Full wwPDB EM Validation Report ⓘ

Sep 18, 2024 – 02:07 pm BST

PDB ID	:	8RX1
EMDB ID	:	EMD-19570
Title	:	CryoEM structure of the gTuRC-CM1dim complex
Authors	:	Llorca, O.; Serna, M.; Gonzalez-Rodriguez, N.
Deposited on	:	2024-02-06
Resolution	:	3.57 Å(reported)
Based on initial models	:	6X0V, 7AS4

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

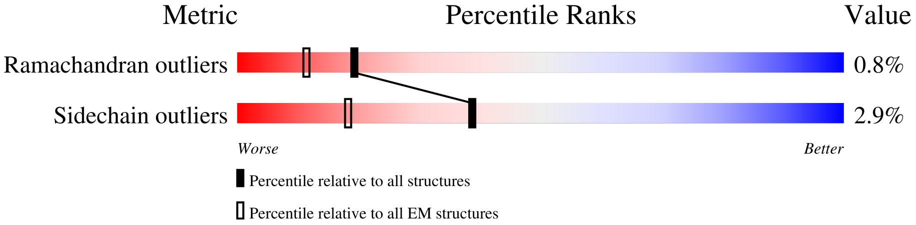
EMDB validation analysis	:	0.0.1.dev112
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

1 Overall quality at a glance ⓘ

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

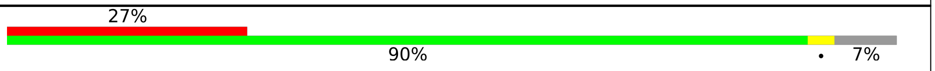
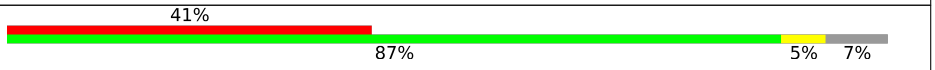
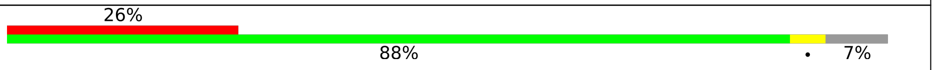
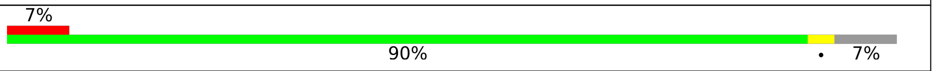
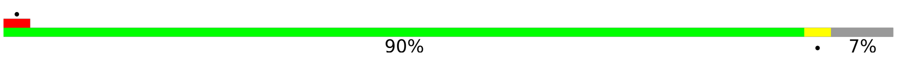
The reported resolution of this entry is 3.57 Å.

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.



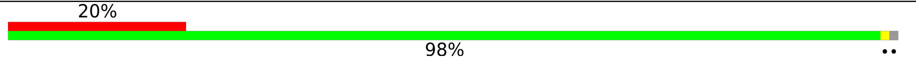
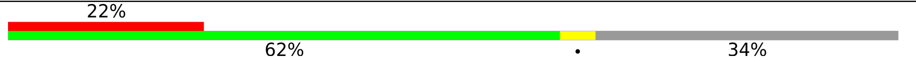
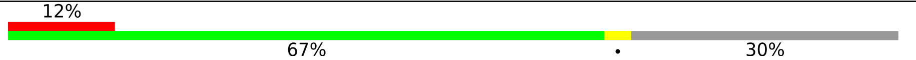
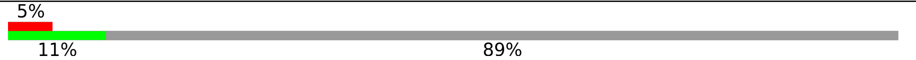
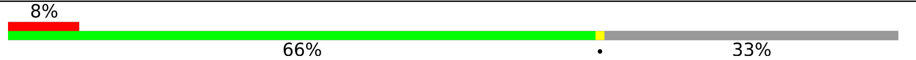
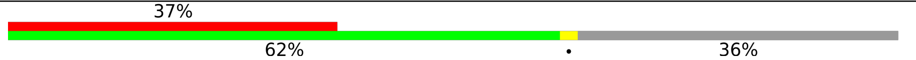
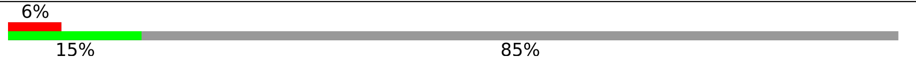
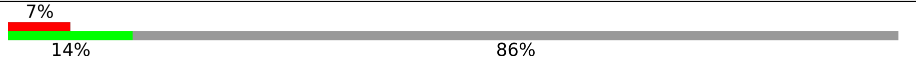
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	451	
1	2	451	
1	O	451	
1	P	451	
1	Q	451	
1	R	451	
1	S	451	
1	T	451	
1	U	451	

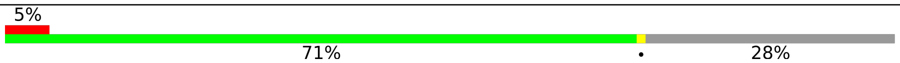
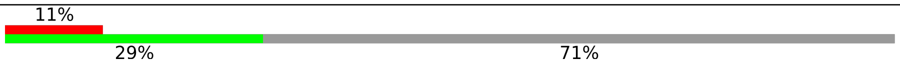
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	V	451	
1	W	451	
1	X	451	
1	Y	451	
1	Z	451	
2	7	364	
3	A	902	
3	C	902	
3	E	902	
3	M	902	
3	f	902	
3	k	902	
4	B	907	
4	D	907	
4	F	907	
4	N	907	
4	b	907	
4	n	907	
5	G	229	
5	H	229	
5	g	229	
5	h	229	
5	i	229	
5	j	229	
5	s	229	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	t	229	
5	u	229	
5	v	229	
6	I	667	
6	K	667	
7	J	1024	
8	L	1819	
8	d	1819	
9	a	82	
9	c	82	
10	e	158	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 123860 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 Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1	420	3365	2130	583	637	15	0	0
1	2	415	3311	2095	574	627	15	0	0
1	O	420	3365	2130	583	637	15	0	0
1	P	420	3359	2127	580	637	15	0	0
1	Q	420	3371	2133	586	637	15	0	0
1	R	420	3365	2130	583	637	15	0	0
1	S	420	3371	2133	586	637	15	0	0
1	T	420	3359	2127	580	637	15	0	0
1	U	420	3365	2130	583	637	15	0	0
1	V	417	3325	2109	571	630	15	0	0
1	W	417	3342	2114	579	634	15	0	0
1	X	420	3371	2133	586	637	15	0	0
1	Y	419	3363	2129	585	634	15	0	0
1	Z	420	3365	2130	583	637	15	0	0

- Molecule 2 is a protein called Actin b.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	7	360	1812	1091	360	361	0	0

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

Mol	Chain	Residues	Atoms	AltConf	Trace
3	A	599	Total C N O S 4846 3135 802 877 32	0	0
3	C	614	Total C N O S 4973 3216 824 901 32	0	0
3	E	638	Total C N O S 5196 3351 870 942 33	0	0
3	M	633	Total C N O S 5158 3325 865 935 33	0	0
3	f	95	Total C N O 481 291 95 95	0	0
3	k	636	Total C N O S 5180 3339 868 940 33	0	0

- Molecule 4 is a protein called Gamma-tubulin complex component 3.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	B	610	Total C N O S 5015 3195 885 910 25	0	0
4	D	581	Total C N O S 4790 3058 839 868 25	0	0
4	F	599	Total C N O S 4921 3140 865 891 25	0	0
4	N	583	Total C N O S 4810 3072 848 865 25	0	0
4	b	116	Total C N O S 933 591 171 169 2	0	0
4	n	594	Total C N O S 4875 3113 852 885 25	0	0

- Molecule 5 is a protein called CM1.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	G	31	Total C N O S 270 173 46 50 1	0	0
5	H	35	Total C N O S 317 202 55 58 2	0	0
5	g	35	Total C N O S 303 192 54 55 2	0	0
5	h	35	Total C N O S 317 202 55 58 2	0	0
5	i	31	Total C N O S 274 176 46 50 2	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	32	Total 290	C 187	N 48	O 54	S 1	0	0
5	s	35	Total 303	C 192	N 54	O 55	S 2	0	0
5	t	35	Total 303	C 192	N 54	O 55	S 2	0	0
5	u	35	Total 317	C 202	N 55	O 58	S 2	0	0
5	v	35	Total 317	C 202	N 55	O 58	S 2	0	0

- Molecule 6 is a protein called Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	521	Total 4203	C 2722	N 714	O 749	S 18	0	0
6	K	562	Total 4573	C 2961	N 778	O 816	S 18	0	0

- Molecule 7 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	601	Total 4837	C 3127	N 811	O 872	S 27	0	0

- Molecule 8 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	617	Total 4928	C 3217	N 830	O 855	S 26	0	0
8	d	147	Total 1152	C 727	N 198	O 219	S 8	0	0

- Molecule 9 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	65	Total 484	C 299	N 85	O 96	S 4	0	0
9	c	59	Total 454	C 281	N 79	O 90	S 4	0	0

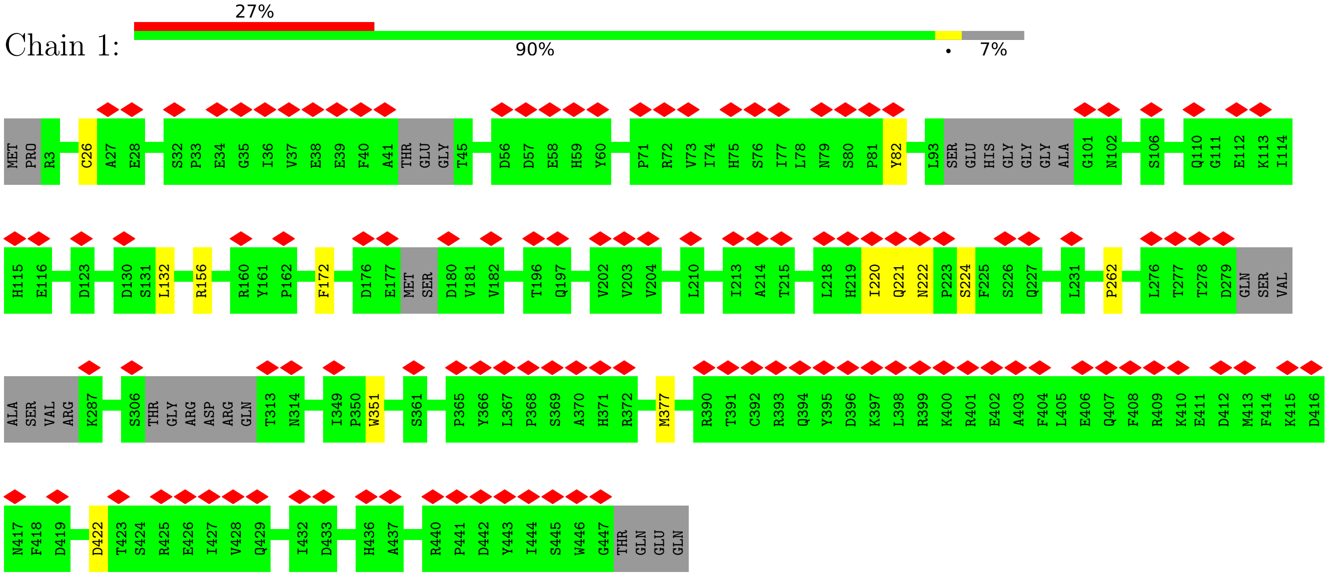
- Molecule 10 is a protein called Mitotic-spindle organizing protein 2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	e	46	231	139	46	46	0	0

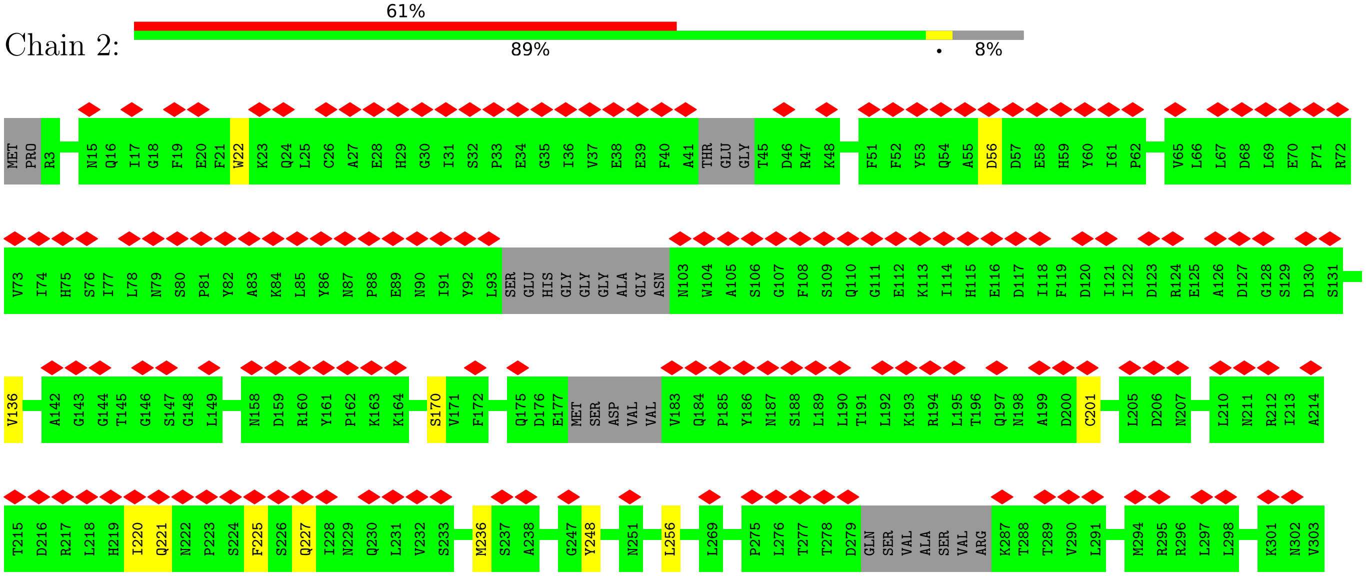
3 Residue-property plots ⓘ

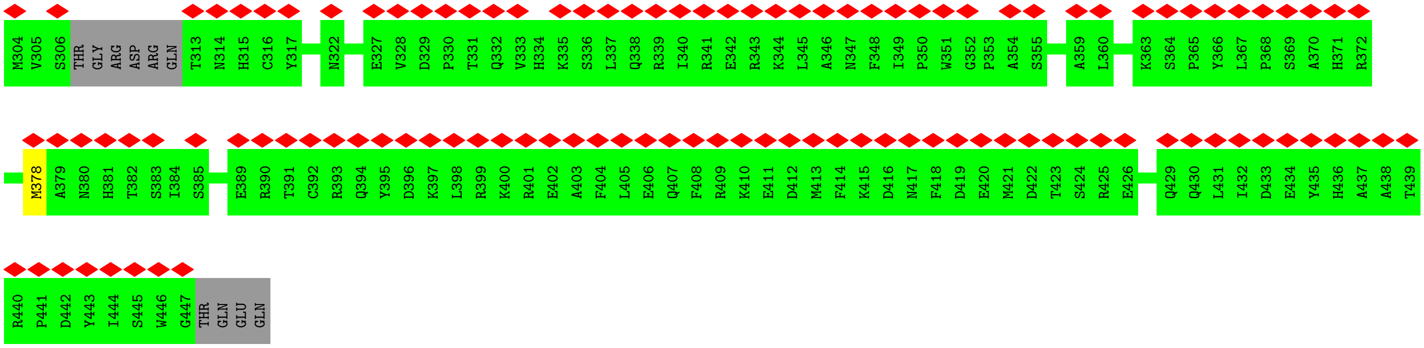
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Tubulin gamma-1 chain

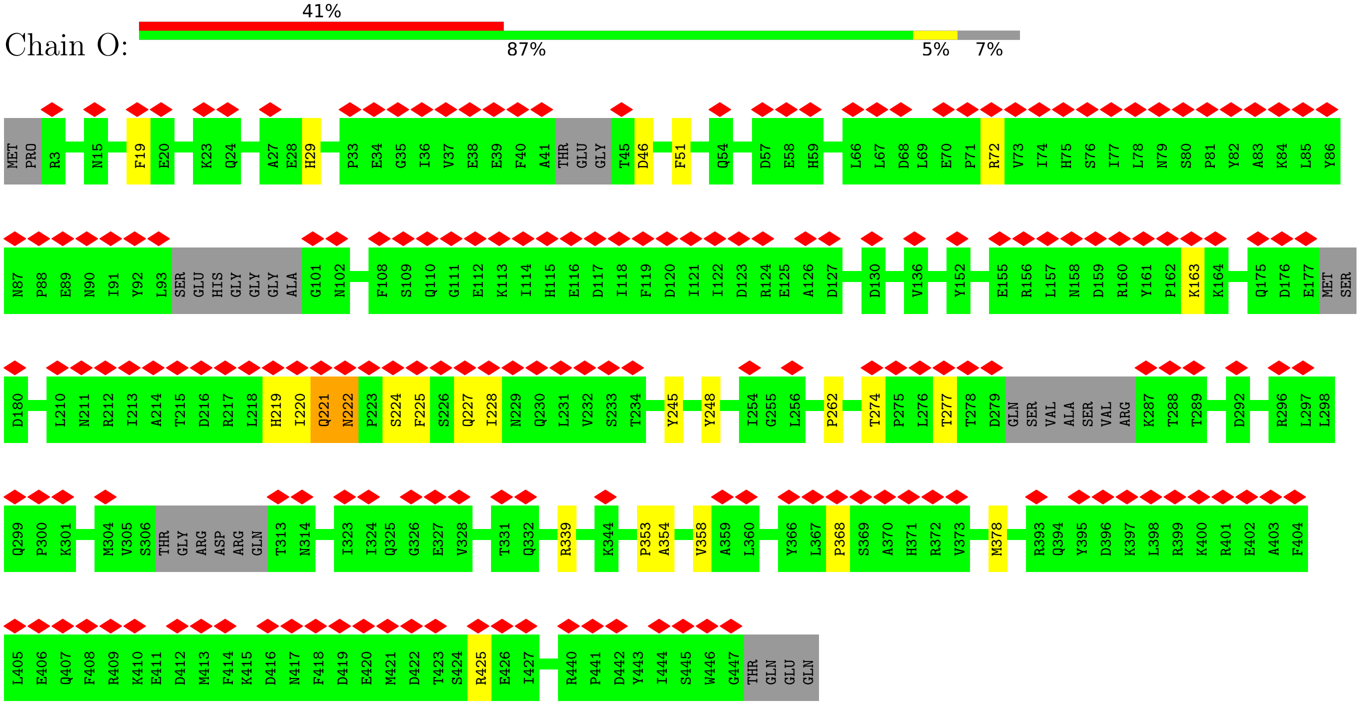


- Molecule 1: Tubulin gamma-1 chain

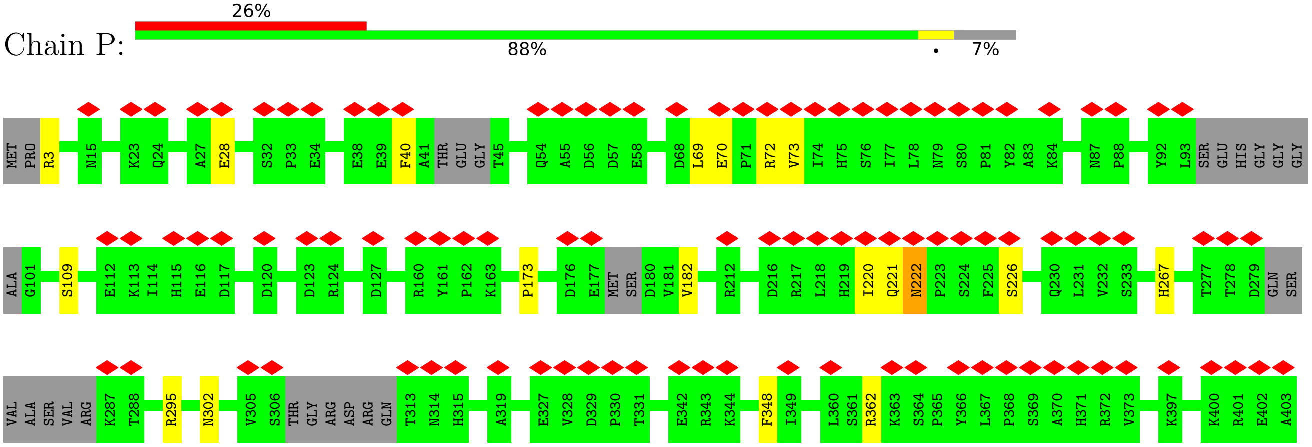


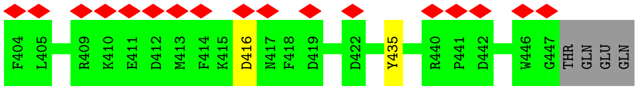


- Molecule 1: Tubulin gamma-1 chain



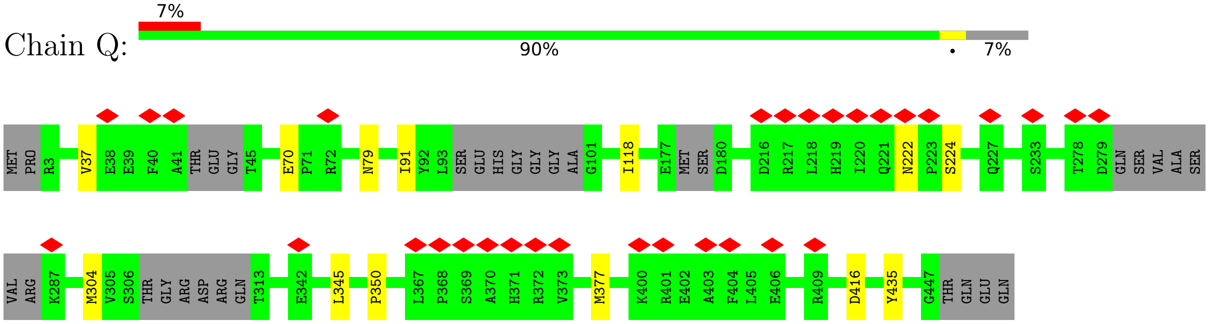
- Molecule 1: Tubulin gamma-1 chain





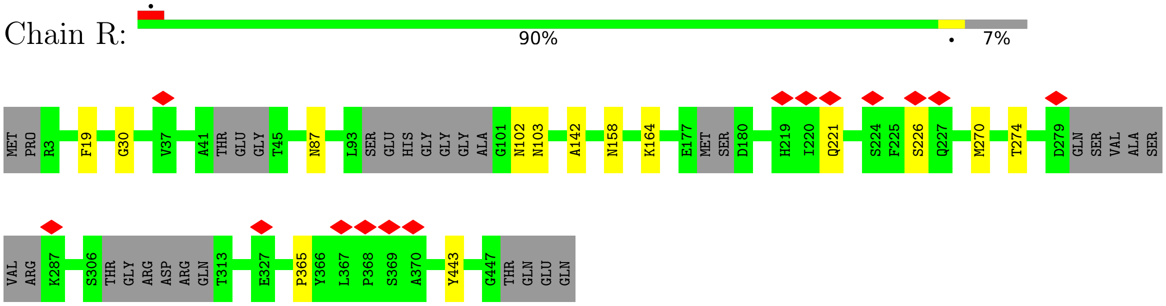
- Molecule 1: Tubulin gamma-1 chain

Chain Q:



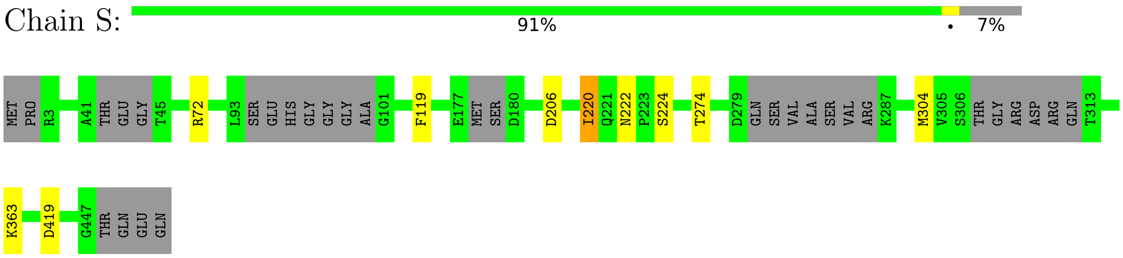
- Molecule 1: Tubulin gamma-1 chain

Chain R:



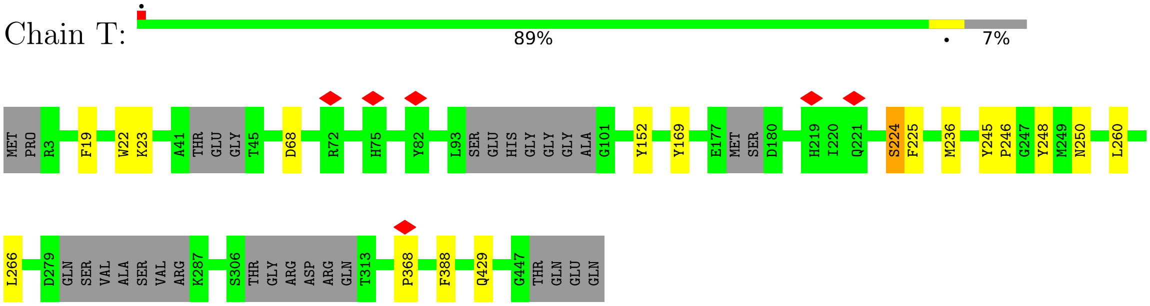
- Molecule 1: Tubulin gamma-1 chain

Chain S:



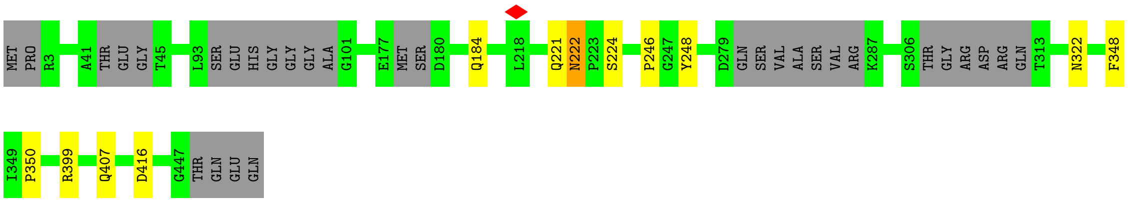
- Molecule 1: Tubulin gamma-1 chain

Chain T:



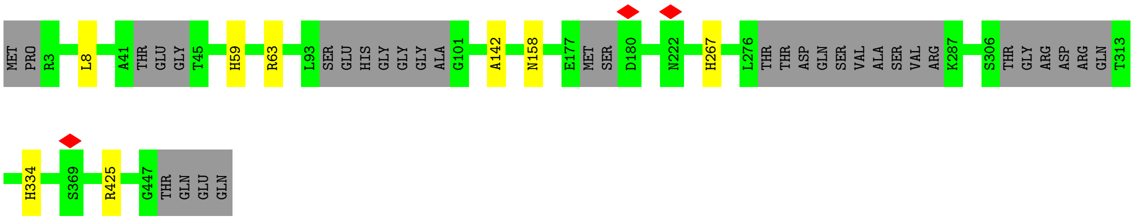
- Molecule 1: Tubulin gamma-1 chain

Chain U:



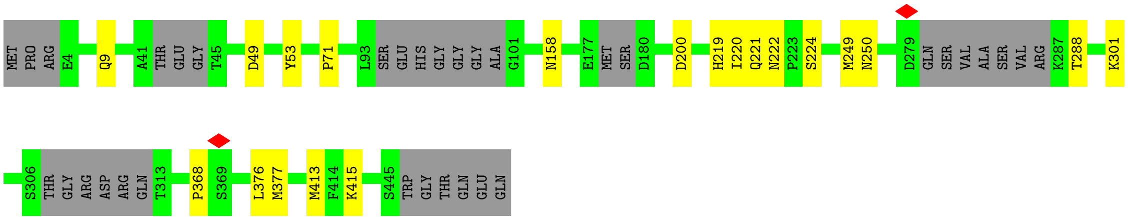
- Molecule 1: Tubulin gamma-1 chain

Chain V:



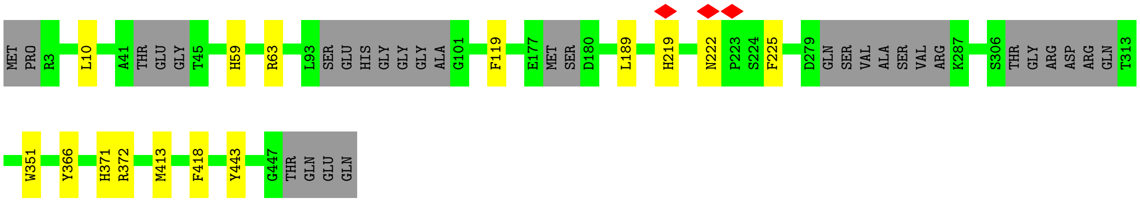
- Molecule 1: Tubulin gamma-1 chain

Chain W:



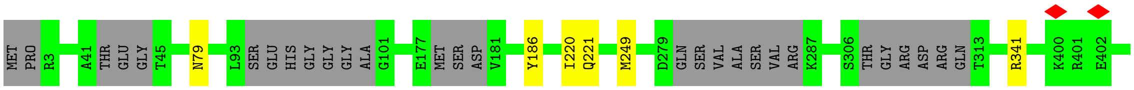
- Molecule 1: Tubulin gamma-1 chain

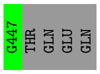
Chain X:



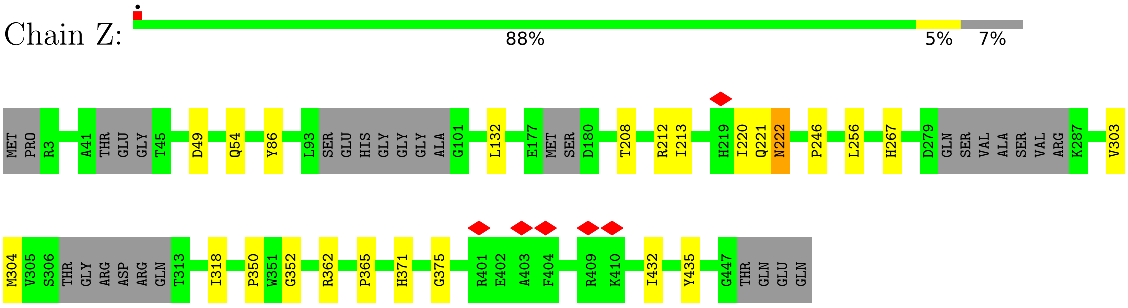
- Molecule 1: Tubulin gamma-1 chain

Chain Y:

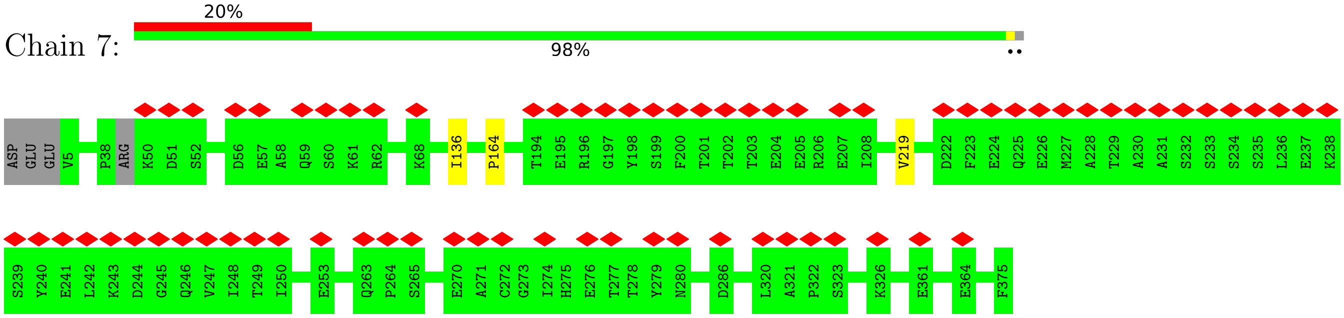




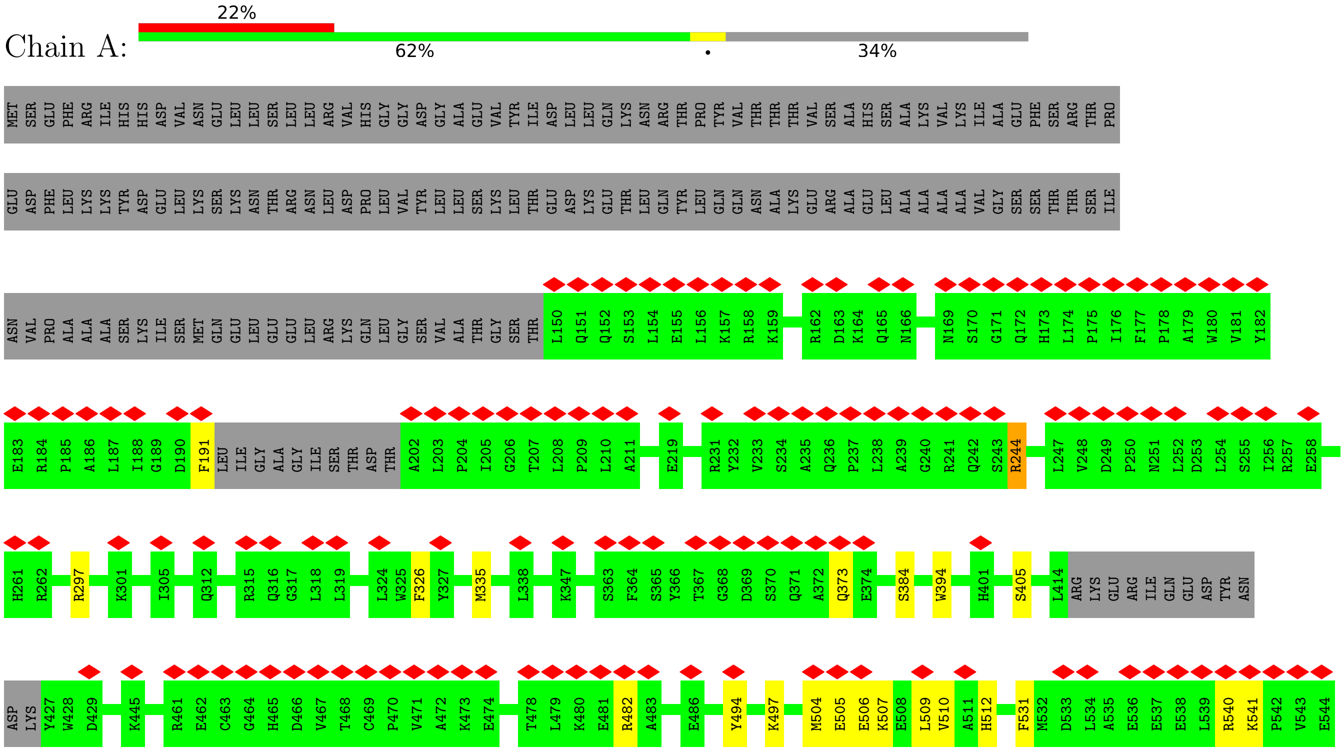
- Molecule 1: Tubulin gamma-1 chain

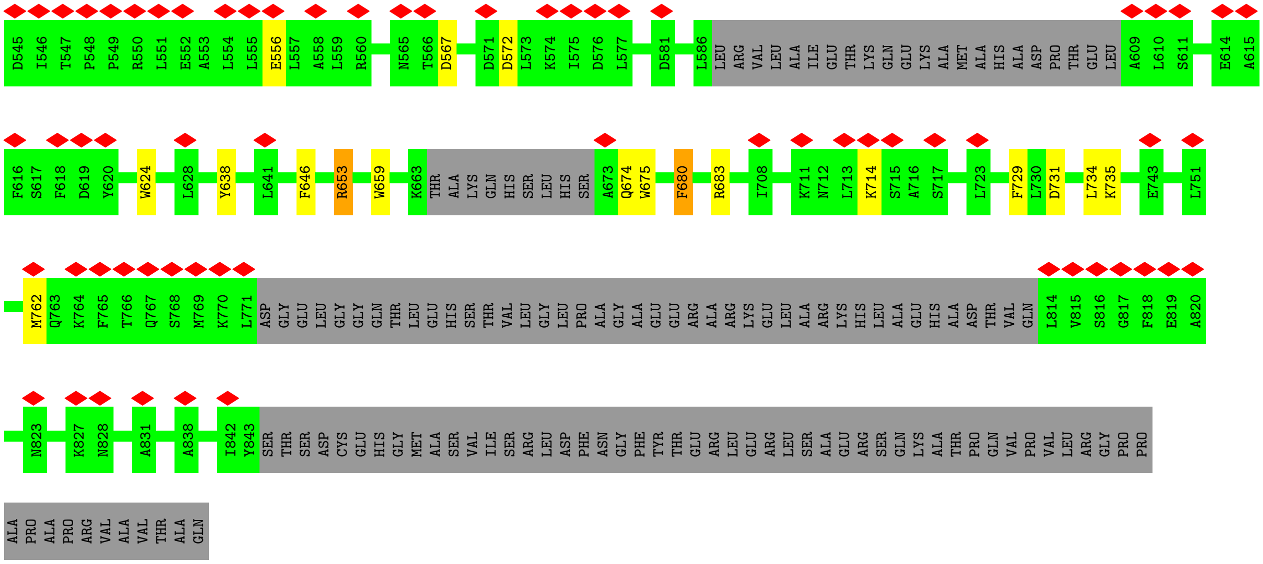


- Molecule 2: Actin b



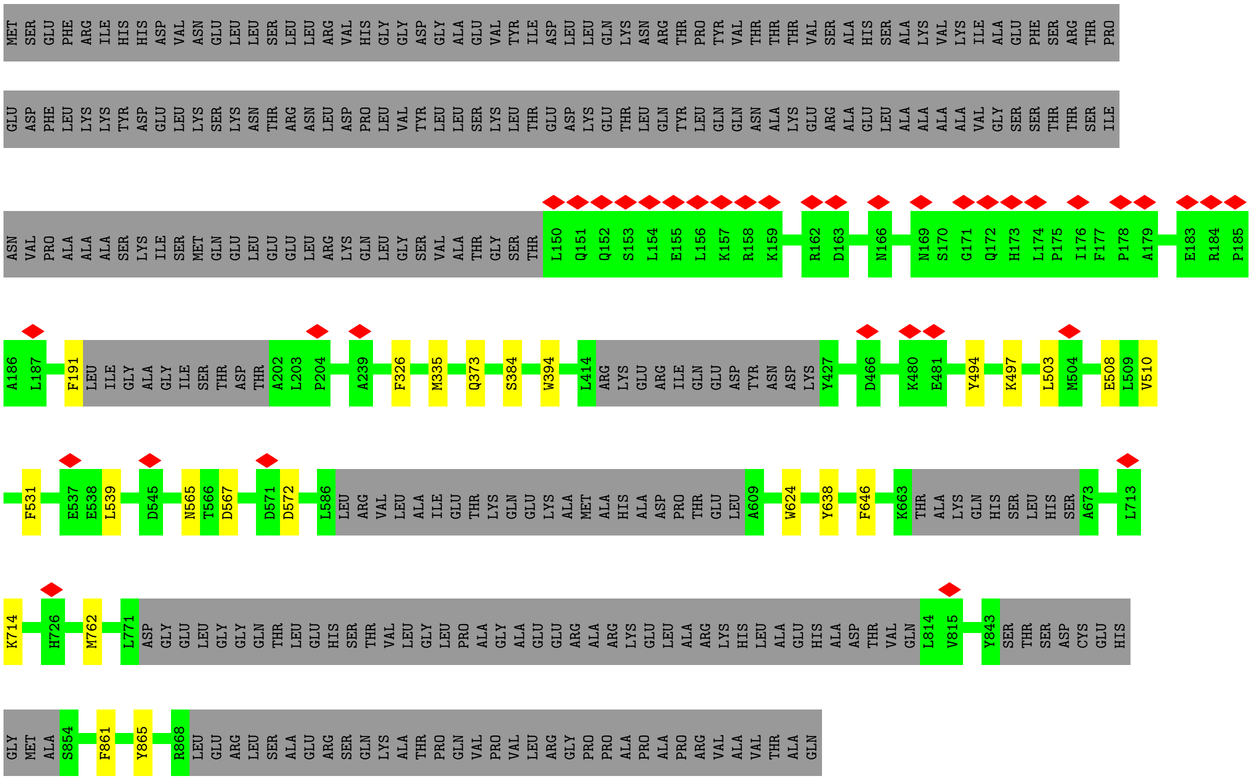
- Molecule 3: Gamma-tubulin complex component 2





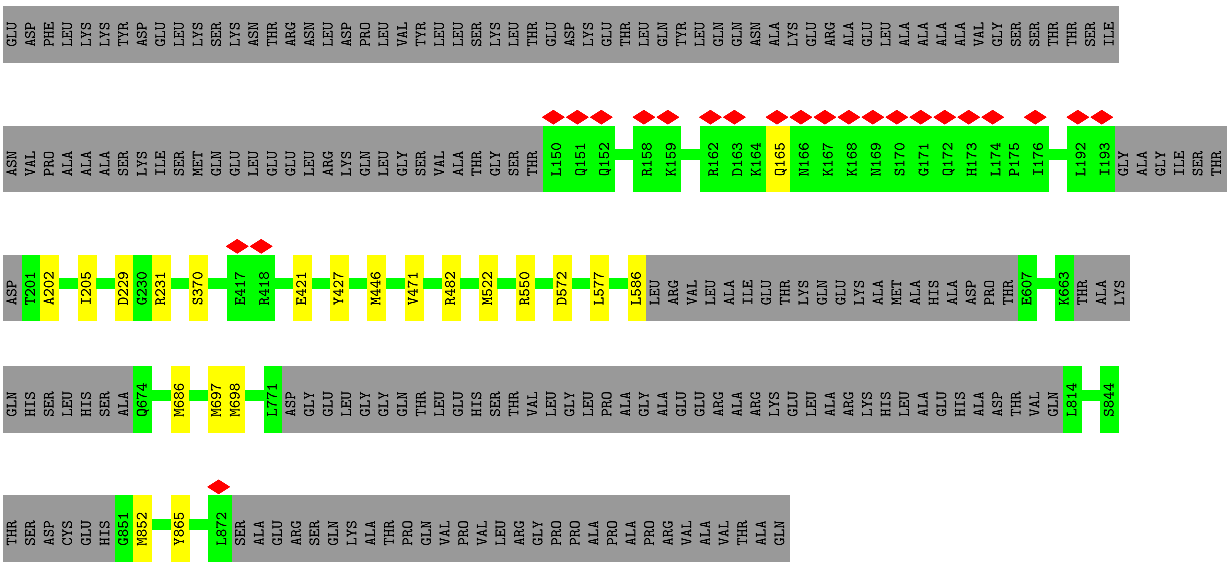
- Molecule 3: Gamma-tubulin complex component 2

Chain C:



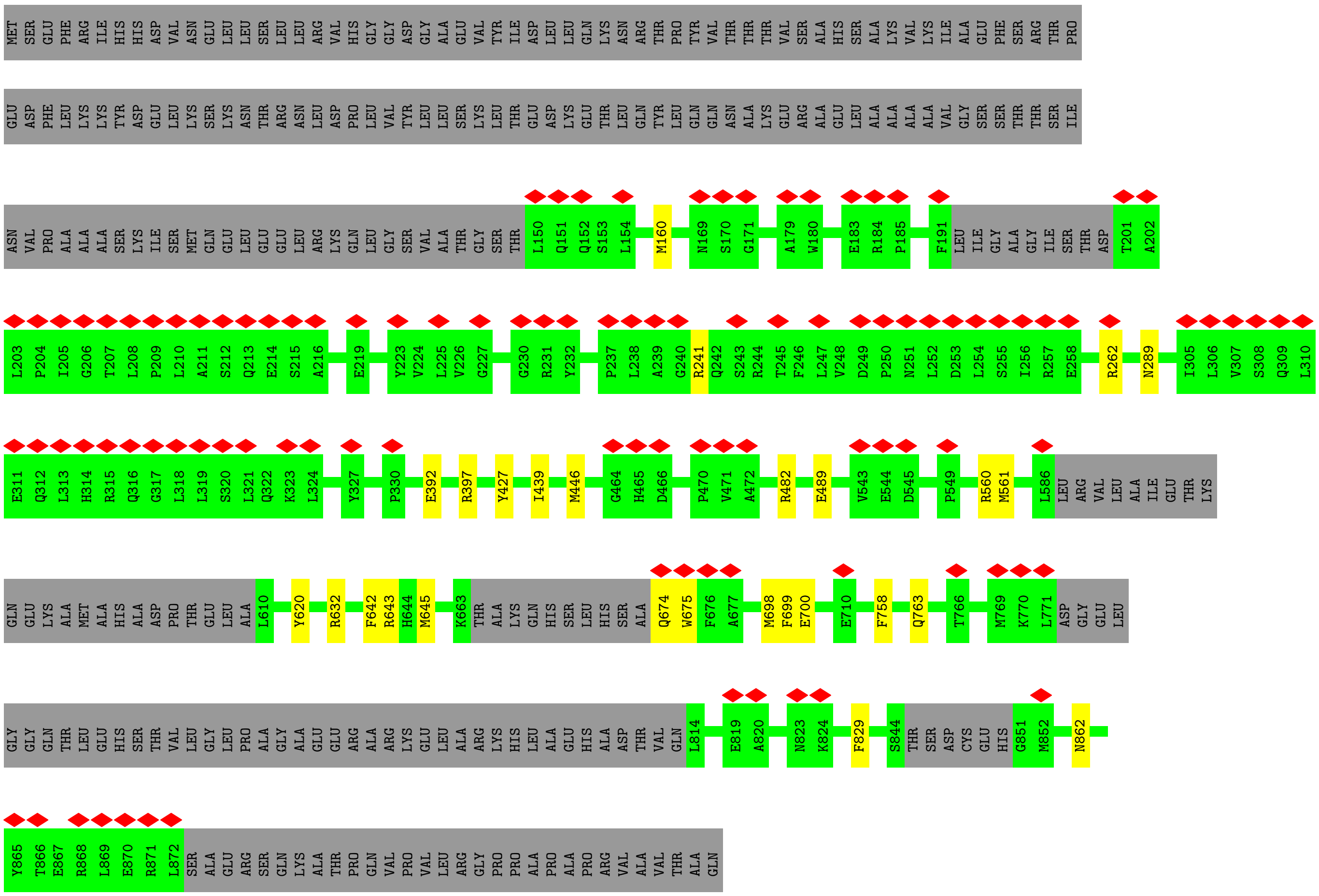
- Molecule 3: Gamma-tubulin complex component 2

