



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:24 PM UTC

PDB ID : 7TNS / pdb_00007tns
EMDB ID : EMD-26019
Title : Subpellicular microtubule from detergent-extract Toxoplasma gondii cells
Authors : Sun, S.Y.; Pintilie, G.D.; Chen, M.; Chiu, W.
Deposited on : 2022-01-21
Resolution : 6.70 Å(reported)
Based on initial model : 7MIZ

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

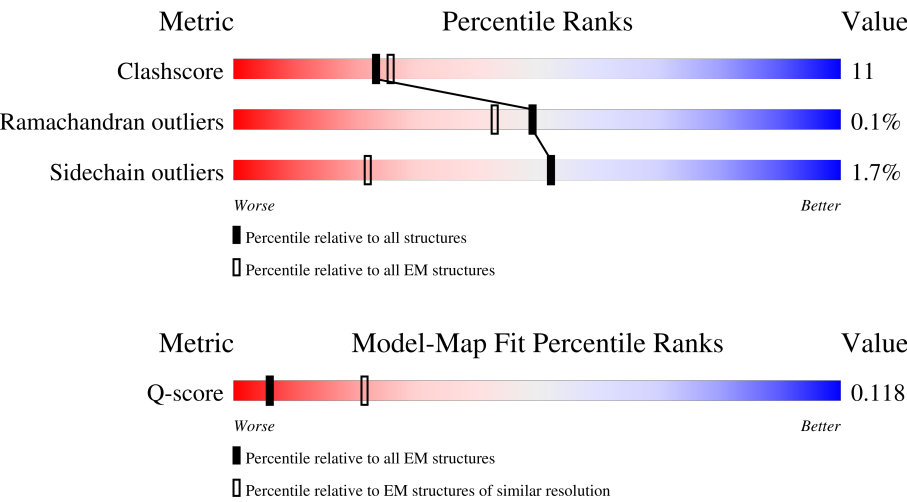
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 6.70 Å.

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



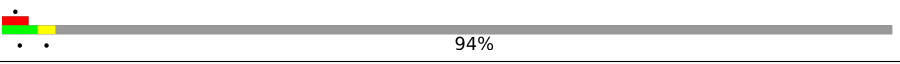
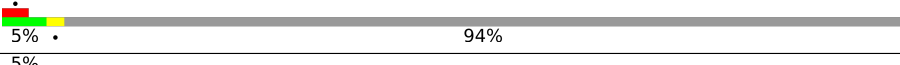
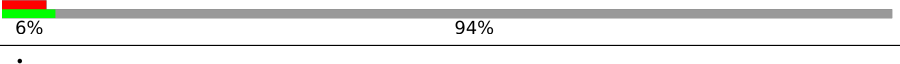
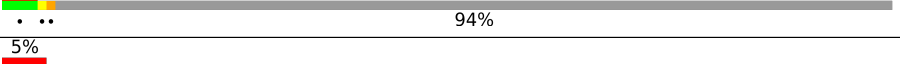
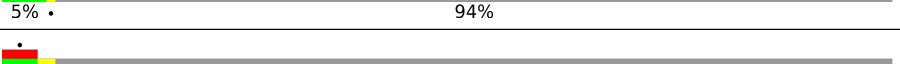
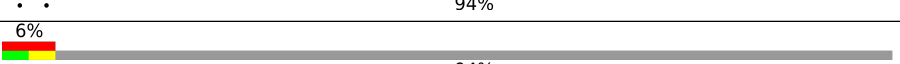
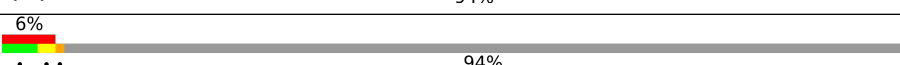
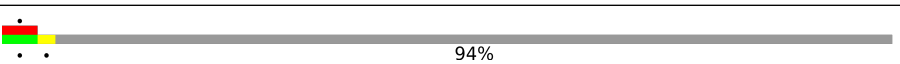
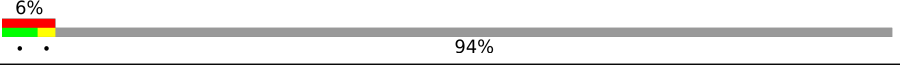
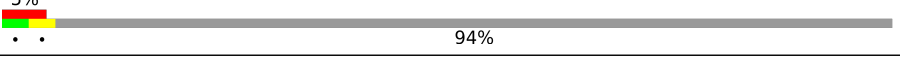
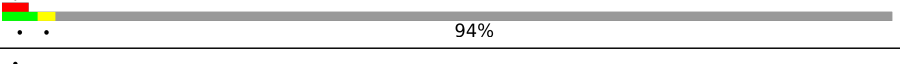
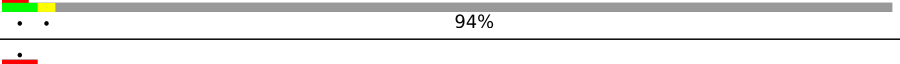
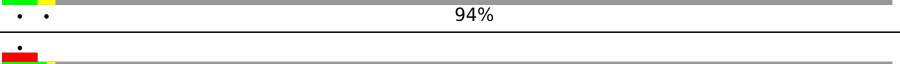
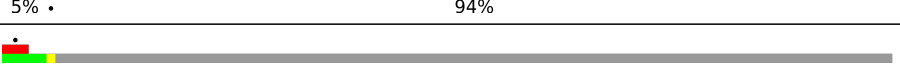
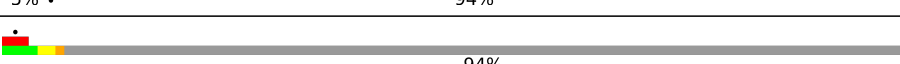
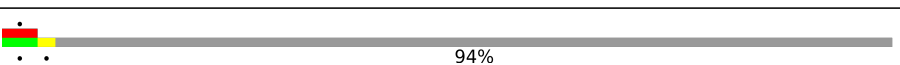
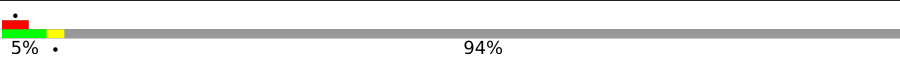
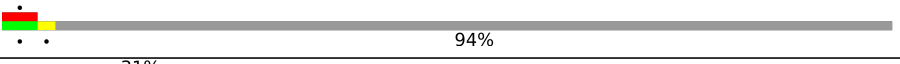
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	523 (6.20 - 7.20)

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

Mol	Chain	Length	Quality of chain
1	0	351	 94%
1	1	351	 5% 94%
1	10	351	 94%
1	11	351	 94%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	12	351	 94%
1	13	351	 94%
1	14	351	 94%
1	15	351	 94%
1	16	351	 94%
1	17	351	 94%
1	18	351	 94%
1	19	351	 94%
1	2	351	 94%
1	20	351	 94%
1	21	351	 94%
1	22	351	 94%
1	23	351	 94%
1	3	351	 94%
1	4	351	 94%
1	5	351	 94%
1	6	351	 94%
1	7	351	 94%
1	8	351	 94%
1	9	351	 94%
2	A0	453	 31% 69% 23% 6%
2	A2	453	 30% 71% 21% 6%
2	A4	453	 29% 75% 18% 6%
2	A6	453	 29% 71% 22% 6%
2	A8	453	 28% 71% 22% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	B0	453	
2	B2	453	
2	B4	453	
2	B6	453	
2	B8	453	
2	C0	453	
2	C2	453	
2	C4	453	
2	C6	453	
2	C8	453	
2	D0	453	
2	D2	453	
2	D4	453	
2	D6	453	
2	D8	453	
2	E0	453	
2	E2	453	
2	E4	453	
2	E6	453	
2	E8	453	
2	F0	453	
3	A1	449	
3	A3	449	
3	A5	449	
3	A7	449	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	A9	449	
3	B1	449	
3	B3	449	
3	B5	449	
3	B7	449	
3	B9	449	
3	C1	449	
3	C3	449	
3	C5	449	
3	C7	449	
3	C9	449	
3	D1	449	
3	D3	449	
3	D5	449	
3	D7	449	
3	D9	449	
3	E1	449	
3	E3	449	
3	E5	449	
3	E7	449	
3	E9	449	
3	F1	449	
4	a	220	
4	b	220	
4	c	220	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	d	220	
4	e	220	
4	f	220	
4	g	220	
4	h	220	
4	i	220	
4	j	220	
4	k	220	
4	l	220	
4	m	220	
4	n	220	
4	o	220	
4	p	220	
4	q	220	
4	r	220	
4	s	220	
4	t	220	
4	u	220	
4	v	220	
4	x	220	
4	y	220	
5	w	189	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 216148 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 Microtubule associated protein SPM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	1	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	10	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	11	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	12	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	13	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	14	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	15	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	16	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	17	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	18	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	19	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	2	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	20	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	21	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	22	20	Total	C	N	O	S	0	0
			160	105	26	28	1		
1	23	20	Total	C	N	O	S	0	0
			160	105	26	28	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	22	Total 174	C 114	N 28	O 31	S 1	0	0
1	4	22	Total 174	C 114	N 28	O 31	S 1	0	0
1	5	22	Total 174	C 114	N 28	O 31	S 1	0	0
1	6	22	Total 174	C 114	N 28	O 31	S 1	0	0
1	7	22	Total 174	C 114	N 28	O 31	S 1	0	0
1	8	22	Total 174	C 114	N 28	O 31	S 1	0	0
1	9	22	Total 174	C 114	N 28	O 31	S 1	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	263	ALA	VAL	conflict	UNP S8F1Y1
1	263	ALA	VAL	conflict	UNP S8F1Y1
10	263	ALA	VAL	conflict	UNP S8F1Y1
11	263	ALA	VAL	conflict	UNP S8F1Y1
12	263	ALA	VAL	conflict	UNP S8F1Y1
13	263	ALA	VAL	conflict	UNP S8F1Y1
14	263	ALA	VAL	conflict	UNP S8F1Y1
15	263	ALA	VAL	conflict	UNP S8F1Y1
16	263	ALA	VAL	conflict	UNP S8F1Y1
17	263	ALA	VAL	conflict	UNP S8F1Y1
18	263	ALA	VAL	conflict	UNP S8F1Y1
19	263	ALA	VAL	conflict	UNP S8F1Y1
2	263	ALA	VAL	conflict	UNP S8F1Y1
20	263	ALA	VAL	conflict	UNP S8F1Y1
21	263	ALA	VAL	conflict	UNP S8F1Y1
22	263	ALA	VAL	conflict	UNP S8F1Y1
23	263	ALA	VAL	conflict	UNP S8F1Y1
3	263	ALA	VAL	conflict	UNP S8F1Y1
4	263	ALA	VAL	conflict	UNP S8F1Y1
5	263	ALA	VAL	conflict	UNP S8F1Y1
6	263	ALA	VAL	conflict	UNP S8F1Y1
7	263	ALA	VAL	conflict	UNP S8F1Y1
8	263	ALA	VAL	conflict	UNP S8F1Y1
9	263	ALA	VAL	conflict	UNP S8F1Y1

- Molecule 2 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	F0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

- Molecule 3 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A1	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A3	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A5	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A7	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A9	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B1	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B3	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B5	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B7	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B9	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C1	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C3	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C5	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C7	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C9	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D1	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D3	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D5	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D7	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D9	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E1	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E3	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E5	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E7	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E9	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	F1	426	Total 3331	C 2094	N 569	O 641	S 27	0	0

- Molecule 4 is a protein called PDI family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	150	Total 1198	C 763	N 213	O 217	S 5	0	0
4	b	150	Total 1198	C 763	N 213	O 217	S 5	0	0
4	c	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	d	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	e	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	f	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	g	201	Total 1608	C 1021	N 283	O 297	S 7	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
4	h	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	i	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	j	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	k	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	l	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	m	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	n	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	o	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	p	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	q	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	r	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	s	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	t	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	u	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	v	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	x	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	y	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		

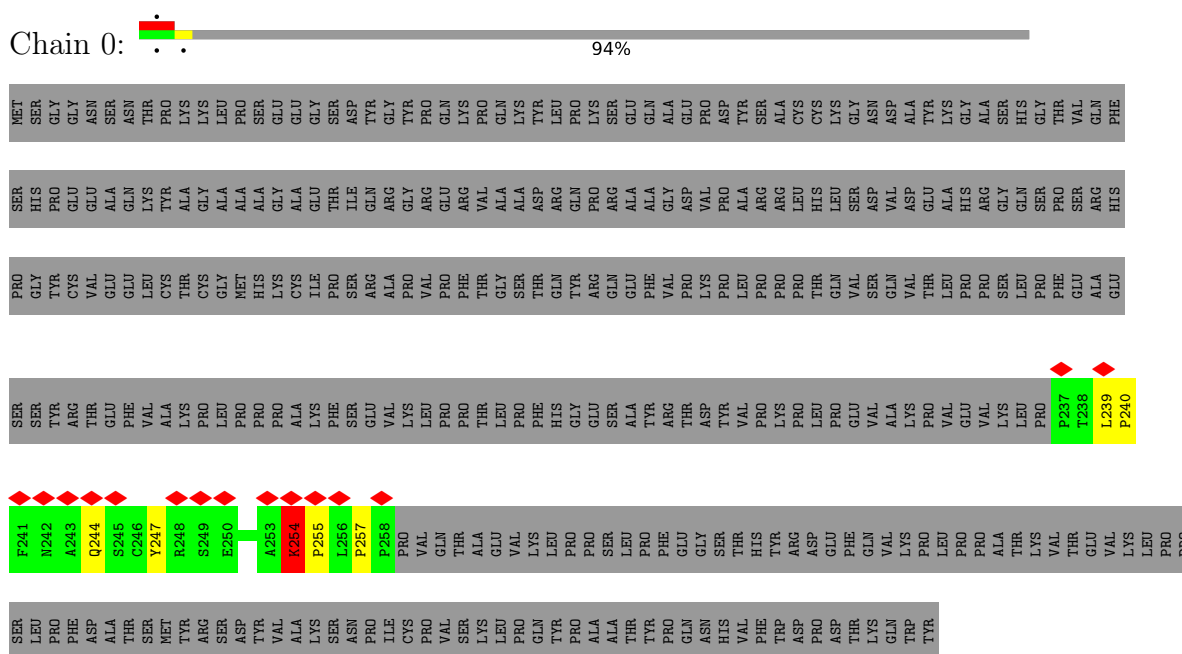
- Molecule 5 is a protein called PDI family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	w	143	Total	C	N	O	S	0	0
			1172	755	207	205	5		

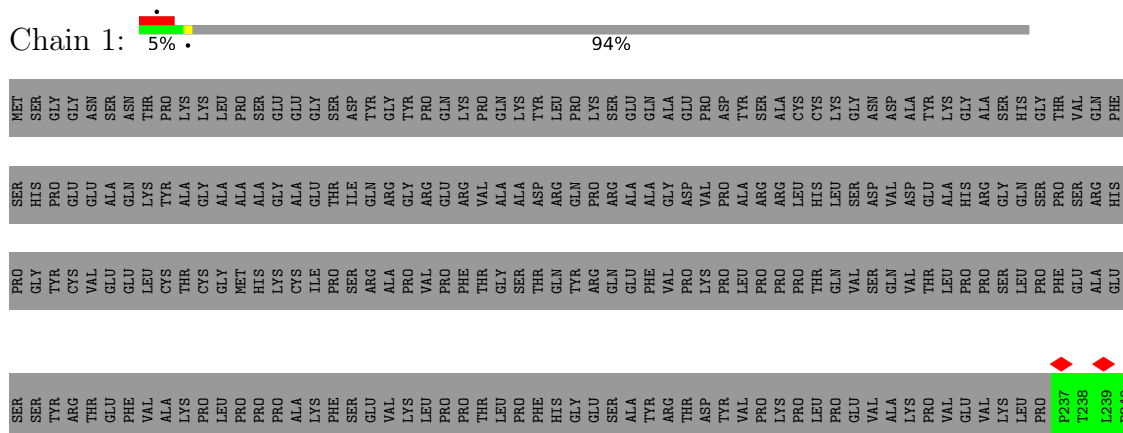
3 Residue-property plots

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: Microtubule associated protein SPM1



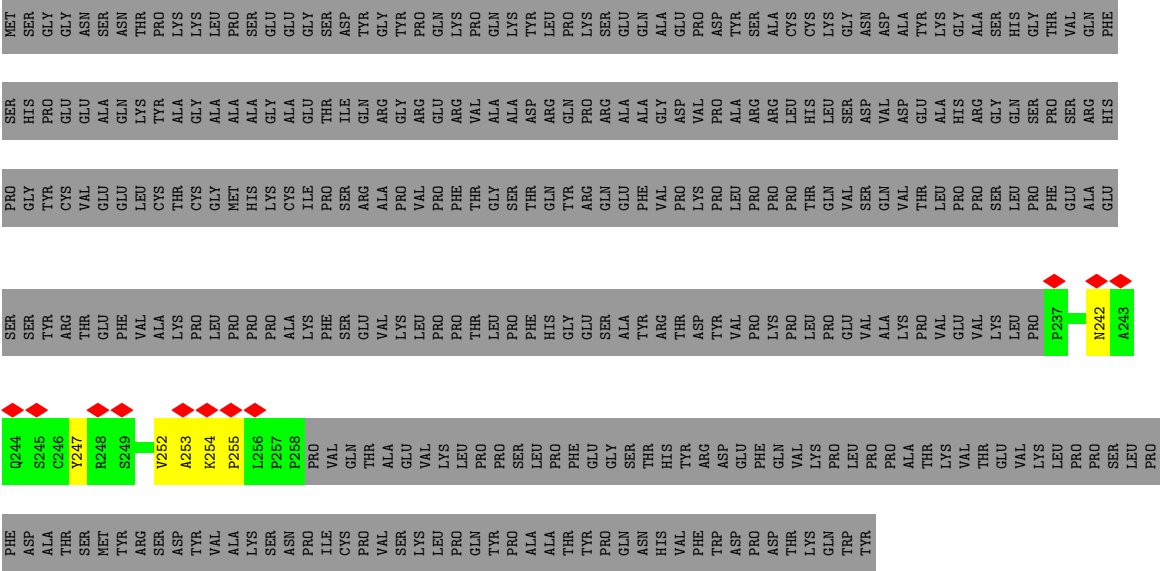
- Molecule 1: Microtubule associated protein SPM1





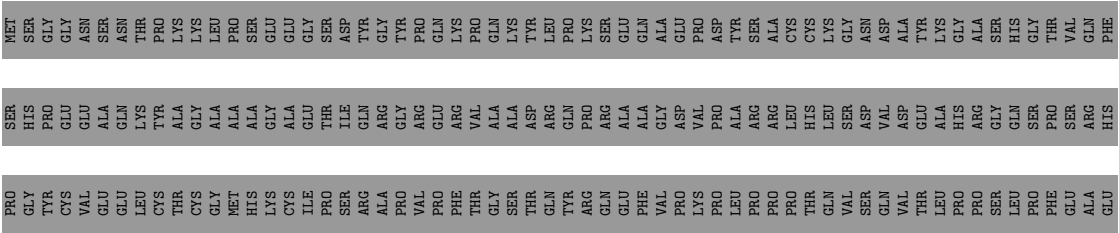
• Molecule 1: Microtubule associated protein SPM1

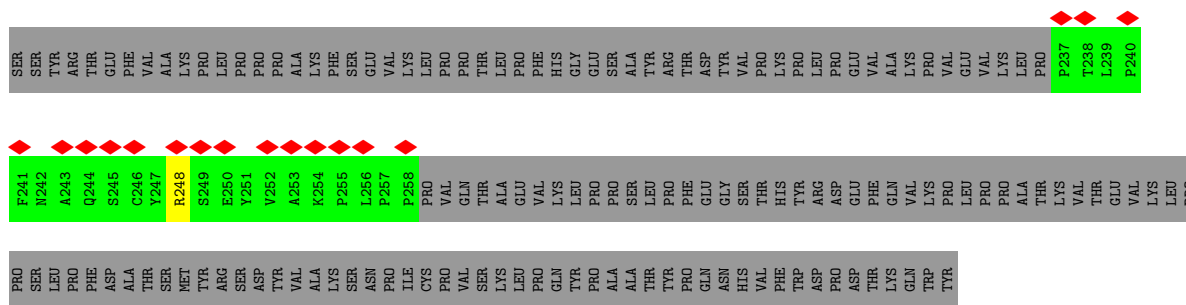
Chain 13: 5% . 94%



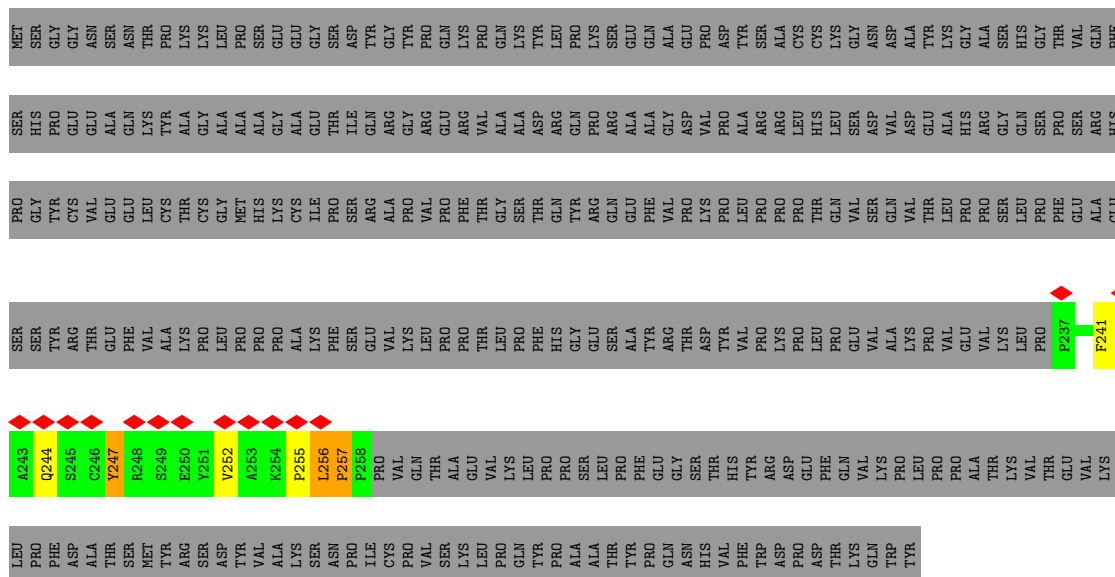
• Molecule 1: Microtubule associated protein SPM1

Chain 14: 5% 6% 94%

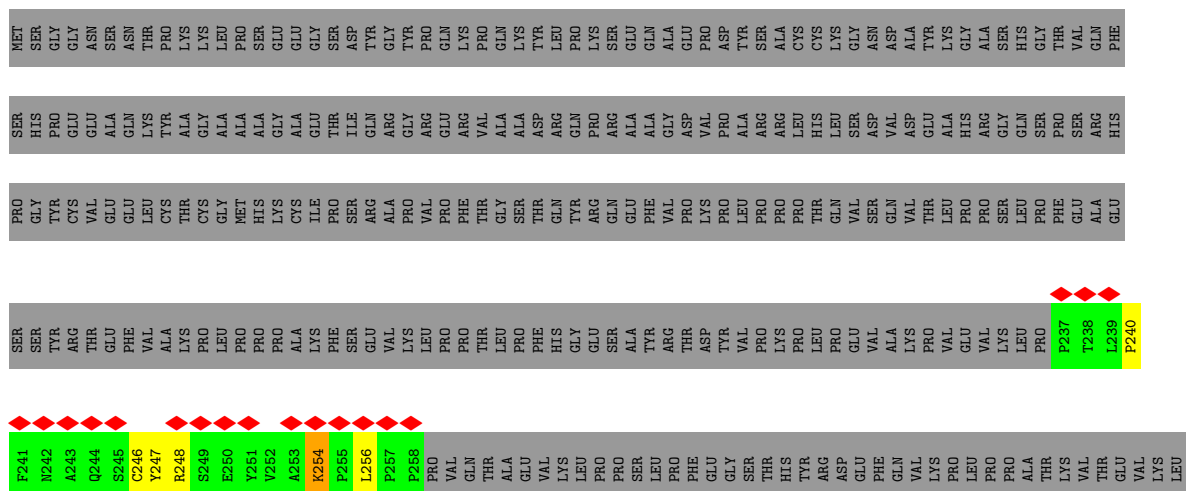




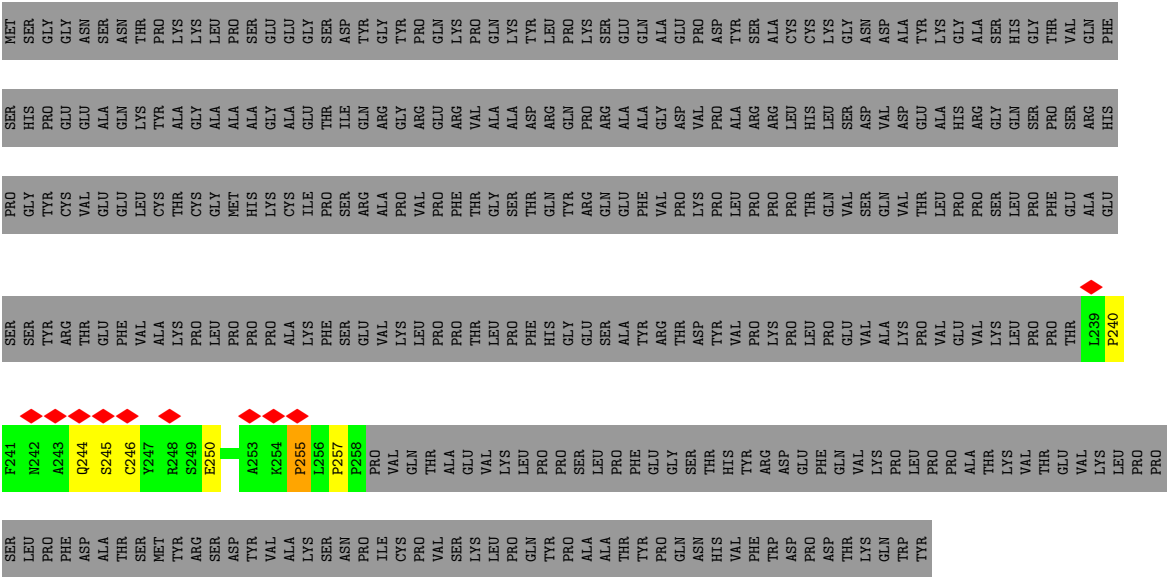
- Molecule 1: Microtubule associated protein SPM1



- Molecule 1: Microtubule associated protein SPM1

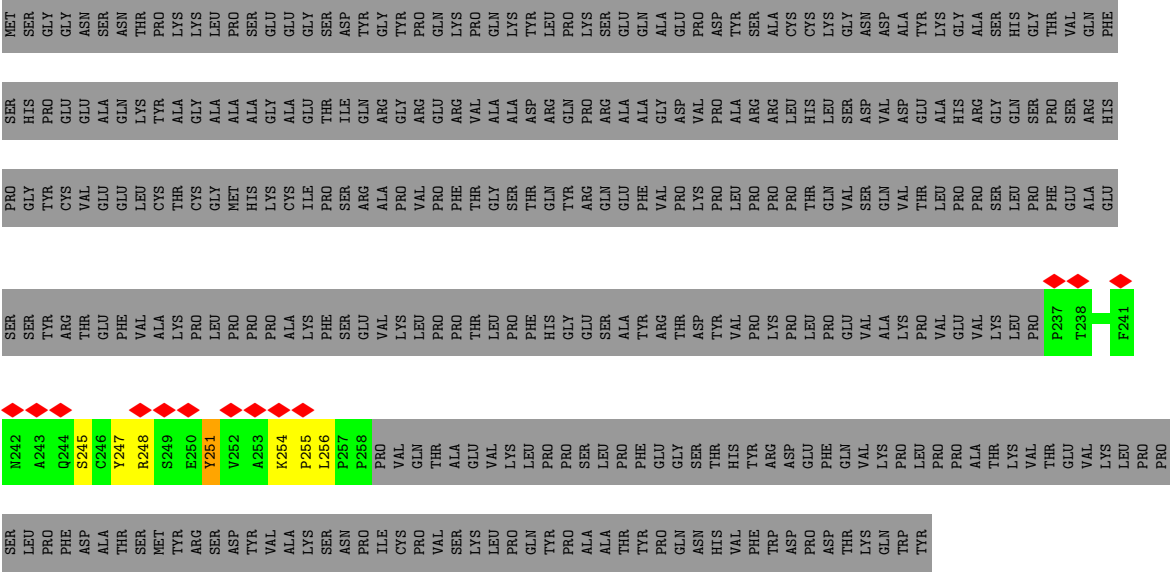






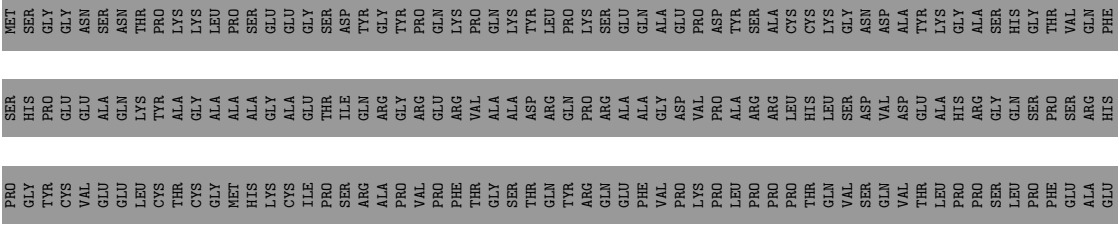
• Molecule 1: Microtubule associated protein SPM1

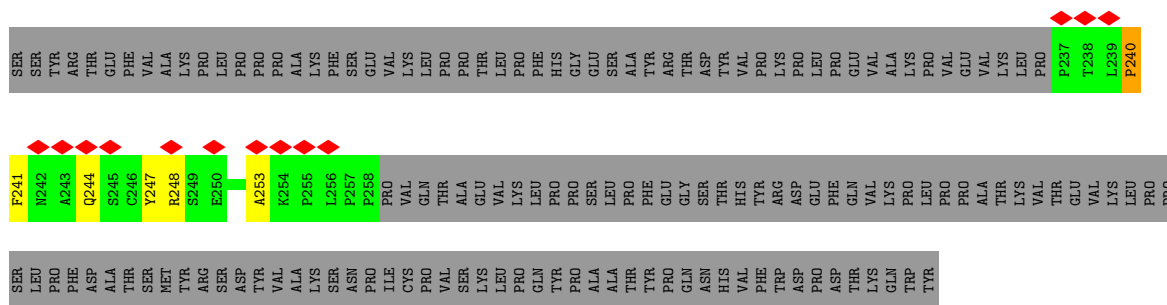
Chain 3:  94%



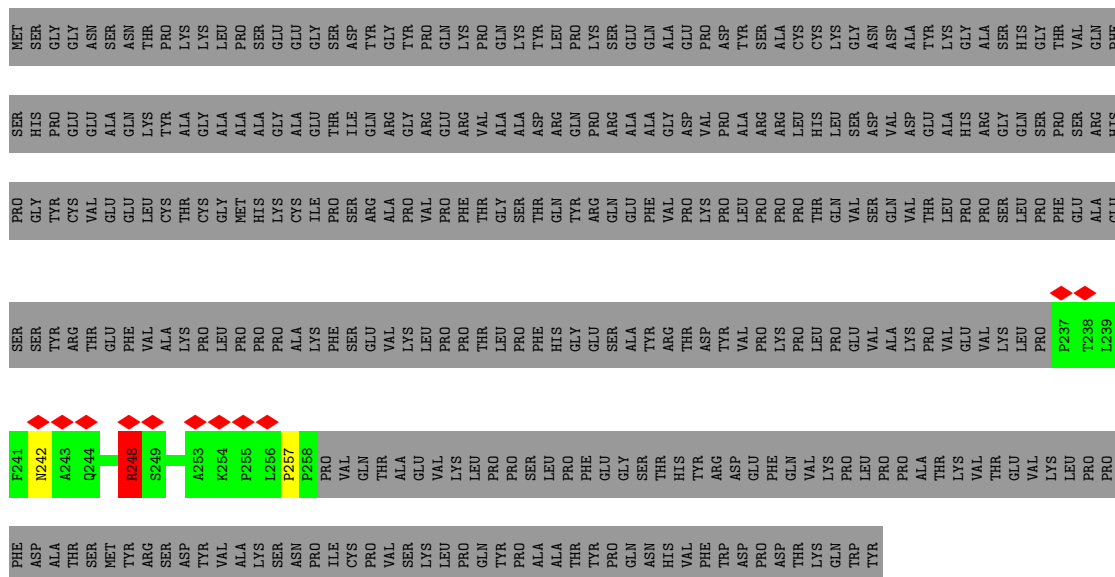
• Molecule 1: Microtubule associated protein SPM1

Chain 4:  5% 94%

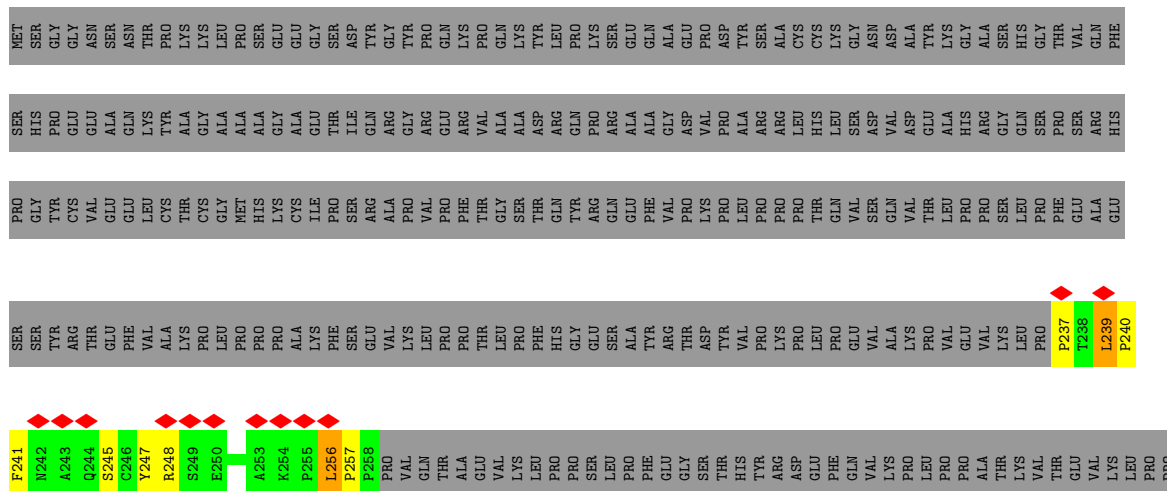




- Molecule 1: Microtubule associated protein SPM1



- Molecule 1: Microtubule associated protein SPM1



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

● Molecule 1: Microtubule associated protein SPM1

Chain 7:  94%

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

SER	HIS	PRO	GLU	GLU	ALA	GLN	LYS	TYR	ALA	GLY	ALA	GLY	ILE	THR	ILE	GLN	ARG	GLY	PRO	ARG	GLU	PRO	VAL	ARG	VAL	ALA	GLN	ASP	TYR	PRO	GLN	PRO	ARG	ALA	TYR	ALA	ARG	ALA	TRP	PRO	CYS	LYS	GLY	ASN	ASP	VAL	ASP	ALA	TYR	GLY	LYS	PRO	GLY	THR	VAL	GLN	ARG	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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

