



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 01:58 AM UTC

PDB ID : 9I8N / pdb_00009i8n
EMDB ID : EMD-52730
Title : NEDD1-bound native vertebrate gamma-tubulin ring complex from *Xenopus laevis*
Authors : Vermeulen, B.J.A.; Pfeffer, S.
Deposited on : 2025-02-05
Resolution : 4.60 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

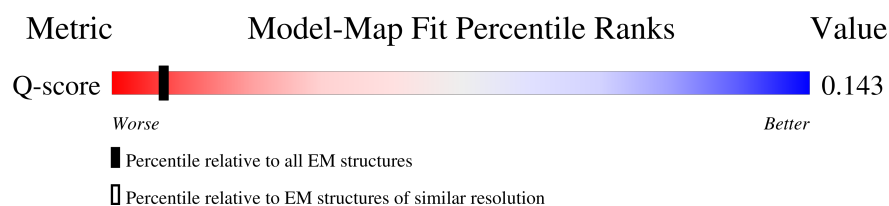
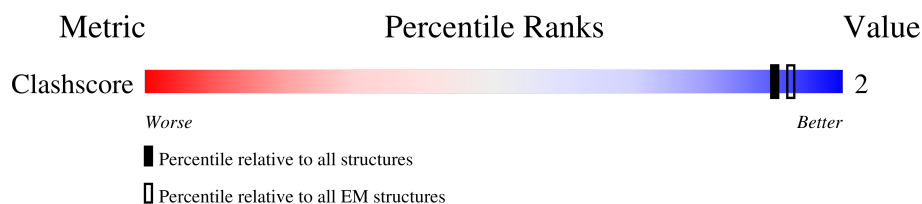
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

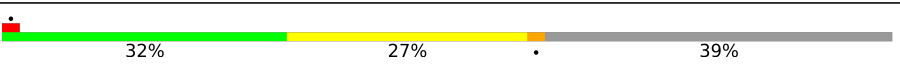
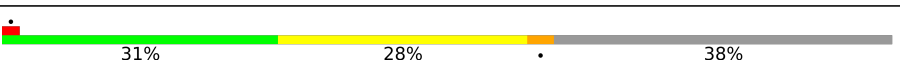
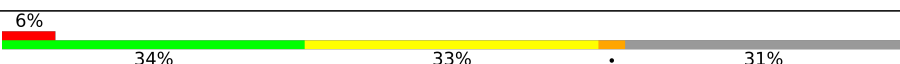
The reported resolution of this entry is 4.60 Å.

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	-
Q-score	-	25397	2407 (4.10 - 5.10)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	896	
1	C	896	
1	E	896	
1	G	896	
1	M	896	
2	B	906	

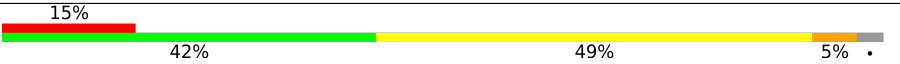
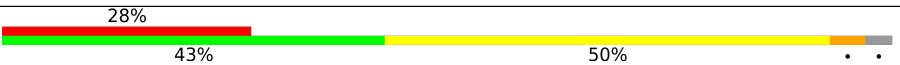
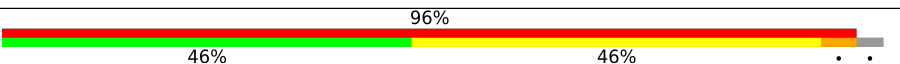
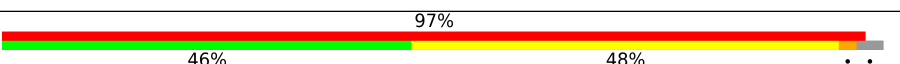
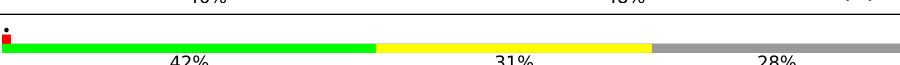
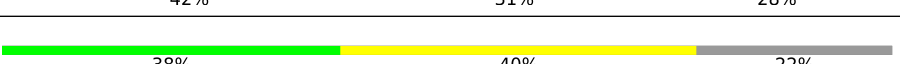
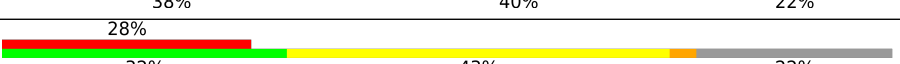
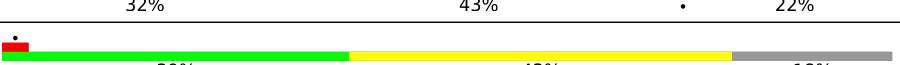
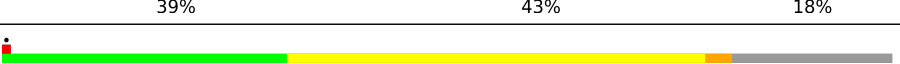
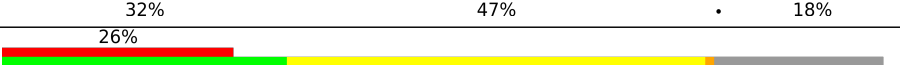
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Mol	Chain	Length	Quality of chain
2	D	906	
2	F	906	
2	H	906	
2	N	906	
2	O	906	
2	Q	906	
2	R	906	
2	S	906	
2	T	906	
3	I	666	
3	K	666	
4	J	1019	
5	L	1698	
6	P	375	
7	U	671	
7	V	671	
7	W	671	
7	X	671	
8	a	451	
8	b	451	
8	c	451	
8	d	451	
8	e	451	
8	f	451	
8	g	451	

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Mol	Chain	Length	Quality of chain
8	h	451	
8	i	451	
8	j	451	
8	k	451	
8	l	451	
8	m	451	
8	n	451	
9	o	72	
9	p	72	
9	q	72	
9	r	72	
9	s	72	
9	t	72	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 129788 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
1	C	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
1	E	551	Total	C	N	O	S	0	0
			4508	2898	740	838	32		
1	G	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
1	M	551	Total	C	N	O	S	0	0
			4503	2894	739	838	32		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	D	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	F	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	H	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	N	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	O	93	Total	C	N	O	S	0	0
			753	480	137	134	2		
2	Q	109	Total	C	N	O	S	0	0
			878	557	160	159	2		
2	R	98	Total	C	N	O	S	0	0
			794	503	144	145	2		
2	S	109	Total	C	N	O	S	0	0
			878	557	160	159	2		
2	T	93	Total	C	N	O	S	0	0
			753	480	137	134	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	571	Total	C	N	O	S	0	0
			4635	2993	790	831	21		
3	K	571	Total	C	N	O	S	0	0
			4635	2993	790	831	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	636	Total	C	N	O	S	0	0
			5252	3406	890	930	26		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	780	Total	C	N	O	S	0	0
			6303	4088	1029	1155	31		

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 6 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	371	Total	C	N	O	S	0	0
			2892	1828	486	557	21		

- Molecule 7 is a protein called NEDD1 gamma-tubulin ring complex targeting factor L homolog.

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

- Molecule 8 is a protein called Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	b	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	c	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	d	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	e	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	f	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	g	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	h	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	i	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	j	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	k	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	l	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	m	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
8	n	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	o	52	Total	C	N	O	S	0	0
			403	248	71	79	5		
9	p	56	Total	C	N	O	S	0	0
			429	263	73	89	4		
9	q	56	Total	C	N	O	S	0	0
			432	266	76	86	4		
9	r	59	Total	C	N	O	S	0	0
			454	278	80	91	5		
9	s	59	Total	C	N	O	S	0	0
			451	277	79	90	5		

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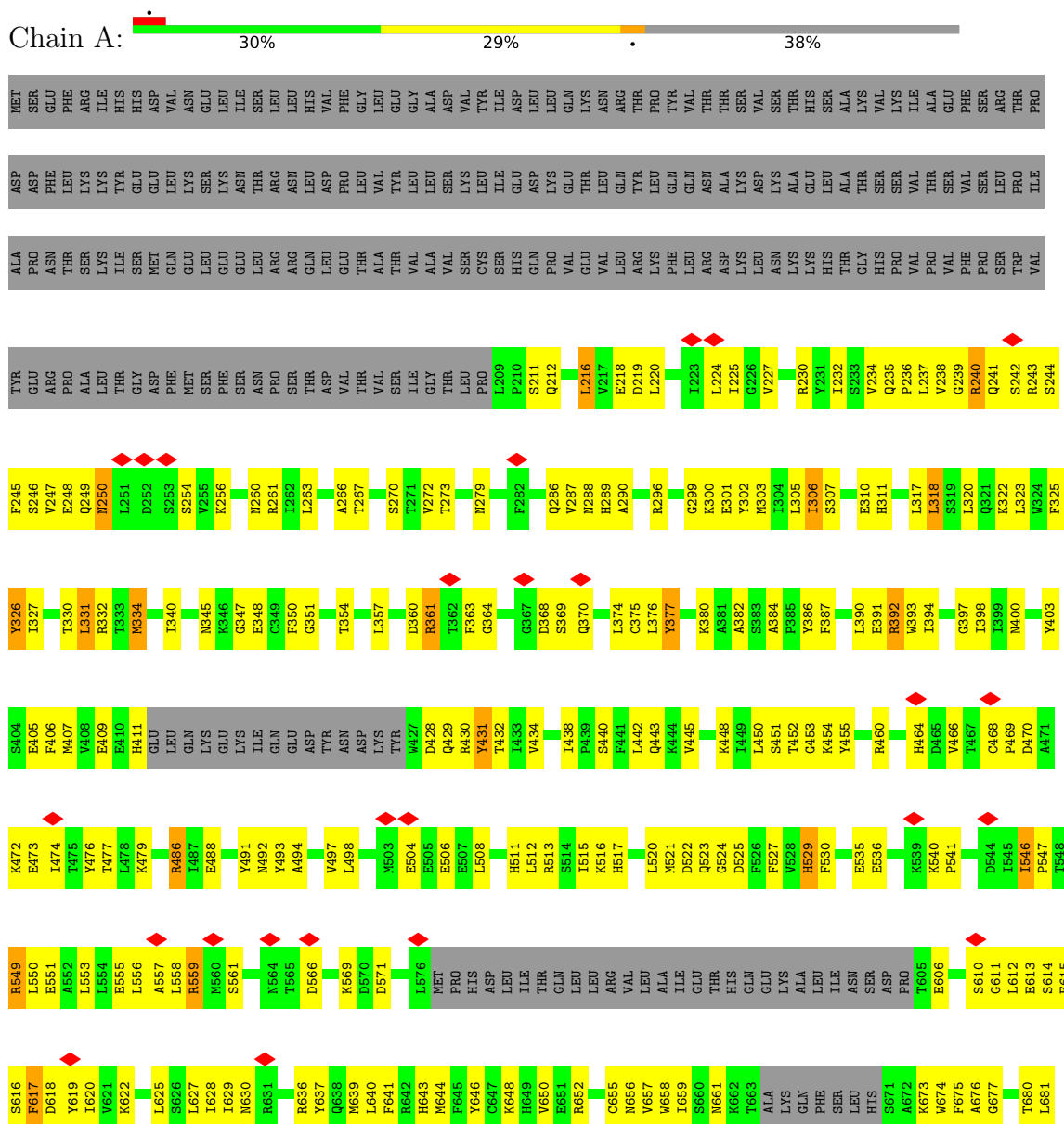
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Mol	Chain	Residues	Atoms					AltConf	Trace
9	t	58	Total	C	N	O	S	0	0
			446	274	78	89	5		

