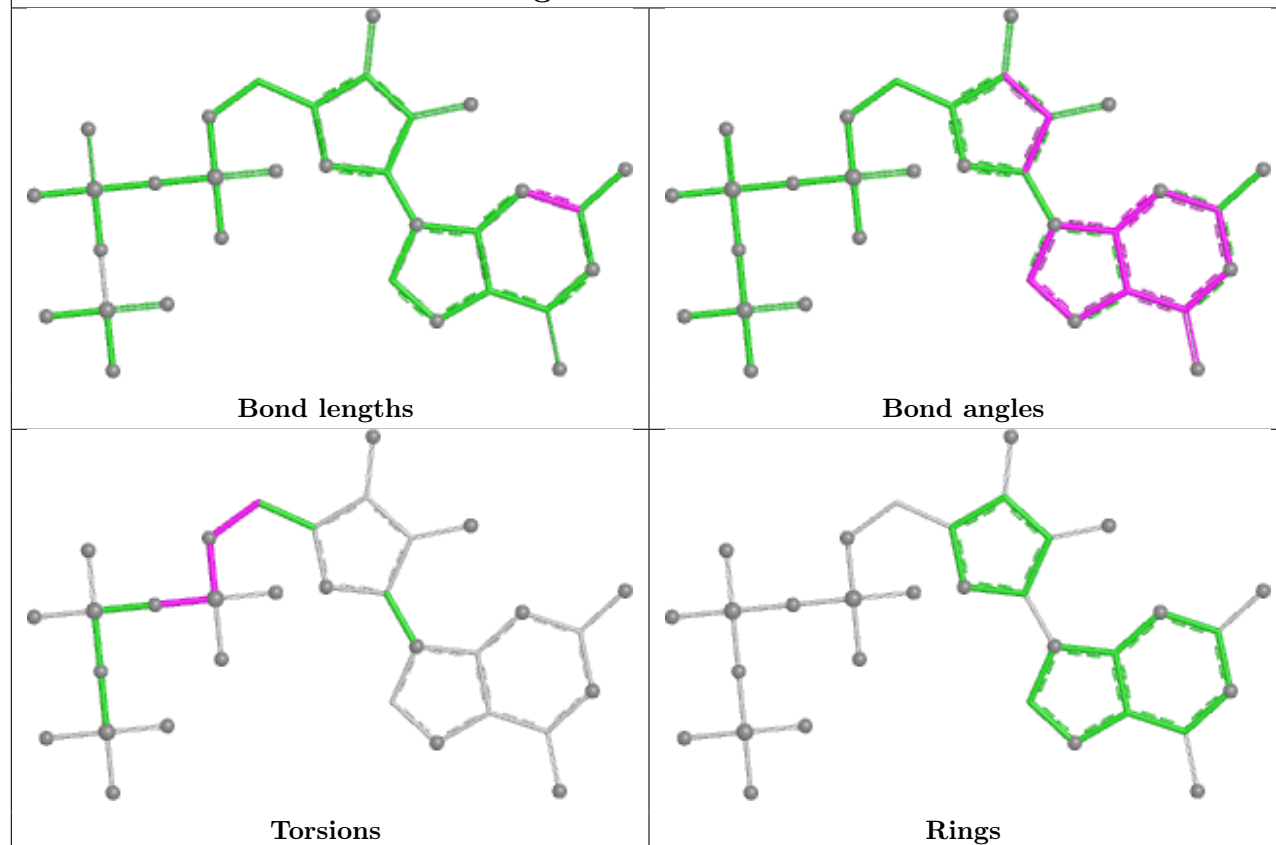
11 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	m	501	GTP	3	0
8	n	501	GTP	2	0
8	d	501	GTP	3	0
8	c	501	GTP	3	0
8	j	501	GTP	1	0
8	e	501	GTP	3	0
8	k	501	GTP	3	0
8	i	501	GTP	3	0
9	a	501	GDP	3	0
8	g	501	GTP	2	0
8	l	501	GTP	1	0

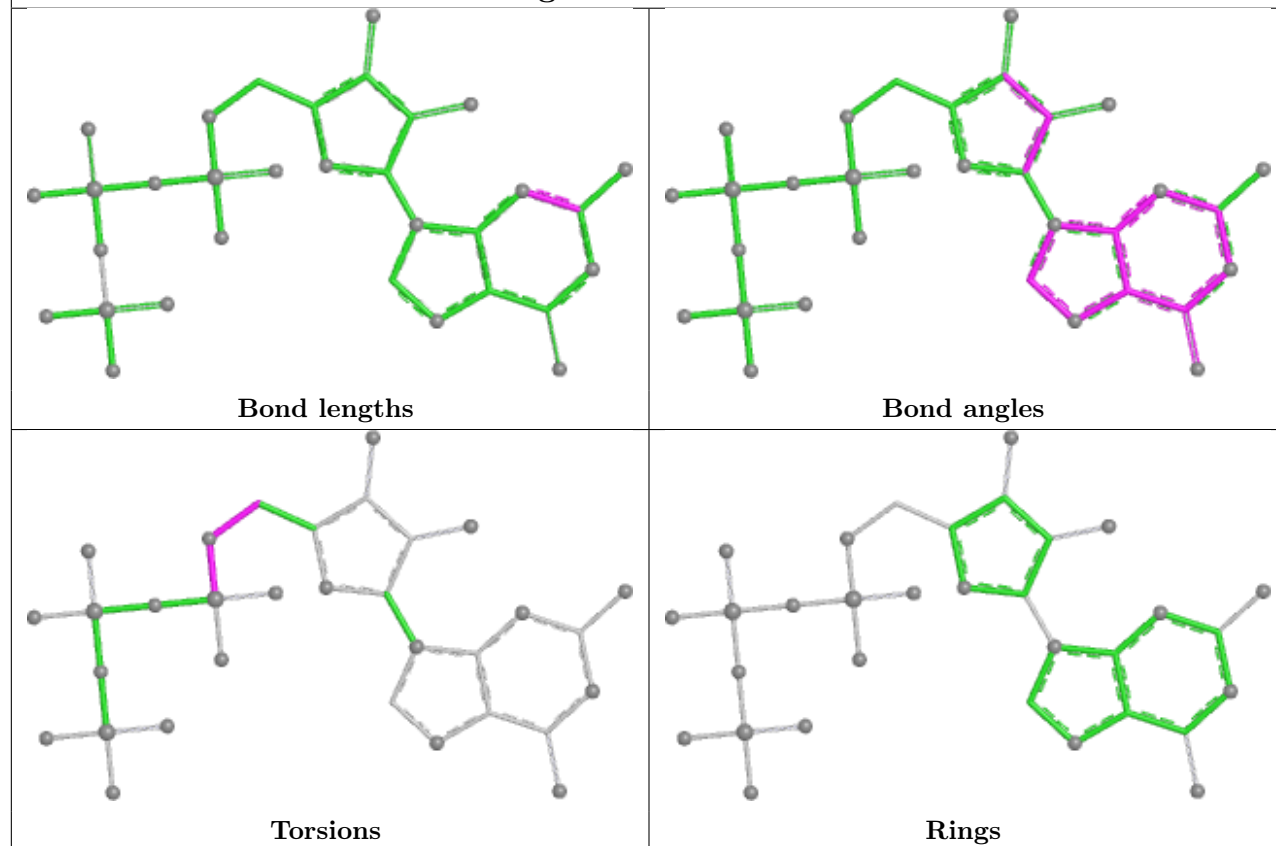
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