F241	N242	A243	Q244	S245	R246	E247	S248	E249	Y250	Y251	Y252	A253	N254	P255	L256	P257	P258	PRO	VAL	GLN	PRO	VAL	THR	ALA	GLY	VAL	GLN	LYS	PRO	LEU	THR	GLY	VAL	ARG	PRO	ALA	GLY	THR	VAL	PRO	PRO	ARG	ALA	TRP	PRO	CYS	LYS	GLY	ASN	ASP	VAL	ASP	ALA	TYR	GLY	LYS	PRO	GLY	THR	VAL	GLN	ARG	HIS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

● Molecule 1: Microtubule associated protein SPM1

Chain 8:  5% . 94%

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

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

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

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

F241	N242	A243	Q244	S245	C246	Y247	R248	Y251	Y252	A253	K254	P255	L256	P257	P258	PRO	VAL	GLN	PRO	VAL	THR	ALA	GLY	VAL	LYS	PRO	LEU	THR	GLY	VAL	ARG	PRO	ALA	GLY	THR	VAL	PRO	PRO	ARG	ALA	TRP	PRO	CYS	LYS	GLY	ASN	ASP	VAL	ASP	ALA	TYR	GLY	LYS	PRO	GLY	THR	VAL	GLN	ARG	HIS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

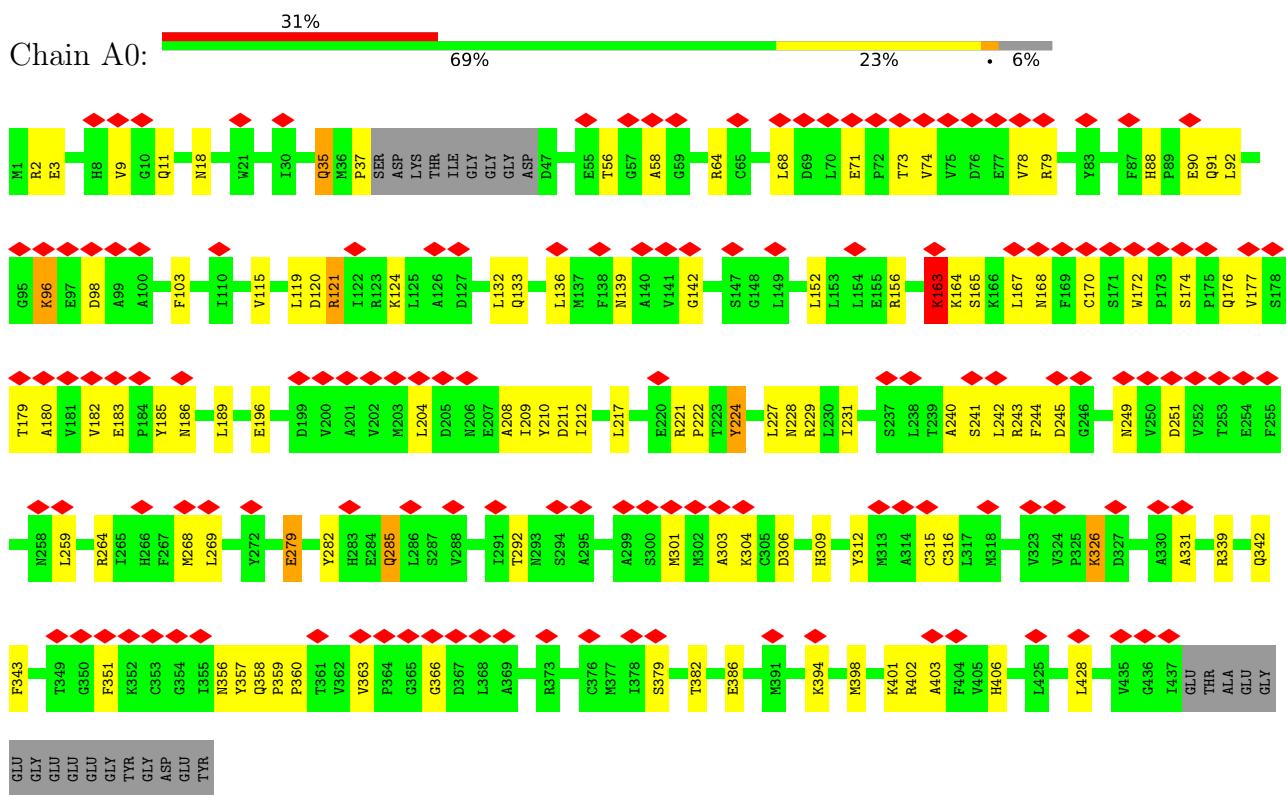
SER	LEU	PRO	PHE	ASP	ALA	THR	SER	MET	TYR	ARG	SER	ASP	TYR	VAL	GLY	LYS	ILE	THR	SER	ASN	PRO	ILE	PRO	CYS	GLY	TYR	PRO	GLN	VAL	THR	ALA	GLY	VAL	ARG	PRO	ALA	GLY	THR	VAL	PRO	PRO	ARG	ALA	TRP	PRO	CYS	LYS	GLY	ASN	ASP	VAL	ASP	ALA	TYR	GLY	LYS	PRO	GLY	THR	VAL	GLN	ARG	HIS
-----	-----	-----	-----	-----	-----	-----	-----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

● Molecule 1: Microtubule associated protein SPM1

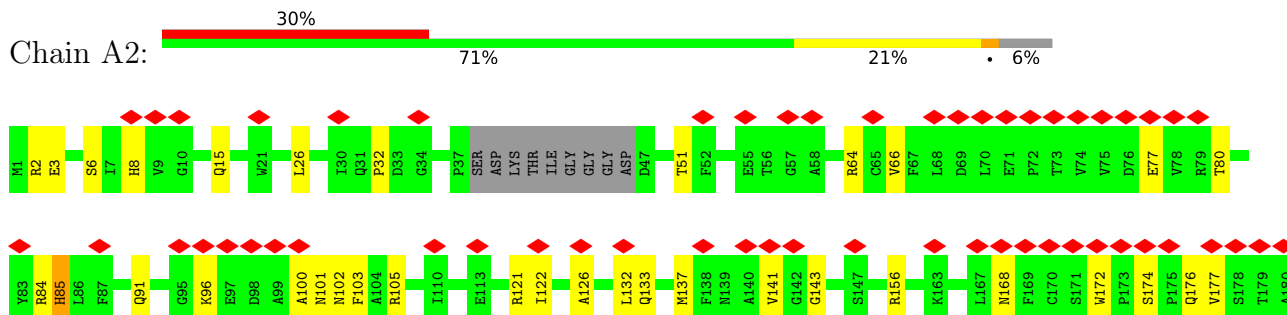
Chain 9:  94%

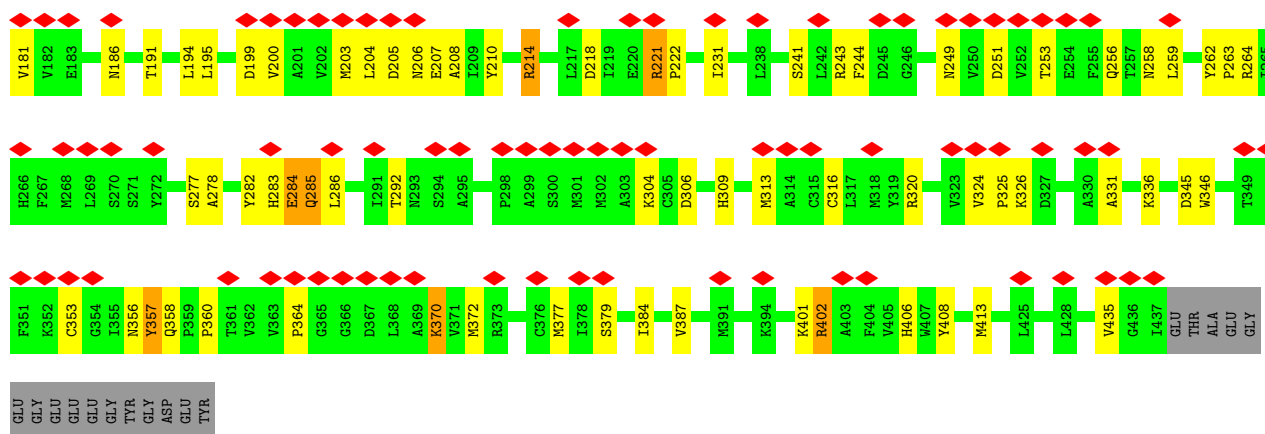
MET	SER	GLY	ASN	ASN	THR	PRO	LYS	LEU	PRO	SER	GLU	GLY	GLY	ASP	TYR	ARG	GLY	TYR	PRO	GLN	PRO	VAL	SER	LYS	LEU	PRO	TYR	PRO	ALA	ALA	THR	TYR	PRO	GLN	ASP	TYR	PRO	GLN	PRO	VAL	ARG	ALA	TRP	PRO	CYS	LYS	GLY	ASN	ASP	VAL	ASP	ALA	TYR	GLY	LYS	PRO	GLY	THR	VAL	GLN	ARG	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----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

- Molecule 2: Tubulin alpha chain

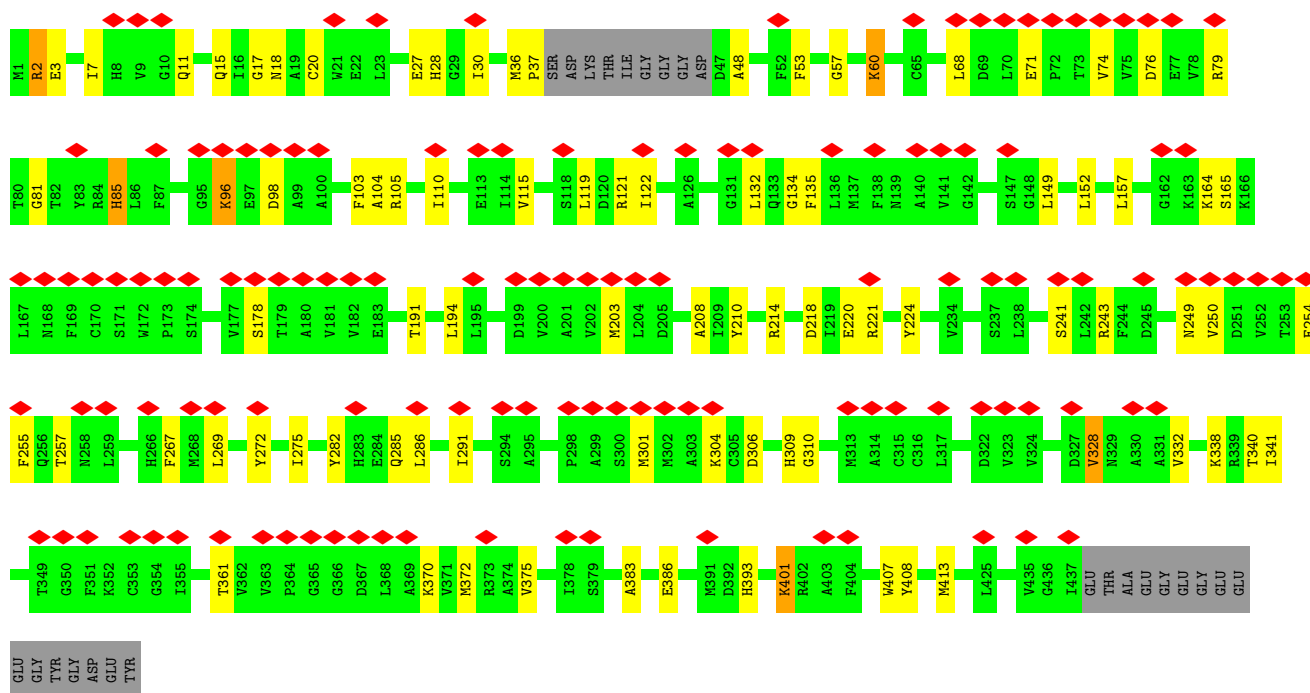
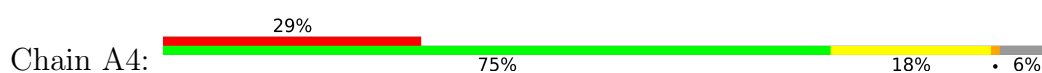


- Molecule 2: Tubulin alpha chain

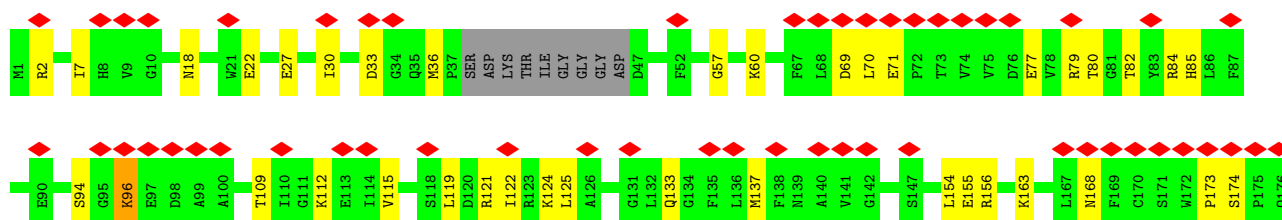
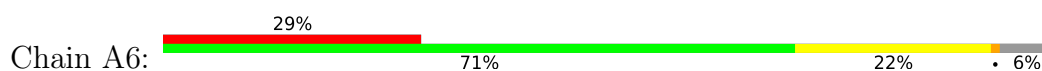


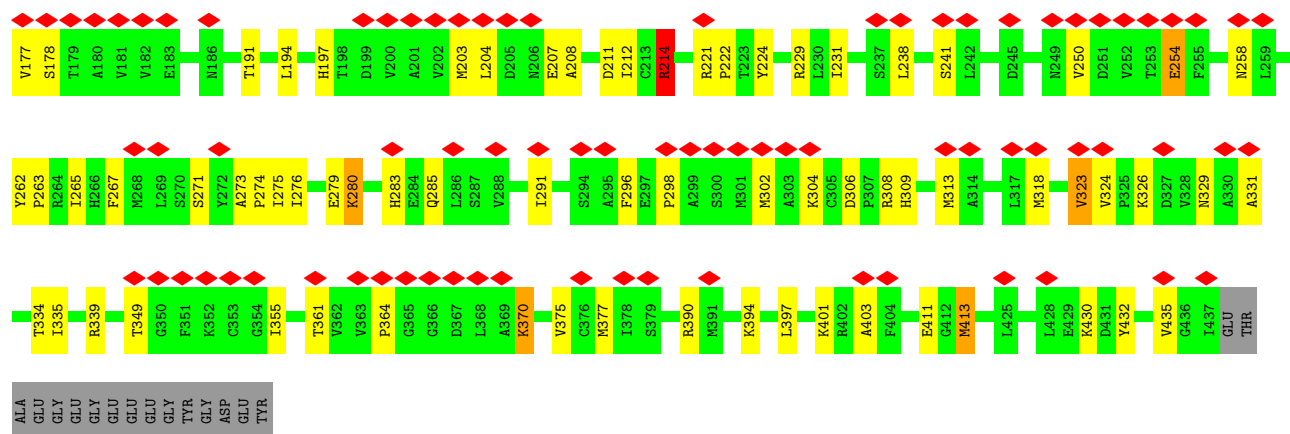


• Molecule 2: Tubulin alpha chain

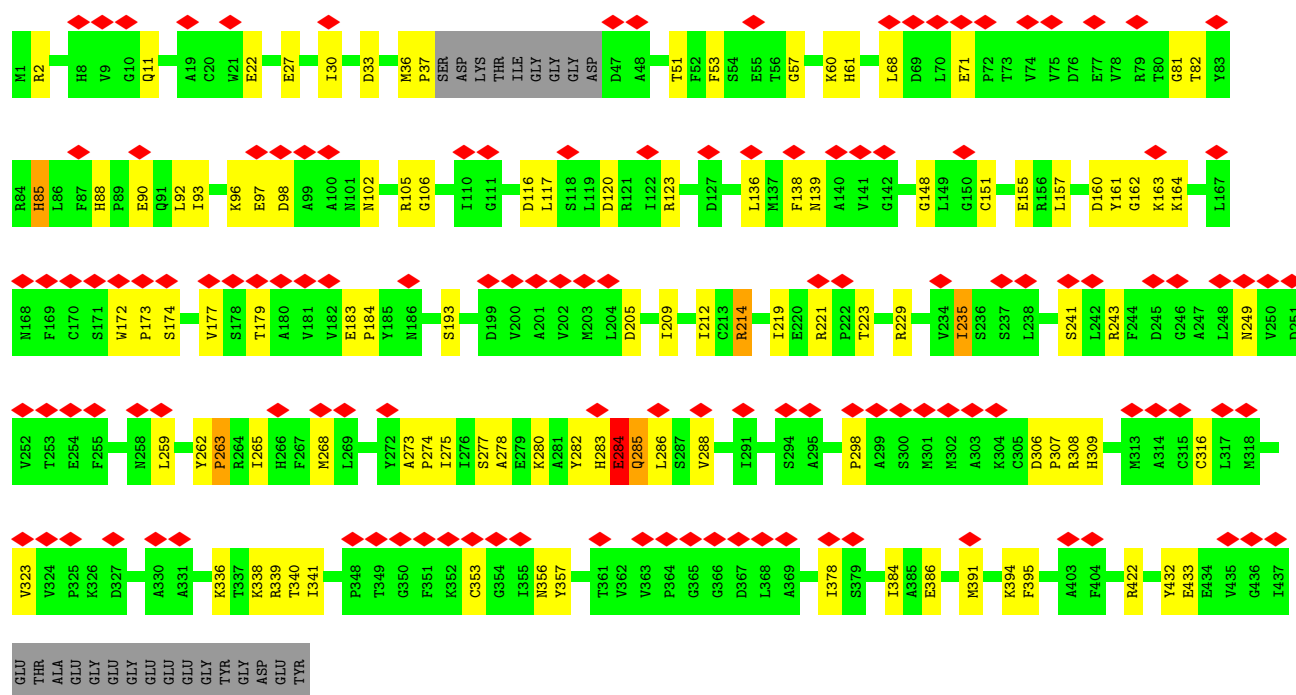
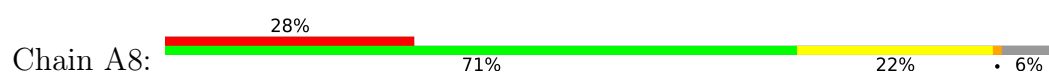


• Molecule 2: Tubulin alpha chain

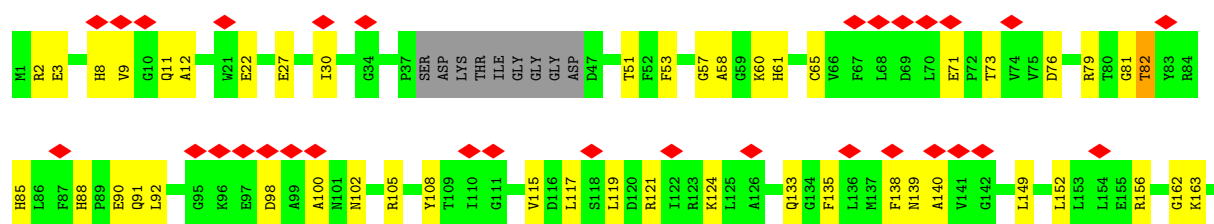
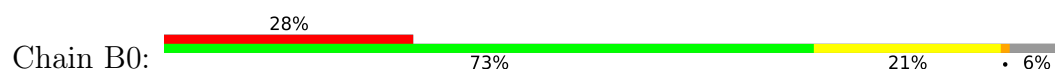


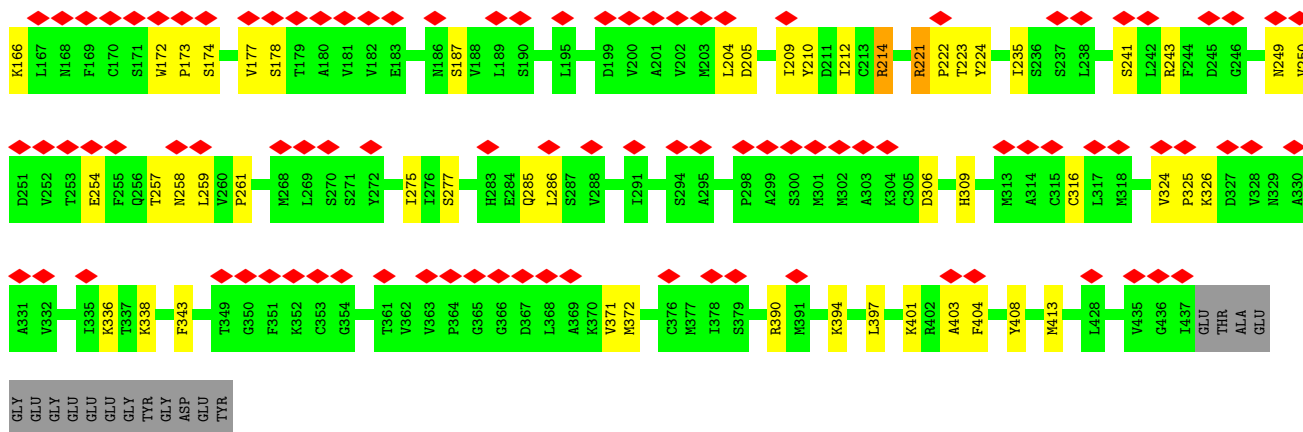


• Molecule 2: Tubulin alpha chain

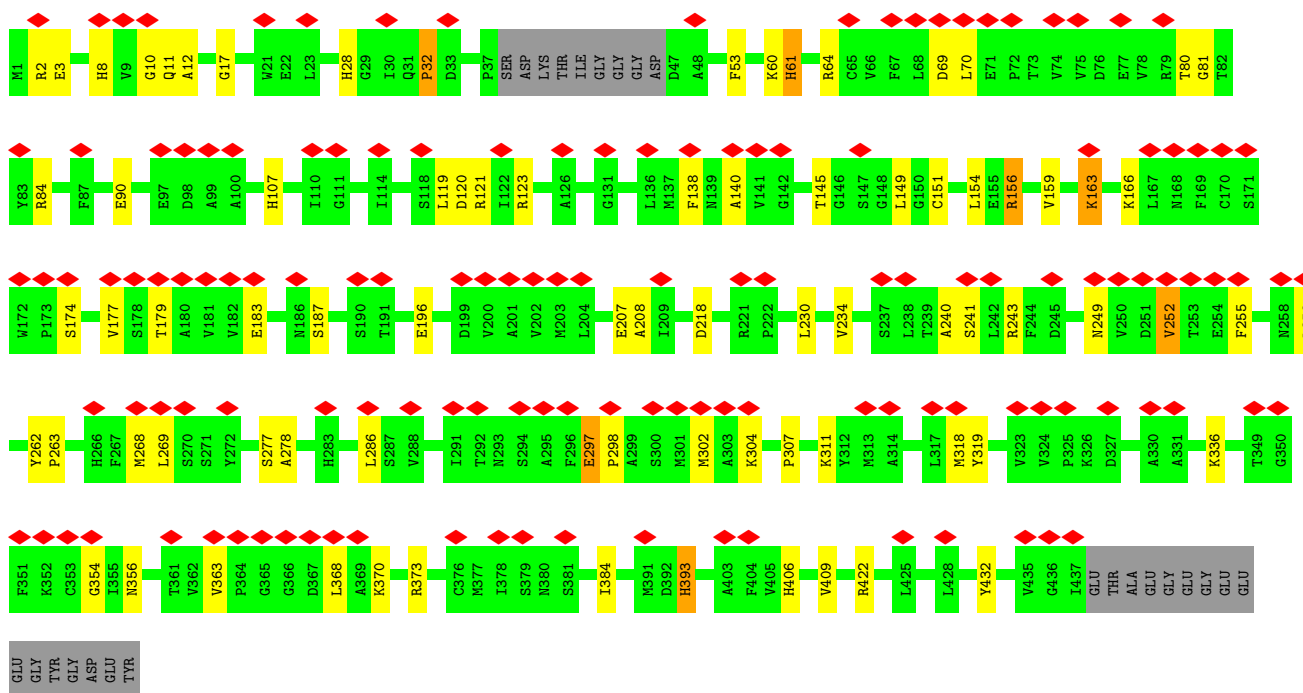
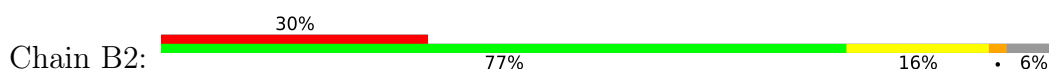


• Molecule 2: Tubulin alpha chain

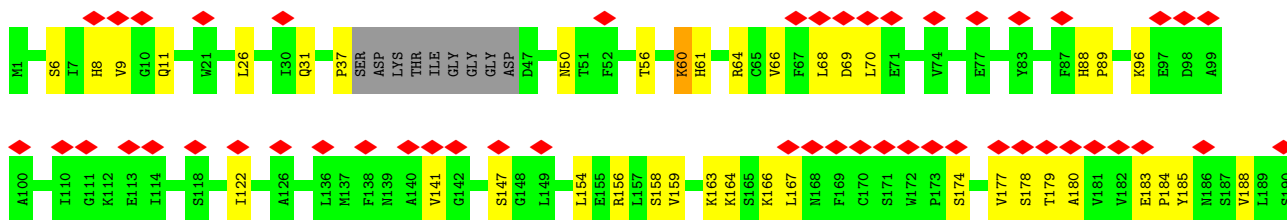
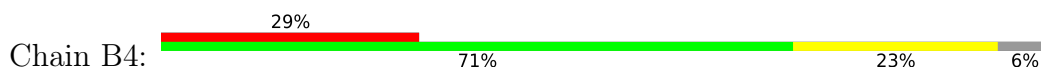


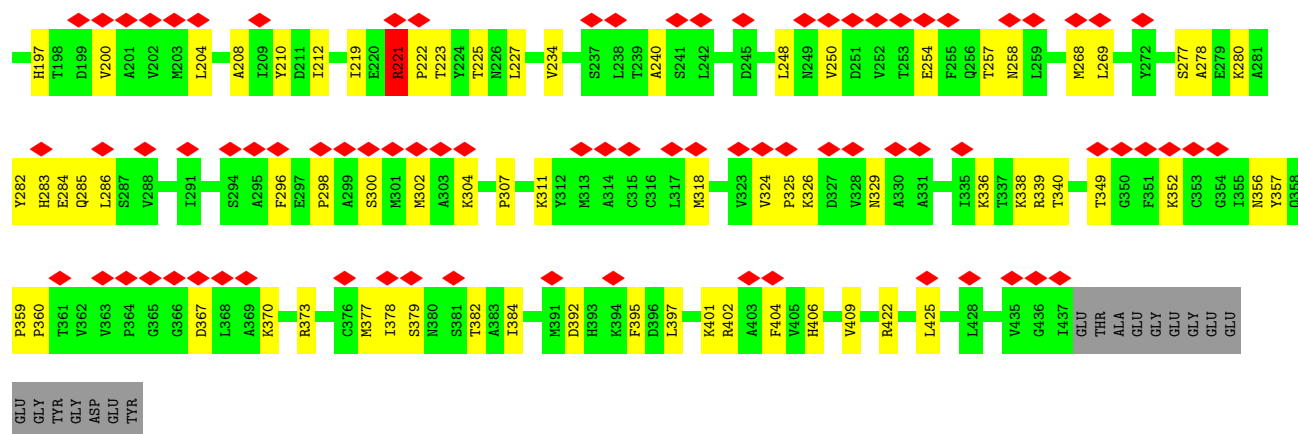


• Molecule 2: Tubulin alpha chain

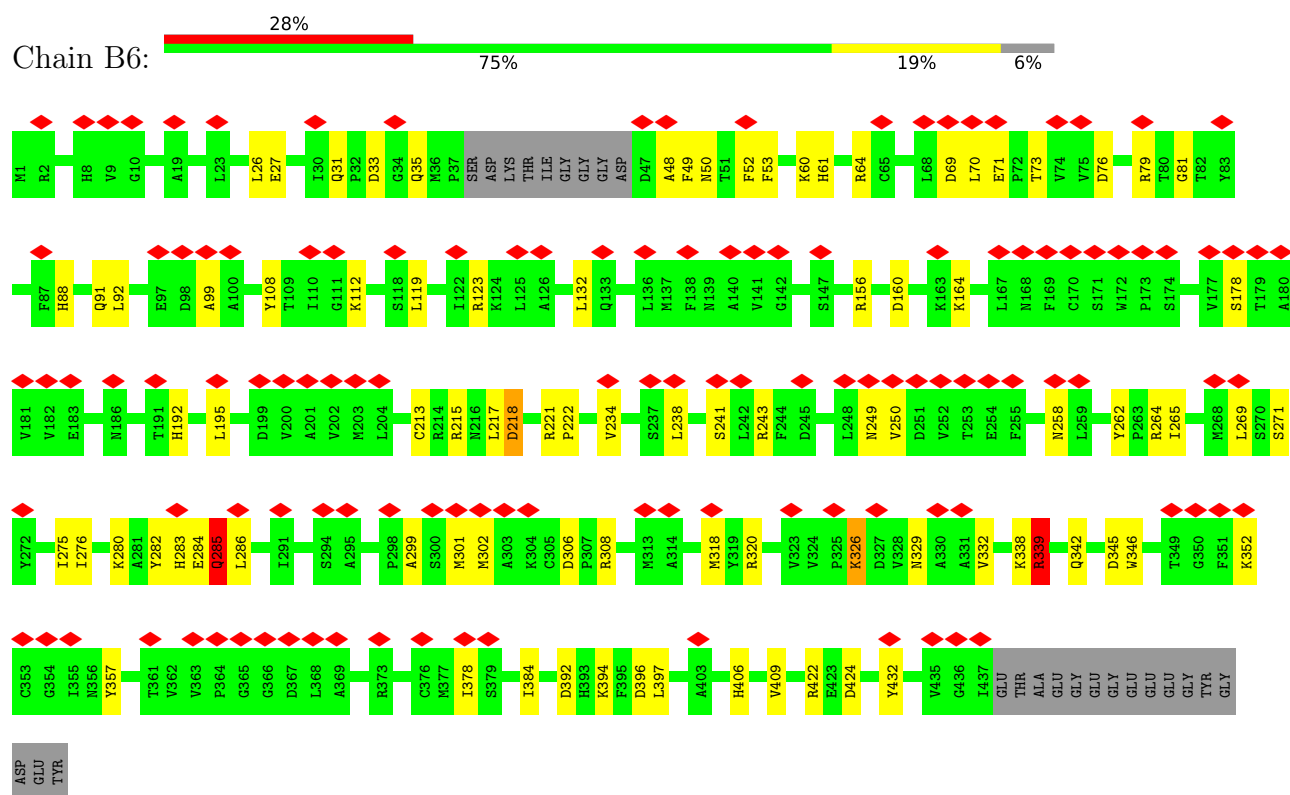


• Molecule 2: Tubulin alpha chain

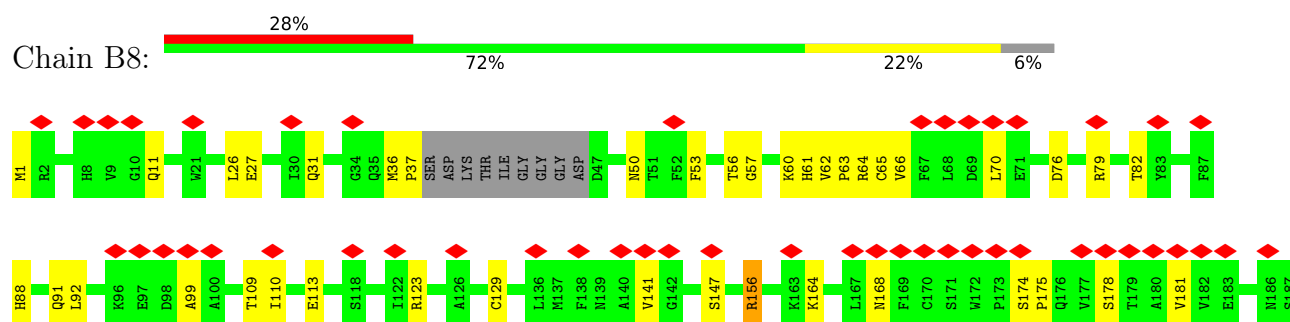




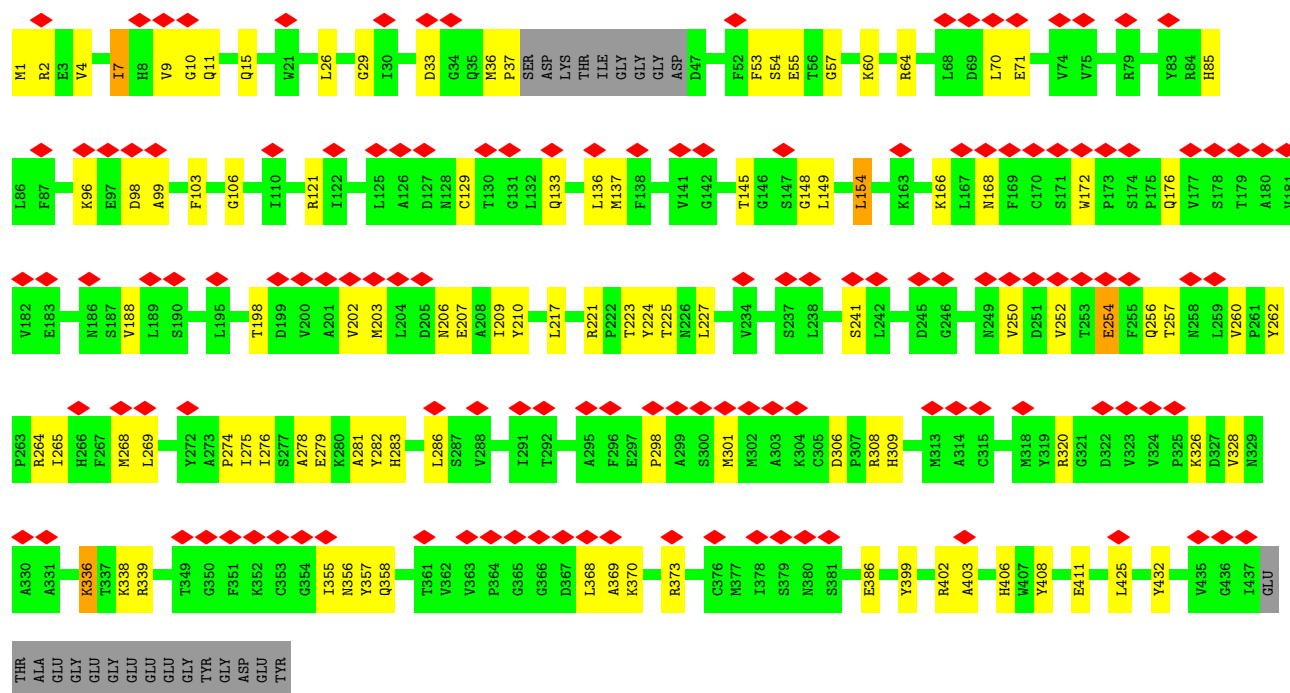
• Molecule 2: Tubulin alpha chain



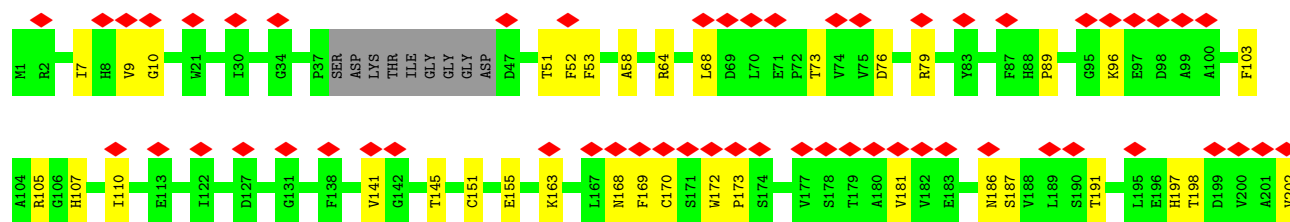
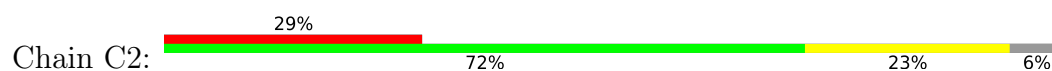
• Molecule 2: Tubulin alpha chain