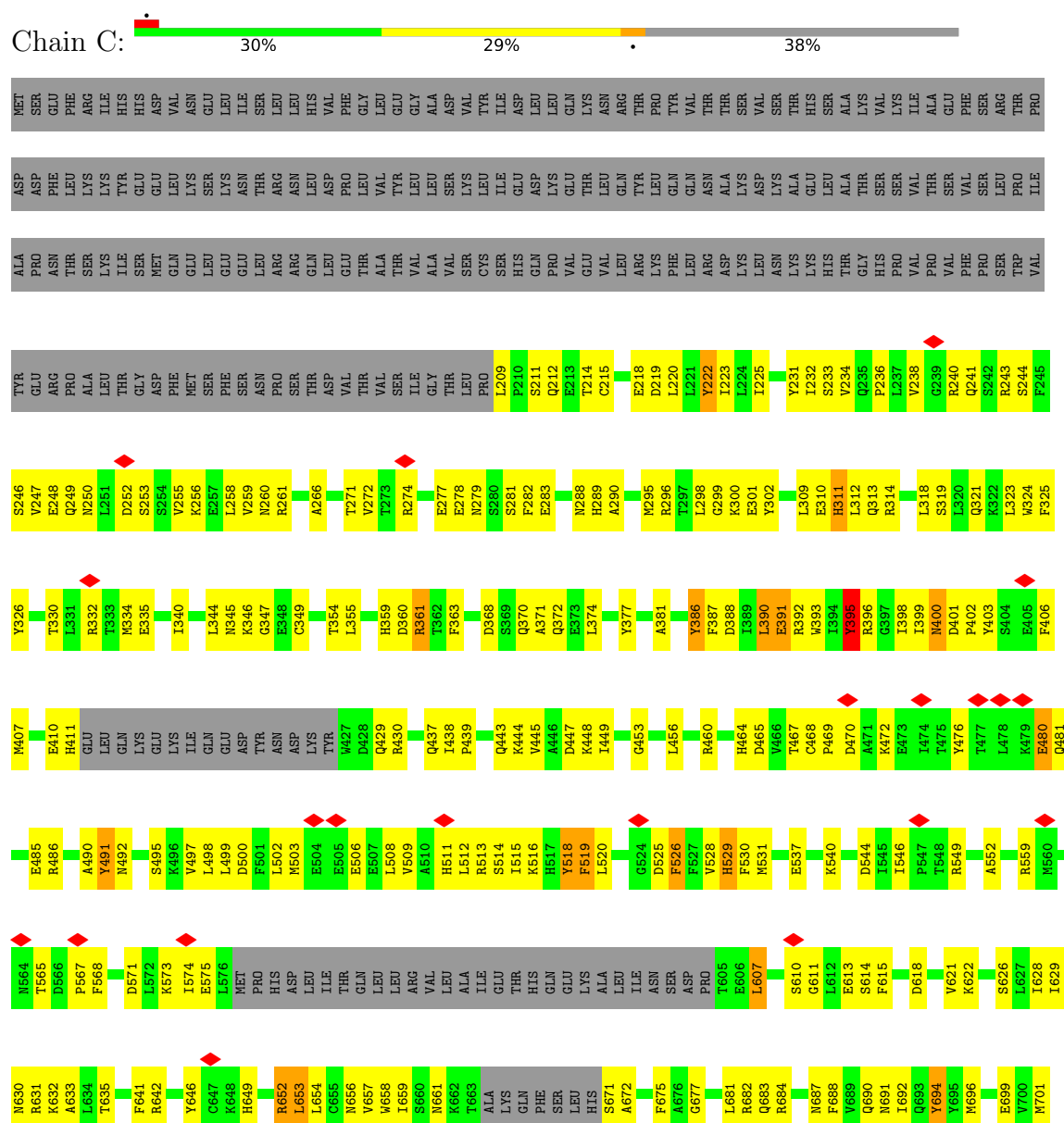
3 Residue-property plots

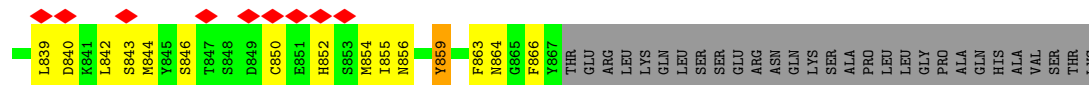
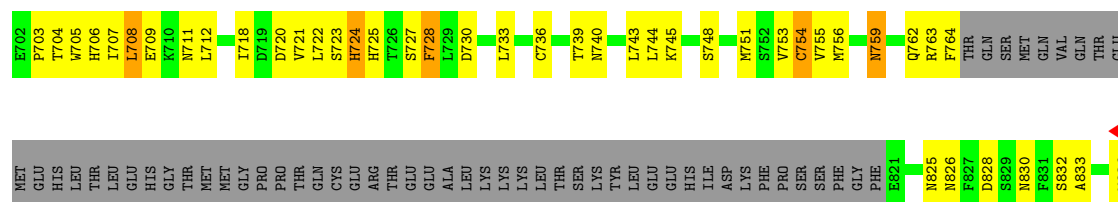
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

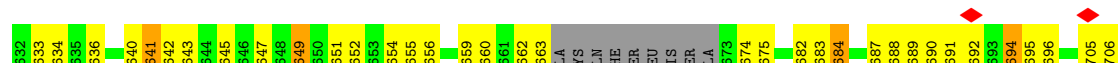
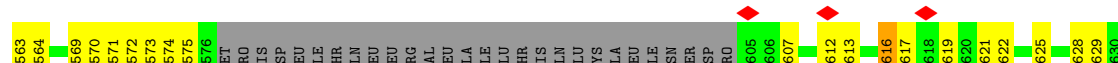
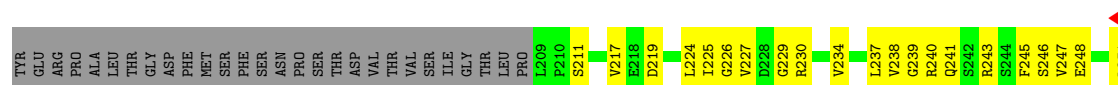
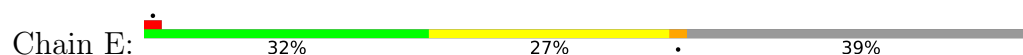


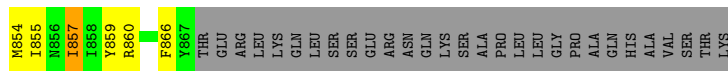
- Molecule 1: Gamma-tubulin complex component



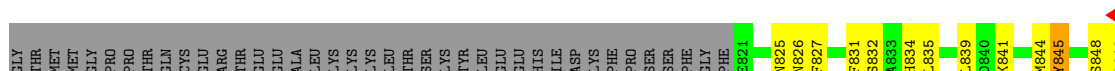
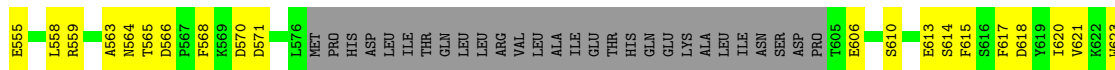
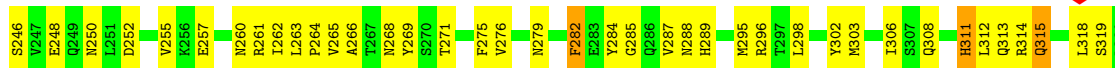
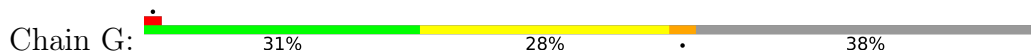


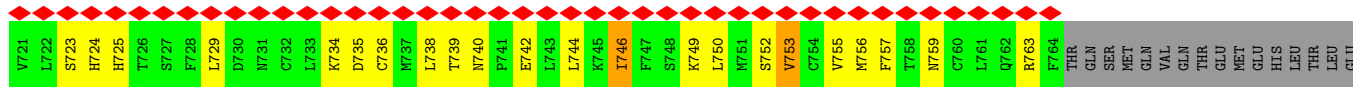
• Molecule 1: Gamma-tubulin complex component