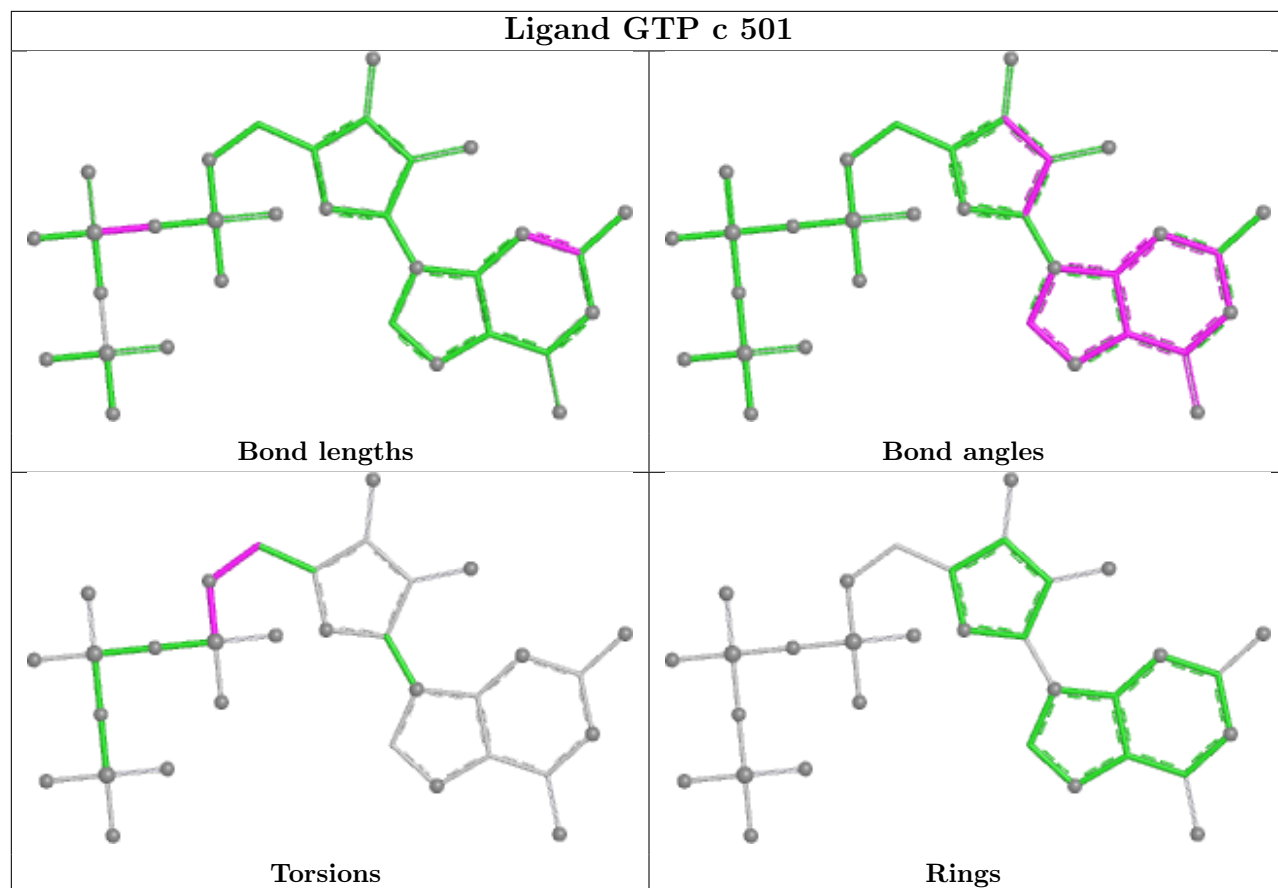
Ligand GTP d 501



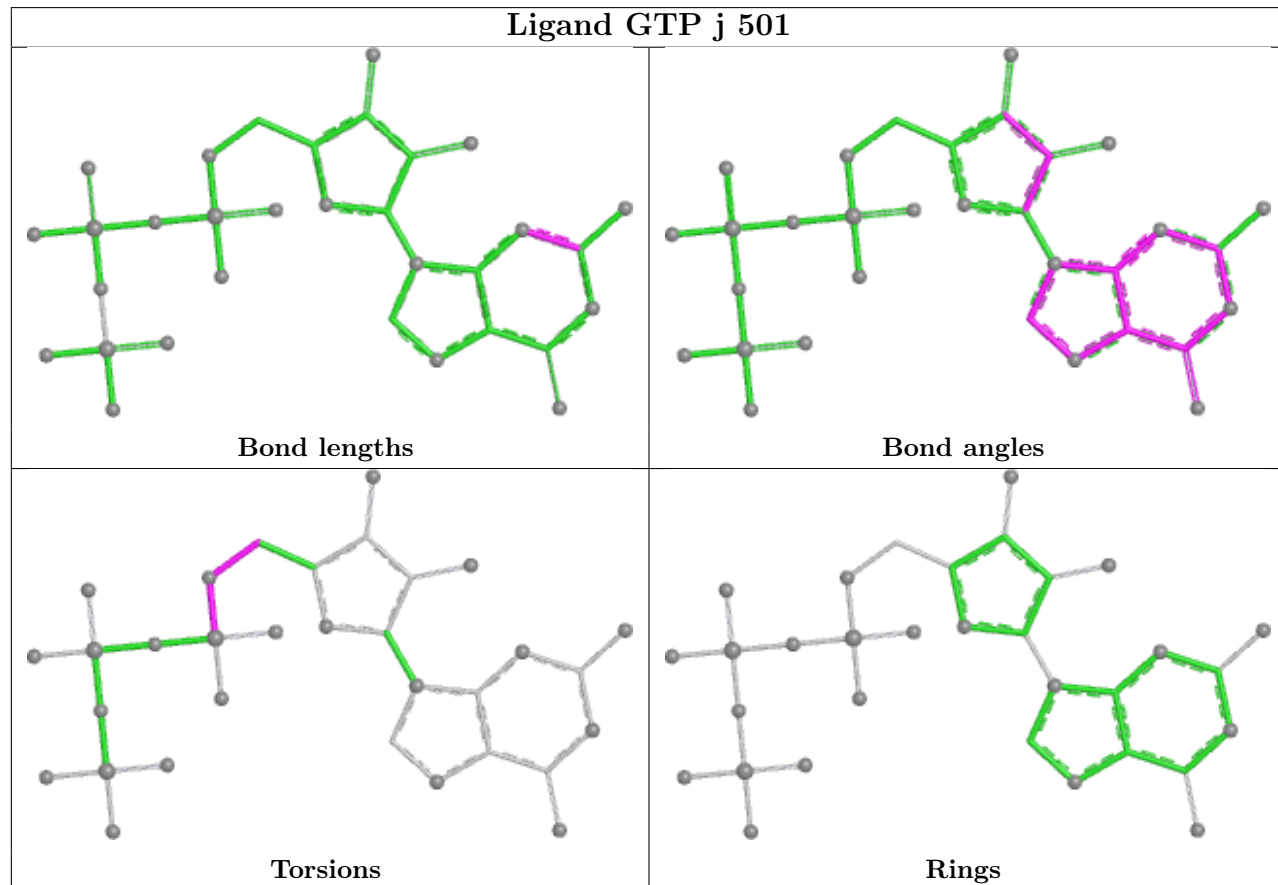
Ligand GTP f 501



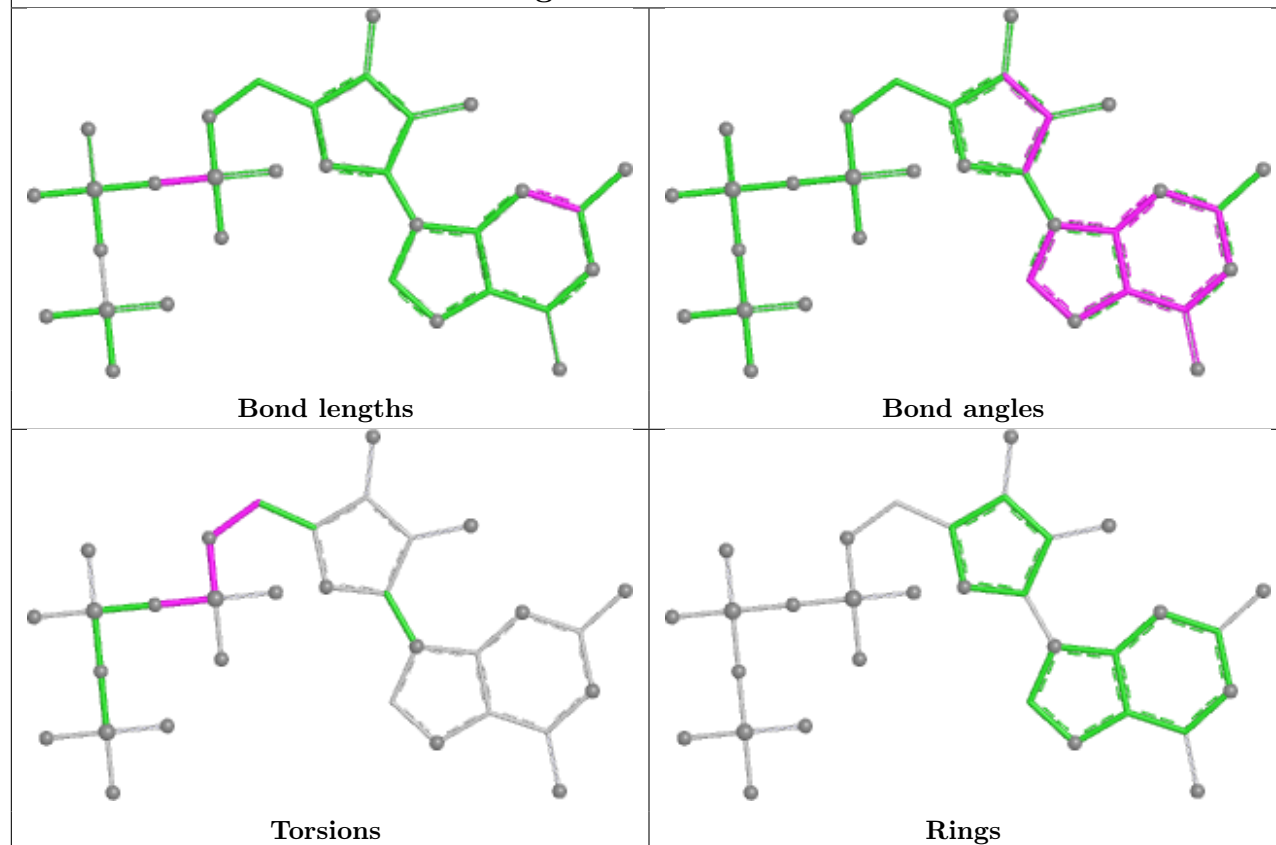
Ligand GTP c 501



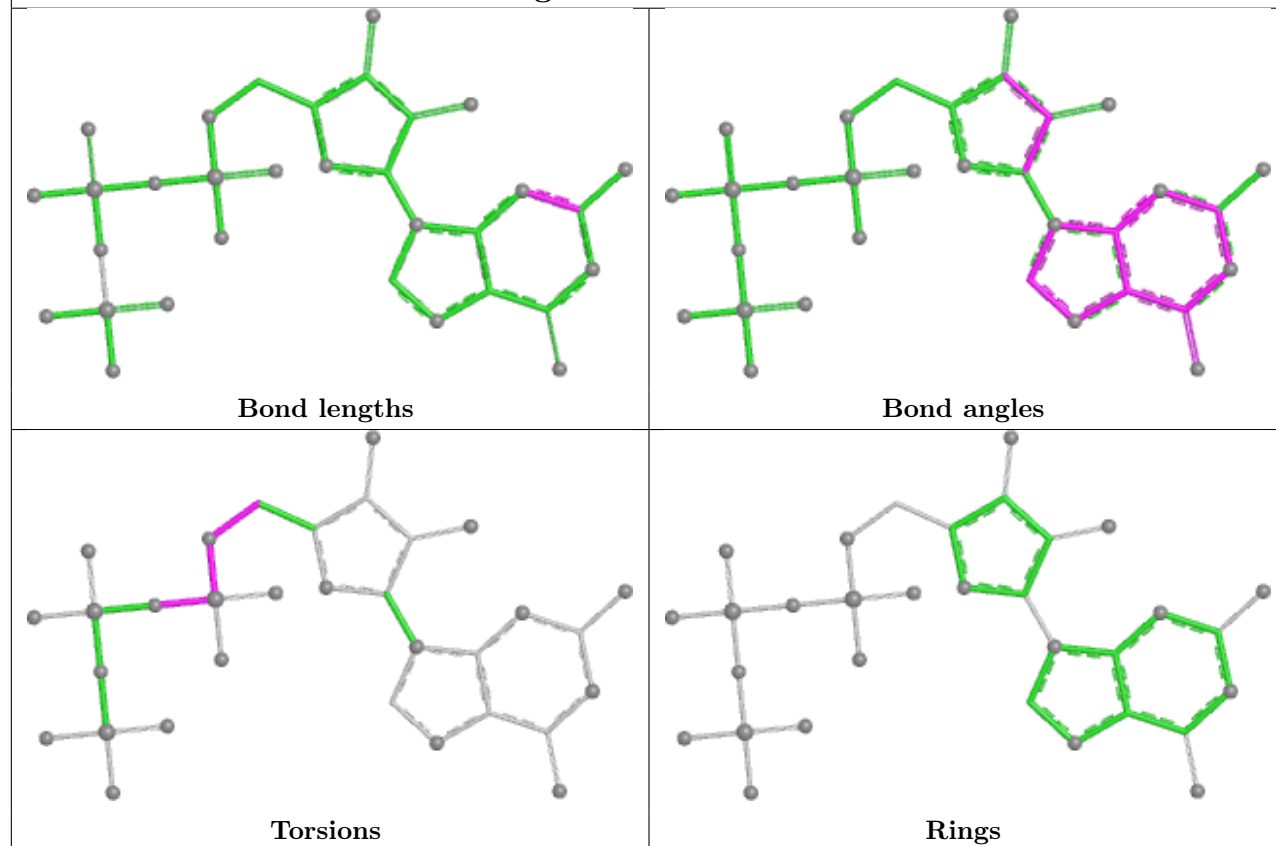
