wwPDB EM Validation Summary Report (i)

Mar 5, 2026 – 01:06 PM UTC

PDB ID	:	9I8M / pdb_00009i8m
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:

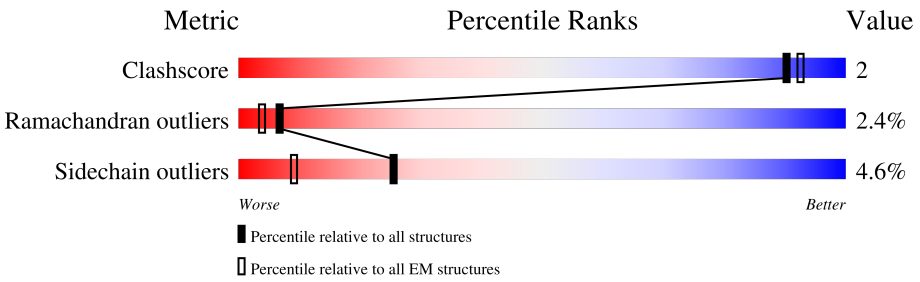
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

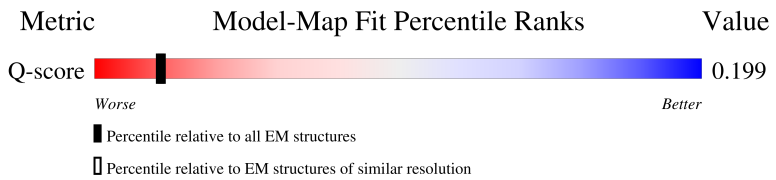
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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% 14% 14% • 69%
1	C	896	7% 13% 13% • 72%
1	E	896	16% 12% 14% • 72%
1	G	896	7% 14% 12% • 72%

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Mol	Chain	Length	Quality of chain
2	B	906	12% 17% 14% 68%
2	D	906	15% 13% 13% 72%
2	F	906	14% 12% 13% 73%
2	H	906	14% 12% 71%
2	O	906	7% 90%
2	Q	906	11% 5% 6% 88%
2	R	906	6% 6% 89%
2	S	906	6% 5% 6% 88%
2	T	906	10% 5% 90%
3	I	666	6% 21% 19% 57%
3	K	666	10% 21% 19% 57%
4	J	1019	6% 16% 15% 65%
5	L	1698	12% 13% 13% 72%
6	U	671	7% 5% 5% 89%
6	V	671	7% 5% 6% 89%
6	W	671	8% 5% 5% 89%
6	X	671	8% 7% 89%
7	o	72	8% 36% 31% 6% 28%
7	p	72	29% 40% 36% 22%
7	q	72	65% 42% 33% 22%
7	r	72	26% 36% 40% 18%
7	s	72	15% 40% 36% 6% 18%
7	t	72	81% 36% 40% 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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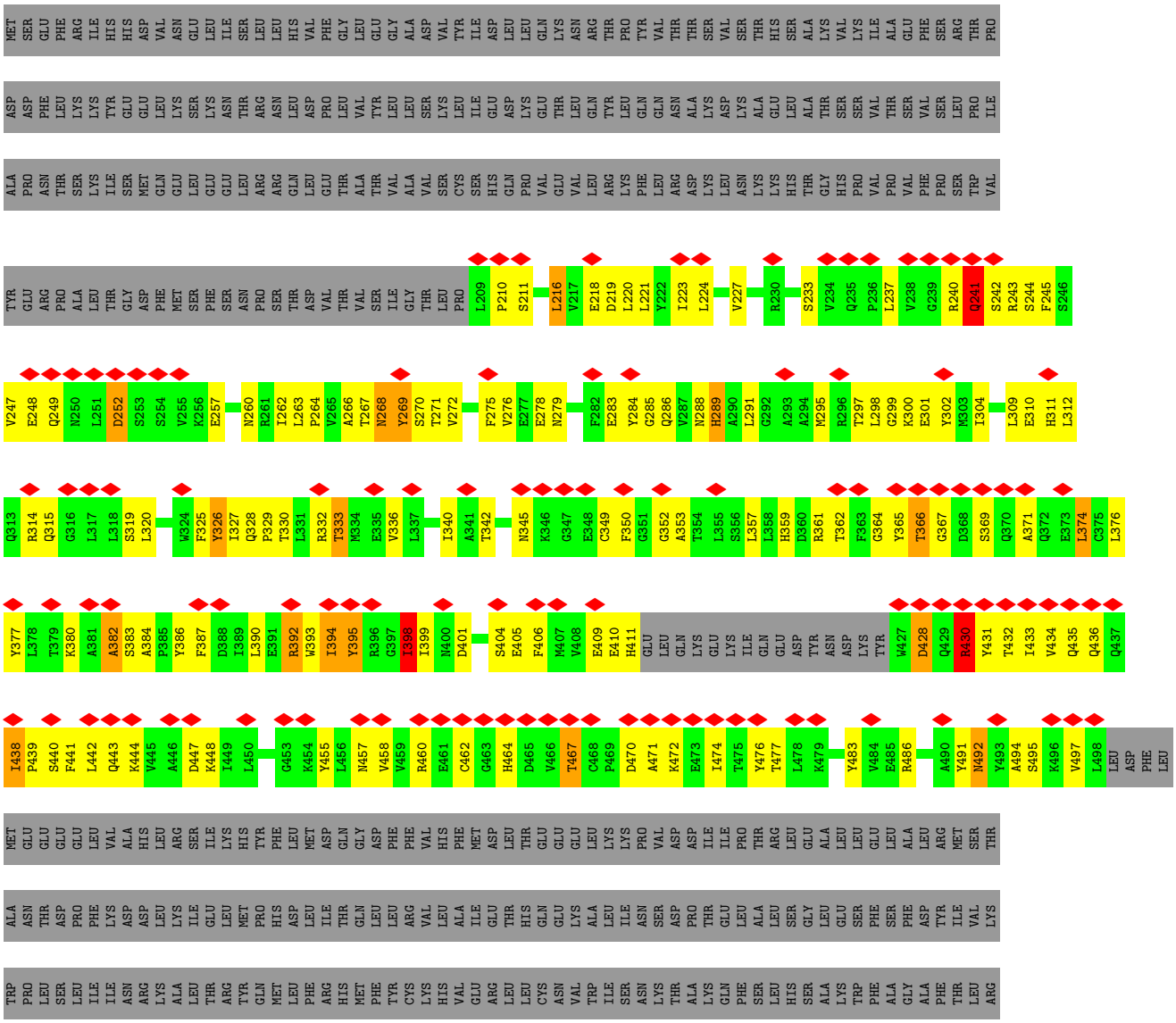
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	q	56	432	266	76	86	4	0	0
			Total	C	N	O	S		
7	r	59	454	278	80	91	5	0	0
			Total	C	N	O	S		
7	s	59	451	277	79	90	5	0	0
			Total	C	N	O	S		
7	t	58	446	274	78	89	5	0	0

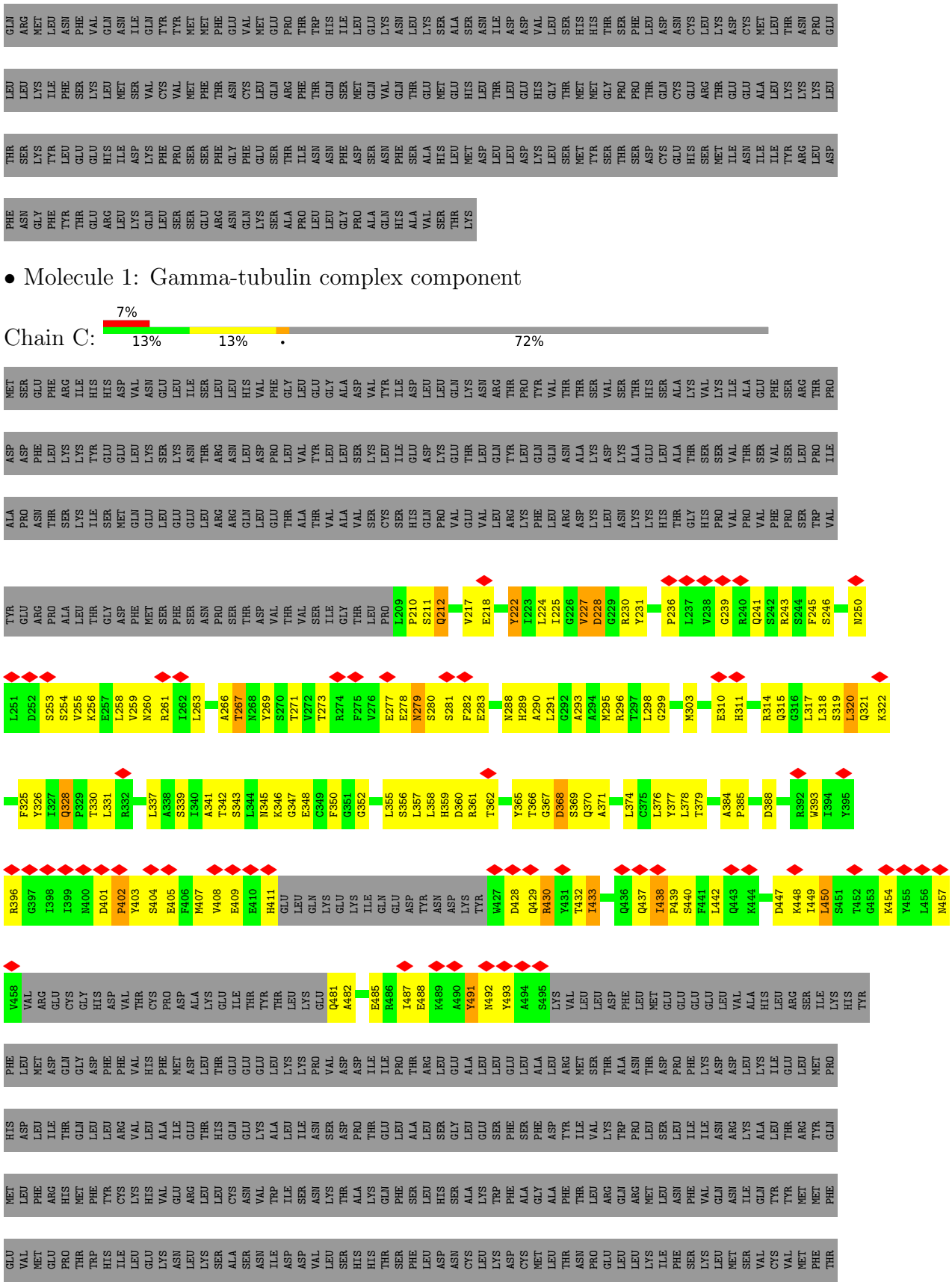
3 Residue-property plots (i)

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

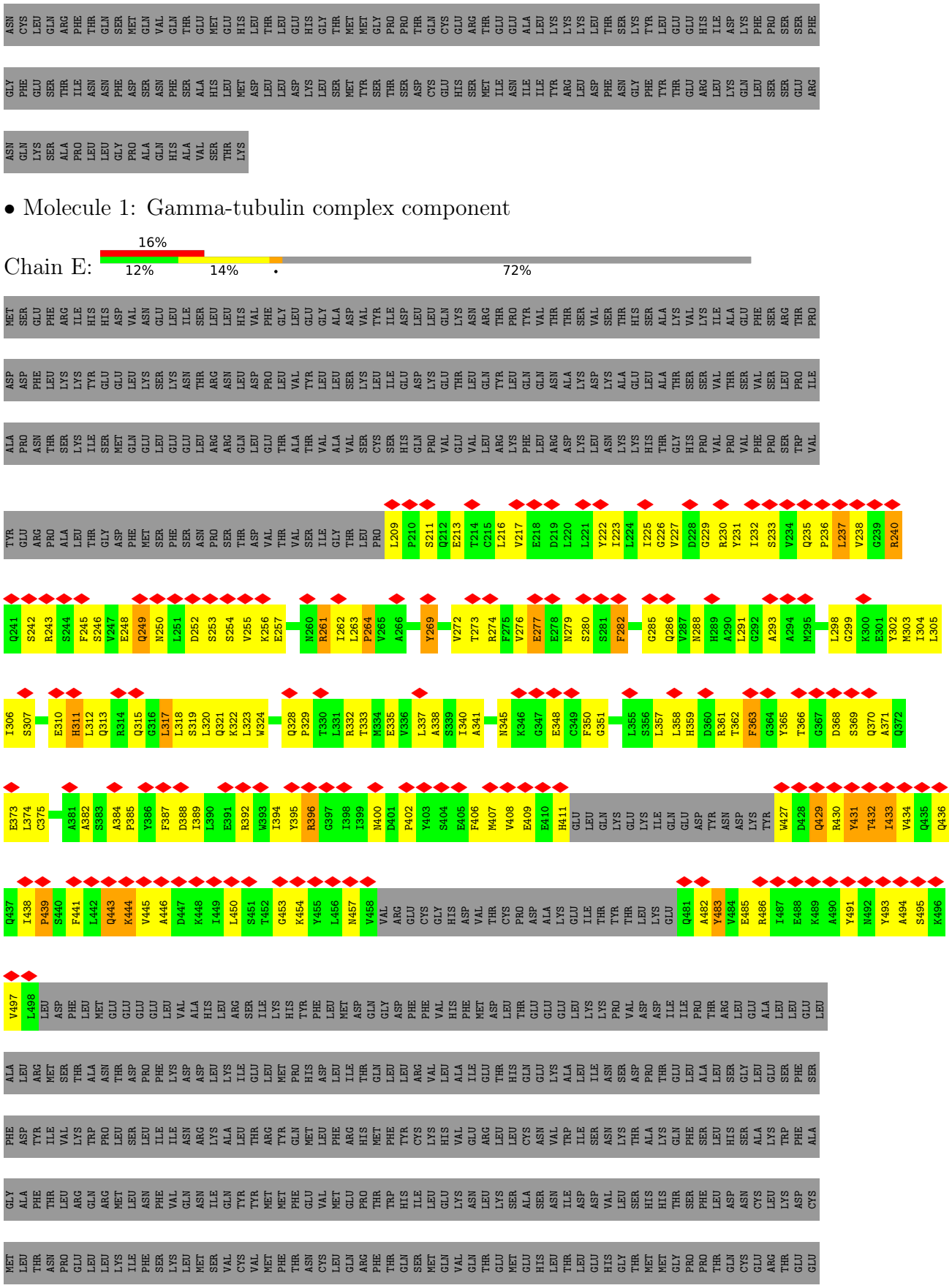
Chain A: 13% 14% 14% • 69%





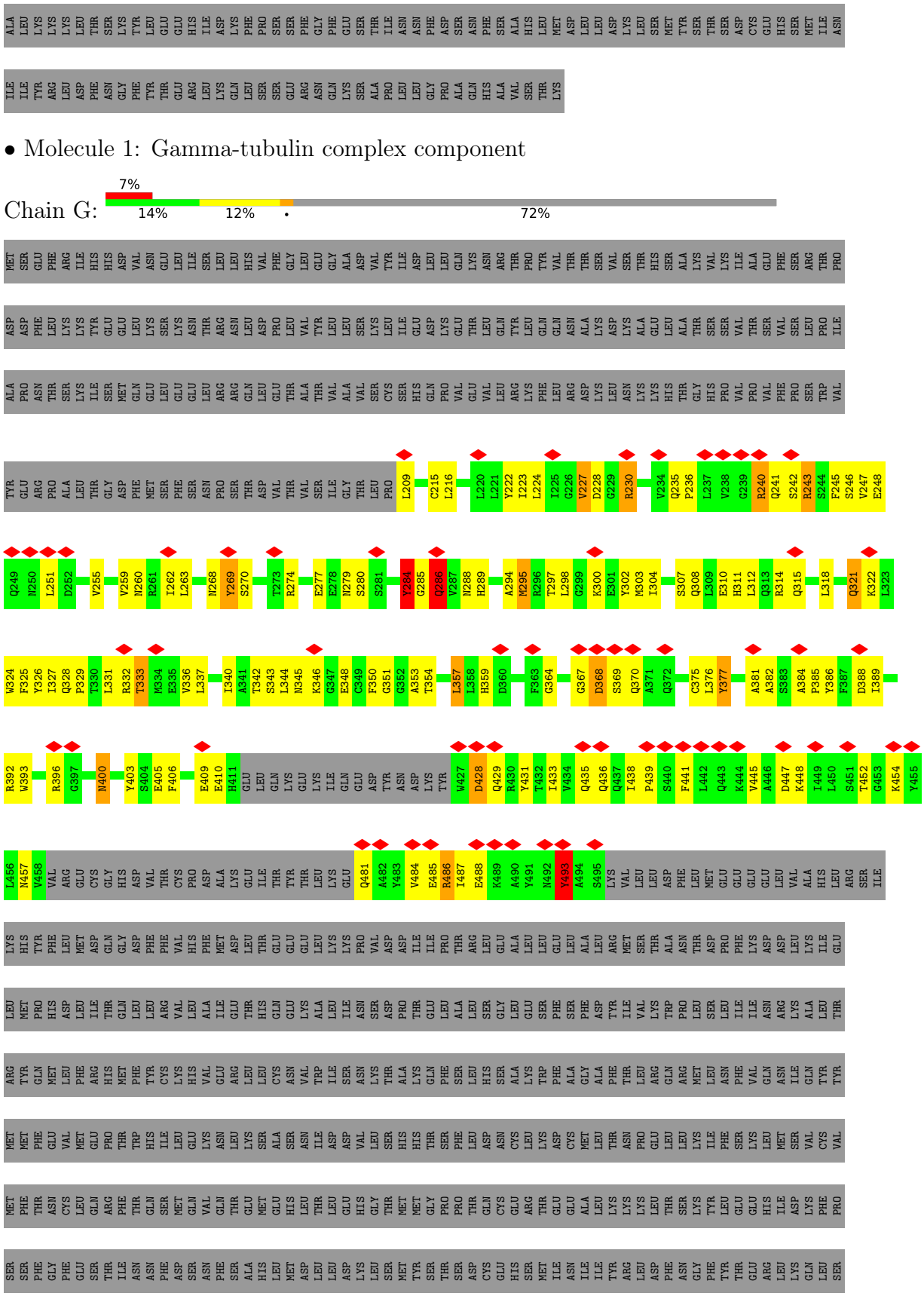
- Molecule 1: Gamma-tubulin complex component