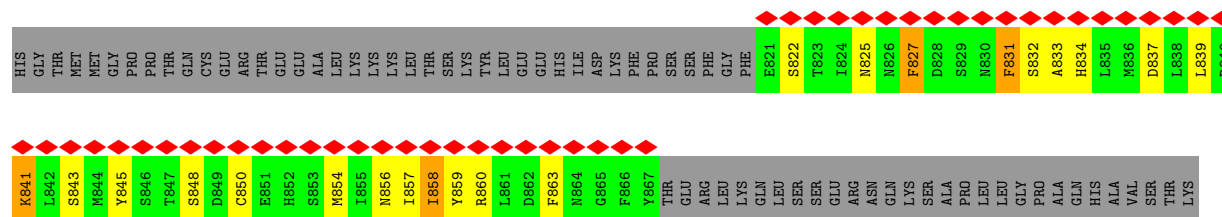




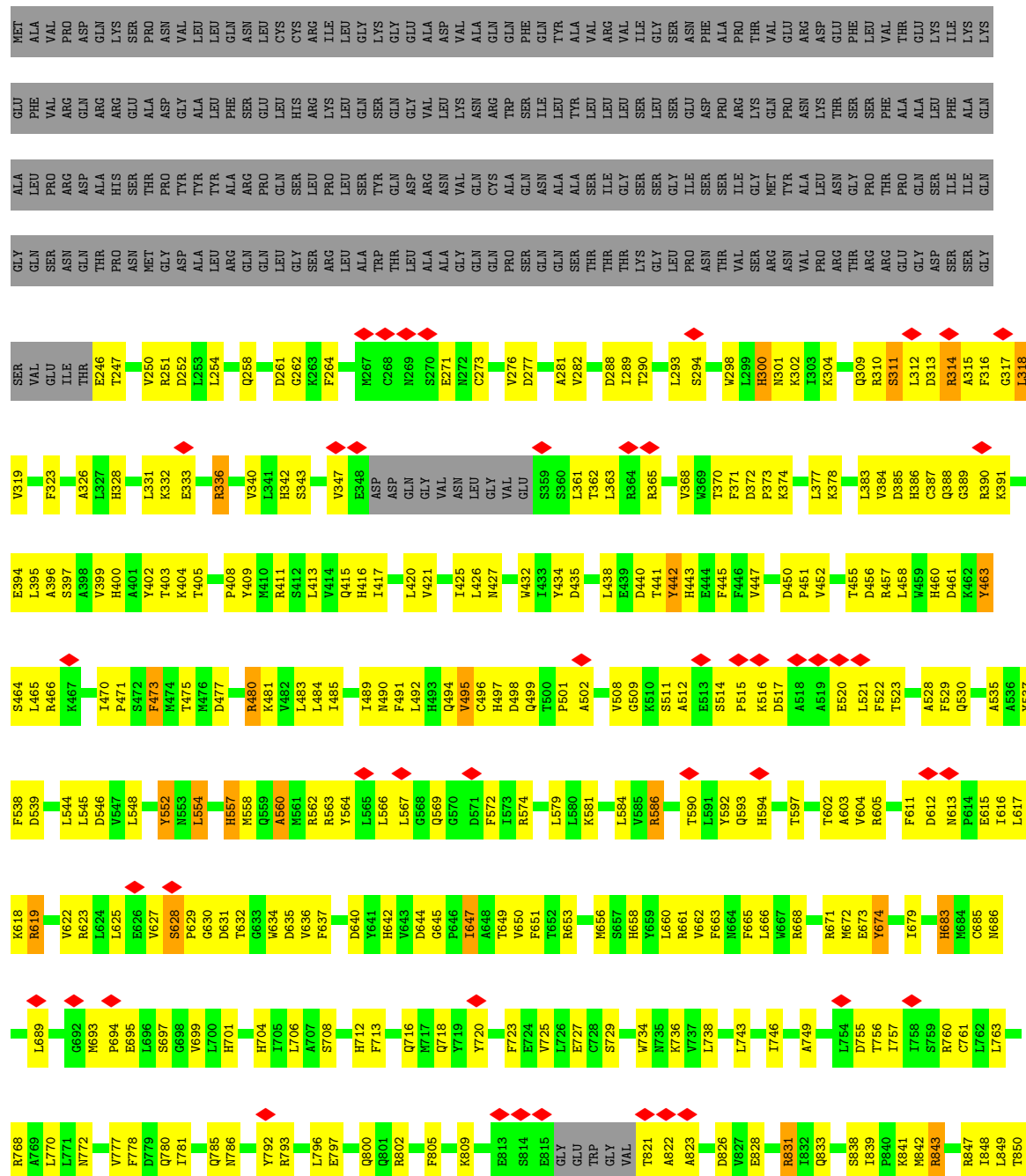
- Molecule 1: Gamma-tubulin complex component



