wwPDB EM Map/Model Validation Report (i)

May 5, 2016 – 10:46 PM EDT

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 Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

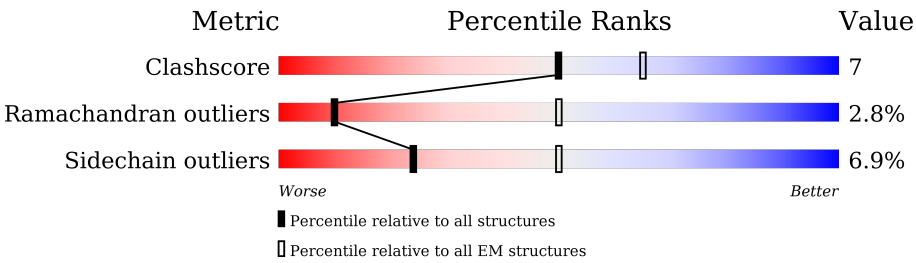
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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%

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%
1	8-A	823	43% 22% 5% • 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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	63% 23% 7% 6%
3	1-D	473	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%
3	6-D	473	62% 27% • • 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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	100%
4	1-F	44	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%
4	9-E	44	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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
			Total	C	N	O	S		
1	1-A	575	4831	3110	806	889	26	0	0
1	2-A	575	4831	3110	806	889	26	0	0
1	3-A	575	4831	3110	806	889	26	0	0
1	4-A	575	4831	3110	806	889	26	0	0
1	5-A	575	4831	3110	806	889	26	0	0
1	6-A	575	4831	3110	806	889	26	0	0
1	7-A	575	4831	3110	806	889	26	0	0
1	8-A	575	4831	3110	806	889	26	0	0
1	9-A	575	4831	3110	806	889	26	0	0
1	10-A	575	4831	3110	806	889	26	0	0

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

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

Continued on next page...

Continued from previous page...

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

- Molecule 3 is a protein called TUBULIN GAMMA CHAIN.

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

Continued on next page...

Continued from previous page...

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

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
			Total	C	N	O		
4	1-E	44	220	132	44	44	0	0
4	2-E	44	220	132	44	44	0	0
4	3-E	44	220	132	44	44	0	0
4	4-E	44	220	132	44	44	0	0
4	5-E	44	220	132	44	44	0	0
4	6-E	44	220	132	44	44	0	0
4	7-E	44	220	132	44	44	0	0
4	8-E	44	220	132	44	44	0	0
4	9-E	44	220	132	44	44	0	0

Continued on next page...

Continued from previous page...

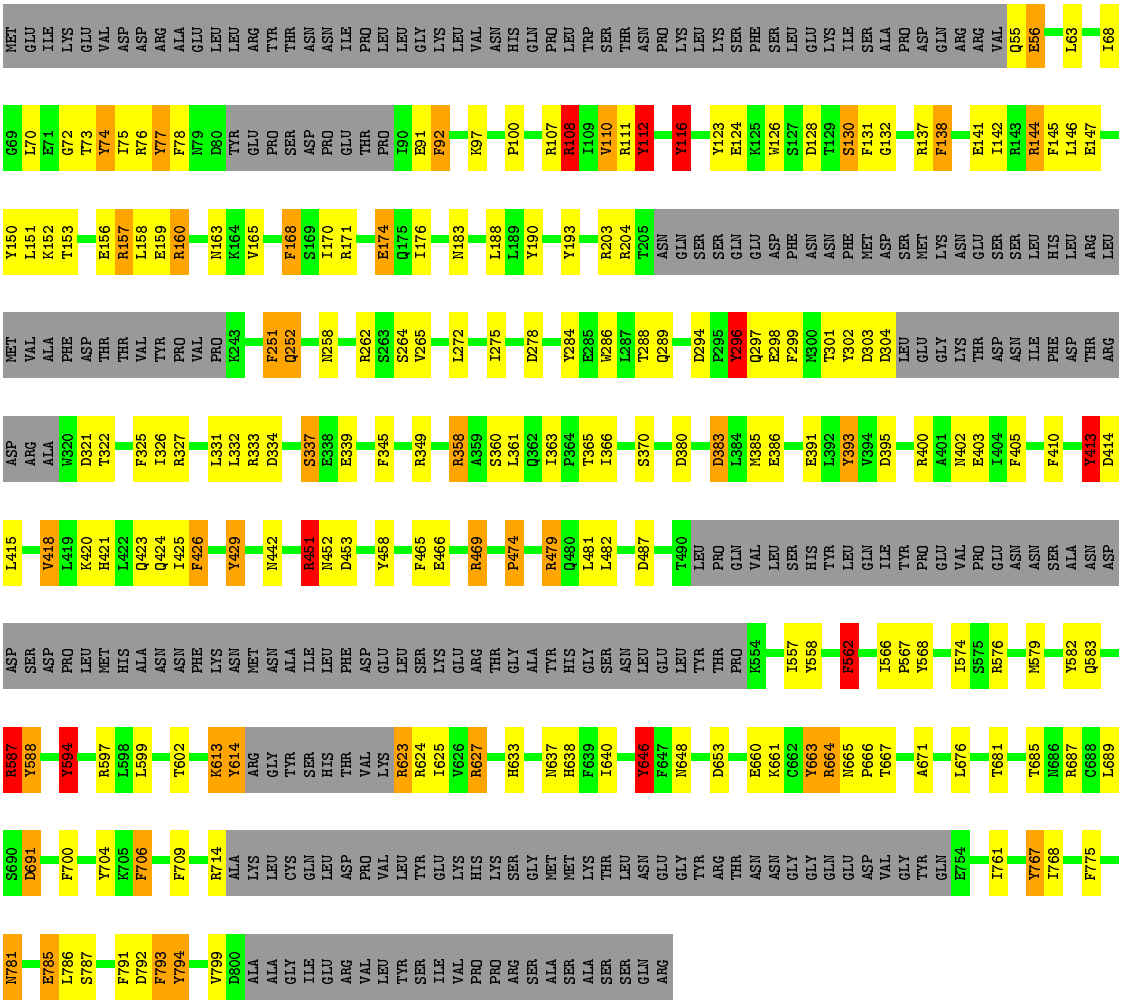
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	10-E	44	220	132	44	44	0	0
4	1-F	44	220	132	44	44	0	0
4	2-F	44	220	132	44	44	0	0
4	3-F	44	220	132	44	44	0	0
4	4-F	44	220	132	44	44	0	0
4	5-F	44	220	132	44	44	0	0
4	6-F	44	220	132	44	44	0	0
4	7-F	44	220	132	44	44	0	0
4	8-F	44	220	132	44	44	0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

3 Residue-property plots (i)

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

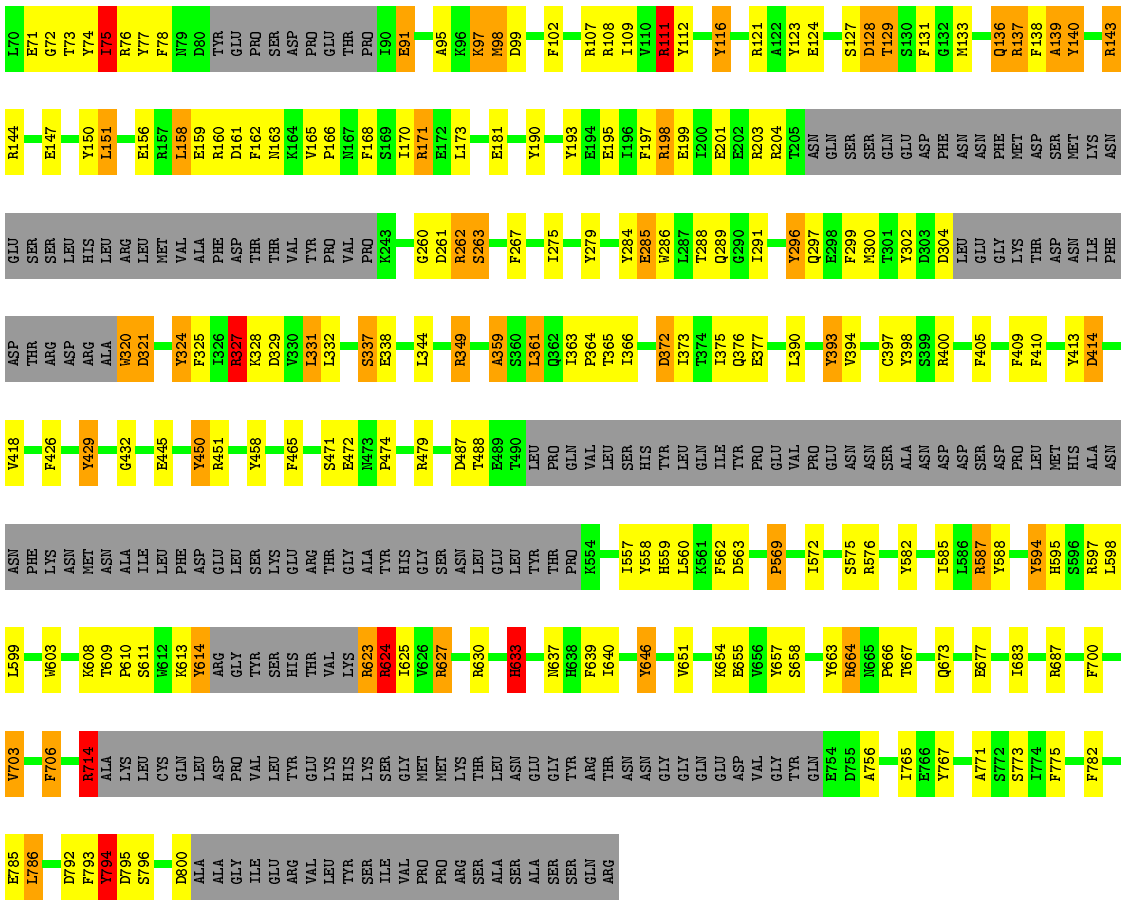
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 1-A: 46% 18% 5% • 30%



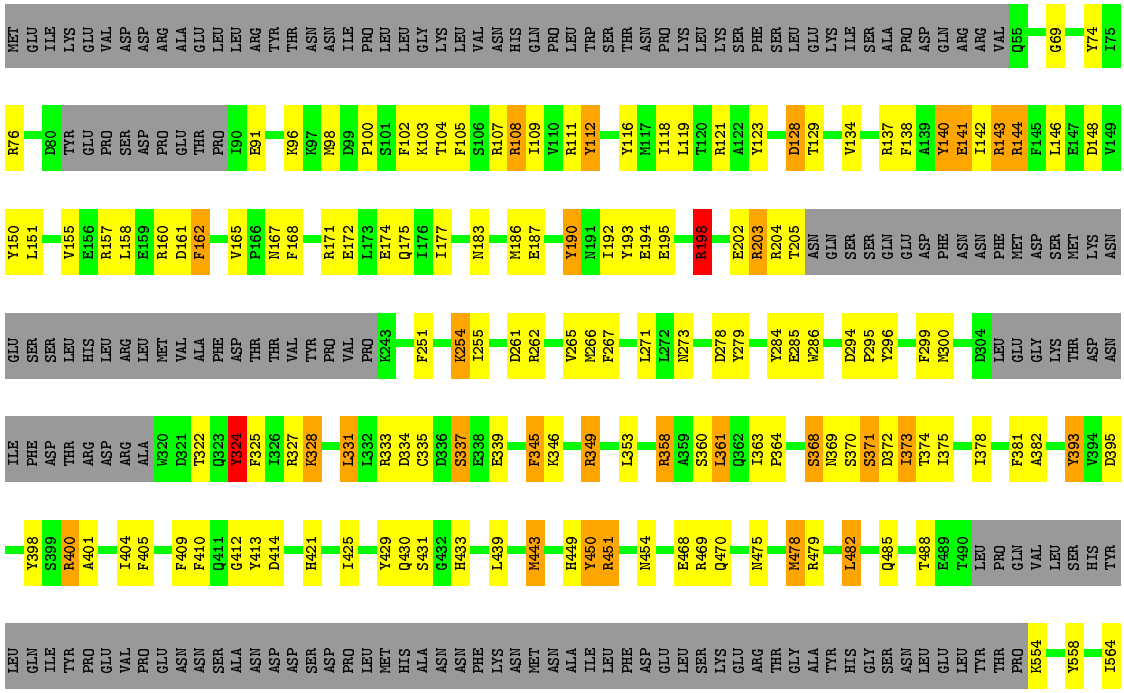
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

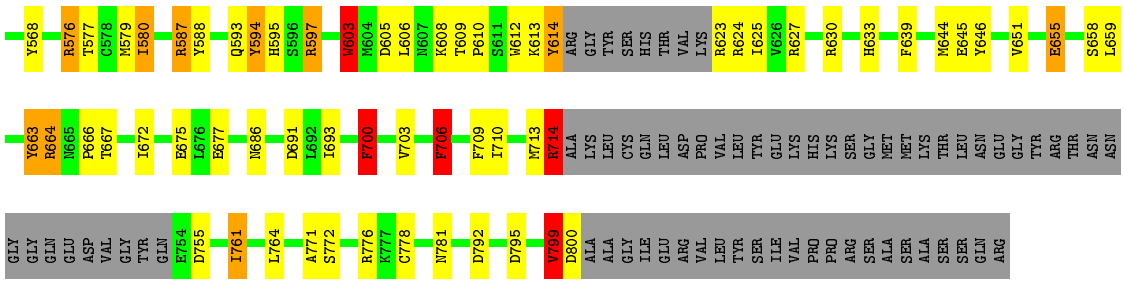
Chain 2-A: 45% 18% 5% • 30%



- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

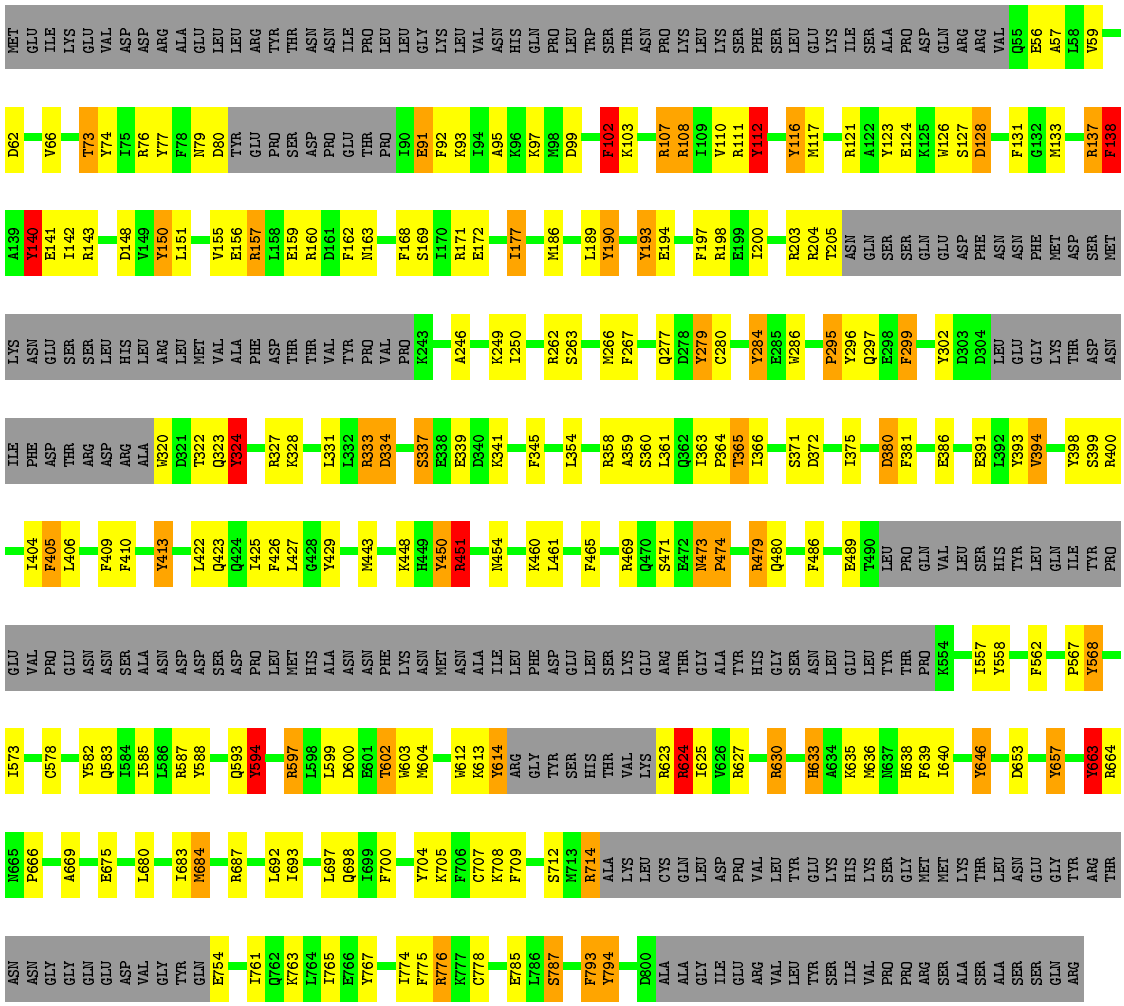
Chain 3-A:





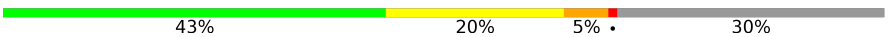
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

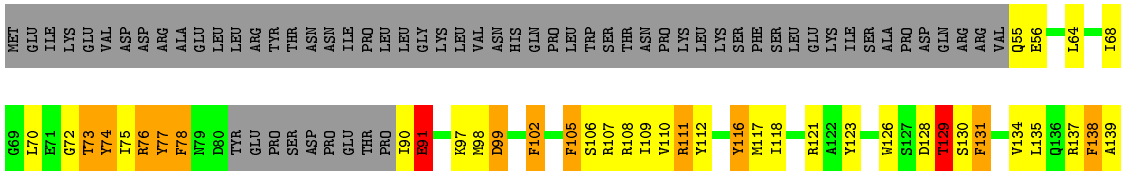
Chain 4-A:

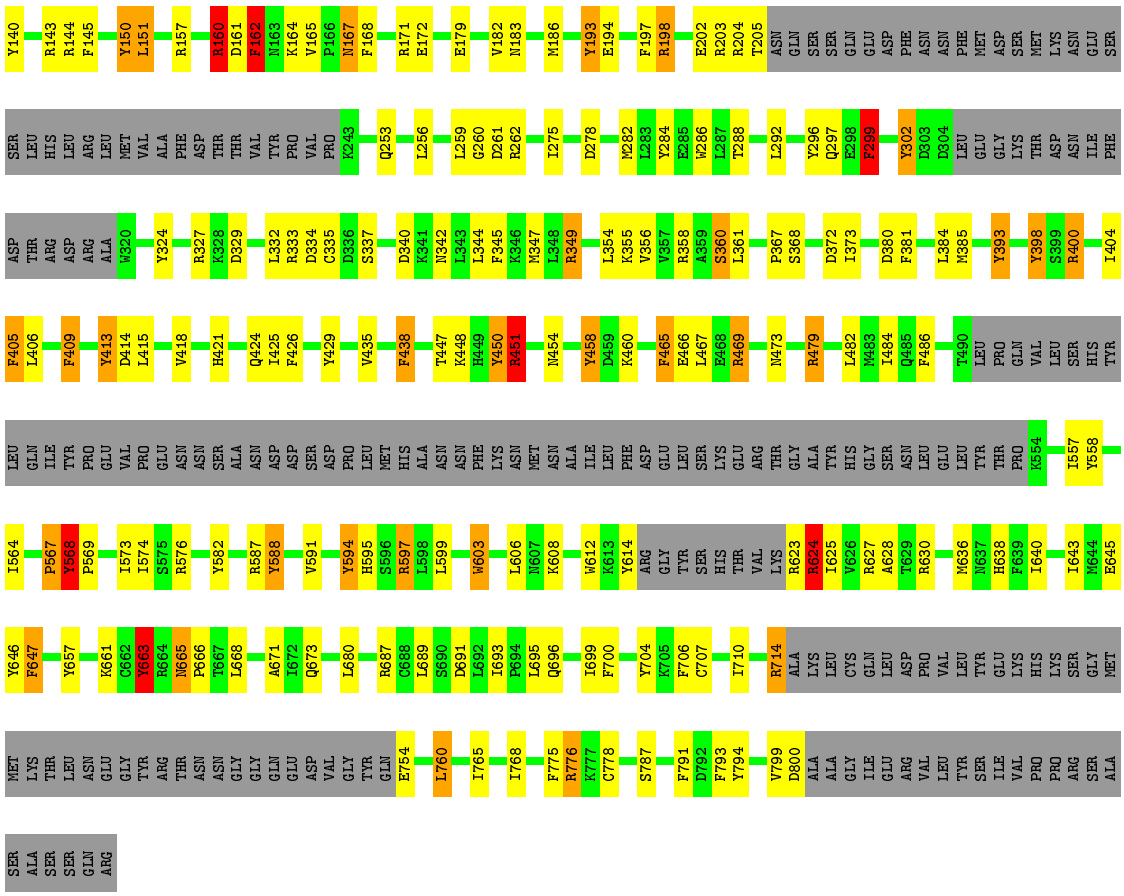


- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 5-A:

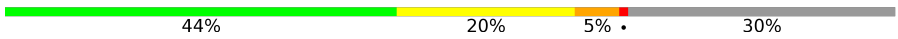


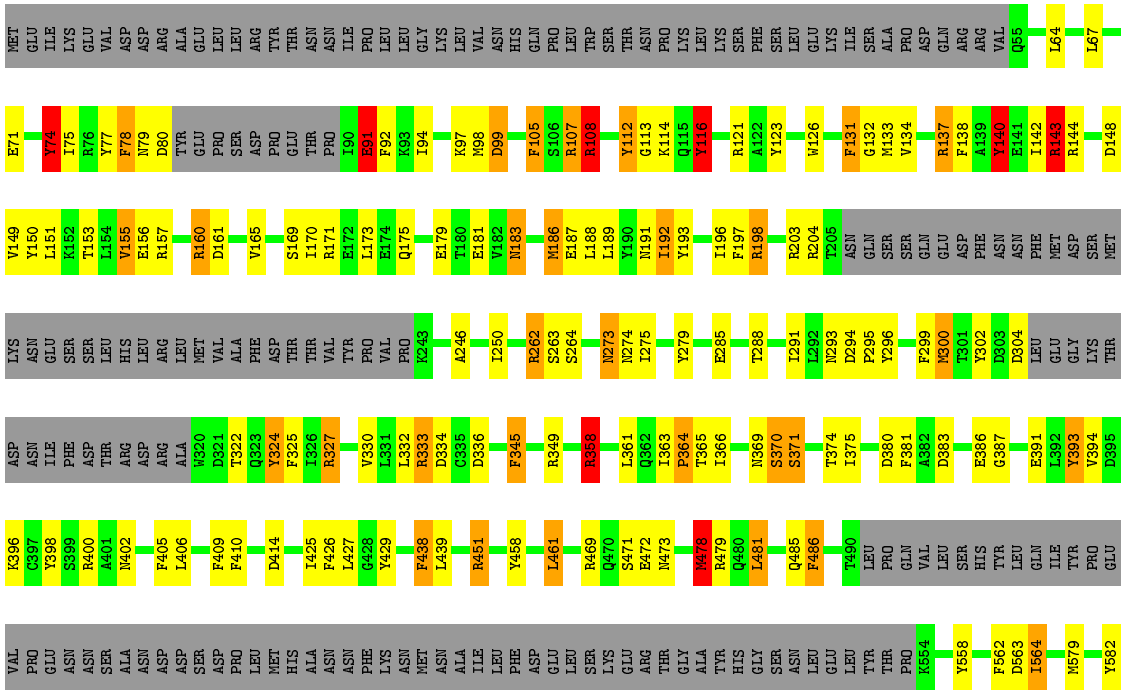


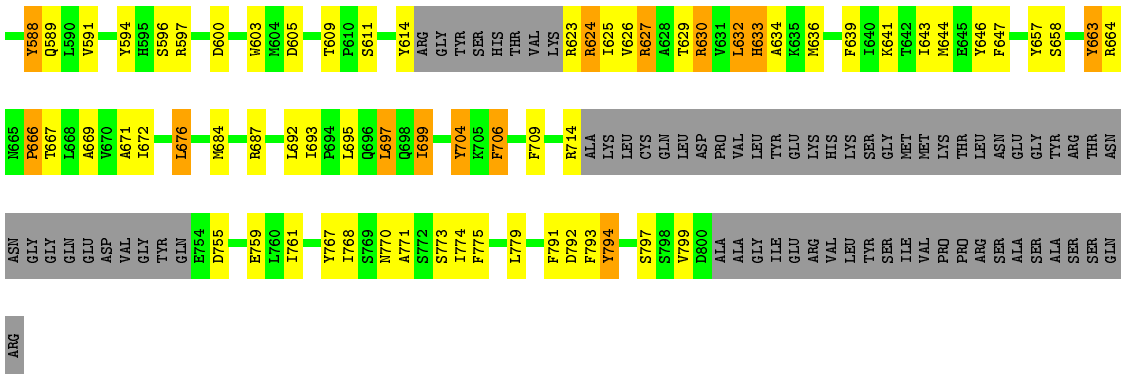


- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 6-A:

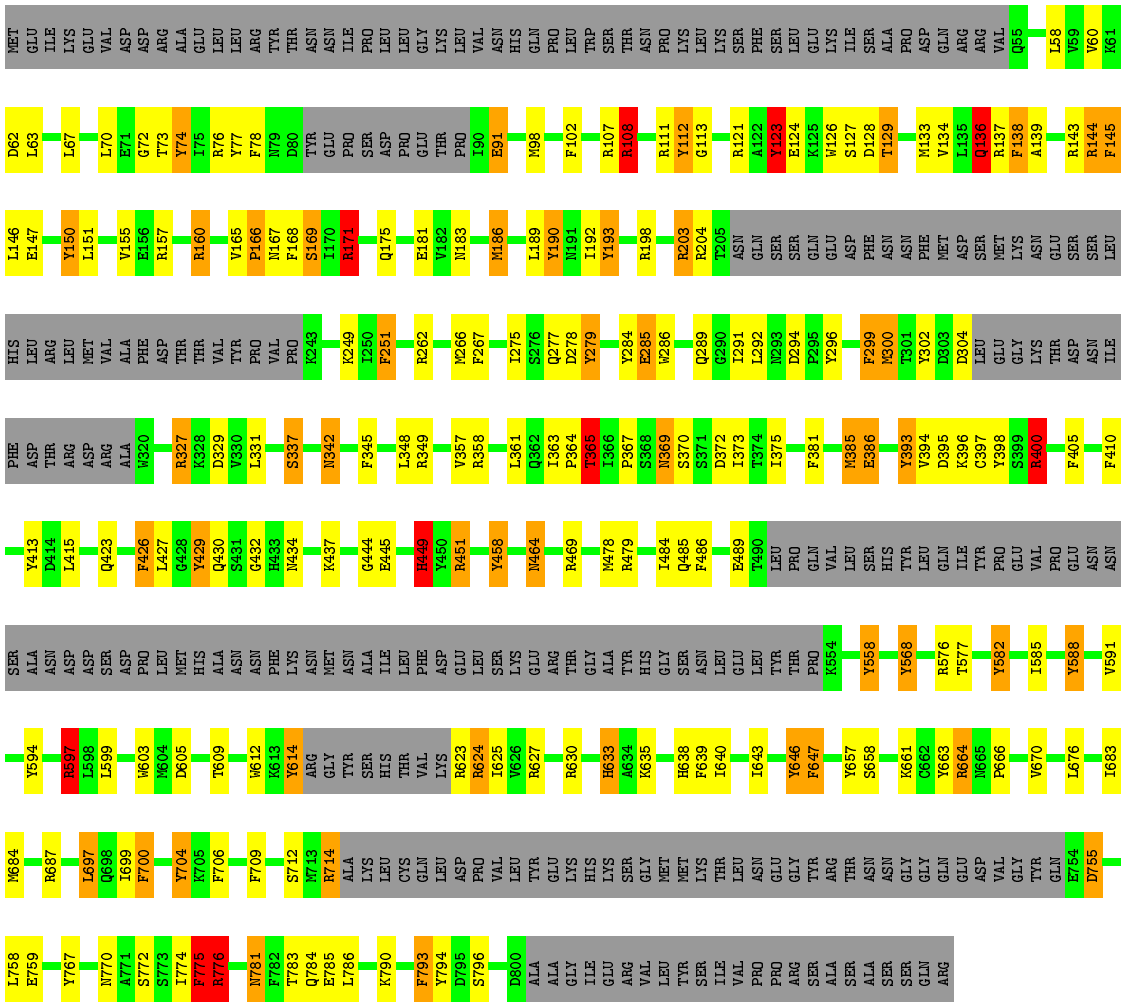






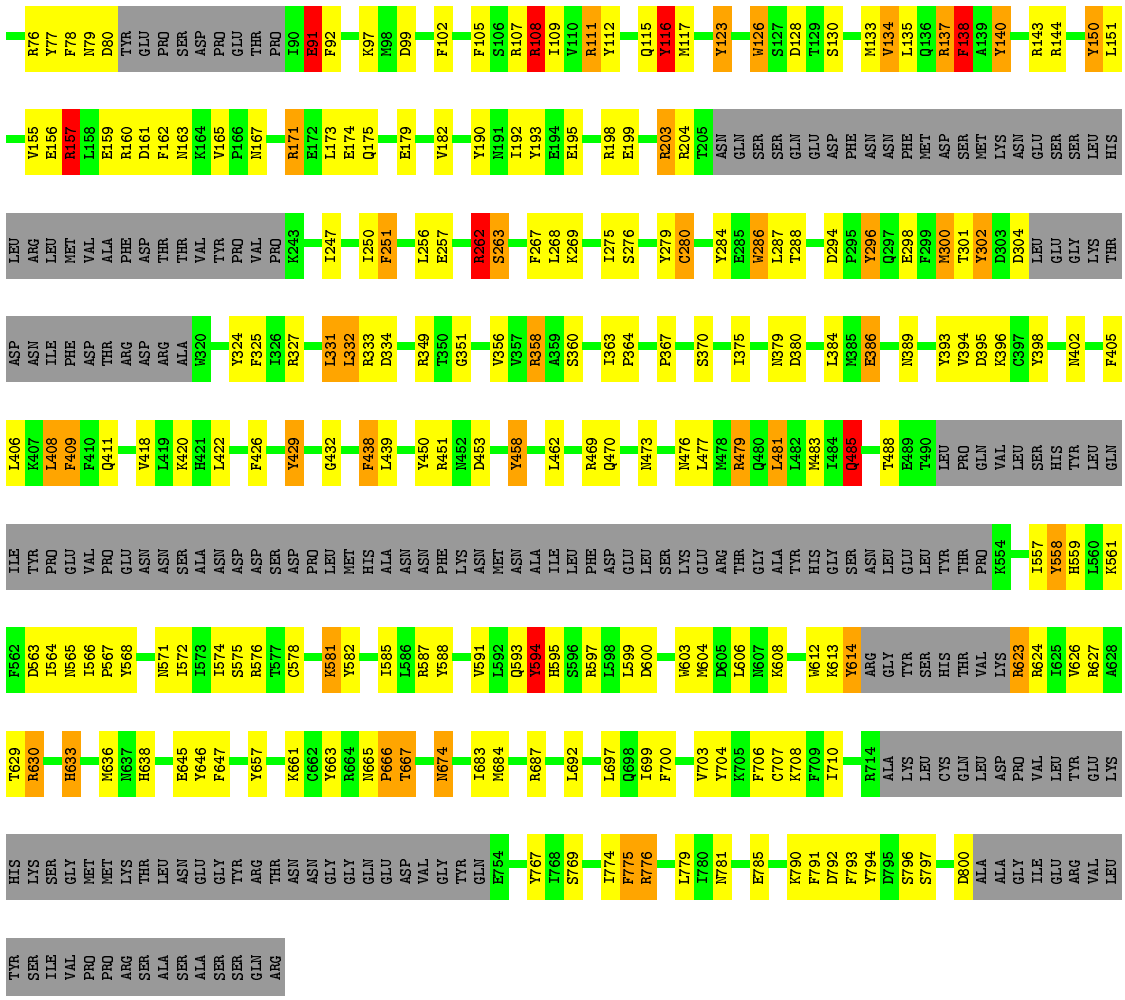
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

Chain 7-A: 45% 17% 6% • 30%



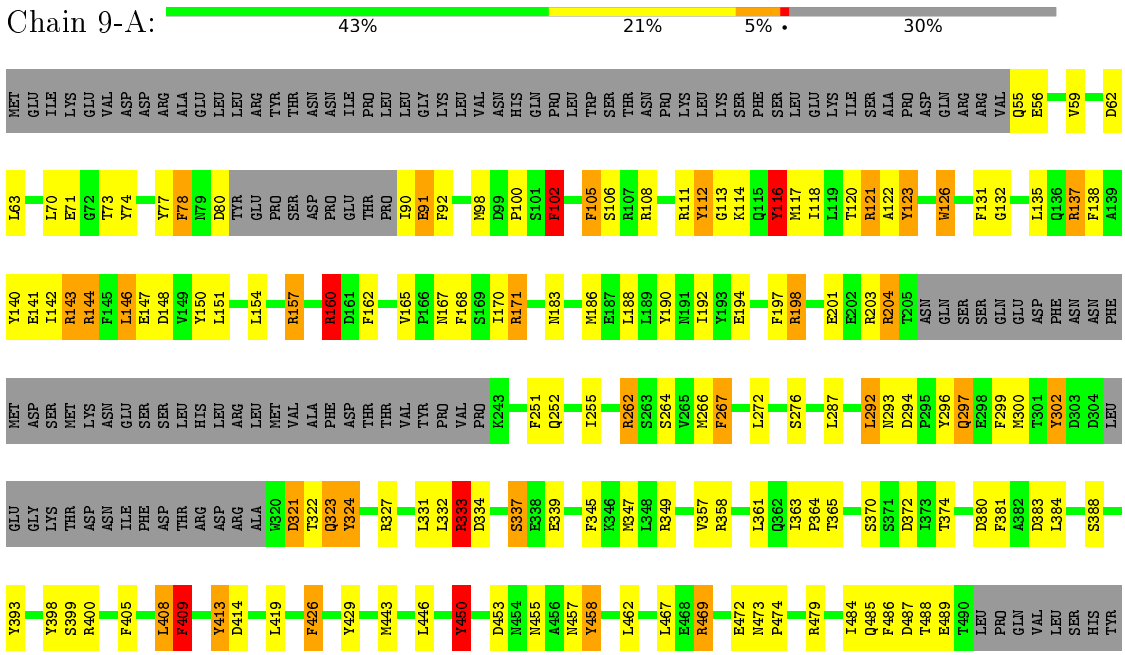
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

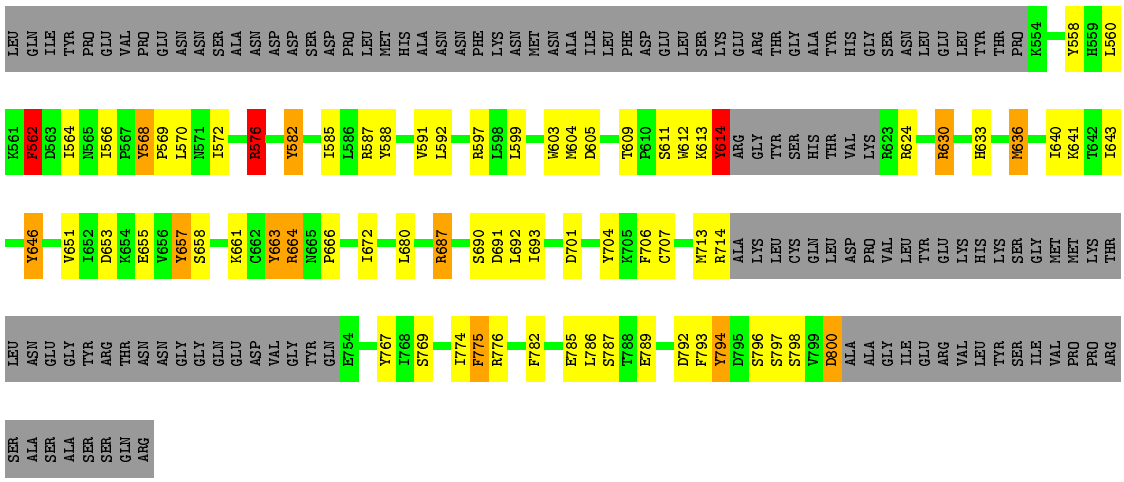
Chain 8-A: 43% 22% 5% • 30%



- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

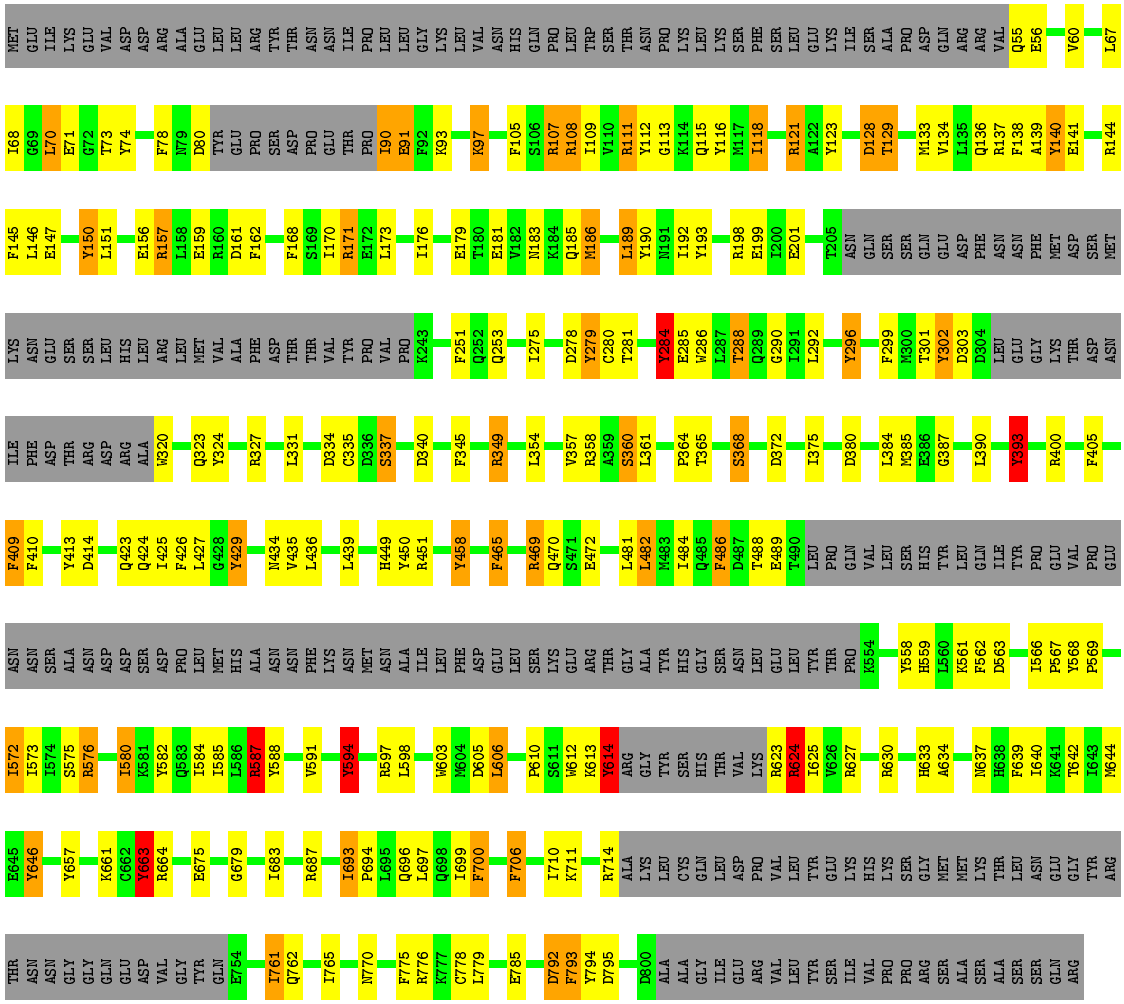
Chain 9-A:





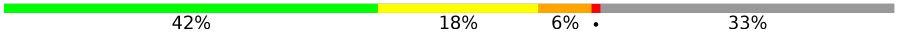
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

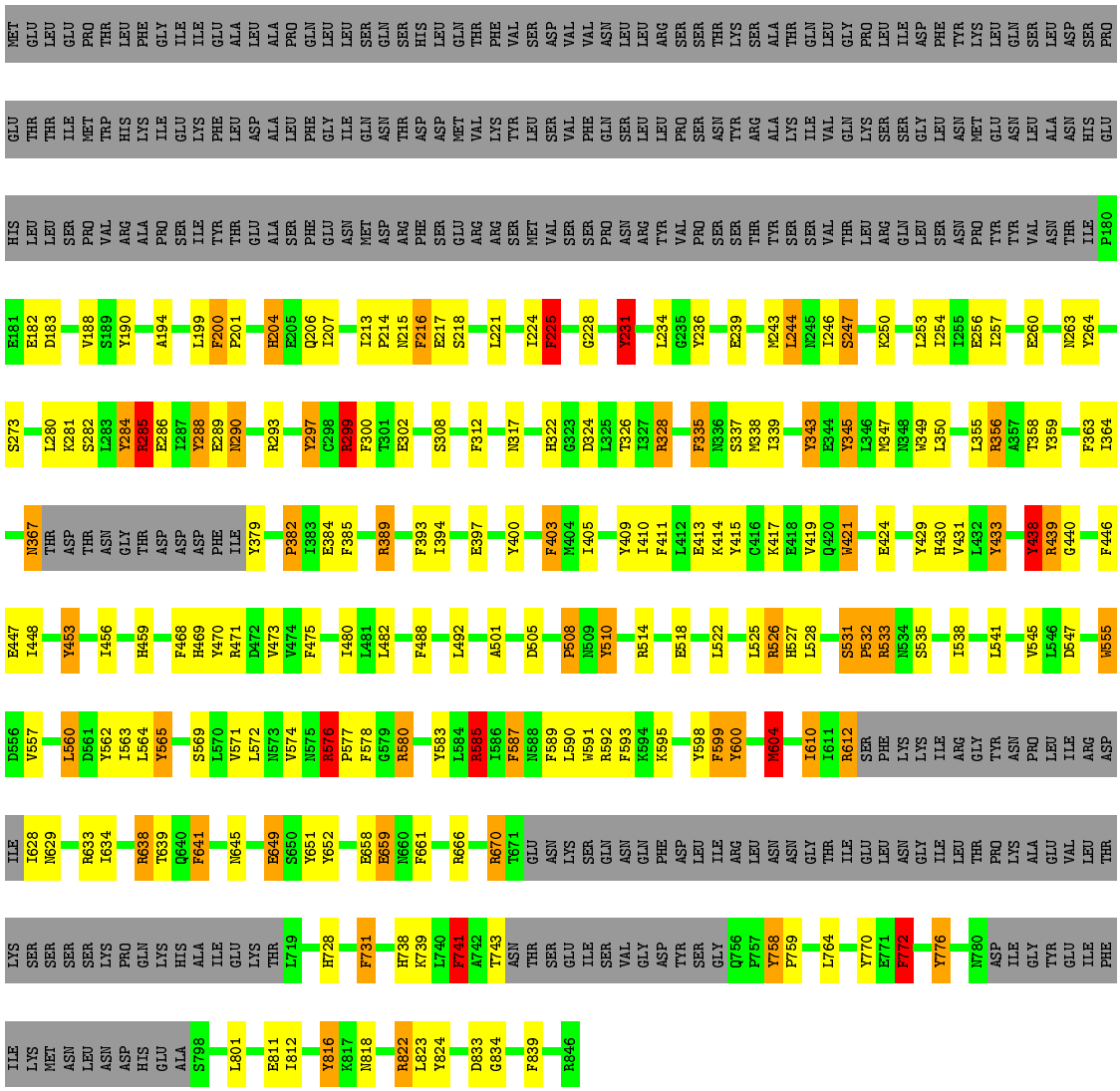
Chain 10-A:



- Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

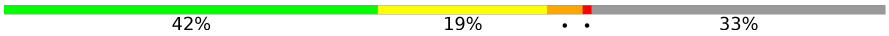
Chain 1-B:

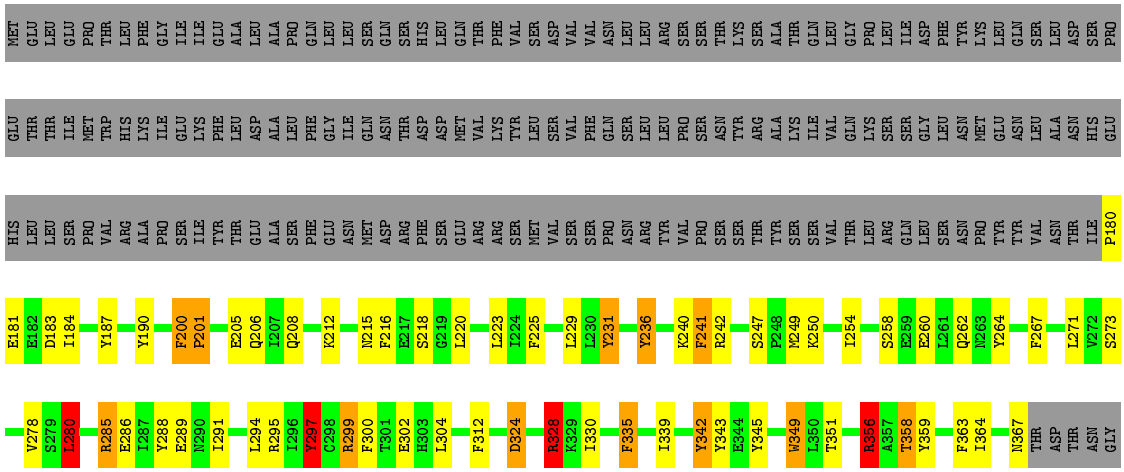


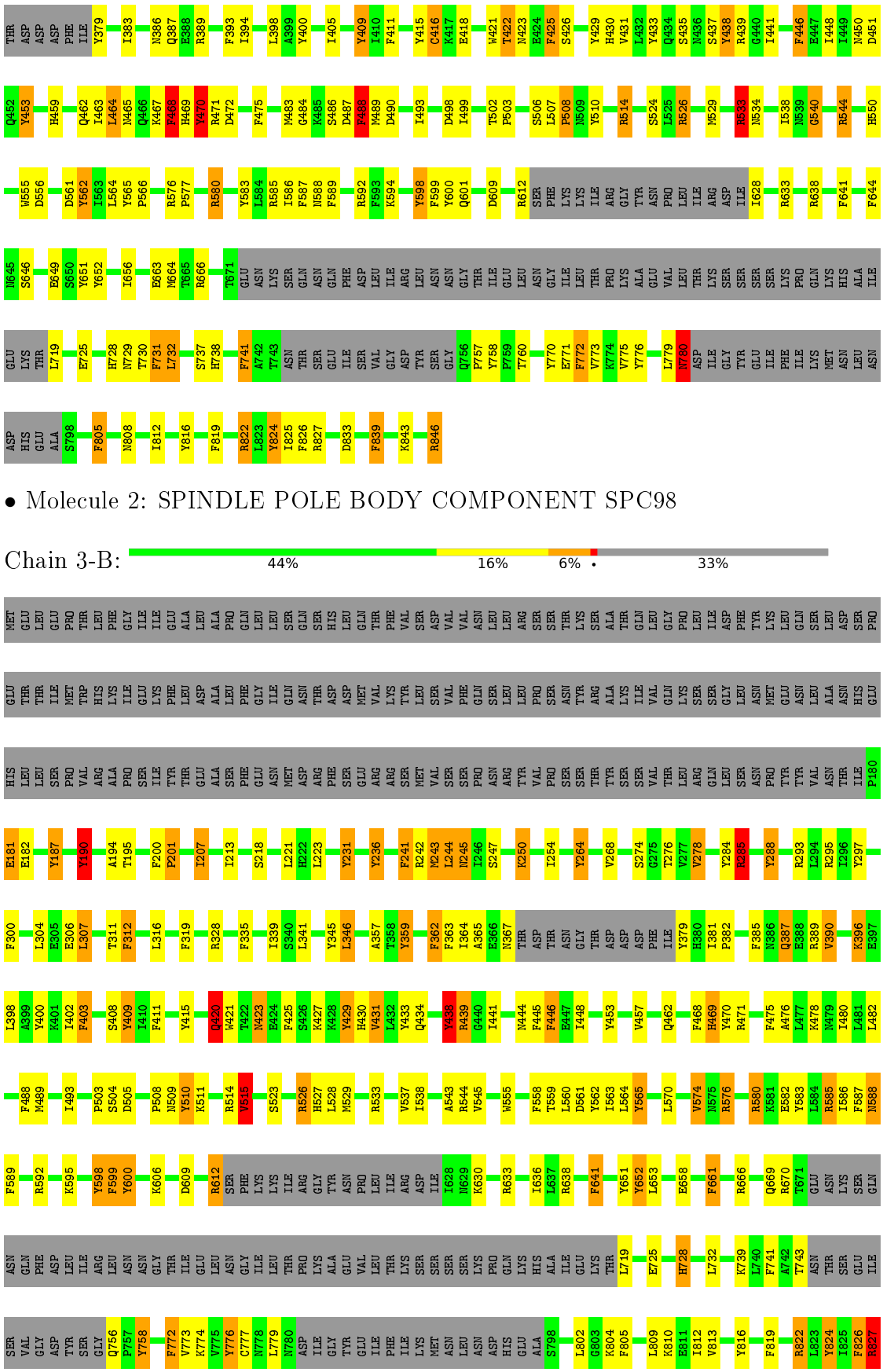


- Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 2-B:





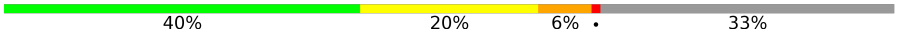


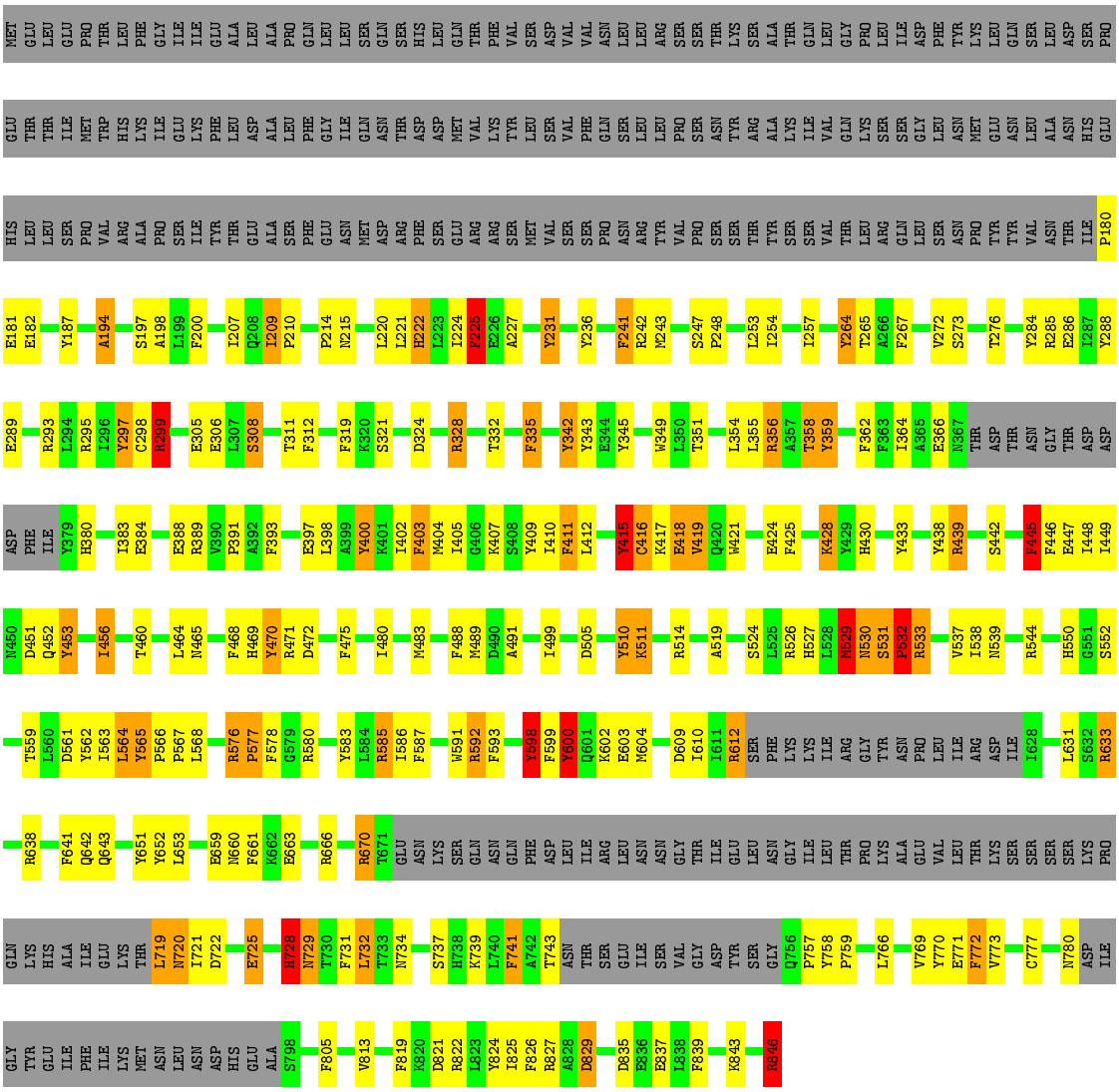
• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 3-B: 44% 16% 6% • 33%

• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

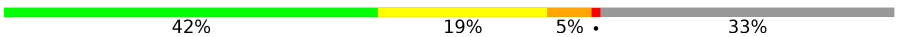
Chain 4-B:

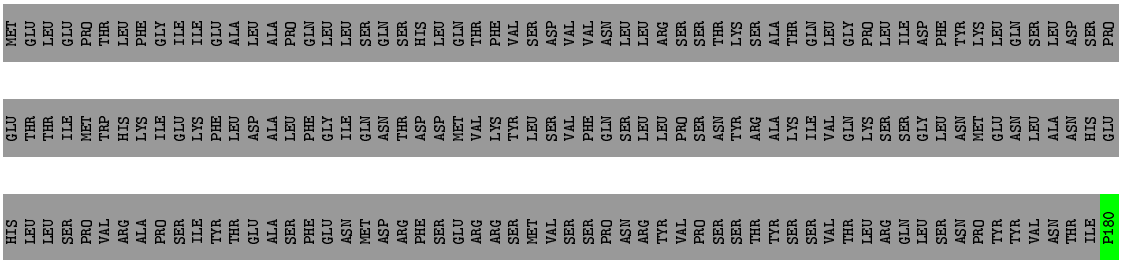


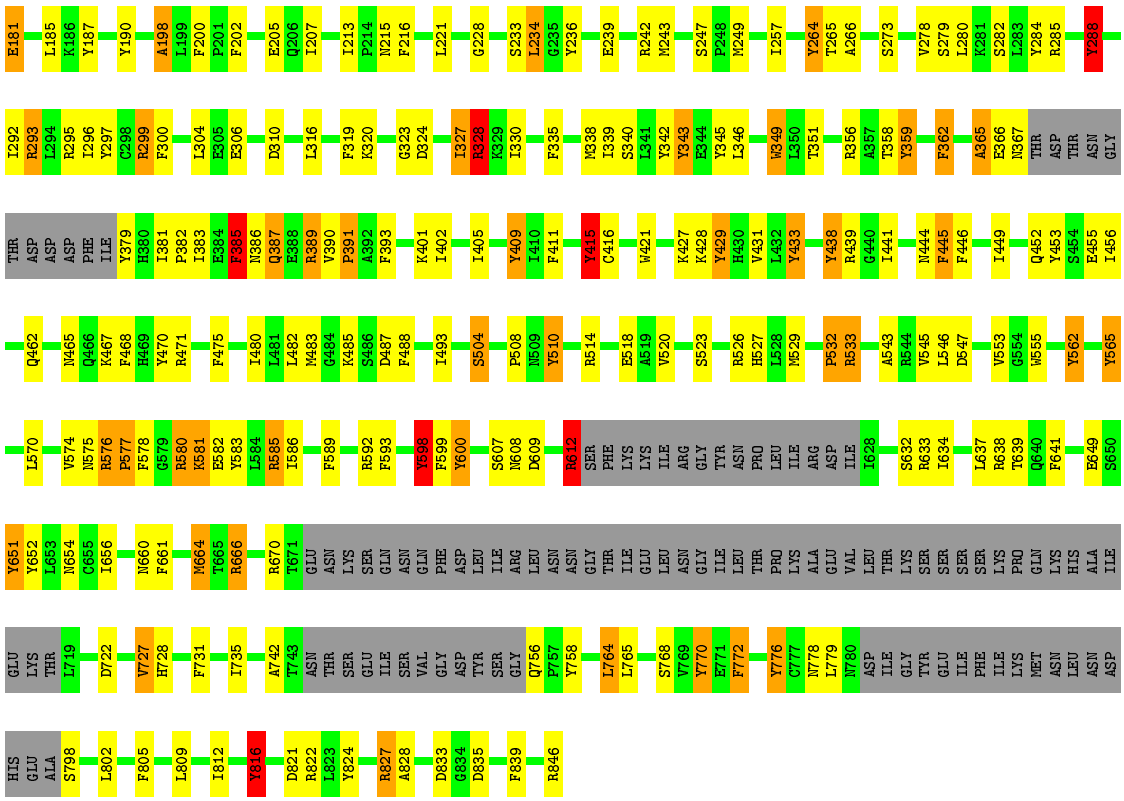


• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 5-B:

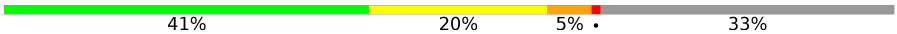


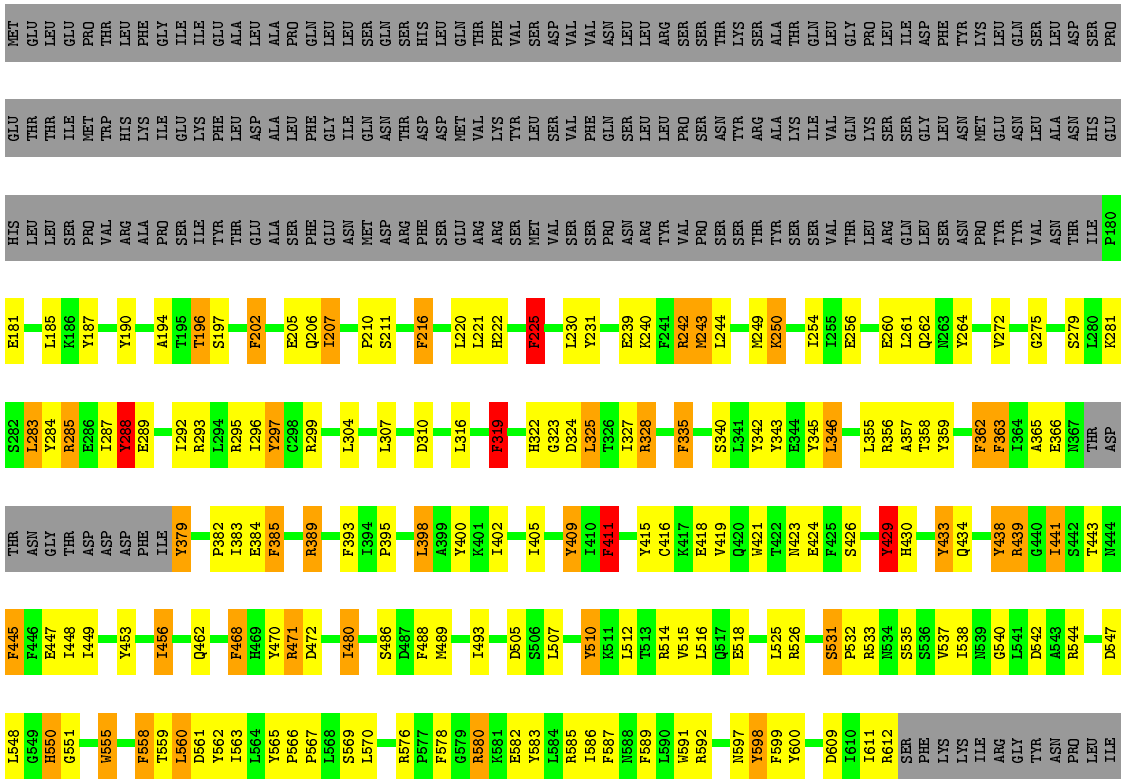


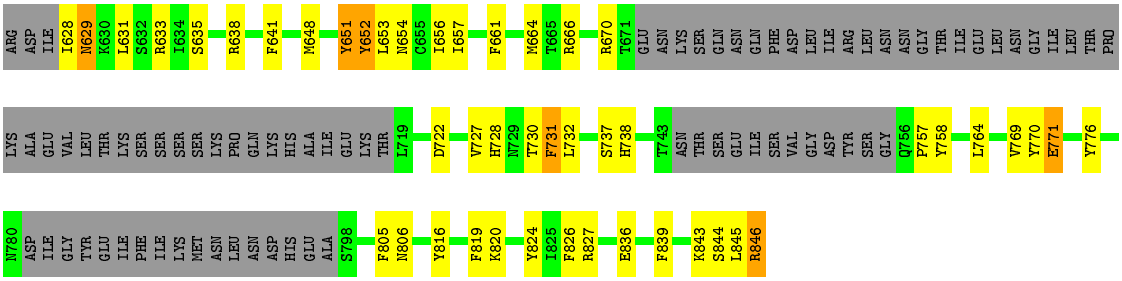


- Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 6-B:

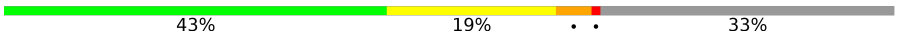


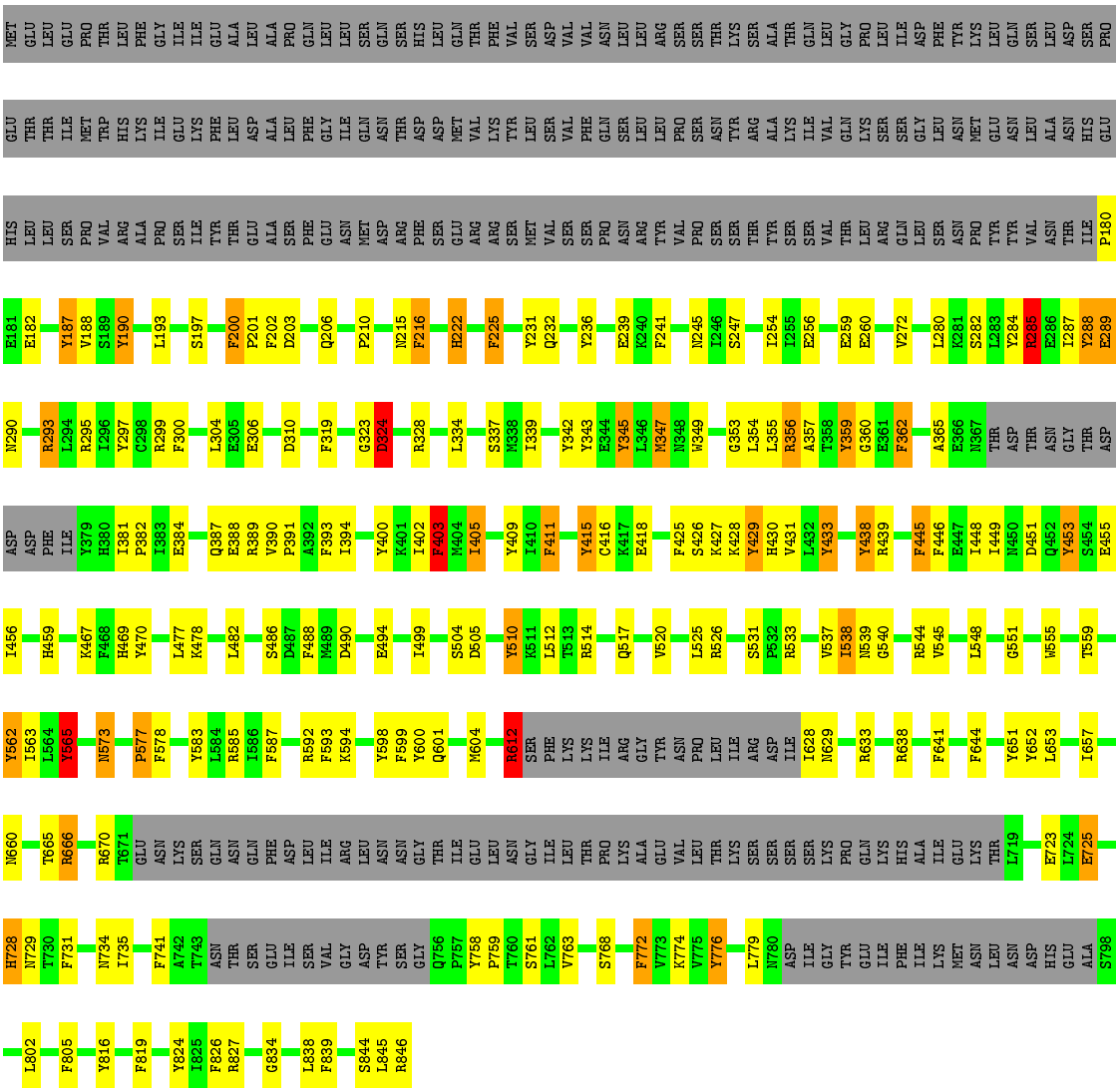




- Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

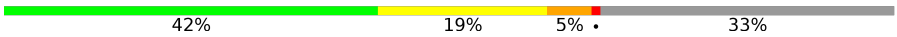
Chain 7-B:

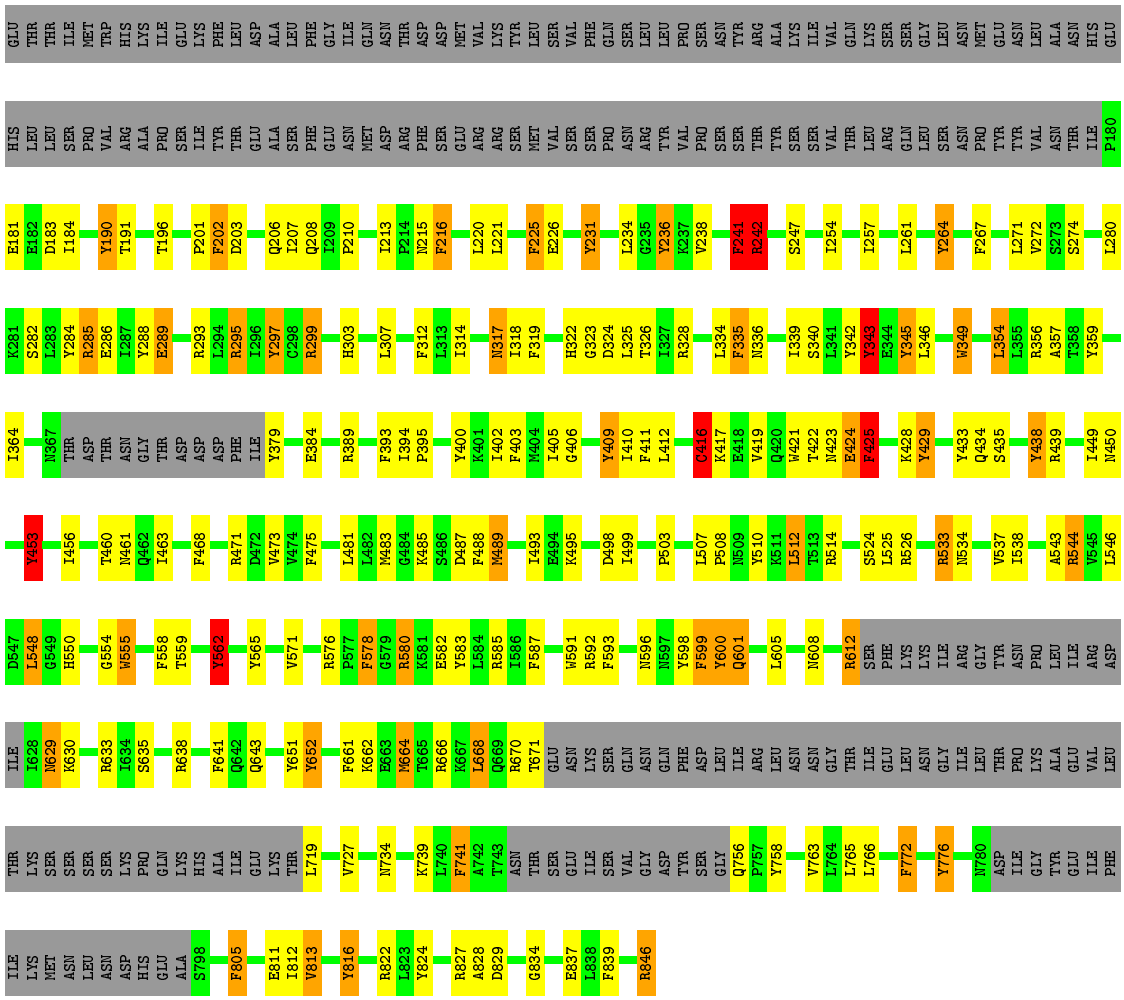




- Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

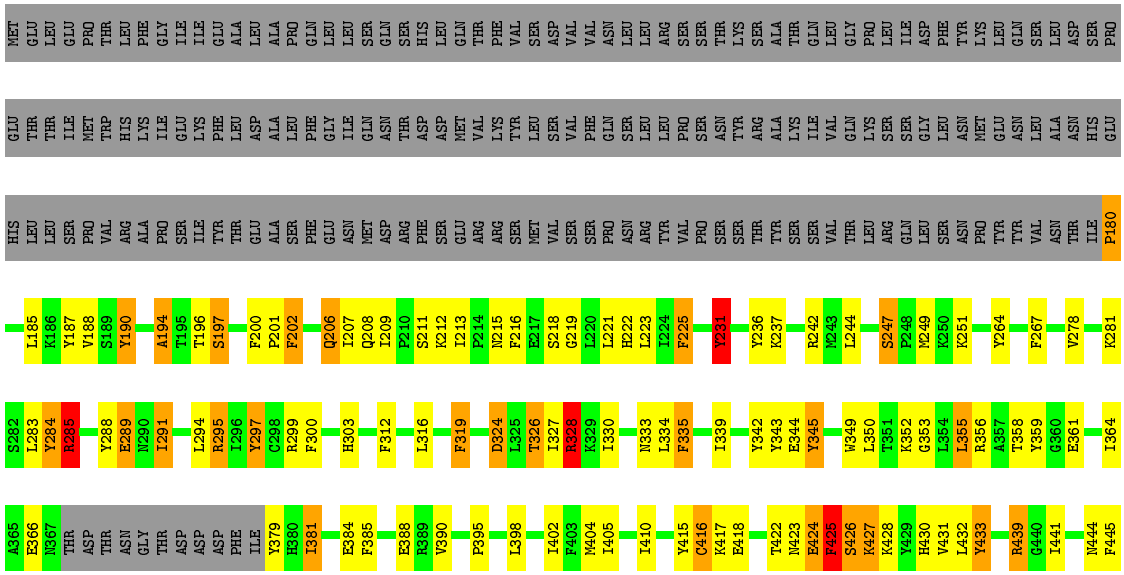
Chain 8-B:

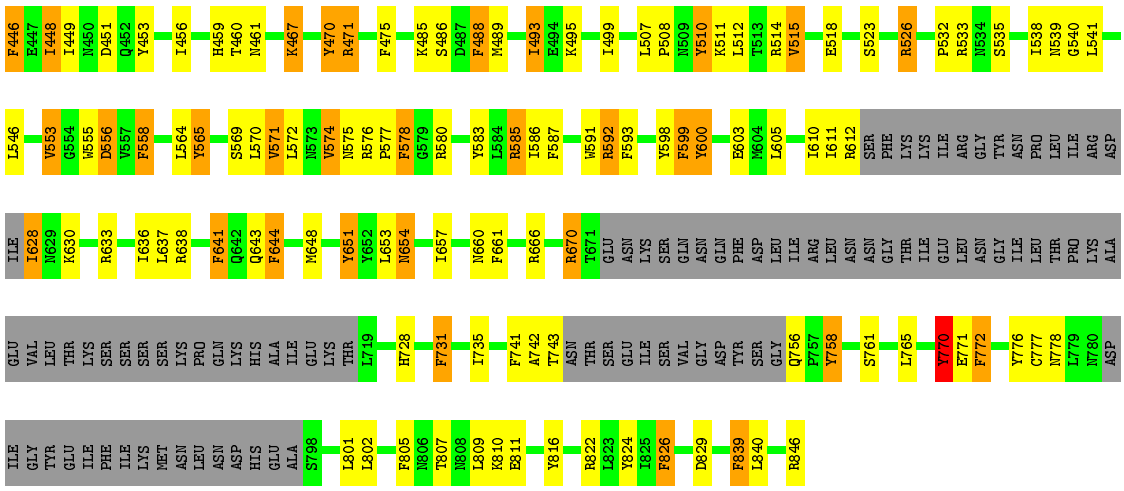




• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

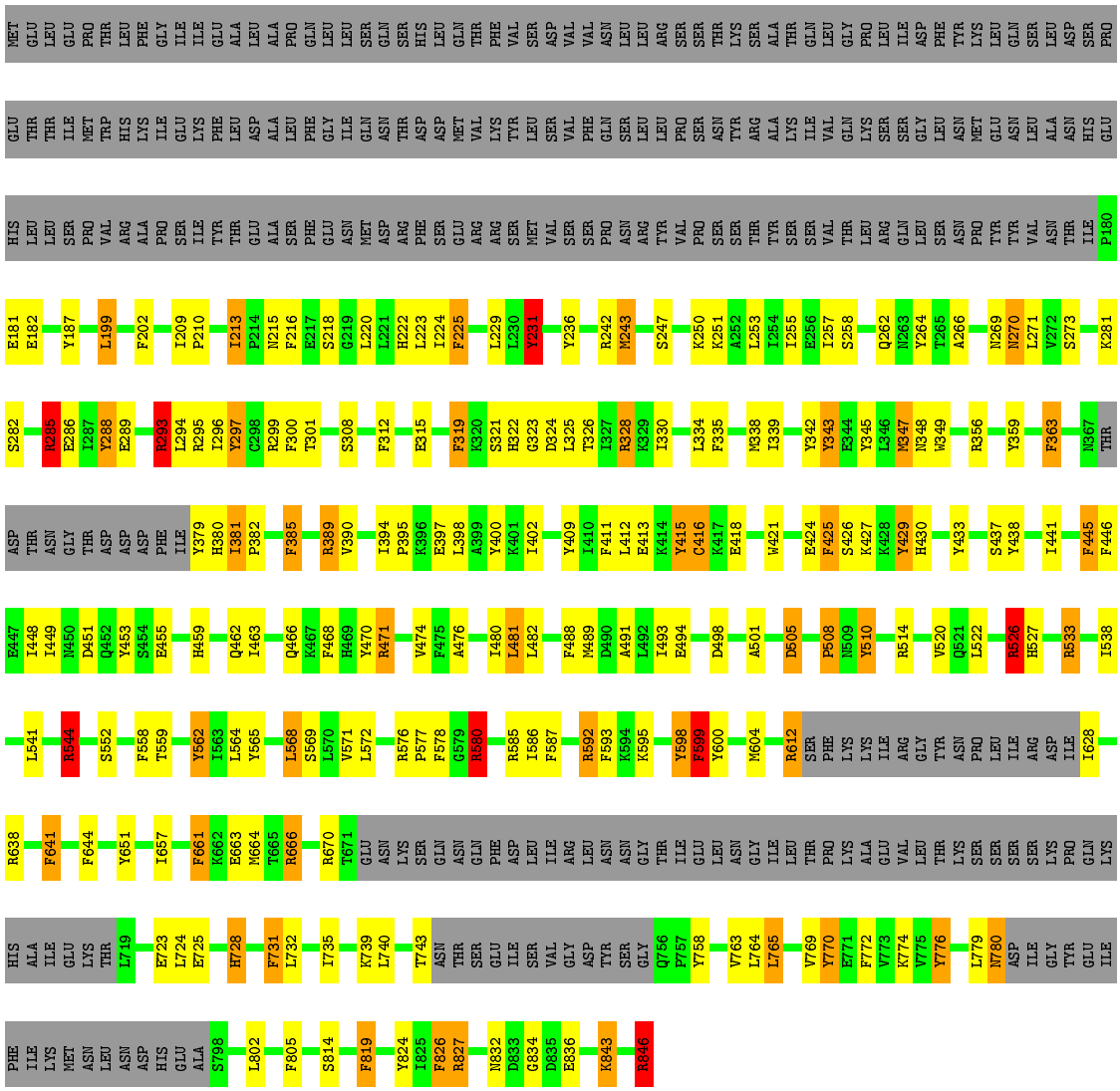
Chain 9-B: 40% 19% 7% • 33%





- Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 10-B: 42% 19% 5% • 33%



- Molecule 3: TUBULIN GAMMA CHAIN

Chain 1-C: 63% 23% 7% 6%

M1 I5 I6 T7 Q12 V17 F20 D34 D48 F53 F54 R55 R59 N60 K61 R65 M68 M69 D70 V75 R84 F87 R90 N91 T92 W93 V94 A95 S96 D97 S104 Y109 D118 I119 L120 I123 E126 I127 F136 Q137

L138 L139 H140 S141 G144 S148 G149 L150 D160 R161 Y162 P163 Y170 F173 R176 Y185 I188 L189 R192 I195 E196 D199 A200 T201 P204 D205 N206 A207 S208 L209 L210 M211 I212 S213 F217 R218 I222 D223 L224 T227 I231 S232 T233 I234

R243 F244 P245 S246 Y247 M248 Y249 S250 S251 M252 S253 S254 I255 Y256 S257 T258 L259 I260 P261 S262 H266 F267 L268 S269 P270 S271 F272 F275 T276 S277 D278 Y279 D282 H289 Y292 D293 L296 N303 S304 L305 V306 S307 Y315 F316 Y319 I322 N325

P328 R329 S332 R333 A334 M335 Q340 R341 F344 P345 S346 W347 I356 G357 R358 R359 S360 P361 Y362 L363 P364 L365 Q366 S373 G374 M375 F387 E388 C391 F394 F398 Y407 N408 V409 G410 M416 Q420 F423 A424 E425 V430 E435 D436 Y437 V438

A439 D443 S444 Y445 LEU ASP ASP VAL LEU VAL ASP ASP GLU ASN MET VAL GLY GLU LEU GLU GLU ASP LEU ASP ALA ASP GLY HIS LYS LEU VAL

- Molecule 3: TUBULIN GAMMA CHAIN

Chain 1-D: 64% 23% 5% • 6%

M1 G2 G3 E4 H16 W22 S23 A30 G35 Q38 D41 S42 S43 T44 E45 R46 D47 F53 F54 R55 E56 R59 F62 T63 P64 R65 A66 I67 M68 M69 D70 S71 E72 I76 E80 F83 R84 G85 F86 F87 R90 W93 V94 W105

Y109 T113 R114 D118 I119 L120 N121 K122 I123 D124 D128 S129 T130 L138 L139 H140 A143 L158 R161 K165 I166 Y170 S171 V172 F173 P174 A175 R176 V180 V181 V182 Q183 S184 Y185 R192 Y203 F204 D205 L209 I212 S213 Y216 F217 R218 N219

I222 I231 I234 S237 V238 F244 Y247 M248 Y249 Y256 P261 S262 P263 E264 L265 H266 F267 F272 T273 P274 S277 D278 Y279 I280 H281 D282 A285 H286 K287 S291 M295 D300 N303 S304 L305 V306 S307 P313 T314 Y315 V318 Y319

I323 G324 N325 P328 R329 Q330 R333 A334 Q339 Q340 R341 I342 M352 H353 V354 R359 S360 Y361 Y362 L363 Q366 E369 N370 E371 M376 M380 S381 T382 V383 V386 F387 T393 F398 Y407 M416 E425 S426 R427 Q431 Y437 D443 S444

Y445 LEU ASP ASP VAL LEU VAL ASP ASP GLU ASN MET VAL GLY GLU LEU GLU GLU ASP LEU ASP ALA ASP GLY ASP HIS LYS LEU VAL

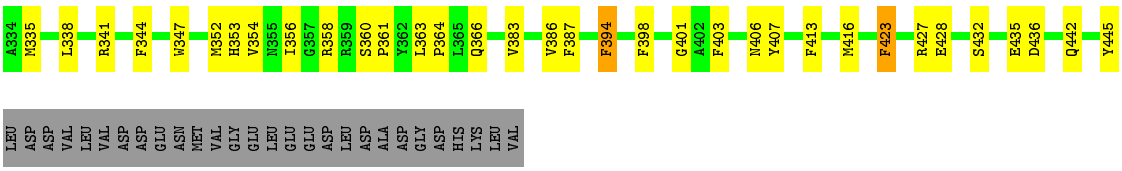
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 2-C: 64% 26% • • 6%

M1 G2 G3 E4 L8 Q12 F20 S23 Q24 I31 G35 D41 S42 S43 T44 E45 R46 K51 F54 R55 C58 R59 W60 K61 F62 R65 A66 D70 V75 I76 A77 D78 F83 R84 G85 F86 F87 D88 P89 W93 V94 A95 S96 D97 G98

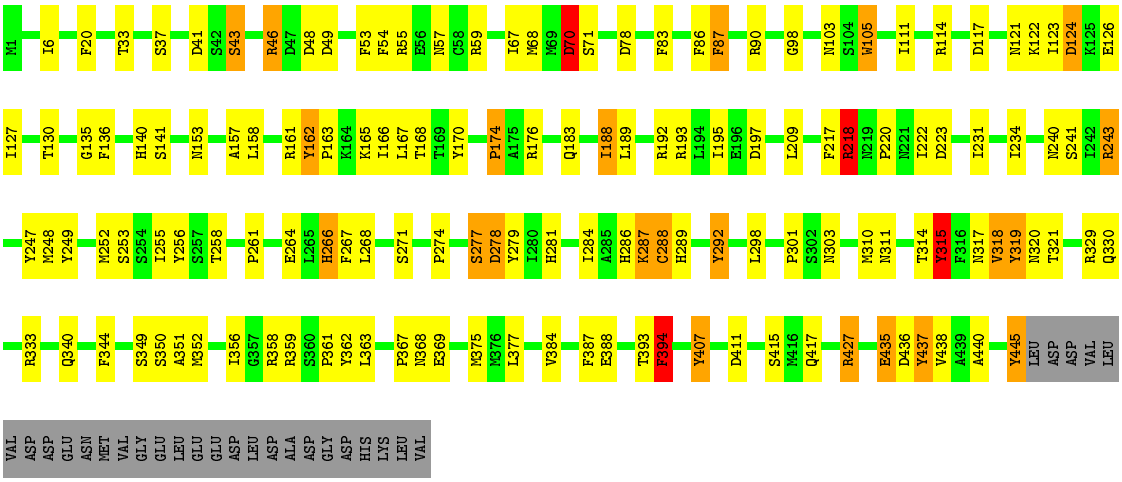
A99 W105 Y109 T113 R114 N115 Q116 D117 D124 K125 E126 I127 D131 N132 H140 G145 L150 D160 R161 Y162 P163 L167 Y170 F173 P174 A175 R176 S177 V181 S184 Y185 I188 L191 R192 R193 L194 I195 D205 G214 F217 R218

D223 L224 Q225 S232 R243 F244 Y247 M248 Y249 S250 S251 Y256 S257 T258 P261 S262 F267 L268 S271 F272 T273 P274 F275 Y279 I280 H281 D282 D283 H289 Y292 D293 P301 S302 V306 S307 M310 N311 Y315 Y319 P328 R329 R333



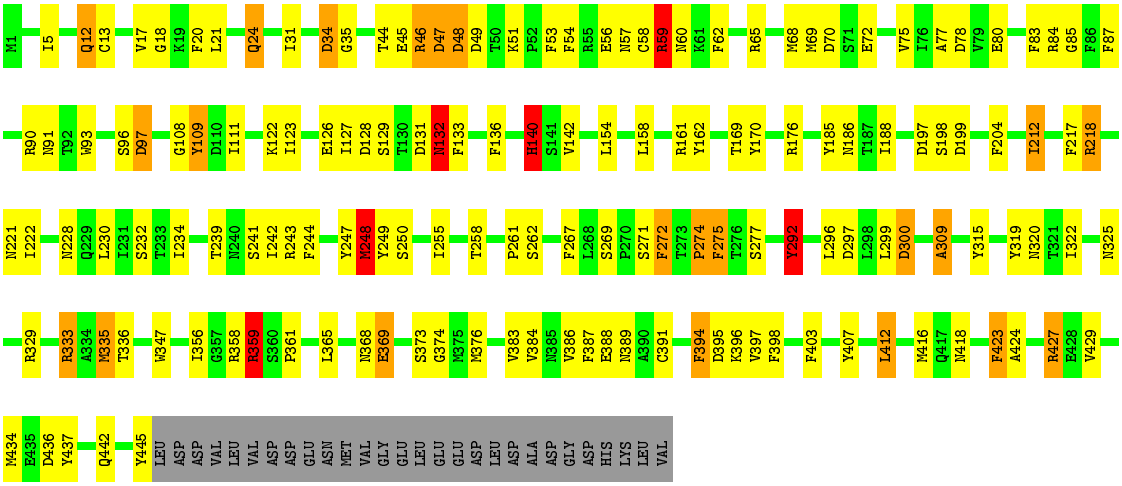
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 2-D:



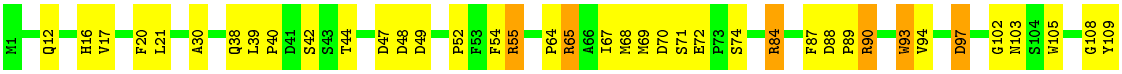
- Molecule 3: TUBULIN GAMMA CHAIN

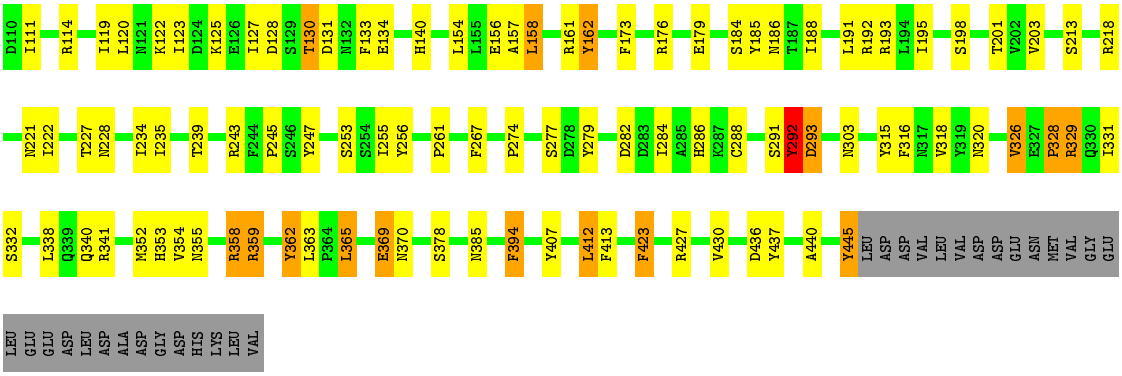
Chain 3-C:



- Molecule 3: TUBULIN GAMMA CHAIN

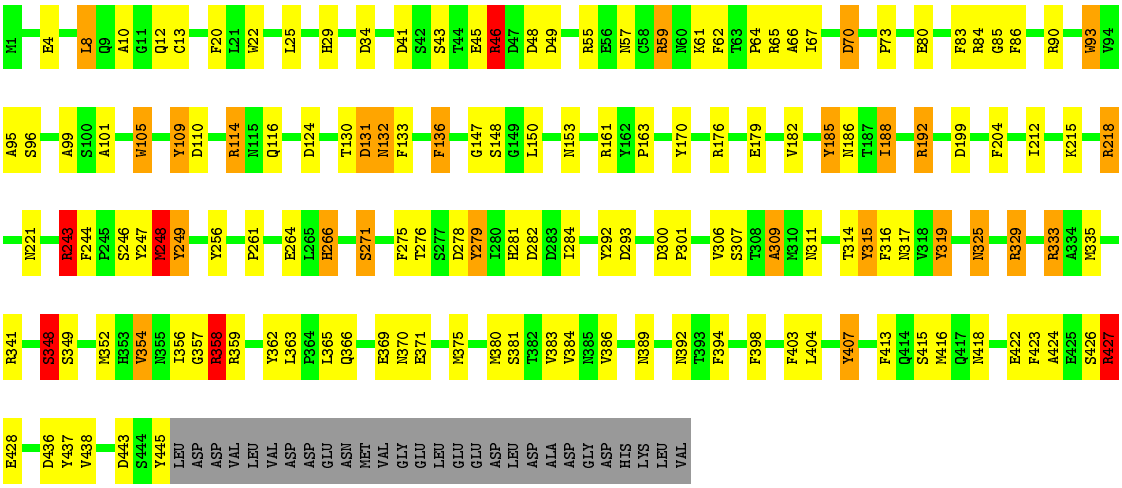
Chain 3-D:





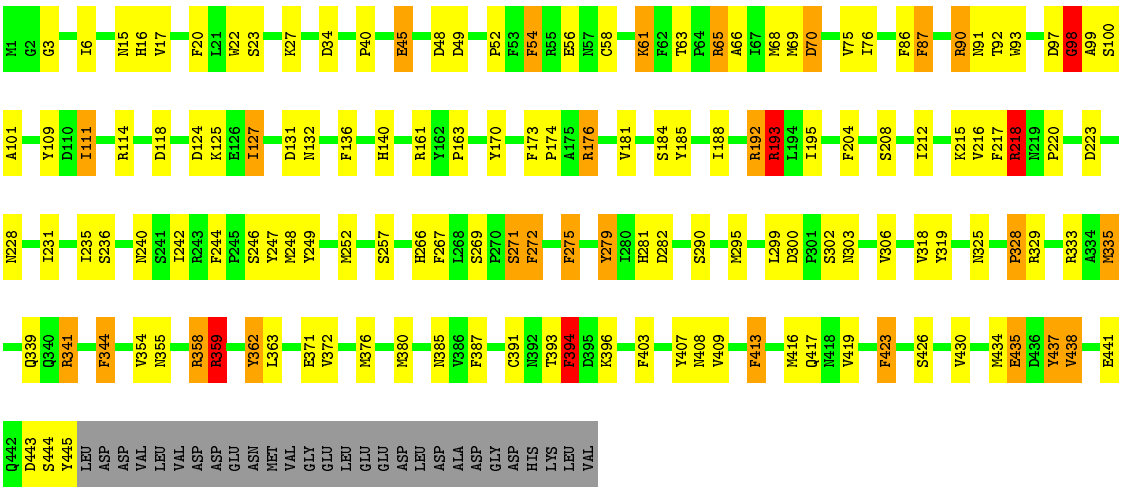
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 4-C:



- Molecule 3: TUBULIN GAMMA CHAIN

Chain 4-D:



- Molecule 3: TUBULIN GAMMA CHAIN

Chain 5-C: 62% 25% 6% 6%

M1 I6 T7 L8 Q9 A10 G11 Q12 F20 L21 W22 I31 L36 L39 P40 D41 R46 D47 N57 C58 R59 F62 T63 P64 R65 A66 I67 D70 V75 N81 T82 F83 R84 G85 F86 F87 R90 N91 T92 W93 V94 A95 S96 D97 G98 A99 S100 A101

G102 N103 S104 N107 G108 Y109 R114 D118 K122 I123 D124 K125 E126 N132 F133 E134 L138 L139 H140 S141 V142 A143 T146 G147 S148 L154 L158 C159 D160 R161 Y162 K165 I166 T169 Y170 P174 A175 R176 S177 V180 Q183 S184 Y185 I188

R192 R193 S198 D199 F204 I212 F217 R218 N219 D223 I235 I242 R243 F244 P245 S246 Y247 M248 Y249 S250 S251 M252 I255 Y256 L259 I260 P261 H266 F267 S271 F275 T276 S277 D278 Y279 I280 D283 S290 S291 Y292 D293 V294 L299 D300 P301

S302 S307 P313 T314 Y315 V318 Y319 I322 R333 A334 M335 R341 I342 K343 F344 H353 I356 G357 R358 R359 S360 P361 Y362 L363 P364 L365 Q366 P367 N368 E369 M375 M376 T382 N385 V386 F387 F394 D395 K396 A402 Y407 N408 V409 F413 Q414

S415 M416 Q417 N418 F423 R427 V430 Q431 Y445 LEU ASP ASP VAL LEU VAL ASP ASP GLU ASN MET VAL GLY GLU LEU GLU GLU ASP LEU ASP ALA ASP GLY ASP HIS LYS LEU VAL

- Molecule 3: TUBULIN GAMMA CHAIN

Chain 5-D: 63% 26% 5% • 6%

M1 I5 V17 G18 K19 F20 L21 D41 E45 R46 D47 K51 F54 R55 C58 R59 R65 A66 I67 M68 M69 D70 S71 E72 P73 S74 V75 I76 A77 D78 R84 G85 F86 R90 N91 T92 D97 G98 A99 S100 A101 G102 N103 Y109 D110 L120

D124 D128 D131 F136 L139 H140 S148 G149 S152 N153 L154 L155 E156 A157 L158 R161 Y162 P163 K164 Y170 S171 V172 F173 R176 V182 Y185 A190 L191 R192 R193 K215 V216 F217 R218 N221 I222 D223 L224 Q225 I231 I235 S236 N240

F244 P245 S246 Y247 M248 Y249 S250 S251 M252 S253 S254 I255 Y256 I260 F267 F272 T273 P274 F275 D278 Y279 I280 H281 D282 D283 I284 A285 H289 Y292 D293 V294 M295 L296 L299 S302 T314 Y315 F316 Y319 N320 G324 N325 V326 E327 P328 R329 R333

A334 M335 Q340 R341 F344 W347 Y354 N355 I356 G357 R358 R359 S360 P361 Y362 L363 P364 L365 Q366 N370 E371 N379 F387 E388 T393 F394 F398 A399 K400 F403 D411 I412 M416 V419 F423 A424 E425 S426 R427 V430 E435 D436 Y437

D443 S444 Y445 LEU ASP ASP VAL LEU VAL ASP ASP GLU ASN MET VAL GLY GLU LEU GLU GLU ASP LEU ASP ALA ASP GLY ASP HIS LYS LEU VAL

- Molecule 3: TUBULIN GAMMA CHAIN

Chain 6-C: 65% 25% • • 6%

M1 E4 I5 I6 A10 F20 L21 L25 E28 D34 S37 D41 E45 R46 D47 F53 F54 R55 E56 N57 C58 R59 N60 K61 M68 M69 D70 P73 S74 V75 E80 F83 R84 G85 F86 F87 R90 W93 V94 A95 S100 S104

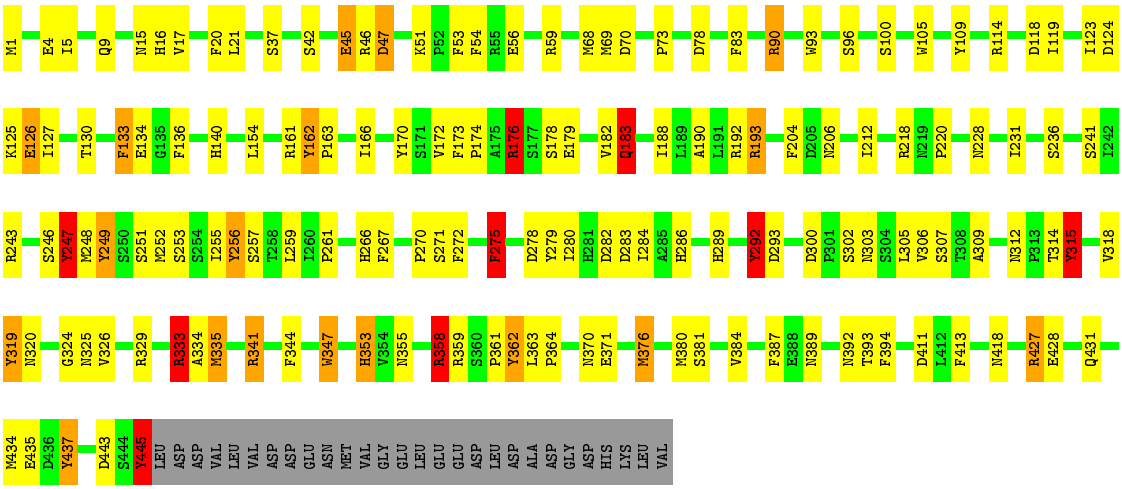
W105 Y109 D110 I111 R114 D118 I123 D124 K125 E126 I127 D128 S129 T130 D131 N132 F133 F136 H140 A143 G147 S148 S152 N153 L154 L158 R161 Y162 K165 T168 T169 P174 A175 R176 Q183 S184 Y185 I188 R192 R193 L194 I195 E196

F204 D205 N206 F217 R218 N219 R243 S246 Y247 M248 Y249 Y256 I260 L265 H266 T273 P274 F275 A285 H289 S290 S291 Y292 D293 V294 M295 S302 S307 M310 N311 N312 P313 T314 Y315 F316 Y319 N320 T321 I322 N325 V326 R333 A334 M335

R341 F344 W347 I356 G357 R358 R359 S360 P361 Y362 P367 N368 E369 N370 E371 V372 S378 V386 F387 F394 D395 K396 V397 F398 F403 Y407 D411 F423 R427 Q431 D436 Y437 A440 D443 S444 Y445 LEU ASP ASP VAL LEU VAL ASP

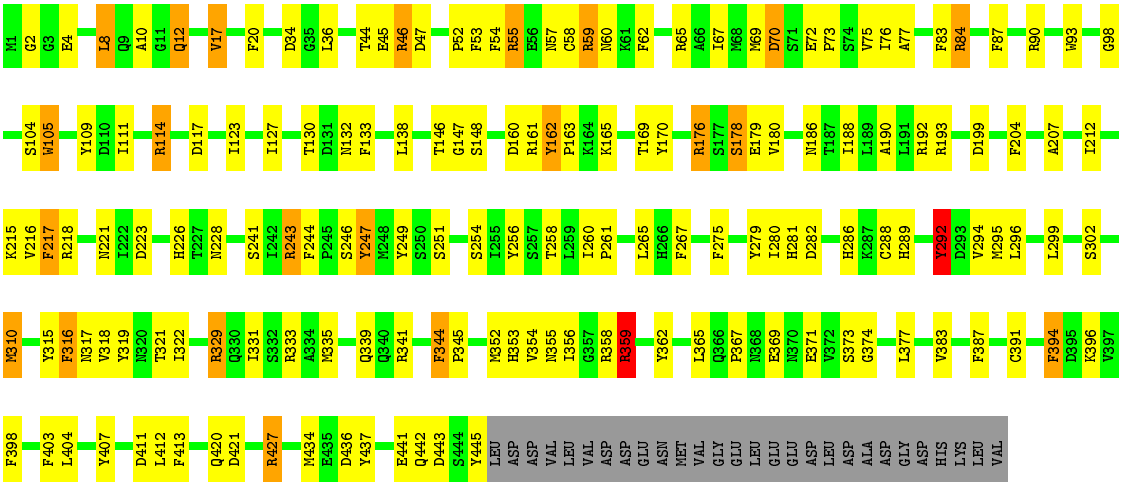
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 6-D:



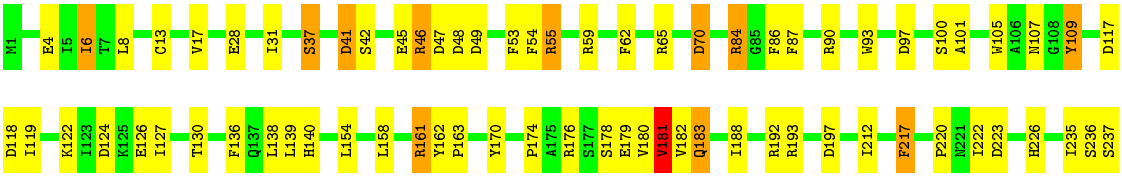
- Molecule 3: TUBULIN GAMMA CHAIN

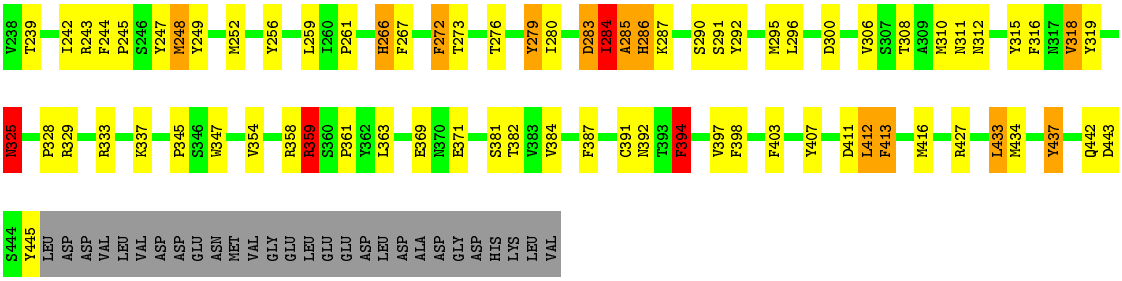
Chain 7-C:



- Molecule 3: TUBULIN GAMMA CHAIN

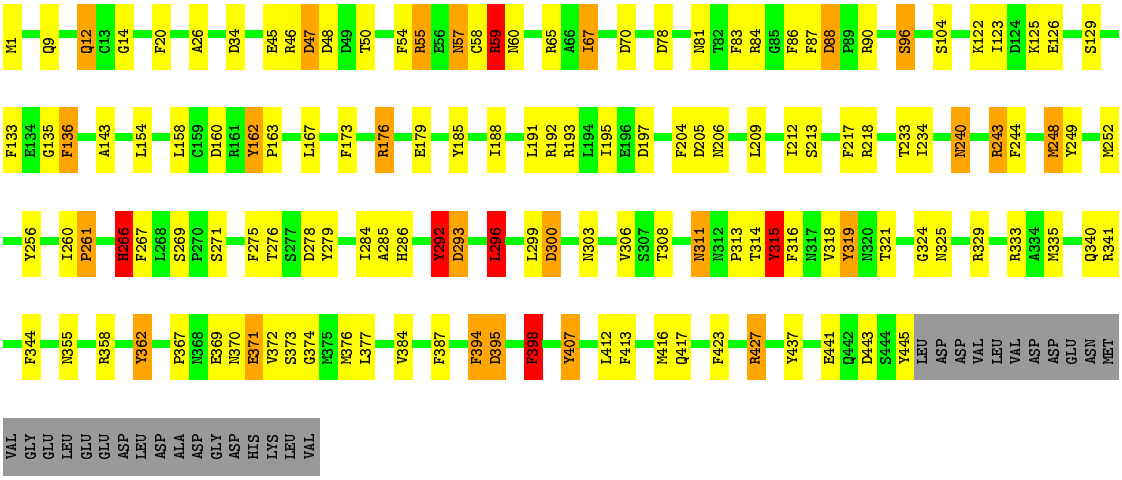
Chain 7-D:





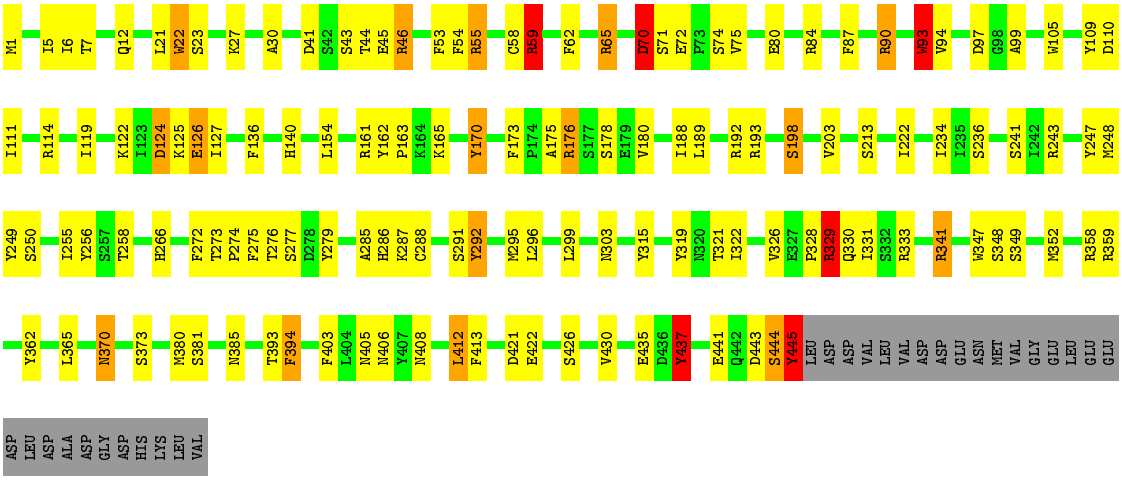
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 8-C:



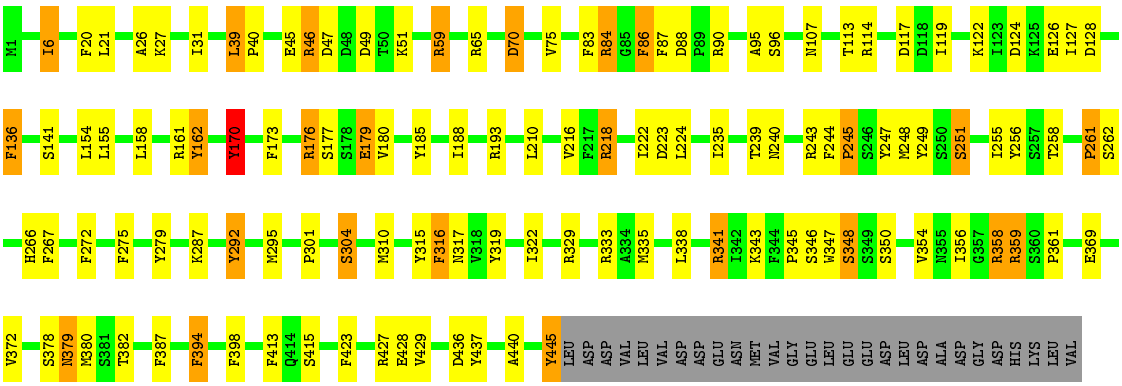
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 8-D:



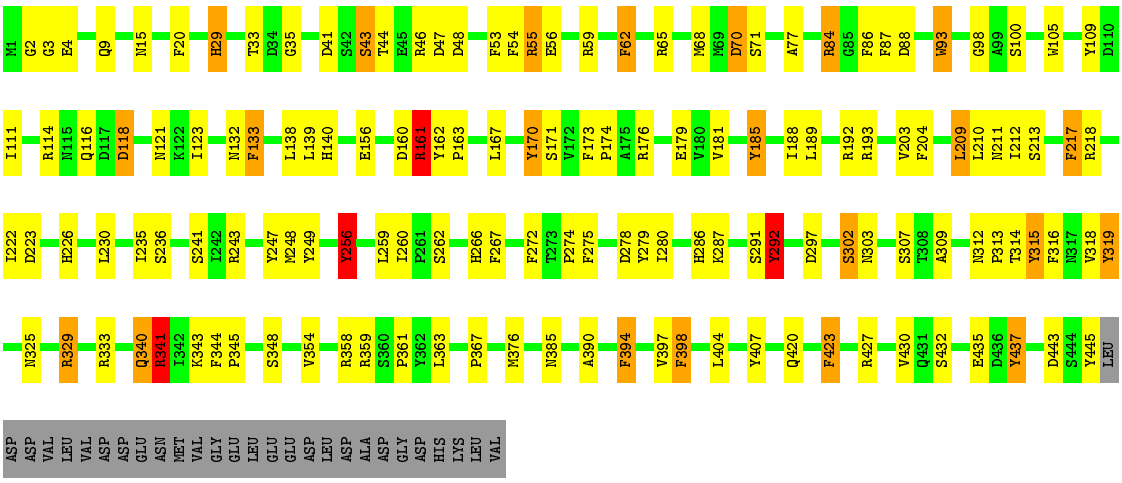
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 9-C:



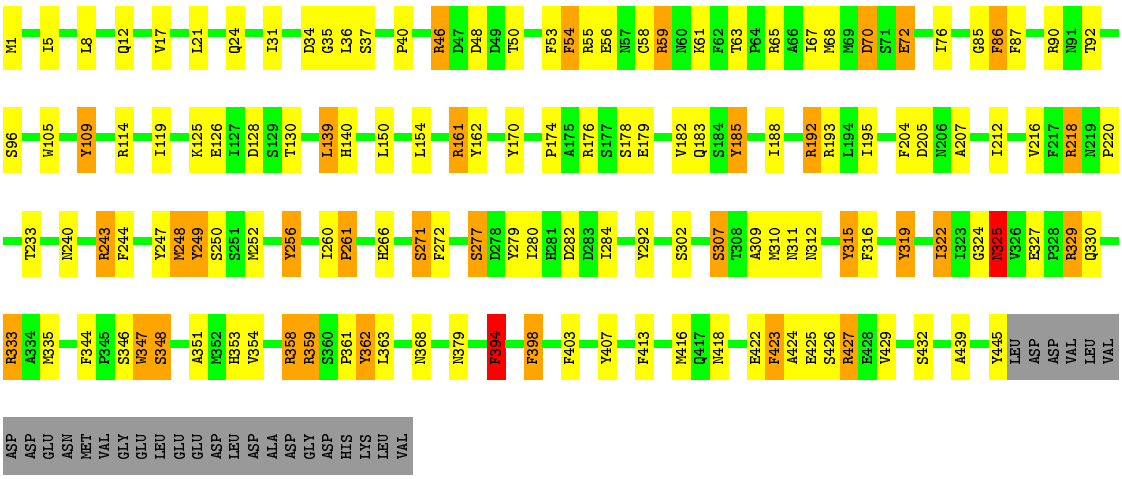
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 9-D:



- Molecule 3: TUBULIN GAMMA CHAIN

Chain 10-C:



- Molecule 3: TUBULIN GAMMA CHAIN

Chain 10-D: 61% 27% 5% 6%

M1 I6 A10 G11 Q12 G13 G14 V17 G18 K19 F20 L25 I31 D34 D41 S42 S43 R46 D49 P52 F53 F54 R55 R59 N60 K61 R65 D70 S71 E72 F73 S74 V75 I76 A77 D78 R84 G85 F86 F87 D88 T92 W93 V94 A95

S96 D97 G98 A101 W105 Y109 R114 I119 D124 K125 E126 I127 D128 S129 T130 F133 F136 L139 H140 S141 V142 T146 G151 L154 L158 R161 Y162 P163 Y170 A175 R176 V180 V181 V182 Q183 S184 Y185 I188 L191 R192 R193

F204 N211 I212 S213 R218 D223 I231 I235 T239 N240 S241 I242 R243 F244 P245 S246 Y247 M248 Y249 S250 Y256 S257 T258 P261 S262 H266 F267 F275 D278 Y279 I280 H281 D282 A285 H286 K287 C288 H289 Y292 L296 L299 S302 N303

S304 N311 T314 Y319 N320 T321 N325 V326 E327 P328 R329 Q330 I331 S332 R333 A334 M335 T336 R341 I342 K343 F344 S349 S350 A351 I356 G357 R358 R359 Y362 L363 P364 L365 Q366 P367 E371 V372 S373 N379 M380 S381 V384 F387 C391 N392 T393 F394

F403 N406 Y407 M416 F423 E435 D436 Y437 V438 A439 A440 E441 Y445 LEU ASP ASP VAL LEU VAL ASP ASP GLU ASN MET VAL GLY GLU LEU GLU GLU GLU ASP LEU ASP ALA ASP GLY ASP HIS LYS LEU VAL

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 1-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 1-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 2-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 2-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 3-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 3-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 4-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 4-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 5-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 5-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 6-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 6-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 7-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 7-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 8-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 8-F: 95% 5%

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 9-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 9-F: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 10-E: 100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 10-F: 100%

There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
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	Not provided	Depositor
Image detector	TVIPS TEMCAM-F816 (8K X 8K)	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| >2	RMSZ	#|Z| >2
1	1-A	1.76	45/4917 (0.9%)	1.98	139/6616 (2.1%)
1	10-A	1.72	38/4917 (0.8%)	1.96	138/6616 (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%)
2	1-B	1.73	52/4803 (1.1%)	1.99	135/6481 (2.1%)
2	10-B	1.76	49/4803 (1.0%)	2.06	143/6481 (2.2%)
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%)
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	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%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >2	RMSZ	#|Z| >2
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%)
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%)
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	10-A	0	19
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
2	1-B	0	27
2	10-B	0	25
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
3	1-C	0	16
3	1-D	0	13
3	10-C	0	13
3	10-D	0	10
3	2-C	0	11
3	2-D	0	12
3	3-C	0	9
3	3-D	0	7

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
3	4-C	0	15
3	4-D	0	14
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
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

Continued on next page...

Continued from previous page...

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%)	7	46
1	2-A	561/823 (68%)	524 (93%)	19 (3%)	18 (3%)	5	41
1	3-A	561/823 (68%)	521 (93%)	24 (4%)	16 (3%)	6	43
1	4-A	561/823 (68%)	523 (93%)	25 (4%)	13 (2%)	8	48
1	5-A	561/823 (68%)	524 (93%)	23 (4%)	14 (2%)	7	46
1	6-A	561/823 (68%)	525 (94%)	26 (5%)	10 (2%)	11	53
1	7-A	561/823 (68%)	519 (92%)	27 (5%)	15 (3%)	6	45
1	8-A	561/823 (68%)	519 (92%)	26 (5%)	16 (3%)	6	43
1	9-A	561/823 (68%)	526 (94%)	23 (4%)	12 (2%)	9	50
1	10-A	561/823 (68%)	528 (94%)	19 (3%)	14 (2%)	7	46
2	1-B	553/846 (65%)	512 (93%)	26 (5%)	15 (3%)	6	45
2	2-B	553/846 (65%)	505 (91%)	41 (7%)	7 (1%)	15	60
2	3-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	9	51
2	4-B	553/846 (65%)	503 (91%)	32 (6%)	18 (3%)	5	40
2	5-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	9	51
2	6-B	553/846 (65%)	502 (91%)	36 (6%)	15 (3%)	6	45
2	7-B	553/846 (65%)	515 (93%)	24 (4%)	14 (2%)	7	46
2	8-B	553/846 (65%)	516 (93%)	29 (5%)	8 (1%)	14	58
2	9-B	553/846 (65%)	505 (91%)	24 (4%)	24 (4%)	3	34
2	10-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	9	51
3	1-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
3	1-D	443/473 (94%)	395 (89%)	37 (8%)	11 (2%)	7	46
3	2-C	443/473 (94%)	395 (89%)	29 (6%)	19 (4%)	3	34
3	2-D	443/473 (94%)	390 (88%)	33 (7%)	20 (4%)	3	33
3	3-C	443/473 (94%)	396 (89%)	33 (7%)	14 (3%)	5	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3-D	443/473 (94%)	393 (89%)	33 (7%)	17 (4%)	4	37
3	4-C	443/473 (94%)	401 (90%)	29 (6%)	13 (3%)	6	43
3	4-D	443/473 (94%)	402 (91%)	29 (6%)	12 (3%)	6	45
3	5-C	443/473 (94%)	400 (90%)	27 (6%)	16 (4%)	4	38
3	5-D	443/473 (94%)	401 (90%)	28 (6%)	14 (3%)	5	41
3	6-C	443/473 (94%)	397 (90%)	34 (8%)	12 (3%)	6	45
3	6-D	443/473 (94%)	396 (89%)	32 (7%)	15 (3%)	5	40
3	7-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
3	7-D	443/473 (94%)	389 (88%)	33 (7%)	21 (5%)	3	32
3	8-C	443/473 (94%)	391 (88%)	29 (6%)	23 (5%)	2	30
3	8-D	443/473 (94%)	408 (92%)	26 (6%)	9 (2%)	9	51
3	9-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
3	9-D	443/473 (94%)	401 (90%)	29 (6%)	13 (3%)	6	43
3	10-C	443/473 (94%)	396 (89%)	29 (6%)	18 (4%)	3	35
3	10-D	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
All	All	20000/26150 (76%)	18292 (92%)	1141 (6%)	567 (3%)	10	44

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%)	15	49

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2-A	542/766 (71%)	502 (93%)	40 (7%)	17	54
1	3-A	542/766 (71%)	510 (94%)	32 (6%)	24	61
1	4-A	542/766 (71%)	499 (92%)	43 (8%)	15	51
1	5-A	542/766 (71%)	508 (94%)	34 (6%)	22	59
1	6-A	542/766 (71%)	487 (90%)	55 (10%)	9	38
1	7-A	542/766 (71%)	501 (92%)	41 (8%)	16	53
1	8-A	542/766 (71%)	497 (92%)	45 (8%)	14	48
1	9-A	542/766 (71%)	505 (93%)	37 (7%)	20	57
1	10-A	542/766 (71%)	497 (92%)	45 (8%)	14	48
2	1-B	528/787 (67%)	492 (93%)	36 (7%)	20	57
2	2-B	528/787 (67%)	492 (93%)	36 (7%)	20	57
2	3-B	528/787 (67%)	490 (93%)	38 (7%)	18	55
2	4-B	528/787 (67%)	482 (91%)	46 (9%)	13	45
2	5-B	528/787 (67%)	493 (93%)	35 (7%)	21	57
2	6-B	528/787 (67%)	479 (91%)	49 (9%)	11	42
2	7-B	528/787 (67%)	487 (92%)	41 (8%)	16	51
2	8-B	528/787 (67%)	491 (93%)	37 (7%)	19	56
2	9-B	528/787 (67%)	486 (92%)	42 (8%)	15	50
2	10-B	528/787 (67%)	475 (90%)	53 (10%)	9	38
3	1-C	396/421 (94%)	369 (93%)	27 (7%)	20	57
3	1-D	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	2-C	396/421 (94%)	371 (94%)	25 (6%)	22	59
3	2-D	396/421 (94%)	373 (94%)	23 (6%)	25	61
3	3-C	396/421 (94%)	374 (94%)	22 (6%)	26	62
3	3-D	396/421 (94%)	371 (94%)	25 (6%)	22	59
3	4-C	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	4-D	396/421 (94%)	366 (92%)	30 (8%)	16	53
3	5-C	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	5-D	396/421 (94%)	369 (93%)	27 (7%)	20	57
3	6-C	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	6-D	396/421 (94%)	376 (95%)	20 (5%)	29	66

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	7-C	396/421 (94%)	380 (96%)	16 (4%)	38	71
3	7-D	396/421 (94%)	379 (96%)	17 (4%)	35	70
3	8-C	396/421 (94%)	376 (95%)	20 (5%)	29	66
3	8-D	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	9-C	396/421 (94%)	372 (94%)	24 (6%)	23	60
3	9-D	396/421 (94%)	377 (95%)	19 (5%)	31	67
3	10-C	396/421 (94%)	368 (93%)	28 (7%)	18	55
3	10-D	396/421 (94%)	366 (92%)	30 (8%)	16	53
All	All	18620/23950 (78%)	17333 (93%)	1287 (7%)	24	56

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

Mol	Chain	Res	Type
3	5-C	84	ARG
2	6-B	652	TYR
2	10-B	315	GLU
3	5-D	19	LYS
1	6-A	369	ASN

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

Mol	Chain	Res	Type
3	5-C	24	GLN
3	6-C	340	GLN
2	10-B	459	HIS
3	5-C	355	ASN
1	6-A	559	HIS

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 carbohydrates 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.