



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 02:02 AM UTC

PDB ID : 7TNQ / pdb_00007tnq
EMDB ID : EMD-26018
Title : The symmetry-released subpellicular microtubule map from detergent-extracted Toxoplasma cells
Authors : Sun, S.Y.; Pintilie, G.D.; Chen, M.
Deposited on : 2022-01-21
Resolution : 8.40 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:

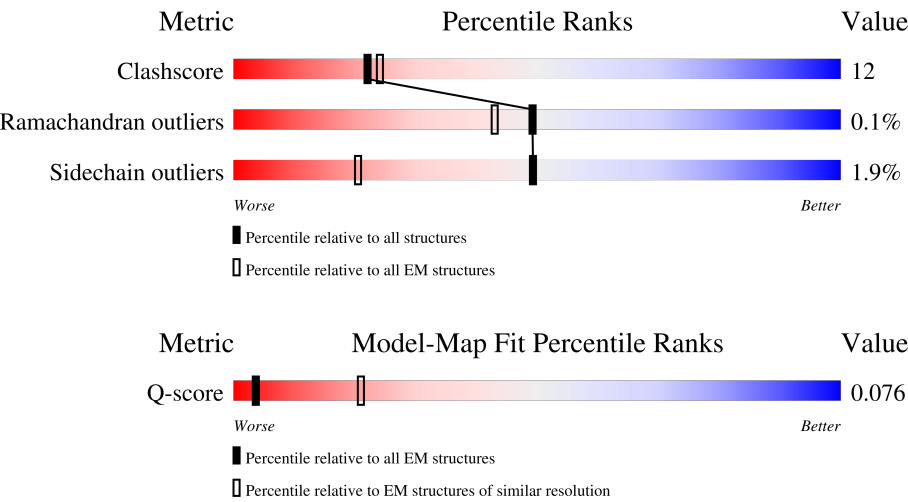
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.40 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	298 (7.90 - 8.90)

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	 5% 6% 94%
1	1	351	 6% 6% 94%
1	10	351	 6% 6% 94%
1	11	351	 6% 6% 94%

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Mol	Chain	Length	Quality of chain
1	12	351	
1	13	351	
1	14	351	
1	15	351	
1	16	351	
1	17	351	
1	18	351	
1	19	351	
1	2	351	
1	20	351	
1	21	351	
1	22	351	
1	23	351	
1	3	351	
1	4	351	
1	5	351	
1	6	351	
1	7	351	
1	8	351	
1	9	351	
2	A0	453	
2	A2	453	
2	A4	453	
2	A6	453	
2	A8	453	

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Mol	Chain	Length	Quality of chain
2	B0	453	51% 74% 18% 6%
2	B2	453	53% 74% 19% 6%
2	B4	453	49% 71% 23% 6%
2	B6	453	52% 75% 19% 6%
2	B8	453	47% 71% 23% 6%
2	C0	453	53% 70% 24% 6%
2	C2	453	46% 69% 25% 6%
2	C4	453	54% 64% 28% 6%
2	C6	453	48% 64% 28% 6%
2	C8	453	57% 70% 24% 6%
2	D0	453	51% 70% 23% 6%
2	D2	453	59% 70% 22% 6%
2	D4	453	53% 68% 24% 6%
2	D6	453	60% 76% 17% 6%
2	D8	453	51% 72% 20% 6%
2	E0	453	65% 75% 18% 6%
2	E2	453	49% 75% 18% 6%
2	E4	453	76% 74% 19% 6%
2	E6	453	45% 73% 21% 6%
2	E8	453	83% 71% 24% 6%
2	F0	453	49% 69% 25% 6%
3	A1	449	51% 69% 26% 5%
3	A3	449	67% 75% 20% 5%
3	A5	449	47% 68% 25% 5%
3	A7	449	60% 76% 17% 5%

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Mol	Chain	Length	Quality of chain
3	A9	449	49% 72% 21% 5%
3	B1	449	56% 75% 19% 5%
3	B3	449	49% 73% 20% 5%
3	B5	449	53% 73% 20% 5%
3	B7	449	40% 75% 19% 5%
3	B9	449	51% 73% 20% 5%
3	C1	449	40% 68% 25% 5%
3	C3	449	46% 69% 25% 5%
3	C5	449	45% 70% 23% 5%
3	C7	449	48% 70% 23% 5%
3	C9	449	51% 68% 25% 5%
3	D1	449	55% 70% 23% 5%
3	D3	449	54% 66% 27% 5%
3	D5	449	55% 62% 29% 5%
3	D7	449	53% 70% 23% 5%
3	D9	449	50% 69% 24% 5%
3	E1	449	46% 74% 20% 5%
3	E3	449	43% 74% 19% 5%
3	E5	449	45% 70% 24% 5%
3	E7	449	40% 69% 24% 5%
3	E9	449	53% 71% 23% 5%
3	F1	449	43% 65% 28% 5%
4	a	220	43% 45% 22% 32%
4	b	220	48% 48% 19% 32%
4	c	220	41% 65% 25% 9%

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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	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	
5	k	189	
5	l	189	
5	w	189	
5	x	189	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 213168 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		

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

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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		

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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

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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	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		

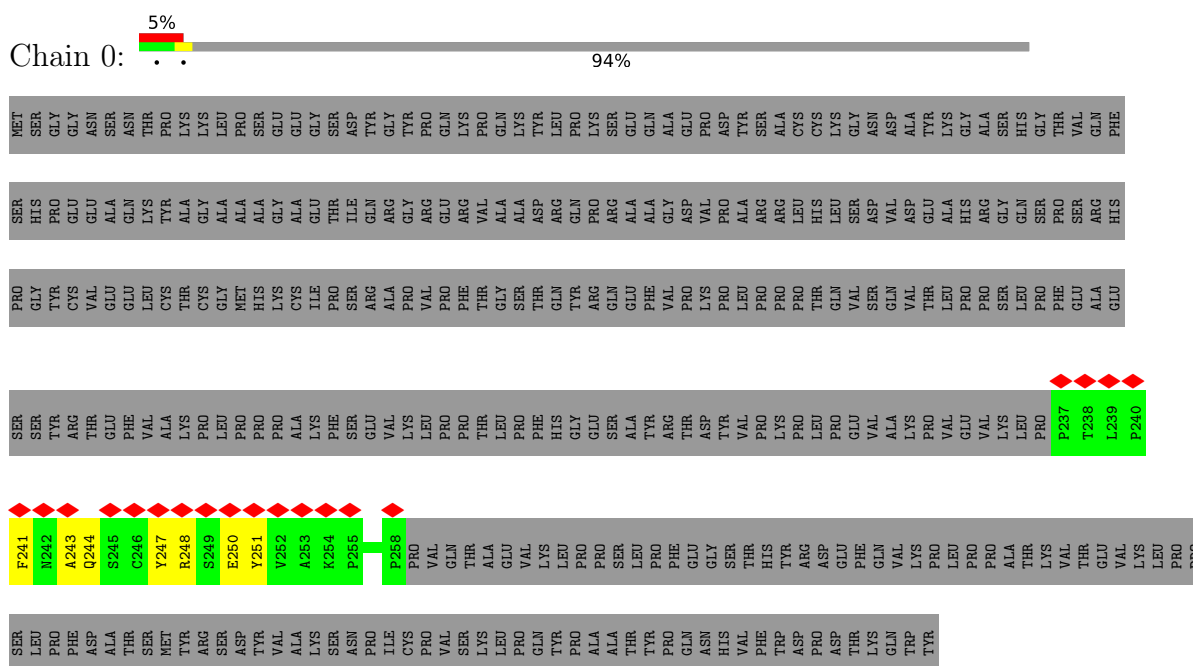
- Molecule 5 is a protein called PDI family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	k	139	Total	C	N	O	S	0	0
			1140	738	203	195	4		
5	l	139	Total	C	N	O	S	0	0
			1140	738	203	195	4		
5	w	143	Total	C	N	O	S	0	0
			1172	755	207	205	5		
5	x	143	Total	C	N	O	S	0	0
			1172	755	207	205	5		

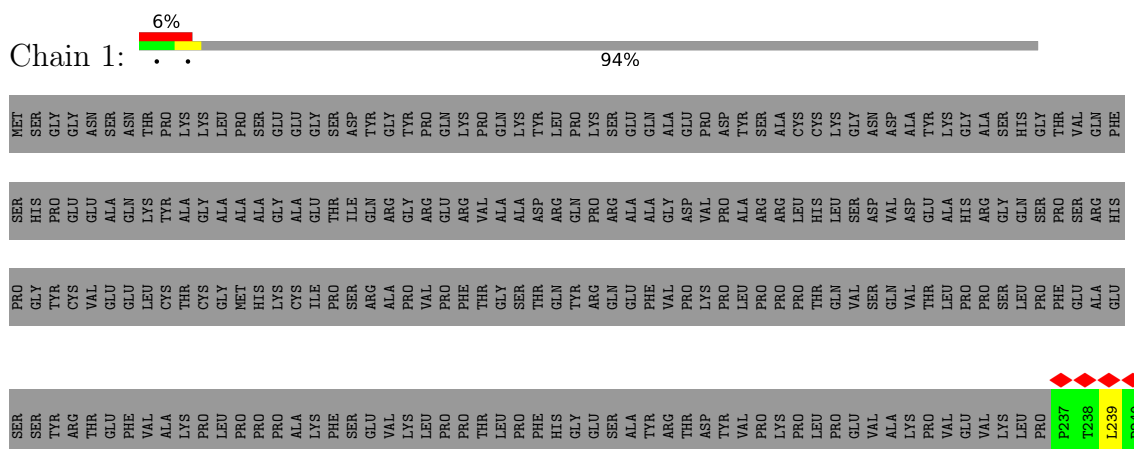
3 Residue-property plots

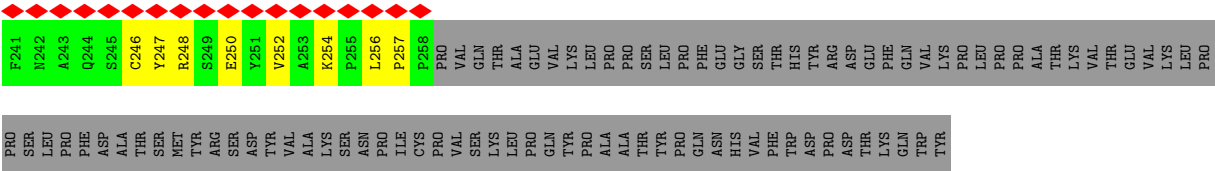
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

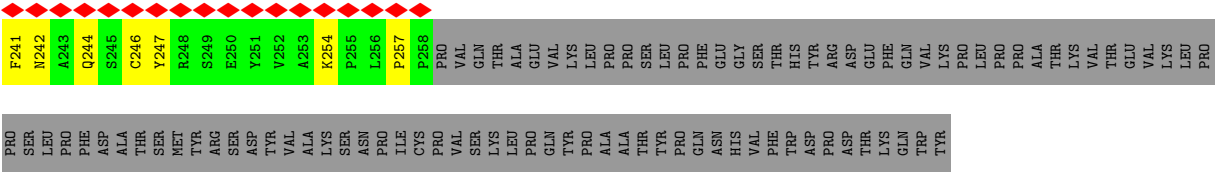
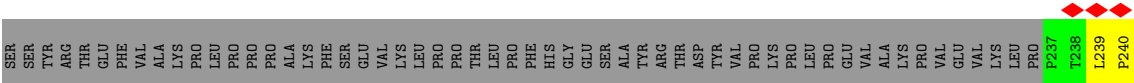
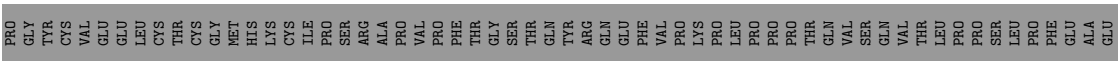
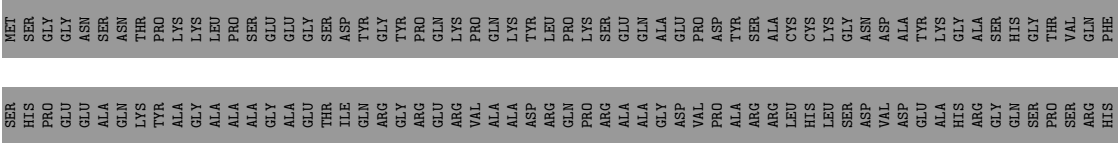


- Molecule 1: Microtubule associated protein SPM1

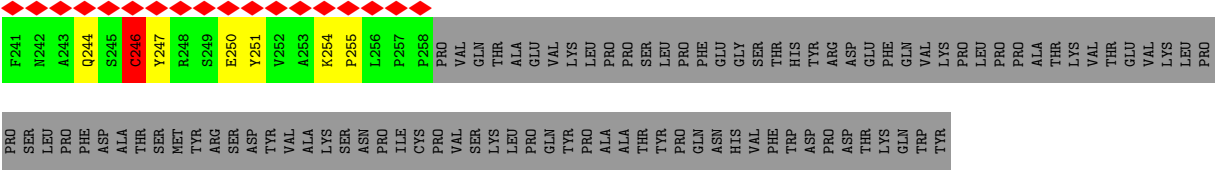
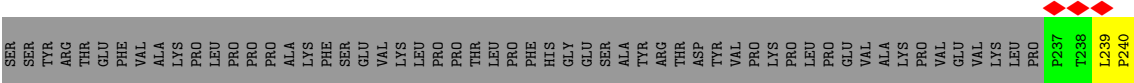
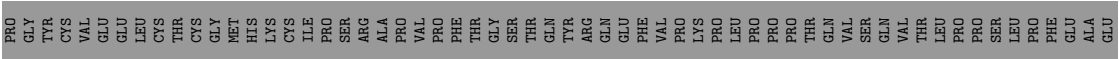
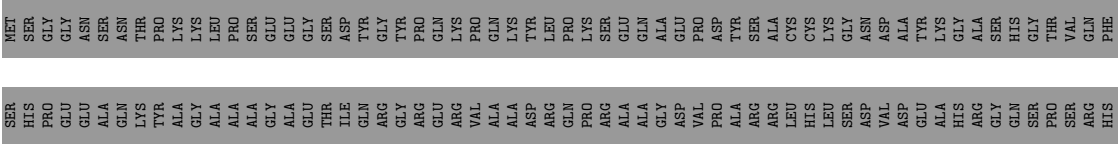




• Molecule 1: Microtubule associated protein SPM1

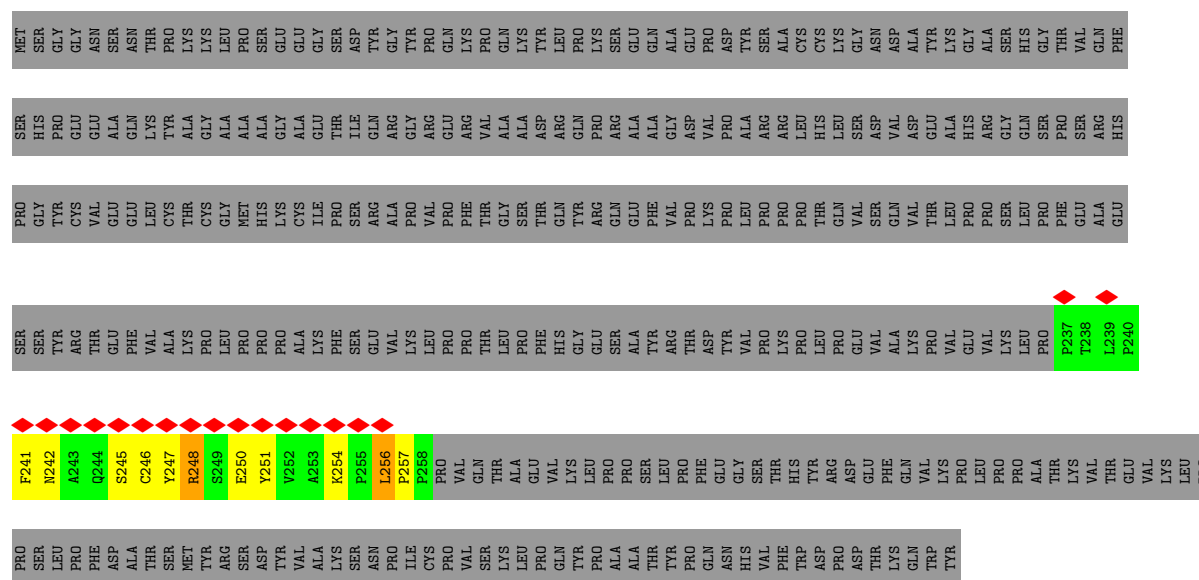


• Molecule 1: Microtubule associated protein SPM1

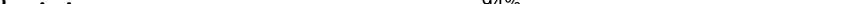


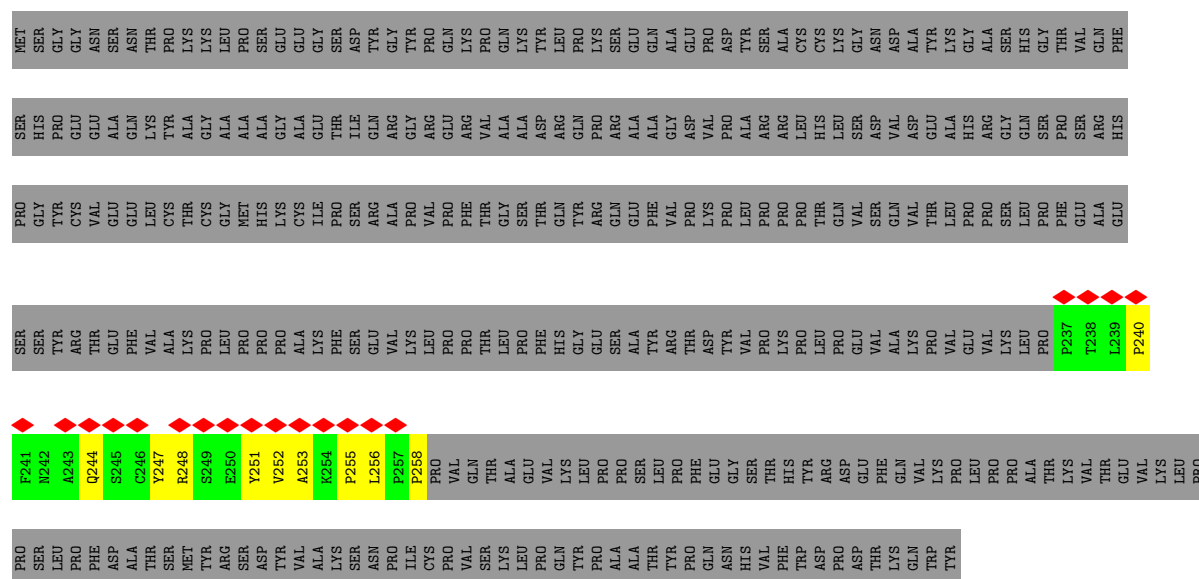
• Molecule 1: Microtubule associated protein SPM1

Chain 12: 5% 94%

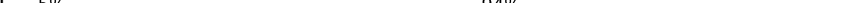


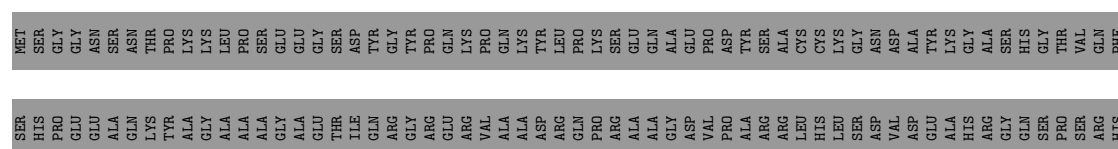
- Molecule 1: Microtubule associated protein SPM1

Chain 13:  5% 94%



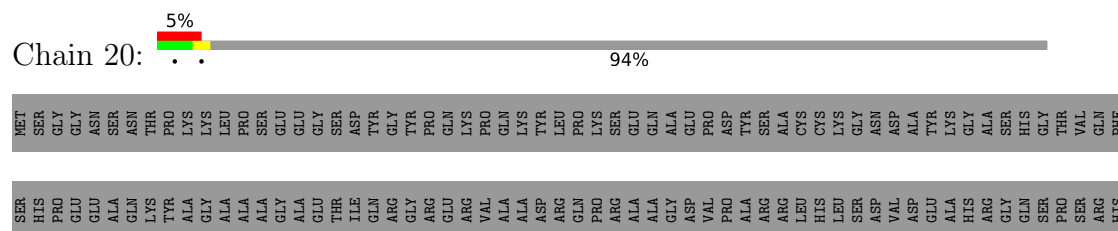
- Molecule 1: Microtubule associated protein SPM1

Chain 14:  6%
5% 94%



- Molecule 1: Microtubule associated protein SPM1

- Molecule 1: Microtubule associated protein SPM1

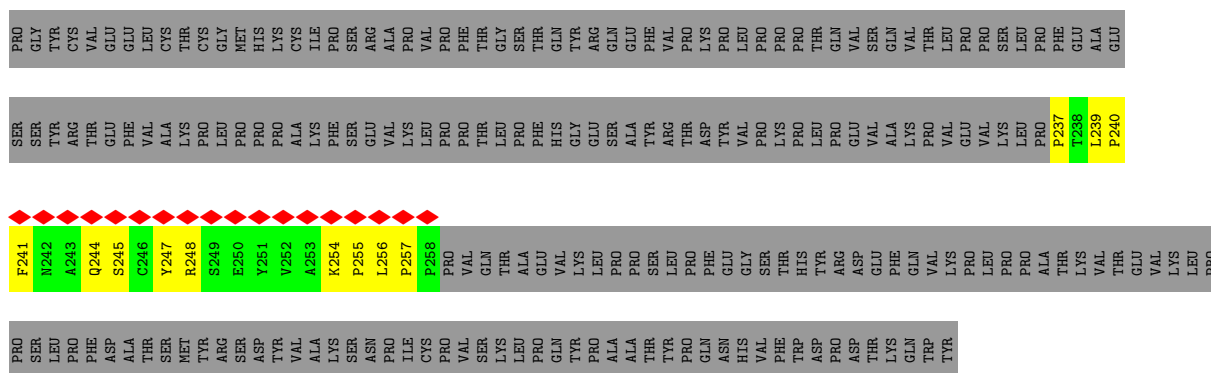


- Molecule 1: Microtubule associated protein SPM1

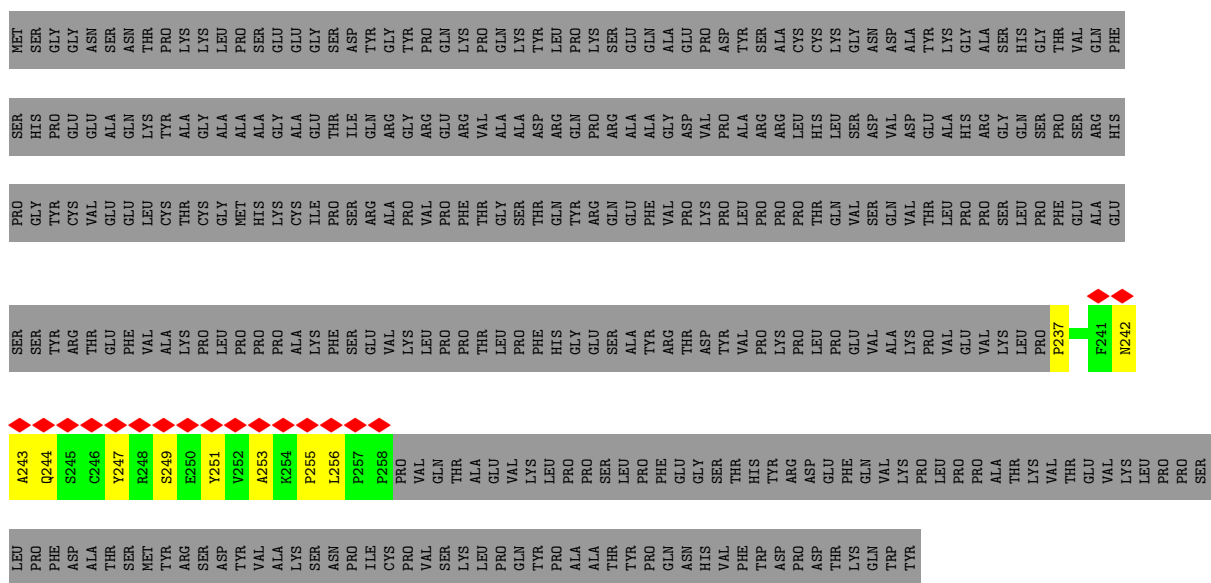
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- Molecule 1: Microtubule associated protein SPM1

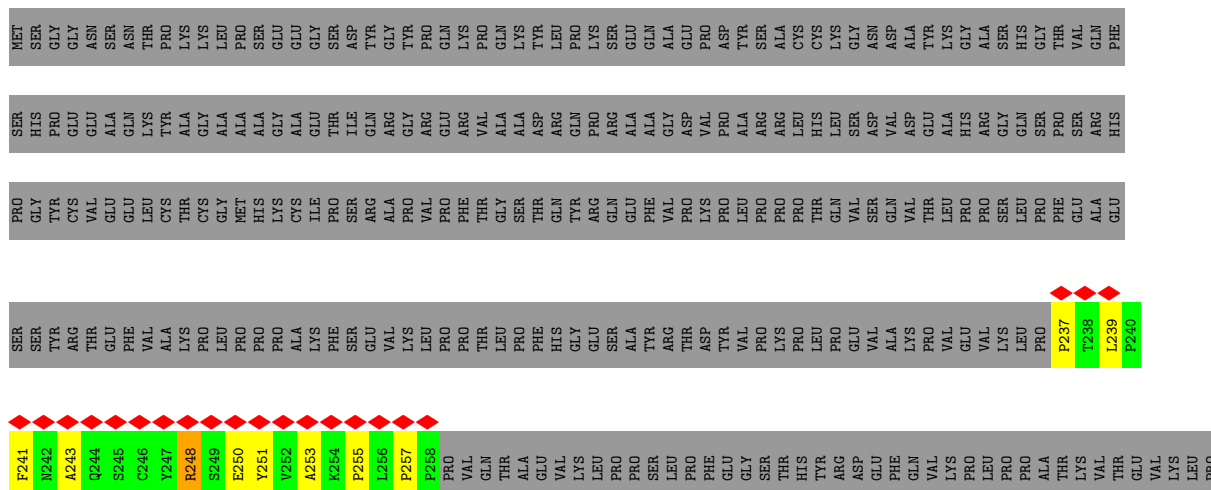
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- Molecule 1: Microtubule associated protein SPM1



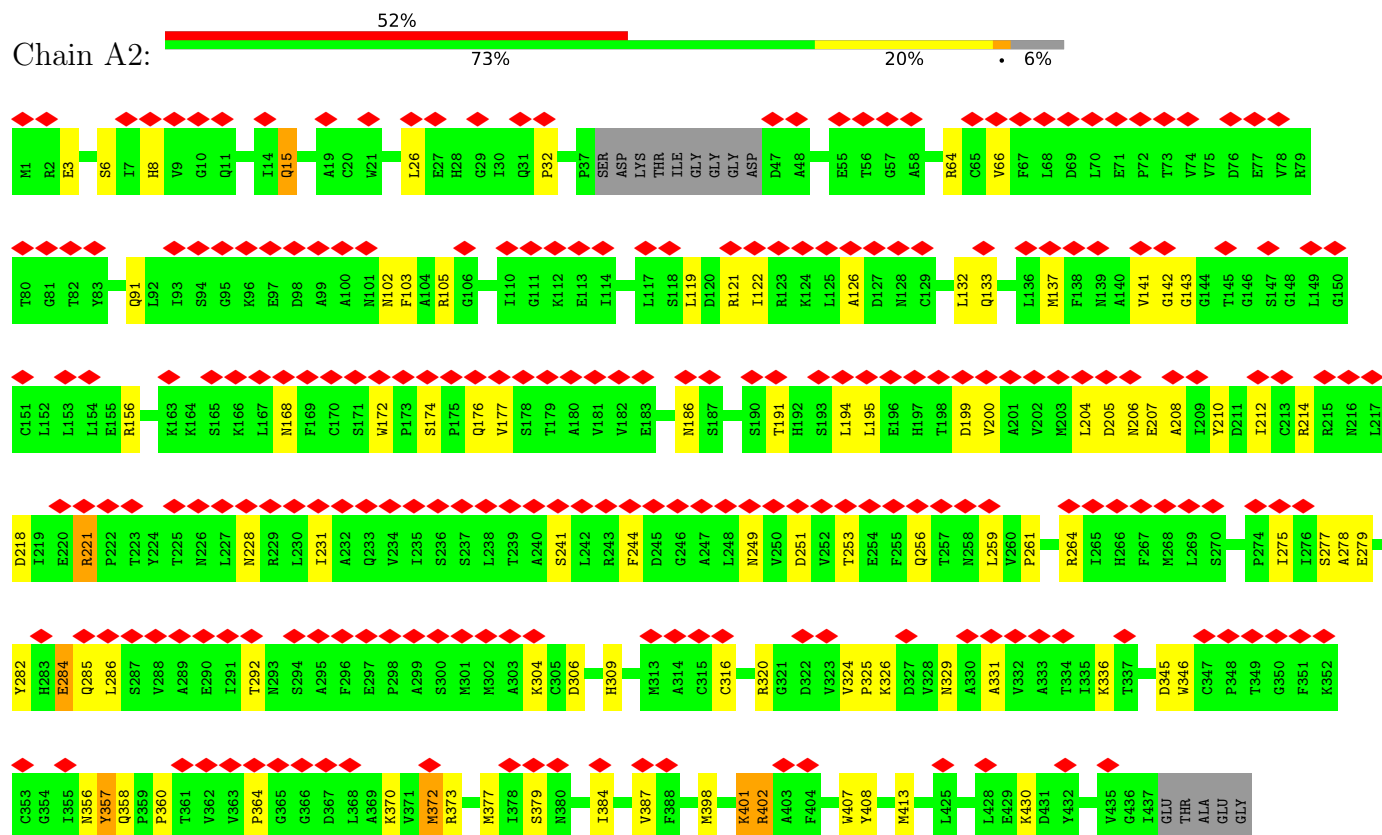
- Molecule 1: Microtubule associated protein SPM1



GLU
TYR

• Molecule 2: Tubulin alpha chain

Chain A2:

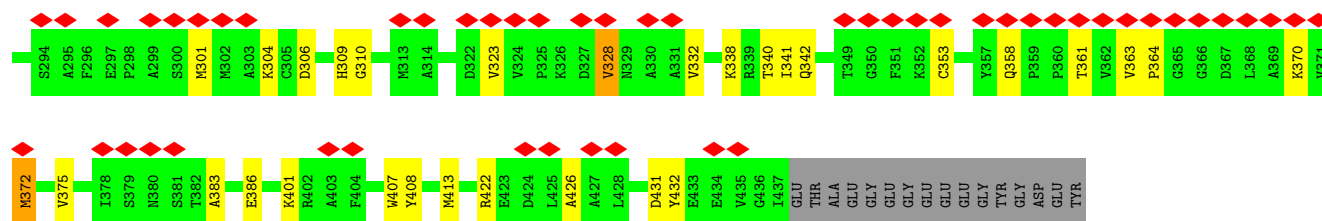


GLU
GLY
GLU
GLU
GLU
GLU
TYR
GLY
ASP
GLU
TYR

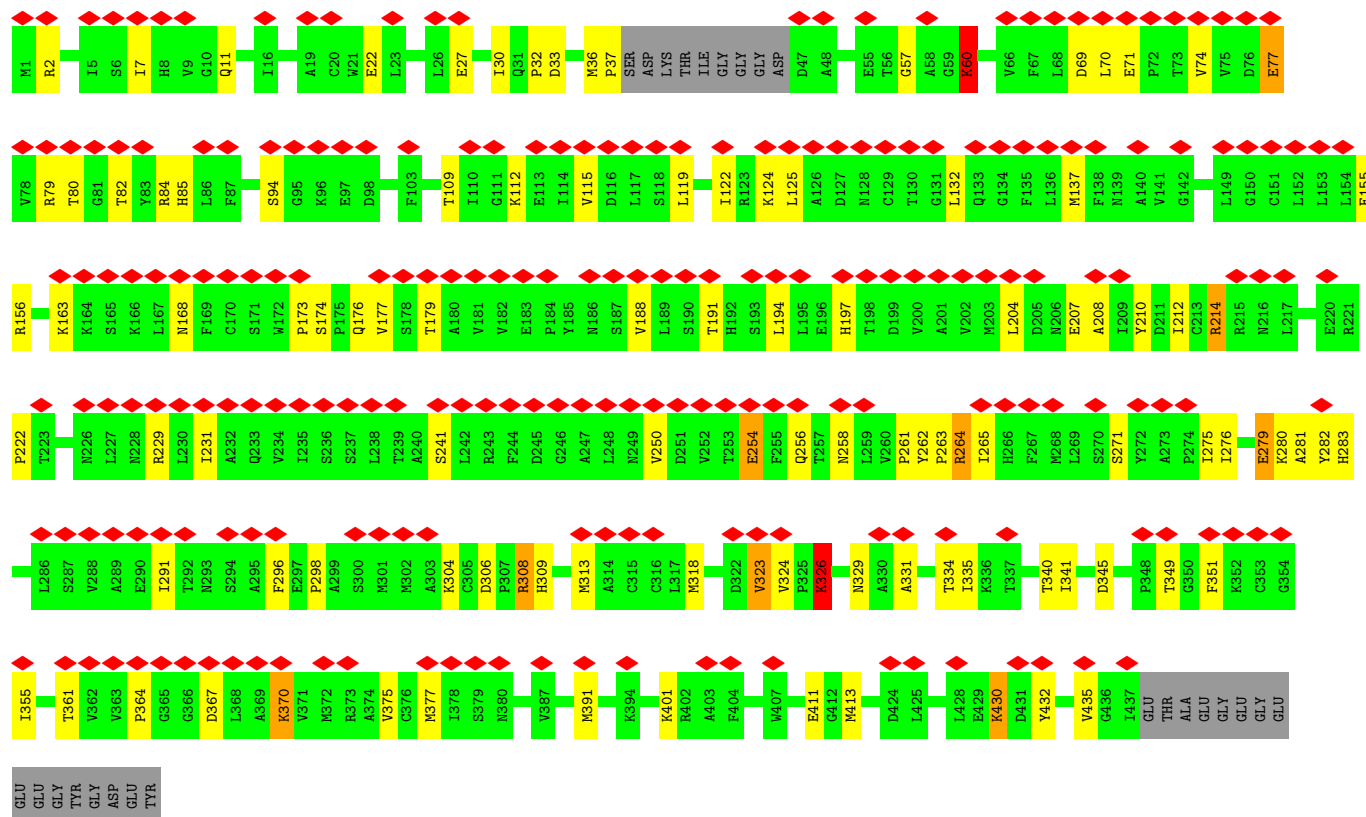
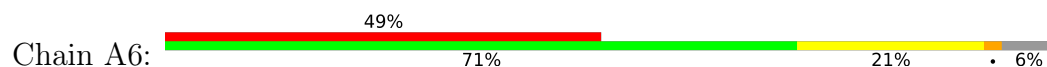
• Molecule 2: Tubulin alpha chain

