wwPDB EM Validation Summary Report (i)

Mar 15, 2025 – 06:21 am GMT

PDB ID	:	9I8M
EMDB ID	:	EMD-52729
Title	:	NEDD1-bound native vertebrate gamma-tubulin ring complex from Xenopus laevis, focused reconstruction
Authors	:	Vermeulen, B.J.A.; Pfeffer, S.
Deposited on	:	2025-02-05
Resolution	:	4.30 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 (i) 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 (i)) were used in the production of this report:

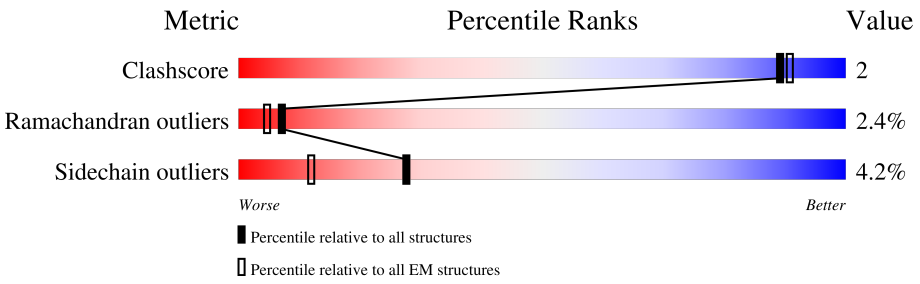
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41

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 4.30 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	A	896	13% 22% 7% • 69%
1	C	896	7% 19% 8% • 72%
1	E	896	16% 20% 7% • 72%
1	G	896	7% 20% 6% • 72%
2	B	906	12% 23% 8% • 68%
2	D	906	15% 20% 6% • 72%
2	F	906	14% 18% 7% • 73%
2	H	906	• 20% 7% • 71%

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Mol	Chain	Length	Quality of chain
2	O	906	8% 90%
2	Q	906	11% 9% 88%
2	R	906	6% 8% 89%
2	S	906	6% 9% 88%
2	T	906	10% 7% 90%
3	I	666	6% 31% 10% 57%
3	K	666	10% 32% 10% 57%
4	J	1019	6% 25% 8% 65%
5	L	1698	12% 21% 6% 72%
6	U	671	7% 8% 89%
6	V	671	7% 9% 89%
6	W	671	8% 8% 89%
6	X	671	8% 9% 89%
7	o	72	8% 60% 11% 28%
7	p	72	29% 68% 10% 22%
7	q	72	65% 69% 6% 22%
7	r	72	26% 58% 21% 18%
7	s	72	15% 65% 14% 18%
7	t	72	81% 65% 14% 19%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 37358 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 Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	275	2211	1412	369	421	9	0	0
1	C	250	2014	1289	336	382	7	0	0
1	E	253	2038	1306	340	385	7	0	0
1	G	250	2014	1289	336	382	7	0	0

- Molecule 2 is a protein called Gamma-tubulin complex component 3 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	294	2363	1517	401	434	11	0	0
2	D	254	2059	1324	351	375	9	0	0
2	F	242	1964	1263	337	355	9	0	0
2	H	263	2135	1374	363	389	9	0	0
2	O	93	753	480	137	134	2	0	0
2	Q	109	878	557	160	159	2	0	0
2	R	98	794	503	144	145	2	0	0
2	S	109	878	557	160	159	2	0	0
2	T	93	753	480	137	134	2	0	0

- Molecule 3 is a protein called Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	I	287	2325	1500	394	418	13	0	0
3	K	287	2325	1500	394	418	13	0	0

- Molecule 4 is a protein called Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	352	2909	1881	493	522	13	0	0

- Molecule 5 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L	478	3794	2449	613	713	19	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	392	ASP	GLU	conflict	UNP A0A974HT83
L	394	VAL	ILE	conflict	UNP A0A974HT83

- Molecule 6 is a protein called NEDD1 gamma-tubulin ring complex targeting factor L homeolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	U	75	634	396	112	122	4	0	0
6	V	75	634	396	112	122	4	0	0
6	W	75	634	396	112	122	4	0	0
6	X	75	634	396	112	122	4	0	0

- Molecule 7 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	o	52	403	248	71	79	5	0	0
7	p	56	429	263	73	89	4	0	0

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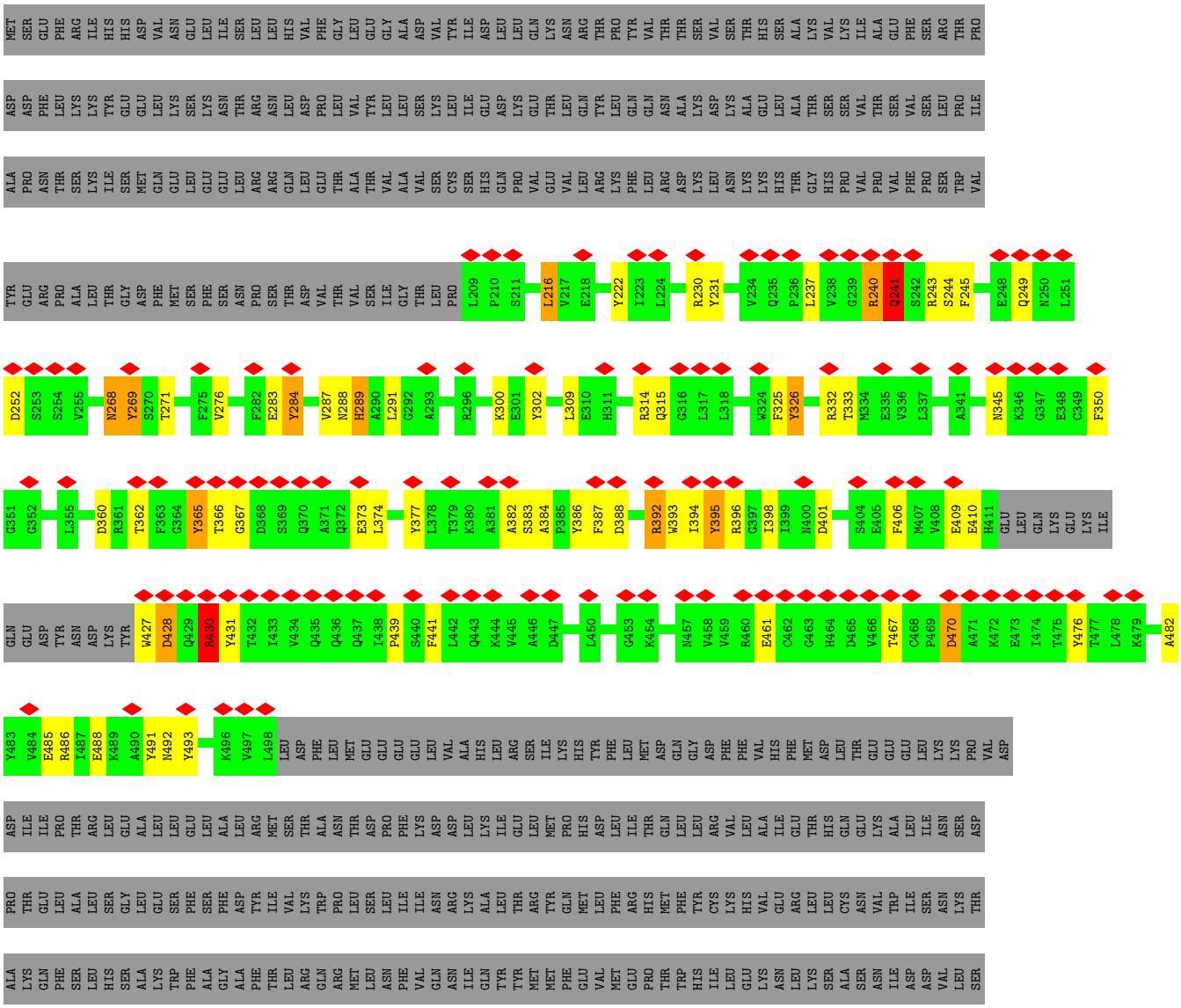
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	q	56	432	266	76	86	4	0	0
			Total	C	N	O	S		
7	r	59	454	278	80	91	5	0	0
			Total	C	N	O	S		
7	s	59	451	277	79	90	5	0	0
			Total	C	N	O	S		
7	t	58	446	274	78	89	5	0	0

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: Gamma-tubulin complex component

Chain A: 13% 22% 7% 69%



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

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

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

- Molecule 1: Gamma-tubulin complex component

Chain C: 7% 19% 8% 72%

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

ASP ASP PHE LEU LYS LYS TYR GLU GLU LEU LYS SER LYS ASN THR ARG ASN LEU ASP PRO LEU VAL TYR LEU LEU SER LYS LEU ILE GLU ASP LYS GLU THR LEU GLN TYR LEU GLN GLN ASN ALA LYS ASP LYS ALA GLU LEU ALA THR THR SER SER VAL SER LEU PRO ILE

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

TYR GLU ARG PRO ALA LEU THR GLY ASP PHE MET SER PHE SER ASN PRO SER THR ASP VAL THR VAL SER ILE GLY THR LEU PRO L209 P210 S211 Q212 E213 T214 E218 D219 Y222 V227 D228 G229 R230 Y231 P236 L237 V238 G239 R240 R243 S244 F245 S246 N250 L251 D252

S253 S254 V255 K256 E257 L258 R261 I262 A266 Y269 R274 F275 V276 E277 E278 N279 S280 S281 F282 E283 M295 R296 Y302 M303 E310 H311 R314 L317 L320 Q321 K322 L323 W324 F325 Y326 I327 Q328 R332 L337 S343 K346 F350 S356 L357

L358 H359 D360 R361 T362 F363 G364 Y365 D368 E373 Y377 L378 T379 S383 D388 R392 W393 I394 Y395 R396 G397 I398 I399 N400 D401 P402 Y403 S404 E405 V408 E409 E410 H411 GLU LEU GLN LYS GLU LYS ILE GLN GLU ASP TYR ASN ASP LYS TYR W427 D428 Q429 R430 Y431

T432 I433 Q436 Q437 I438 P439 S440 F441 L442 Q443 K444 D447 K448 T452 G453 K454 Y455 L456 M457 V458 VAL ARG GLU CYS GLY HIS ASP VAL THR CYS PRO ASP ALA LYS GLU ILE THR TYR THR LEU LYS GLU Q481 A482 Y483 I487 E488 K489 A490 Y491 N492 Y493 A494 S495 LYS VAL

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

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

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

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

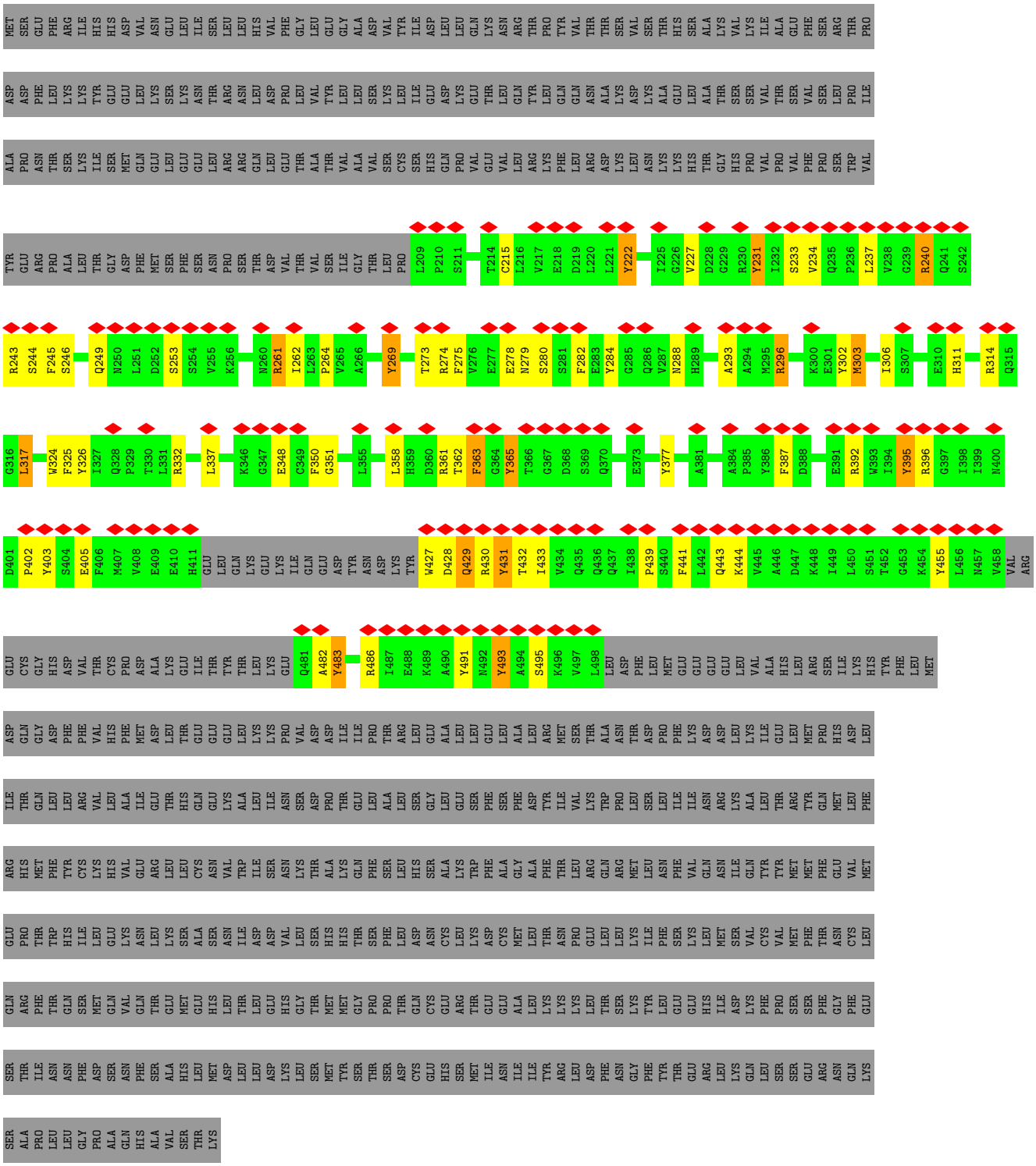
LEU THR ASN PRO GLU GLU LEU LYS ILE PHE SER LYS LEU MET SER VAL CYS VAL MET PHE THR ASN CYS LEU GLN ARG PHE THR GLN SER MET GLU GLN VAL GLN THR GLU MET GLU HIS GLY THR MET MET GLY PRO PRO THR GLN CYS GLU ARG THR GLU GLU ALA

LEU LYS LYS LYS LEU THR SER LYS TYR LEU GLU GLU HIS ILE ASP LYS LYS SER SER SER PHE GLY PHE GLU SER THR ILE ASN ASN PHE ASP SER ASN PHE SER LYS LYS LEU SER SER MET TYR SER THR SER ASP CYS GLU HIS SER MET ILE ASN ILE

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

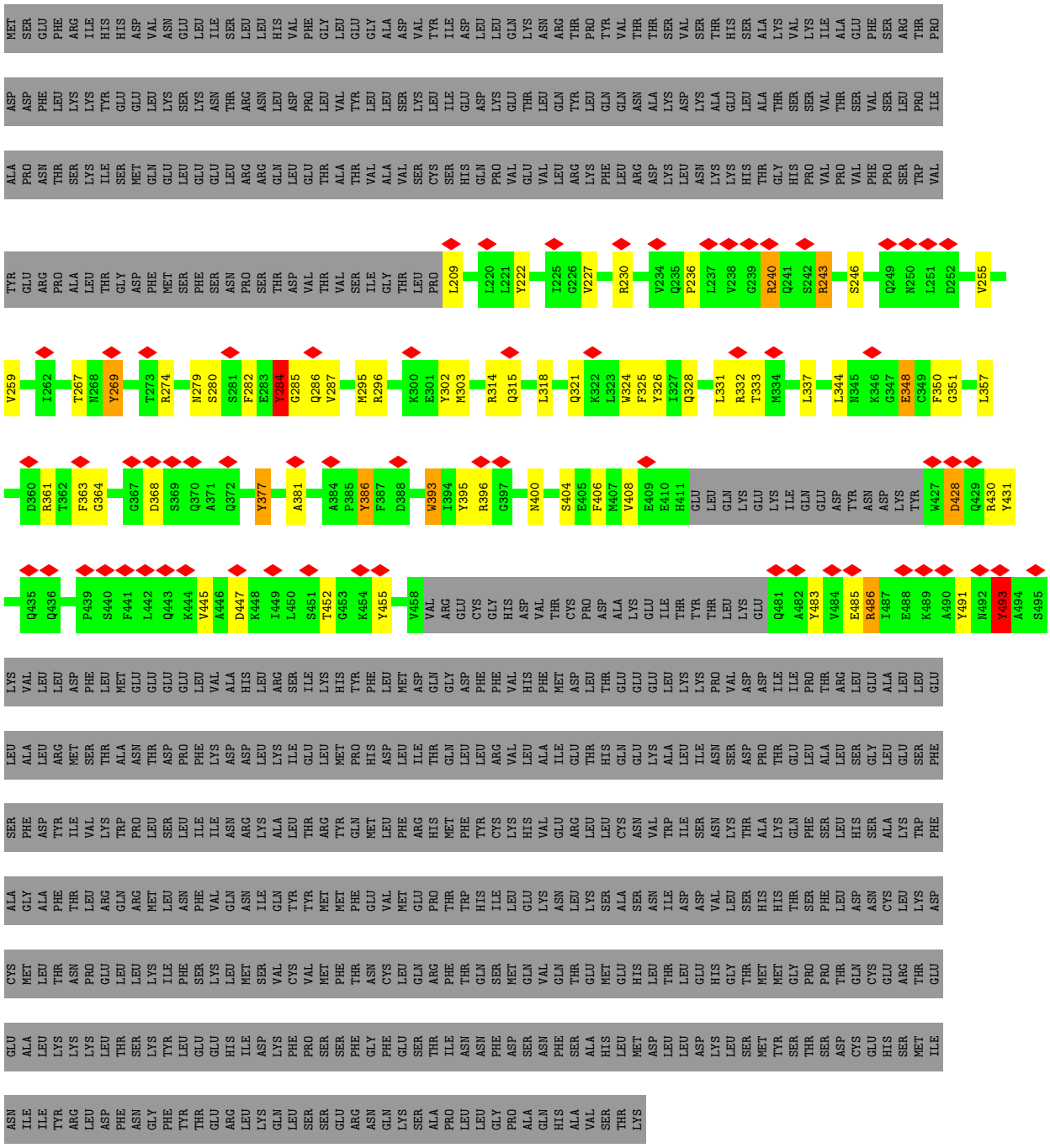
- Molecule 1: Gamma-tubulin complex component

Chain E:



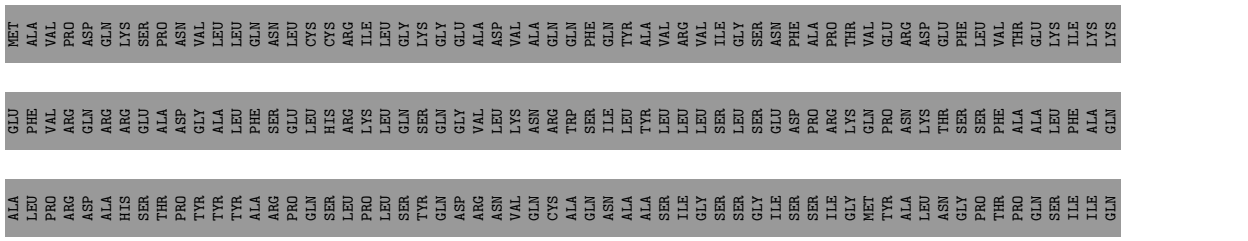
- Molecule 1: Gamma-tubulin complex component

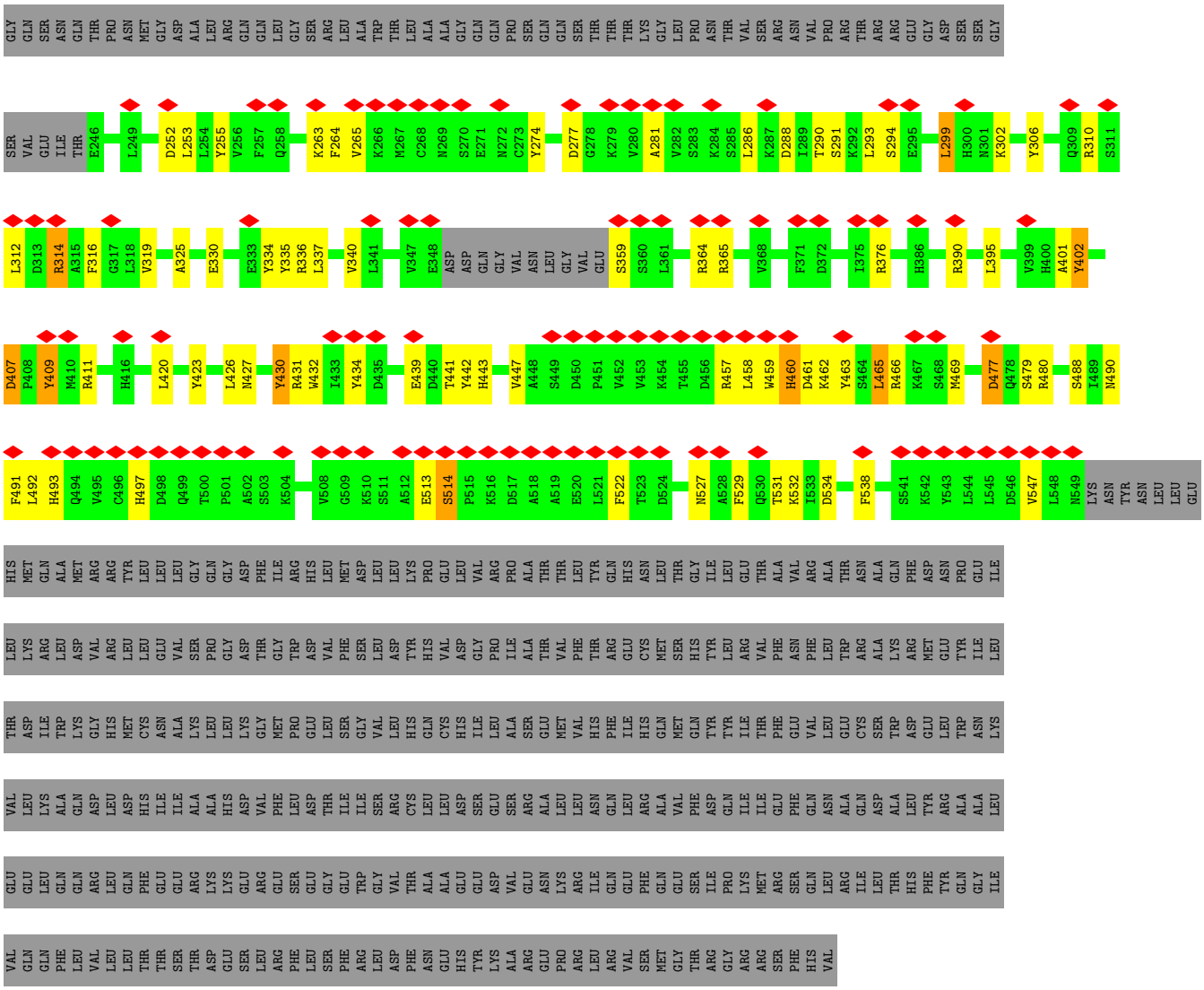
Chain G:



- Molecule 2: Gamma-tubulin complex component 3 homolog

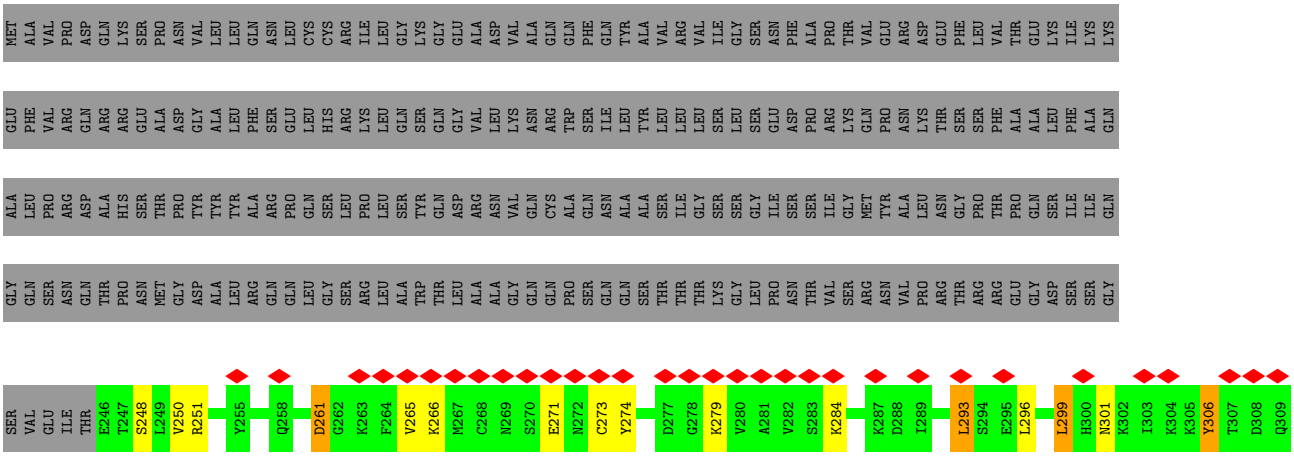
Chain B:

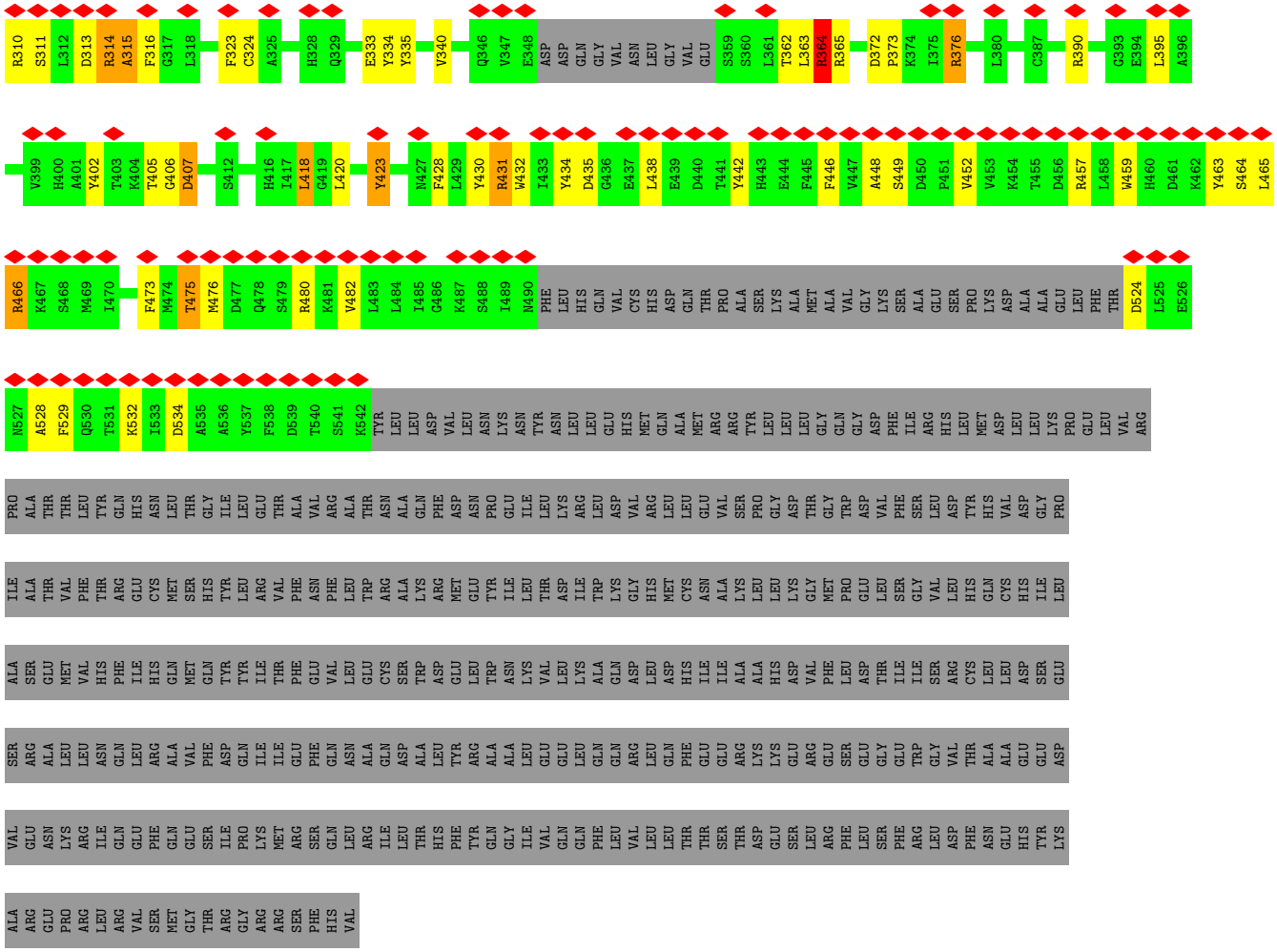




- Molecule 2: Gamma-tubulin complex component 3 homolog

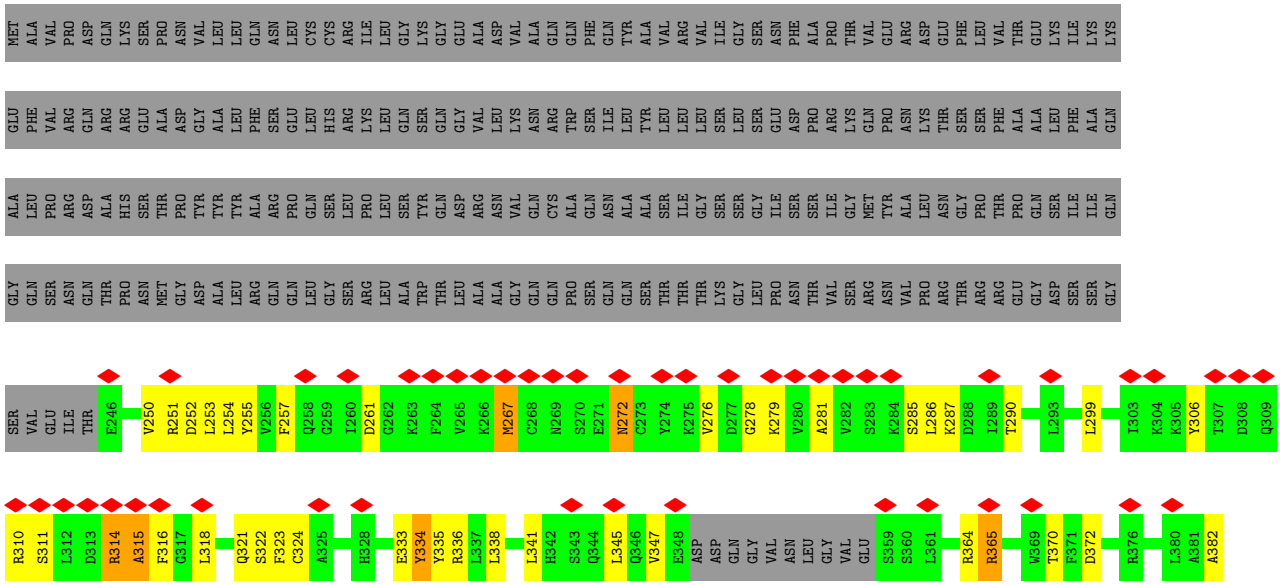
Chain D:

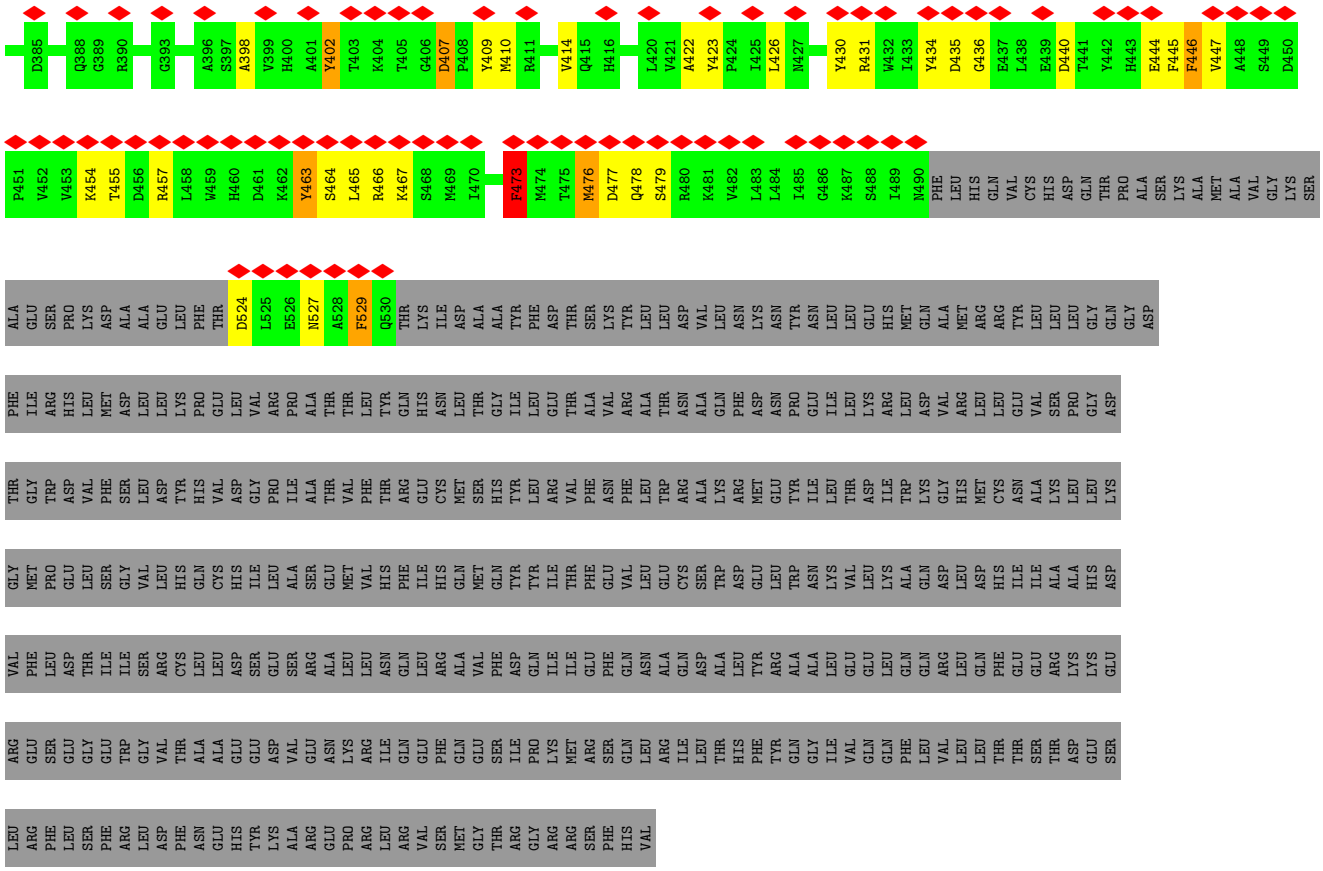




• Molecule 2: Gamma-tubulin complex component 3 homolog

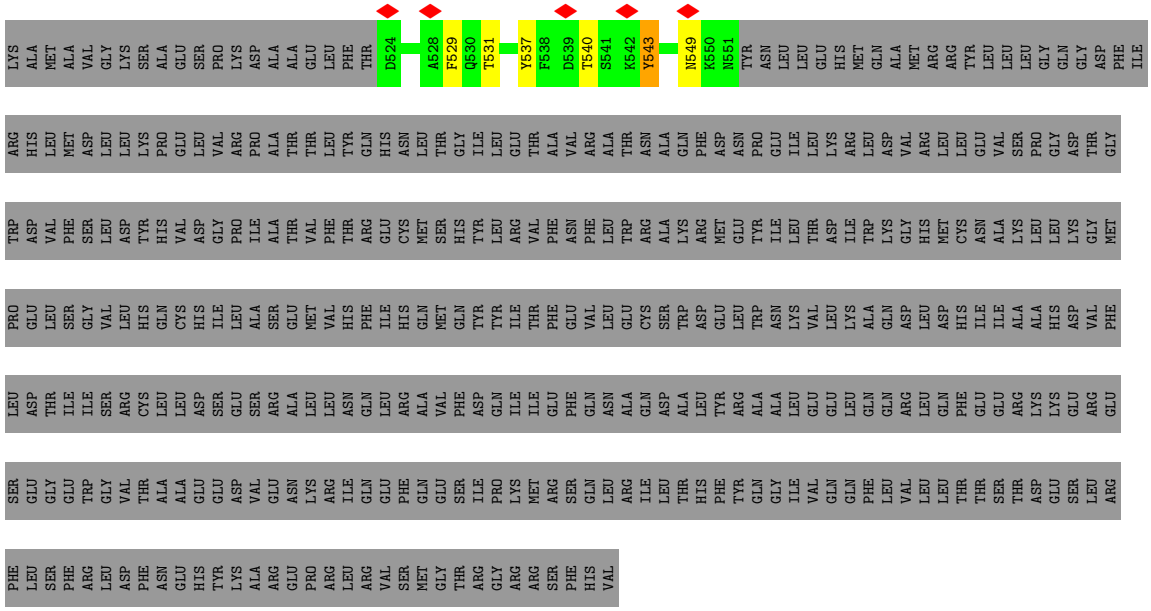
Chain F:





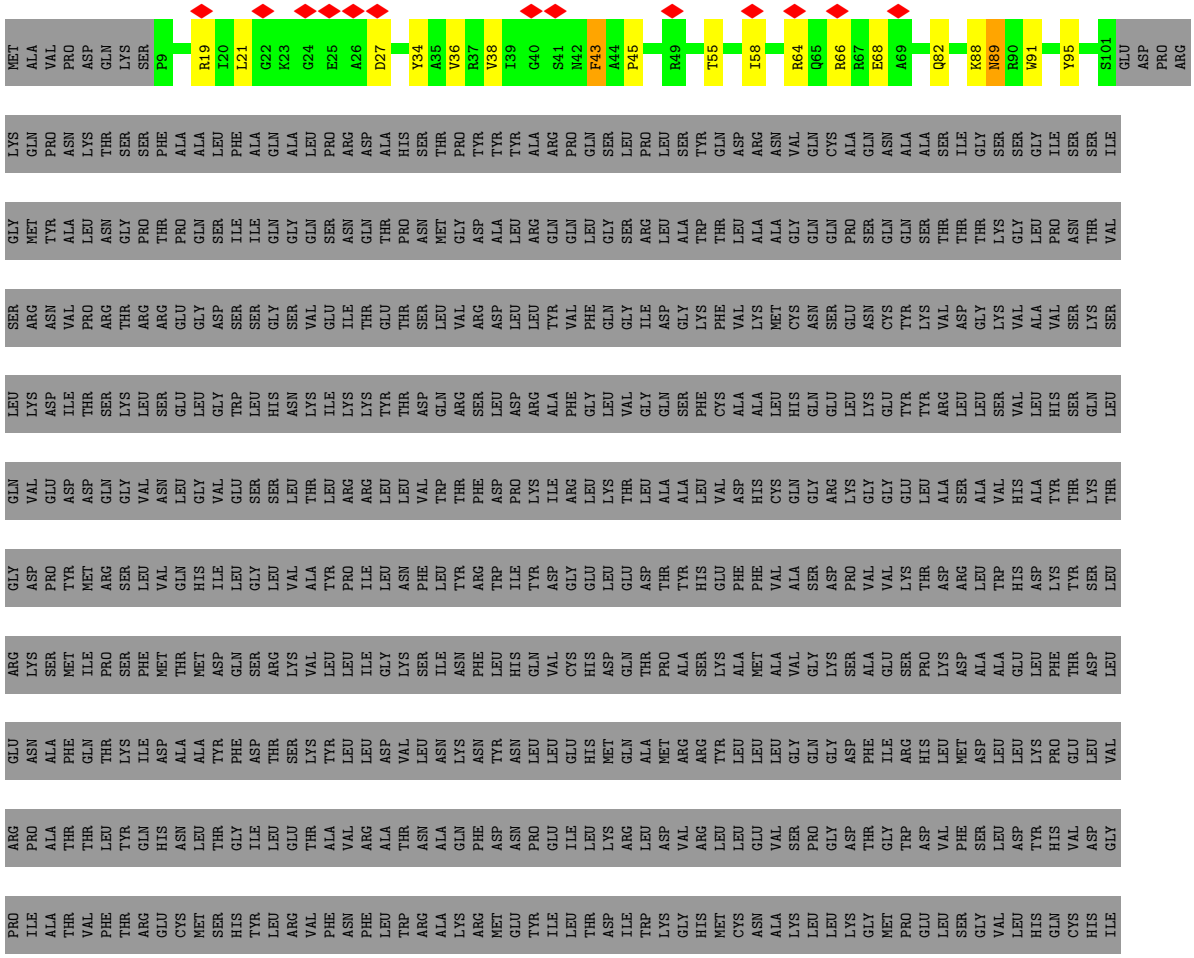
- Molecule 2: Gamma-tubulin complex component 3 homolog

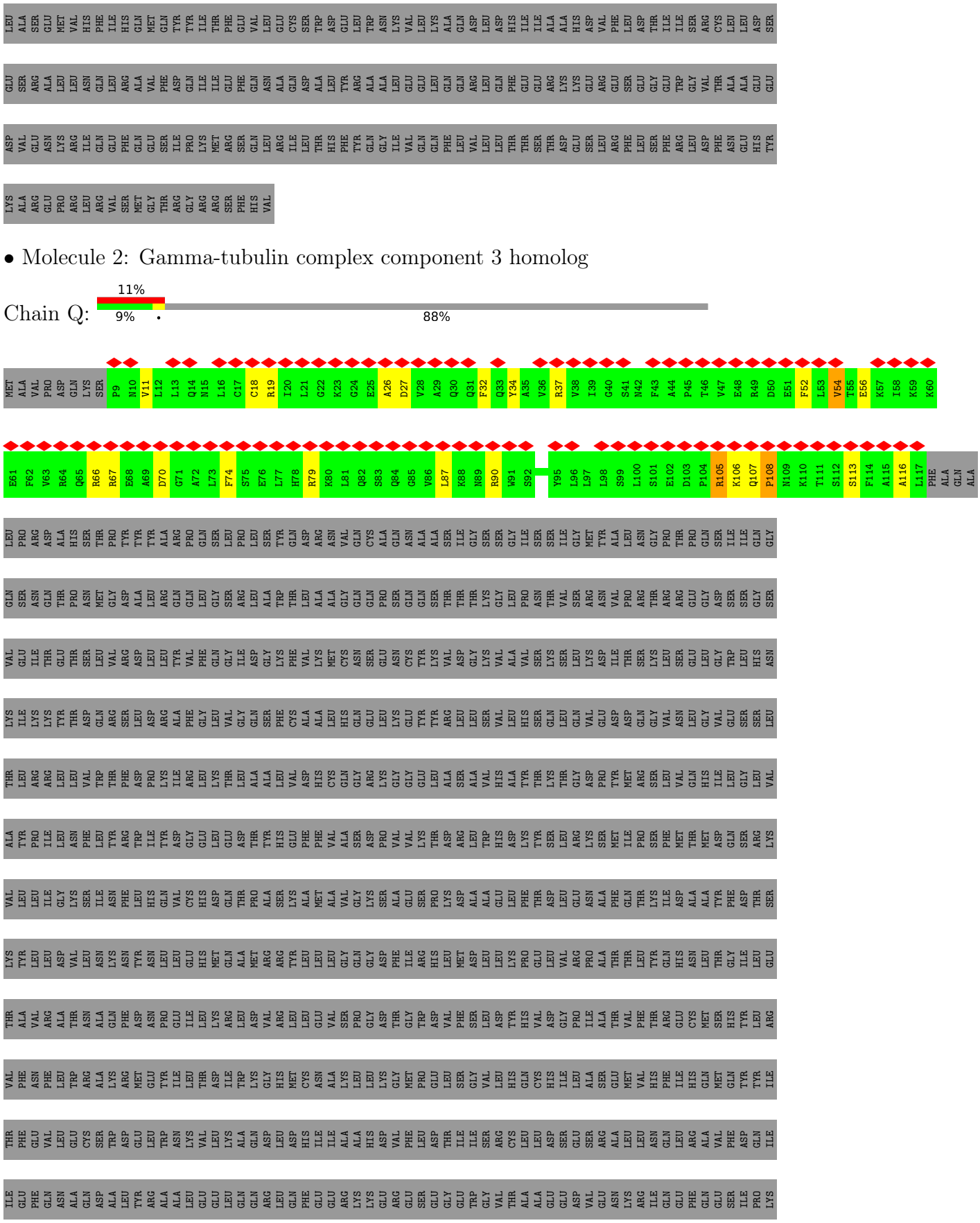
Chain H:



- Molecule 2: Gamma-tubulin complex component 3 homolog

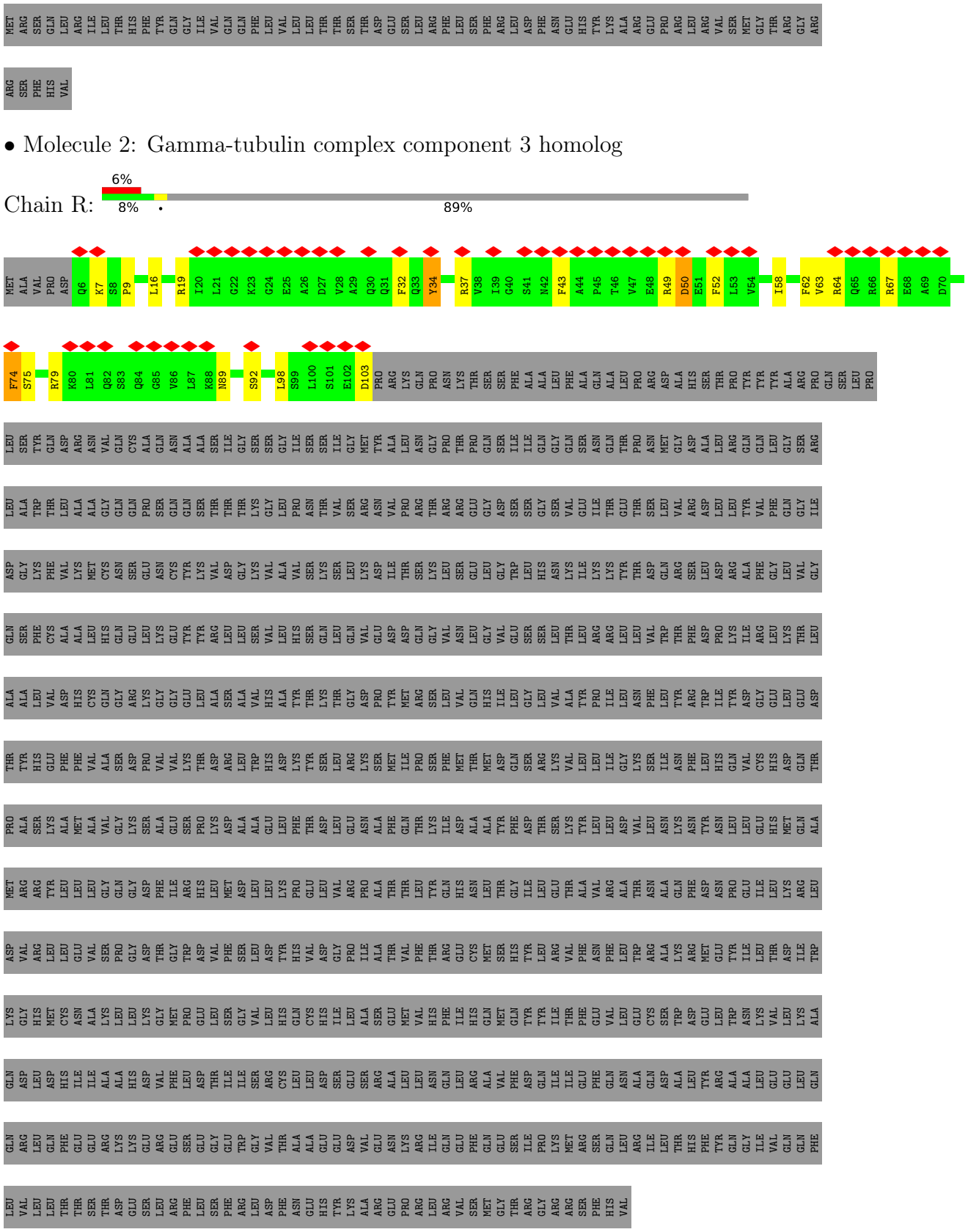
Chain O:





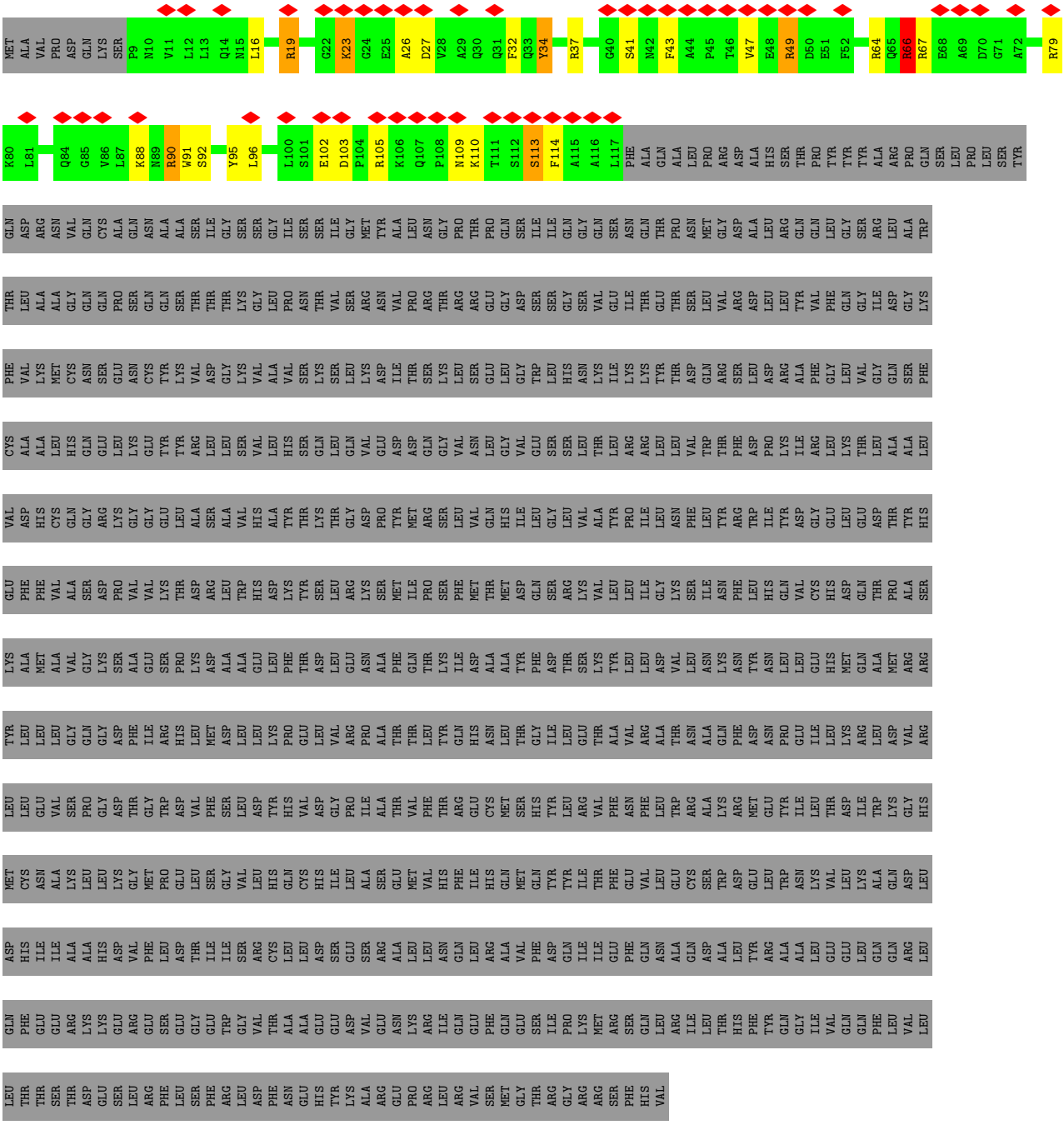
- Molecule 2: Gamma-tubulin complex component 3 homolog

Chain Q: 11% 9% 88%



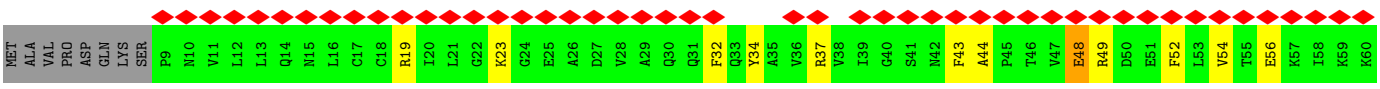
• Molecule 2: Gamma-tubulin complex component 3 homolog

