wwPDB EM Validation Summary Report (i)

Mar 5, 2026 – 02:00 PM UTC

PDB ID	:	9QZF / pdb_00009qzf
EMDB ID	:	EMD-53471
Title	:	Proximal A-C linker of Tetrahymena centriole, six repeating units
Authors	:	Cai, B.; Xu, J.W.; Luo, L.; Aarts, E.; Leitner, A.; Ishikawa, T.; Beltro, P.; Pilhofer, M.; Wieczorek, M.
Deposited on	:	2025-04-22
Resolution	:	3.80 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:

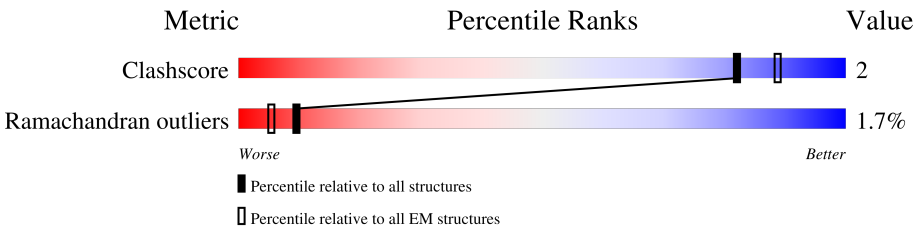
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

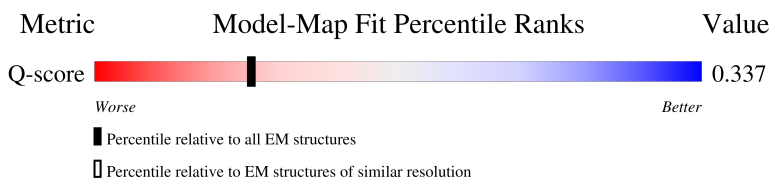
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 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	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	452	11% 83% 10% • 5%
1	BD	452	6% 83% 11% • 5%
1	C	452	10% 82% 11% • 5%
1	CP	452	5% 82% 11% • 5%
1	Ca	452	11% 82% 11% • 5%

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Mol	Chain	Length	Quality of chain
1	i	452	85% 9% 5%
2	BK	380	6% 65% 7% 25%
2	BR	380	8% 58% 7% 32%
2	CW	380	5% 64% 8% 25%
2	Cd	380	7% 55% 8% 32%
2	Ch	380	9% 64% 7% 25%
2	D	380	8% 65% 7% 25%
2	f	380	11% 56% 8% 32%
2	k	380	15% 61% 11% 25%
2	q	380	68% 5% 25%
2	s	380	19% 57% 8% 32%
2	y	380	6% 56% 10% 32%
2	z	380	11% 56% 10% 32%
3	1	937	20% 56% 9% 34%
3	7	937	14% 73% 12% 13%
3	BY	937	15% 70% 10% 18%
3	E	937	14% 66% 9% 23%
3	I	937	22% 75% 10% 13%
3	n	937	21% 59% 10% 29%
4	BO	151	91% 9%
4	BZ	151	92% 8%
4	Bw	151	94% 6%
4	F	151	6% 93% 7%
4	d	151	5% 93% 7%
4	o	151	45% 95% 5%

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Mol	Chain	Length	Quality of chain
5	9	1202	5% 20% 75%
5	AB	1202	16% 25% 71%
5	AE	1202	36% 5% 57%
5	AO	1202	17% 24% 5% 71%
5	AU	1202	14% 24% 71%
5	Bf	1202	33% 5% 61%
5	Bt	1202	15% 24% 71%
5	G	1202	29% 66%
5	L	1202	5% 36% 6% 57%
5	M	1202	13% 24% 5% 71%
5	R	1202	17% 25% 71%
5	v	1202	25% 70%
6	B4	164	12% 99%
6	BV	164	12% 99%
6	Bg	164	12% 99%
6	H	164	14% 99%
6	l	164	17% 99%
6	w	164	17% 99%
7	4	634	15% 44% 12% 42%
7	AG	634	16% 43% 12% 42%
7	AM	634	11% 44% 12% 42%
7	Bm	634	13% 43% 12% 42%
7	J	634	11% 44% 10% 42%
7	O	634	18% 47% 8% 42%
8	5	167	12% 100%

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Mol	Chain	Length	Quality of chain
8	Bc	167	10% 100%
8	Bn	167	9% 100%
8	CA	167	8% 100%
8	K	167	14% 100%
8	t	167	15% 100%
9	2	161	98%
9	AC	161	99%
9	Bj	161	100%
9	Bu	161	100%
9	CH	161	100%
9	N	161	100%
10	AJ	32	12% 100%
10	AW	32	100%
10	Ac	32	100%
10	B1	32	100%
10	P	32	100%
10	U	32	9% 100%
11	0	105	7% 99%
11	AK	105	8% 98%
11	B2	105	5% 99%
11	Bq	105	99%
11	CO	105	6% 99%
11	Q	105	7% 98%
12	AR	33	9% 100%
12	Ae	33	15% 100%

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Mol	Chain	Length	Quality of chain
12	Ak	33	12% 100%
12	B8	33	6% 100%
12	S	33	6% 100%
12	X	33	12% 100%
13	AH	127	98%
13	AS	127	22% 99%
13	B9	127	98%
13	Bx	127	98%
13	CV	127	98%
13	T	127	98%
14	AZ	153	9% 95% 5%
14	Am	153	33% 90% 10%
14	As	153	95% 5%
14	CE	153	95% 5%
14	V	153	6% 96%
14	a	153	8% 95% 5%
15	AP	102	6% 94% 5%
15	Aa	102	21% 98%
15	B5	102	96%
15	CF	102	95%
15	Cc	102	97%
15	W	102	7% 97%
16	A7	230	7% 57% 10% 31%
16	Ai	230	8% 54% 8% 34%
16	An	230	10% 55% 8% 34%

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Mol	Chain	Length	Quality of chain
16	Aq	230	11% 58% 8% • 31%
16	Av	230	15% 57% 8% • 31%
16	Az	230	7% 55% 8% • 34%
16	CB	230	6% 55% 8% • 34%
16	CI	230	11% 56% 10% • 31%
16	CM	230	5% 53% 9% • 34%
16	CT	230	8% 58% 8% • 31%
16	Z	230	5% 53% 9% • 34%
16	c	230	11% 57% 10% • 31%

2 Entry composition (i)

There are 16 unique types of molecules in this entry. The entry contains 130144 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 WD repeat WRAP73-like protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	429	2129	1271	429	429	0	0
1	C	429	2129	1271	429	429	0	0
1	i	429	2129	1271	429	429	0	0
1	BD	429	2129	1271	429	429	0	0
1	CP	429	2129	1271	429	429	0	0
1	Ca	429	2129	1271	429	429	0	0

- Molecule 2 is a protein called Centrosomal protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	D	284	1415	847	284	284	0	0
2	f	258	1288	772	258	258	0	0
2	k	284	1415	847	284	284	0	0
2	q	284	1415	847	284	284	0	0
2	s	258	1288	772	258	258	0	0
2	y	258	1288	772	258	258	0	0
2	BK	284	1415	847	284	284	0	0
2	BR	258	1288	772	258	258	0	0
2	CW	284	1415	847	284	284	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	Cd	258	1288	772	258	258	0	0
2	Ch	284	1415	847	284	284	0	0
2	z	258	1288	772	258	258	0	0

- Molecule 3 is a protein called Rab-GAP TBC domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	E	724	3597	2149	724	724	0	0
3	I	813	4040	2414	813	813	0	0
3	n	665	3302	1972	665	665	0	0
3	1	621	3082	1840	621	621	0	0
3	7	813	4040	2414	813	813	0	0
3	BY	773	3841	2295	773	773	0	0

- Molecule 4 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	F	151	755	453	151	151	0	0
4	d	151	755	453	151	151	0	0
4	o	151	755	453	151	151	0	0
4	BO	151	755	453	151	151	0	0
4	BZ	151	755	453	151	151	0	0
4	Bw	151	755	453	151	151	0	0

- Molecule 5 is a protein called TBC1 domain family member 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	G	414	2064	1236	414	414	0	0
5	L	518	2584	1548	518	518	0	0
5	M	354	1752	1044	354	354	0	0
5	R	354	1752	1044	354	354	0	0
5	v	359	1790	1072	359	359	0	0
5	9	303	1510	904	303	303	0	0
5	AB	354	1752	1044	354	354	0	0
5	AE	518	2584	1548	518	518	0	0
5	AO	354	1752	1044	354	354	0	0
5	AU	354	1752	1044	354	354	0	0
5	Bf	468	2334	1398	468	468	0	0
5	Bt	354	1752	1044	354	354	0	0

- Molecule 6 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	H	164	820	492	164	164	0	0
6	l	164	820	492	164	164	0	0
6	w	164	820	492	164	164	0	0
6	BV	164	820	492	164	164	0	0
6	Bg	164	820	492	164	164	0	0
6	B4	164	820	492	164	164	0	0

- Molecule 7 is a protein called POC1 centriolar protein homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	J	365	1806	1076	365	365	0	0
7	O	365	1806	1076	365	365	0	0
7	4	365	1806	1076	365	365	0	0
7	AG	365	1806	1076	365	365	0	0
7	AM	365	1806	1076	365	365	0	0
7	Bm	365	1806	1076	365	365	0	0

- Molecule 8 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	K	167	835	501	167	167	0	0
8	t	167	835	501	167	167	0	0
8	5	167	835	501	167	167	0	0
8	Bc	167	835	501	167	167	0	0
8	Bn	167	835	501	167	167	0	0
8	CA	167	835	501	167	167	0	0

- Molecule 9 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	N	161	805	483	161	161	0	0
9	2	161	805	483	161	161	0	0
9	AC	161	805	483	161	161	0	0
9	Bj	161	805	483	161	161	0	0
9	Bu	161	805	483	161	161	0	0
9	CH	161	805	483	161	161	0	0

- Molecule 10 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	P	32	160	96	32	32	0	0
10	U	32	160	96	32	32	0	0
10	AJ	32	160	96	32	32	0	0
10	AW	32	160	96	32	32	0	0
10	Ac	32	160	96	32	32	0	0
10	B1	32	160	96	32	32	0	0

- Molecule 11 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	Q	105	525	315	105	105	0	0
11	0	105	525	315	105	105	0	0
11	AK	105	525	315	105	105	0	0
11	Bq	105	525	315	105	105	0	0
11	B2	105	525	315	105	105	0	0
11	CO	105	525	315	105	105	0	0

- Molecule 12 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	S	33	165	99	33	33	0	0
12	X	33	165	99	33	33	0	0
12	AR	33	165	99	33	33	0	0
12	Ae	33	165	99	33	33	0	0
12	Ak	33	165	99	33	33	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	B8	33	165	99	33	33	0	0

- Molecule 13 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	T	127	635	381	127	127	0	0
13	AH	127	635	381	127	127	0	0
13	AS	127	635	381	127	127	0	0
13	Bx	127	635	381	127	127	0	0
13	B9	127	635	381	127	127	0	0
13	CV	127	635	381	127	127	0	0

- Molecule 14 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	V	153	765	459	153	153	0	0
14	a	153	765	459	153	153	0	0
14	AZ	153	765	459	153	153	0	0
14	Am	153	765	459	153	153	0	0
14	As	153	765	459	153	153	0	0
14	CE	153	765	459	153	153	0	0

- Molecule 15 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	W	102	510	306	102	102	0	0
15	AP	102	510	306	102	102	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	Aa	102	510	306	102	102	0	0
15	B5	102	510	306	102	102	0	0
15	CF	102	510	306	102	102	0	0
15	Cc	102	510	306	102	102	0	0

- Molecule 16 is a protein called SWIM-type domain-containing protein.

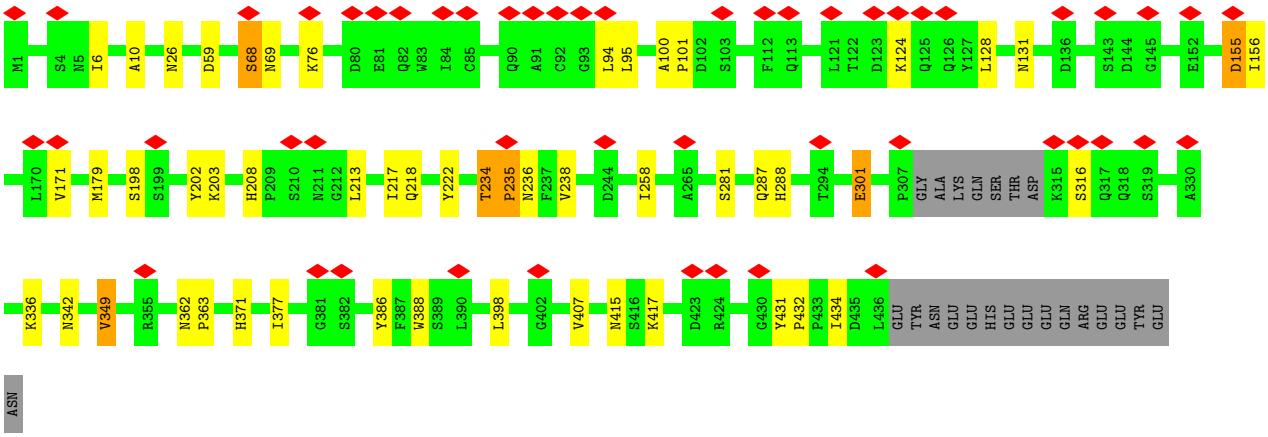
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	Z	151	748	446	151	151	0	0
16	c	158	783	467	158	158	0	0
16	Ai	151	748	446	151	151	0	0
16	An	151	748	446	151	151	0	0
16	Aq	158	783	467	158	158	0	0
16	Av	158	783	467	158	158	0	0
16	Az	151	748	446	151	151	0	0
16	A7	158	783	467	158	158	0	0
16	CB	151	748	446	151	151	0	0
16	CI	158	783	467	158	158	0	0
16	CM	151	748	446	151	151	0	0
16	CT	158	783	467	158	158	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.

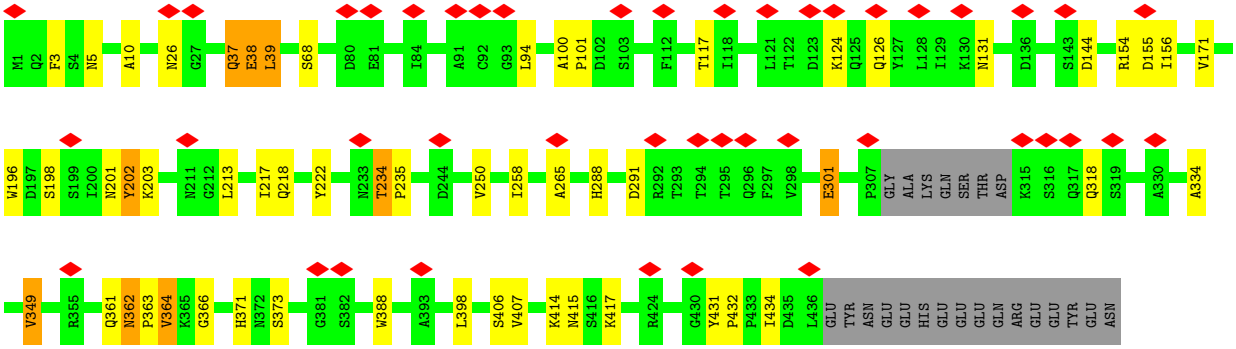
• Molecule 1: WD repeat WRAP73-like protein, putative

Chain A:



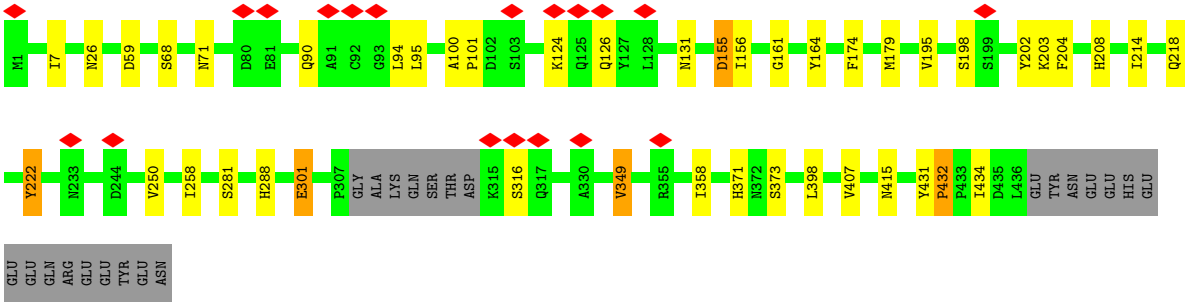
• Molecule 1: WD repeat WRAP73-like protein, putative

Chain C:



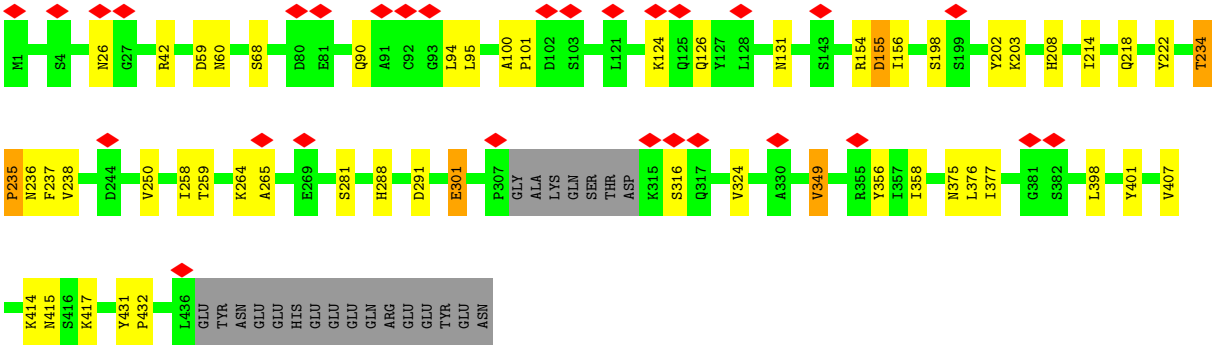
• Molecule 1: WD repeat WRAP73-like protein, putative

Chain i:



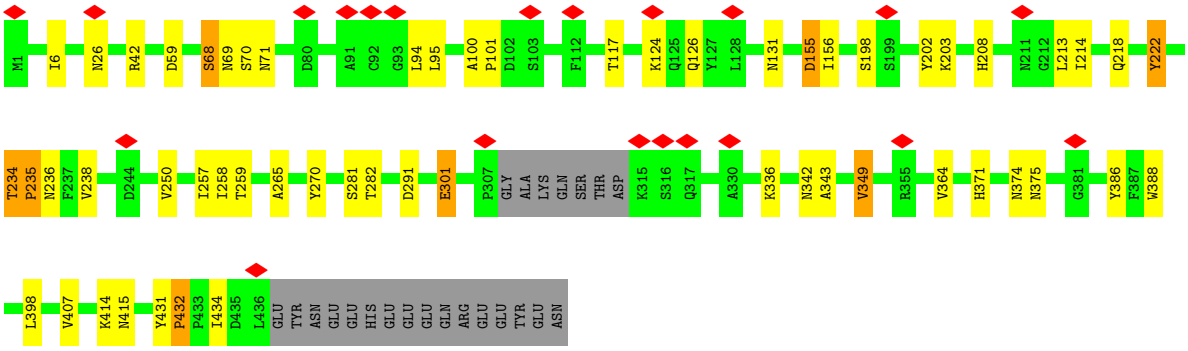
• Molecule 1: WD repeat WRAP73-like protein, putative

Chain BD:



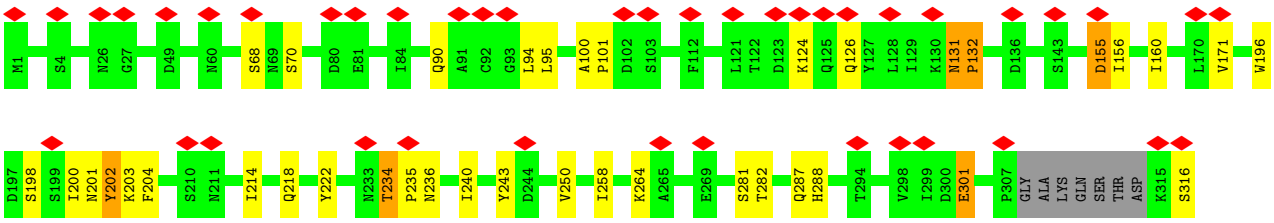
• Molecule 1: WD repeat WRAP73-like protein, putative

Chain CP:



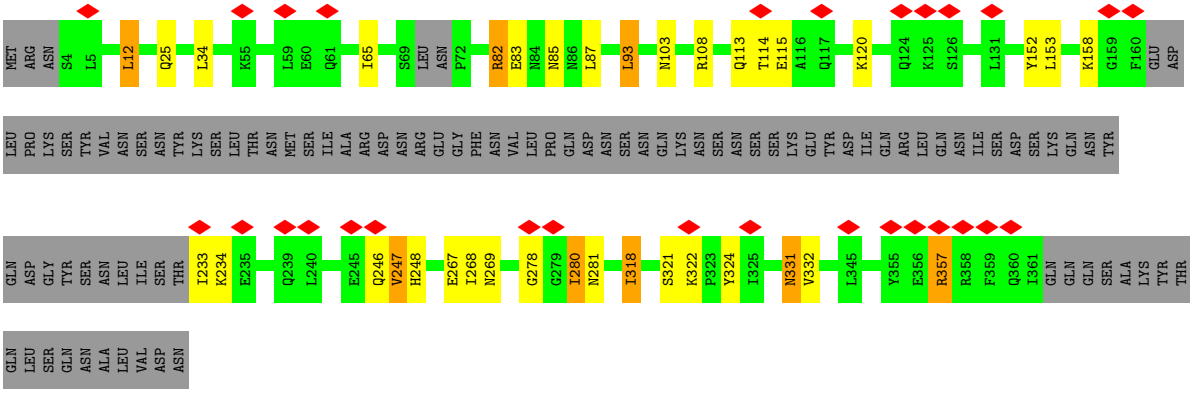
• Molecule 1: WD repeat WRAP73-like protein, putative

Chain Ca:



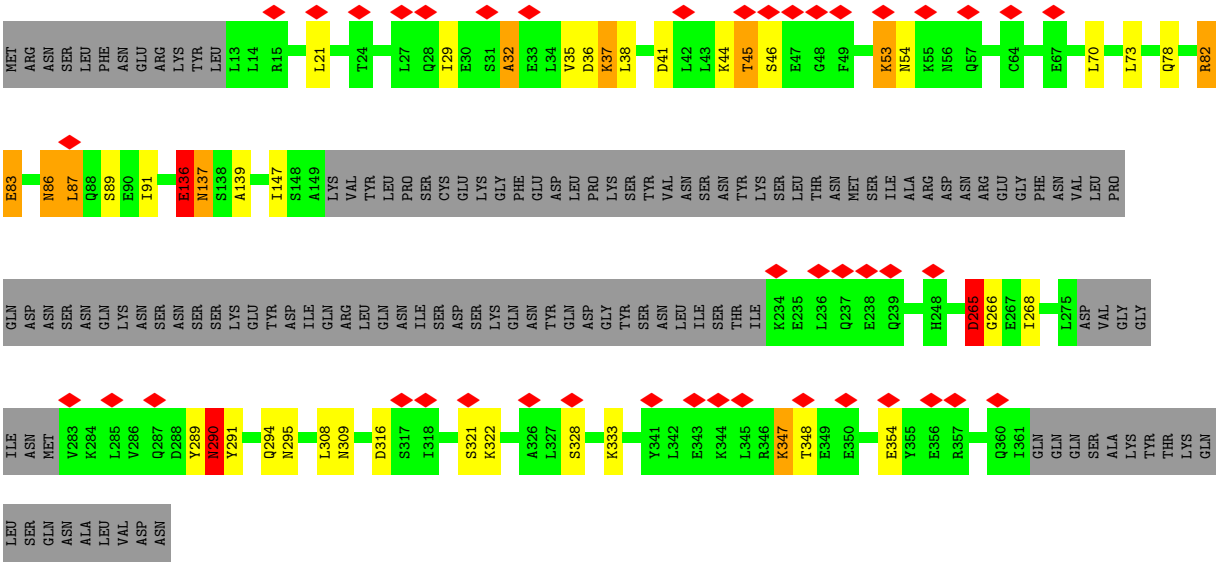
- Molecule 2: Centrosomal protein, putative

Chain D:



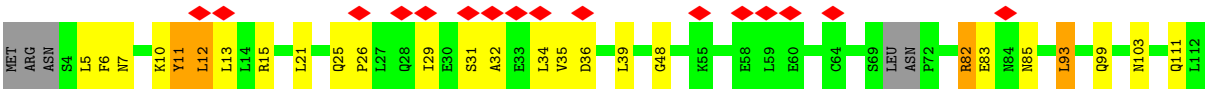
- Molecule 2: Centrosomal protein, putative

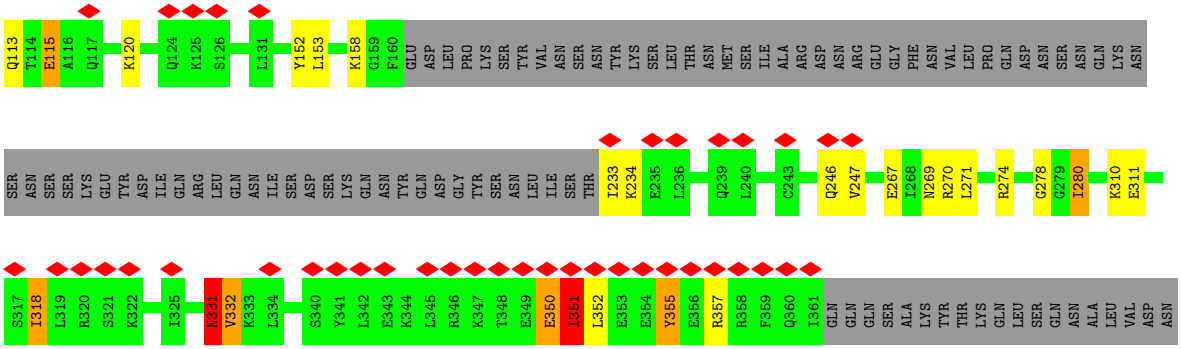
Chain f:



- Molecule 2: Centrosomal protein, putative

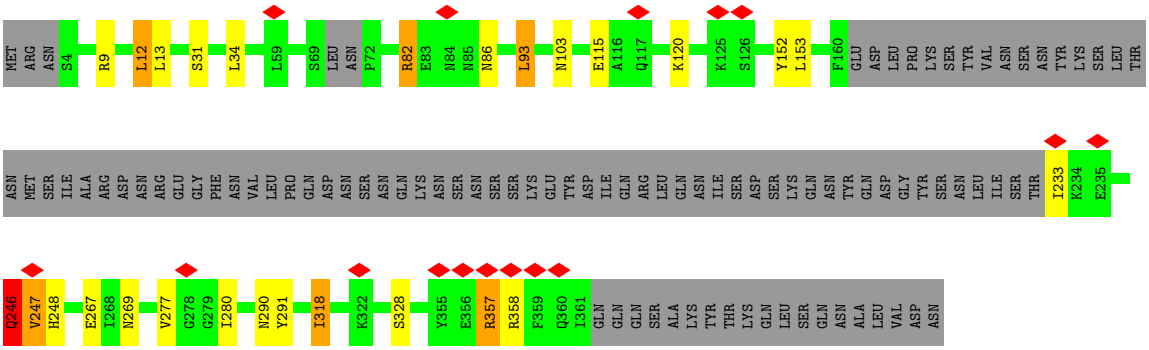
Chain k:





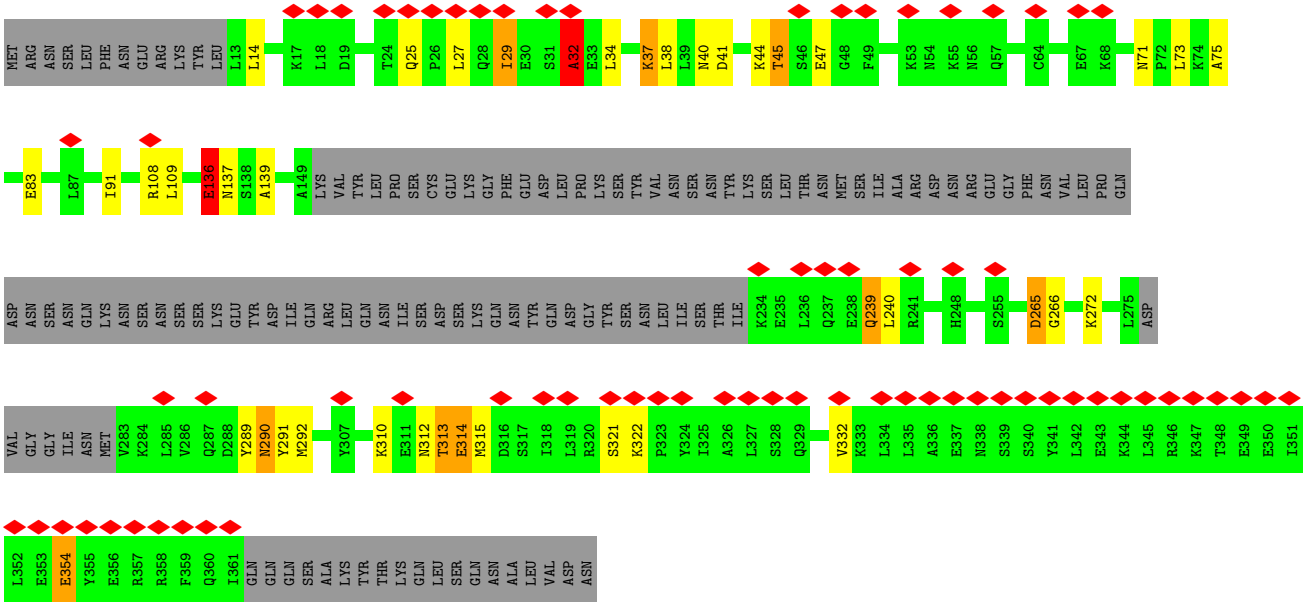
- Molecule 2: Centrosomal protein, putative

Chain q:



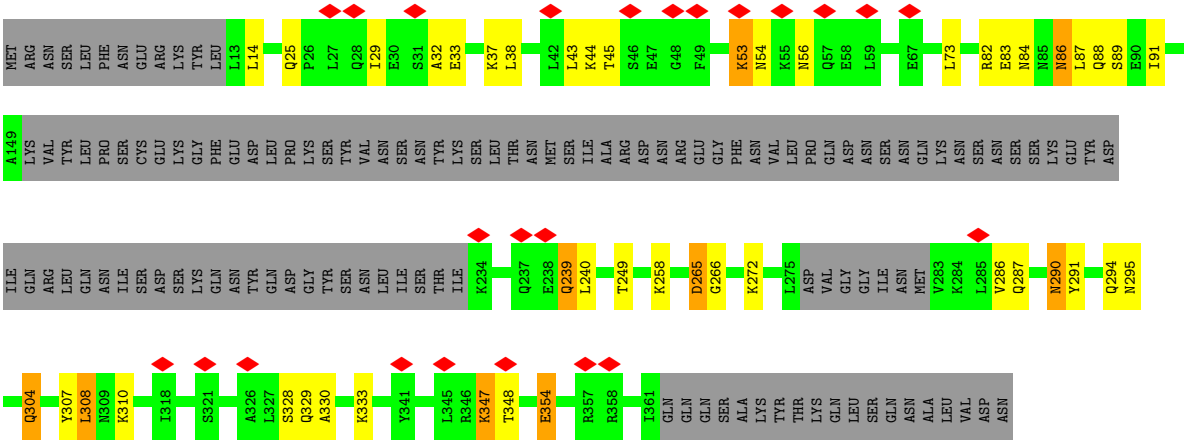
- Molecule 2: Centrosomal protein, putative

Chain s:



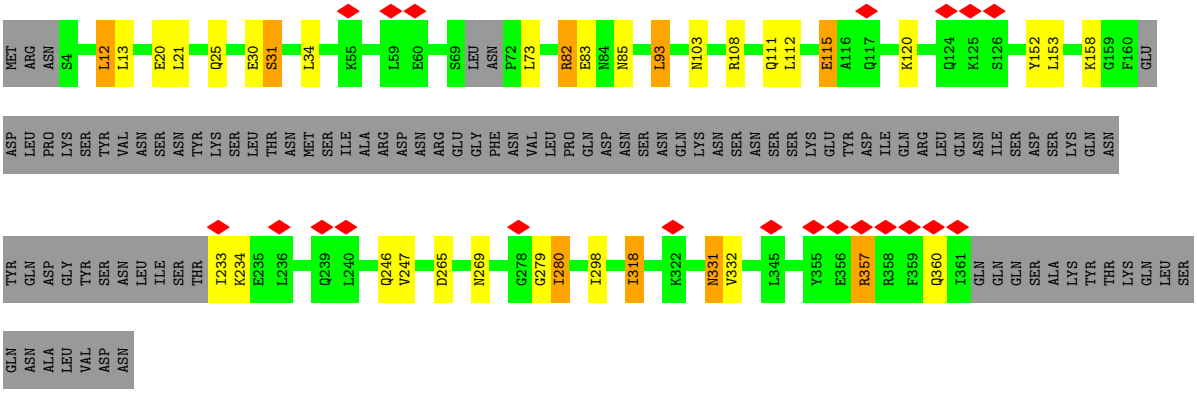
- Molecule 2: Centrosomal protein, putative

Chain y:



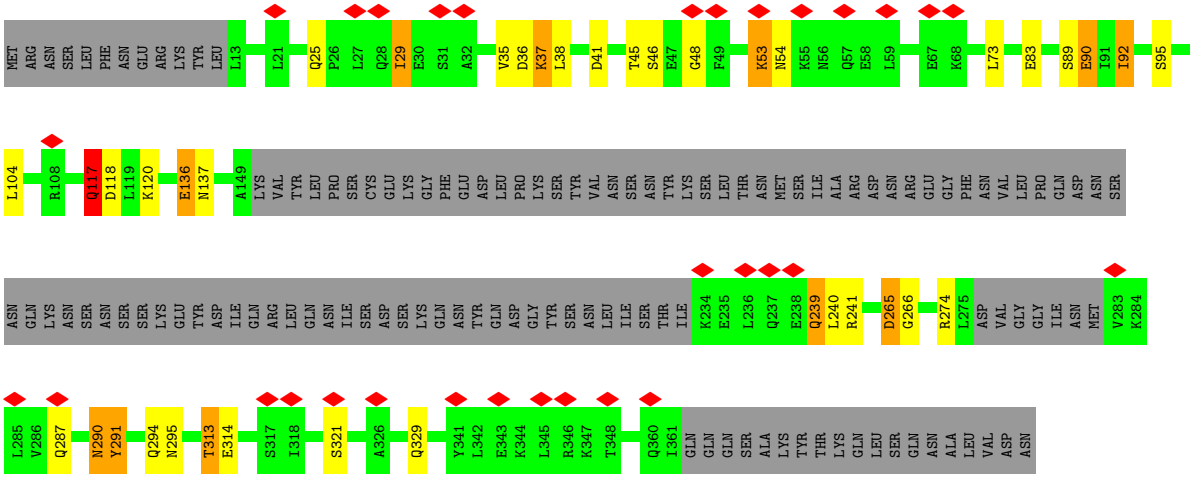
• Molecule 2: Centrosomal protein, putative

Chain BK:



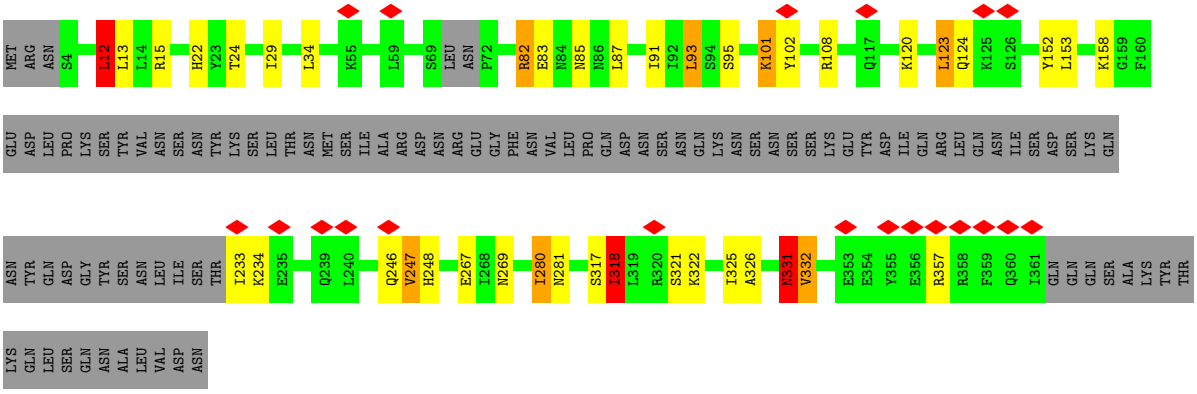
• Molecule 2: Centrosomal protein, putative

Chain BR:



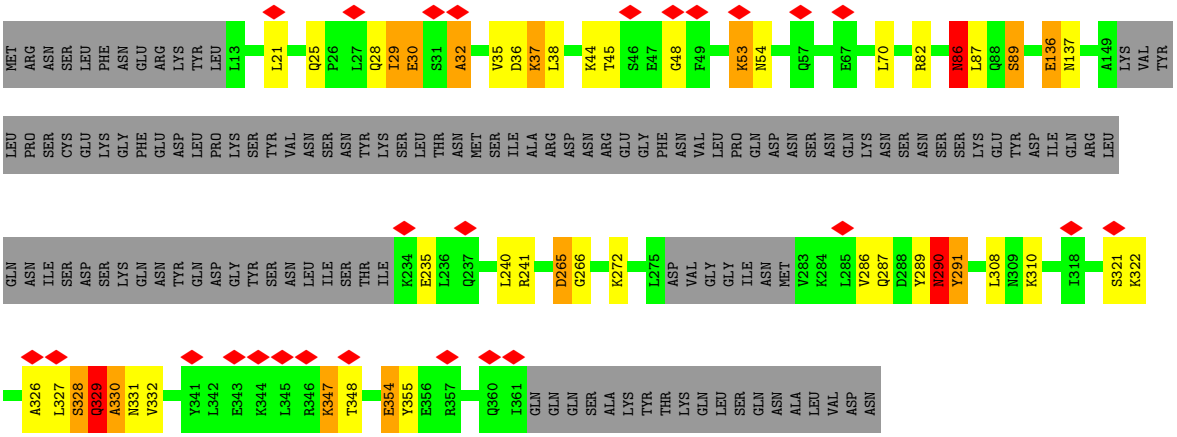
• Molecule 2: Centrosomal protein, putative

Chain CW:



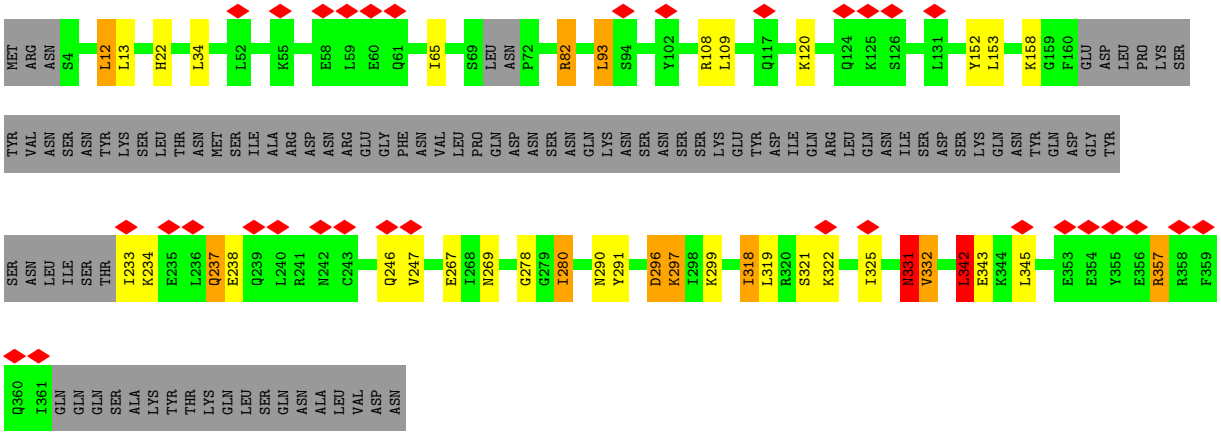
• Molecule 2: Centrosomal protein, putative

Chain Cd:



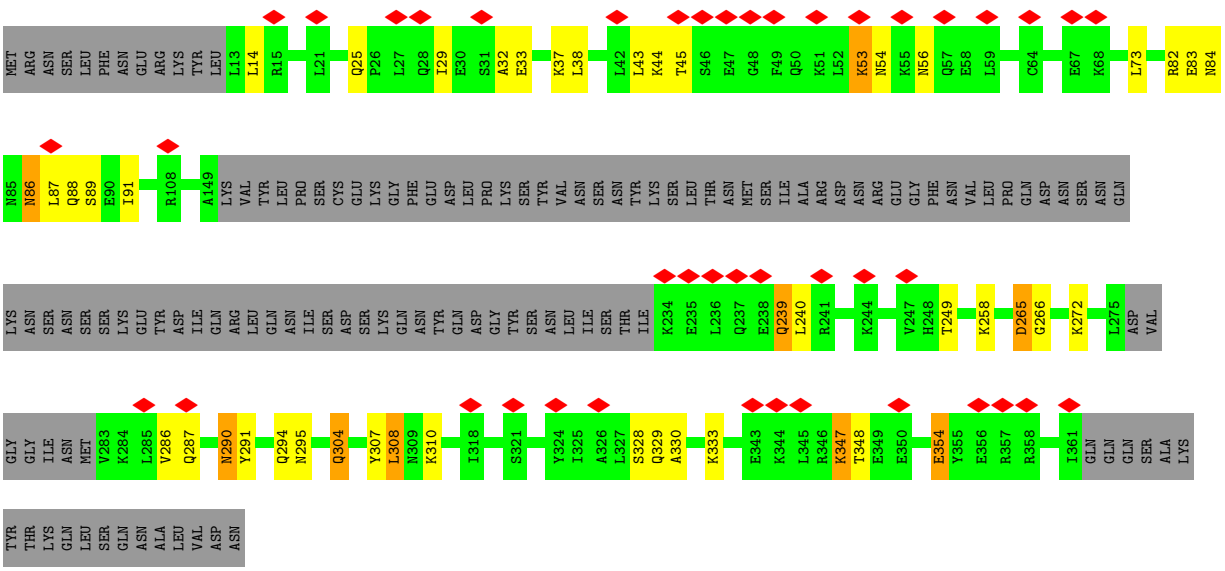
• Molecule 2: Centrosomal protein, putative

Chain Ch:



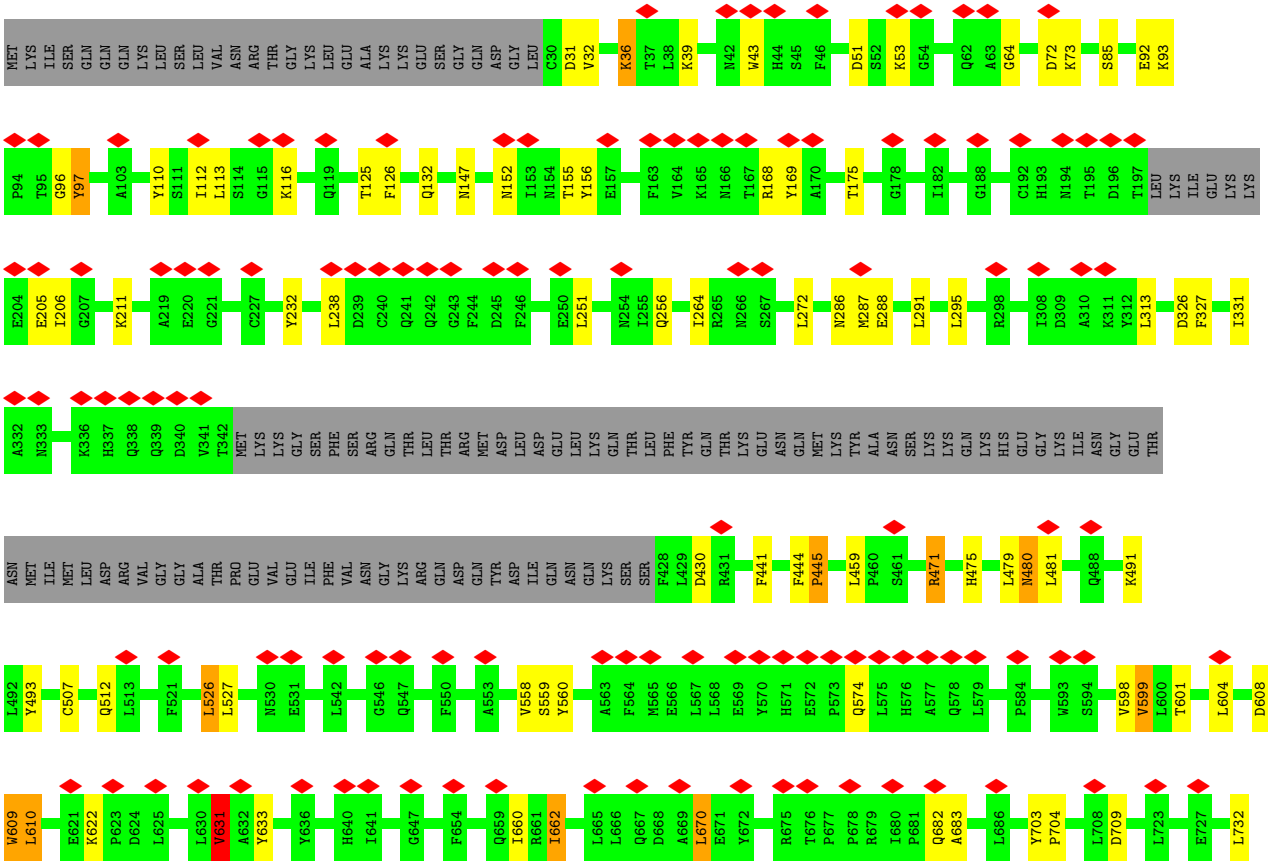
- Molecule 2: Centrosomal protein, putative

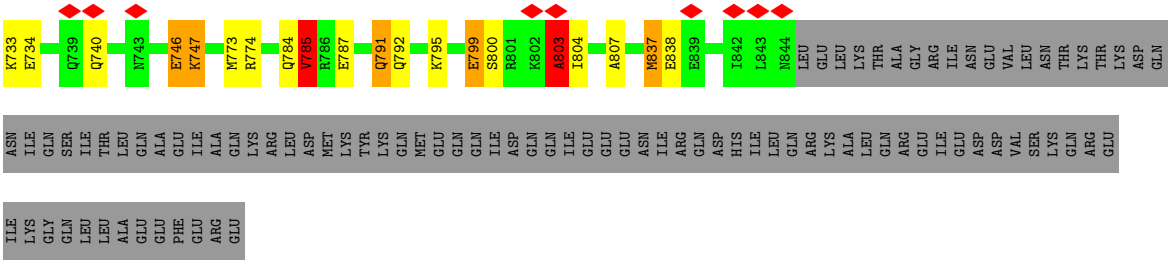
Chain z:



- Molecule 3: Rab-GAP TBC domain-containing protein

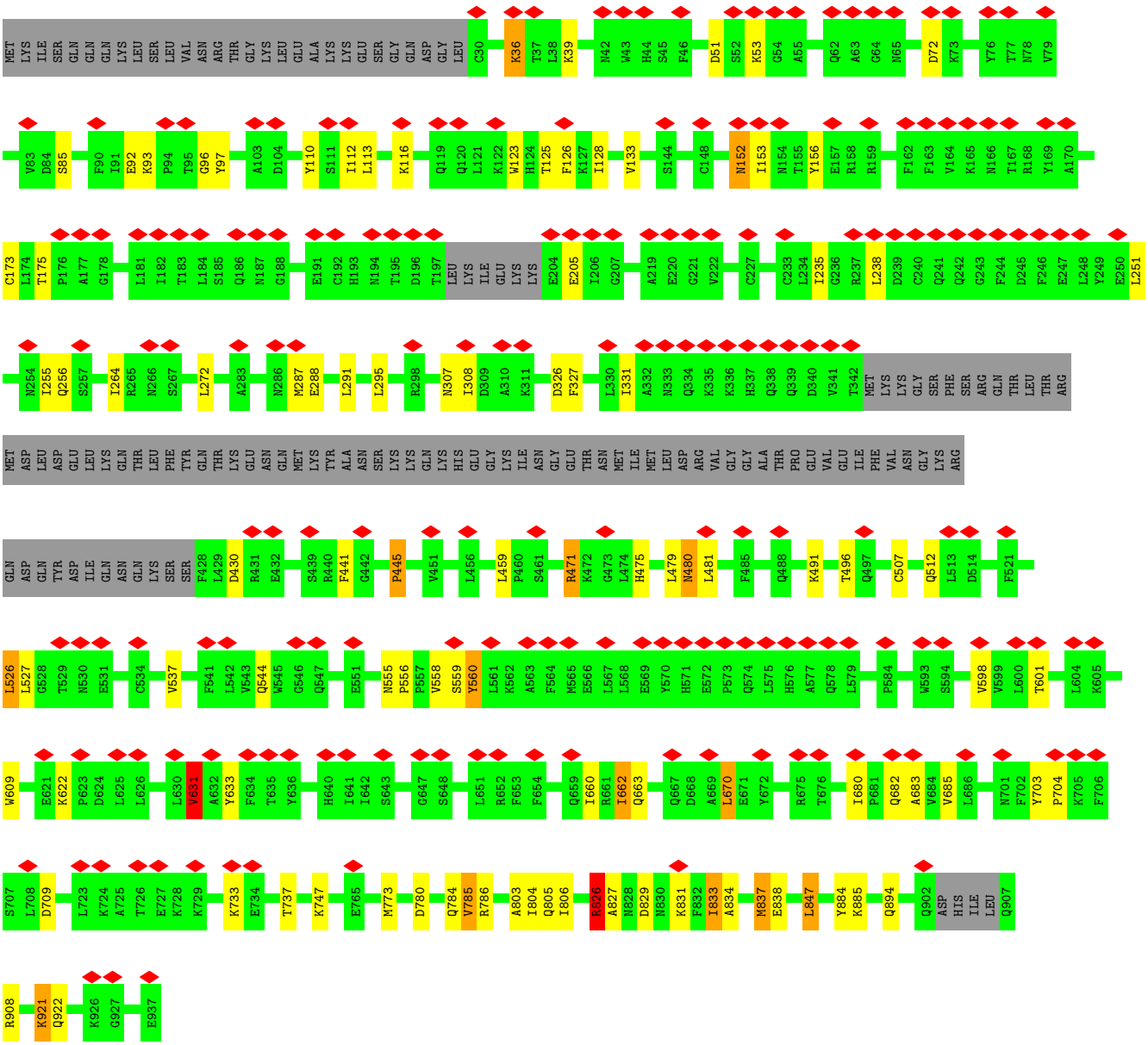
Chain E:





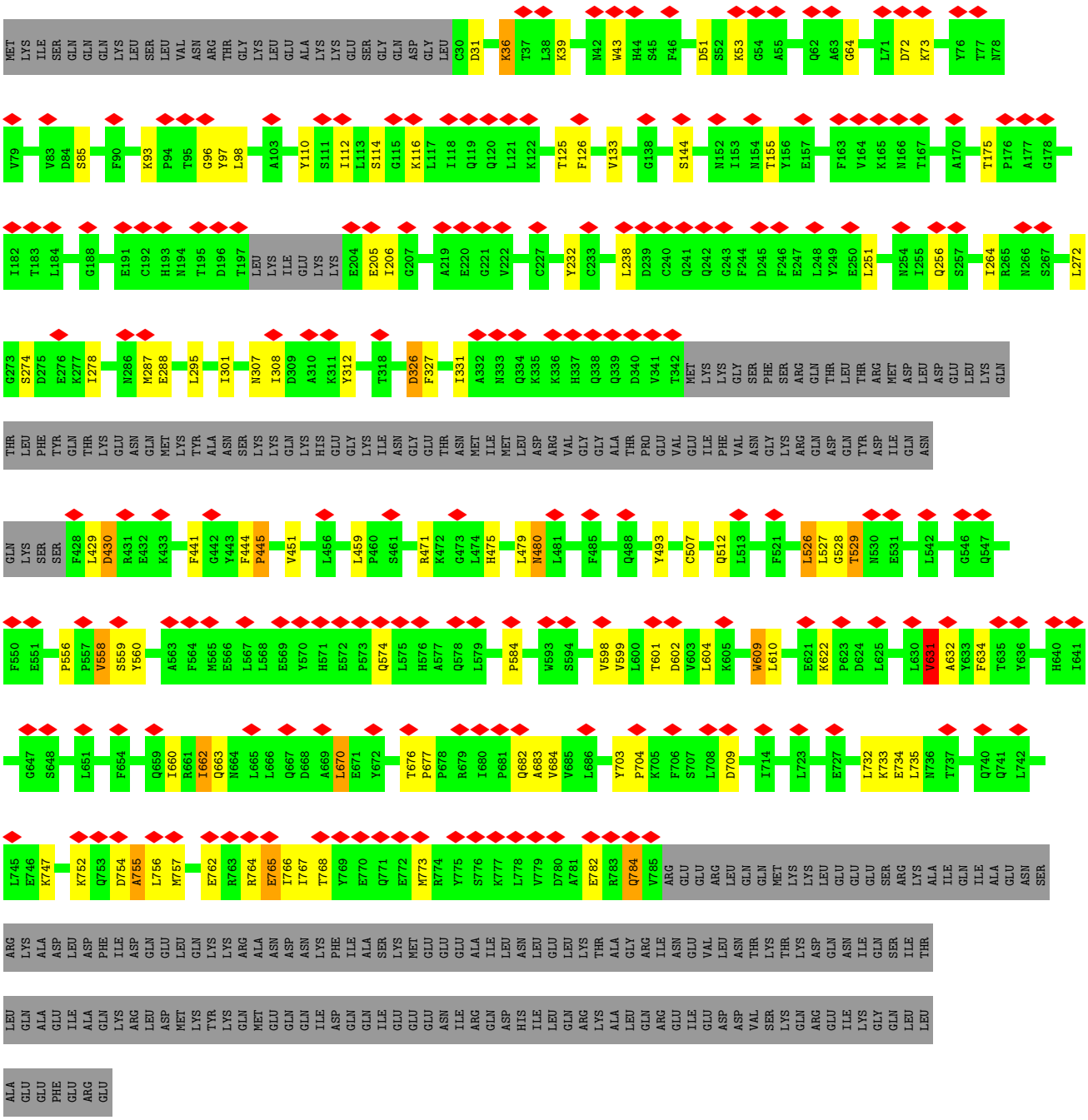
• Molecule 3: Rab-GAP TBC domain-containing protein

Chain I:



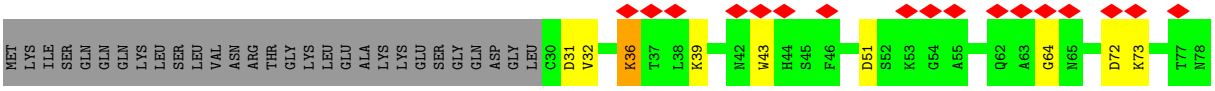
• Molecule 3: Rab-GAP TBC domain-containing protein

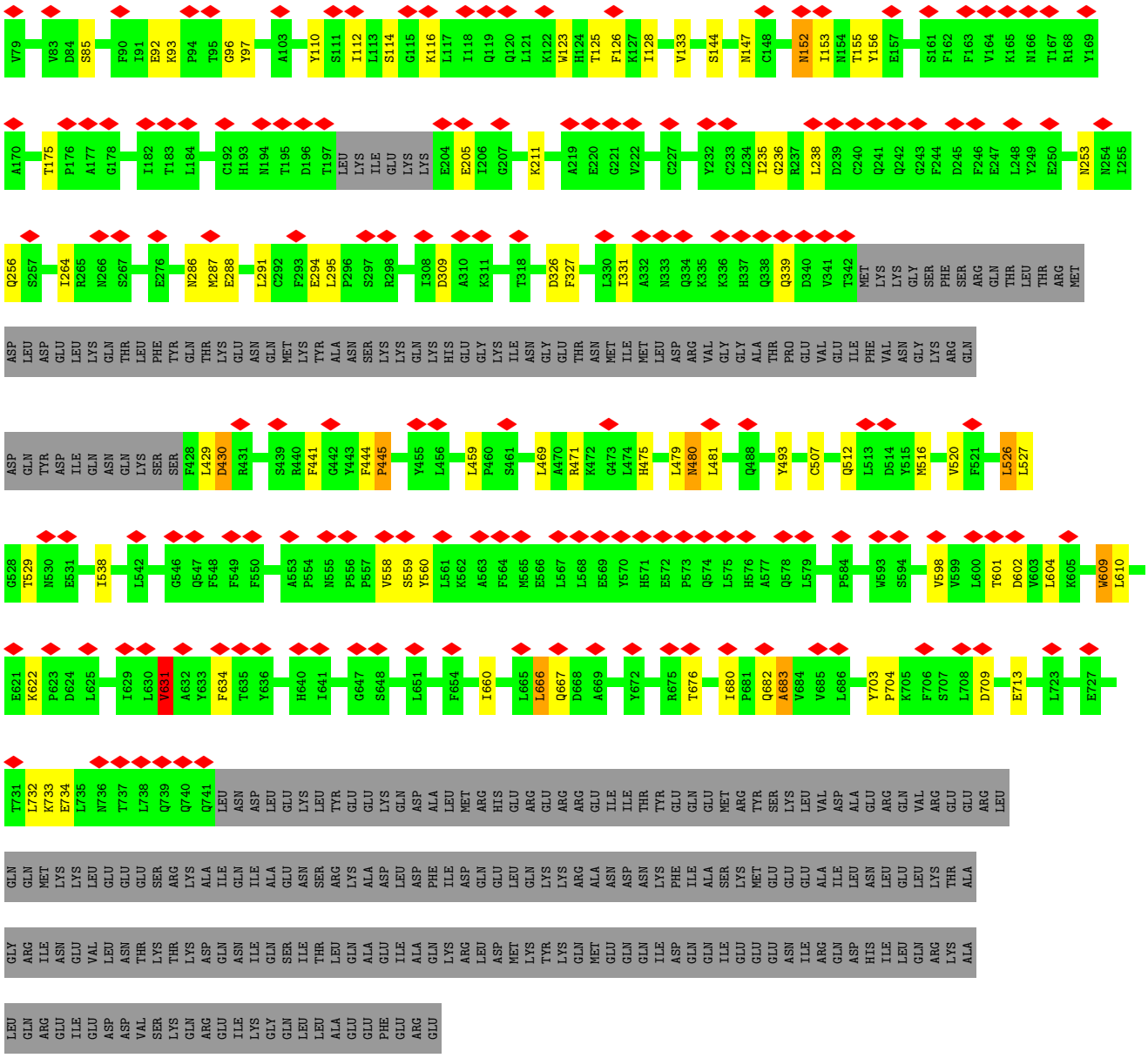
Chain n:



- Molecule 3: Rab-GAP TBC domain-containing protein

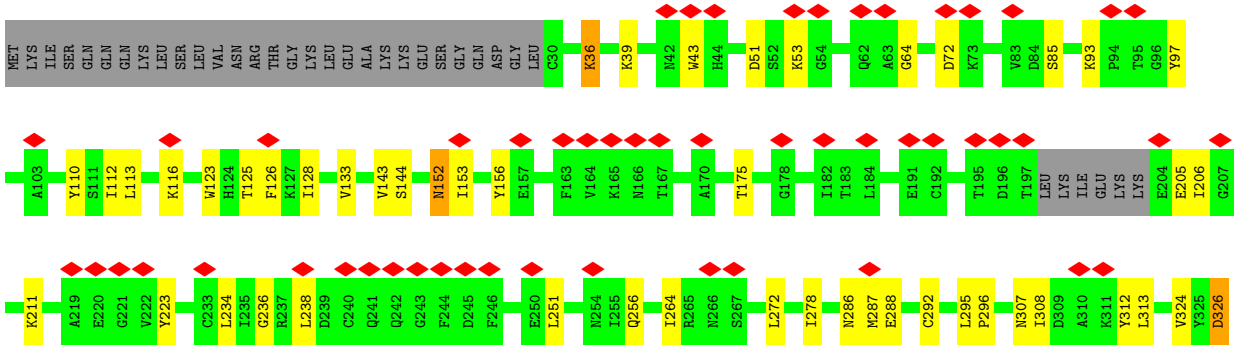
Chain 1:

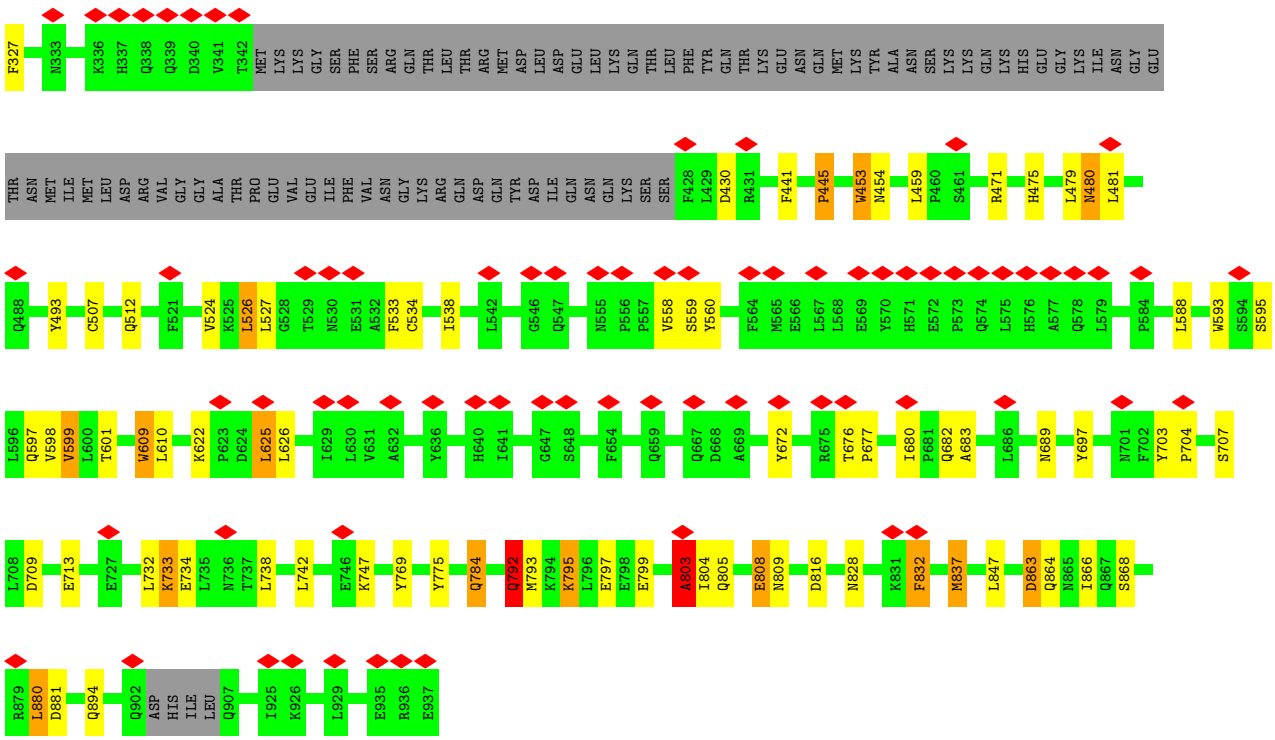




- Molecule 3: Rab-GAP TBC domain-containing protein

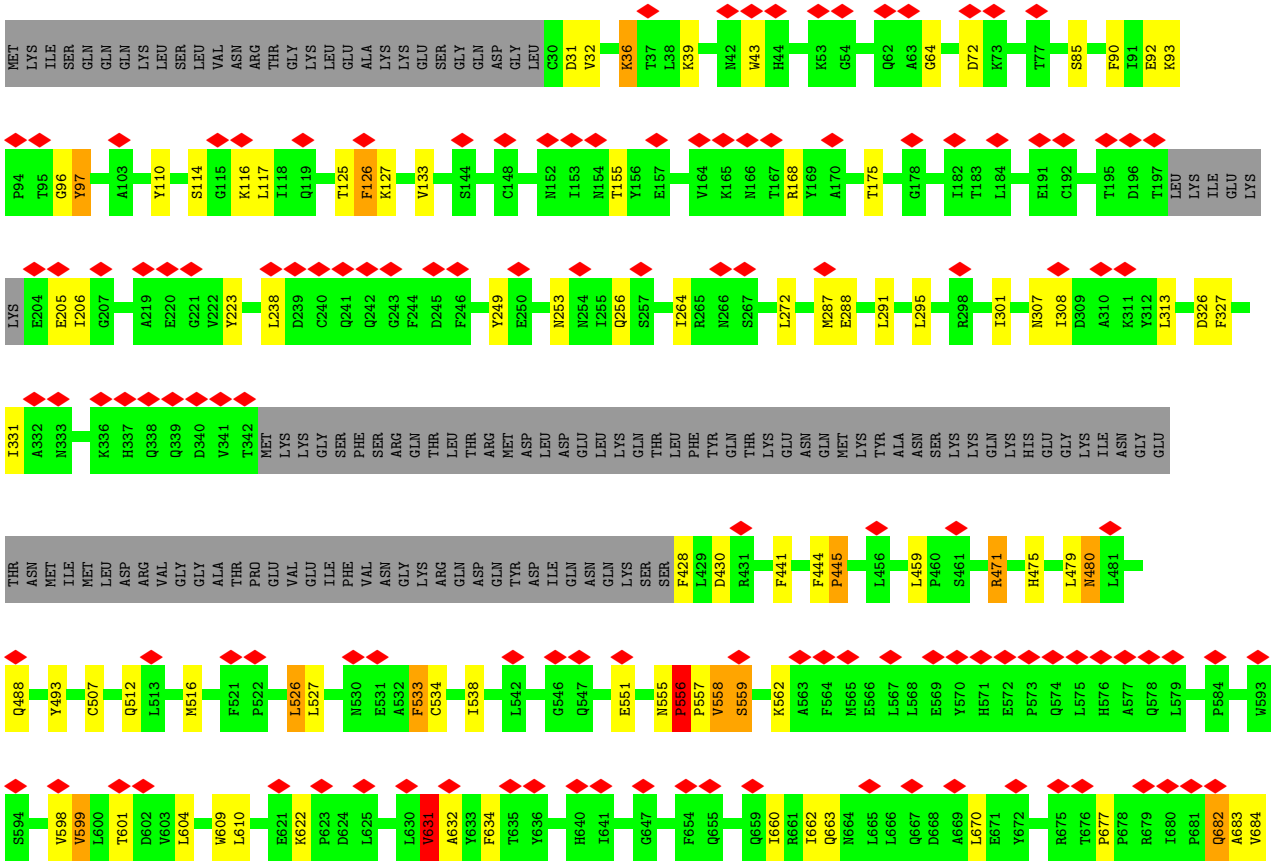
Chain 7:

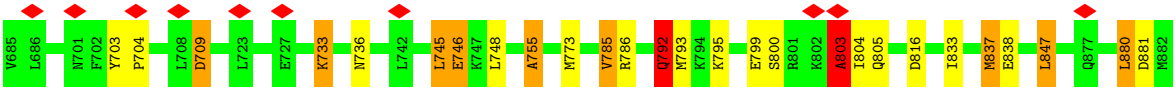


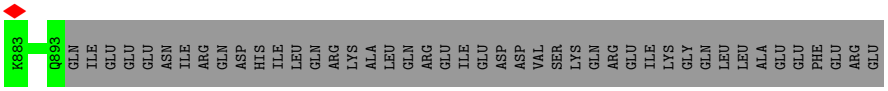


• Molecule 3: Rab-GAP TBC domain-containing protein

Chain BY:







• Molecule 4: Unknown Protein Chain

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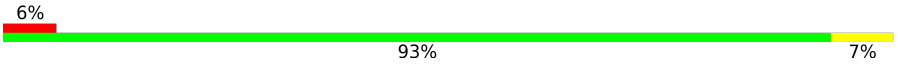
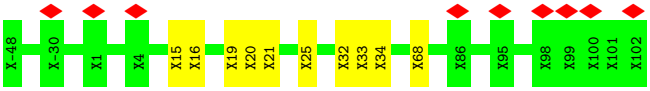
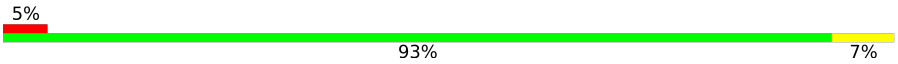
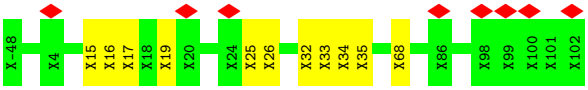




• Molecule 4: Unknown Protein Chain

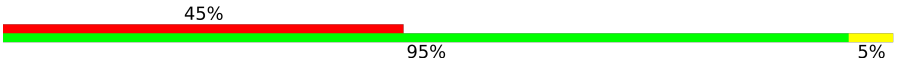
Chain d:

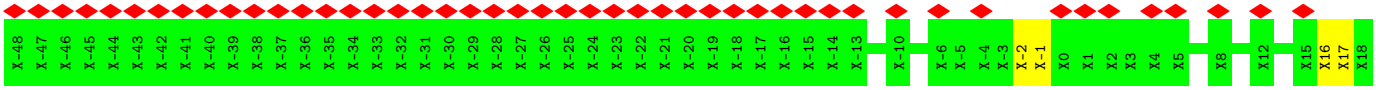


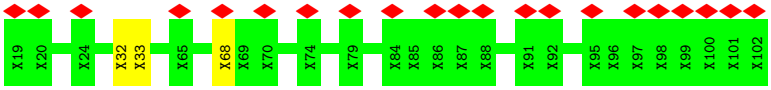


• Molecule 4: Unknown Protein Chain

Chain o:







• Molecule 4: Unknown Protein Chain

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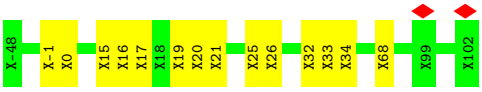

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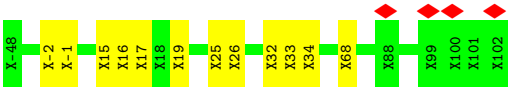

• Molecule 4: Unknown Protein Chain

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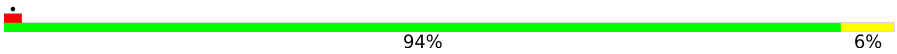
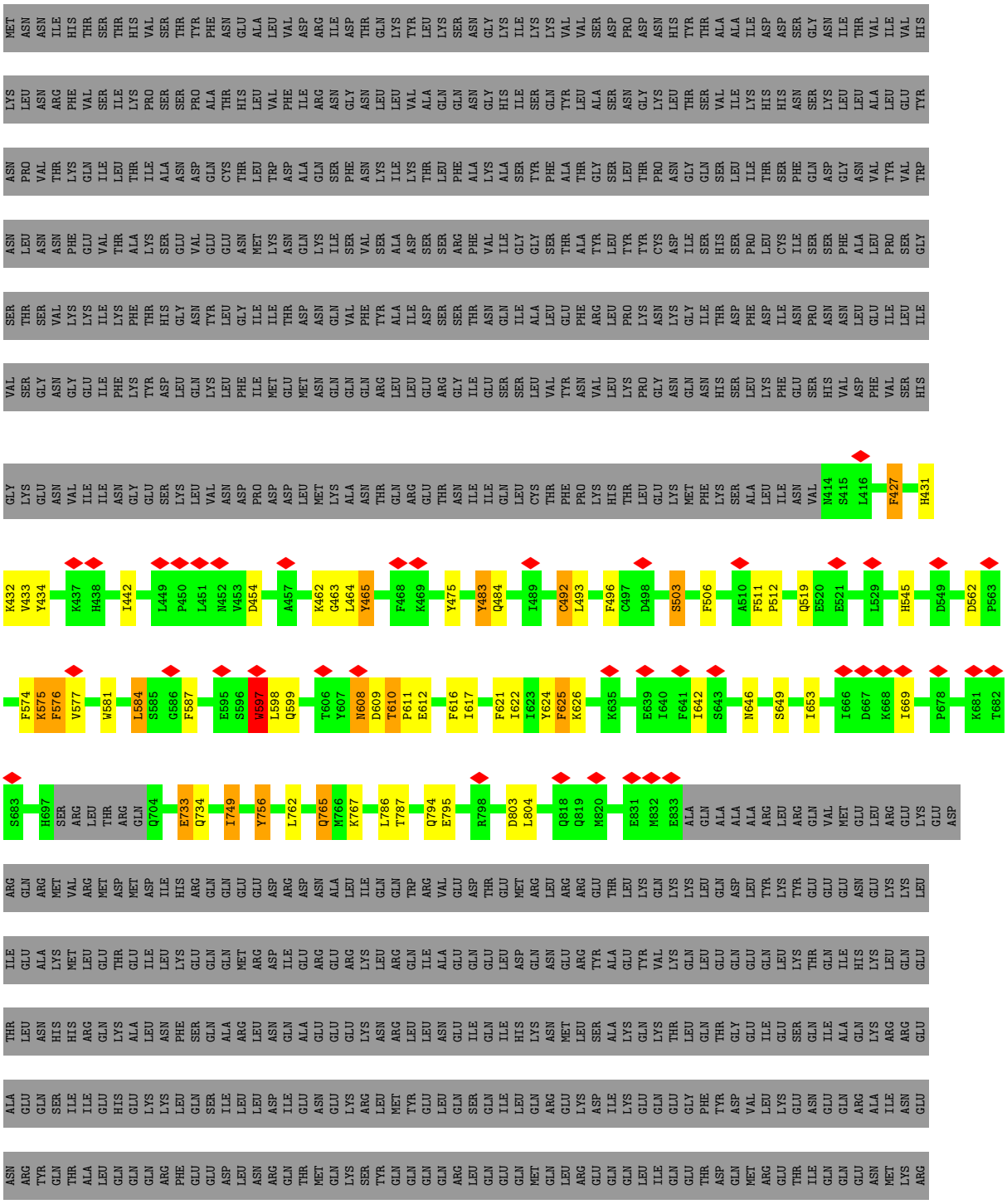
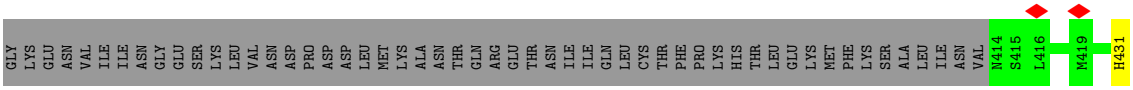


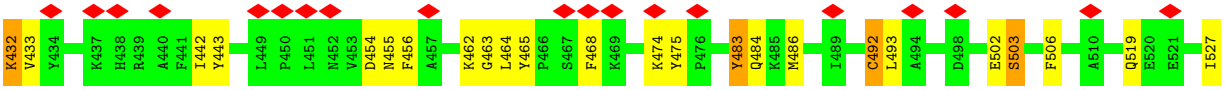
• Molecule 5: TBC1 domain family member 31

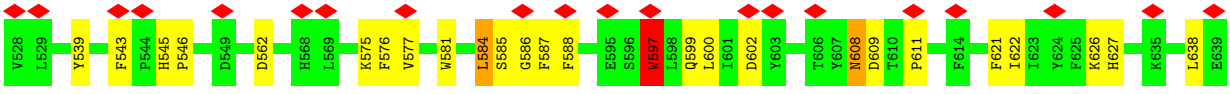
Chain G:

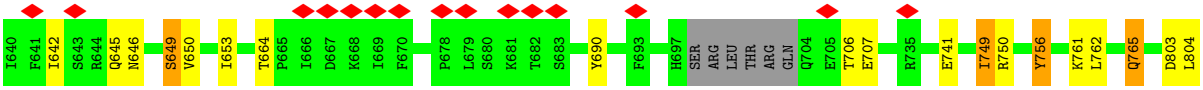


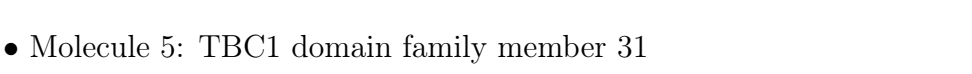
- Molecule 5: TBC1 domain family member 31







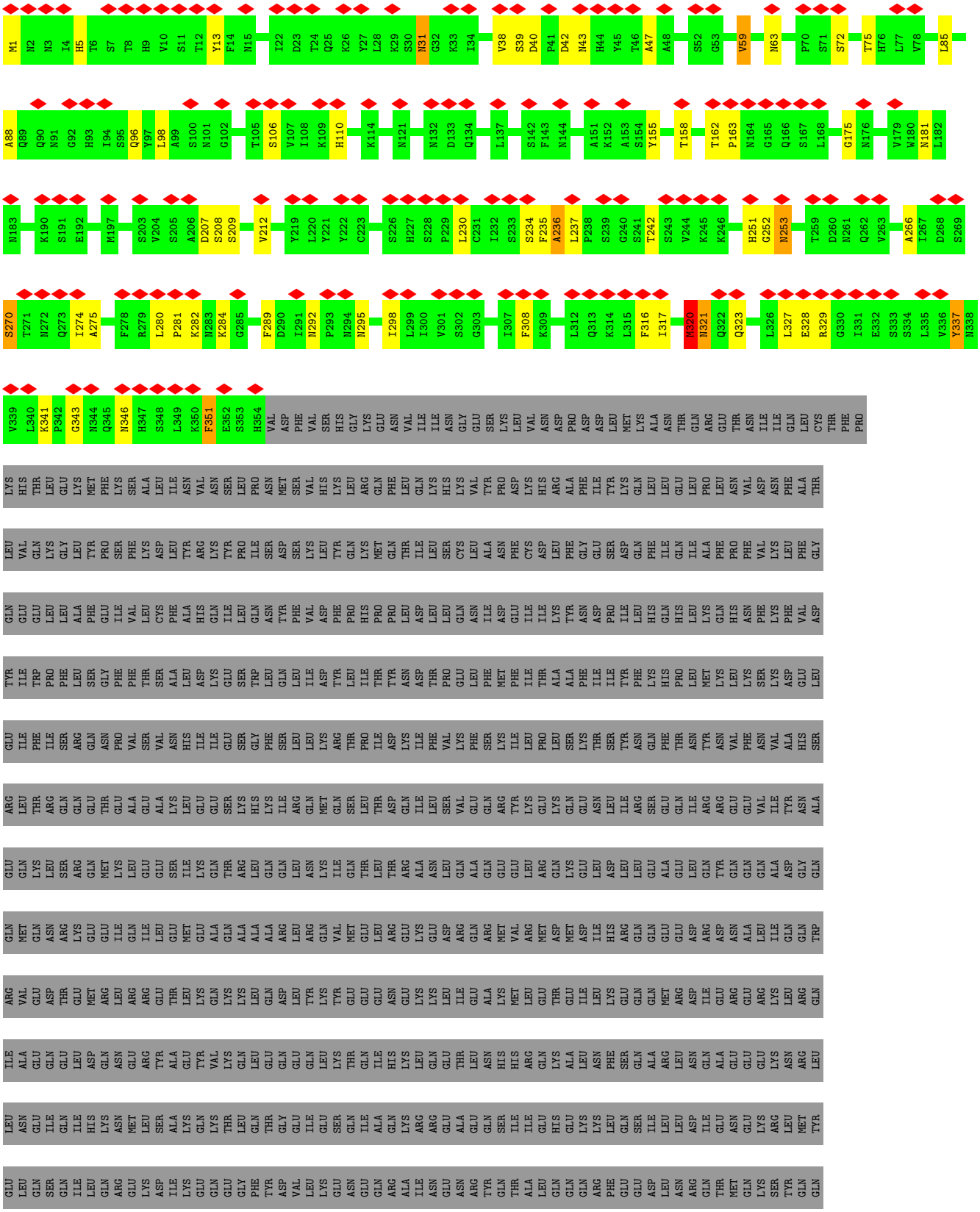




- Molecule 5: TBC1 domain family member 31

Chain M:

13%
24%
5%
71%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N183 K190 S191 E192 M197 S203 V204 S205 A206 D207 S208 S209 V212 Y219 L220 Y221 Y222 C223 S226 H227 S228 P229 L230 C231 I232 S233 S234 F235 A236 L237 P238 S239 G240 S241 T242 S243 V244 K245 K246 H251 G252 N253 T259 D260 N261 Q262 V263 A266 I267 D268 S269
S270 T271 N272 Q273 I274 A275 F278 R279 L280 P281 K282 N283 K284 G285 F289 D290 I291 N292 P293 N294 N295 I298 L299 I300 V301 S302 G303 I307 F308 K309 L312 Q313 K314 L315 F316 I317 M320 N321 Q322 Q323 L326 L327 E328 R329 G330 I331 E332 S333 S334 L335 V336 Y337 N338
V339 L340 K341 P342 G343 N344 Q345 N346 H347 S348 L349 K350 F351 E352 S353 H354 VAL ASP PHE VAL SER HIS GLY LYS GLU ASN VAL ILE ILE ASN GLY GLU SER LYS LEU VAL ASN ASP PRO ASP ASP LEU MET LYS ALA ASN THR GLN ARG GLU THR ASN ILE ILE GLN LEU CYS THR PHE PRO
LYS HIS THR LEU GLU LYS MET PHE LYS SER ALA LEU ILE ASN VAL ASN SER LEU PRO ASN MET SER VAL HIS LYS LEU ARG GLN PHE LEU GLN LYS HIS LYS VAL TYR PRO ASP LYS HIS ARG ALA PHE ILE TYR LYS GLN LEU LEU GLU LEU PRO LEU ASN VAL ASP ASN PHE ALA THR
LEU VAL GLN LYS GLY LEU TYR PRO SER PHE LYS ASP LEU TYR ARG LYS TYR PRO ILE SER ASP SER LYS LEU TYR GLN LYS MET GLN THR ILE LEU SER CYS LEU ALA ASN PHE CYS ASP LEU PHE GLY GLU SER ASP GLN PHE ILE GLN ILE ALA PHE PRO PHE VAL LYS LEU PHE GLY
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TYR ILE TRP PRO PHE LEU SER GLY PHE PHE THR SER ALA LEU ASP LYS GLU GLU SER TRP LEU LEU GLN LEU ILE ASP TYR LEU ILE THR TYR ASN ASP THR PRO GLU GLU LEU PHE MET PHE ILE THR ALA ALA PHE ILE ILE TYR PHE LYS HIS PRO LEU MET LYS LEU LYS SER LYS ASP GLU LEU
GLU ILE PHE ILE SER ARG GLN ASN PRO VAL SER VAL ASN HIS ILE ILE GLU GLU SER GLY PHE SER LEU LEU LYS ARG THR PRO ILE ASP LYS ILE PHE VAL LYS PHE SER LYS ILE LEU PRO LEU ALA SER LYS THR SER TYR ASN GLN PHE THR ASN TYR ASN VAL PHE ASN VAL ALA HIS SER
ARG LEU THR ARG GLN GLN GLU THR GLU ALA GLU ALA LYS LEU GLU GLU SER LYS HIS LYS ILE ARG GLN MET GLN SER LEU THR ASP GLN ILE LEU SER VAL GLU GLN ARG TYR LYS GLU LYS GLN GLU ASN LEU ILE ARG SER GLU GLN ILE ARG ARG GLU GLU GLU VAL ILE TYR ASN ALA
GLU GLN LYS LEU SER ARG GLN MET LYS LEU GLU GLU SER ILE LYS GLN THR ARG LEU GLN GLN LEU ASN LYS ILE GLN THR LEU THR ARG ALA ASN LEU GLN ALA GLN GLU GLU LEU LYS GLU LEU ARG GLN LYS GLU LEU ASP LEU LEU GLN TYR GLN GLU ALA GLU GLN LEU GLN ALA ASP GLY GLN
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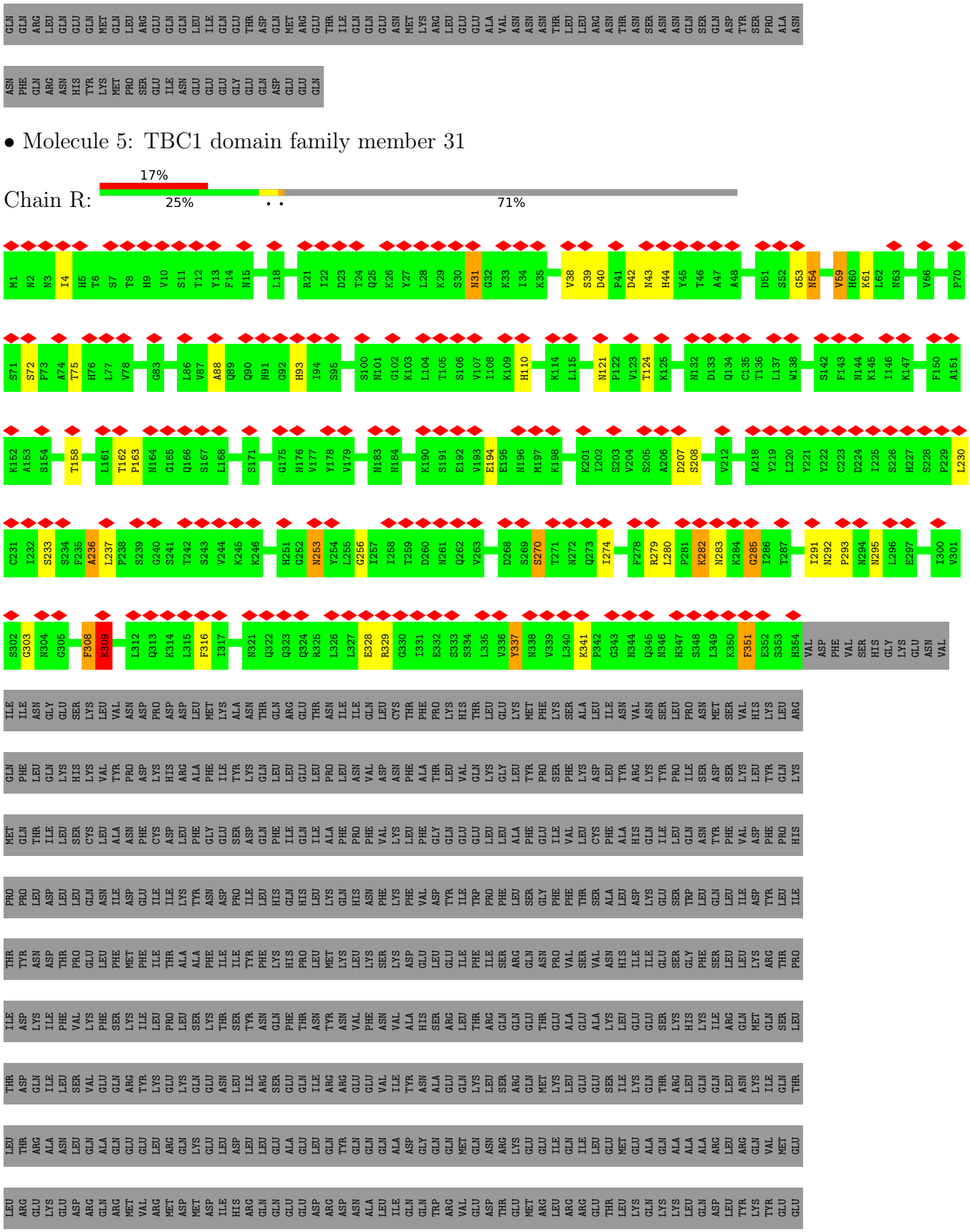
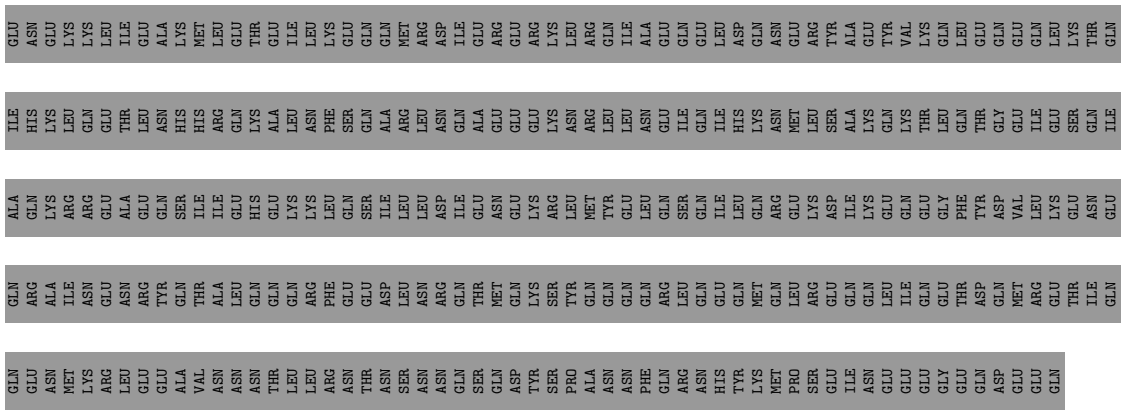
ARG VAL GLU ASP THR GLU MET ARG LEU ARG ARG GLU THR LEU LYS GLN LYS LYS LEU GLN ASP LEU TYR LYS TYR GLU GLU GLU GLU ASN GLU LYS LYS LEU ILE GLU ILE THR GLU ILE LEU LYS GLU GLN GLN MET GLU GLU ASP ILE ALA GLU ARG GLU GLU ARG LYS LEU GLN ARG
ILE ALA GLU GLN GLU LEU ASP GLN ASN GLU ARG TYR ALA GLU TYR VAL LYS GLN LEU GLU GLN GLN LEU LYS THR GLN ILE ILE HIS LYS LEU GLN GLU THR LEU ASN HIS HIS ARG GLN LYS ALA LEU ASN PHE SER GLN ALA ARG LEU ASN GLN ALA GLU GLU GLU ARG LYS ASN ARG LEU
LEU ASN GLU ILE GLN ILE HIS LYS ASN MET LEU SER ALA LYS GLN LYS THR LEU GLN THR GLY GLU ILE GLU HIS GLU SER GLN ILE ALA GLN LYS ARG GLU ALA GLN SER ILE ILE GLU HIS GLU LYS LYS LEU GLN GLN ILE LEU LEU LEU ASP ILE GLU ASN ARG GLU GLU LYS GLN LEU
GLU LEU GLN SER GLN ILE LEU GLN ARG GLU LYS ASP ILE LYS GLU GLN GLY PHE TYR ASP VAL LEU LYS GLU ASN GLU GLN ARG ALA ILE ASN GLU ASN ARG TYR GLN THR ALA LEU GLN GLN GLN ARG PHE GLU GLU ASP LEU ASN ARG GLN THR MET GLN LYS GLU LEU ARG GLN TYR