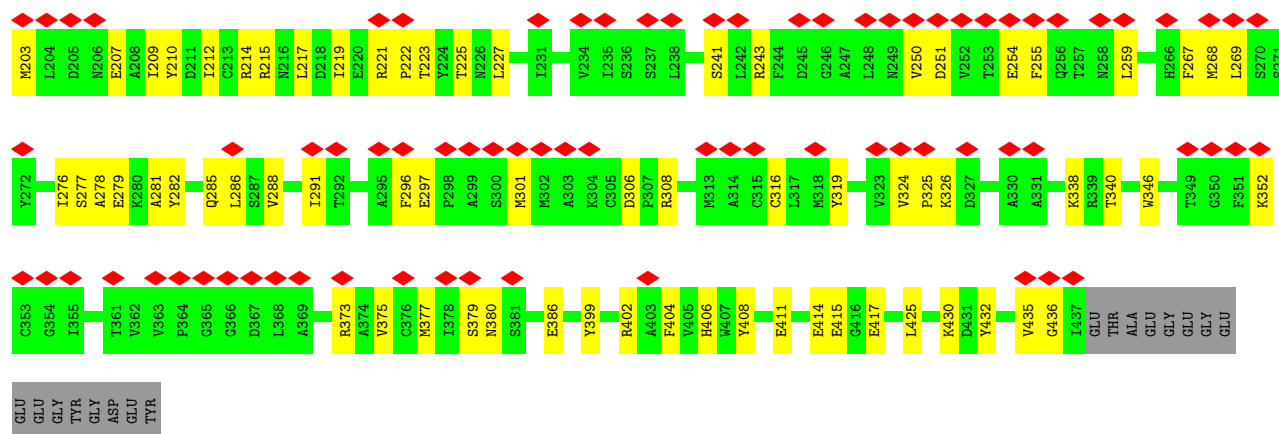


- Molecule 2: Tubulin alpha chain

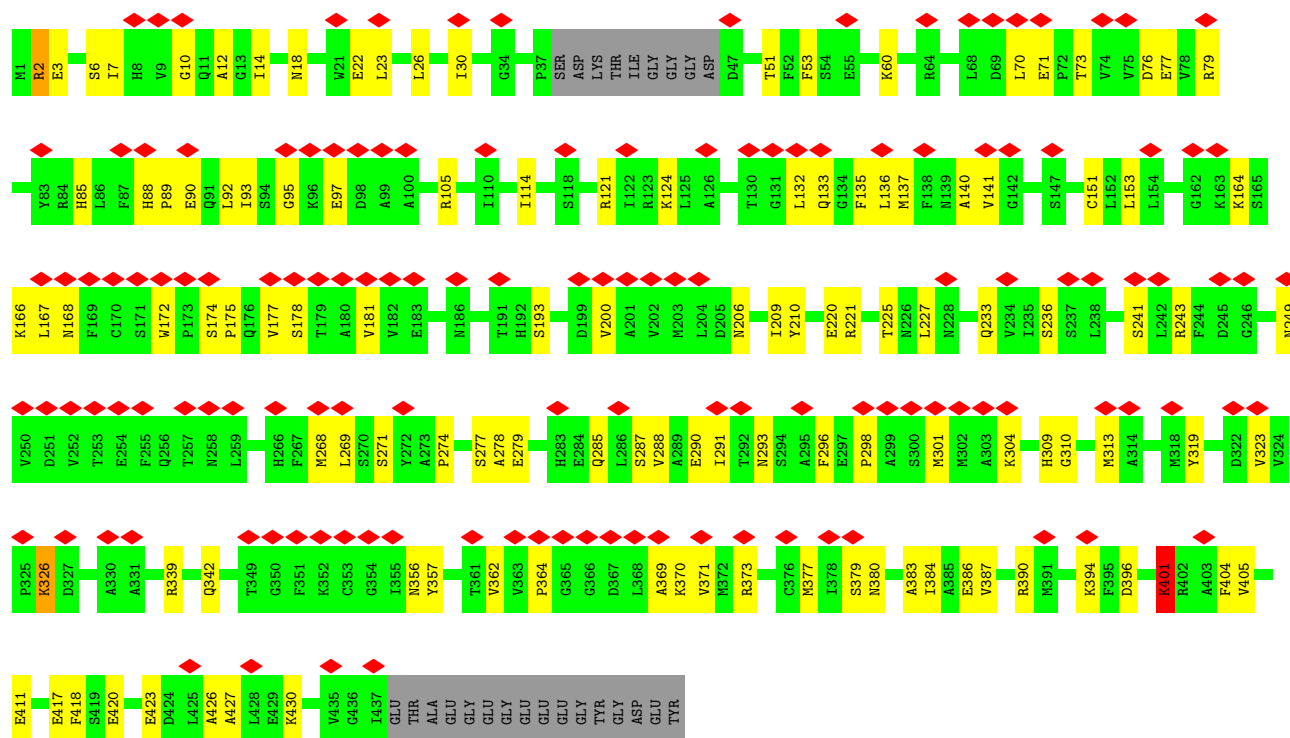


- Molecule 2: Tubulin alpha chain

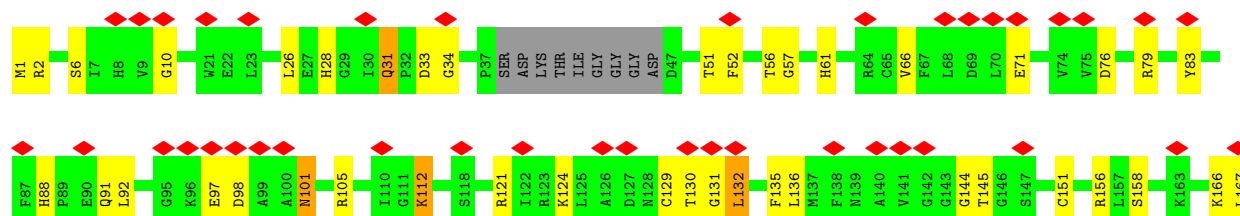


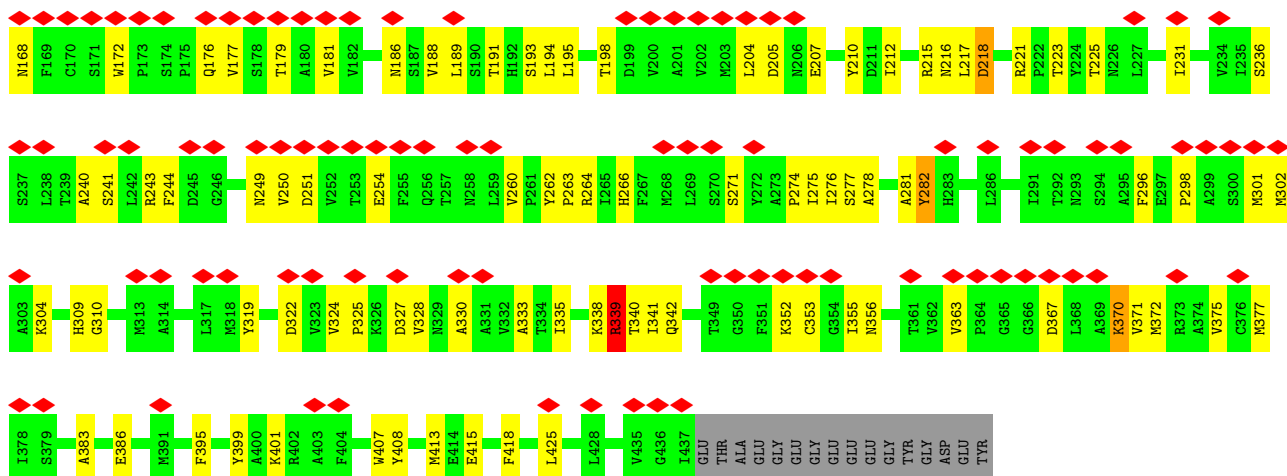


• Molecule 2: Tubulin alpha chain

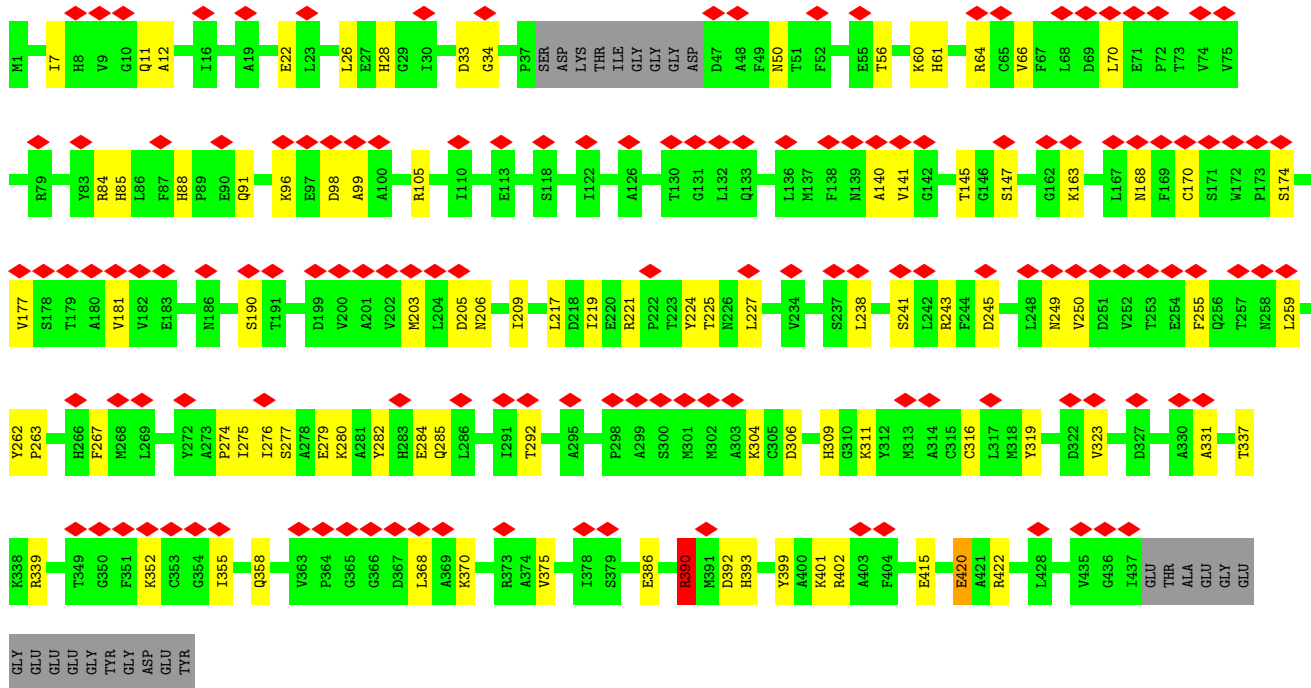
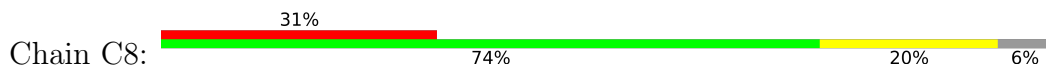


• Molecule 2: Tubulin alpha chain

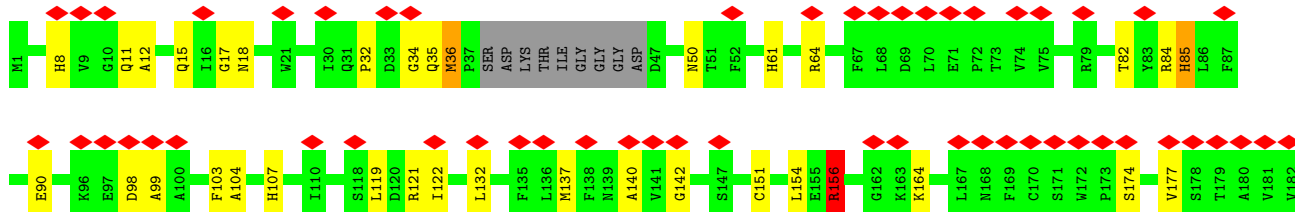
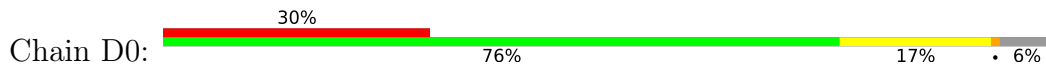


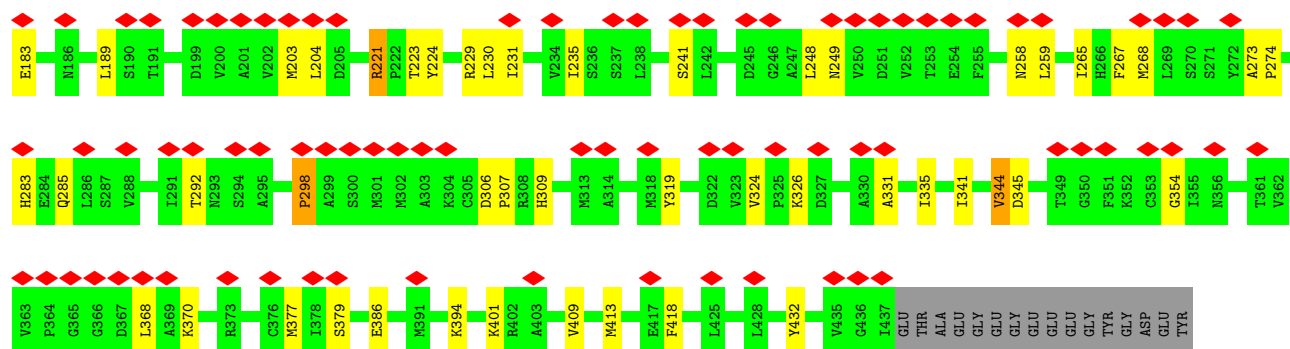


• Molecule 2: Tubulin alpha chain

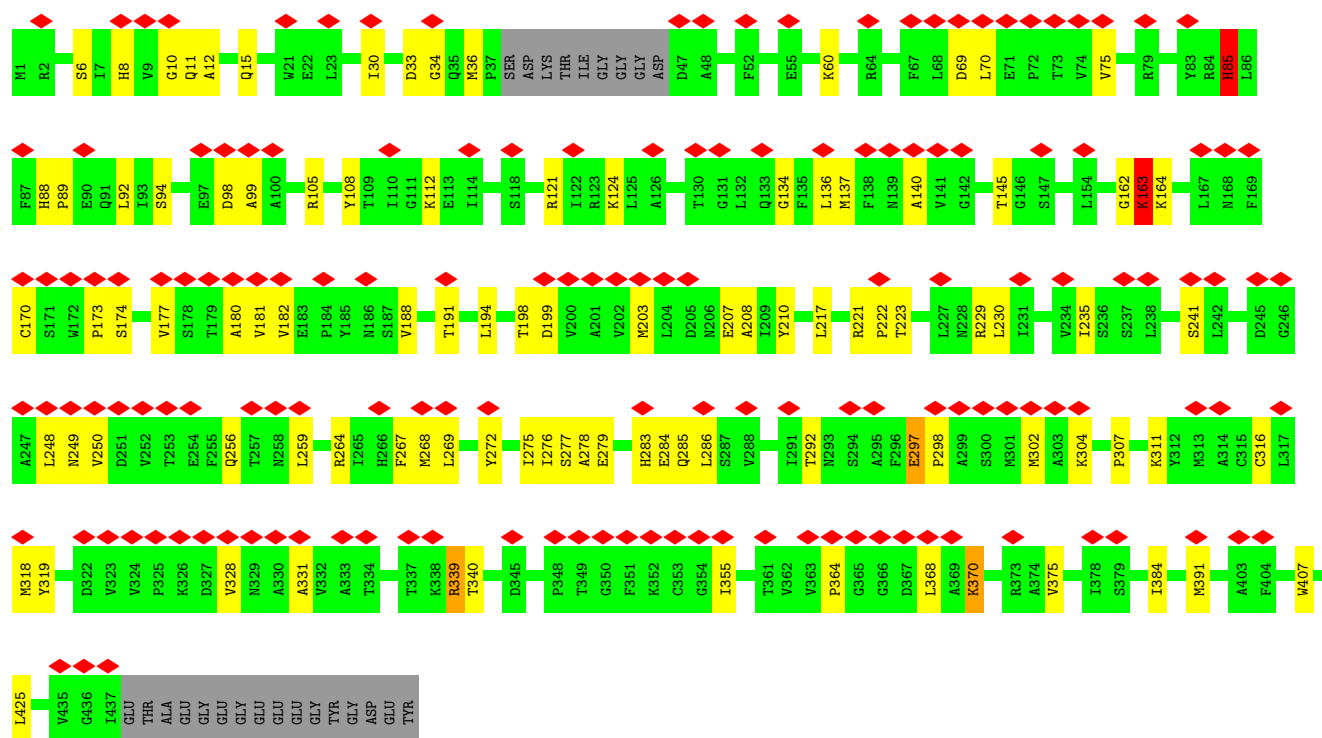
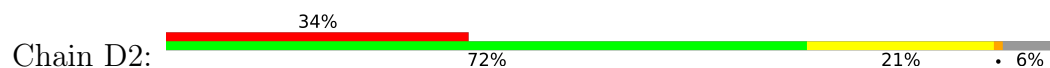


• Molecule 2: Tubulin alpha chain

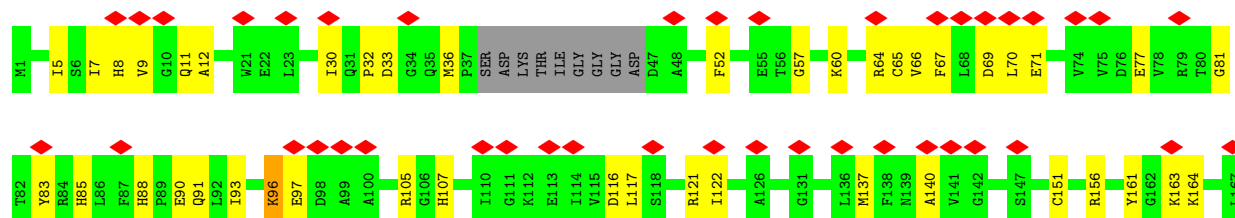
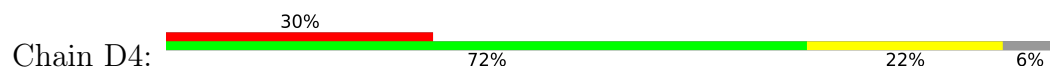


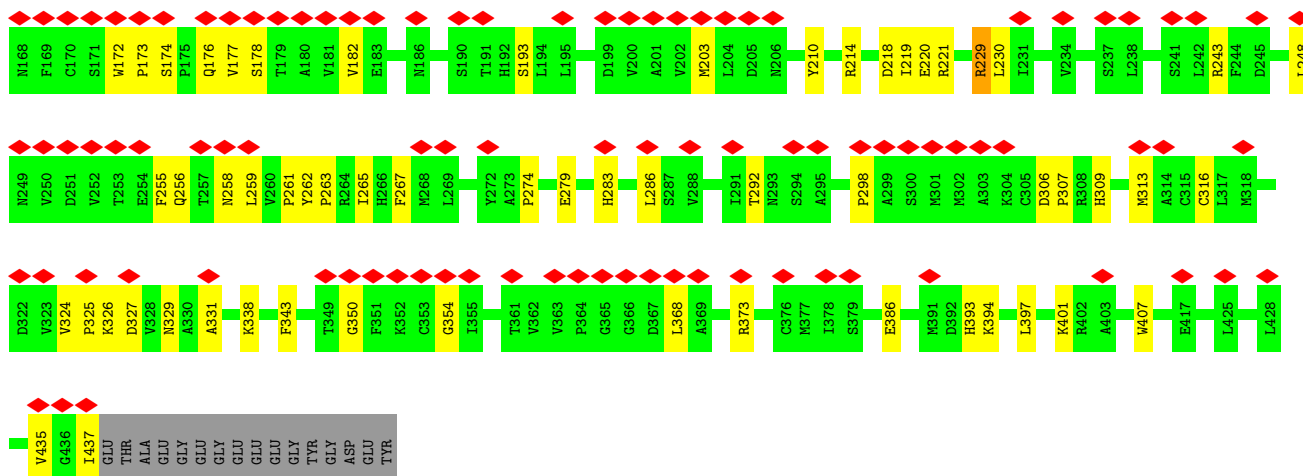


• Molecule 2: Tubulin alpha chain

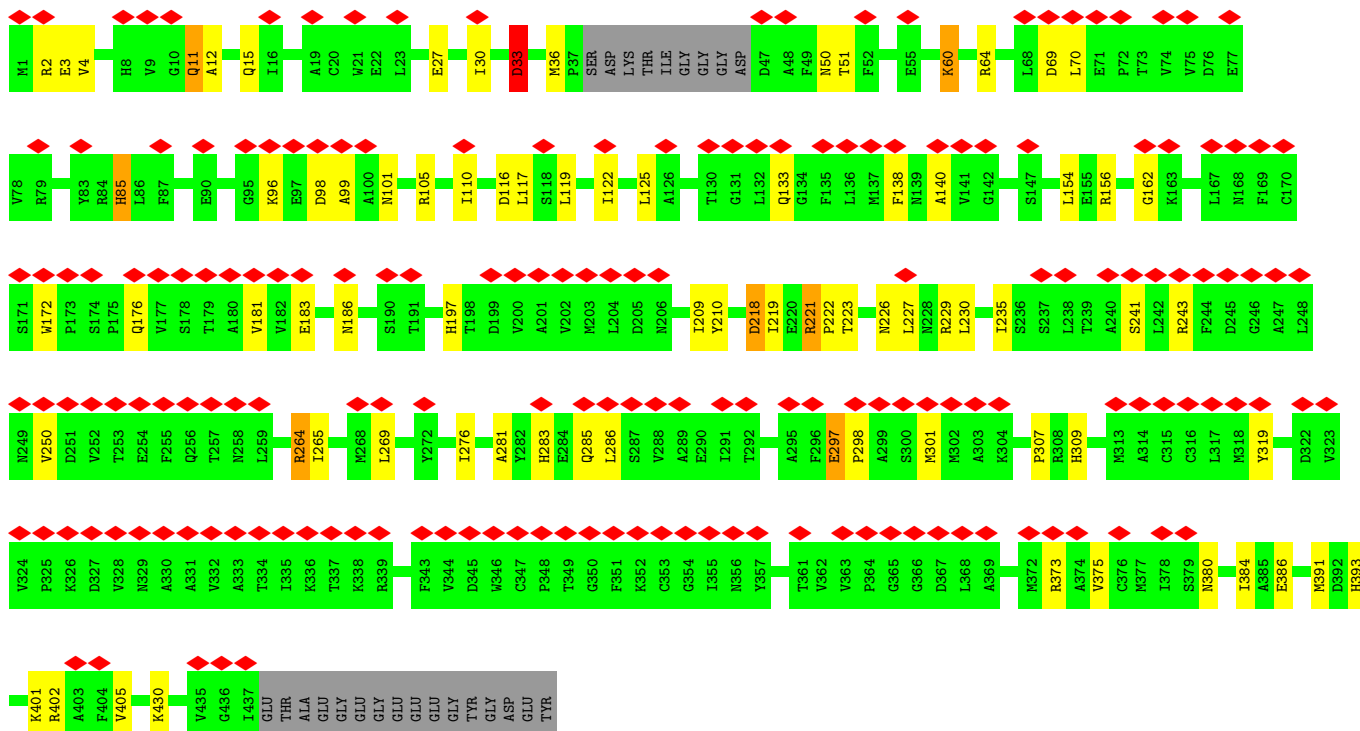
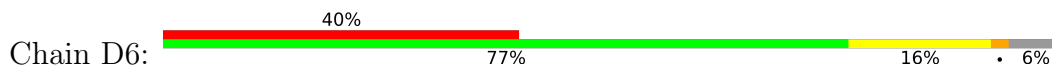


• Molecule 2: Tubulin alpha chain

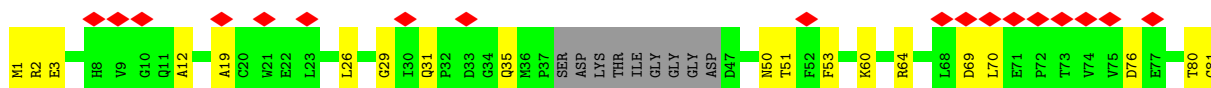
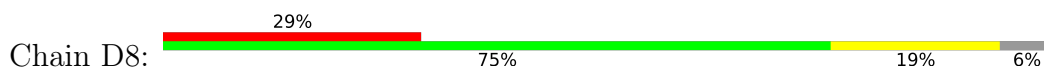


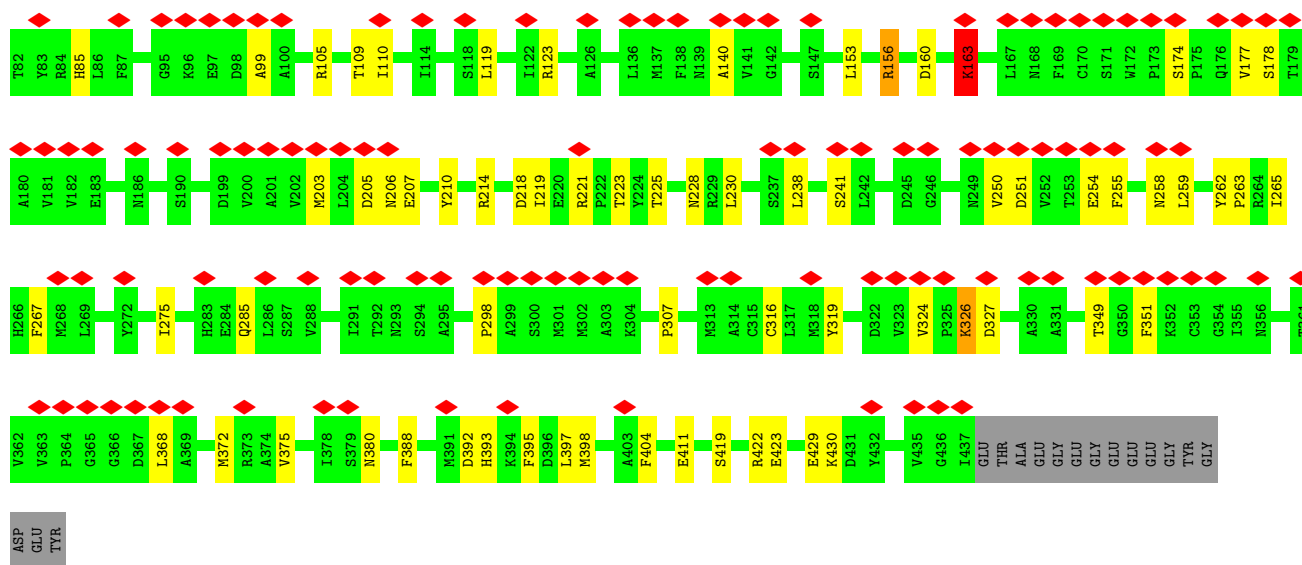


• Molecule 2: Tubulin alpha chain

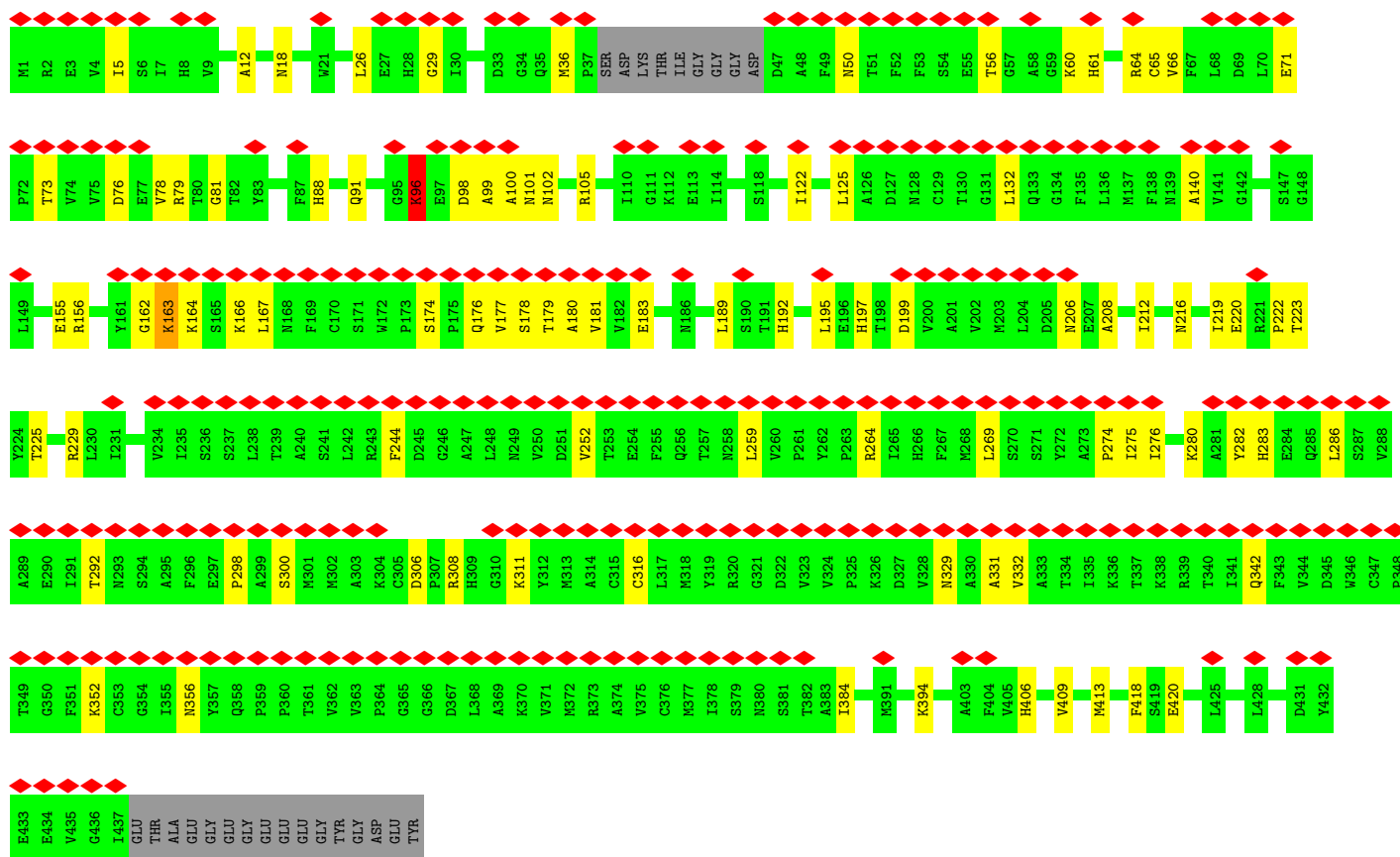
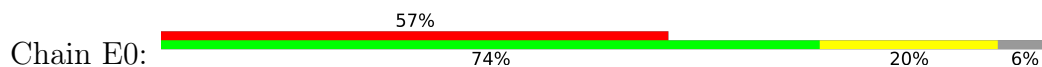