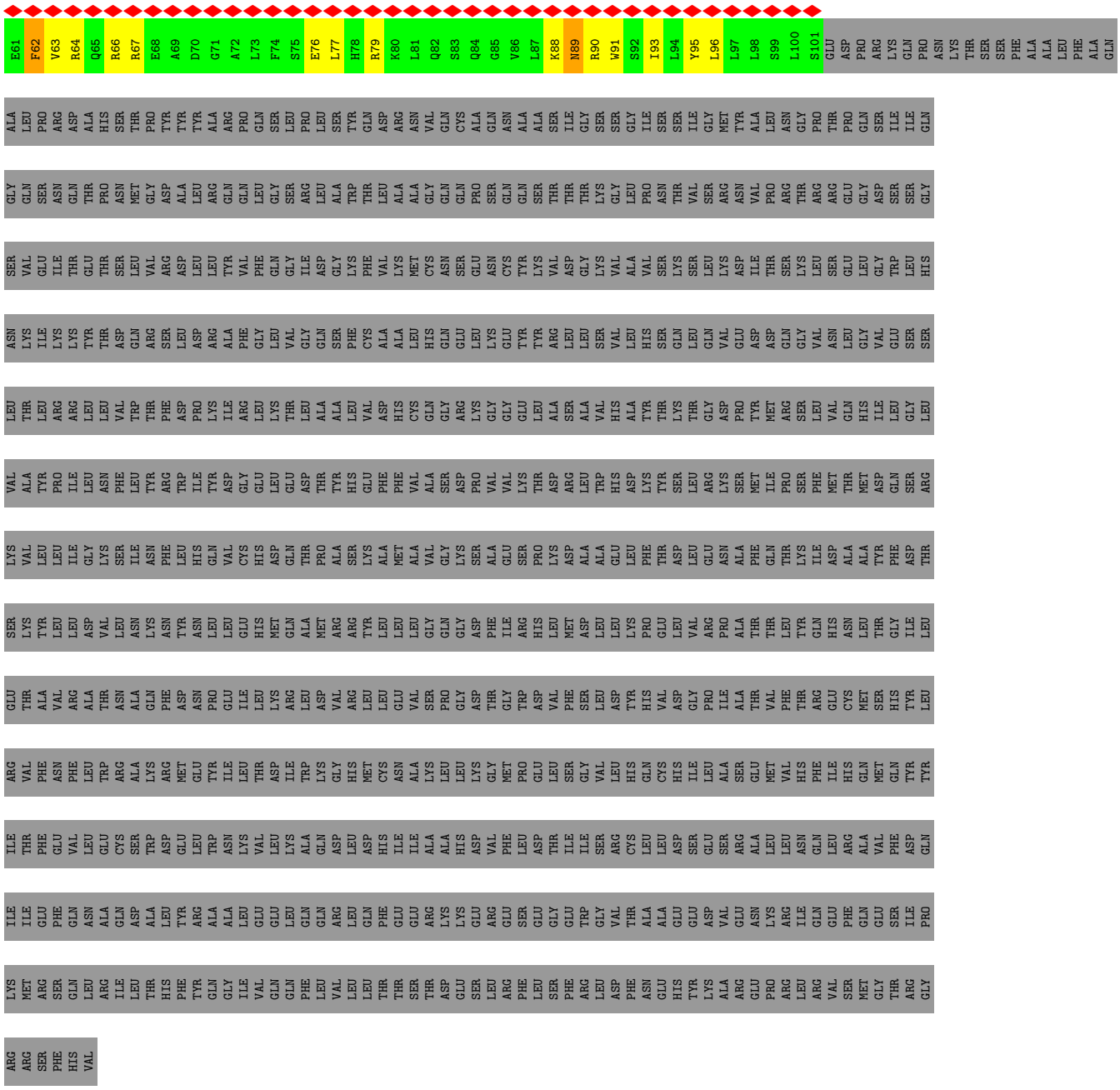
Chain S: 6% 9% 88%



• Molecule 2: Gamma-tubulin complex component 3 homolog

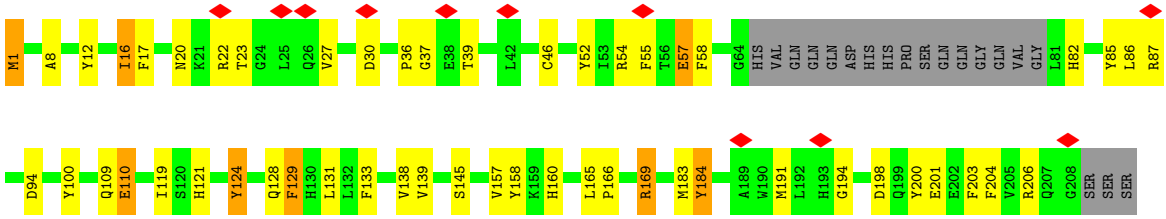
Chain T: 10% 7% 90%

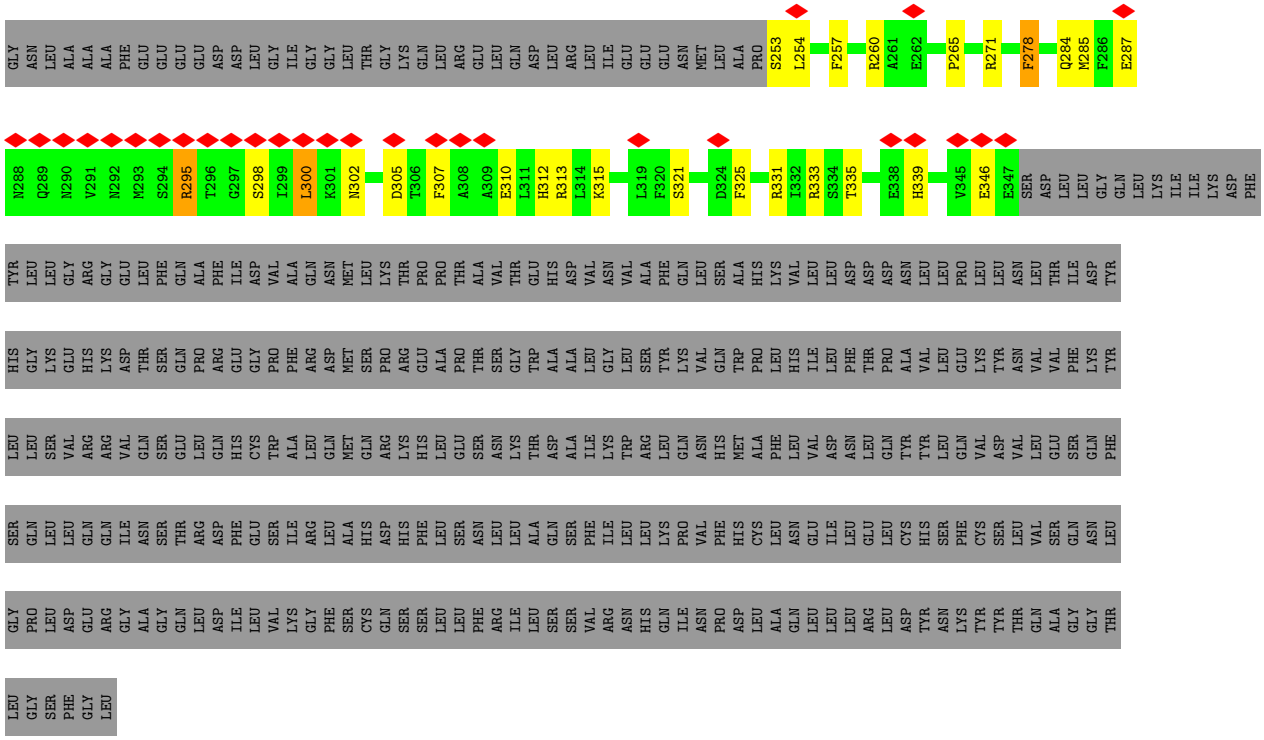




- Molecule 3: Gamma-tubulin complex component

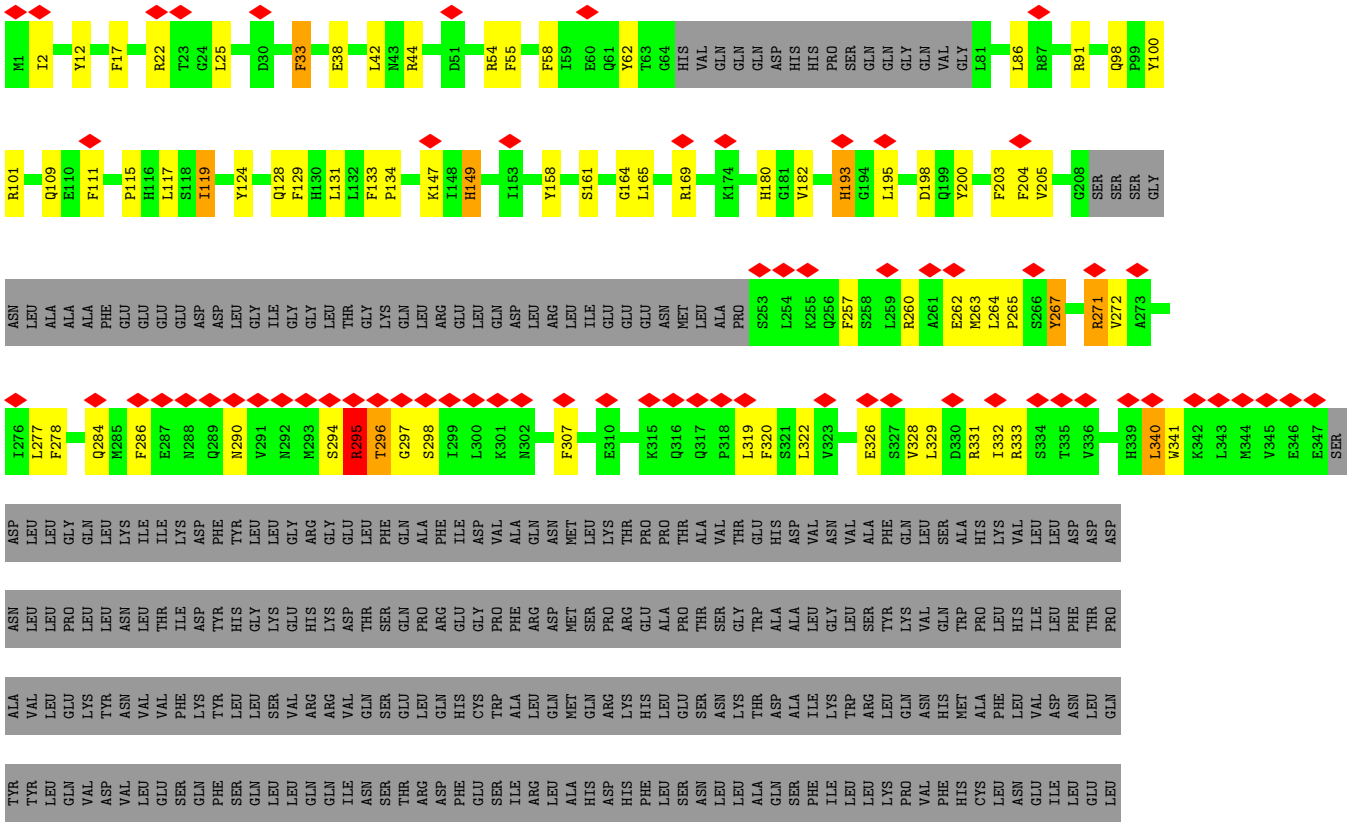
Chain I:

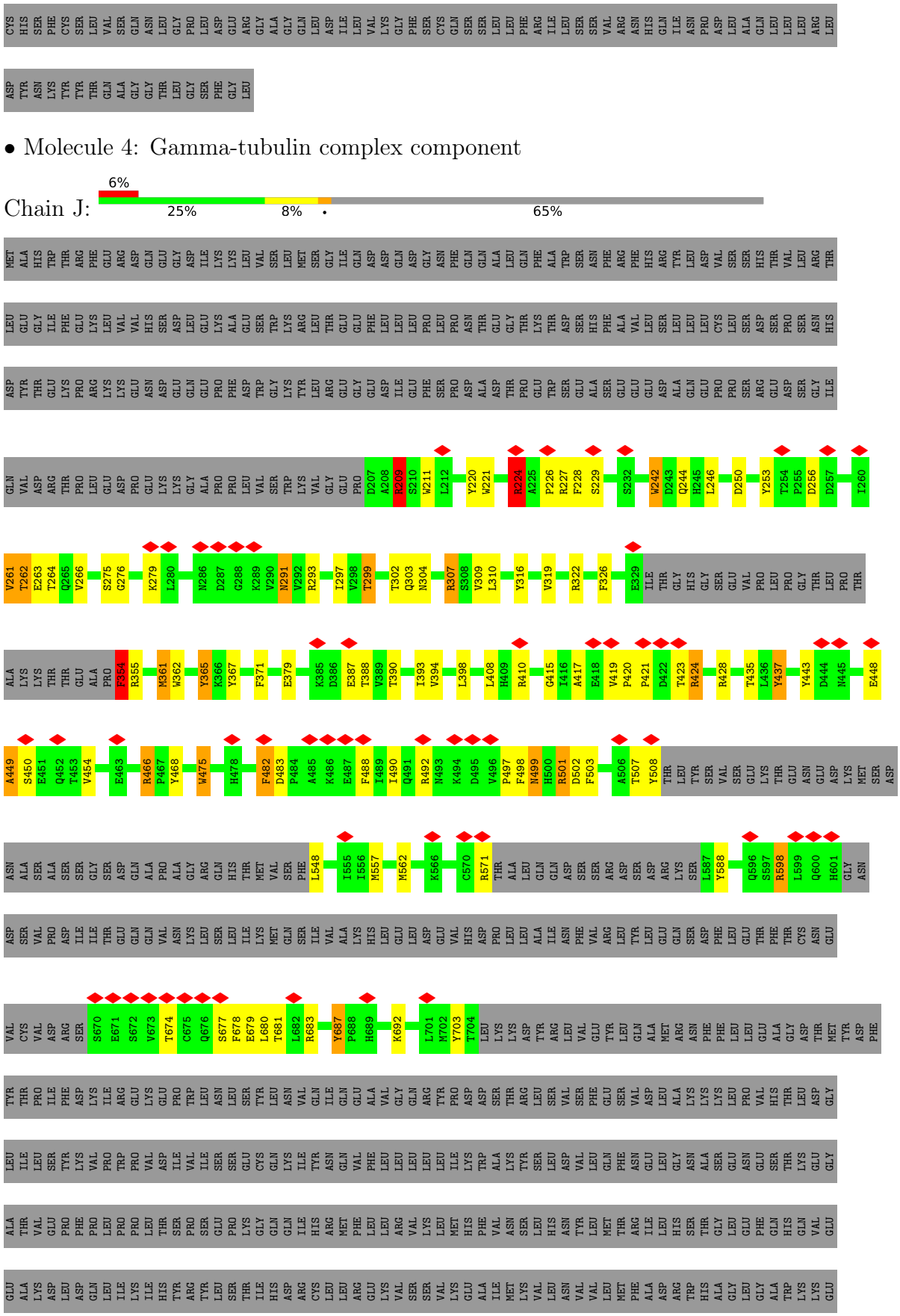




• Molecule 3: Gamma-tubulin complex component

Chain K:




CYS HIS SER PHE CYS SER LEU VAL SER GLN ASN LEU GLY PRO LEU ASP GLU ARG GLY ALA GLY GLN LEU ASP ILE LEU VAL LYS GLY PHE SER CYS GLN SER SER LEU LEU PHE ARG ILE LEU SER SER VAL ARG ASN HIS GLN ILE ASN PRO ASP LEU ALA GLN LEU LEU LEU ARG LEU
ASP TYR ASN LYS TYR TYR THR GLN ALA GLY GLY THR LEU GLY SER PHE GLY LEU
• Molecule 4: Gamma-tubulin complex component
Chain J:
6%
25%
8%
65%
MET ALA HIS TRP THR ARG PHE GLU ARG ASP GLN GLU GLY ASP ILE LYS LYS LEU VAL SER LEU MET SER GLY ILE GLN ASP ASP GLN ASP GLY ASN PHE GLN GLN ALA LEU GLN PHE ALA TRP SER ASN PHE ARG PHE HIS ARG TYR LEU ASP VAL SER SER HIS THR VAL LEU ARG THR
LEU GLU GLY ILE PHE GLU LYS LEU VAL VAL HIS SER ASP LEU GLU LYS LYS ALA GLU SER TRP LYS ARG LEU THR GLU GLU GLU PHE LEU LEU LEU PRO LEU PRO ASN THR GLU GLY THR LYS THR ASP SER HIS PHE ALA VAL LEU SER LEU LEU LEU CYS LEU SER ASP SER PRO SER ASN HIS
ASP TYR THR GLU LYS PRO ARG LYS LYS GLU ASN ASP GLU GLN GLU PRO PHE ASP TRP GLY LYS TYR LEU ARG GLU GLY GLU ASP ILE GLU PHE SER PRO ASP ALA ASP THR PRO GLU TRP SER GLU ALA SER GLU GLU GLU ASP ALA GLN GLU PRO PRO SER ARG GLU ASP SER GLY ILE
GLN VAL ASP ARG THR PRO LEU GLU ASP PRO GLU LYS LYS GLY ALA PRO PRO LEU VAL SER TRP LYS VAL GLY GLU PRO D207 A208 R209 S210 W211 L212 Y220 W221 R224 A225 P226 R227 F228 S229 S232 W242 D243 Q244 H245 L246 D250 Y253 T254 P255 D256 D257 I260
V261 T262 E263 T264 Q265 V266 S275 G276 K279 L280 N286 D287 G288 K289 V290 N291 V292 R293 I297 V298 T299 T302 Q303 N304 R307 S308 V309 L310 Y316 V319 R322 F326 E329 ILE THR GLY HIS GLY SER GLU VAL PRO LEU PRO GLY THR LEU PRO THR
ALA LYS LYS THR THR GLU ALA PRO F354 R355 M361 W362 Y365 K366 Y367 F371 E379 K385 D386 E387 T388 V389 T390 I393 V394 L398 L408 H409 R410 G415 I416 A417 E418 V419 P420 P421 D422 T423 R424 R428 T435 L436 Y437 Y443 D444 N445 E448
A449 S450 E451 Q452 T453 V454 E463 R466 P467 Y468 W475 H478 F482 D483 P484 A485 K486 E487 F488 I489 I490 Q491 R492 N493 K494 D495 V496 P497 F498 N499 H500 R501 D502 F503 A506 T507 Y508 THR LEU TYR SER VAL SER GLU LYS THR GLU ASN GLU ASP LYS MET SER ASP
ASN ALA SER ALA SER SER GLY SER ASP GLN ALA PRO ALA GLY ARG GLN HIS THR MET VAL SER PHE L548 I555 I556 M557 M562 K566 C570 R571 THR ALA LEU GLN GLN ASP SER SER ARG ASP SER ASP ARG LYS SER L587 Y588 Q596 S597 R598 L599 Q600 H601 GLY ASN
ASP SER VAL PRO ASP ILE ILE THR GLU GLN GLN VAL ASN LYS LEU SER LEU ILE LYS MET GLN SER ILE VAL ALA LYS HIS LEU GLU LEU ASP GLU VAL HIS ASP PRO LEU LEU ALA ILE ASN PHE VAL ARG LEU TYR LEU GLU GLN SER ASP PHE LEU GLU THR PHE THR CYS ASN GLU
VAL CYS VAL ASP ARG SER S670 E671 S672 V673 T674 G675 Q676 S677 F678 E679 L680 T681 L682 R683 Y687 P688 H689 K692 L701 M702 Y703 T704 LEU LYS LYS ASP TYR ARG LEU VAL GLU TYR LEU GLN ALA MET ARG ASN PHE PHE LEU LEU GLU VAL ASP ALA LEU ALA LYS LYS LEU PRO VAL HIS THR MET TYR ASP PHE
TYR THR PRO ILE PHE ASP LYS ILE ARG GLU LYS GLU PRO TRP LEU ASN LEU SER TYR LEU ASN VAL GLN ILE GLN GLU ALA VAL GLY GLN ARG TYR PRO ASP ASP SER THR ARG LEU SER VAL SER PHE GLU SER VAL ASP LEU ALA LYS LYS LEU PRO VAL HIS THR LEU ASP GLY
LEU ILE LEU SER TYR LYS VAL PRO TRP PRO VAL ASP ILE VAL ILE SER SER GLU CYS GLN LYS ILE TYR ASN GLN VAL PHE LEU LEU LEU LEU LEU ILE LYS TRP ALA LYS TYR SER LEU ASP VAL LEU GLN PHE ASN GLU LEU GLY ASN ALA SER GLU ASN VAL GLU SER THR LYS GLU GLY
ALA THR VAL GLU PRO PHE PRO PRO LEU PRO PRO LEU THR SER PRO PRO SER GLU PRO LYS GLY GLN GLN ILE HIS ARG MET PHE LEU LEU ARG VAL LYS LEU MET HIS PHE VAL ASN SER LEU HIS ASN TYR LEU MET THR ARG ILE LEU GLU PHE GLN HIS GLN VAL GLU
GLU ALA LYS ASP LEU ASP GLN LEU ILE HIS TYR ARG TYR LEU SER THR ILE HIS ASP ARG CYS LEU LEU ARG GLU LYS VAL SER SER VAL LYS GLU ALA ILE MET LYS VAL LEU ASN VAL LEU MET PHE ALA ASP ARG TRP HIS ALA GLY LEU GLY ALA TRP LYS LYS GLU
ww PDB PROTEIN DATA BANK