Chain E:



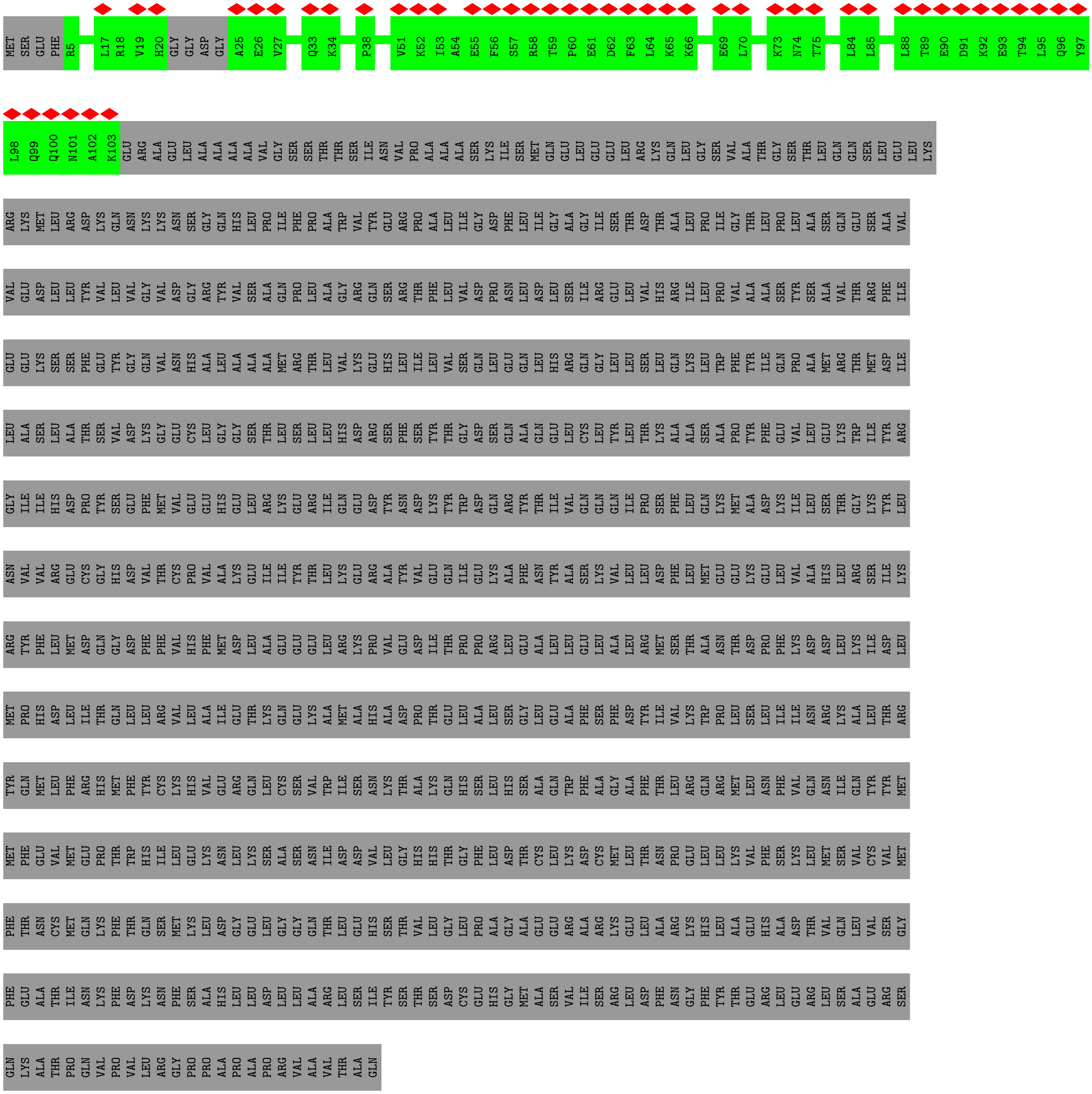
- Molecule 3: Gamma-tubulin complex component 2

Chain M:



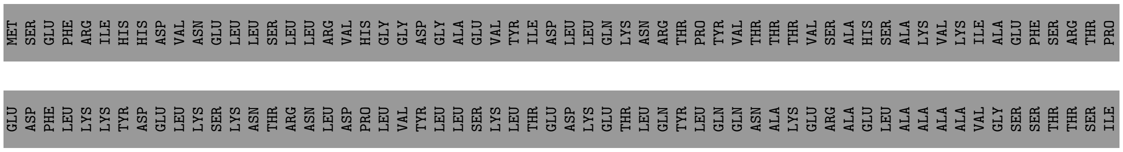
- Molecule 3: Gamma-tubulin complex component 2

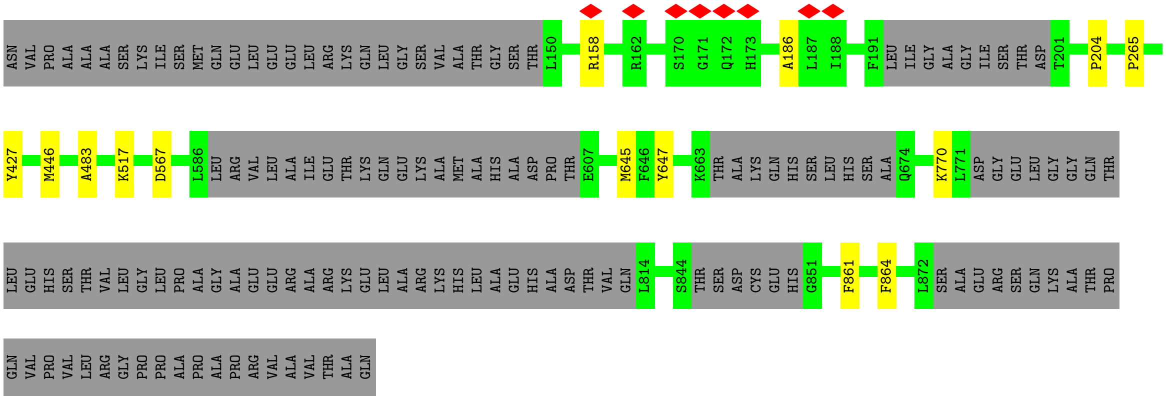
Chain f:



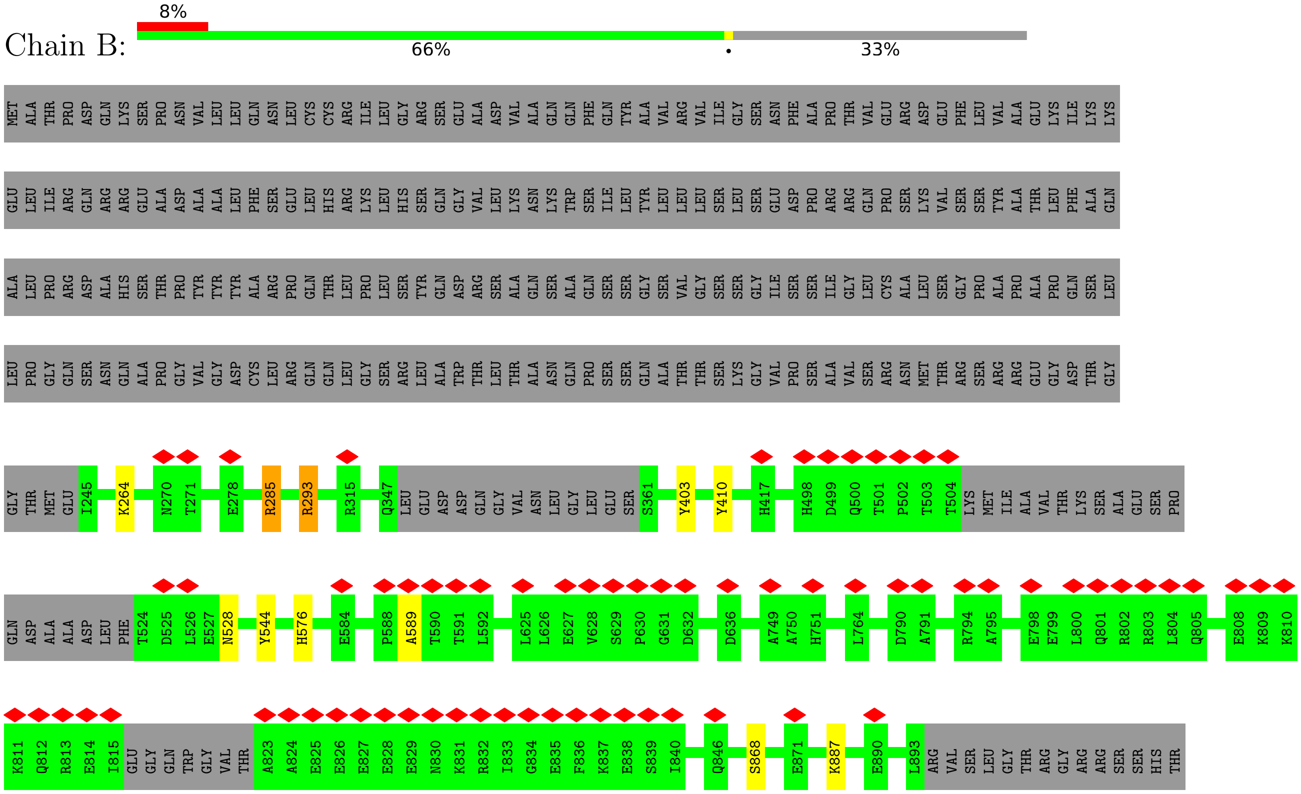
- Molecule 3: Gamma-tubulin complex component 2

Chain k:

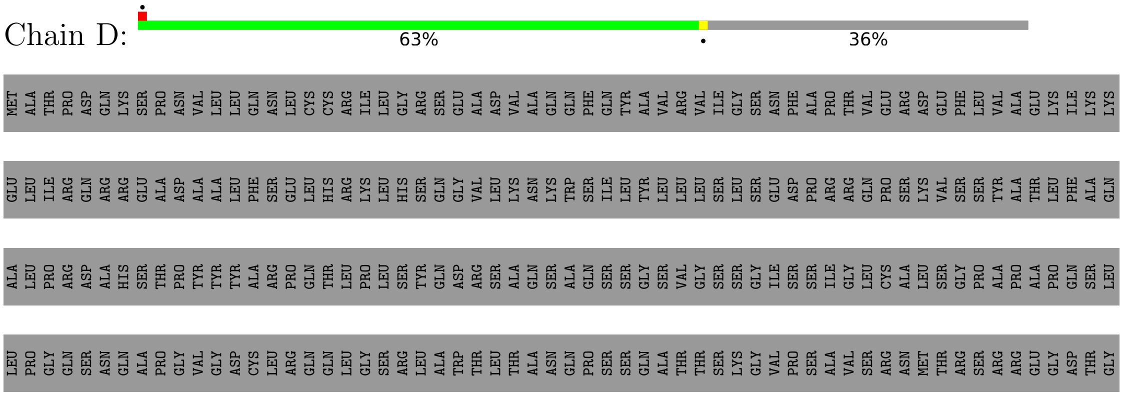


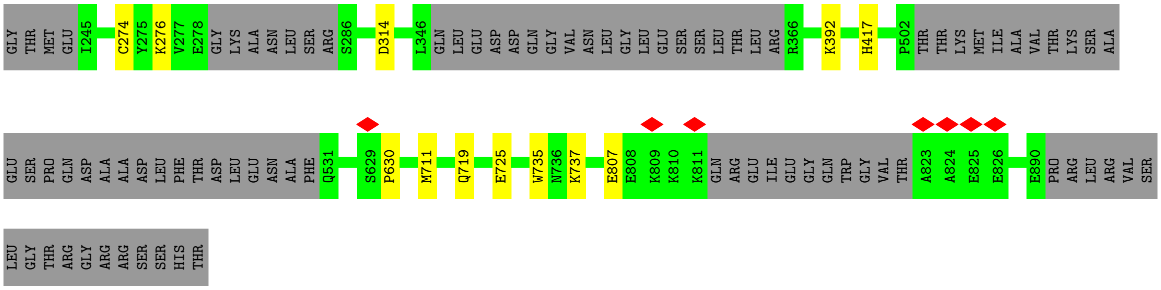


- Molecule 4: Gamma-tubulin complex component 3

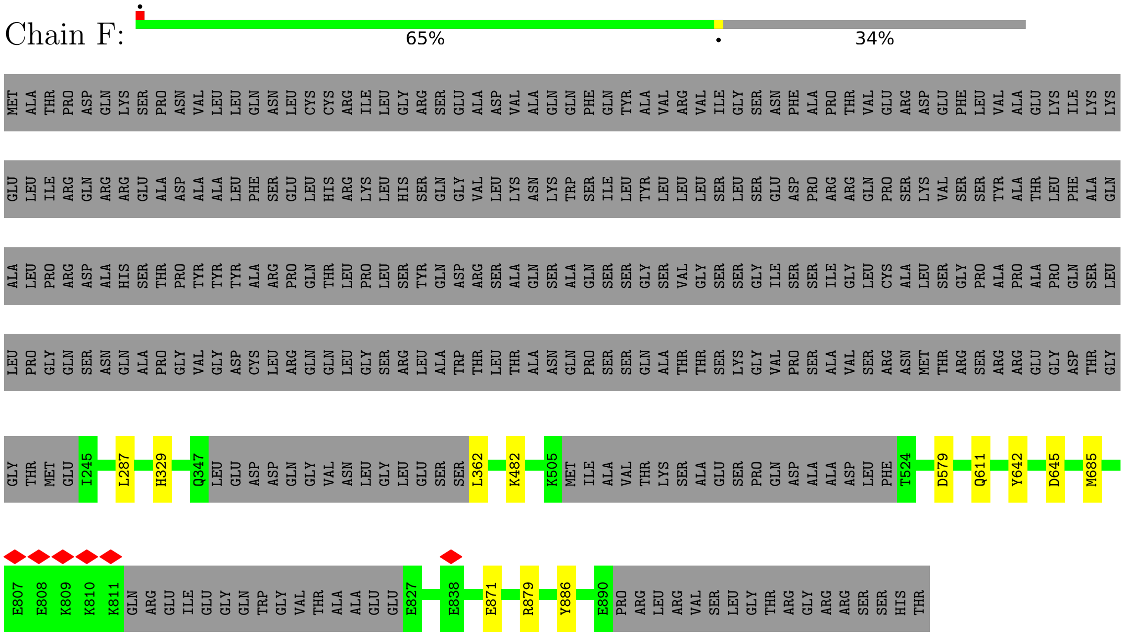


- Molecule 4: Gamma-tubulin complex component 3

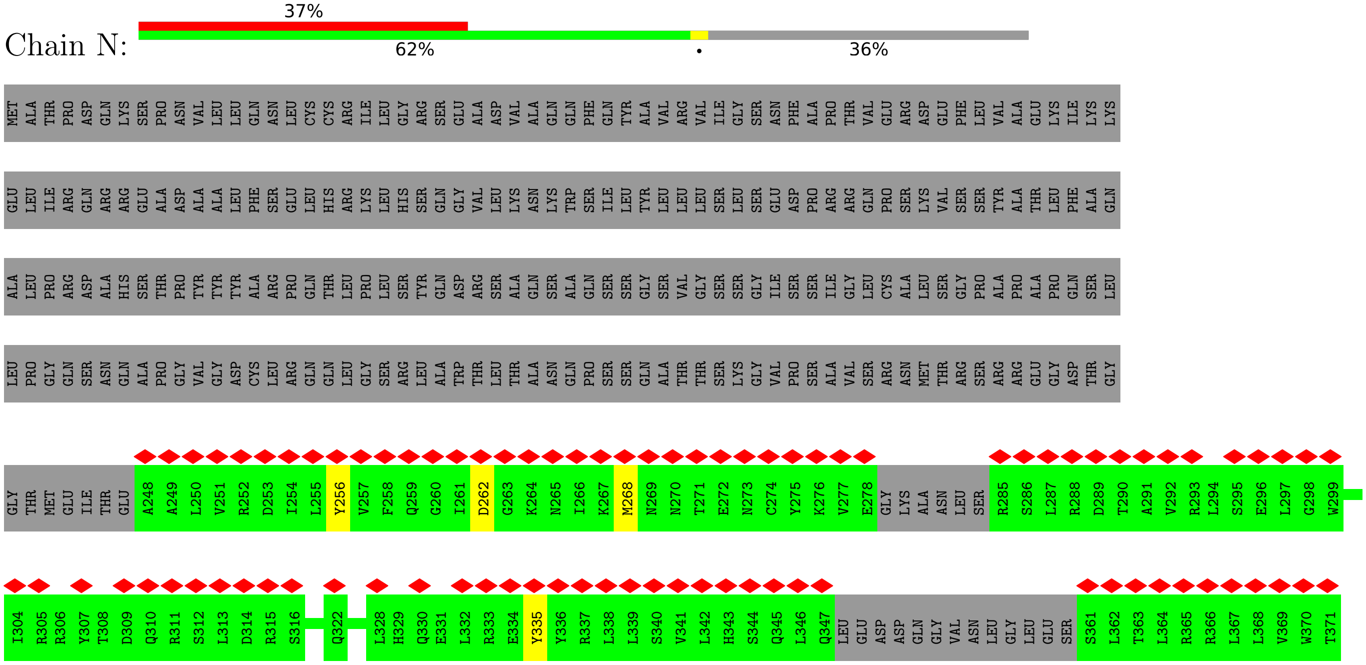


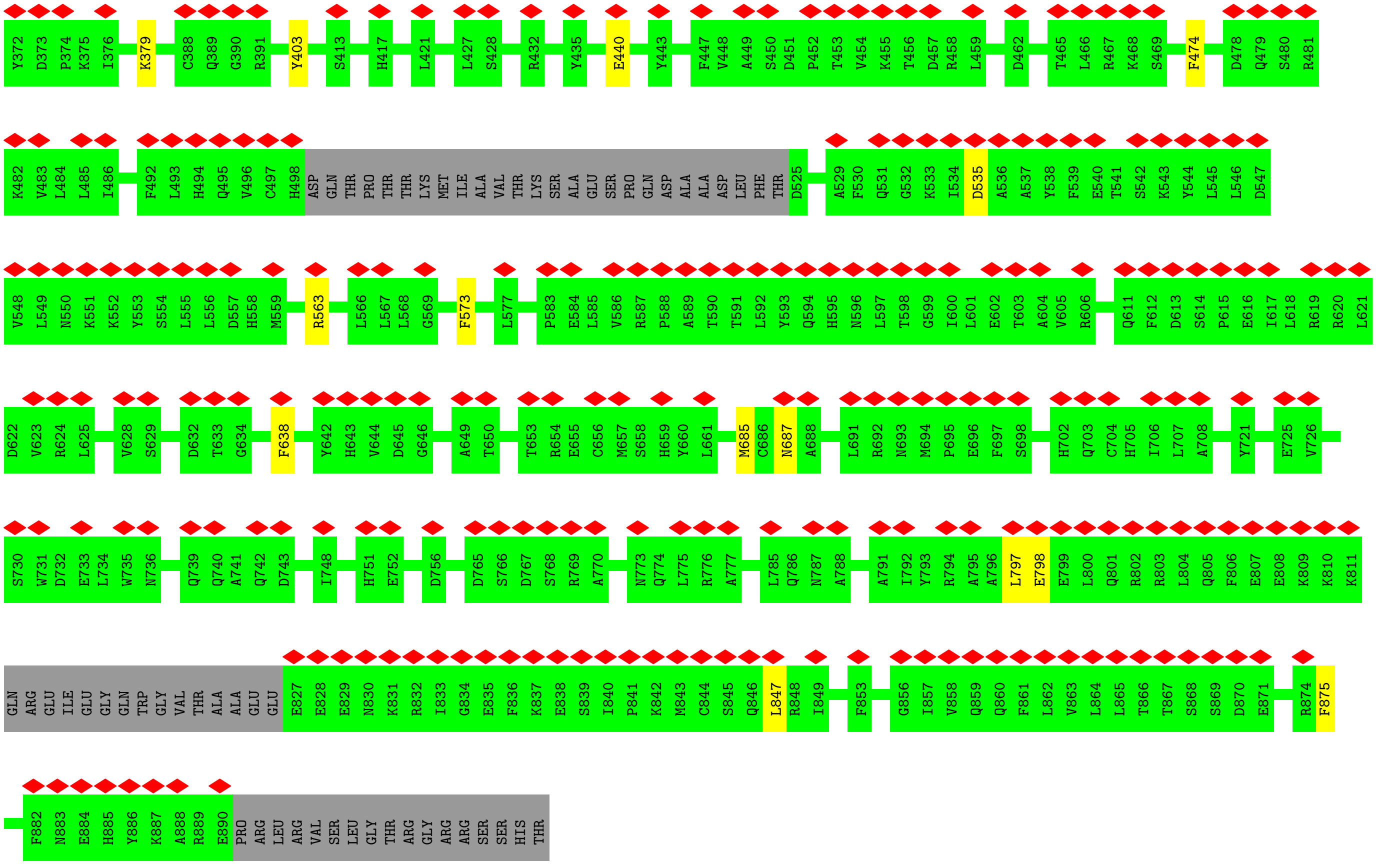


- Molecule 4: Gamma-tubulin complex component 3



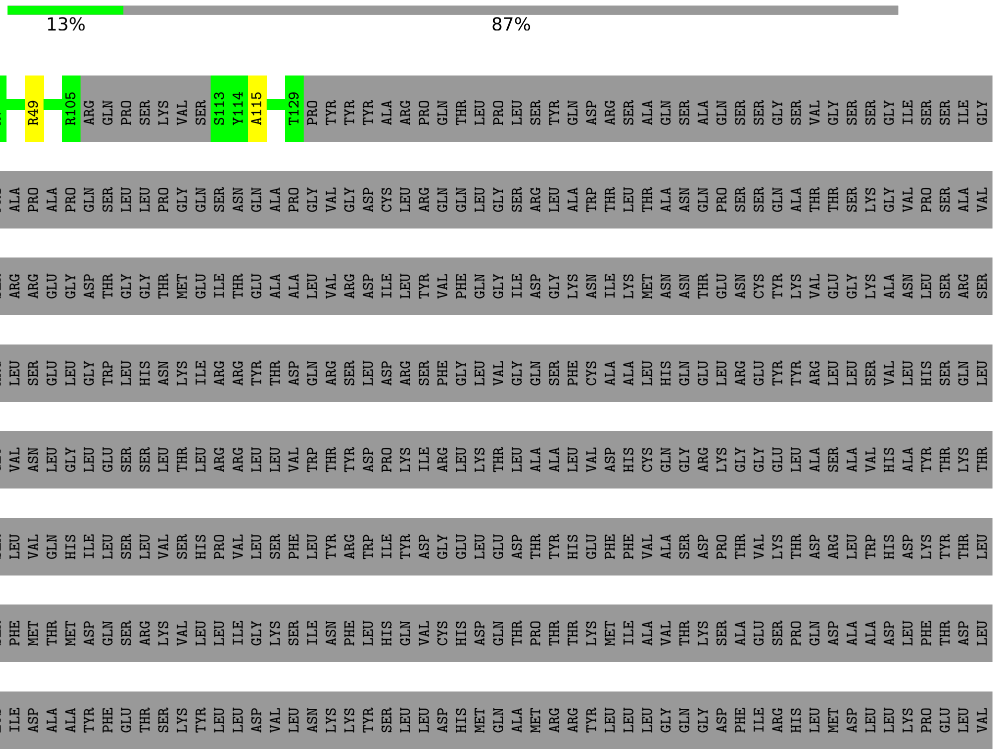
- Molecule 4: Gamma-tubulin complex component 3