Chain A4:

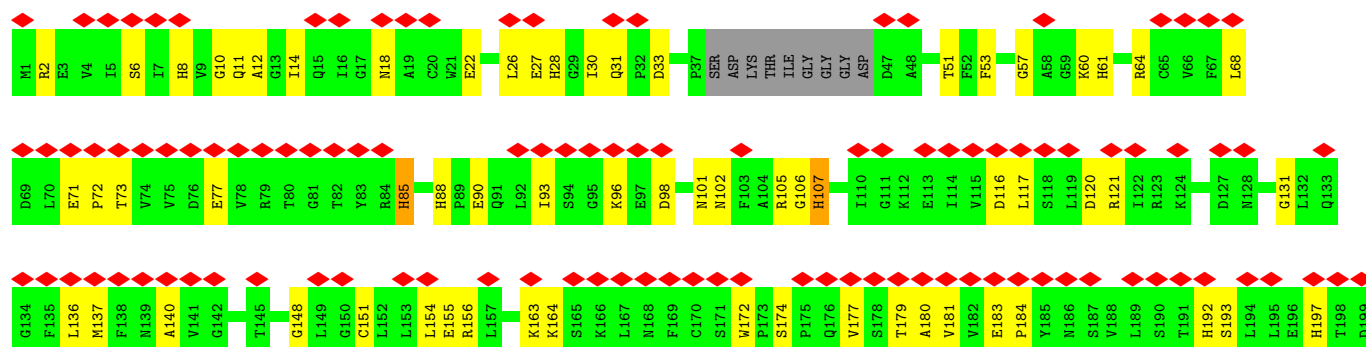


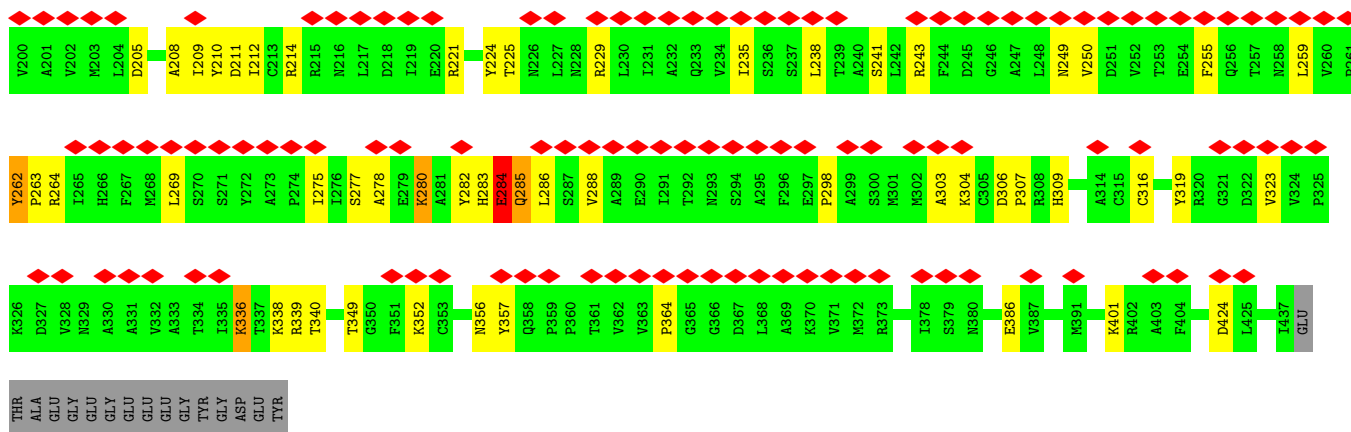


• Molecule 2: Tubulin alpha chain

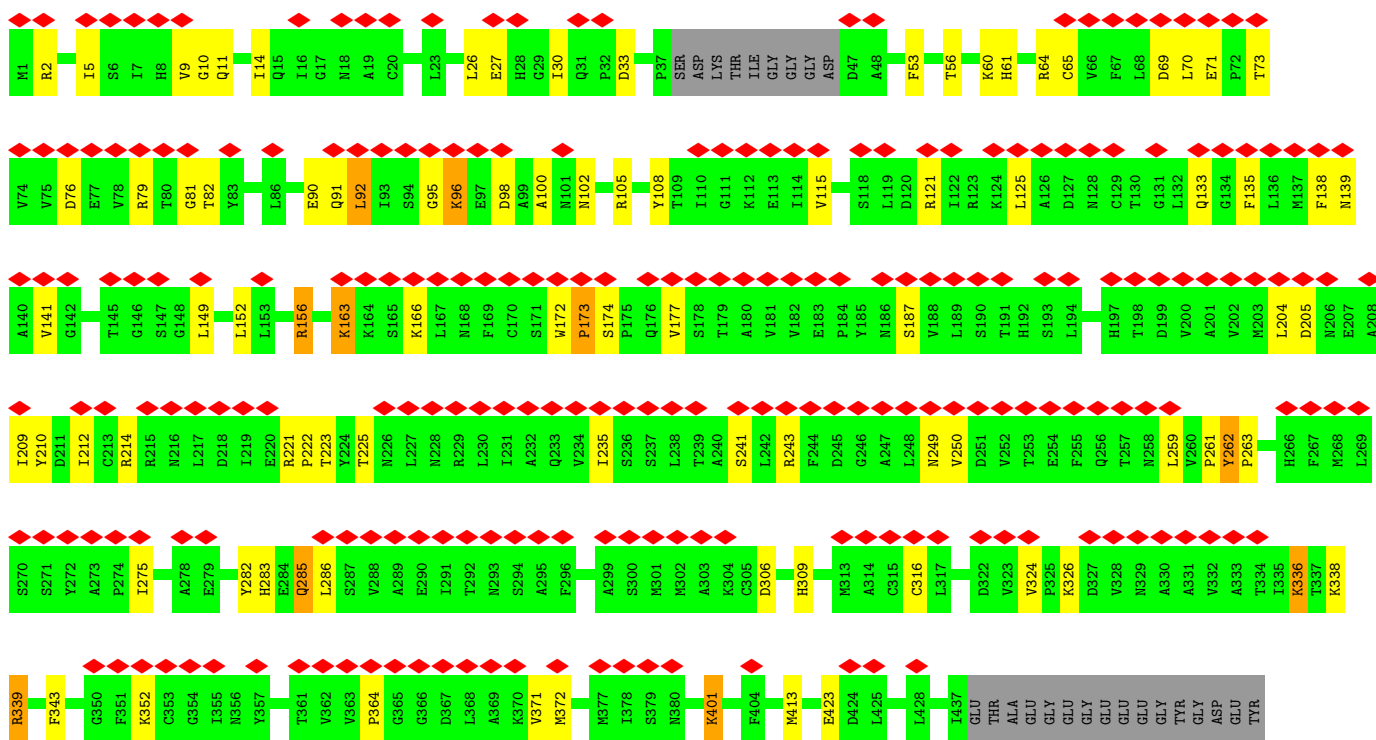
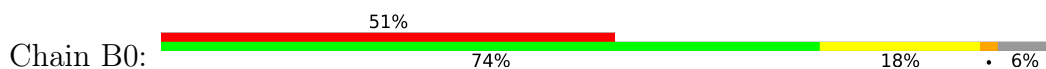


• Molecule 2: Tubulin alpha chain

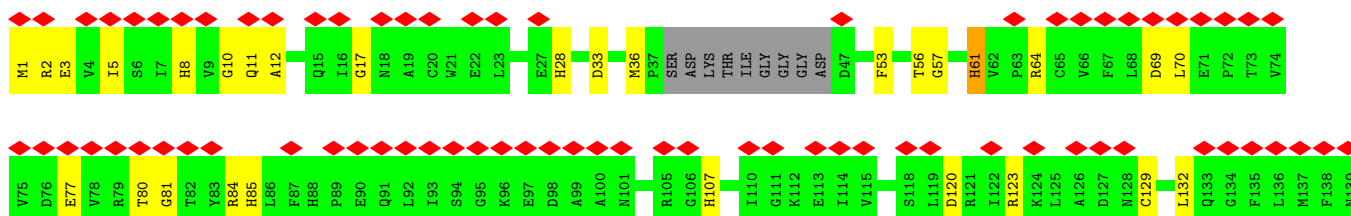
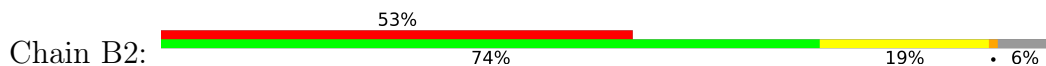


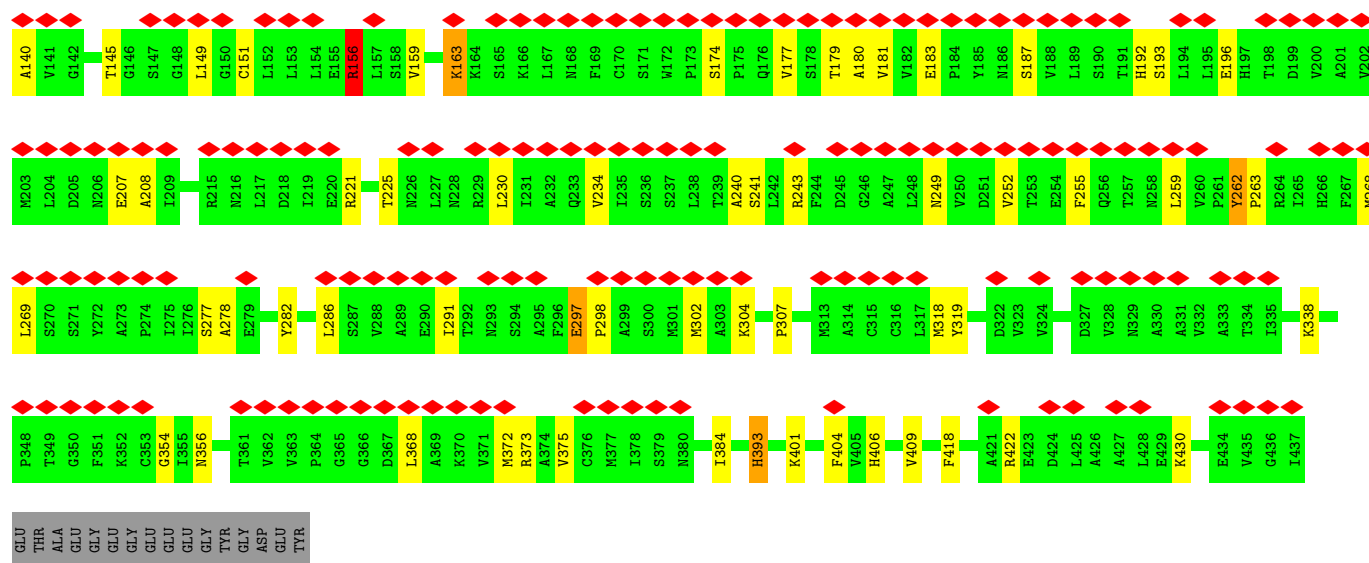


• Molecule 2: Tubulin alpha chain



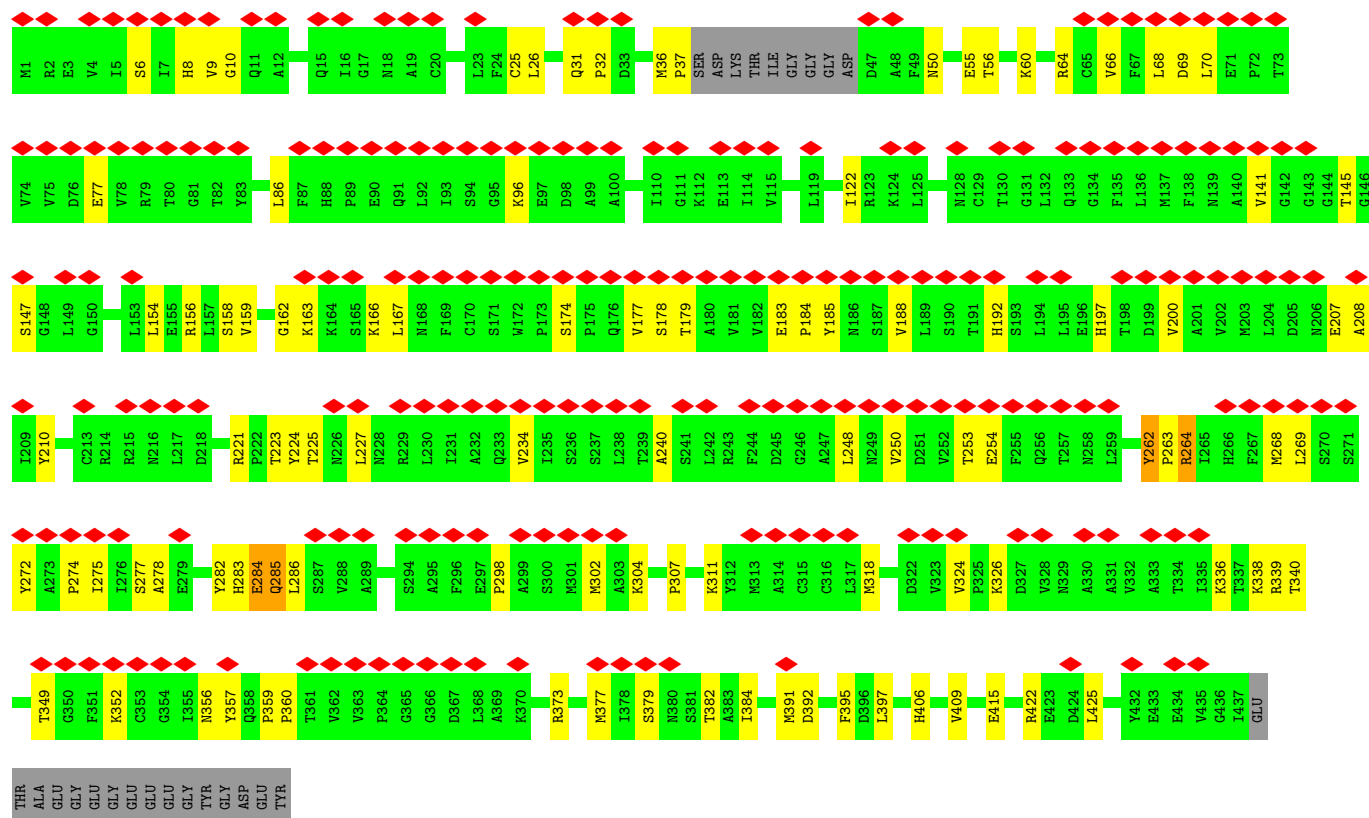
• Molecule 2: Tubulin alpha chain





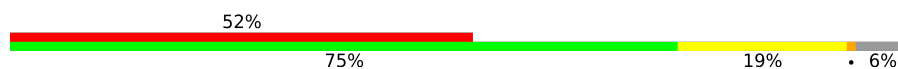
• Molecule 2: Tubulin alpha chain

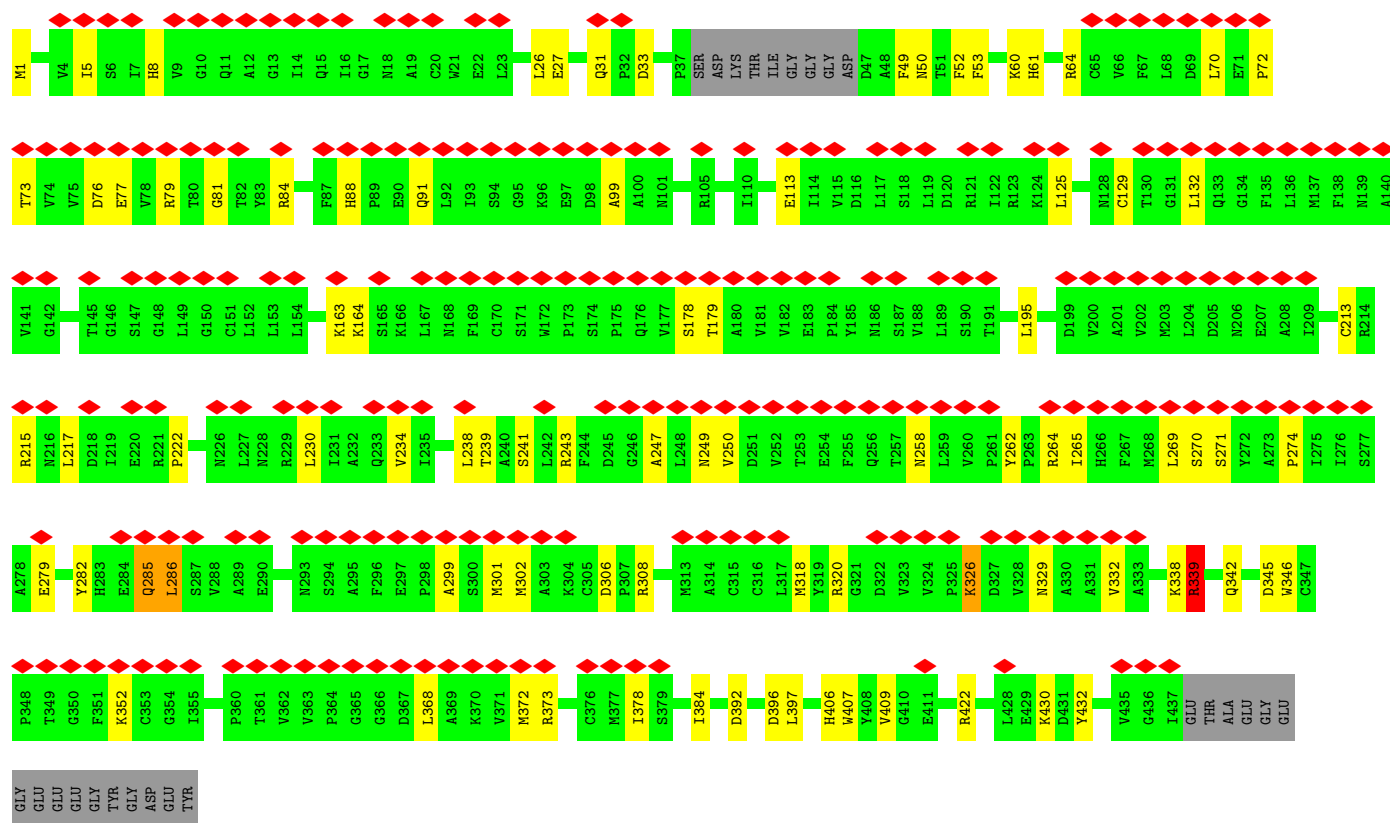
Chain B4:



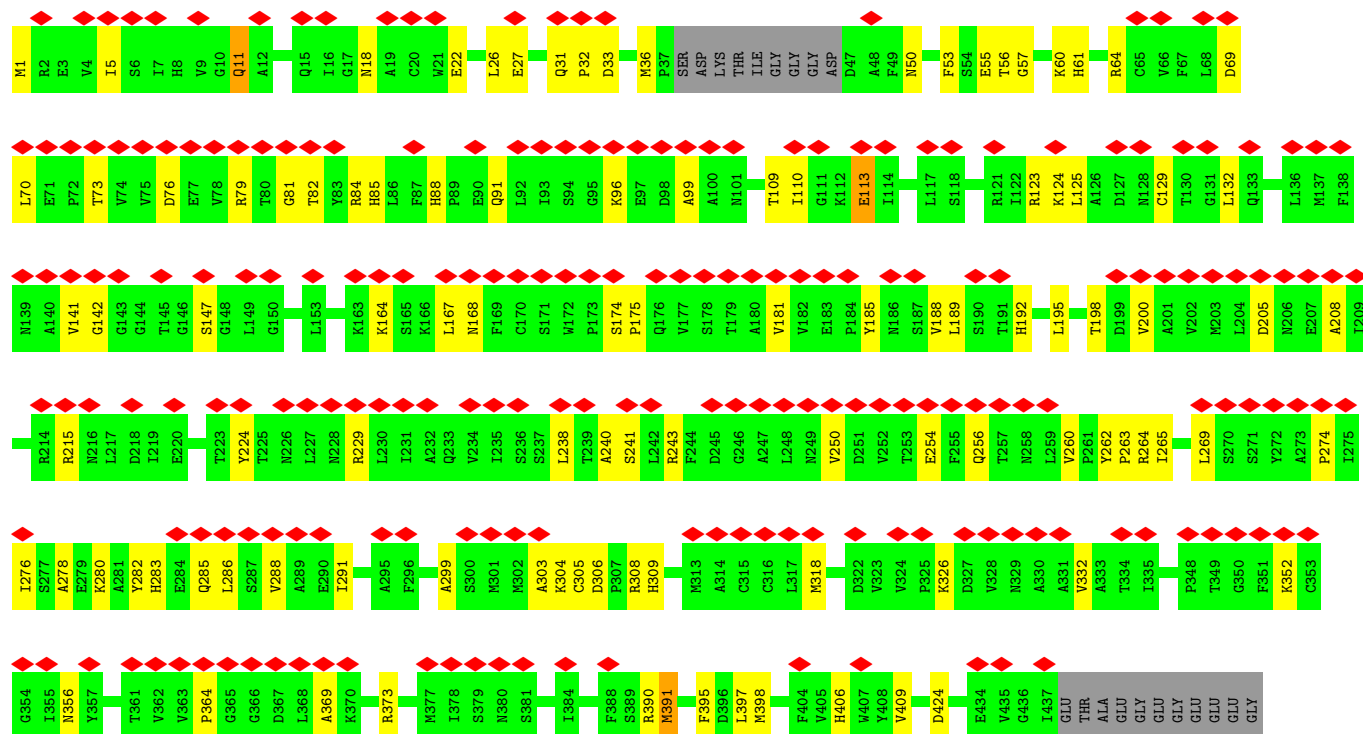
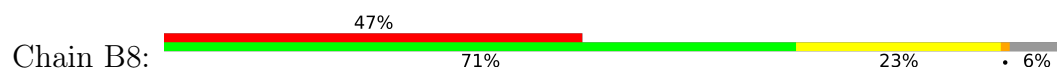
• Molecule 2: Tubulin alpha chain

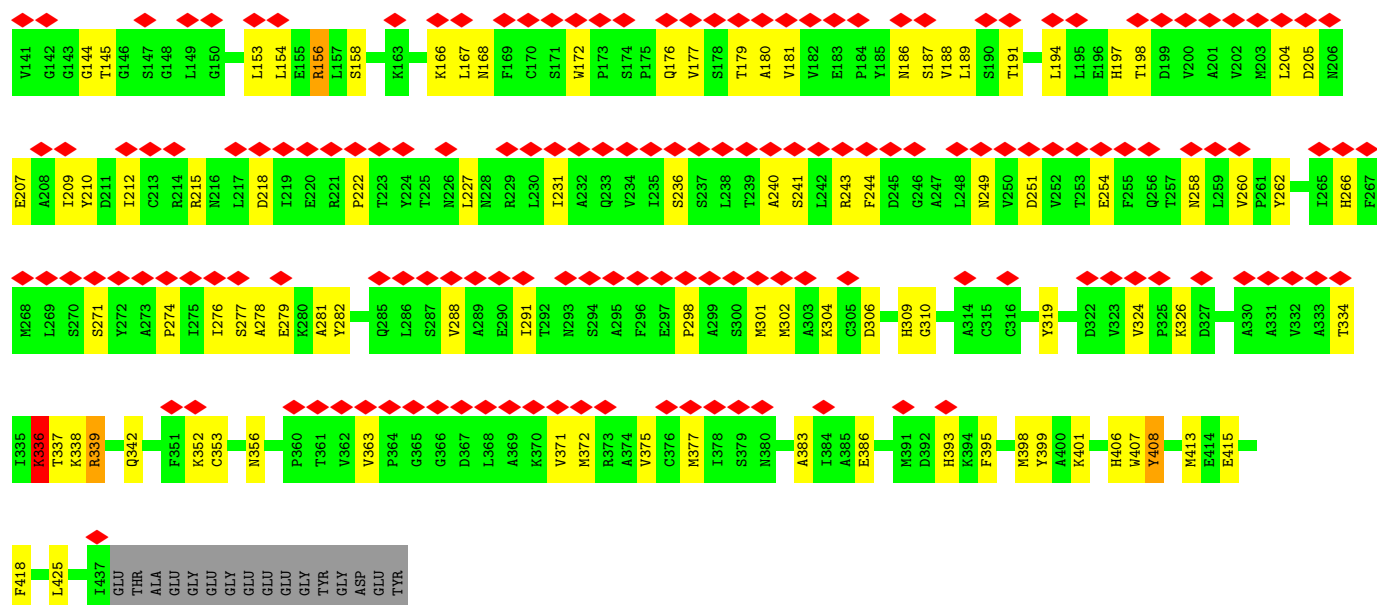
Chain B6:



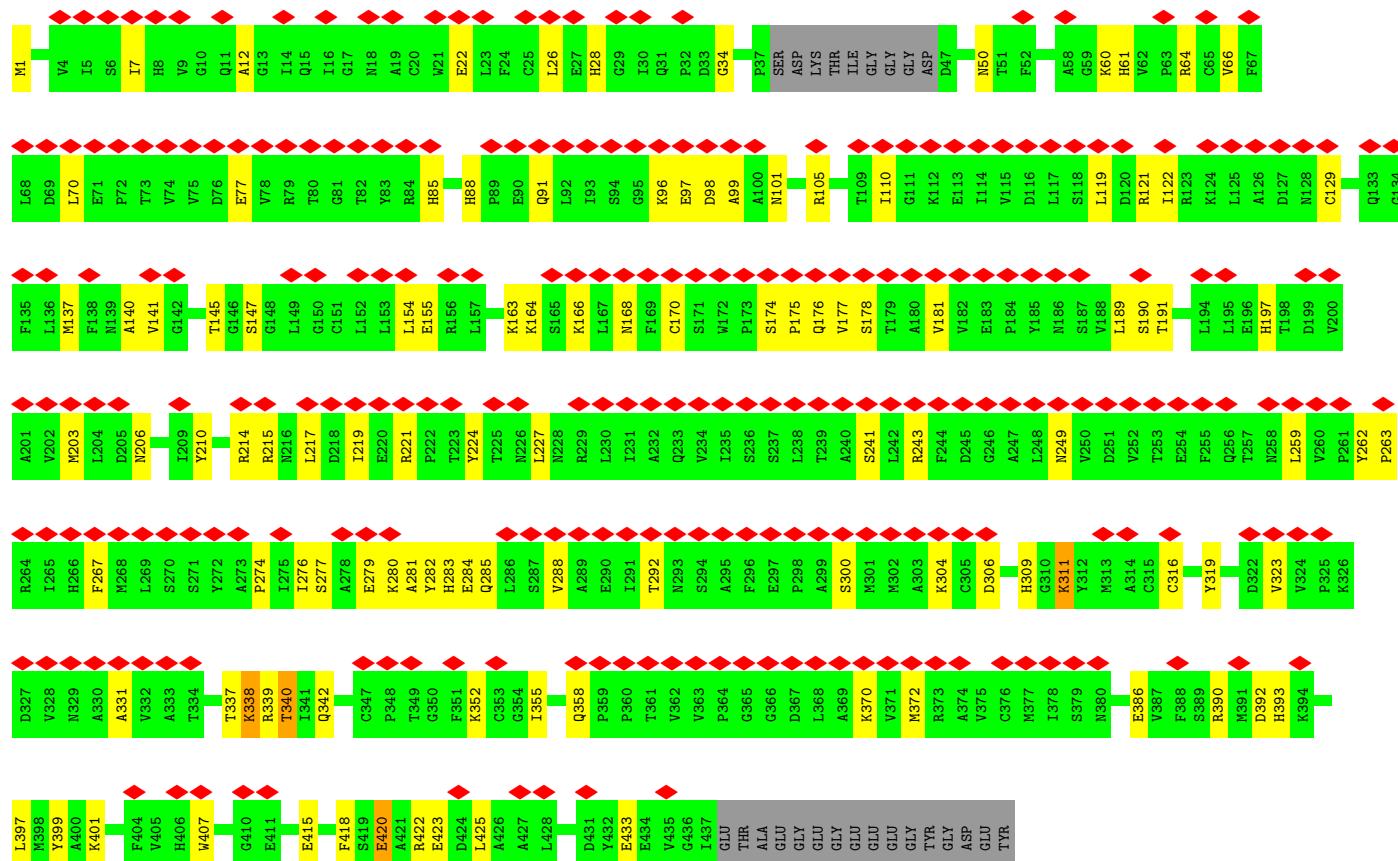


• Molecule 2: Tubulin alpha chain



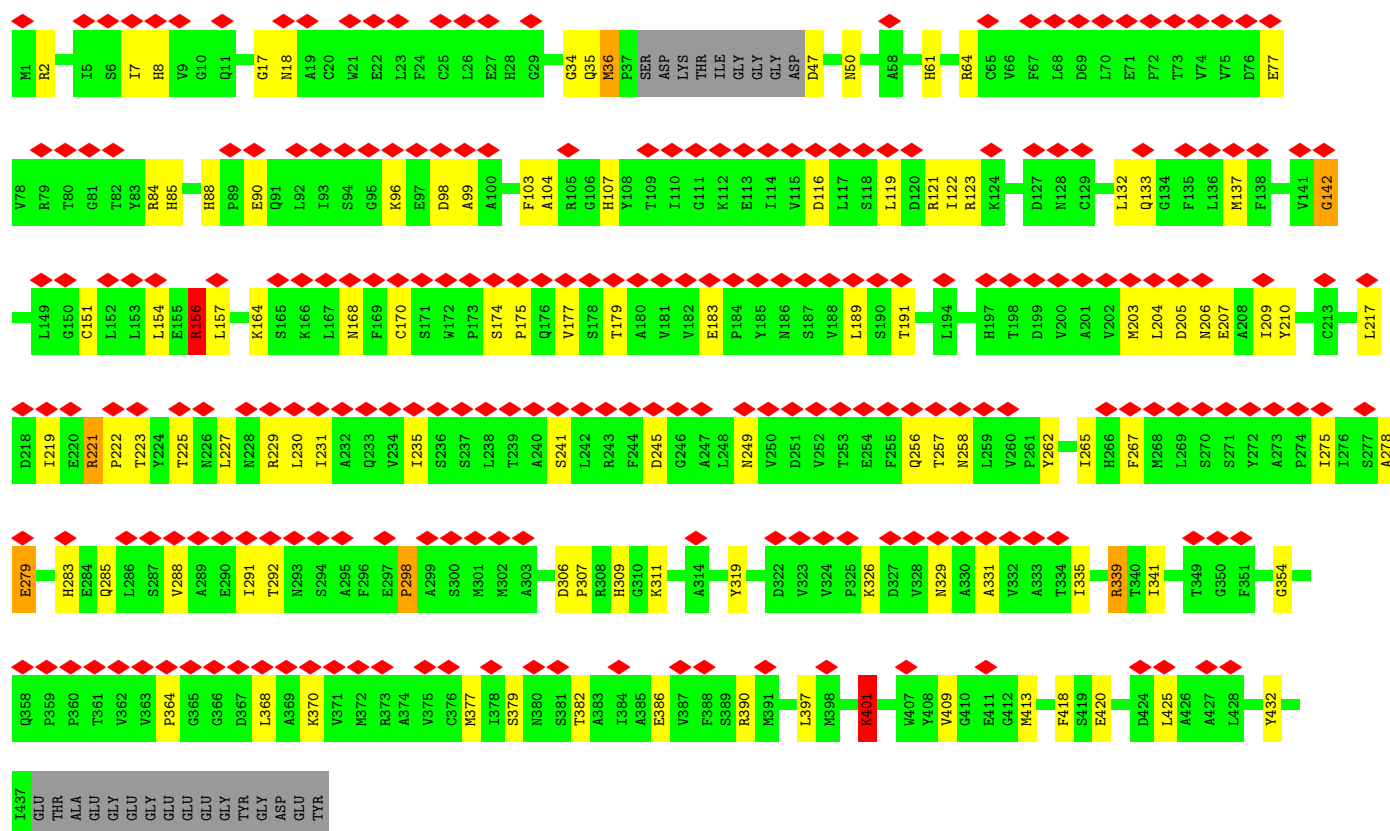


• Molecule 2: Tubulin alpha chain



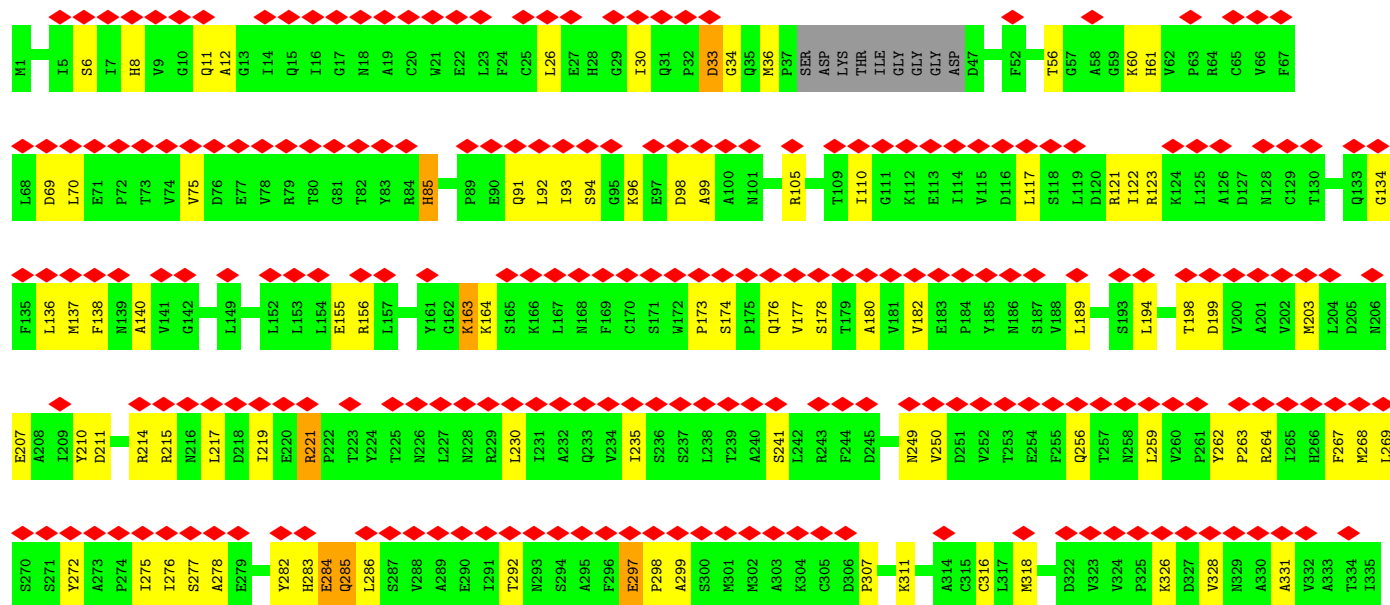
• Molecule 2: Tubulin alpha chain

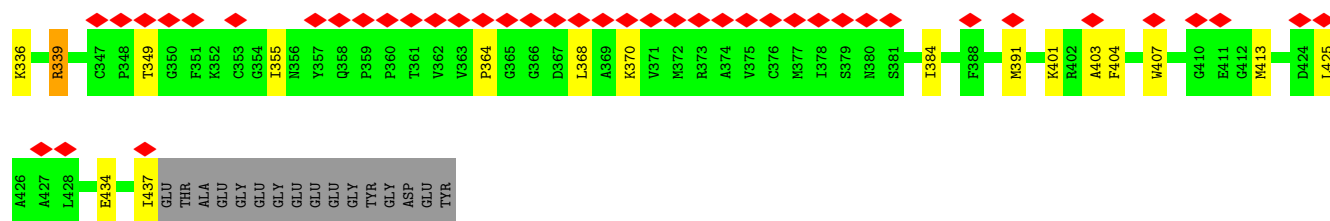
Chain D0: 