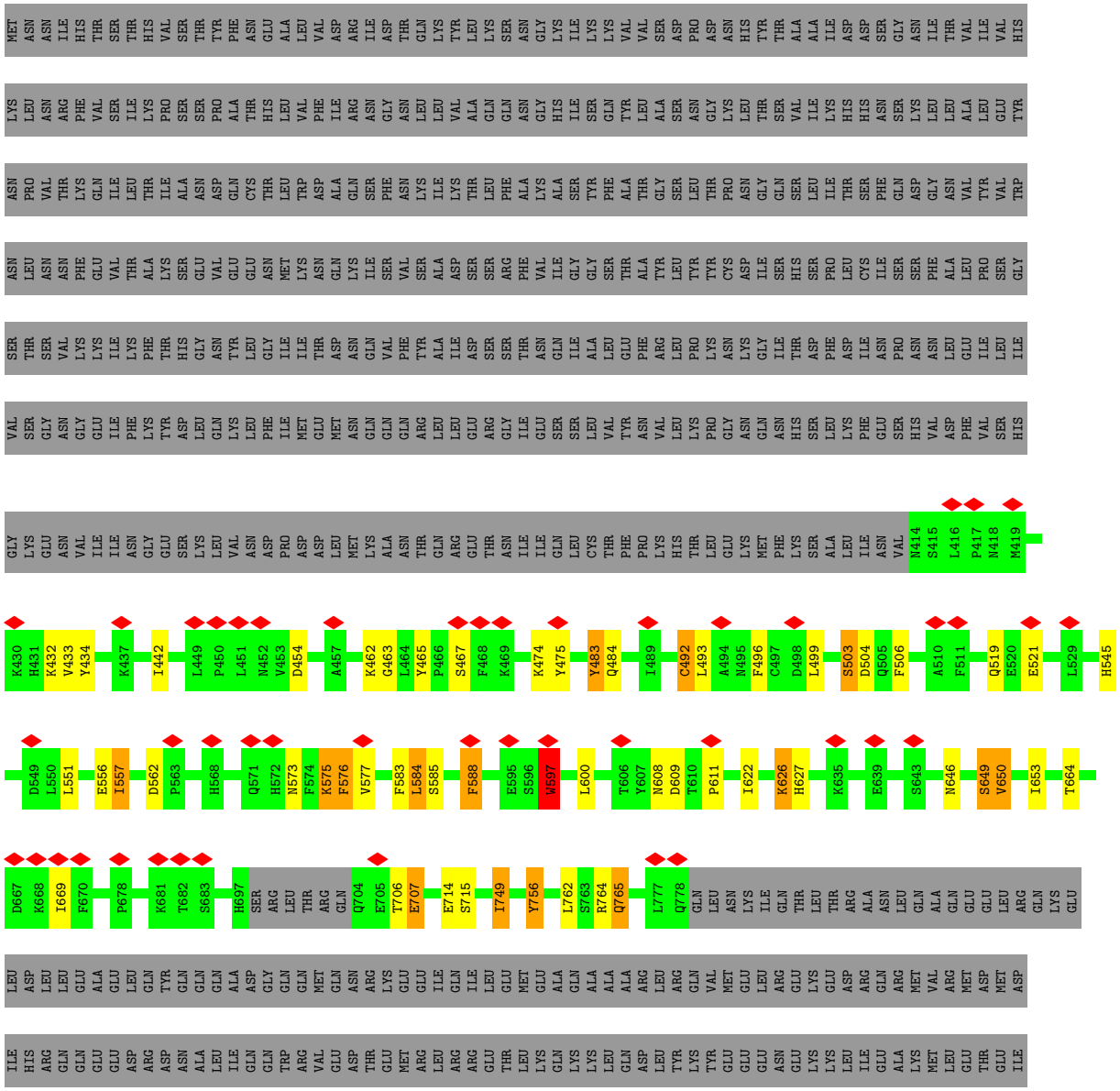


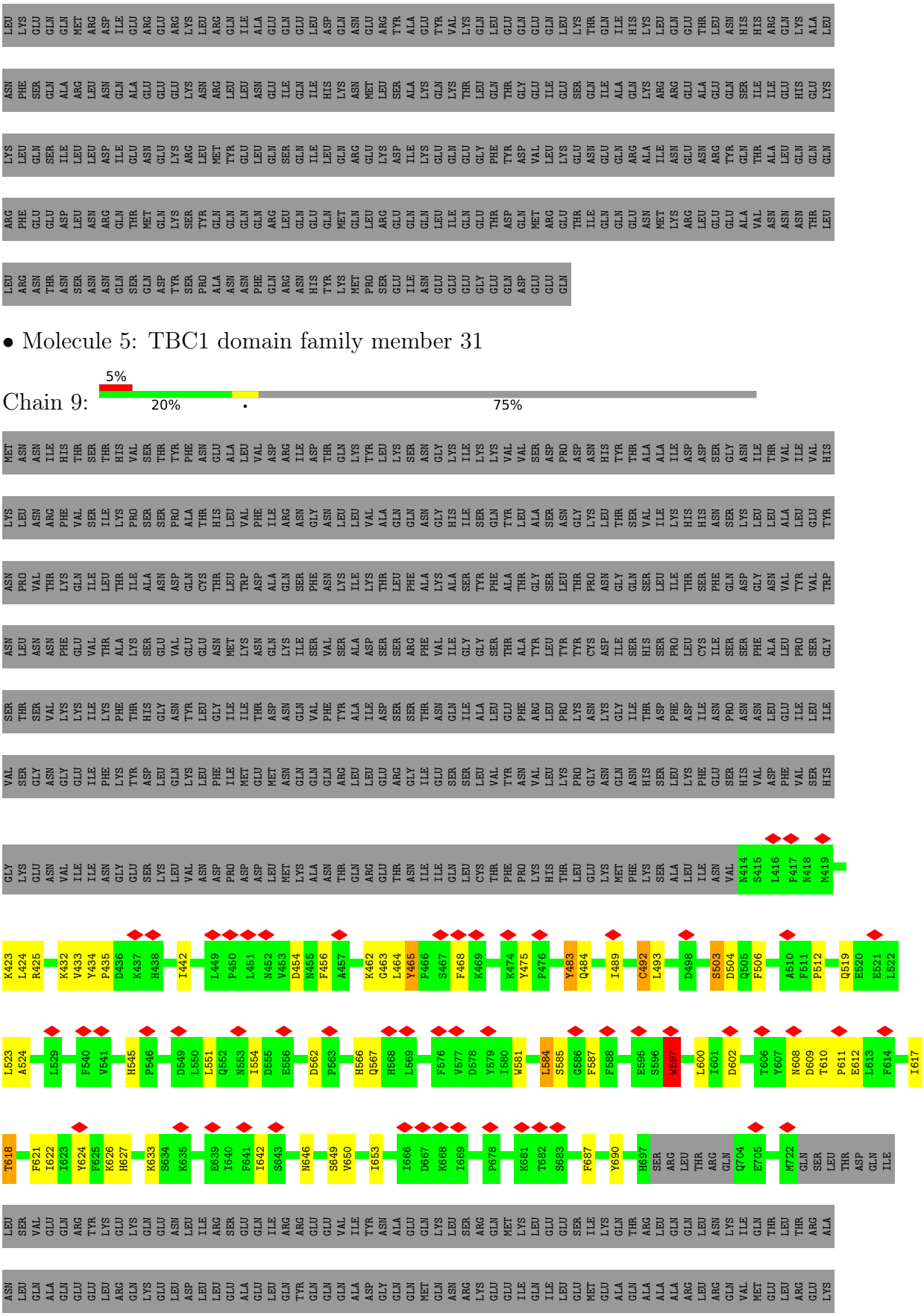
• Molecule 5: TBC1 domain family member 31



- Molecule 5: TBC1 domain family member 31

Chain v:



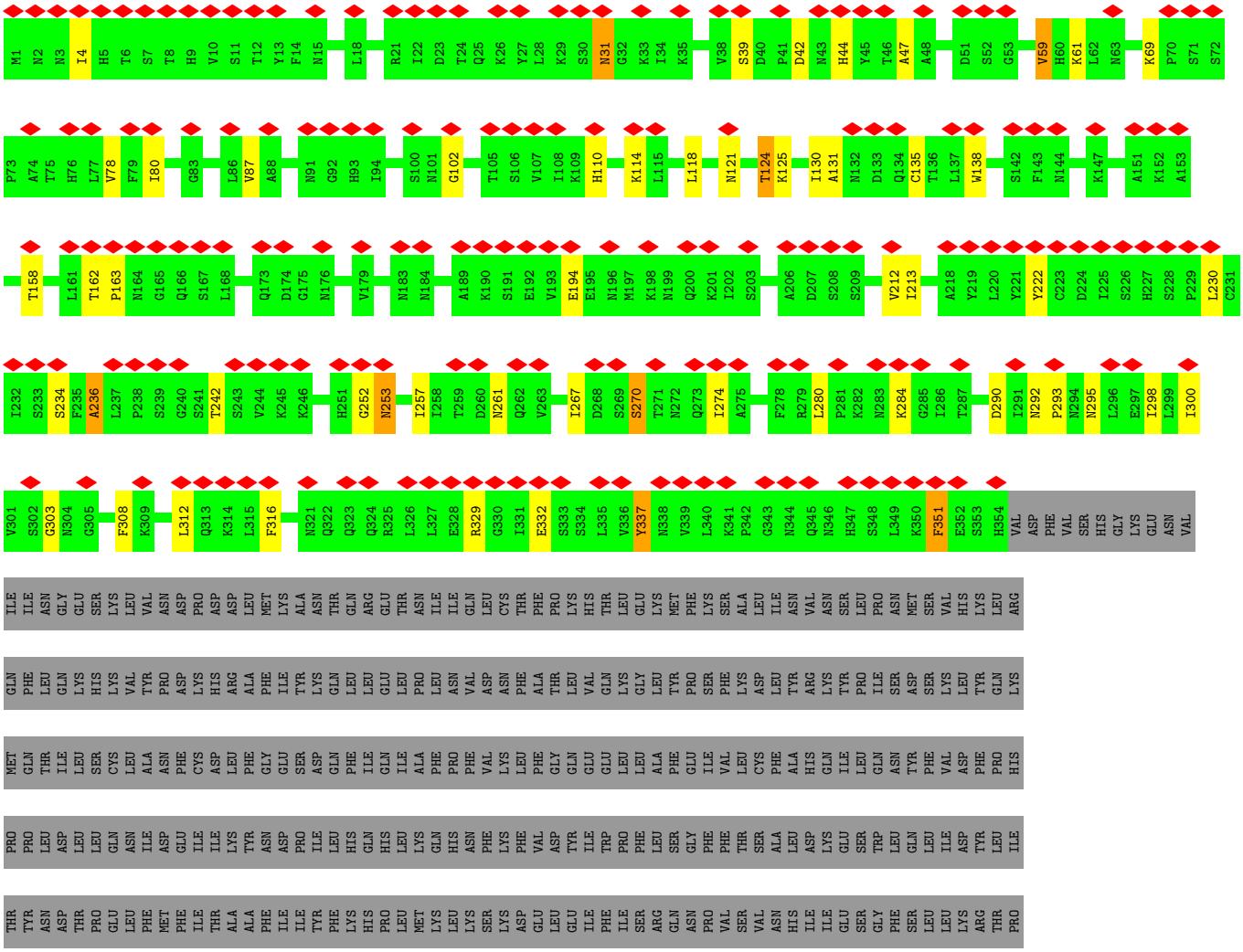


• Molecule 5: TBC1 domain family member 31

Chain 9:

- Molecule 5: TBC1 domain family member 31

Chain AB:



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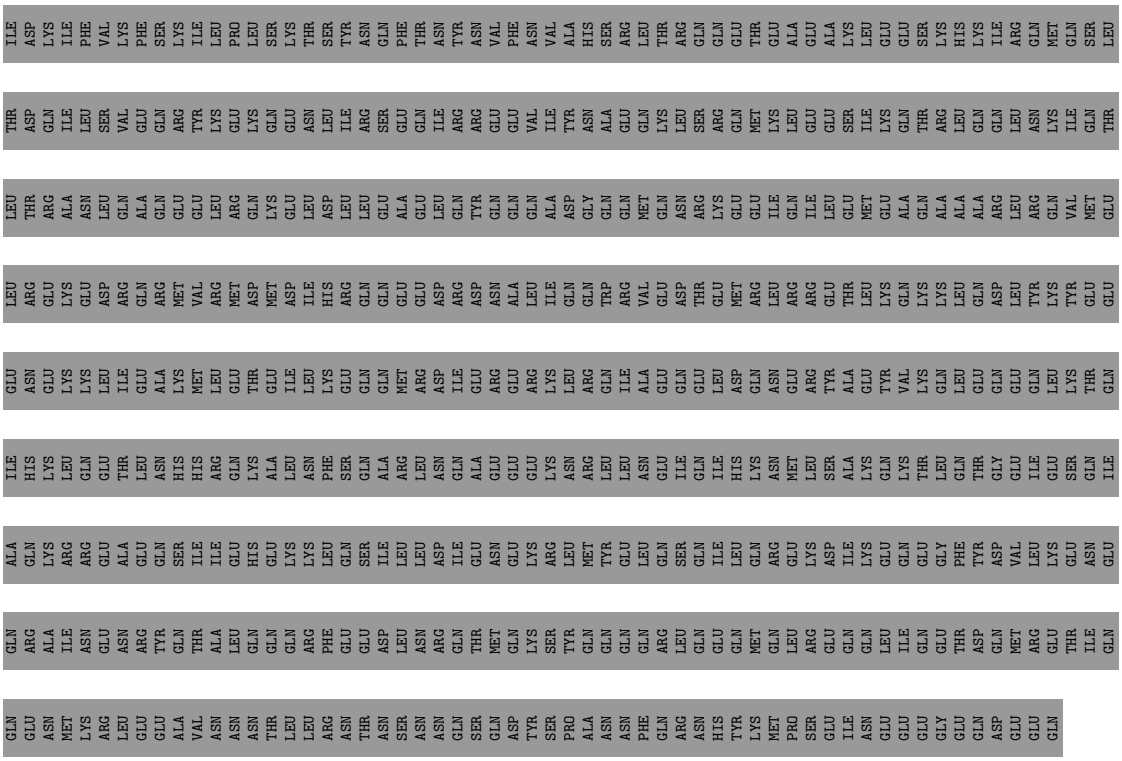
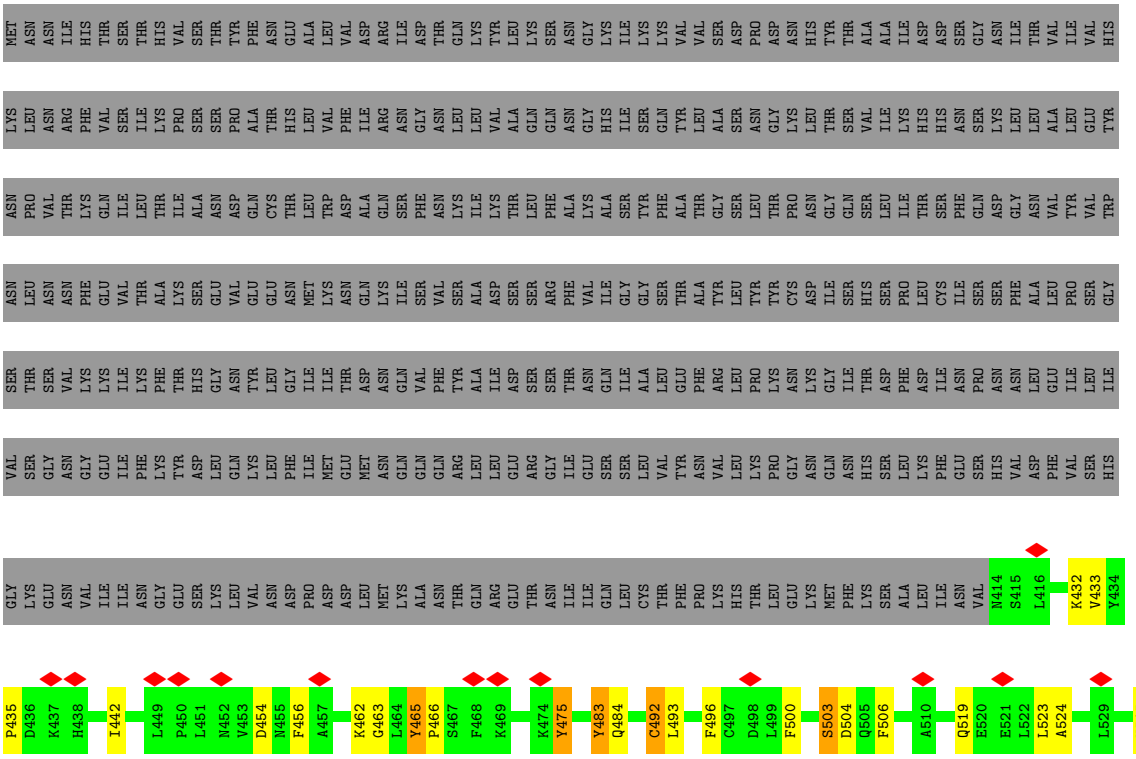
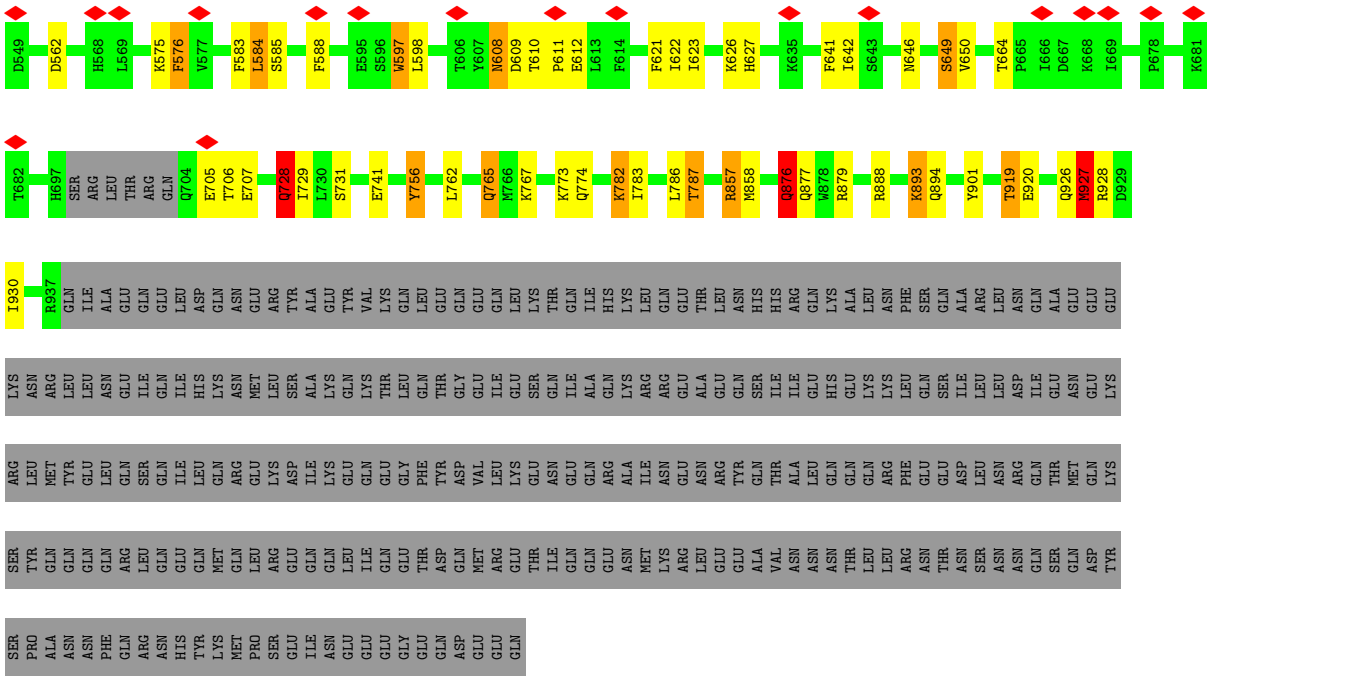


- Molecule 5: TBC1 domain family member 31

Chain AE:





- Molecule 5: TBC1 domain family member 31

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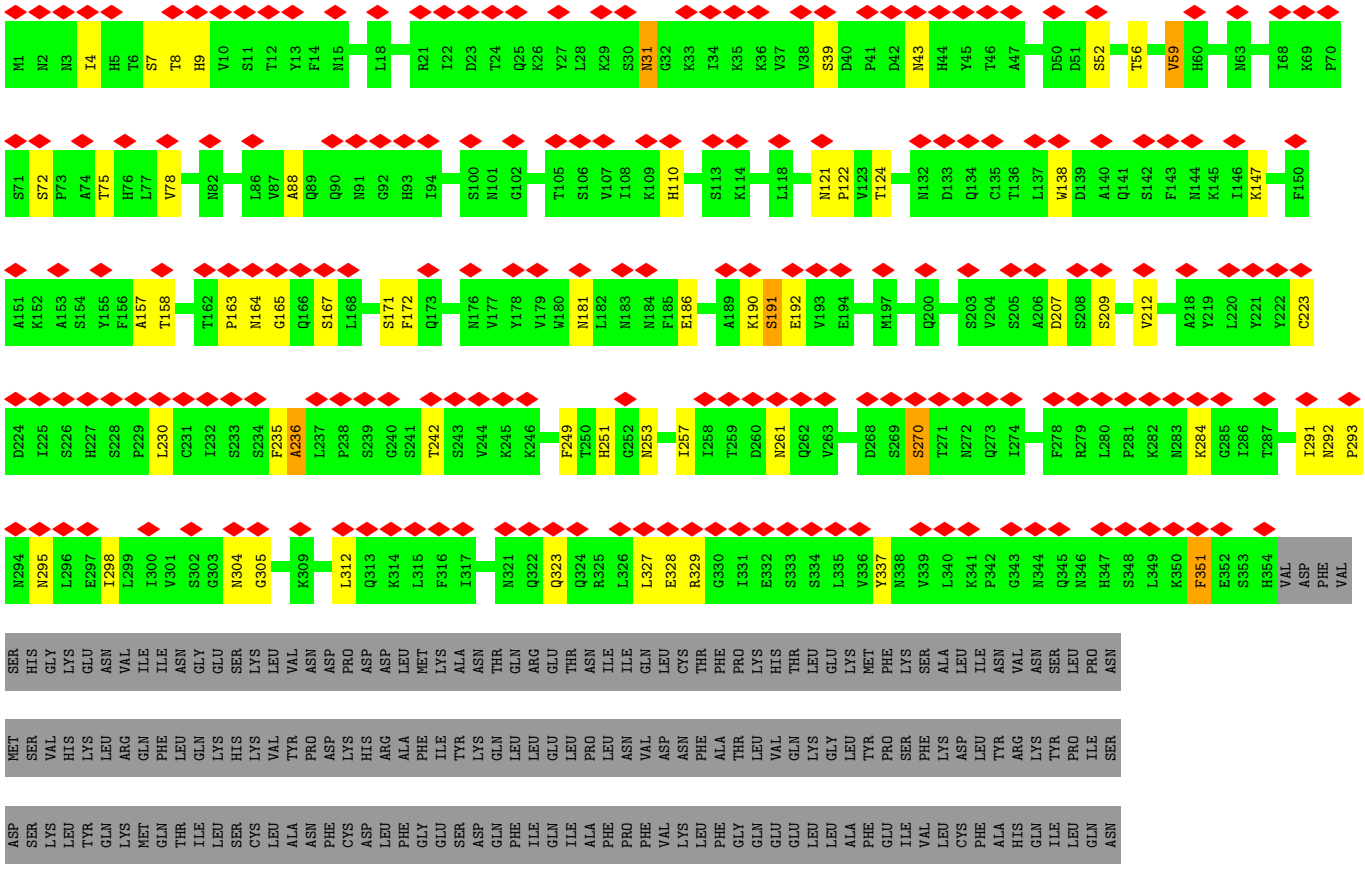
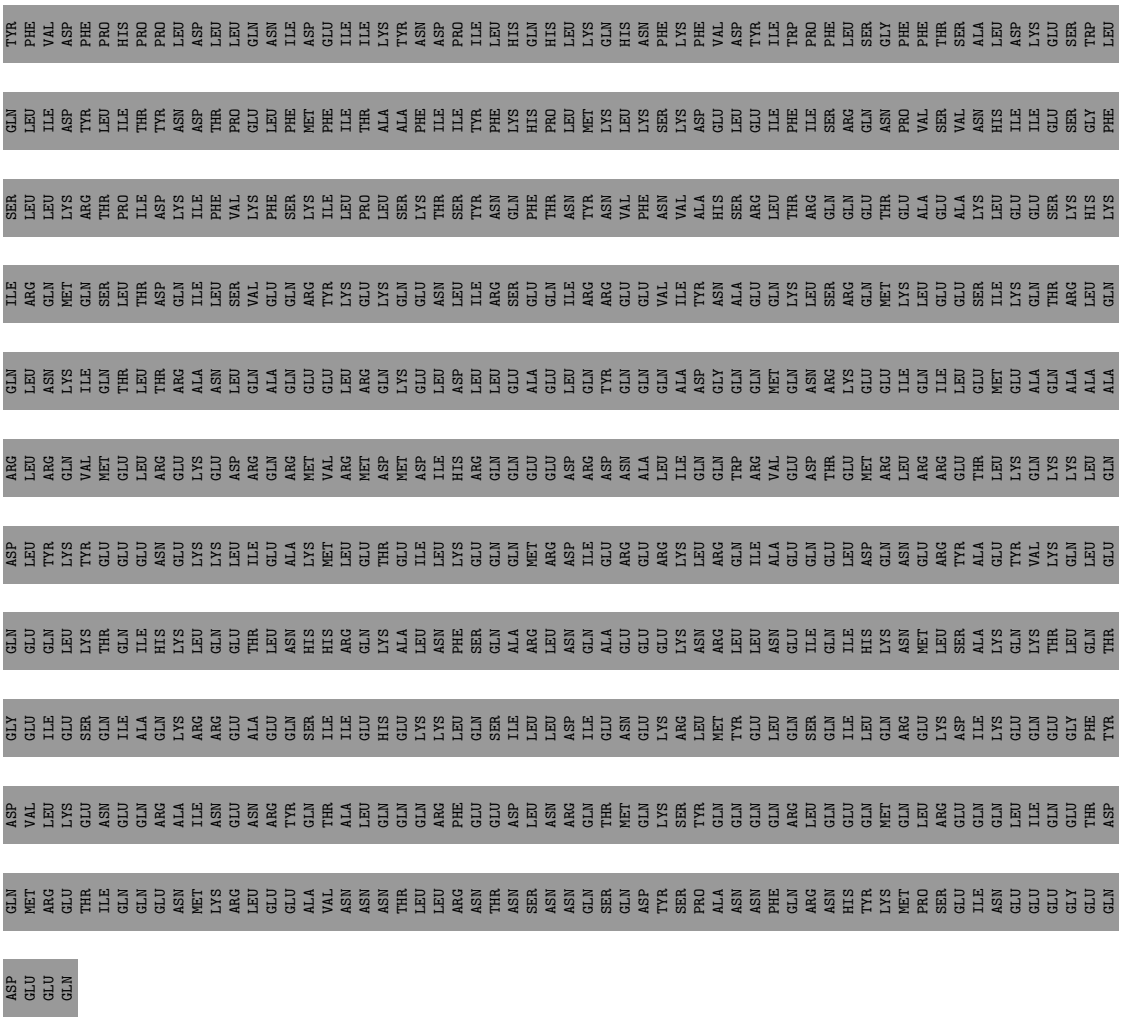
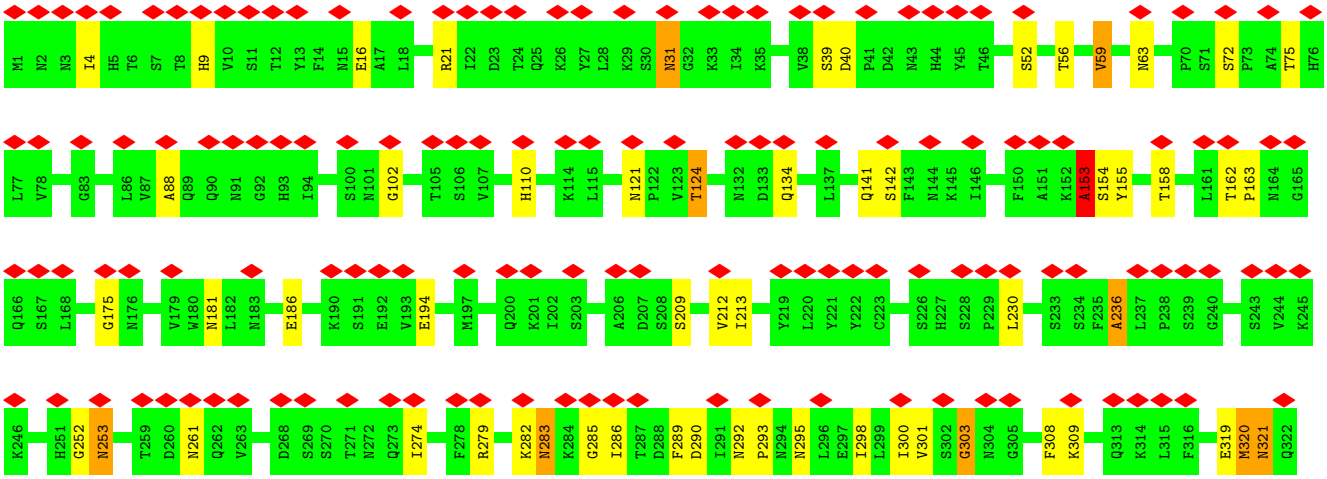
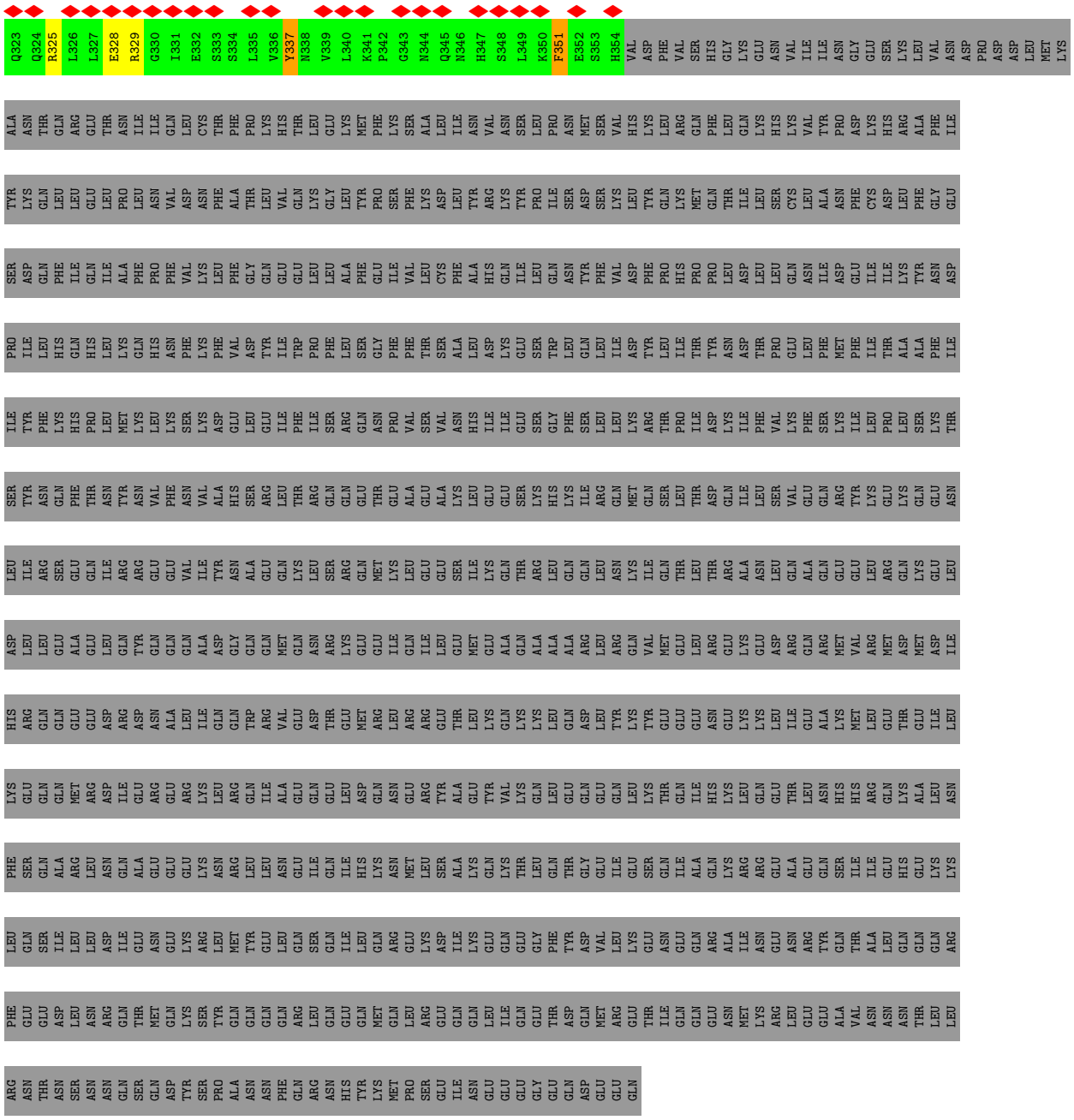