- Molecule 4: Gamma-tubulin complex component 3

Chain b:



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

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

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

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

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

LYS ALA ARG GLU PRO ARG LEU ARG VAL SER LEU GLY THR ARG GLY ARG ARG SER SER HIS THR

- Molecule 4: Gamma-tubulin complex component 3

Chain n:

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

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

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

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

GLY THR MET GLU I245 D253 Y275 E278 GLY LYS ALA ASN LEU SER R285 Q347 LEU GLU ASP ASP GLN GLY VAL ASN LEU GLY LEU GLU SER S361 R366 L367 L378 K379 T380 P409 L439 K505 MET ILE ALA VAL THR LYS SER ALA GLU SER PRO GLN ASP

ALA ALA ASP LEU PHE T524 Y538 R575 H595 L667 F697 L763 F806 K811 GLN ARG GLU ILE GLU GLY GLN TRP GLY VAL THR ALA ALA GLU GLU E827 F836 E890 PRO ARG LEU ARG VAL SER LEU GLY THR ARG GLY ARG ARG SER SER HIS THR

- Molecule 5: CM1

Chain G:

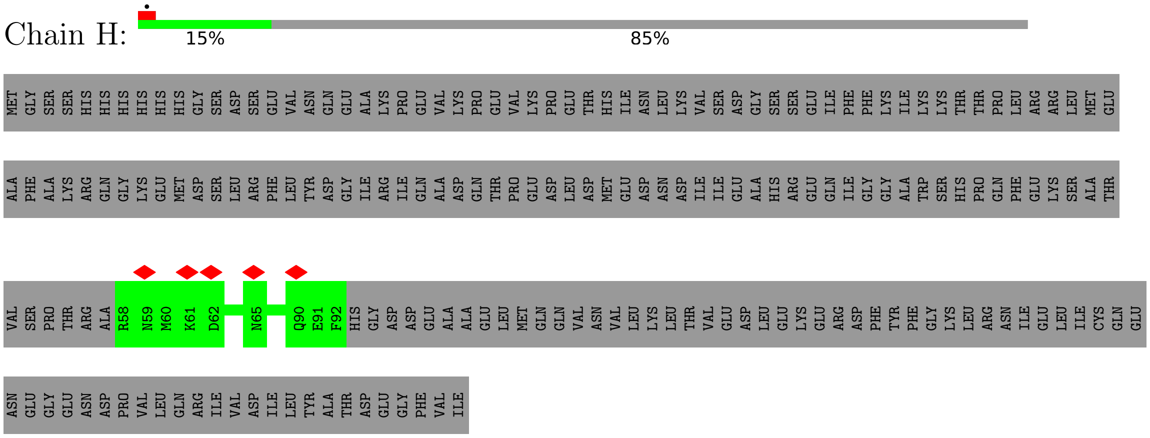
MET GLY SER SER HIS HIS HIS HIS HIS HIS GLY SER ASP SER GLU VAL ASN GLN GLU ALA LYS PRO GLU VAL LYS PRO GLU VAL LYS PRO GLU THR HIS ILE ASN LEU LYS VAL SER ASP GLY SER SER GLU ILE PHE PHE LYS ILE LYS LYS THR THR PRO LEU ARG ARG LEU MET GLU

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

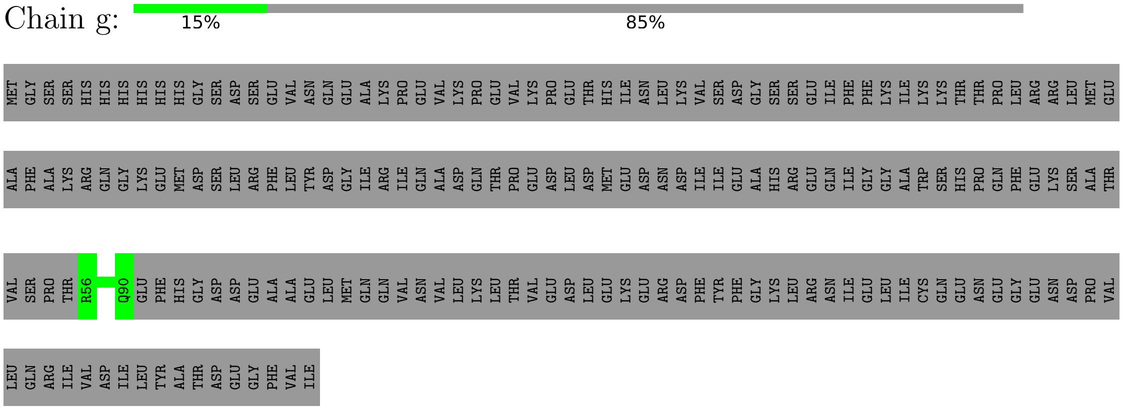
VAL SER PRO THR R56 A57 E69 R80 E86 ARG MET GLN GLN GLU PHE HIS GLY ASP ASP GLU ALA ALA GLU LEU MET GLN GLN VAL ASN VAL LEU LYS LEU THR VAL GLU ASP LEU GLU LYS GLU ARG ASP PHE TYR PHE GLY LYS LEU ARG ASN ILE GLU LEU ILE CYS GLN

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

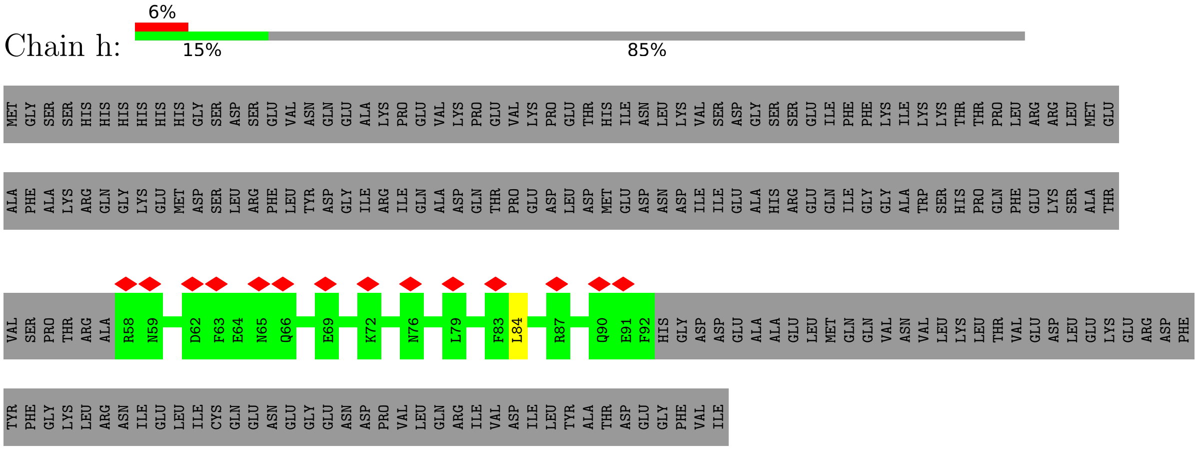
- Molecule 5: CM1



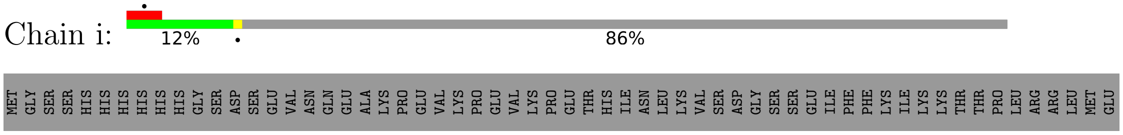
- Molecule 5: CM1

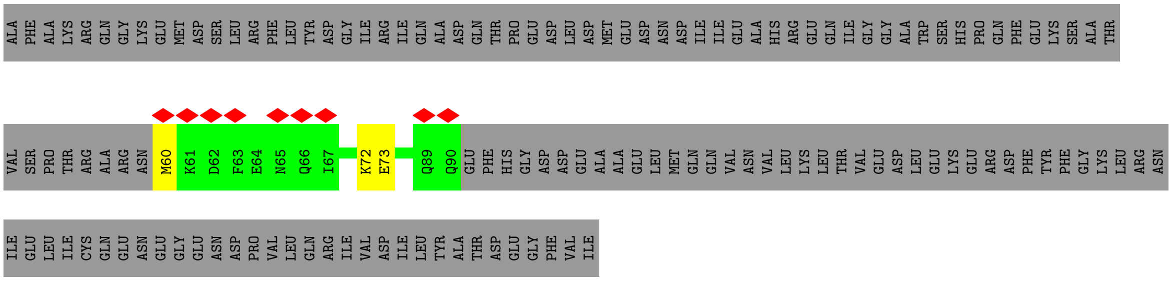


- Molecule 5: CM1



- Molecule 5: CM1





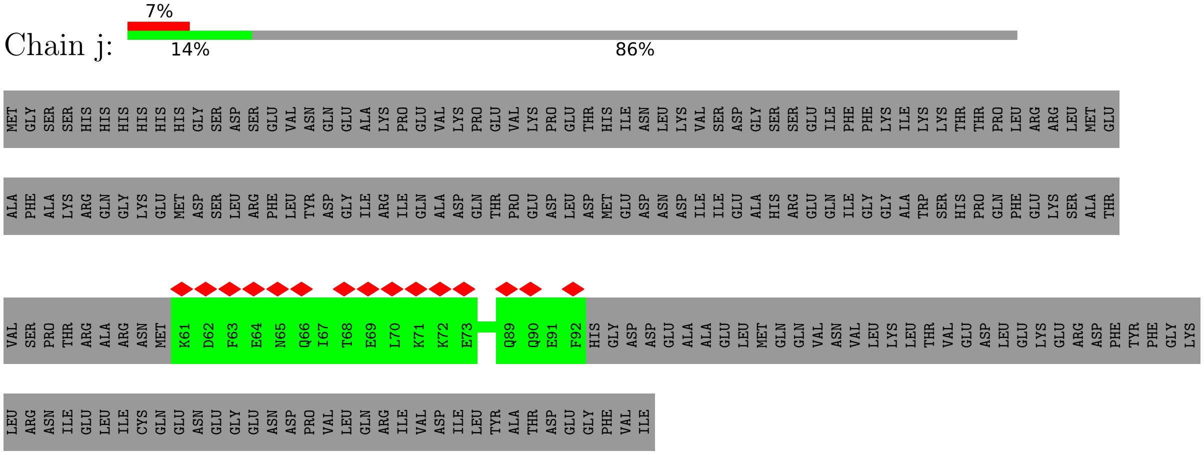
ALA PHE ALA LYS ARG GLN GLY LYS GLU MET ASP SER LEU ARG PHE LEU TYR ASP GLY ILE ARG ILE GLN ALA ASP GLN THR PRO GLU ASP LEU ASP MET GLU ASP ASN ASP ILE ILE GLU ALA HIS ARG GLU GLN ILE GLY GLY ALA TRP SER HIS PRO GLN PHE GLU LYS SER ALA THR

VAL SER PRO THR ARG ALA ARG ASN M60 K61 D62 F63 E64 N65 Q66 I67 K72 E73 Q89 Q90 GLU PHE HIS GLY ASP ASP GLU ALA ALA GLU LEU MET GLN GLN VAL ASN VAL LEU LYS LEU THR VAL GLU ASP LEU GLU LYS GLU ARG ASP PHE TYR PHE GLY LYS LEU ARG ASN

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

- Molecule 5: CM1

Chain j:



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

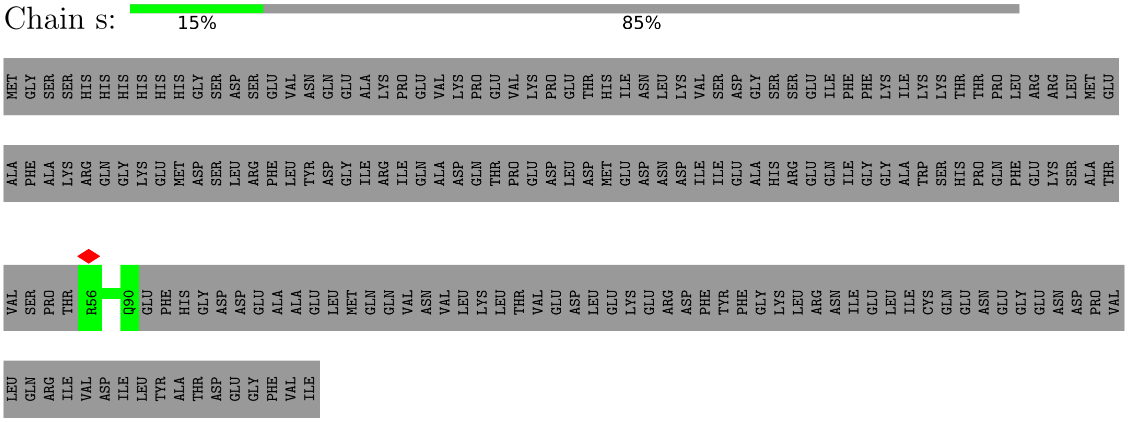
ALA PHE ALA LYS ARG GLN GLY LYS GLU MET ASP SER LEU ARG PHE LEU TYR ASP GLY ILE ARG ILE GLN ALA ASP GLN THR PRO GLU ASP LEU ASP MET GLU ASP ASN ASP ILE ILE GLU ALA HIS ARG GLU GLN ILE GLY GLY ALA TRP SER HIS PRO GLN PHE GLU LYS SER ALA THR

VAL SER PRO THR ARG ALA ARG ASN MET K61 D62 F63 E64 N65 Q66 I67 T68 E69 L70 K71 K72 E73 Q89 Q90 E91 F92 HIS GLY ASP ASP GLU ALA ALA GLU LEU MET GLN GLN VAL ASN VAL LEU LYS LEU THR VAL GLU ASP LEU GLU LYS GLU ARG ASP PHE TYR PHE GLY LYS

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

- Molecule 5: CM1

Chain s:



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

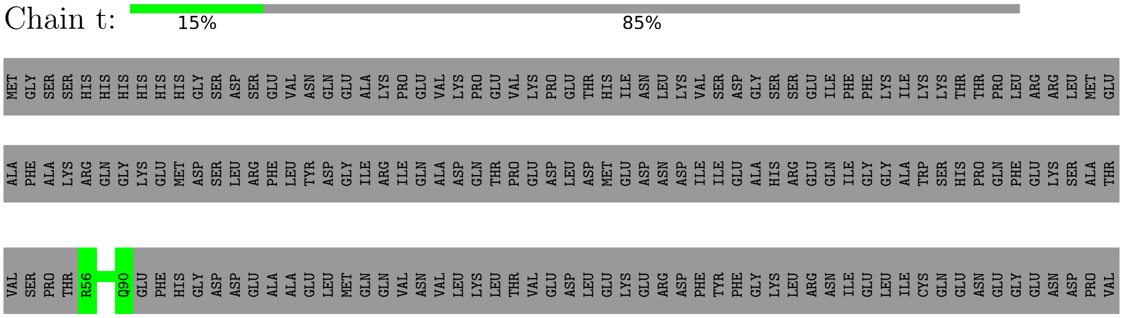
ALA PHE ALA LYS ARG GLN GLY LYS GLU MET ASP SER LEU ARG PHE LEU TYR ASP GLY ILE ARG ILE GLN ALA ASP GLN THR PRO GLU ASP LEU ASP MET GLU ASP ASN ASP ILE ILE GLU ALA HIS ARG GLU GLN ILE GLY GLY ALA TRP SER HIS PRO GLN PHE GLU LYS SER ALA THR

VAL SER PRO THR R56 Q90 GLU PHE HIS GLY ASP ASP GLU ALA ALA GLU LEU MET GLN GLN VAL ASN VAL LEU LYS LEU THR VAL GLU ASP LEU GLU LYS GLU ARG ASP PHE TYR PHE GLY LYS LEU ARG ASN ILE GLU LEU ILE CYS GLN GLU ASN GLU GLY GLU ASN ASP PRO VAL

LEU GLN ARG ILE VAL ASP ILE LEU TYR ALA THR ASP GLU GLY PHE VAL ILE

- Molecule 5: CM1

Chain t:

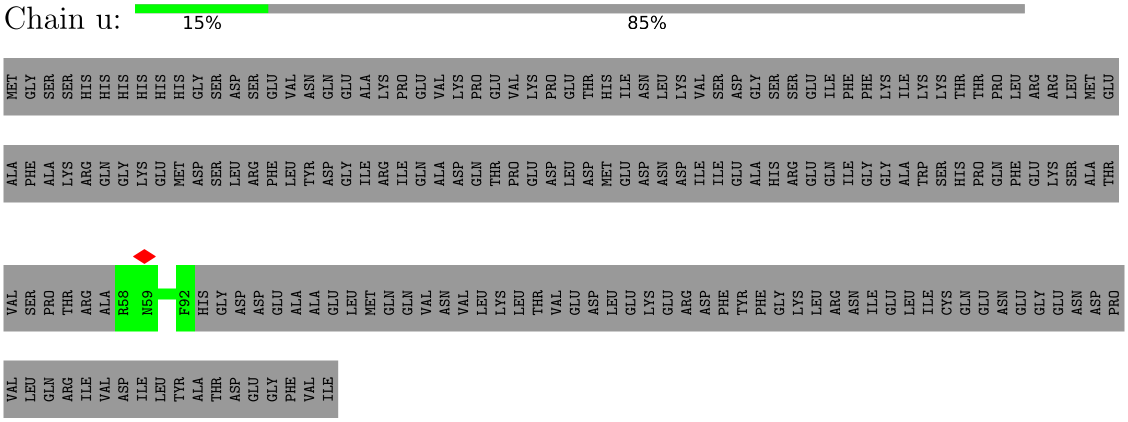


MET GLY SER SER HIS HIS HIS HIS HIS HIS GLY SER ASP SER GLU VAL ASN GLN GLU ALA LYS PRO GLU VAL LYS PRO GLU VAL LYS PRO GLU THR HIS ILE ASN LEU LYS VAL SER ASP GLY SER SER GLU ILE PHE PHE LYS ILE LYS LYS THR THR PRO LEU ARG ARG LEU MET GLU

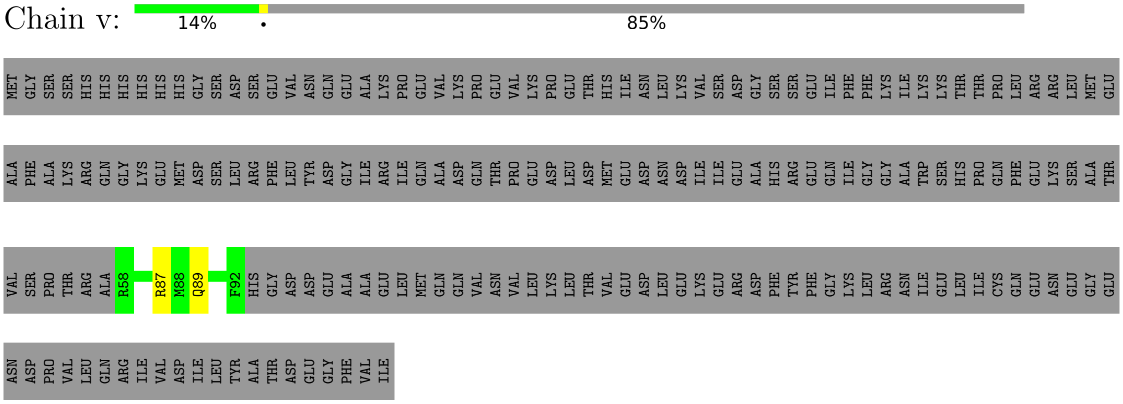
ALA PHE ALA LYS ARG GLN GLY LYS GLU MET ASP SER LEU ARG PHE LEU TYR ASP GLY ILE ARG ILE GLN ALA ASP GLN THR PRO GLU ASP LEU ASP MET GLU ASP ASN ASP ILE ILE GLU ALA HIS ARG GLU GLN ILE GLY GLY ALA TRP SER HIS PRO GLN PHE GLU LYS SER ALA THR

VAL SER PRO THR R56 Q90 GLU PHE HIS GLY ASP ASP GLU ALA ALA GLU LEU MET GLN GLN VAL ASN VAL LEU LYS LEU THR VAL GLU ASP LEU GLU LYS GLU ARG ASP PHE TYR PHE GLY LYS LEU ARG ASN ILE GLU LEU ILE CYS GLN GLU ASN GLU GLY GLU ASN ASP PRO VAL