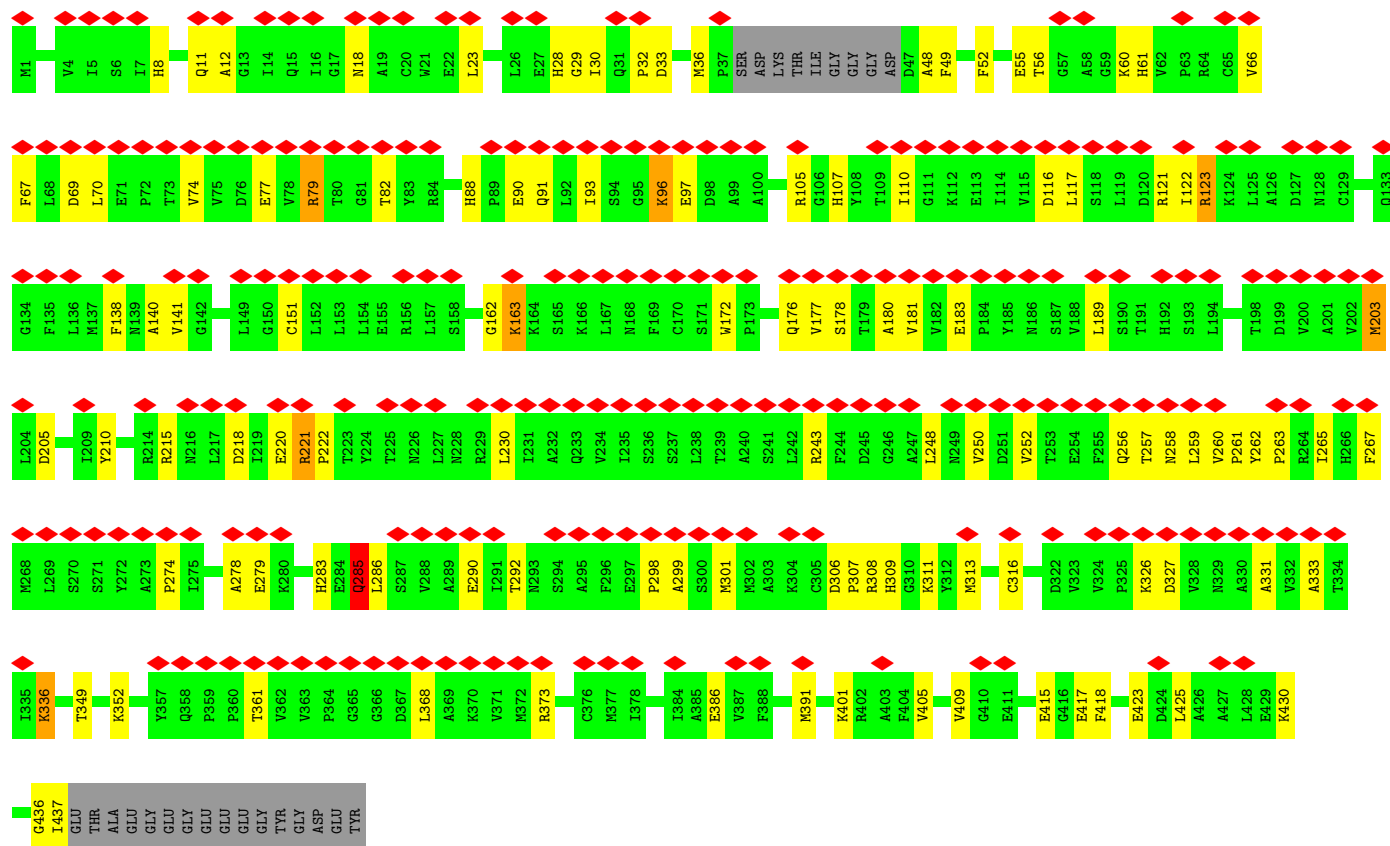
• Molecule 2: Tubulin alpha chain

Chain D2: 

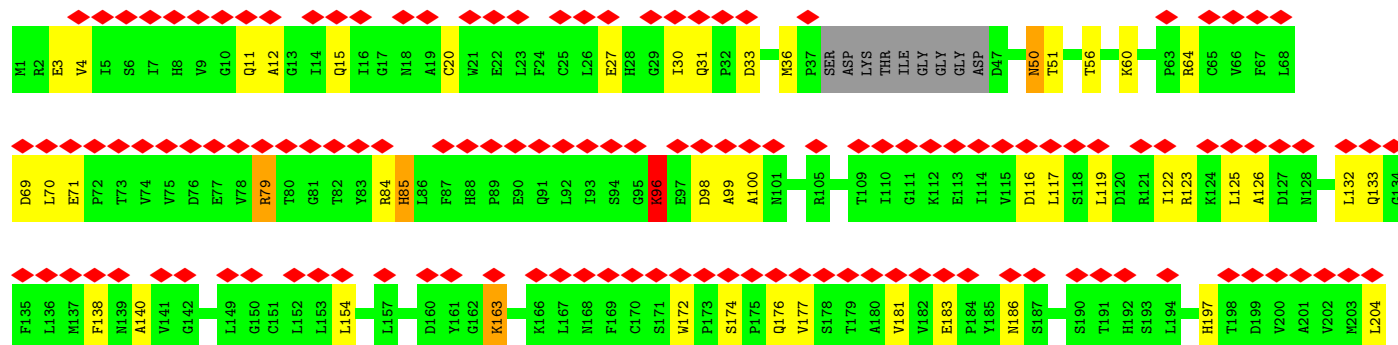
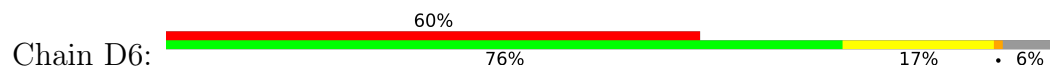


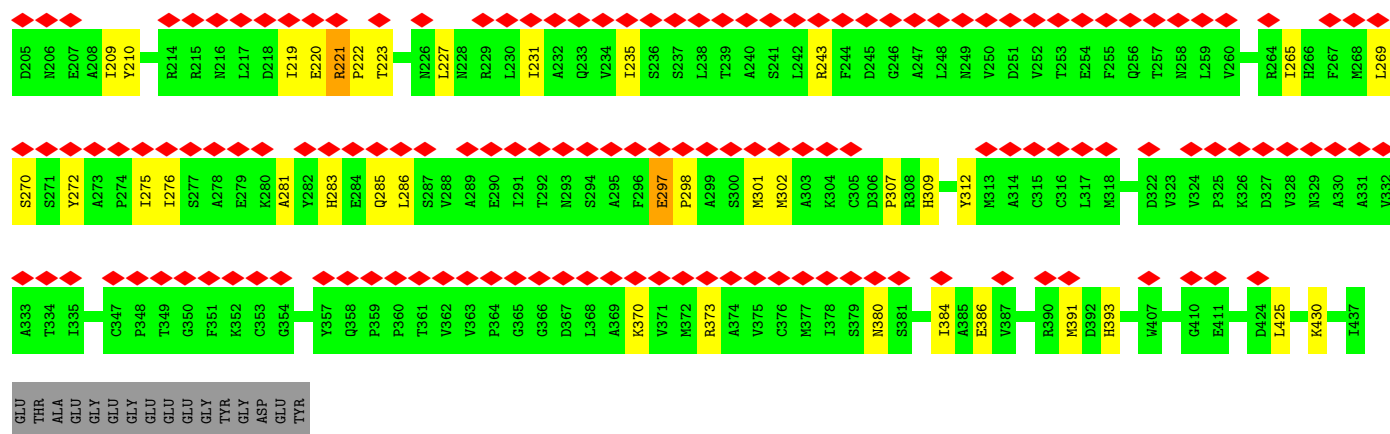


• Molecule 2: Tubulin alpha chain

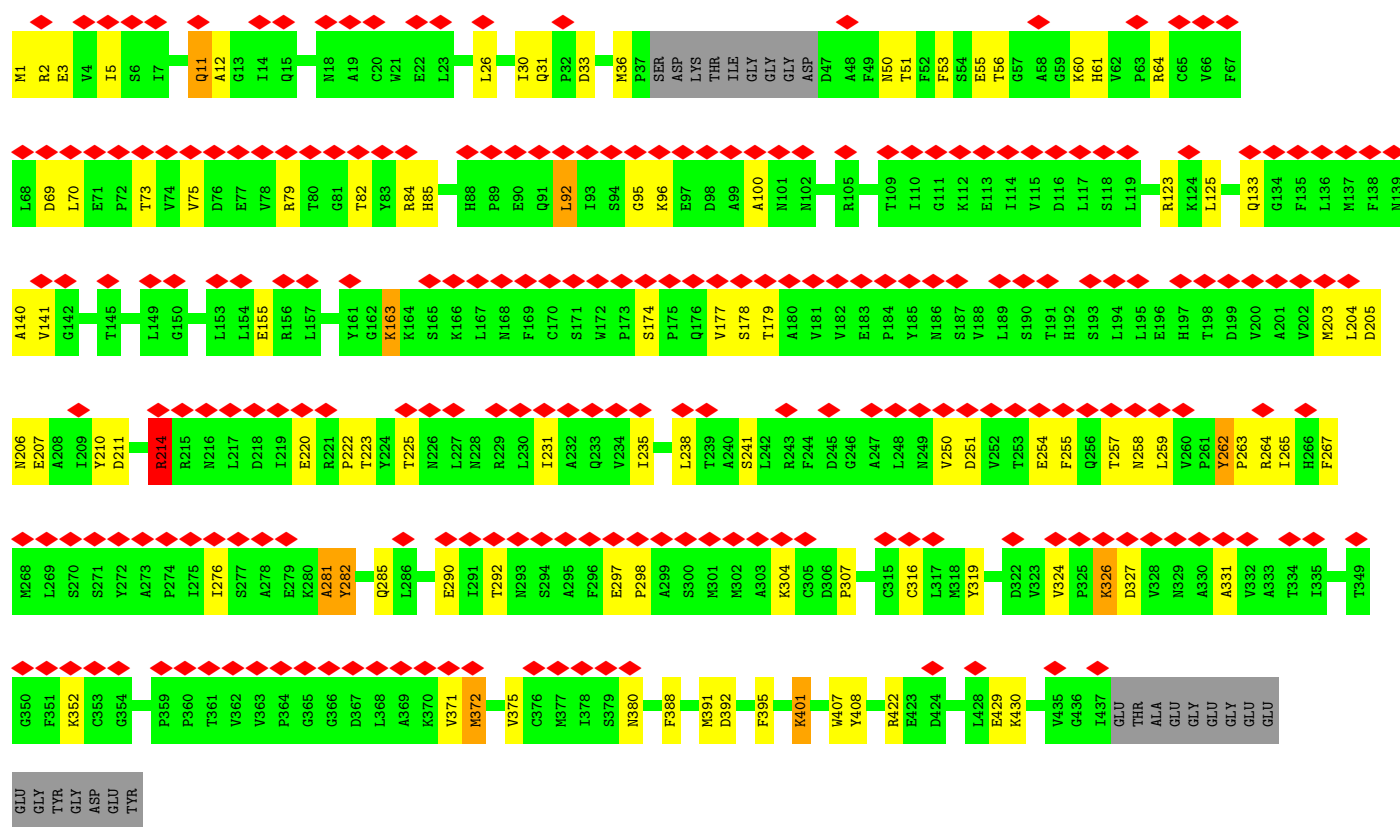
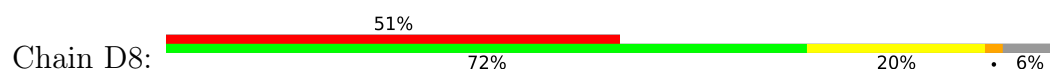


• Molecule 2: Tubulin alpha chain

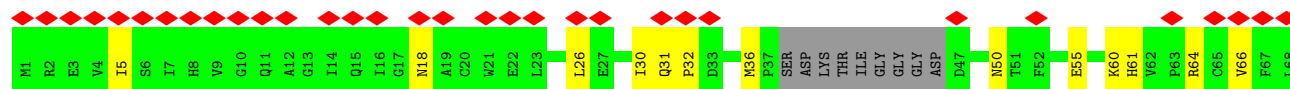
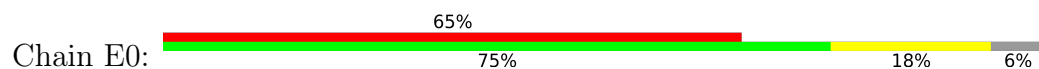


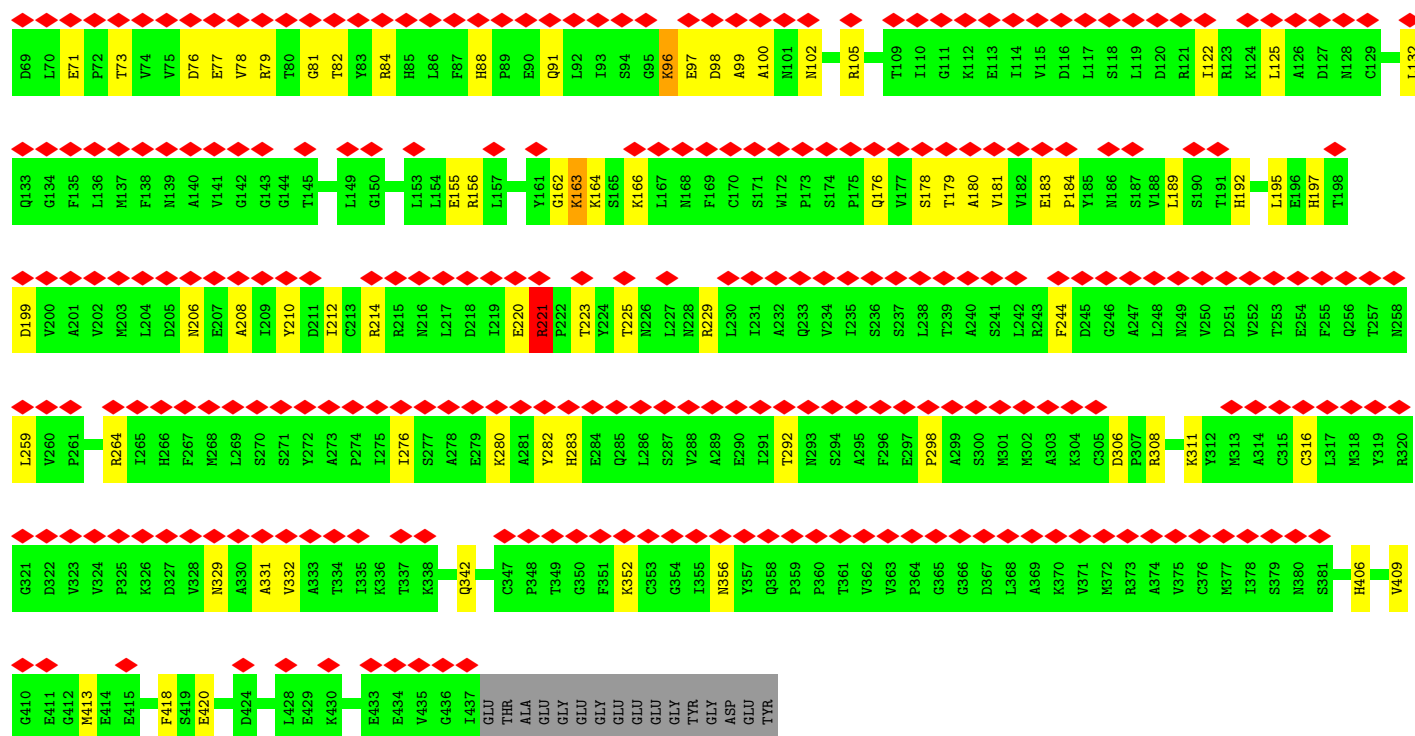


• Molecule 2: Tubulin alpha chain

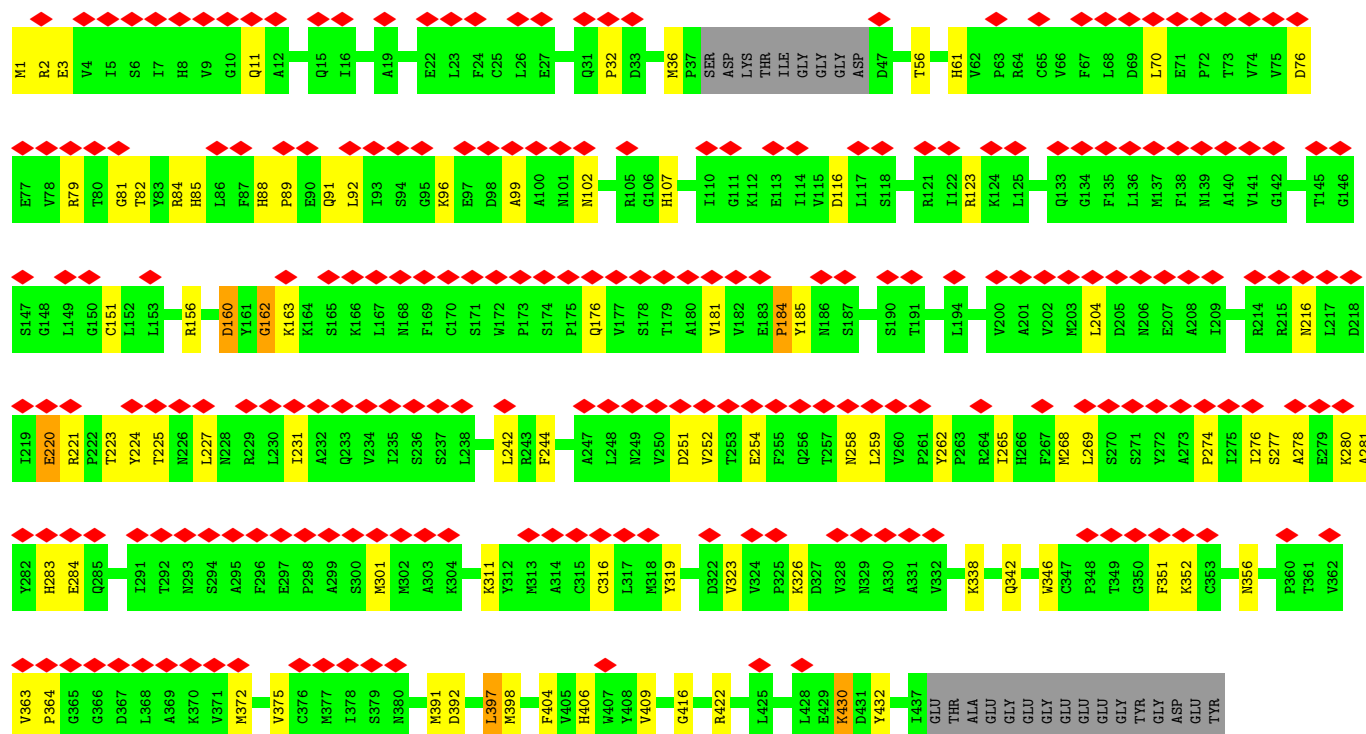
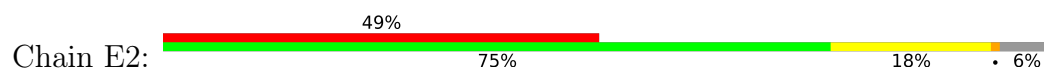


• Molecule 2: Tubulin alpha chain



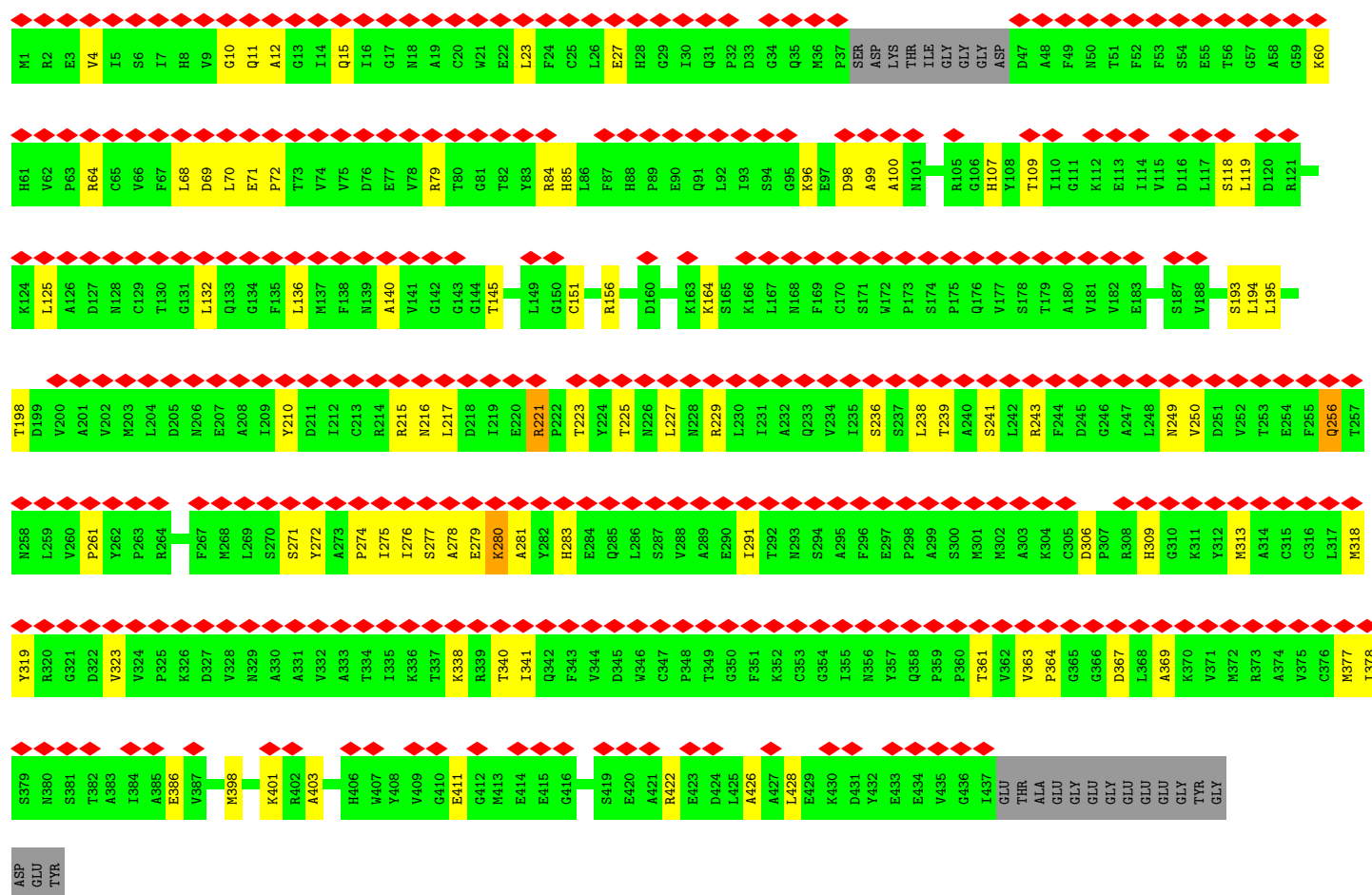


• Molecule 2: Tubulin alpha chain



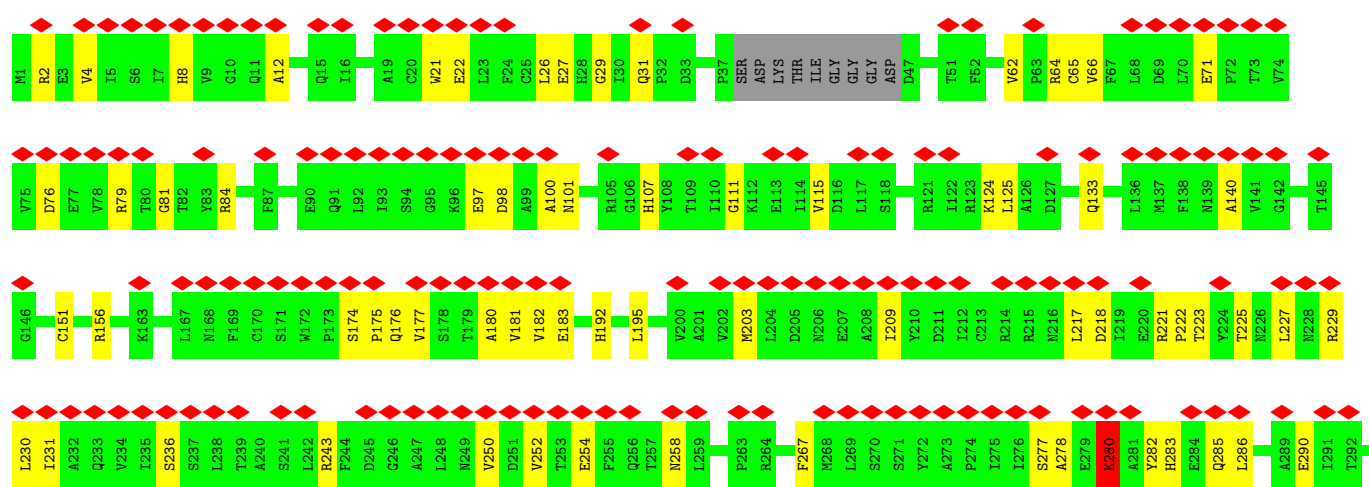
• Molecule 2: Tubulin alpha chain

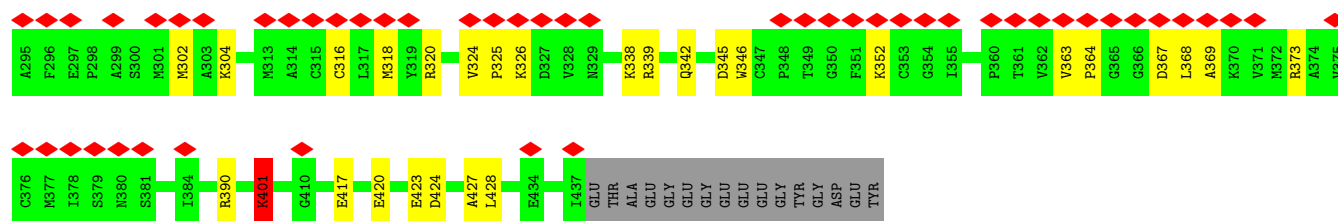
Chain E4: 



• Molecule 2: Tubulin alpha chain

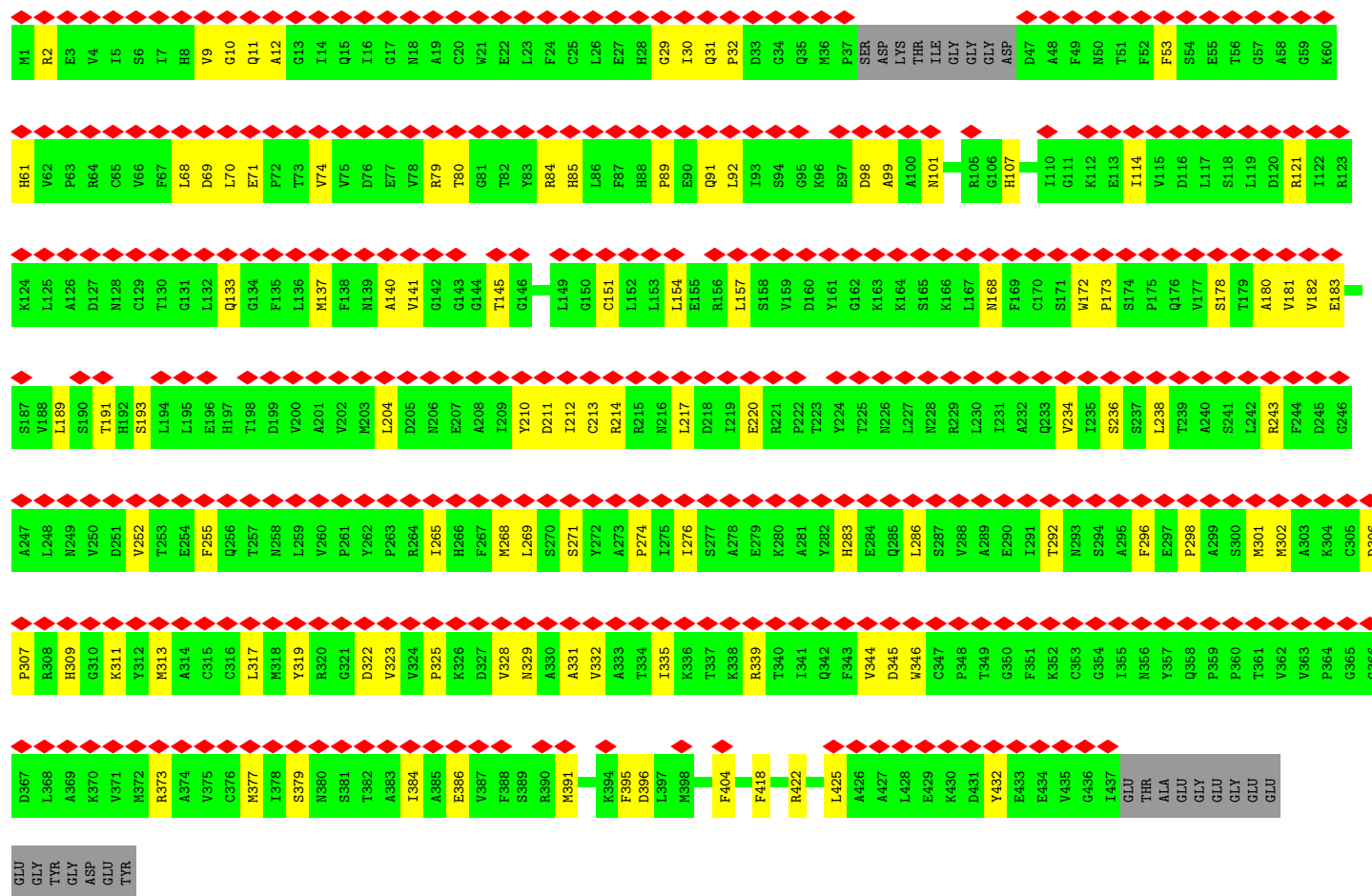
Chain E6: 