Ligand GTP j 501



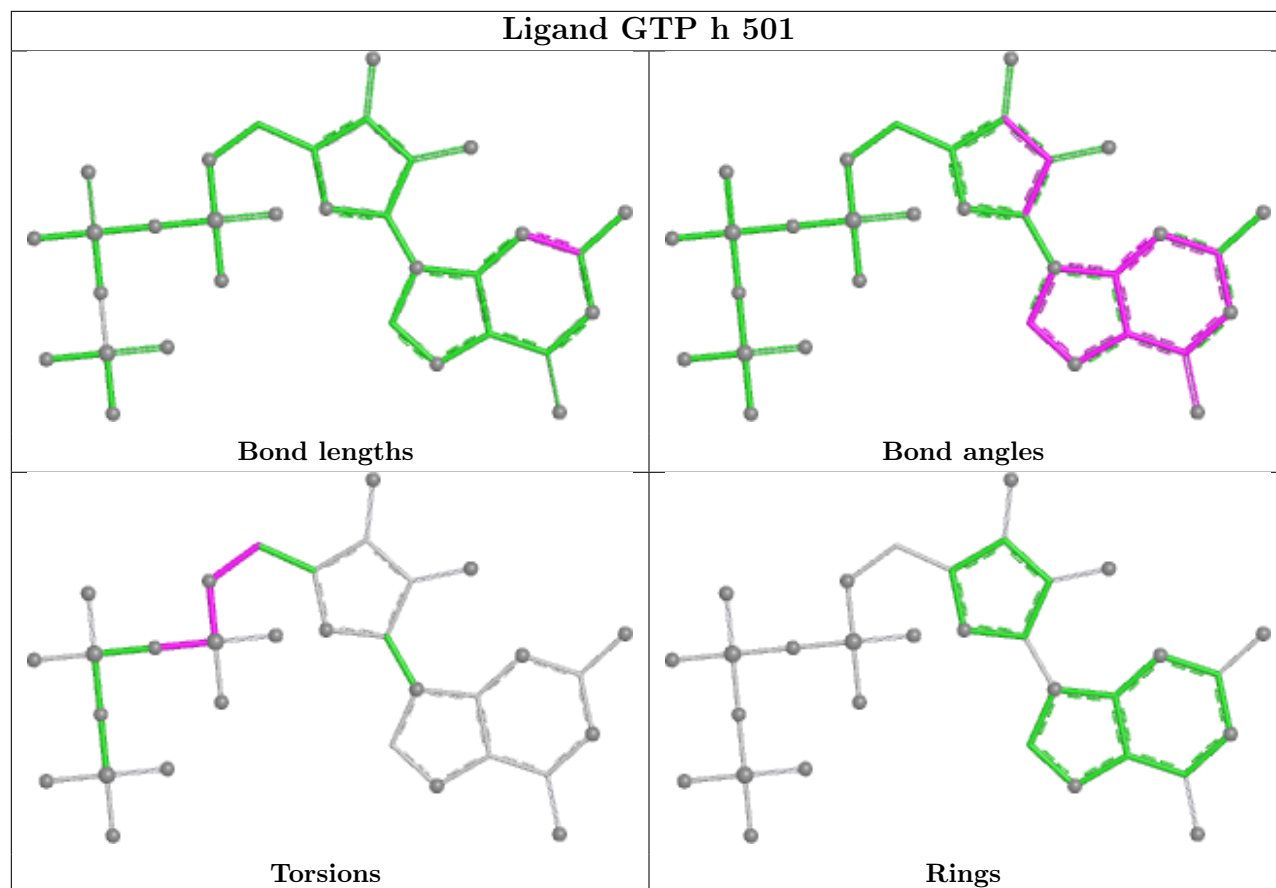
Ligand GTP e 501



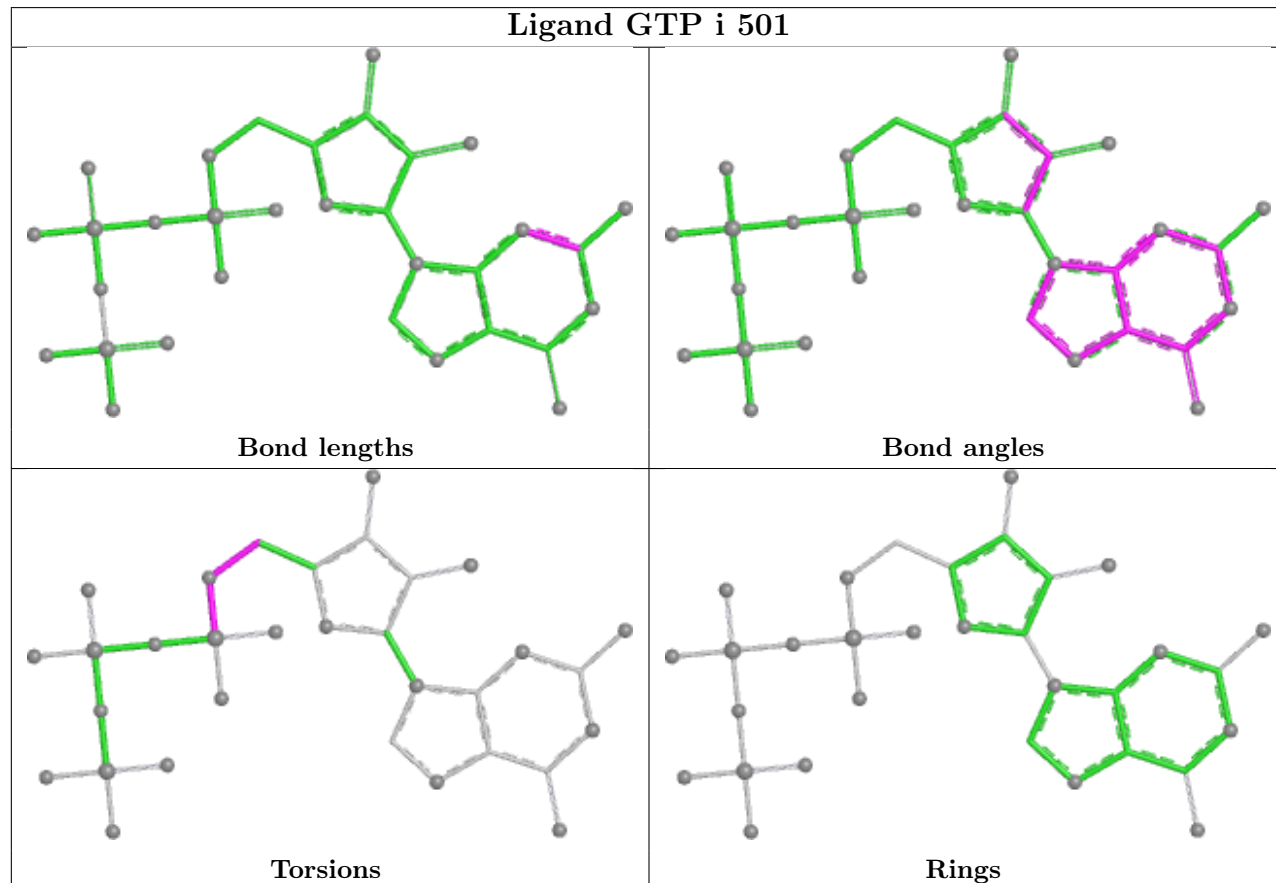
Ligand GTP k 501

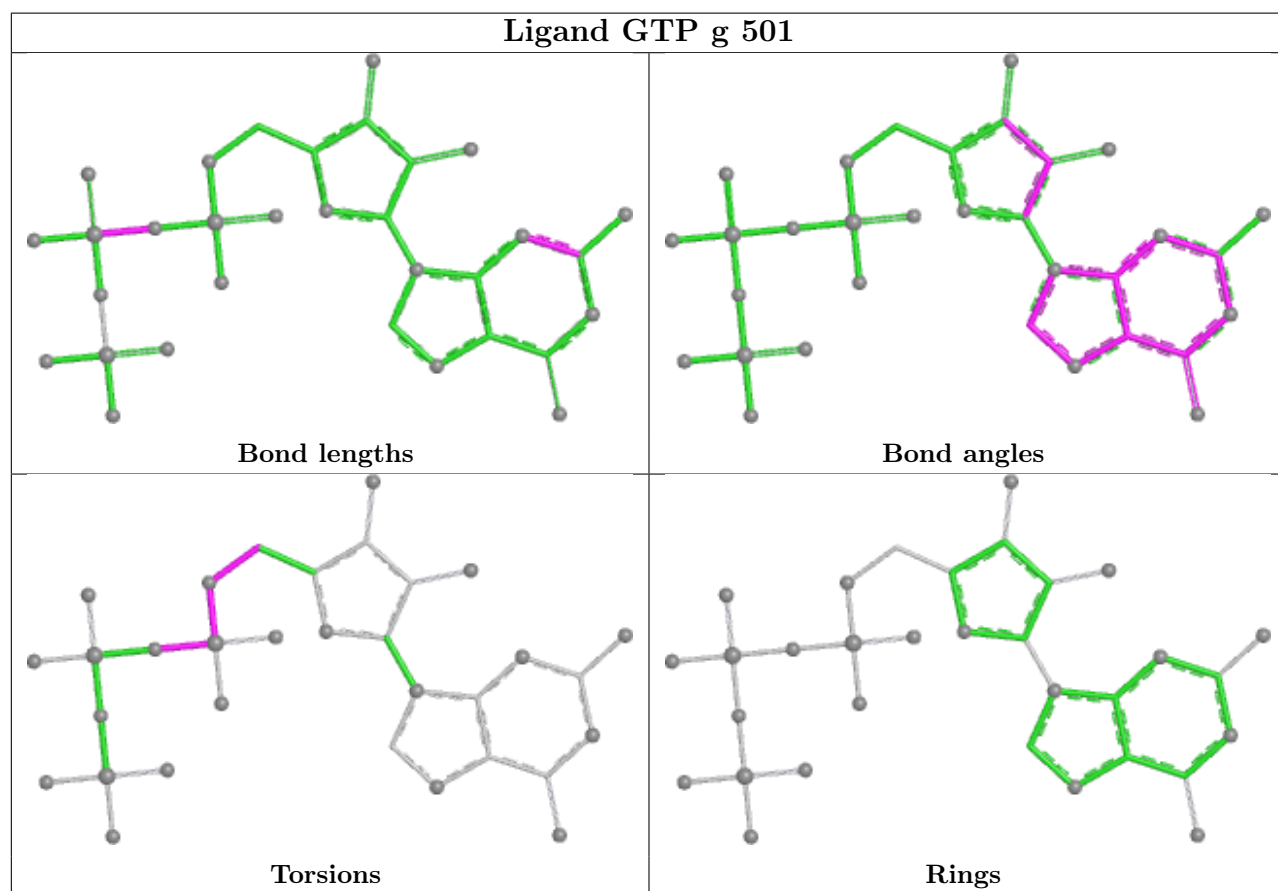
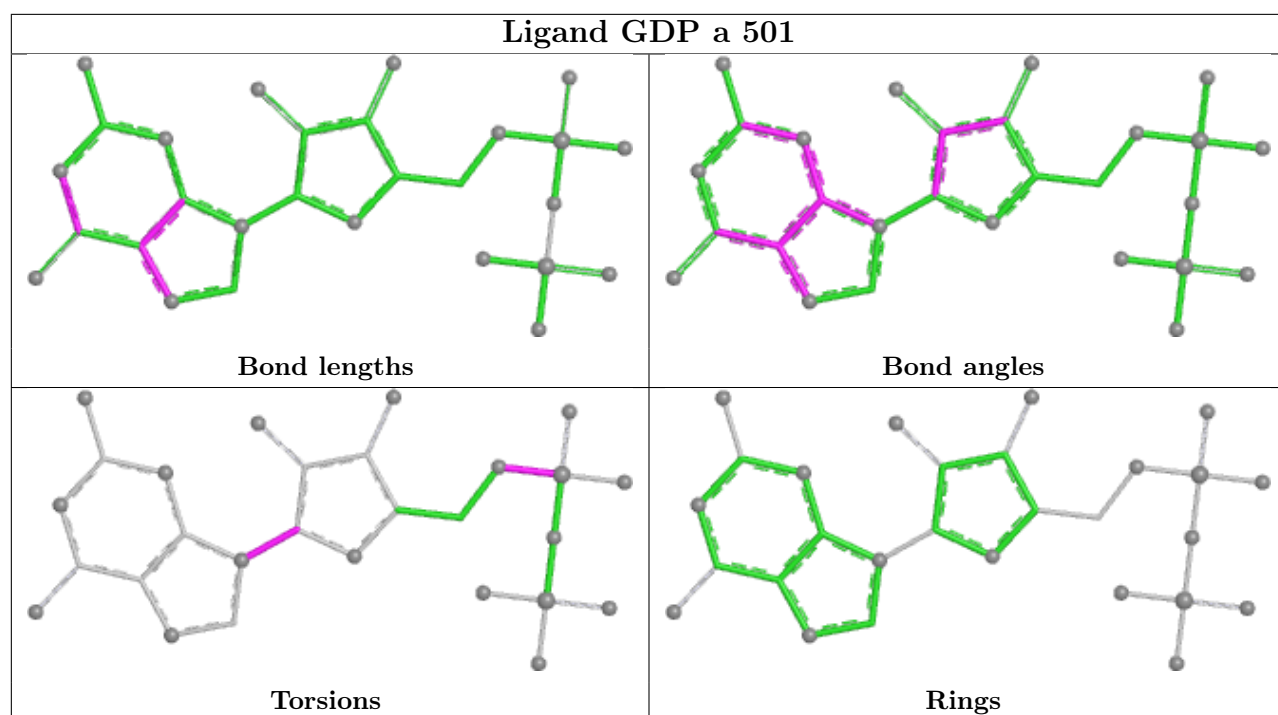