• Molecule 2: Tubulin alpha chain

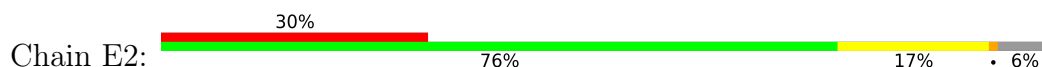


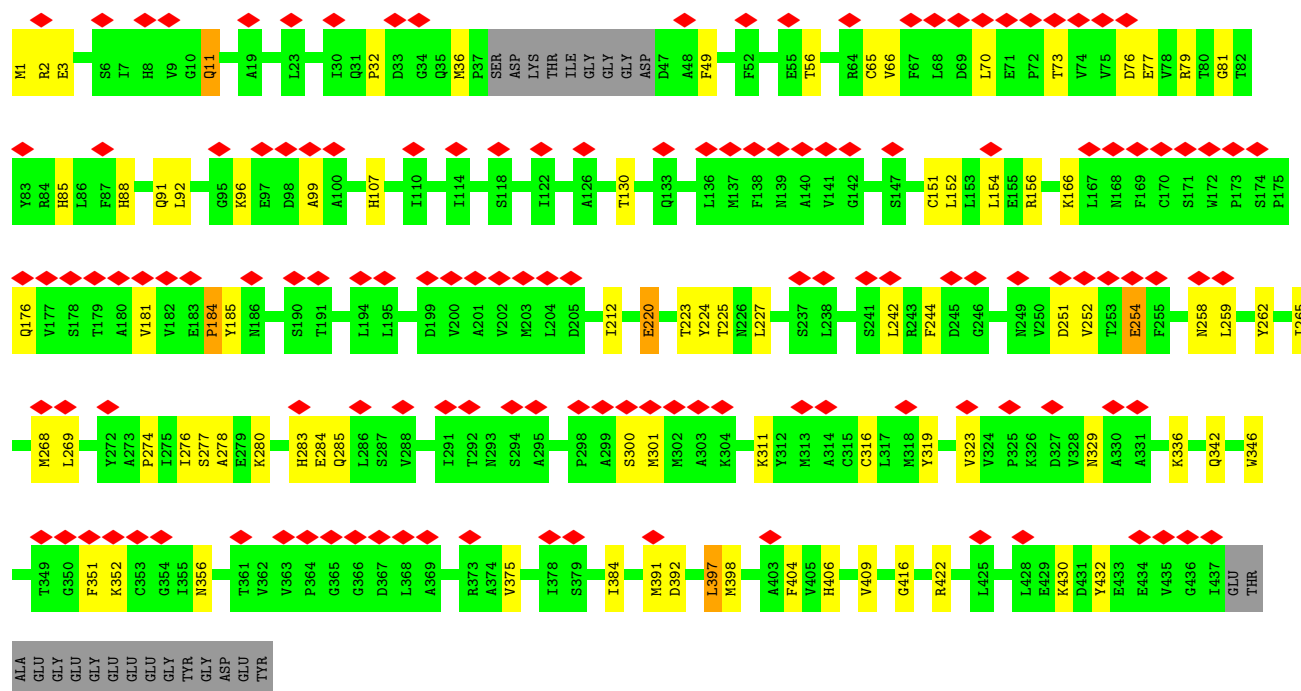


• Molecule 2: Tubulin alpha chain

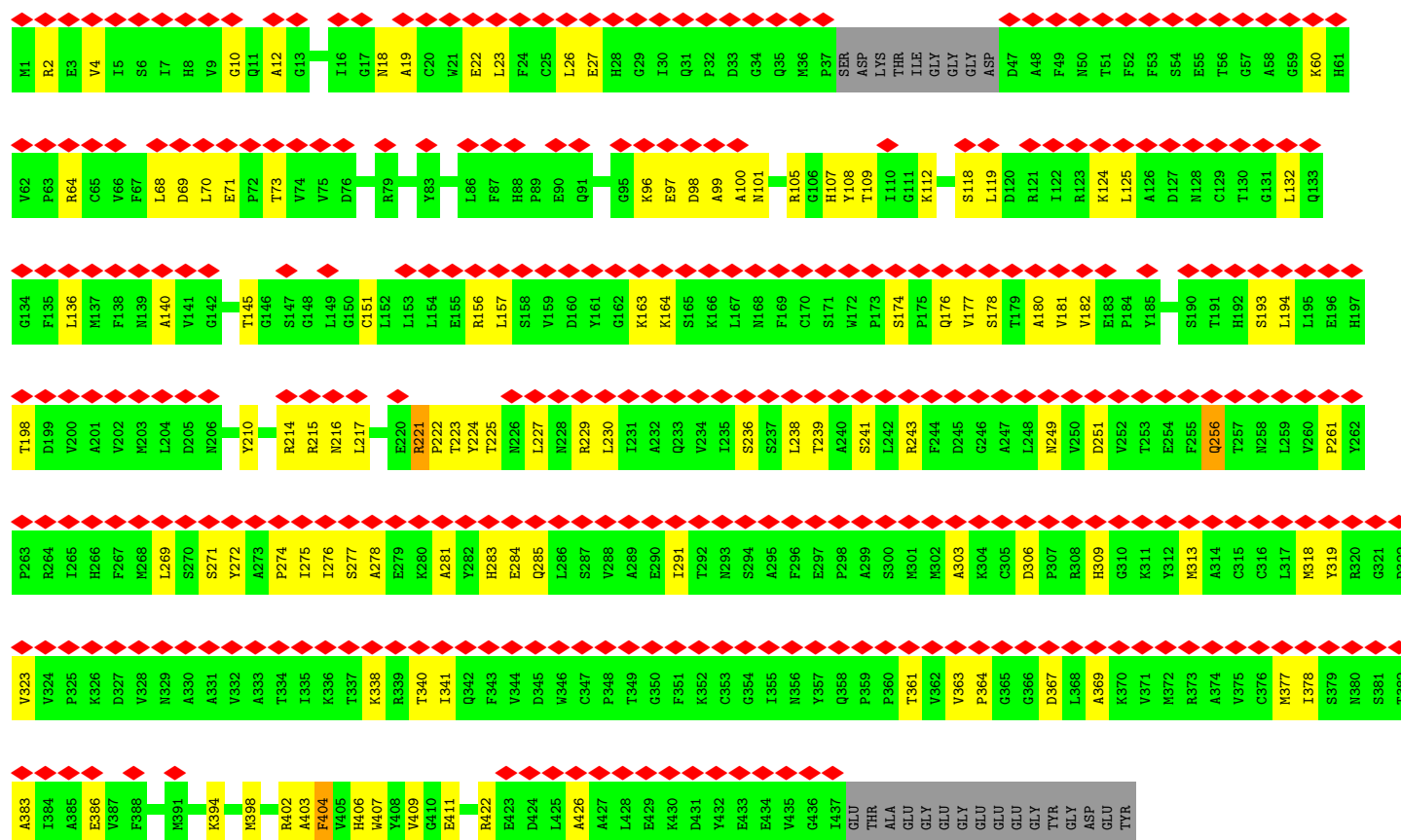
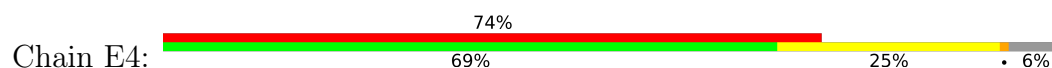


• Molecule 2: Tubulin alpha chain



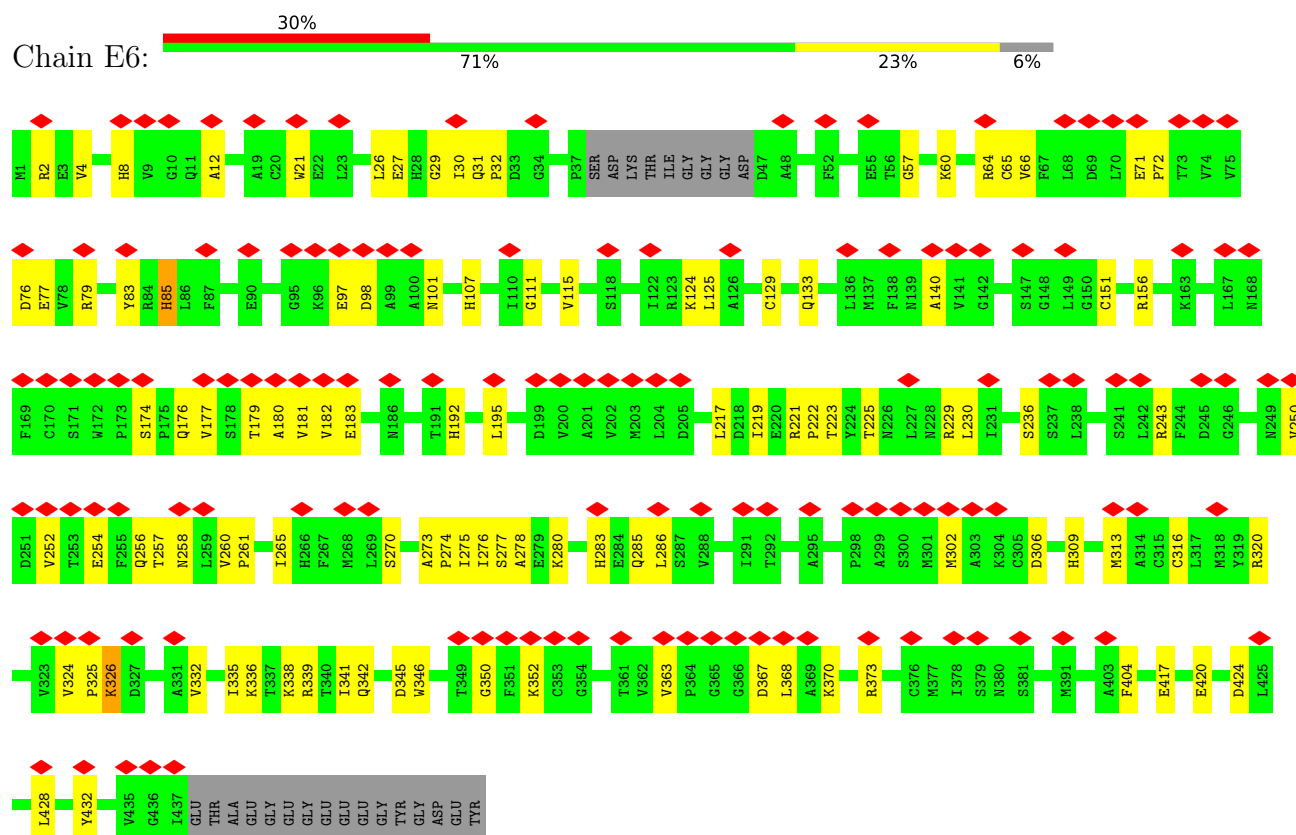


• Molecule 2: Tubulin alpha chain



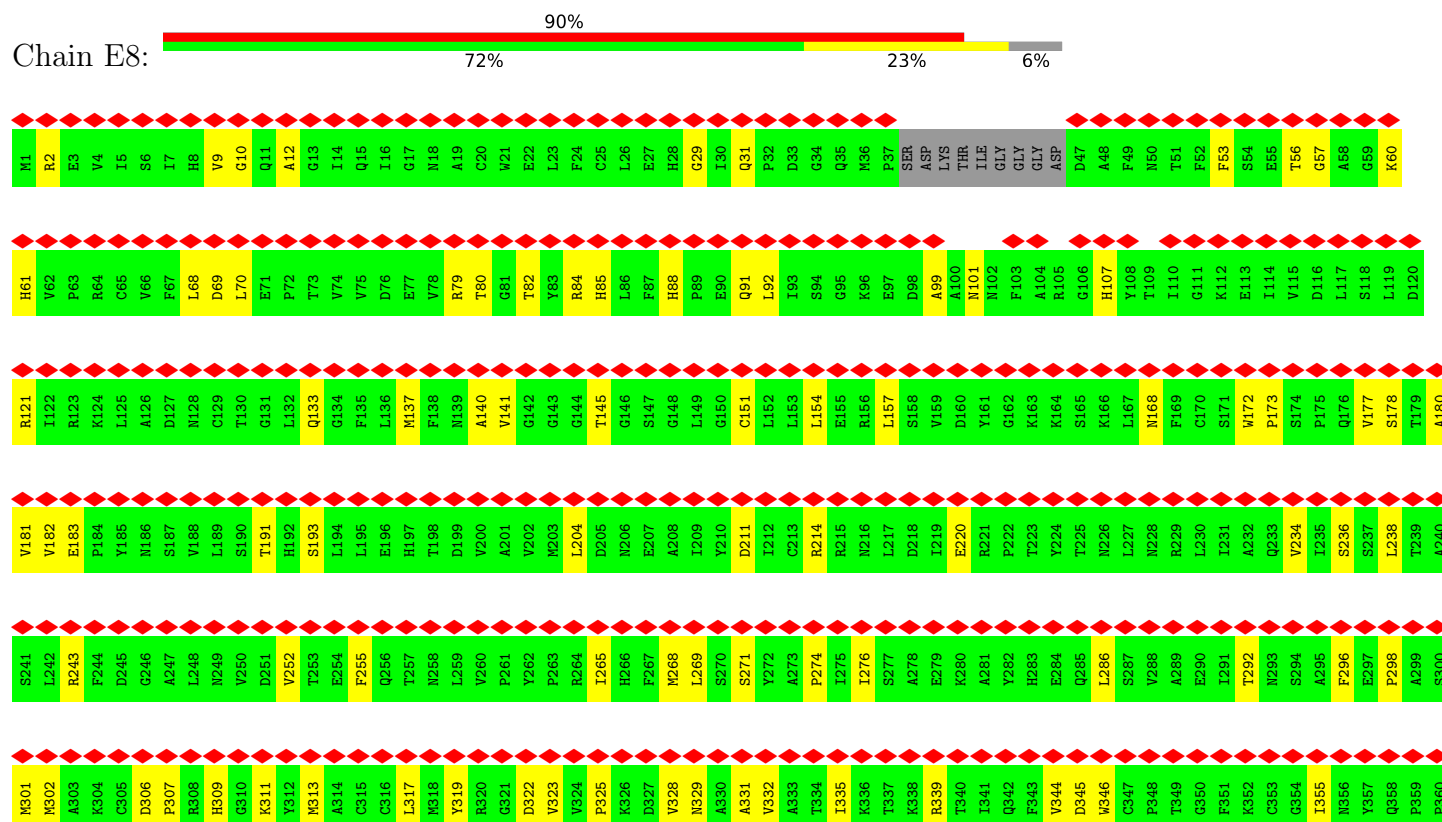
- Molecule 2: Tubulin alpha chain

Chain E6:



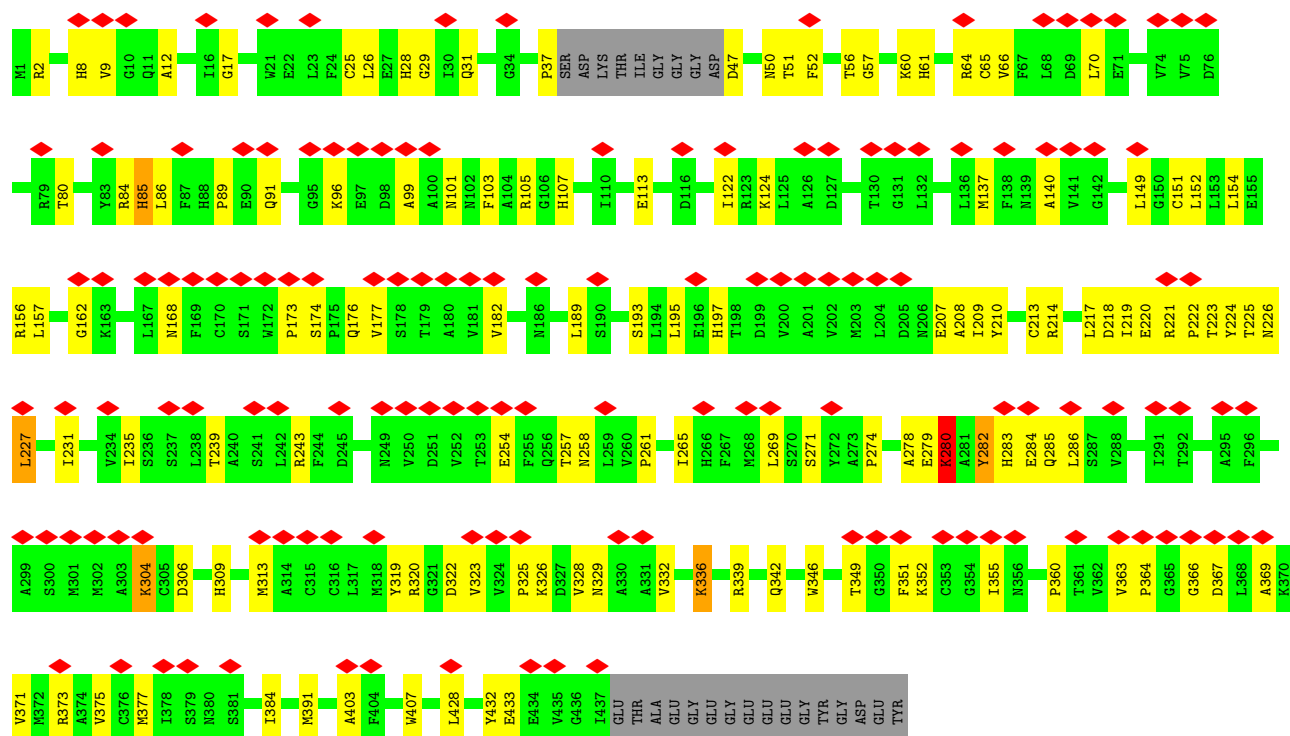
- Molecule 2: Tubulin alpha chain

Chain E8:

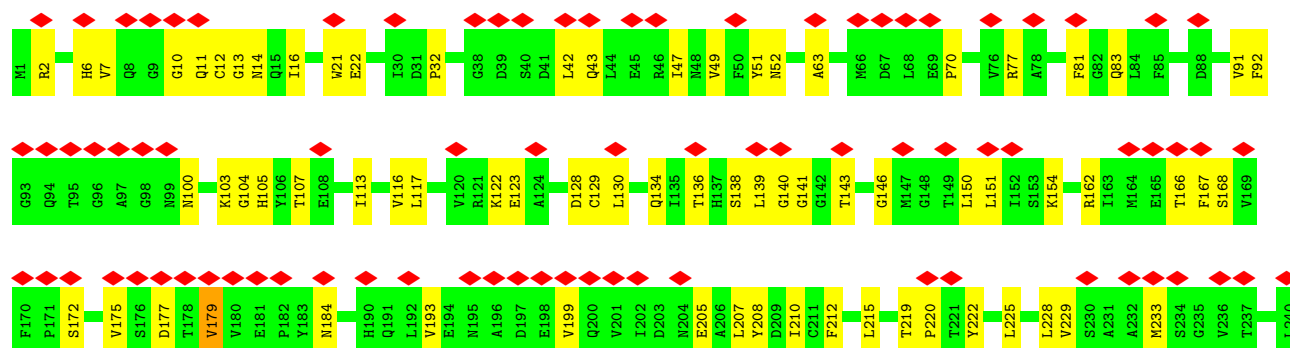


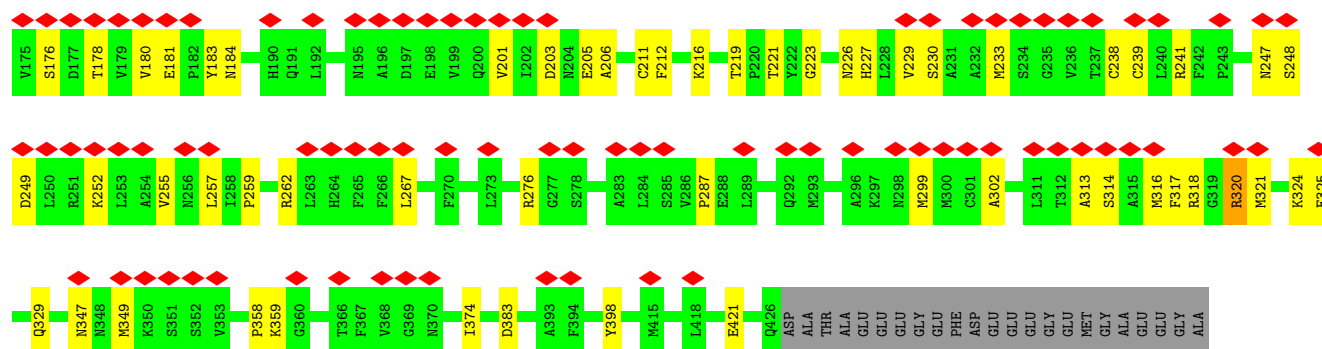


• Molecule 2: Tubulin alpha chain

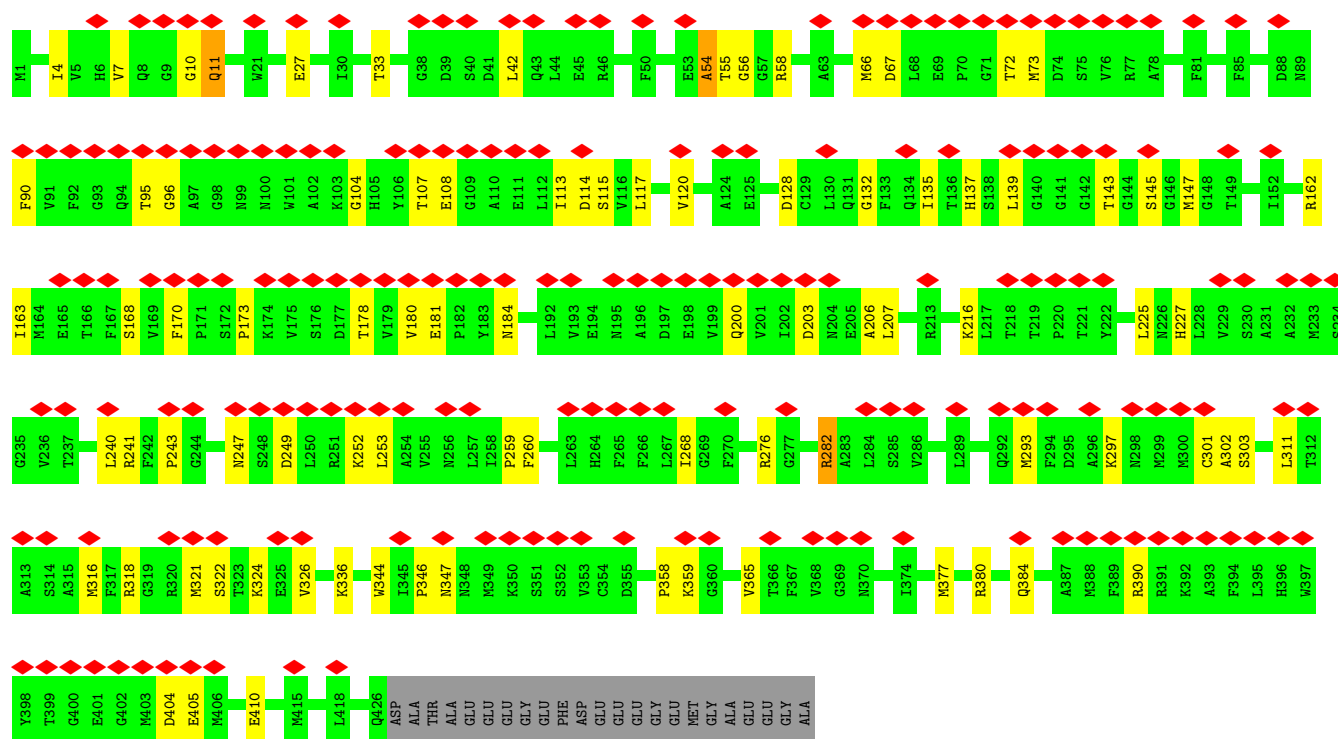
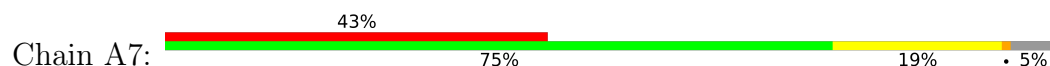


• Molecule 3: Tubulin beta chain

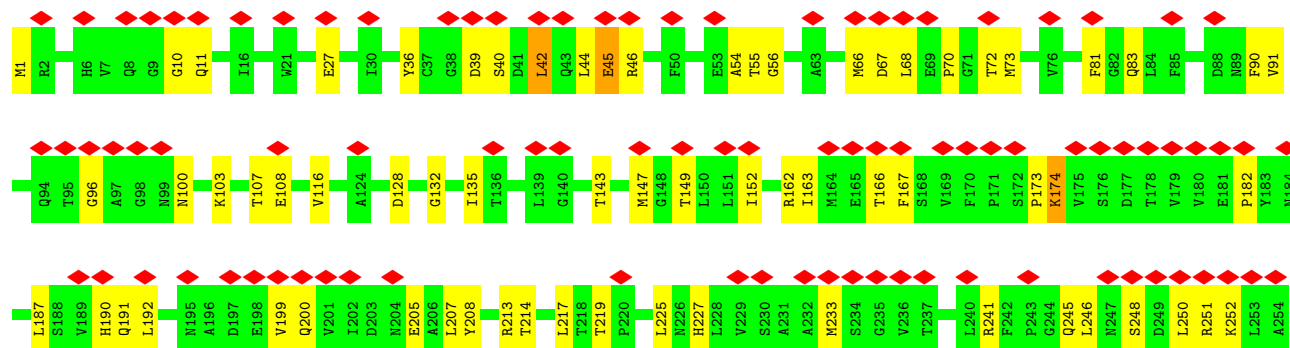


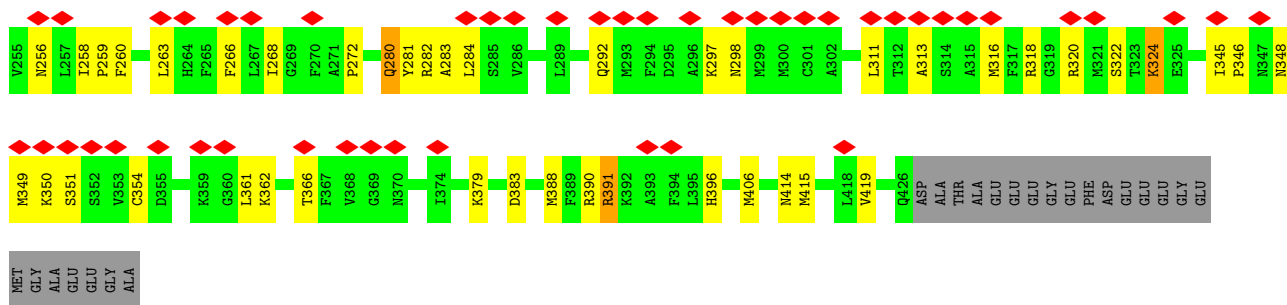


• Molecule 3: Tubulin beta chain

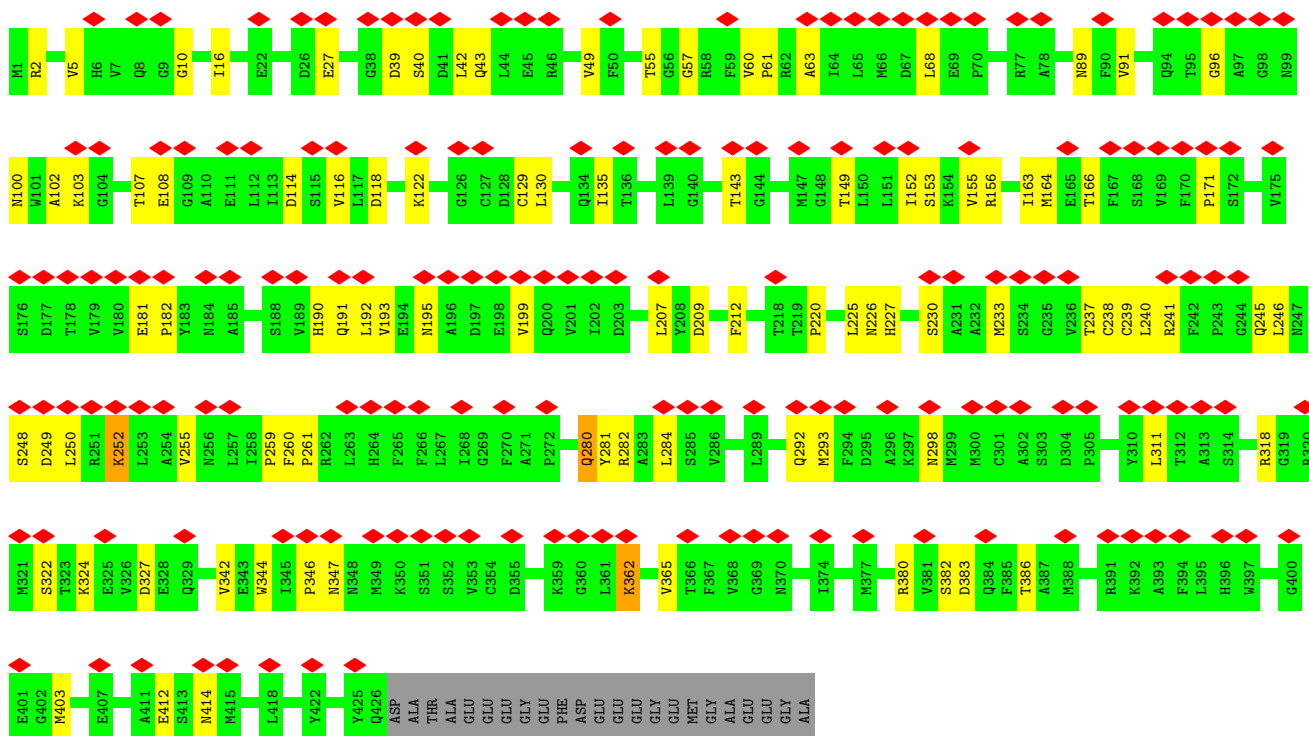
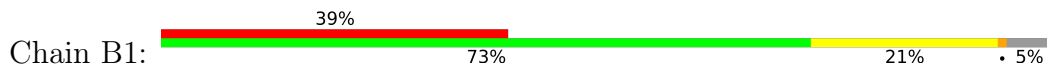


• Molecule 3: Tubulin beta chain

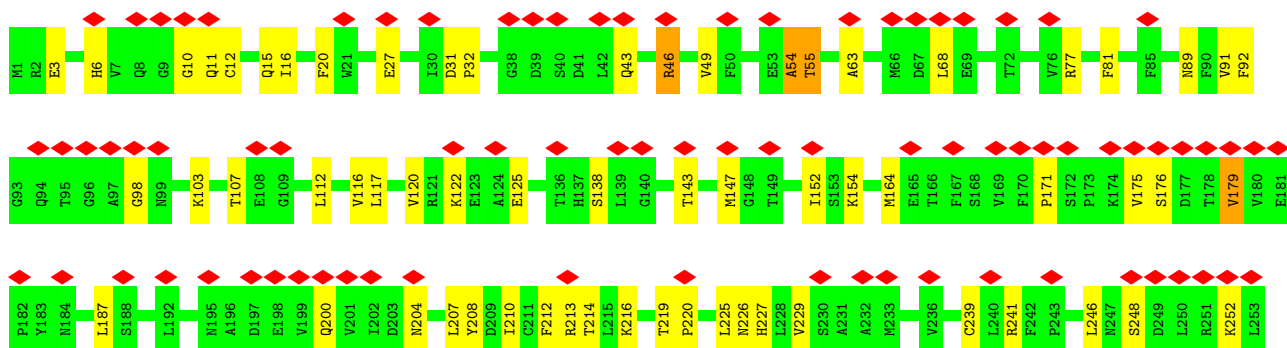
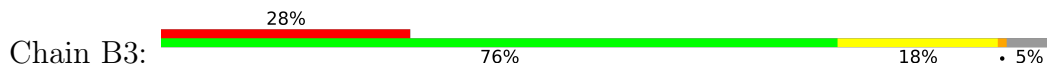