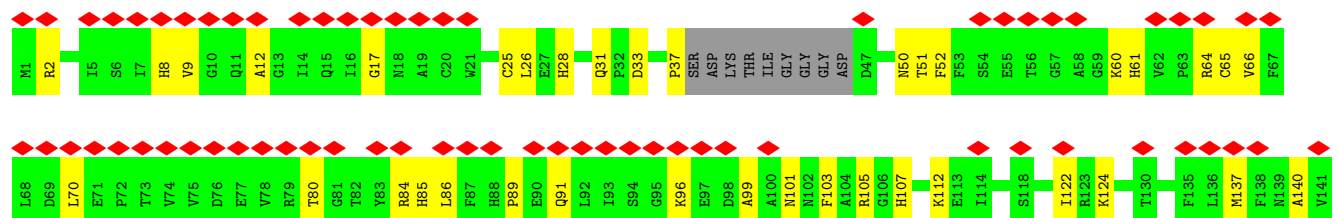
• Molecule 2: Tubulin alpha chain

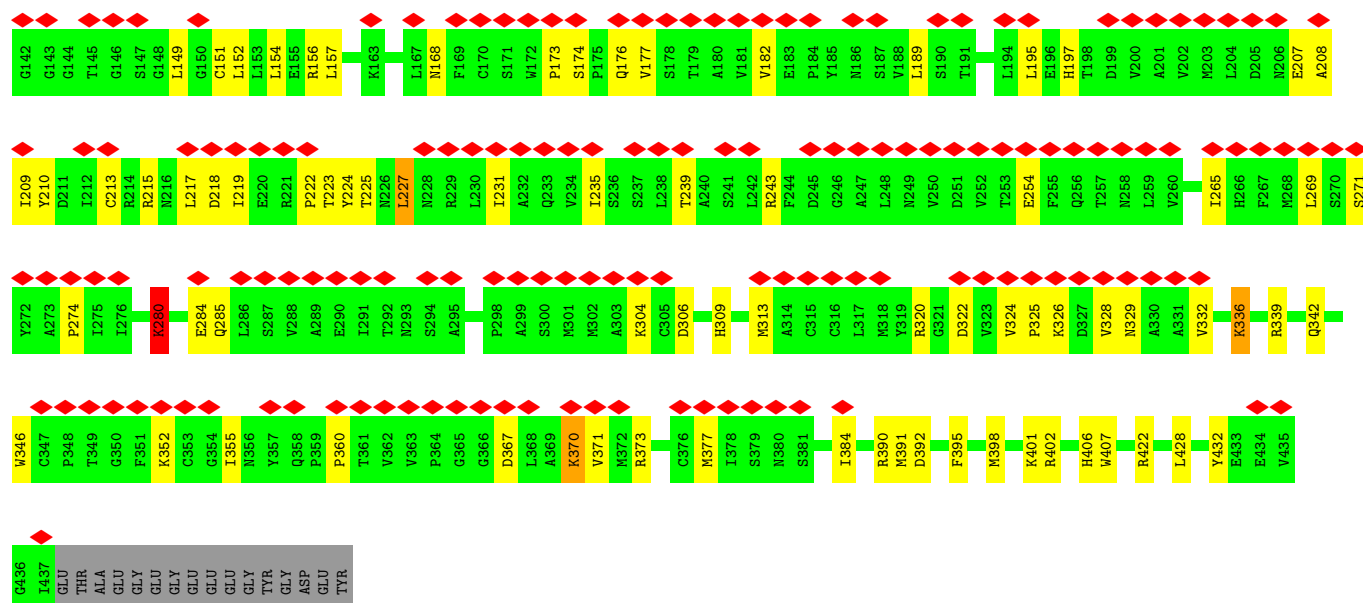
Chain E8: 71% 83% 24% 6%



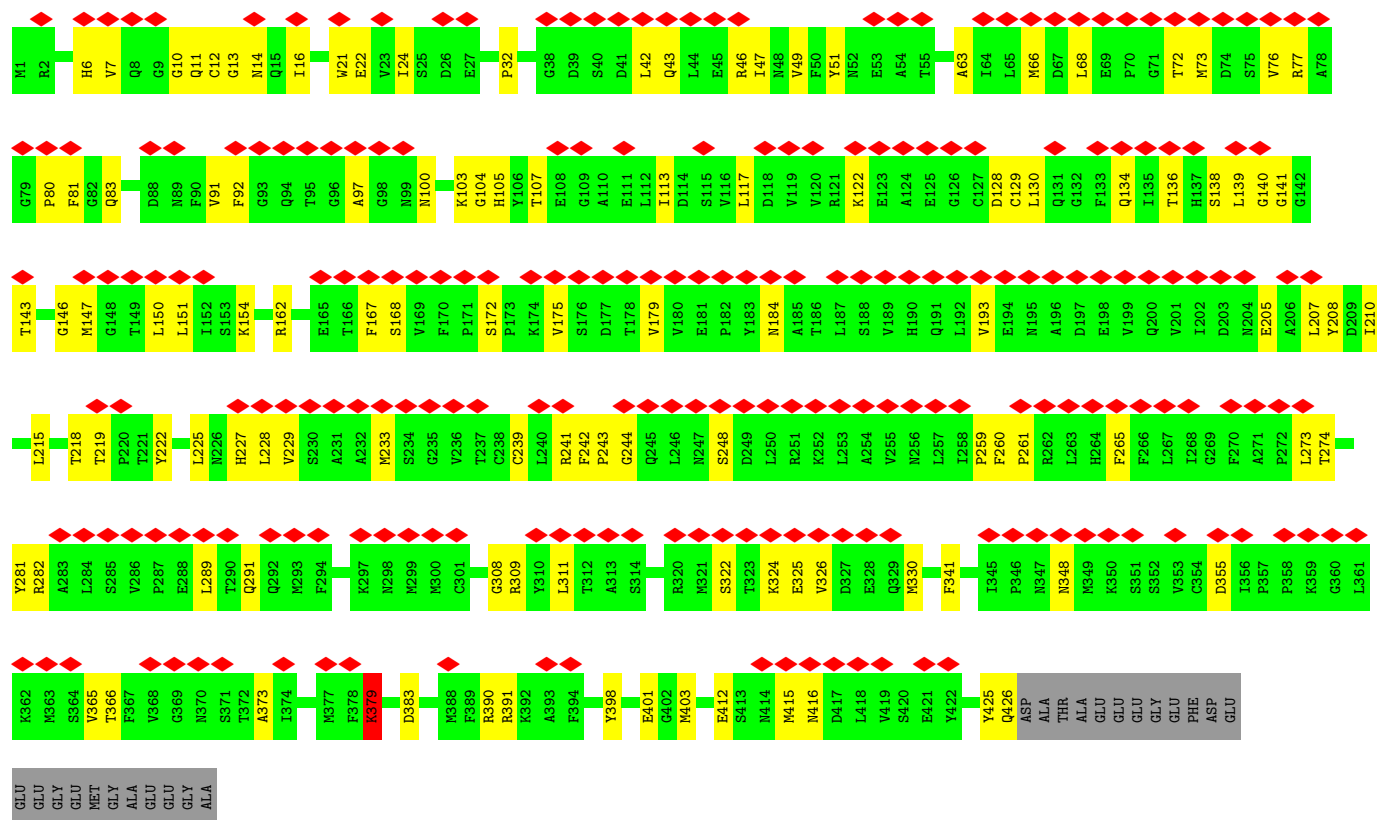
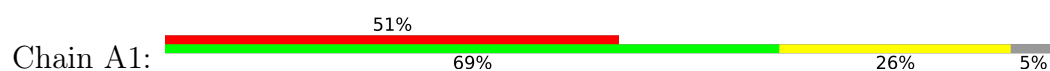
• Molecule 2: Tubulin alpha chain

Chain F0: 69% 49% 25% 6%

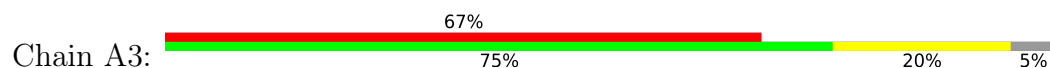


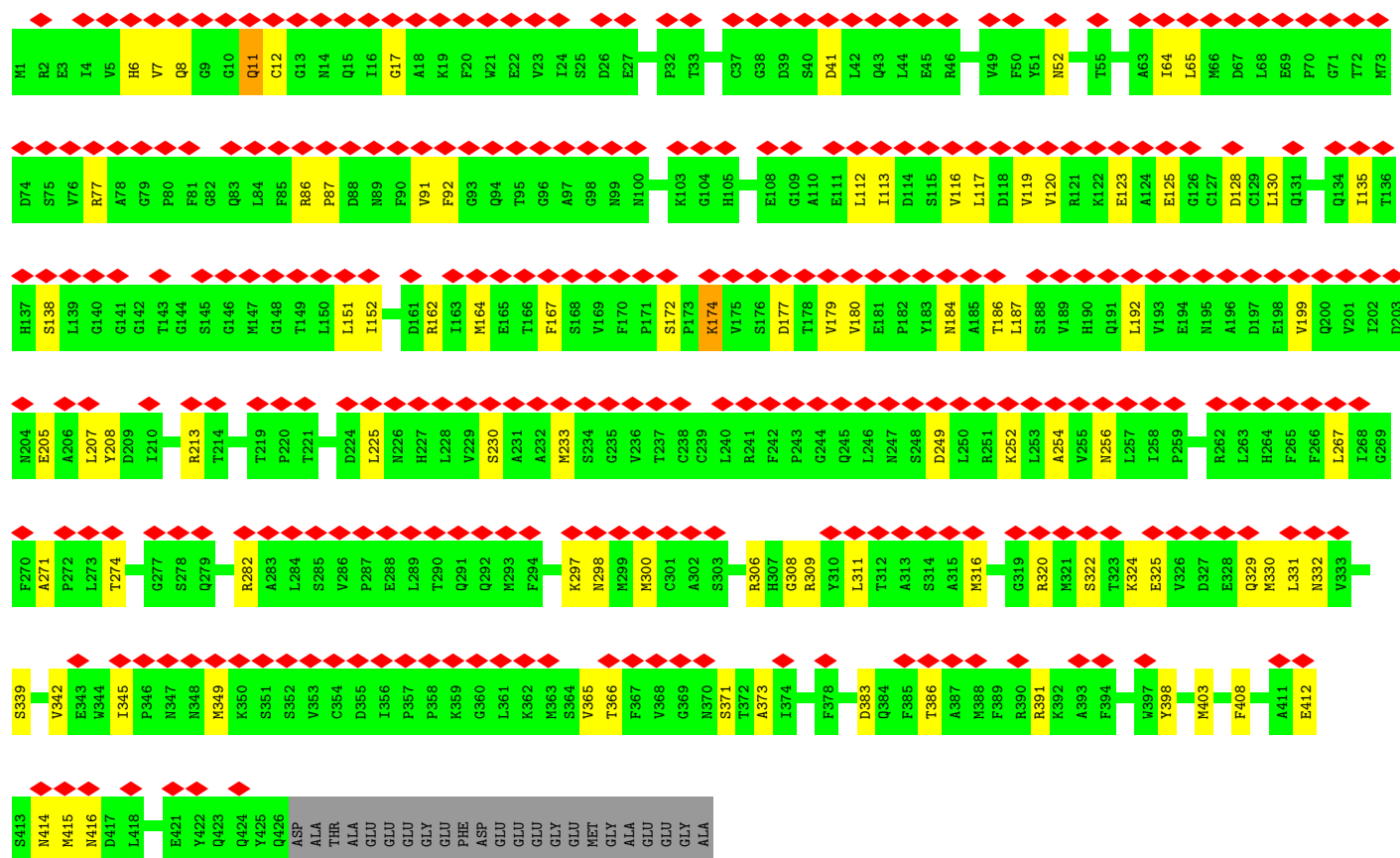


• Molecule 3: Tubulin beta chain

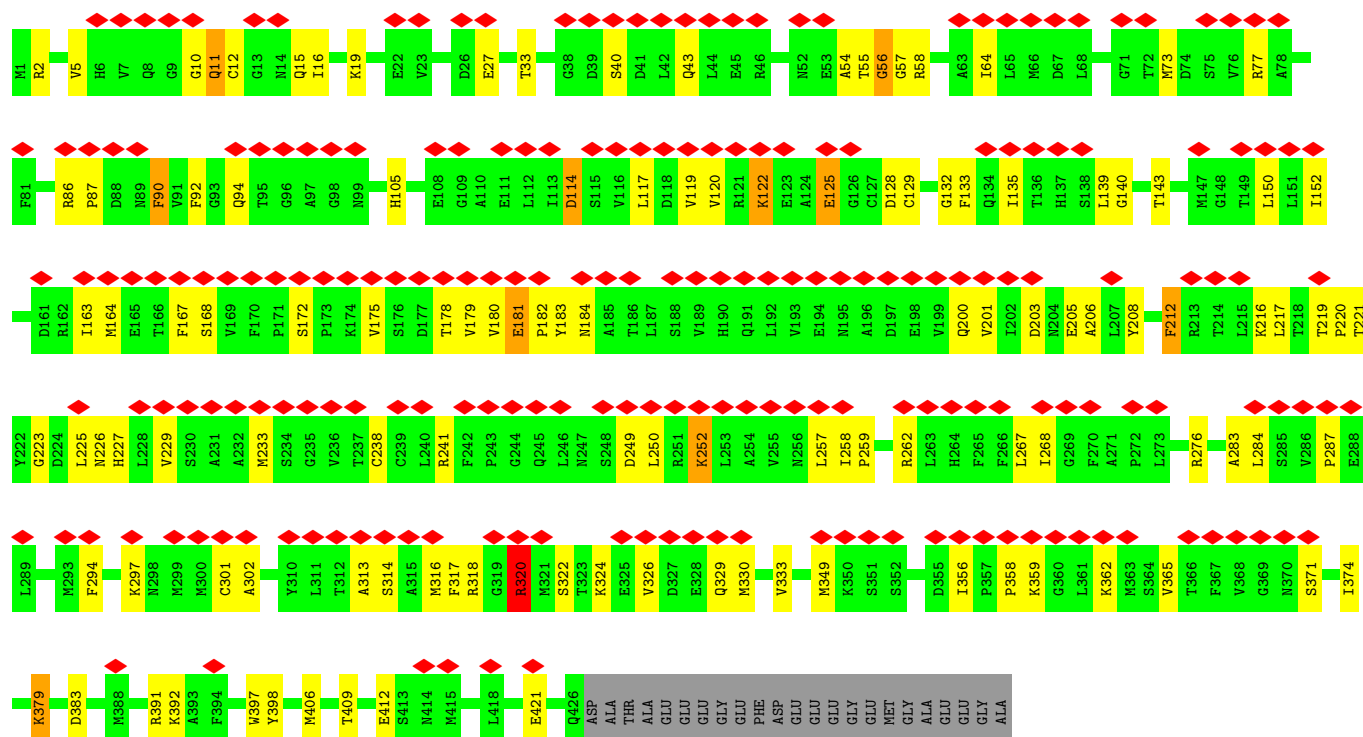


• Molecule 3: Tubulin beta chain

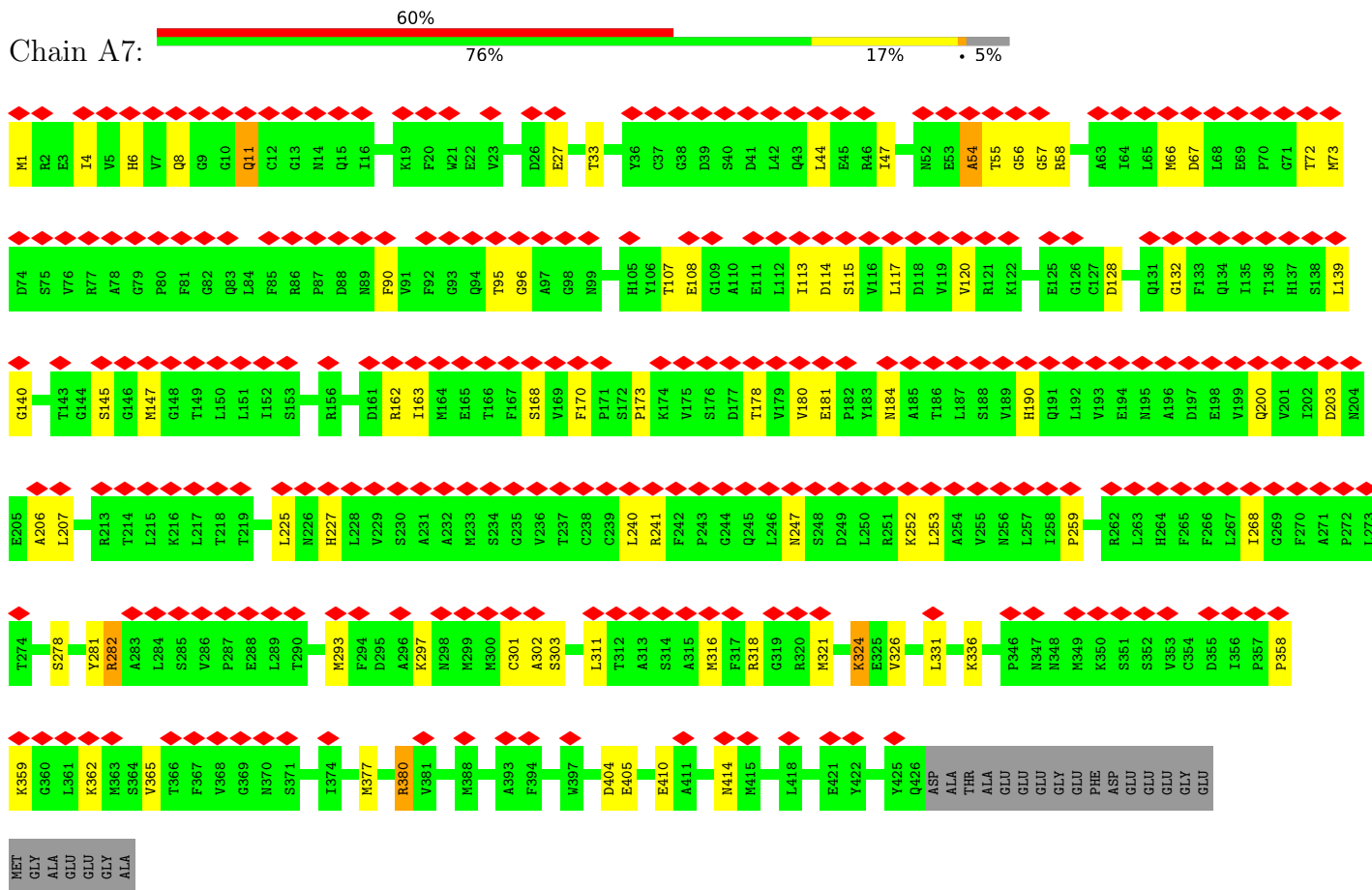




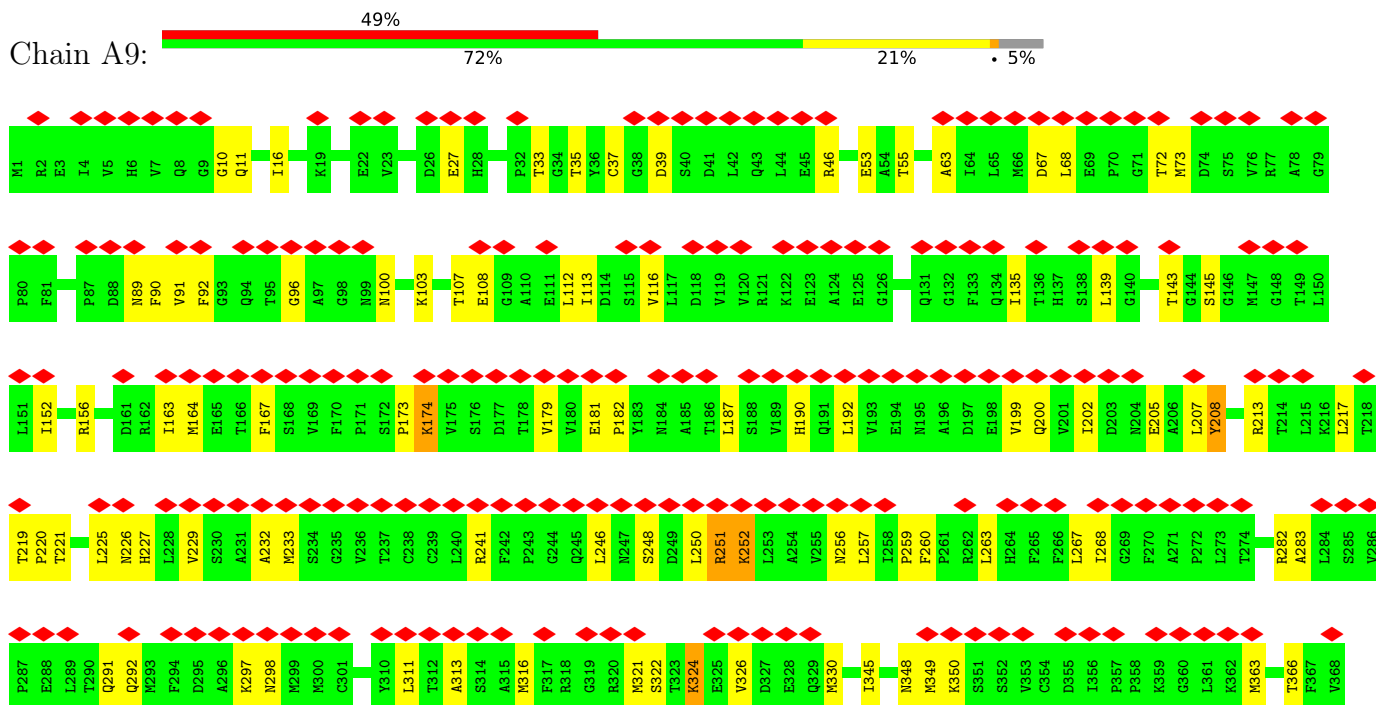
• Molecule 3: Tubulin beta chain

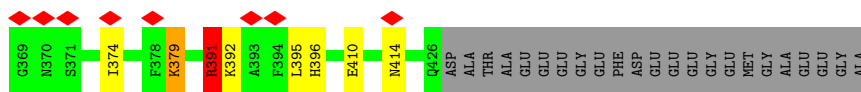


Chain A7:

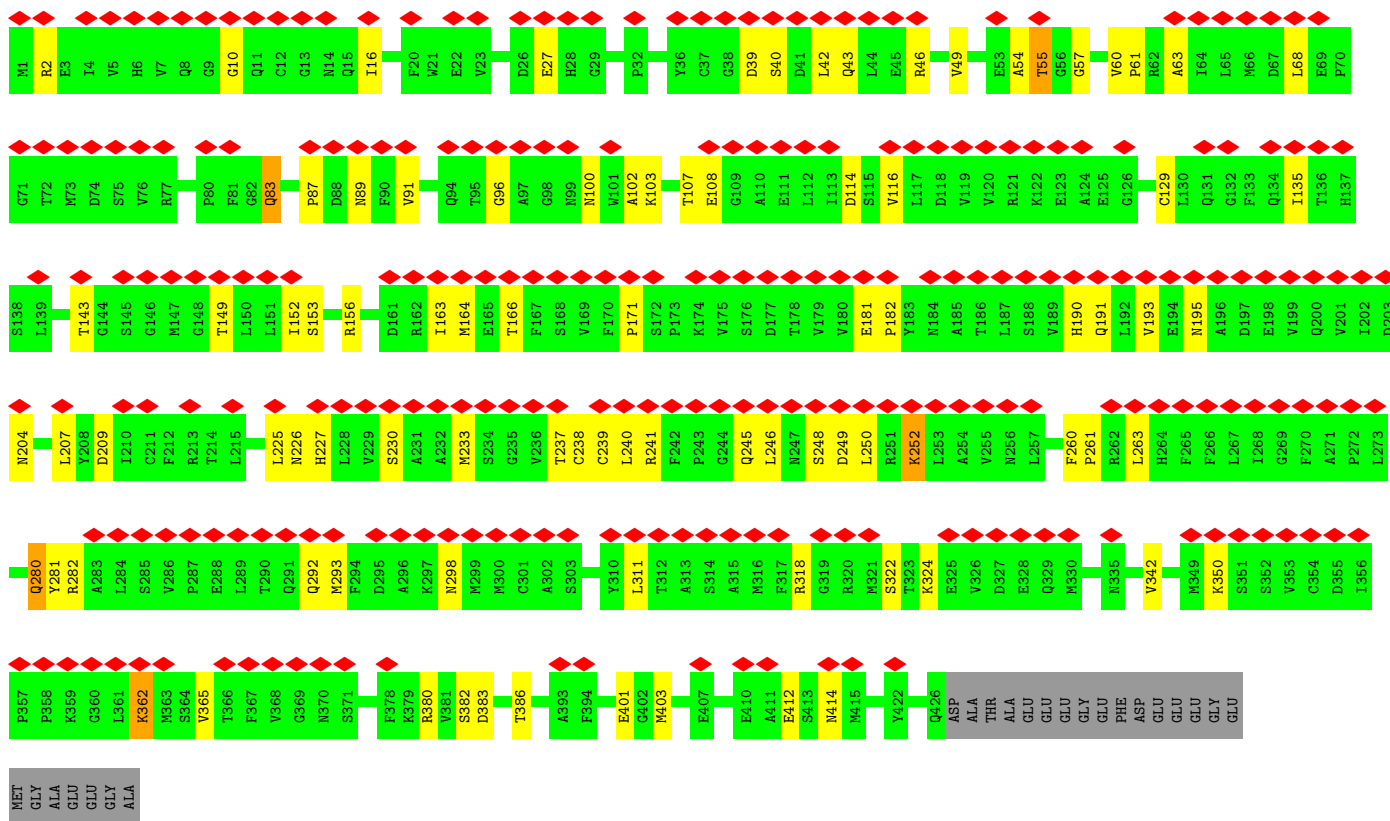
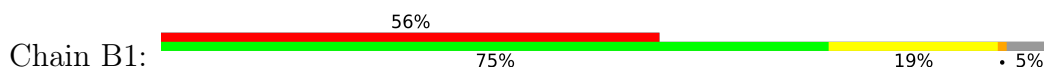


Chain A9:

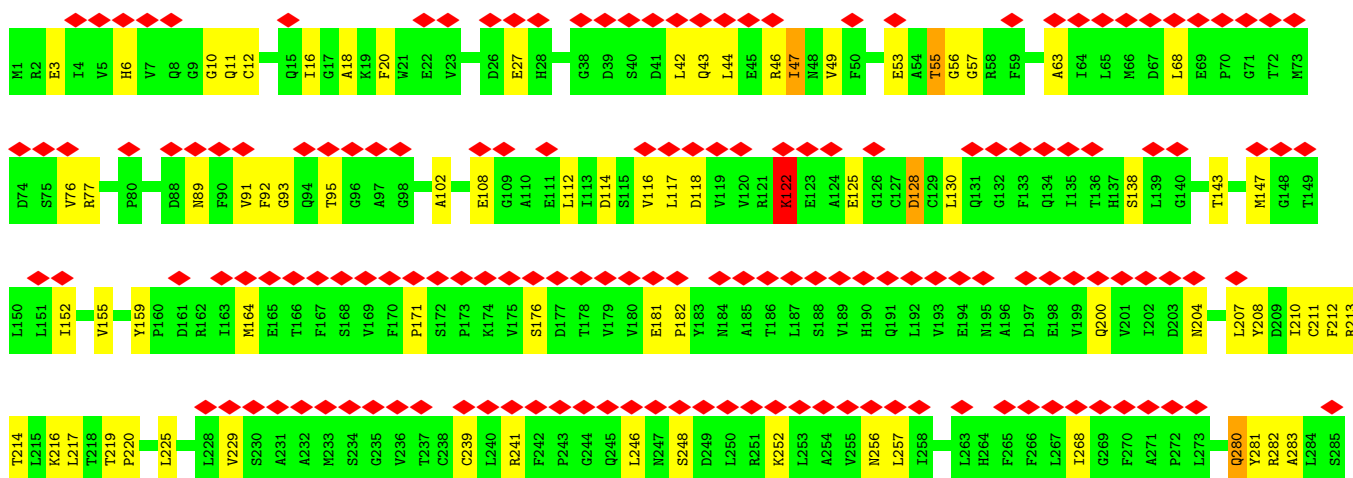
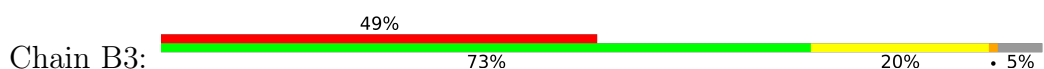


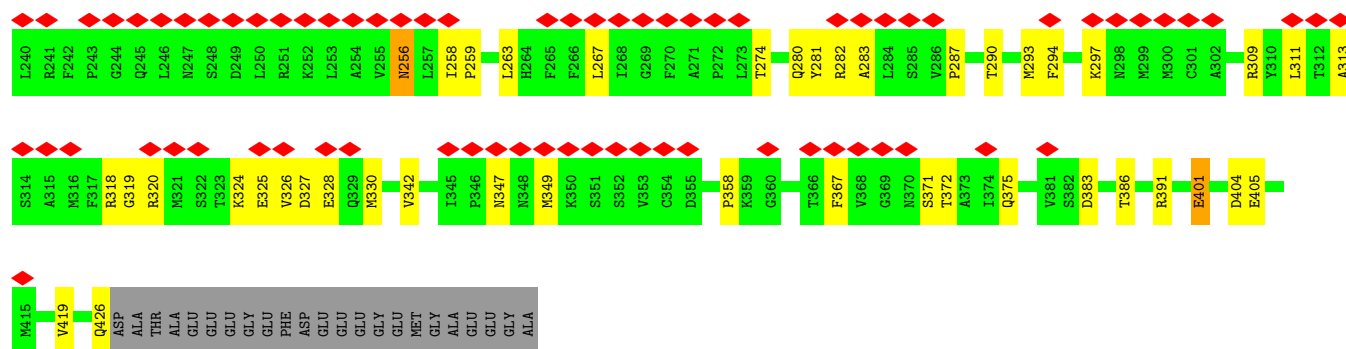


• Molecule 3: Tubulin beta chain

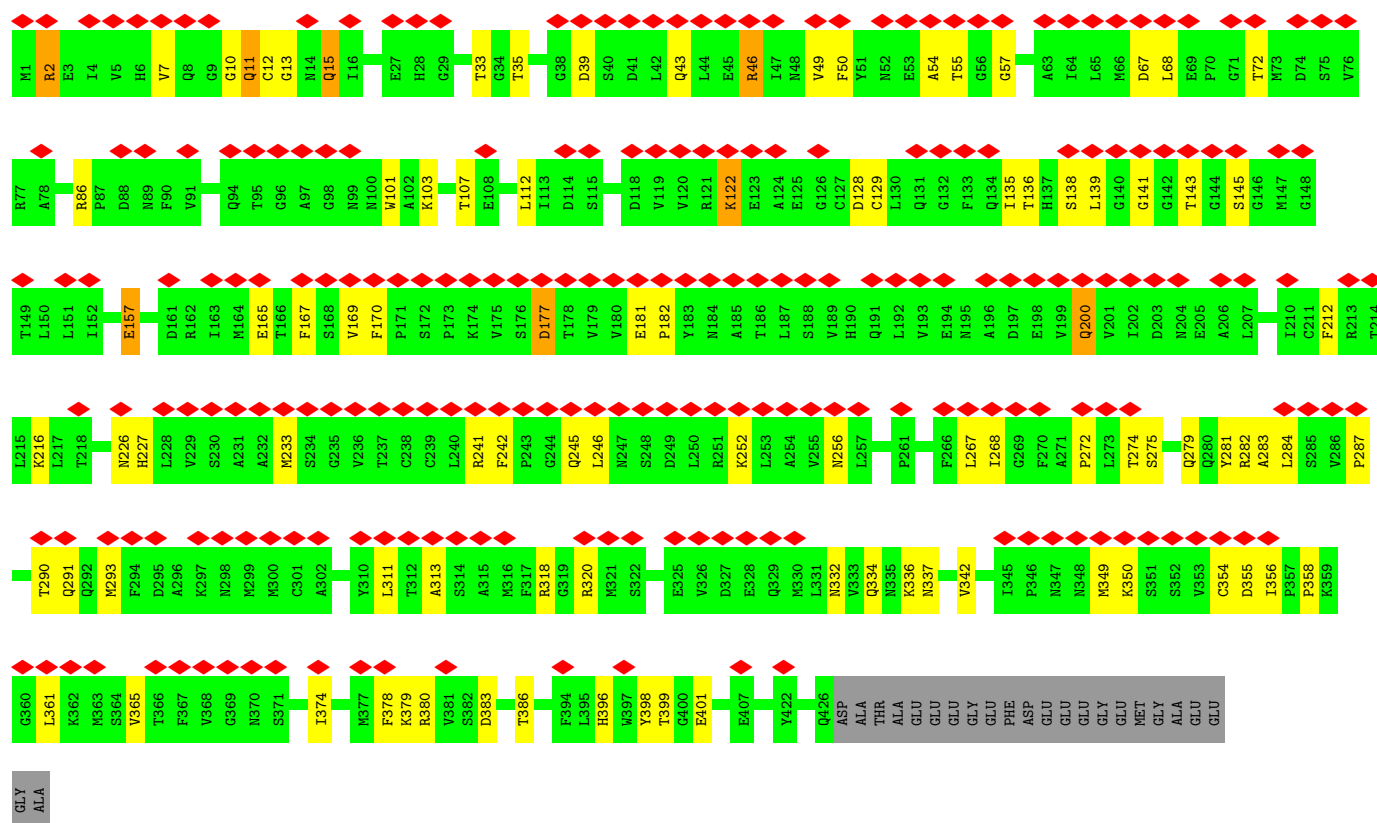
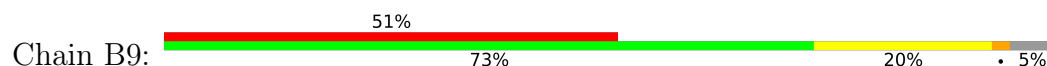