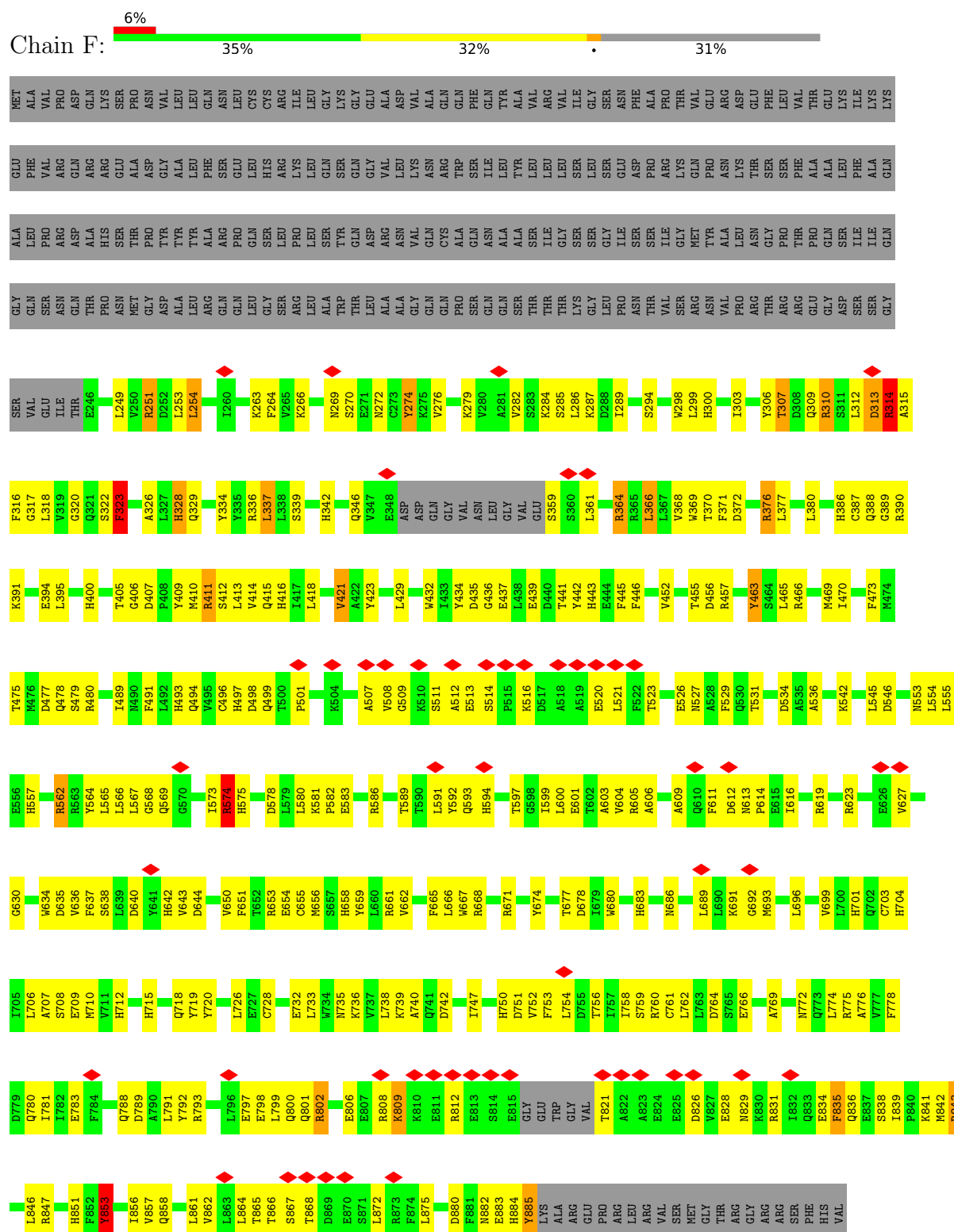




• Molecule 2: Gamma-tubulin complex component 3 homolog

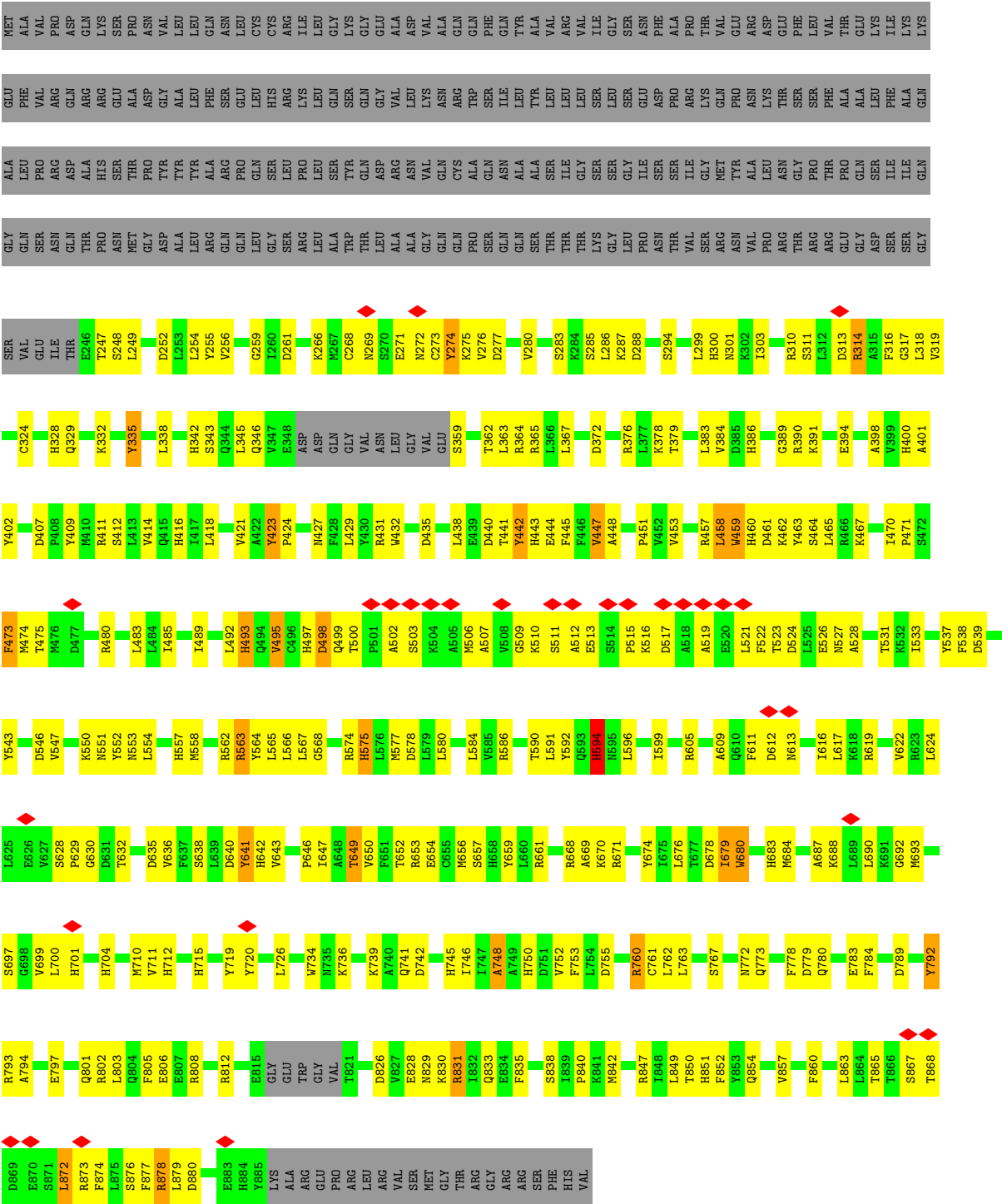


- Molecule 2: Gamma-tubulin complex component 3 homolog



- Molecule 2: Gamma-tubulin complex component 3 homolog







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PDB
PROTEIN DATA BANK

VAL	ARG	ASP	GLN	THR	THR	THR	GLY	ASP	GLY	VAL	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY</
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● Molecule 2: Gamma-tubulin complex component 3 homolog

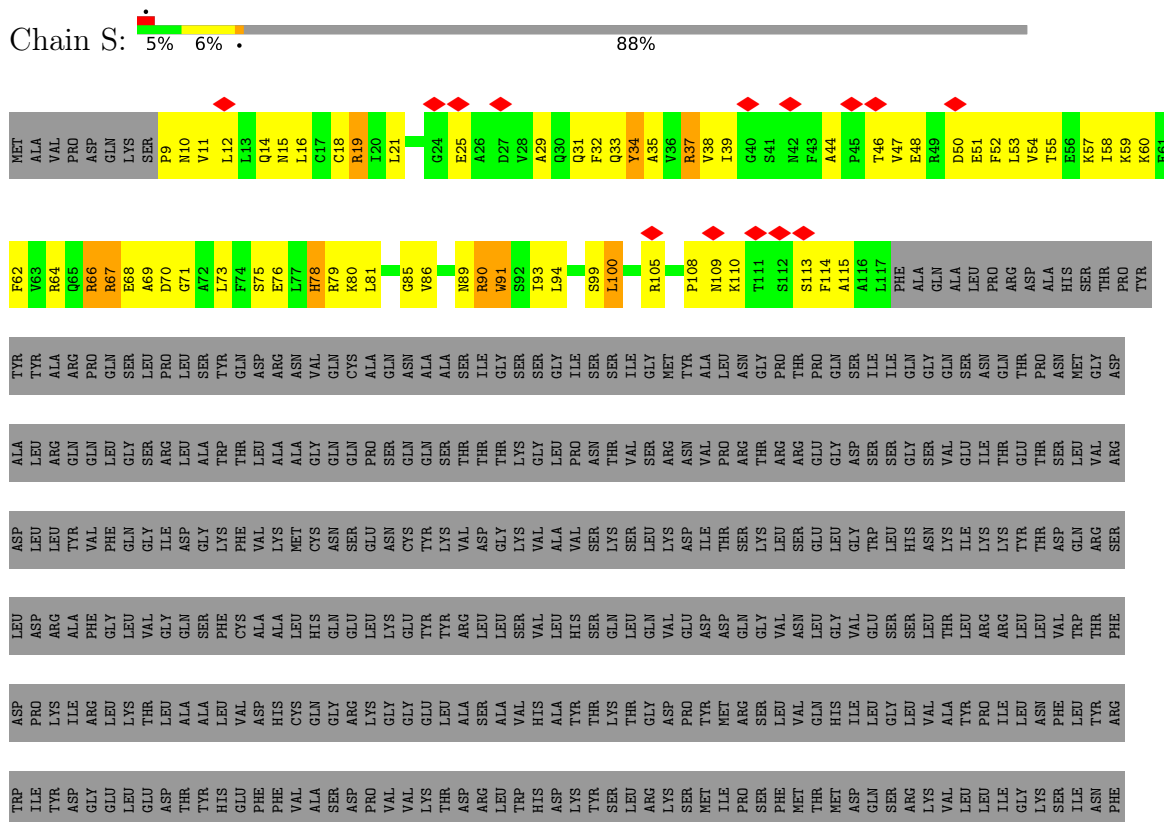


MET	ALA	VAL	PRO	ASP	GLN	LYS	SER	P9	N10	V11	L12	L13	C18	R19	I20	L21	G22	K23	G24	E25	A26	D27	V28	A29	Q30	Q31	F32	Q33	Y34	R37	V38	I39	G40	S41	F43	A44	P45	T46	V47	E48	R49	D50	L53	V54	T55	E56	K57	I58	K59	R64	Q65	R66	R67	E68		
A69	D70	F74	S75	H78	R79	K80	L81	Q82	S83	Q84	C85	V86	L87	K88	R89	R90	N91	S92	Y95	L96	I97	L98	S99	L100	S101	D102	P103	P104	R105	K106	Q107	P108	M109	K110	T111	S112	S113	F114	A115	A116	L117	PHE	ALA	GLN	VAL	LEU	PRO	ARG	ASP	ALA	HIS	SER	THR	PRO	TYR	TYR



[illegible]

- Molecule 2: Gamma-tubulin complex component 3 homolog

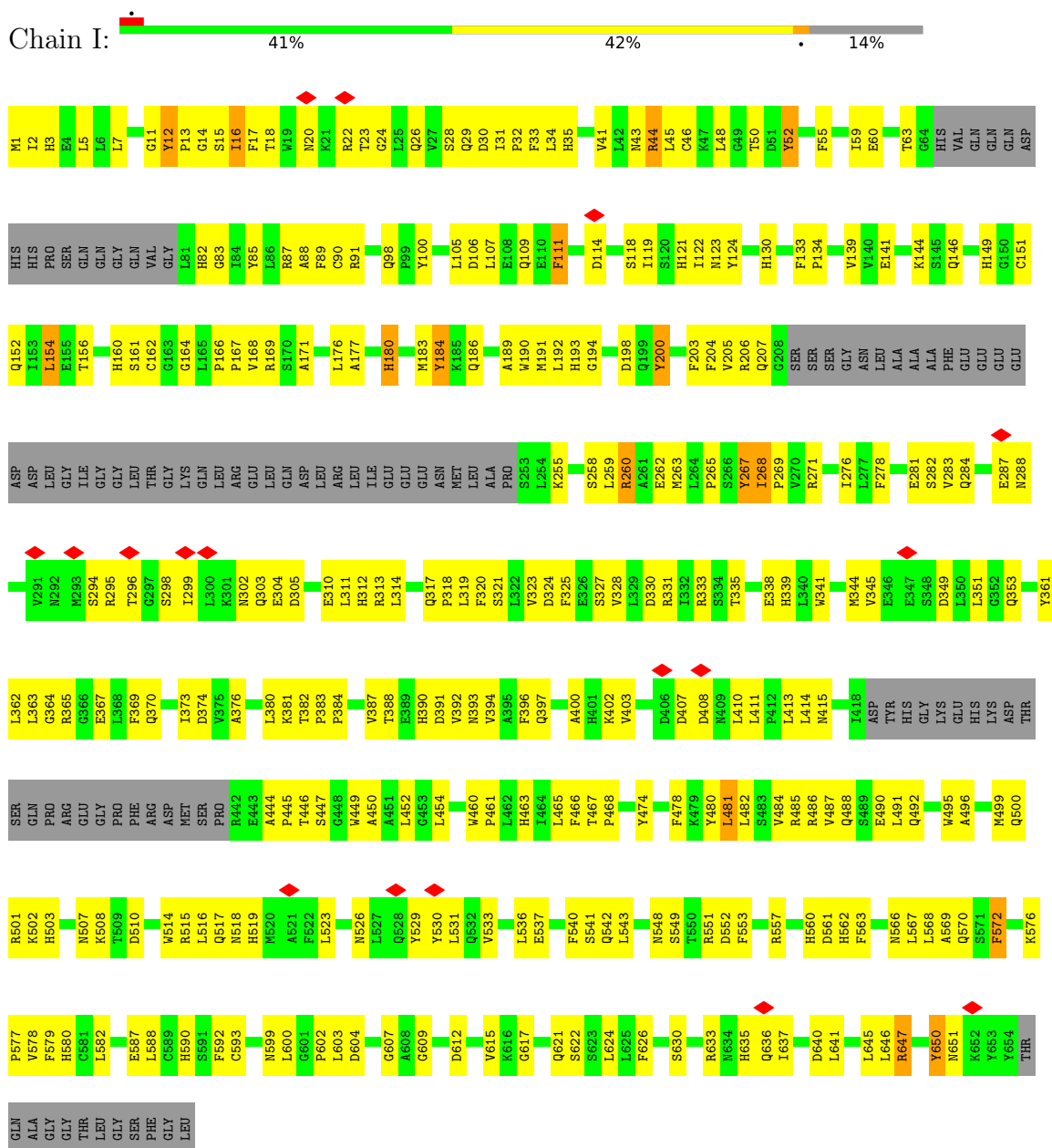


- Molecule 2: Gamma-tubulin complex component 3 homolog

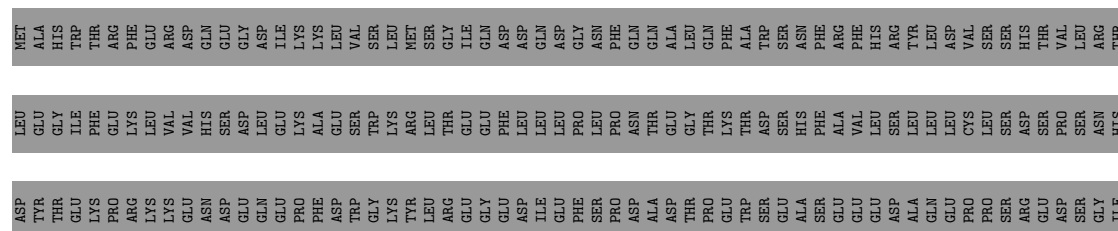
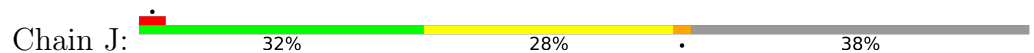
[illegible]