Chain C: 7% 13% 13% • 72%



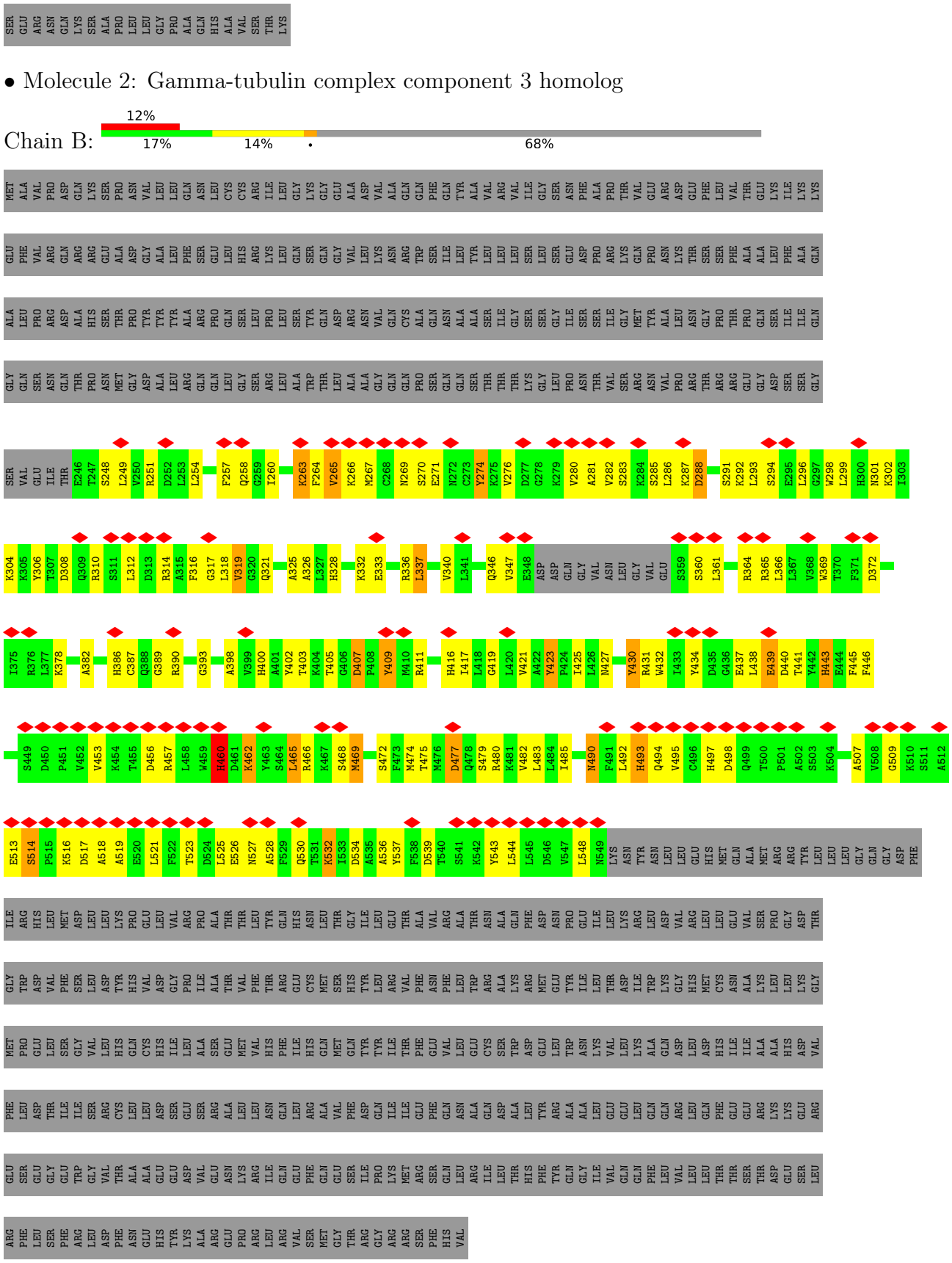
• Molecule 1: Gamma-tubulin complex component

Chain E: 16% 12% 14% • 72%



• Molecule 1: Gamma-tubulin complex component

Chain G: 7% 14% 12% • 72%


SER GLU ARG ASN GLN LYS SER ALA PRO LEU LEU GLY PRO ALA GLN HIS ALA VAL SER THR LYS
• Molecule 2: Gamma-tubulin complex component 3 homolog
Chain B:
12%
17%
14%
68%
MET ALA VAL PRO ASP GLN LYS SER PRO ASN VAL LEU LEU GLN ASN LEU CYS CYS ARG ILE LEU GLY LYS GLY GLU ALA ASP VAL ALA GLN GLN PHE GLN TYR ALA VAL ARG VAL ILE GLY SER ASN PHE ALA PRO THR VAL GLU ARG ASP GLU PHE LEU VAL THR GLU LYS ILE LYS LYS
GLU PHE VAL ARG GLN ARG ARG GLU ALA ASP GLY ALA LEU PHE SER GLU LEU HIS ARG LYS LEU GLN SER GLN GLY GLY VAL LEU LYS ASN ARG TRP SER ILE LEU TYR LEU LEU LEU SER LEU SER GLU ASP PRO ARG LYS GLN PRO ASN LYS THR SER SER PHE ALA ALA LEU PHE ALA GLN
ALA LEU PRO ARG ASP ALA HIS SER THR PRO TYR TYR TYR ALA ARG PRO GLN SER LEU PRO LEU SER SER TYR GLN ASP ARG ASN VAL GLN CYS ALA GLN ASN ALA ALA SER ILE GLY SER SER GLY ILE SER SER ILE GLY MET TYR ALA LEU ASN GLY PRO THR PRO GLN SER ILE ILE GLN
GLY GLN SER ASN GLN THR PRO ASN MET GLY ASP ALA LEU ARG GLN GLN LEU GLY SER ARG LEU ALA TRP THR LEU ALA ALA GLY GLN GLN PRO SER GLN SER SER THR THR THR LYS GLY LEU PRO ASN THR VAL SER ARG ASN VAL PRO ARG THR ARG ARG GLU GLY ASP SER SER GLY
SER VAL GLU ILE THR E246 T247 S248 L249 V250 R251 D252 L253 L254 F257 Q258 G259 I260 K263 F264 V265 K266 M267 C268 N269 S270 E271 N272 C273 Y274 K275 V276 D277 G278 K279 V280 A281 V282 S283 K284 S285 L286 K287 D288 S291 K292 L293 S294 E295 L296 G297 W298 L299 H300 N301 K302 I303
K304 K305 Y306 T307 D308 Q309 R310 S311 L312 D313 R314 A315 F316 G317 L318 V319 G320 Q321 A325 A326 L327 H328 K332 E333 R336 L337 V340 L341 Q346 V347 E348 ASP ASP GLN GLY VAL ASN LEU GLY VAL GLU S359 S360 L361 R364 R365 L366 L367 V368 W369 T370 F371 D372
I375 R376 L377 K378 A382 H386 C387 Q388 G389 R390 G393 A398 V399 H400 A401 Y402 T403 K404 T405 G406 D407 P408 Y409 M410 R411 H416 I417 I418 G419 L420 V421 A422 Y423 P424 I425 L426 N427 Y430 R431 W432 I433 Y434 D435 G436 E437 L438 E439 D440 T441 Y442 H443 E444 F445 F446
S449 D450 P451 V452 V453 K454 T455 D456 R457 L458 W459 H460 D461 K462 Y463 S464 L465 R466 K467 S468 M469 S472 F473 M474 T475 M476 D477 Q478 S479 R480 K481 V482 L483 L484 I485 N490 F491 L492 H493 Q494 V495 C496 H497 D498 Q499 T500 P501 A502 S503 K504 A507 V508 G509 K510 S511 A512
E513 S514 P515 K516 D517 A518 A519 E520 L521 F522 T523 D524 L525 E526 N527 A528 F529 Q530 T531 K532 I533 D534 A535 A536 Y537 F538 D539 T540 S541 K542 Y543 L544 L545 D546 V547 L548 N549 LYS ASN TYR ASN LEU LEU GLU HIS MET GLN ALA MET ARG ARG TYR LEU LEU LEU GLY GLN GLY ASP PHE
ILE ARG HIS LEU MET ASP LEU LEU LYS PRO GLU LEU VAL ARG PRO ALA THR THR LEU TYR GLN HIS ASN LEU THR GLY ILE LEU GLU THR ALA VAL ARG ALA THR ASN ALA GLN PHE ASP ASN PRO GLU ILE LEU LEU LYS ARG LEU ASP VAL ARG LEU LEU GLU VAL SER PRO GLY ASP THR
GLY TRP ASP VAL PHE SER LEU ASP TYR HIS VAL ASP GLY PRO ILE ALA THR VAL PHE THR ARG GLU CYS MET SER HIS TYR LEU ARG VAL PHE ASN PHE LEU TRP ARG ALA LYS ARG MET GLU TYR ILE LEU THR ASP ILE TRP LYS GLY HIS MET CYS ASN ALA LYS LEU LEU LYS GLY
MET PRO GLU LEU SER GLY VAL LEU HIS GLN CYS HIS ILE LEU ALA SER GLU MET VAL HIS PHE ILE HIS GLN MET GLN TYR TYR ILE THR PHE GLU VAL LEU CYS SER TRP ASP GLU LEU TRP ASN LYS VAL LEU LYS ALA GLN ASP LEU ASP HIS ILE ILE ALA ALA HIS ASP VAL
PHE LEU ASP THR ILE ILE SER ARG CYS LEU LEU ASP SER GLU SER ARG ALA LEU LEU ASN GLN LEU ARG ALA VAL PHE ASP GLN ILE ILE GLU PHE GLN GLN ASN ALA GLN ASP ALA LEU TYR ARG ALA ALA LEU GLU GLU LEU GLN GLN ARG LEU GLN PHE GLU GLU ARG LYS LYS GLU ARG
GLU SER GLU GLY GLU TRP GLY VAL THR ALA ALA GLU GLU ASP VAL GLU ASN LYS ARG ILE GLN GLU PHE GLN GLU SER ILE PRO LYS MET ARG SER GLN LEU ARG ILE LEU THR HIS PHE TYR GLN GLY ILE VAL GLN GLN PHE LEU VAL LEU LEU THR THR SER THR ASP GLU SER LEU
ARG PHE LEU SER PHE ARG LEU ASP PHE ASN GLU HIS TYR LYS ALA ARG GLU PRO ARG LEU ARG VAL SER MET GLY THR ARG GLY ARG ARG SER PHE HIS VAL
• Molecule 2: Gamma-tubulin complex component 3 homolog

Chain D: 15% 13% 13% • 72%

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

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

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

GLY GLN SER ASN GLN THR PRO ASN MET GLY ASP ALA LEU ARG GLN GLN LEU GLY SER ARG LEU ALA TRP THR LEU ALA ALA GLY GLN GLN PRO SER GLN GLN SER THR THR THR LYS GLY LEU PRO ASN THR VAL SER ARG ASN VAL PRO ARG THR ARG ARG GLU GLY ASP SER SER GLY

SER VAL GLU ILE THR E246 T247 V250 R251 L254 Y255 V256 F257 Q258 D261 G262 K263 F264 V265 K266 M267 C268 N269 S270 E271 N272 C273 Y274 D277 G278 K279 V280 A281 V282 S283 K284 K287 D288 I289 T290 S291 K292 L293 S294 E295 L296 G297 W298 L299 H300 N301 K302 I303 K304 K305

Y306 T307 D308 Q309 R310 S311 L312 D313 R314 A315 F316 G317 L318 Q321 S322 F323 C324 A325 H328 Q329 K332 E333 Y334 Y335 S339 V340 L341 H342 S343 Q344 L345 Q346 V347 E348 ASP ASP GLN GLY VAL ASN LEU GLY VAL GLU S359 S360 L361 T362 L363 R364 R365 D372 P373 K374 I375

R376 L377 L380 A381 A382 L383 V384 C387 Q388 G389 R390 K391 G392 G393 E394 L395 A396 S397 A398 V399 H400 T403 K404 T405 G406 D407 P408 R411 S412 L413 H416 I417 L418 G419 Y423 P424 I425 L426 N427 F428 L429 Y430 R431 W432 I433 Y434 D435 G436 E437 L438 E439 D440 T441 Y442

H443 E444 F445 F446 V447 A448 S449 D450 P451 V452 V453 K454 T455 D456 R457 L458 W459 H460 D461 K462 Y463 S464 L465 R466 K467 S468 M469 I470 F473 M474 T475 M476 D477 Q478 S479 R480 K481 V482 L483 L484 I485 G486 K487 S488 I489 N490 PHE LEU HIS GLN VAL CYS HIS ASP GLN THR PRO ALA SER

LYS ALA MET ALA VAL GLY LYS SER ALA GLU SER PRO LYS ASP ALA ALA GLU LEU PHE THR D524 L525 E526 N527 A528 F529 Q530 T531 K532 I533 D534 A535 A536 Y537 F538 D539 T540 S541 K542 TYR LEU LEU ASP VAL LEU ASN LYS ASN TYR ASN LEU LEU LEU GLU HIS MET GLN ALA MET ARG ARG

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

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

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

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

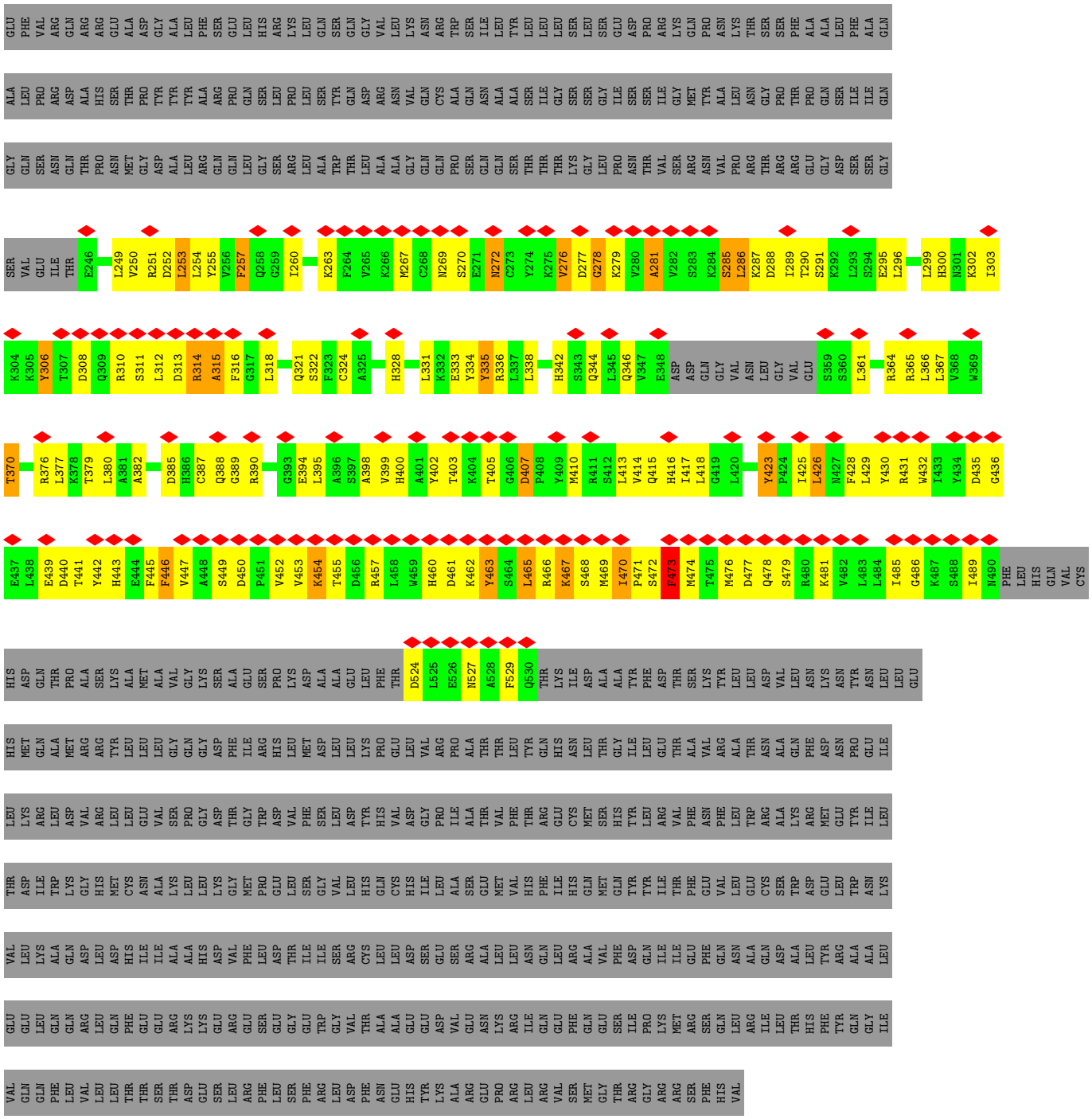
GLN PHE GLU GLU ARG LYS GLU ARG GLU SER GLU GLY GLU TRP GLY VAL THR ALA ALA GLU GLU ASP VAL GLU ASN LYS ARG ILE GLN GLU PHE GLN GLU SER ILE PRO LYS MET ARG SER GLN LEU ARG ILE LEU THR HIS PHE TYR GLN GLY ILE VAL GLN GLN PHE LEU VAL LEU