- Molecule 5: TBC1 domain family member 31

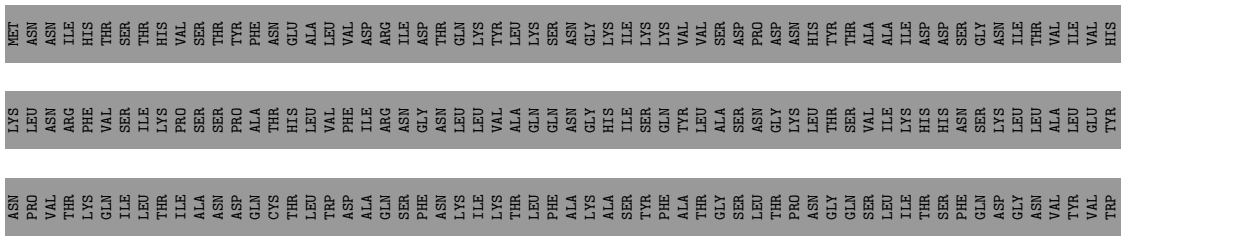
Chain AU:

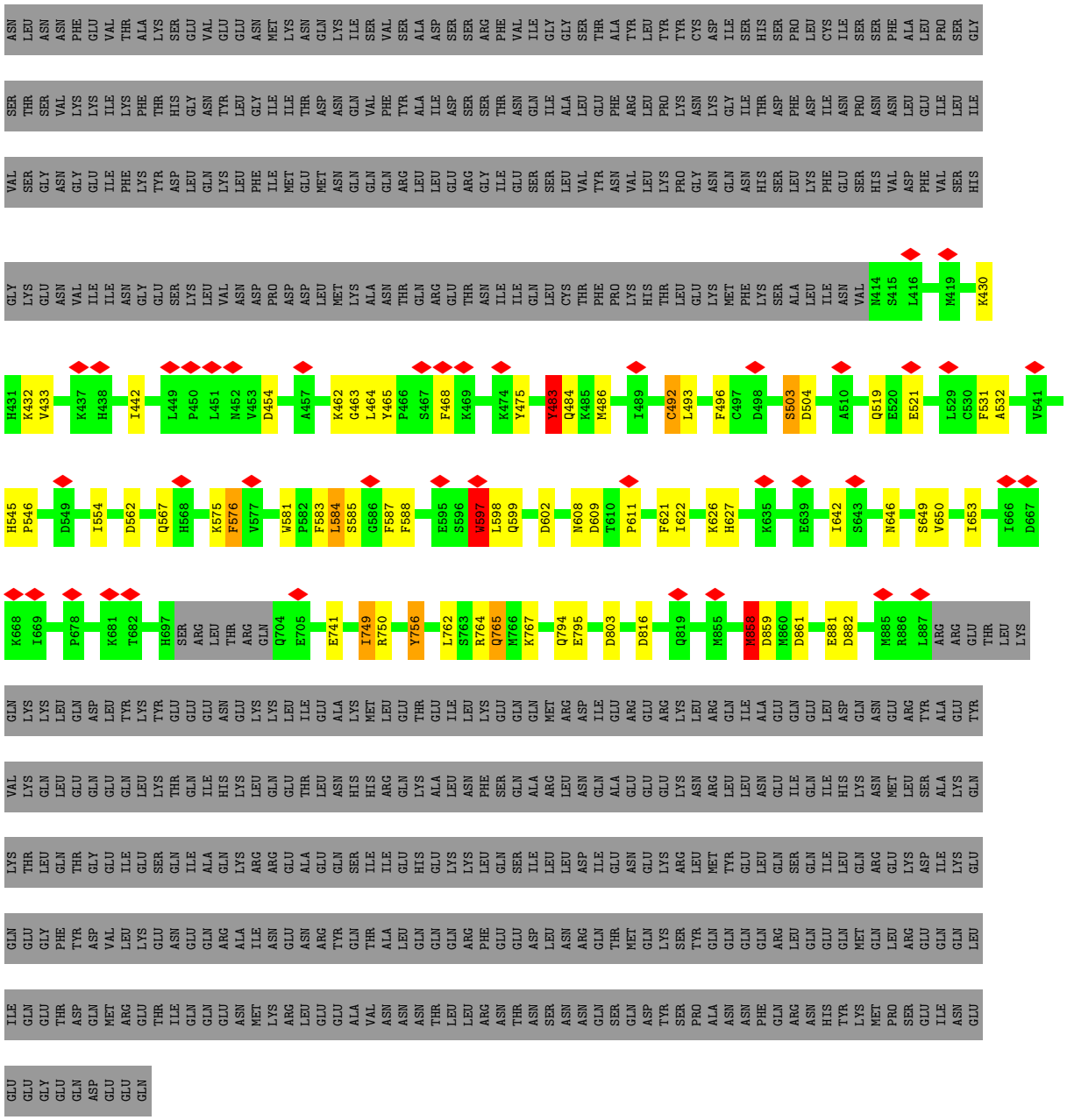




- Molecule 5: TBC1 domain family member 31

Chain Bf:





• Molecule 5: TBC1 domain family member 31

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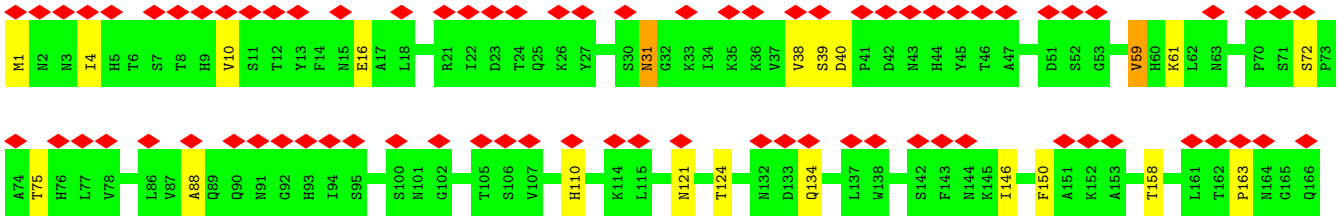
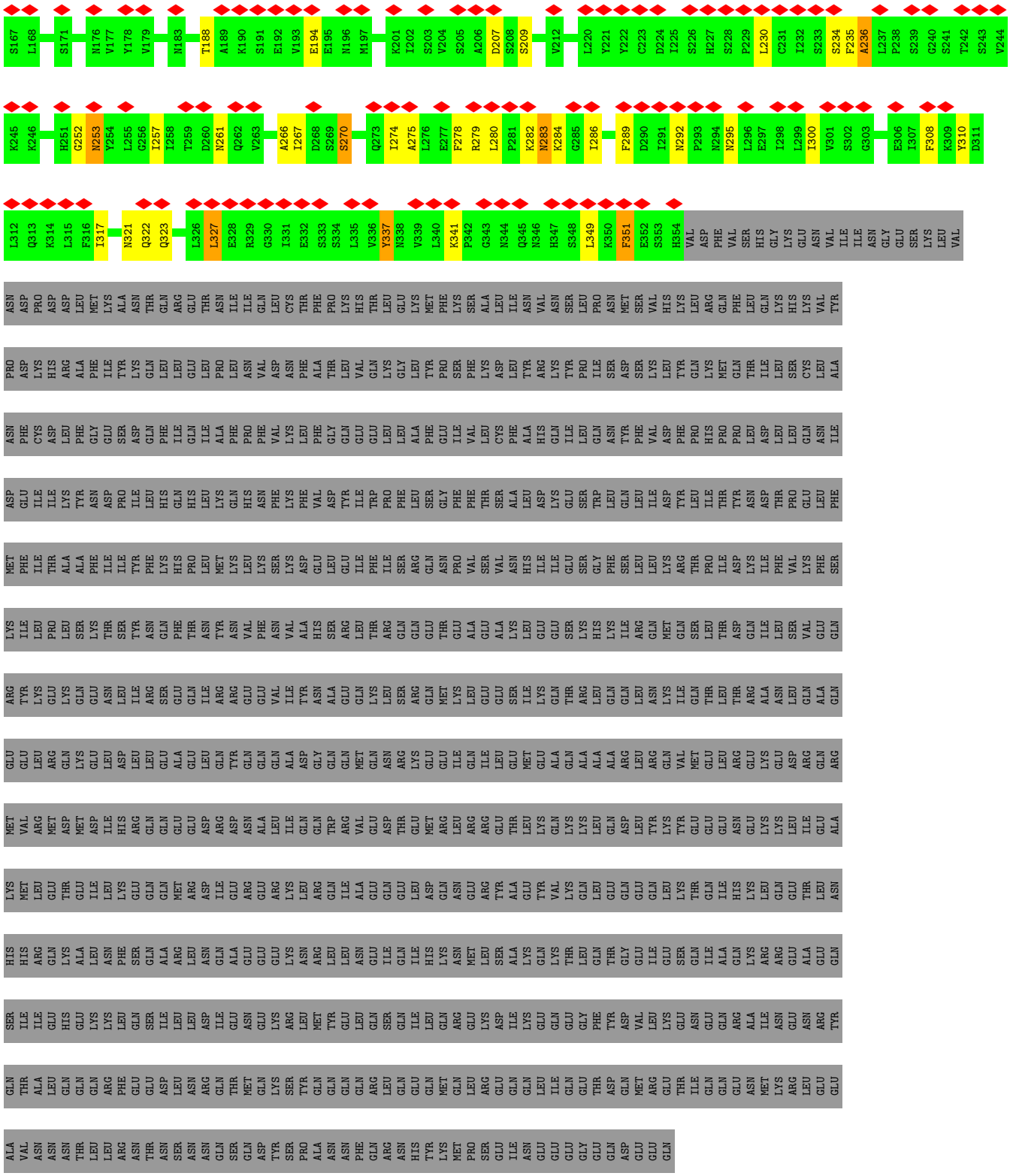
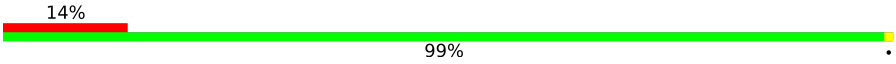
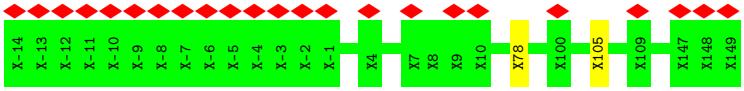




- Molecule 6: Unknown Protein Chain

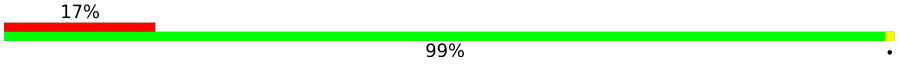
Chain H:

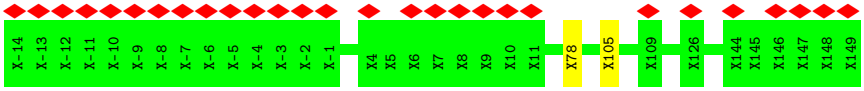




• Molecule 6: Unknown Protein Chain

Chain l:





• Molecule 6: Unknown Protein Chain

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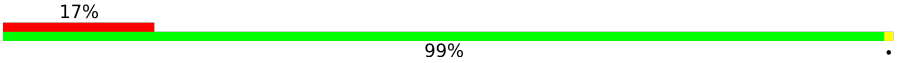
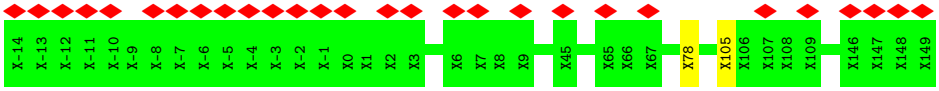
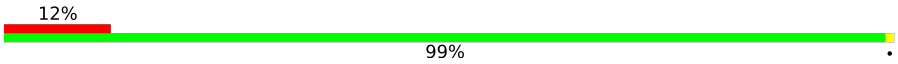
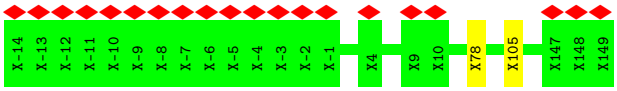




• Molecule 6: Unknown Protein Chain

Chain BV:





• Molecule 6: Unknown Protein Chain

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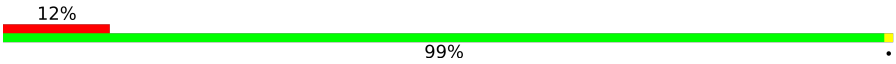
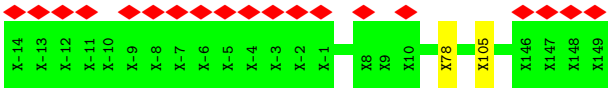
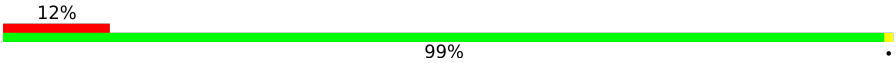
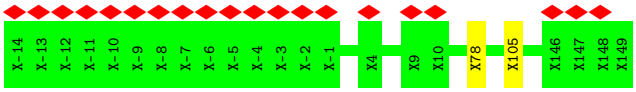




• Molecule 6: Unknown Protein Chain

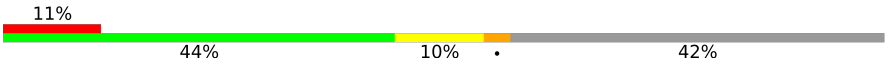
Chain B4:

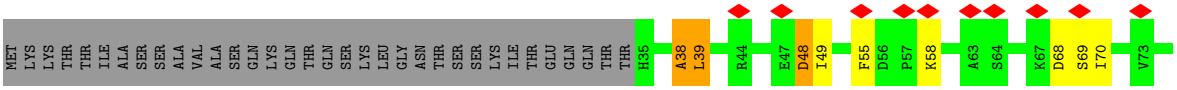


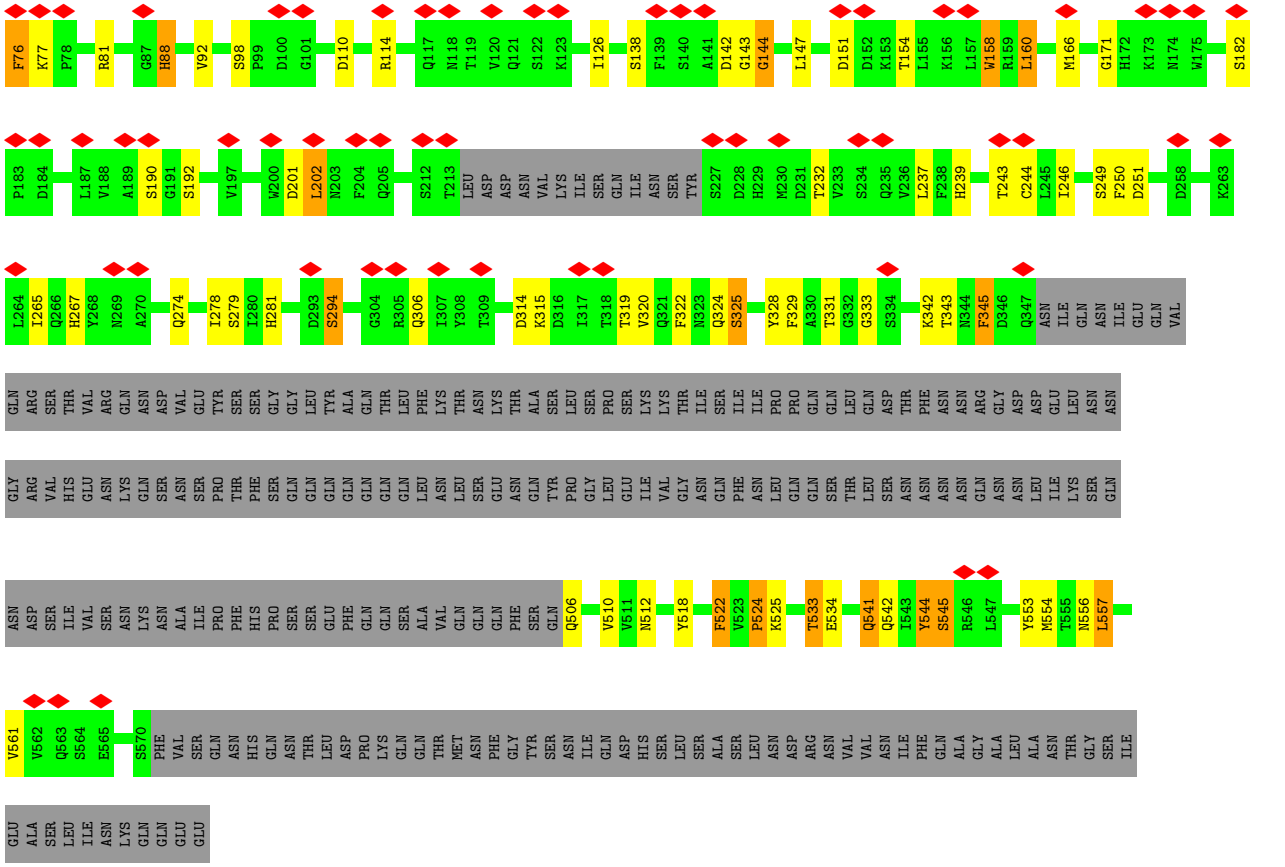


• Molecule 7: POC1 centriolar protein homolog

Chain J:

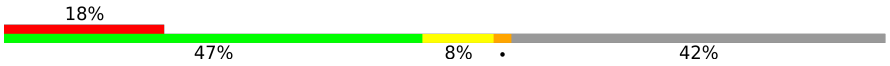


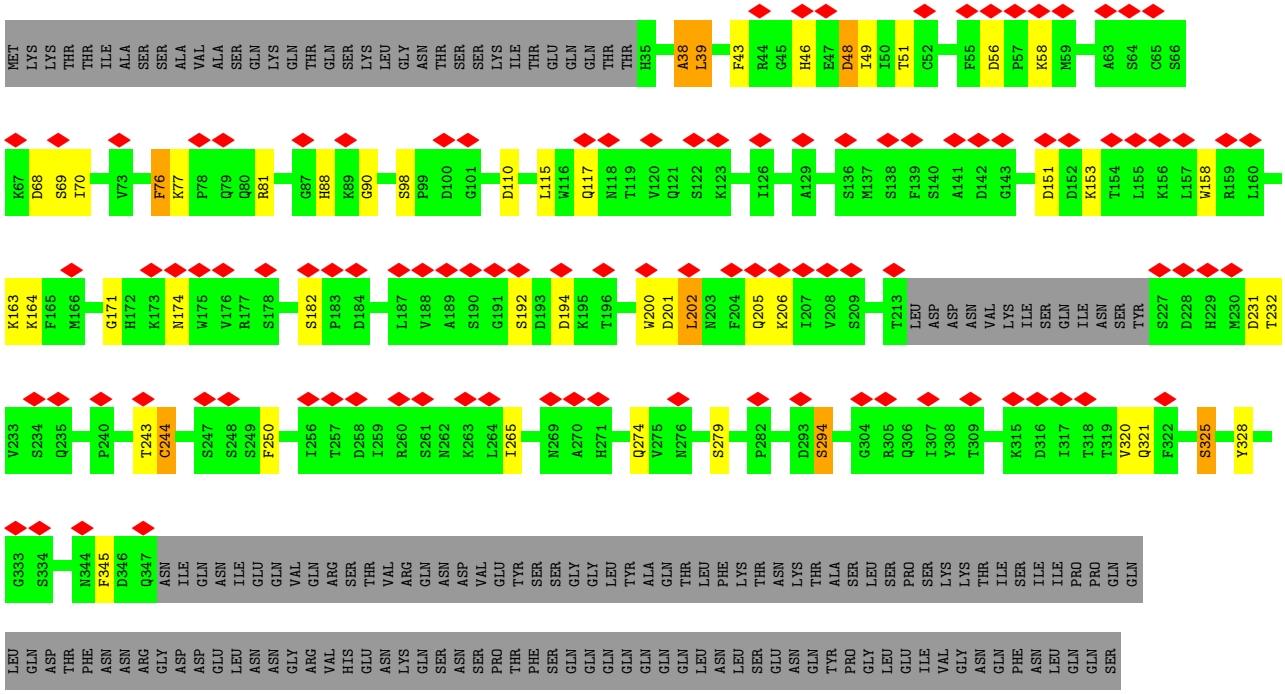


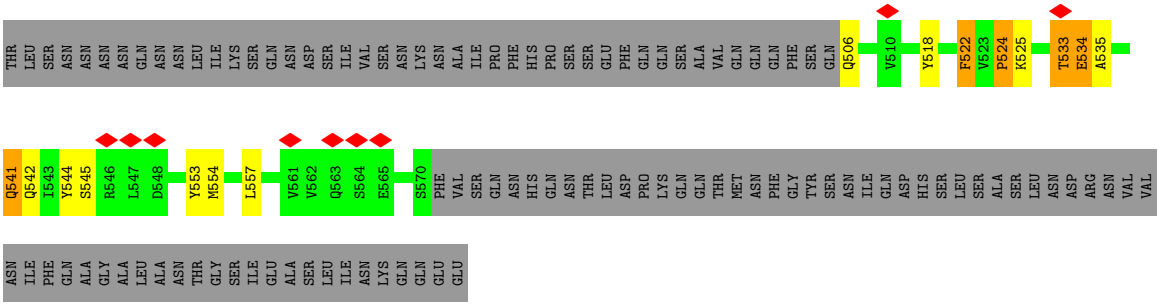


- Molecule 7: POC1 centriolar protein homolog

Chain O:

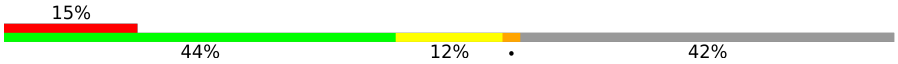


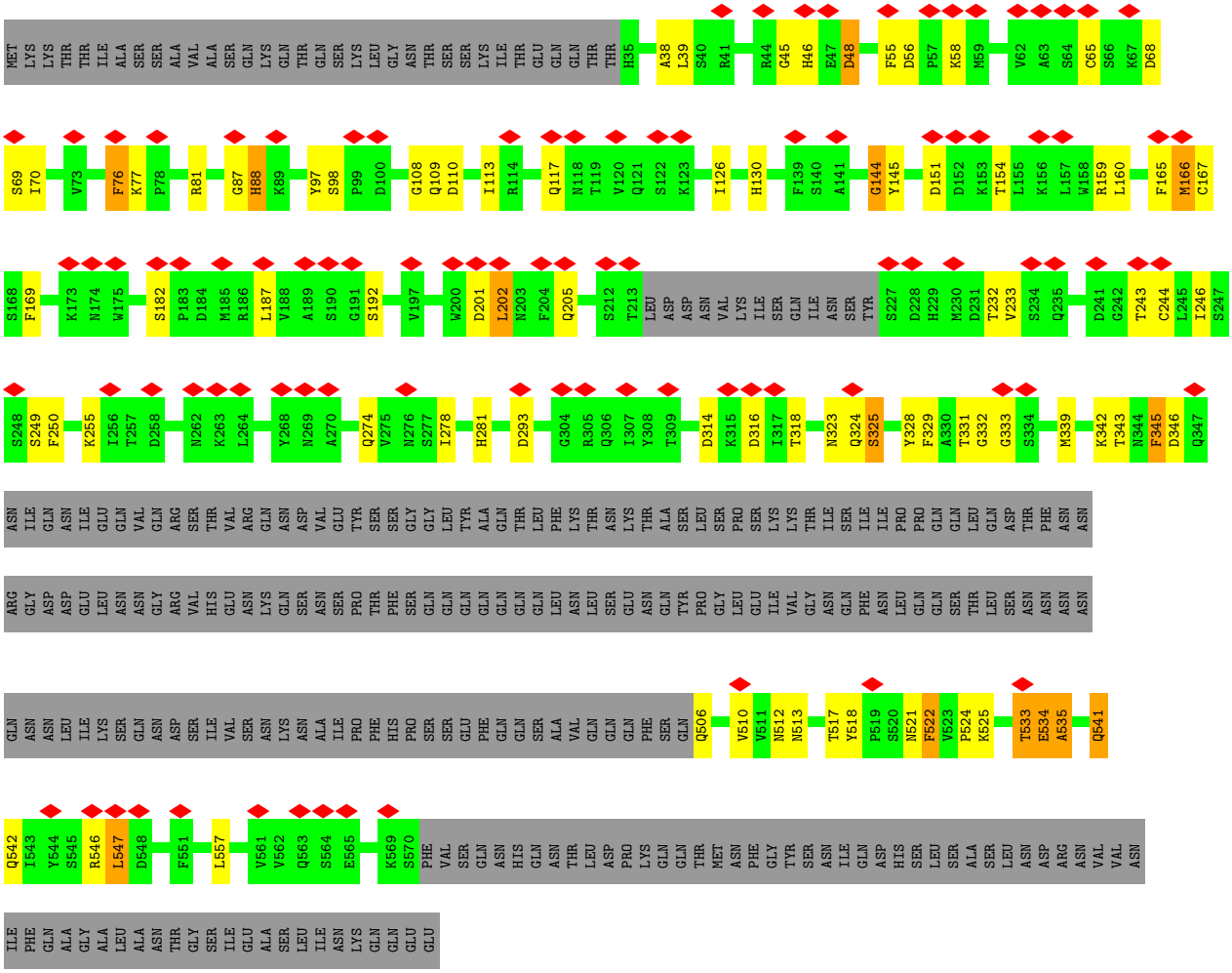




- Molecule 7: POC1 centriolar protein homolog

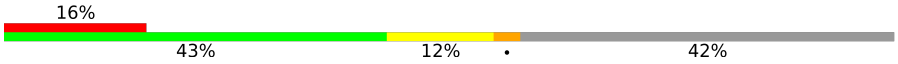
Chain 4:

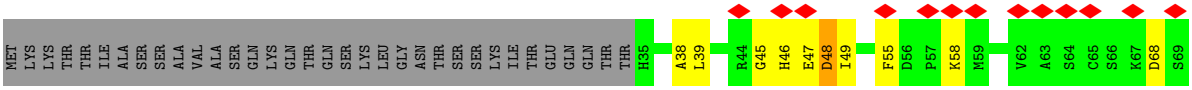


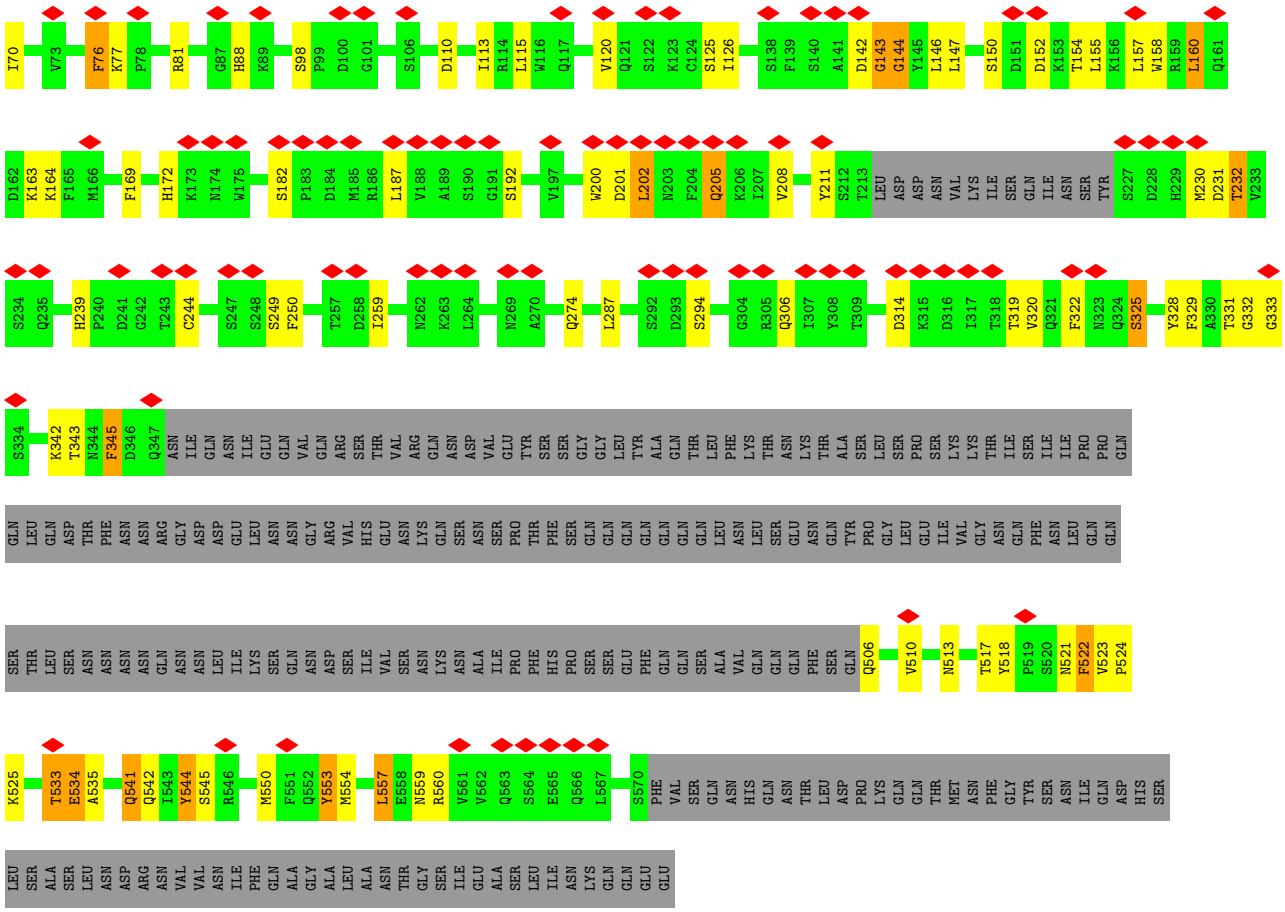


- Molecule 7: POC1 centriolar protein homolog

Chain AG:

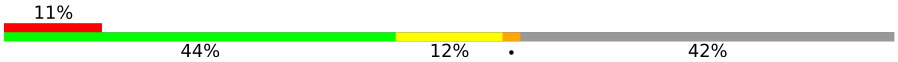


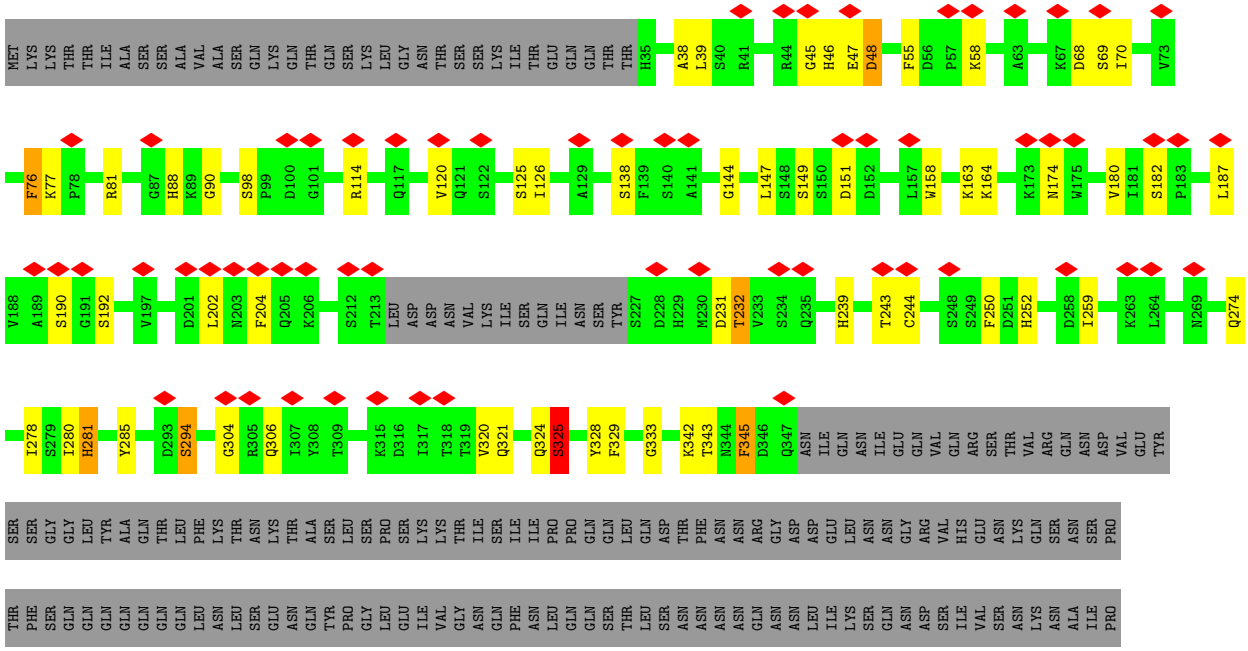


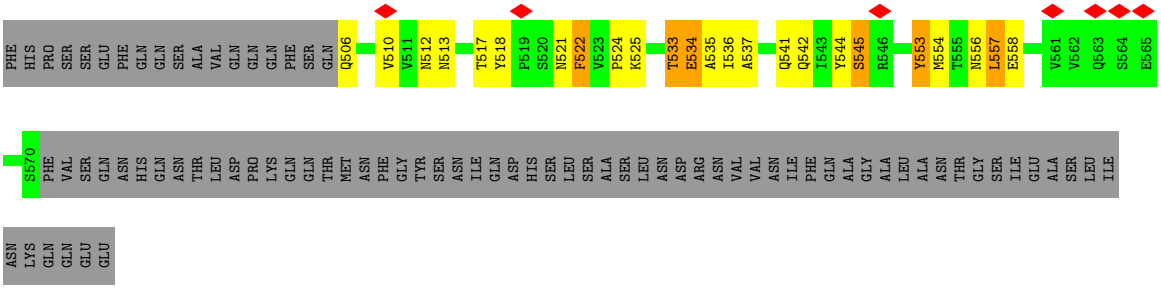


- Molecule 7: POC1 centriolar protein homolog

Chain AM:

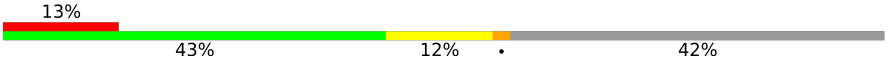


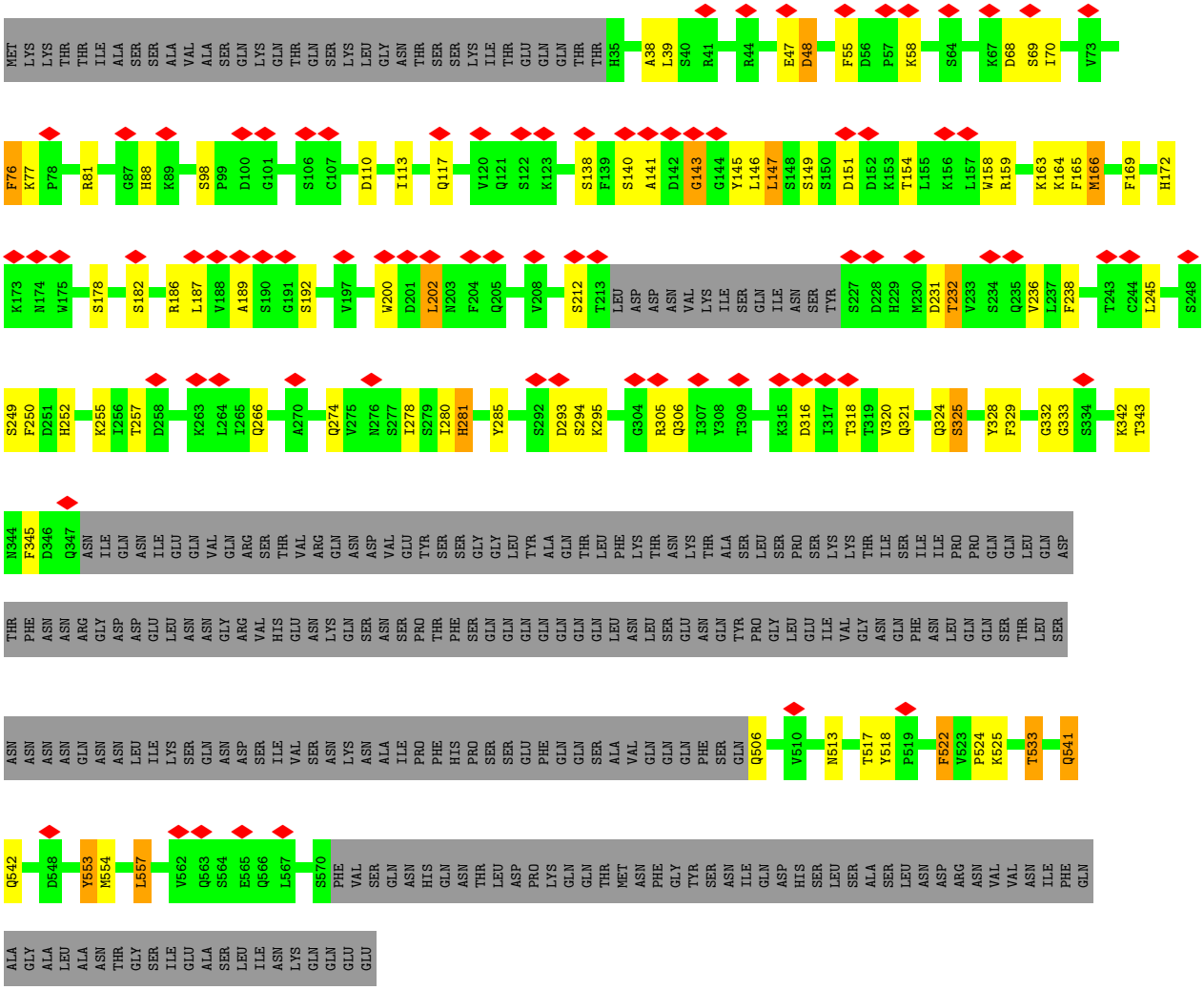




• Molecule 7: POC1 centriolar protein homolog

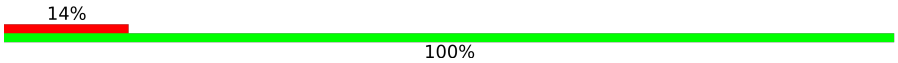
Chain Bm:

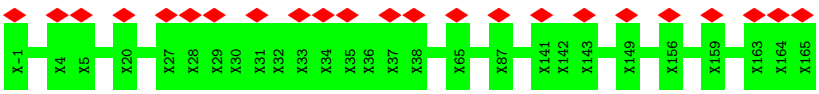




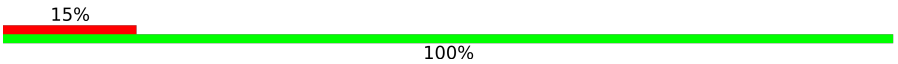
• Molecule 8: Unknown Protein Chain

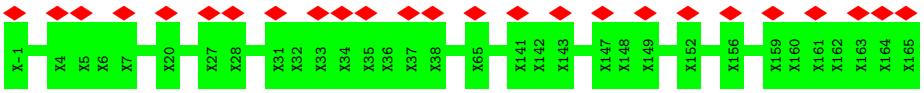
Chain K:



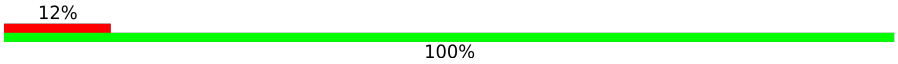


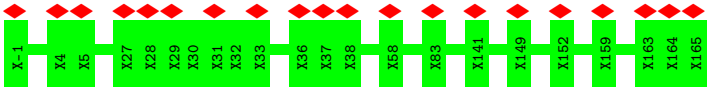
• Molecule 8: Unknown Protein Chain

Chain t: 

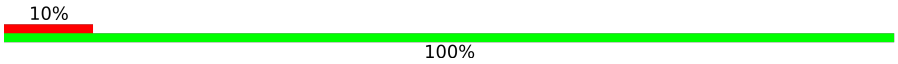


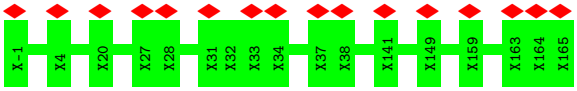
• Molecule 8: Unknown Protein Chain

Chain 5: 

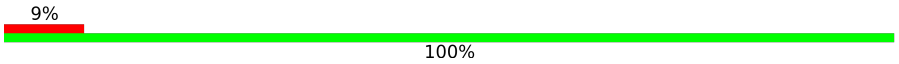


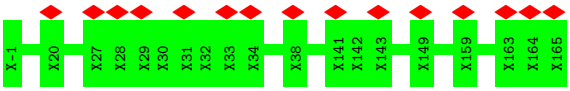
• Molecule 8: Unknown Protein Chain

Chain Bc: 

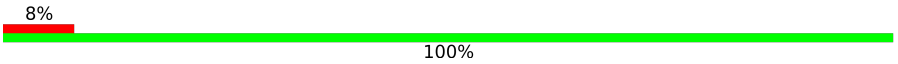


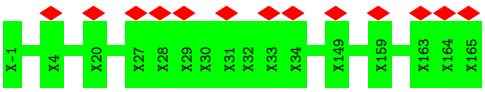
• Molecule 8: Unknown Protein Chain

Chain Bn: 

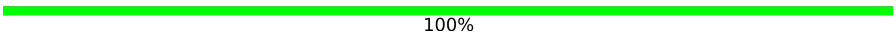


• Molecule 8: Unknown Protein Chain

Chain CA: 

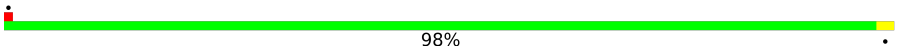


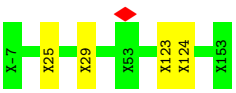
• Molecule 9: Unknown Protein Chain

Chain N: 

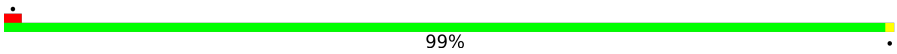
There are no outlier residues recorded for this chain.

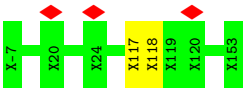
• Molecule 9: Unknown Protein Chain

Chain 2: 

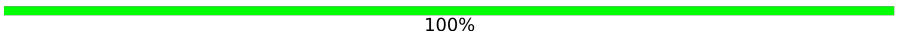


• Molecule 9: Unknown Protein Chain

Chain AC: 



• Molecule 9: Unknown Protein Chain

Chain Bj: 

There are no outlier residues recorded for this chain.

• Molecule 9: Unknown Protein Chain

Chain Bu:

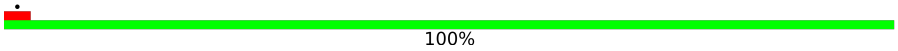
There are no outlier residues recorded for this chain.

• Molecule 9: Unknown Protein Chain

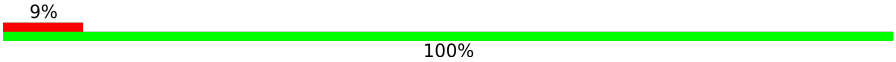
Chain CH:

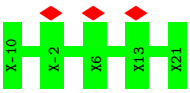
There are no outlier residues recorded for this chain.

• Molecule 10: Unknown Protein Chain

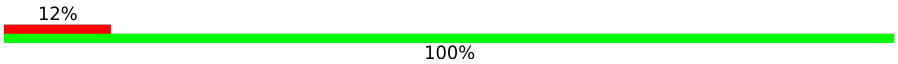
Chain P: 

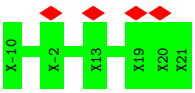
• Molecule 10: Unknown Protein Chain

Chain U: 

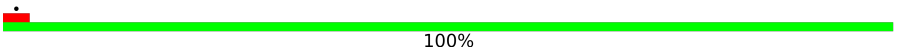


• Molecule 10: Unknown Protein Chain

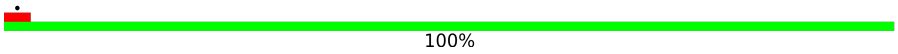
Chain AJ: 



• Molecule 10: Unknown Protein Chain

Chain AW: 

• Molecule 10: Unknown Protein Chain

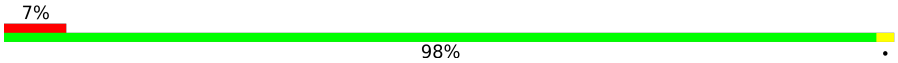
Chain Ac: 

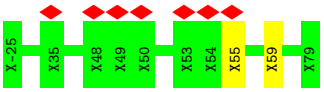
• Molecule 10: Unknown Protein Chain

Chain B1:

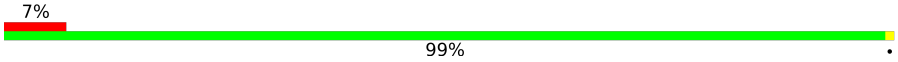
There are no outlier residues recorded for this chain.

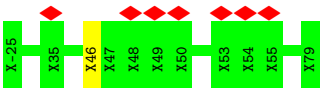
• Molecule 11: Unknown Protein Chain

Chain Q: 

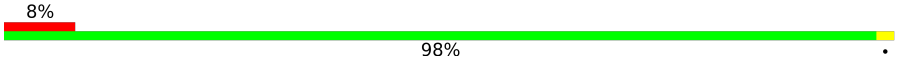


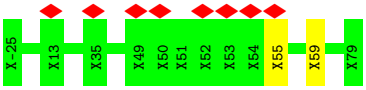
• Molecule 11: Unknown Protein Chain

Chain 0: 

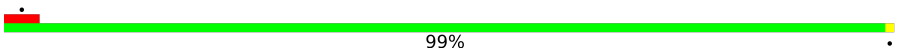


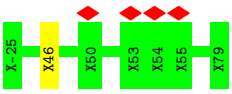
• Molecule 11: Unknown Protein Chain

Chain AK: 

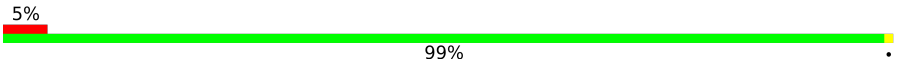


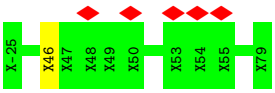
• Molecule 11: Unknown Protein Chain

Chain Bq: 

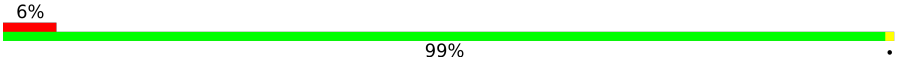


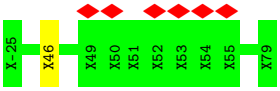
• Molecule 11: Unknown Protein Chain

Chain B2: 

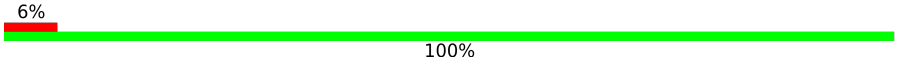


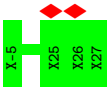
• Molecule 11: Unknown Protein Chain

Chain CO: 

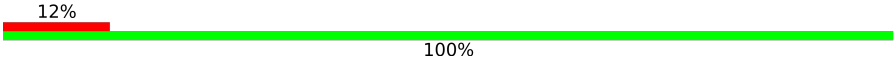


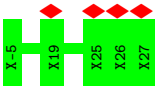
• Molecule 12: Unknown Protein Chain

Chain S: 

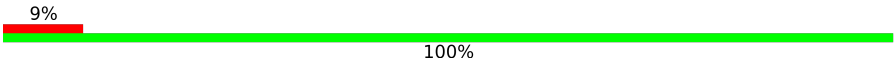


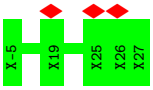
• Molecule 12: Unknown Protein Chain

Chain X: 

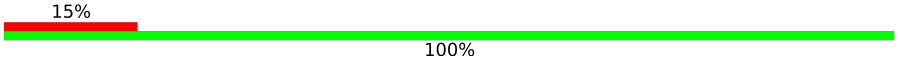


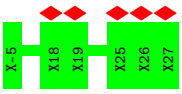
• Molecule 12: Unknown Protein Chain

Chain AR: 

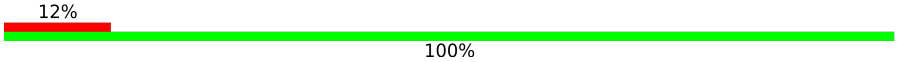


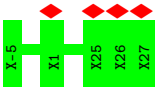
• Molecule 12: Unknown Protein Chain

Chain Ae: 

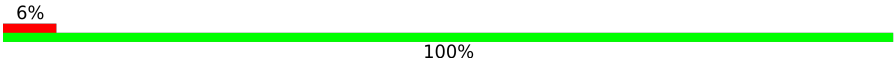


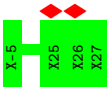
• Molecule 12: Unknown Protein Chain

Chain Ak: 

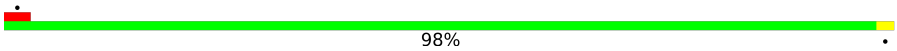


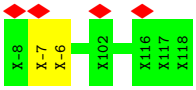
• Molecule 12: Unknown Protein Chain

Chain B8: 

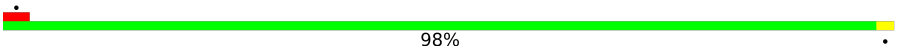


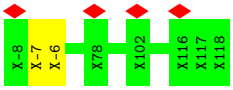
• Molecule 13: Unknown Protein Chain

Chain T: 

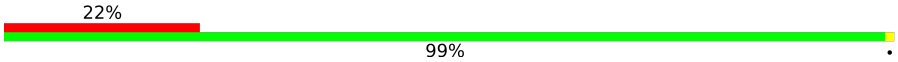


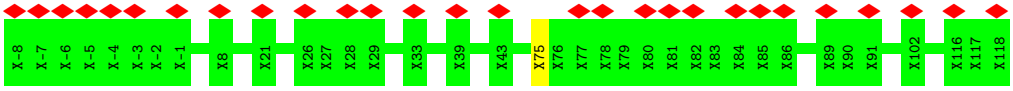
• Molecule 13: Unknown Protein Chain

Chain AH: 

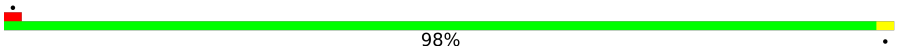


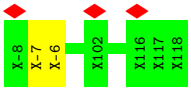
• Molecule 13: Unknown Protein Chain

Chain AS: 

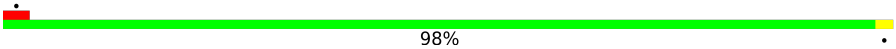


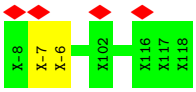
• Molecule 13: Unknown Protein Chain

Chain Bx: 

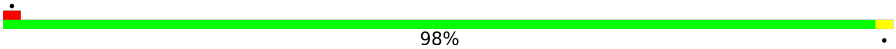


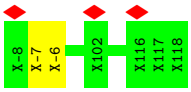
• Molecule 13: Unknown Protein Chain

Chain B9: 

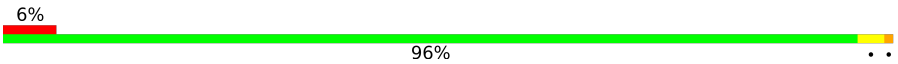


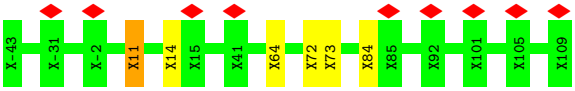
• Molecule 13: Unknown Protein Chain

Chain CV: 

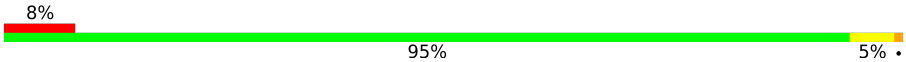


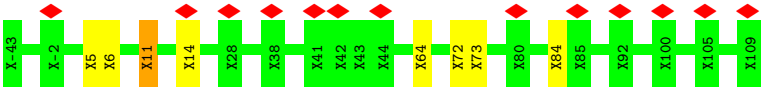
- Molecule 14: Unknown Protein Chain

Chain V: 

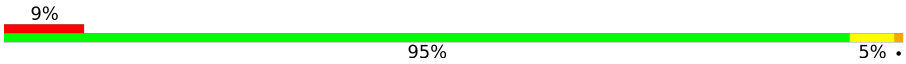


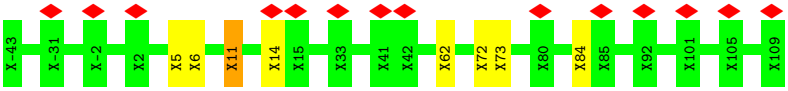
- Molecule 14: Unknown Protein Chain

Chain a: 

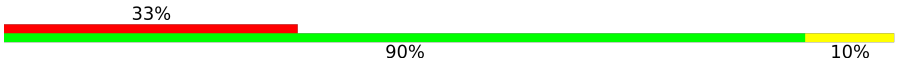


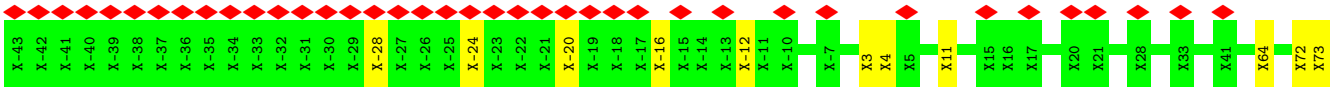
- Molecule 14: Unknown Protein Chain

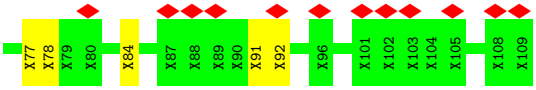
Chain AZ: 



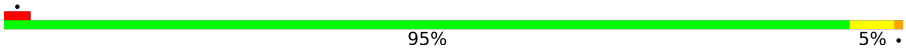
- Molecule 14: Unknown Protein Chain

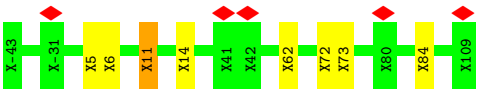
Chain Am: 



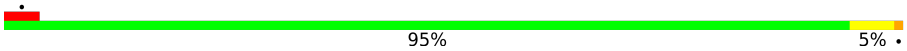


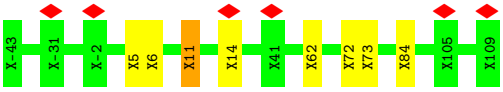
- Molecule 14: Unknown Protein Chain

Chain As: 



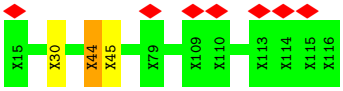
- Molecule 14: Unknown Protein Chain

Chain CE: 



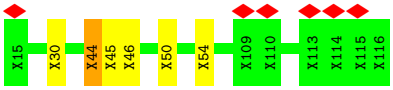
- Molecule 15: Unknown Protein Chain

Chain W: 7% 97%



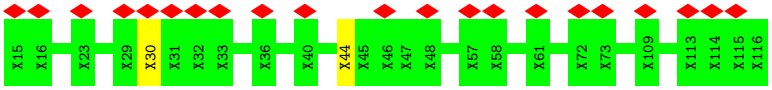
• Molecule 15: Unknown Protein Chain

Chain AP: 6% 94% 5%



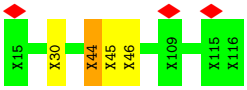
• Molecule 15: Unknown Protein Chain

Chain Aa: 21% 98%



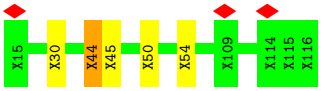
• Molecule 15: Unknown Protein Chain

Chain B5: 96%



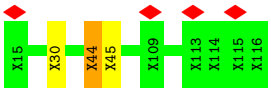
• Molecule 15: Unknown Protein Chain

Chain CF: 95%



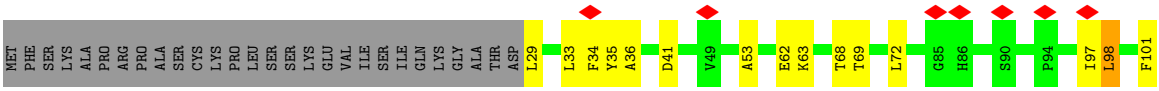
• Molecule 15: Unknown Protein Chain

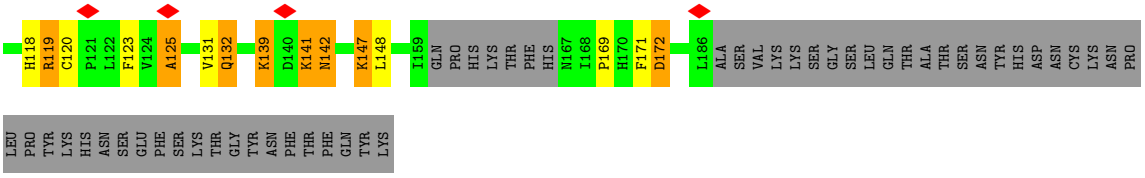
Chain Cc: 97%



• Molecule 16: SWIM-type domain-containing protein

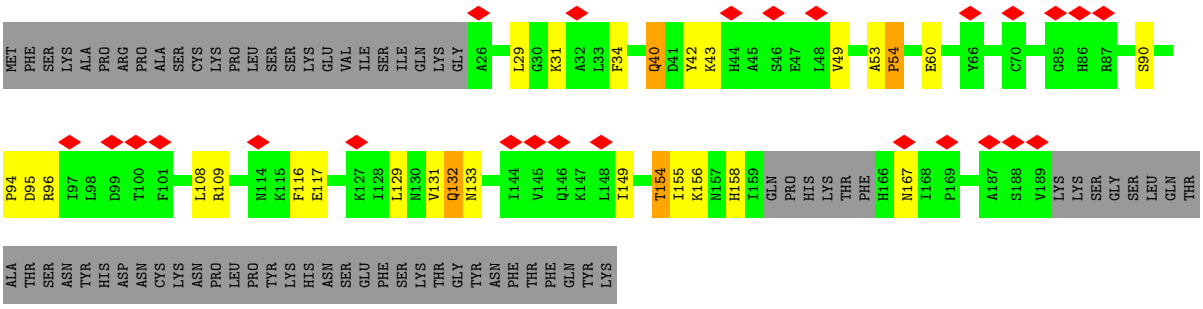
Chain Z: 5% 53% 9% 34%





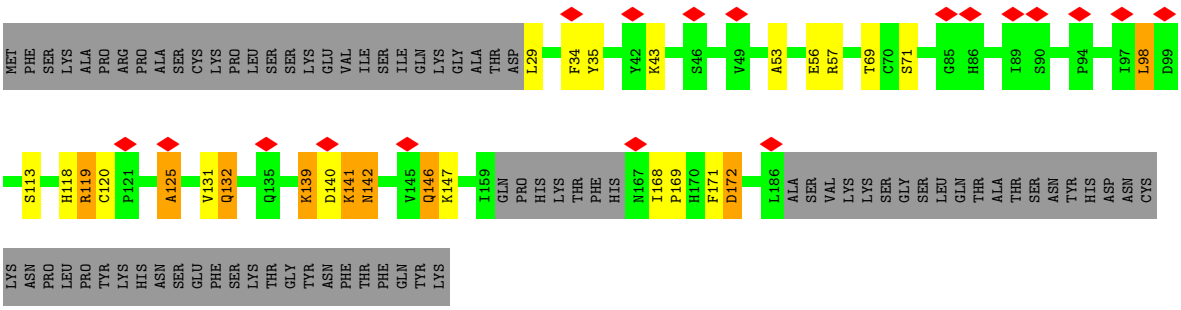
• Molecule 16: SWIM-type domain-containing protein