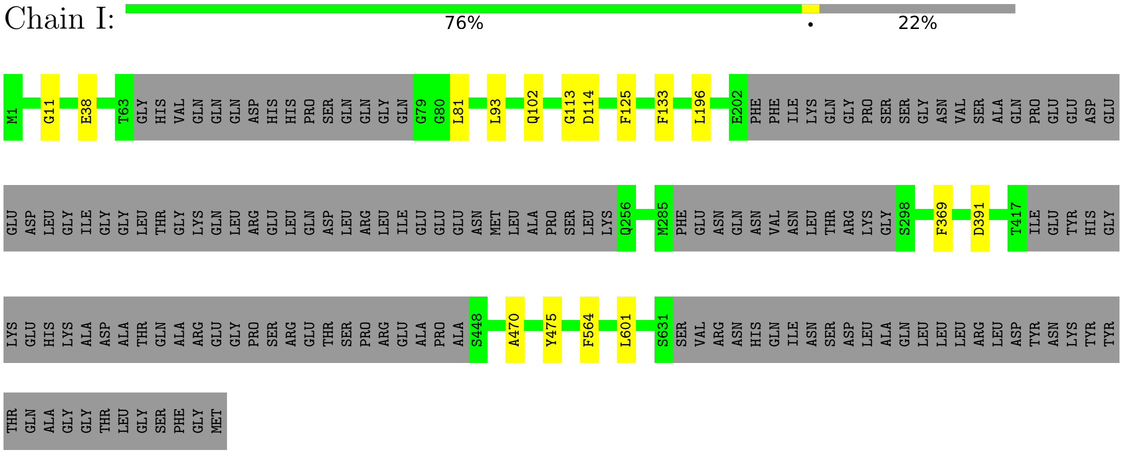
- Molecule 5: CM1



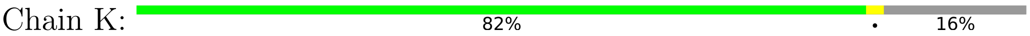
- Molecule 5: CM1

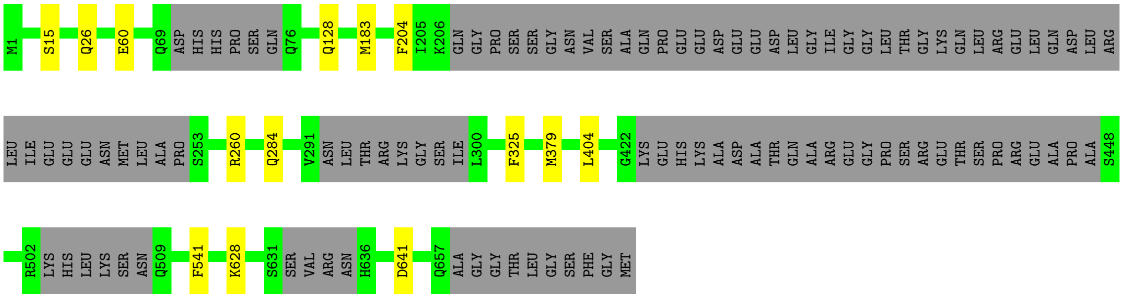


- Molecule 6: Gamma-tubulin complex component 4



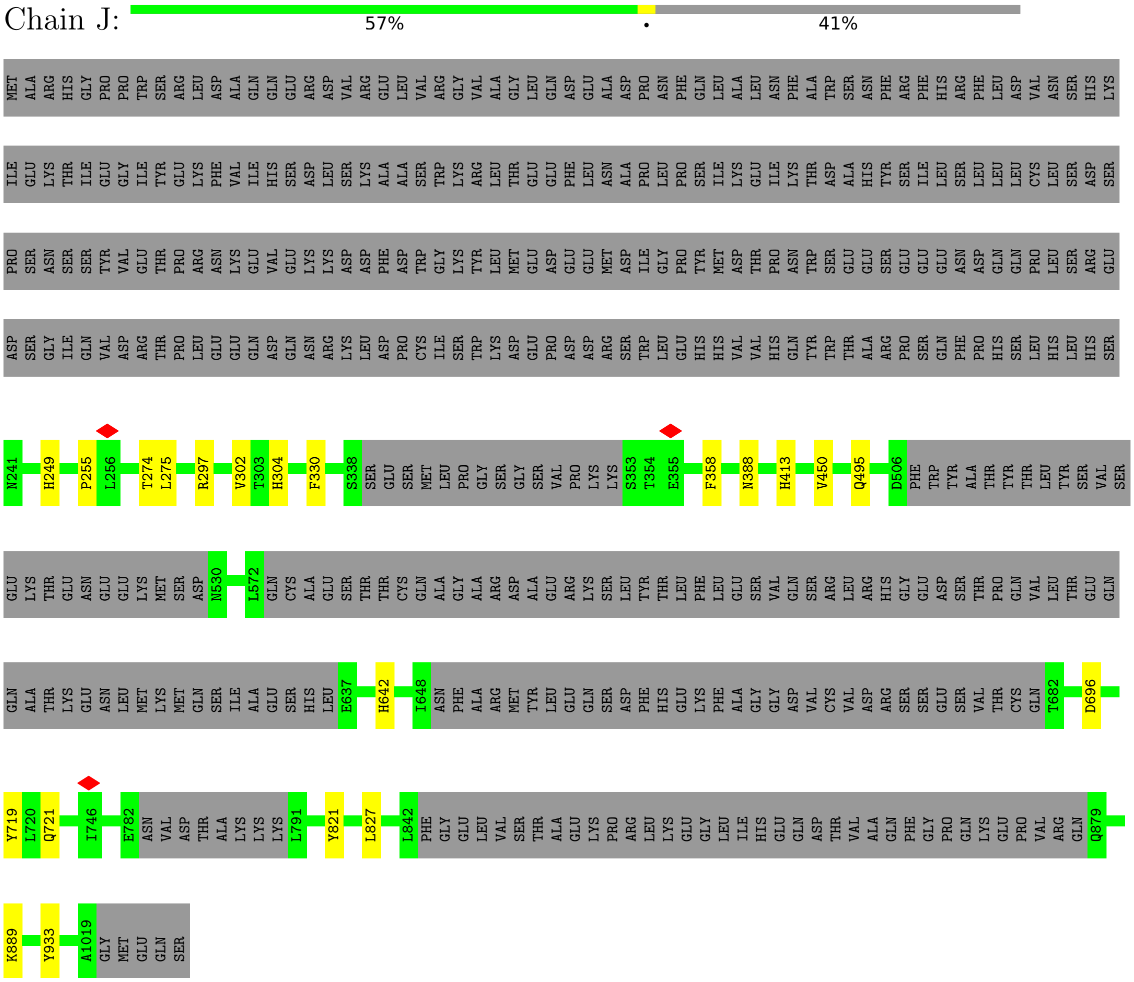
- Molecule 6: Gamma-tubulin complex component 4





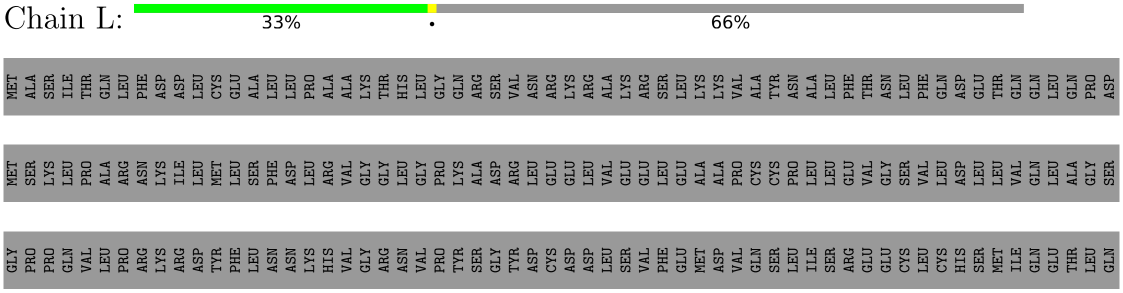
- Molecule 7: Gamma-tubulin complex component 5

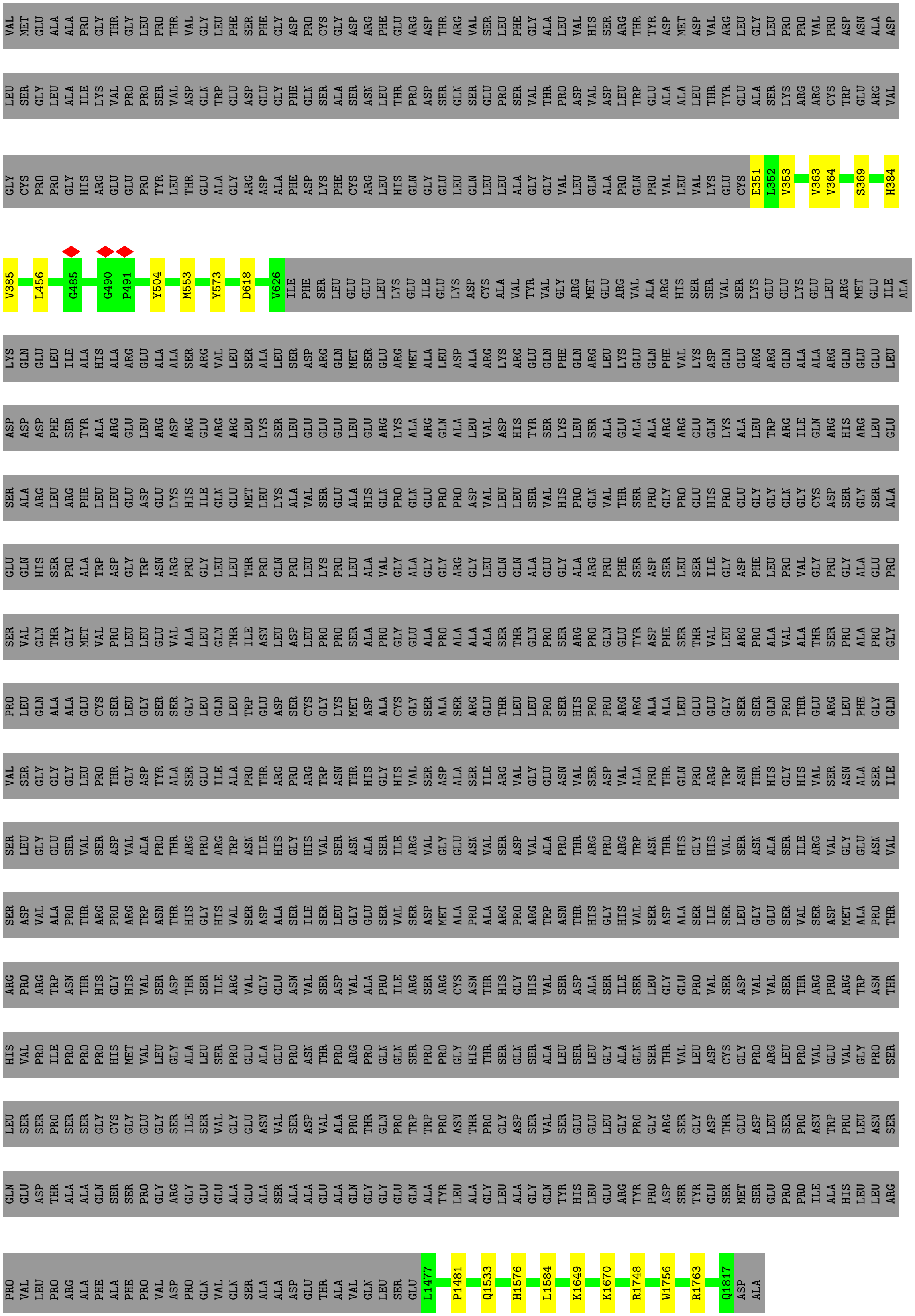
Chain J:



- Molecule 8: Gamma-tubulin complex component 6

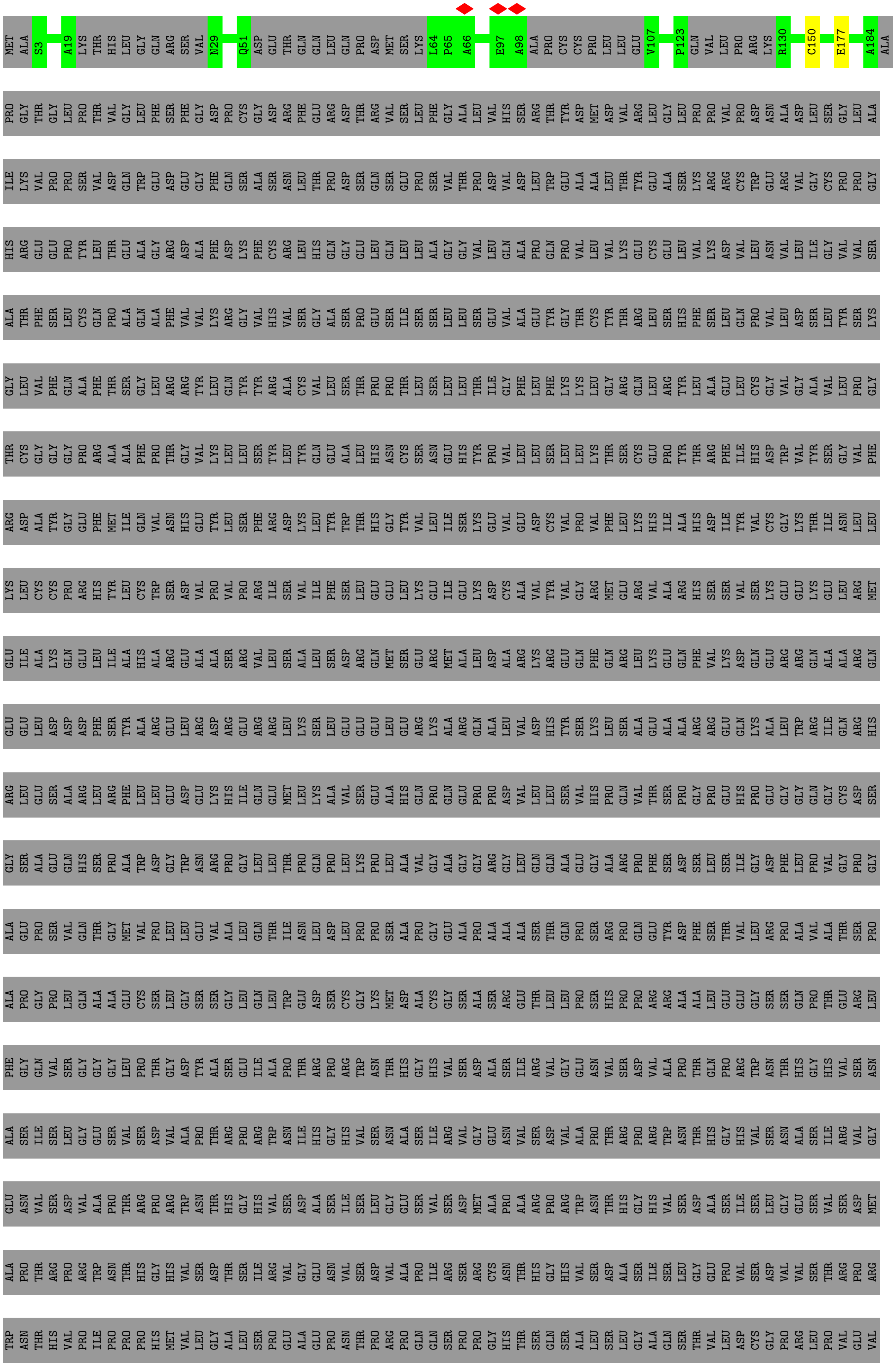
Chain L:

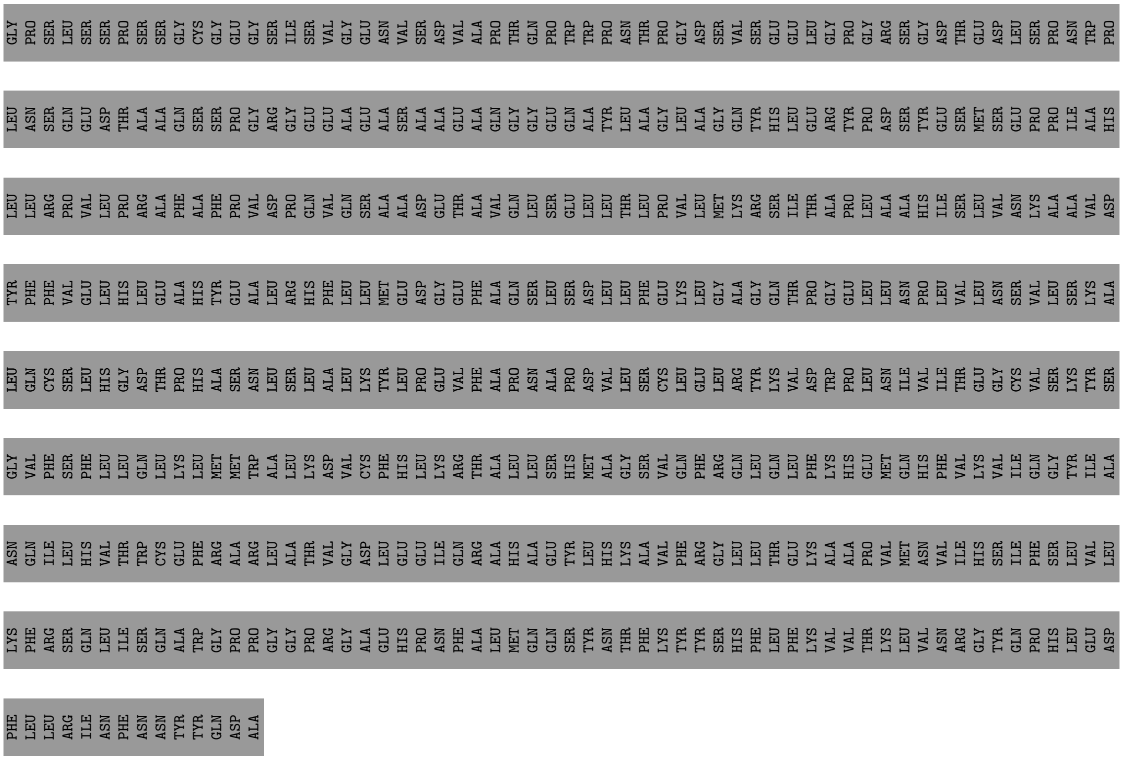




- Molecule 8: Gamma-tubulin complex component 6

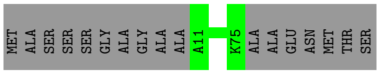
Chain d:


MET ALA S3 A19 LYS THR HIS LEU GLY GLN ARG SER VAL N29 Q51 ASP GLU THR GLN GLN LEU GLN PRO ASP MET SER LYS L64 P65 A66 E97 A98 ALA PRO CYS CYS PRO LEU LEU GLU V107 P123 GLN VAL LEU PRO ARG LYS R130 C150 E177 A184 ALA
PRO GLY THR GLY LEU PRO THR VAL GLY LEU PHE SER PHE GLY ASP PRO CYS GLY ASP ARG PHE GLU ARG ASP THR ARG VAL SER LEU PHE GLY ALA LEU VAL HIS SER ARG THR TYR ASP MET ASP VAL ARG LEU GLY LEU PRO PRO VAL PRO ASP ASN ALA ASP LEU SER GLY LEU ALA
ILE LYS VAL PRO PRO SER VAL ASP GLN TRP GLU ASP GLU GLY PHE GLN SER ALA SER ASN LEU THR PRO ASP SER GLN SER GLU PRO SER VAL THR PRO ASP VAL ASP LEU TRP GLU ALA ALA LEU THR TYR GLU ALA SER LYS ARG ARG CYS TRP GLU ARG VAL GLY CYS PRO PRO GLY
HIS ARG GLU GLU PRO TYR LEU THR GLU ALA GLY ARG ASP ALA PHE ASP LYS PHE CYS ARG LEU HIS GLN GLY GLU LEU GLN LEU LEU ALA GLY GLY VAL LEU GLN ALA PRO GLN PRO VAL LEU VAL LYS GLU CYS GLU LEU VAL LYS ASP VAL LEU ASN VAL LEU ILE GLY VAL VAL SER
ALA THR PHE SER LEU CYS GLN PRO ALA GLN ALA PHE VAL VAL LYS ARG GLY VAL HIS VAL SER GLY ALA SER PRO GLU SER ILE SER SER LEU LEU SER GLU VAL ALA GLU TYR GLY THR CYS TYR THR ARG LEU SER HIS PHE SER LEU GLN PRO VAL LEU ASP SER LEU TYR SER LYS
GLY LEU VAL PHE GLN ALA PHE THR SER GLY LEU ARG ARG TYR LEU GLN TYR TYR ARG ALA CYS VAL LEU SER THR PRO PRO THR LEU SER LEU LEU THR ILE GLY PHE LEU PHE LYS LYS LEU GLY ARG GLN LEU ARG TYR LEU ALA GLU LEU CYS GLY VAL GLY ALA VAL LEU PRO GLY
THR CYS GLY GLY GLY PRO ARG ALA ALA PHE PRO THR GLY VAL LYS LEU LEU SER TYR LEU TYR GLN GLU ALA LEU HIS ASN CYS SER ASN GLU HIS TYR PRO VAL LEU LEU SER LEU LEU LYS THR SER CYS GLU PRO TYR THR ARG PHE ILE HIS ASP TRP VAL TYR SER GLY VAL PHE
ARG ASP ALA TYR GLY GLU PHE MET ILE GLN VAL ASN HIS GLU TYR LEU SER PHE ARG ASP LYS LEU TYR TRP THR HIS GLY TYR VAL LEU ILE SER LYS GLU VAL GLU ASP CYS VAL PRO VAL PHE LEU LYS HIS ILE ALA HIS ASP ILE TYR VAL CYS GLY LYS THR ILE ASN LEU LEU
LYS LEU CYS CYS PRO ARG HIS TYR LEU CYS TRP SER ASP VAL PRO VAL PRO ARG ILE SER VAL ILE PHE SER LEU GLU GLU LEU LYS GLU ILE GLU LYS ASP CYS ALA VAL TYR VAL GLY ARG MET GLU ARG VAL ALA ARG HIS SER SER VAL SER LYS GLU GLU LYS GLU LEU ARG MET
GLU ILE ALA LYS GLN GLU LEU ILE ALA HIS ALA ARG GLU ALA ALA SER ARG VAL LEU SER ALA LEU SER ASP ARG GLN MET SER GLU ARG MET ALA LEU ASP ALA ARG LYS ARG GLU GLN PHE GLN ARG LEU LYS GLU GLN PHE VAL LYS ASP GLN GLU ARG ARG GLN ALA ALA ARG GLN
GLU GLU LEU ASP ASP ASP PHE SER TYR ALA ARG GLU LEU ARG ASP ARG GLU ARG ARG LEU LYS SER LEU GLU GLU GLU LEU GLU ARG LYS ALA ARG GLN ALA LEU VAL ASP HIS TYR SER LYS LEU SER ALA GLU ALA ALA ARG ARG GLU GLN LYS ALA LEU TRP ARG ILE GLN ARG HIS
ARG LEU GLU SER ALA ARG LEU ARG PHE LEU LEU GLU ASP GLU LYS HIS ILE GLN GLU MET LEU LYS ALA VAL SER GLU ALA HIS GLN PRO GLN GLU PRO PRO ASP VAL LEU LEU SER VAL HIS PRO GLN VAL THR SER PRO GLY PRO GLU HIS PRO GLU GLY GLY GLN GLY CYS ASP SER
GLY SER ALA GLU GLN HIS SER PRO ALA TRP ASP GLY TRP ASN ARG PRO GLY LEU LEU THR PRO GLN PRO LEU LYS PRO LEU ALA VAL GLY ALA GLY GLY ARG GLY LEU GLN GLN ALA GLU GLY ALA ARG PRO PHE SER ASP SER LEU SER ILE GLY ASP PHE LEU PRO VAL GLY PRO GLY
ALA GLU PRO SER VAL GLN THR GLY MET VAL PRO LEU LEU GLU VAL ALA LEU GLN THR ILE ASN LEU ASP LEU PRO PRO SER ALA PRO GLY GLU ALA PRO ALA ALA ALA SER THR GLN PRO SER ARG PRO GLN GLU TYR ASP PHE SER THR VAL LEU ARG PRO ALA VAL ALA THR SER PRO
ALA PRO GLY PRO LEU GLN ALA ALA GLU CYS SER LEU GLY SER SER GLY LEU GLN LEU TRP GLU ASP SER CYS GLY LYS MET ASP ALA CYS GLY SER ALA SER ARG GLU THR LEU LEU PRO SER HIS PRO PRO ARG ARG ALA ALA LEU GLU GLU GLY SER SER GLN PRO THR GLU ARG LEU
PHE GLY GLN VAL SER GLY GLY GLY LEU PRO THR GLY ASP TYR ALA SER GLU ILE ALA PRO THR ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASP ALA SER ILE ARG VAL GLY GLU ASN VAL SER ASP VAL ALA PRO THR GLN PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASN
ALA SER ILE SER LEU GLY GLU SER VAL SER ASP VAL ALA PRO THR ARG PRO ARG TRP ASN ILE HIS GLY HIS VAL SER ASN ALA SER ILE ARG VAL GLY GLU ASN VAL SER ASP VAL ALA PRO THR ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASN ALA SER ILE ARG VAL GLY
GLU ASN VAL SER ASP VAL ALA PRO THR ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASP ALA SER ILE SER LEU GLY GLU SER VAL SER ASP MET ALA PRO ALA ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASP ALA SER ILE SER LEU GLY GLU SER VAL SER ASP MET
ALA PRO THR ARG PRO ARG TRP ASN THR HIS GLY HIS VAL SER ASP THR SER ILE ARG VAL GLY GLU ASN VAL SER ASP VAL ALA PRO ILE ARG SER ARG CYS ASN THR HIS GLY HIS VAL SER ASP ALA SER ILE SER LEU GLY GLU PRO VAL SER ASP VAL VAL SER THR ARG PRO ARG
TRP ASN THR HIS VAL PRO ILE PRO PRO PRO HIS MET VAL LEU GLY ALA LEU SER PRO GLU ALA GLU PRO ASN THR PRO ARG PRO GLN GLN SER PRO PRO GLY HIS THR SER GLN SER ALA LEU SER LEU GLY ALA GLN SER THR VAL LEU ASP CYS GLY PRO ARG LEU PRO VAL GLU VAL