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

• Molecule 2: Gamma-tubulin complex component 3 homolog

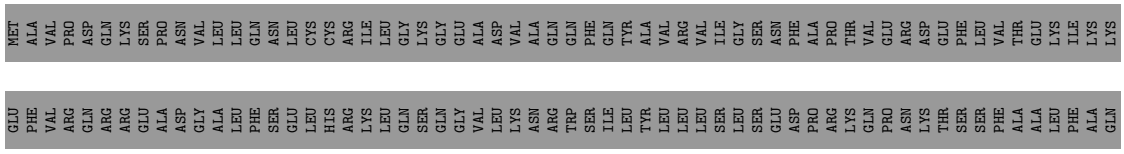
Chain F: 14% 12% 13% • 73%

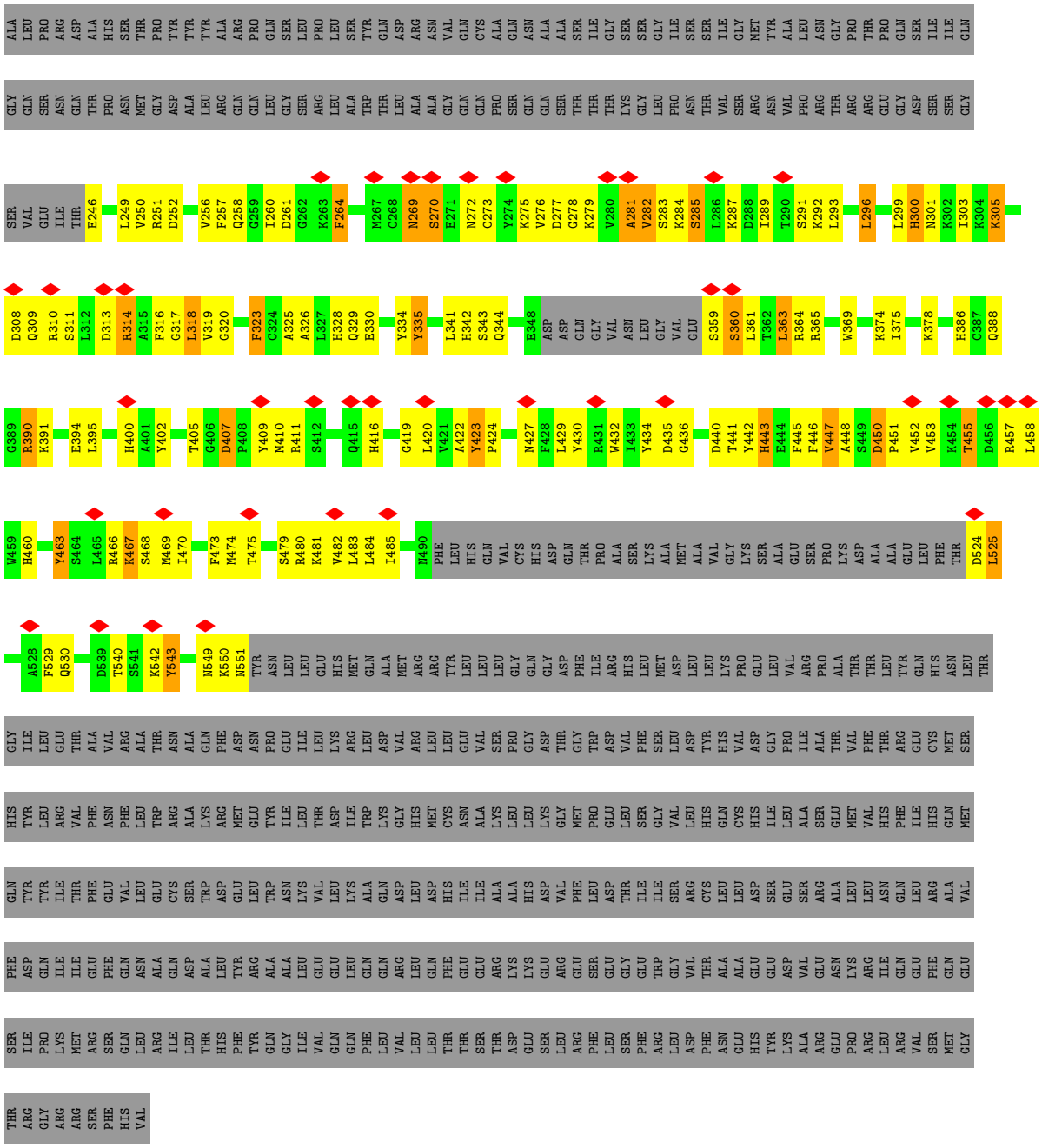
MET ALA VAL PRO ASP GLN LYS SER PRO ASN VAL LEU LEU GLN ASN LEU CYS CYS ARG ILE LEU GLY LYS GLY GLU ALA ASP VAL ALA GLN GLN PHE GLN TYR ALA VAL ARG VAL ILE GLY SER ASN PHE ALA PRO THR VAL GLU ARG ASP GLU PHE LEU VAL THR GLU LYS ILE LYS LYS



• Molecule 2: Gamma-tubulin complex component 3 homolog

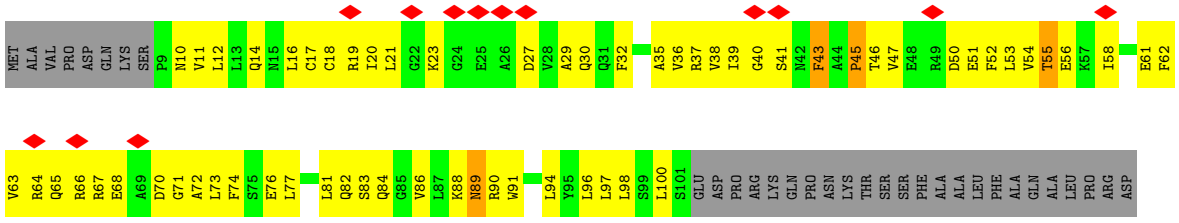
Chain H:

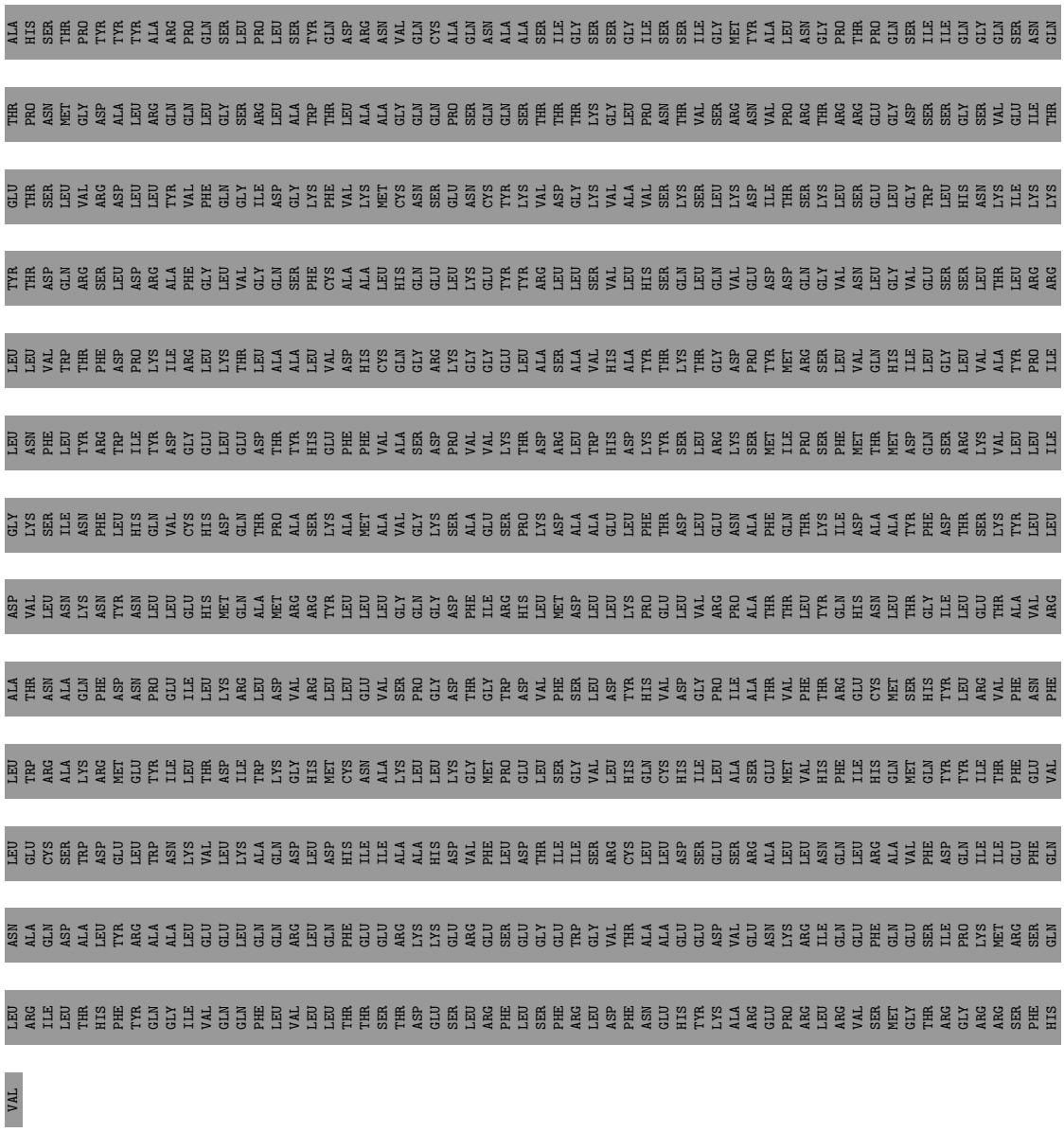




• Molecule 2: Gamma-tubulin complex component 3 homolog

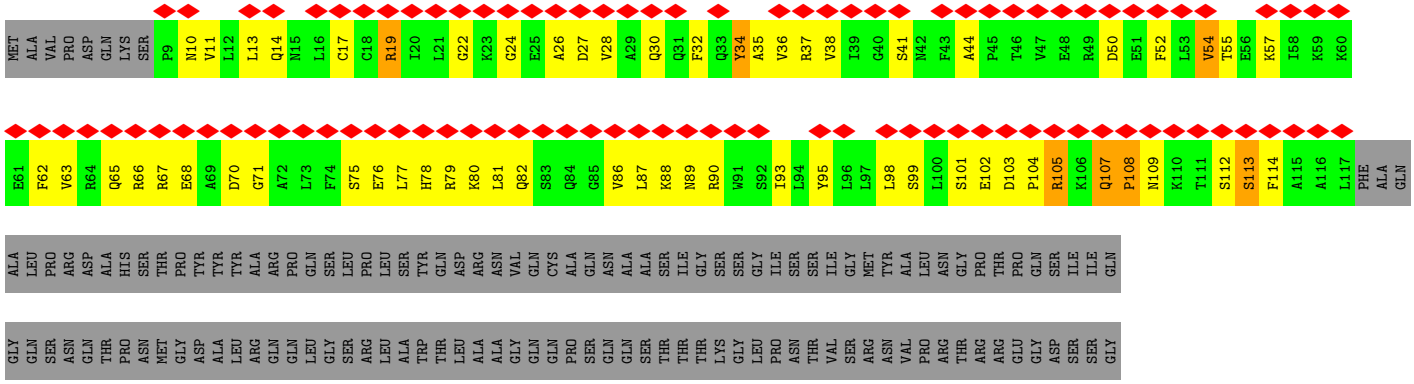
Chain O: 7% 90%





- Molecule 2: Gamma-tubulin complex component 3 homolog

Chain Q: 11% 5% 6% 88%



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

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

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

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

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

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

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

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

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

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

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

ARG ARG SER PHE HIS VAL

- Molecule 2: Gamma-tubulin complex component 3 homolog

Chain R: 6% 6% 89%

MET ALA VAL PRO ASP Q6 K7 S8 P9 N10 V11 L12 N15 L16 R19 T20 L21 G22 K23 G24 E25 A26 D27 V28 A29 Q30 Q31 F32 Q33 Y34 R37 V38 I39 G40 S41 N42 F43 A44 P45 T46 V47 E48 R49 D50 E51 F52 L53 V54 T55 E56 K57 I58 K59 K60 E61 F62 V63

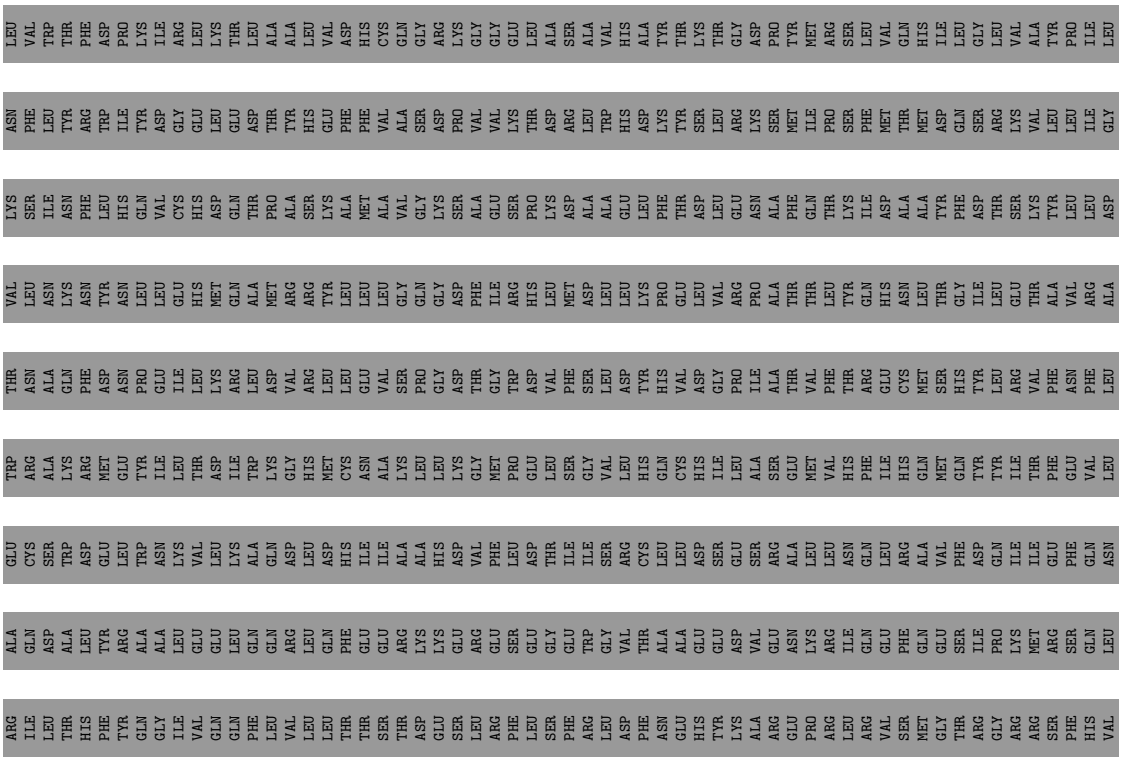
R64 Q65 R66 R67 E68 A69 D70 G71 F74 S75 E76 L77 H78 R79 K80 L81 Q82 S83 Q84 G85 V86 L87 K88 N89 R90 W91 S92 L96 L97 L98 S99 L100 S101 E102 D103 PRO ARG LYS GLN PRO ASN LYS THR SER SER PHE ALA ALA LEU PHE ALA GLN ALA LEU PRO ARG ASP ALA

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

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

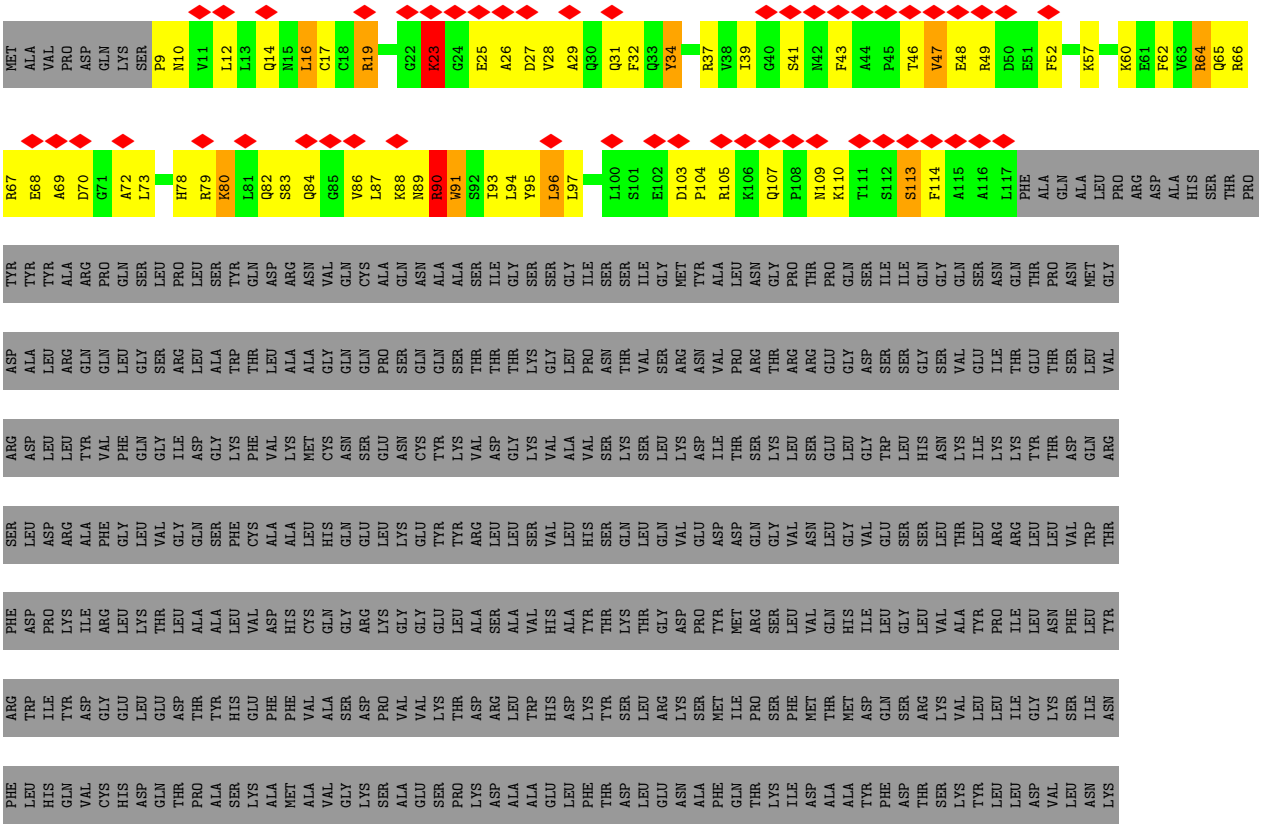
THR SER LEU VAL ARG ASP LEU LEU TYR VAL PHE GLN GLY ILE ASP GLY LYS PHE VAL LYS MET CYS ASN SER GLU ASN CYS TYR LYS VAL ASP GLY LYS VAL ALA VAL SER LYS SER LEU LYS ASP ILE THR SER LYS LEU SER GLU LEU GLY TRP LEU HIS ASN LYS ILE LYS LYS TYR