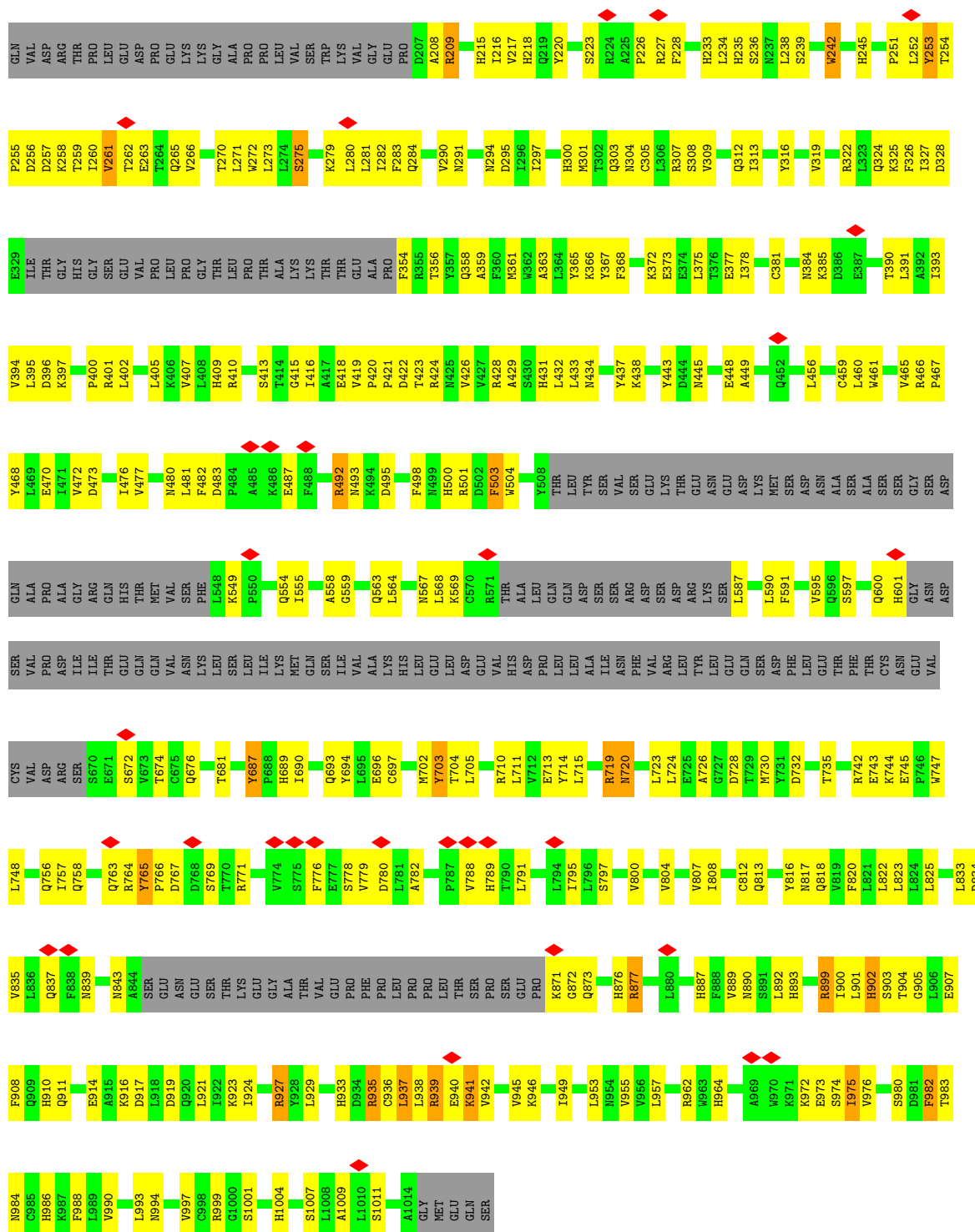
HIS	VAL	GLN	LEU	ASN	GLN	VAL	PHE
		LEU	ASN	LEU	LEU	TRP	TRP
HIS	VAL	ARG	ARG	ALA	GLN	CYS	ARG
		ILE	LEU	ASP	ALA	TRP	ALA
HIS	VAL	THR	LEU	LEU	ASP	ASP	ARG
		HIS	TYR	GLU	GLU	GLU	MET
HIS	VAL	TYR	ARG	ALA	TRP	TYR	TYR
		GLN	ALA	ALA	TRP	ILE	ILE
HIS	VAL	GLY	ALA	ASN	ASN	LYS	LEU
		ILE	LEU	LYS	VAL	THR	THR
HIS	VAL	VAL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

- Molecule 3: Gamma-tubulin complex component

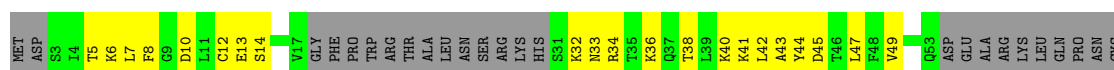


Chain K: 6% 42% 41% 14%

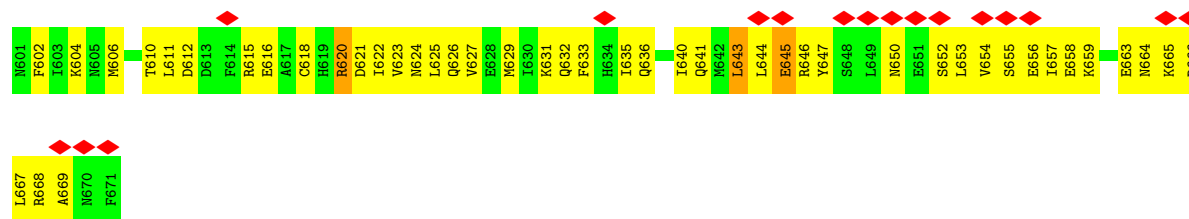




• Molecule 5: Gamma-tubulin complex component 6

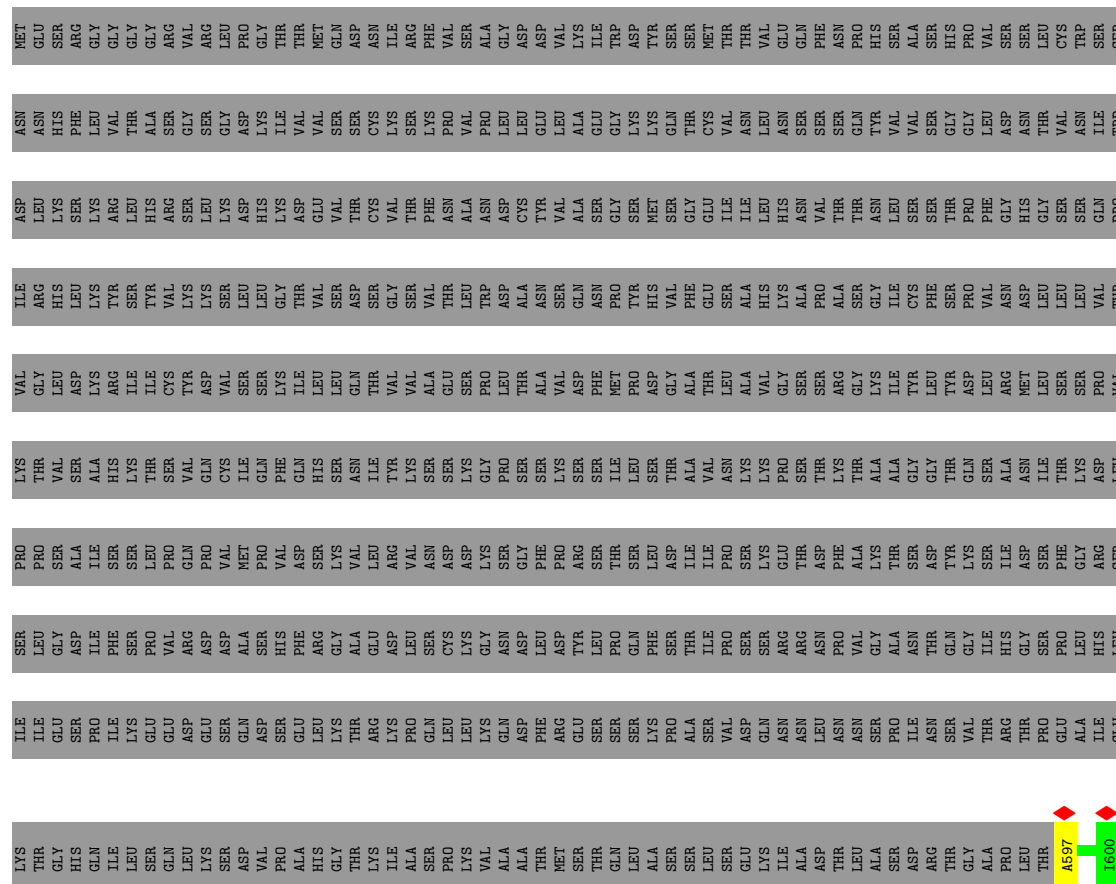






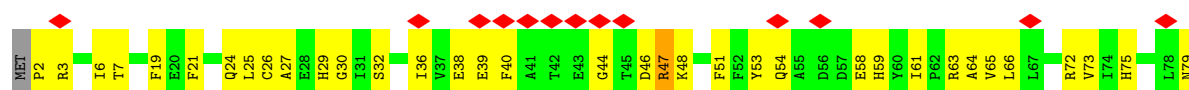
• Molecule 7: NEDD1 gamma-tubulin ring complex targeting factor L homeolog