Ligand GTP h 501

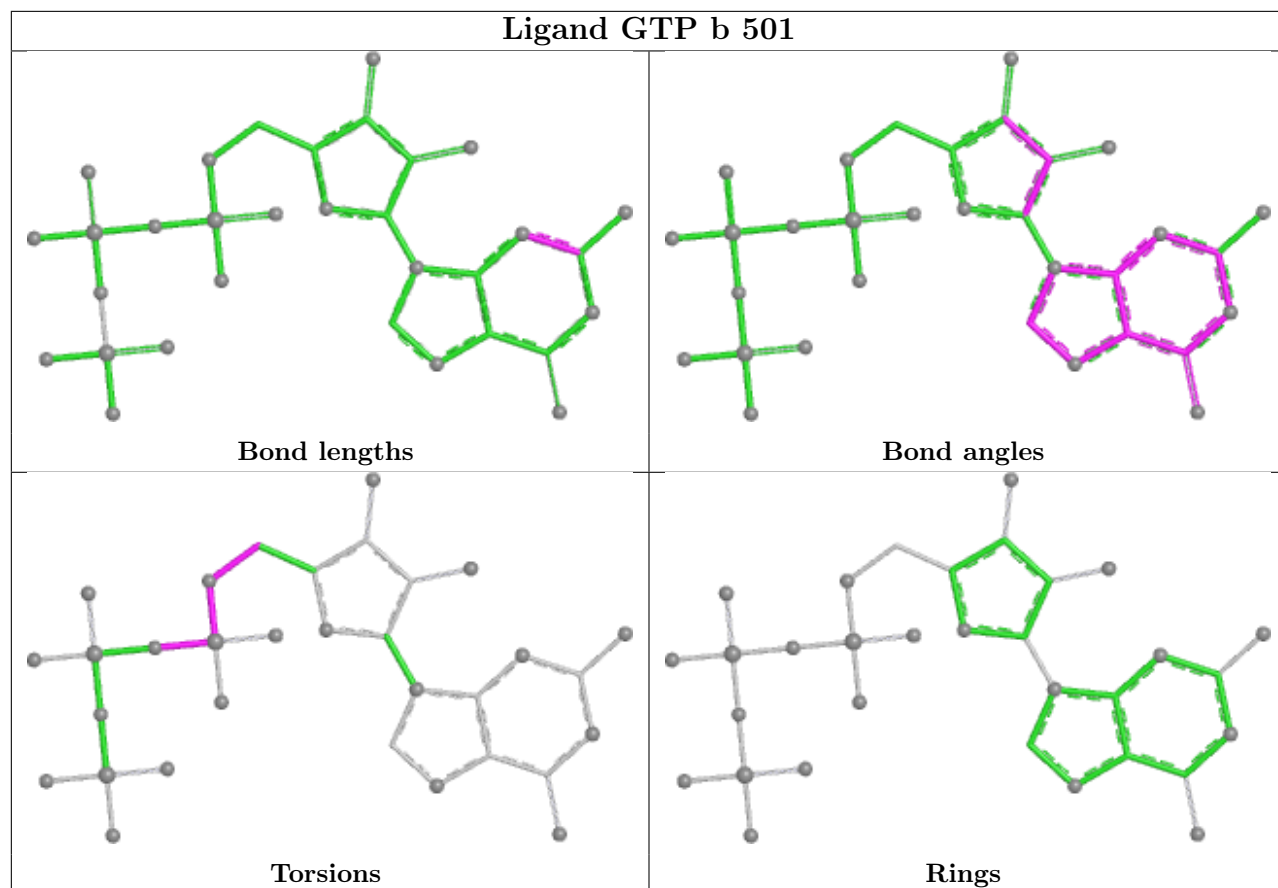


Ligand GTP i 501

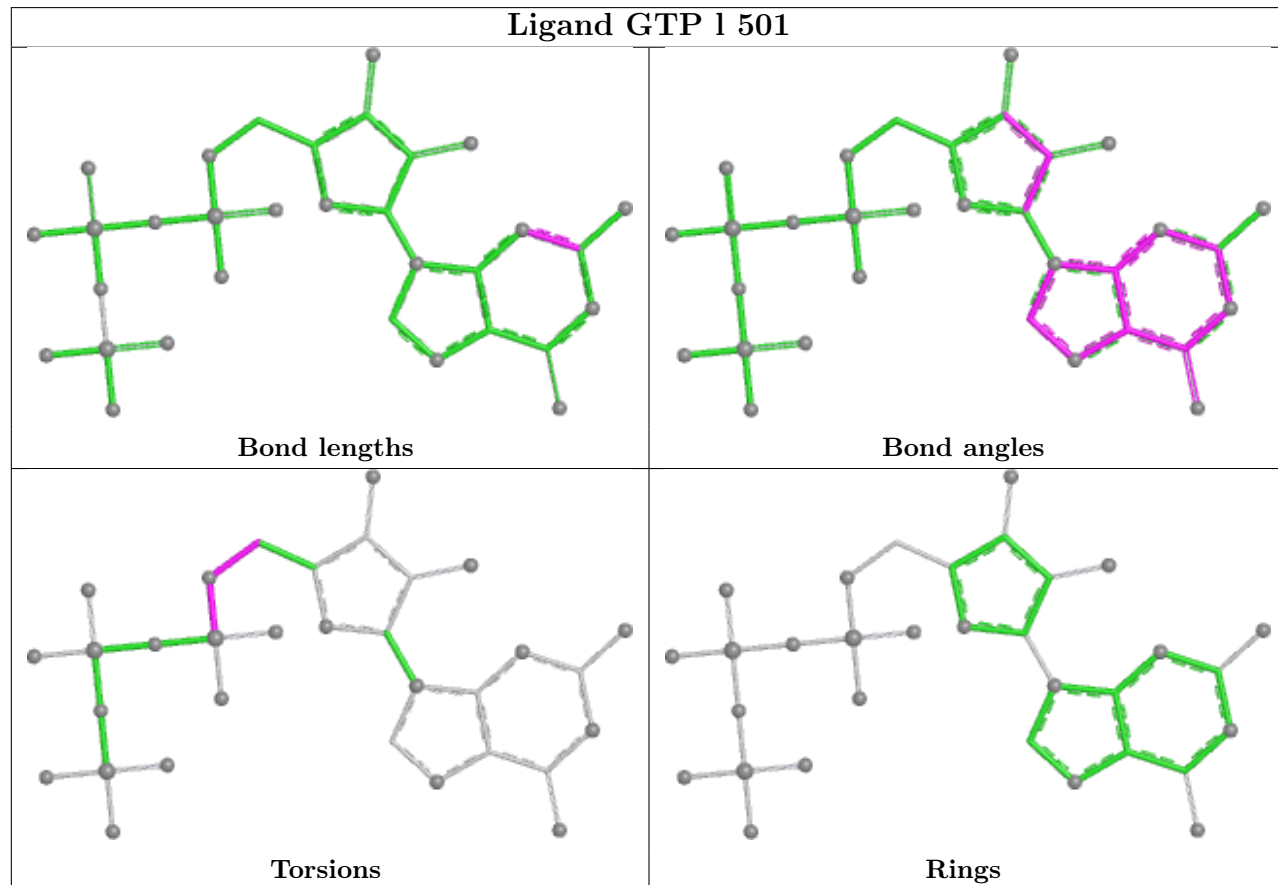




Ligand GTP b 501



Ligand GTP l 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.

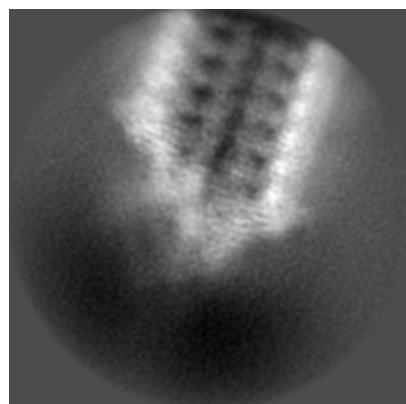
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18665. These allow visual inspection of the internal detail of the map and identification of artifacts.