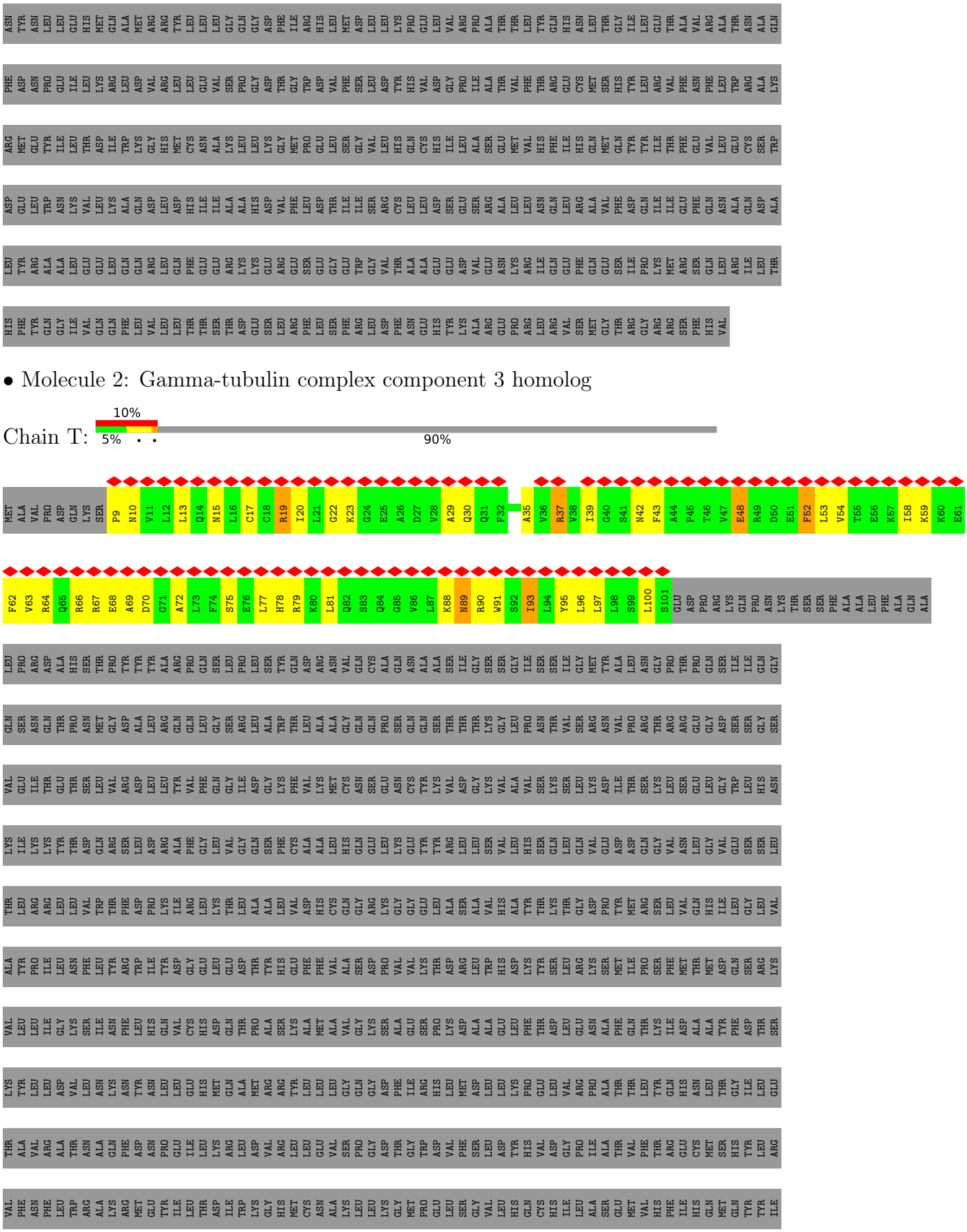
THR ASP GLN ARG SER LEU ASP ARG ALA PHE GLY LEU VAL GLY GLN SER PHE CYS ALA ALA LEU HIS GLN GLU LEU LYS GLU TYR TYR ARG LEU LEU SER VAL LEU HIS SER GLN LEU GLN VAL GLU ASP ASP GLN GLY VAL ASN LEU GLY VAL GLU SER SER LEU THR LEU ARG ARG ASP LEU



- Molecule 2: Gamma-tubulin complex component 3 homolog

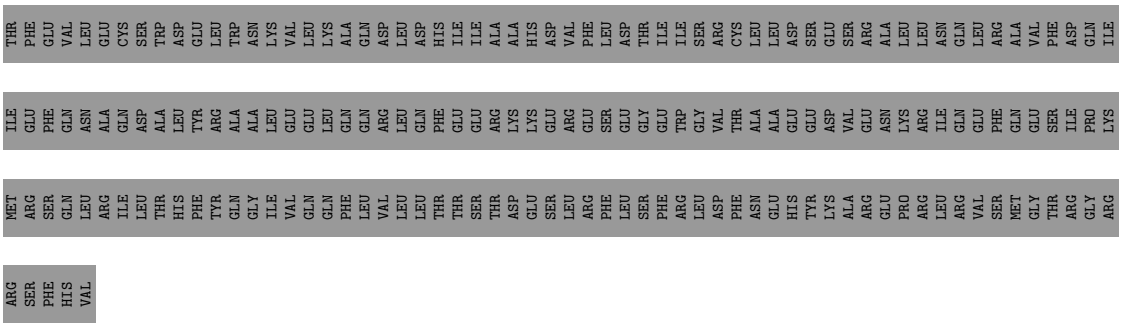
Chain S:





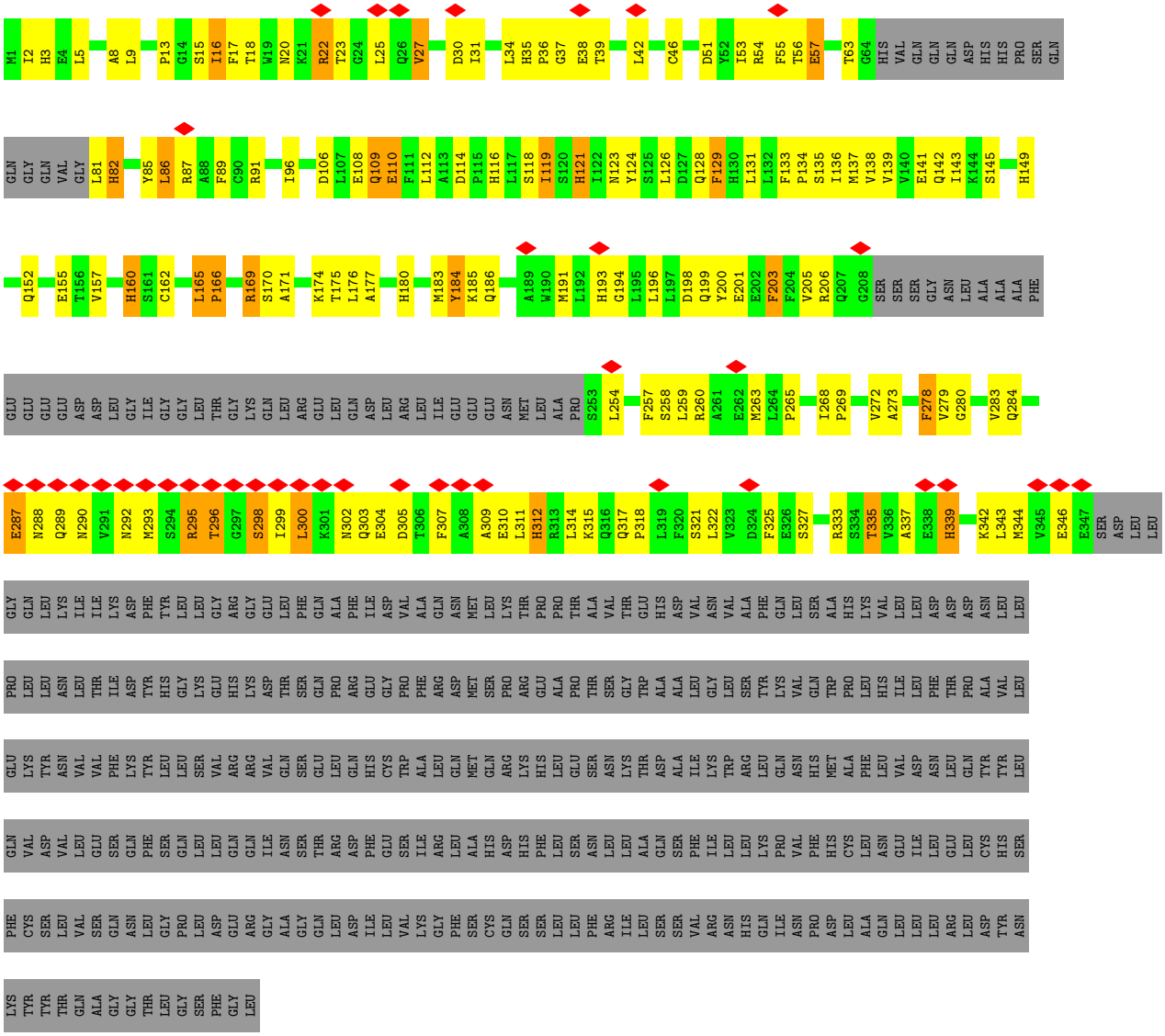
• Molecule 2: Gamma-tubulin complex component 3 homolog

Chain T: 10% 5% 90%



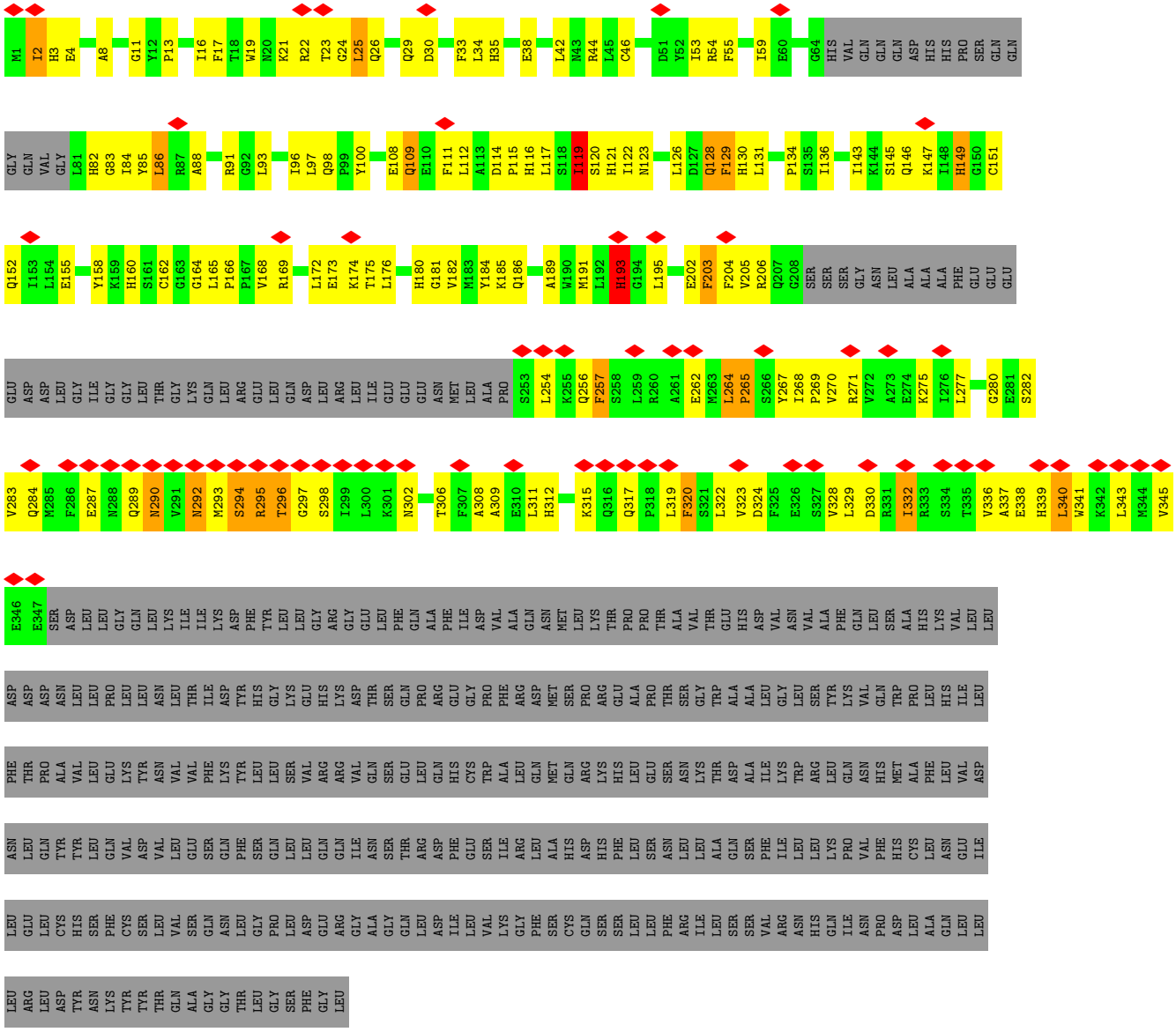
- Molecule 3: Gamma-tubulin complex component

Chain I:



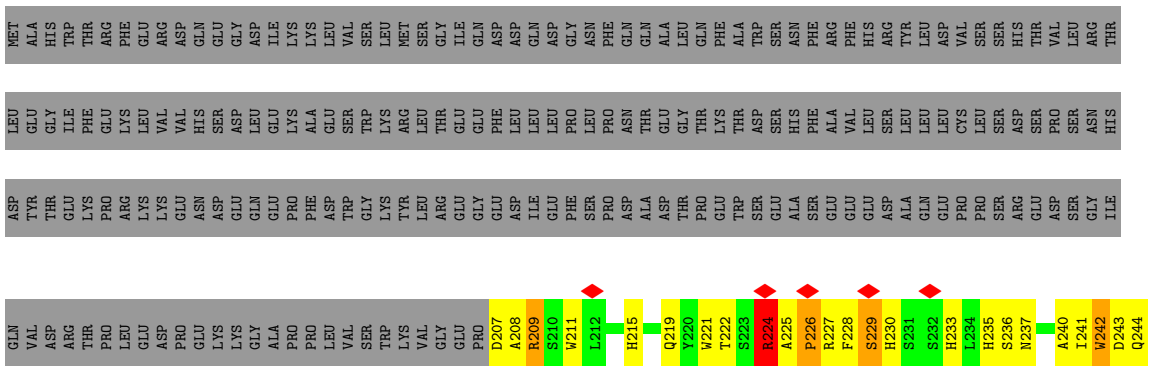
- Molecule 3: Gamma-tubulin complex component

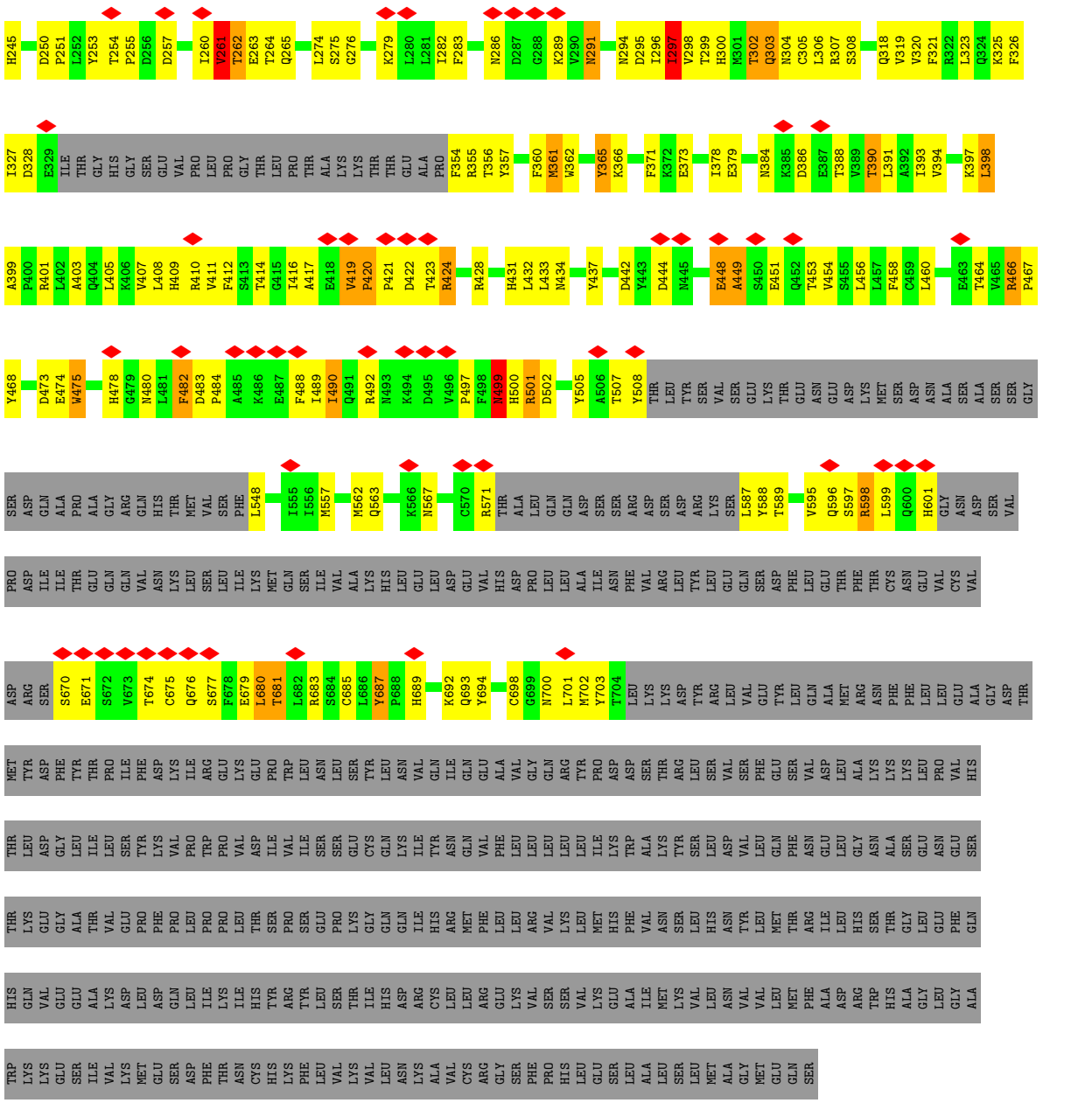
Chain K:



- Molecule 4: Gamma-tubulin complex component

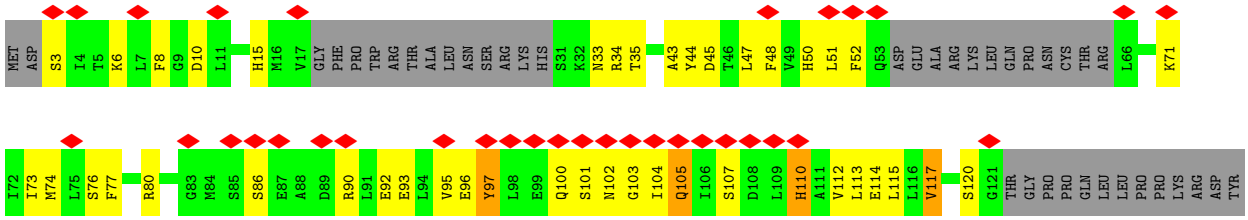
Chain J:

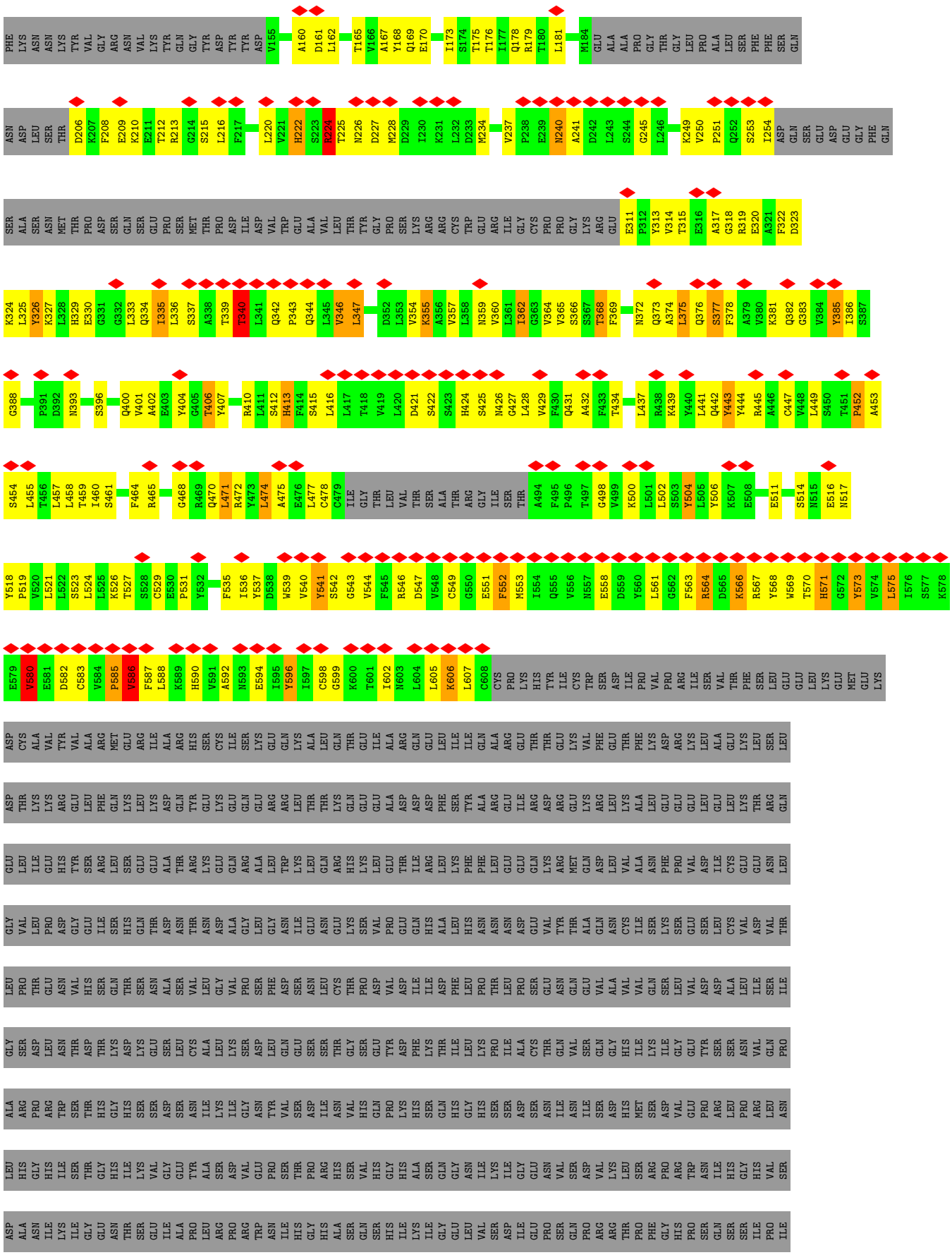


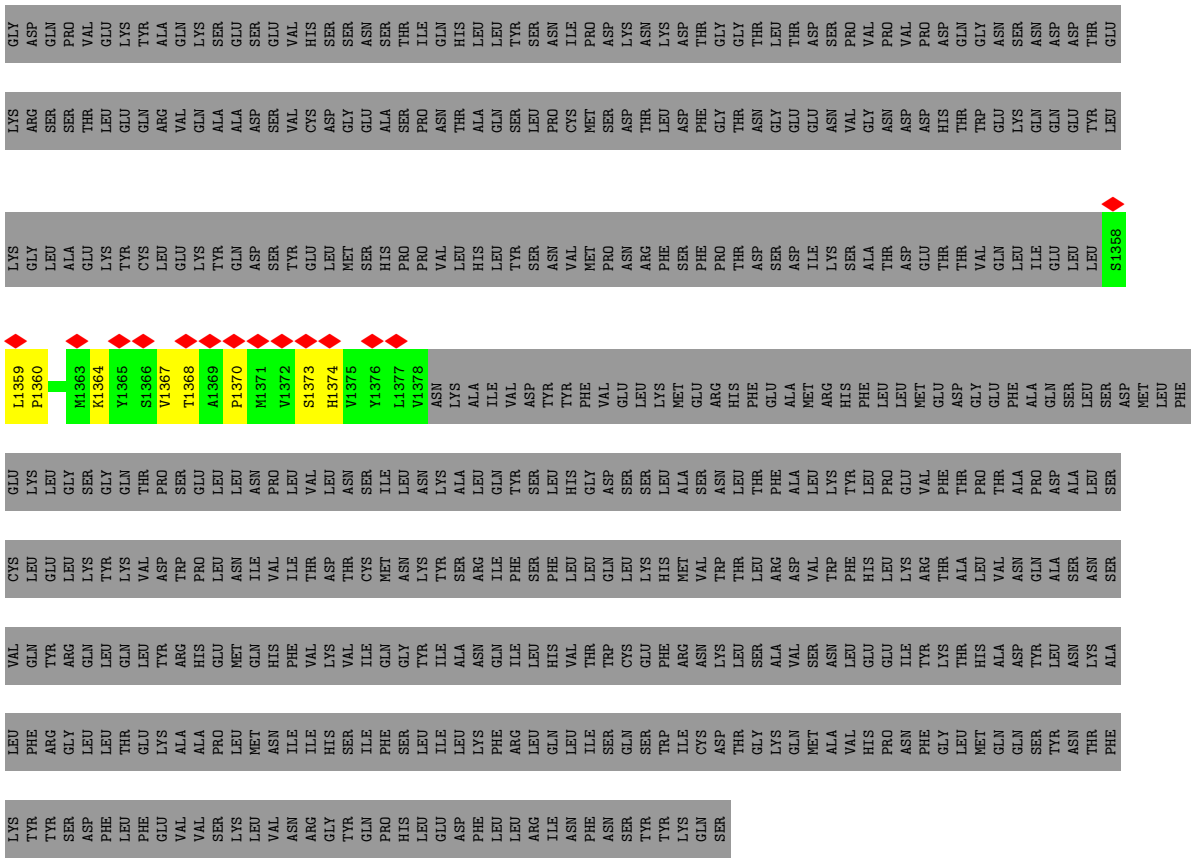


- Molecule 5: Gamma-tubulin complex component 6

Chain L:

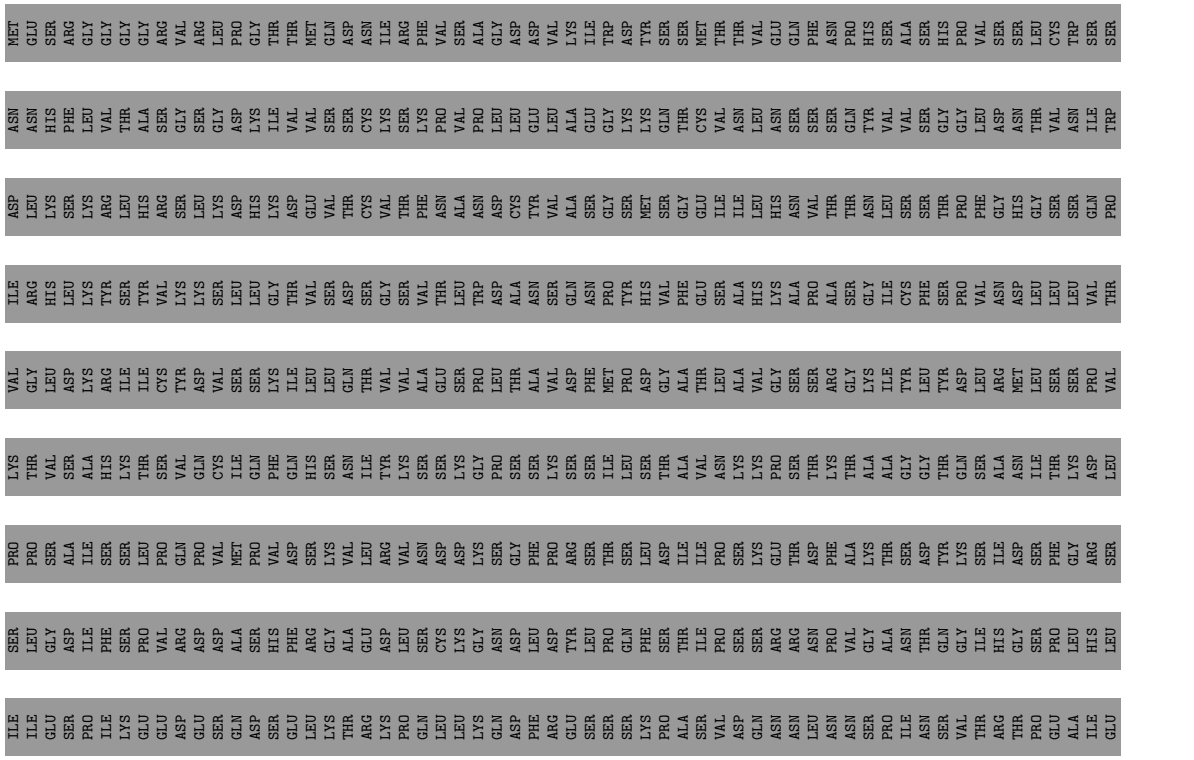


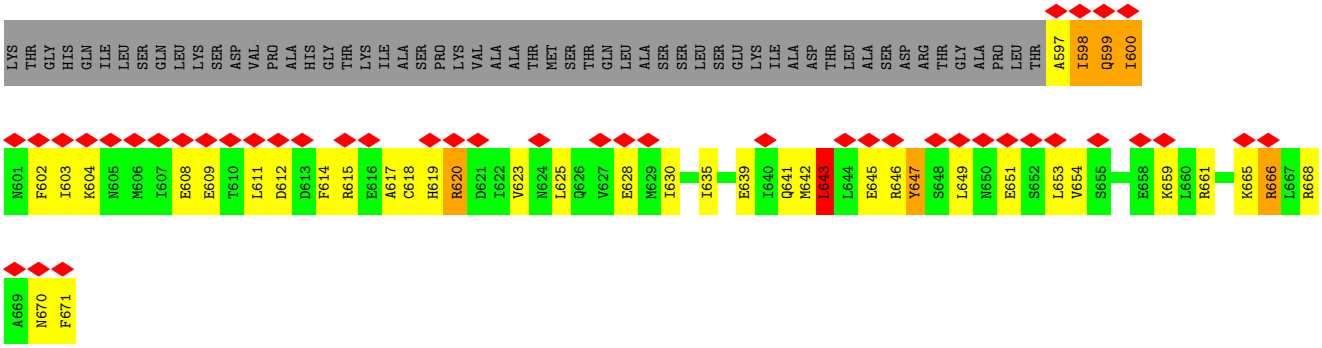

PHE LYS ASN ASN LYS TYR VAL GLY ARG ASN VAL LYS TYR GLN GLY TYR ASP TYR TYR ASP V155 A160 D161 L162 T165 V166 A167 Y168 Q169 E170 I173 S174 T175 T176 I177 Q178 R179 T180 L181 M184 GLU ALA ALA PRO GLY THR GLY LEU PRO ALA LEU SER PHE PHE SER GLN
ASN ASP LEU SER THR D206 K207 F208 E209 K210 E211 T212 R213 G214 S215 L216 F217 L220 V221 H222 S223 R224 T225 N226 D227 M228 D229 I230 K231 L232 D233 M234 V237 P238 E239 N240 A241 D242 L243 S244 G245 L246 K249 V250 P251 Q252 S253 T254 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 G318 R319 E320 A321 F322 D323
K324 L325 Y326 K327 L328 H329 E330 G331 G332 L333 Q334 I335 L336 S337 A338 T339 T340 L341 Q342 P343 Q344 L345 V346 L347 D352 L353 V354 K355 A356 V357 L358 N359 V360 L361 T362 G363 V364 V365 S366 S367 T368 F369 N372 Q373 A374 L375 Q376 S377 F378 A379 V380 K381 Q382 G383 V384 Y385 I386 S387
G388 P391 D392 N393 S396 Q400 V401 A402 E403 Y404 G405 T406 Y407 R410 L411 S412 H413 F414 S415 L416 L417 T418 V419 L420 D421 S422 S423 H424 S425 N426 G427 L428 V429 F430 Q431 A432 F433 T434 L437 R438 K439 Y440 L441 Q442 Y443 Y444 R445 A446 C447 V448 L449 S450 T451 P452 A453
S454 L455 T456 L457 L458 T459 I460 S461 F464 R465 G468 R469 Q470 L471 R472 Y473 L474 A475 E476 L477 C478 C479 ILE GLY THR LEU VAL THR SER ALA THR ARG GLY ILE SER THR A494 F495 P496 T497 G498 V499 K500 L501 L502 S503 Y504 L505 Y506 K507 E508 E511 S514 N515 E516 N517
Y518 P519 V520 L521 L522 S523 L524 L525 K526 T527 S528 C529 E530 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 Y574 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 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 LEU LYS LEU GLU LEU LYS THR ARG GLN
GLU LEU ILE GLU HIS TYR SER ARG LEU SER GLU 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 PRO VAL ASP ILE CYS GLU GLU GLU ASN LEU
GLY VAL LEU PRO ASP GLY 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 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 GLY VAL PRO SER ASP SER ASN LEU CYS THR PRO ASP VAL ASP ILE ILE ASP PHE LEU PRO THR LEU PRO GLU SER GLU ASN GLN GLU VAL ALA VAL VAL GLN SER LEU VAL ASP ASP ALA LEU ILE SER SER ILE
GLY SER ASP LEU ASN THR ASP THR LYS ASP GLU SER LEU CYS ALA LEU LYS SER ASP LEU GLN SER SER THR GLY SER GLU TYR ASP PHE LYS THR ILE LEU LYS PRO ILE ALA CYS THR GLN VAL SER GLN GLY HIS ILE LYS ILE GLY GLU TYR SER ARG ASN ASN VAL GLU ARG
ALA ARG PRO ARG TRP SER THR HIS SER GLY HIS ILE ASP SER ASN TYR VAL SER GLY ASP ILE ASN ASN VAL HIS SER GLN PRO LYS HIS SER GLN HIS GLY HIS SER ILE ASN ILE ASN ILE SER ASP VAL GLU PRO SER ARG LEU ASN
LEU HIS GLY HIS ILE SER THR GLY HIS ILE LYS VAL HIS GLU ARG ASP VAL GLU ASN VAL HIS SER VAL HIS GLY HIS ALA SER GLN LYS ILE GLY GLU ASN VAL SER ASP VAL LYS LEU SER ARG PRO ARG TRP ASN ILE SER GLN PRO
ASP ALA ASN ILE LYS ILE GLY HIS ILE SER GLU ILE ALA PRO LEU ARG PRO ARG TRP ASN ILE HIS GLY HIS ALA SER GLN SER HIS ILE LYS ILE GLY GLU LEU VAL SER ASP ILE GLU GLU PRO SER GLN SER SER ILE PRO ILE ILE PRO SER ARG ARG THR PRO PHE GLY HIS PRO SER GLN SER SER ILE PRO ILE