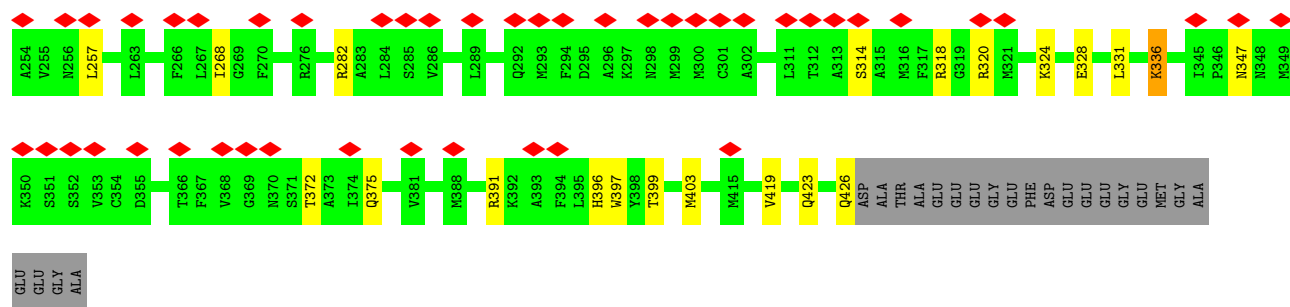


• Molecule 3: Tubulin beta chain



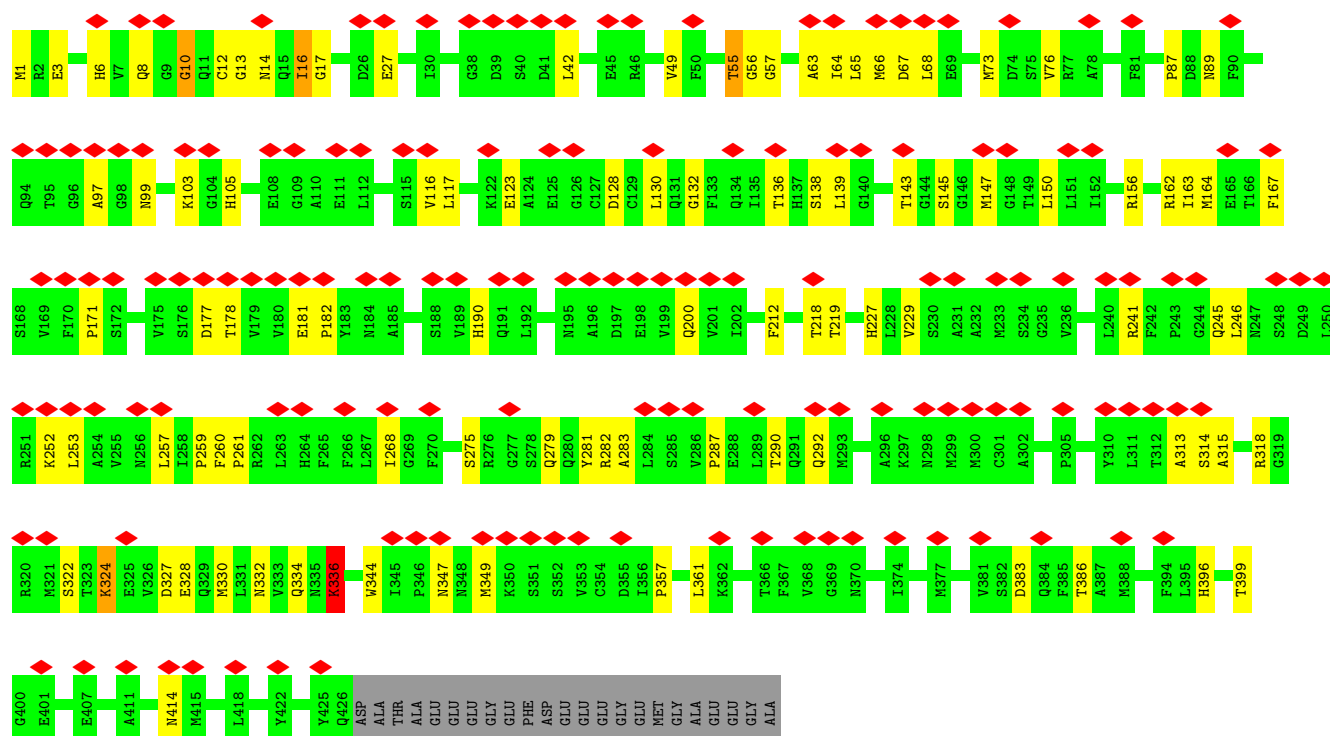
• Molecule 3: Tubulin beta chain





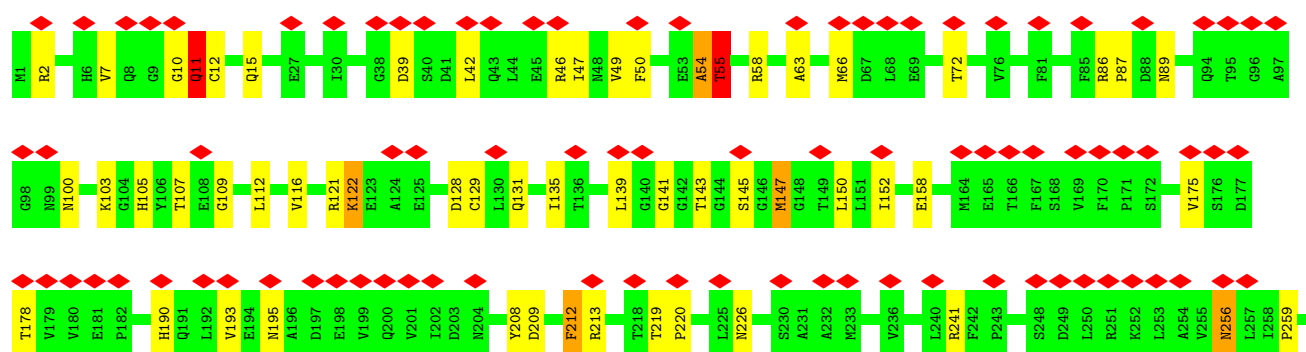
• Molecule 3: Tubulin beta chain

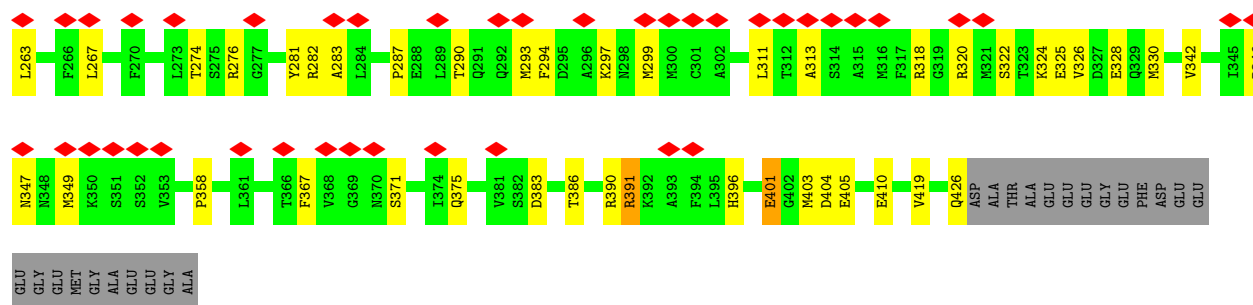
Chain B5: 34% 73% 21% • 5%



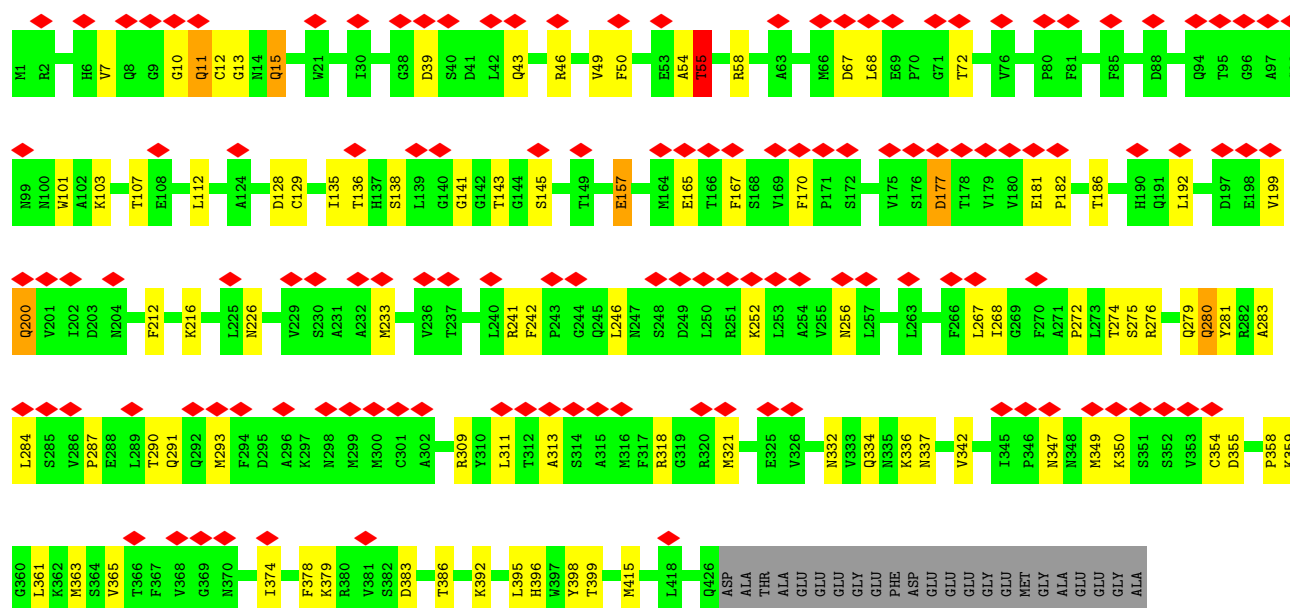
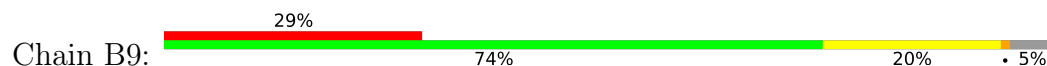
• Molecule 3: Tubulin beta chain

Chain B7: 29% 73% 20% • 5%

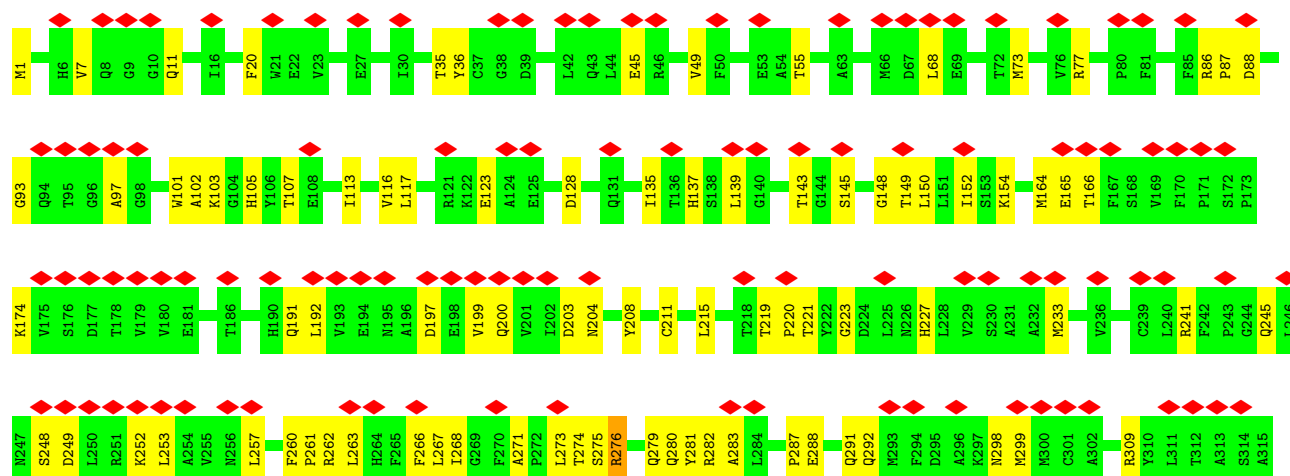


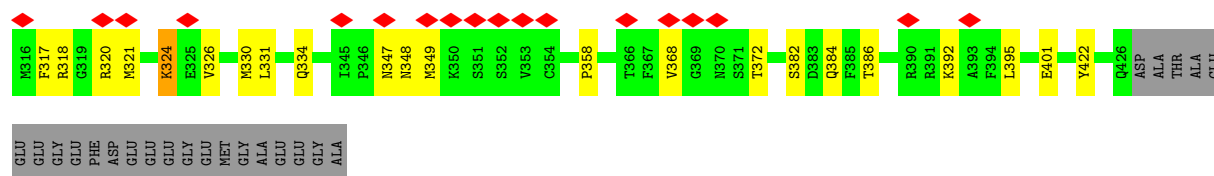


• Molecule 3: Tubulin beta chain

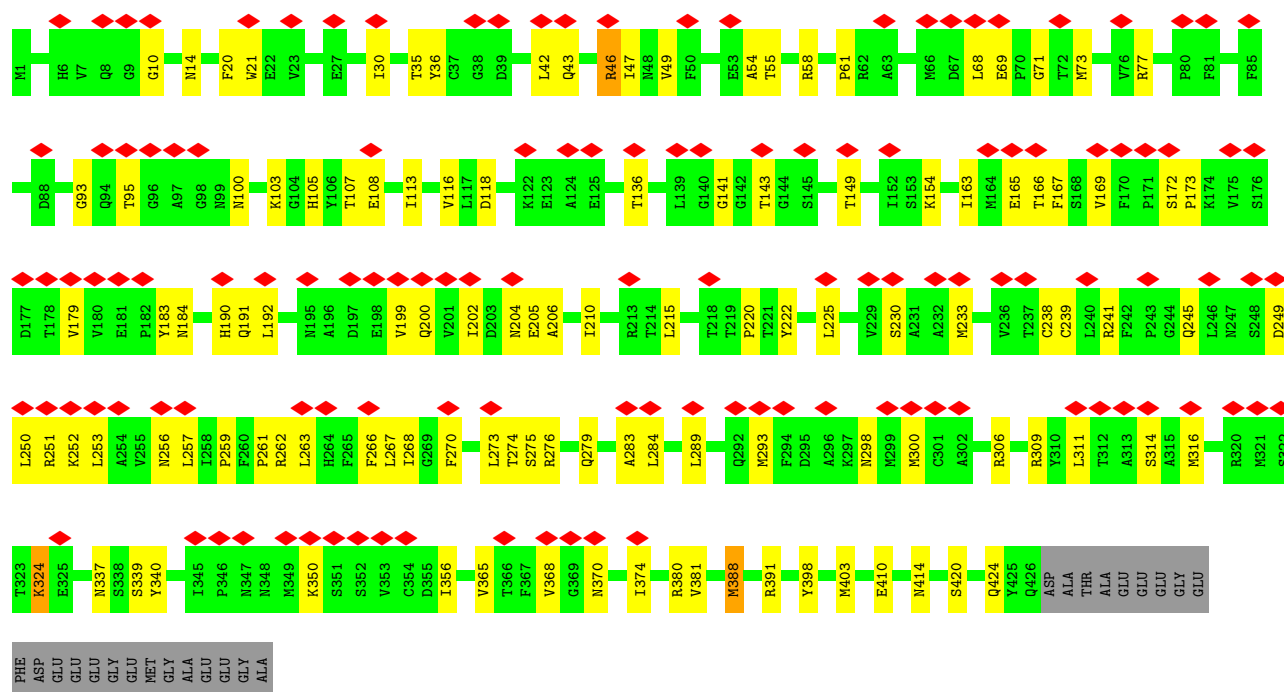


• Molecule 3: Tubulin beta chain

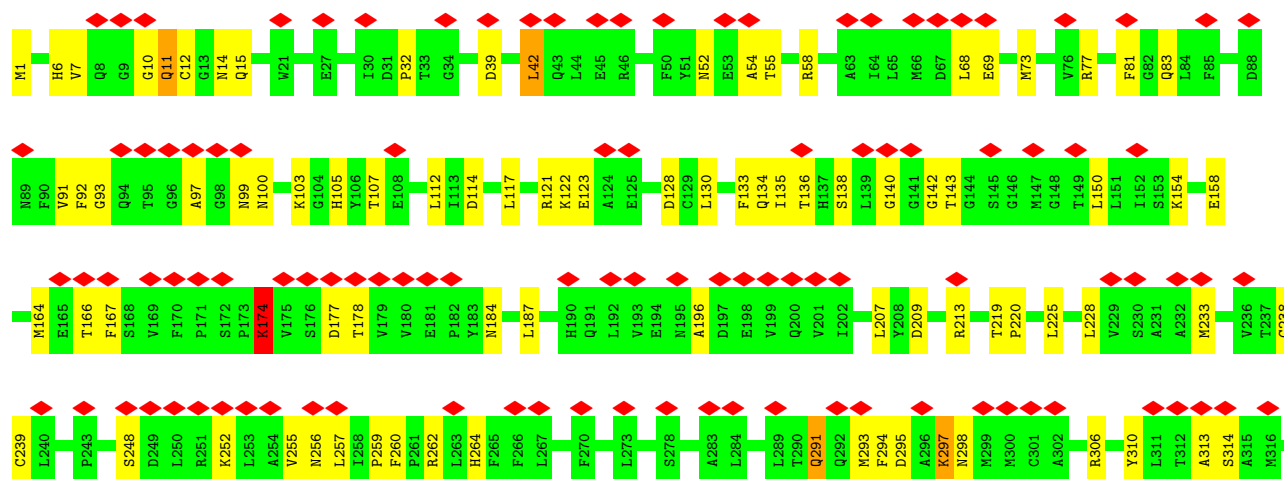
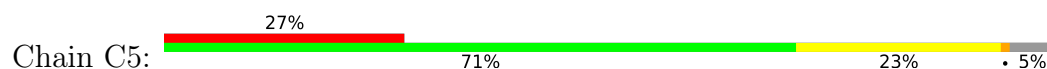


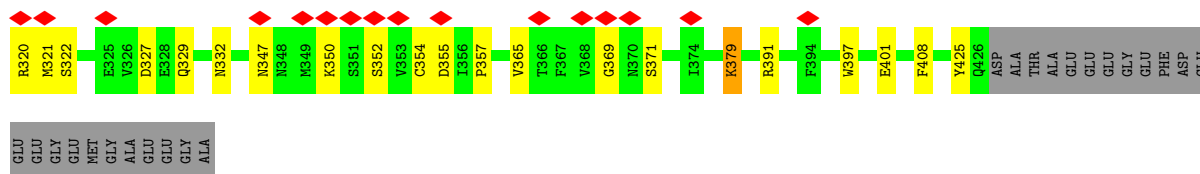


• Molecule 3: Tubulin beta chain

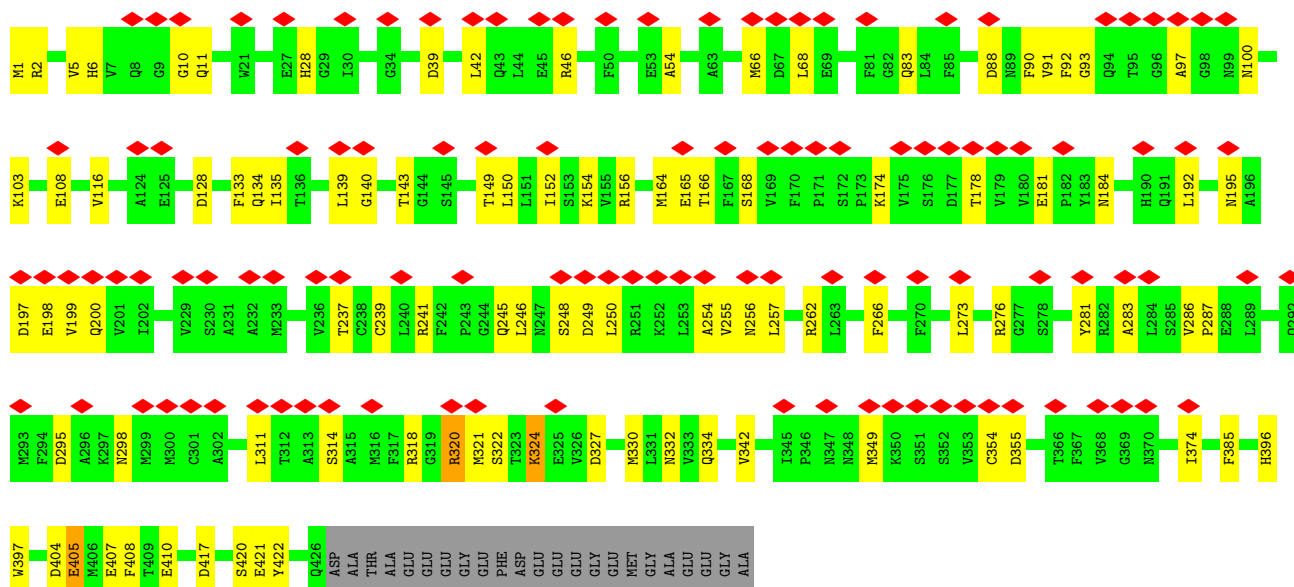
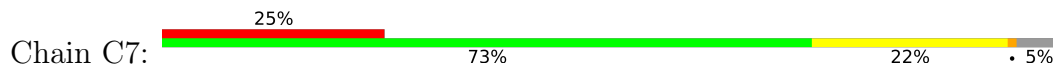


• Molecule 3: Tubulin beta chain

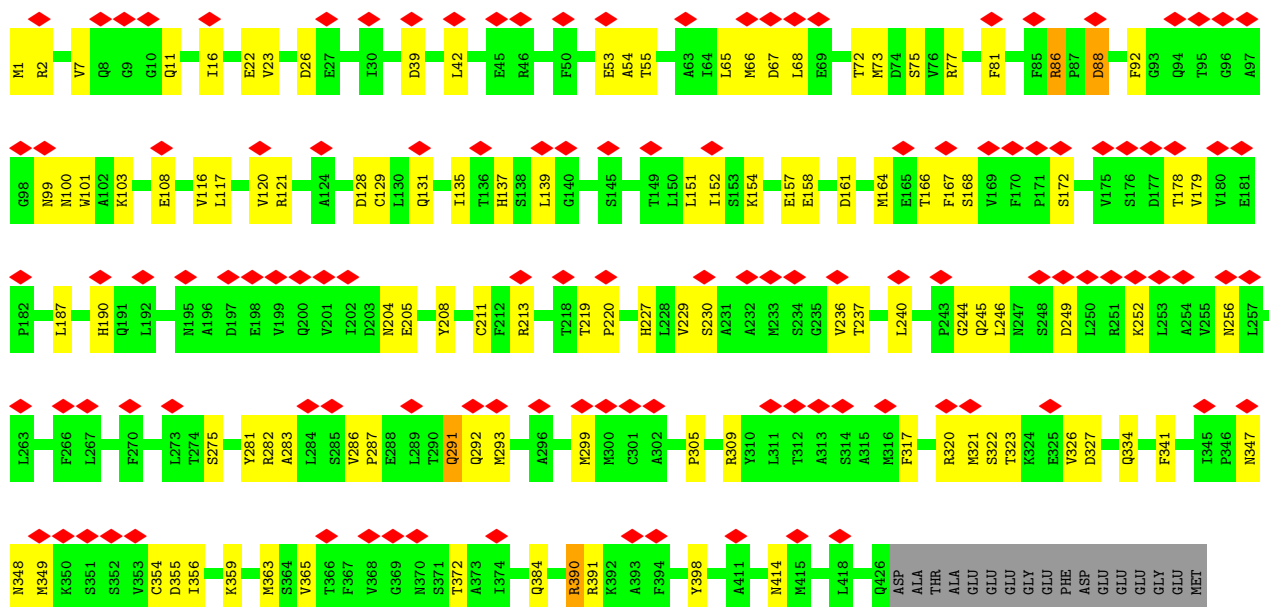




• Molecule 3: Tubulin beta chain



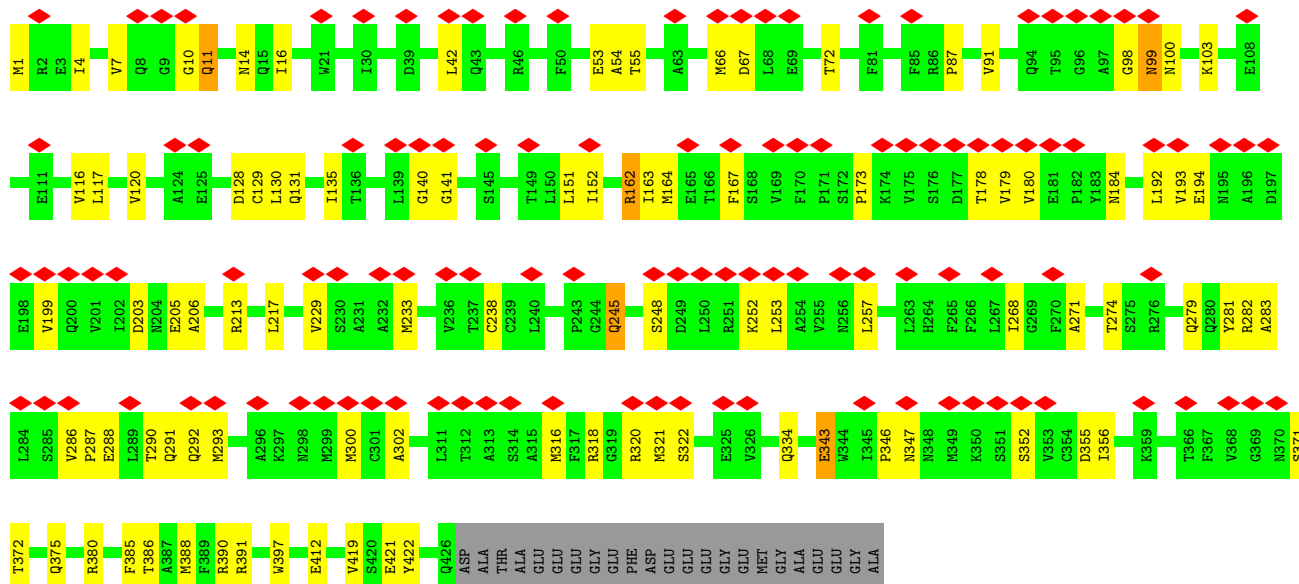
• Molecule 3: Tubulin beta chain



GLY
ALA
GLU
GLY
GLY
ALA

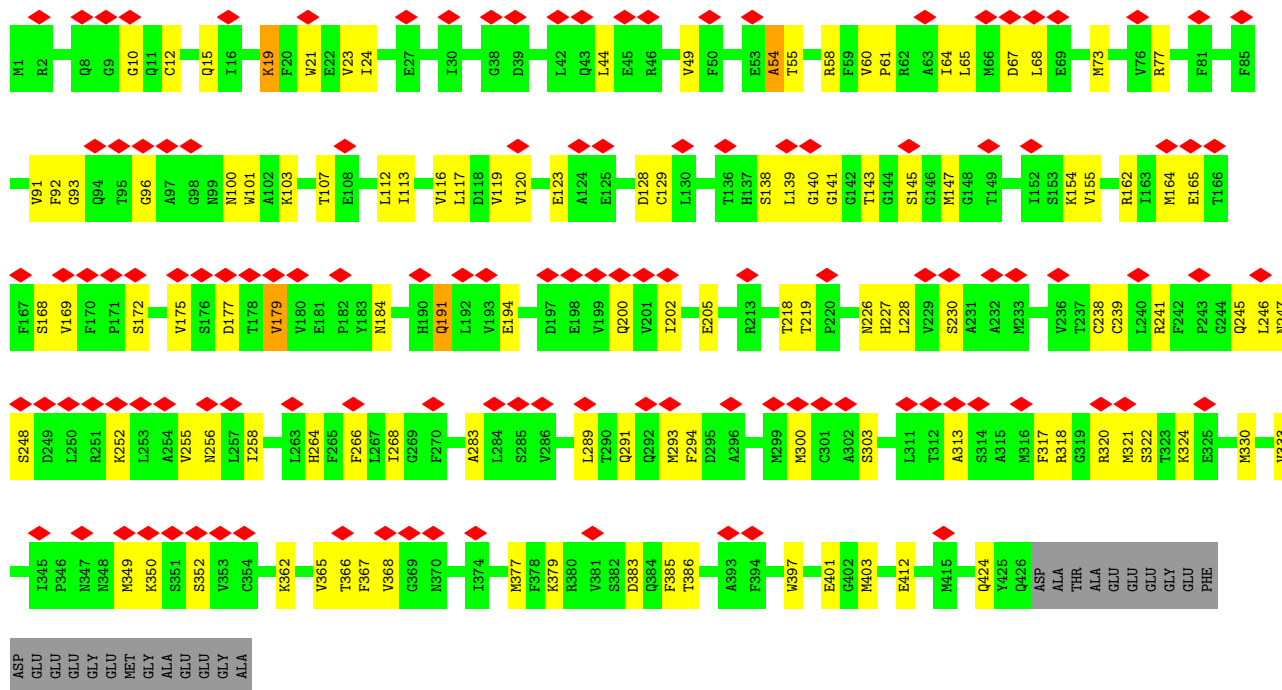
• Molecule 3: Tubulin beta chain

Chain D1: 26% 73% 21% 5%



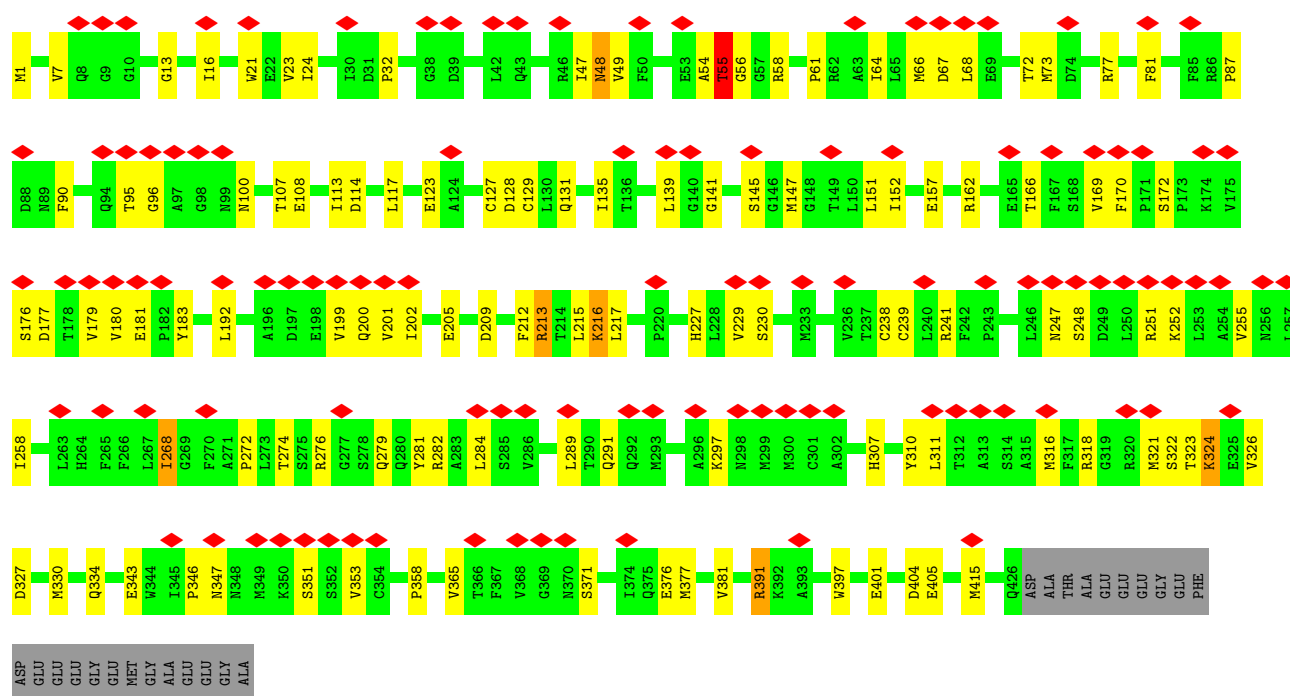
• Molecule 3: Tubulin beta chain

Chain D3: 27% 69% 25% 5%



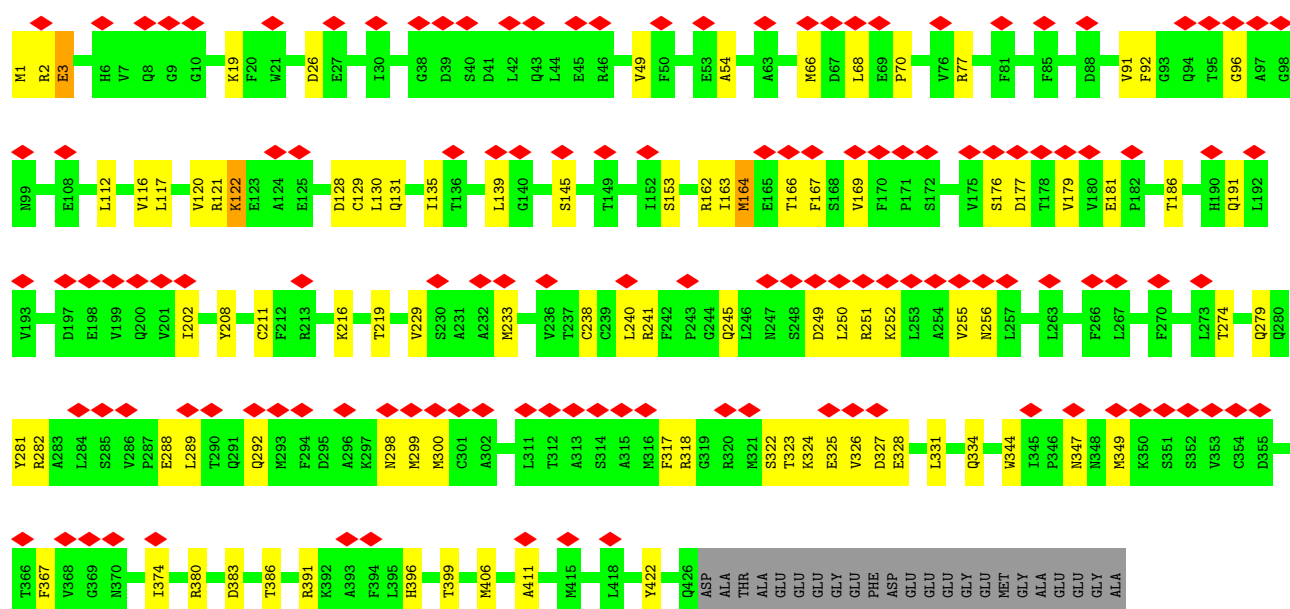
• Molecule 3: Tubulin beta chain

Chain D5: 



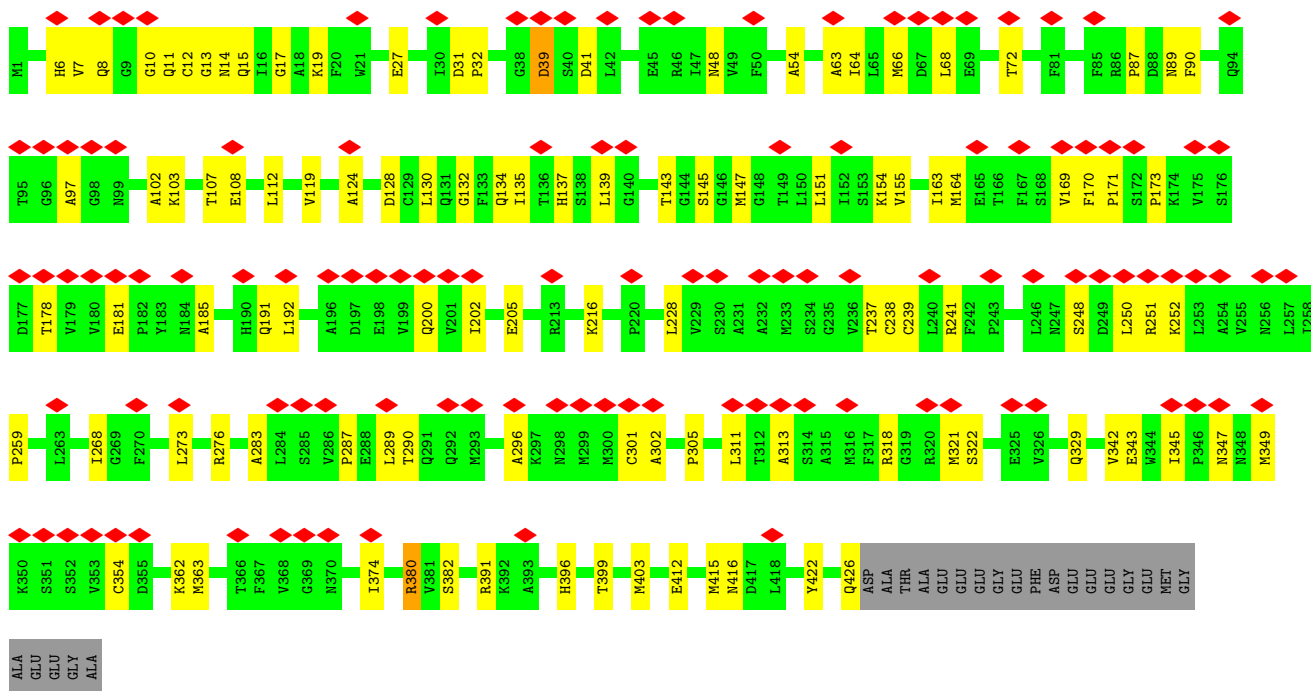
• Molecule 3: Tubulin beta chain

Chain D7: 