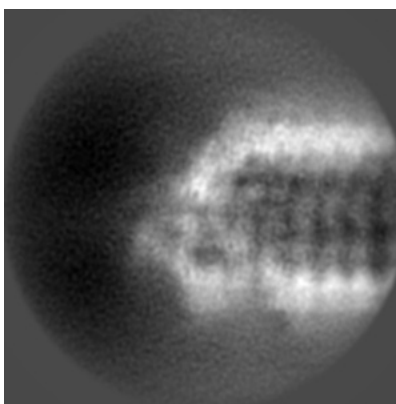
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

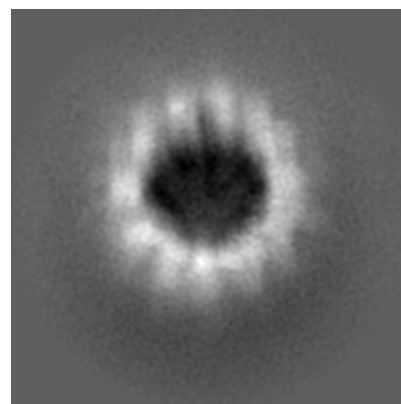
6.1.1 Primary map



X

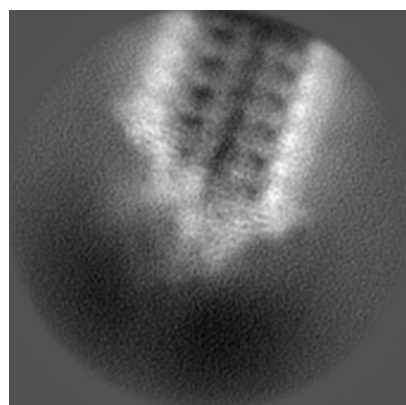


Y

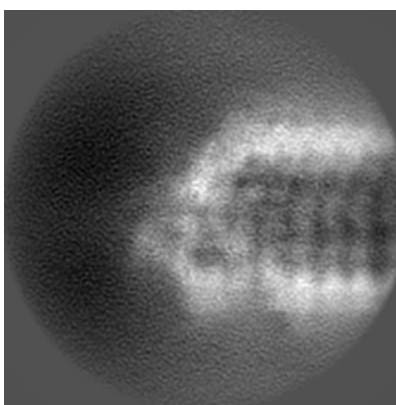


Z

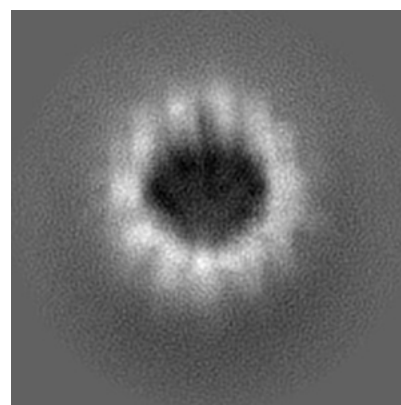
6.1.2 Raw map



X



Y

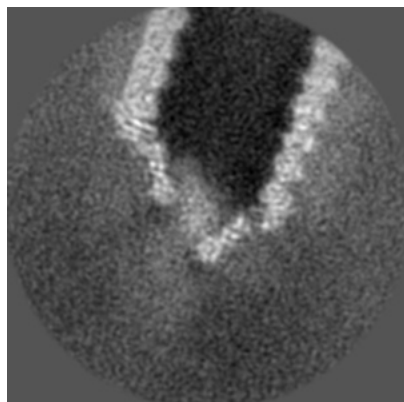


Z

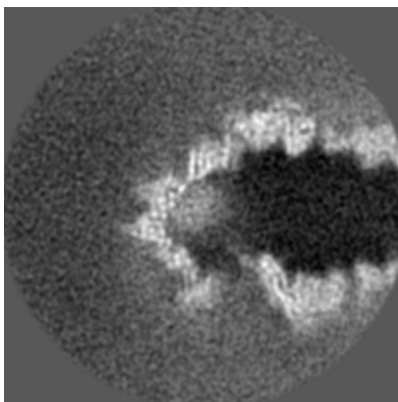
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

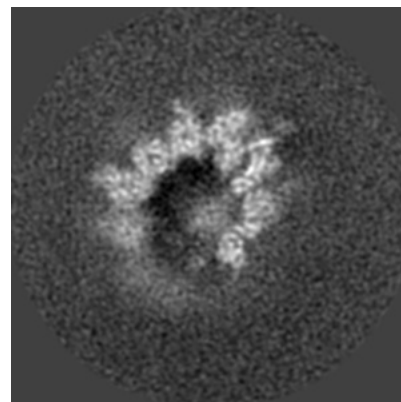
6.2.1 Primary map



X Index: 84

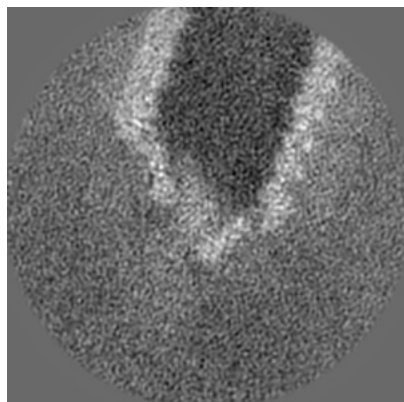


Y Index: 84

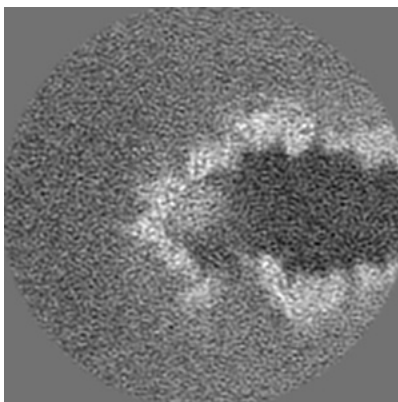


Z Index: 84

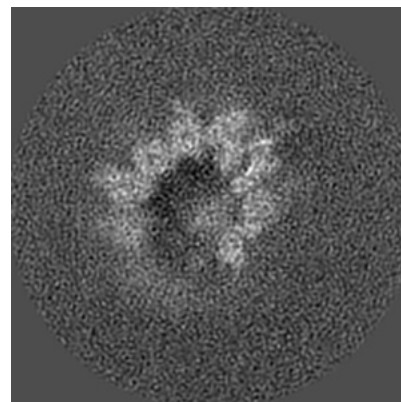
6.2.2 Raw map



X Index: 84



Y Index: 84

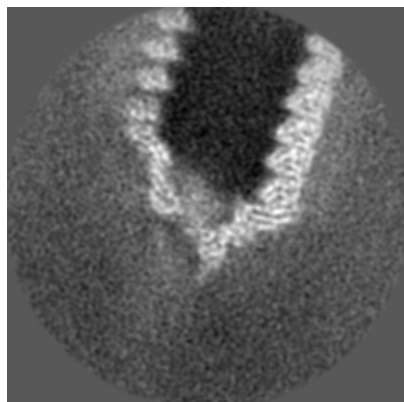


Z Index: 84

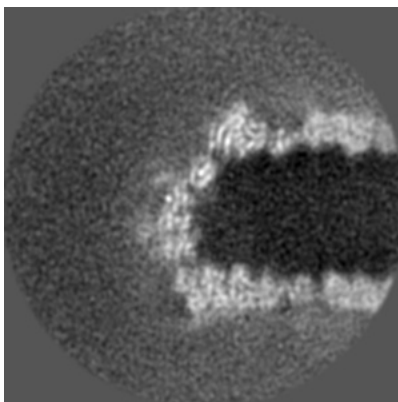
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

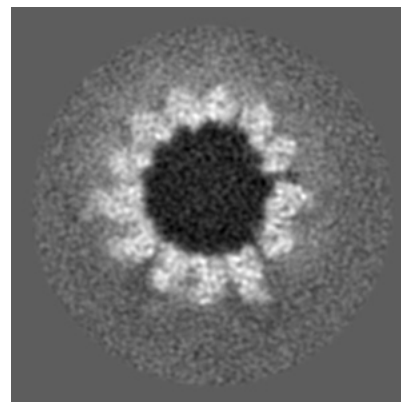
6.3.1 Primary map



X Index: 89

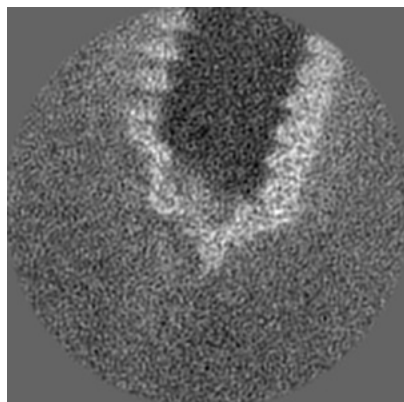


Y Index: 94

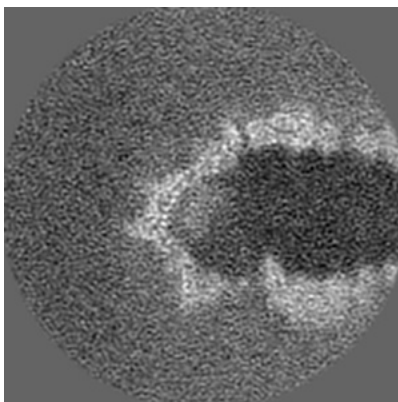


Z Index: 124

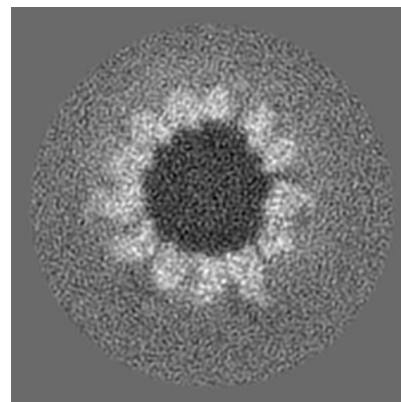
6.3.2 Raw map



X Index: 89



Y Index: 86

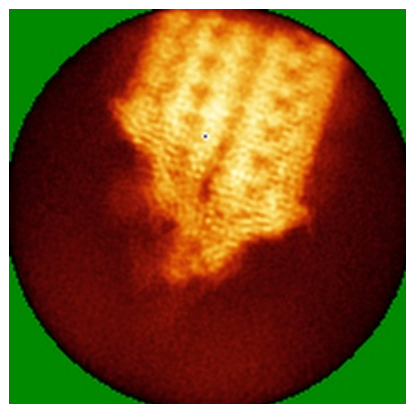


Z Index: 123

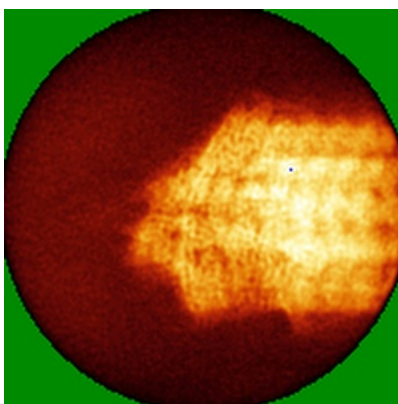
The images above show the largest variance slices of the map in three orthogonal directions.