• Molecule 3: Tubulin beta chain

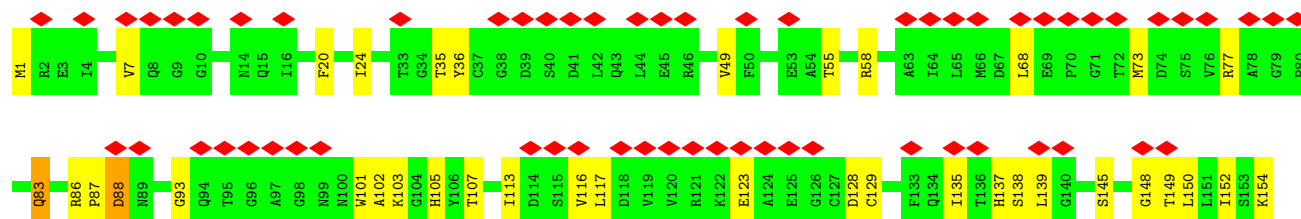
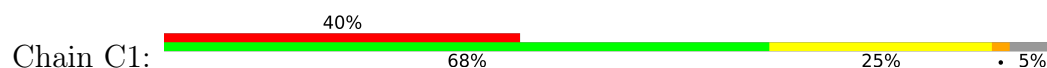


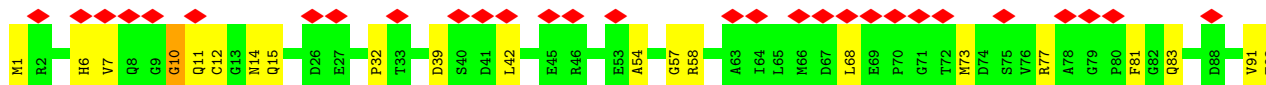


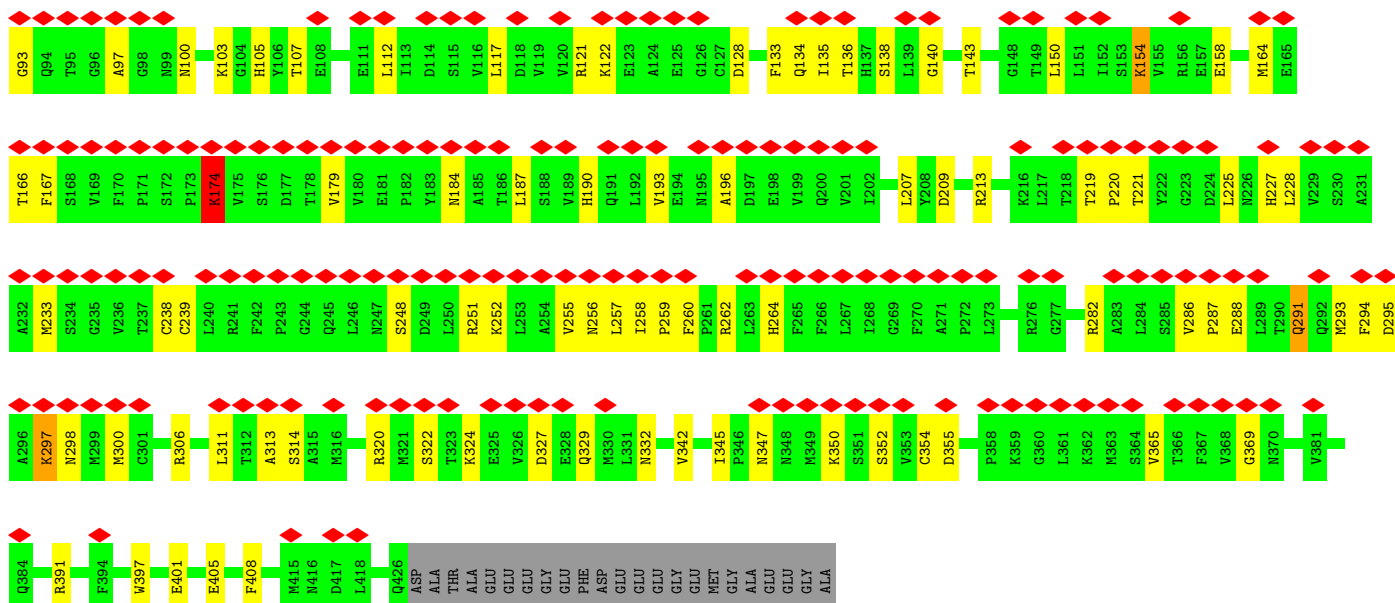
• Molecule 3: Tubulin beta chain



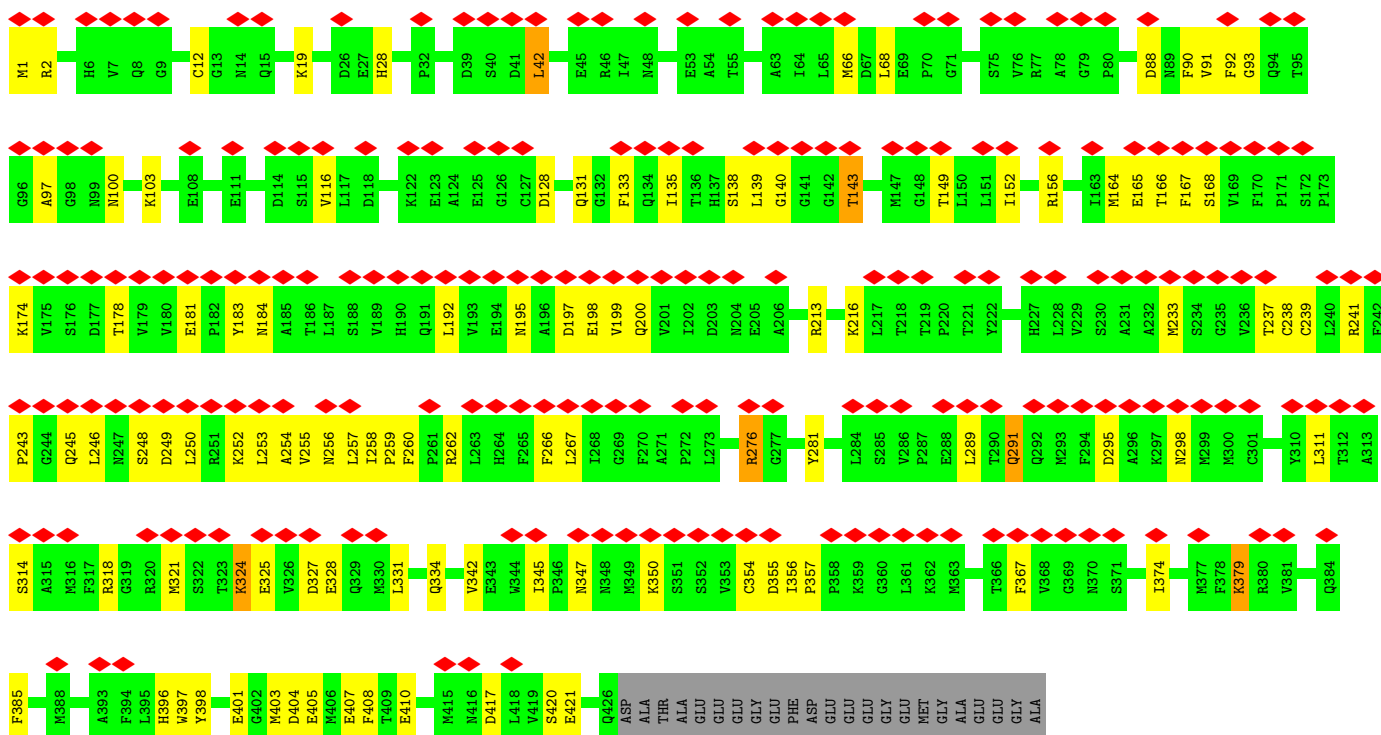
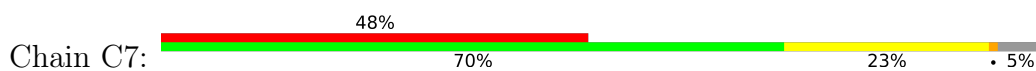
• Molecule 3: Tubulin beta chain



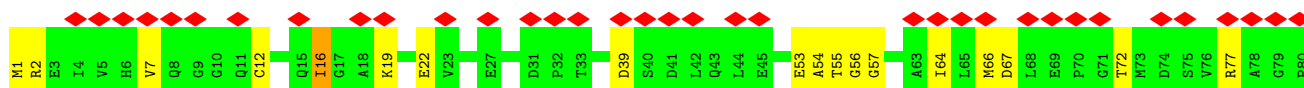


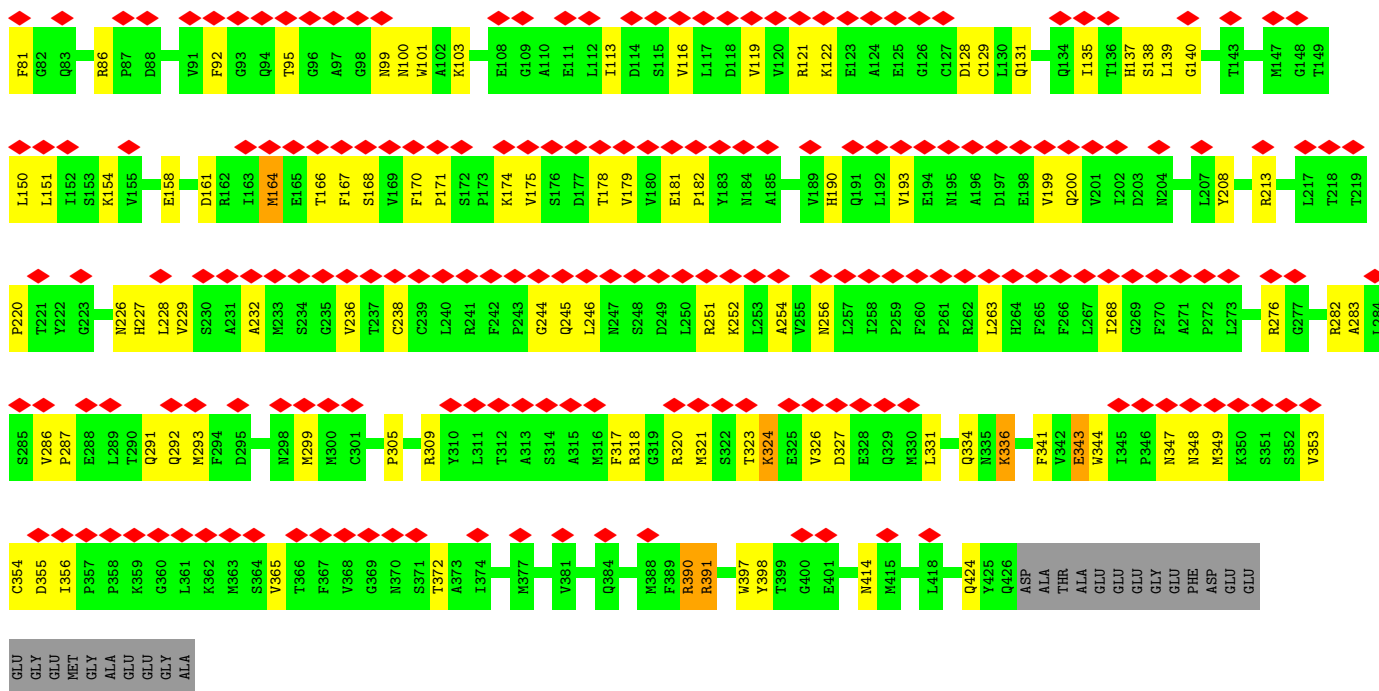


• Molecule 3: Tubulin beta chain

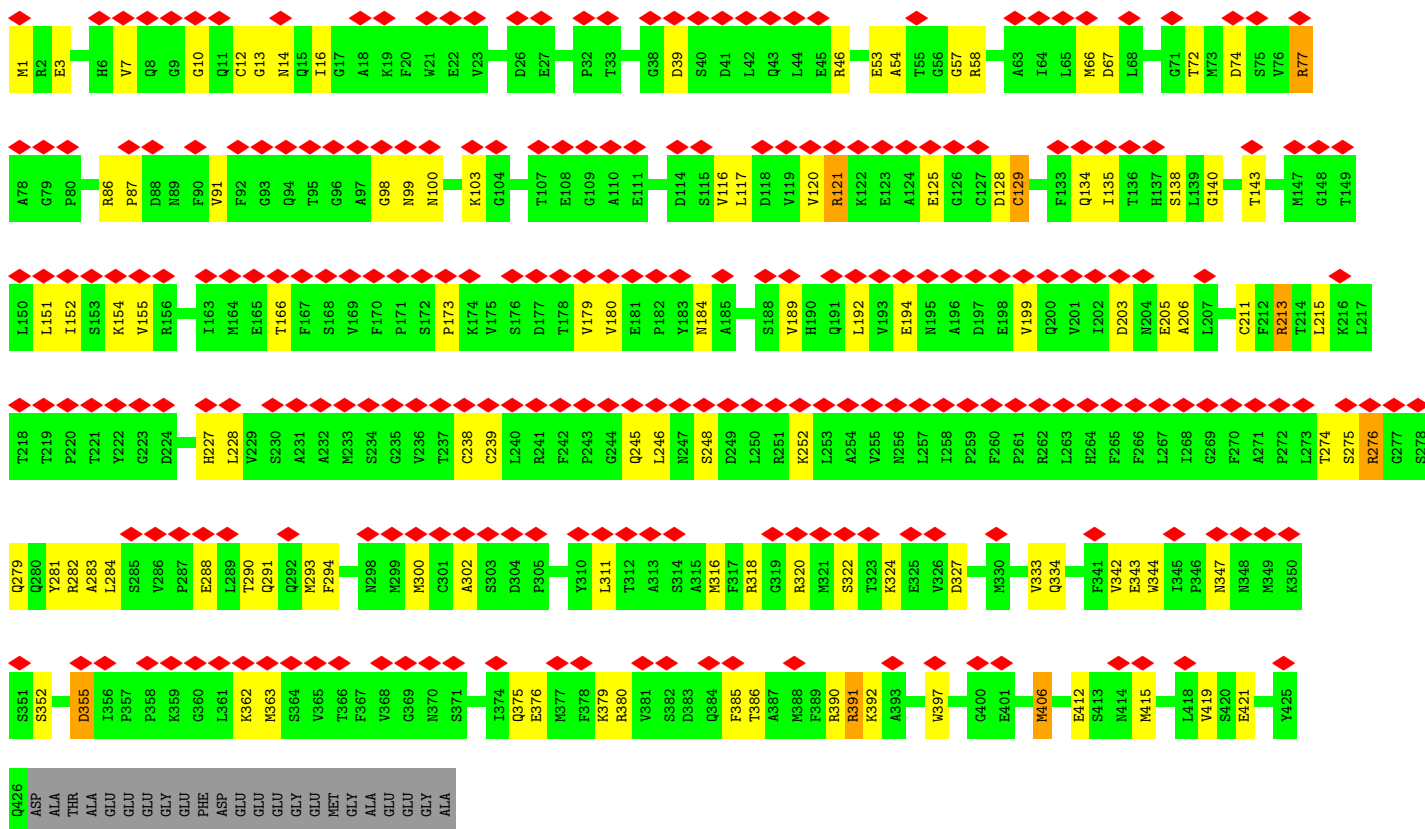
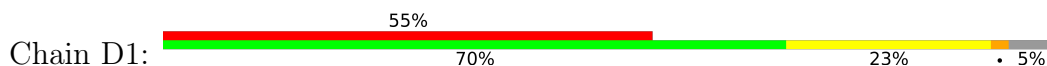


• Molecule 3: Tubulin beta chain

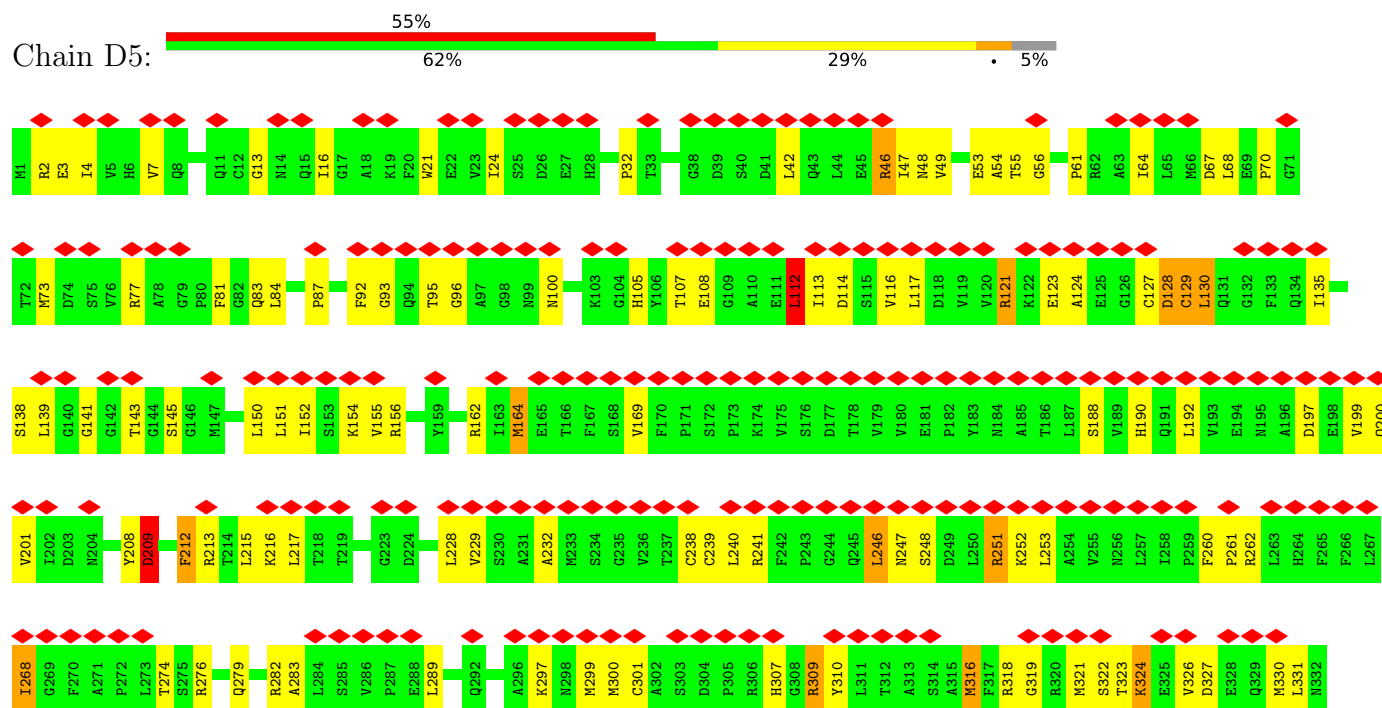


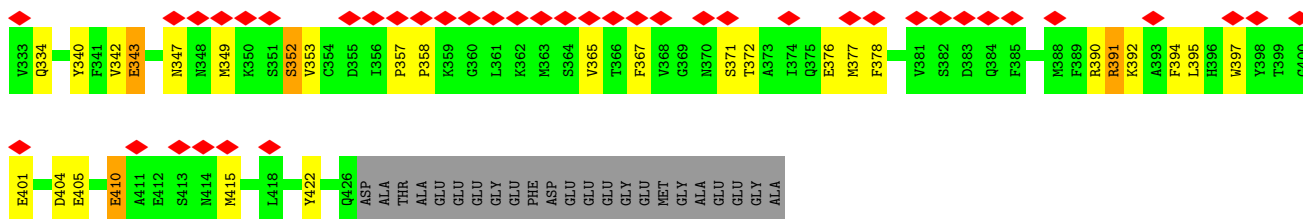


• Molecule 3: Tubulin beta chain

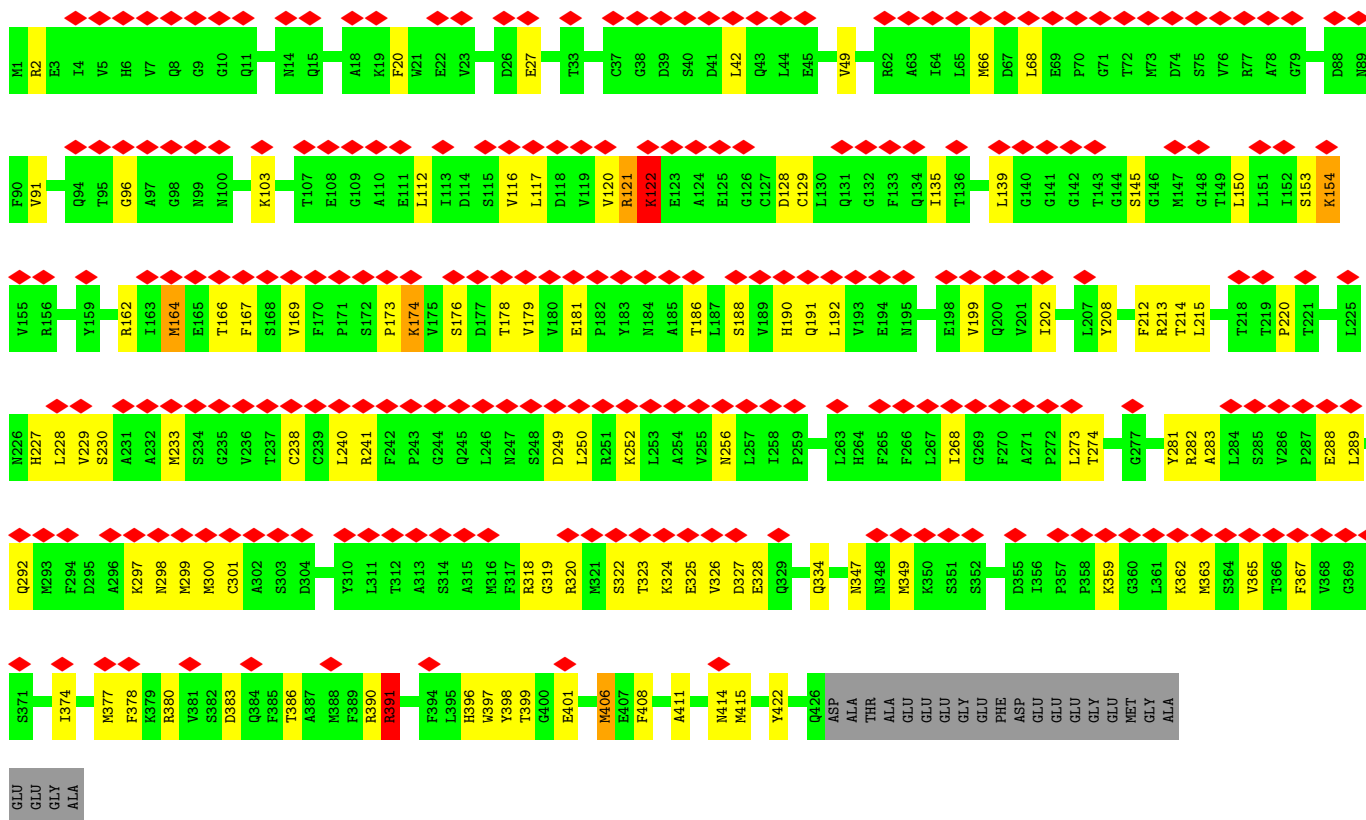
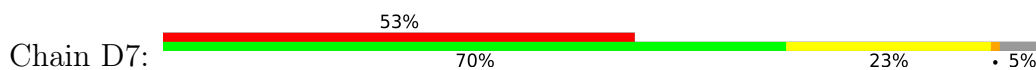


• Molecule 3: Tubulin beta chain

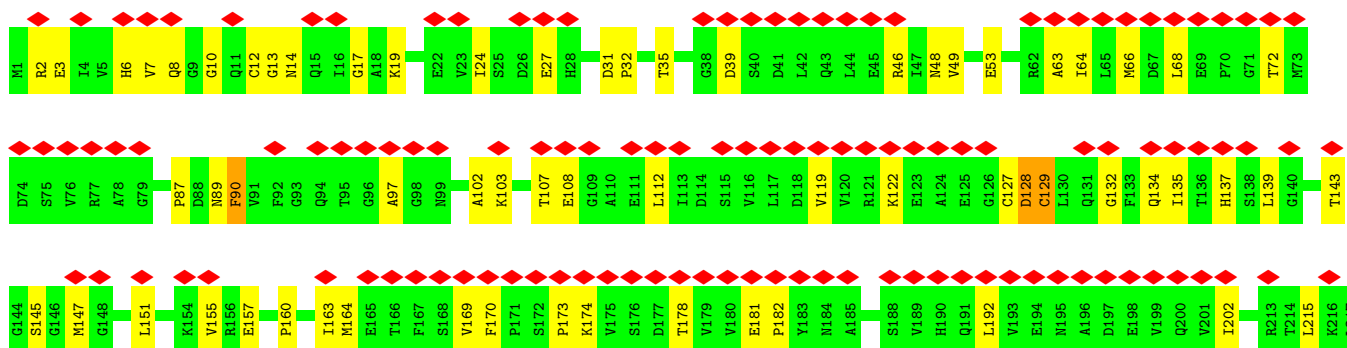
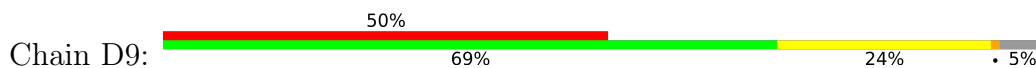