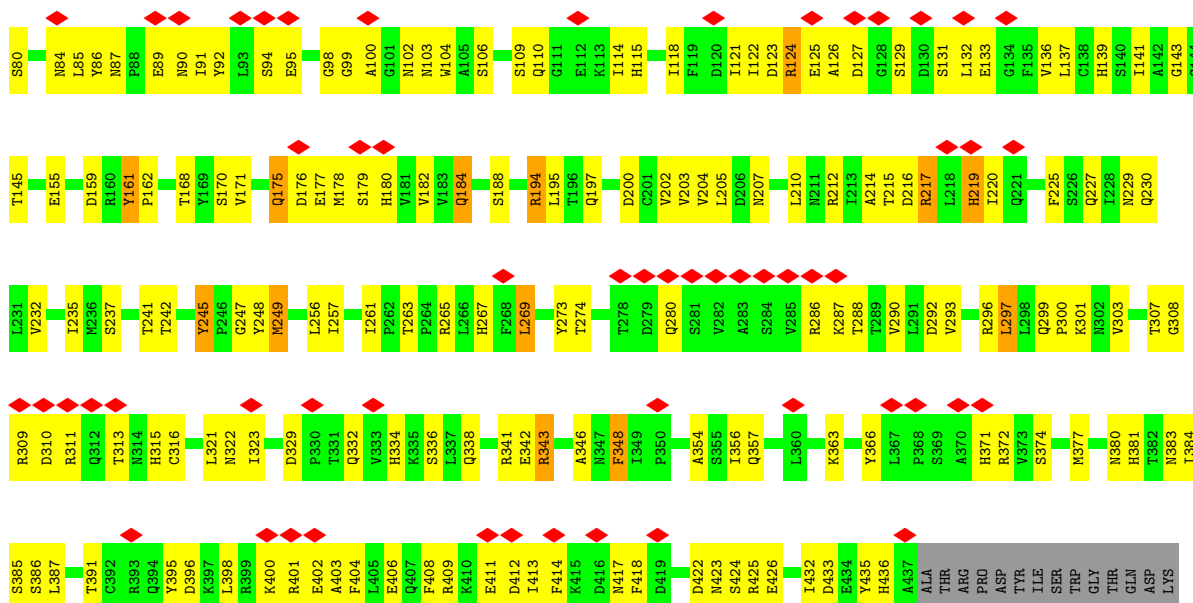
Chain X: 89%



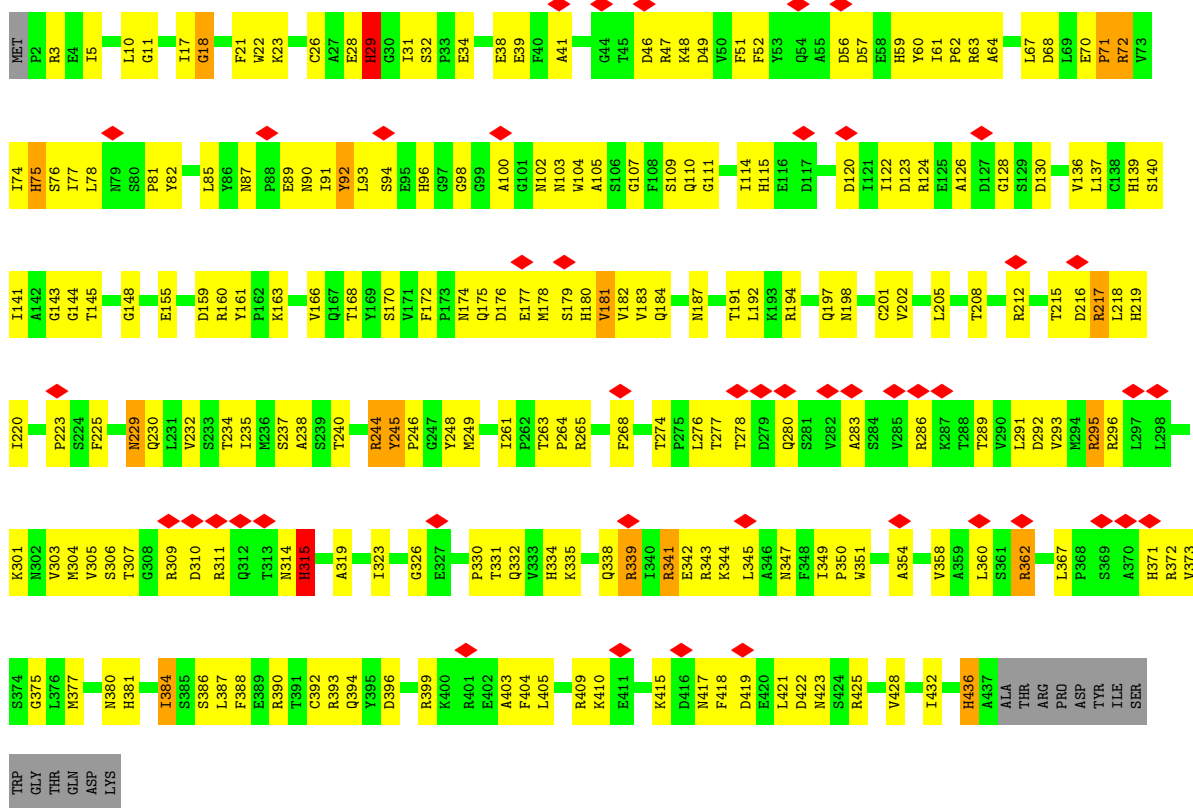
• Molecule 8: Tubulin gamma-1 chain

Chain a: 15% 51% 43%

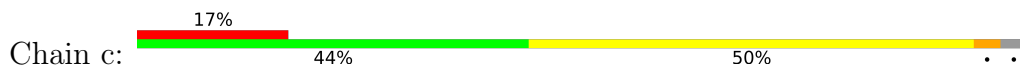


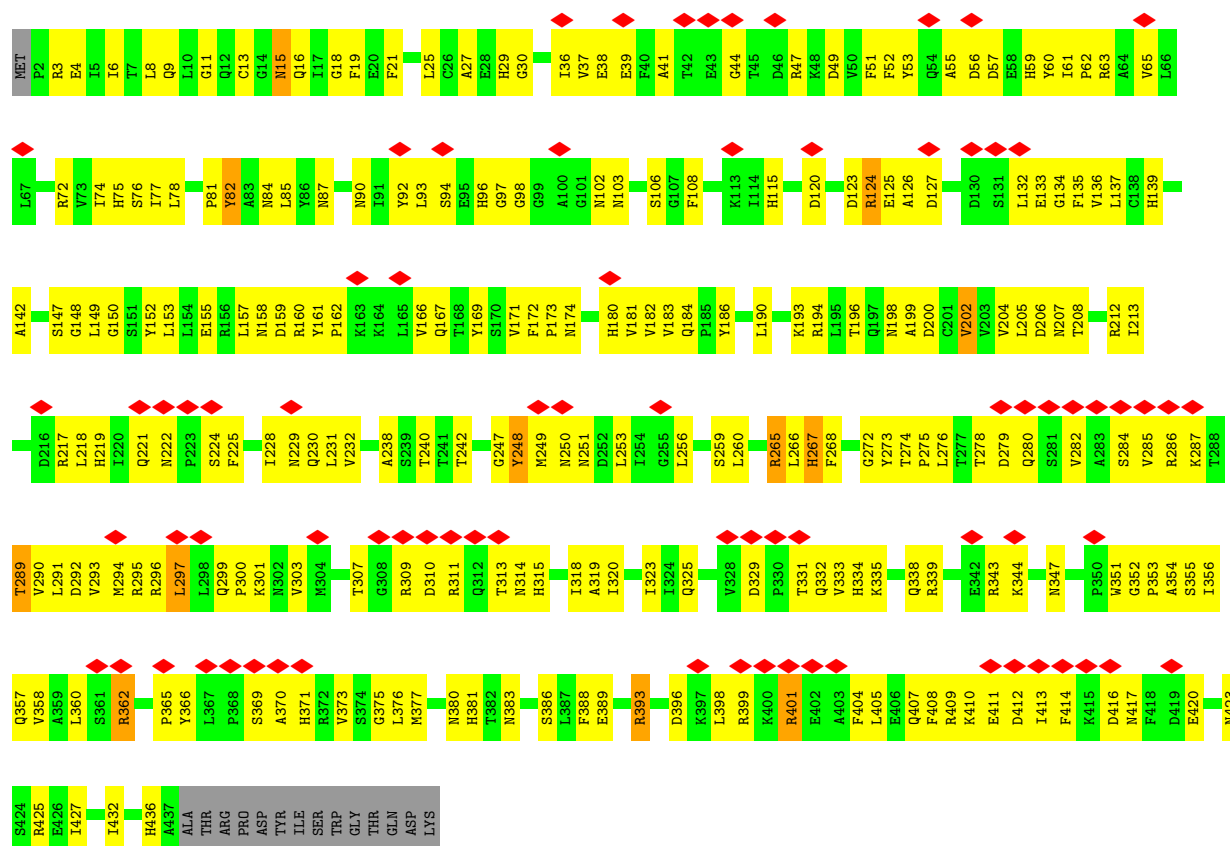


• Molecule 8: Tubulin gamma-1 chain

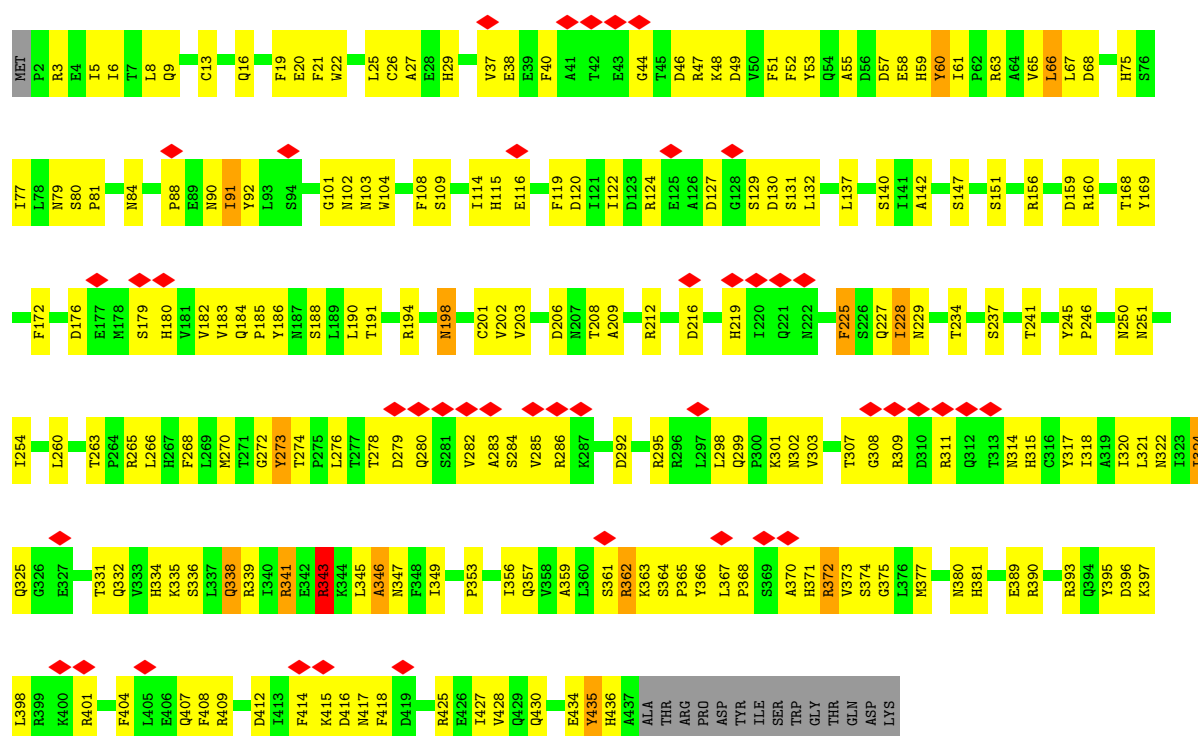