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

- Molecule 5: Gamma-tubulin complex component 6

Chain L:

MET ASP S3 T4 L7 F8 L11 V17 GLY PHE PRO TRP ARG THR ALA LEU ASN SER ARG LYS HIS S31 R34 L42 A43 Y44 F48 L51 F52 Q53 ASP GLU ALA ARG LYS LEU GLN PRO ASN CYS THR ARG L66 K71 L75 S76 F77 G83 M84 S85

S86 E87 A88 D89 R90 V95 E96 Y97 L98 E99 Q100 S101 N102 G103 I104 Q105 I106 S107 D108 L109 H110 V117 G121 THR GLY PRO PRO GLN LEU LEU PRO PRO LYS ARG ARG ASP TYR PHE LYS ASN ASN LYS TYR VAL GLY ARG ASN VAL LYS TYR GLN GLY TYR ASP TYR TYR ASP V155

F158 E159 A160 D161 Y168 T175 R179 T180 L181 M184 GLU ALA ALA PRO GLY THR GLY LEU PRO ALA LEU SER PHE PHE SER GLN ASN ASP LEU SER THR D206 E209 T212 R213 G214 S215 L216 F217 L220 V221 H222 S223 R224 T225 N226 D227 M228 D229 I230 K231 L232

P238 E239 N240 A241 D242 L243 S244 G245 L246 P251 Q252 S253 I254 ASP GLN SER GLU ASP GLU GLY PHE GLN SER ALA SER ASN MET THR PRO ASP SER GLN SER GLU PRO SER MET THR PRO ASP ILE ASP VAL TRP GLU ALA VAL LEU THR TYR GLY PRO SER LYS ARG ARG CYS TRP

GLU ARG ILE GLY CYS PRO PRO GLY LYS ARG GLU E311 P312 Y313 V314 T315 E316 A317 F322 Y326 H329 G332 I335 L336 S337 A338 T339 T340 L341 Q342 P343 Q344 L345 V346 L347 T351 D352 K355 N359 I362 S366 S367 T368 Y371 N372 Q373 A374 L375 Q376

S377 F378 A379 Q382 G383 V384 Y385 G388 P391 D392 N393 S396 Y404 G405 T406 Y407 Y408 T409 R410 H413 F414 S415 L416 L417 T418 V419 L420 D421 S422 S423 H424 S425 N426 G427 L428 V429 A432 F433 R438 K439 Y440 Y443 Y444 R445 A446 C447 T451 P452 A453 S454

L455 F462 R465 K466 L467 G468 R469 Q470 L471 R472 Y473 L474 A475 E476 C479 ILE GLY THR LEU VAL THR SER ALA THR ARG GLY ILE SER THR A494 F495 P496 T497 G498 V499 K500 L501 Y504 L505 Y506 K507 E508 E516 N517 Y518 P519 S523 T527 S528 P531 Y532

F535 I536 Y537 D538 W539 V540 Y541 S542 G543 V544 F545 R546 D547 V548 C549 G550 E551 F552 M553 I554 Q555 V556 N557 E558 D559 Y560 L561 G562 F563 R564 D565 K566 R567 Y568 W569 T570 H571 G572 Y573 V574 L575 I576 S577 K578 E579 V580 E581 D582 C583 V584 P585 V586 F587 L588 K589 H590 V591 A592 N593 E594

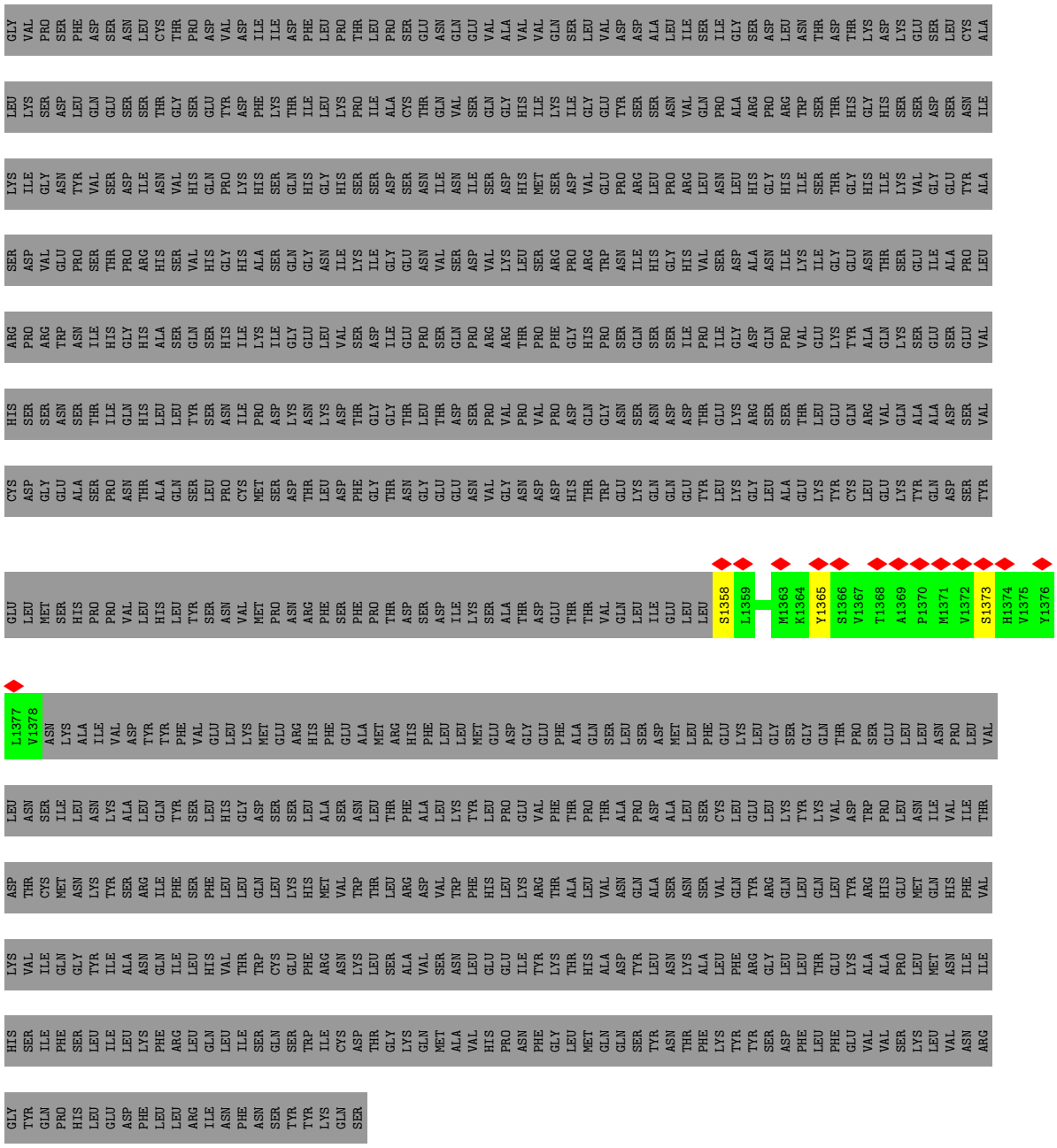
I595 Y596 I597 C598 G599 K600 T601 I602 N603 L604 L605 K606 L607 C608 CYS PRO LYS HIS TYR ILE CYS TRP SER ASP ILE PRO VAL PRO ARG ILE SER VAL THR PHE SER LEU GLU GLU LEU LYS GLU MET GLU LYS ASP CYS ALA VAL TYR VAL ALA ARG MET GLU ARG ILE ALA ARG HIS SER

CYS ILE SER LYS GLU GLN LYS ALA LEU GLN THR GLU ILE ALA ARG GLN GLU LEU ILE ILE GLN ALA ARG GLU THR THR GLU LYS VAL PHE GLU THR PHE LYS ASP ARG LYS LEU ALA GLU LYS LEU SER LEU ASP THR LYS LYS ARG GLU LEU PHE GLN LYS LEU LYS ASP GLN TYR GLU

LYS GLU GLN GLU ARG ARG LEU THR THR LYS GLN GLU GLU ALA ASP ASP ASP PHE SER TYR ALA ARG GLU ILE ARG ASP ARG GLU LYS ARG LEU LYS ALA LEU GLU GLU GLU GLU LEU GLU LEU LYS THR ARG GLN GLU LEU ILE GLU HIS TYR SER ARG LEU SER GLU GLU ALA THR ARG LYS

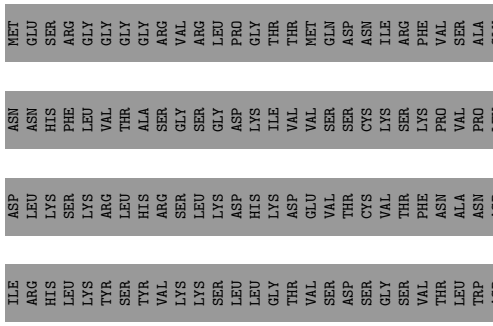
GLU GLN ARG ALA LEU TRP LYS LEU GLN ARG HIS LYS LEU GLU THR ILE ARG LEU LYS PHE PHE LEU GLU GLU GLN LYS ARG MET GLN ASP LEU VAL ALA ASN PHE PRO VAL ASP ILE CYS GLU GLU ASN LEU GLY VAL LEU PRO ASP GLY GLU ILE SER HIS GLN THR ASP ASN THR ASN

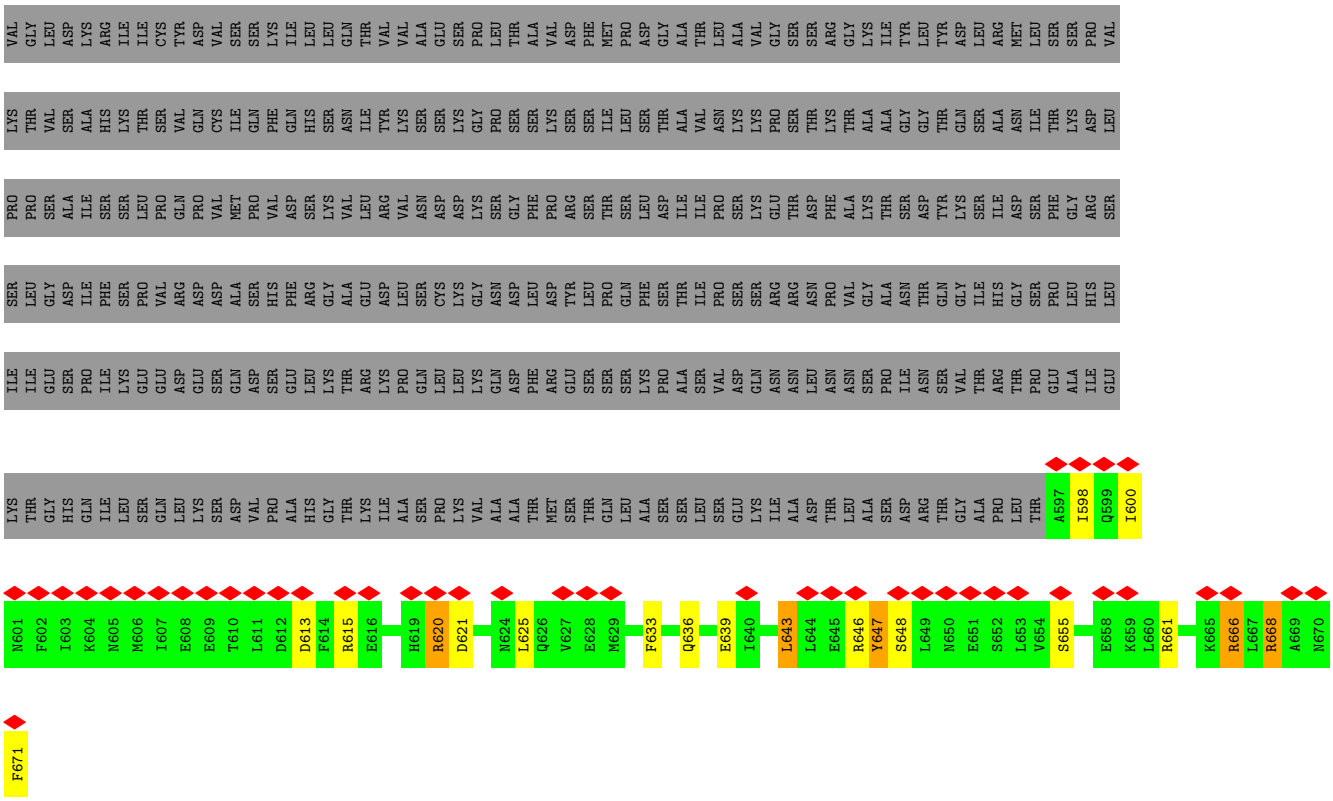
ASP ALA GLY LEU GLY ASN ILE GLU ASN GLU LYS SER VAL PRO GLU GLN HIS ALA LEU HIS ASN ASN ASP GLU VAL TYR THR ALA GLN ASN CYS ILE SER LYS SER GLU SER LEU CYS VAL ASP VAL THR LEU PRO THR GLU ASN VAL HIS SER GLN THR SER ASN ALA SER VAL LEU



• Molecule 6: NEDD1 gamma-tubulin ring complex targeting factor L homeolog

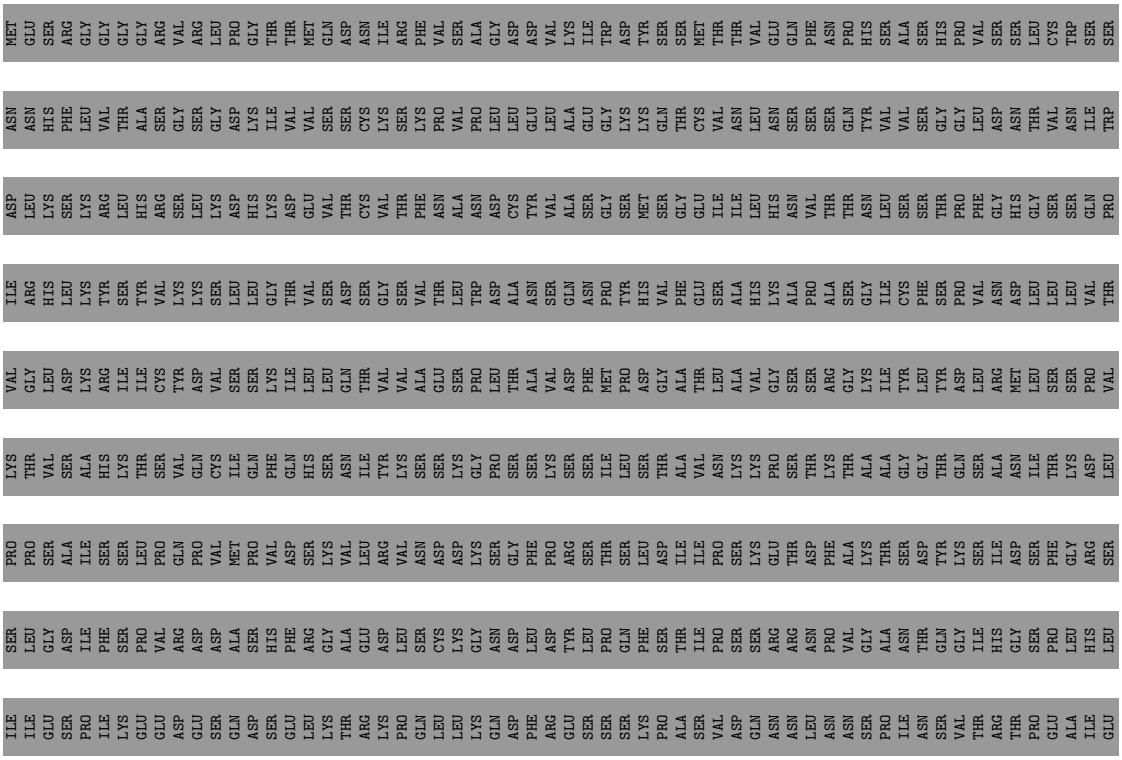
Chain U: 7% 8% 89%

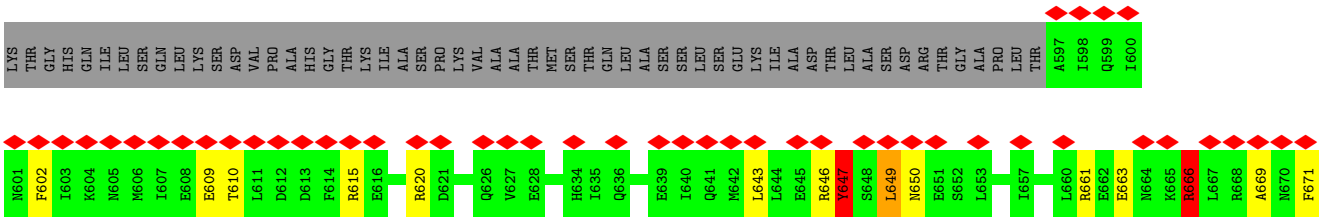




• Molecule 6: NEDD1 gamma-tubulin ring complex targeting factor L homeolog

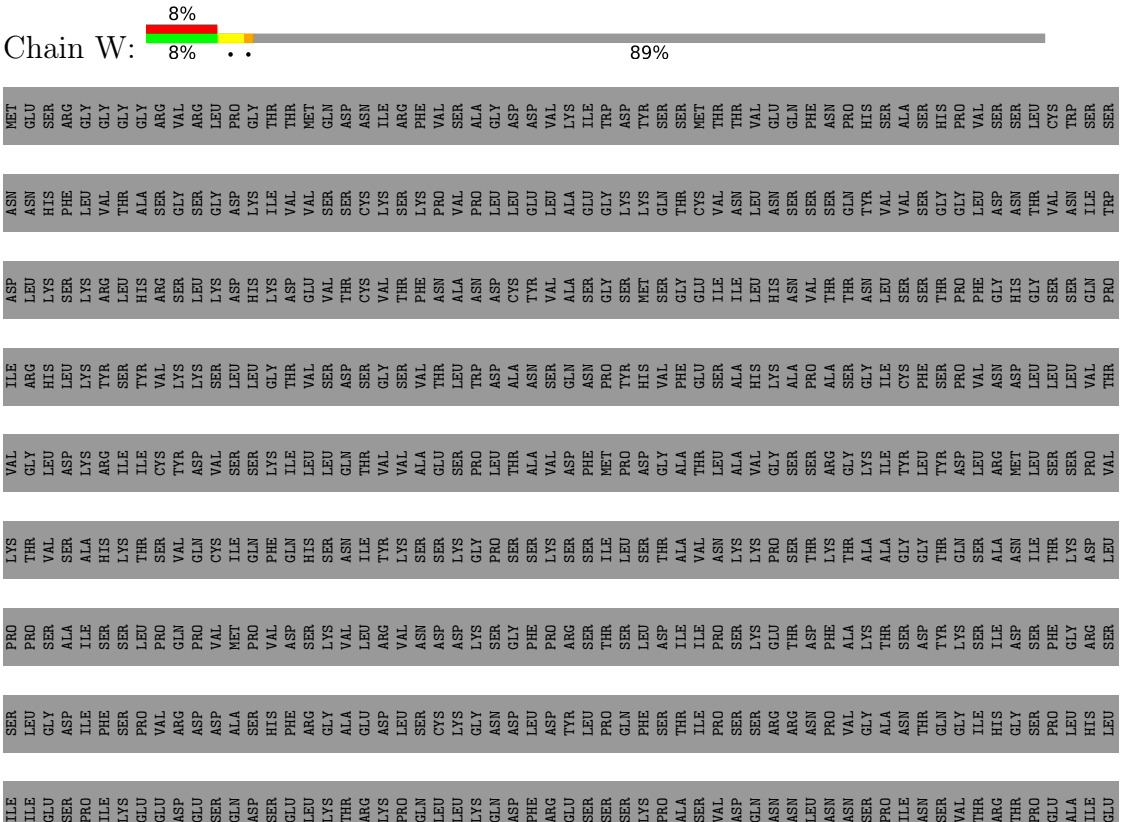
Chain V:





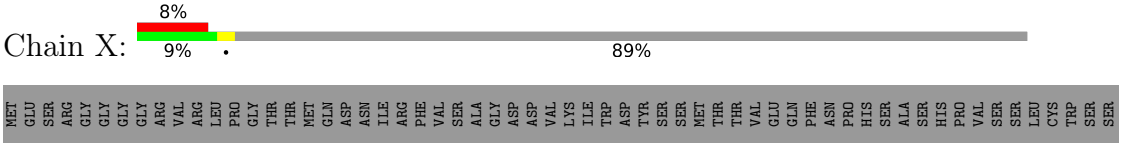
• Molecule 6: NEDD1 gamma-tubulin ring complex targeting factor L homeolog

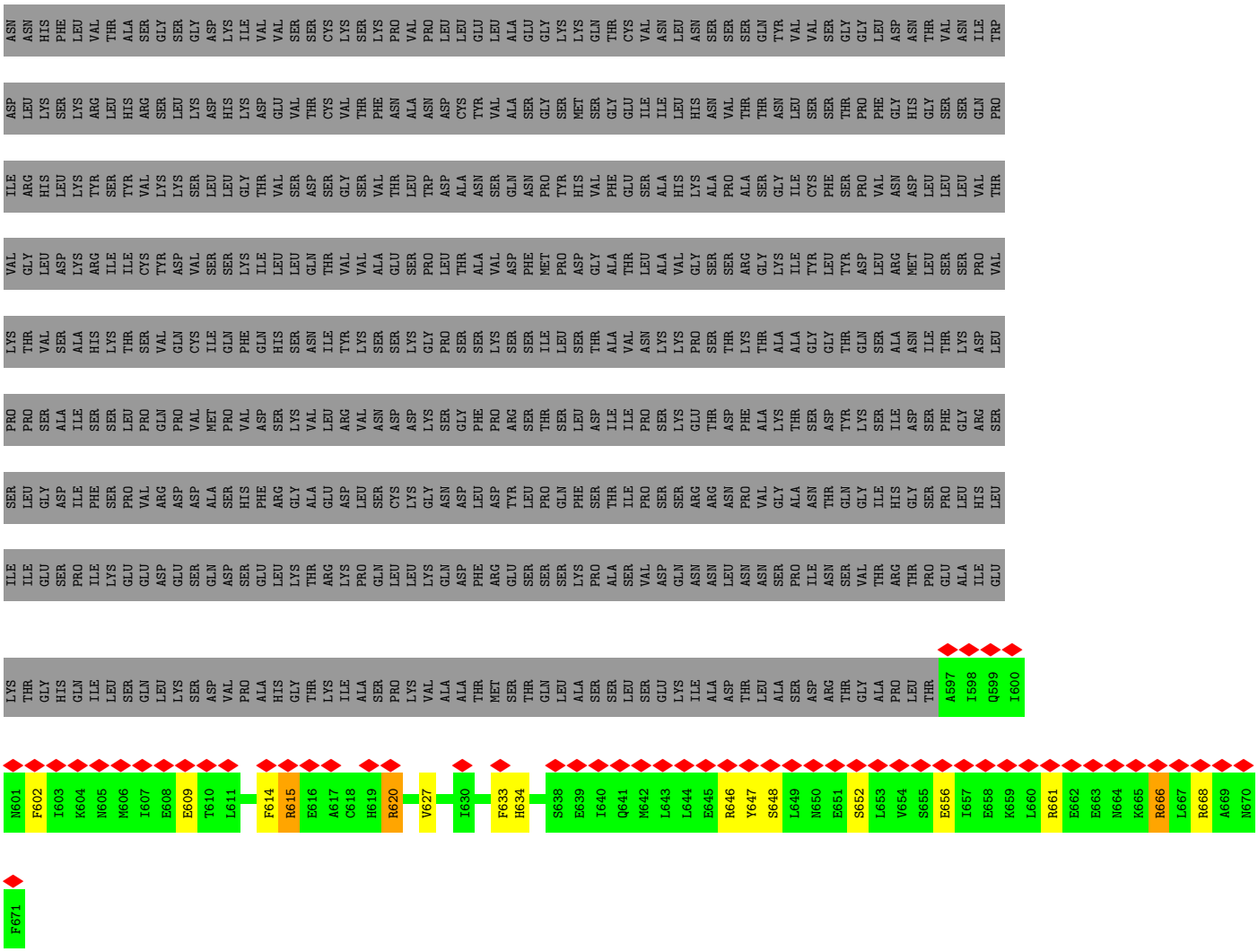
Chain W:



• Molecule 6: NEDD1 gamma-tubulin ring complex targeting factor L homeolog

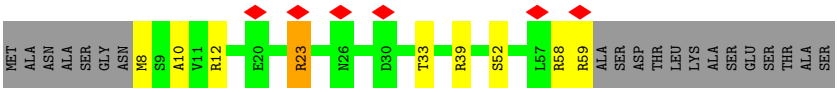
Chain X:





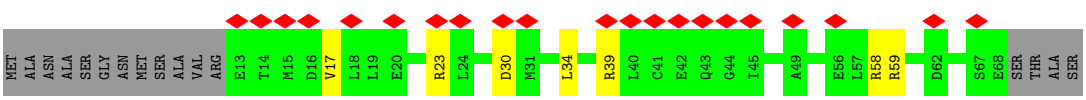
• Molecule 7: Mitotic-spindle organizing protein 1

Chain o:



• Molecule 7: Mitotic-spindle organizing protein 1

Chain p:

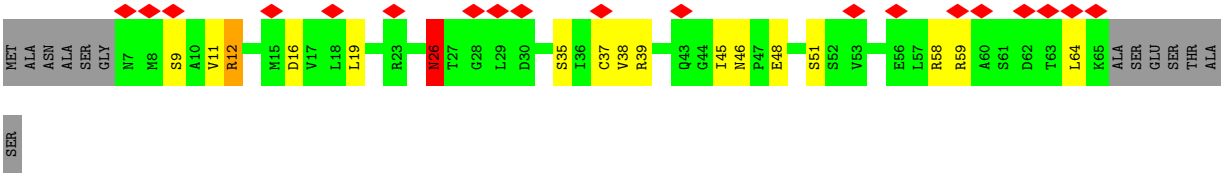


• Molecule 7: Mitotic-spindle organizing protein 1

Chain q:

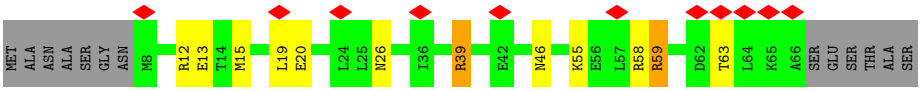
- Molecule 7: Mitotic-spindle organizing protein 1

Chain r:



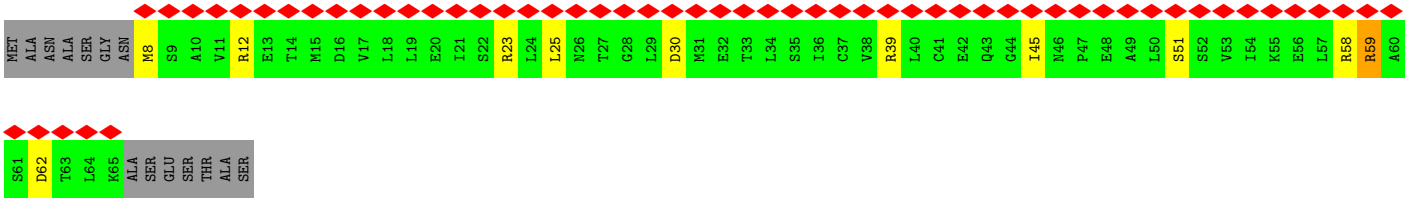
- Molecule 7: Mitotic-spindle organizing protein 1

Chain s:



- Molecule 7: Mitotic-spindle organizing protein 1

Chain t:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	299022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.404	Depositor
Minimum map value	-0.286	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0421	Depositor
Map size (Å)	365.9392, 365.9392, 365.9392	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.42945, 1.42945, 1.42945	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	A	1.74	16/2254 (0.7%)	1.92	55/3055 (1.8%)
1	C	1.74	20/2053 (1.0%)	1.99	54/2781 (1.9%)
1	E	1.80	22/2077 (1.1%)	2.02	67/2813 (2.4%)
1	G	1.76	21/2053 (1.0%)	2.06	62/2781 (2.2%)
2	B	1.72	23/2413 (1.0%)	1.99	65/3257 (2.0%)
2	D	1.74	19/2101 (0.9%)	1.96	60/2831 (2.1%)
2	F	1.65	11/2004 (0.5%)	1.93	53/2700 (2.0%)
2	H	1.71	21/2178 (1.0%)	2.02	54/2936 (1.8%)
2	O	1.65	3/764 (0.4%)	1.82	13/1026 (1.3%)
2	Q	1.72	8/892 (0.9%)	1.90	16/1199 (1.3%)
2	R	1.73	8/805 (1.0%)	2.01	22/1081 (2.0%)
2	S	1.70	5/892 (0.6%)	1.92	18/1199 (1.5%)
2	T	1.75	6/764 (0.8%)	1.98	22/1026 (2.1%)
3	I	1.73	16/2377 (0.7%)	1.92	50/3212 (1.6%)
3	K	1.68	14/2377 (0.6%)	1.88	46/3212 (1.4%)
4	J	2.16	32/2976 (1.1%)	2.03	83/4037 (2.1%)
5	L	1.73	37/3862 (1.0%)	1.89	92/5228 (1.8%)
6	U	1.67	6/640 (0.9%)	2.00	17/854 (2.0%)
6	V	1.68	4/640 (0.6%)	2.12	14/854 (1.6%)
6	W	1.68	2/640 (0.3%)	1.82	18/854 (2.1%)
6	X	1.73	4/640 (0.6%)	2.01	17/854 (2.0%)
7	o	1.63	2/403 (0.5%)	1.97	8/541 (1.5%)
7	p	1.69	1/429 (0.2%)	1.96	9/577 (1.6%)
7	q	1.64	3/432 (0.7%)	1.96	10/581 (1.7%)
7	r	1.76	10/454 (2.2%)	1.91	12/610 (2.0%)
7	s	1.71	6/451 (1.3%)	1.72	9/606 (1.5%)
7	t	1.58	1/446 (0.2%)	2.11	14/599 (2.3%)
All	All	1.76	321/38017 (0.8%)	1.96	960/51304 (1.9%)

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	A	0	6
1	C	0	6
1	E	0	8
1	G	0	10
2	B	0	5
2	D	0	6
2	F	0	10
2	H	0	11
2	O	0	2
2	Q	0	2
2	R	0	3
2	S	0	3
2	T	0	2
3	I	0	9
3	K	0	6
4	J	0	16
5	L	0	20
6	U	0	4
6	V	0	2
6	W	0	4
6	X	0	4
7	o	0	2
7	q	0	2
7	r	0	1
7	s	0	1
7	t	0	1
All	All	0	146

The worst 5 of 321 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	242	TRP	CD2-CE3	35.46	1.93	1.40
4	J	242	TRP	CD2-CE2	31.73	1.79	1.41
4	J	242	TRP	CE2-CZ2	30.77	1.92	1.39
4	J	242	TRP	CZ3-CH2	26.52	1.82	1.40
4	J	242	TRP	CE3-CZ3	26.23	1.83	1.38

The worst 5 of 960 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	364	ARG	NE-CZ-NH2	-21.14	109.73	120.30
6	V	661	ARG	NE-CZ-NH1	20.07	130.33	120.30
4	J	571	ARG	NE-CZ-NH1	20.02	130.31	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	L	410	ARG	NE-CZ-NH1	19.87	130.23	120.30
4	J	501	ARG	NE-CZ-NH1	18.54	129.57	120.30

There are no chirality outliers.

5 of 146 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	269	TYR	Sidechain
1	A	284	TYR	Sidechain
1	A	326	TYR	Sidechain
1	A	365	TYR	Sidechain
1	A	395	TYR	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	A	2211	0	2199	6	0
1	C	2014	0	1998	5	0
1	E	2038	0	2031	5	0
1	G	2014	0	1998	6	0
2	B	2363	0	2379	6	0
2	D	2059	0	2080	8	0
2	F	1964	0	1988	8	0
2	H	2135	0	2160	4	0
2	O	753	0	779	1	0
2	Q	878	0	903	1	0
2	R	794	0	814	1	0
2	S	878	0	903	4	0
2	T	753	0	779	3	0
3	I	2325	0	2335	34	0
3	K	2325	0	2335	9	0
4	J	2909	0	2916	42	0
5	L	3794	0	3844	6	0
6	U	634	0	635	2	0
6	V	634	0	635	1	0
6	W	634	0	635	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	X	634	0	635	0	0
7	o	403	0	426	0	0
7	p	429	0	446	0	0
7	q	432	0	457	0	0
7	r	454	0	477	0	0
7	s	451	0	476	0	0
7	t	446	0	471	0	0
All	All	37358	0	37734	120	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 2.

The worst 5 of 120 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:242:TRP:CZ3	4:J:242:TRP:CE3	1.83	1.66
4:J:242:TRP:CZ2	4:J:242:TRP:CH2	1.87	1.61
4:J:242:TRP:CZ3	4:J:242:TRP:CH2	1.82	1.59
4:J:242:TRP:CZ2	4:J:242:TRP:CE2	1.92	1.57
4:J:242:TRP:CE3	4:J:242:TRP:CD2	1.93	1.56

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	271/896 (30%)	250 (92%)	14 (5%)	7 (3%)	4 26
1	C	244/896 (27%)	217 (89%)	21 (9%)	6 (2%)	4 27
1	E	247/896 (28%)	229 (93%)	12 (5%)	6 (2%)	5 28
1	G	244/896 (27%)	232 (95%)	11 (4%)	1 (0%)	30 67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	290/906 (32%)	261 (90%)	20 (7%)	9 (3%)	3	23
2	D	248/906 (27%)	224 (90%)	17 (7%)	7 (3%)	4	25
2	F	236/906 (26%)	214 (91%)	13 (6%)	9 (4%)	2	20
2	H	257/906 (28%)	227 (88%)	20 (8%)	10 (4%)	2	19
2	O	91/906 (10%)	85 (93%)	5 (6%)	1 (1%)	12	46
2	Q	107/906 (12%)	97 (91%)	6 (6%)	4 (4%)	2	21
2	R	96/906 (11%)	90 (94%)	4 (4%)	2 (2%)	5	31
2	S	107/906 (12%)	96 (90%)	8 (8%)	3 (3%)	4	25
2	T	91/906 (10%)	85 (93%)	4 (4%)	2 (2%)	5	30
3	I	281/666 (42%)	255 (91%)	20 (7%)	6 (2%)	5	31
3	K	281/666 (42%)	259 (92%)	13 (5%)	9 (3%)	3	22
4	J	342/1019 (34%)	317 (93%)	15 (4%)	10 (3%)	3	24
5	L	462/1698 (27%)	422 (91%)	26 (6%)	14 (3%)	3	23
6	U	73/671 (11%)	73 (100%)	0	0	100	100
6	V	73/671 (11%)	72 (99%)	0	1 (1%)	9	40
6	W	73/671 (11%)	71 (97%)	1 (1%)	1 (1%)	9	40
6	X	73/671 (11%)	72 (99%)	1 (1%)	0	100	100
7	o	50/72 (69%)	50 (100%)	0	0	100	100
7	p	54/72 (75%)	54 (100%)	0	0	100	100
7	q	54/72 (75%)	53 (98%)	1 (2%)	0	100	100
7	r	57/72 (79%)	54 (95%)	1 (2%)	2 (4%)	3	21
7	s	57/72 (79%)	54 (95%)	3 (5%)	0	100	100
7	t	56/72 (78%)	55 (98%)	1 (2%)	0	100	100
All	All	4515/18903 (24%)	4168 (92%)	237 (5%)	110 (2%)	7	28

5 of 110 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	ASP
1	A	428	ASP
2	B	312	LEU
2	D	314	ARG
2	F	281	ALA

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	A	244/824 (30%)	232 (95%)	12 (5%)	21	43
1	C	221/824 (27%)	213 (96%)	8 (4%)	30	52
1	E	224/824 (27%)	213 (95%)	11 (5%)	21	43
1	G	221/824 (27%)	215 (97%)	6 (3%)	40	60
2	B	260/798 (33%)	246 (95%)	14 (5%)	18	41
2	D	227/798 (28%)	219 (96%)	8 (4%)	31	53
2	F	217/798 (27%)	202 (93%)	15 (7%)	13	34
2	H	236/798 (30%)	224 (95%)	12 (5%)	20	43
2	O	82/798 (10%)	81 (99%)	1 (1%)	67	79
2	Q	96/798 (12%)	93 (97%)	3 (3%)	35	56
2	R	87/798 (11%)	86 (99%)	1 (1%)	70	80
2	S	96/798 (12%)	89 (93%)	7 (7%)	11	32
2	T	82/798 (10%)	79 (96%)	3 (4%)	29	51
3	I	259/595 (44%)	241 (93%)	18 (7%)	13	34
3	K	259/595 (44%)	247 (95%)	12 (5%)	23	46
4	J	326/933 (35%)	313 (96%)	13 (4%)	27	49
5	L	431/1539 (28%)	417 (97%)	14 (3%)	34	55
6	U	72/598 (12%)	69 (96%)	3 (4%)	25	48
6	V	72/598 (12%)	70 (97%)	2 (3%)	38	59
6	W	72/598 (12%)	69 (96%)	3 (4%)	25	48
6	X	72/598 (12%)	70 (97%)	2 (3%)	38	59
7	o	48/62 (77%)	46 (96%)	2 (4%)	25	48
7	p	51/62 (82%)	51 (100%)	0	100	100
7	q	51/62 (82%)	51 (100%)	0	100	100
7	r	54/62 (87%)	52 (96%)	2 (4%)	29	51
7	s	53/62 (86%)	50 (94%)	3 (6%)	17	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
7	t	53/62 (86%)	53 (100%)	0	100 100
All	All	4166/16904 (25%)	3991 (96%)	175 (4%)	27 48

5 of 175 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	J	681	THR
2	O	45	PRO
3	K	117	LEU
5	L	240	ASN
2	S	66	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
3	K	180	HIS
5	L	413	HIS
7	r	46	ASN
3	K	193	HIS
5	L	105	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

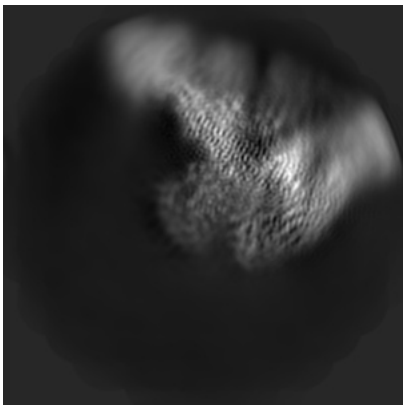
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-52729. These allow visual inspection of the internal detail of the map and identification of artifacts.