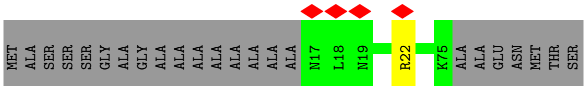
- Molecule 9: Mitotic-spindle organizing protein 1

Chain a:



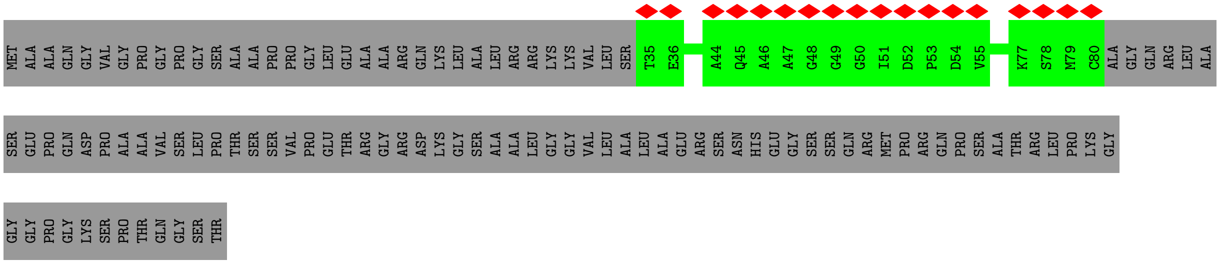
- Molecule 9: Mitotic-spindle organizing protein 1

Chain c:



- Molecule 10: Mitotic-spindle organizing protein 2A

Chain e:



4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	579078	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	55.4	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	601.2, 601.2, 601.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6700001, 1.6700001, 1.6700001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	1	0.46	0/3433	0.76	0/4651
1	2	0.54	0/3377	0.81	0/4575
1	O	0.52	0/3433	0.80	0/4651
1	P	0.49	0/3427	0.76	0/4644
1	Q	0.44	0/3439	0.78	0/4658
1	R	0.48	0/3433	0.77	0/4651
1	S	0.45	0/3439	0.78	0/4658
1	T	0.49	0/3427	0.80	0/4644
1	U	0.48	0/3433	0.81	0/4651
1	V	0.46	0/3393	0.76	0/4599
1	W	0.47	0/3408	0.84	0/4616
1	X	0.43	0/3439	0.77	0/4658
1	Y	0.49	0/3431	0.80	0/4647
1	Z	0.52	0/3433	0.84	0/4651
2	7	0.30	0/1828	0.52	0/2554
3	A	0.49	0/4951	0.75	0/6692
3	C	0.46	0/5080	0.76	0/6864
3	E	0.46	0/5305	0.77	0/7162
3	M	0.50	0/5267	0.78	0/7110
3	f	0.26	0/482	0.44	0/674
3	k	0.52	0/5289	0.81	0/7140
4	B	0.45	0/5119	0.75	0/6912
4	D	0.43	0/4891	0.77	0/6603
4	F	0.46	0/5024	0.80	0/6784
4	N	0.46	0/4911	0.77	0/6627
4	b	0.46	0/948	0.80	0/1277
4	n	0.48	0/4977	0.79	0/6722
5	G	0.59	0/273	0.81	0/362
5	H	0.45	0/321	0.76	0/424
5	g	0.42	0/306	0.72	0/405
5	h	0.41	0/321	0.60	0/424
5	i	0.53	0/277	0.70	0/366
5	j	0.43	0/294	0.63	0/389
5	s	0.45	0/306	0.82	0/405

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	t	0.47	0/306	0.78	0/405
5	u	0.45	0/321	0.80	0/424
5	v	0.45	0/321	0.82	0/424
6	I	0.50	0/4299	0.84	0/5824
6	K	0.43	0/4677	0.74	0/6331
7	J	0.50	0/4939	0.82	0/6693
8	L	0.45	0/5062	0.77	0/6877
8	d	0.47	0/1165	0.81	0/1566
9	a	0.40	0/484	0.78	0/653
9	c	0.50	0/454	0.84	0/611
10	e	0.29	0/232	0.36	0/323
All	All	0.47	0/126375	0.78	0/170981

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
3	A	0	4
4	B	0	2
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	244	ARG	Sidechain
3	A	540	ARG	Sidechain
3	A	653	ARG	Sidechain
3	A	683	ARG	Sidechain
4	B	285	ARG	Sidechain
4	B	293	ARG	Sidechain

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	408/451 (90%)	373 (91%)	32 (8%)	3 (1%)	19	53
1	2	403/451 (89%)	363 (90%)	40 (10%)	0	100	100
1	O	408/451 (90%)	357 (88%)	43 (10%)	8 (2%)	6	34
1	P	408/451 (90%)	359 (88%)	43 (10%)	6 (2%)	8	39
1	Q	408/451 (90%)	370 (91%)	32 (8%)	6 (2%)	8	39
1	R	408/451 (90%)	363 (89%)	40 (10%)	5 (1%)	11	43
1	S	408/451 (90%)	356 (87%)	49 (12%)	3 (1%)	19	53
1	T	408/451 (90%)	362 (89%)	42 (10%)	4 (1%)	13	46
1	U	408/451 (90%)	365 (90%)	39 (10%)	4 (1%)	13	46
1	V	405/451 (90%)	356 (88%)	46 (11%)	3 (1%)	19	53
1	W	405/451 (90%)	363 (90%)	35 (9%)	7 (2%)	7	36
1	X	408/451 (90%)	360 (88%)	47 (12%)	1 (0%)	44	74
1	Y	407/451 (90%)	353 (87%)	53 (13%)	1 (0%)	44	74
1	Z	408/451 (90%)	355 (87%)	44 (11%)	9 (2%)	5	32
2	7	356/364 (98%)	305 (86%)	48 (14%)	3 (1%)	16	51
3	A	587/902 (65%)	542 (92%)	43 (7%)	2 (0%)	37	67
3	C	600/902 (66%)	549 (92%)	45 (8%)	6 (1%)	13	46
3	E	626/902 (69%)	558 (89%)	64 (10%)	4 (1%)	22	55
3	M	621/902 (69%)	555 (89%)	65 (10%)	1 (0%)	44	74
3	f	91/902 (10%)	81 (89%)	10 (11%)	0	100	100
3	k	624/902 (69%)	564 (90%)	55 (9%)	5 (1%)	16	51
4	B	602/907 (66%)	544 (90%)	57 (10%)	1 (0%)	44	74
4	D	571/907 (63%)	529 (93%)	40 (7%)	2 (0%)	30	62
4	F	591/907 (65%)	535 (90%)	55 (9%)	1 (0%)	44	74
4	N	573/907 (63%)	521 (91%)	51 (9%)	1 (0%)	44	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	b	112/907 (12%)	104 (93%)	7 (6%)	1 (1%)	14	48
4	n	584/907 (64%)	526 (90%)	54 (9%)	4 (1%)	19	53
5	G	29/229 (13%)	25 (86%)	4 (14%)	0	100	100
5	H	33/229 (14%)	32 (97%)	1 (3%)	0	100	100
5	g	33/229 (14%)	31 (94%)	2 (6%)	0	100	100
5	h	33/229 (14%)	30 (91%)	3 (9%)	0	100	100
5	i	29/229 (13%)	26 (90%)	3 (10%)	0	100	100
5	j	30/229 (13%)	30 (100%)	0	0	100	100
5	s	33/229 (14%)	31 (94%)	2 (6%)	0	100	100
5	t	33/229 (14%)	30 (91%)	3 (9%)	0	100	100
5	u	33/229 (14%)	33 (100%)	0	0	100	100
5	v	33/229 (14%)	31 (94%)	2 (6%)	0	100	100
6	I	511/667 (77%)	436 (85%)	69 (14%)	6 (1%)	11	43
6	K	548/667 (82%)	504 (92%)	41 (8%)	3 (0%)	25	59
7	J	587/1024 (57%)	499 (85%)	82 (14%)	6 (1%)	13	46
8	L	613/1819 (34%)	537 (88%)	69 (11%)	7 (1%)	12	45
8	d	137/1819 (8%)	128 (93%)	8 (6%)	1 (1%)	19	53
9	a	63/82 (77%)	60 (95%)	3 (5%)	0	100	100
9	c	57/82 (70%)	54 (95%)	3 (5%)	0	100	100
10	e	44/158 (28%)	40 (91%)	4 (9%)	0	100	100
All	All	15117/26140 (58%)	13525 (90%)	1478 (10%)	114 (1%)	19	51

All (114) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	589	ALA
4	D	314	ASP
3	E	370	SER
4	F	287	LEU
6	I	470	ALA
7	J	297	ARG
6	K	15	SER
8	L	363	VAL
1	W	49	ASP
1	W	368	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Z	246	PRO
1	1	221	GLN
6	I	11	GLY
8	L	385	VAL
1	O	221	GLN
1	O	274	THR
1	P	267	HIS
1	T	224	SER
1	T	250	ASN
1	W	250	ASN
1	Z	303	VAL
1	Z	318	ILE
1	Z	371	HIS
3	k	483	ALA
4	n	763	LEU
3	C	503	LEU
3	C	565	ASN
3	E	421	GLU
6	I	93	LEU
6	I	113	GLY
7	J	249	HIS
8	L	369	SER
1	O	262	PRO
1	O	277	THR
1	O	354	ALA
1	Q	118	ILE
1	R	226	SER
1	U	222	ASN
1	V	8	LEU
1	W	288	THR
2	7	164	PRO
3	A	680	PHE
3	C	539	LEU
7	J	302	VAL
6	K	404	LEU
8	L	384	HIS
3	M	241	ARG
4	N	687	ASN
1	P	40	PHE
1	P	222	ASN
1	Q	345	LEU
1	R	142	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	S	220	ILE
1	S	222	ASN
1	U	246	PRO
1	U	350	PRO
1	W	415	LYS
1	X	371	HIS
3	k	186	ALA
3	k	427	TYR
4	n	367	LEU
4	n	380	THR
1	1	224	SER
3	C	865	TYR
3	E	202	ALA
6	I	81	LEU
6	I	601	LEU
7	J	255	PRO
7	J	450	VAL
7	J	495	GLN
6	K	204	PHE
8	L	1481	PRO
1	O	222	ASN
1	Q	350	PRO
1	R	365	PRO
1	S	274	THR
1	U	407	GLN
1	V	142	ALA
1	W	71	PRO
1	Y	220	ILE
1	Z	365	PRO
8	d	150	CYS
1	1	262	PRO
3	C	510	VAL
3	C	861	PHE
8	L	353	VAL
8	L	364	VAL
1	P	72	ARG
1	R	87	ASN
1	V	63	ARG
1	W	224	SER
4	b	115	ALA
2	7	136	ILE
4	D	630	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Q	37	VAL
1	Q	70	GLU
1	T	368	PRO
1	Z	222	ASN
3	E	471	VAL
1	O	228	ILE
1	Z	375	GLY
3	k	204	PRO
3	k	265	PRO
4	n	409	PRO
2	7	219	VAL
3	A	510	VAL
1	P	173	PRO
1	Z	352	GLY
1	O	368	PRO
1	P	182	VAL
1	Q	91	ILE
1	R	30	GLY
1	T	246	PRO
1	Z	350	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	374/400 (94%)	364 (97%)	10 (3%)	40	65
1	2	367/400 (92%)	354 (96%)	13 (4%)	31	60
1	O	374/400 (94%)	354 (95%)	20 (5%)	19	48
1	P	373/400 (93%)	357 (96%)	16 (4%)	25	54
1	Q	375/400 (94%)	368 (98%)	7 (2%)	52	73
1	R	374/400 (94%)	365 (98%)	9 (2%)	44	68
1	S	375/400 (94%)	367 (98%)	8 (2%)	48	71
1	T	373/400 (93%)	358 (96%)	15 (4%)	27	56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	U	374/400 (94%)	365 (98%)	9 (2%)	44	68
1	V	368/400 (92%)	363 (99%)	5 (1%)	62	80
1	W	373/400 (93%)	360 (96%)	13 (4%)	31	60
1	X	375/400 (94%)	361 (96%)	14 (4%)	29	58
1	Y	374/400 (94%)	369 (99%)	5 (1%)	65	82
1	Z	374/400 (94%)	358 (96%)	16 (4%)	25	54
2	7	18/310 (6%)	18 (100%)	0	100	100
3	A	533/791 (67%)	496 (93%)	37 (7%)	13	40
3	C	547/791 (69%)	530 (97%)	17 (3%)	35	62
3	E	573/791 (72%)	556 (97%)	17 (3%)	36	63
3	M	569/791 (72%)	543 (95%)	26 (5%)	23	51
3	f	3/791 (0%)	3 (100%)	0	100	100
3	k	571/791 (72%)	562 (98%)	9 (2%)	58	77
4	B	547/798 (68%)	537 (98%)	10 (2%)	54	74
4	D	524/798 (66%)	514 (98%)	10 (2%)	52	73
4	F	537/798 (67%)	526 (98%)	11 (2%)	50	72
4	N	525/798 (66%)	508 (97%)	17 (3%)	34	62
4	b	101/798 (13%)	100 (99%)	1 (1%)	73	85
4	n	532/798 (67%)	520 (98%)	12 (2%)	45	69
5	G	29/207 (14%)	27 (93%)	2 (7%)	13	40
5	H	35/207 (17%)	35 (100%)	0	100	100
5	g	32/207 (16%)	32 (100%)	0	100	100
5	h	35/207 (17%)	34 (97%)	1 (3%)	37	63
5	i	30/207 (14%)	27 (90%)	3 (10%)	6	28
5	j	32/207 (16%)	32 (100%)	0	100	100
5	s	32/207 (16%)	32 (100%)	0	100	100
5	t	32/207 (16%)	32 (100%)	0	100	100
5	u	35/207 (17%)	35 (100%)	0	100	100
5	v	35/207 (17%)	33 (94%)	2 (6%)	17	46
6	I	468/594 (79%)	458 (98%)	10 (2%)	48	71
6	K	508/594 (86%)	497 (98%)	11 (2%)	47	70

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	J	531/933 (57%)	516 (97%)	15 (3%)	38	64
8	L	540/1546 (35%)	526 (97%)	14 (3%)	41	66
8	d	128/1546 (8%)	127 (99%)	1 (1%)	79	89
9	a	53/62 (86%)	53 (100%)	0	100	100
9	c	53/62 (86%)	52 (98%)	1 (2%)	52	73
10	e	2/118 (2%)	2 (100%)	0	100	100
All	All	13413/22969 (58%)	13026 (97%)	387 (3%)	39	63

All (387) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	26	CYS
1	1	82	TYR
1	1	132	LEU
1	1	156	ARG
1	1	172	PHE
1	1	220	ILE
1	1	222	ASN
1	1	351	TRP
1	1	377	MET
1	1	422	ASP
1	2	22	TRP
1	2	56	ASP
1	2	136	VAL
1	2	170	SER
1	2	201	CYS
1	2	220	ILE
1	2	221	GLN
1	2	225	PHE
1	2	227	GLN
1	2	236	MET
1	2	248	TYR
1	2	256	LEU
1	2	378	MET
3	A	191	PHE
3	A	244	ARG
3	A	297	ARG
3	A	326	PHE
3	A	335	MET
3	A	373	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	A	384	SER
3	A	394	TRP
3	A	405	SER
3	A	482	ARG
3	A	494	TYR
3	A	497	LYS
3	A	504	MET
3	A	505	GLU
3	A	506	GLU
3	A	507	LYS
3	A	509	LEU
3	A	512	HIS
3	A	531	PHE
3	A	541	LYS
3	A	556	GLU
3	A	567	ASP
3	A	572	ASP
3	A	624	TRP
3	A	638	TYR
3	A	646	PHE
3	A	653	ARG
3	A	659	TRP
3	A	674	GLN
3	A	675	TRP
3	A	680	PHE
3	A	714	LYS
3	A	729	PHE
3	A	731	ASP
3	A	734	LEU
3	A	735	LYS
3	A	762	MET
4	B	264	LYS
4	B	285	ARG
4	B	293	ARG
4	B	403	TYR
4	B	410	TYR
4	B	528	ASN
4	B	544	TYR
4	B	576	HIS
4	B	868	SER
4	B	887	LYS
3	C	191	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	326	PHE
3	C	335	MET
3	C	373	GLN
3	C	384	SER
3	C	394	TRP
3	C	494	TYR
3	C	497	LYS
3	C	508	GLU
3	C	531	PHE
3	C	567	ASP
3	C	572	ASP
3	C	624	TRP
3	C	638	TYR
3	C	646	PHE
3	C	714	LYS
3	C	762	MET
4	D	274	CYS
4	D	276	LYS
4	D	392	LYS
4	D	417	HIS
4	D	711	MET
4	D	719	GLN
4	D	725	GLU
4	D	735	TRP
4	D	737	LYS
4	D	807	GLU
3	E	165	GLN
3	E	205	ILE
3	E	229	ASP
3	E	231	ARG
3	E	427	TYR
3	E	446	MET
3	E	482	ARG
3	E	522	MET
3	E	550	ARG
3	E	572	ASP
3	E	577	LEU
3	E	586	LEU
3	E	686	MET
3	E	697	MET
3	E	698	MET
3	E	852	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	E	865	TYR
4	F	329	HIS
4	F	362	LEU
4	F	482	LYS
4	F	579	ASP
4	F	611	GLN
4	F	642	TYR
4	F	645	ASP
4	F	685	MET
4	F	871	GLU
4	F	879	ARG
4	F	886	TYR
5	G	69	GLU
5	G	80	ARG
6	I	38	GLU
6	I	102	GLN
6	I	114	ASP
6	I	125	PHE
6	I	133	PHE
6	I	196	LEU
6	I	369	PHE
6	I	391	ASP
6	I	475	TYR
6	I	564	PHE
7	J	274	THR
7	J	275	LEU
7	J	304	HIS
7	J	330	PHE
7	J	358	PHE
7	J	388	ASN
7	J	413	HIS
7	J	642	HIS
7	J	696	ASP
7	J	719	TYR
7	J	721	GLN
7	J	821	TYR
7	J	827	LEU
7	J	889	LYS
7	J	933	TYR
6	K	26	GLN
6	K	60	GLU
6	K	128	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	K	183	MET
6	K	260	ARG
6	K	284	GLN
6	K	325	PHE
6	K	379	MET
6	K	541	PHE
6	K	628	LYS
6	K	641	ASP
8	L	351	GLU
8	L	456	LEU
8	L	504	TYR
8	L	553	MET
8	L	573	TYR
8	L	618	ASP
8	L	1533	GLN
8	L	1576	HIS
8	L	1584	LEU
8	L	1649	LYS
8	L	1670	LYS
8	L	1748	ARG
8	L	1756	TRP
8	L	1763	ARG
3	M	160	MET
3	M	262	ARG
3	M	289	ASN
3	M	392	GLU
3	M	397	ARG
3	M	427	TYR
3	M	439	ILE
3	M	446	MET
3	M	482	ARG
3	M	489	GLU
3	M	560	ARG
3	M	561	MET
3	M	620	TYR
3	M	632	ARG
3	M	642	PHE
3	M	643	ARG
3	M	645	MET
3	M	674	GLN
3	M	675	TRP
3	M	698	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	M	699	PHE
3	M	700	GLU
3	M	758	PHE
3	M	763	GLN
3	M	829	PHE
3	M	862	ASN
4	N	256	TYR
4	N	262	ASP
4	N	268	MET
4	N	335	TYR
4	N	379	LYS
4	N	403	TYR
4	N	440	GLU
4	N	474	PHE
4	N	535	ASP
4	N	563	ARG
4	N	573	PHE
4	N	638	PHE
4	N	685	MET
4	N	797	LEU
4	N	798	GLU
4	N	847	LEU
4	N	875	PHE
1	O	19	PHE
1	O	29	HIS
1	O	46	ASP
1	O	51	PHE
1	O	72	ARG
1	O	163	LYS
1	O	219	HIS
1	O	220	ILE
1	O	221	GLN
1	O	222	ASN
1	O	224	SER
1	O	225	PHE
1	O	227	GLN
1	O	245	TYR
1	O	248	TYR
1	O	339	ARG
1	O	353	PRO
1	O	358	VAL
1	O	378	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	O	425	ARG
1	P	3	ARG
1	P	28	GLU
1	P	69	LEU
1	P	70	GLU
1	P	73	VAL
1	P	109	SER
1	P	220	ILE
1	P	221	GLN
1	P	222	ASN
1	P	226	SER
1	P	295	ARG
1	P	302	ASN
1	P	348	PHE
1	P	362	ARG
1	P	416	ASP
1	P	435	TYR
1	Q	79	ASN
1	Q	222	ASN
1	Q	224	SER
1	Q	304	MET
1	Q	377	MET
1	Q	416	ASP
1	Q	435	TYR
1	R	19	PHE
1	R	102	ASN
1	R	103	ASN
1	R	158	ASN
1	R	164	LYS
1	R	221	GLN
1	R	270	MET
1	R	274	THR
1	R	443	TYR
1	S	72	ARG
1	S	119	PHE
1	S	206	ASP
1	S	220	ILE
1	S	224	SER
1	S	304	MET
1	S	363	LYS
1	S	419	ASP
1	T	19	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	T	22	TRP
1	T	23	LYS
1	T	68	ASP
1	T	152	TYR
1	T	169	TYR
1	T	224	SER
1	T	225	PHE
1	T	236	MET
1	T	245	TYR
1	T	248	TYR
1	T	260	LEU
1	T	266	LEU
1	T	388	PHE
1	T	429	GLN
1	U	184	GLN
1	U	221	GLN
1	U	222	ASN
1	U	224	SER
1	U	248	TYR
1	U	322	ASN
1	U	348	PHE
1	U	399	ARG
1	U	416	ASP
1	V	59	HIS
1	V	158	ASN
1	V	267	HIS
1	V	334	HIS
1	V	425	ARG
1	W	9	GLN
1	W	53	TYR
1	W	158	ASN
1	W	200	ASP
1	W	219	HIS
1	W	220	ILE
1	W	221	GLN
1	W	222	ASN
1	W	249	MET
1	W	301	LYS
1	W	376	LEU
1	W	377	MET
1	W	413	MET
1	X	10	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	X	59	HIS
1	X	63	ARG
1	X	119	PHE
1	X	189	LEU
1	X	219	HIS
1	X	222	ASN
1	X	225	PHE
1	X	351	TRP
1	X	366	TYR
1	X	372	ARG
1	X	413	MET
1	X	418	PHE
1	X	443	TYR
1	Y	79	ASN
1	Y	186	TYR
1	Y	221	GLN
1	Y	249	MET
1	Y	341	ARG
1	Z	49	ASP
1	Z	54	GLN
1	Z	86	TYR
1	Z	132	LEU
1	Z	208	THR
1	Z	212	ARG
1	Z	213	ILE
1	Z	220	ILE
1	Z	221	GLN
1	Z	222	ASN
1	Z	256	LEU
1	Z	267	HIS
1	Z	304	MET
1	Z	362	ARG
1	Z	432	ILE
1	Z	435	TYR
4	b	49	ARG
9	c	22	ARG
8	d	177	GLU
5	h	84	LEU
5	i	60	MET
5	i	72	LYS
5	i	73	GLU
3	k	158	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	k	446	MET
3	k	517	LYS
3	k	567	ASP
3	k	645	MET
3	k	647	TYR
3	k	770	LYS
3	k	861	PHE
3	k	864	PHE
4	n	253	ASP
4	n	275	TYR
4	n	366	ARG
4	n	378	LEU
4	n	439	LEU
4	n	538	TYR
4	n	575	ARG
4	n	595	HIS
4	n	667	LEU
4	n	697	PHE
4	n	806	PHE
4	n	836	PHE
5	v	87	ARG
5	v	89	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	373	GLN
3	A	465	HIS
3	A	684	GLN
3	C	373	GLN
4	D	789	GLN
3	E	165	GLN
6	I	370	GLN
6	I	464	HIS
6	I	494	HIS
7	J	307	HIS
6	K	378	HIS
8	L	1681	GLN
3	M	401	HIS
3	M	760	ASN
4	N	846	GLN
1	O	334	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	P	221	GLN
1	P	332	GLN
1	U	184	GLN
1	U	221	GLN
1	U	334	HIS
1	W	251	ASN
1	Y	184	GLN
1	Y	221	GLN
1	Z	219	HIS
1	Z	221	GLN
4	b	82	HIS
4	n	417	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