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

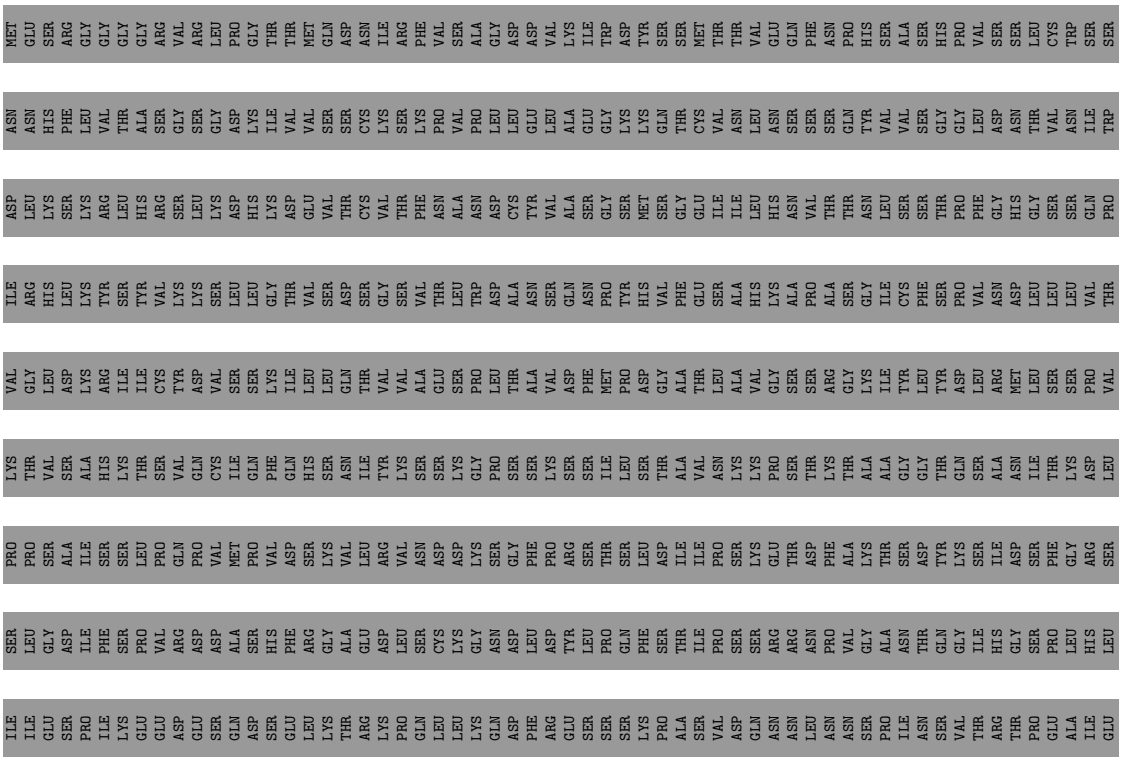
Chain U: 7% 5% 5% • 89%





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

Chain V: 7% 5% 6% 89%



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

Chain W: 8% 5% 5% • 89%

MET GLU SER ARG GLY GLY GLY GLY ARG VAL ARG LEU PRO GLY THR THR MET GLN ASP ASN ILE ARG PHE VAL SER ALA GLY ASP ASP VAL LYS ILE TRP ASP TYR SER SER MET THR THR VAL GLU GLN PHE ASN PRO HIS SER ALA SER HIS PRO VAL SER SER LEU CYS TRP SER SER
ASN ASN HIS PHE LEU VAL THR ALA SER GLY SER GLY ASP LYS ILE VAL VAL SER SER CYS LYS SER LYS PRO VAL PRO LEU LEU GLU LEU ALA GLU GLY LYS LYS GLN THR CYS VAL ASN LEU ASN SER SER SER GLN TYR VAL VAL SER GLY GLY LEU ASP ASN THR VAL ASN ILE TRP
ASP LEU LYS SER LYS ARG LEU HIS ARG SER LEU LYS ASP HIS LYS ASP GLU VAL THR CYS VAL THR PHE ASN ALA ASN ASP CYS TYR VAL ALA SER GLY SER MET SER GLY GLU ILE ILE LEU HIS ASN VAL THR THR ASN LEU SER SER THR PRO PHE GLY HIS GLY SER SER GLN PRO
ILE ARG HIS LEU LYS TYR SER TYR VAL LYS LYS SER LEU LEU GLY THR VAL SER ASP SER GLY SER VAL THR LEU TRP ASP ALA ASN SER GLN ASN PRO TYR HIS VAL PHE GLU SER ALA HIS LYS ALA PRO ALA SER GLY ILE CYS PHE SER PRO VAL ASN ASP LEU LEU VAL THR
VAL GLY LEU ASP LYS ARG ILE ILE CYS TYR ASP VAL SER SER LYS ILE LEU LEU GLN THR VAL VAL ALA GLU SER PRO LEU THR ALA VAL ASP PHE MET PRO ASP GLY ALA THR LEU ALA VAL GLY SER SER ARG GLY LYS ILE TYR LEU TYR ASP LEU ARG MET LEU SER SER PRO VAL
LYS THR VAL SER ALA HIS LYS THR SER VAL GLN CYS ILE GLN PHE GLN HIS SER ASN ILE TYR LYS SER SER LYS LYS GLY PRO SER SER LYS SER SER THR ALA VAL ASN LYS LYS PRO SER THR LYS THR ALA ALA GLY GLY THR GLN SER ALA ASN ILE THR LYS ASP LEU
PRO PRO SER ALA ILE SER SER LEU PRO GLN PRO VAL MET PRO VAL ASP SER LYS VAL LEU ARG VAL ASN ASP ASP LYS SER GLY PHE PRO ARG SER THR SER LEU ASP ILE ILE PRO SER LYS GLU THR ASP PHE ALA LYS THR SER ASP TYR LYS SER ILE ASP SER PHE GLY ARG SER
SER LEU GLY ASP ILE PHE SER PRO VAL ARG ASP ASP ALA SER HIS PHE ARG GLY ALA GLU ASP LEU SER CYS LYS GLY ASN ASP LEU ASP TYR LEU PRO GLN PHE SER THR ILE PRO SER SER ARG ARG ASN PRO VAL GLY ALA ASN THR GLN GLY ILE HIS GLY SER PRO LEU HIS LEU
ILE ILE GLU SER PRO ILE LYS GLU GLU ASP GLU SER GLN ASP SER GLU LEU LYS THR ARG LYS PRO GLN LEU LEU LYS GLN ASP PHE ARG GLU SER SER VAL ASP GLN ASN ASN LEU ASN ASN SER PRO ILE ASN SER VAL THR ARG THR PRO GLU ALA ILE GLU
LYS THR GLY HIS GLN ILE LEU SER GLN LEU LYS SER ASP VAL PRO ALA HIS GLY THR LYS ILE ALA SER PRO LYS VAL ALA ALA THR MET SER THR GLN LEU ALA SER SER LEU SER GLU LYS ILE ALA ASP THR LEU ALA SER ASP ARG THR GLY ALA PRO LEU THR A597 I598 Q599 I600

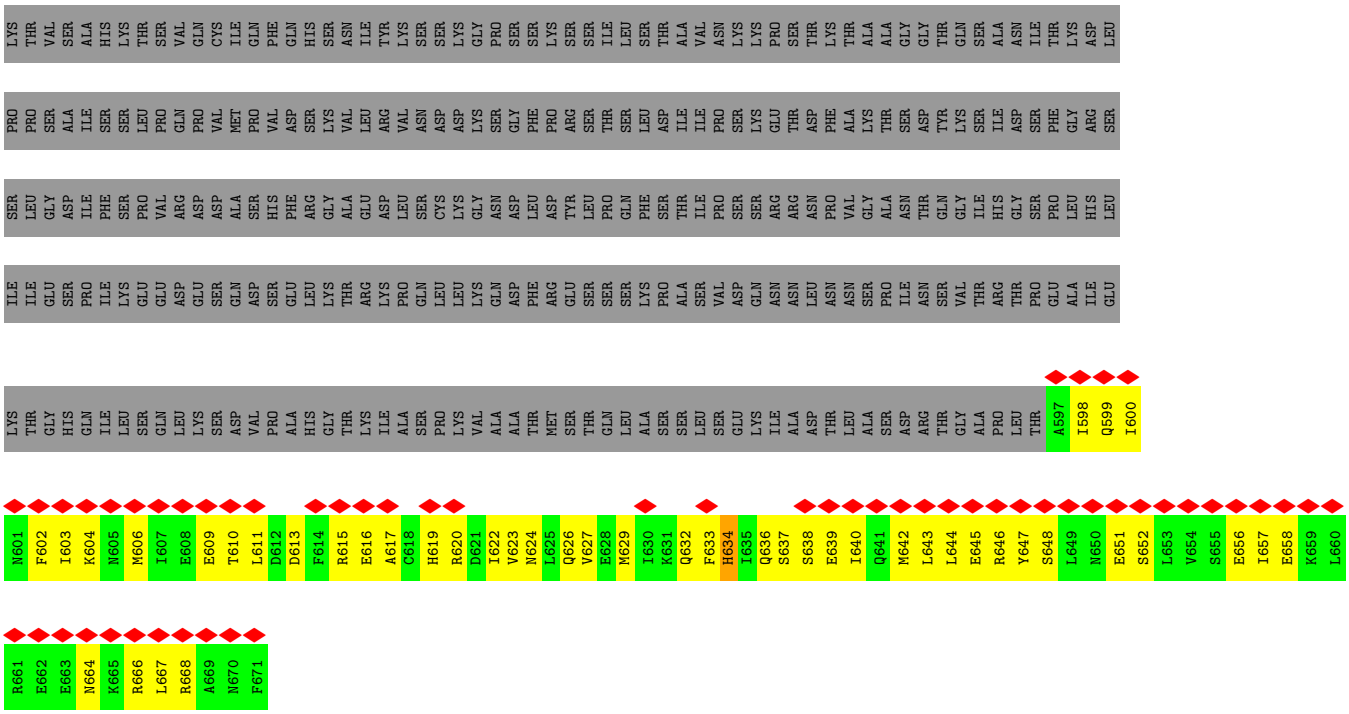
N601 F602 I603 K604 M605 M606 I607 E608 E609 T610 L611 D612 D613 F614 R615 E616 A617 C618 H619 R620 D621 I622 V623 N624 L625 Q626 V627 E628 M629 I630 K631 Q632 F633 H634 I635 Q636 S637 S638 E639 I640 Q641 M642 L643 L644 E645 R646 Y647 S648 L649 N650 E651 S652 L653 V654 S655 E656 I657 E658 K659 L660

R661 E662 E663 N664 K665 R666 L667 R668 A669 N670 F671

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

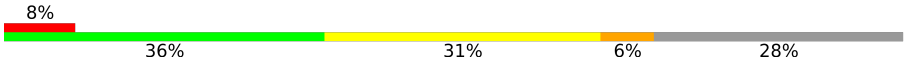
Chain X: 8% • 7% 89%

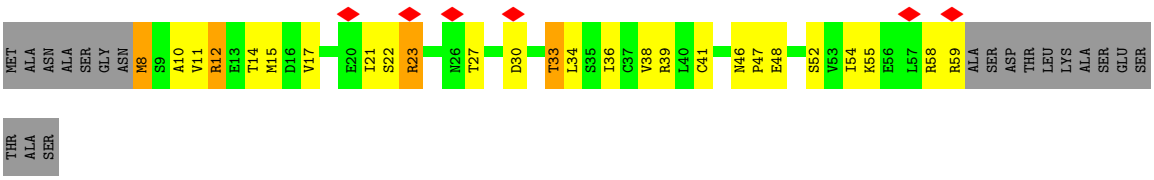
MET GLU SER ARG GLY GLY GLY GLY ARG VAL ARG LEU PRO GLY THR THR MET GLN ASP ASN ILE ARG PHE VAL SER ALA GLY ASP ASP VAL LYS ILE TRP ASP TYR SER SER MET THR THR VAL GLU GLN PHE ASN PRO HIS SER ALA SER HIS PRO VAL SER SER LEU CYS TRP SER SER
ASN ASN HIS PHE LEU VAL THR ALA SER GLY SER GLY ASP LYS ILE VAL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



- Molecule 7: Mitotic-spindle organizing protein 1

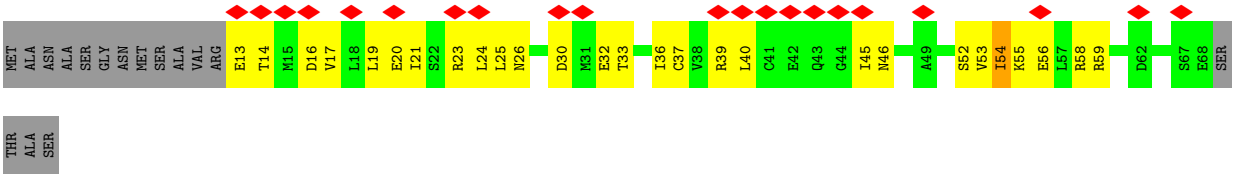
Chain o:





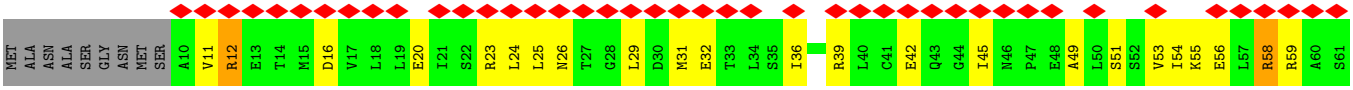
- Molecule 7: Mitotic-spindle organizing protein 1

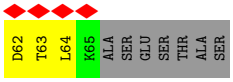
Chain p:



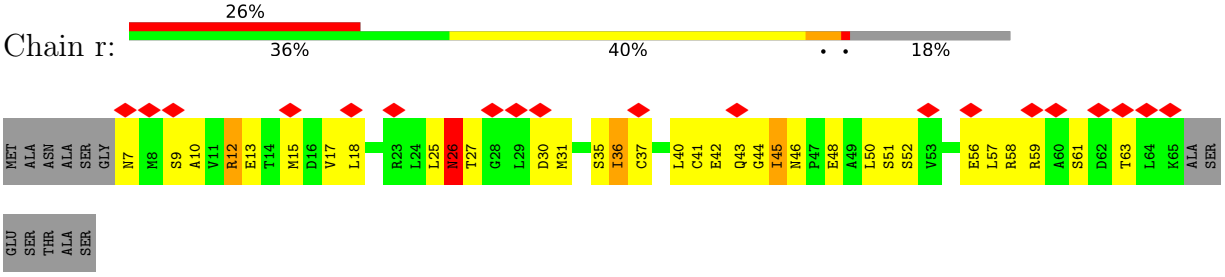
- Molecule 7: Mitotic-spindle organizing protein 1

Chain q:

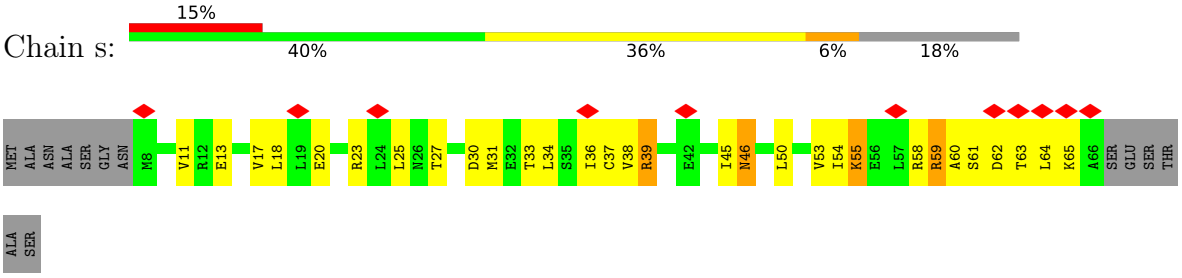




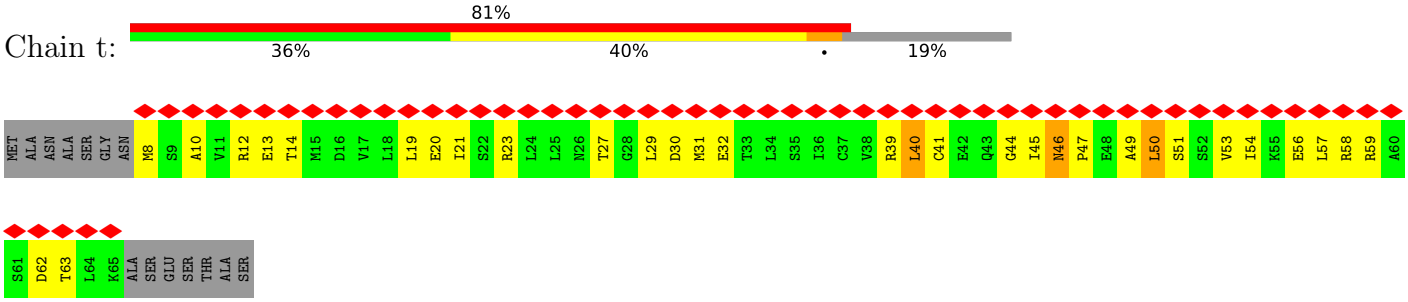
• Molecule 7: Mitotic-spindle organizing protein 1



• Molecule 7: Mitotic-spindle organizing protein 1



• Molecule 7: Mitotic-spindle organizing protein 1



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	2.24	75/2254 (3.3%)	2.41	150/3055 (4.9%)
1	C	2.26	80/2053 (3.9%)	2.42	121/2781 (4.4%)
1	E	2.24	63/2077 (3.0%)	2.38	135/2813 (4.8%)
1	G	2.22	64/2053 (3.1%)	2.35	112/2781 (4.0%)
2	B	2.22	81/2413 (3.4%)	2.32	113/3257 (3.5%)
2	D	2.20	68/2101 (3.2%)	2.33	121/2831 (4.3%)
2	F	2.18	71/2004 (3.5%)	2.33	101/2700 (3.7%)
2	H	2.18	71/2178 (3.3%)	2.34	108/2936 (3.7%)
2	O	2.21	21/764 (2.7%)	2.60	69/1026 (6.7%)
2	Q	2.23	27/892 (3.0%)	2.61	82/1199 (6.8%)
2	R	2.30	30/805 (3.7%)	2.45	41/1081 (3.8%)
2	S	2.23	25/892 (2.8%)	2.53	69/1199 (5.8%)
2	T	2.27	25/764 (3.3%)	2.59	53/1026 (5.2%)
3	I	2.25	70/2377 (2.9%)	2.38	154/3212 (4.8%)
3	K	2.24	81/2377 (3.4%)	2.30	116/3212 (3.6%)
4	J	2.45	98/2976 (3.3%)	2.43	176/4037 (4.4%)
5	L	2.22	143/3862 (3.7%)	2.42	257/5228 (4.9%)
6	U	2.24	19/640 (3.0%)	2.66	62/854 (7.3%)
6	V	2.18	18/640 (2.8%)	2.65	53/854 (6.2%)
6	W	2.27	21/640 (3.3%)	2.44	41/854 (4.8%)
6	X	2.29	26/640 (4.1%)	2.61	49/854 (5.7%)
7	o	2.26	14/403 (3.5%)	2.45	27/541 (5.0%)
7	p	2.27	12/429 (2.8%)	2.66	42/577 (7.3%)
7	q	2.32	18/432 (4.2%)	2.50	24/581 (4.1%)
7	r	2.28	16/454 (3.5%)	2.65	41/610 (6.7%)
7	s	2.38	25/451 (5.5%)	2.40	31/606 (5.1%)
7	t	2.24	12/446 (2.7%)	2.72	41/599 (6.8%)
All	All	2.25	1274/38017 (3.4%)	2.42	2389/51304 (4.7%)

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 1274 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	16	ILE	CG1-CD1	33.79	2.83	1.51
4	J	242	TRP	CD2-CE3	33.30	1.93	1.40
4	J	242	TRP	CZ2-CH2	26.19	1.87	1.37
4	J	242	TRP	CE2-CZ2	24.86	1.92	1.39
4	J	242	TRP	CD2-CE2	22.39	1.79	1.41

The worst 5 of 2389 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	R	86	VAL	N-CA-C	-11.89	101.07	112.96
2	D	361	LEU	N-CA-C	-11.25	99.54	113.38
4	J	228	PHE	CA-CB-CG	11.13	124.93	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	441	PHE	CA-CB-CG	-11.03	102.77	113.80
1	A	327	ILE	N-CA-C	-10.53	102.54	111.91

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	3	0
2	O	753	0	779	1	0
2	Q	878	0	903	1	0
2	R	794	0	814	2	0
2	S	878	0	903	4	0
2	T	753	0	779	4	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	3	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	1	0
7	q	432	0	457	0	0
7	r	454	0	477	1	0
7	s	451	0	476	0	0
7	t	446	0	471	4	0
All	All	37358	0	37734	126	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 126 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 25
1	C	244/896 (27%)	217 (89%)	21 (9%)	6 (2%)	4 26
1	E	247/896 (28%)	229 (93%)	12 (5%)	6 (2%)	4 27
1	G	244/896 (27%)	232 (95%)	11 (4%)	1 (0%)	30 66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	290/906 (32%)	261 (90%)	20 (7%)	9 (3%)	3	22
2	D	248/906 (27%)	224 (90%)	17 (7%)	7 (3%)	4	24
2	F	236/906 (26%)	214 (91%)	13 (6%)	9 (4%)	2	19
2	H	257/906 (28%)	227 (88%)	20 (8%)	10 (4%)	2	19
2	O	91/906 (10%)	85 (93%)	5 (6%)	1 (1%)	11	45
2	Q	107/906 (12%)	97 (91%)	6 (6%)	4 (4%)	2	20
2	R	96/906 (11%)	90 (94%)	4 (4%)	2 (2%)	5	30
2	S	107/906 (12%)	96 (90%)	8 (8%)	3 (3%)	4	24
2	T	91/906 (10%)	85 (93%)	4 (4%)	2 (2%)	5	29
3	I	281/666 (42%)	255 (91%)	20 (7%)	6 (2%)	5	30
3	K	281/666 (42%)	259 (92%)	13 (5%)	9 (3%)	3	21
4	J	342/1019 (34%)	317 (93%)	15 (4%)	10 (3%)	3	23
5	L	462/1698 (27%)	422 (91%)	26 (6%)	14 (3%)	3	22
6	U	73/671 (11%)	73 (100%)	0	0	100	100
6	V	73/671 (11%)	72 (99%)	0	1 (1%)	9	39
6	W	73/671 (11%)	71 (97%)	1 (1%)	1 (1%)	9	39
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	20
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	27

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%)	230 (94%)	14 (6%)	18	41
1	C	221/824 (27%)	210 (95%)	11 (5%)	22	44
1	E	224/824 (27%)	214 (96%)	10 (4%)	24	47
1	G	221/824 (27%)	211 (96%)	10 (4%)	24	47
2	B	260/798 (33%)	249 (96%)	11 (4%)	26	48
2	D	227/798 (28%)	219 (96%)	8 (4%)	32	54
2	F	217/798 (27%)	202 (93%)	15 (7%)	14	37
2	H	236/798 (30%)	222 (94%)	14 (6%)	18	41
2	O	82/798 (10%)	80 (98%)	2 (2%)	43	63
2	Q	96/798 (12%)	94 (98%)	2 (2%)	47	65
2	R	87/798 (11%)	86 (99%)	1 (1%)	65	74
2	S	96/798 (12%)	87 (91%)	9 (9%)	8	27
2	T	82/798 (10%)	80 (98%)	2 (2%)	43	63
3	I	259/595 (44%)	245 (95%)	14 (5%)	20	43
3	K	259/595 (44%)	247 (95%)	12 (5%)	24	46
4	J	326/933 (35%)	308 (94%)	18 (6%)	19	43
5	L	431/1539 (28%)	414 (96%)	17 (4%)	28	50
6	U	72/598 (12%)	69 (96%)	3 (4%)	26	48
6	V	72/598 (12%)	70 (97%)	2 (3%)	38	59
6	W	72/598 (12%)	67 (93%)	5 (7%)	14	37
6	X	72/598 (12%)	70 (97%)	2 (3%)	38	59
7	o	48/62 (77%)	45 (94%)	3 (6%)	16	38
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%)	30	51
7	s	53/62 (86%)	49 (92%)	4 (8%)	12	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	t	53/62 (86%)	53 (100%)	0	100	100
All	All	4166/16904 (25%)	3975 (95%)	191 (5%)	25	46

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	J	421	PRO
5	L	368	THR
4	J	598	ARG
3	K	134	PRO
5	L	573	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 134 such sidechains are listed below:

Mol	Chain	Res	Type
6	U	619	HIS
6	V	632	GLN
7	r	7	ASN
2	F	300	HIS
1	E	481	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.

