wwPDB EM Validation Summary Report

Dec 10, 2022 – 09:41 am GMT

PDB ID	:	5FLZ
EMDB ID	:	EMD-2799
Title	:	Cryo-EM structure of gamma-TuSC oligomers in a closed conformation
Authors	:	Greenberg, C.H.; Kollman, J.; Zelter, A.; Johnson, R.; MacCoss, M.J.; Davis, T.N.; Agard, D.A.; Sali, A.
Deposited on	:	2015-10-29
Resolution	:	6.90 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

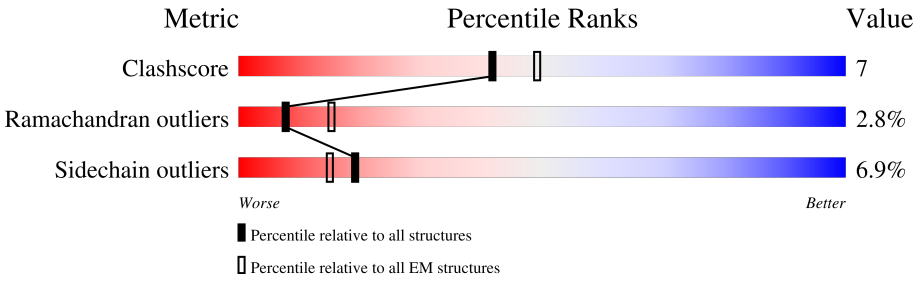
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 6.90 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	1-A	823	46% 18% 5% • 30%
1	10-A	823	44% 20% 5% • 30%
1	2-A	823	45% 18% 5% • 30%
1	3-A	823	44% 20% 5% • 30%
1	4-A	823	44% 20% 5% • 30%
1	5-A	823	43% 20% 5% • 30%
1	6-A	823	44% 20% 5% • 30%
1	7-A	823	45% 17% 6% • 30%

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Mol	Chain	Length	Quality of chain
1	8-A	823	43% 22% 5% • 30%
1	9-A	823	43% 21% 5% • 30%
2	1-B	846	• 42% 18% 6% • 33%
2	10-B	846	42% 19% 5% • 33%
2	2-B	846	42% 19% • • 33%
2	3-B	846	44% 16% 6% • 33%
2	4-B	846	40% 20% 6% • 33%
2	5-B	846	42% 19% 5% • 33%
2	6-B	846	41% 20% 5% • 33%
2	7-B	846	43% 19% • • 33%
2	8-B	846	42% 19% 5% • 33%
2	9-B	846	40% 19% 7% • 33%
3	1-C	473	13% 63% 23% 7% 6%
3	1-D	473	14% 64% 23% 5% • 6%
3	10-C	473	65% 22% 7% 6%
3	10-D	473	61% 27% 5% 6%
3	2-C	473	64% 26% • • 6%
3	2-D	473	64% 25% 5% • 6%
3	3-C	473	62% 27% 5% • 6%
3	3-D	473	65% 24% 5% 6%
3	4-C	473	63% 25% 5% • 6%
3	4-D	473	63% 24% 5% • 6%
3	5-C	473	62% 25% 6% 6%
3	5-D	473	63% 26% 5% • 6%
3	6-C	473	65% 25% • • 6%

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Mol	Chain	Length	Quality of chain
3	6-D	473	62% 27% 6%
3	7-C	473	60% 29% 5% 6%
3	7-D	473	63% 25% 5% 6%
3	8-C	473	65% 23% 5% 6%
3	8-D	473	65% 25% 6%
3	9-C	473	68% 21% 5% 6%
3	9-D	473	64% 25% 5% 6%
4	1-E	44	20% 100%
4	1-F	44	20% 100%
4	10-E	44	100%
4	10-F	44	100%
4	2-E	44	100%
4	2-F	44	100%
4	3-E	44	100%
4	3-F	44	100%
4	4-E	44	100%
4	4-F	44	100%
4	5-E	44	100%
4	5-F	44	100%
4	6-E	44	100%
4	6-F	44	100%
4	7-E	44	100%
4	7-F	44	100%
4	8-E	44	100%
4	8-F	44	95% 5%

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Mol	Chain	Length	Quality of chain
4	9-E	44	100%
4	9-F	44	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 169420 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 SPINDLE POLE BODY COMPONENT SPC97.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	2-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	3-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	4-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	5-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	6-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	7-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	8-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	9-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	10-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		

- Molecule 2 is a protein called SPINDLE POLE BODY COMPONENT SPC98.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	2-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	3-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	4-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	5-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	7-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	8-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	9-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	10-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		

- Molecule 3 is a protein called TUBULIN GAMMA CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	2-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	3-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	4-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	5-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	6-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	7-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	8-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	9-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	10-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	1-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	2-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	3-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	4-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	5-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	6-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	7-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	8-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	9-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	10-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	58	CYS	SER	engineered mutation	UNP P53378
C	288	CYS	GLY	engineered mutation	UNP P53378
D	58	CYS	SER	engineered mutation	UNP P53378
D	288	CYS	GLY	engineered mutation	UNP P53378

- Molecule 4 is a protein called SPINDLE POLE BODY COMPONENT 110.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	1-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	2-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	3-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	4-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	5-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	6-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	7-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	8-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	9-E	44	Total	C	N	O	0	0
			220	132	44	44		

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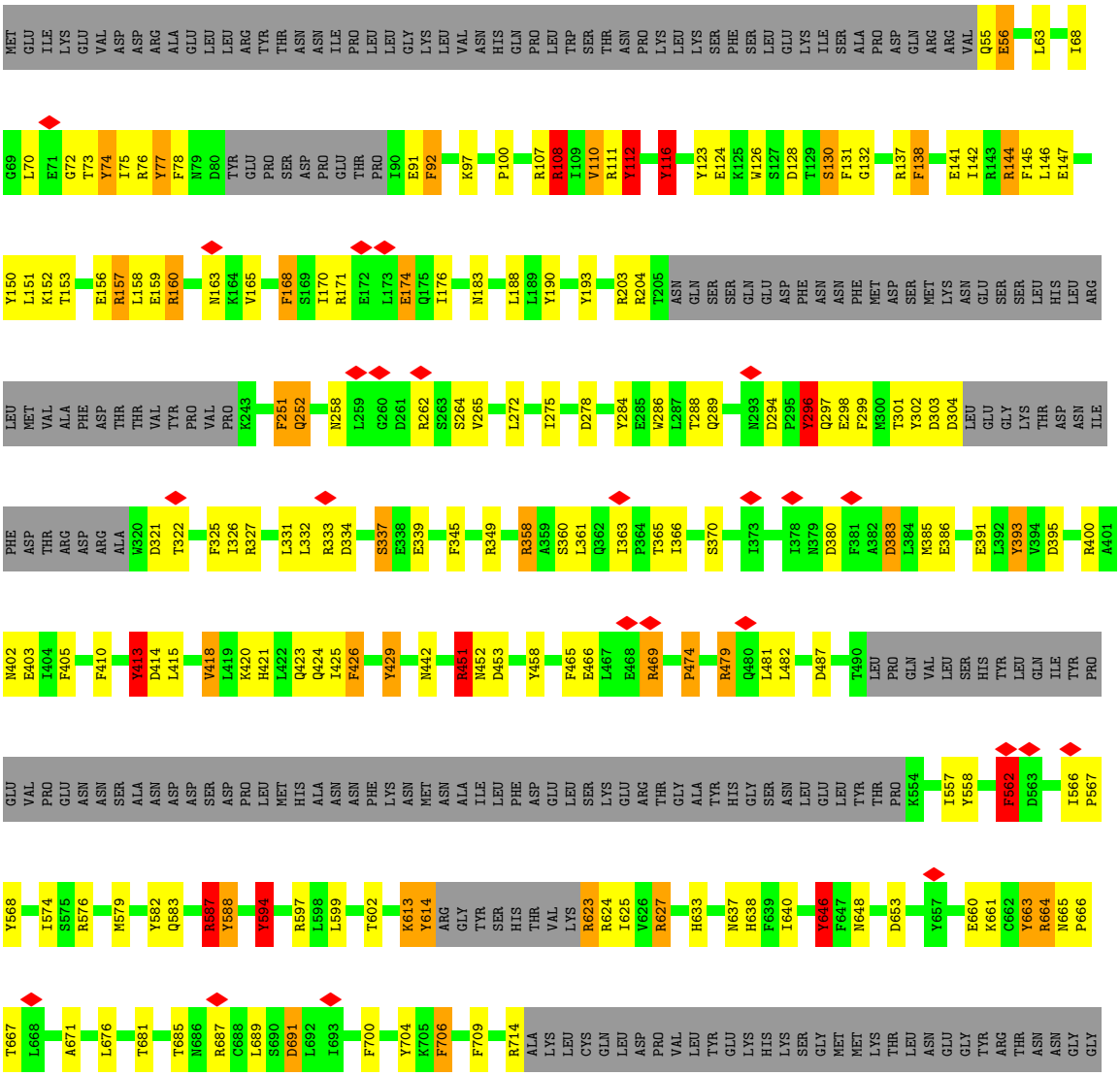
Mol	Chain	Residues	Atoms				AltConf	Trace
4	10-E	44	Total 220	C 132	N 44	O 44	0	0
4	1-F	44	Total 220	C 132	N 44	O 44	0	0
4	2-F	44	Total 220	C 132	N 44	O 44	0	0
4	3-F	44	Total 220	C 132	N 44	O 44	0	0
4	4-F	44	Total 220	C 132	N 44	O 44	0	0
4	5-F	44	Total 220	C 132	N 44	O 44	0	0
4	6-F	44	Total 220	C 132	N 44	O 44	0	0
4	7-F	44	Total 220	C 132	N 44	O 44	0	0
4	8-F	44	Total 220	C 132	N 44	O 44	0	0
4	9-F	44	Total 220	C 132	N 44	O 44	0	0
4	10-F	44	Total 220	C 132	N 44	O 44	0	0

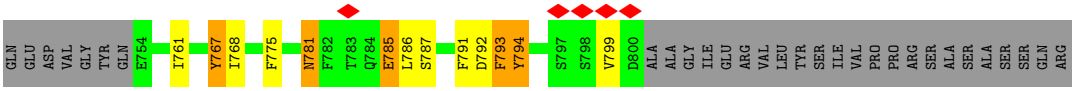
3 Residue-property plots (i)

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: SPINDLE POLE BODY COMPONENT SPC97

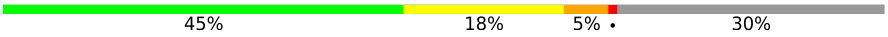
Chain 1-A:

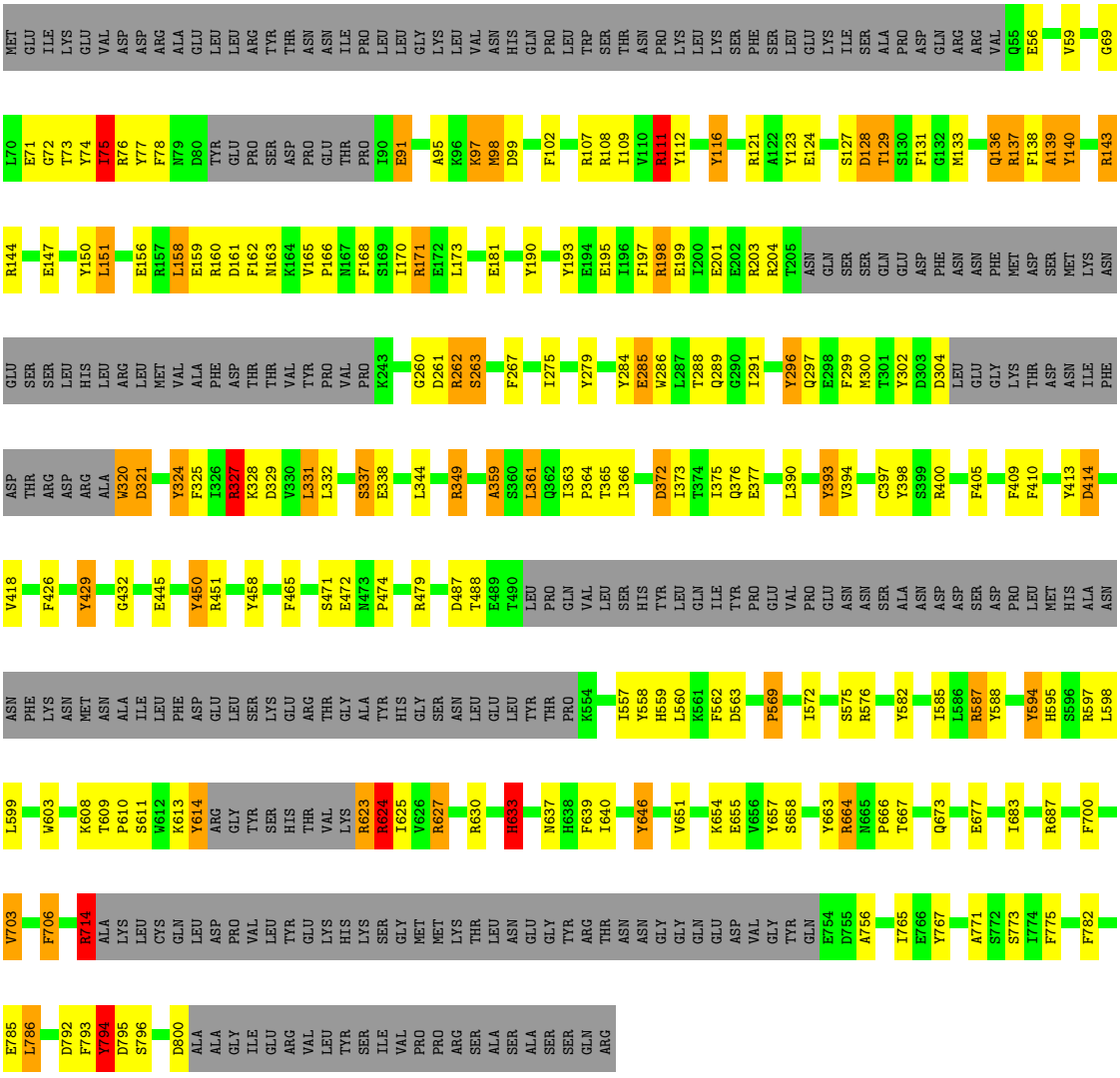




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

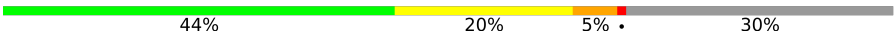
Chain 2-A:

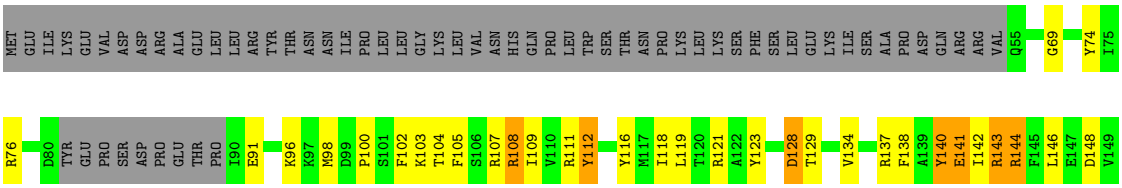


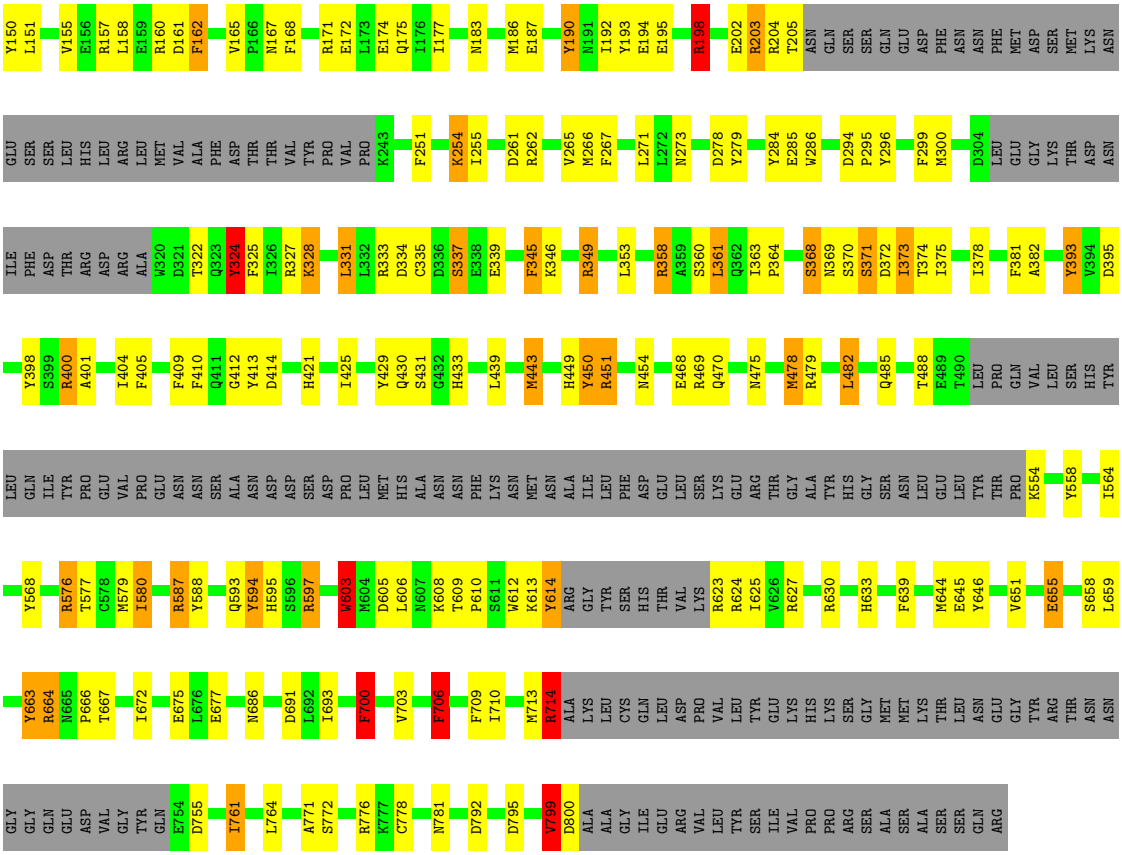


• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 3-A:

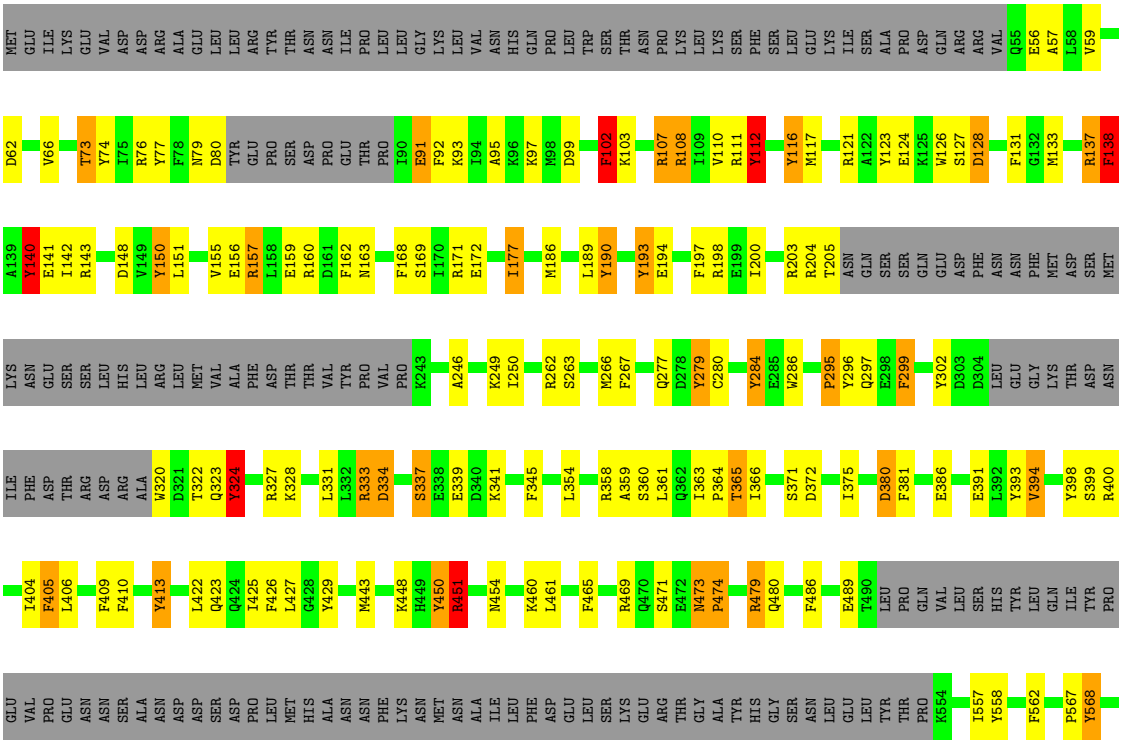


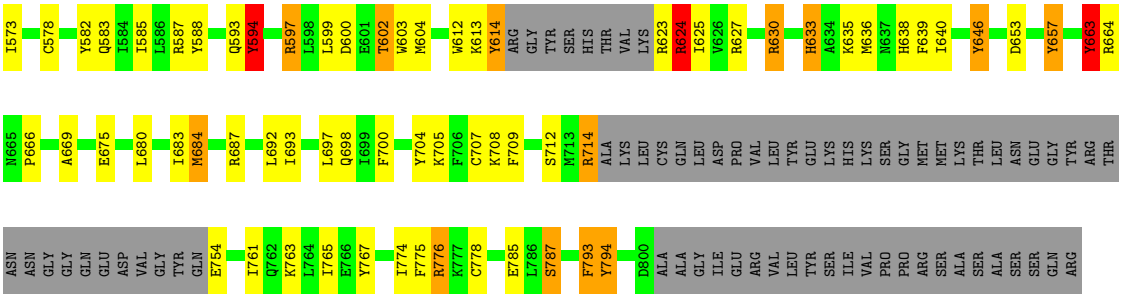




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

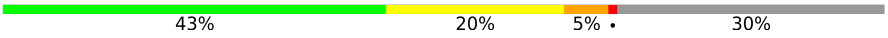
Chain 4-A:

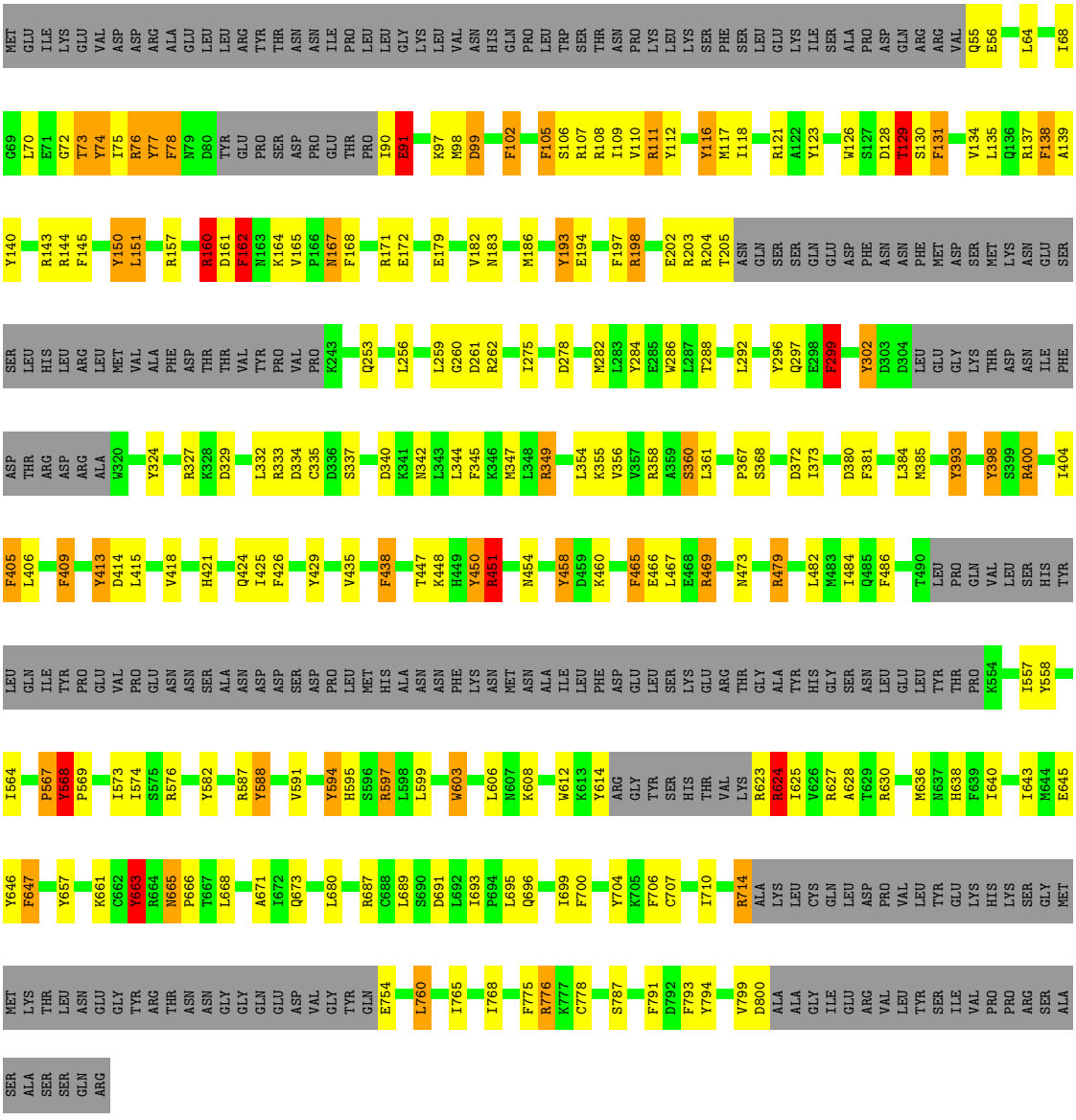




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

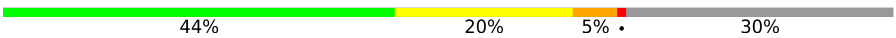
Chain 5-A:

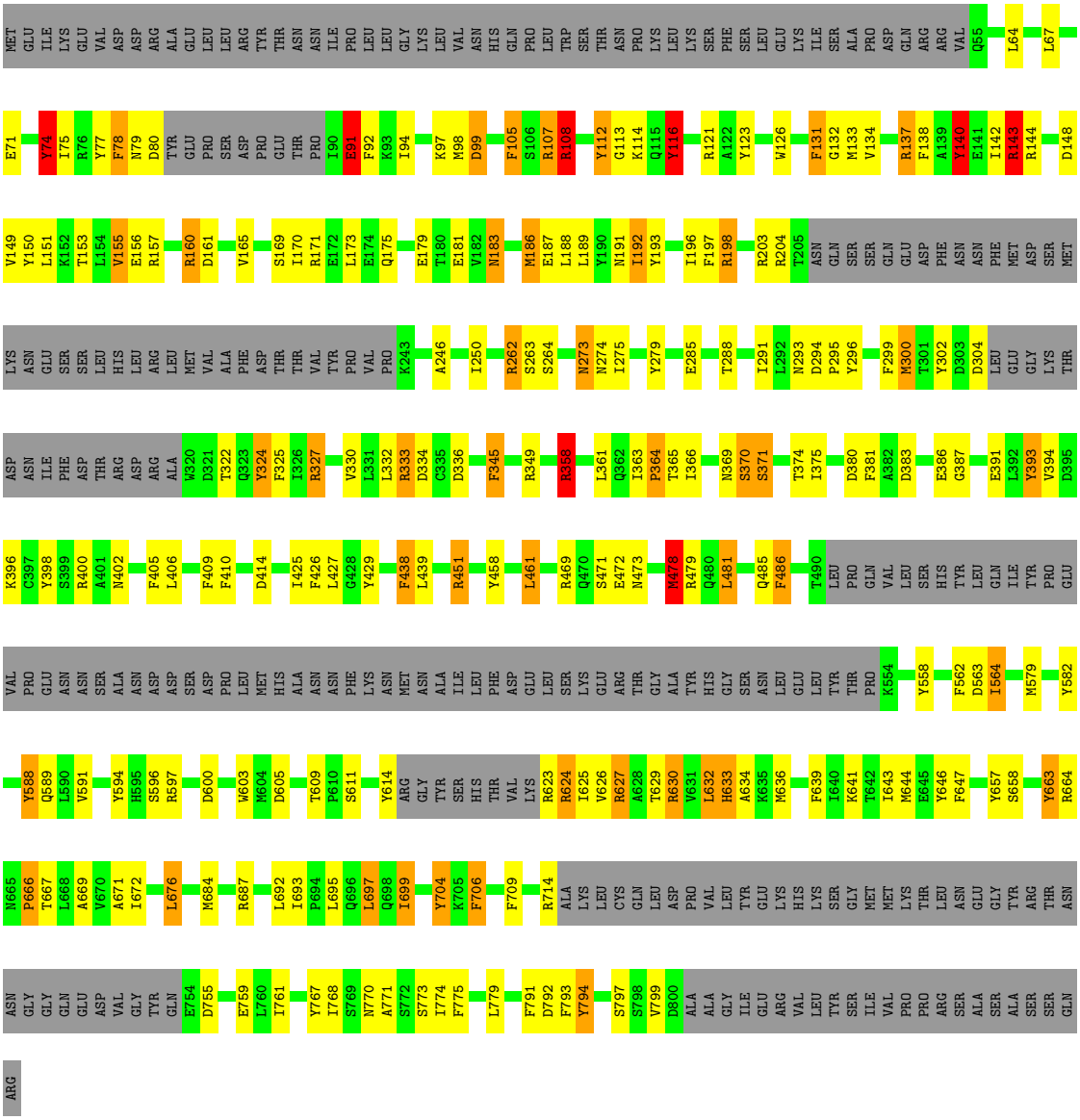




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

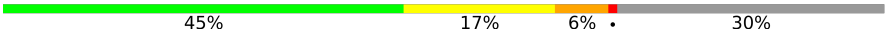
Chain 6-A:

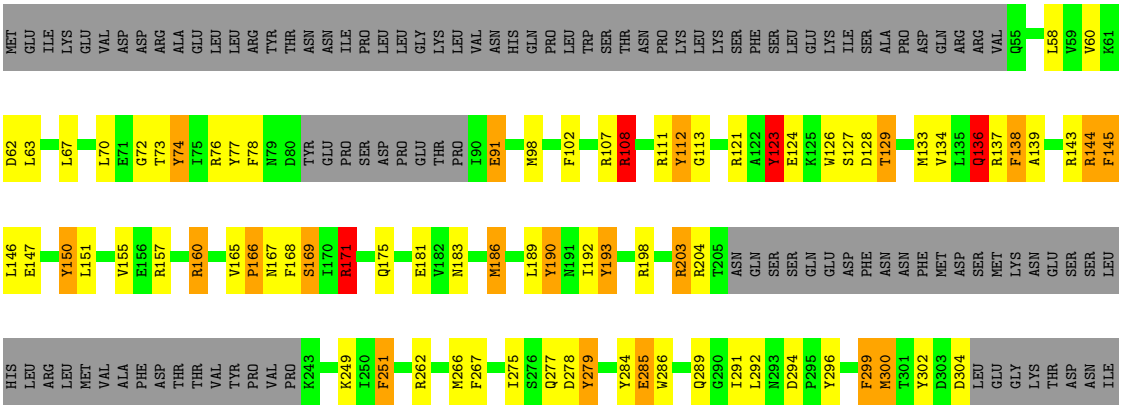


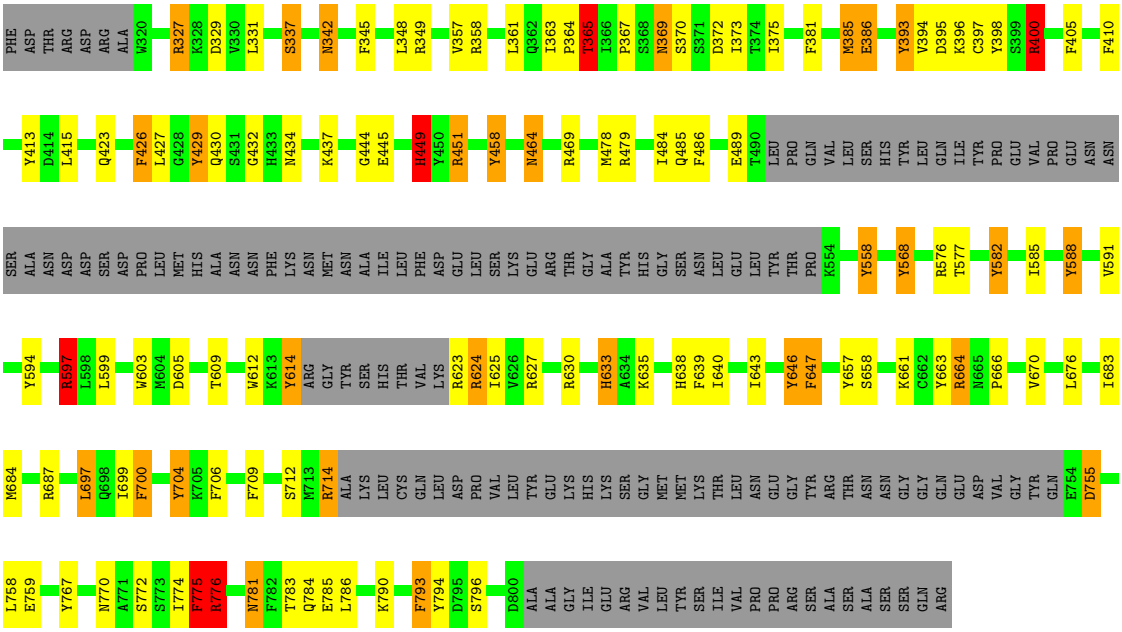


• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 7-A:

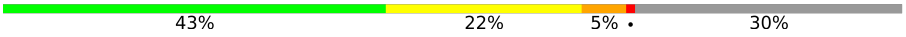


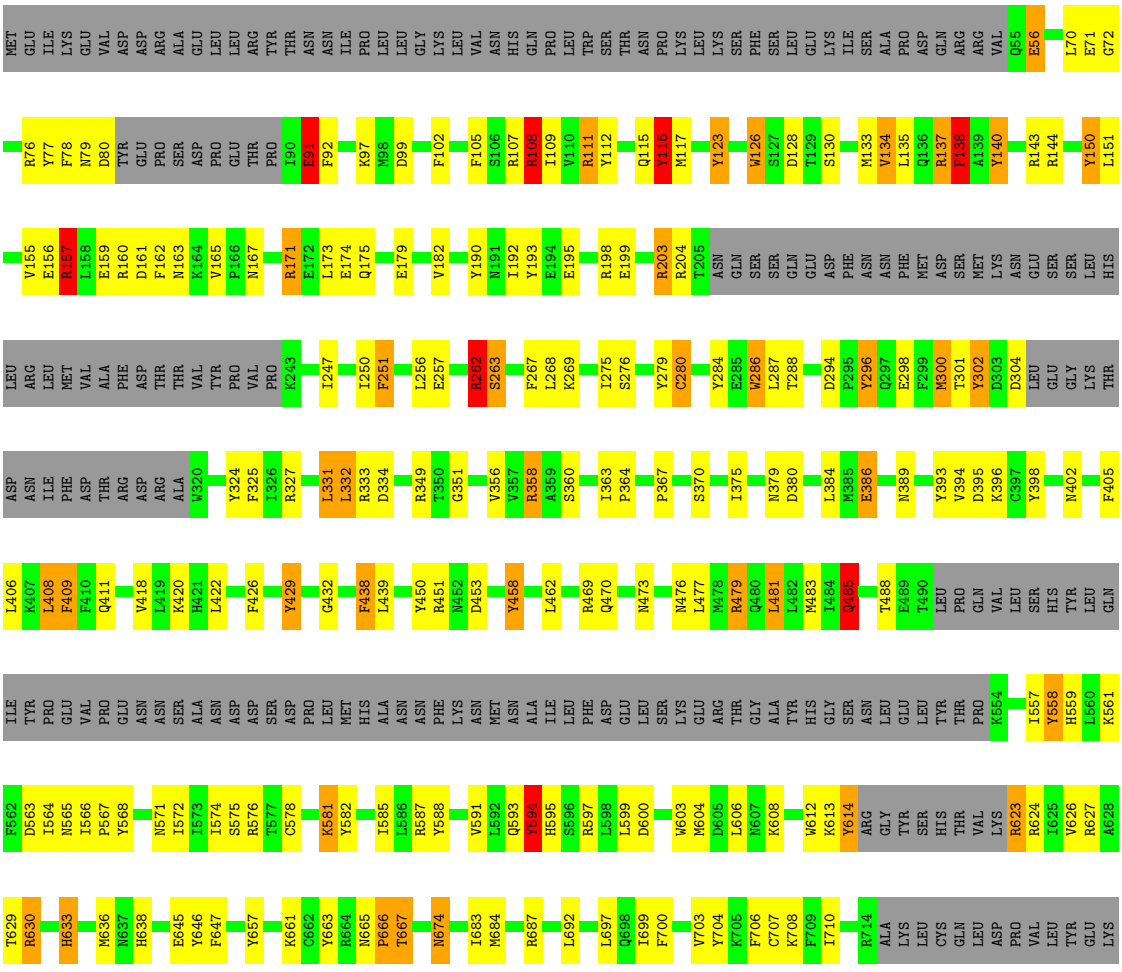


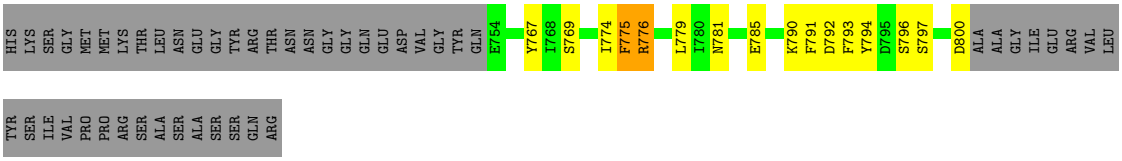


• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 8-A:

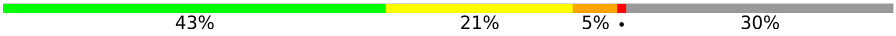


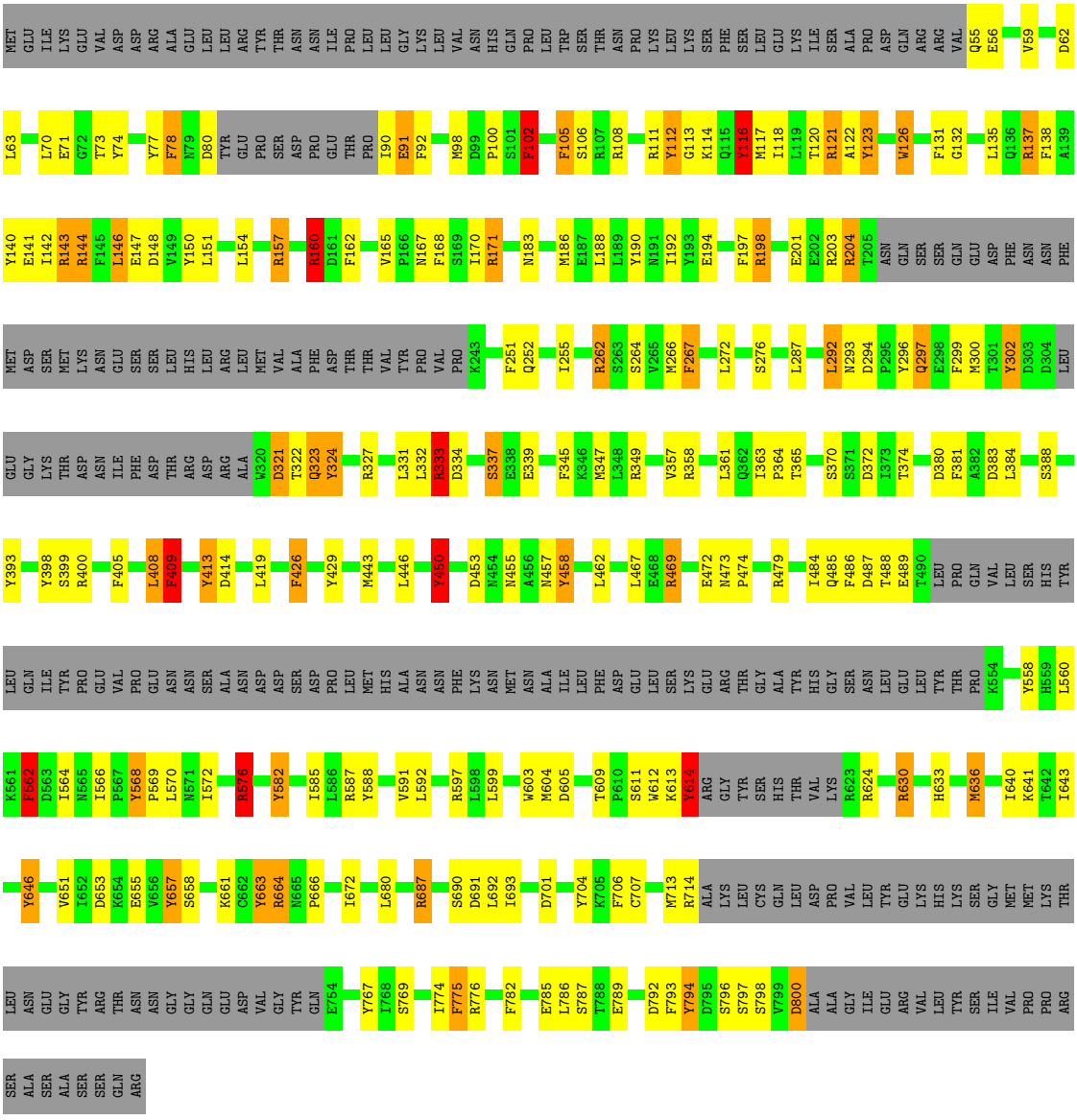




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

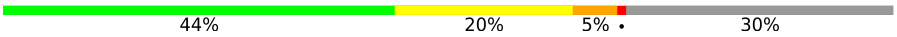
Chain 9-A:

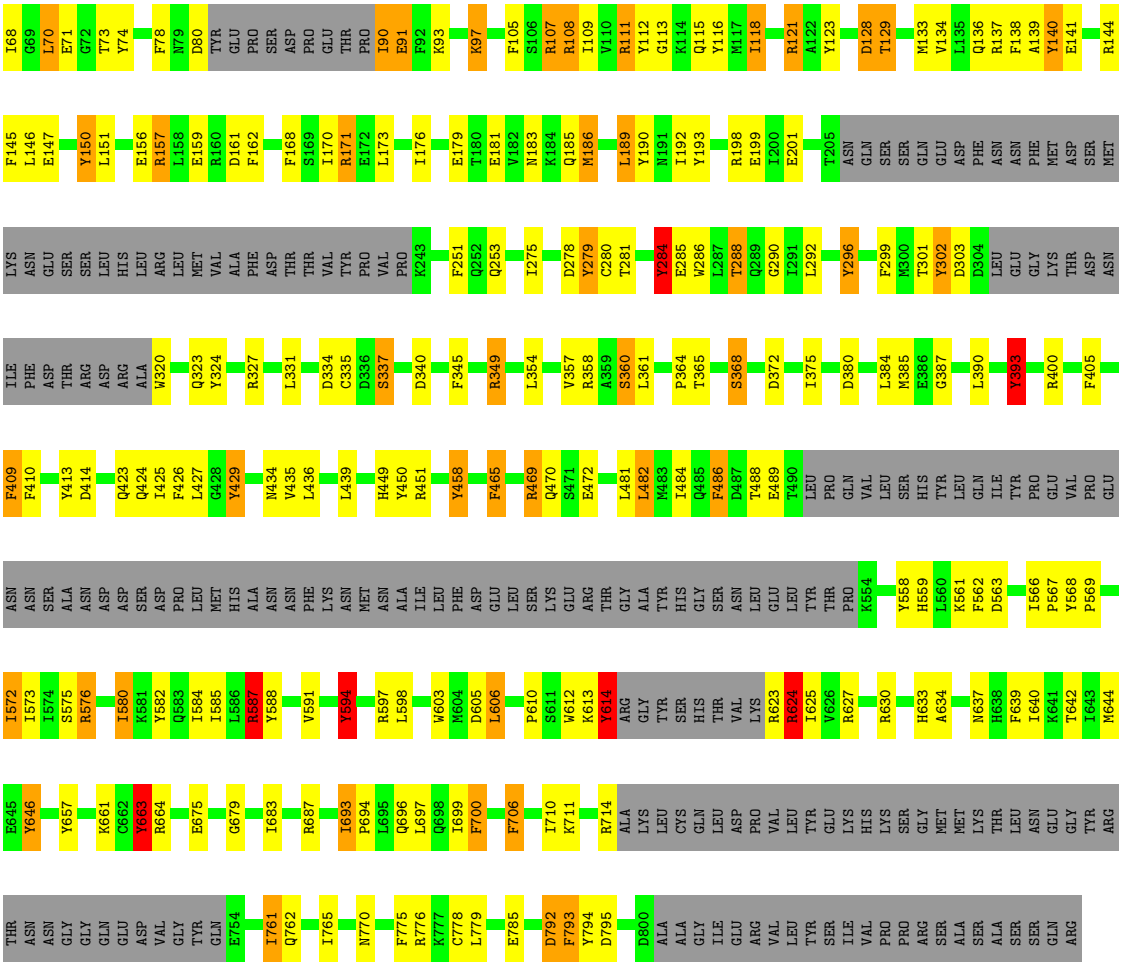




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

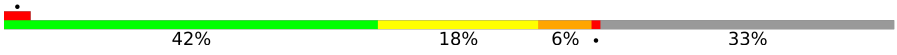
Chain 10-A:

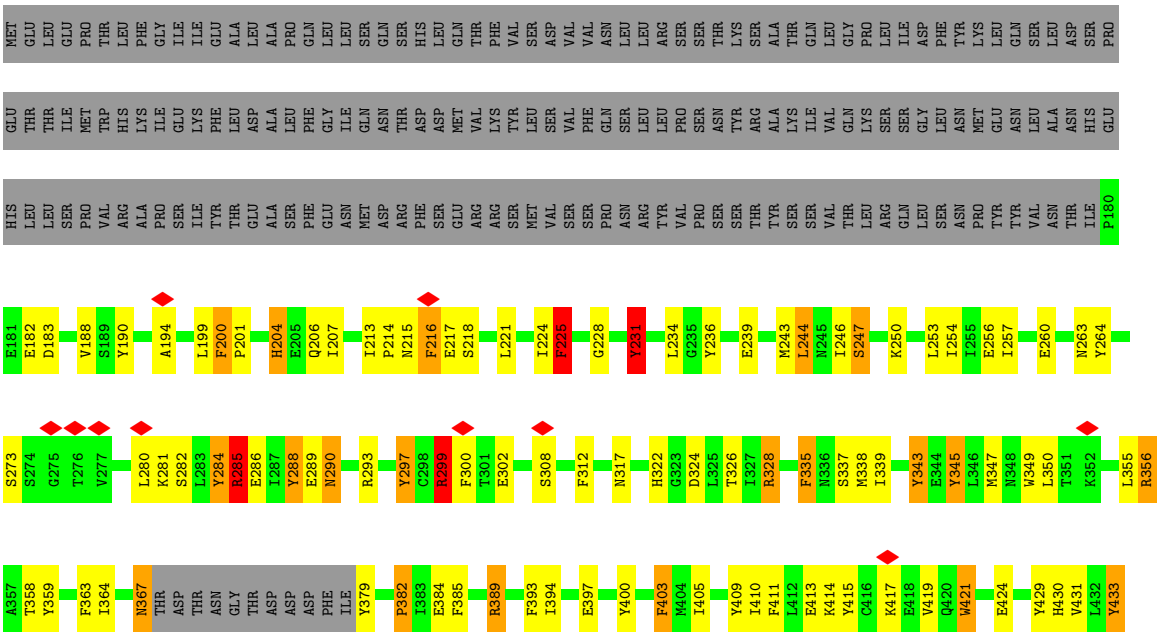


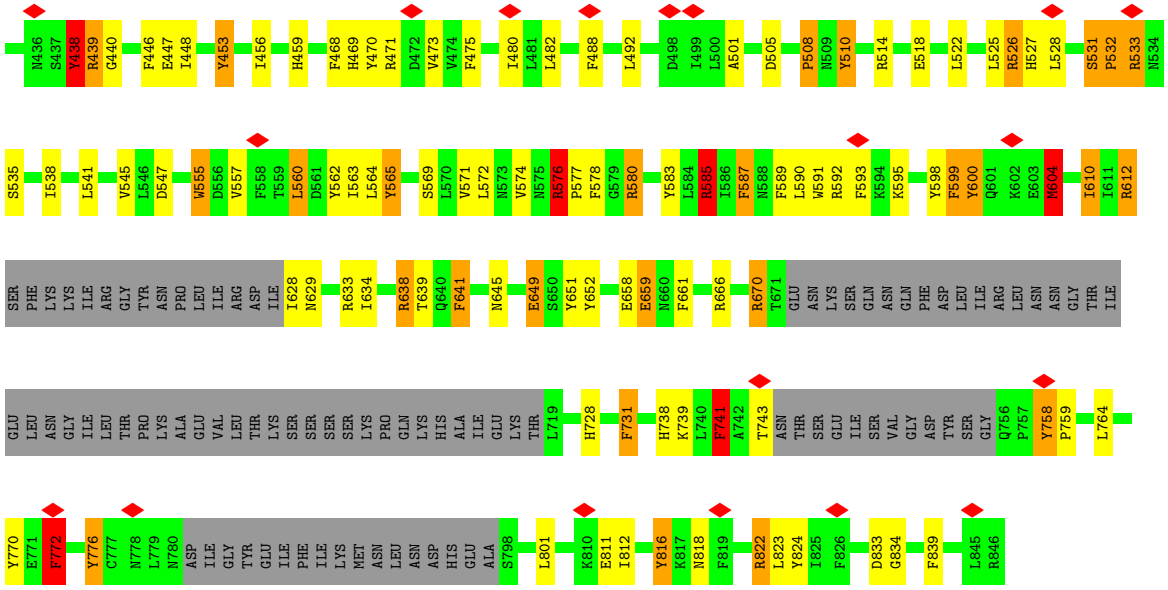


• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 1-B:

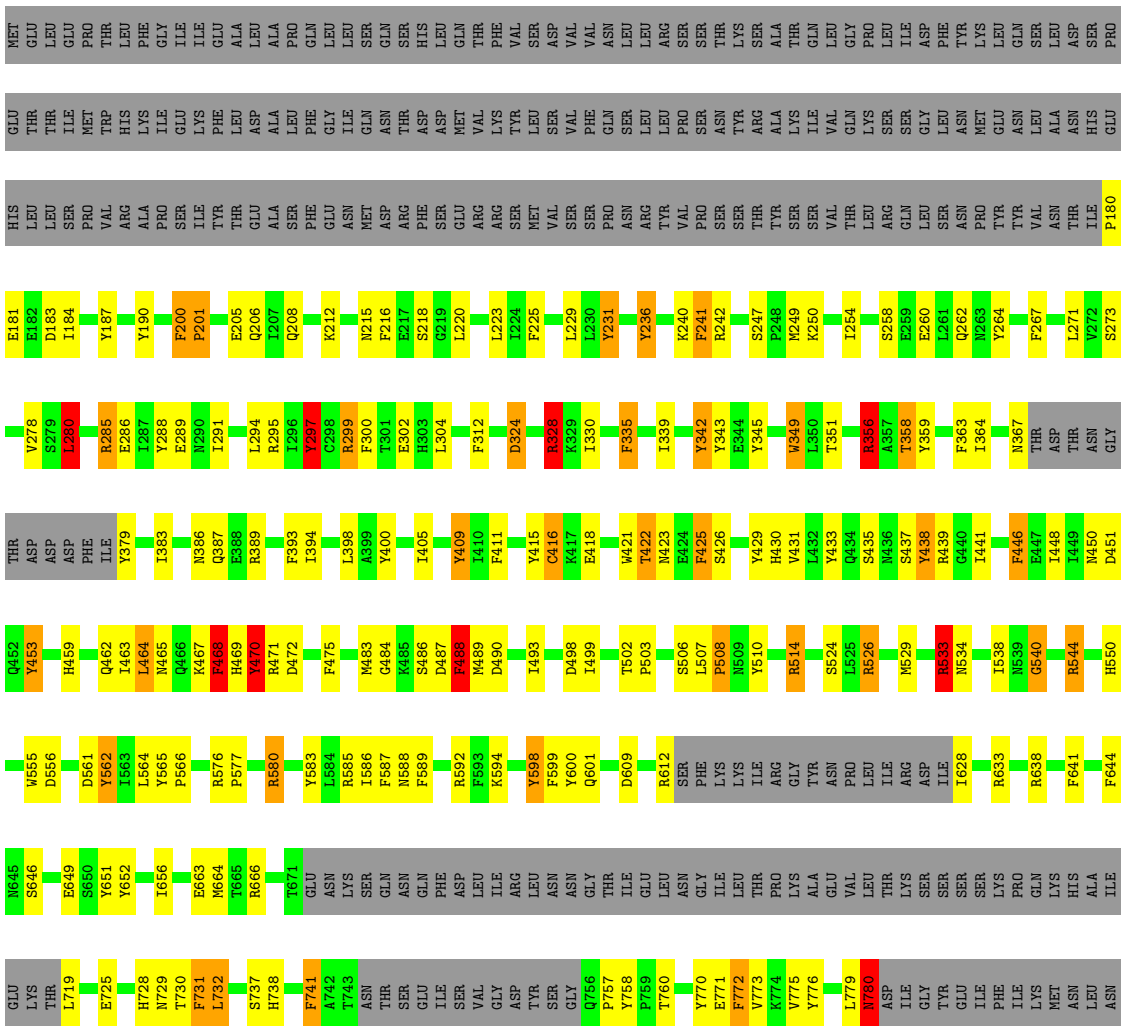






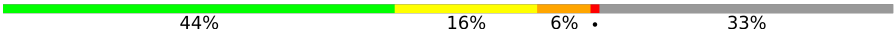
• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

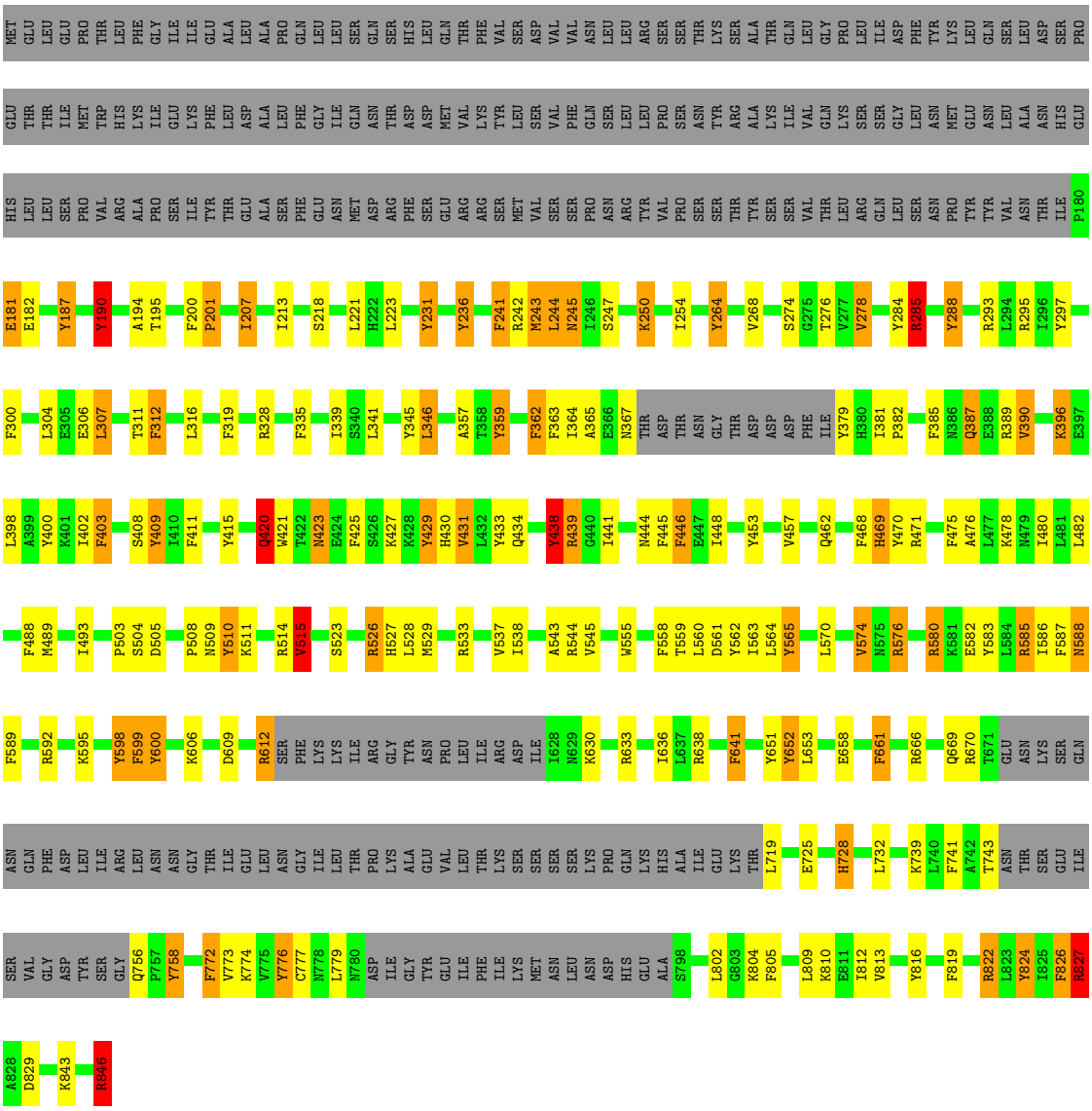
Chain 2-B: 42% 19% 33%



• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

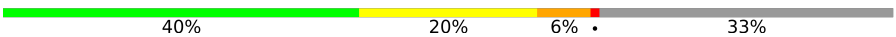
Chain 3-B:

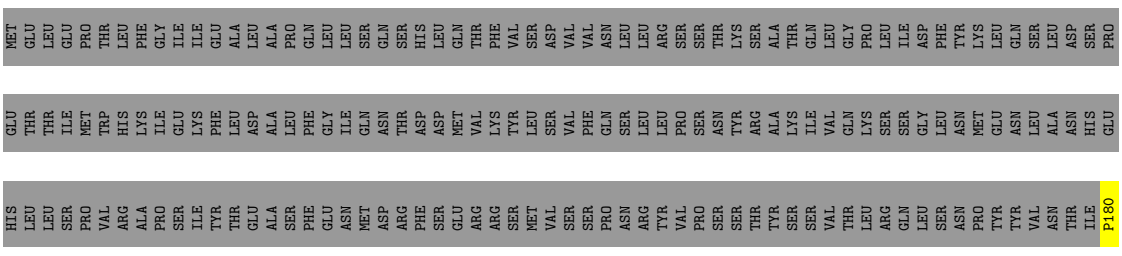


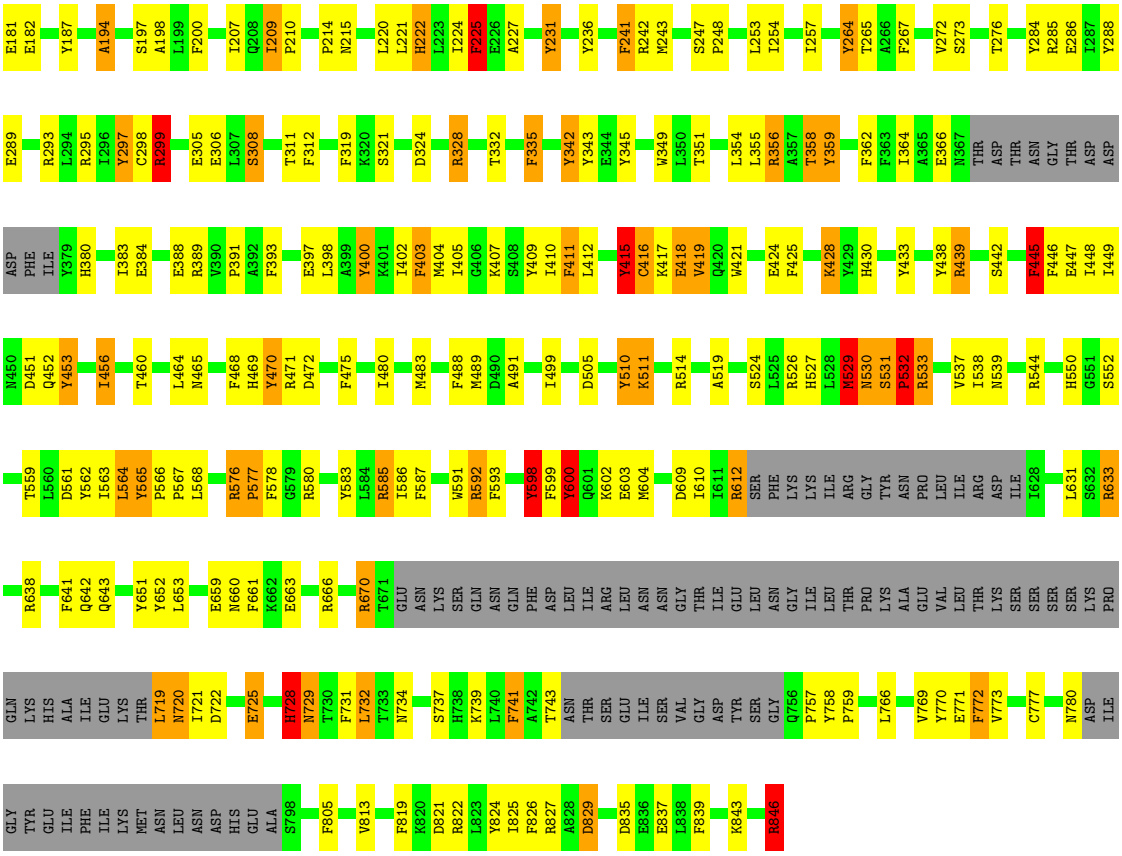


• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 4-B:

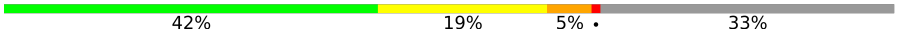


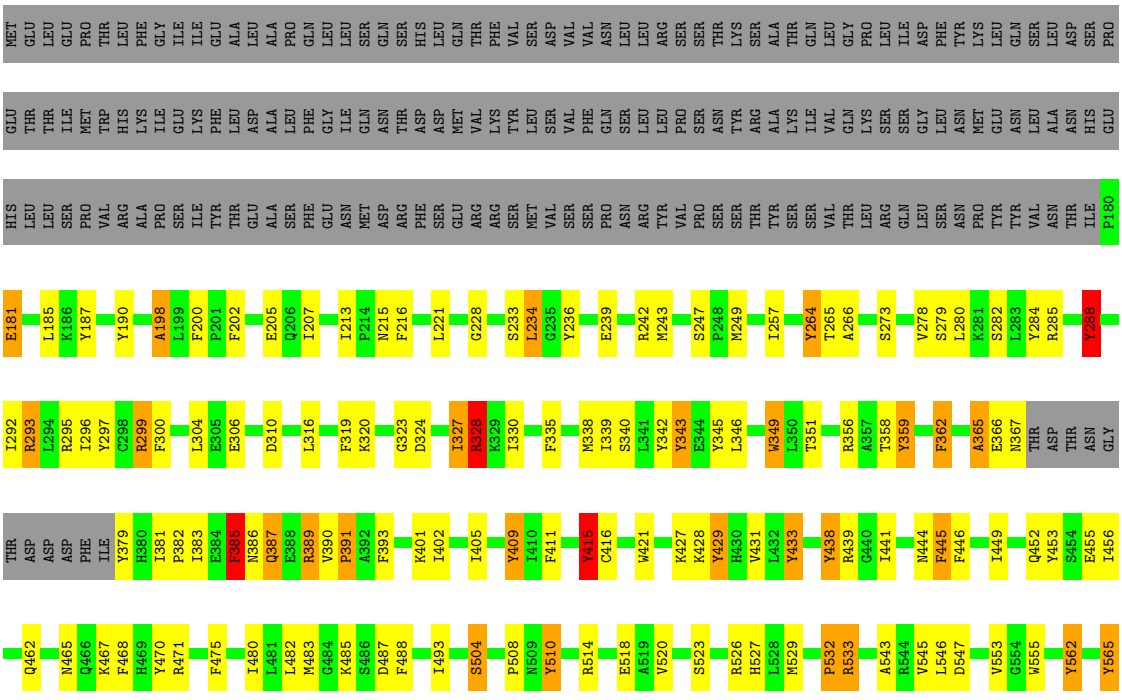


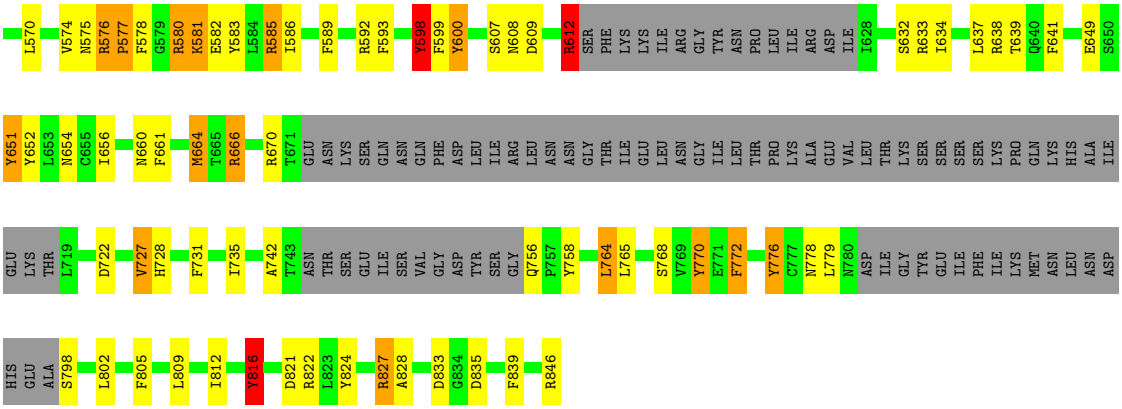


• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 5-B:

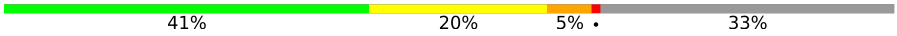


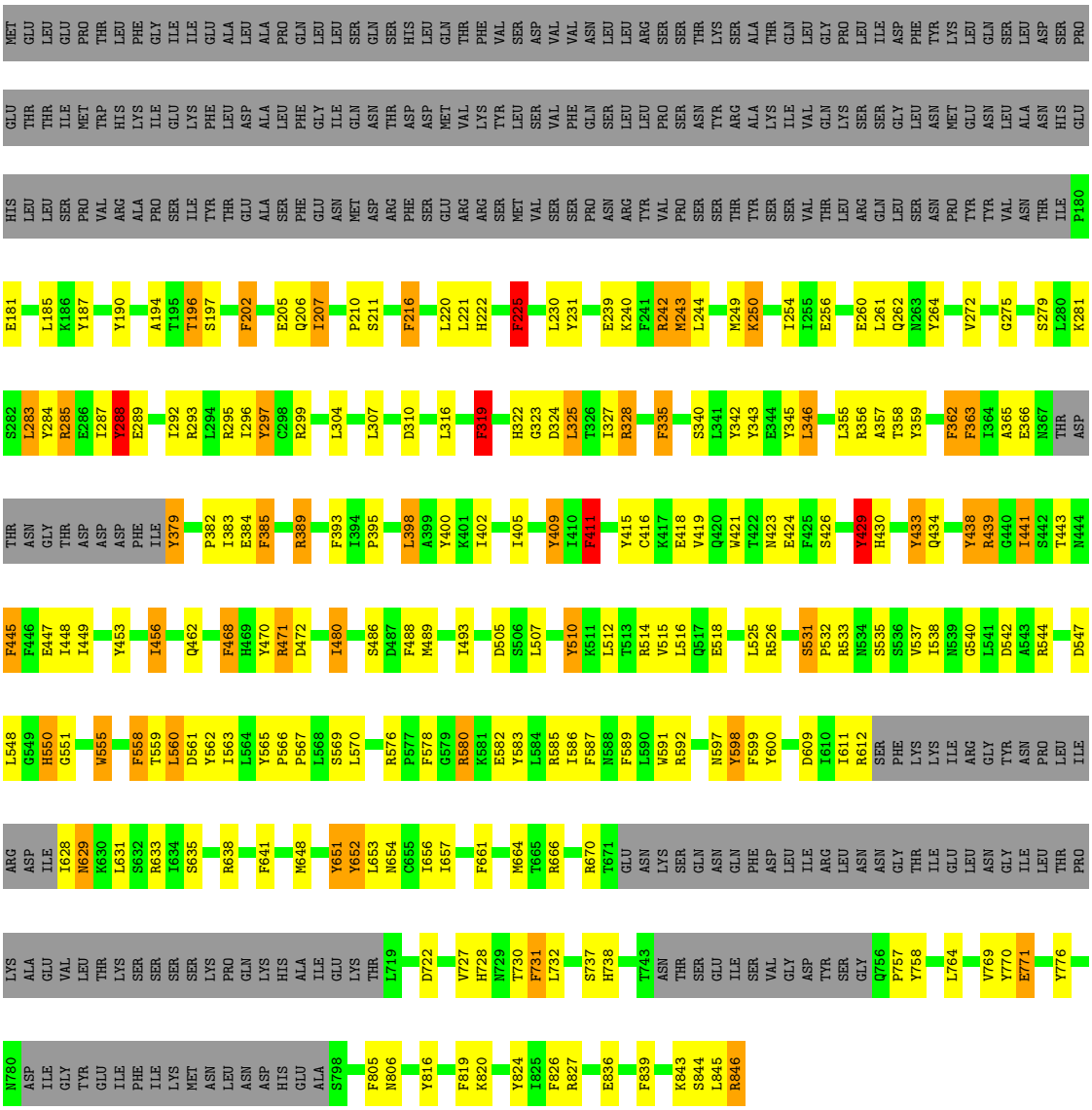




• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

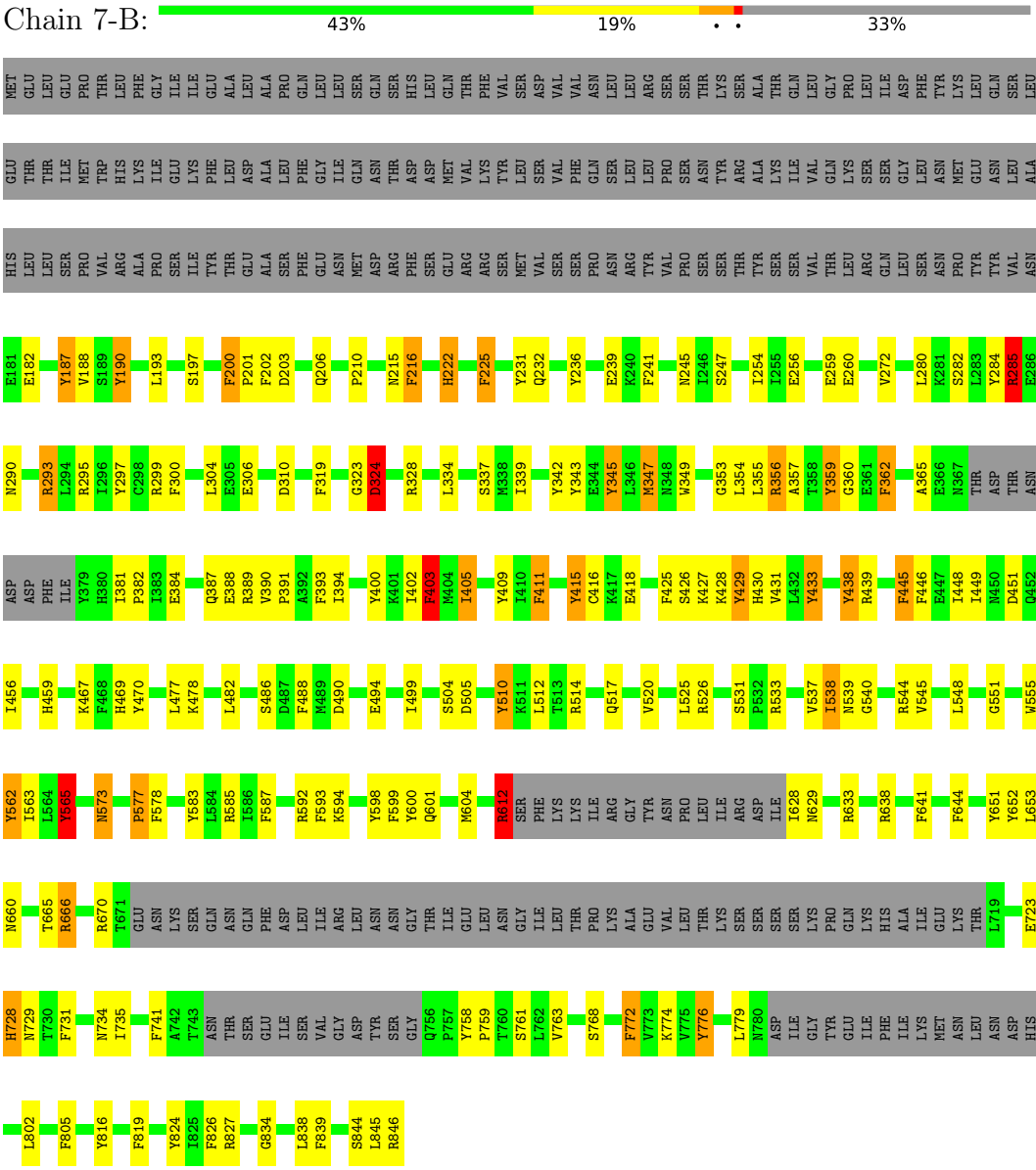
Chain 6-B:





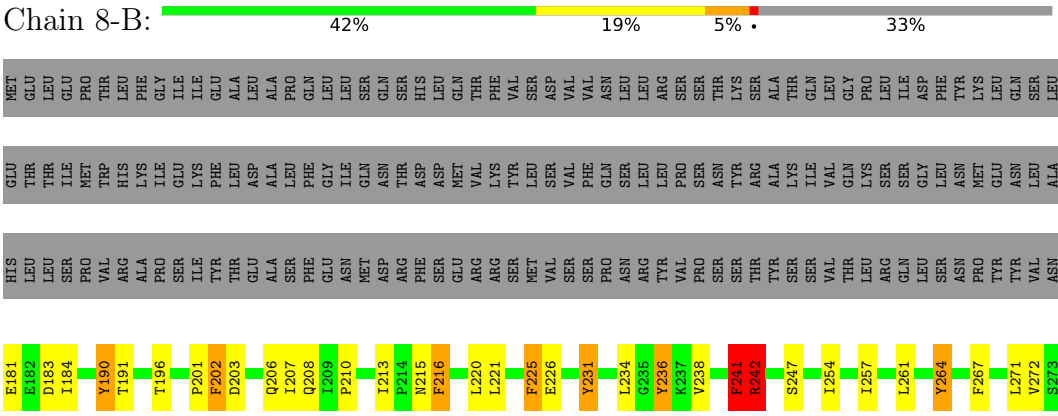
• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

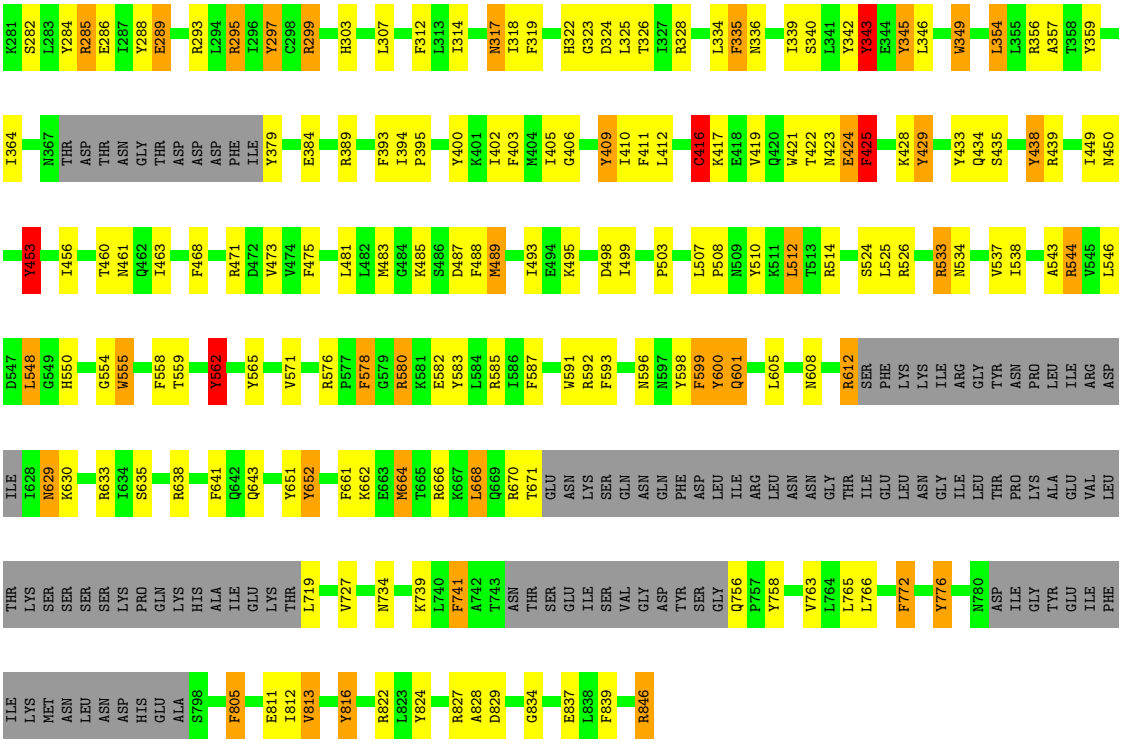
Chain 7-B:



• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

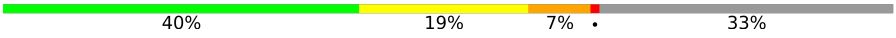
Chain 8-B:

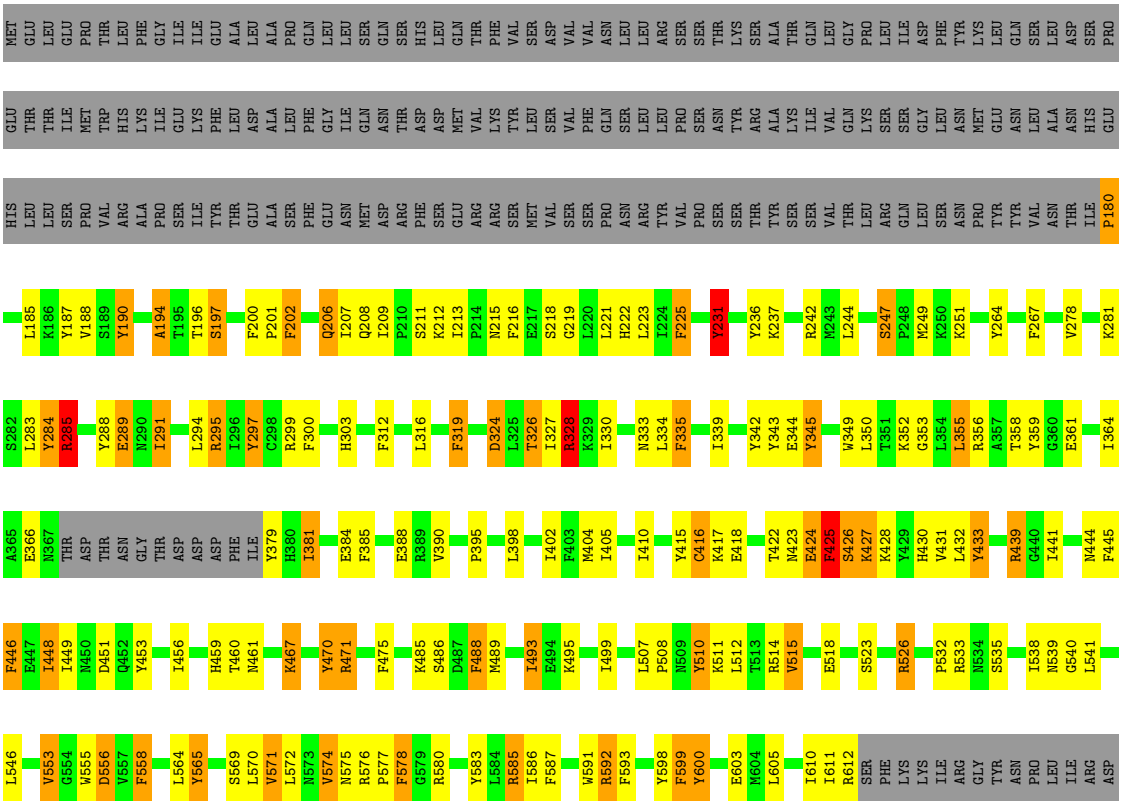


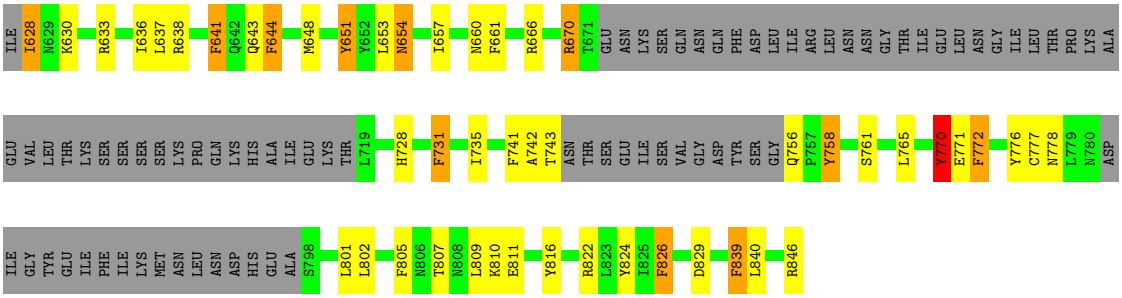


• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 9-B:

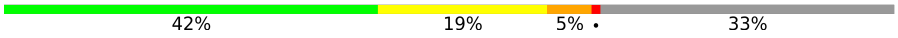


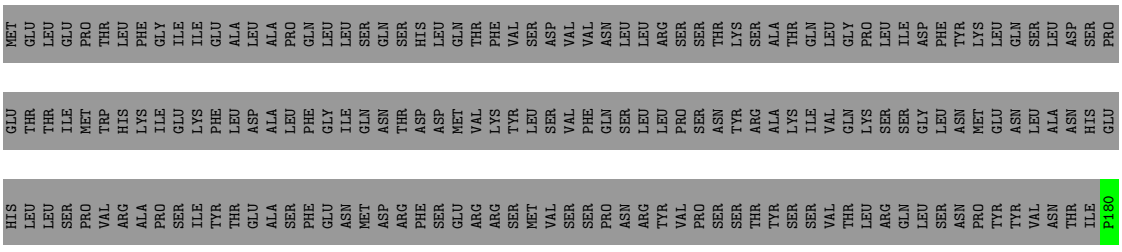


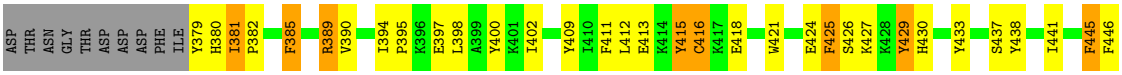


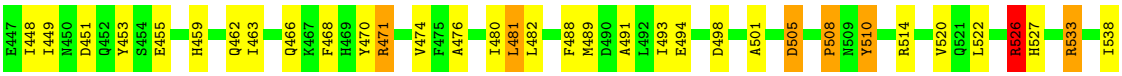
• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