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

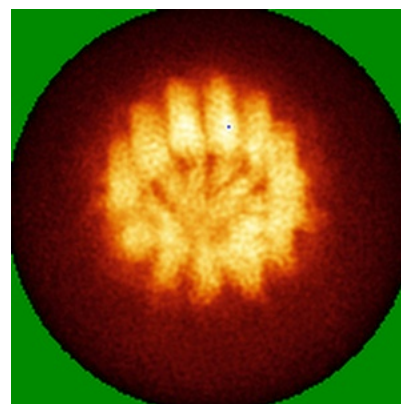
6.4.1 Primary map



X

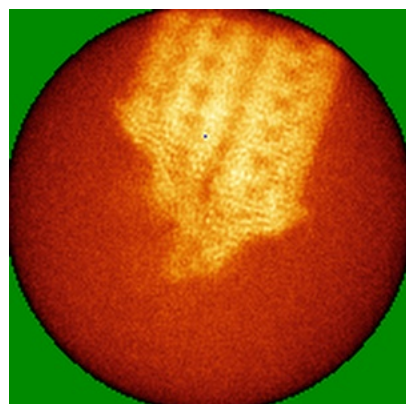


Y

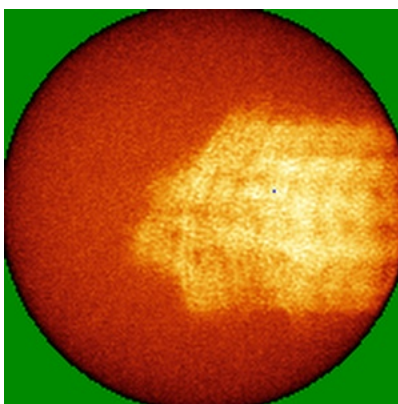


Z

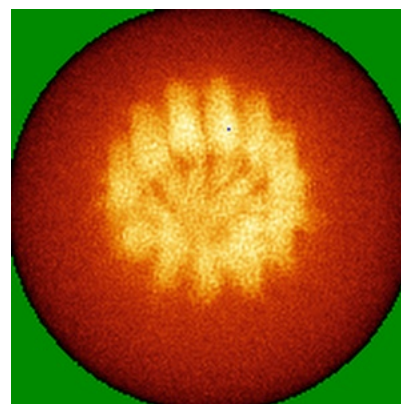
6.4.2 Raw map



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.

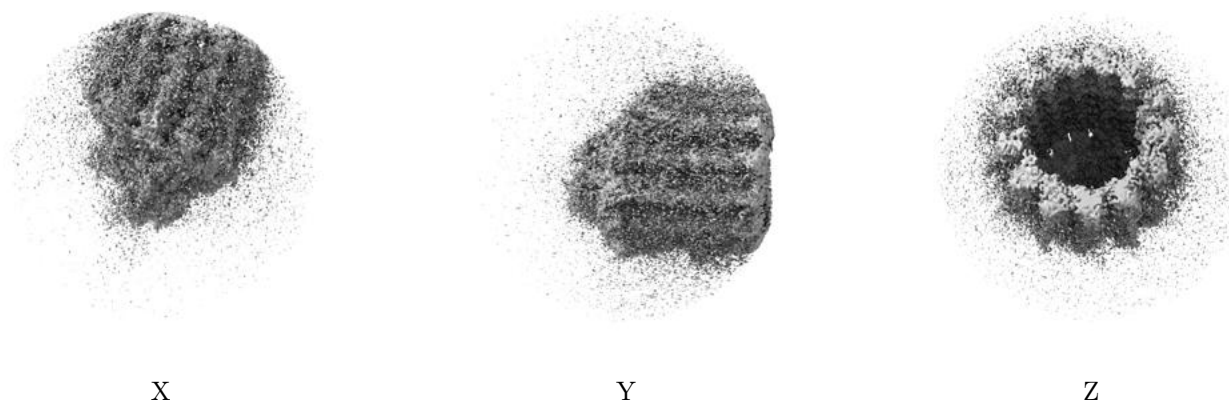
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.243. 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.

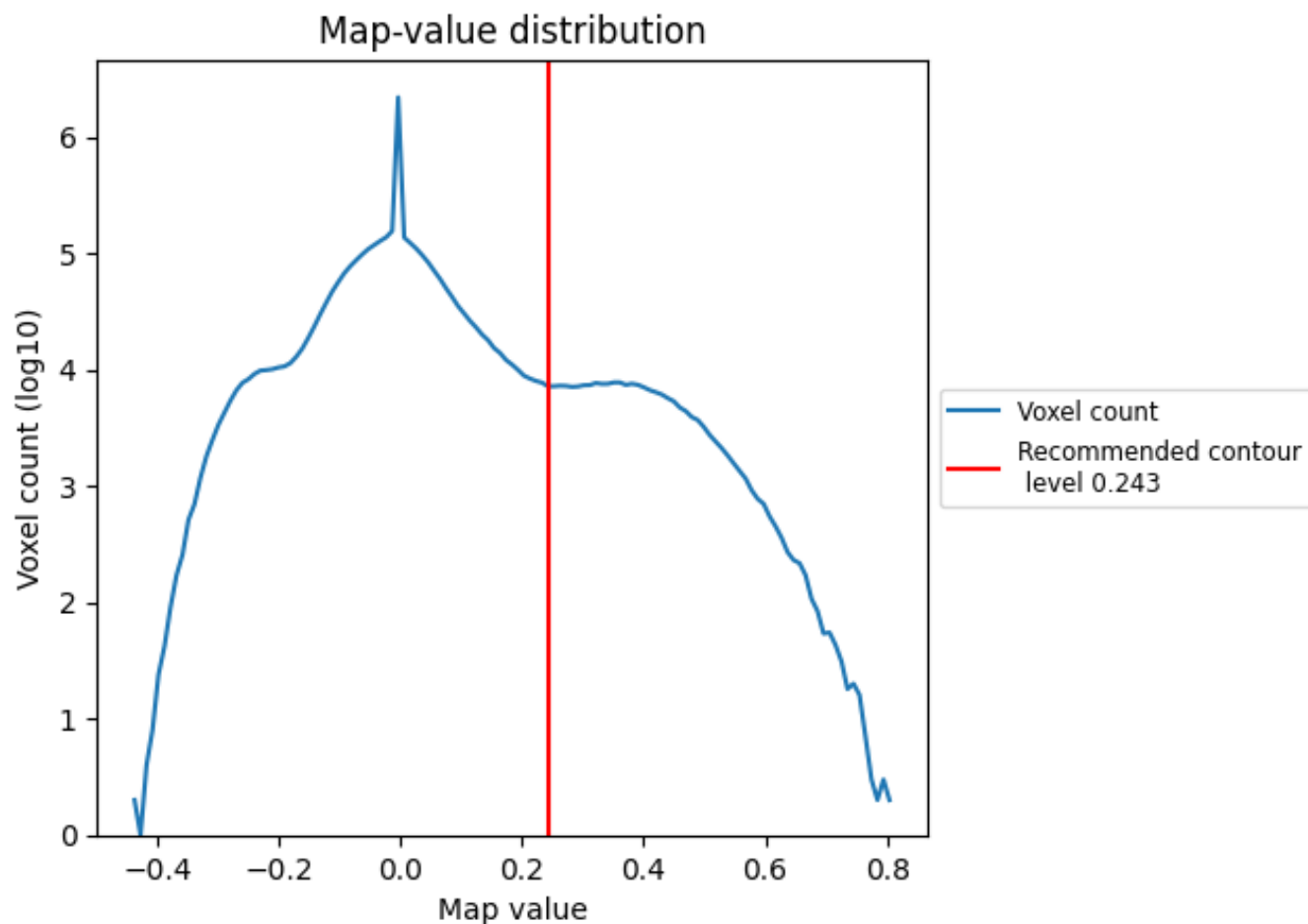
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

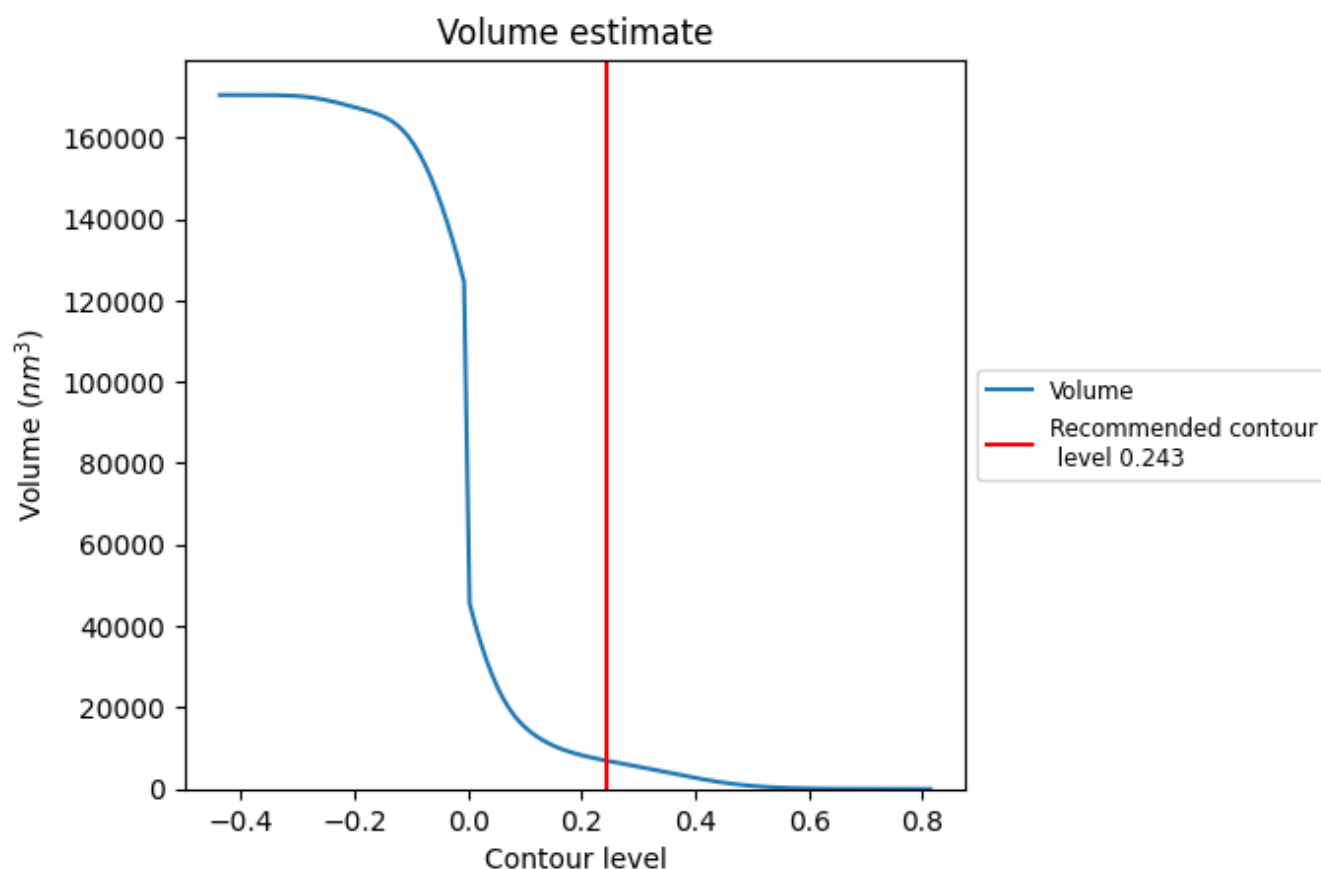
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