Chain c:



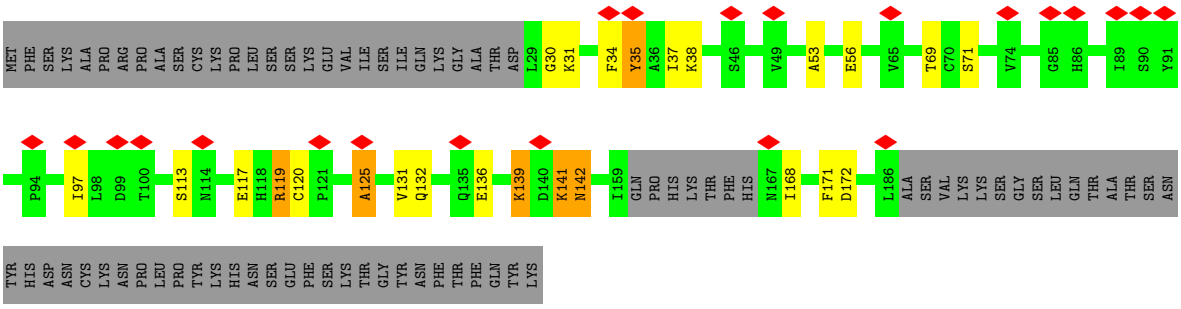
• Molecule 16: SWIM-type domain-containing protein

Chain Ai:



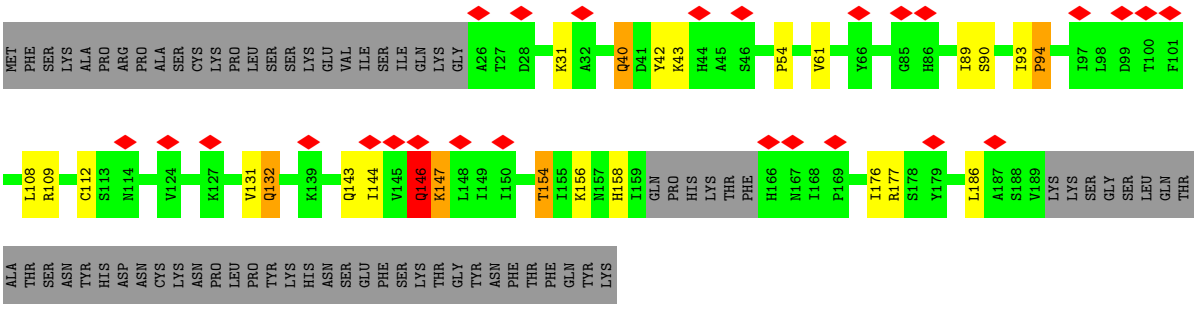
• Molecule 16: SWIM-type domain-containing protein

Chain An:



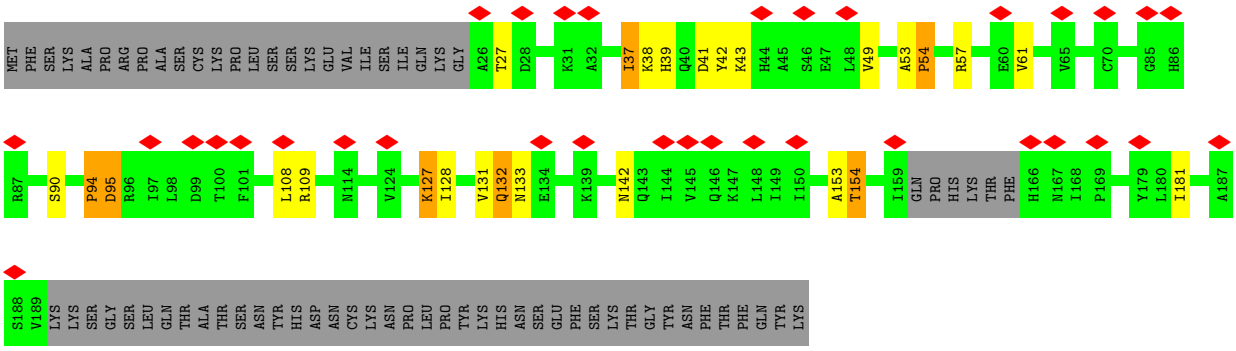
• Molecule 16: SWIM-type domain-containing protein

Chain Aq:



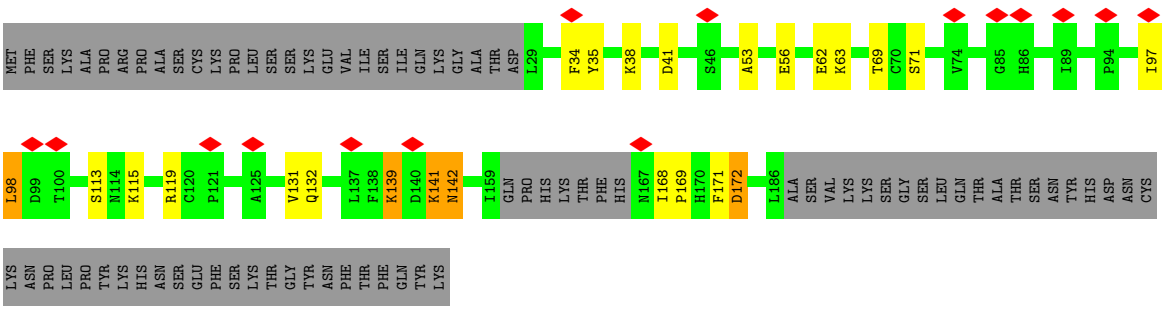
- Molecule 16: SWIM-type domain-containing protein

Chain Av:



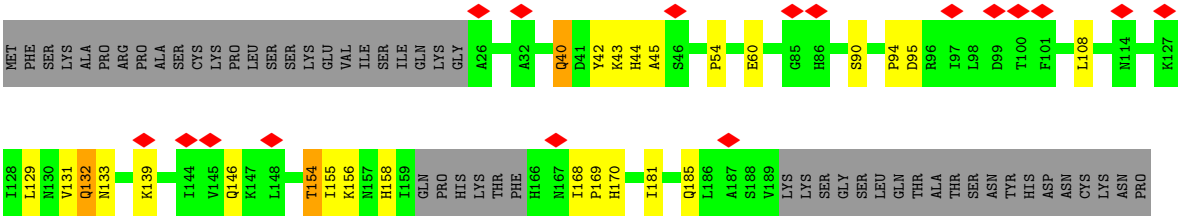
- Molecule 16: SWIM-type domain-containing protein

Chain Az:



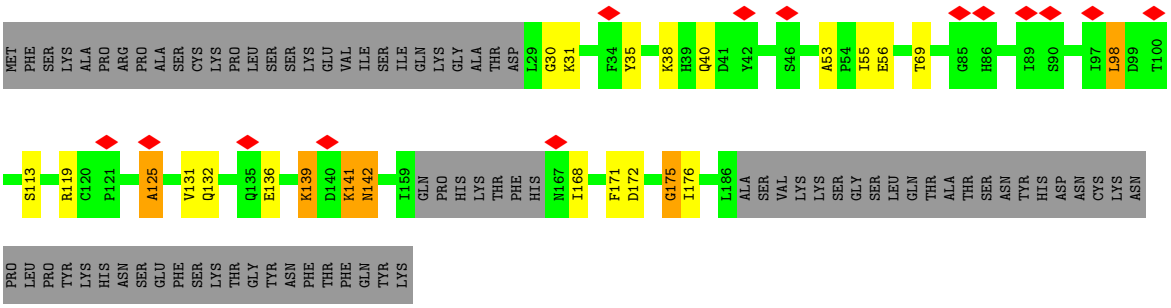
- Molecule 16: SWIM-type domain-containing protein

Chain A7:



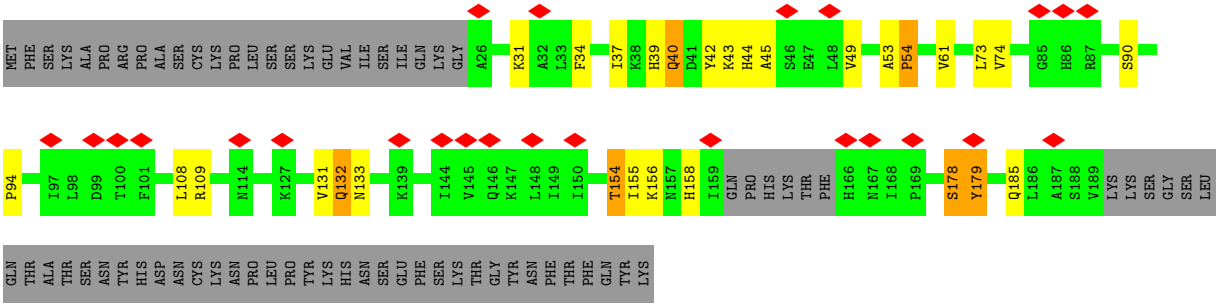
• Molecule 16: SWIM-type domain-containing protein

Chain CB:



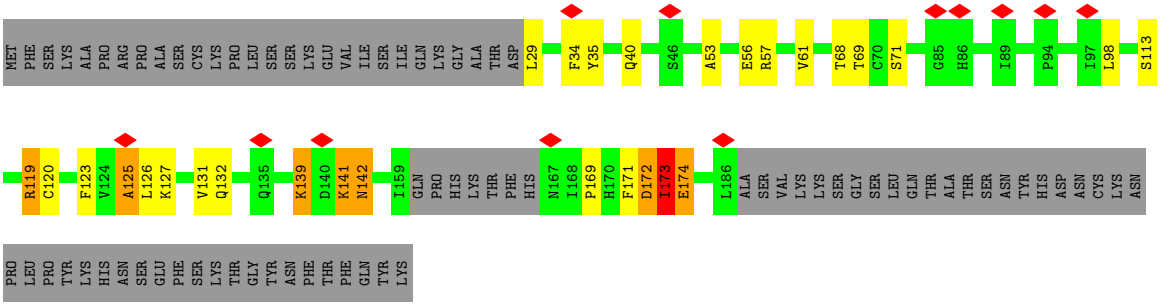
• Molecule 16: SWIM-type domain-containing protein

Chain CI:



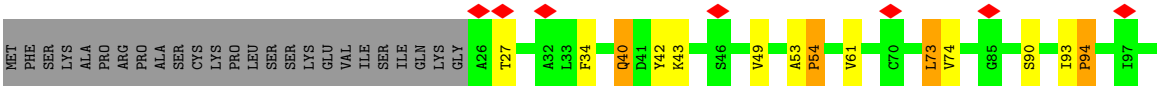
• Molecule 16: SWIM-type domain-containing protein

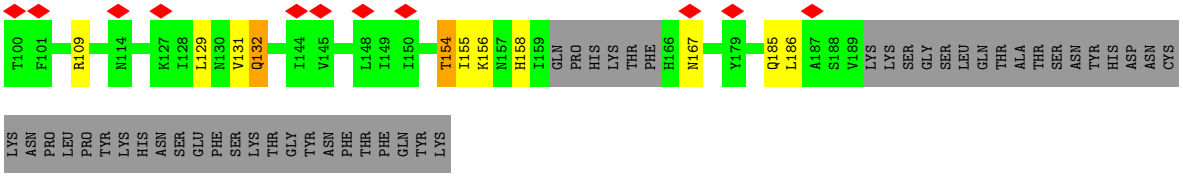
Chain CM:



• Molecule 16: SWIM-type domain-containing protein

Chain CT:




T100
F101
R109
N114
K127
I128
L129
N130
V131
Q132
I144
V145
L148
I149
I150
T154
I155
K156
N157
H158
I159
GLN
PRO
HIS
LYS
THR
PHE
H166
N167
Y179
Q185
L186
A187
S188
V189
LYS
LYS
SER
GLY
SER
LEU
GLN
THR
ALA
THR
SER
ASN
TYR
HIS
ASP
ASN
CYS
LYS
ASN
PRO
LEU
PRO
TYR
LYS
HIS
ASN
SER
GLU
PHE
SER
LYS
THR
GLY
TYR
ASN
PHE
THR
PHE
GLN
TYR
LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	155485	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 ($e^-/Å^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	13.599	Depositor
Minimum map value	0.000	Depositor
Average map value	0.223	Depositor
Map value standard deviation	1.035	Depositor
Recommended contour level	5	Depositor
Map size (Å)	631.2, 631.2, 631.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.315, 1.315, 1.315	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	1.44	3/2127 (0.1%)	1.93	50/2965 (1.7%)
1	BD	1.53	4/2127 (0.2%)	1.91	42/2965 (1.4%)
1	C	1.50	1/2127 (0.0%)	1.87	48/2965 (1.6%)
1	CP	1.55	2/2127 (0.1%)	1.99	53/2965 (1.8%)
1	Ca	1.51	2/2127 (0.1%)	1.96	51/2965 (1.7%)
1	i	1.59	4/2127 (0.2%)	1.88	38/2965 (1.3%)
2	BK	1.32	1/1412 (0.1%)	1.71	33/1969 (1.7%)
2	BR	1.38	0/1285	2.08	43/1793 (2.4%)
2	CW	1.39	4/1412 (0.3%)	1.89	37/1969 (1.9%)
2	Cd	1.45	1/1285 (0.1%)	1.90	47/1793 (2.6%)
2	Ch	1.31	3/1412 (0.2%)	1.74	34/1969 (1.7%)
2	D	1.28	2/1412 (0.1%)	1.74	34/1969 (1.7%)
2	f	1.34	2/1285 (0.2%)	1.92	42/1793 (2.3%)
2	k	1.35	3/1412 (0.2%)	1.90	52/1969 (2.6%)
2	q	1.30	0/1412	1.65	21/1969 (1.1%)
2	s	1.31	0/1285	1.77	39/1793 (2.2%)
2	y	1.42	0/1285	2.07	44/1793 (2.5%)
2	z	1.42	0/1285	2.07	44/1793 (2.5%)
3	1	1.32	1/3079 (0.0%)	1.91	97/4292 (2.3%)
3	7	1.34	6/4036 (0.1%)	1.84	112/5629 (2.0%)
3	BY	1.36	5/3838 (0.1%)	1.93	109/5354 (2.0%)
3	E	1.38	4/3594 (0.1%)	1.91	101/5013 (2.0%)
3	I	1.25	4/4036 (0.1%)	1.88	103/5629 (1.8%)
3	n	1.36	6/3299 (0.2%)	2.00	111/4600 (2.4%)
5	9	1.36	1/1508 (0.1%)	2.02	65/2105 (3.1%)
5	AB	1.40	5/1751 (0.3%)	2.02	74/2439 (3.0%)
5	AE	1.33	1/2582 (0.0%)	1.91	82/3608 (2.3%)
5	AO	1.34	1/1751 (0.1%)	1.94	64/2439 (2.6%)
5	AU	1.38	9/1751 (0.5%)	1.99	70/2439 (2.9%)
5	Bf	1.33	0/2332	1.87	71/3258 (2.2%)
5	Bt	1.40	4/1751 (0.2%)	2.07	69/2439 (2.8%)
5	G	1.38	2/2062 (0.1%)	1.96	75/2880 (2.6%)
5	L	1.24	0/2582	1.88	91/3608 (2.5%)
5	M	1.39	6/1751 (0.3%)	2.00	64/2439 (2.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	R	1.29	1/1751 (0.1%)	1.94	55/2439 (2.3%)
5	v	1.35	0/1788	2.04	68/2497 (2.7%)
7	4	1.55	8/1803 (0.4%)	2.06	81/2508 (3.2%)
7	AG	1.55	12/1803 (0.7%)	2.10	90/2508 (3.6%)
7	AM	1.55	2/1803 (0.1%)	2.05	74/2508 (3.0%)
7	Bm	1.51	5/1803 (0.3%)	2.08	84/2508 (3.3%)
7	J	1.52	11/1803 (0.6%)	2.09	80/2508 (3.2%)
7	O	1.44	5/1803 (0.3%)	1.91	53/2508 (2.1%)
16	A7	1.49	1/781 (0.1%)	2.03	26/1086 (2.4%)
16	Ai	1.38	0/746	2.02	35/1037 (3.4%)
16	An	1.36	0/746	1.94	26/1037 (2.5%)
16	Aq	1.48	1/781 (0.1%)	2.07	27/1086 (2.5%)
16	Av	1.52	2/781 (0.3%)	2.00	23/1086 (2.1%)
16	Az	1.35	0/746	2.02	25/1037 (2.4%)
16	CB	1.39	1/746 (0.1%)	2.01	28/1037 (2.7%)
16	CI	1.51	1/781 (0.1%)	2.05	29/1086 (2.7%)
16	CM	1.38	0/746	2.09	34/1037 (3.3%)
16	CT	1.54	1/781 (0.1%)	1.99	23/1086 (2.1%)
16	Z	1.39	1/746 (0.1%)	2.16	34/1037 (3.3%)
16	c	1.52	1/781 (0.1%)	1.96	22/1086 (2.0%)
All	All	1.40	140/94166 (0.1%)	1.95	3027/131255 (2.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	BD	0	7
1	C	0	5
1	CP	0	7
1	Ca	0	8
1	i	0	6
2	BK	0	9
2	BR	0	10
2	CW	0	11
2	Cd	0	15
2	Ch	0	11
2	D	0	8
2	f	0	11
2	k	0	11

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	q	0	7
2	s	0	10
2	y	0	11
2	z	0	11
3	1	0	10
3	7	0	18
3	BY	0	18
3	E	0	17
3	I	0	18
3	n	0	12
4	BO	0	1
4	BZ	0	1
4	Bw	0	1
4	F	0	1
4	d	0	1
4	o	0	1
5	9	0	9
5	AB	0	9
5	AE	0	18
5	AO	0	9
5	AU	0	9
5	Bf	0	11
5	Bt	0	8
5	G	0	12
5	L	0	17
5	M	0	9
5	R	0	11
5	v	0	10
6	B4	0	3
6	BV	0	3
6	Bg	0	3
6	H	0	3
6	l	0	3
6	w	0	3
7	4	0	13
7	AG	0	10
7	AM	0	13
7	Bm	0	13
7	J	0	10
7	O	0	12
11	0	0	1
11	B2	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	Bq	0	1
11	CO	0	1
13	AS	0	1
14	AZ	0	3
14	Am	0	3
14	As	0	3
14	CE	0	3
14	V	0	3
14	a	0	3
15	AP	0	2
15	Aa	0	2
15	B5	0	2
15	CF	0	2
15	Cc	0	2
15	W	0	2
16	A7	0	5
16	Ai	0	5
16	An	0	5
16	Aq	0	6
16	Av	0	6
16	Az	0	3
16	CB	0	5
16	CI	0	5
16	CM	0	4
16	CT	0	5
16	Z	0	5
16	c	0	5
All	All	0	579

The worst 5 of 140 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	n	752	LYS	CA-C	9.79	1.57	1.52
7	4	144	GLY	CA-C	-7.76	1.43	1.52
5	Bt	283	ASN	CA-C	-7.34	1.43	1.53
1	Ca	204	PHE	CA-C	-7.05	1.44	1.52
7	4	130	HIS	CA-C	-6.99	1.49	1.53

The worst 5 of 3027 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	301	GLU	CA-C-O	-35.50	84.00	120.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BD	301	GLU	CA-C-O	-35.40	84.11	120.92
1	i	301	GLU	CA-C-O	-33.51	84.04	121.58
1	CP	301	GLU	CA-C-O	-33.50	84.06	121.58
1	Ca	301	GLU	CA-C-O	-33.44	84.12	121.58

There are no chirality outliers.

5 of 579 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	155	ASP	Mainchain
1	A	222	TYR	Mainchain,Peptide
1	A	301	GLU	Mainchain
1	A	349	VAL	Mainchain
1	A	94	LEU	Mainchain

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	2129	0	926	2	0
1	BD	2129	0	926	2	0
1	C	2129	0	926	7	0
1	CP	2129	0	926	4	0
1	Ca	2129	0	926	5	0
1	i	2129	0	926	1	0
2	BK	1415	0	597	4	0
2	BR	1288	0	542	5	0
2	CW	1415	0	596	6	0
2	Cd	1288	0	542	10	0
2	Ch	1415	0	597	8	0
2	D	1415	0	597	4	0
2	f	1288	0	542	9	0
2	k	1415	0	597	9	0
2	q	1415	0	597	4	0
2	s	1288	0	542	10	0
2	y	1288	0	542	5	0
2	z	1288	0	542	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	1	3082	0	1317	8	0
3	7	4040	0	1741	15	0
3	BY	3841	0	1655	18	0
3	E	3597	0	1547	14	0
3	I	4040	0	1741	10	0
3	n	3302	0	1411	12	0
4	BO	755	0	158	7	0
4	BZ	755	0	158	6	0
4	Bw	755	0	158	5	0
4	F	755	0	157	5	0
4	d	755	0	159	6	0
4	o	755	0	157	3	0
5	9	1510	0	629	6	0
5	AB	1752	0	772	1	0
5	AE	2584	0	1093	11	0
5	AO	1752	0	772	3	0
5	AU	1752	0	772	7	0
5	Bf	2334	0	990	8	0
5	Bt	1752	0	772	5	0
5	G	2064	0	867	9	0
5	L	2584	0	1093	10	0
5	M	1752	0	772	6	0
5	R	1752	0	772	4	0
5	v	1790	0	744	5	0
6	B4	820	0	167	0	0
6	BV	820	0	167	0	0
6	Bg	820	0	167	0	0
6	H	820	0	167	0	0
6	l	820	0	167	0	0
6	w	820	0	166	0	0
7	4	1806	0	792	15	0
7	AG	1806	0	792	17	0
7	AM	1806	0	792	17	0
7	Bm	1806	0	792	17	0
7	J	1806	0	792	10	0
7	O	1806	0	792	10	0
8	5	835	0	169	0	0
8	Bc	835	0	169	0	0
8	Bn	835	0	169	0	0
8	CA	835	0	169	0	0
8	K	835	0	169	0	0
8	t	835	0	169	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	2	805	0	165	2	0
9	AC	805	0	165	1	0
9	Bj	805	0	165	0	0
9	Bu	805	0	165	0	0
9	CH	805	0	165	0	0
9	N	805	0	165	0	0
10	AJ	160	0	34	0	0
10	AW	160	0	34	0	0
10	Ac	160	0	35	0	0
10	B1	160	0	34	0	0
10	P	160	0	34	0	0
10	U	160	0	34	0	0
11	0	525	0	107	0	0
11	AK	525	0	107	1	0
11	B2	525	0	107	0	0
11	Bq	525	0	107	0	0
11	CO	525	0	107	0	0
11	Q	525	0	107	1	0
12	AR	165	0	35	0	0
12	Ae	165	0	35	0	0
12	Ak	165	0	35	0	0
12	B8	165	0	35	0	0
12	S	165	0	35	0	0
12	X	165	0	35	0	0
13	AH	635	0	129	1	0
13	AS	635	0	130	0	0
13	B9	635	0	129	1	0
13	Bx	635	0	129	1	0
13	CV	635	0	129	1	0
13	T	635	0	129	1	0
14	AZ	765	0	158	3	0
14	Am	765	0	157	7	0
14	As	765	0	158	3	0
14	CE	765	0	157	4	0
14	V	765	0	157	2	0
14	a	765	0	158	3	0
15	AP	510	0	105	3	0
15	Aa	510	0	104	0	0
15	B5	510	0	104	2	0
15	CF	510	0	104	2	0
15	Cc	510	0	104	1	0
15	W	510	0	104	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	A7	783	0	350	3	0
16	Ai	748	0	330	1	0
16	An	748	0	330	2	0
16	Aq	783	0	350	4	0
16	Av	783	0	350	3	0
16	Az	748	0	330	1	0
16	CB	748	0	330	1	0
16	CI	783	0	350	5	0
16	CM	748	0	330	3	0
16	CT	783	0	350	4	0
16	Z	748	0	330	2	0
16	c	783	0	350	4	0
All	All	130144	0	48035	442	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 442 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)
2:Cd:330:ALA:H	2:Cd:332:VAL:H	1.41	0.69
1:BD:234:THR:O	1:BD:235:PRO:C	2.43	0.62
1:CP:234:THR:O	1:CP:235:PRO:C	2.43	0.62
1:A:234:THR:O	1:A:235:PRO:C	2.43	0.61
14:CE:72:UNK:O	14:CE:73:UNK:C	2.48	0.61

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	425/452 (94%)	373 (88%)	41 (10%)	11 (3%)	4	27
1	BD	425/452 (94%)	374 (88%)	37 (9%)	14 (3%)	3	24
1	C	425/452 (94%)	369 (87%)	44 (10%)	12 (3%)	4	26
1	CP	425/452 (94%)	369 (87%)	43 (10%)	13 (3%)	3	25
1	Ca	425/452 (94%)	375 (88%)	40 (9%)	10 (2%)	4	29
1	i	425/452 (94%)	371 (87%)	45 (11%)	9 (2%)	5	31
2	BK	278/380 (73%)	269 (97%)	5 (2%)	4 (1%)	9	37
2	BR	252/380 (66%)	244 (97%)	7 (3%)	1 (0%)	30	62
2	CW	278/380 (73%)	262 (94%)	12 (4%)	4 (1%)	9	37
2	Cd	252/380 (66%)	243 (96%)	3 (1%)	6 (2%)	4	29
2	Ch	278/380 (73%)	263 (95%)	12 (4%)	3 (1%)	11	41
2	D	278/380 (73%)	266 (96%)	8 (3%)	4 (1%)	9	37
2	f	252/380 (66%)	244 (97%)	6 (2%)	2 (1%)	16	48
2	k	278/380 (73%)	262 (94%)	12 (4%)	4 (1%)	9	37
2	q	278/380 (73%)	266 (96%)	8 (3%)	4 (1%)	9	37
2	s	252/380 (66%)	244 (97%)	6 (2%)	2 (1%)	16	48
2	y	252/380 (66%)	244 (97%)	6 (2%)	2 (1%)	16	48
2	z	252/380 (66%)	244 (97%)	6 (2%)	2 (1%)	16	48
3	1	615/937 (66%)	577 (94%)	23 (4%)	15 (2%)	4	29
3	7	805/937 (86%)	761 (94%)	28 (4%)	16 (2%)	6	32
3	BY	767/937 (82%)	724 (94%)	27 (4%)	16 (2%)	5	31
3	E	718/937 (77%)	677 (94%)	25 (4%)	16 (2%)	5	30
3	I	805/937 (86%)	765 (95%)	26 (3%)	14 (2%)	7	34
3	n	659/937 (70%)	620 (94%)	25 (4%)	14 (2%)	5	31
5	9	299/1202 (25%)	272 (91%)	23 (8%)	4 (1%)	9	38
5	AB	352/1202 (29%)	332 (94%)	17 (5%)	3 (1%)	14	45
5	AE	514/1202 (43%)	479 (93%)	27 (5%)	8 (2%)	7	35
5	AO	352/1202 (29%)	335 (95%)	13 (4%)	4 (1%)	11	41
5	AU	352/1202 (29%)	334 (95%)	15 (4%)	3 (1%)	14	45
5	Bf	464/1202 (39%)	432 (93%)	27 (6%)	5 (1%)	11	41
5	Bt	352/1202 (29%)	330 (94%)	20 (6%)	2 (1%)	21	54
5	G	410/1202 (34%)	382 (93%)	26 (6%)	2 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	L	514/1202 (43%)	484 (94%)	25 (5%)	5 (1%)	12	43
5	M	352/1202 (29%)	326 (93%)	23 (6%)	3 (1%)	14	45
5	R	352/1202 (29%)	329 (94%)	19 (5%)	4 (1%)	11	41
5	v	355/1202 (30%)	327 (92%)	22 (6%)	6 (2%)	7	34
7	4	359/634 (57%)	315 (88%)	38 (11%)	6 (2%)	7	34
7	AG	359/634 (57%)	316 (88%)	35 (10%)	8 (2%)	5	30
7	AM	359/634 (57%)	319 (89%)	36 (10%)	4 (1%)	11	41
7	Bm	359/634 (57%)	317 (88%)	37 (10%)	5 (1%)	9	37
7	J	359/634 (57%)	317 (88%)	34 (10%)	8 (2%)	5	30
7	O	359/634 (57%)	317 (88%)	36 (10%)	6 (2%)	7	34
16	A7	154/230 (67%)	143 (93%)	9 (6%)	2 (1%)	9	38
16	Ai	147/230 (64%)	133 (90%)	10 (7%)	4 (3%)	4	27
16	An	147/230 (64%)	133 (90%)	9 (6%)	5 (3%)	3	23
16	Aq	154/230 (67%)	141 (92%)	12 (8%)	1 (1%)	21	54
16	Av	154/230 (67%)	143 (93%)	7 (4%)	4 (3%)	4	27
16	Az	147/230 (64%)	129 (88%)	13 (9%)	5 (3%)	3	23
16	CB	147/230 (64%)	130 (88%)	13 (9%)	4 (3%)	4	27
16	CI	154/230 (67%)	144 (94%)	9 (6%)	1 (1%)	21	54
16	CM	147/230 (64%)	127 (86%)	15 (10%)	5 (3%)	3	23
16	CT	154/230 (67%)	142 (92%)	11 (7%)	1 (1%)	21	54
16	Z	147/230 (64%)	133 (90%)	10 (7%)	4 (3%)	4	27
16	c	154/230 (67%)	143 (93%)	9 (6%)	2 (1%)	9	38
All	All	18727/33882 (55%)	17310 (92%)	1095 (6%)	322 (2%)	9	34

5 of 322 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	SER
1	A	101	PRO
1	C	68	SER
1	C	101	PRO
2	D	234	LYS

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

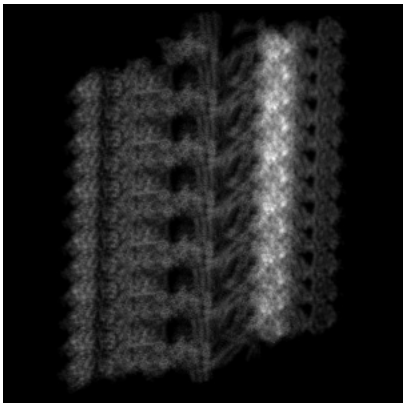
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-53471. These allow visual inspection of the internal detail of the map and identification of artifacts.