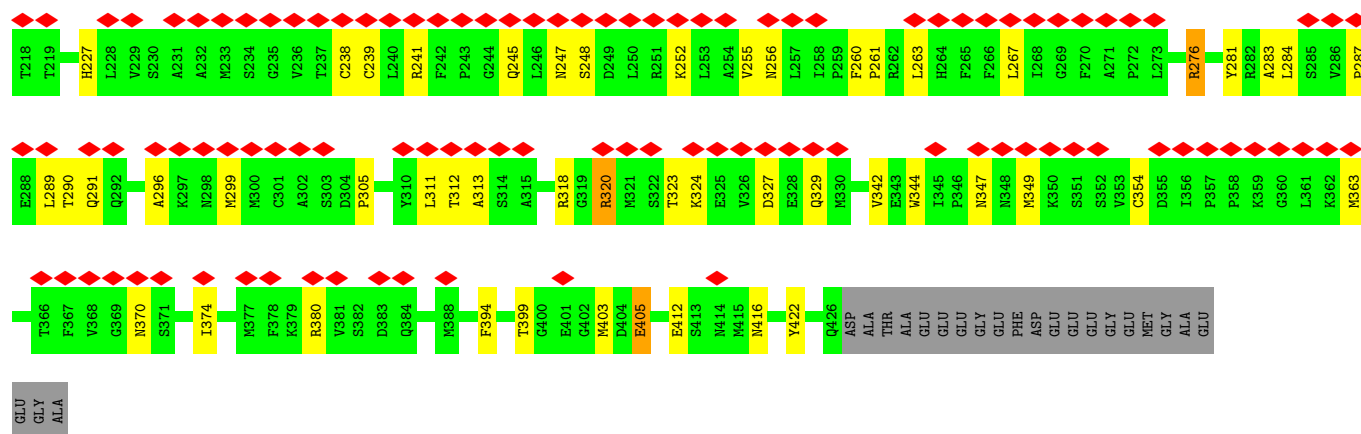


• Molecule 3: Tubulin beta chain



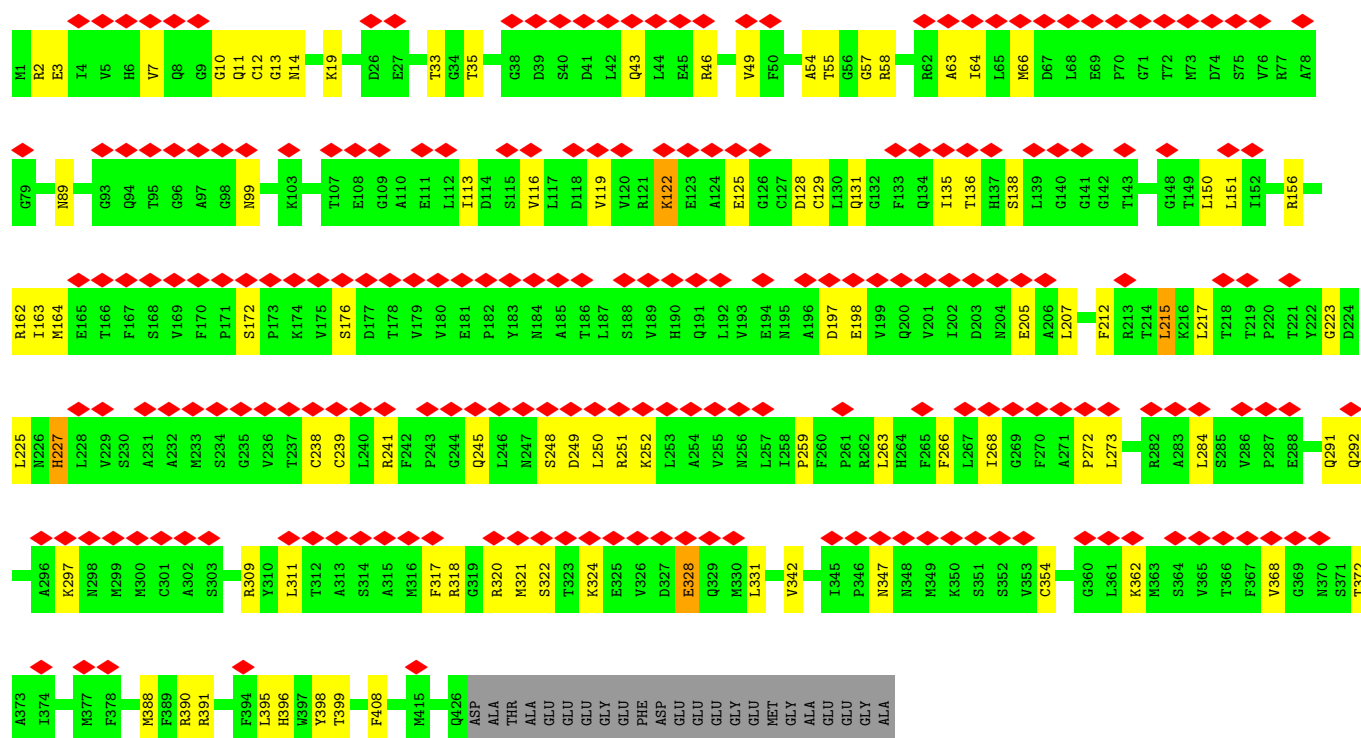
• Molecule 3: Tubulin beta chain





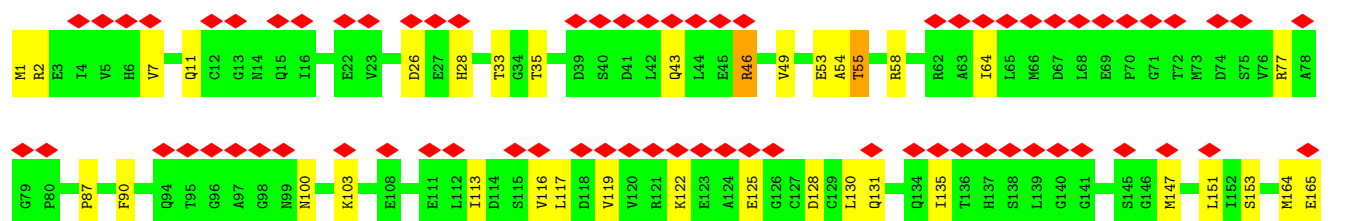
• Molecule 3: Tubulin beta chain

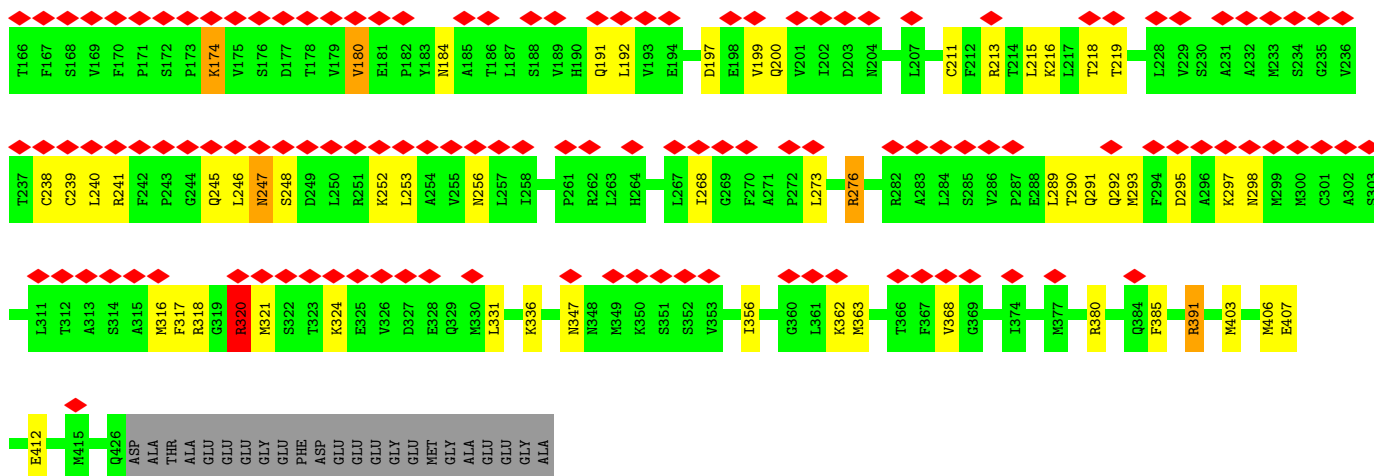
Chain E1: 46% 74% 20% 5%



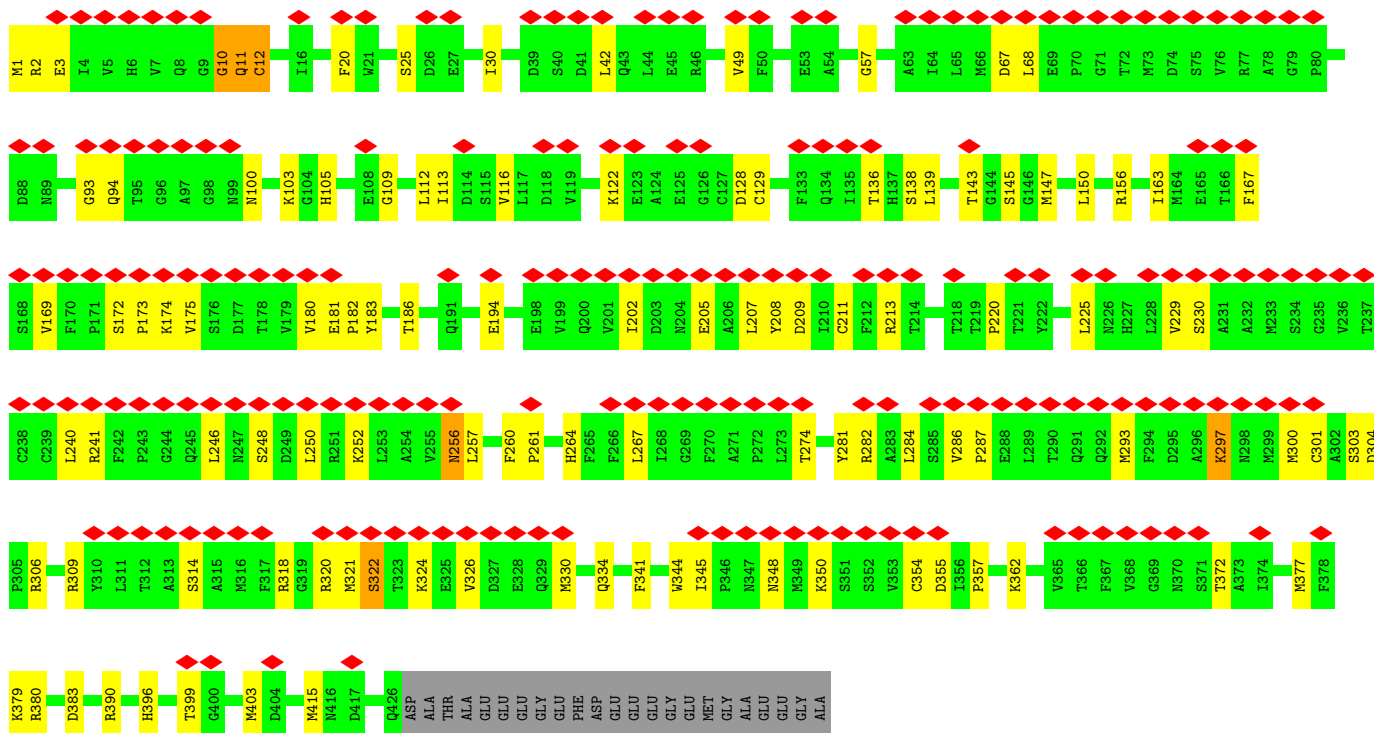
• Molecule 3: Tubulin beta chain

Chain E3: 43% 74% 19% 5%

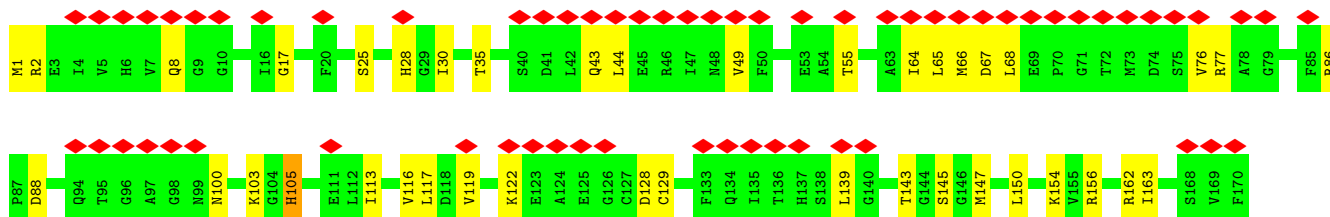
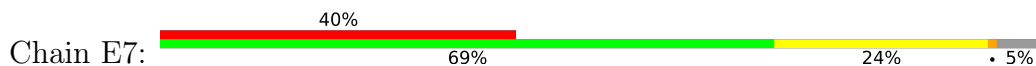


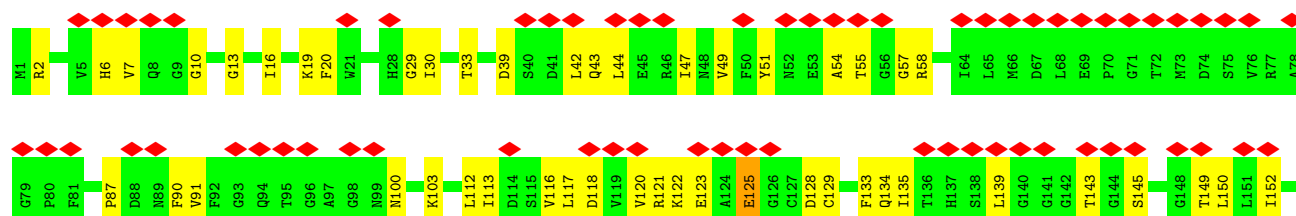


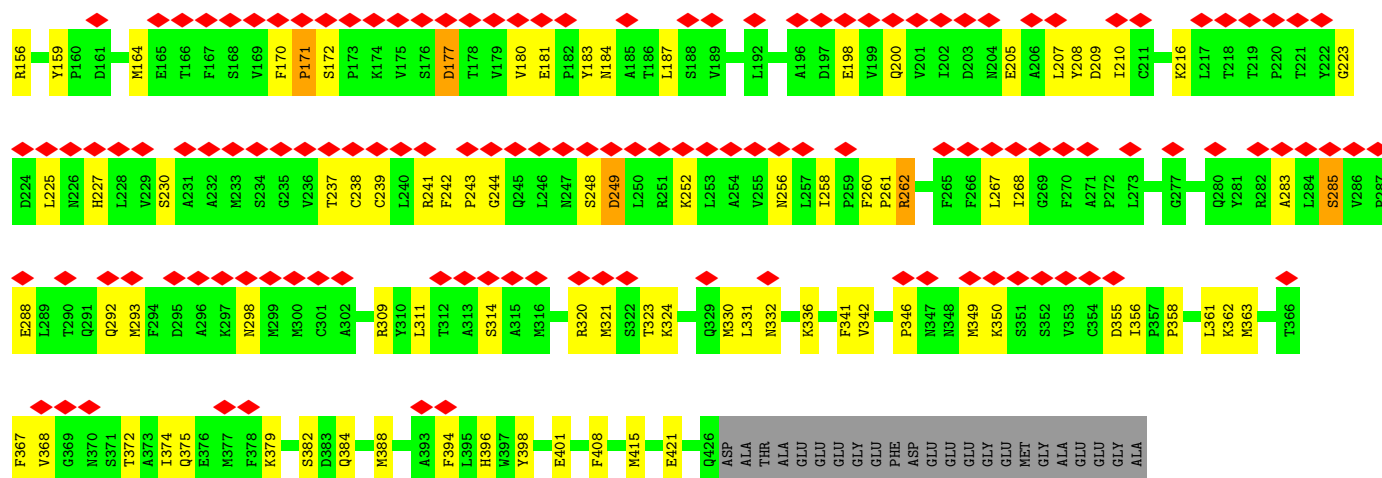
• Molecule 3: Tubulin beta chain



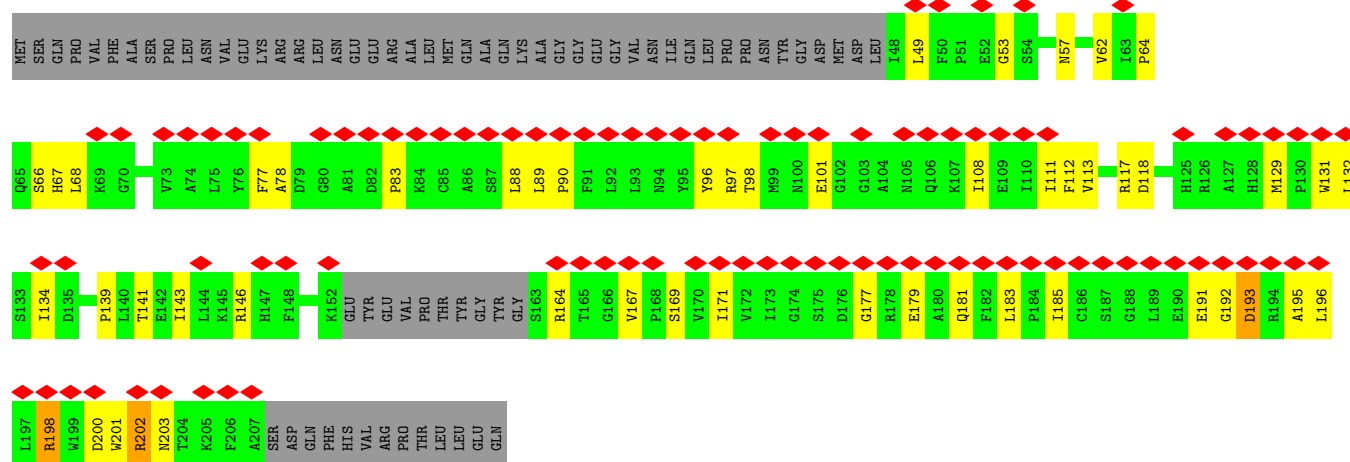
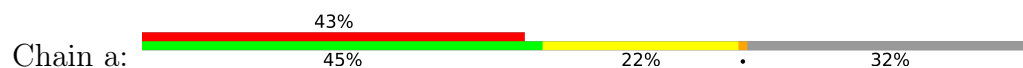
• Molecule 3: Tubulin beta chain



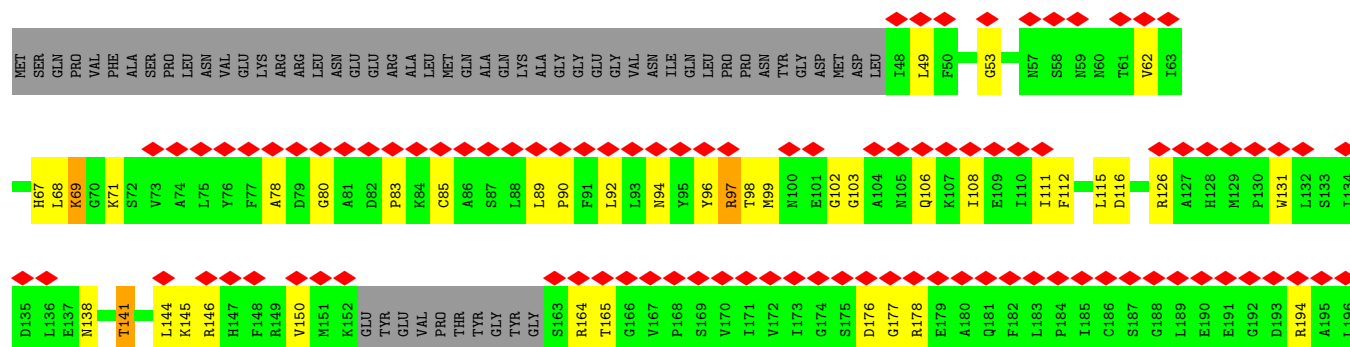


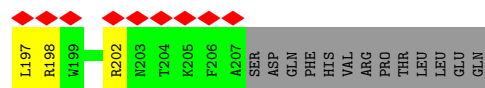


• Molecule 4: PDI family protein

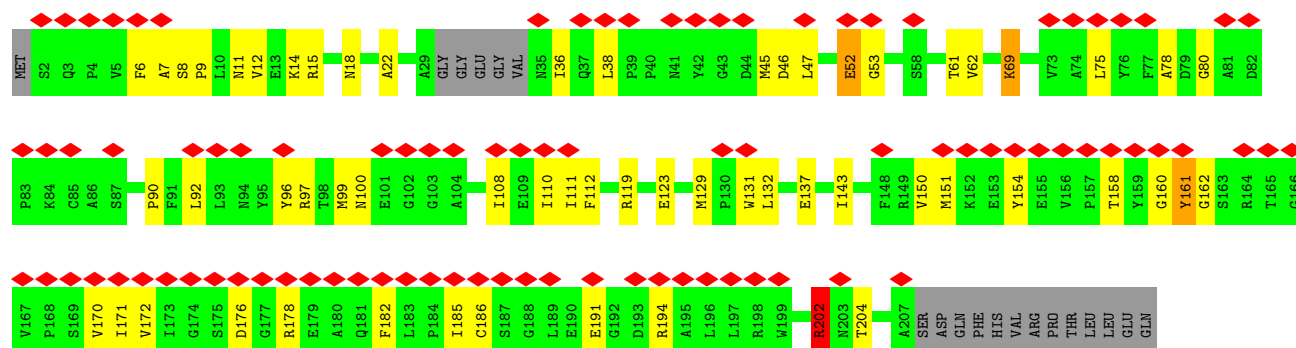
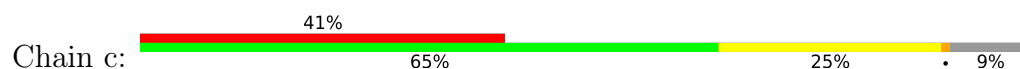


• Molecule 4: PDI family protein

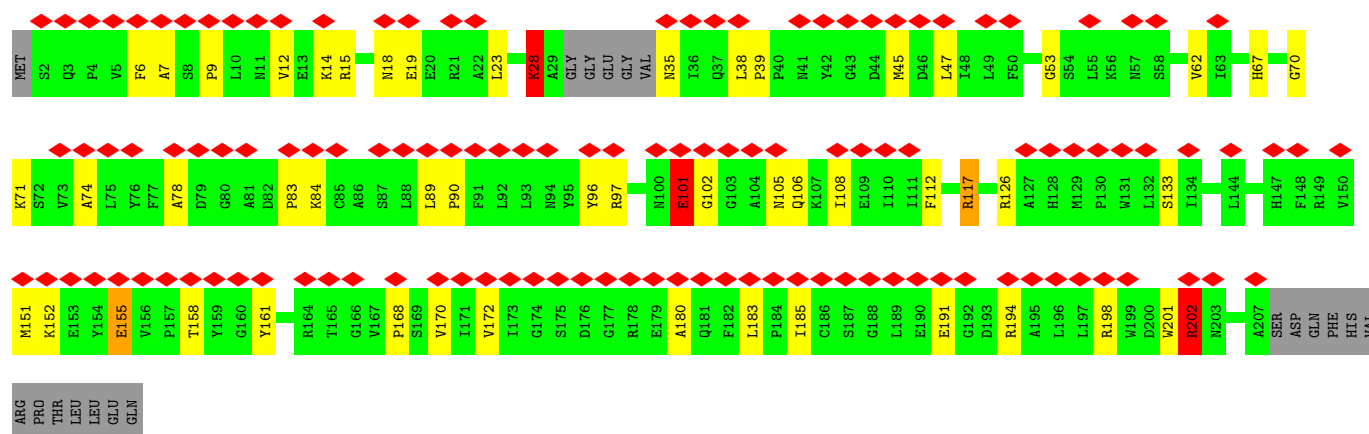




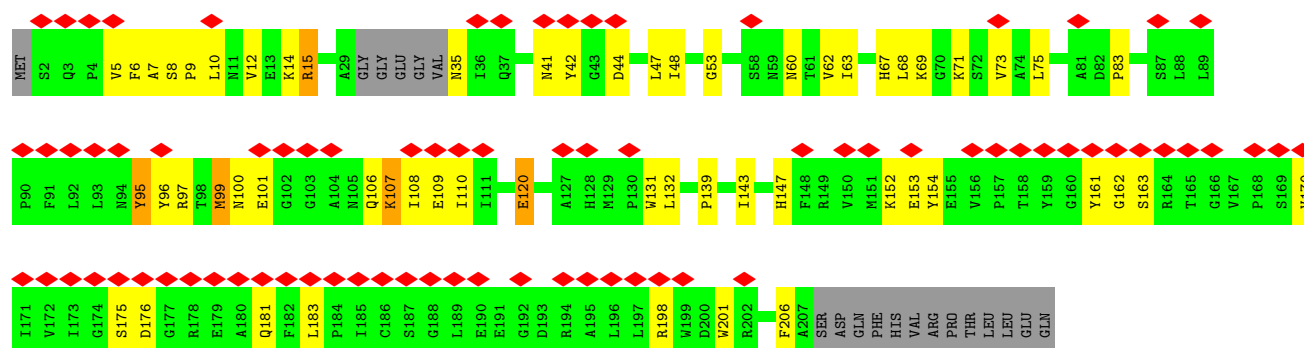
• Molecule 4: PDI family protein



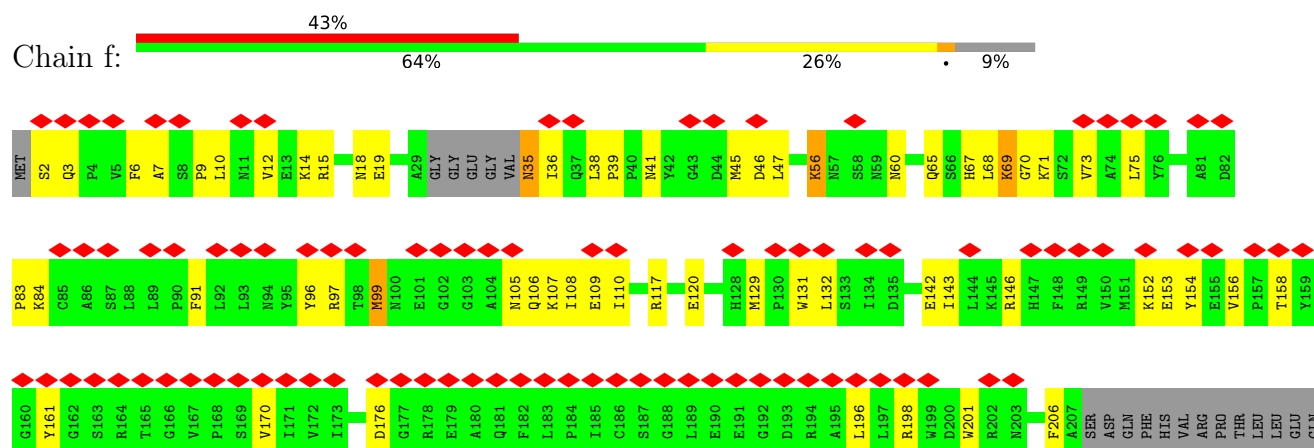
• Molecule 4: PDI family protein



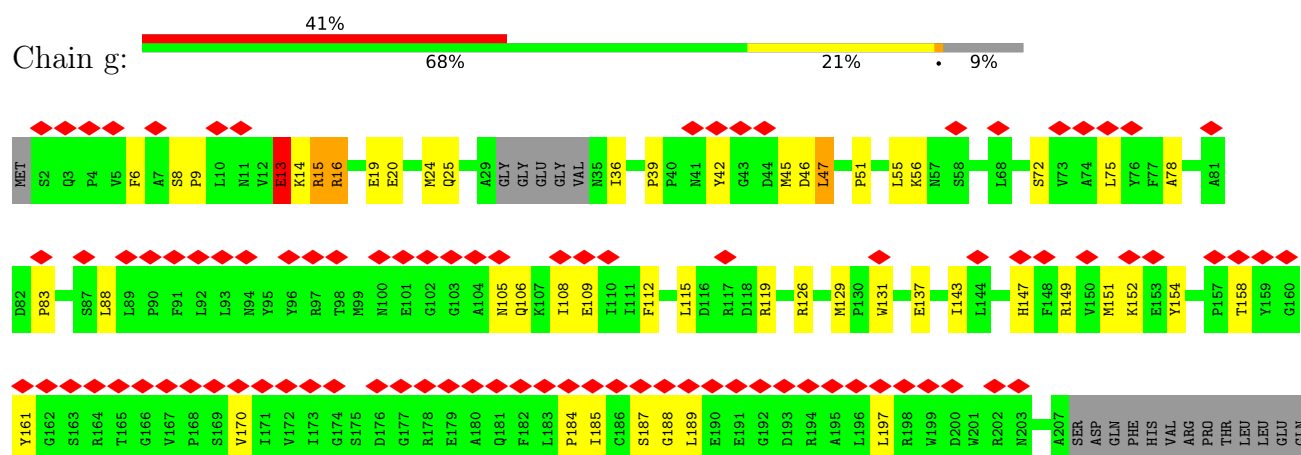
• Molecule 4: PDI family protein



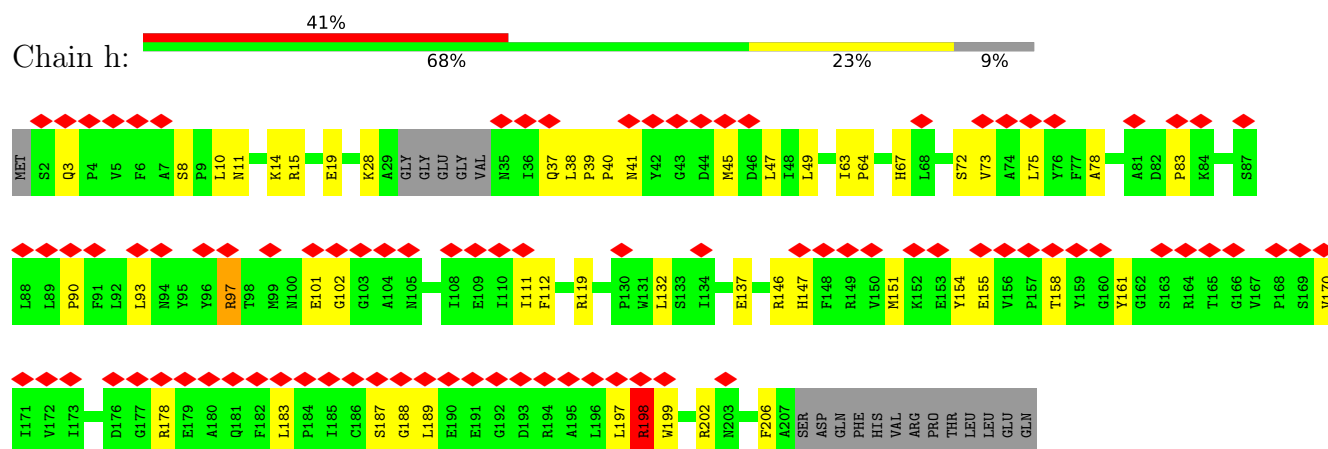
- Molecule 4: PDI family protein



- Molecule 4: PDI family protein

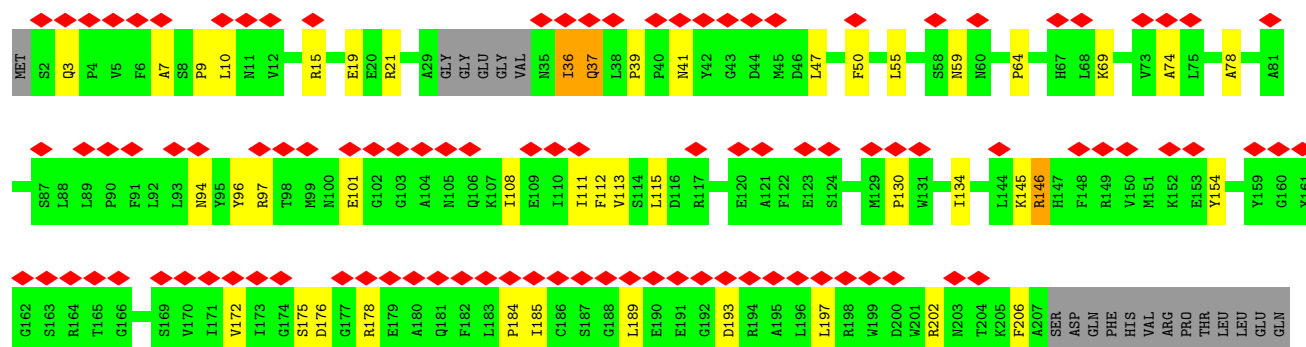


- Molecule 4: PDI family protein

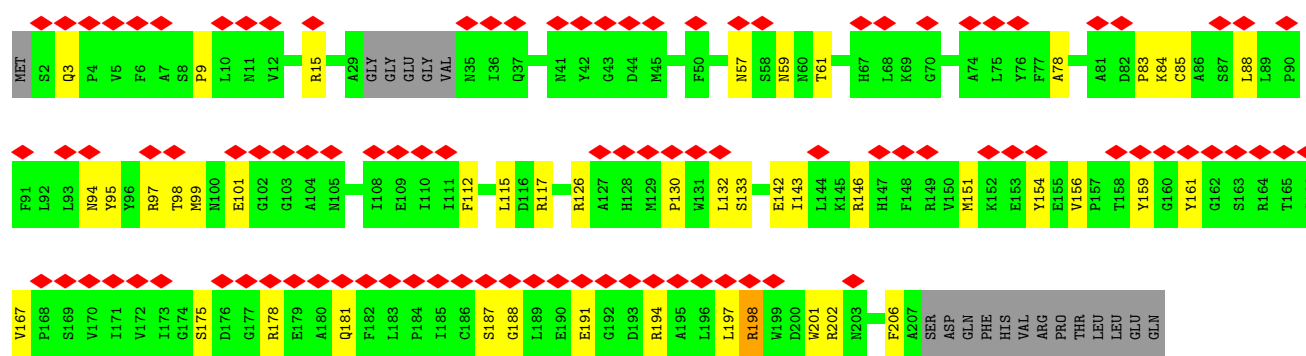
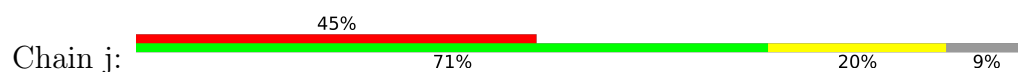


- Molecule 4: PDI family protein

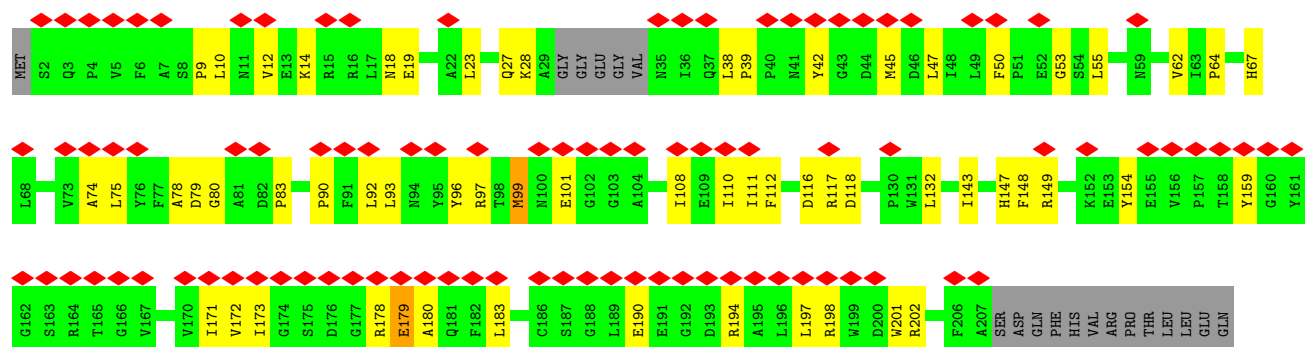
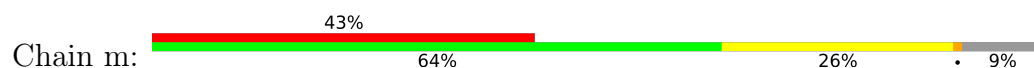