• Molecule 8: Tubulin gamma-1 chain

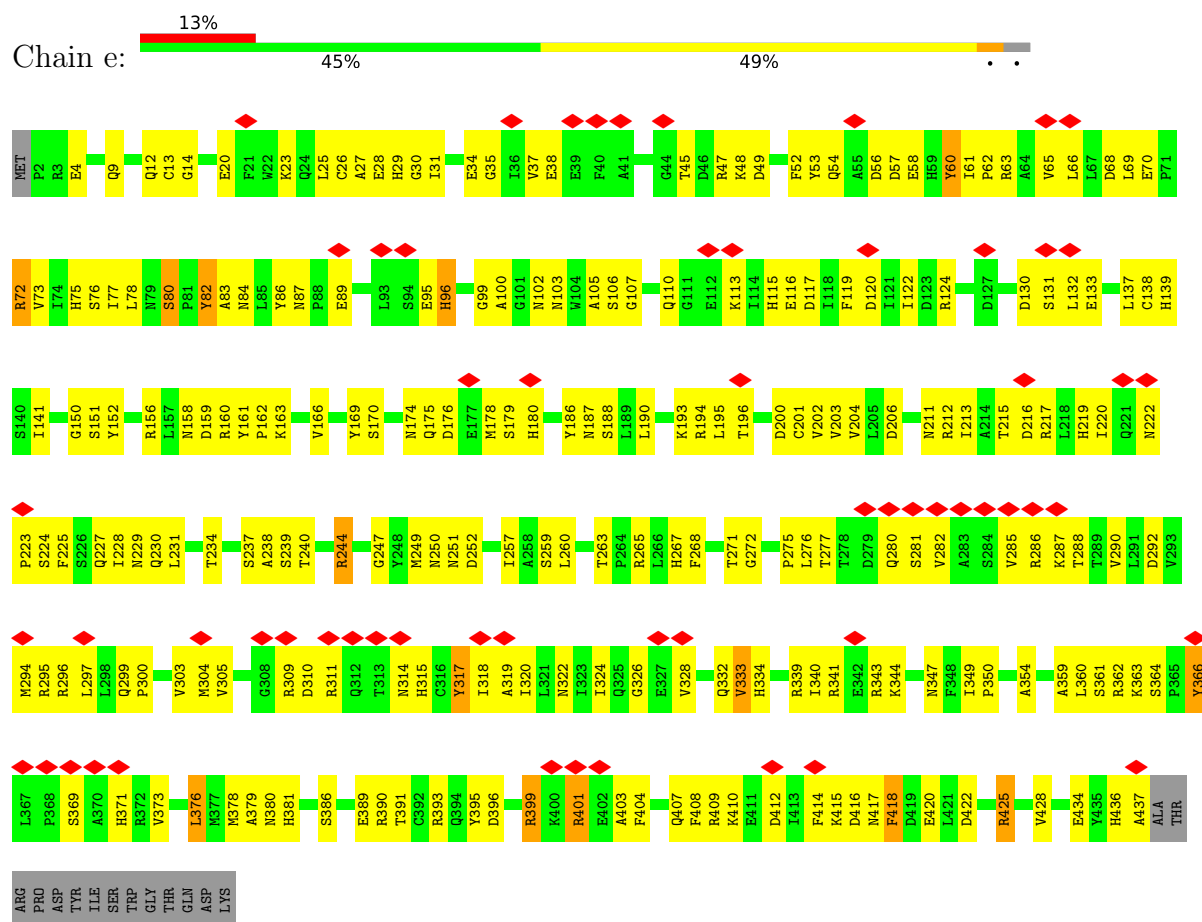




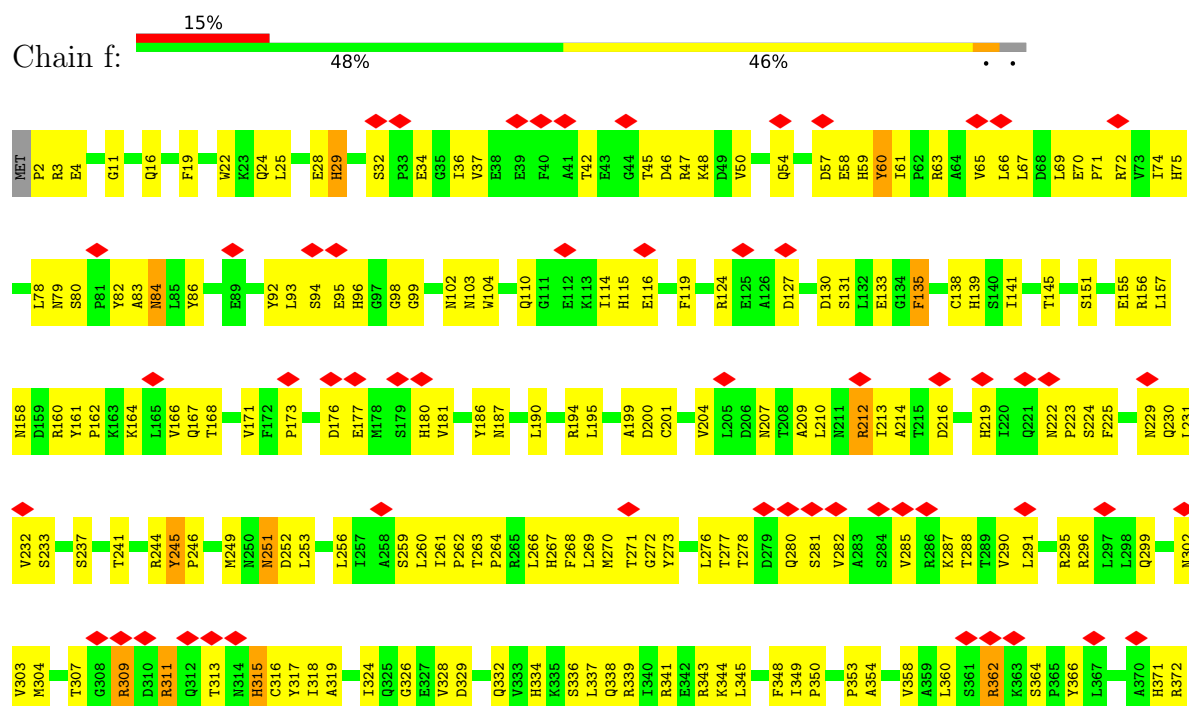
• Molecule 8: Tubulin gamma-1 chain

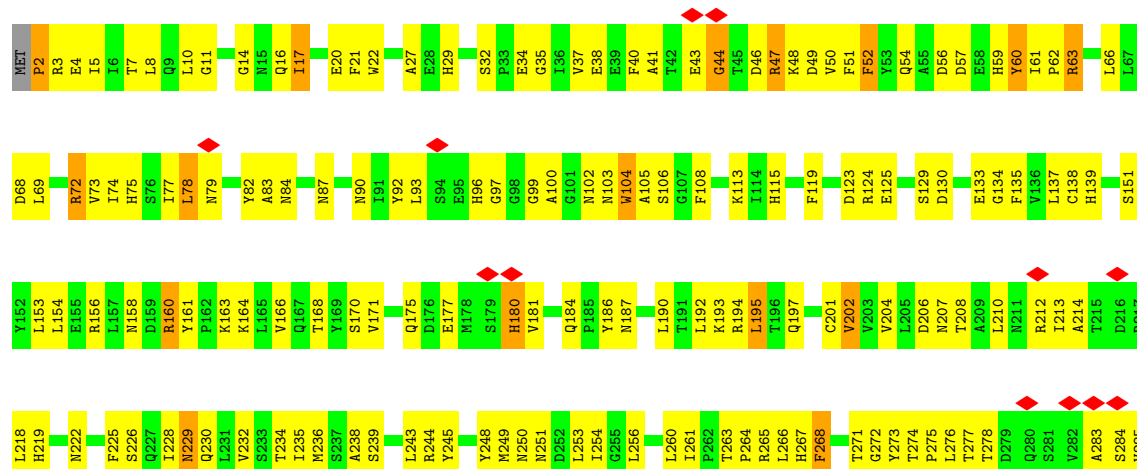


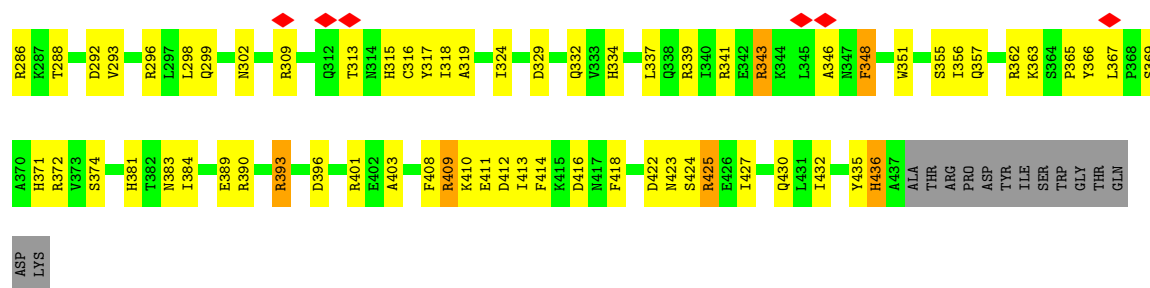
- Molecule 8: Tubulin gamma-1 chain



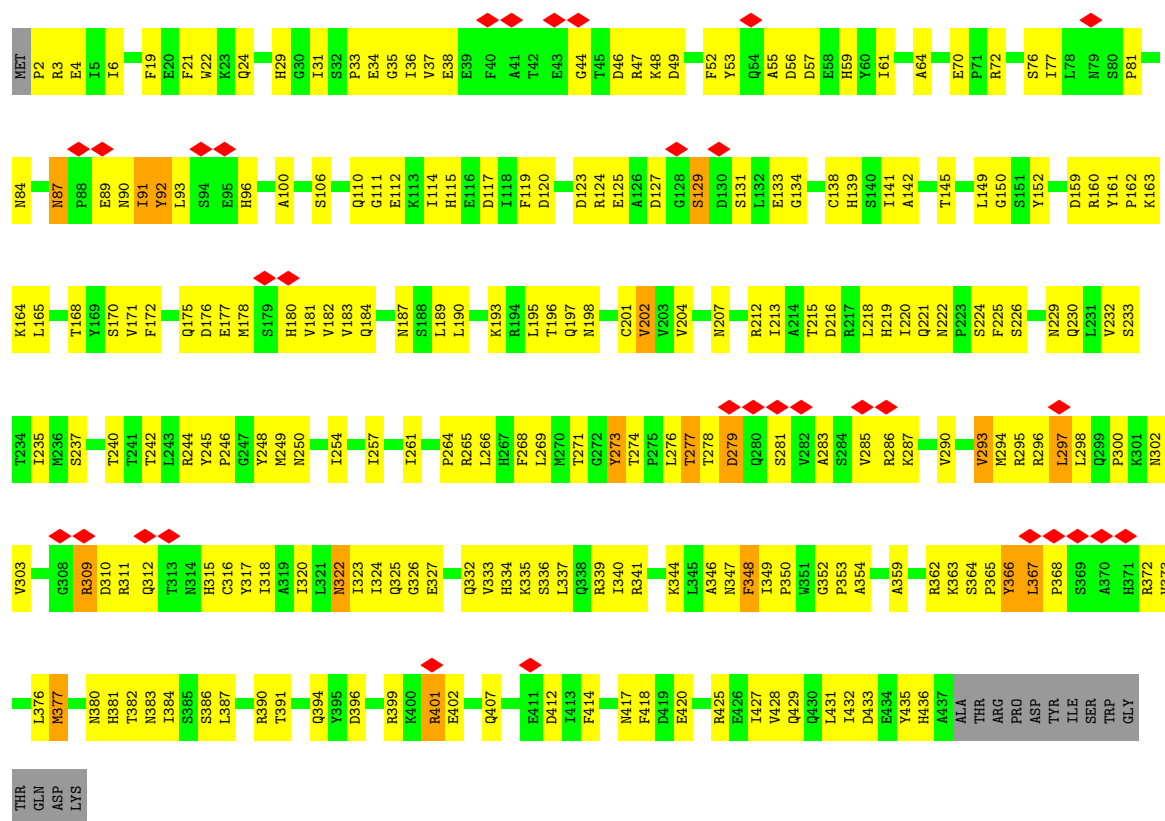