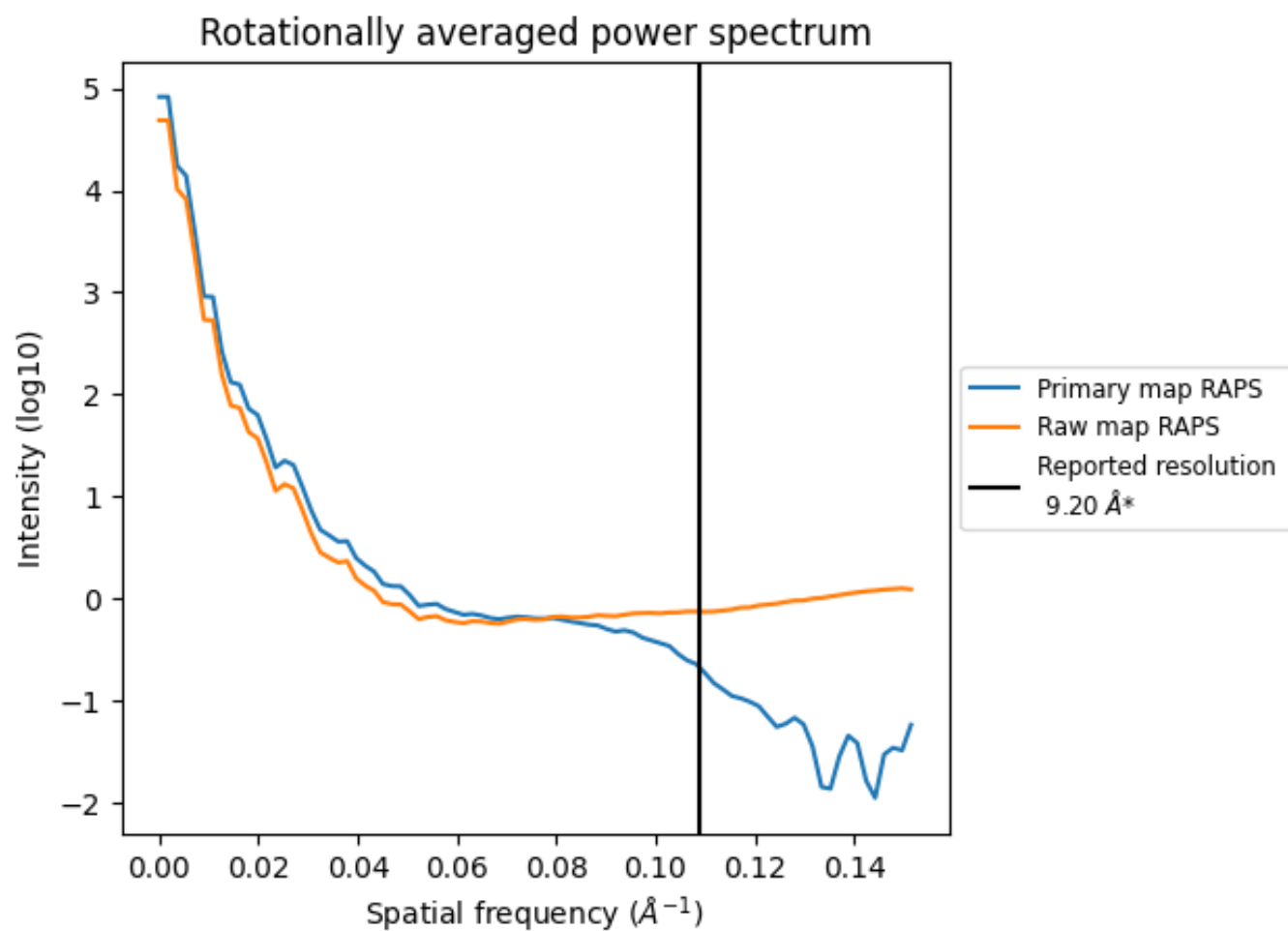
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6972 nm^3 ; this corresponds to an approximate mass of 6298 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 ⓘ

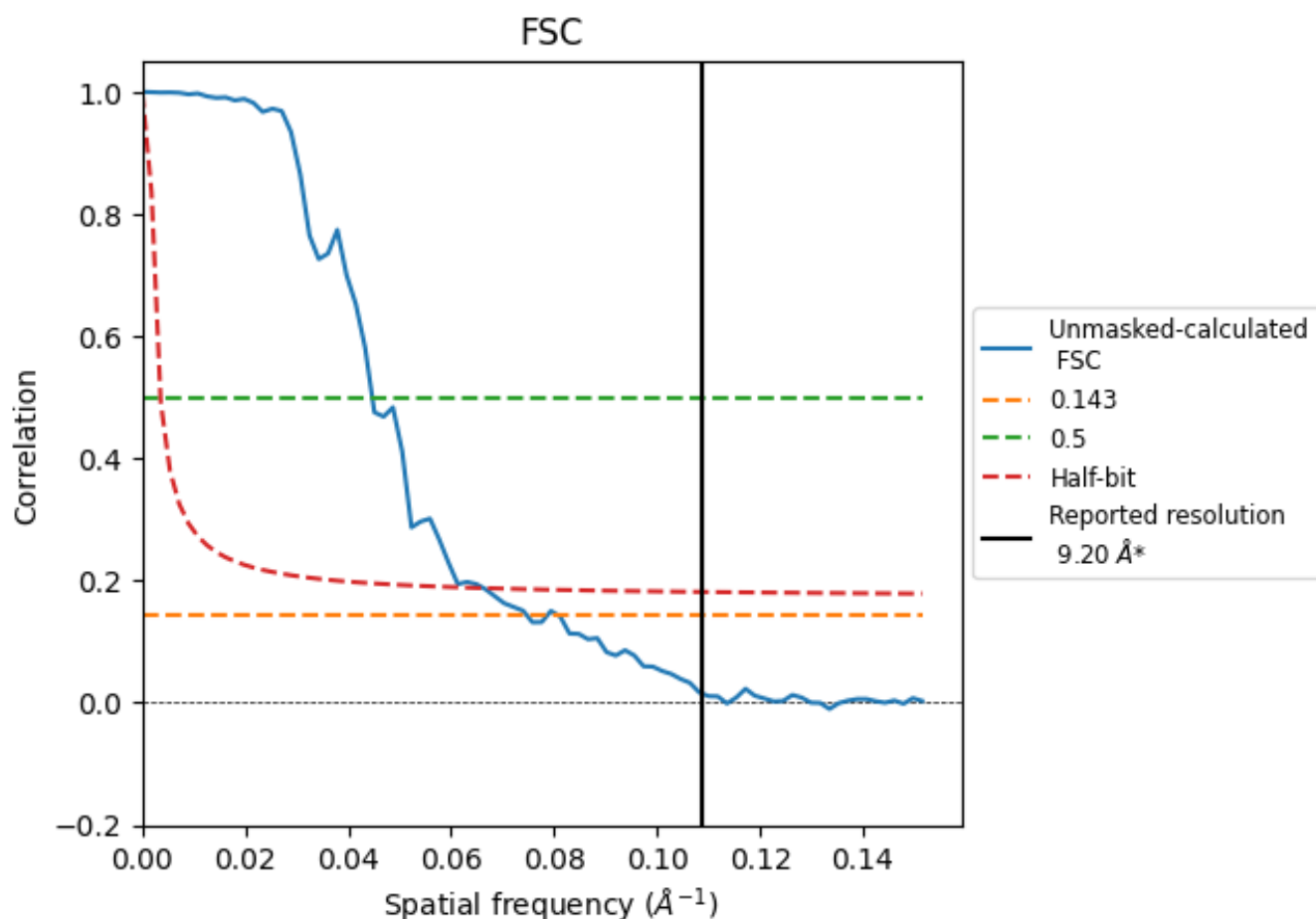


*Reported resolution corresponds to spatial frequency of 0.109 Å⁻¹

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 0.109 Å⁻¹

8.2 Resolution estimates [i](#)

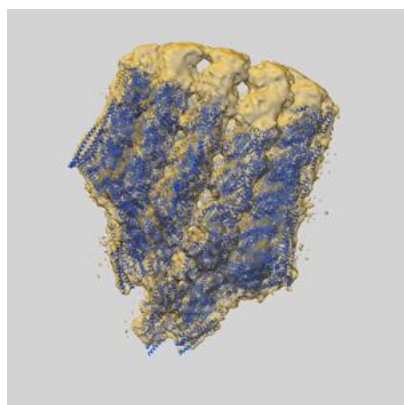
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	13.39	22.37	15.08

*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 13.39 differs from the reported value 9.2 by more than 10 %

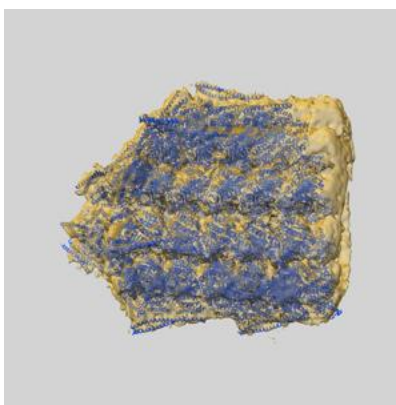
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18665 and PDB model 8QV2. Per-residue inclusion information can be found in section 3 on page 15.