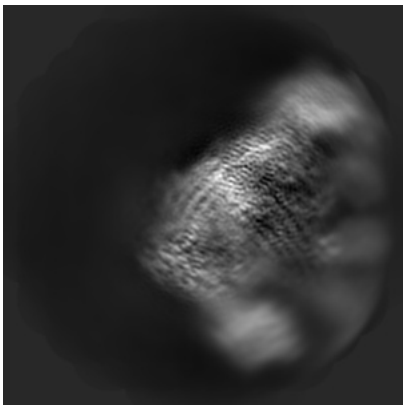
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

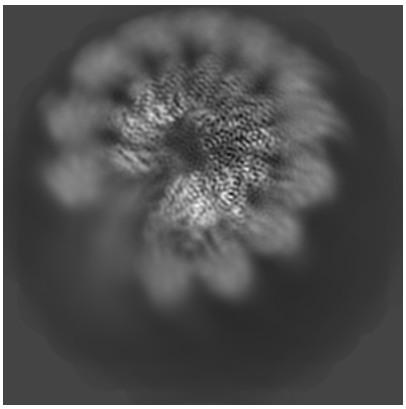
6.1.1 Primary map



X

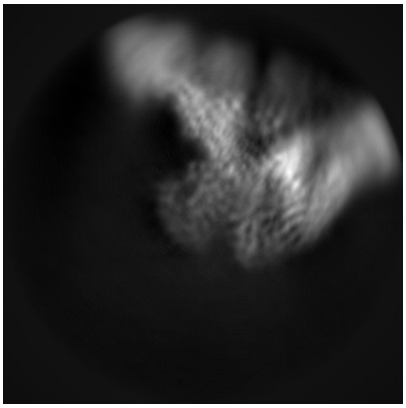


Y

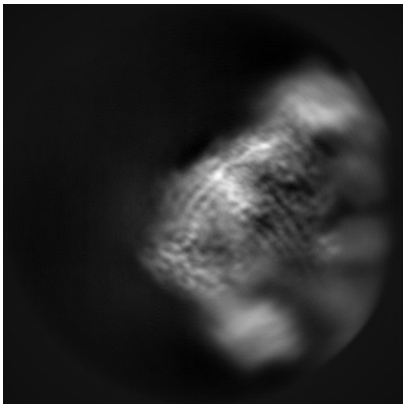


Z

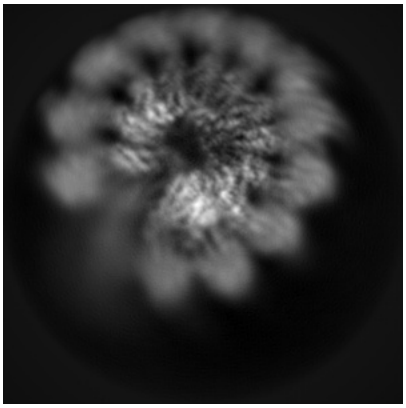
6.1.2 Raw map



X



Y

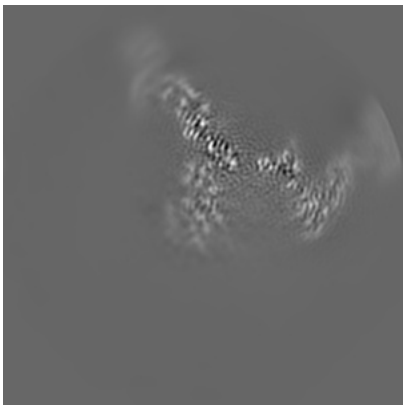


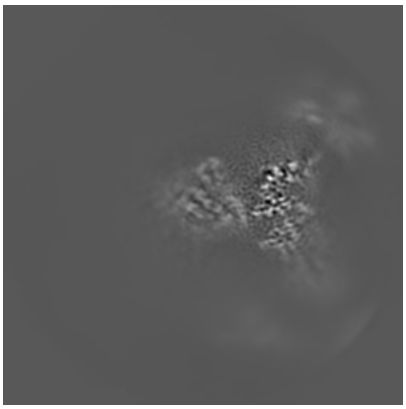
Z

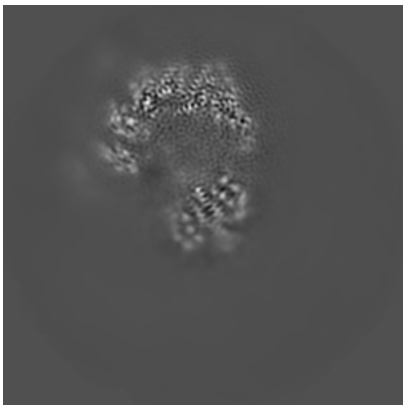
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

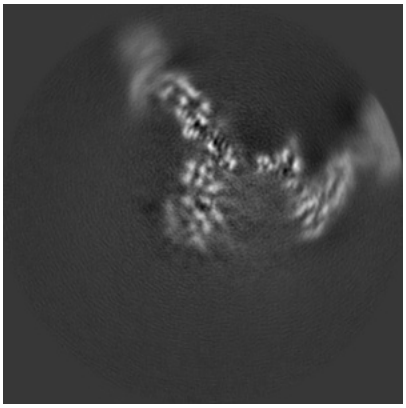
6.2.1 Primary map

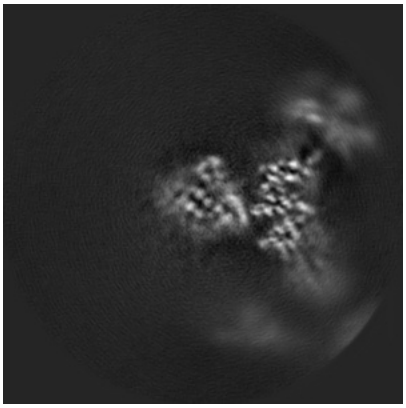

X Index: 128

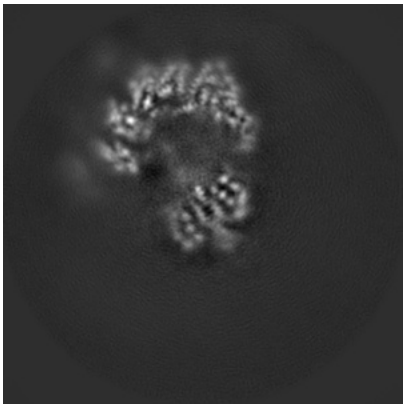

Y Index: 128


Z Index: 128

6.2.2 Raw map


X Index: 128


Y Index: 128

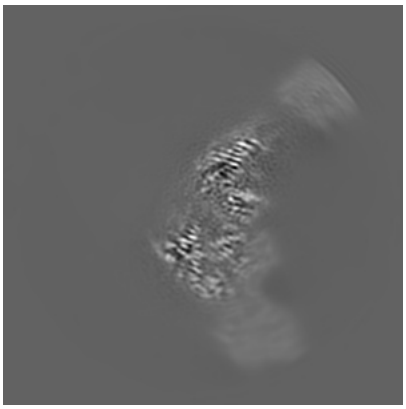

Z Index: 128

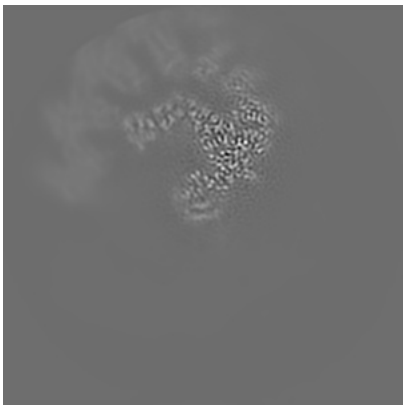
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

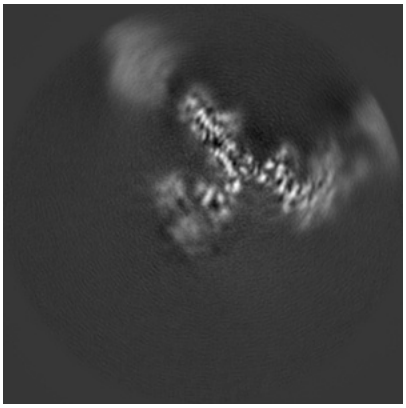
6.3.1 Primary map

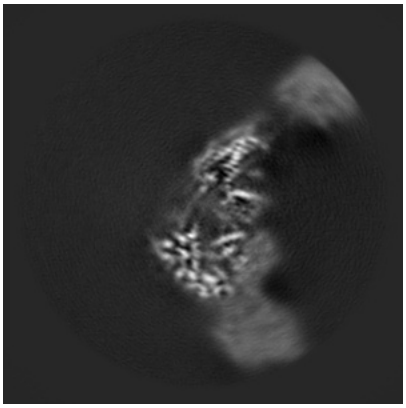
X Index: 148

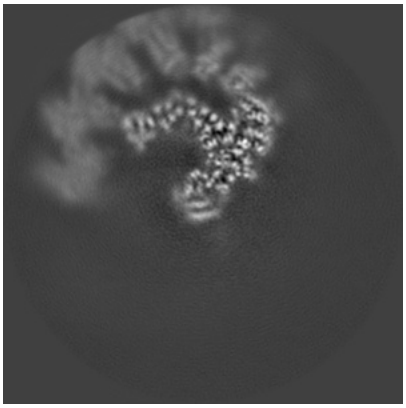

Y Index: 184


Z Index: 150

6.3.2 Raw map


X Index: 145

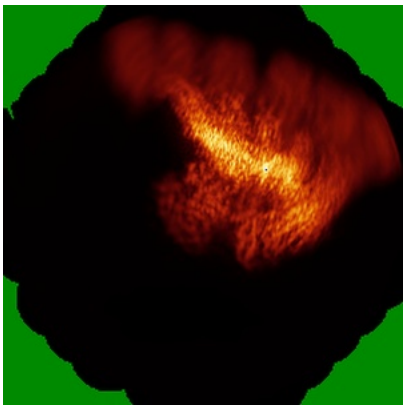

Y Index: 183

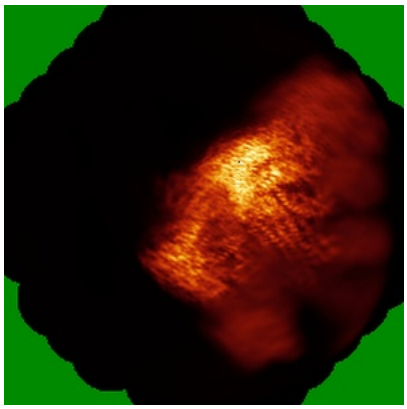

Z Index: 151

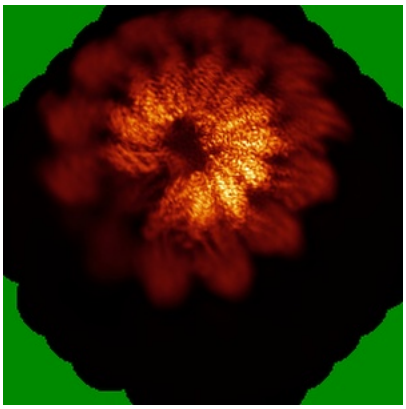
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

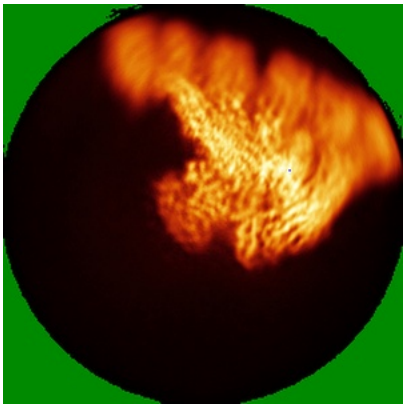
6.4.1 Primary map

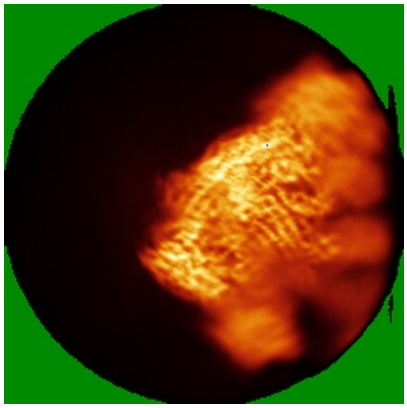

X

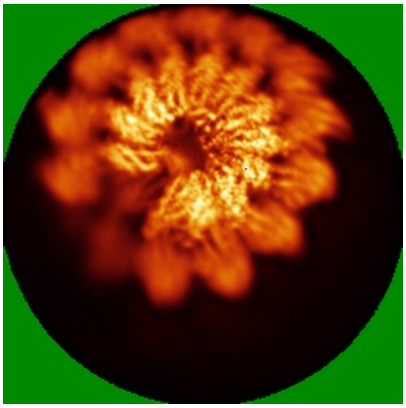

Y


Z

6.4.2 Raw map


X


Y


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0421. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

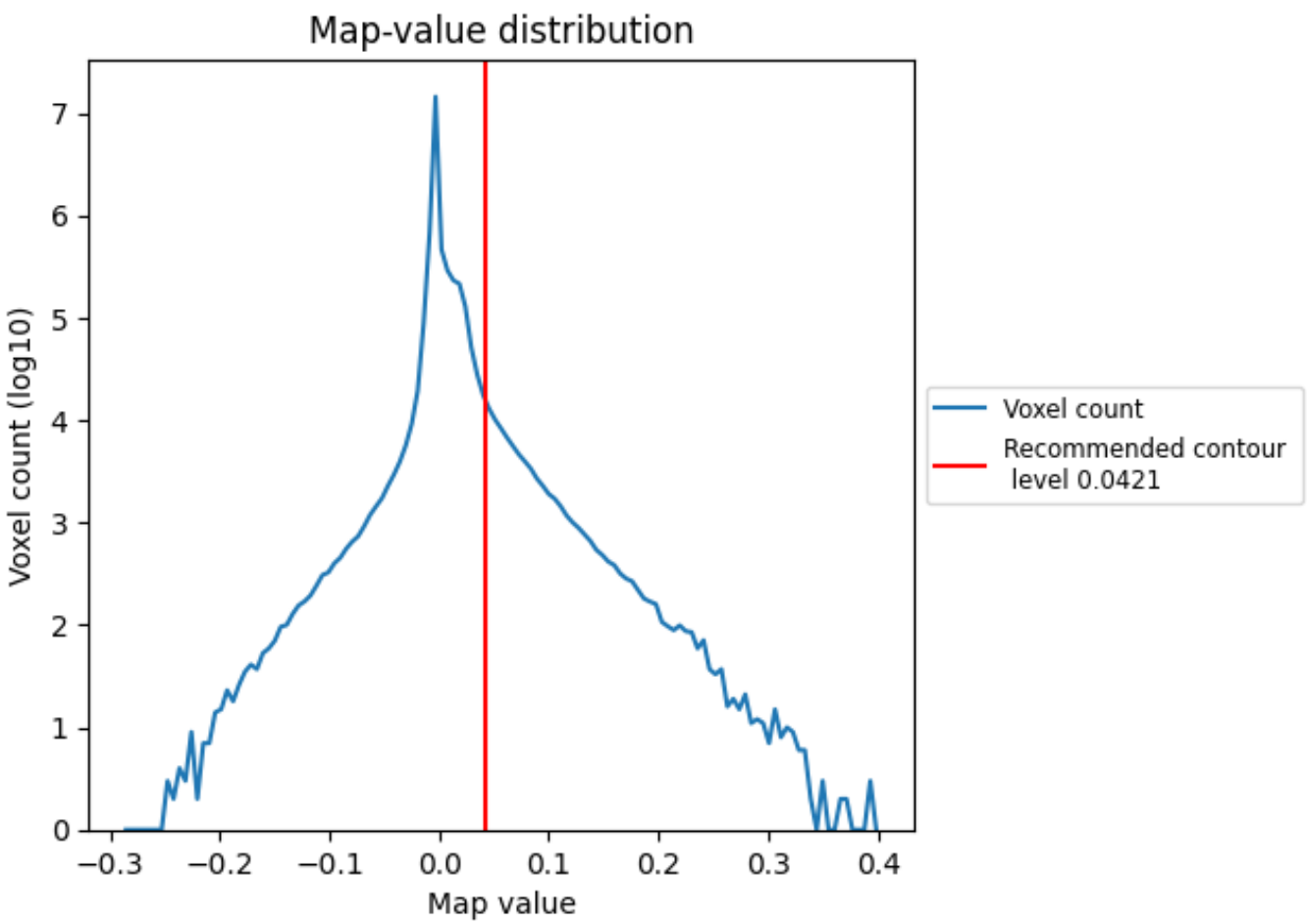
6.6 Mask visualisation (i)