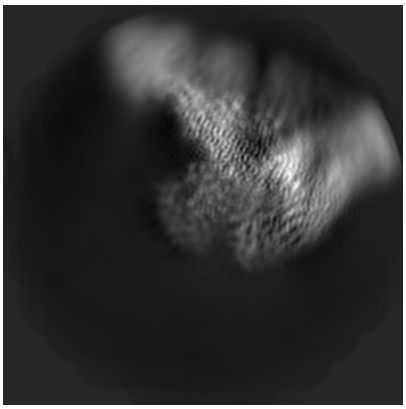
6 Map visualisation (i)

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.

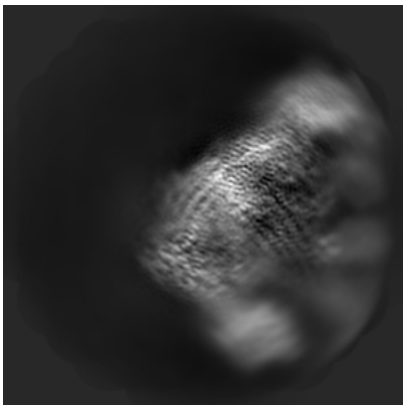
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

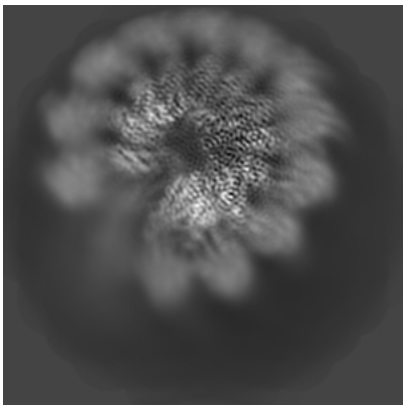
6.1.1 Primary map



X

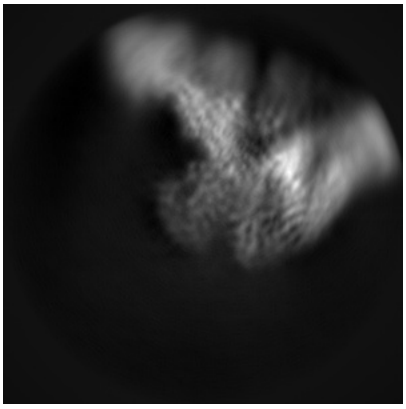


Y

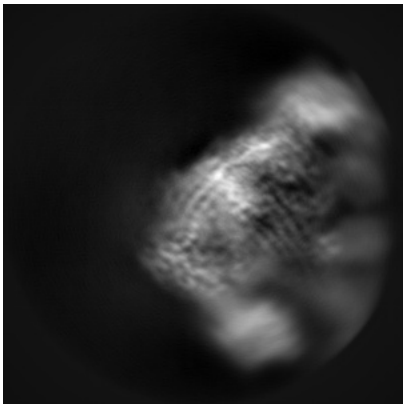


Z

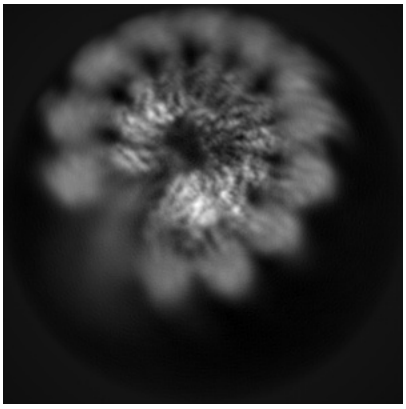
6.1.2 Raw map



X



Y

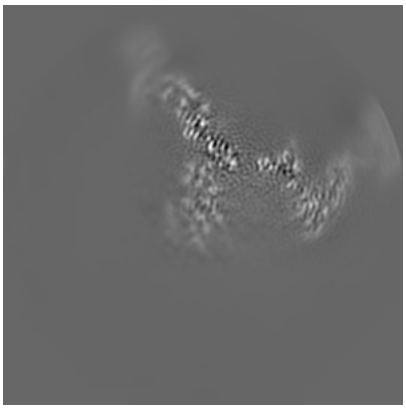


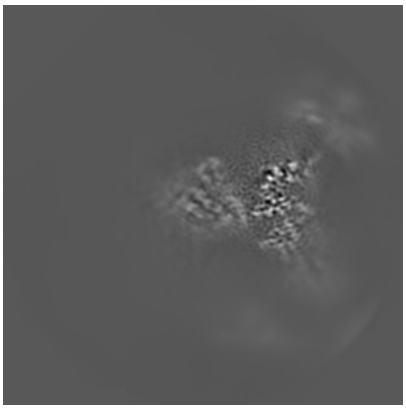
Z

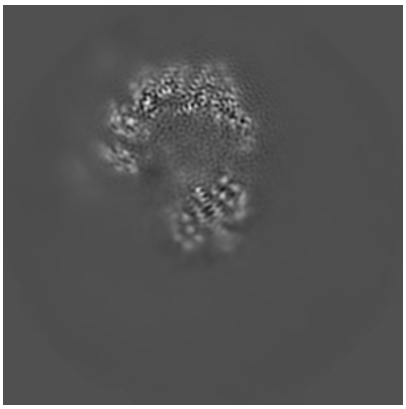
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

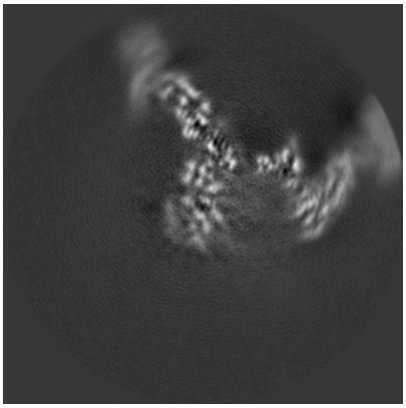
6.2.1 Primary map

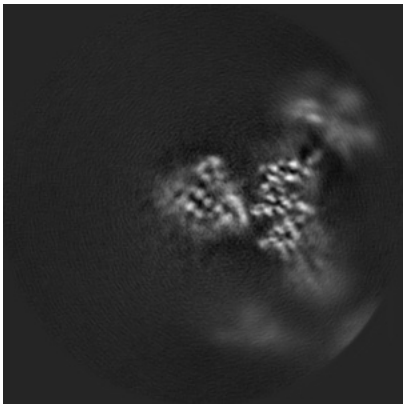

X Index: 128

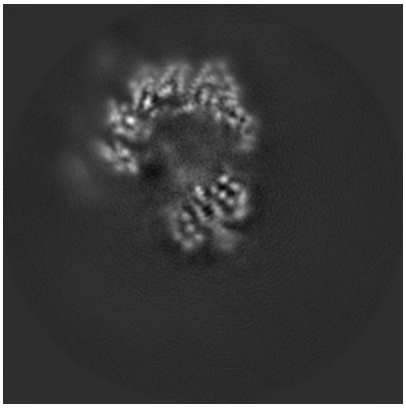

Y Index: 128


Z Index: 128

6.2.2 Raw map


X Index: 128


Y Index: 128

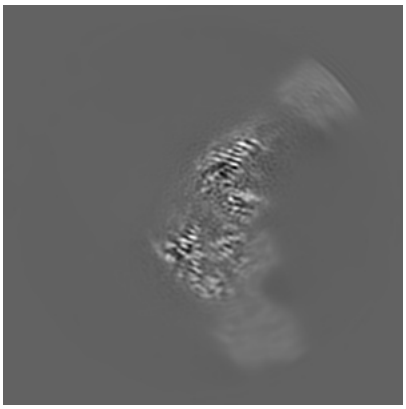

Z Index: 128

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

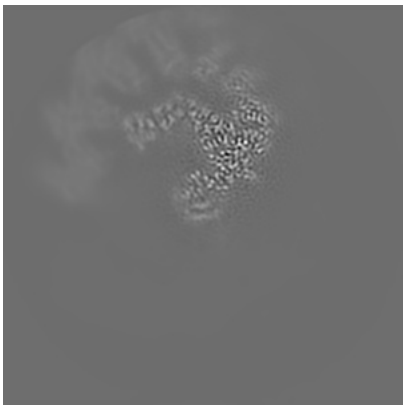
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 148

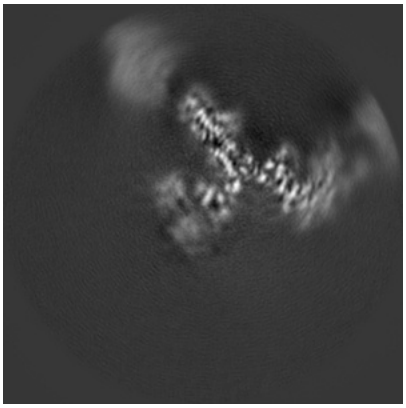


Y Index: 184

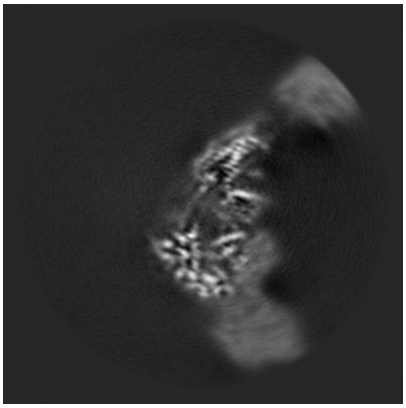


Z Index: 150

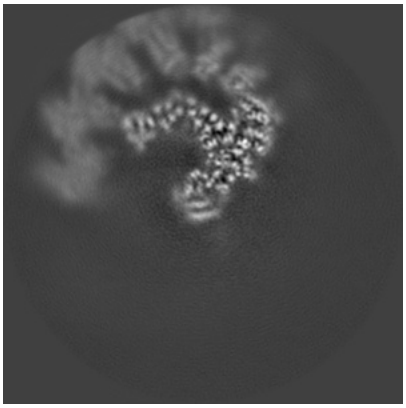
6.3.2 Raw map



X Index: 145



Y Index: 183

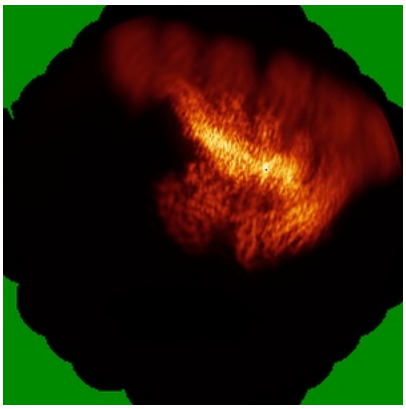


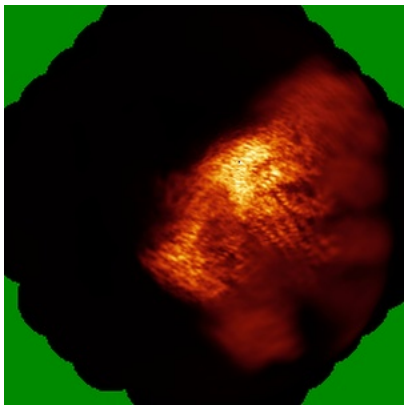
Z Index: 151

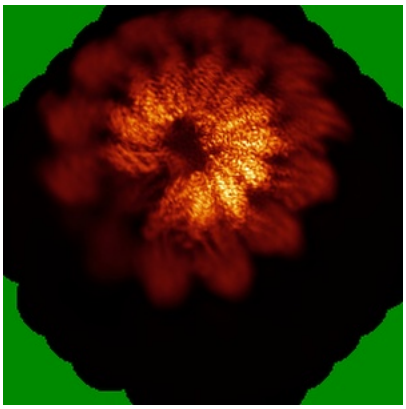
The images above show the largest variance slices of the map in three orthogonal directions.

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

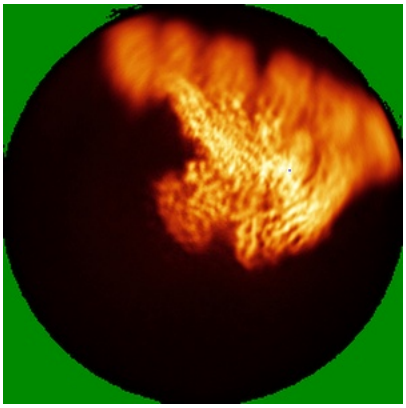
6.4.1 Primary map

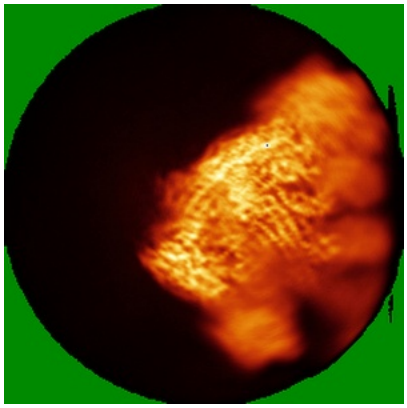

X

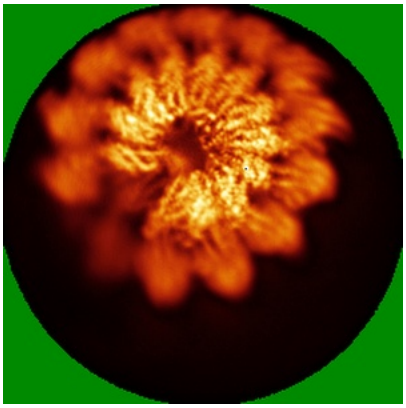

Y


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.

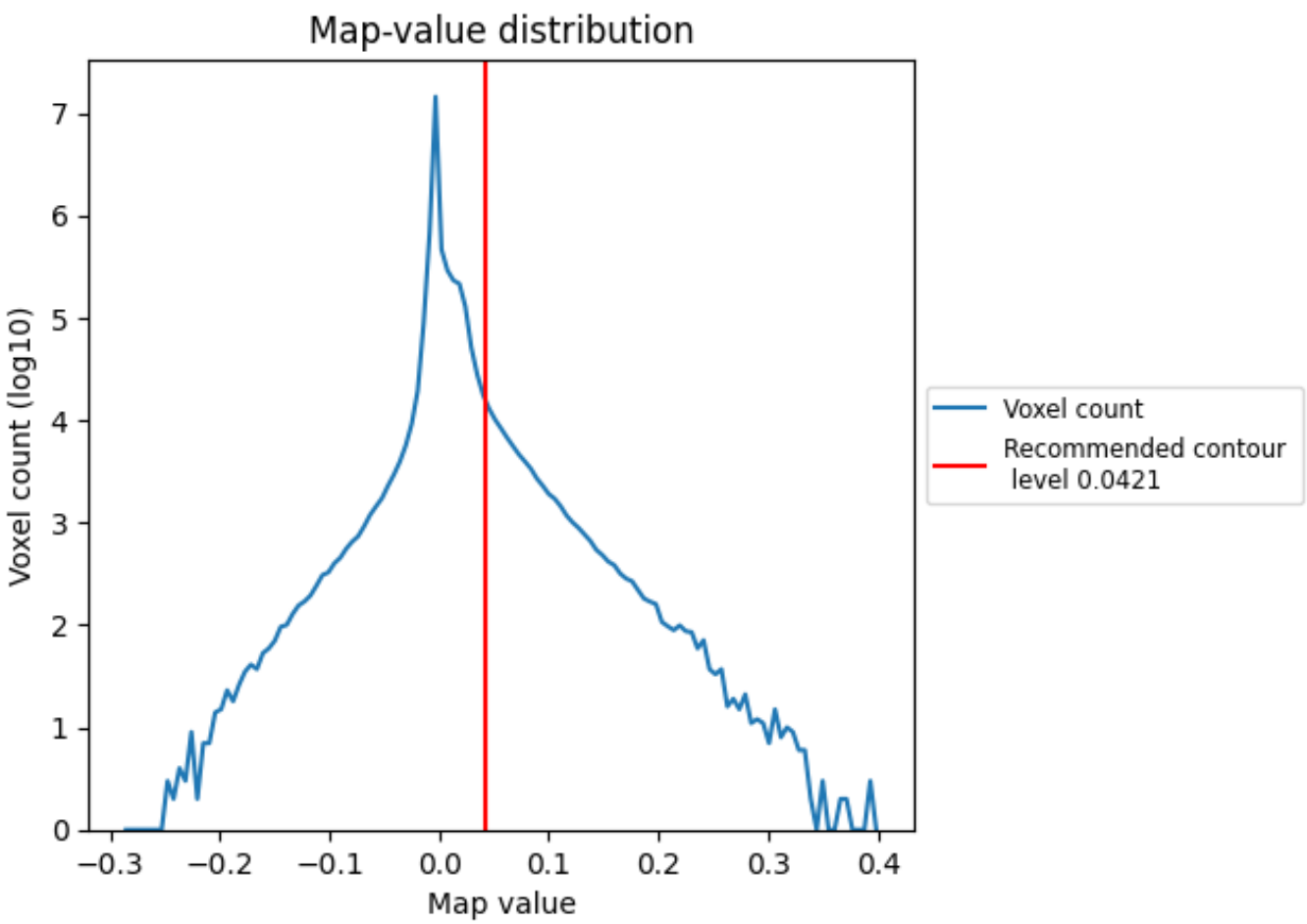
6.6 Mask visualisation (i)