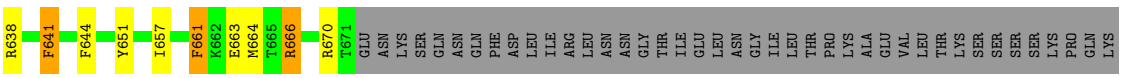
Chain 10-B:

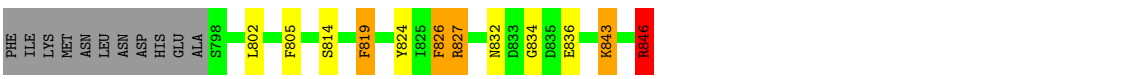






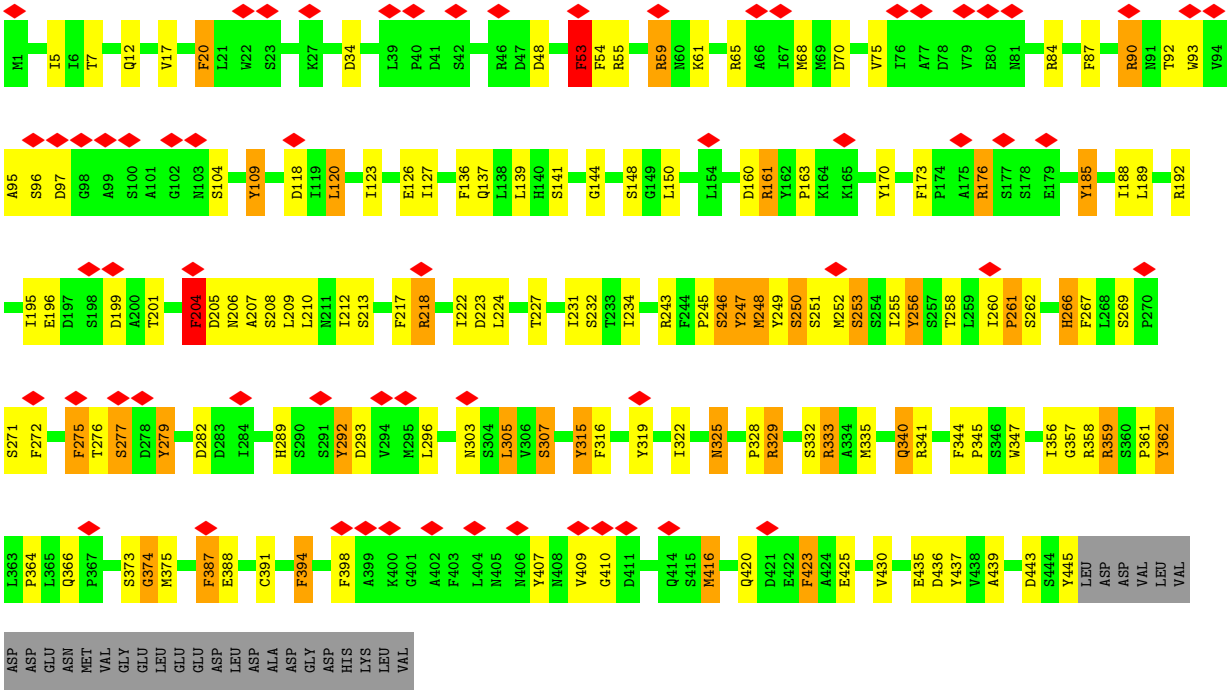






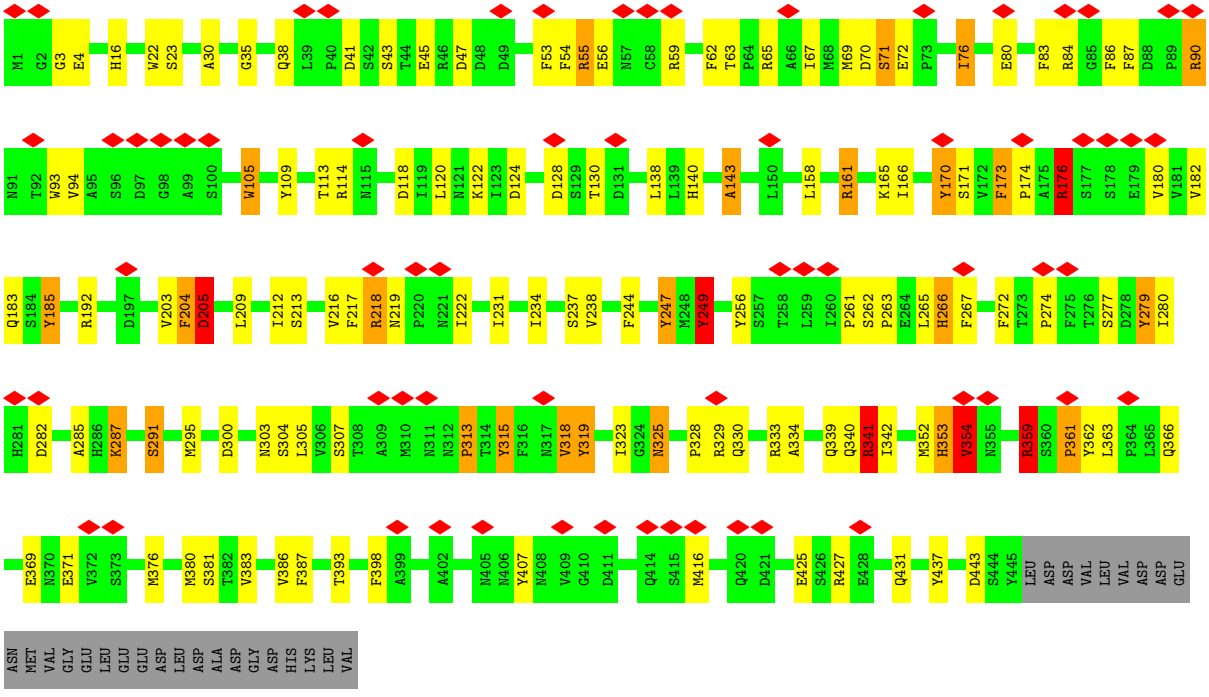
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 1-C:



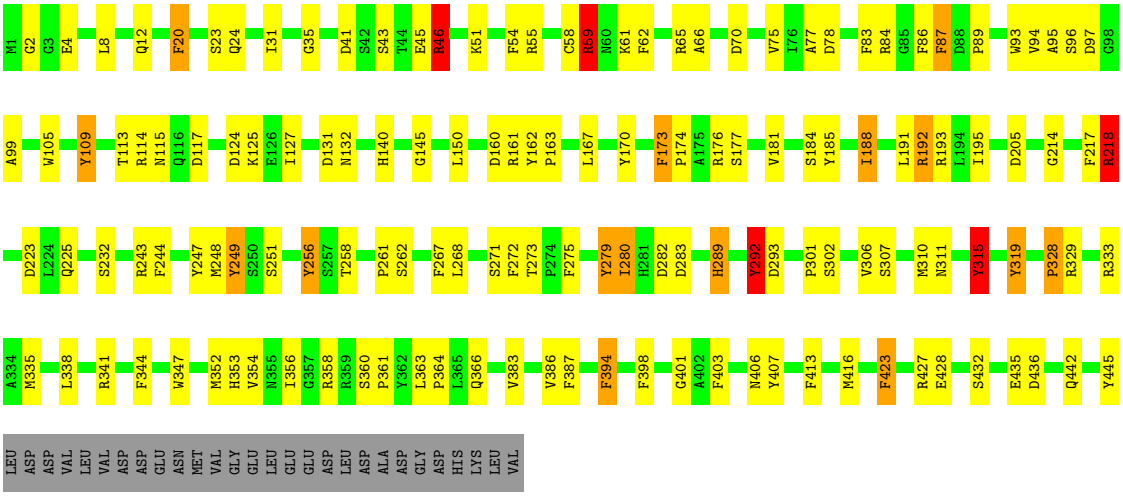
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 1-D:



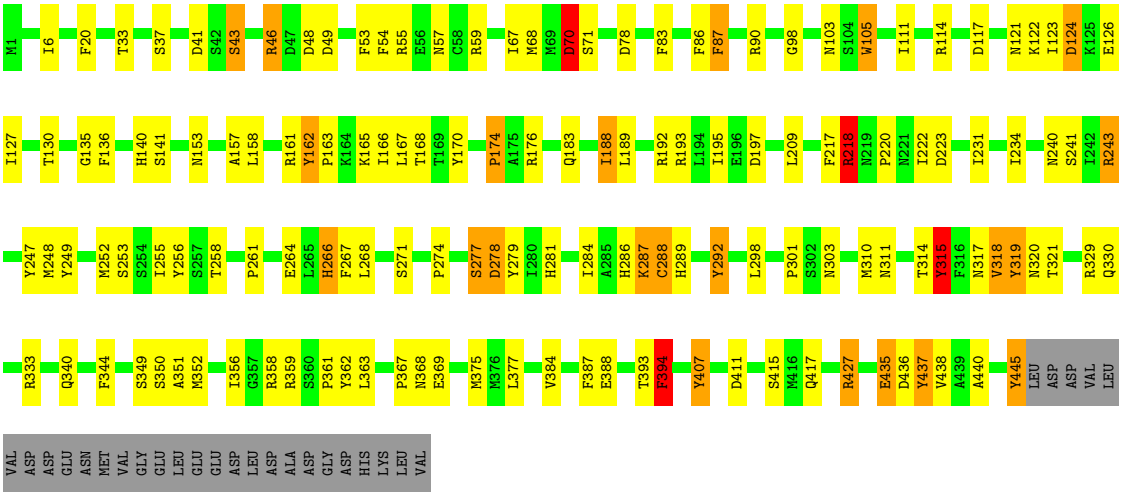
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 2-C:



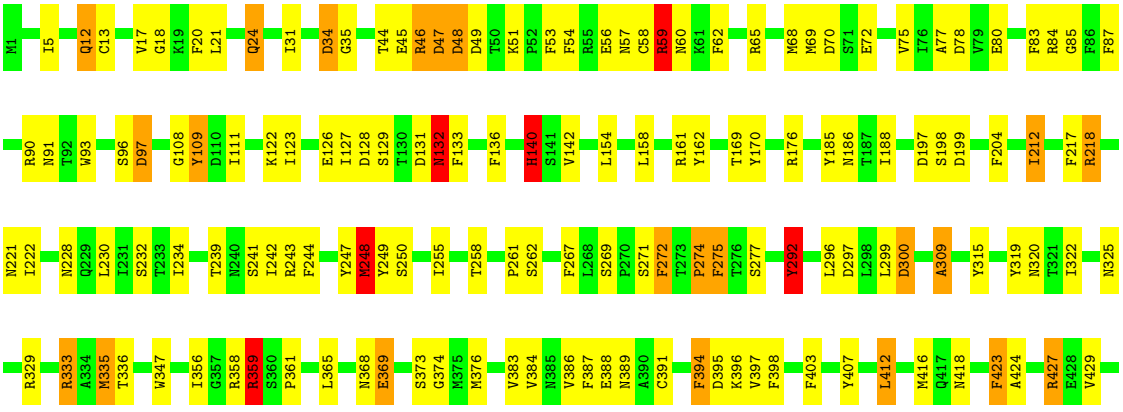
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 2-D:



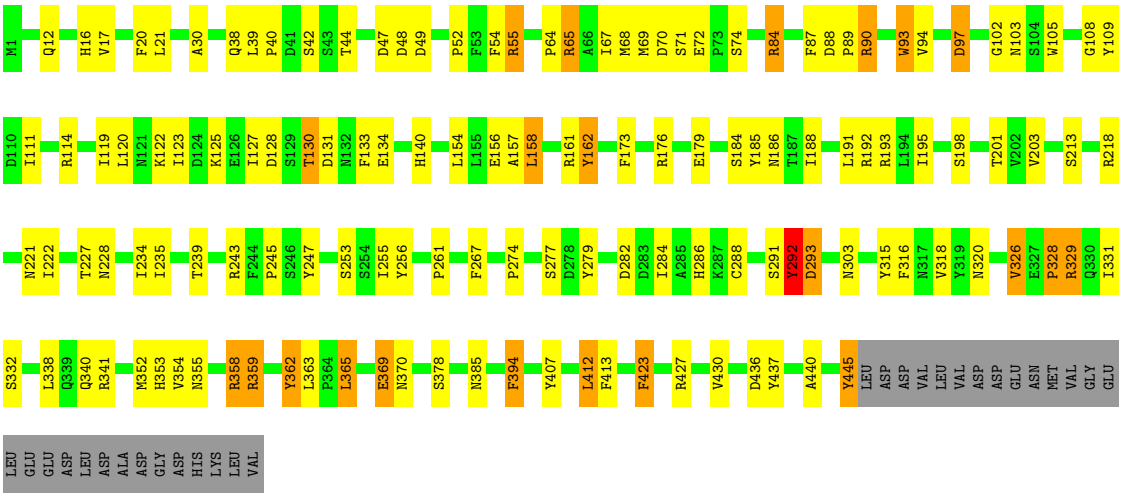
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 3-C:



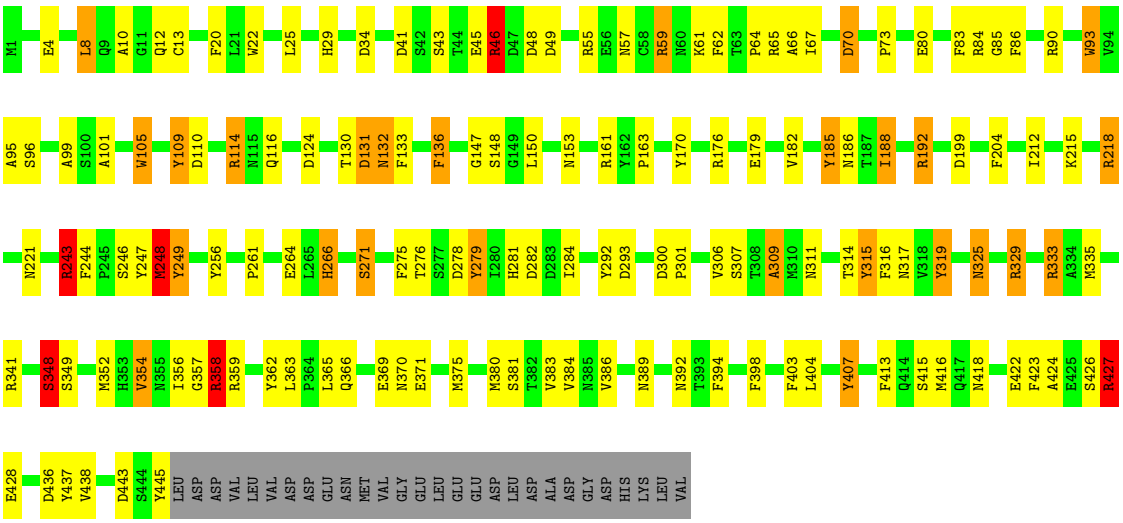
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 3-D:



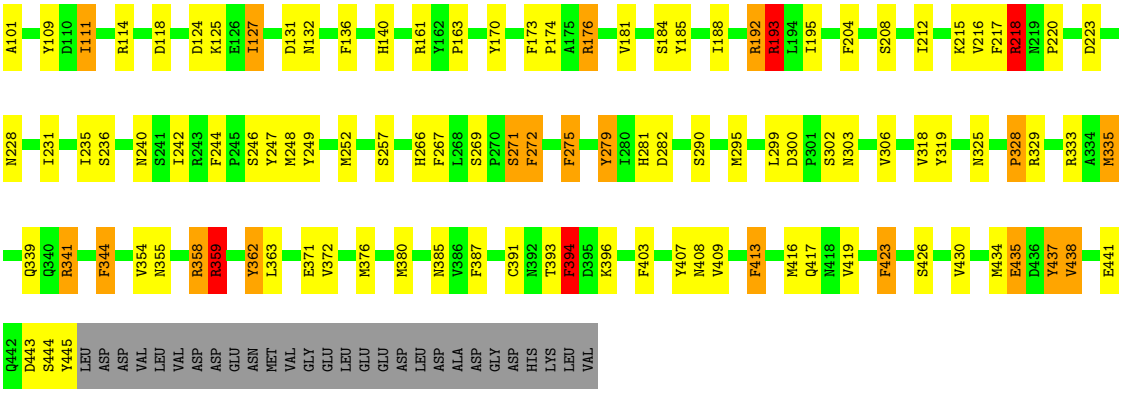
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 4-C:



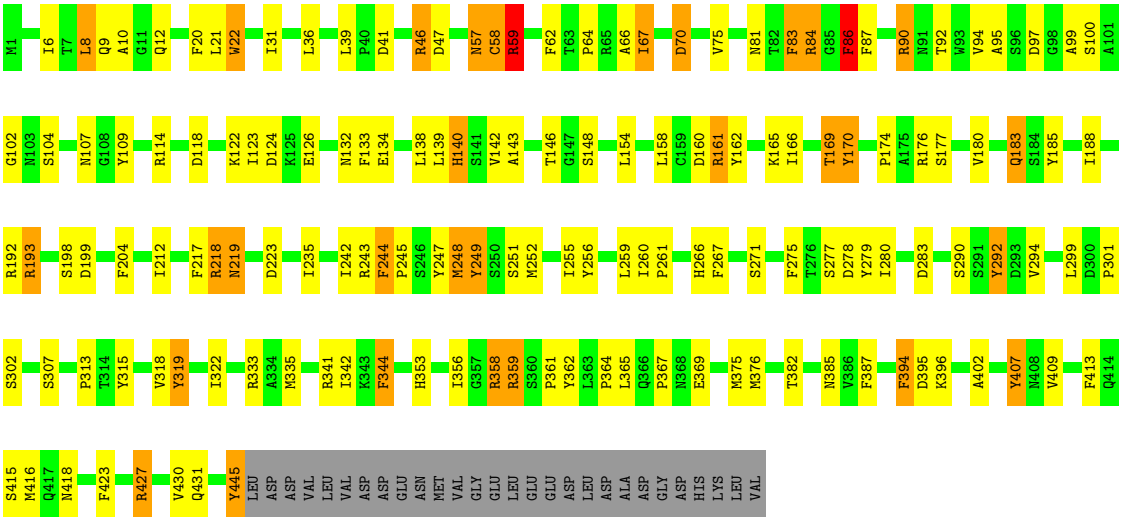
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 4-D:



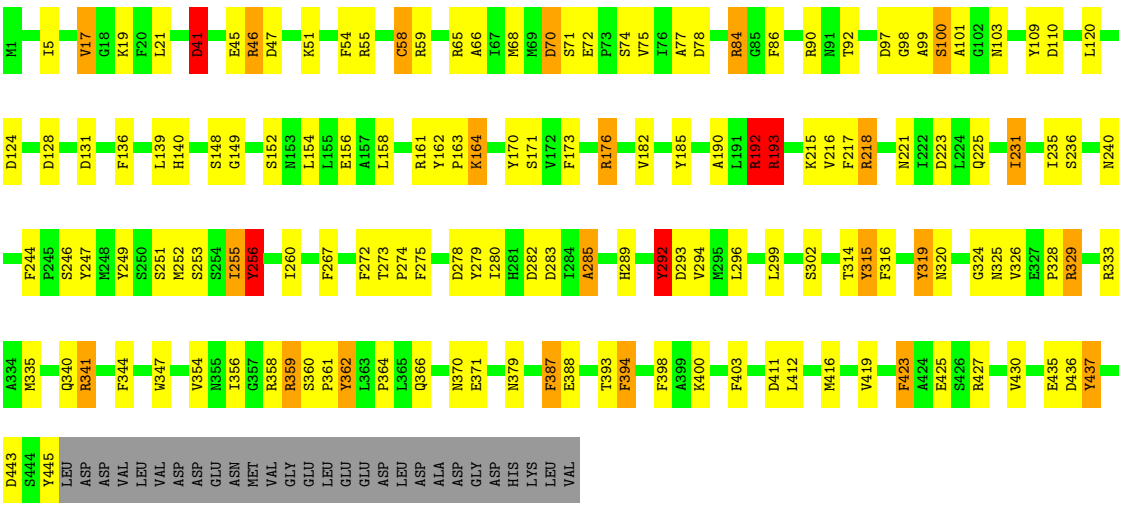
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 5-C:



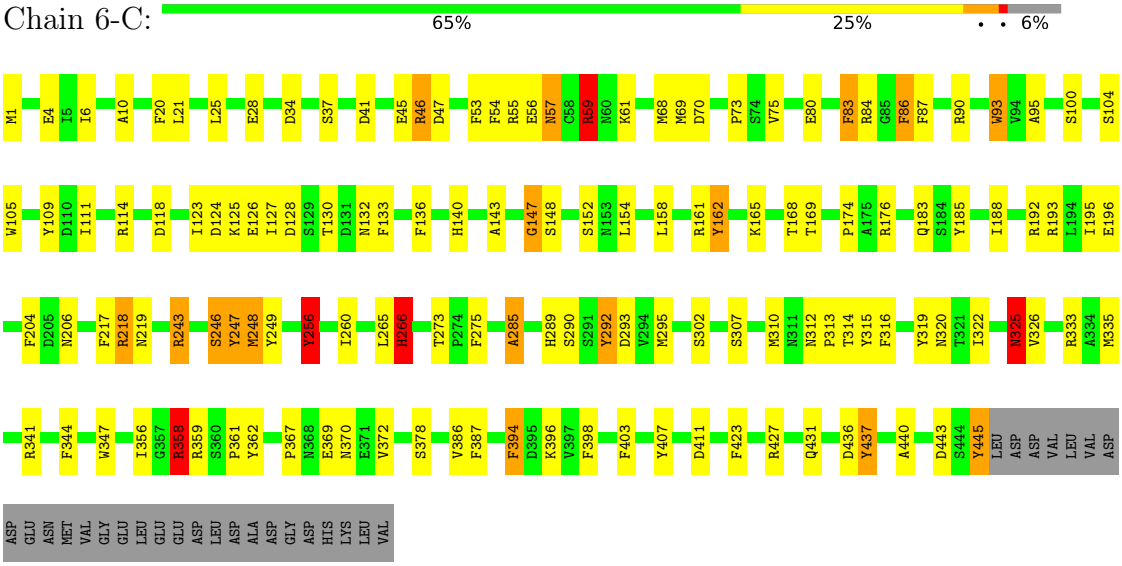
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 5-D:



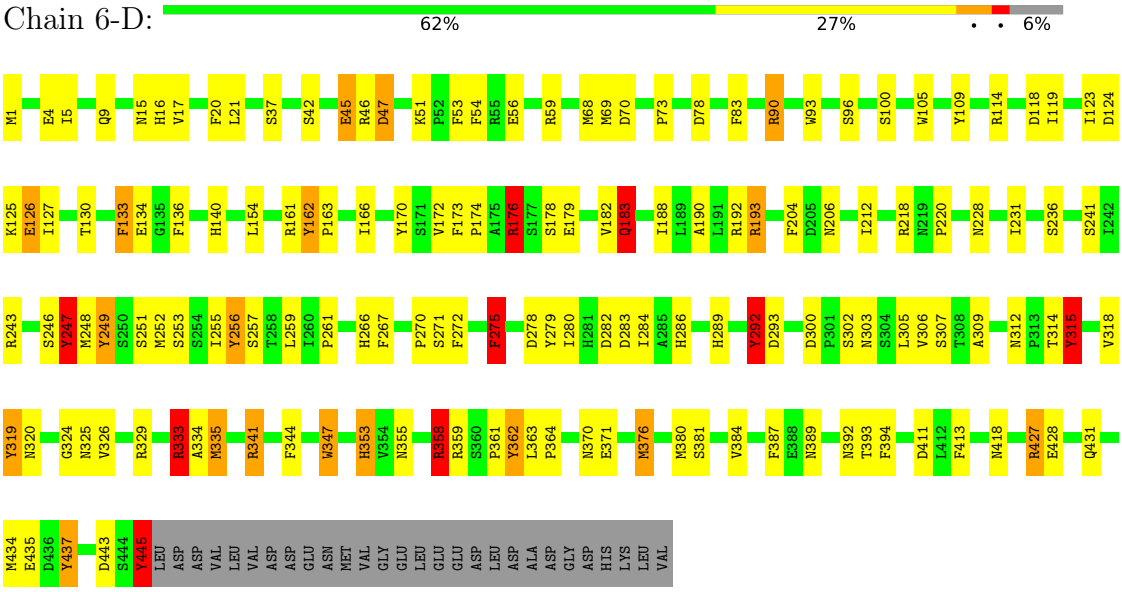
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 6-C:



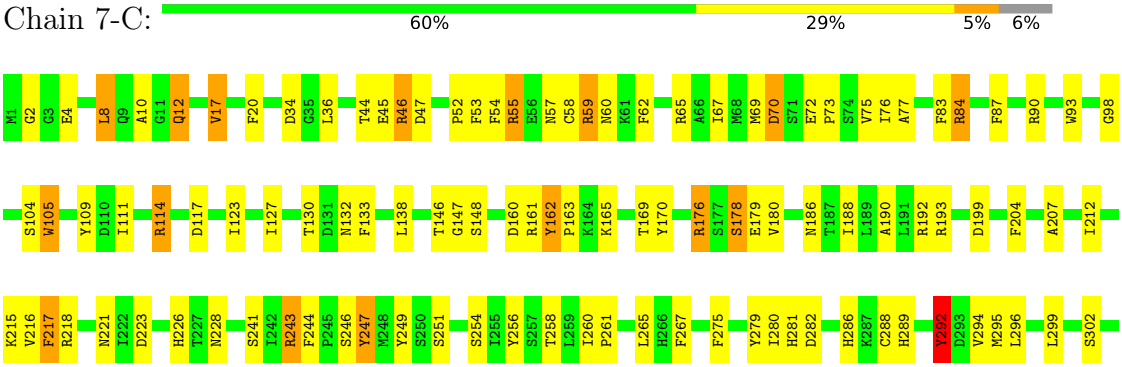
• Molecule 3: TUBULIN GAMMA CHAIN

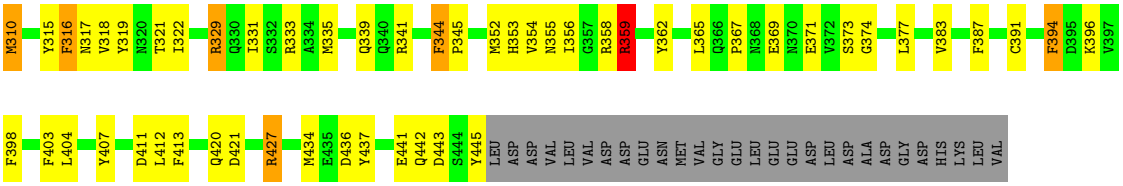
Chain 6-D:



• Molecule 3: TUBULIN GAMMA CHAIN

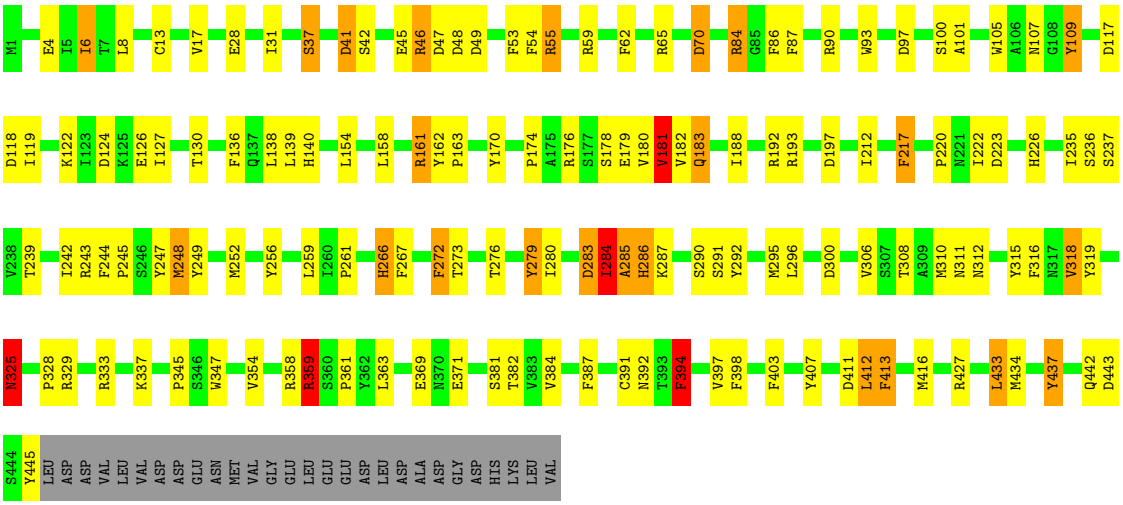
Chain 7-C:





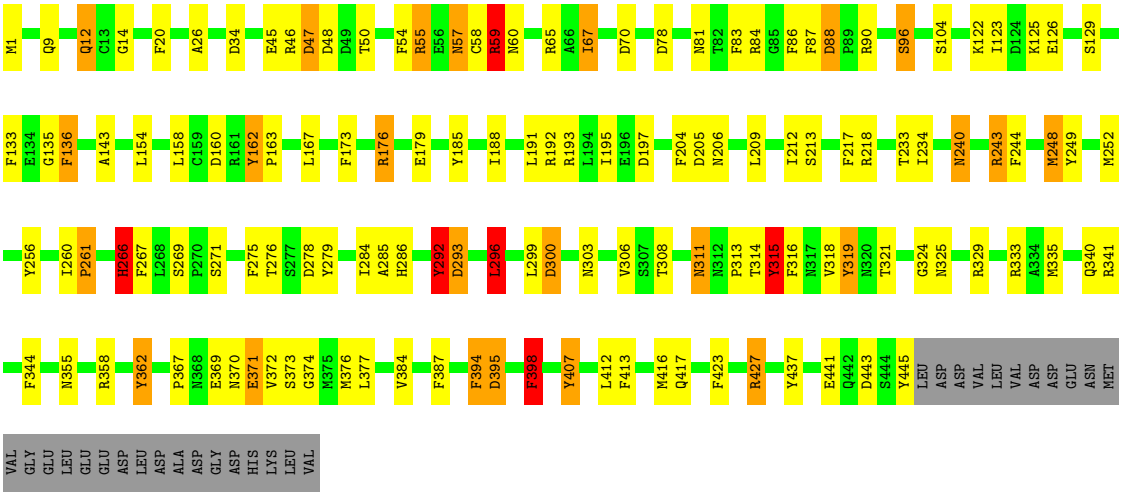
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 7-D:



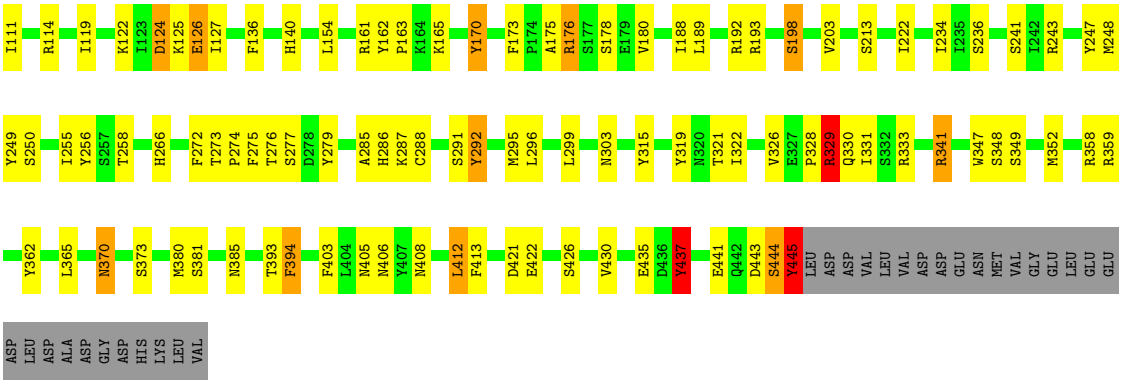
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 8-C:



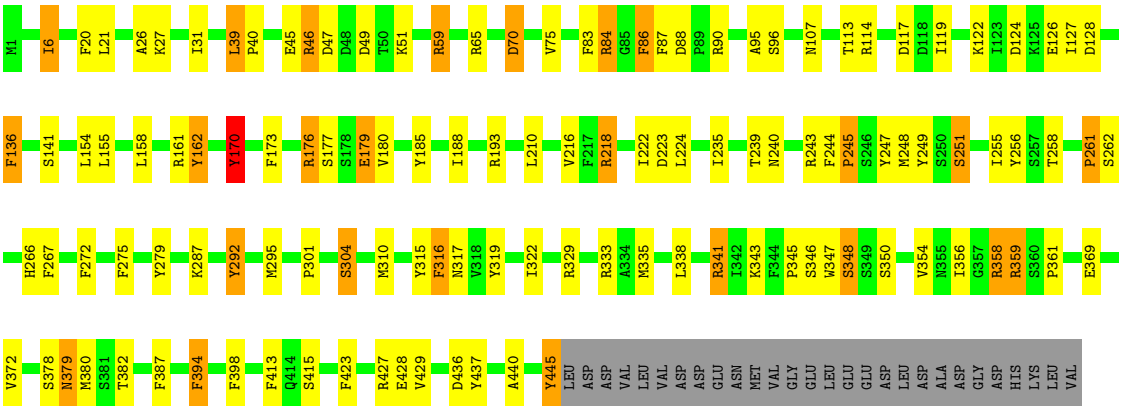
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 8-D:



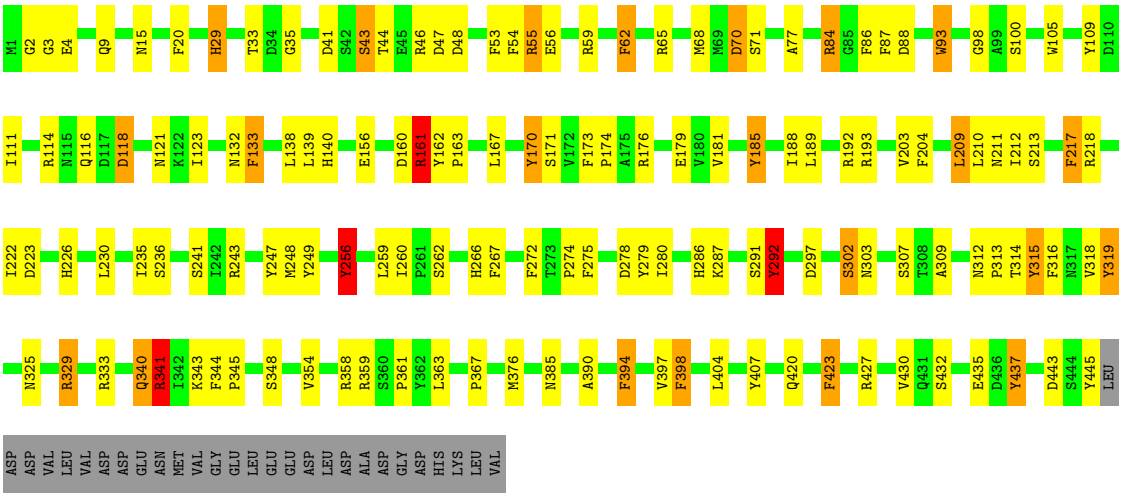
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 9-C:



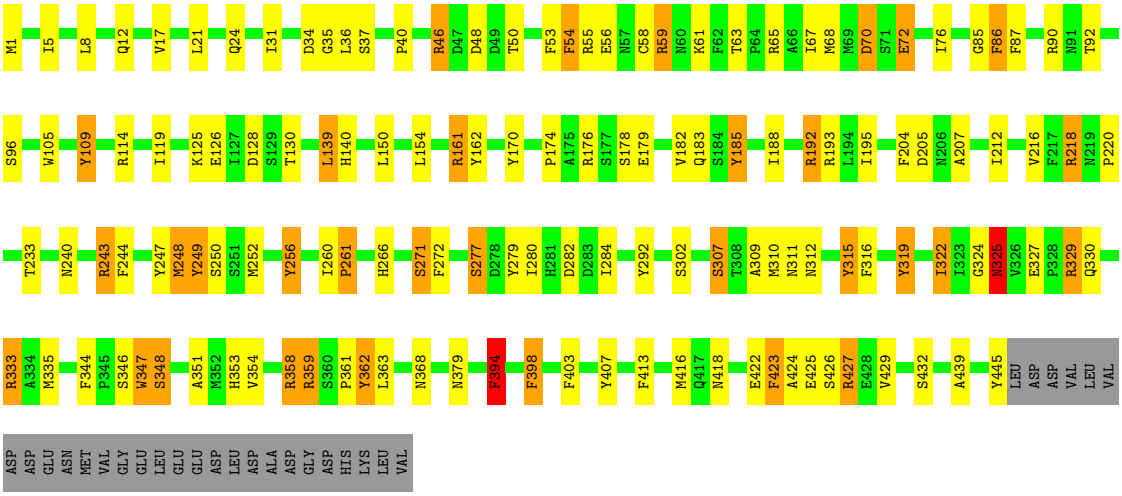
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 9-D:



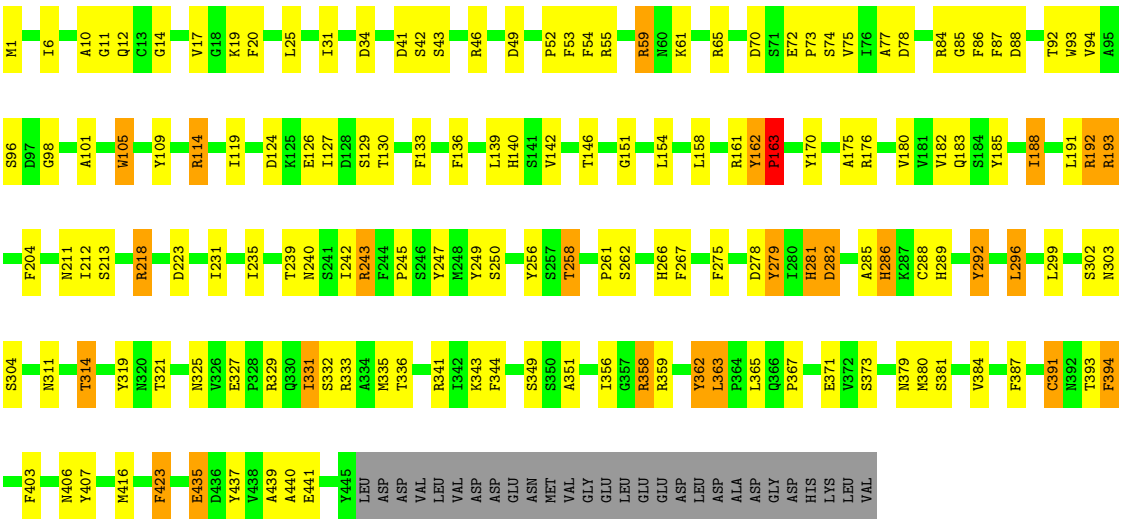
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 10-C:



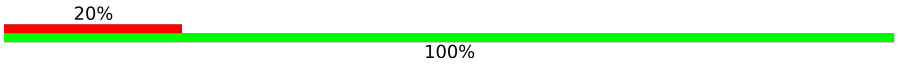
• Molecule 3: TUBULIN GAMMA CHAIN

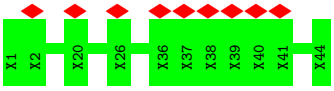
Chain 10-D:



• Molecule 4: SPINDLE POLE BODY COMPONENT 110

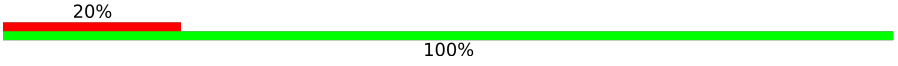
Chain 1-E:

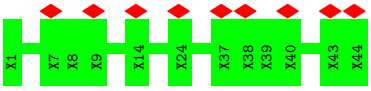




• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 1-F:



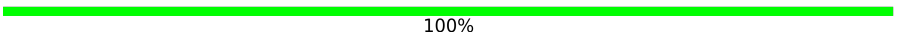


• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 2-E: 

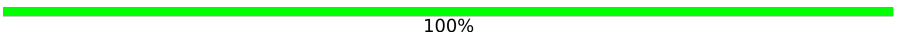
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 2-F: 

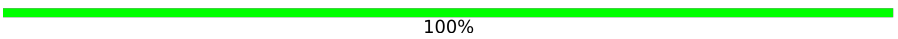
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 3-E: 

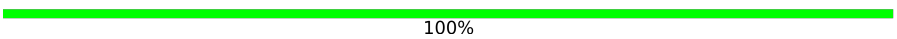
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 3-F: 

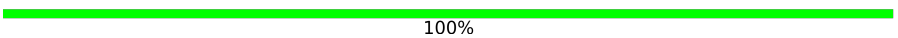
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 4-E: 

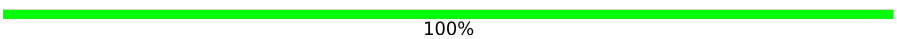
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 4-F: 

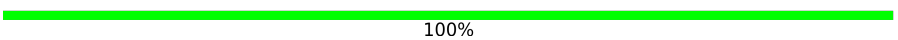
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 5-E: 

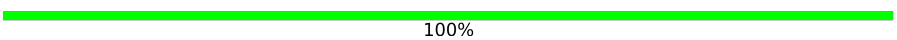
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 5-F: 

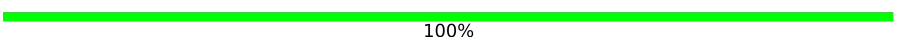
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 6-E: 

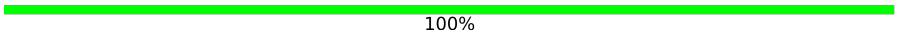
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 6-F: 

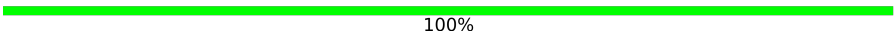
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 7-E: 

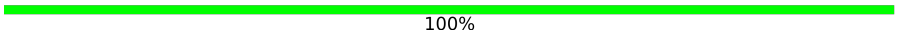
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 7-F: 

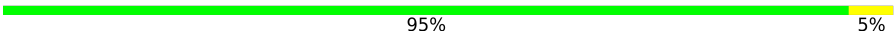
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

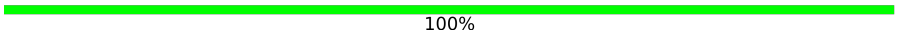
Chain 8-E: 

There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

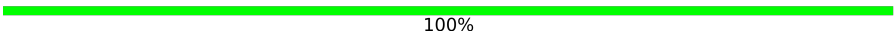
Chain 8-F: 

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 9-E: 

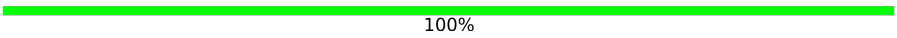
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 9-F: 

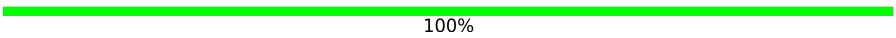
There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 10-E: 

There are no outlier residues recorded for this chain.

• Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 10-F: 

There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	EACH MICROGRAPH	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	94000	Depositor
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor
Maximum map value	3.045	Depositor
Minimum map value	-1.944	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.314	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	398.56, 398.56, 398.56	wwPDB
Map dimensions	212, 212, 212	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.88, 1.88, 1.88	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1-A	1.76	45/4917 (0.9%)	1.98	139/6616 (2.1%)
1	2-A	1.75	66/4917 (1.3%)	2.00	129/6616 (1.9%)
1	3-A	1.75	49/4917 (1.0%)	1.98	139/6616 (2.1%)
1	4-A	1.75	48/4917 (1.0%)	2.07	156/6616 (2.4%)
1	5-A	1.74	50/4917 (1.0%)	2.01	144/6616 (2.2%)
1	6-A	1.76	54/4917 (1.1%)	2.01	146/6616 (2.2%)
1	7-A	1.72	40/4917 (0.8%)	2.06	154/6616 (2.3%)
1	8-A	1.77	58/4917 (1.2%)	2.06	158/6616 (2.4%)
1	9-A	1.75	53/4917 (1.1%)	2.00	140/6616 (2.1%)
1	10-A	1.72	38/4917 (0.8%)	1.96	138/6616 (2.1%)
2	1-B	1.73	52/4803 (1.1%)	1.99	135/6481 (2.1%)
2	2-B	1.76	54/4803 (1.1%)	1.99	144/6481 (2.2%)
2	3-B	1.73	42/4803 (0.9%)	2.01	136/6481 (2.1%)
2	4-B	1.74	48/4803 (1.0%)	2.07	147/6481 (2.3%)
2	5-B	1.75	58/4803 (1.2%)	2.07	162/6481 (2.5%)
2	6-B	1.71	51/4803 (1.1%)	2.03	147/6481 (2.3%)
2	7-B	1.75	49/4803 (1.0%)	2.02	144/6481 (2.2%)
2	8-B	1.73	40/4803 (0.8%)	2.00	141/6481 (2.2%)
2	9-B	1.75	45/4803 (0.9%)	2.09	151/6481 (2.3%)
2	10-B	1.76	49/4803 (1.0%)	2.06	143/6481 (2.2%)
3	1-C	1.73	27/3560 (0.8%)	1.95	92/4834 (1.9%)
3	1-D	1.72	29/3560 (0.8%)	1.93	92/4834 (1.9%)
3	2-C	1.76	43/3560 (1.2%)	1.98	93/4834 (1.9%)
3	2-D	1.70	28/3560 (0.8%)	1.94	86/4834 (1.8%)
3	3-C	1.73	40/3560 (1.1%)	1.93	89/4834 (1.8%)
3	3-D	1.74	29/3560 (0.8%)	1.95	83/4834 (1.7%)
3	4-C	1.73	29/3560 (0.8%)	1.92	95/4834 (2.0%)
3	4-D	1.72	31/3560 (0.9%)	1.94	85/4834 (1.8%)
3	5-C	1.71	29/3560 (0.8%)	1.99	99/4834 (2.0%)
3	5-D	1.77	48/3560 (1.3%)	1.93	86/4834 (1.8%)
3	6-C	1.74	32/3560 (0.9%)	2.01	102/4834 (2.1%)
3	6-D	1.69	22/3560 (0.6%)	1.98	89/4834 (1.8%)
3	7-C	1.75	39/3560 (1.1%)	1.97	102/4834 (2.1%)
3	7-D	1.72	16/3560 (0.4%)	1.98	102/4834 (2.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
3	8-C	1.71	22/3560 (0.6%)	1.97	88/4834 (1.8%)
3	8-D	1.73	35/3560 (1.0%)	1.92	81/4834 (1.7%)
3	9-C	1.71	32/3560 (0.9%)	1.93	77/4834 (1.6%)
3	9-D	1.70	29/3560 (0.8%)	1.98	95/4834 (2.0%)
3	10-C	1.68	27/3560 (0.8%)	1.99	99/4834 (2.0%)
3	10-D	1.75	35/3560 (1.0%)	1.94	86/4834 (1.8%)
All	All	1.74	1611/168400 (1.0%)	1.99	4714/227650 (2.1%)

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	1-A	0	25
1	2-A	0	20
1	3-A	0	22
1	4-A	0	25
1	5-A	0	27
1	6-A	0	18
1	7-A	0	26
1	8-A	0	19
1	9-A	0	29
1	10-A	0	19
2	1-B	0	27
2	2-B	0	21
2	3-B	0	28
2	4-B	0	23
2	5-B	0	22
2	6-B	0	23
2	7-B	0	20
2	8-B	0	19
2	9-B	0	28
2	10-B	0	25
3	1-C	0	16
3	1-D	0	13
3	2-C	0	11
3	2-D	0	12
3	3-C	0	9
3	3-D	0	7
3	4-C	0	15
3	4-D	0	14

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	5-C	0	14
3	5-D	0	17
3	6-C	0	16
3	6-D	0	12
3	7-C	0	13
3	7-D	0	13
3	8-C	0	12
3	8-D	0	13
3	9-C	0	6
3	9-D	0	15
3	10-C	0	13
3	10-D	0	10
All	All	0	717

The worst 5 of 1611 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	7-B	592	ARG	CZ-NH2	9.95	1.46	1.33
1	3-A	141	GLU	CD-OE2	9.33	1.35	1.25
1	7-A	160	ARG	CD-NE	9.23	1.62	1.46
2	1-B	585	ARG	CZ-NH1	9.02	1.44	1.33
3	10-D	192	ARG	CD-NE	8.88	1.61	1.46

The worst 5 of 4714 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	10-B	433	TYR	CB-CG-CD2	-20.70	108.58	121.00
1	1-A	107	ARG	NE-CZ-NH1	20.67	130.63	120.30
3	9-D	256	TYR	CB-CG-CD2	20.54	133.32	121.00
3	9-D	256	TYR	CB-CG-CD1	-19.19	109.48	121.00
2	10-B	264	TYR	CB-CG-CD1	18.97	132.38	121.00

There are no chirality outliers.

5 of 717 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	112	TYR	Sidechain
1	1-A	116	TYR	Sidechain
1	1-A	123	TYR	Sidechain
1	1-A	77	TYR	Sidechain
1	1-A	78	PHE	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	4831	0	4863	62	0
1	2-A	4831	0	4863	79	0
1	3-A	4831	0	4863	77	0
1	4-A	4831	0	4863	61	0
1	5-A	4831	0	4863	105	0
1	6-A	4831	0	4863	97	0
1	7-A	4831	0	4863	99	0
1	8-A	4831	0	4863	120	0
1	9-A	4831	0	4863	76	0
1	10-A	4831	0	4863	112	0
2	1-B	4701	0	4731	92	0
2	2-B	4701	0	4731	93	0
2	3-B	4701	0	4731	61	0
2	4-B	4701	0	4731	100	0
2	5-B	4701	0	4731	84	0
2	6-B	4701	0	4731	86	0
2	7-B	4701	0	4731	80	0
2	8-B	4701	0	4730	105	0
2	9-B	4701	0	4731	128	0
2	10-B	4701	0	4731	100	0
3	1-C	3485	0	3342	62	0
3	1-D	3485	0	3342	41	0
3	2-C	3485	0	3340	36	0
3	2-D	3485	0	3342	43	0
3	3-C	3485	0	3341	68	0
3	3-D	3485	0	3342	74	0
3	4-C	3485	0	3342	38	0
3	4-D	3485	0	3342	43	0
3	5-C	3485	0	3342	60	0
3	5-D	3485	0	3342	34	0
3	6-C	3485	0	3342	32	0
3	6-D	3485	0	3342	68	0
3	7-C	3485	0	3340	61	0
3	7-D	3485	0	3341	59	0
3	8-C	3485	0	3340	31	0
3	8-D	3485	0	3341	28	0
3	9-C	3485	0	3342	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	9-D	3485	0	3342	35	0
3	10-C	3485	0	3342	46	0
3	10-D	3485	0	3342	53	0
4	1-E	220	0	46	0	0
4	1-F	220	0	46	0	0
4	2-E	220	0	46	0	0
4	2-F	220	0	46	0	0
4	3-E	220	0	46	0	0
4	3-F	220	0	46	0	0
4	4-E	220	0	46	0	0
4	4-F	220	0	46	0	0
4	5-E	220	0	46	0	0
4	5-F	220	0	46	0	0
4	6-E	220	0	46	0	0
4	6-F	220	0	46	0	0
4	7-E	220	0	46	0	0
4	7-F	220	0	46	0	0
4	8-E	220	0	46	0	0
4	8-F	220	0	46	1	0
4	9-E	220	0	46	0	0
4	9-F	220	0	46	0	0
4	10-E	220	0	46	0	0
4	10-F	220	0	46	0	0
All	All	169420	0	163690	2439	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 7.

The worst 5 of 2439 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:A:143:ARG:HH22	2:B:292:ILE:CD1	1.12	1.60
1:A:585:ILE:CD1	1:A:683:ILE:HD13	1.26	1.56
1:A:70:LEU:CD2	2:B:216:PHE:CG	1.87	1.53
3:C:59:ARG:HG3	3:D:280:ILE:CD1	1.40	1.51
1:A:143:ARG:CZ	2:B:292:ILE:HD11	1.38	1.49

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	1-A	561/823 (68%)	526 (94%)	21 (4%)	14 (2%)	5 32
1	2-A	561/823 (68%)	524 (93%)	19 (3%)	18 (3%)	4 26
1	3-A	561/823 (68%)	521 (93%)	24 (4%)	16 (3%)	4 29
1	4-A	561/823 (68%)	523 (93%)	25 (4%)	13 (2%)	6 34
1	5-A	561/823 (68%)	524 (93%)	23 (4%)	14 (2%)	5 32
1	6-A	561/823 (68%)	525 (94%)	26 (5%)	10 (2%)	8 40
1	7-A	561/823 (68%)	519 (92%)	27 (5%)	15 (3%)	5 31
1	8-A	561/823 (68%)	519 (92%)	26 (5%)	16 (3%)	4 29
1	9-A	561/823 (68%)	526 (94%)	23 (4%)	12 (2%)	7 36
1	10-A	561/823 (68%)	528 (94%)	19 (3%)	14 (2%)	5 32
2	1-B	553/846 (65%)	512 (93%)	26 (5%)	15 (3%)	5 31
2	2-B	553/846 (65%)	505 (91%)	41 (7%)	7 (1%)	12 48
2	3-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	7 38
2	4-B	553/846 (65%)	503 (91%)	32 (6%)	18 (3%)	4 26
2	5-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	7 38
2	6-B	553/846 (65%)	502 (91%)	36 (6%)	15 (3%)	5 31
2	7-B	553/846 (65%)	515 (93%)	24 (4%)	14 (2%)	5 32
2	8-B	553/846 (65%)	516 (93%)	29 (5%)	8 (1%)	11 46
2	9-B	553/846 (65%)	505 (91%)	24 (4%)	24 (4%)	2 22
2	10-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	7 38
3	1-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	5 32
3	1-D	443/473 (94%)	395 (89%)	37 (8%)	11 (2%)	5 32
3	2-C	443/473 (94%)	395 (89%)	29 (6%)	19 (4%)	2 22
3	2-D	443/473 (94%)	390 (88%)	33 (7%)	20 (4%)	2 22
3	3-C	443/473 (94%)	396 (89%)	33 (7%)	14 (3%)	4 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	3-D	443/473 (94%)	393 (89%)	33 (7%)	17 (4%)	3 24
3	4-C	443/473 (94%)	401 (90%)	29 (6%)	13 (3%)	4 29
3	4-D	443/473 (94%)	402 (91%)	29 (6%)	12 (3%)	5 31
3	5-C	443/473 (94%)	400 (90%)	27 (6%)	16 (4%)	3 25
3	5-D	443/473 (94%)	401 (90%)	28 (6%)	14 (3%)	4 26
3	6-C	443/473 (94%)	397 (90%)	34 (8%)	12 (3%)	5 31
3	6-D	443/473 (94%)	396 (89%)	32 (7%)	15 (3%)	3 26
3	7-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	5 32
3	7-D	443/473 (94%)	389 (88%)	33 (7%)	21 (5%)	2 21
3	8-C	443/473 (94%)	391 (88%)	29 (6%)	23 (5%)	2 19
3	8-D	443/473 (94%)	408 (92%)	26 (6%)	9 (2%)	7 38
3	9-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	5 32
3	9-D	443/473 (94%)	401 (90%)	29 (6%)	13 (3%)	4 29
3	10-C	443/473 (94%)	396 (89%)	29 (6%)	18 (4%)	3 22
3	10-D	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	5 32
All	All	20000/26150 (76%)	18292 (92%)	1141 (6%)	567 (3%)	8 30

5 of 567 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	91	GLU
1	1-A	97	LYS
1	1-A	130	SER
1	1-A	785	GLU
2	1-B	247	SER

5.3.2 Protein sidechains (i)

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	1-A	542/766 (71%)	498 (92%)	44 (8%)	11 35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	2-A	542/766 (71%)	502 (93%)	40 (7%)	13 38
1	3-A	542/766 (71%)	510 (94%)	32 (6%)	19 45
1	4-A	542/766 (71%)	499 (92%)	43 (8%)	12 35
1	5-A	542/766 (71%)	508 (94%)	34 (6%)	18 43
1	6-A	542/766 (71%)	487 (90%)	55 (10%)	7 25
1	7-A	542/766 (71%)	501 (92%)	41 (8%)	13 37
1	8-A	542/766 (71%)	497 (92%)	45 (8%)	11 34
1	9-A	542/766 (71%)	505 (93%)	37 (7%)	16 41
1	10-A	542/766 (71%)	497 (92%)	45 (8%)	11 34
2	1-B	528/787 (67%)	492 (93%)	36 (7%)	16 41
2	2-B	528/787 (67%)	492 (93%)	36 (7%)	16 41
2	3-B	528/787 (67%)	490 (93%)	38 (7%)	14 39
2	4-B	528/787 (67%)	482 (91%)	46 (9%)	10 31
2	5-B	528/787 (67%)	493 (93%)	35 (7%)	16 41
2	6-B	528/787 (67%)	479 (91%)	49 (9%)	9 28
2	7-B	528/787 (67%)	487 (92%)	41 (8%)	12 36
2	8-B	528/787 (67%)	491 (93%)	37 (7%)	15 40
2	9-B	528/787 (67%)	486 (92%)	42 (8%)	12 35
2	10-B	528/787 (67%)	475 (90%)	53 (10%)	7 26
3	1-C	396/421 (94%)	369 (93%)	27 (7%)	16 41
3	1-D	396/421 (94%)	375 (95%)	21 (5%)	22 47
3	2-C	396/421 (94%)	371 (94%)	25 (6%)	18 43
3	2-D	396/421 (94%)	373 (94%)	23 (6%)	20 45
3	3-C	396/421 (94%)	374 (94%)	22 (6%)	21 46
3	3-D	396/421 (94%)	371 (94%)	25 (6%)	18 43
3	4-C	396/421 (94%)	375 (95%)	21 (5%)	22 47
3	4-D	396/421 (94%)	366 (92%)	30 (8%)	13 37
3	5-C	396/421 (94%)	375 (95%)	21 (5%)	22 47
3	5-D	396/421 (94%)	369 (93%)	27 (7%)	16 41
3	6-C	396/421 (94%)	375 (95%)	21 (5%)	22 47
3	6-D	396/421 (94%)	376 (95%)	20 (5%)	24 48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	7-C	396/421 (94%)	380 (96%)	16 (4%)	31	55
3	7-D	396/421 (94%)	379 (96%)	17 (4%)	29	53
3	8-C	396/421 (94%)	376 (95%)	20 (5%)	24	48
3	8-D	396/421 (94%)	375 (95%)	21 (5%)	22	47
3	9-C	396/421 (94%)	372 (94%)	24 (6%)	18	44
3	9-D	396/421 (94%)	377 (95%)	19 (5%)	25	51
3	10-C	396/421 (94%)	368 (93%)	28 (7%)	14	39
3	10-D	396/421 (94%)	366 (92%)	30 (8%)	13	37
All	All	18620/23950 (78%)	17333 (93%)	1287 (7%)	19	40

5 of 1287 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	8-A	697	LEU
1	10-A	253	GLN
2	8-B	537	VAL
1	8-A	692	LEU
1	9-A	661	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 310 such sidechains are listed below:

Mol	Chain	Res	Type
2	8-B	629	ASN
2	10-B	459	HIS
3	8-C	317	ASN
2	9-B	597	ASN
3	10-C	186	ASN

5.3.3 RNA (i)

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 monosaccharides 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.

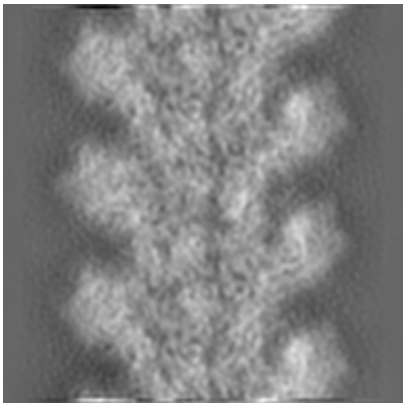
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-2799. These allow visual inspection of the internal detail of the map and identification of artifacts.

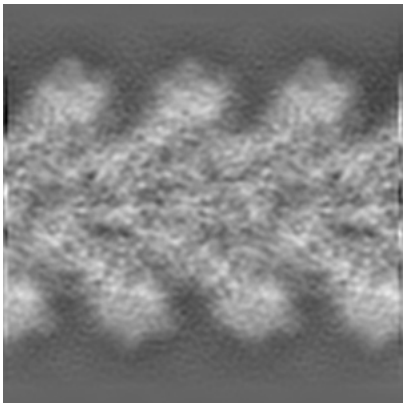
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

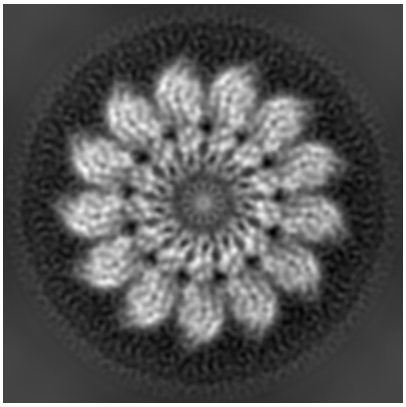
6.1.1 Primary map



X



Y

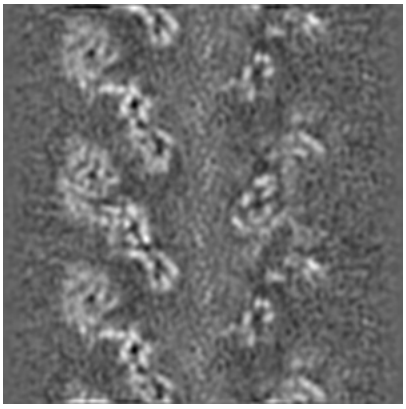


Z

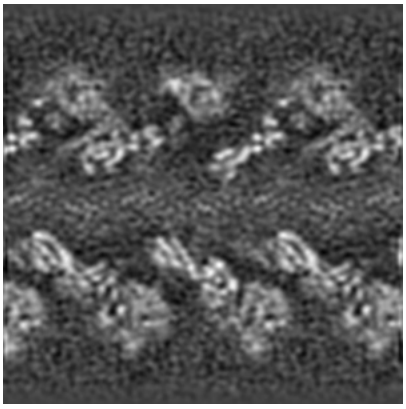
The images above show the map projected in three orthogonal directions.