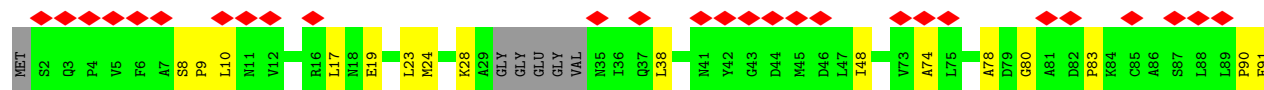
• Molecule 4: PDI family protein

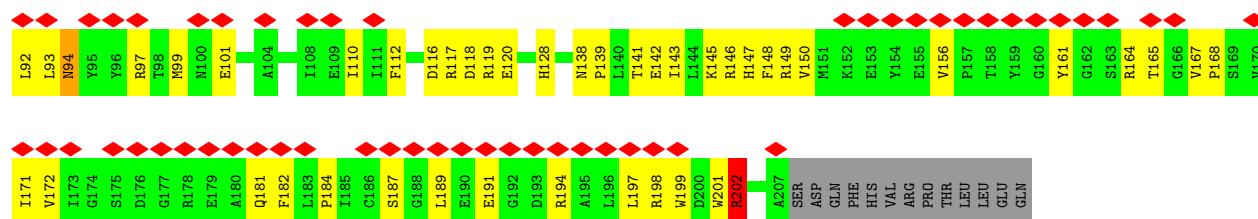


• Molecule 4: PDI family protein

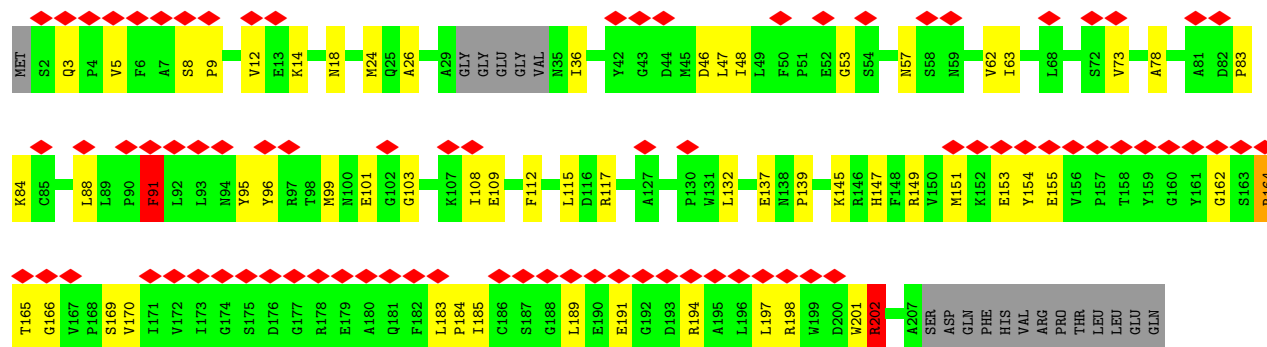


• Molecule 4: PDI family protein

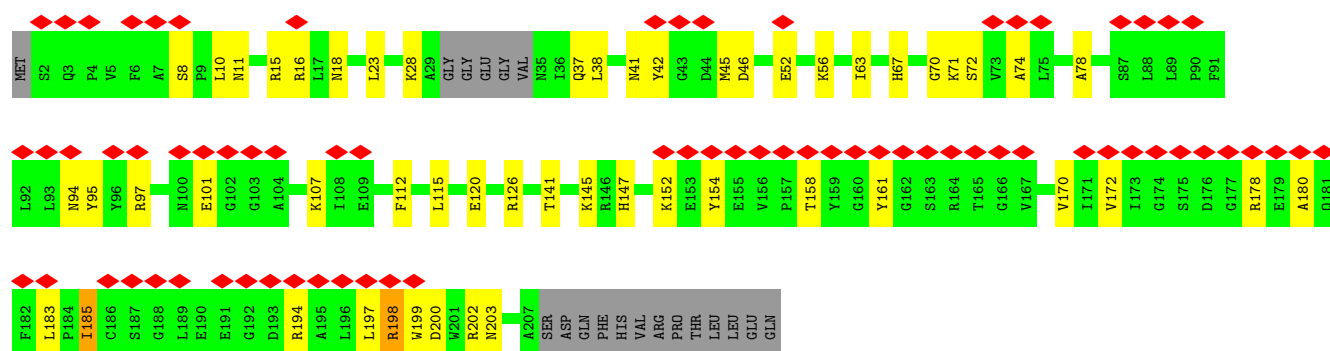




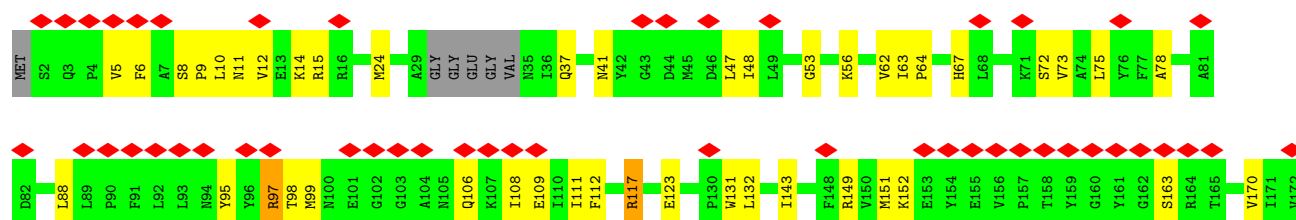
• Molecule 4: PDI family protein

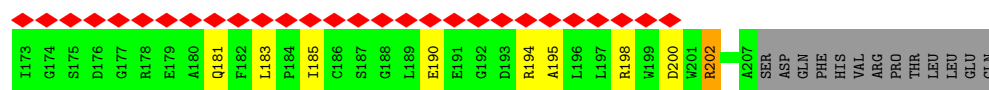


• Molecule 4: PDI family protein

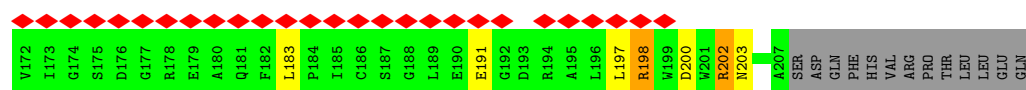
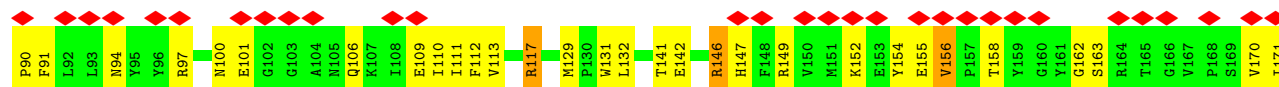
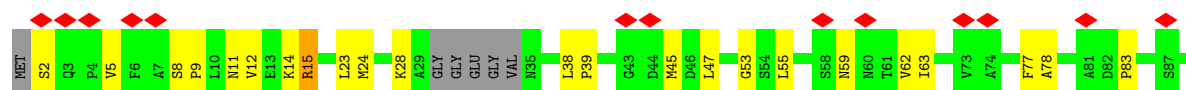


• Molecule 4: PDI family protein

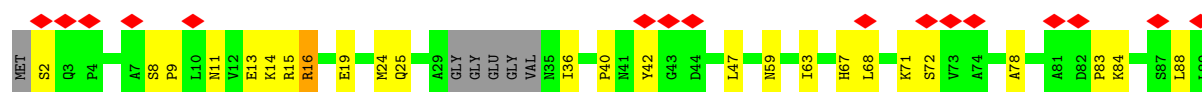




• Molecule 4: PDI family protein



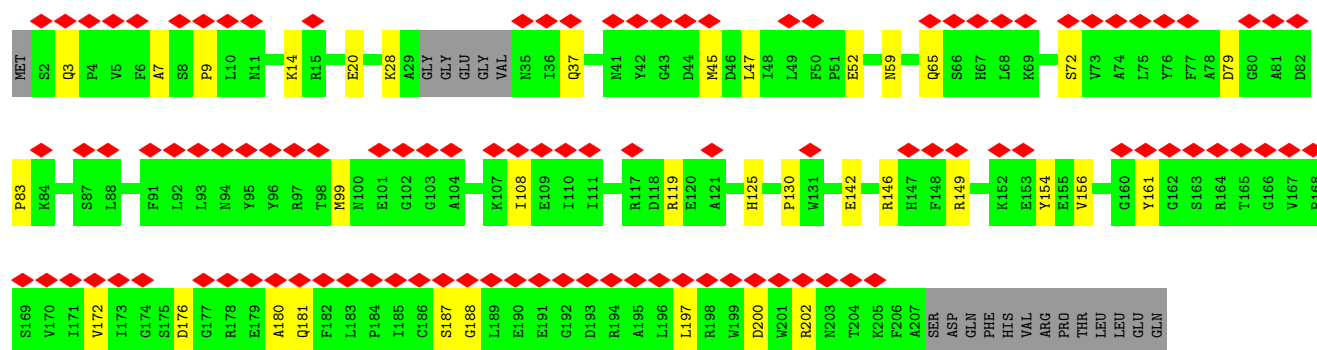
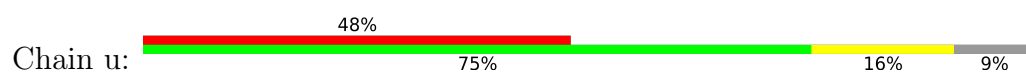
• Molecule 4: PDI family protein



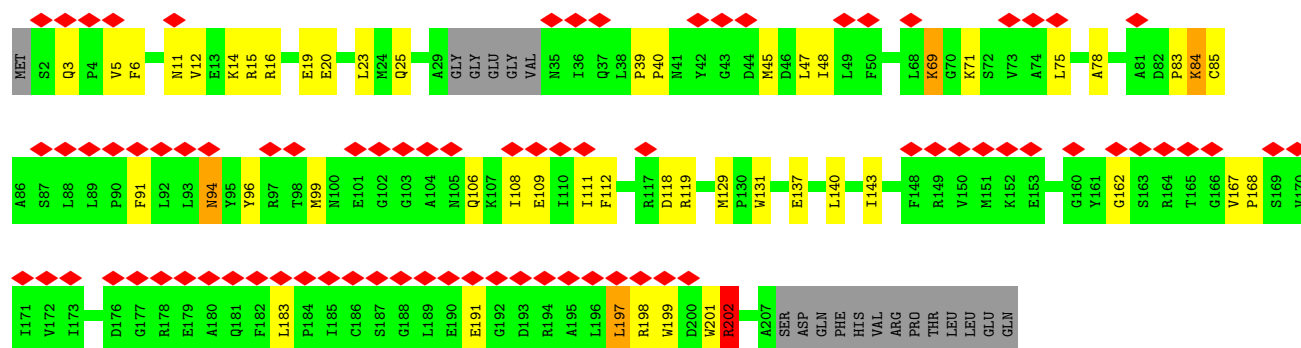
• Molecule 4: PDI family protein



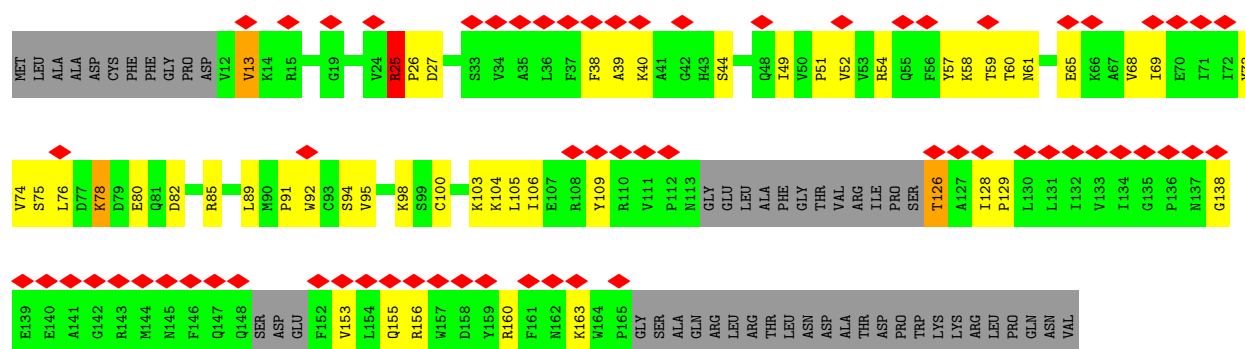
• Molecule 4: PDI family protein



• Molecule 4: PDI family protein

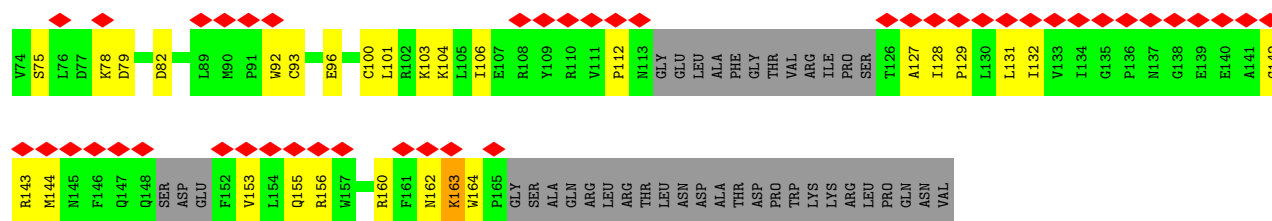


• Molecule 5: PDI family protein

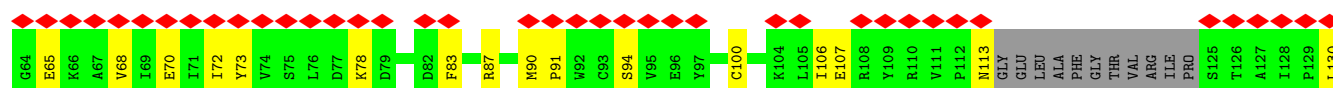


• Molecule 5: PDI family protein

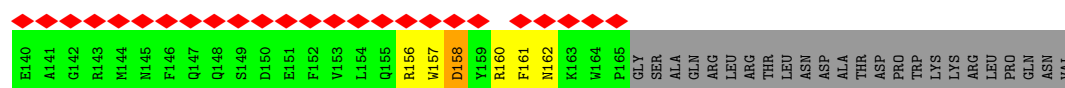
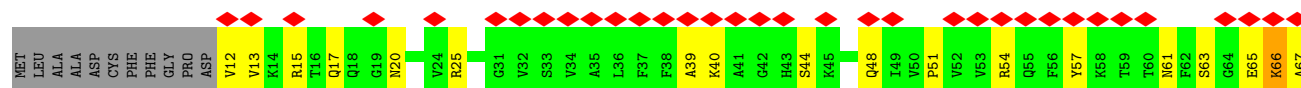




• Molecule 5: PDI family protein



• Molecule 5: PDI family protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	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	10.004	Depositor
Minimum map value	-8.373	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.892	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	447.444, 447.444, 447.444	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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	0.72	0/181	1.40	1/248 (0.4%)
1	1	0.68	0/181	1.40	2/248 (0.8%)
1	10	0.60	0/181	1.25	0/248
1	11	0.73	0/181	1.53	2/248 (0.8%)
1	12	0.74	0/181	1.73	6/248 (2.4%)
1	13	0.74	0/181	1.43	1/248 (0.4%)
1	14	0.65	0/181	1.11	1/248 (0.4%)
1	15	0.78	0/181	1.64	3/248 (1.2%)
1	16	0.62	0/181	1.25	1/248 (0.4%)
1	17	0.75	0/181	1.60	3/248 (1.2%)
1	18	0.69	0/181	1.37	0/248
1	19	1.09	2/181 (1.1%)	1.42	3/248 (1.2%)
1	2	0.75	0/181	1.41	0/248
1	20	0.59	0/181	1.05	0/248
1	21	0.85	0/181	1.39	2/248 (0.8%)
1	22	0.81	0/166	1.61	1/227 (0.4%)
1	23	0.67	0/166	1.34	0/227
1	3	0.65	0/181	1.20	0/248
1	4	0.67	0/181	1.43	2/248 (0.8%)
1	5	0.63	0/181	1.44	2/248 (0.8%)
1	6	0.67	0/181	1.56	4/248 (1.6%)
1	7	0.69	0/181	1.40	0/248
1	8	0.71	0/181	1.40	1/248 (0.4%)
1	9	0.70	0/181	1.32	1/248 (0.4%)
2	A0	0.71	0/3398	1.31	20/4606 (0.4%)
2	A2	0.66	1/3398 (0.0%)	1.18	13/4606 (0.3%)
2	A4	0.85	6/3398 (0.2%)	1.33	17/4606 (0.4%)
2	A6	0.67	1/3398 (0.0%)	1.23	17/4606 (0.4%)
2	A8	0.83	4/3398 (0.1%)	1.37	31/4606 (0.7%)
2	B0	0.67	1/3398 (0.0%)	1.19	15/4606 (0.3%)
2	B2	0.74	4/3398 (0.1%)	1.21	9/4606 (0.2%)
2	B4	0.62	1/3398 (0.0%)	1.09	6/4606 (0.1%)
2	B6	0.66	3/3398 (0.1%)	1.09	8/4606 (0.2%)
2	B8	0.60	0/3398	1.07	7/4606 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	C0	0.62	0/3398	1.09	3/4606 (0.1%)
2	C2	0.61	0/3398	1.09	3/4606 (0.1%)
2	C4	0.76	6/3398 (0.2%)	1.14	10/4606 (0.2%)
2	C6	0.68	0/3398	1.20	13/4606 (0.3%)
2	C8	0.70	1/3398 (0.0%)	1.18	8/4606 (0.2%)
2	D0	0.72	1/3398 (0.0%)	1.24	13/4606 (0.3%)
2	D2	0.64	0/3398	1.16	15/4606 (0.3%)
2	D4	0.79	2/3398 (0.1%)	1.33	22/4606 (0.5%)
2	D6	0.66	2/3398 (0.1%)	1.09	10/4606 (0.2%)
2	D8	0.70	1/3398 (0.0%)	1.23	20/4606 (0.4%)
2	E0	0.53	0/3398	0.96	6/4606 (0.1%)
2	E2	0.65	2/3398 (0.1%)	1.13	12/4606 (0.3%)
2	E4	0.53	0/3398	0.93	4/4606 (0.1%)
2	E6	0.60	0/3398	1.06	3/4606 (0.1%)
2	E8	0.50	0/3398	0.88	0/4606
2	F0	0.65	2/3398 (0.1%)	1.07	6/4606 (0.1%)
3	A1	0.69	4/3404 (0.1%)	1.19	12/4606 (0.3%)
3	A3	0.57	0/3404	1.08	7/4606 (0.2%)
3	A5	0.77	4/3404 (0.1%)	1.32	22/4606 (0.5%)
3	A7	0.58	0/3404	1.07	9/4606 (0.2%)
3	A9	0.72	3/3404 (0.1%)	1.20	8/4606 (0.2%)
3	B1	0.63	0/3404	1.13	7/4606 (0.2%)
3	B3	0.65	0/3404	1.21	10/4606 (0.2%)
3	B5	0.64	1/3404 (0.0%)	1.16	9/4606 (0.2%)
3	B7	0.60	0/3404	1.13	11/4606 (0.2%)
3	B9	0.58	2/3404 (0.1%)	1.09	11/4606 (0.2%)
3	C1	0.61	0/3404	1.12	14/4606 (0.3%)
3	C3	0.62	0/3404	1.14	10/4606 (0.2%)
3	C5	0.64	2/3404 (0.1%)	1.13	11/4606 (0.2%)
3	C7	0.68	2/3404 (0.1%)	1.18	11/4606 (0.2%)
3	C9	0.67	2/3404 (0.1%)	1.21	16/4606 (0.3%)
3	D1	0.83	7/3404 (0.2%)	1.39	27/4606 (0.6%)
3	D3	0.73	3/3404 (0.1%)	1.32	31/4606 (0.7%)
3	D5	0.81	3/3404 (0.1%)	1.42	33/4606 (0.7%)
3	D7	0.68	4/3404 (0.1%)	1.16	12/4606 (0.3%)
3	D9	0.72	3/3404 (0.1%)	1.24	12/4606 (0.3%)
3	E1	0.57	1/3404 (0.0%)	1.01	4/4606 (0.1%)
3	E3	0.64	1/3404 (0.0%)	1.14	16/4606 (0.3%)
3	E5	0.57	0/3404	1.07	9/4606 (0.2%)
3	E7	0.66	1/3404 (0.0%)	1.16	13/4606 (0.3%)
3	E9	0.58	0/3404	1.06	8/4606 (0.2%)
3	F1	0.68	1/3404 (0.0%)	1.25	19/4606 (0.4%)
4	a	0.78	3/1225 (0.2%)	1.28	8/1654 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	b	0.73	2/1225 (0.2%)	1.18	8/1654 (0.5%)
4	c	1.11	3/1645 (0.2%)	1.53	14/2225 (0.6%)
4	d	0.81	2/1645 (0.1%)	1.27	9/2225 (0.4%)
4	e	0.69	0/1645	1.25	9/2225 (0.4%)
4	f	0.67	0/1645	1.20	5/2225 (0.2%)
4	g	0.68	1/1645 (0.1%)	1.24	8/2225 (0.4%)
4	h	0.70	3/1645 (0.2%)	1.24	6/2225 (0.3%)
4	i	0.79	2/1645 (0.1%)	1.26	14/2225 (0.6%)
4	j	0.83	2/1645 (0.1%)	1.19	7/2225 (0.3%)
4	m	0.66	0/1645	1.19	10/2225 (0.4%)
4	n	0.82	3/1645 (0.2%)	1.28	15/2225 (0.7%)
4	o	0.66	0/1645	1.26	13/2225 (0.6%)
4	p	1.01	2/1645 (0.1%)	1.36	14/2225 (0.6%)
4	q	0.80	2/1645 (0.1%)	1.24	7/2225 (0.3%)
4	r	0.72	1/1645 (0.1%)	1.24	10/2225 (0.4%)
4	s	0.63	0/1645	1.19	9/2225 (0.4%)
4	t	0.83	2/1645 (0.1%)	1.25	6/2225 (0.3%)
4	u	0.65	0/1645	1.19	5/2225 (0.2%)
4	v	0.81	2/1645 (0.1%)	1.32	6/2225 (0.3%)
5	k	0.69	0/1168	1.31	10/1578 (0.6%)
5	l	0.68	1/1168 (0.1%)	1.23	5/1578 (0.3%)
5	w	0.63	1/1201 (0.1%)	1.08	1/1623 (0.1%)
5	x	0.75	0/1201	1.34	9/1623 (0.6%)
All	All	0.69	116/217964 (0.1%)	1.19	887/295182 (0.3%)

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	13	0	1
1	15	0	2
1	18	0	1
1	23	0	2
1	4	0	1
1	7	0	1
2	A0	0	1
2	A2	0	2
2	A4	0	2
2	A8	0	3
2	B0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	B4	0	1
2	B6	0	1
2	C4	0	1
2	C8	0	1
2	D0	0	2
2	D2	0	1
2	E2	0	1
3	B3	0	1
3	B9	0	1
3	E5	0	2
4	c	0	1
4	e	0	1
4	o	0	1
4	t	0	1
5	k	0	1
5	l	0	1
All	All	0	35

The worst 5 of 116 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	c	178	ARG	NE-CZ	28.66	1.64	1.33
4	p	97	ARG	NE-CZ	26.48	1.62	1.33
4	j	97	ARG	NE-CZ	18.65	1.53	1.33
4	t	97	ARG	NE-CZ	17.93	1.52	1.33
2	C4	2	ARG	CD-NE	17.05	1.70	1.46

The worst 5 of 887 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	c	178	ARG	NE-CZ-NH1	20.78	142.28	121.50
2	C4	2	ARG	CG-CD-NE	17.47	150.43	112.00
3	D1	213	ARG	CG-CD-NE	-15.03	78.93	112.00
4	t	97	ARG	CD-NE-CZ	14.87	145.22	124.40
3	C9	291	GLN	CB-CG-CD	14.39	137.06	112.60

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	13	255	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	15	237	PRO	Peptide
1	15	240	PRO	Peptide
1	18	242	ASN	Peptide
1	23	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	25	0
1	1	174	0	171	6	0
1	10	174	0	171	29	0
1	11	174	0	171	28	0
1	12	174	0	171	9	0
1	13	174	0	171	16	0
1	14	174	0	171	8	0
1	15	174	0	171	20	0
1	16	174	0	171	18	0
1	17	174	0	171	12	0
1	18	174	0	171	8	0
1	19	174	0	171	24	0
1	2	174	0	171	29	0
1	20	174	0	171	13	0
1	21	174	0	171	20	0
1	22	160	0	156	8	0
1	23	160	0	156	11	0
1	3	174	0	171	8	0
1	4	174	0	171	28	0
1	5	174	0	171	23	0
1	6	174	0	171	22	0
1	7	174	0	171	23	0
1	8	174	0	171	32	0
1	9	174	0	171	33	0
2	A0	3325	0	3252	99	0
2	A2	3325	0	3252	80	0
2	A4	3325	0	3252	86	0
2	A6	3325	0	3252	100	0
2	A8	3325	0	3252	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B0	3325	0	3252	85	0
2	B2	3325	0	3252	77	0
2	B4	3325	0	3252	89	0
2	B6	3325	0	3252	76	0
2	B8	3325	0	3252	98	0
2	C0	3325	0	3252	87	0
2	C2	3325	0	3252	108	0
2	C4	3325	0	3252	107	0
2	C6	3325	0	3252	125	0
2	C8	3325	0	3252	91	0
2	D0	3325	0	3252	114	0
2	D2	3325	0	3252	88	0
2	D4	3325	0	3252	126	0
2	D6	3325	0	3252	66	0
2	D8	3325	0	3252	107	0
2	E0	3325	0	3252	81	0
2	E2	3325	0	3252	64	0
2	E4	3325	0	3252	72	0
2	E6	3325	0	3252	95	0
2	E8	3325	0	3252	78	0
2	F0	3325	0	3252	101	0
3	A1	3331	0	3207	99	0
3	A3	3331	0	3209	58	0
3	A5	3331	0	3207	103	0
3	A7	3331	0	3207	71	0
3	A9	3331	0	3207	88	0
3	B1	3331	0	3209	75	0
3	B3	3331	0	3207	89	0
3	B5	3331	0	3207	73	0
3	B7	3331	0	3209	66	0
3	B9	3331	0	3209	66	0
3	C1	3331	0	3209	115	0
3	C3	3331	0	3209	99	0
3	C5	3331	0	3209	86	0
3	C7	3331	0	3209	96	0
3	C9	3331	0	3209	110	0
3	D1	3331	0	3209	89	0
3	D3	3331	0	3207	111	0
3	D5	3331	0	3207	121	0
3	D7	3331	0	3207	91	0
3	D9	3331	0	3207	84	0
3	E1	3331	0	3207	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E3	3331	0	3209	65	0
3	E5	3331	0	3207	80	0
3	E7	3331	0	3207	97	0
3	E9	3331	0	3207	84	0
3	F1	3331	0	3207	96	0
4	a	1198	0	1194	46	0
4	b	1198	0	1194	48	0
4	c	1608	0	1590	59	0
4	d	1608	0	1590	66	0
4	e	1608	0	1590	75	0
4	f	1608	0	1590	77	0
4	g	1608	0	1590	65	0
4	h	1608	0	1590	54	0
4	i	1608	0	1590	32	0
4	j	1608	0	1590	41	0
4	m	1608	0	1590	59	0
4	n	1608	0	1590	62	0
4	o	1608	0	1590	41	0
4	p	1608	0	1590	44	0
4	q	1608	0	1590	33	0
4	r	1608	0	1590	50	0
4	s	1608	0	1590	36	0
4	t	1608	0	1590	68	0
4	u	1608	0	1590	30	0
4	v	1608	0	1588	58	0
5	k	1140	0	1143	50	0
5	l	1140	0	1143	39	0
5	w	1172	0	1171	35	0
5	x	1172	0	1171	33	0
All	All	213168	0	207664	4846	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 12.

The worst 5 of 4846 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:19:241:PHE:CZ	3:E7:356:ILE:HG23	1.28	1.68
4:v:202:ARG:CD	4:v:202:ARG:NE	1.67	1.56
2:C4:2:ARG:CG	2:C4:2:ARG:CD	1.76	1.56
3:A9:252:LYS:CG	3:A9:252:LYS:CD	1.84	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:19:241:PHE:HZ	3:E7:356:ILE:CG2	1.03	1.54

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%)	16 (80%)	4 (20%)	0	100	100
1	12	20/351 (6%)	19 (95%)	1 (5%)	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%)	18 (90%)	2 (10%)	0	100	100
1	16	20/351 (6%)	20 (100%)	0	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%)	19 (95%)	1 (5%)	0	100	100
1	2	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	20	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	21	20/351 (6%)	18 (90%)	1 (5%)	1 (5%)	1	16
1	22	18/351 (5%)	16 (89%)	2 (11%)	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
1	4	20/351 (6%)	20 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	5	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	6	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	7	20/351 (6%)	20 (100%)	0	0	100	100
1	8	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	9	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
2	A0	424/453 (94%)	398 (94%)	26 (6%)	0	100	100
2	A2	424/453 (94%)	405 (96%)	18 (4%)	1 (0%)	43	78
2	A4	424/453 (94%)	393 (93%)	31 (7%)	0	100	100
2	A6	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
2	A8	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
2	B0	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	B2	424/453 (94%)	405 (96%)	19 (4%)	0	100	100
2	B4	424/453 (94%)	408 (96%)	16 (4%)	0	100	100
2	B6	424/453 (94%)	405 (96%)	19 (4%)	0	100	100
2	B8	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	C0	424/453 (94%)	402 (95%)	21 (5%)	1 (0%)	43	78
2	C2	424/453 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
2	C4	424/453 (94%)	386 (91%)	37 (9%)	1 (0%)	43	78
2	C6	424/453 (94%)	397 (94%)	27 (6%)	0	100	100
2	C8	424/453 (94%)	396 (93%)	28 (7%)	0	100	100
2	D0	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	D2	424/453 (94%)	404 (95%)	20 (5%)	0	100	100
2	D4	424/453 (94%)	409 (96%)	15 (4%)	0	100	100
2	D6	424/453 (94%)	408 (96%)	16 (4%)	0	100	100
2	D8	424/453 (94%)	407 (96%)	17 (4%)	0	100	100
2	E0	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
2	E2	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
2	E4	424/453 (94%)	399 (94%)	25 (6%)	0	100	100
2	E6	424/453 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
2	E8	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
2	F0	424/453 (94%)	401 (95%)	23 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A1	424/449 (94%)	397 (94%)	27 (6%)	0	100	100
3	A3	424/449 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
3	A5	424/449 (94%)	388 (92%)	34 (8%)	2 (0%)	24	63
3	A7	424/449 (94%)	397 (94%)	26 (6%)	1 (0%)	43	78
3	A9	424/449 (94%)	400 (94%)	23 (5%)	1 (0%)	43	78
3	B1	424/449 (94%)	401 (95%)	22 (5%)	1 (0%)	43	78
3	B3	424/449 (94%)	400 (94%)	22 (5%)	2 (0%)	24	63
3	B5	424/449 (94%)	394 (93%)	28 (7%)	2 (0%)	24	63
3	B7	424/449 (94%)	396 (93%)	28 (7%)	0	100	100
3	B9	424/449 (94%)	407 (96%)	17 (4%)	0	100	100
3	C1	424/449 (94%)	401 (95%)	23 (5%)	0	100	100
3	C3	424/449 (94%)	396 (93%)	27 (6%)	1 (0%)	43	78
3	C5	424/449 (94%)	402 (95%)	22 (5%)	0	100	100
3	C7	424/449 (94%)	396 (93%)	28 (7%)	0	100	100
3	C9	424/449 (94%)	396 (93%)	27 (6%)	1 (0%)	43	78
3	D1	424/449 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
3	D3	424/449 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
3	D5	424/449 (94%)	396 (93%)	28 (7%)	0	100	100
3	D7	424/449 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
3	D9	424/449 (94%)	402 (95%)	22 (5%)	0	100	100
3	E1	424/449 (94%)	402 (95%)	22 (5%)	0	100	100
3	E3	424/449 (94%)	402 (95%)	21 (5%)	1 (0%)	43	78
3	E5	424/449 (94%)	392 (92%)	32 (8%)	0	100	100
3	E7	424/449 (94%)	397 (94%)	26 (6%)	1 (0%)	43	78
3	E9	424/449 (94%)	388 (92%)	36 (8%)	0	100	100
3	F1	424/449 (94%)	389 (92%)	34 (8%)	1 (0%)	43	78
4	a	146/220 (66%)	135 (92%)	11 (8%)	0	100	100
4	b	146/220 (66%)	137 (94%)	9 (6%)	0	100	100
4	c	197/220 (90%)	188 (95%)	9 (5%)	0	100	100
4	d	197/220 (90%)	179 (91%)	18 (9%)	0	100	100
4	e	197/220 (90%)	183 (93%)	13 (7%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	f	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	g	197/220 (90%)	185 (94%)	11 (6%)	1 (0%)	24	63
4	h	197/220 (90%)	183 (93%)	14 (7%)	0	100	100
4	i	197/220 (90%)	186 (94%)	11 (6%)	0	100	100
4	j	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	m	197/220 (90%)	180 (91%)	17 (9%)	0	100	100
4	n	197/220 (90%)	186 (94%)	11 (6%)	0	100	100
4	o	197/220 (90%)	179 (91%)	18 (9%)	0	100	100
4	p	197/220 (90%)	182 (92%)	15 (8%)	0	100	100
4	q	197/220 (90%)	187 (95%)	10 (5%)	0	100	100
4	r	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	s	197/220 (90%)	179 (91%)	18 (9%)	0	100	100
4	t	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	u	197/220 (90%)	189 (96%)	7 (4%)	1 (0%)	24	63
4	v	197/220 (90%)	183 (93%)	14 (7%)	0	100	100
5	k	133/189 (70%)	127 (96%)	6 (4%)	0	100	100
5	l	133/189 (70%)	128 (96%)	5 (4%)	0	100	100
5	w	139/189 (74%)	133 (96%)	6 (4%)	0	100	100
5	x	139/189 (74%)	129 (93%)	10 (7%)	0	100	100
All	All	26906/37032 (73%)	25298 (94%)	1580 (6%)	28 (0%)	49	83

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A3	179	VAL
3	A5	55	THR
3	A7	55	THR
3	B3	55	THR
3	C3	179	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	20/304 (7%)	20 (100%)	0	100	100
1	1	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	10	20/304 (7%)	20 (100%)	0	100	100
1	11	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	12	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	13	20/304 (7%)	20 (100%)	0	100	100
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%)	17 (94%)	1 (6%)	19	40
1	23	18/304 (6%)	18 (100%)	0	100	100
1	3	20/304 (7%)	20 (100%)	0	100	100
1	4	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	5	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	6	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	7	20/304 (7%)	20 (100%)	0	100	100
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%)	351 (98%)	8 (2%)	45	64
2	A2	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	A4	359/379 (95%)	346 (96%)	13 (4%)	31	52
2	A6	359/379 (95%)	348 (97%)	11 (3%)	35	56
2	A8	359/379 (95%)	358 (100%)	1 (0%)	86	86
2	B0	359/379 (95%)	351 (98%)	8 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B2	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	B4	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	B6	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	B8	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	C0	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	C2	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	C4	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	C6	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	C8	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	D0	359/379 (95%)	354 (99%)	5 (1%)	59	72
2	D2	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	D4	359/379 (95%)	349 (97%)	10 (3%)	38	60
2	D6	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	D8	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	E0	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	E2	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	E4	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	E6	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	E8	359/379 (95%)	358 (100%)	1 (0%)	86	86
2	F0	359/379 (95%)	353 (98%)	6 (2%)	53	69
3	A1	364/381 (96%)	362 (100%)	2 (0%)	81	83
3	A3	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	A5	364/381 (96%)	356 (98%)	8 (2%)	45	64
3	A7	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	A9	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	B1	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	B3	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	B5	364/381 (96%)	356 (98%)	8 (2%)	45	64
3	B7	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	B9	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	C1	364/381 (96%)	358 (98%)	6 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C3	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	C5	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	C7	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	C9	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	D1	364/381 (96%)	353 (97%)	11 (3%)	36	57
3	D3	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	D5	364/381 (96%)	351 (96%)	13 (4%)	31	52
3	D7	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	D9	364/381 (96%)	356 (98%)	8 (2%)	45	64
3	E1	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	E3	364/381 (96%)	353 (97%)	11 (3%)	36	57
3	E5	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	E7	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	E9	364/381 (96%)	362 (100%)	2 (0%)	81	83
3	F1	364/381 (96%)	357 (98%)	7 (2%)	50	67
4	a	130/190 (68%)	128 (98%)	2 (2%)	57	72
4	b	130/190 (68%)	128 (98%)	2 (2%)	57	72
4	c	174/190 (92%)	168 (97%)	6 (3%)	32	54
4	d	174/190 (92%)	165 (95%)	9 (5%)	21	42
4	e	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	f	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	g	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	h	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	i	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	j	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	m	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	n	174/190 (92%)	169 (97%)	5 (3%)	37	58
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%)	169 (97%)	5 (3%)	37	58
4	r	174/190 (92%)	168 (97%)	6 (3%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	s	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	t	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	u	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	v	174/190 (92%)	168 (97%)	6 (3%)	32	54
5	k	122/164 (74%)	116 (95%)	6 (5%)	22	43
5	l	122/164 (74%)	119 (98%)	3 (2%)	42	63
5	w	127/164 (77%)	122 (96%)	5 (4%)	28	49
5	x	127/164 (77%)	123 (97%)	4 (3%)	35	56
All	All	23164/31512 (74%)	22724 (98%)	440 (2%)	49	67

5 of 440 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D3	362	LYS
2	E0	163	LYS
5	x	110	ARG
4	o	117	ARG
2	D4	248	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 355 such sidechains are listed below:

Mol	Chain	Res	Type
3	D9	291	GLN
3	F1	337	ASN
3	E1	191	GLN
2	E6	35	GLN
4	e	106	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

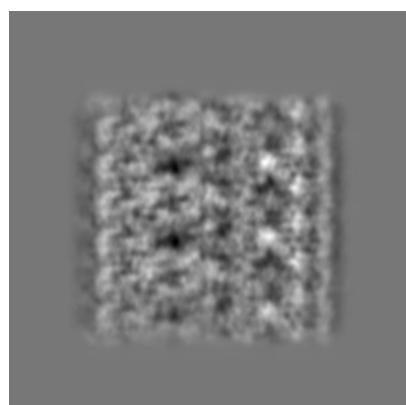
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26018. These allow visual inspection of the internal detail of the map and identification of artifacts.