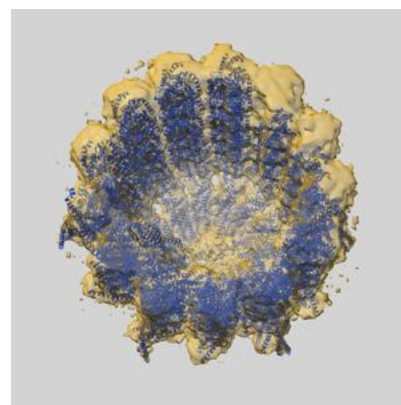
9.1 Map-model overlay [i](#)



X



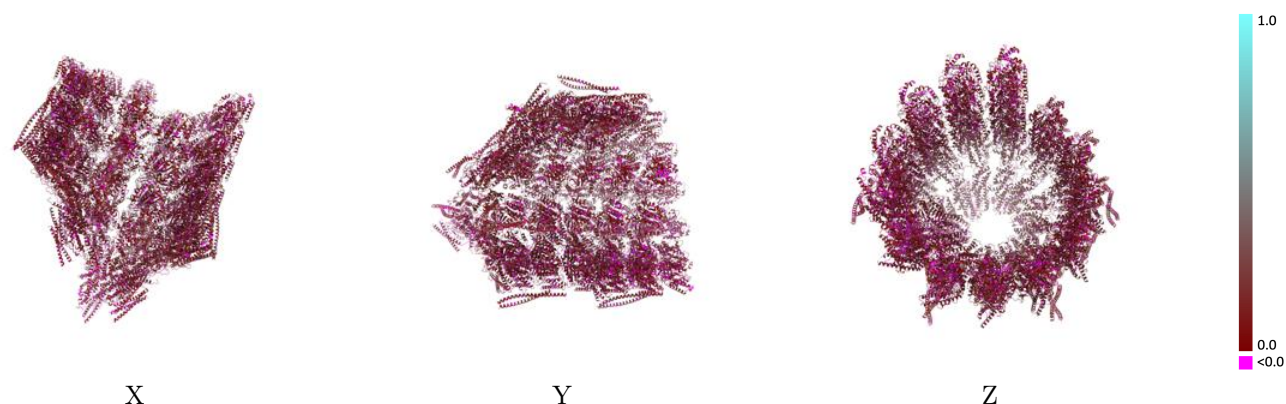
Y



Z

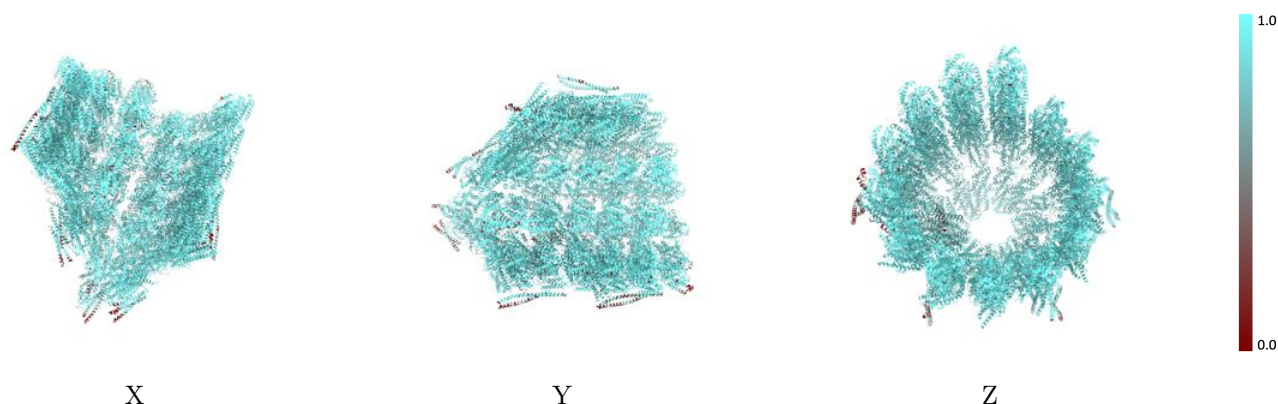
The images above show the 3D surface view of the map at the recommended contour level 0.243 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



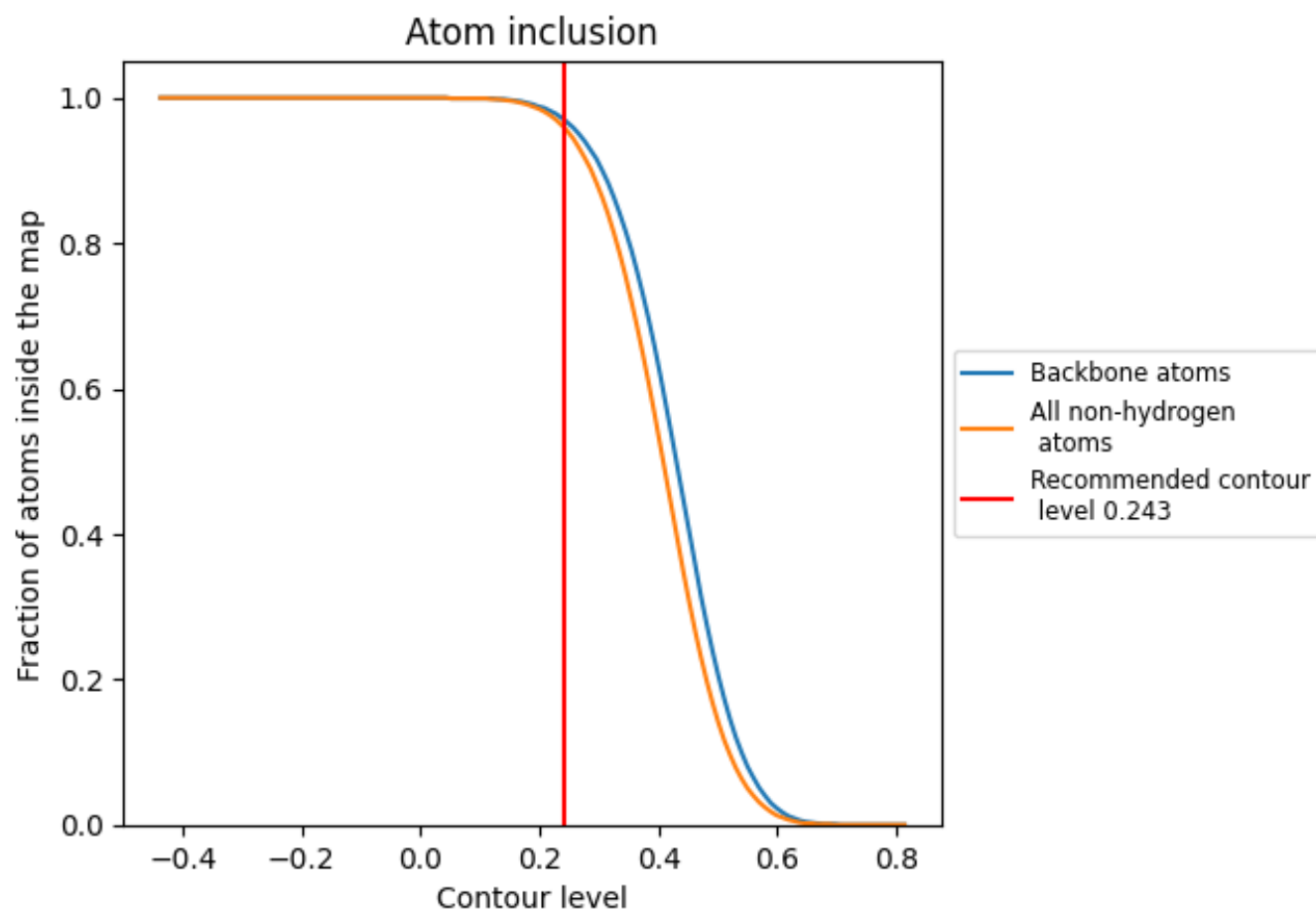
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.243).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.243) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.1120
Ab	 0.9440	 0.1110
Ac	 0.9720	 0.1250
Ad	 0.9880	 0.1140
Ae	 0.9940	 0.1170
Af	 0.9880	 0.1180
Ag	 0.9860	 0.1160
Ah	 0.9790	 0.1150
Ai	 0.9870	 0.1150
Aj	 0.9910	 0.1020
Ak	 0.9880	 0.1080
Al	 0.9900	 0.0960
Am	 0.9730	 0.0950
An	 0.9640	 0.0940
Ao	 0.9520	 0.0980
Ap	 0.9870	 0.1090
Aq	 0.9920	 0.0910
Ar	 0.9890	 0.1050
Bb	 0.9670	 0.1060
Bc	 0.9830	 0.1210
Bd	 0.9910	 0.1180
Be	 0.9910	 0.1130
Bf	 0.9940	 0.1190
Bg	 0.9900	 0.1190
Bh	 0.9800	 0.1190
Bi	 0.9850	 0.1030
Bj	 0.9860	 0.1090
Bk	 0.9840	 0.1030
Bl	 0.9850	 0.0960
Bm	 0.9530	 0.0870
Bn	 0.8850	 0.0870
Bo	 0.9550	 0.0980
Bp	 0.9610	 0.0930
Bq	 0.9810	 0.1080
Br	 0.9800	 0.0970



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
C	 0.8970	 0.0510
D	 0.9500	 0.1130
E	 0.9780	 0.1230
F	 0.9750	 0.1350
G	 0.9860	 0.1310
H	 0.9740	 0.1320
I	 0.9820	 0.1320
J	 0.9640	 0.1390
K	 0.9770	 0.1360
L	 0.9680	 0.1340
M	 0.9820	 0.1290
N	 0.9630	 0.1240
O	 0.9490	 0.1110
P	 0.8820	 0.1170
Sa	 0.5480	 0.0830
Sb	 0.5750	 0.0560
Sc	 0.7580	 0.0840
Sd	 0.8080	 0.0790
Se	 0.8440	 0.1210
Sf	 0.8570	 0.1040
Sg	 0.8820	 0.1220
Sh	 0.8240	 0.1100
Si	 0.8100	 0.0930
Sj	 0.8550	 0.0980
Sk	 0.7870	 0.1070
Sl	 0.7450	 0.0870
Sm	 0.7280	 0.1040
Sn	 0.8090	 0.0680
Ua	 0.8810	 0.1450
Ub	 0.4550	 0.1070
Uc	 0.9370	 0.1680
Ud	 0.7850	 0.1590
Ue	 0.8840	 0.1860
Uf	 0.7420	 0.1810
Ug	 0.9070	 0.1510
Uh	 0.8440	 0.1800
Ui	 0.8240	 0.1680
Uj	 0.6150	 0.1720
Uk	 0.8660	 0.1610
Ul	 0.5340	 0.1570
Um	 0.5490	 0.1280
Un	 0.3450	 0.0990

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
a	 0.7820	 0.0430
b	 0.9450	 0.1000
c	 0.9670	 0.1090
d	 0.9830	 0.1120
e	 0.9850	 0.1230
f	 0.9810	 0.1180
g	 0.9620	 0.1230
h	 0.9670	 0.1140
i	 0.9750	 0.1140
j	 0.9820	 0.1150
k	 0.9800	 0.1030
l	 0.9750	 0.1010
m	 0.9700	 0.1050
n	 0.9450	 0.0920