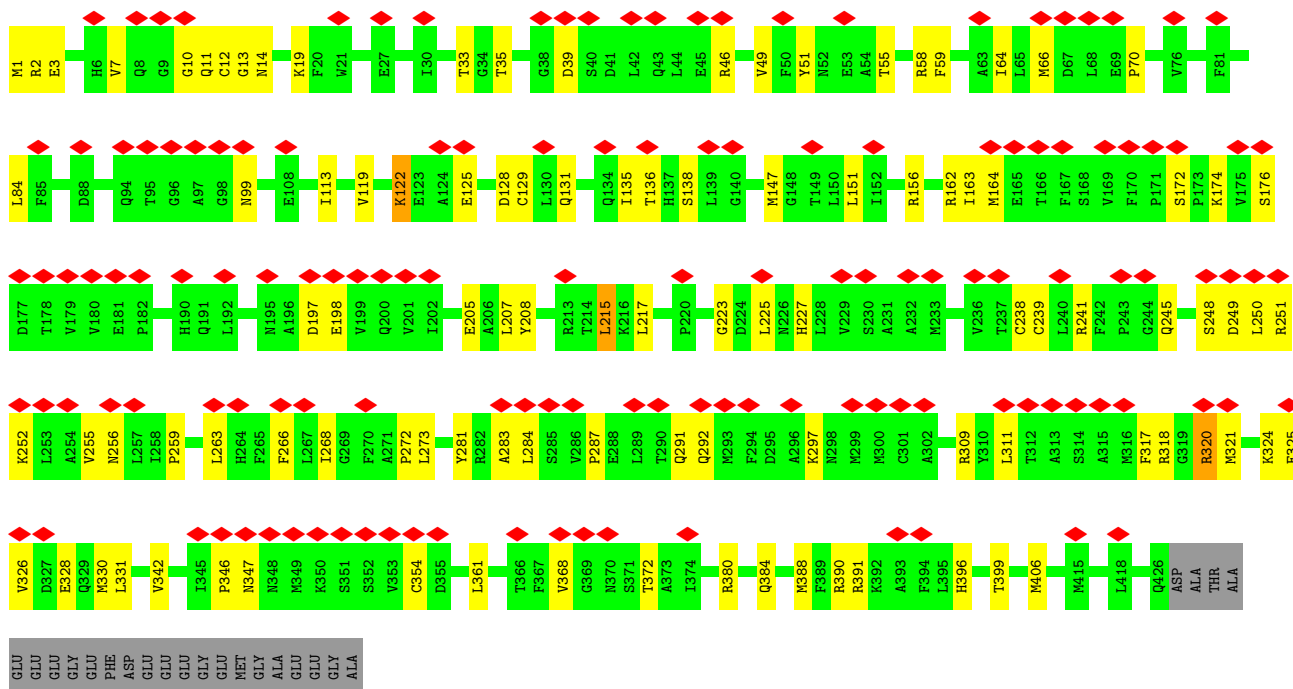
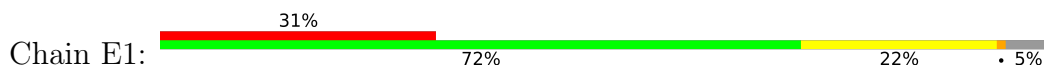


• Molecule 3: Tubulin beta chain

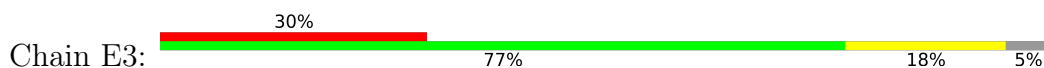
Chain D9: 



- Molecule 3: Tubulin beta chain



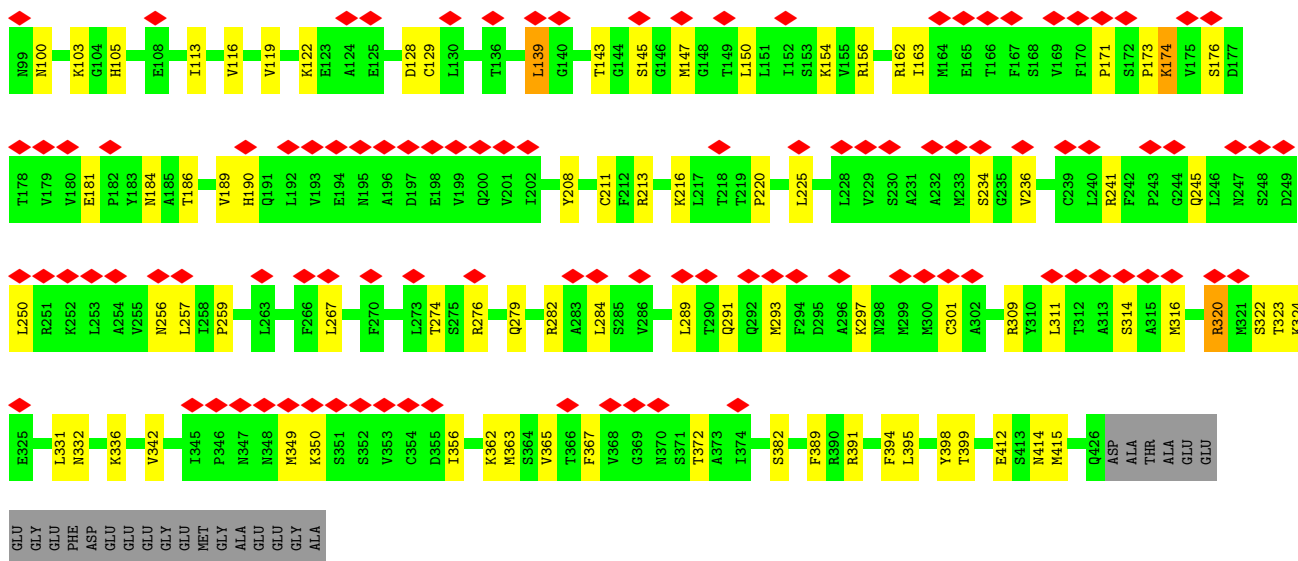
- Molecule 3: Tubulin beta chain



[illegible]

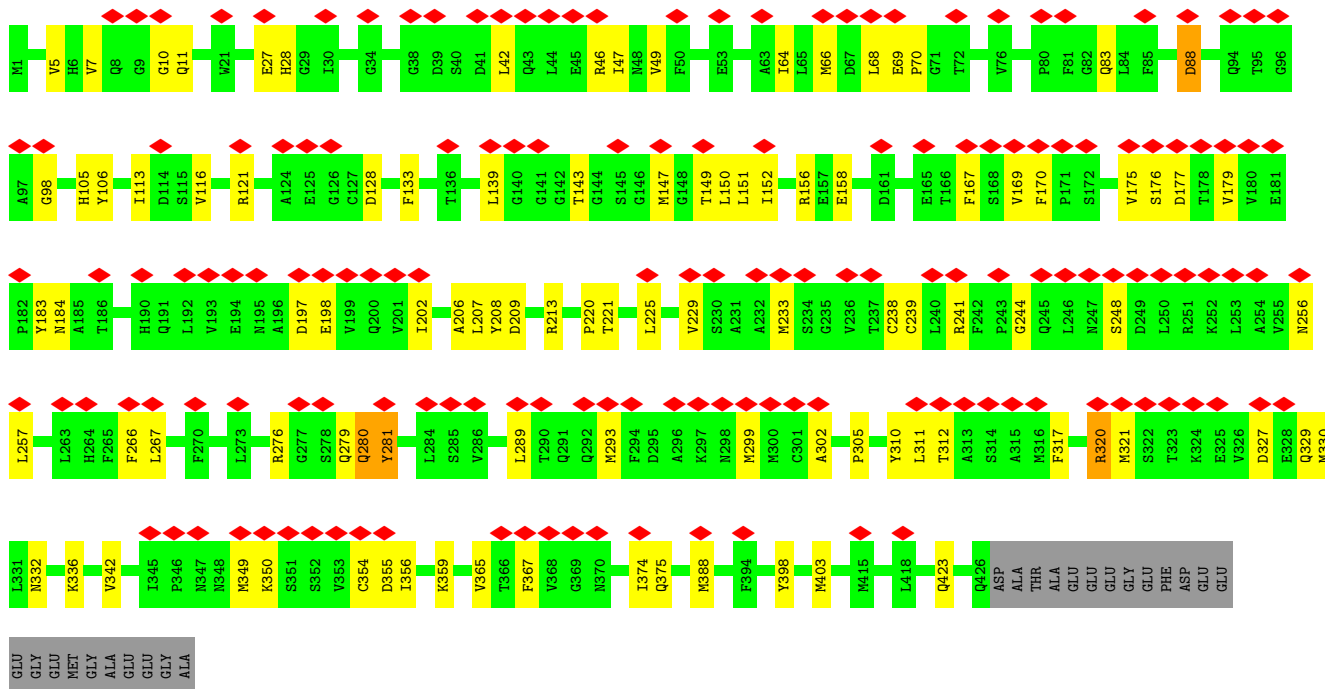
- Molecule 3: Tubulin beta chain

Category	Count
W1	10
W2	10
W3	10
W4	10
W5	10
W6	10
W7	10
W8	10
W9	10
W10	10
W11	10
W12	10
W13	10
W14	10
W15	10
W16	15
W17	12
W18	10
W19	10
W20	10
W21	10
W22	10
W23	10
W24	15
W25	12
W26	10
W27	10
W28	10
W29	10
W30	10
W31	10
W32	10
W33	10
W34	10
W35	10
W36	10
W37	10
W38	15
W39	12
W40	15
W41	12
W42	15
W43	12
W44	15
W45	12
W46	15
W47	12
W48	15
W49	12
W50	15
W51	12
W52	15
W53	12
W54	15
W55	12
W56	15
W57	12
W58	15
W59	12
W60	15
W61	12
W62	15
W63	12
W64	15
W65	12
W66	15
W67	12
W68	15
W69	12
W70	15
W71	12
W72	15
W73	12
W74	15
W75	12
W76	15
W77	12
W78	15
W79	12
W80	15
W81	12
W82	15
W83	12
W84	15
W85	12
W86	15
W87	12
W88	15
W89	12
W90	15
W91	12
W92	15
W93	12
W94	15
W95	12
W96	15
W97	12
W98	15
W99	12
W100	15
A1	12
A2	15
A3	12
A4	15
A5	12
A6	15
A7	12
A8	15
A9	12
A10	15
A11	12
A12	15
A13	12
A14	15
A15	12
A16	15
A17	12
A18	15
A19	12
A20	15
A21	12
A22	15
A23	12
A24	15
A25	12
A26	15
A27	12
A28	15
A29	12
A30	15
A31	12
A32	15
A33	12
A34	15



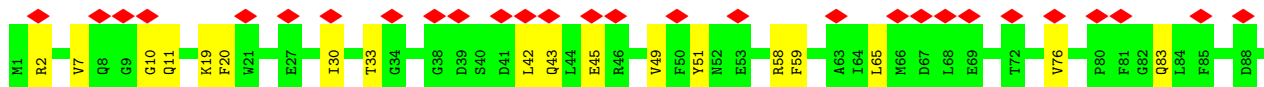
• Molecule 3: Tubulin beta chain

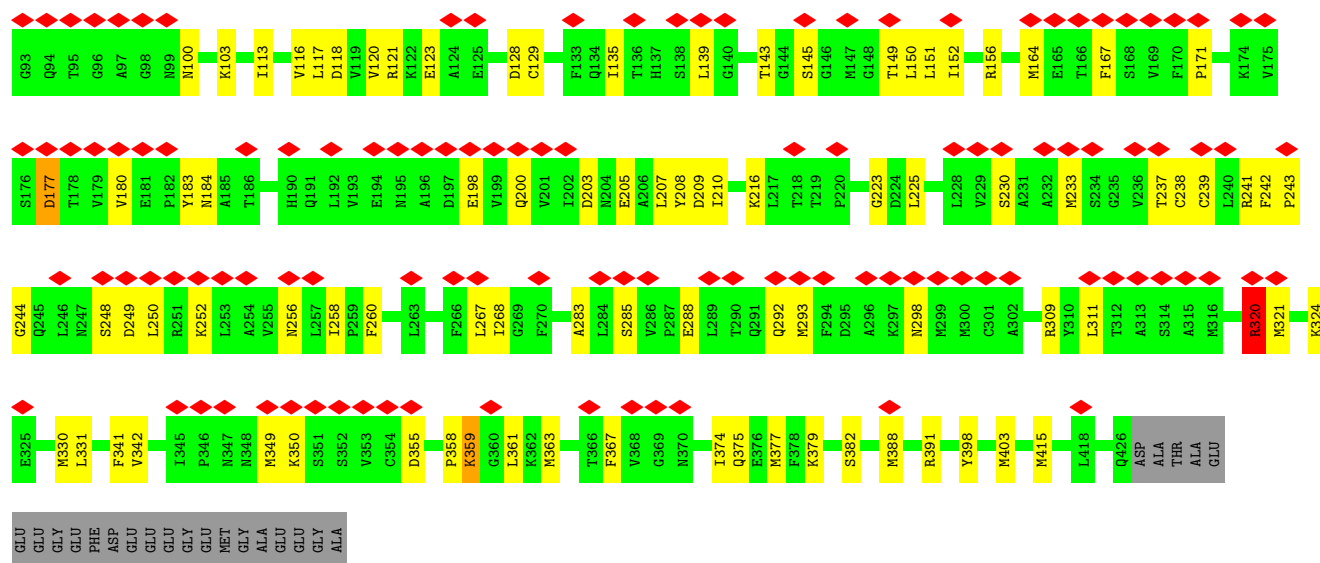
Chain E9: 35% 73% 21% 5%



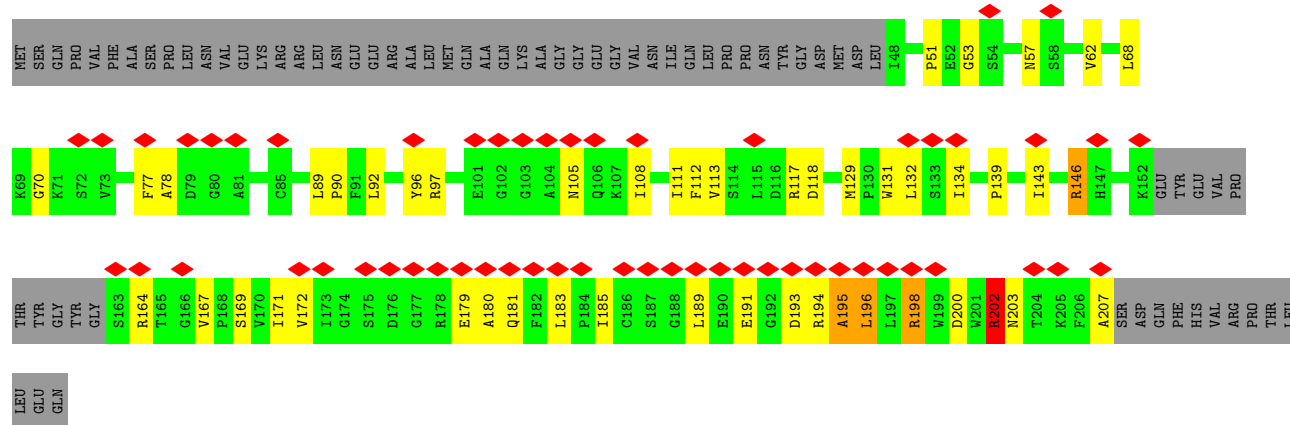
• Molecule 3: Tubulin beta chain

Chain F1: 32% 71% 23% 5%

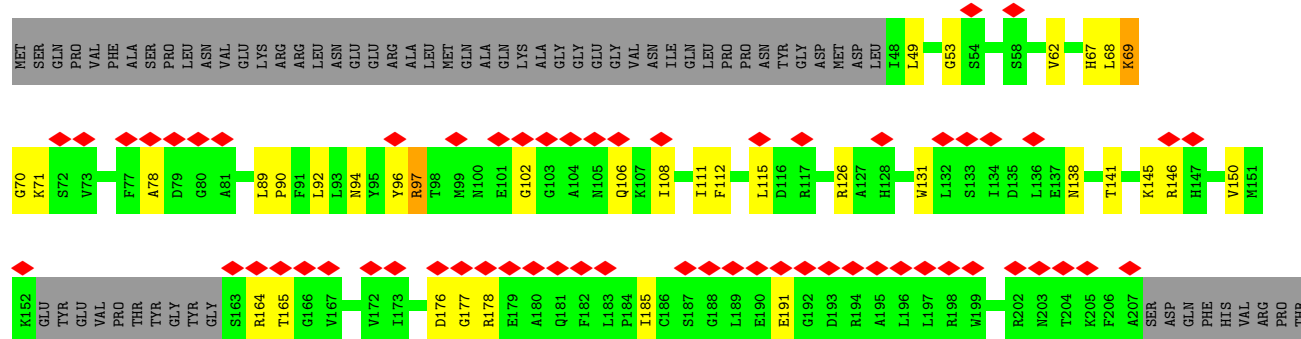




• Molecule 4: PDI family protein



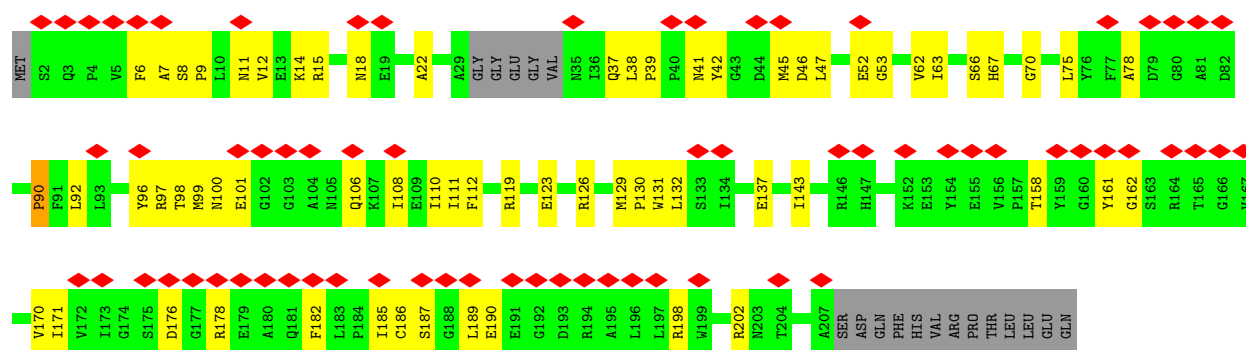
• Molecule 4: PDI family protein



LEU
LEU
GLU
GLN

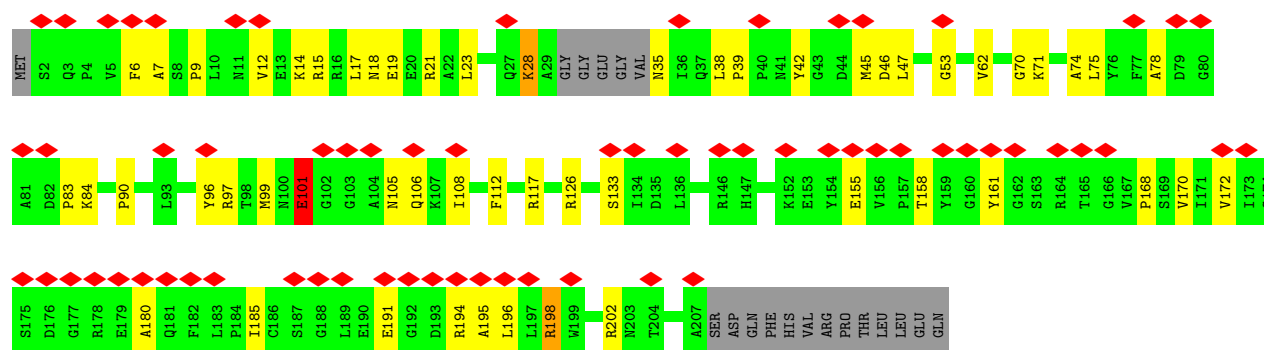
• Molecule 4: PDI family protein

Chain c: 



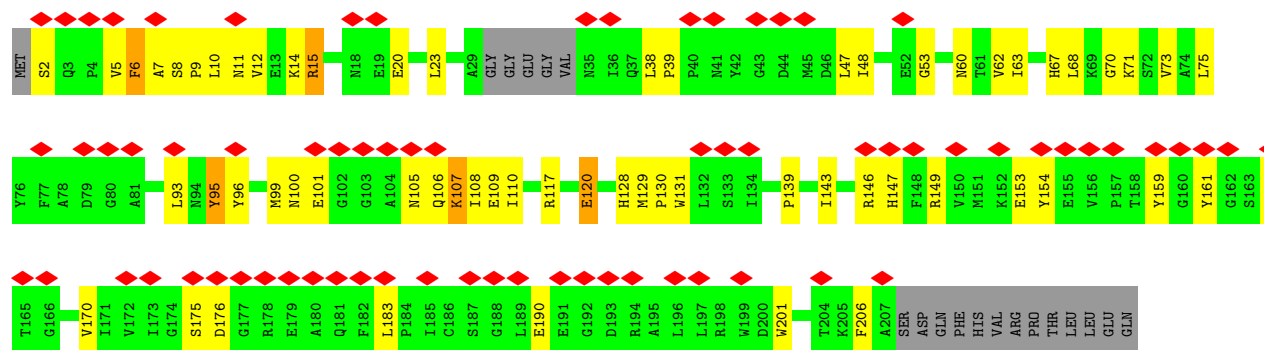
• Molecule 4: PDI family protein

Chain d: 



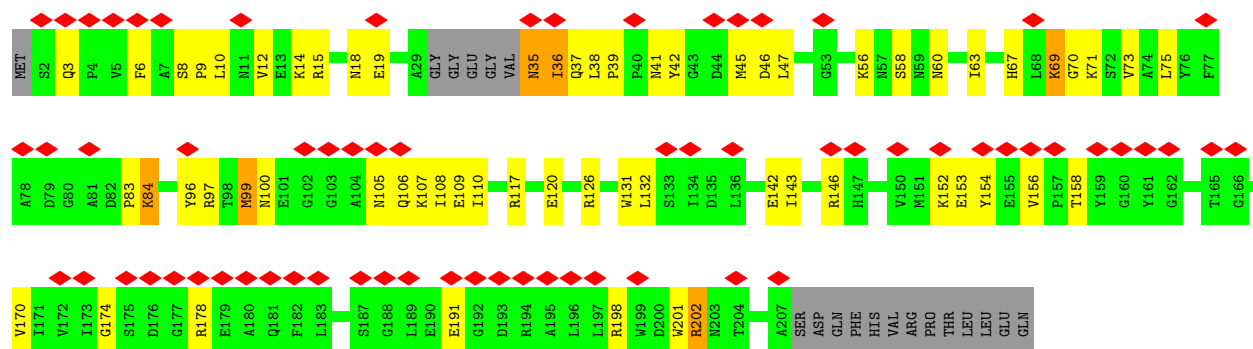
• Molecule 4: PDI family protein

Chain e: 

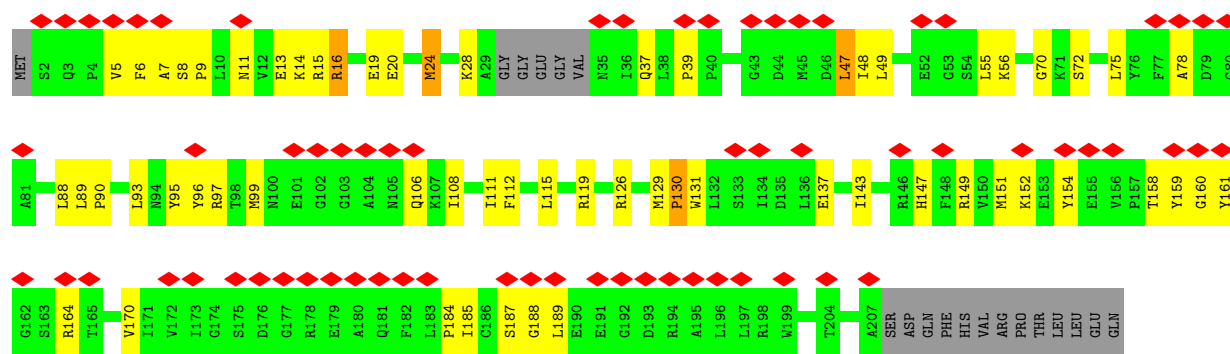


• Molecule 4: PDI family protein

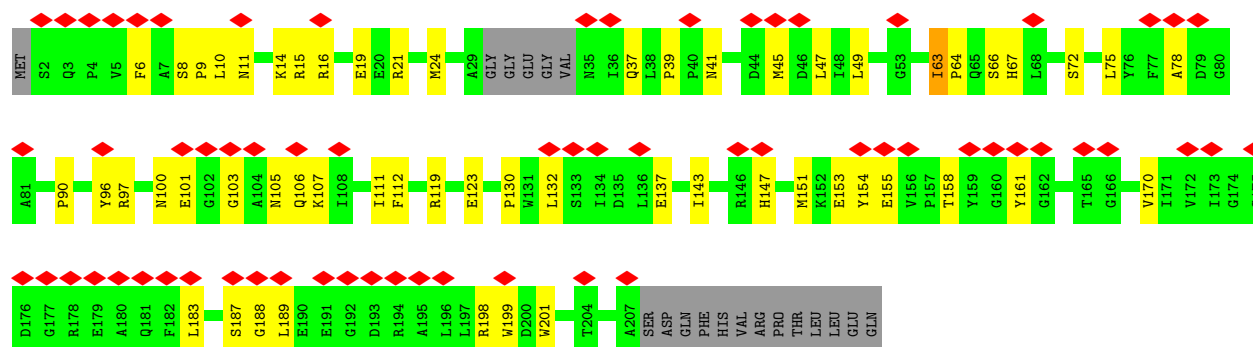
Chain f: 