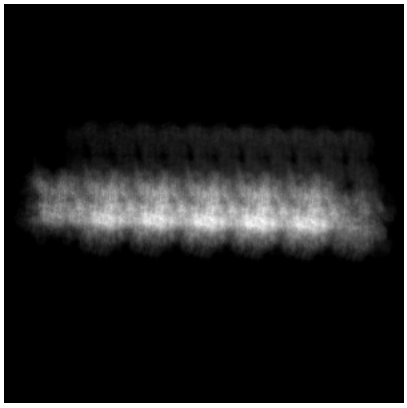
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map



X



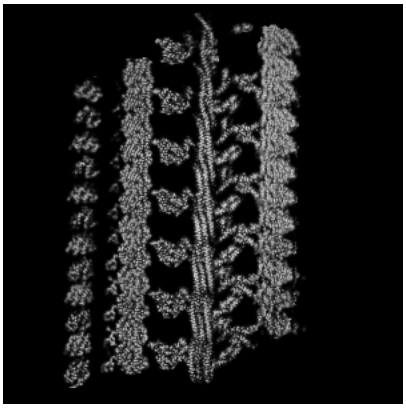
Y

Z

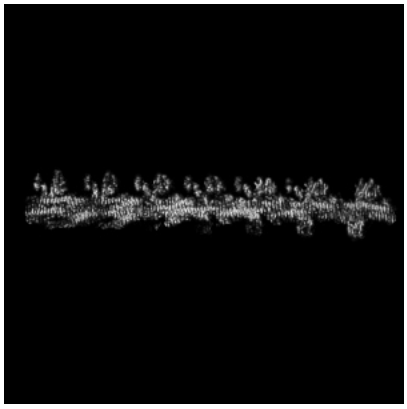
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

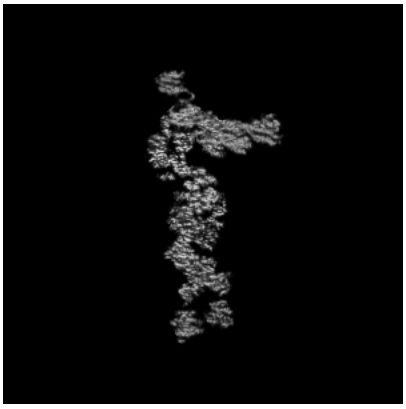
6.2.1 Primary map



X Index: 240



Y Index: 240

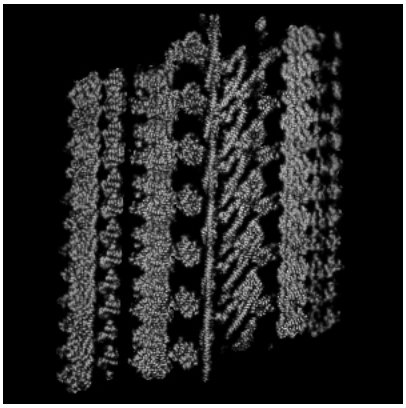


Z Index: 240

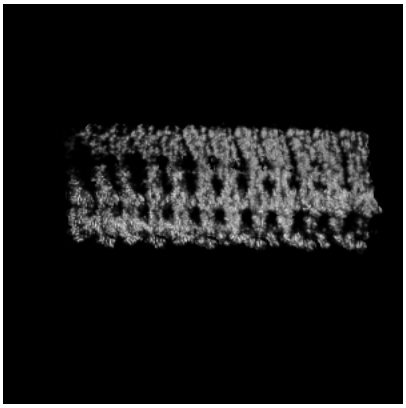
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

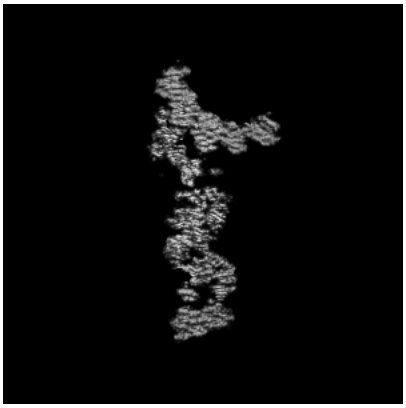
6.3.1 Primary map



X Index: 218



Y Index: 335

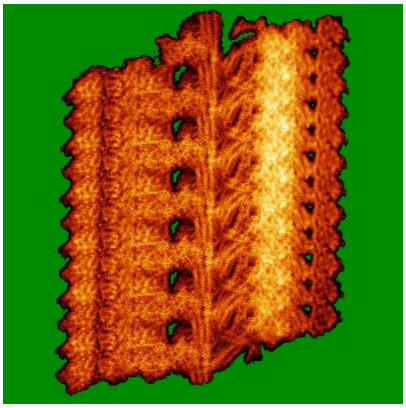


Z Index: 311

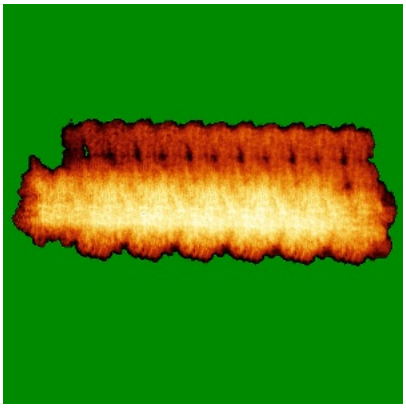
The images above show the largest variance slices of the map in three orthogonal directions.

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

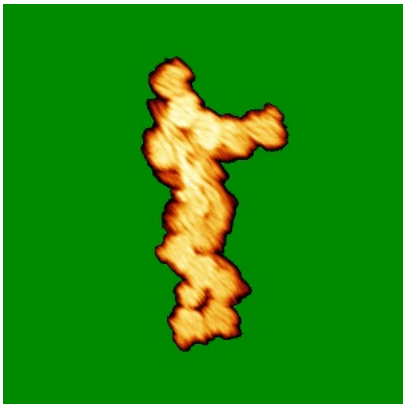
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

This section was not generated.

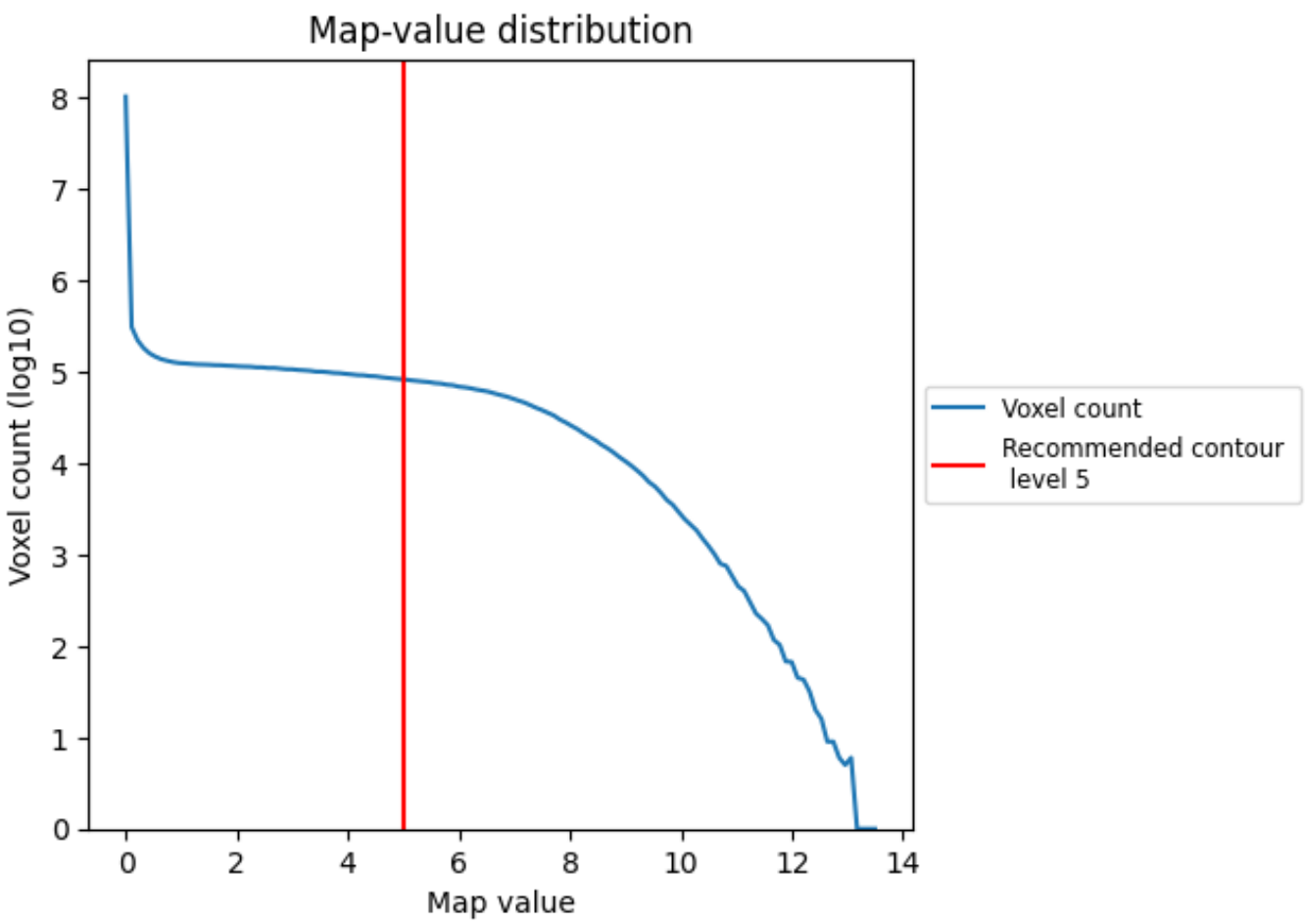
6.6 Mask visualisation (i)

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

7 Map analysis (i)

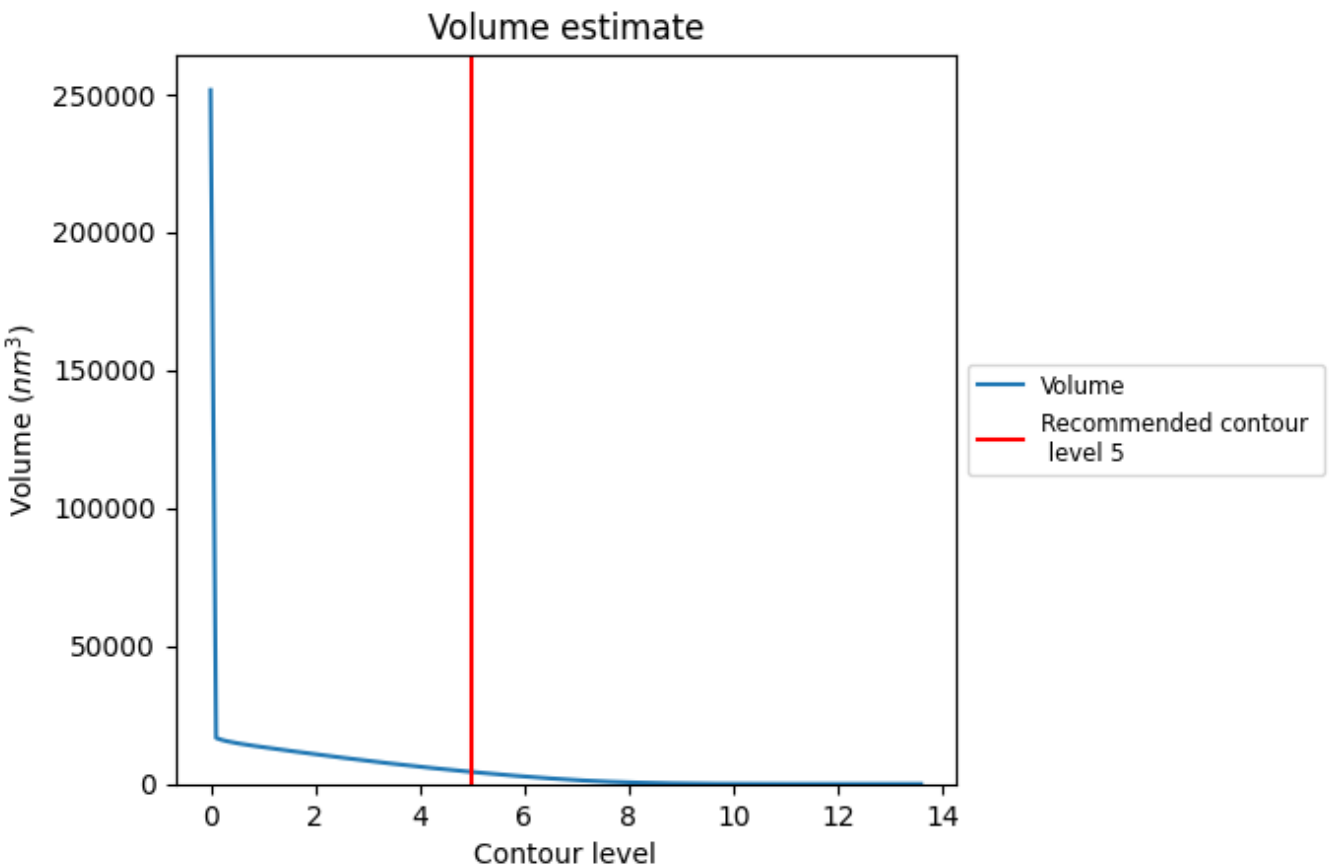
This section contains the results of statistical analysis of the map.

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.

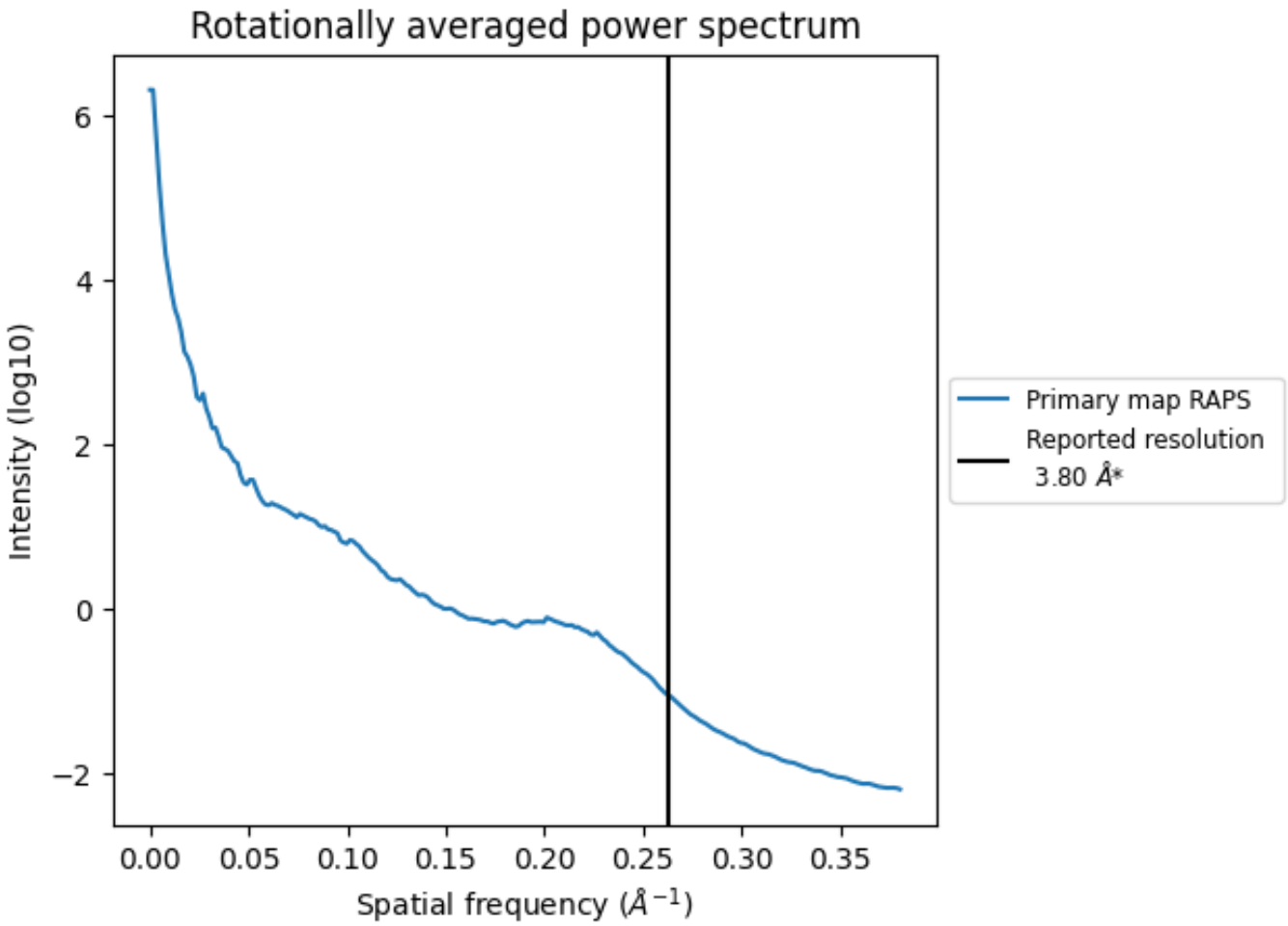
7.2 Volume estimate (i)



The volume at the recommended contour level is 4355 nm^3; this corresponds to an approximate mass of 3934 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 0.263 Å^{-1}

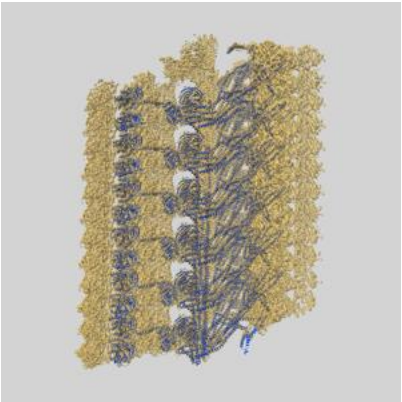
8 Fourier-Shell correlation (i)

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

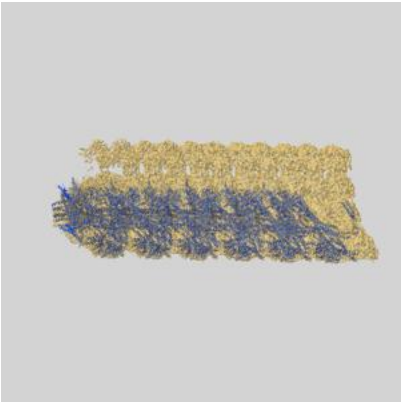
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-53471 and PDB model 9QZF. Per-residue inclusion information can be found in section 3 on page 15.

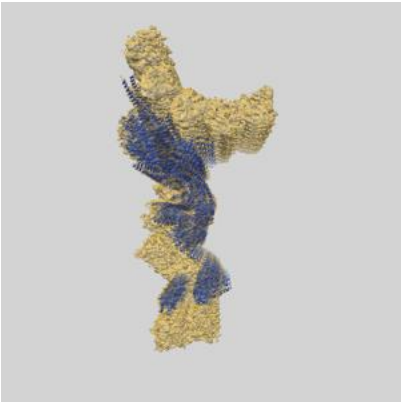
9.1 Map-model overlay (i)



X



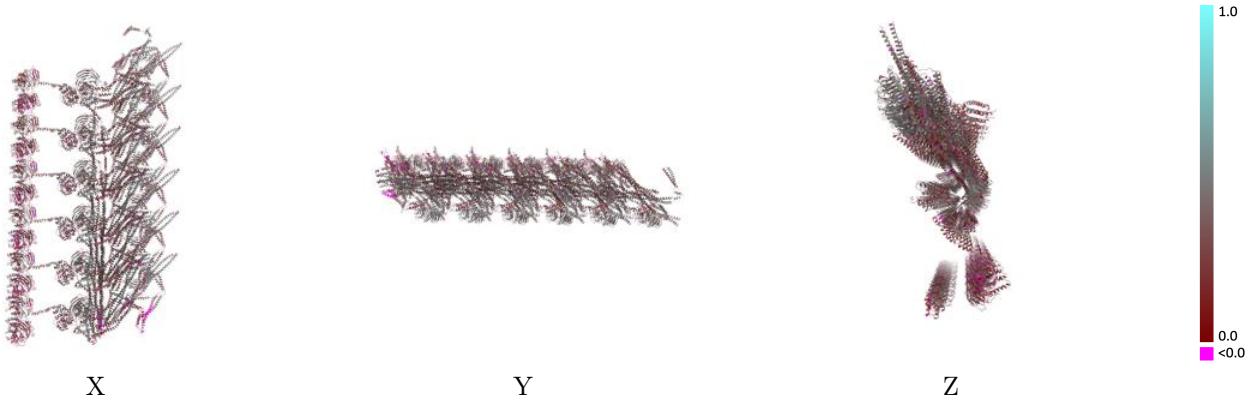
Y



Z

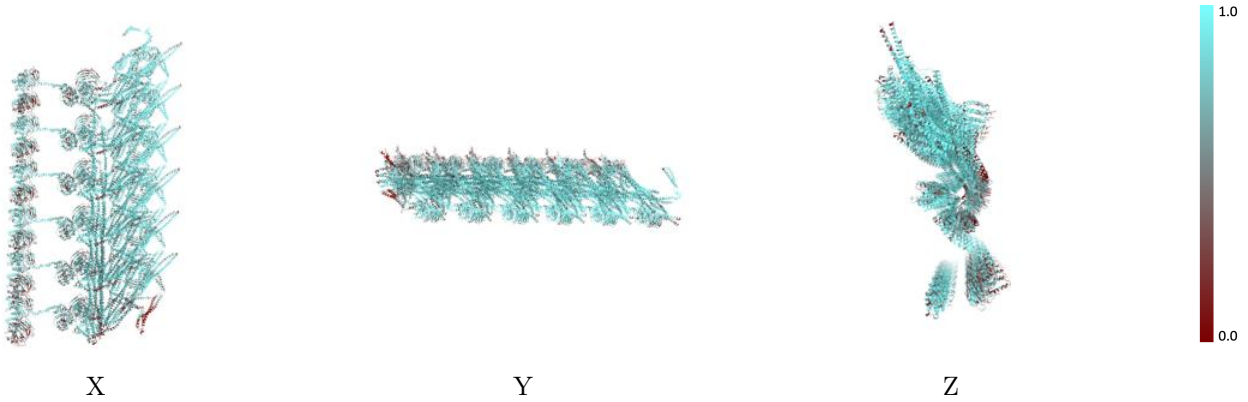
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



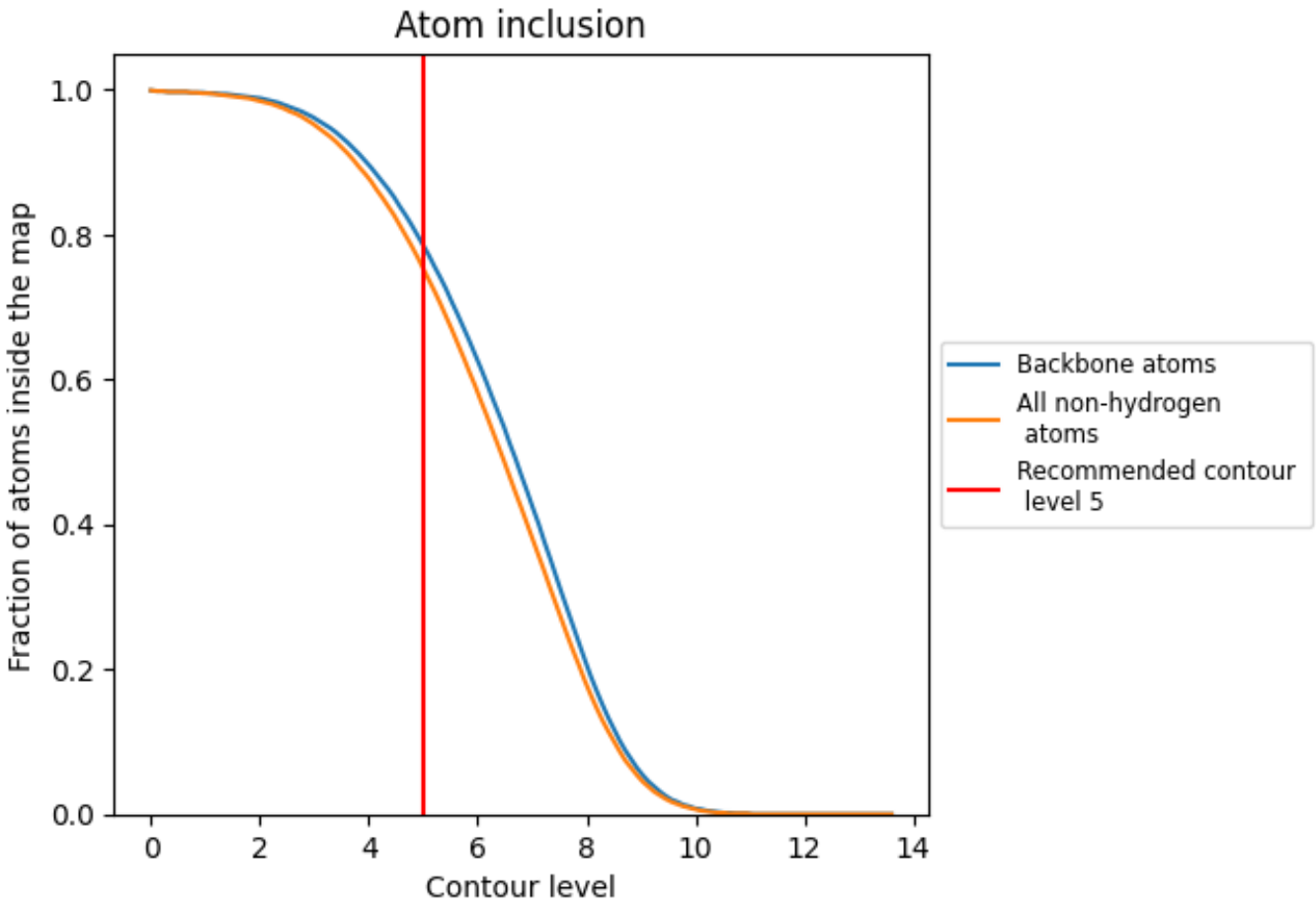
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 75% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7530	0.3370
0	0.8930	0.3640
1	0.5950	0.3520
2	0.9020	0.3790
4	0.6570	0.2890
5	0.7290	0.4000
7	0.7440	0.3410
9	0.7150	0.3350
A	0.7590	0.3960
A7	0.7940	0.3400
AB	0.4420	0.2140
AC	0.8560	0.4000
AE	0.8500	0.3580
AG	0.6470	0.2890
AH	0.8900	0.3500
AJ	0.7690	0.4220
AK	0.8020	0.3780
AM	0.7320	0.2870
AO	0.4300	0.2210
AP	0.8800	0.3710
AR	0.8490	0.3760
AS	0.6830	0.3720
AU	0.5010	0.2150
AW	0.7810	0.4480
AZ	0.8180	0.3400
Aa	0.7060	0.3870
Ac	0.8440	0.4140
Ae	0.7880	0.3640
Ai	0.7740	0.3300
Ak	0.7880	0.3420
Am	0.5520	0.2930
An	0.7430	0.3270
Aq	0.7230	0.3400
As	0.8990	0.3380
Av	0.6900	0.3360

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Chain	Atom inclusion	Q-score
Az	0.7940	0.3240
B1	0.8500	0.4240
B2	0.9330	0.3680
B4	0.8520	0.3670
B5	0.9250	0.3690
B8	0.8730	0.3710
B9	0.9180	0.3590
BD	0.8410	0.3990
BK	0.8620	0.3480
BO	0.9420	0.3710
BR	0.8200	0.3130
BV	0.8540	0.3530
BY	0.7140	0.3540
BZ	0.9010	0.3710
Bc	0.8380	0.3660
Bf	0.8210	0.3570
Bg	0.8460	0.3710
Bj	0.9580	0.3760
Bm	0.6990	0.2870
Bn	0.8480	0.3750
Bq	0.9390	0.3630
Bt	0.4650	0.1940
Bu	0.9490	0.3970
Bw	0.9430	0.3710
Bx	0.9290	0.3460
C	0.7660	0.4030
CA	0.8520	0.3760
CB	0.8010	0.3260
CE	0.8850	0.3430
CF	0.9120	0.3650
CH	0.9430	0.3910
CI	0.7480	0.3350
CM	0.8050	0.3230
CO	0.9330	0.3750
CP	0.8500	0.3950
CT	0.8050	0.3370
CV	0.9200	0.3590
CW	0.8710	0.3560
Ca	0.7740	0.3950
Cc	0.9250	0.3730
Cd	0.8200	0.3150
Ch	0.8010	0.3510

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Chain	Atom inclusion	Q-score
D	0.8070	0.3360
E	0.7170	0.3540
F	0.8720	0.3760
G	0.8170	0.3510
H	0.7910	0.3620
I	0.6590	0.3400
J	0.7180	0.2830
K	0.7750	0.3750
L	0.8080	0.3430
M	0.5110	0.2000
N	0.9200	0.3900
O	0.6220	0.2700
P	0.8250	0.4210
Q	0.8910	0.3580
R	0.4080	0.2080
S	0.8610	0.3590
T	0.8740	0.3600
U	0.7810	0.4140
V	0.8690	0.3470
W	0.8760	0.3700
X	0.7390	0.3470
Z	0.8210	0.3170
a	0.8520	0.3460
c	0.7330	0.3350
d	0.8910	0.3640
f	0.7520	0.3050
i	0.8760	0.3990
k	0.7040	0.3330
l	0.7910	0.3620
n	0.5920	0.3350
o	0.4950	0.2430
q	0.8820	0.3490
s	0.6480	0.2900
t	0.7750	0.3690
v	0.7590	0.3600
w	0.7290	0.3830
y	0.8370	0.3210
z	0.7550	0.3040