6.2 Central slices

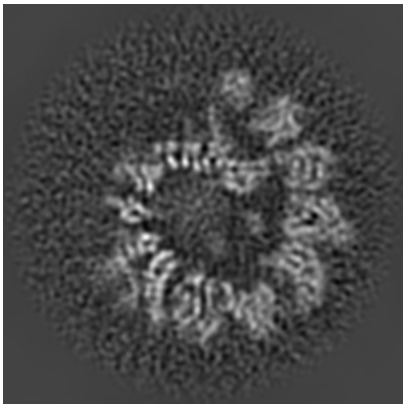
6.2.1 Primary map



X Index: 106



Y Index: 106

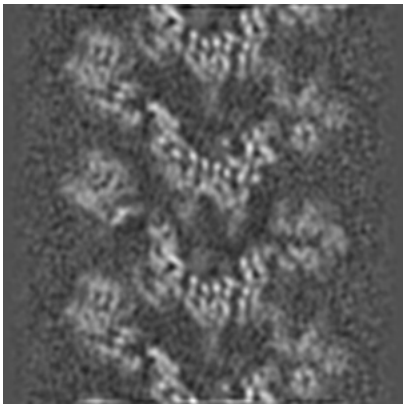


Z Index: 106

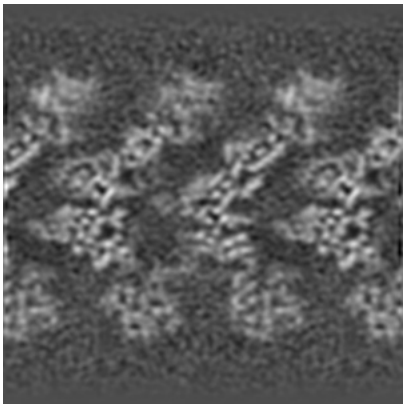
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

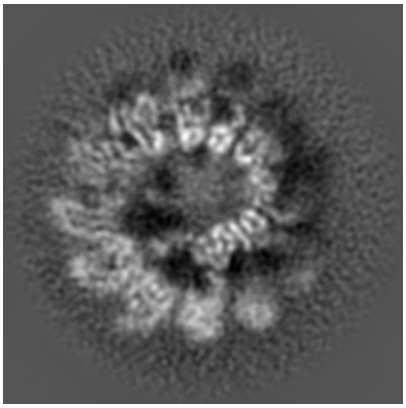
6.3.1 Primary map



X Index: 131



Y Index: 135

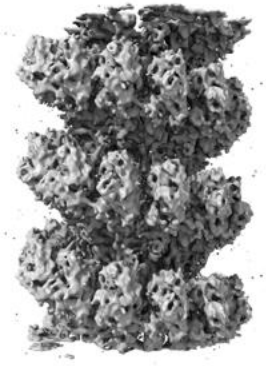


Z Index: 1

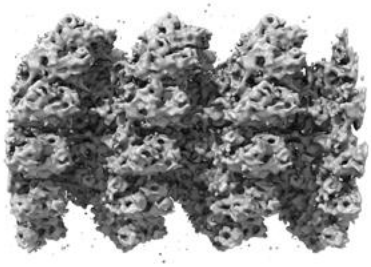
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

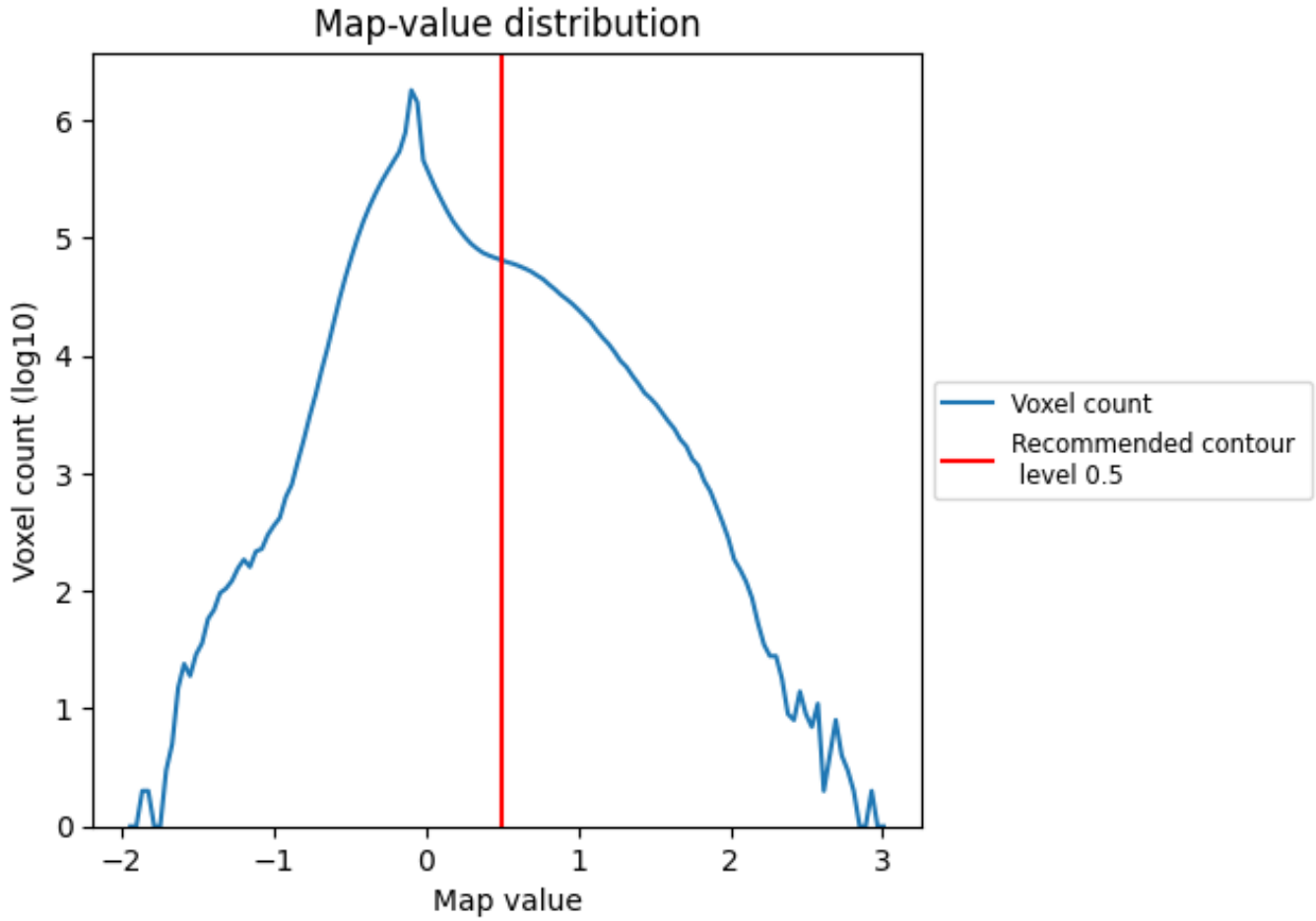
6.5 Mask visualisation (i)

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

7 Map analysis

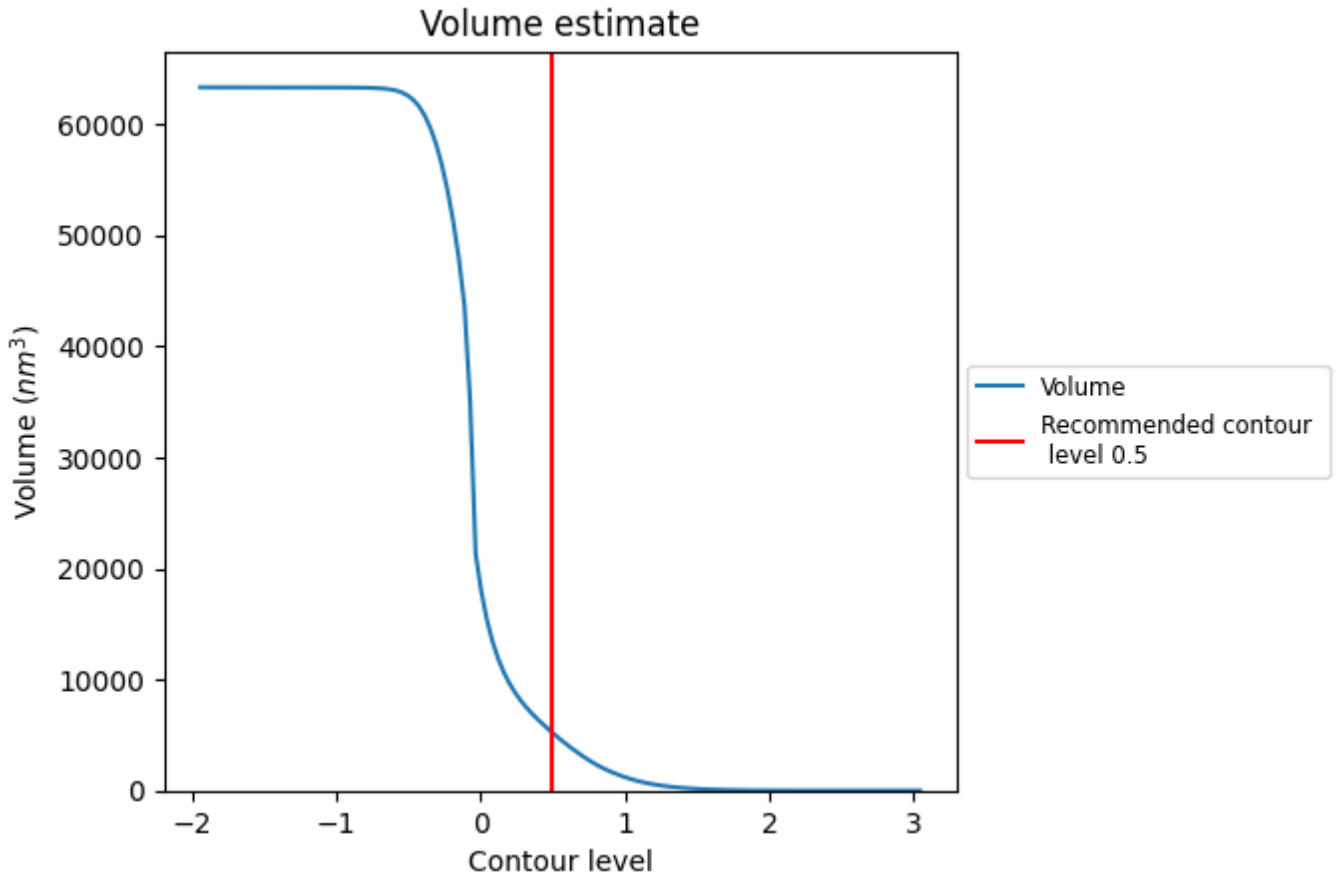
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

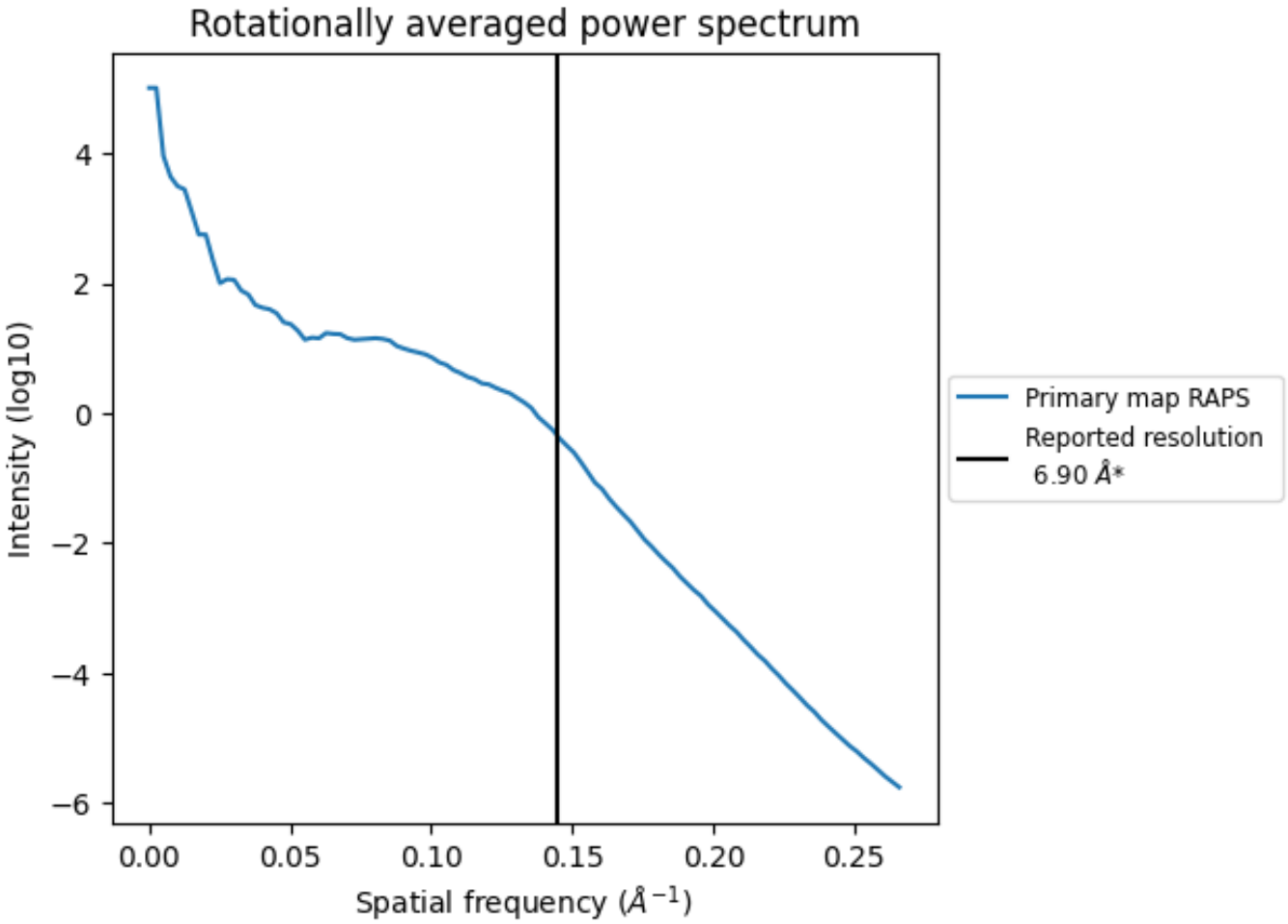
7.2 Volume estimate (i)



The volume at the recommended contour level is 5183 nm^3; this corresponds to an approximate mass of 4682 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 (i)



*Reported resolution corresponds to spatial frequency of 0.145 Å^{-1}

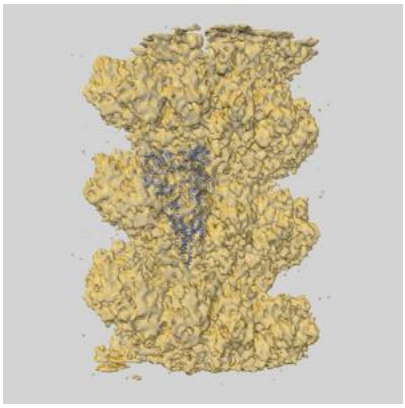
8 Fourier-Shell correlation (i)

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

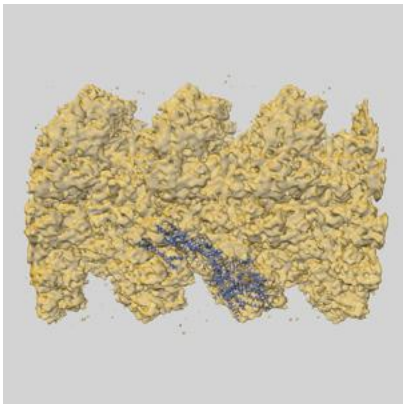
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-2799 and PDB model 5FLZ. Per-residue inclusion information can be found in section 3 on page 10.

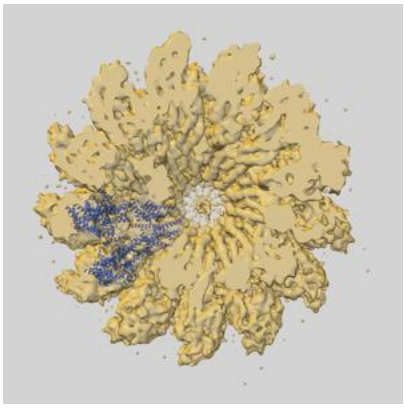
9.1 Map-model overlay



X



Y



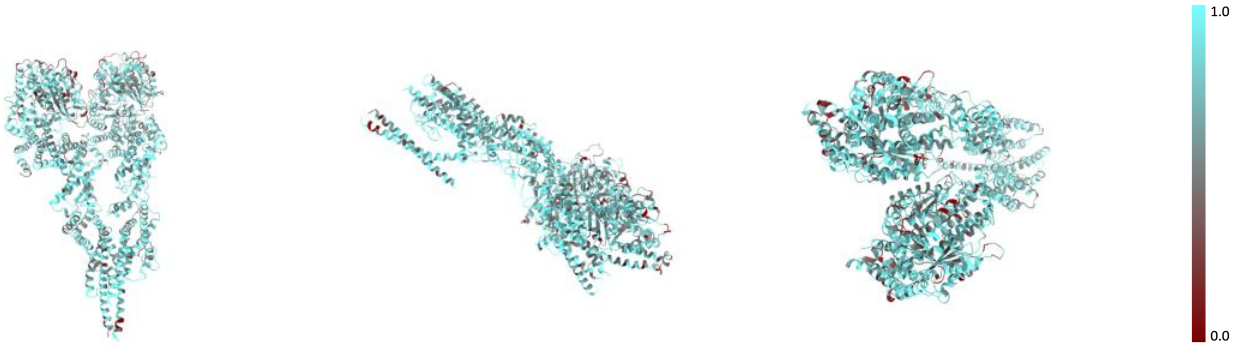
Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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)

This section was not generated.

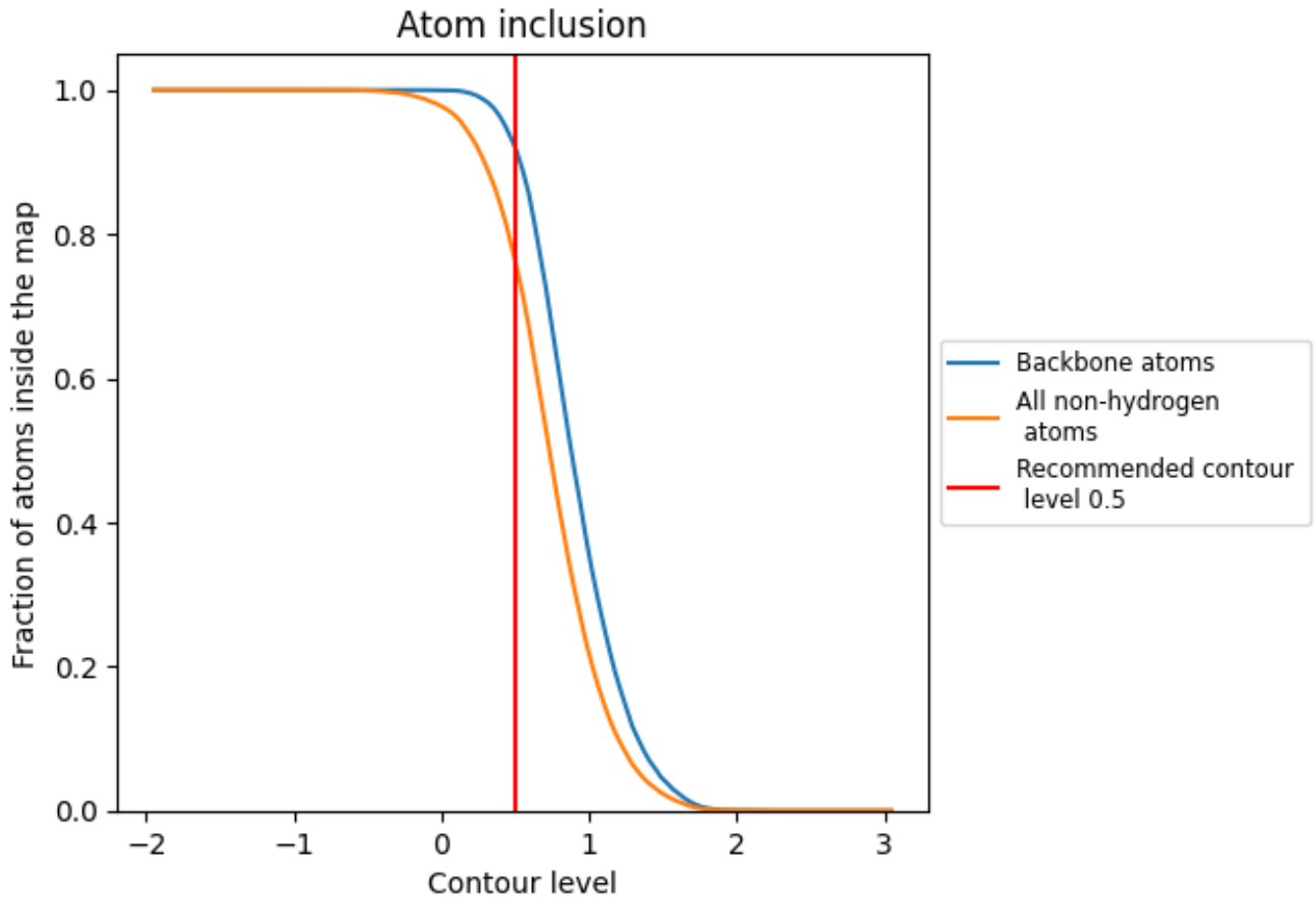
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	0.7619
A	0.7895
B	0.8096
C	0.7214
D	0.7016
E	0.7591
F	0.7409