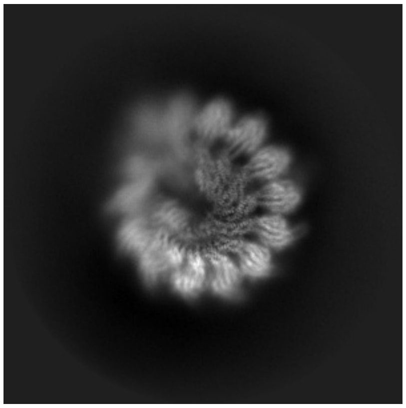
6 Map visualisation ⓘ

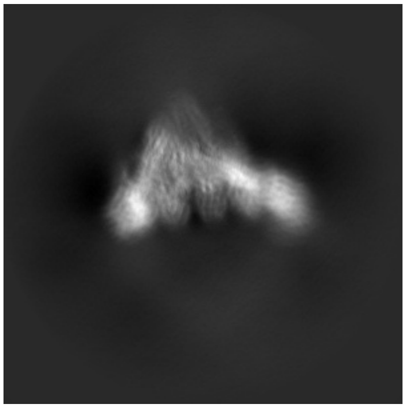
This section contains visualisations of the EMDB entry EMD-19570. These allow visual inspection of the internal detail of the map and identification of artifacts.

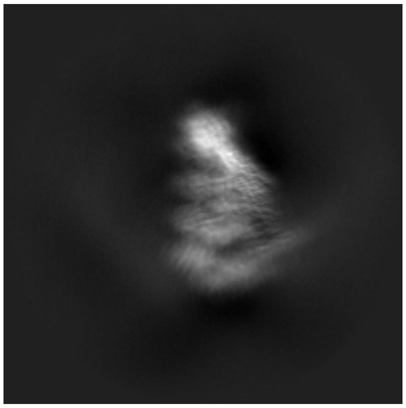
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections ⓘ

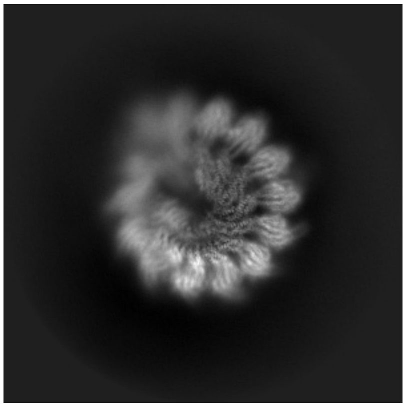
6.1.1 Primary map

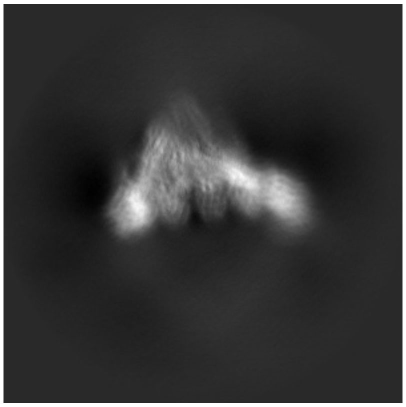

X

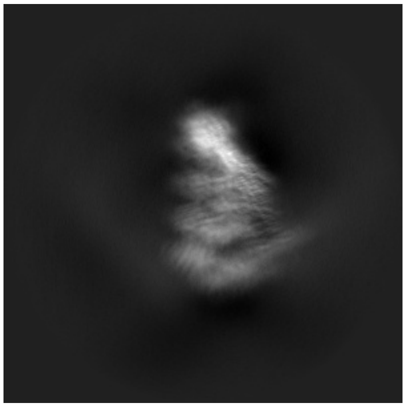

Y


Z

6.1.2 Raw map


X

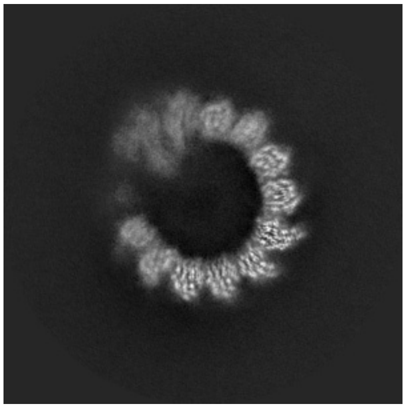

Y


Z

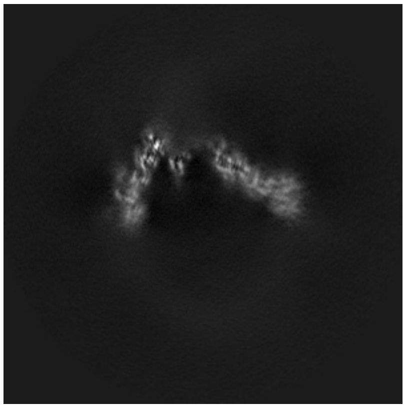
The images above show the map projected in three orthogonal directions.

6.2 Central slices

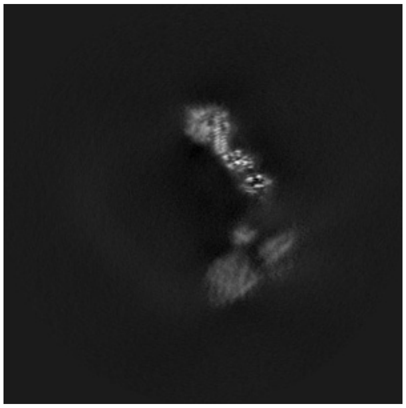
6.2.1 Primary map



X Index: 180

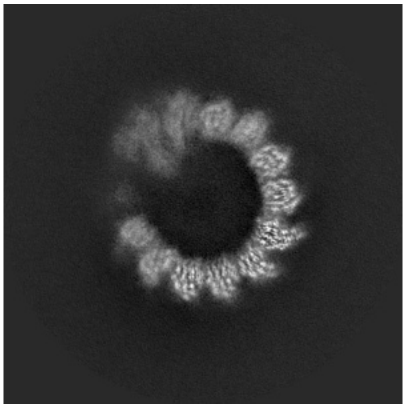


Y Index: 180

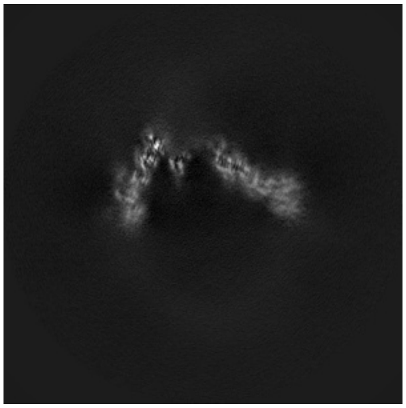


Z Index: 180

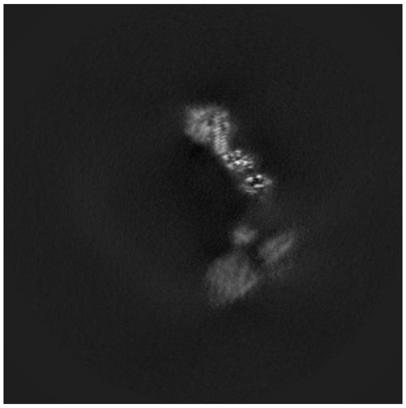
6.2.2 Raw map



X Index: 180



Y Index: 180

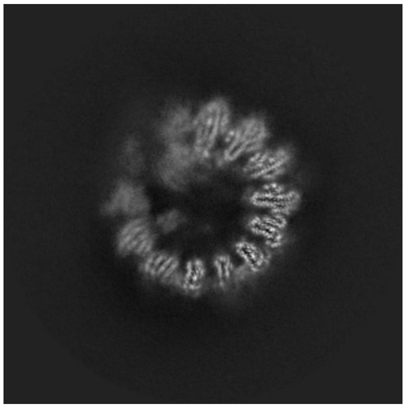


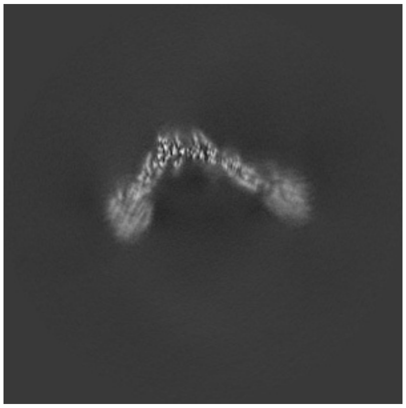
Z Index: 180

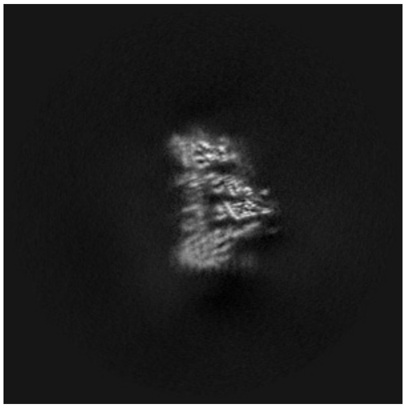
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

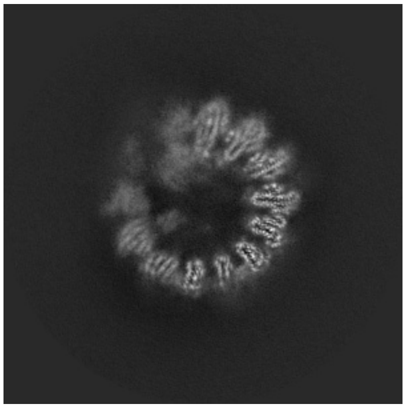
6.3.1 Primary map

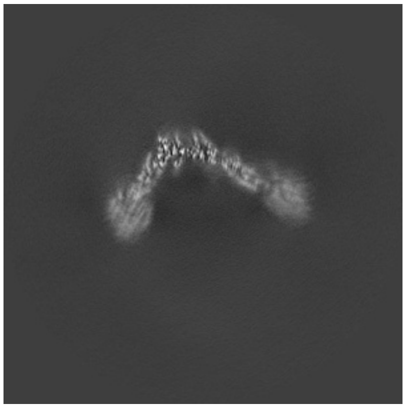

X Index: 195

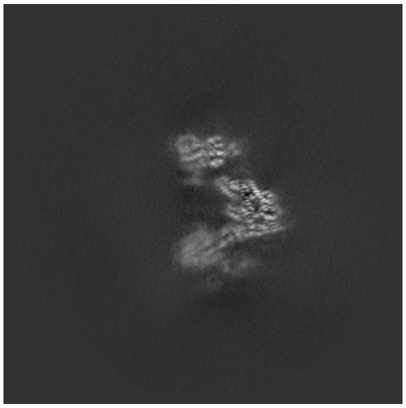

Y Index: 200


Z Index: 126

6.3.2 Raw map


X Index: 195

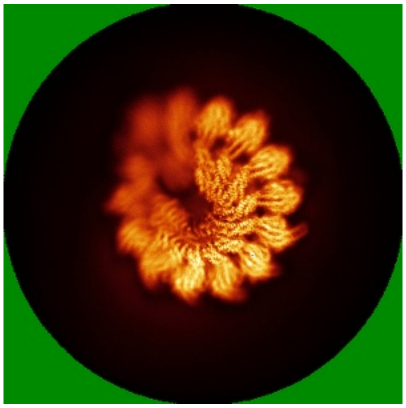

Y Index: 200

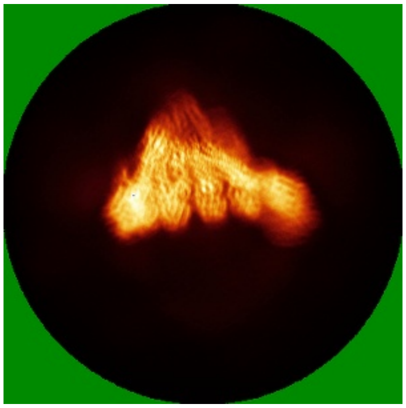

Z Index: 132

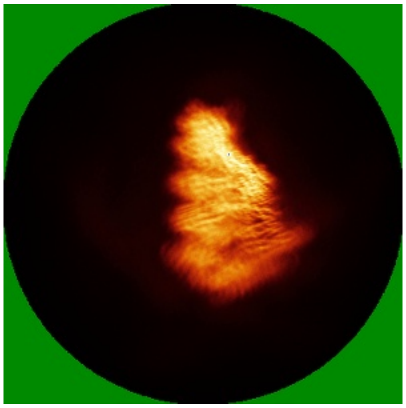
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color)

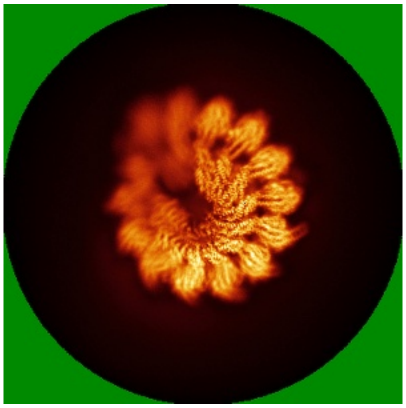
6.4.1 Primary map

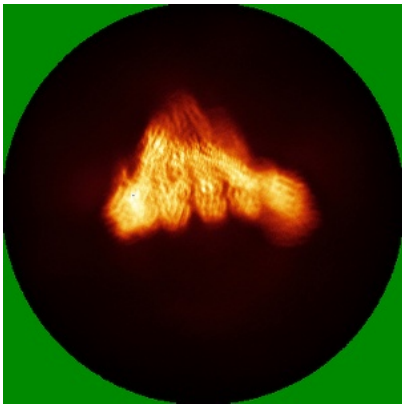

X

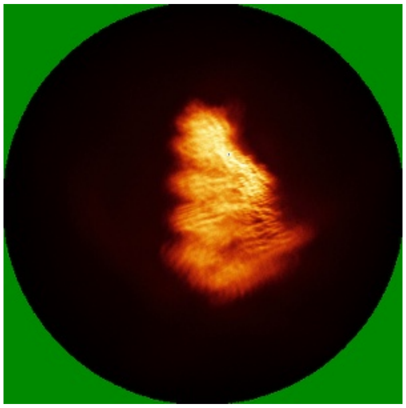

Y


Z

6.4.2 Raw map


X

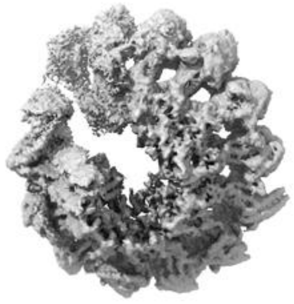

Y


Z

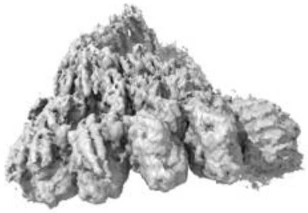
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views ⓘ

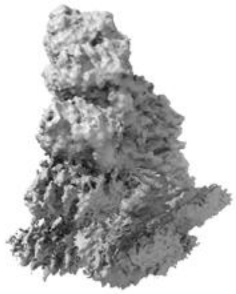
6.5.1 Primary map



X



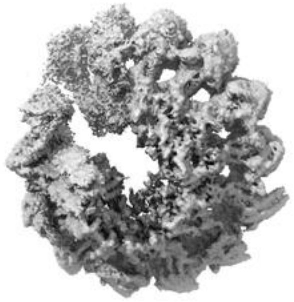
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X

Y

Z

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

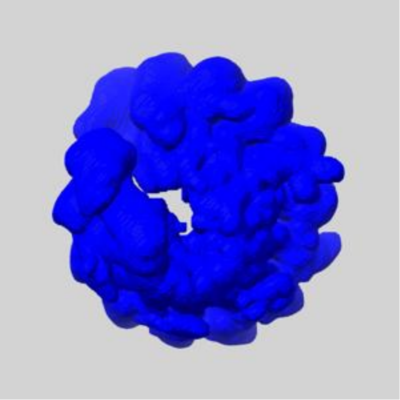
6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

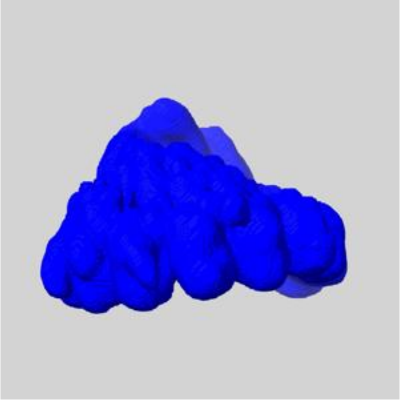
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