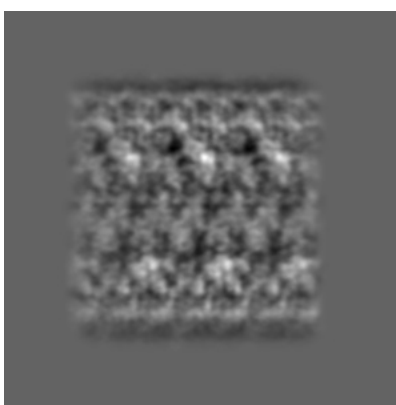
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

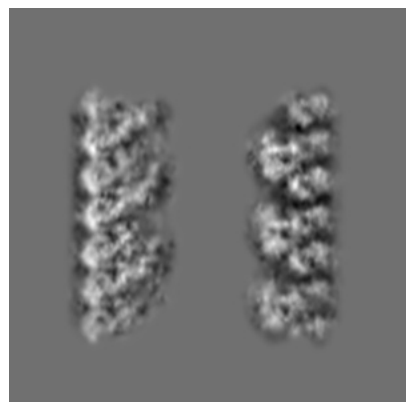


Z

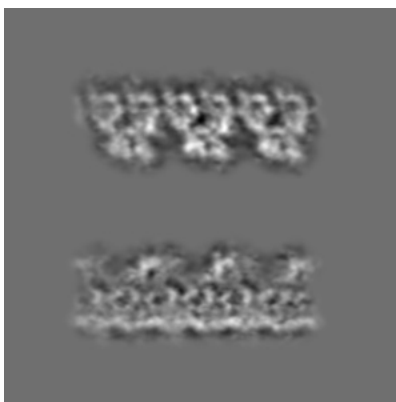
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 108



Y Index: 108

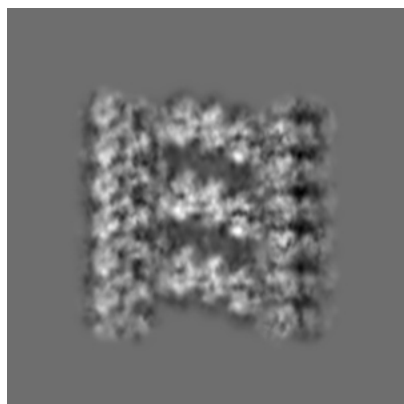


Z Index: 108

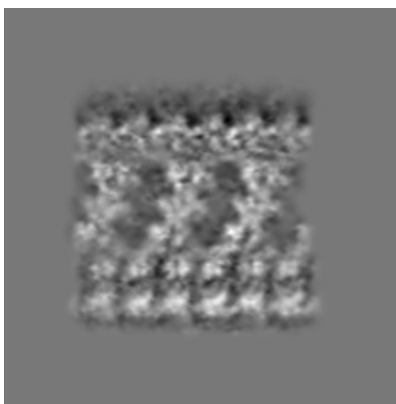
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 137



Y Index: 139

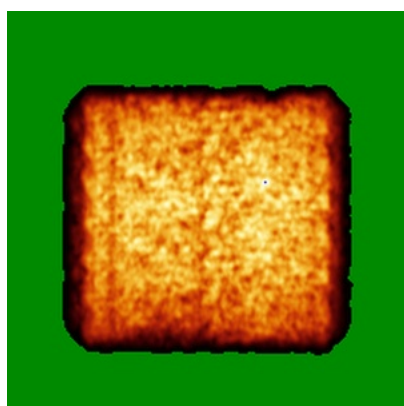


Z Index: 114

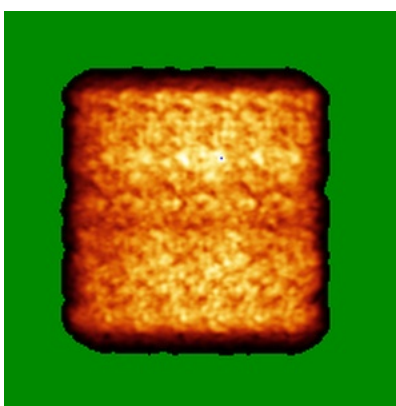
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

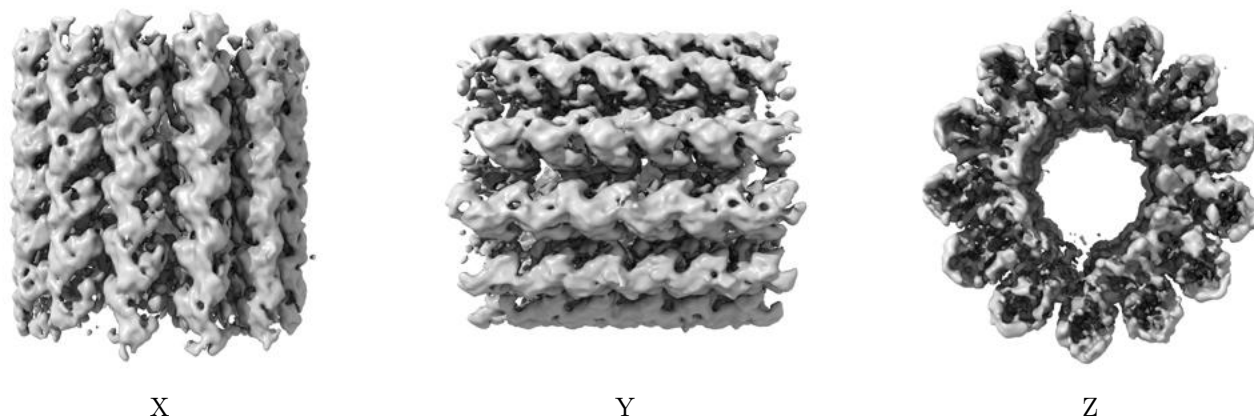


Z

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.

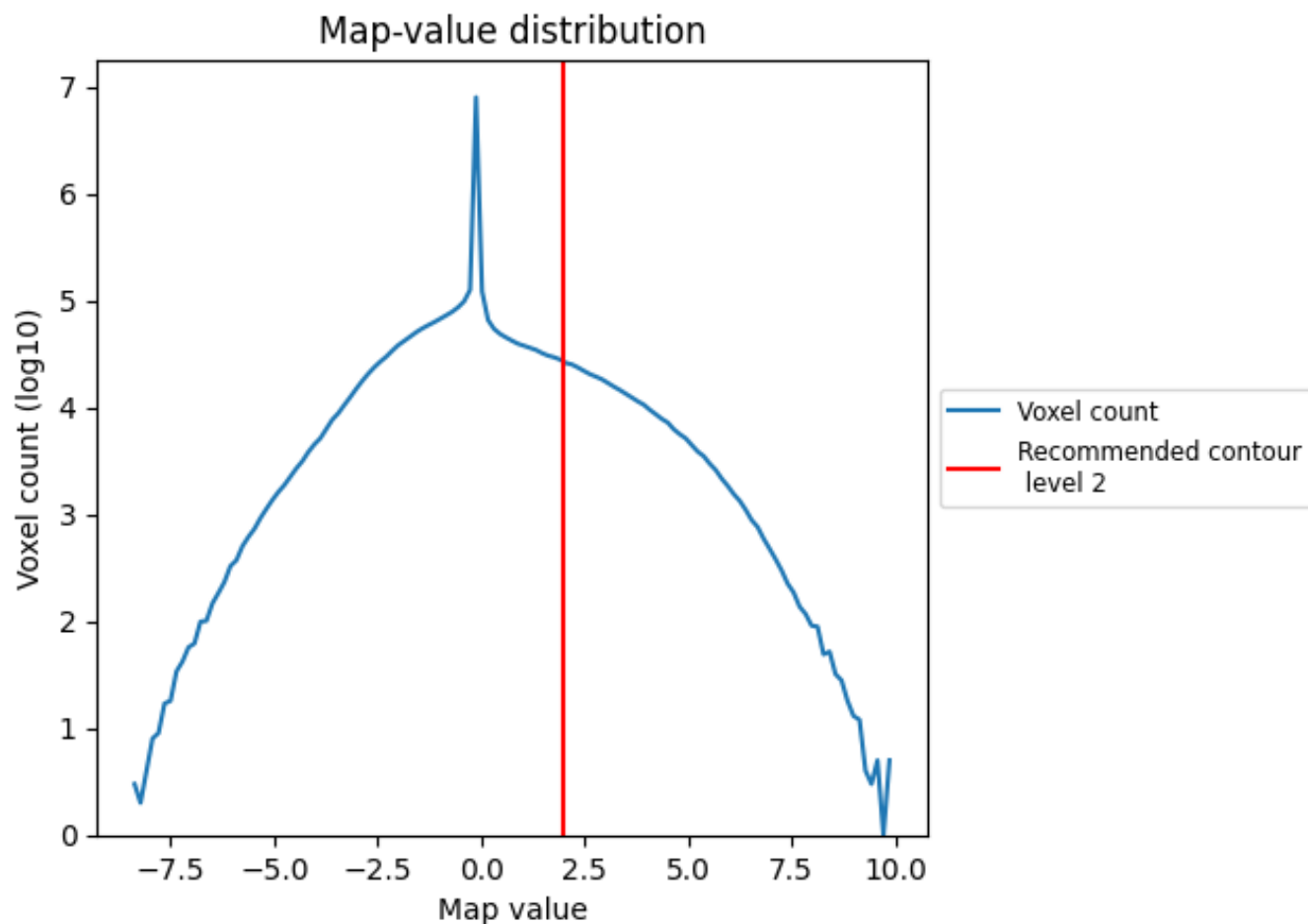
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

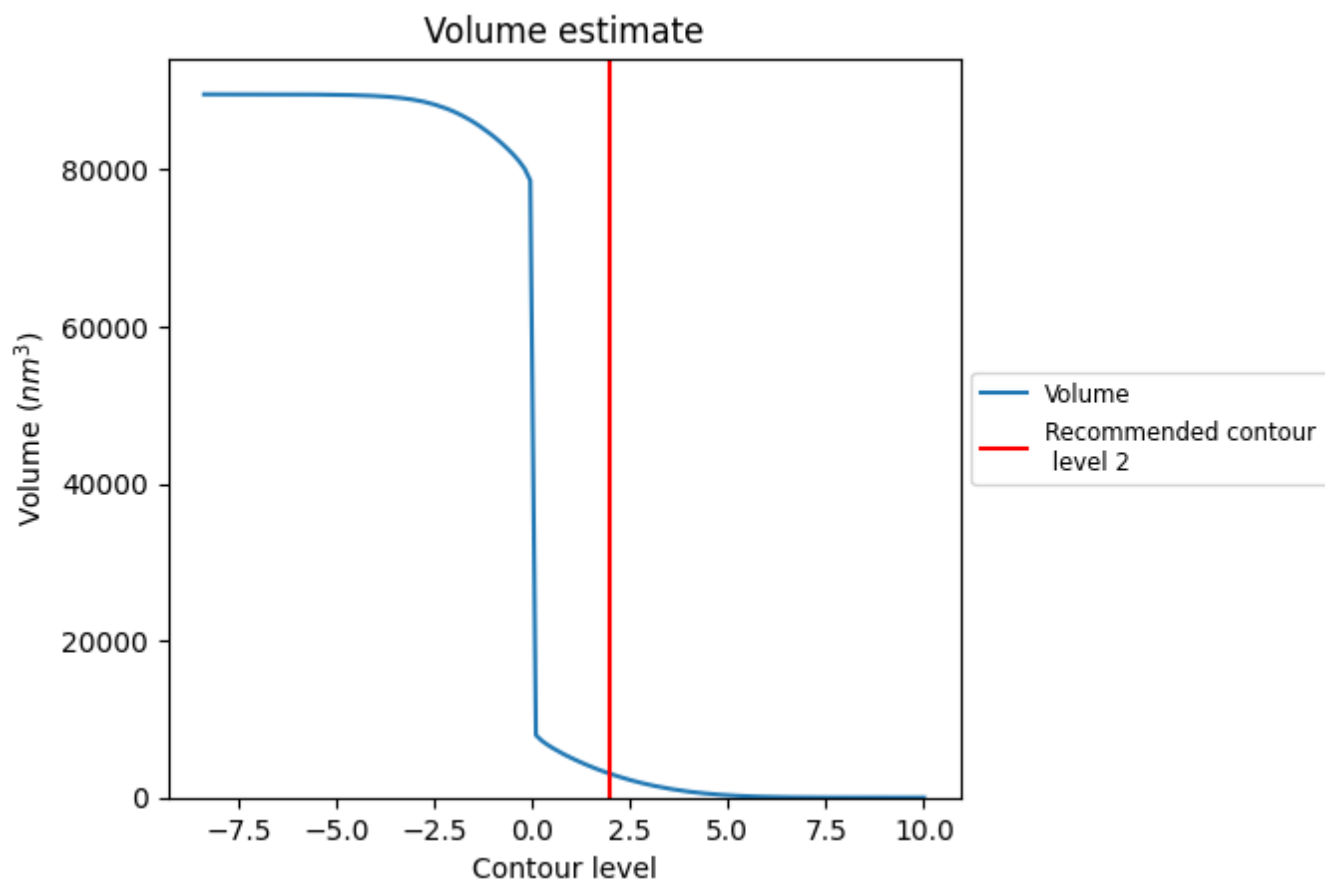
This section contains the results of statistical analysis of the map.

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.

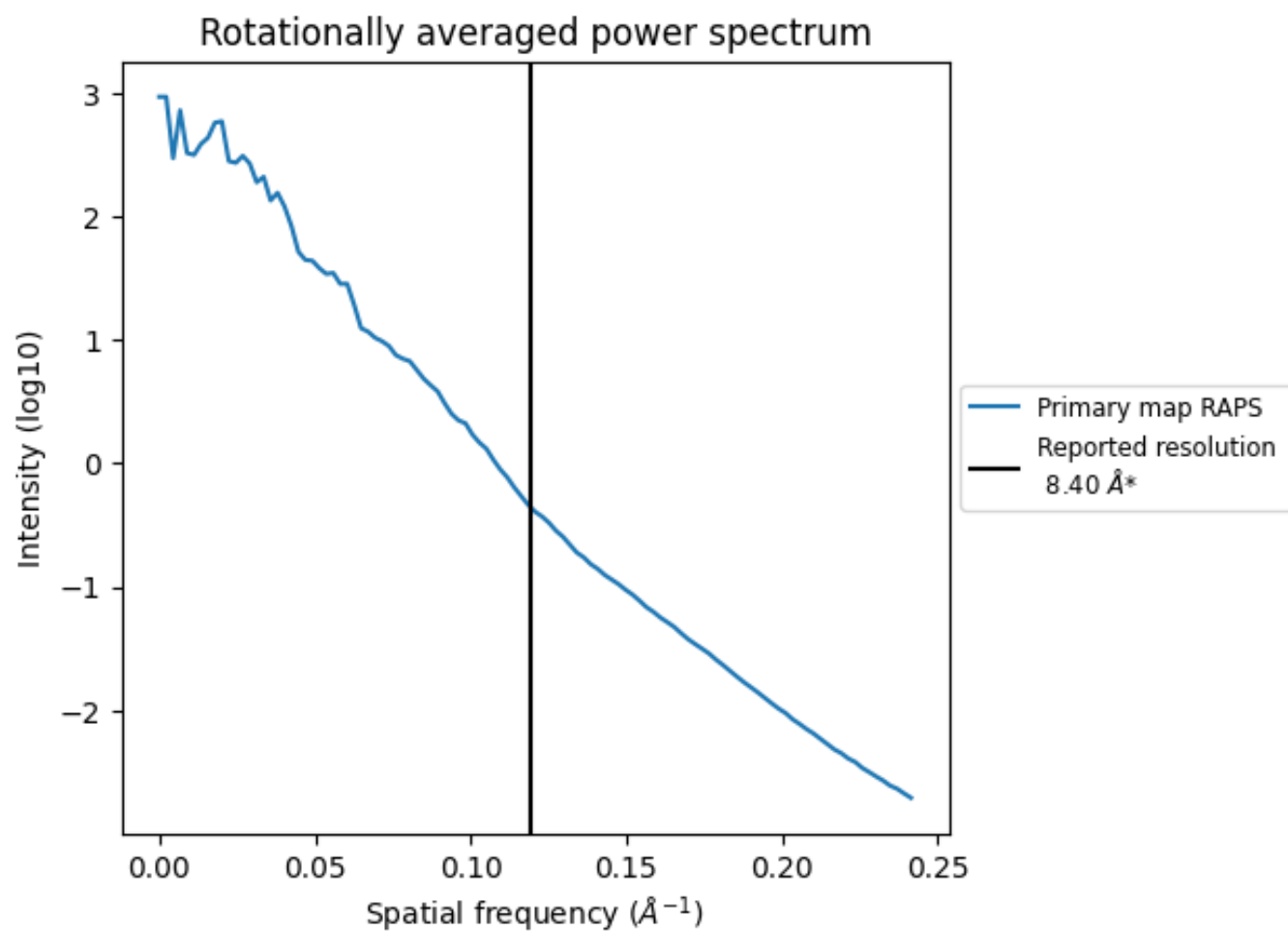
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3015 nm³; this corresponds to an approximate mass of 2724 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 0.119 Å⁻¹

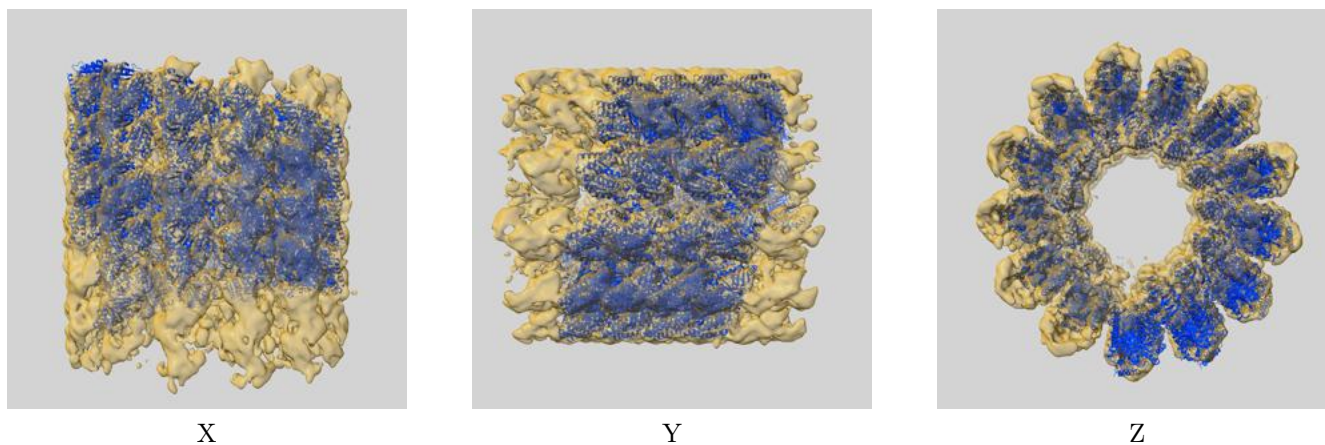
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

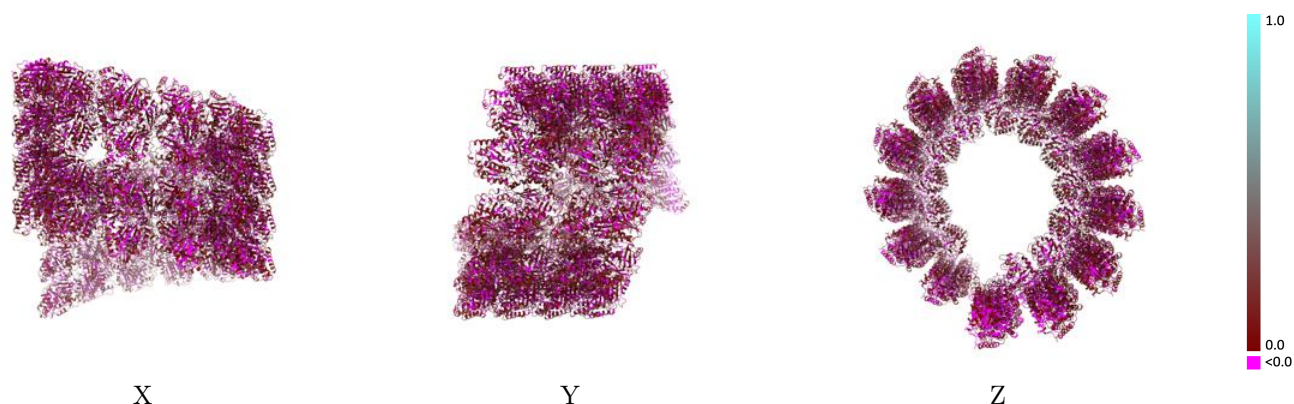
This section contains information regarding the fit between EMDB map EMD-26018 and PDB model 7TNQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



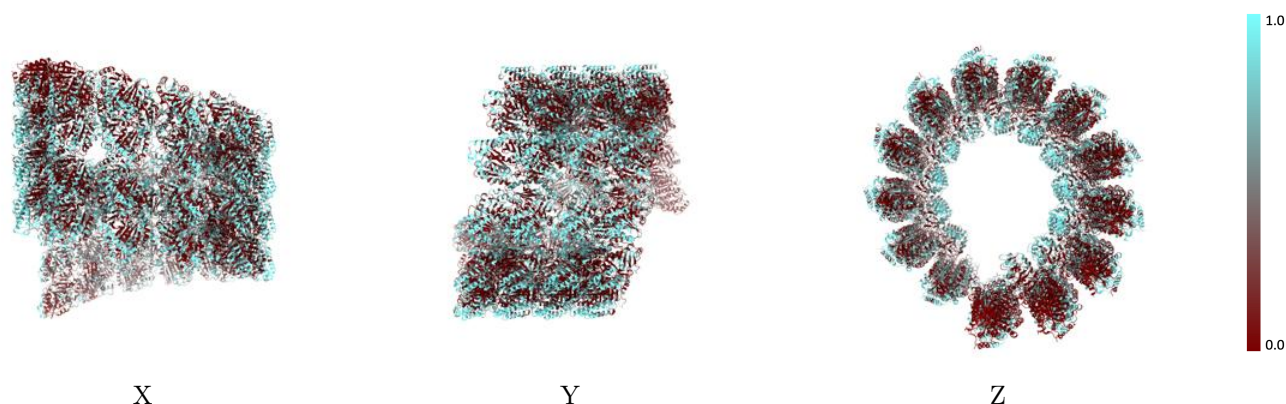
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



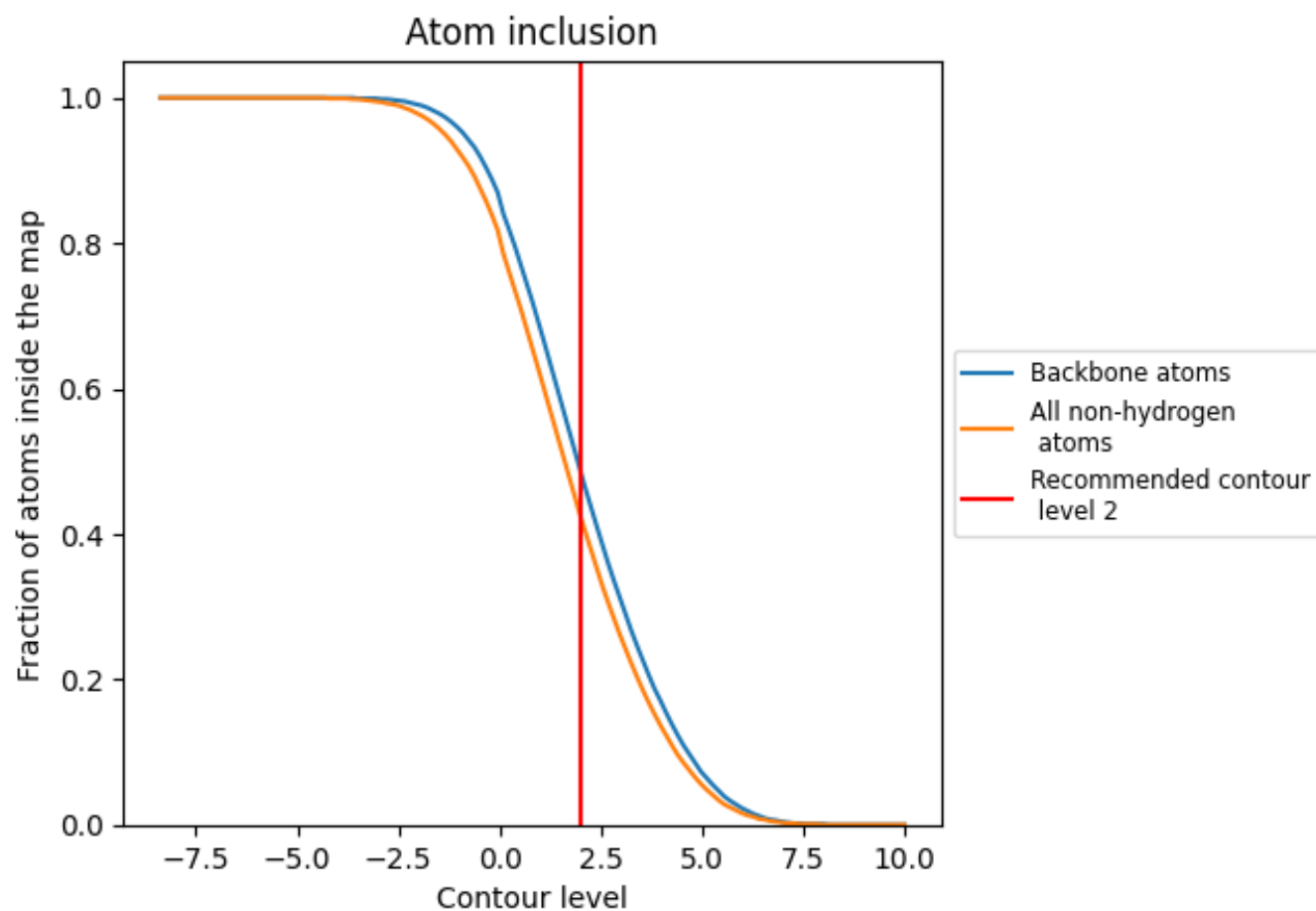
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 49% of all backbone atoms, 42% 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	 0.4240	 0.0760
0	 0.1290	 0.1680
1	 0.0000	 0.0940
10	 0.0820	 0.0720
11	 0.0470	 0.1110
12	 0.1710	 0.1250
13	 0.1470	 0.1000
14	 0.0180	 0.0900
15	 0.0940	 0.1000
16	 0.1350	 0.1160
17	 0.2590	 0.1140
18	 0.1820	 0.0380
19	 0.2410	 0.0440
2	 0.1120	 0.1250
20	 0.1410	 0.0080
21	 0.4230	 0.0670
22	 0.0190	 0.0960
23	 0.0130	 0.1160
3	 0.0650	 0.1040
4	 0.1290	 0.1020
5	 0.1180	 0.1400
6	 0.1290	 0.0710
7	 0.1470	 0.1150
8	 0.0760	 0.0500
9	 0.0290	 0.0540
A0	 0.4570	 0.0780
A1	 0.4220	 0.0750
A2	 0.4210	 0.0760
A3	 0.2960	 0.0730
A4	 0.4700	 0.0730
A5	 0.4630	 0.0750
A6	 0.4380	 0.0780
A7	 0.3430	 0.0670
A8	 0.4370	 0.0720
A9	 0.4450	 0.0830



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Chain	Atom inclusion	Q-score
B0	0.4220	0.0810
B1	0.3690	0.0780
B2	0.4200	0.0800
B3	0.4480	0.0790
B4	0.4340	0.0810
B5	0.3970	0.0760
B6	0.4140	0.0790
B7	0.5220	0.0920
B8	0.4770	0.0920
B9	0.4330	0.0850
C0	0.4230	0.0770
C1	0.5340	0.0910
C2	0.4690	0.0920
C3	0.4730	0.0890
C4	0.4010	0.0880
C5	0.4720	0.0910
C6	0.4550	0.0830
C7	0.4460	0.0890
C8	0.3750	0.0630
C9	0.4450	0.0740
D0	0.4290	0.0600
D1	0.3940	0.0560
D2	0.3460	0.0480
D3	0.4020	0.0600
D4	0.4090	0.0630
D5	0.3920	0.0520
D6	0.3360	0.0680
D7	0.4160	0.0710
D8	0.4200	0.0730
D9	0.4310	0.0690
E0	0.2840	0.0700
E1	0.4700	0.0890
E2	0.4410	0.0810
E3	0.4960	0.0820
E4	0.1810	0.0390
E5	0.4740	0.0670
E6	0.4780	0.0800
E7	0.5310	0.0850
E8	0.1180	-0.0050
E9	0.4120	0.0750
F0	0.4420	0.0840
F1	0.5000	0.0860

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Chain	Atom inclusion	Q-score
a	 0.3480	 0.1010
b	 0.2640	 0.0810
c	 0.4900	 0.1010
d	 0.3900	 0.0780
e	 0.5520	 0.0950
f	 0.4870	 0.0930
g	 0.5360	 0.0850
h	 0.5170	 0.0850
i	 0.4540	 0.0550
j	 0.4620	 0.0640
k	 0.4650	 0.0850
l	 0.4770	 0.0960
m	 0.4800	 0.0800
n	 0.5180	 0.1010
o	 0.5300	 0.0910
p	 0.5650	 0.1010
q	 0.5510	 0.0870
r	 0.5860	 0.1040
s	 0.5570	 0.0850
t	 0.6030	 0.0800
u	 0.4430	 0.0570
v	 0.5680	 0.0740
w	 0.1920	 0.0270
x	 0.2870	 0.0190