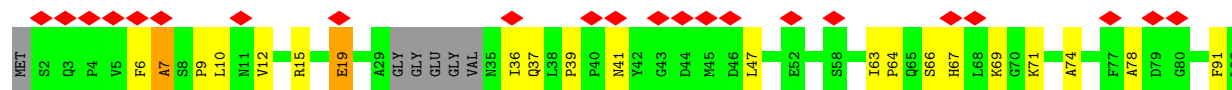
• Molecule 4: PDI family protein

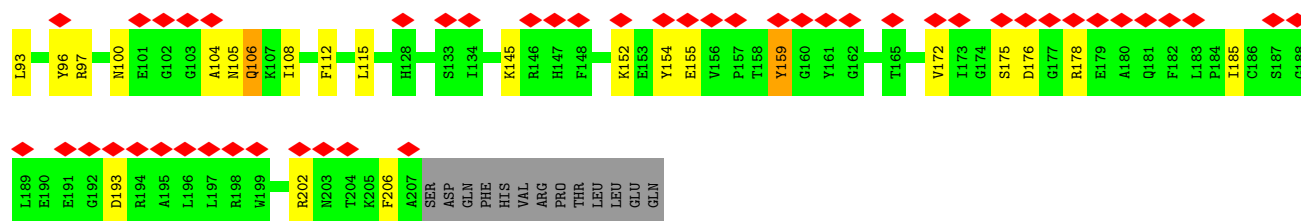


• Molecule 4: PDI family protein

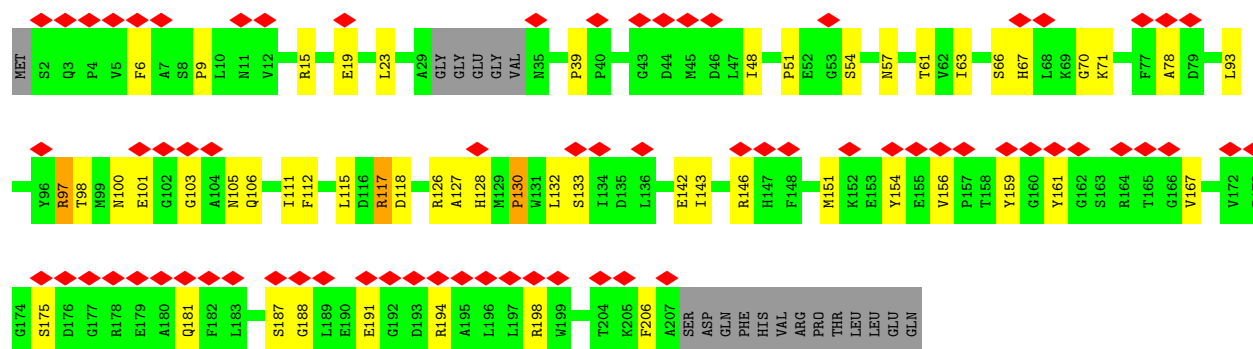


• Molecule 4: PDI family protein

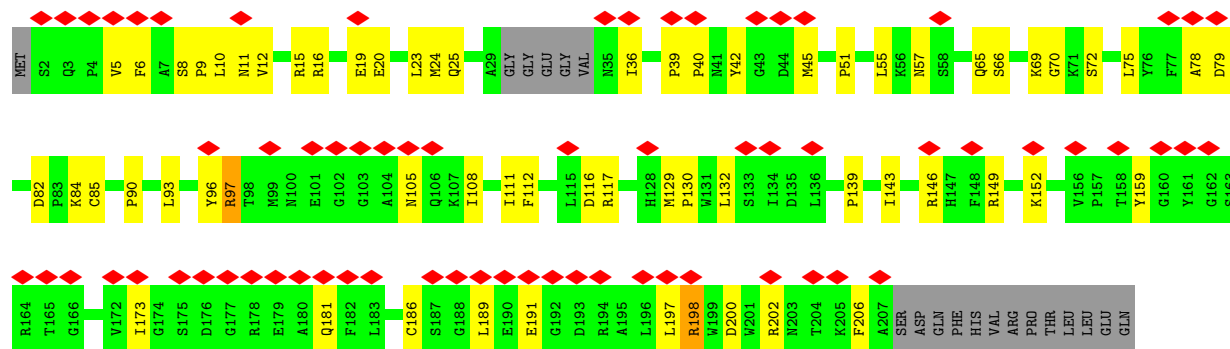




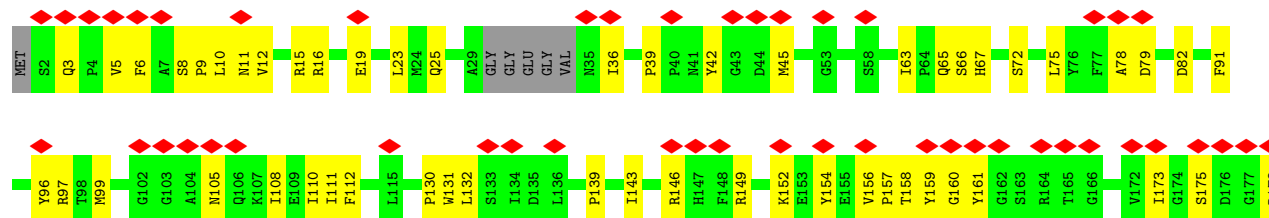
• Molecule 4: PDI family protein



• Molecule 4: PDI family protein

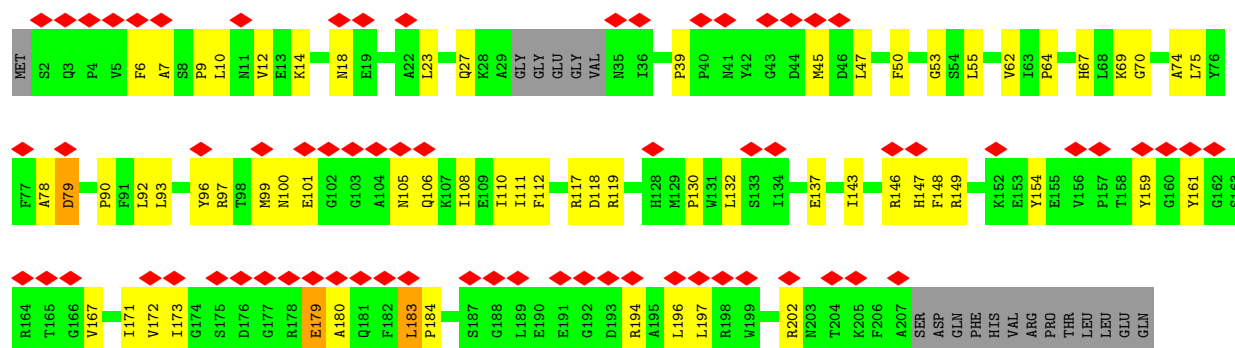


• Molecule 4: PDI family protein

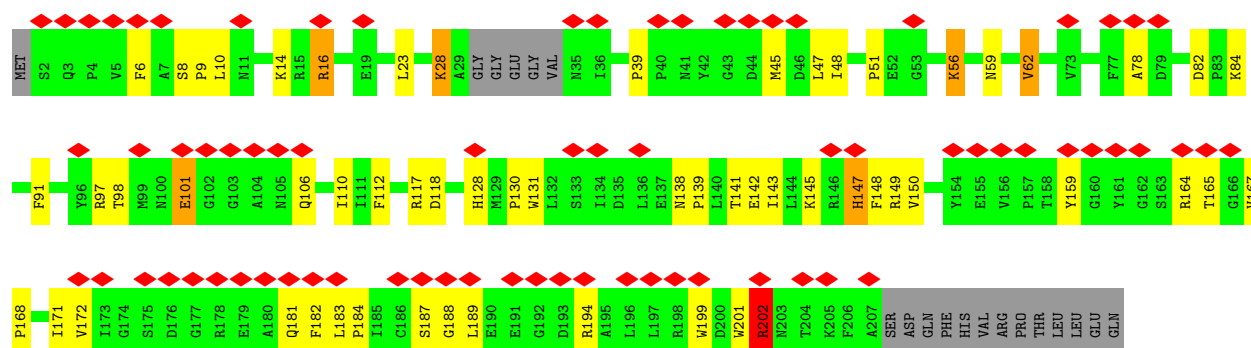




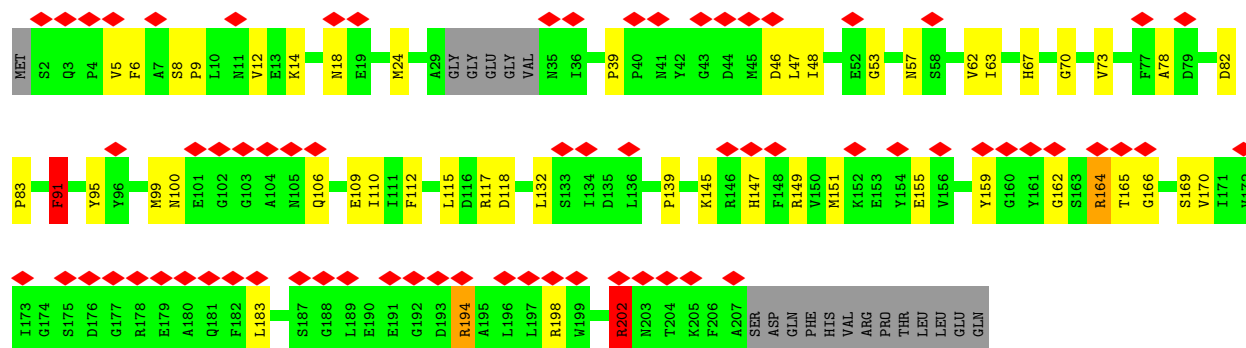
• Molecule 4: PDI family protein



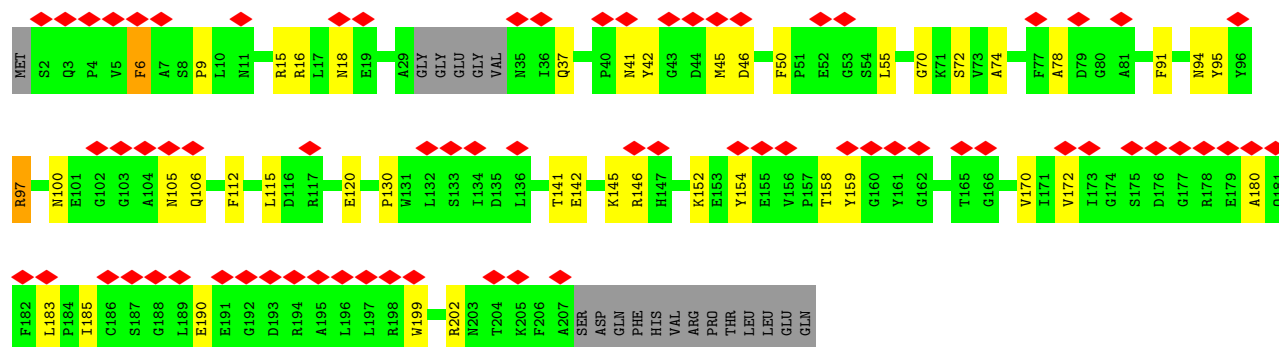
• Molecule 4: PDI family protein



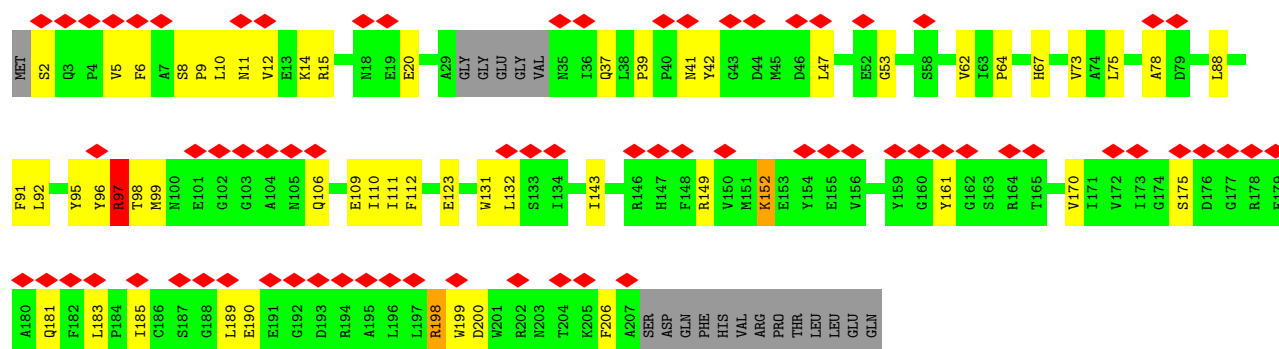
• Molecule 4: PDI family protein



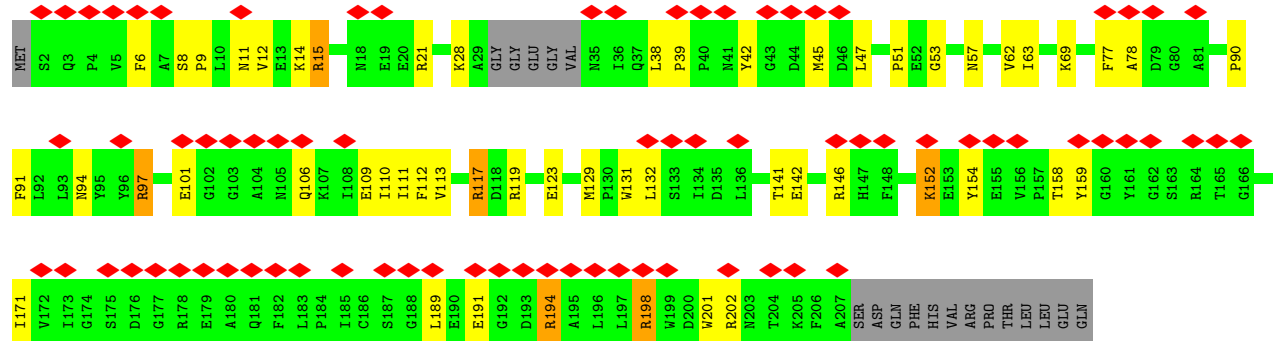
• Molecule 4: PDI family protein



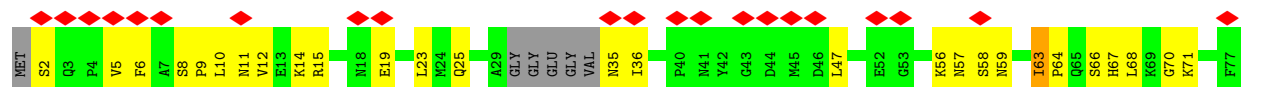
• Molecule 4: PDI family protein

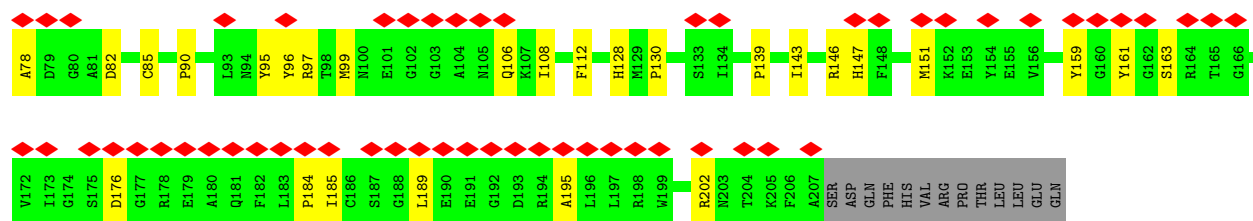


• Molecule 4: PDI family protein

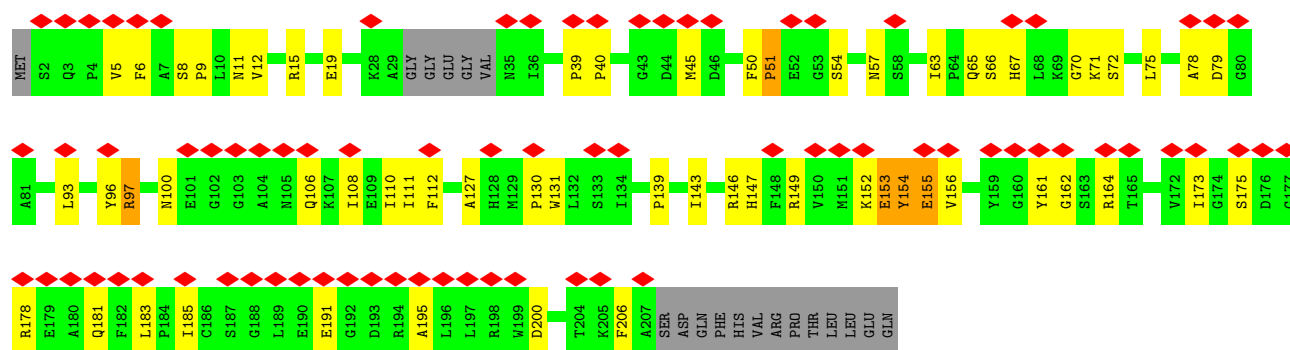


• Molecule 4: PDI family protein

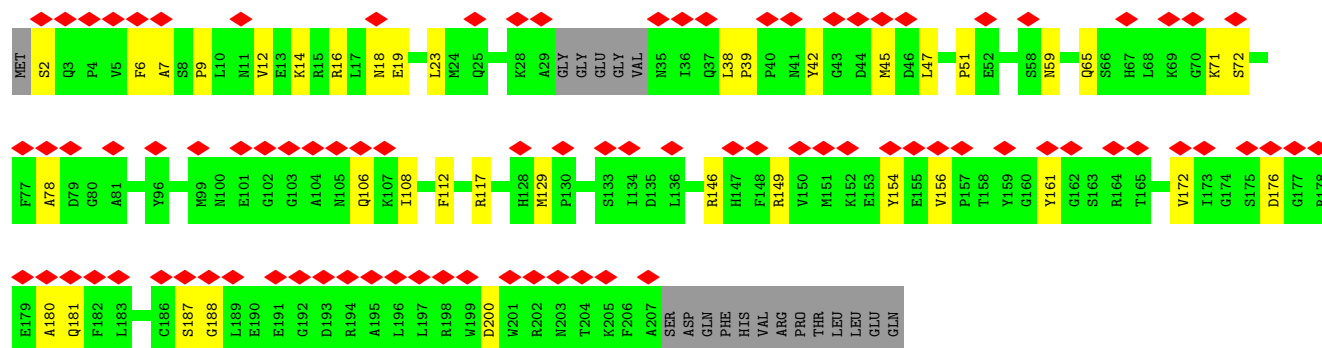
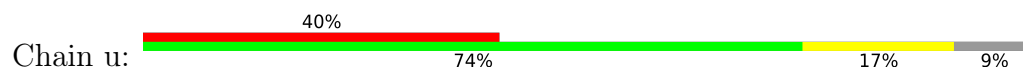




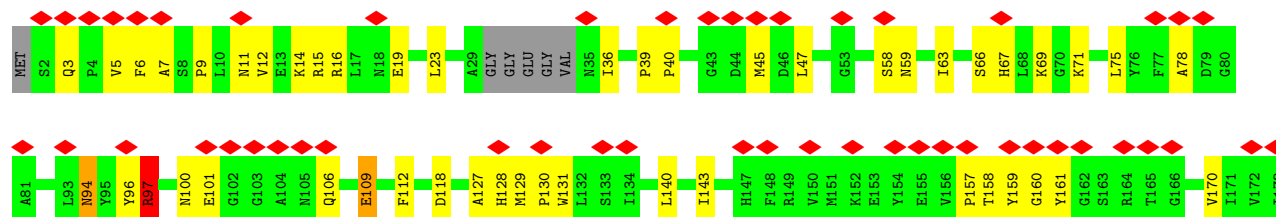
• Molecule 4: PDI family protein

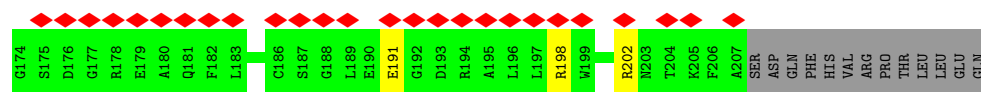


• Molecule 4: PDI family protein

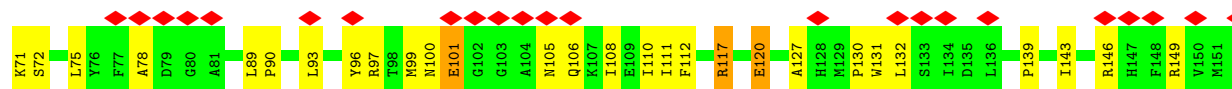
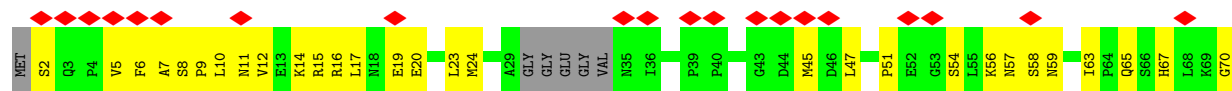


• Molecule 4: PDI family protein



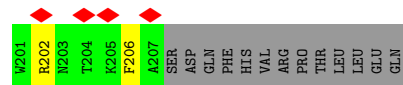
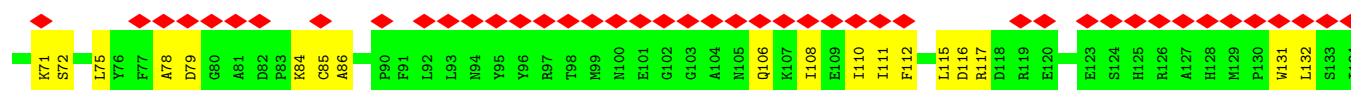
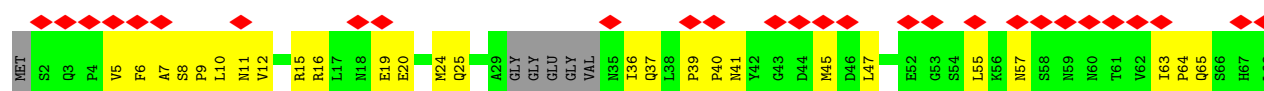


• Molecule 4: PDI family protein

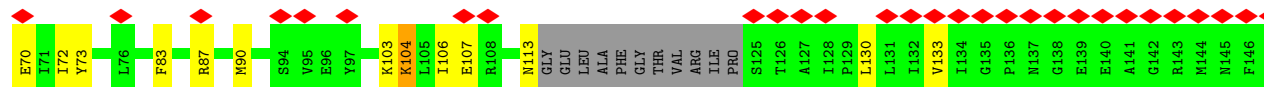
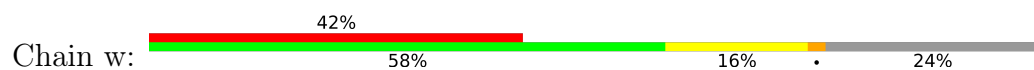


LEU
GLU
GLN

• Molecule 4: PDI family protein



• Molecule 5: PDI family protein



Q148	S149	D150	E151	F152	V153	L154	Q155	R156	W157	D158	Y159	R160	F161	N162	K163	W164	P165	GLY	SER	ALA	GLN	ARG	LEU	ARG	THR	LEU	ASN	ASP	ALA	THR	ASP	PRO	TRP	LYS	LYS	ARG	LEU	PRO	GLN	ASN	VAL
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	HELICAL, twist=27.7°, rise=80 Å, axial sym=C13	Depositor
Number of subtomograms used	39122	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	132	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.064	Depositor
Minimum map value	-13.513	Depositor
Average map value	0.056	Depositor
Map value standard deviation	0.986	Depositor
Recommended contour level	2	Depositor
Map size (Å)	447.444, 447.444, 447.444	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.0715, 2.0715, 2.0715	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.69	0/181	1.31	2/248 (0.8%)
1	1	0.62	0/181	1.12	0/248
1	10	0.61	0/181	1.41	3/248 (1.2%)
1	11	0.70	0/181	1.62	4/248 (1.6%)
1	12	0.58	0/181	1.36	3/248 (1.2%)
1	13	0.63	0/181	1.37	1/248 (0.4%)
1	14	0.59	0/181	1.07	0/248
1	15	0.64	0/181	1.73	8/248 (3.2%)
1	16	0.60	0/181	1.26	1/248 (0.4%)
1	17	1.00	2/181 (1.1%)	1.66	7/248 (2.8%)
1	18	0.64	0/181	1.08	0/248
1	19	0.76	0/181	1.41	0/248
1	2	0.66	0/181	1.43	2/248 (0.8%)
1	20	0.61	0/181	1.04	0/248
1	21	0.74	0/181	1.22	0/248
1	22	0.92	1/166 (0.6%)	1.51	3/227 (1.3%)
1	23	0.66	0/166	1.40	0/227
1	3	0.63	0/181	1.21	0/248
1	4	0.66	0/181	1.48	3/248 (1.2%)
1	5	0.60	0/181	1.44	3/248 (1.2%)
1	6	0.55	0/181	1.40	4/248 (1.6%)
1	7	0.60	0/181	1.23	1/248 (0.4%)
1	8	0.67	0/181	1.33	2/248 (0.8%)
1	9	0.71	0/181	1.21	1/248 (0.4%)
2	A0	0.64	0/3398	1.17	11/4606 (0.2%)
2	A2	0.62	0/3398	1.12	8/4606 (0.2%)
2	A4	0.70	3/3398 (0.1%)	1.24	7/4606 (0.2%)
2	A6	0.61	1/3398 (0.0%)	1.14	16/4606 (0.3%)
2	A8	0.69	2/3398 (0.1%)	1.24	11/4606 (0.2%)
2	B0	0.63	1/3398 (0.0%)	1.16	14/4606 (0.3%)
2	B2	0.64	2/3398 (0.1%)	1.13	4/4606 (0.1%)
2	B4	0.59	1/3398 (0.0%)	1.05	2/4606 (0.0%)
2	B6	0.57	0/3398	1.06	6/4606 (0.1%)
2	B8	0.57	0/3398	1.05	6/4606 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	C0	0.62	3/3398 (0.1%)	1.06	7/4606 (0.2%)
2	C2	0.61	1/3398 (0.0%)	1.04	2/4606 (0.0%)
2	C4	0.78	2/3398 (0.1%)	1.15	8/4606 (0.2%)
2	C6	0.62	0/3398	1.14	12/4606 (0.3%)
2	C8	0.61	0/3398	1.10	9/4606 (0.2%)
2	D0	0.61	0/3398	1.15	14/4606 (0.3%)
2	D2	0.57	0/3398	1.09	13/4606 (0.3%)
2	D4	0.61	0/3398	1.13	12/4606 (0.3%)
2	D6	0.58	1/3398 (0.0%)	1.04	13/4606 (0.3%)
2	D8	0.61	0/3398	1.13	9/4606 (0.2%)
2	E0	0.53	0/3398	0.96	5/4606 (0.1%)
2	E2	0.58	0/3398	1.05	7/4606 (0.2%)
2	E4	0.53	0/3398	1.01	4/4606 (0.1%)
2	E6	0.56	0/3398	1.04	7/4606 (0.2%)
2	E8	0.49	0/3398	0.89	0/4606
2	F0	0.60	1/3398 (0.0%)	1.06	9/4606 (0.2%)
3	A1	0.59	0/3404	1.12	5/4606 (0.1%)
3	A3	0.52	0/3404	1.02	6/4606 (0.1%)
3	A5	0.63	0/3404	1.19	8/4606 (0.2%)
3	A7	0.57	1/3404 (0.0%)	1.07	8/4606 (0.2%)
3	A9	0.61	1/3404 (0.0%)	1.13	9/4606 (0.2%)
3	B1	0.60	0/3404	1.12	5/4606 (0.1%)
3	B3	0.56	0/3404	1.13	12/4606 (0.3%)
3	B5	0.59	0/3404	1.12	9/4606 (0.2%)
3	B7	0.57	0/3404	1.11	10/4606 (0.2%)
3	B9	0.56	0/3404	1.07	8/4606 (0.2%)
3	C1	0.60	2/3404 (0.1%)	1.09	9/4606 (0.2%)
3	C3	0.59	0/3404	1.10	7/4606 (0.2%)
3	C5	0.60	0/3404	1.10	10/4606 (0.2%)
3	C7	0.59	0/3404	1.11	8/4606 (0.2%)
3	C9	0.59	0/3404	1.16	15/4606 (0.3%)
3	D1	0.63	0/3404	1.16	15/4606 (0.3%)
3	D3	0.60	3/3404 (0.1%)	1.10	5/4606 (0.1%)
3	D5	0.68	0/3404	1.28	19/4606 (0.4%)
3	D7	0.59	0/3404	1.06	4/4606 (0.1%)
3	D9	0.60	2/3404 (0.1%)	1.13	15/4606 (0.3%)
3	E1	0.55	0/3404	1.02	5/4606 (0.1%)
3	E3	0.63	2/3404 (0.1%)	1.09	8/4606 (0.2%)
3	E5	0.56	0/3404	1.05	4/4606 (0.1%)
3	E7	0.60	0/3404	1.10	12/4606 (0.3%)
3	E9	0.56	0/3404	1.07	10/4606 (0.2%)
3	F1	0.61	1/3404 (0.0%)	1.14	10/4606 (0.2%)
4	a	0.72	2/1225 (0.2%)	1.28	9/1654 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	b	0.68	2/1225 (0.2%)	1.14	7/1654 (0.4%)
4	c	0.85	2/1645 (0.1%)	1.41	13/2225 (0.6%)
4	d	0.67	0/1645	1.23	7/2225 (0.3%)
4	e	0.67	0/1645	1.25	5/2225 (0.2%)
4	f	0.70	2/1645 (0.1%)	1.16	6/2225 (0.3%)
4	g	0.62	1/1645 (0.1%)	1.23	8/2225 (0.4%)
4	h	0.62	1/1645 (0.1%)	1.15	4/2225 (0.2%)
4	i	0.60	0/1645	1.18	7/2225 (0.3%)
4	j	0.61	0/1645	1.14	2/2225 (0.1%)
4	k	0.65	1/1645 (0.1%)	1.17	1/2225 (0.0%)
4	l	0.59	0/1645	1.13	4/2225 (0.2%)
4	m	0.76	3/1645 (0.2%)	1.23	13/2225 (0.6%)
4	n	0.70	1/1645 (0.1%)	1.30	8/2225 (0.4%)
4	o	0.61	0/1645	1.25	10/2225 (0.4%)
4	p	0.70	0/1645	1.33	11/2225 (0.5%)
4	q	0.69	2/1645 (0.1%)	1.20	6/2225 (0.3%)
4	r	0.68	0/1645	1.27	10/2225 (0.4%)
4	s	0.58	0/1645	1.14	2/2225 (0.1%)
4	t	0.63	0/1645	1.24	7/2225 (0.3%)
4	u	0.62	0/1645	1.13	3/2225 (0.1%)
4	v	0.61	0/1645	1.14	2/2225 (0.1%)
4	x	0.57	1/1645 (0.1%)	1.15	5/2225 (0.2%)
4	y	0.54	0/1645	1.09	1/2225 (0.0%)
5	w	0.58	0/1201	1.13	8/1623 (0.5%)
All	All	0.61	51/221007 (0.0%)	1.13	659/299303 (0.2%)

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
1	12	0	1
1	19	0	1
1	2	0	1
1	20	0	2
1	21	0	1
1	23	0	1
1	7	0	1
1	8	0	1
2	A0	0	1
2	A2	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A4	0	1
2	A8	0	1
2	B4	0	1
2	B6	0	2
2	C4	0	1
2	C8	0	1
2	D2	0	2
2	D8	0	1
2	E4	0	1
2	F0	0	1
3	B3	0	1
3	B9	0	1
3	E5	0	2
3	E9	0	1
4	o	0	1
4	s	0	1
All	All	0	31

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C4	2	ARG	NE-CZ	22.48	1.57	1.33
2	C4	2	ARG	CD-NE	19.88	1.74	1.46
4	c	178	ARG	NE-CZ	17.46	1.52	1.33
2	C2	221	ARG	NE-CZ	12.31	1.46	1.33
4	m	202	ARG	NE-CZ	11.61	1.45	1.33

The worst 5 of 659 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C4	2	ARG	CD-NE-CZ	20.03	152.44	124.40
4	c	178	ARG	CD-NE-CZ	17.47	148.85	124.40
2	C4	2	ARG	NE-CZ-NH1	17.38	138.88	121.50
2	D2	85	HIS	CA-CB-CG	13.45	127.25	113.80
2	C4	2	ARG	CG-CD-NE	13.44	141.57	112.00

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	12	255	PRO	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	19	257	PRO	Peptide
1	2	239	LEU	Peptide
1	20	238	THR	Peptide
1	20	239	LEU	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	0	174	0	171	17	0
1	1	174	0	171	6	0
1	10	174	0	171	16	0
1	11	174	0	171	9	0
1	12	174	0	171	4	0
1	13	174	0	171	7	0
1	14	174	0	171	0	0
1	15	174	0	171	11	0
1	16	174	0	171	10	0
1	17	174	0	171	5	0
1	18	174	0	171	28	0
1	19	174	0	171	28	0
1	2	174	0	171	10	0
1	20	174	0	171	8	0
1	21	174	0	171	25	0
1	22	160	0	156	6	0
1	23	160	0	156	13	0
1	3	174	0	171	5	0
1	4	174	0	171	19	0
1	5	174	0	171	7	0
1	6	174	0	171	15	0
1	7	174	0	171	7	0
1	8	174	0	171	10	0
1	9	174	0	171	8	0
2	A0	3325	0	3252	87	0
2	A2	3325	0	3252	89	0
2	A4	3325	0	3252	60	0
2	A6	3325	0	3252	85	0
2	A8	3325	0	3252	78	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B0	3325	0	3252	92	0
2	B2	3325	0	3252	54	0
2	B4	3325	0	3252	84	0
2	B6	3325	0	3252	71	0
2	B8	3325	0	3252	75	0
2	C0	3325	0	3252	73	0
2	C2	3325	0	3252	73	0
2	C4	3325	0	3252	88	0
2	C6	3325	0	3252	104	0
2	C8	3325	0	3252	59	0
2	D0	3325	0	3252	81	0
2	D2	3325	0	3252	71	0
2	D4	3325	0	3252	97	0
2	D6	3325	0	3252	60	0
2	D8	3325	0	3252	63	0
2	E0	3325	0	3252	95	0
2	E2	3325	0	3252	68	0
2	E4	3325	0	3252	153	0
2	E6	3325	0	3252	94	0
2	E8	3325	0	3252	76	0
2	F0	3325	0	3252	111	0
3	A1	3331	0	3207	88	0
3	A3	3331	0	3209	70	0
3	A5	3331	0	3207	66	0
3	A7	3331	0	3207	62	0
3	A9	3331	0	3207	86	0
3	B1	3331	0	3209	95	0
3	B3	3331	0	3207	59	0
3	B5	3331	0	3207	84	0
3	B7	3331	0	3209	80	0
3	B9	3331	0	3209	61	0
3	C1	3331	0	3209	86	0
3	C3	3331	0	3209	82	0
3	C5	3331	0	3209	80	0
3	C7	3331	0	3209	70	0
3	C9	3331	0	3209	88	0
3	D1	3331	0	3209	72	0
3	D3	3331	0	3207	96	0
3	D5	3331	0	3207	91	0
3	D7	3331	0	3207	79	0
3	D9	3331	0	3207	75	0
3	E1	3331	0	3207	96	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E3	3331	0	3209	55	0
3	E5	3331	0	3207	159	0
3	E7	3331	0	3207	74	0
3	E9	3331	0	3207	70	0
3	F1	3331	0	3207	71	0
4	a	1198	0	1194	35	0
4	b	1198	0	1194	42	0
4	c	1608	0	1590	71	0
4	d	1608	0	1590	68	0
4	e	1608	0	1590	75	0
4	f	1608	0	1590	79	0
4	g	1608	0	1590	73	0
4	h	1608	0	1590	71	0
4	i	1608	0	1590	67	0
4	j	1608	0	1590	84	0
4	k	1608	0	1590	82	0
4	l	1608	0	1590	90	0
4	m	1608	0	1590	57	0
4	n	1608	0	1590	57	0
4	o	1608	0	1590	39	0
4	p	1608	0	1590	33	0
4	q	1608	0	1590	43	0
4	r	1608	0	1590	44	0
4	s	1608	0	1590	61	0
4	t	1608	0	1590	68	0
4	u	1608	0	1590	49	0
4	v	1608	0	1590	88	0
4	x	1608	0	1590	109	0
4	y	1608	0	1590	86	0
5	w	1172	0	1171	20	0
All	All	216148	0	210569	4710	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 11.