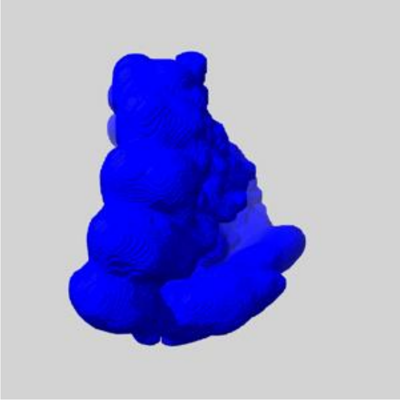
6.6.1 emd_19570_msk_1.map



X



Y

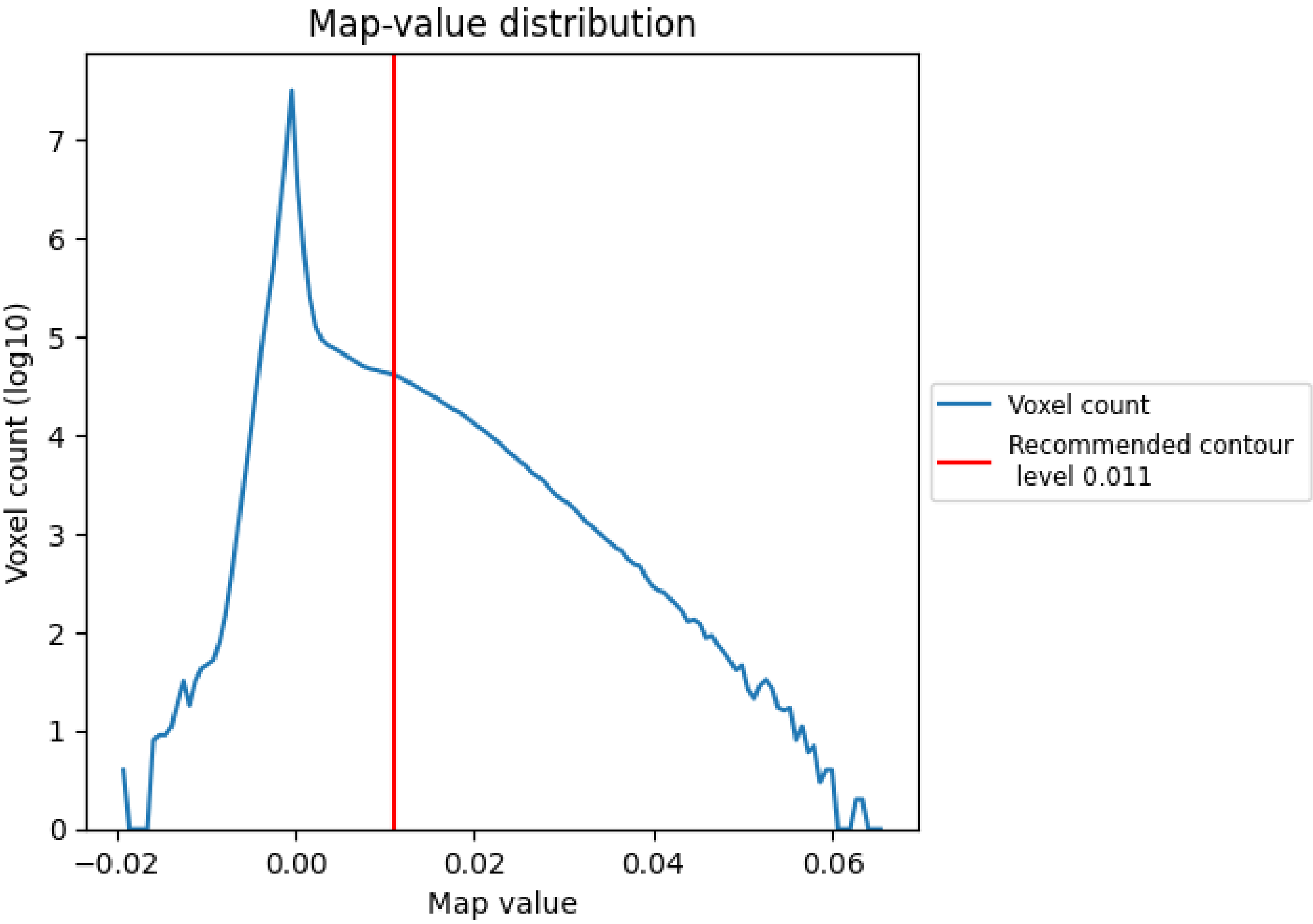


Z

7 Map analysis ⓘ

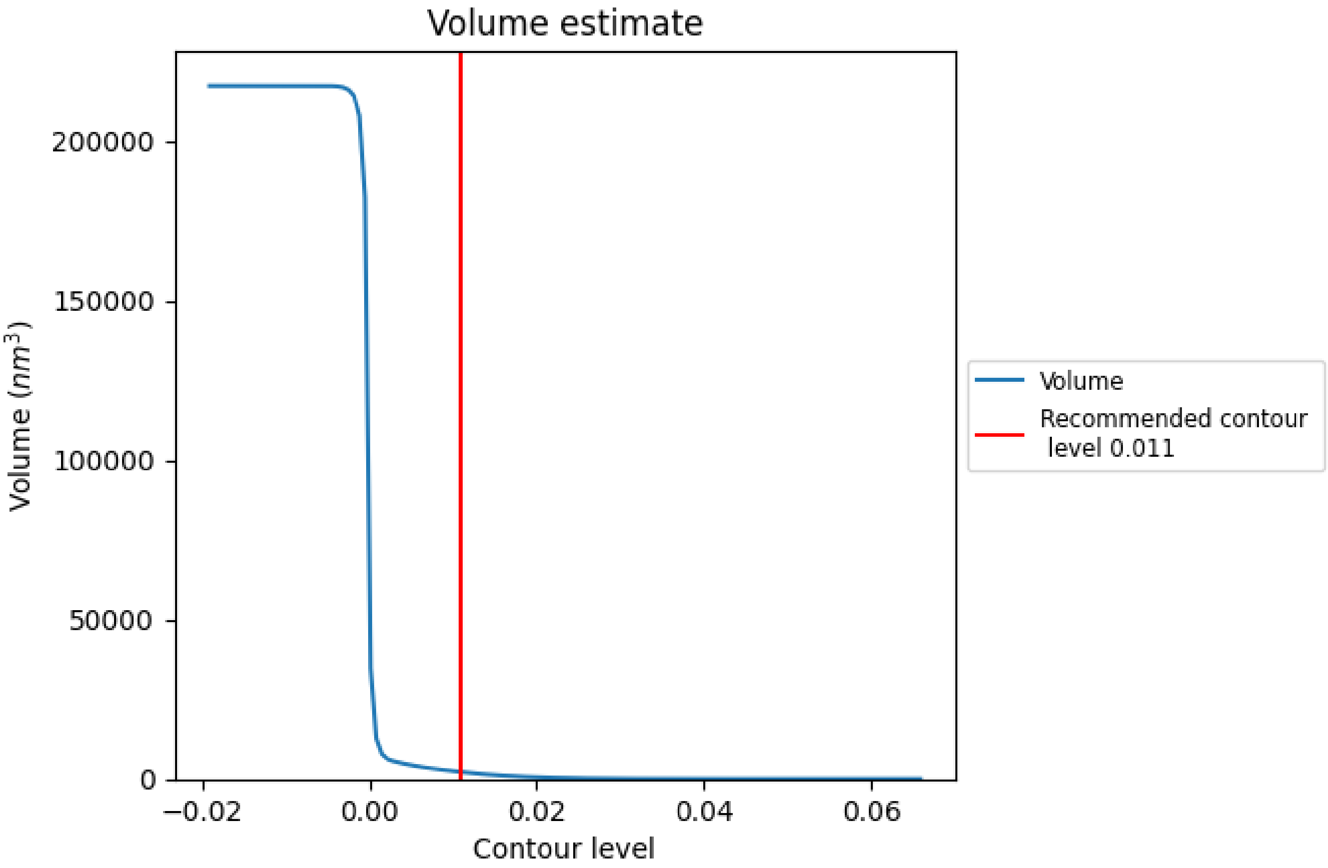
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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

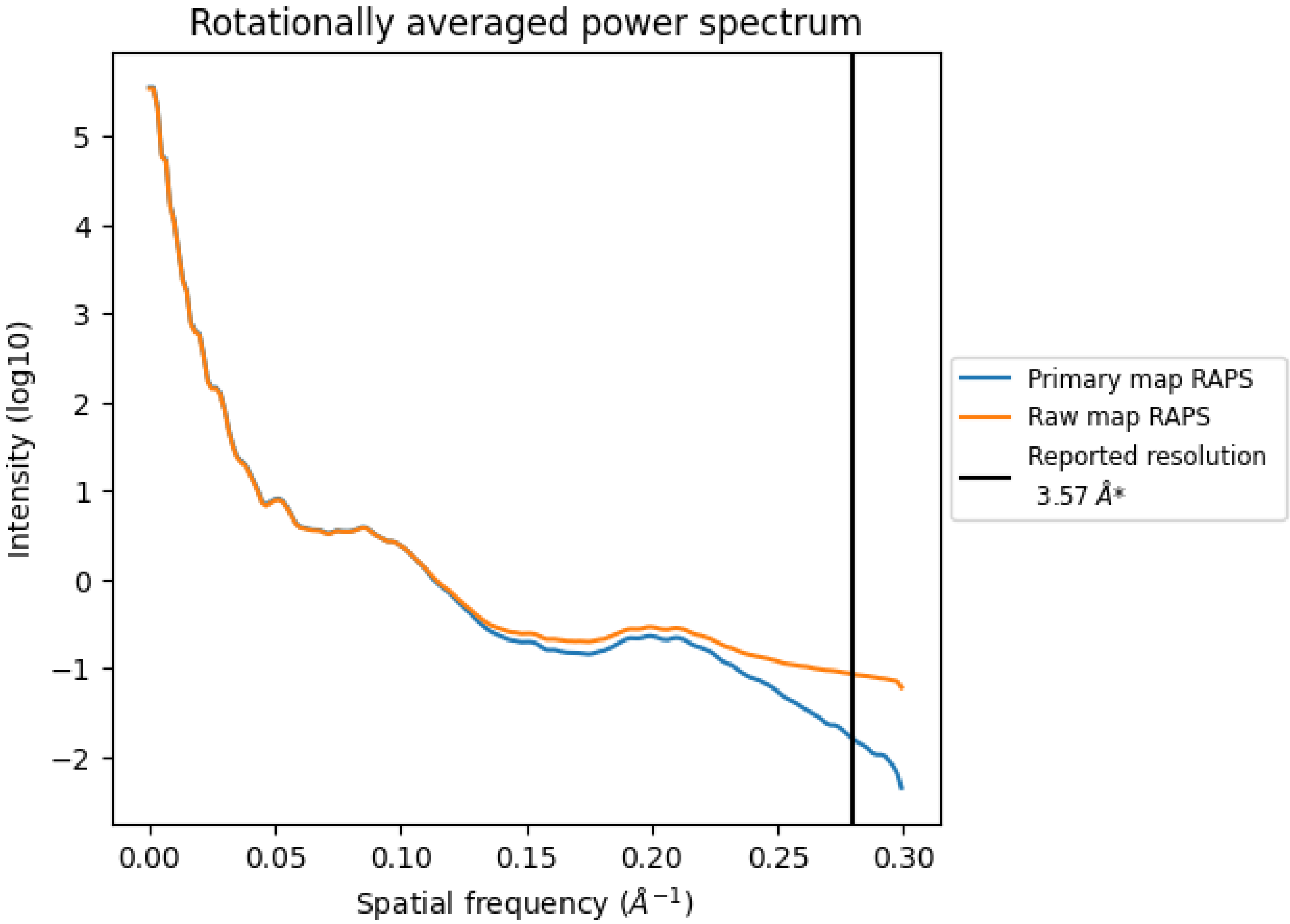
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 2186 nm^3; this corresponds to an approximate mass of 1974 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 ⓘ

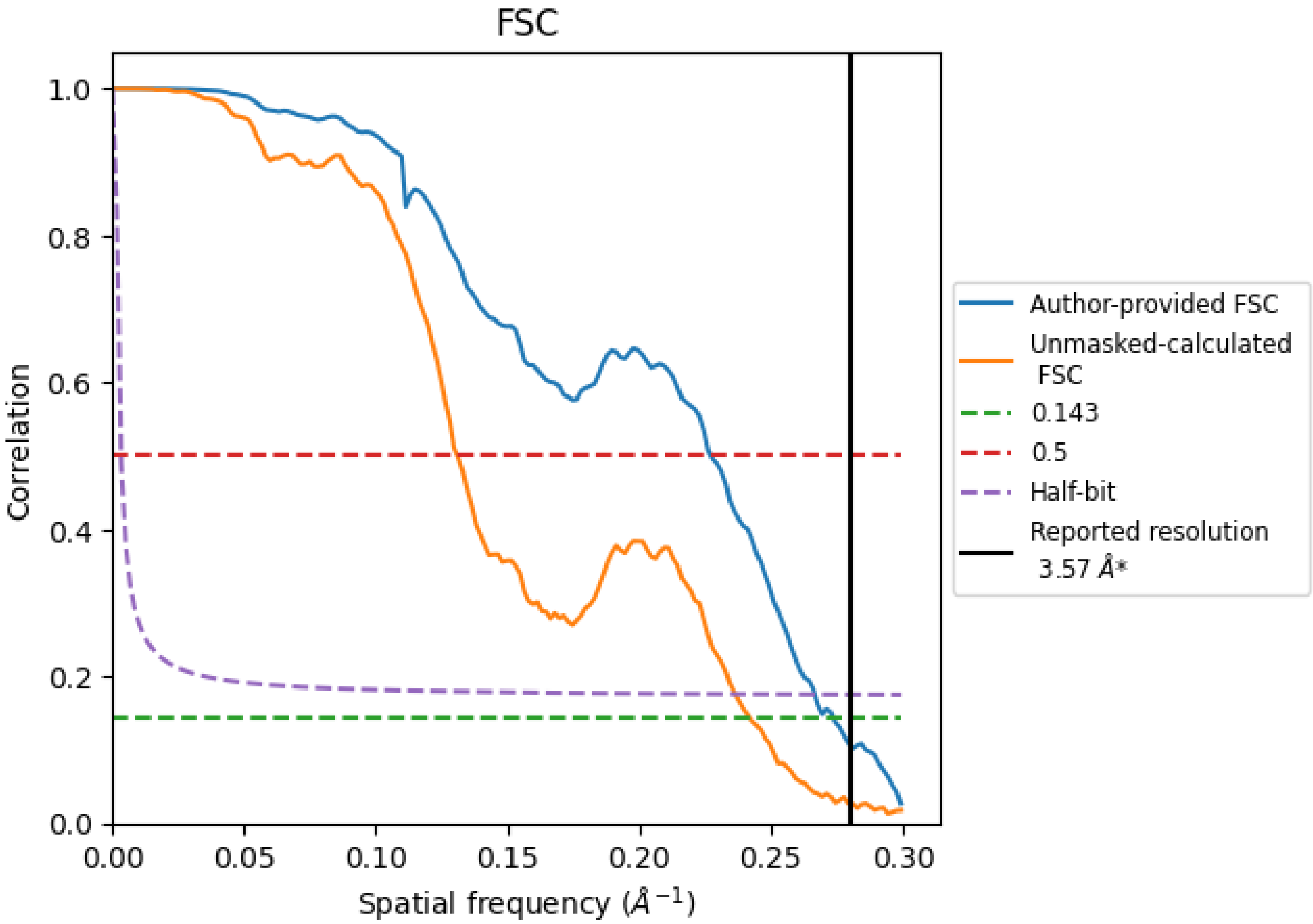


*Reported resolution corresponds to spatial frequency of 0.280 $Å^{-1}$

8 Fourier-Shell correlation ⓘ

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

8.1 FSC ⓘ



*Reported resolution corresponds to spatial frequency of 0.280 Å^{-1}

8.2 Resolution estimates ⓘ

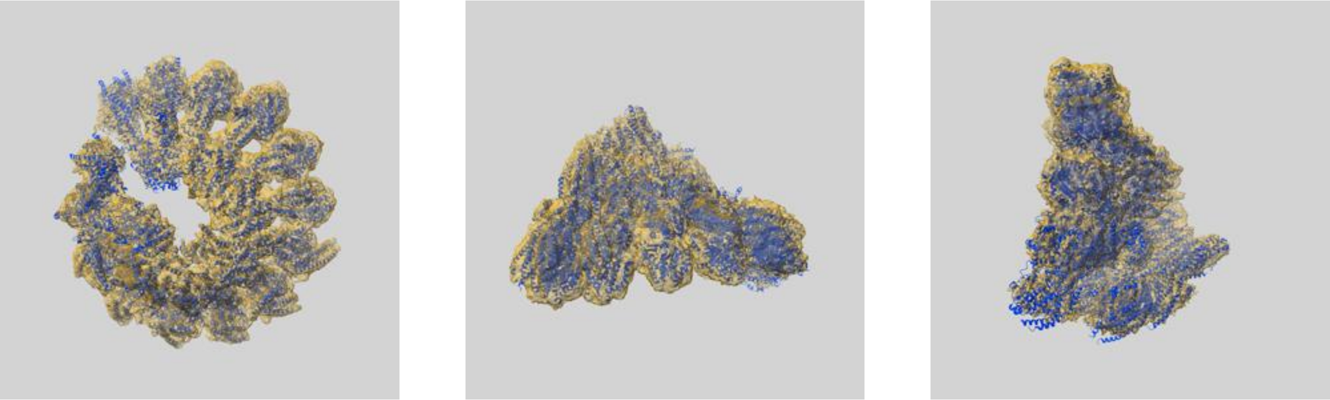
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.57	-	-
Author-provided FSC curve	3.65	4.40	3.75
Unmasked-calculated*	4.13	7.63	4.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.13 differs from the reported value 3.57 by more than 10 %

9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-19570 and PDB model 8RX1. Per-residue inclusion information can be found in section 3 on page 9.

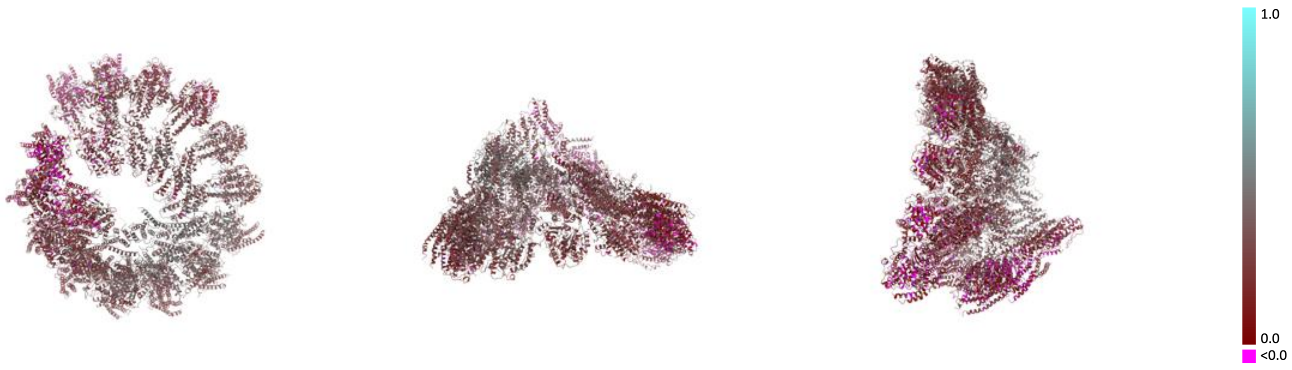
9.1 Map-model overlay



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.011 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.

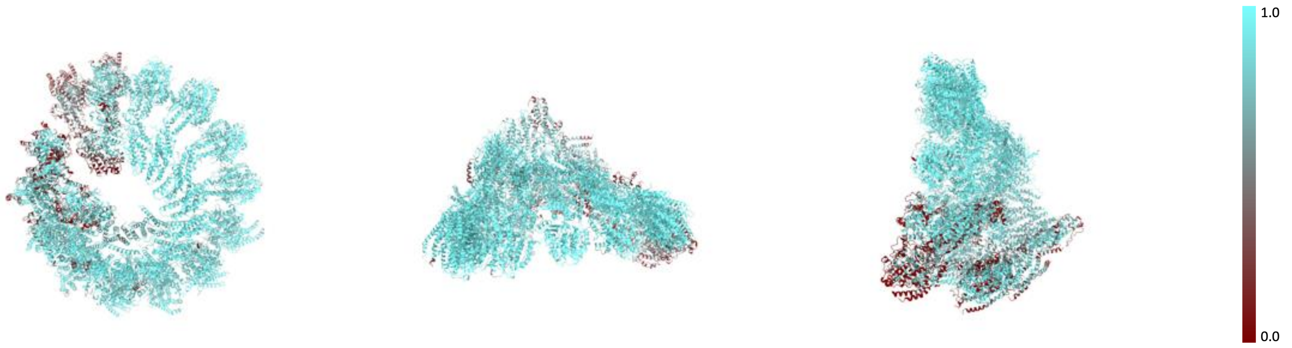
9.2 Q-score mapped to coordinate model



X Y Z

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

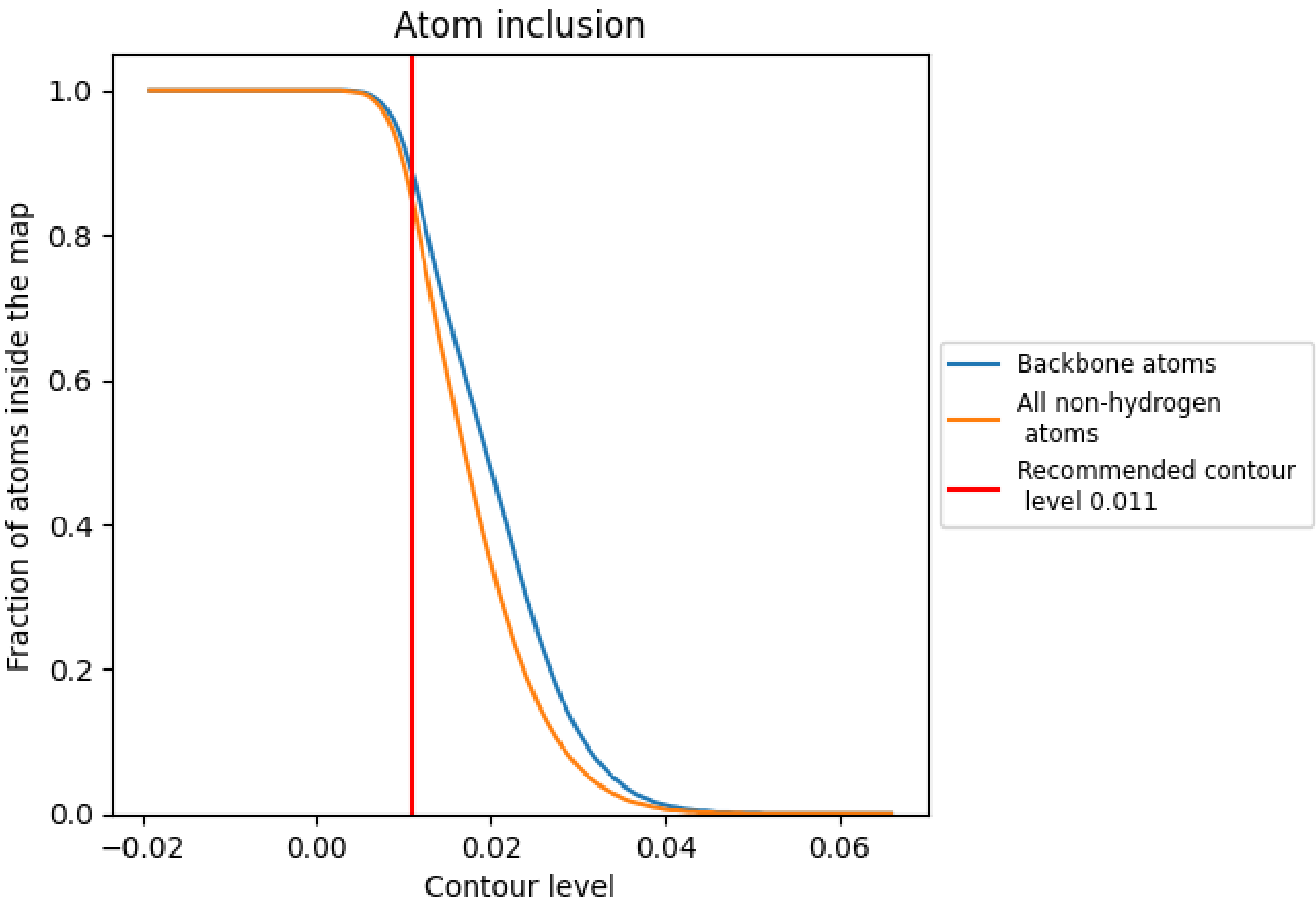
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.011).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8470	0.2420
1	0.6500	0.1390
2	0.2930	0.1280
7	0.7740	0.2890
A	0.5960	0.0970
B	0.7720	0.2080
C	0.8890	0.2370
D	0.9390	0.2560
E	0.9270	0.3150
F	0.9630	0.3150
G	0.8450	0.2400
H	0.7190	0.2450
I	0.9670	0.3310
J	0.9680	0.3030
K	0.9860	0.2860
L	0.9870	0.2510
M	0.7860	0.1870
N	0.3640	0.1570
O	0.5060	0.1430
P	0.6560	0.1500
Q	0.8800	0.1800
R	0.9380	0.1760
S	0.9840	0.2480
T	0.9640	0.2310
U	0.9760	0.2810
V	0.9640	0.3260
W	0.9760	0.2510
X	0.9800	0.2330
Y	0.9780	0.1470
Z	0.9680	0.1580
a	0.8470	0.3880
b	0.8690	0.4020
c	0.7440	0.2880
d	0.8240	0.3470
e	0.5630	0.3180

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	0.5280	0.2940
g	0.9560	0.2570
h	0.5900	0.2510
i	0.5990	0.2530
j	0.4390	0.2430
k	0.9510	0.3560
n	0.9730	0.3800
s	0.9260	0.2890
t	0.9830	0.3430
u	0.8680	0.2570
v	0.9520	0.2860