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

7 Map analysis (i)

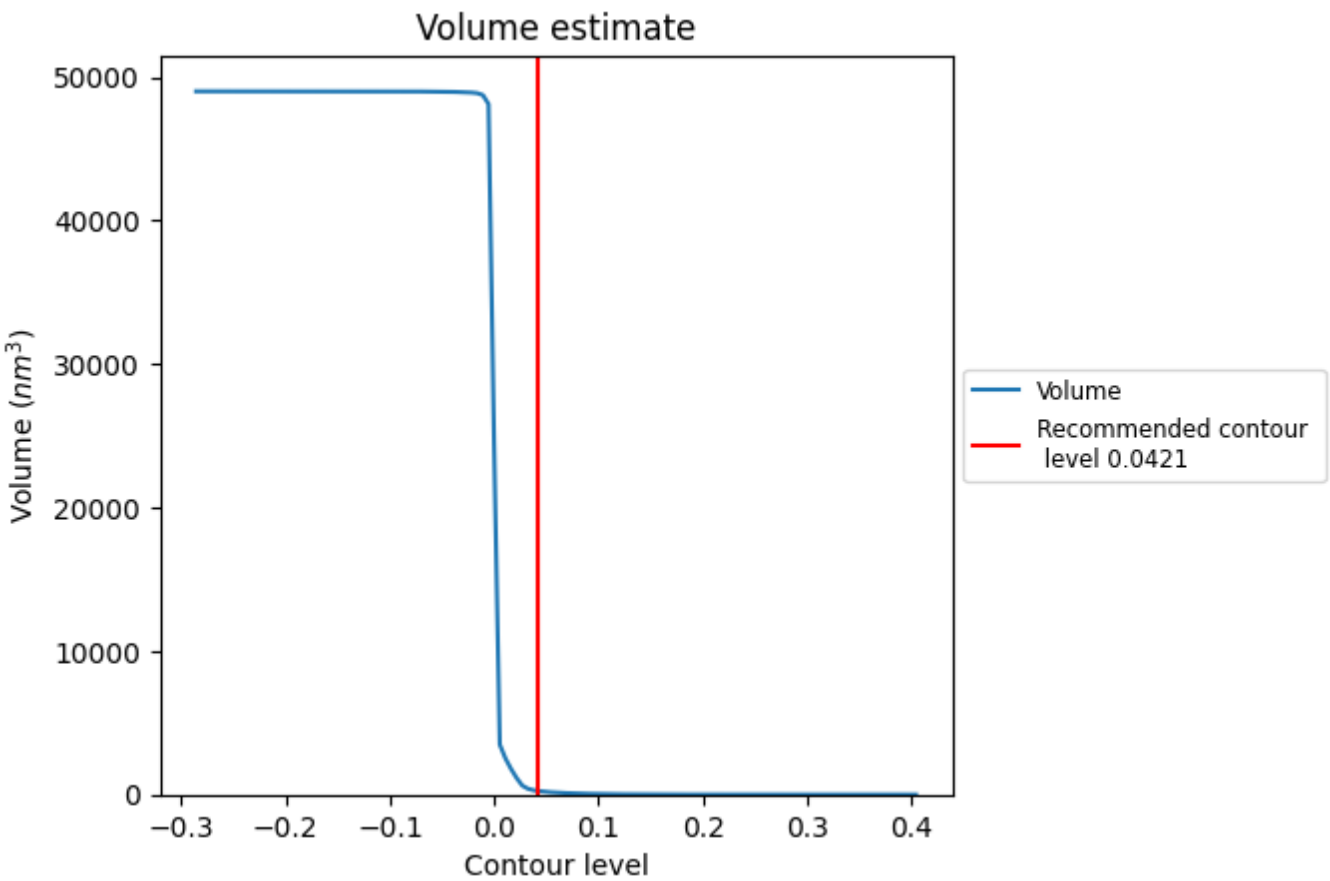
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

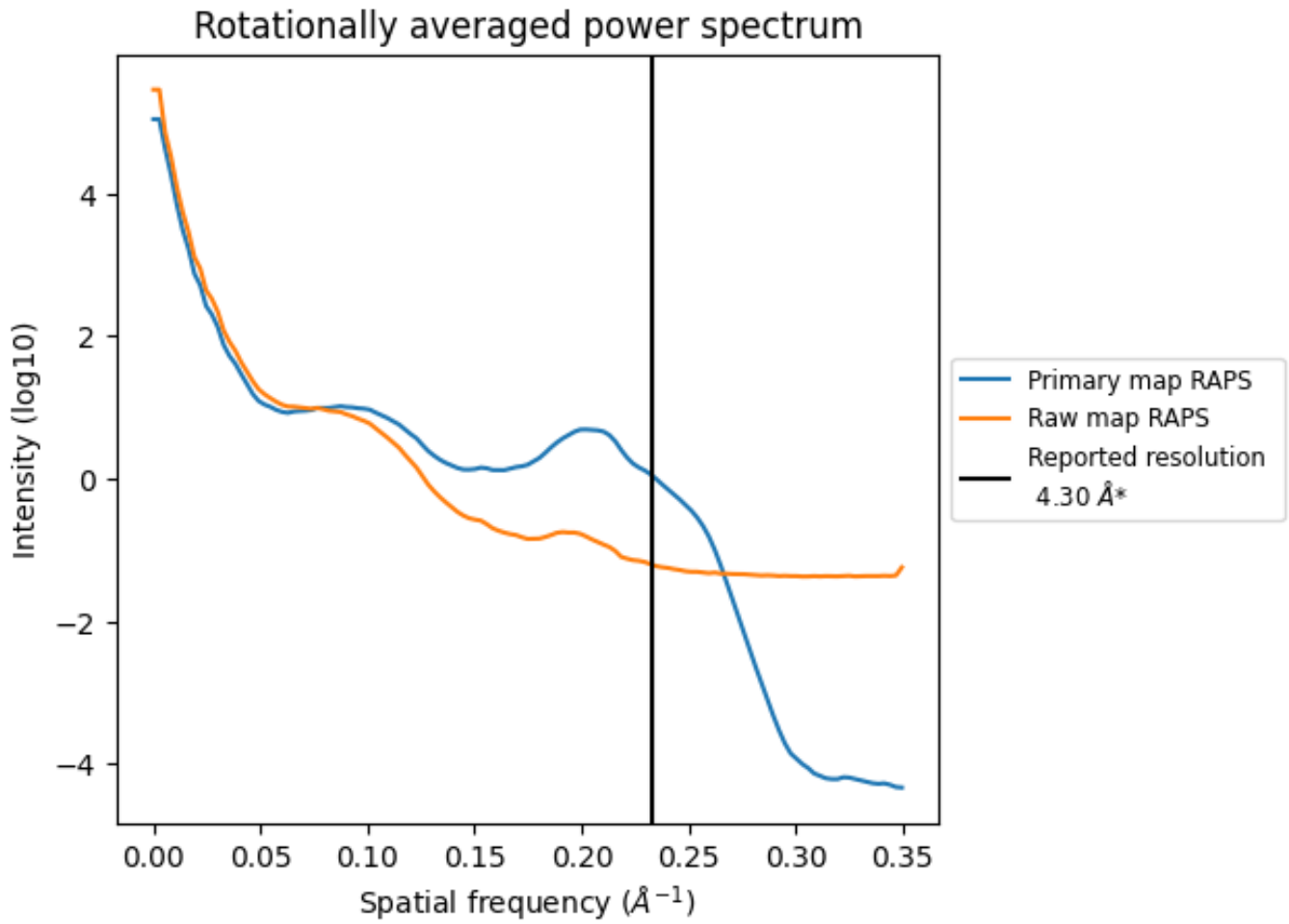
7.2 Volume estimate (i)



The volume at the recommended contour level is 252 nm^3; this corresponds to an approximate mass of 227 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)

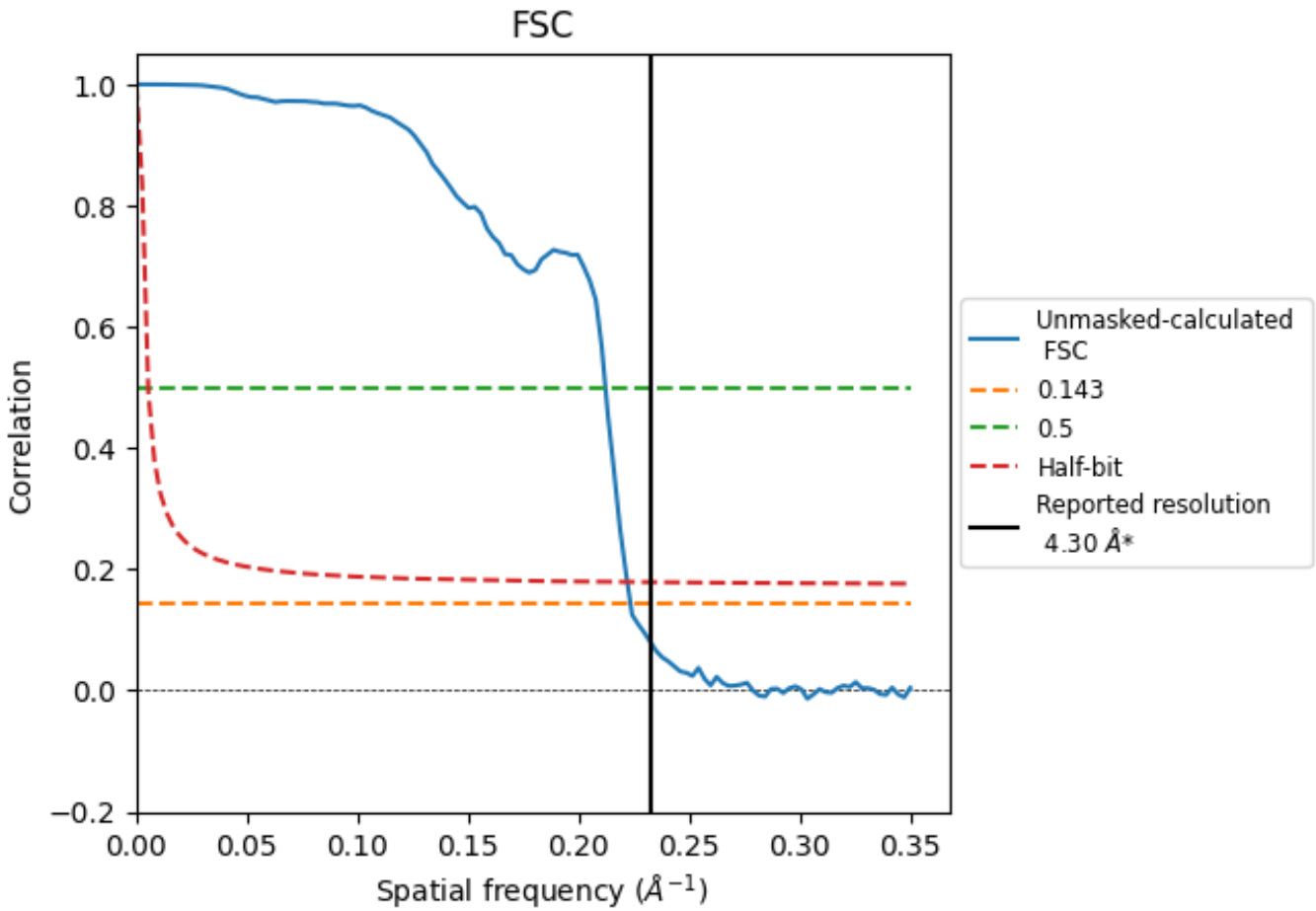


*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

8.2 Resolution estimates (i)

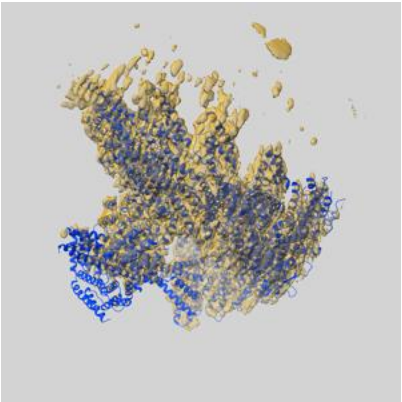
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	4.72	4.50

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

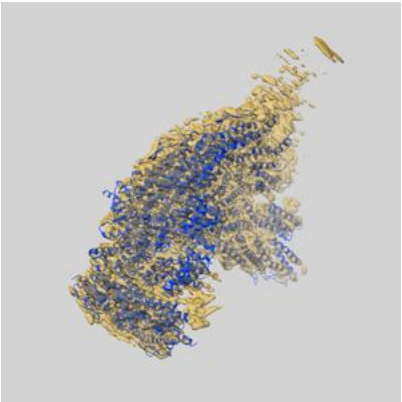
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-52729 and PDB model 9I8M. Per-residue inclusion information can be found in section 3 on page 7.

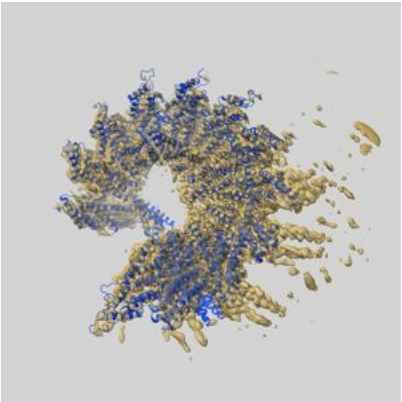
9.1 Map-model overlay (i)



X



Y



Z

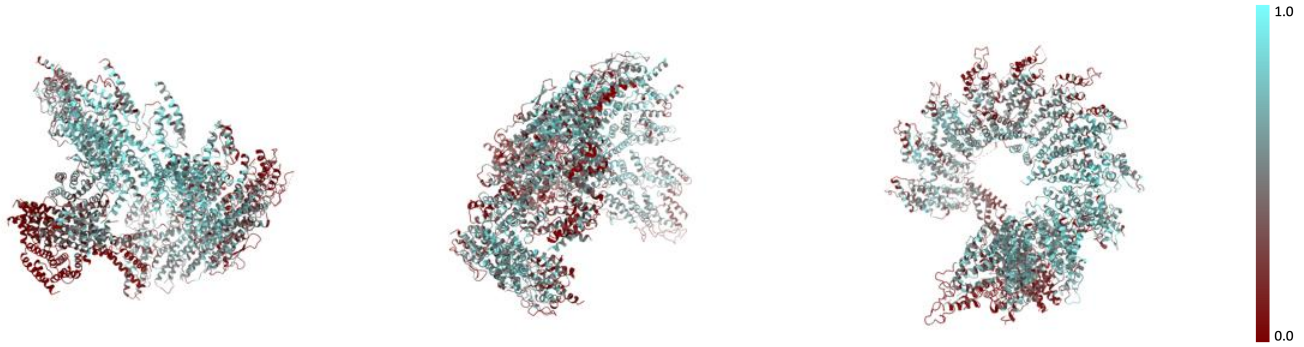
The images above show the 3D surface view of the map at the recommended contour level 0.0421 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)

X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

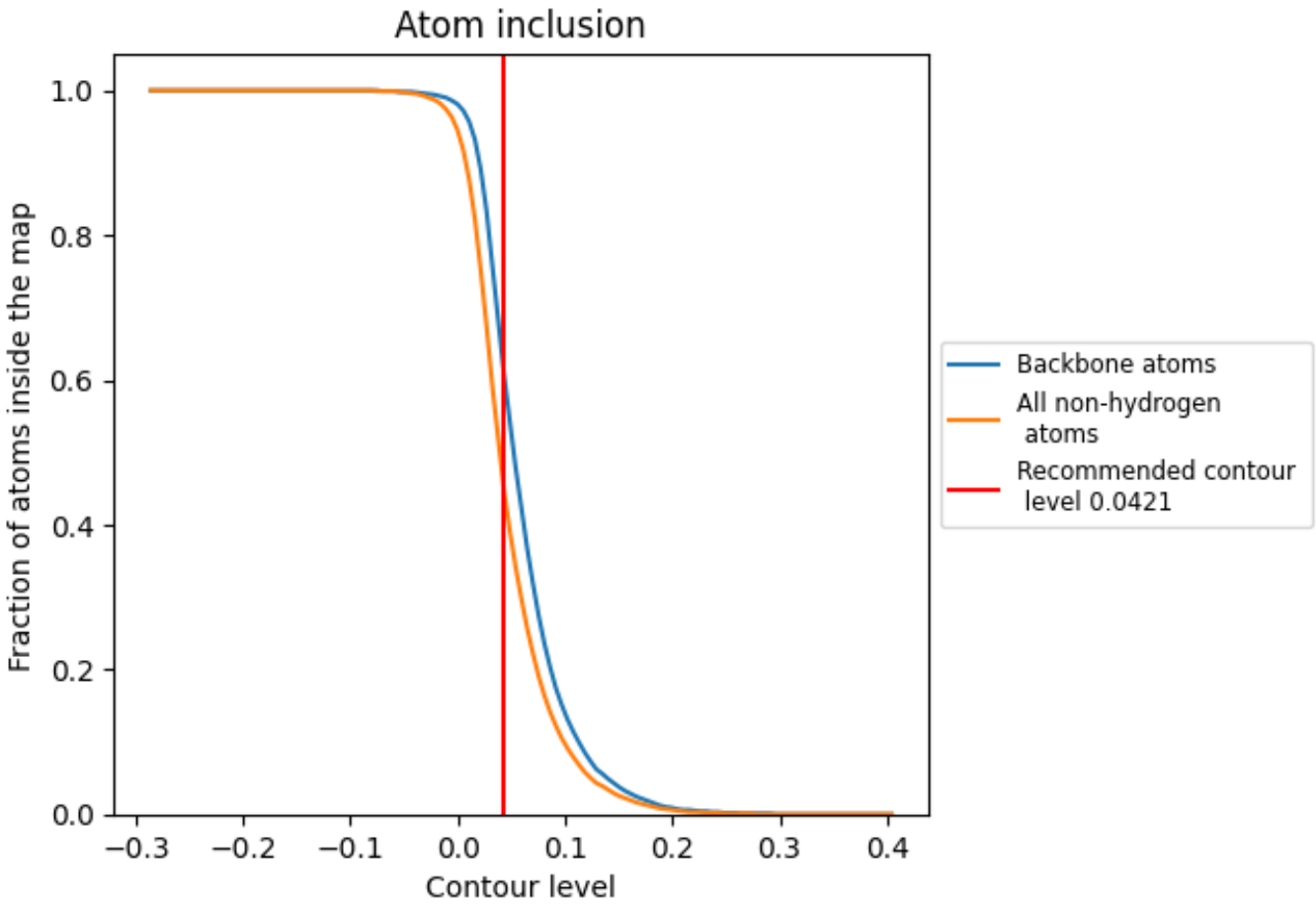
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0421).

9.4 Atom inclusion (i)



At the recommended contour level, 62% of all backbone atoms, 46% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0421) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4610	0.1990
A	0.4370	0.1340
B	0.4790	0.1530
C	0.5550	0.1810
D	0.3590	0.1690
E	0.3630	0.1960
F	0.3810	0.2020
G	0.5550	0.2200
H	0.6540	0.2460
I	0.6440	0.2650
J	0.6320	0.2690
K	0.5640	0.2530
L	0.4320	0.2020
O	0.6400	0.2920
Q	0.1310	0.1250
R	0.3820	0.1750
S	0.4280	0.1670
T	0.0490	0.0990
U	0.3300	0.1960
V	0.2790	0.1550
W	0.2160	0.1210
X	0.1970	0.1160
o	0.6900	0.3130
p	0.4750	0.2310
q	0.1470	0.0950
r	0.4640	0.1750
s	0.5460	0.1970
t	0.0230	0.1270