The worst 5 of 4710 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)
4:b:97:ARG:NH1	4:d:6:PHE:HB3	1.24	1.50
2:C4:2:ARG:NE	2:C4:2:ARG:CD	1.74	1.46
1:4:240:PRO:CB	4:g:154:TYR:HB3	1.50	1.38

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:i:63:ILE:CD1	4:k:16:ARG:HG3	1.53	1.38
1:4:240:PRO:HB2	4:g:154:TYR:CB	1.56	1.35

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	0	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	1	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	10	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	11	20/351 (6%)	15 (75%)	5 (25%)	0	100	100
1	12	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	13	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	14	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	15	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	16	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	17	20/351 (6%)	20 (100%)	0	0	100	100
1	18	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	19	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	2	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	20	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	21	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	22	18/351 (5%)	14 (78%)	4 (22%)	0	100	100
1	23	18/351 (5%)	15 (83%)	3 (17%)	0	100	100
1	3	20/351 (6%)	18 (90%)	1 (5%)	1 (5%)	1	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	4	20/351 (6%)	20 (100%)	0	0	100	100
1	5	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	6	20/351 (6%)	20 (100%)	0	0	100	100
1	7	20/351 (6%)	20 (100%)	0	0	100	100
1	8	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	9	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
2	A0	424/453 (94%)	397 (94%)	27 (6%)	0	100	100
2	A2	424/453 (94%)	406 (96%)	17 (4%)	1 (0%)	43	78
2	A4	424/453 (94%)	398 (94%)	26 (6%)	0	100	100
2	A6	424/453 (94%)	399 (94%)	25 (6%)	0	100	100
2	A8	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	B0	424/453 (94%)	404 (95%)	20 (5%)	0	100	100
2	B2	424/453 (94%)	406 (96%)	18 (4%)	0	100	100
2	B4	424/453 (94%)	407 (96%)	17 (4%)	0	100	100
2	B6	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
2	B8	424/453 (94%)	404 (95%)	20 (5%)	0	100	100
2	C0	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	C2	424/453 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
2	C4	424/453 (94%)	390 (92%)	33 (8%)	1 (0%)	43	78
2	C6	424/453 (94%)	396 (93%)	28 (7%)	0	100	100
2	C8	424/453 (94%)	393 (93%)	31 (7%)	0	100	100
2	D0	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	D2	424/453 (94%)	405 (96%)	18 (4%)	1 (0%)	43	78
2	D4	424/453 (94%)	406 (96%)	18 (4%)	0	100	100
2	D6	424/453 (94%)	409 (96%)	15 (4%)	0	100	100
2	D8	424/453 (94%)	409 (96%)	15 (4%)	0	100	100
2	E0	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
2	E2	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	E4	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	E6	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	E8	424/453 (94%)	400 (94%)	24 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F0	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
3	A1	424/449 (94%)	390 (92%)	34 (8%)	0	100	100
3	A3	424/449 (94%)	402 (95%)	21 (5%)	1 (0%)	43	78
3	A5	424/449 (94%)	388 (92%)	34 (8%)	2 (0%)	24	63
3	A7	424/449 (94%)	394 (93%)	29 (7%)	1 (0%)	43	78
3	A9	424/449 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
3	B1	424/449 (94%)	401 (95%)	23 (5%)	0	100	100
3	B3	424/449 (94%)	397 (94%)	25 (6%)	2 (0%)	24	63
3	B5	424/449 (94%)	394 (93%)	28 (7%)	2 (0%)	24	63
3	B7	424/449 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
3	B9	424/449 (94%)	405 (96%)	18 (4%)	1 (0%)	43	78
3	C1	424/449 (94%)	399 (94%)	25 (6%)	0	100	100
3	C3	424/449 (94%)	398 (94%)	25 (6%)	1 (0%)	43	78
3	C5	424/449 (94%)	403 (95%)	21 (5%)	0	100	100
3	C7	424/449 (94%)	394 (93%)	29 (7%)	1 (0%)	43	78
3	C9	424/449 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
3	D1	424/449 (94%)	398 (94%)	25 (6%)	1 (0%)	43	78
3	D3	424/449 (94%)	394 (93%)	28 (7%)	2 (0%)	24	63
3	D5	424/449 (94%)	396 (93%)	26 (6%)	2 (0%)	24	63
3	D7	424/449 (94%)	404 (95%)	20 (5%)	0	100	100
3	D9	424/449 (94%)	398 (94%)	25 (6%)	1 (0%)	43	78
3	E1	424/449 (94%)	402 (95%)	21 (5%)	1 (0%)	43	78
3	E3	424/449 (94%)	400 (94%)	23 (5%)	1 (0%)	43	78
3	E5	424/449 (94%)	396 (93%)	28 (7%)	0	100	100
3	E7	424/449 (94%)	400 (94%)	23 (5%)	1 (0%)	43	78
3	E9	424/449 (94%)	393 (93%)	31 (7%)	0	100	100
3	F1	424/449 (94%)	391 (92%)	32 (8%)	1 (0%)	43	78
4	a	146/220 (66%)	134 (92%)	11 (8%)	1 (1%)	18	56
4	b	146/220 (66%)	134 (92%)	12 (8%)	0	100	100
4	c	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	d	197/220 (90%)	180 (91%)	17 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	e	197/220 (90%)	185 (94%)	11 (6%)	1 (0%)	24	63
4	f	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	g	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	h	197/220 (90%)	183 (93%)	14 (7%)	0	100	100
4	i	197/220 (90%)	182 (92%)	14 (7%)	1 (0%)	24	63
4	j	197/220 (90%)	182 (92%)	15 (8%)	0	100	100
4	k	197/220 (90%)	183 (93%)	13 (7%)	1 (0%)	24	63
4	l	197/220 (90%)	186 (94%)	11 (6%)	0	100	100
4	m	197/220 (90%)	181 (92%)	16 (8%)	0	100	100
4	n	197/220 (90%)	182 (92%)	14 (7%)	1 (0%)	24	63
4	o	197/220 (90%)	180 (91%)	17 (9%)	0	100	100
4	p	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	q	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	r	197/220 (90%)	184 (93%)	12 (6%)	1 (0%)	24	63
4	s	197/220 (90%)	181 (92%)	16 (8%)	0	100	100
4	t	197/220 (90%)	188 (95%)	7 (4%)	2 (1%)	12	48
4	u	197/220 (90%)	188 (95%)	8 (4%)	1 (0%)	24	63
4	v	197/220 (90%)	180 (91%)	17 (9%)	0	100	100
4	x	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	y	197/220 (90%)	184 (93%)	12 (6%)	1 (0%)	24	63
5	w	139/189 (74%)	133 (96%)	6 (4%)	0	100	100
All	All	27289/37345 (73%)	25630 (94%)	1620 (6%)	39 (0%)	49	83

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A3	179	VAL
3	A5	55	THR
3	A7	55	THR
3	A9	55	THR
3	B3	55	THR

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	0	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	1	20/304 (7%)	20 (100%)	0	100	100
1	10	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	11	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	12	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	13	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	14	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	15	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	16	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	17	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	18	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	19	20/304 (7%)	17 (85%)	3 (15%)	3	12
1	2	20/304 (7%)	20 (100%)	0	100	100
1	20	20/304 (7%)	20 (100%)	0	100	100
1	21	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	22	18/304 (6%)	18 (100%)	0	100	100
1	23	18/304 (6%)	18 (100%)	0	100	100
1	3	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	4	20/304 (7%)	20 (100%)	0	100	100
1	5	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	6	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	7	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	8	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	9	20/304 (7%)	20 (100%)	0	100	100
2	A0	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	A2	359/379 (95%)	352 (98%)	7 (2%)	50	67

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A4	359/379 (95%)	347 (97%)	12 (3%)	33	55
2	A6	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	A8	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	B0	359/379 (95%)	349 (97%)	10 (3%)	38	60
2	B2	359/379 (95%)	349 (97%)	10 (3%)	38	60
2	B4	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	B6	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	B8	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	C0	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	C2	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	C4	359/379 (95%)	357 (99%)	2 (1%)	78	83
2	C6	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	C8	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	D0	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	D2	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	D4	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	D6	359/379 (95%)	354 (99%)	5 (1%)	59	72
2	D8	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	E0	359/379 (95%)	357 (99%)	2 (1%)	78	83
2	E2	359/379 (95%)	354 (99%)	5 (1%)	59	72
2	E4	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	E6	359/379 (95%)	357 (99%)	2 (1%)	78	83
2	E8	359/379 (95%)	358 (100%)	1 (0%)	86	86
2	F0	359/379 (95%)	351 (98%)	8 (2%)	45	64
3	A1	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	A3	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	A5	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	A7	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	A9	364/381 (96%)	355 (98%)	9 (2%)	42	63
3	B1	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	B3	364/381 (96%)	360 (99%)	4 (1%)	65	76

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	B5	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	B7	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	B9	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	C1	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	C3	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	C5	364/381 (96%)	356 (98%)	8 (2%)	45	64
3	C7	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	C9	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	D1	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	D3	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	D5	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	D7	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	D9	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	E1	364/381 (96%)	355 (98%)	9 (2%)	42	63
3	E3	364/381 (96%)	355 (98%)	9 (2%)	42	63
3	E5	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	E7	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	E9	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	F1	364/381 (96%)	359 (99%)	5 (1%)	59	72
4	a	130/190 (68%)	127 (98%)	3 (2%)	44	64
4	b	130/190 (68%)	128 (98%)	2 (2%)	57	72
4	c	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	d	174/190 (92%)	168 (97%)	6 (3%)	32	54
4	e	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	f	174/190 (92%)	169 (97%)	5 (3%)	37	58
4	g	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	h	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	i	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	j	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	k	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	l	174/190 (92%)	173 (99%)	1 (1%)	78	83

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	m	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	n	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	o	174/190 (92%)	167 (96%)	7 (4%)	28	49
4	p	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	q	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	r	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	s	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	t	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	u	174/190 (92%)	174 (100%)	0	100	100
4	v	174/190 (92%)	169 (97%)	5 (3%)	37	58
4	x	174/190 (92%)	168 (97%)	6 (3%)	32	54
4	y	174/190 (92%)	171 (98%)	3 (2%)	53	69
5	w	127/164 (77%)	124 (98%)	3 (2%)	43	64
All	All	23489/31780 (74%)	23093 (98%)	396 (2%)	52	69

5 of 396 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D3	379	LYS
3	E3	362	LYS
3	D5	157	GLU
3	D9	154	LYS
3	E7	174	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 409 such sidechains are listed below:

Mol	Chain	Res	Type
2	D6	102	ASN
2	E4	128	ASN
4	v	67	HIS
3	D7	204	ASN
2	E0	406	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

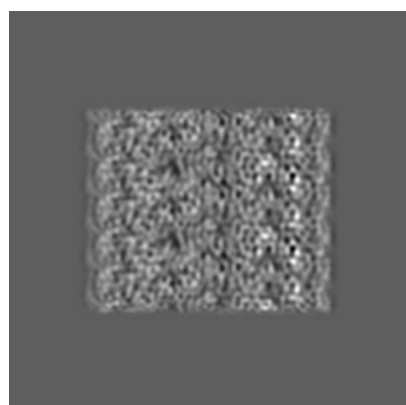
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26019. These allow visual inspection of the internal detail of the map and identification of artifacts.

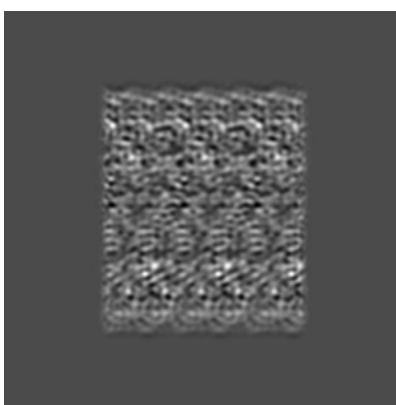
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 108



Y Index: 108



Z Index: 108

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: 156



Y Index: 153

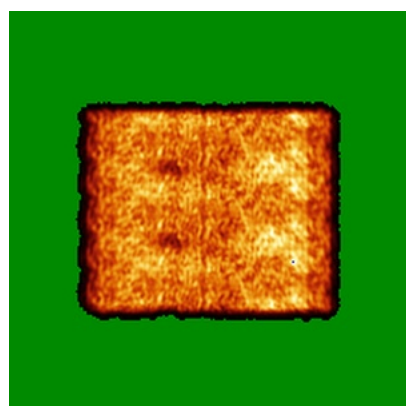


Z Index: 155

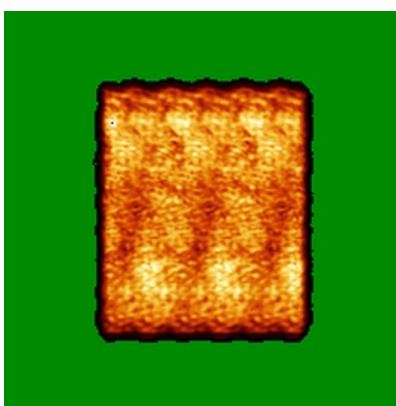
The images above show the largest variance slices of the map in three orthogonal directions.

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

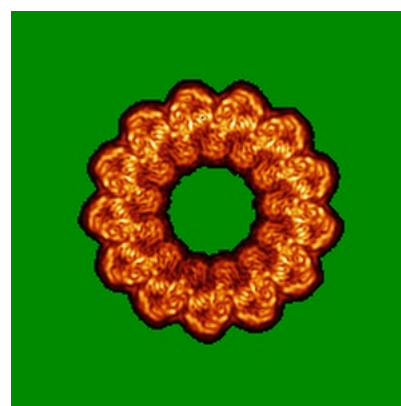
6.4.1 Primary map



X



Y

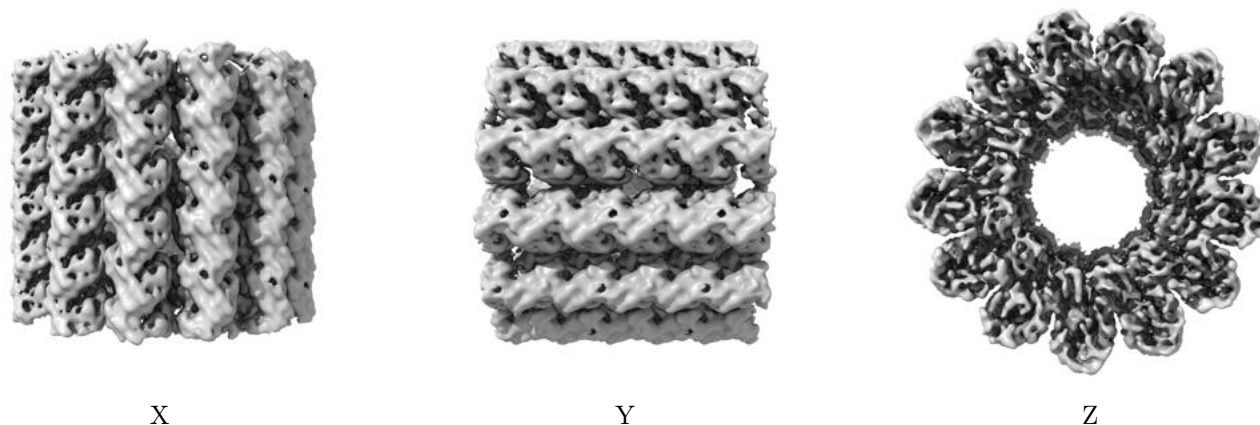


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

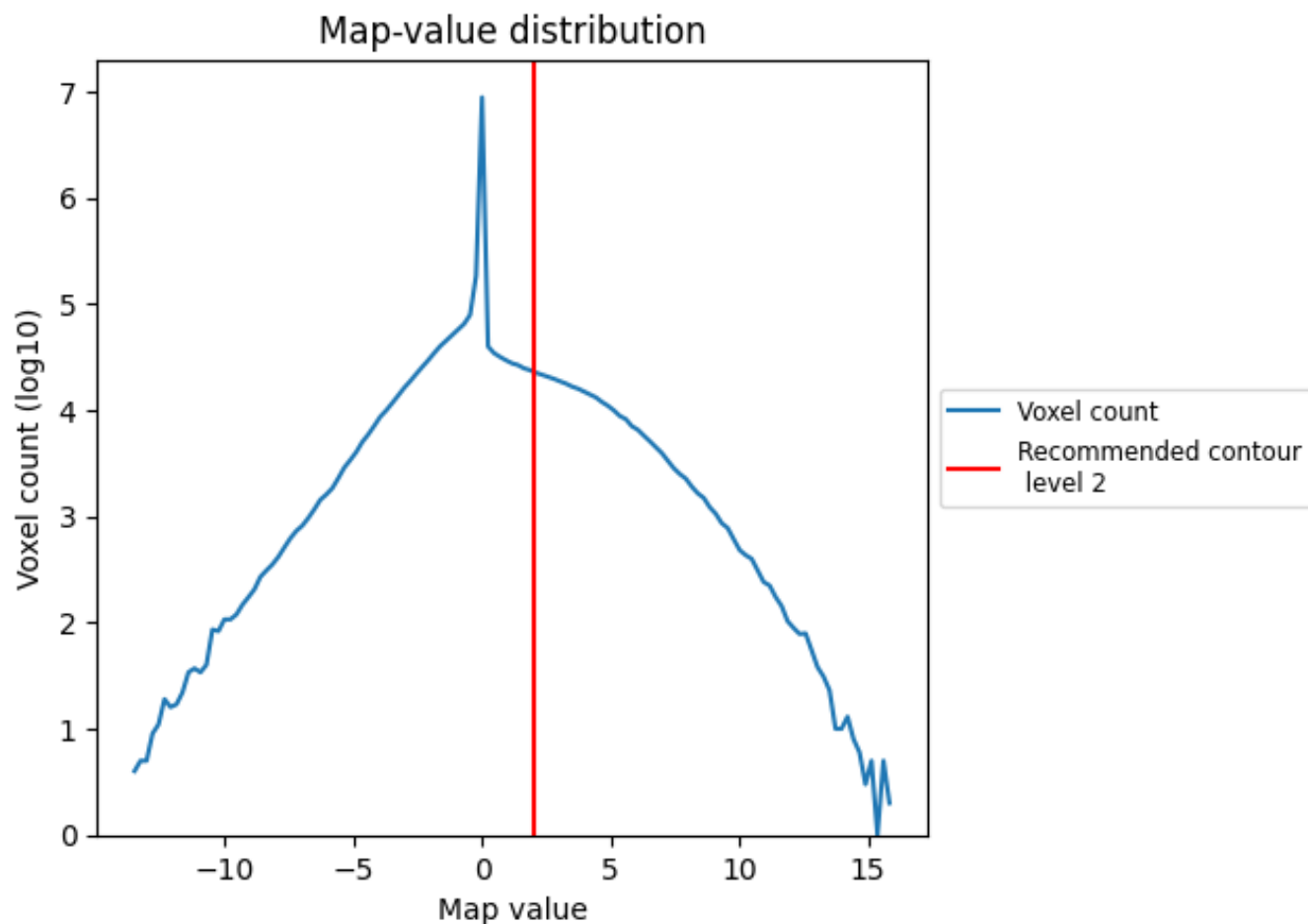
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

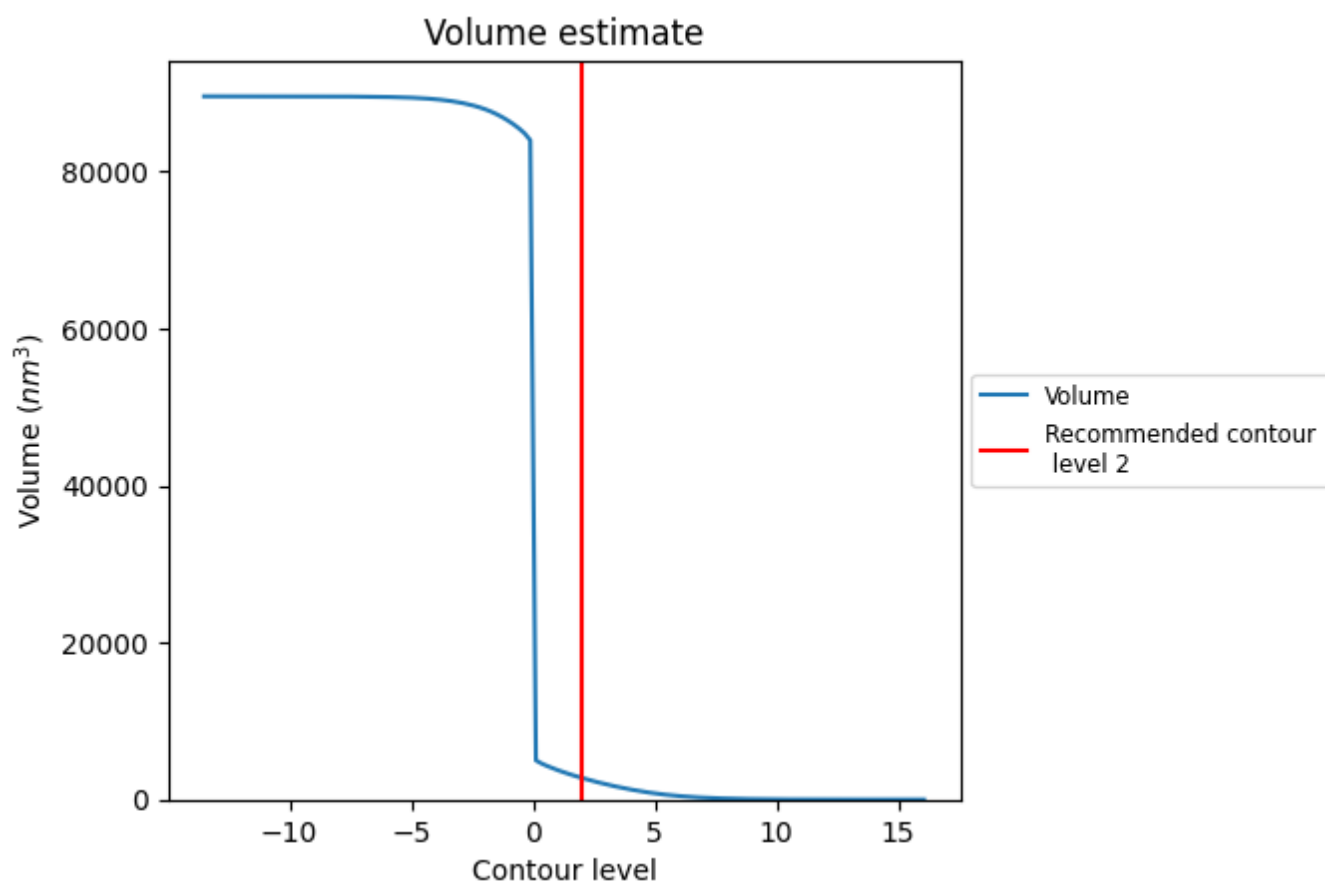
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

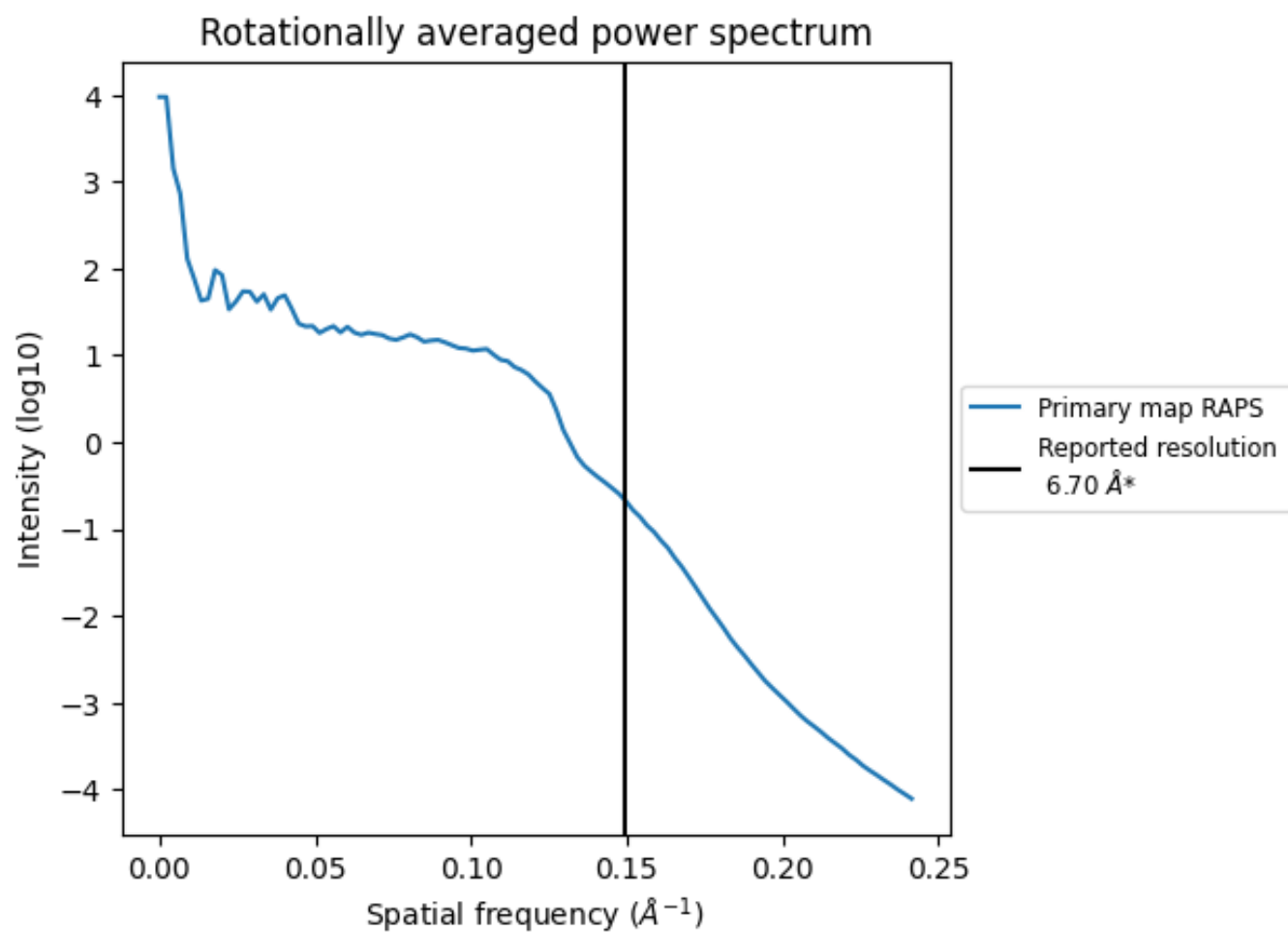
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2760 nm³; this corresponds to an approximate mass of 2494 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 0.149 Å⁻¹

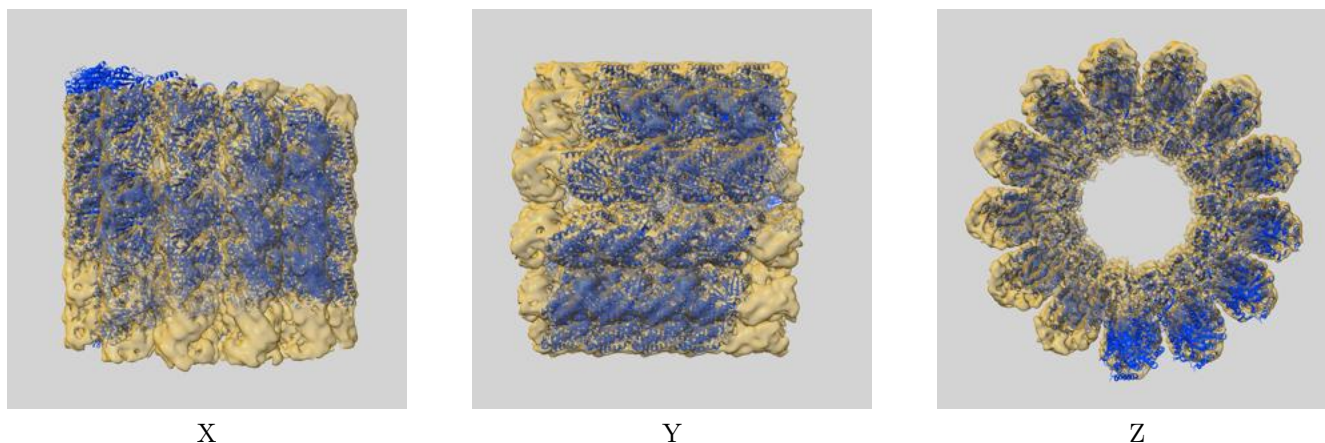
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

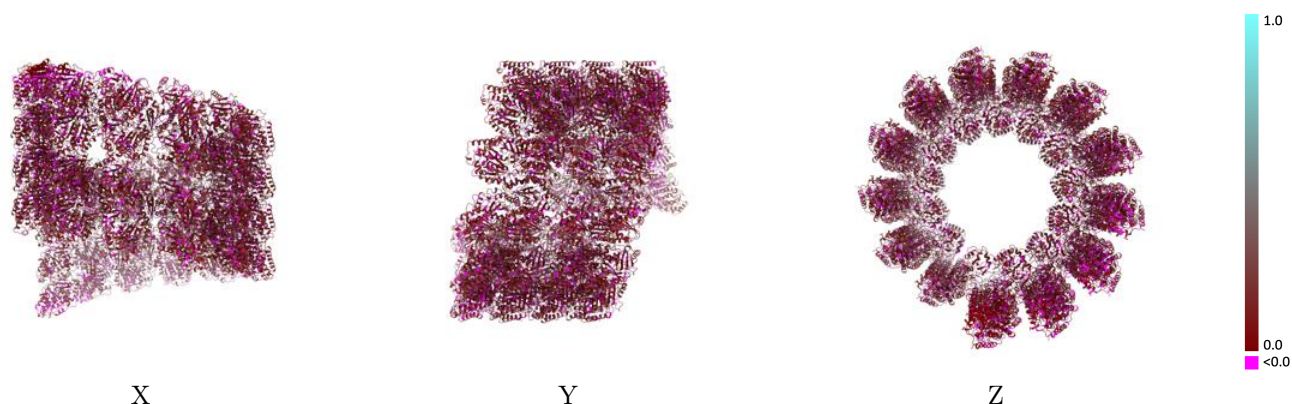
This section contains information regarding the fit between EMDB map EMD-26019 and PDB model 7TNS. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



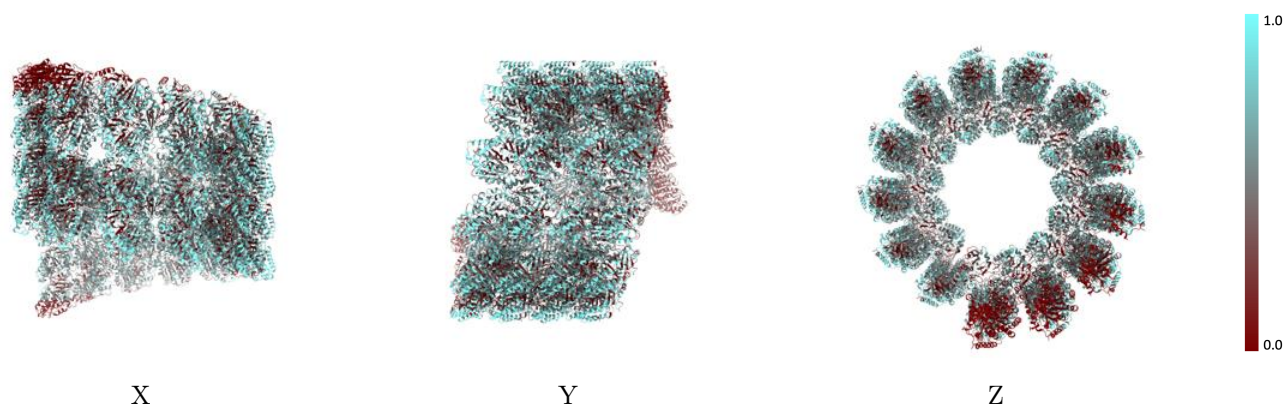
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



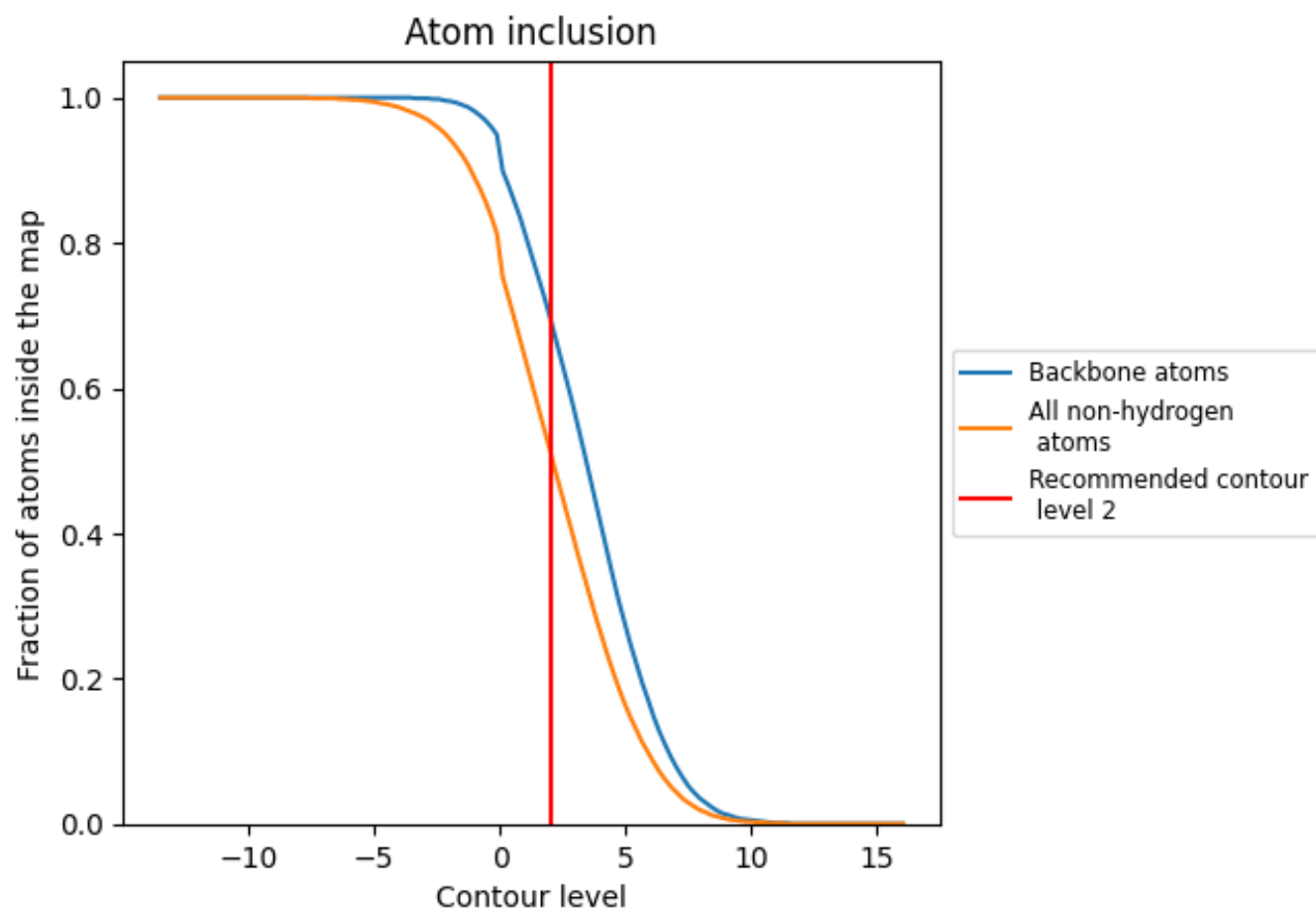
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 52% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5150	 0.1180
0	 0.2880	 0.1450
1	 0.3000	 0.1410
10	 0.3880	 0.1250
11	 0.3770	 0.1420
12	 0.3710	 0.1570
13	 0.3470	 0.1610
14	 0.2770	 0.1400
15	 0.3350	 0.1650
16	 0.2120	 0.1180
17	 0.3000	 0.1450
18	 0.0470	 0.0790
19	 0.1000	 0.0800
2	 0.3240	 0.1350
20	 0.0000	 0.0610
21	 0.1710	 0.0210
22	 0.3650	 0.1020
23	 0.3590	 0.1330
3	 0.3410	 0.1590
4	 0.3350	 0.1460
5	 0.3880	 0.1640
6	 0.3710	 0.1390
7	 0.3180	 0.1220
8	 0.3470	 0.1410
9	 0.3180	 0.1130
A0	 0.5410	 0.1270
A1	 0.5410	 0.1220
A2	 0.5450	 0.1240
A3	 0.3160	 0.0720
A4	 0.5640	 0.1300
A5	 0.5420	 0.1250
A6	 0.5610	 0.1270
A7	 0.4440	 0.0970
A8	 0.5680	 0.1290
A9	 0.5510	 0.1270



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
B0	 0.5640	 0.1260
B1	 0.4770	 0.0940
B2	 0.5620	 0.1280
B3	 0.5590	 0.1210
B4	 0.5620	 0.1260
B5	 0.5190	 0.1020
B6	 0.5520	 0.1200
B7	 0.5630	 0.1200
B8	 0.5570	 0.1190
B9	 0.5680	 0.1170
C0	 0.5670	 0.1310
C1	 0.5730	 0.1230
C2	 0.5620	 0.1300
C3	 0.5730	 0.1200
C4	 0.5620	 0.1310
C5	 0.5810	 0.1280
C6	 0.5520	 0.1250
C7	 0.5840	 0.1230
C8	 0.5470	 0.1270
C9	 0.5890	 0.1300
D0	 0.5540	 0.1270
D1	 0.5910	 0.1260
D2	 0.5270	 0.1210
D3	 0.5800	 0.1270
D4	 0.5520	 0.1280
D5	 0.5880	 0.1260
D6	 0.4660	 0.1050
D7	 0.5750	 0.1290
D8	 0.5500	 0.1300
D9	 0.5760	 0.1250
E0	 0.3190	 0.0770
E1	 0.5510	 0.1200
E2	 0.5540	 0.1280
E3	 0.5630	 0.1200
E4	 0.1930	 0.0440
E5	 0.5400	 0.1200
E6	 0.5510	 0.1250
E7	 0.5400	 0.1200
E8	 0.0500	 0.0060
E9	 0.5170	 0.1160
F0	 0.5540	 0.1250
F1	 0.5370	 0.1200

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
a	 0.4960	 0.1230
b	 0.4710	 0.1120
c	 0.4990	 0.1250
d	 0.5070	 0.1220
e	 0.5110	 0.1290
f	 0.5110	 0.1280
g	 0.5130	 0.1210
h	 0.5280	 0.1240
i	 0.5250	 0.1290
j	 0.5190	 0.1320
k	 0.5070	 0.1260
l	 0.5190	 0.1290
m	 0.5110	 0.1300
n	 0.5060	 0.1300
o	 0.4990	 0.1310
p	 0.4990	 0.1290
q	 0.4920	 0.1250
r	 0.4930	 0.1310
s	 0.4880	 0.1280
t	 0.4650	 0.1220
u	 0.4320	 0.1110
v	 0.4830	 0.1240
w	 0.3220	 0.0780
x	 0.4590	 0.1250
y	 0.3440	 0.1120