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

7 Map analysis (i)

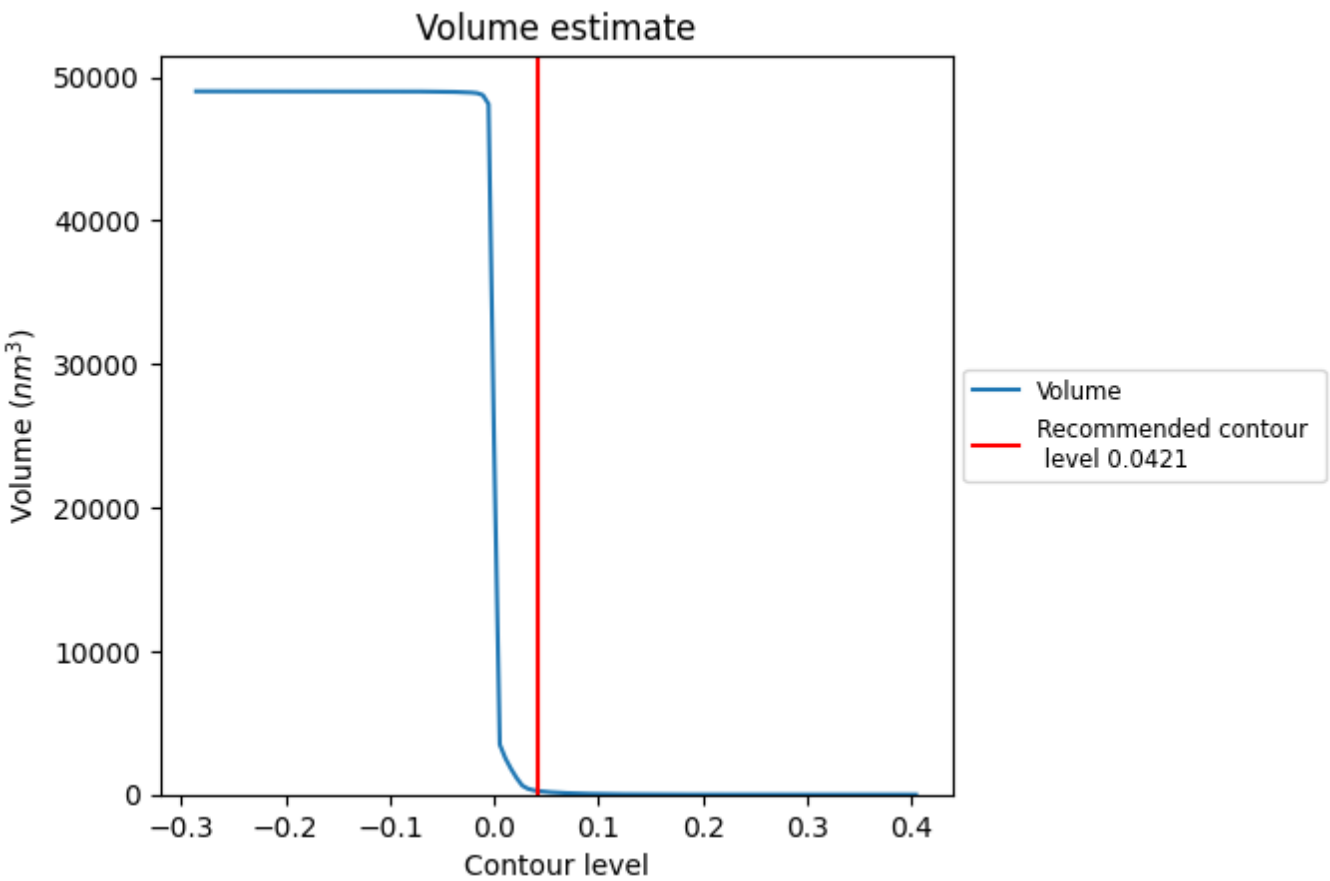
This section contains the results of statistical analysis of the map.

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.

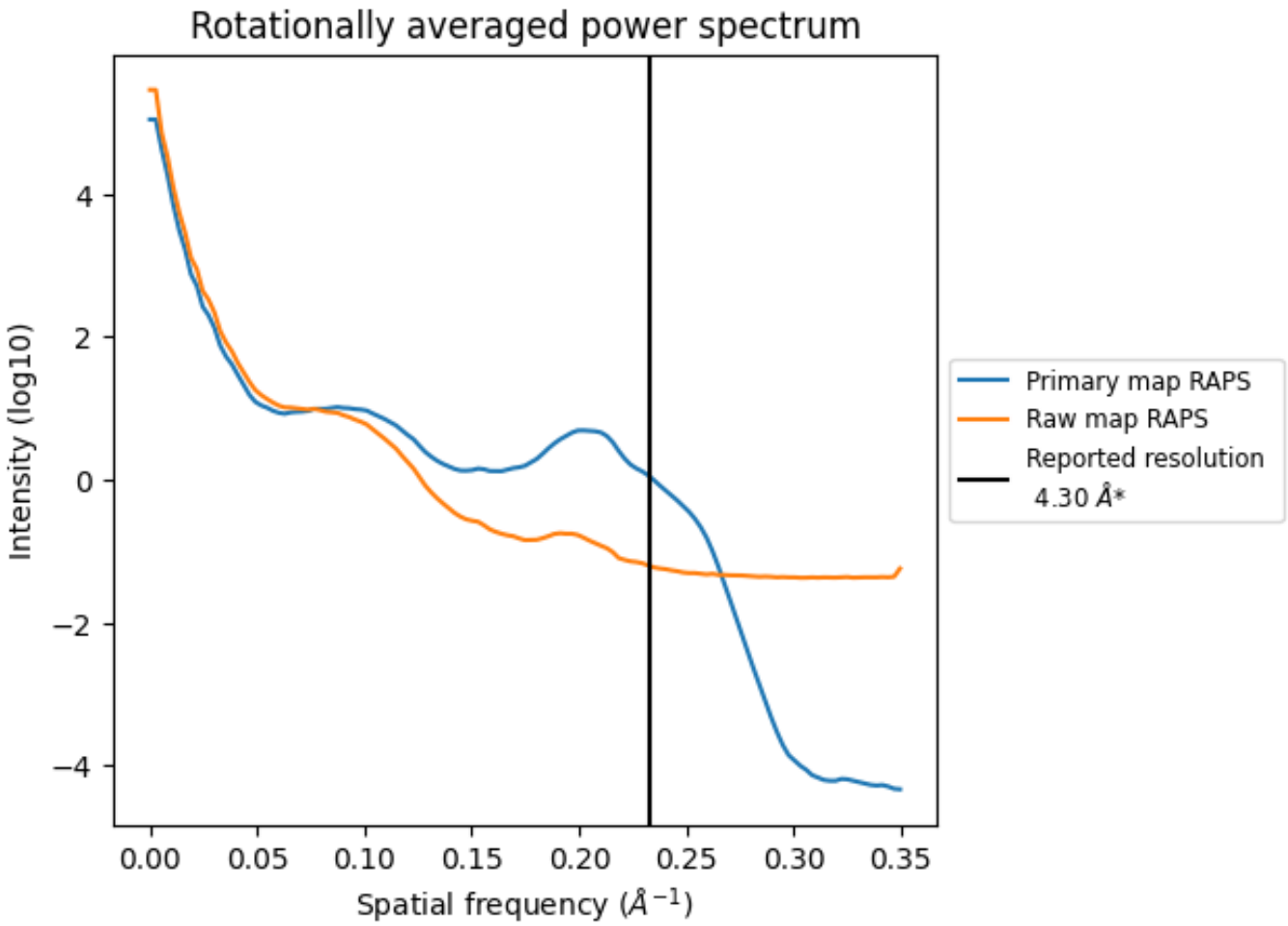
7.2 Volume estimate (i)



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)

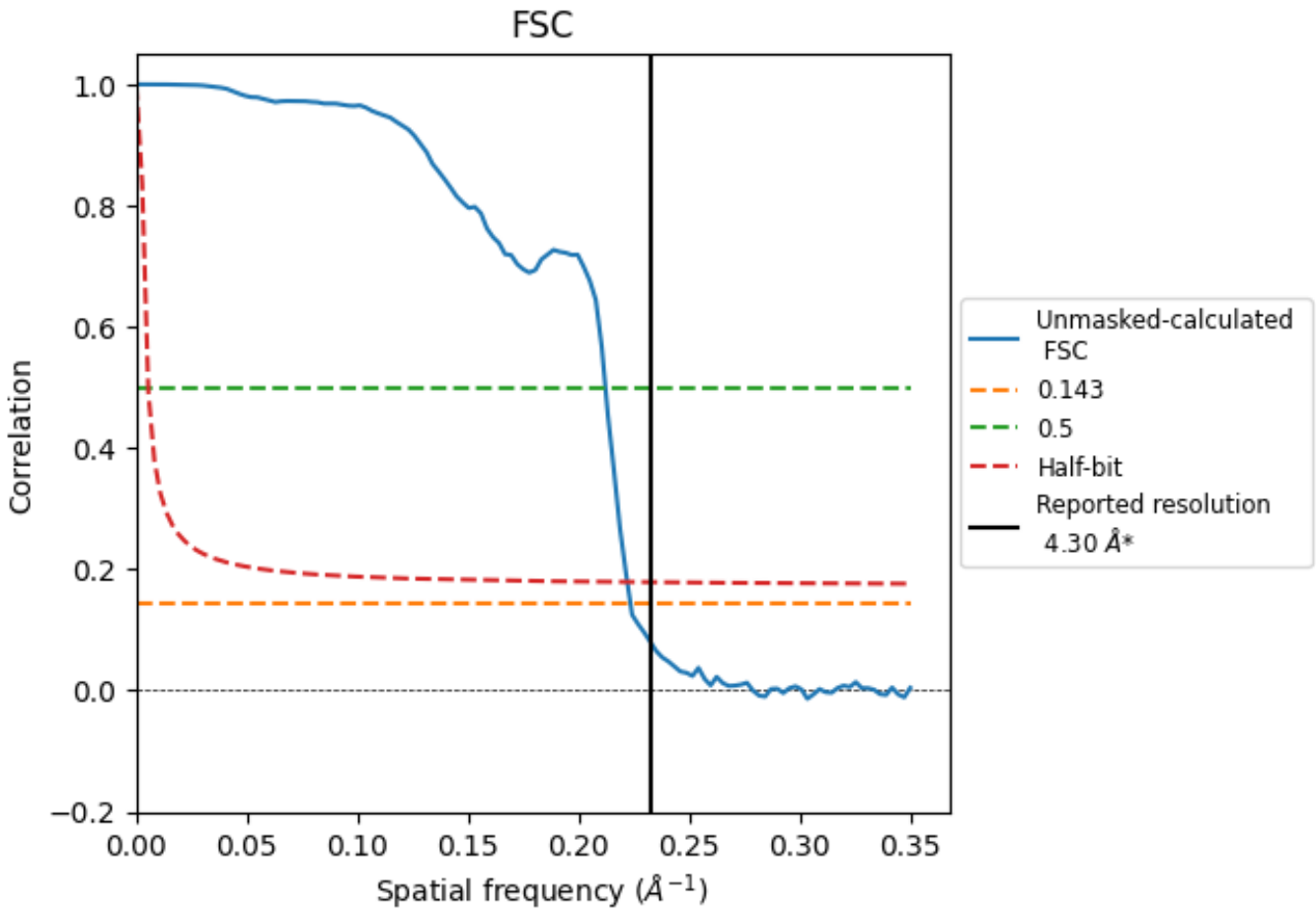


*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

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)

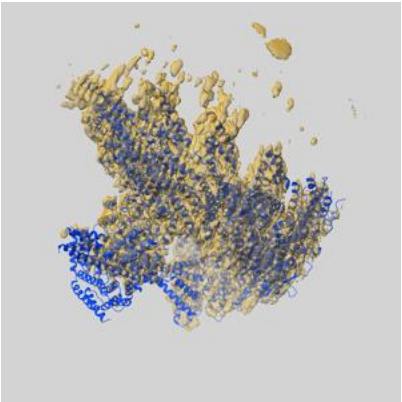
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	4.72	4.50

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

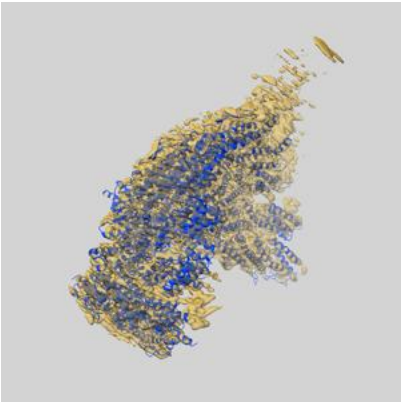
9 Map-model fit (i)

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.

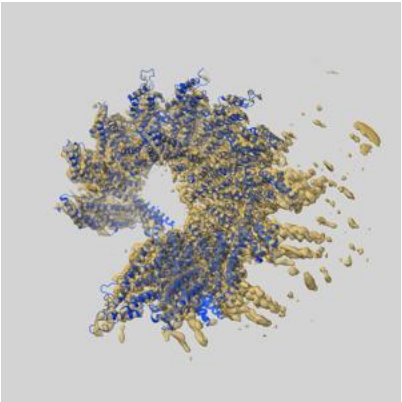
9.1 Map-model overlay (i)



X



Y



Z

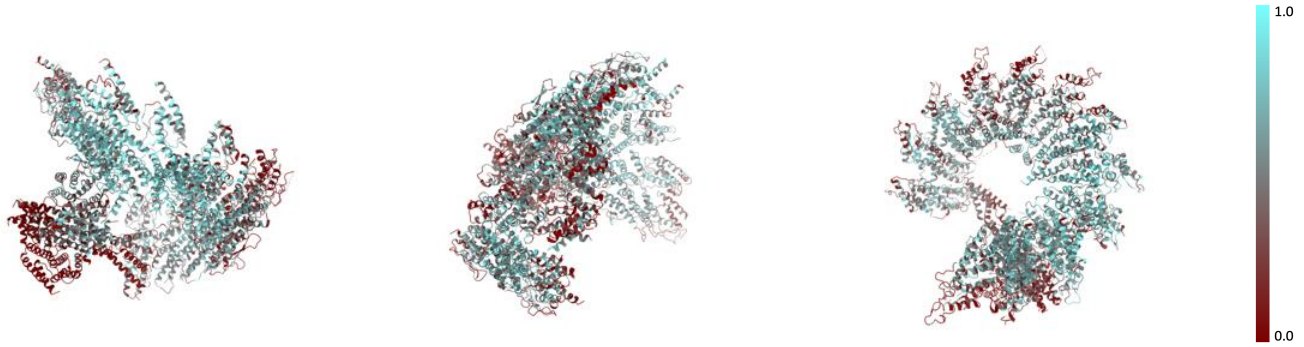
The images above show the 3D surface view of the map at the recommended contour level 0.0421 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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.

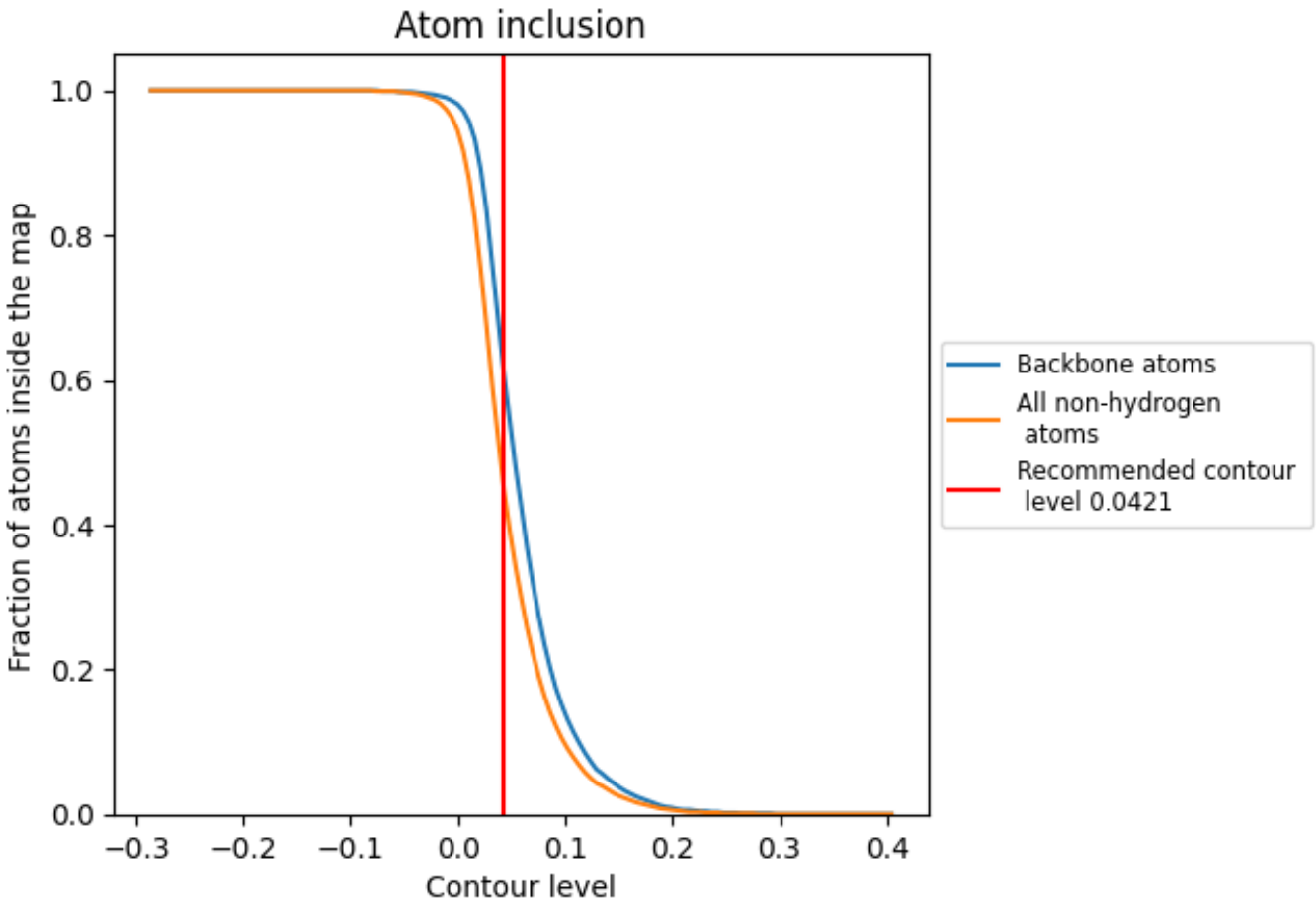
9.3 Atom inclusion mapped to coordinate model (i)



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