- Molecule 8: Tubulin gamma-1 chain



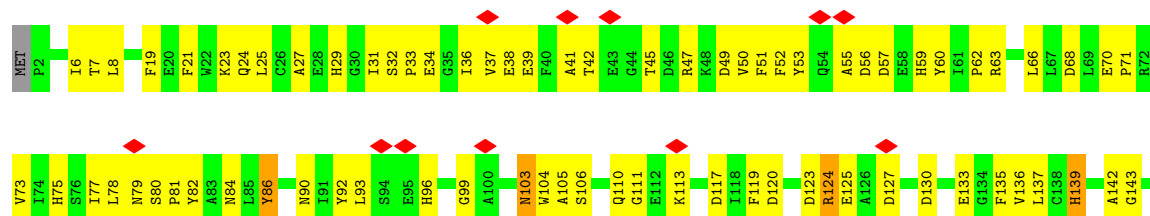
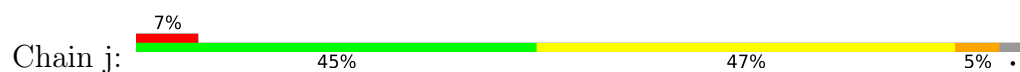


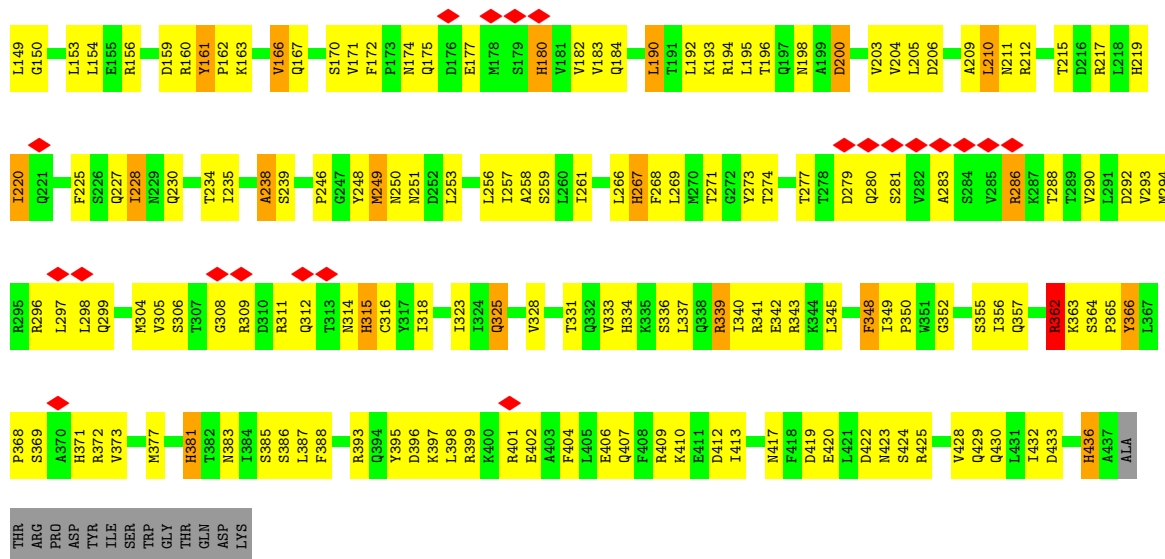


• Molecule 8: Tubulin gamma-1 chain

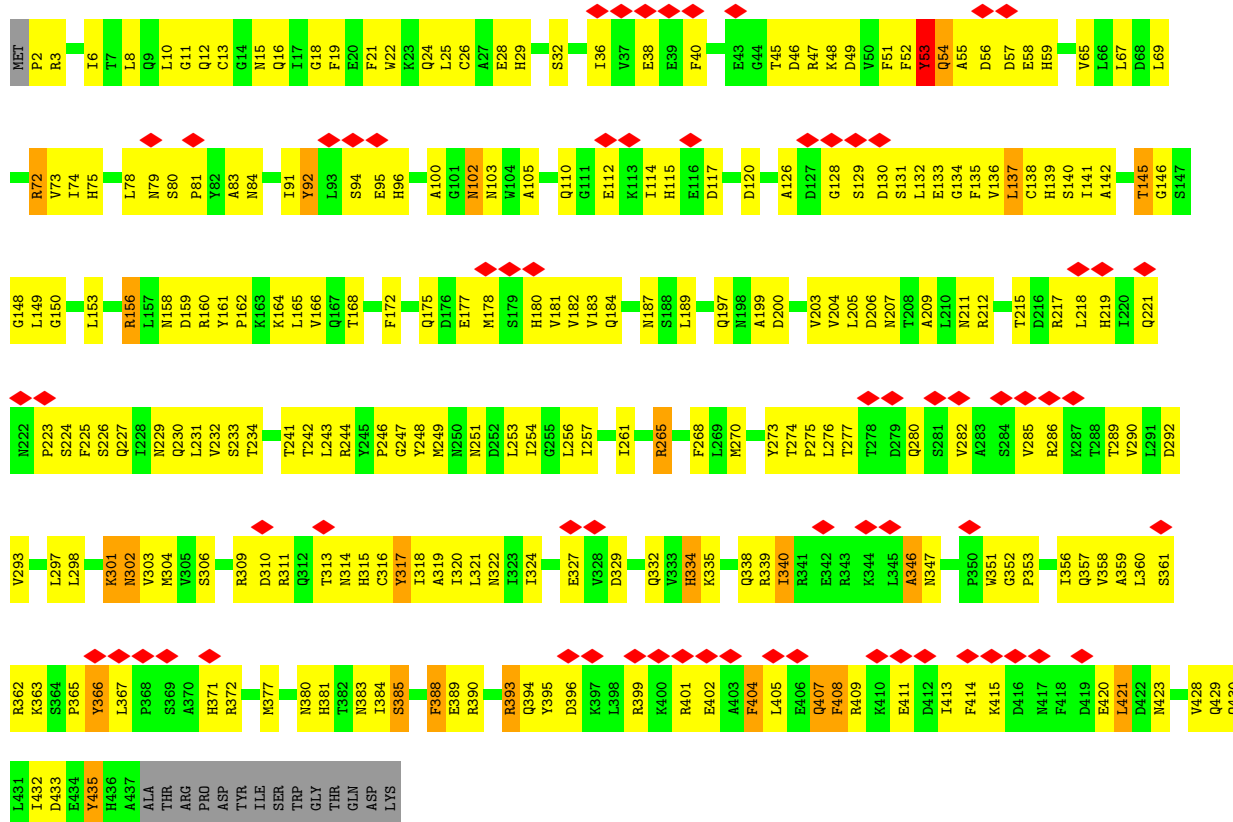


• Molecule 8: Tubulin gamma-1 chain





• Molecule 8: Tubulin gamma-1 chain

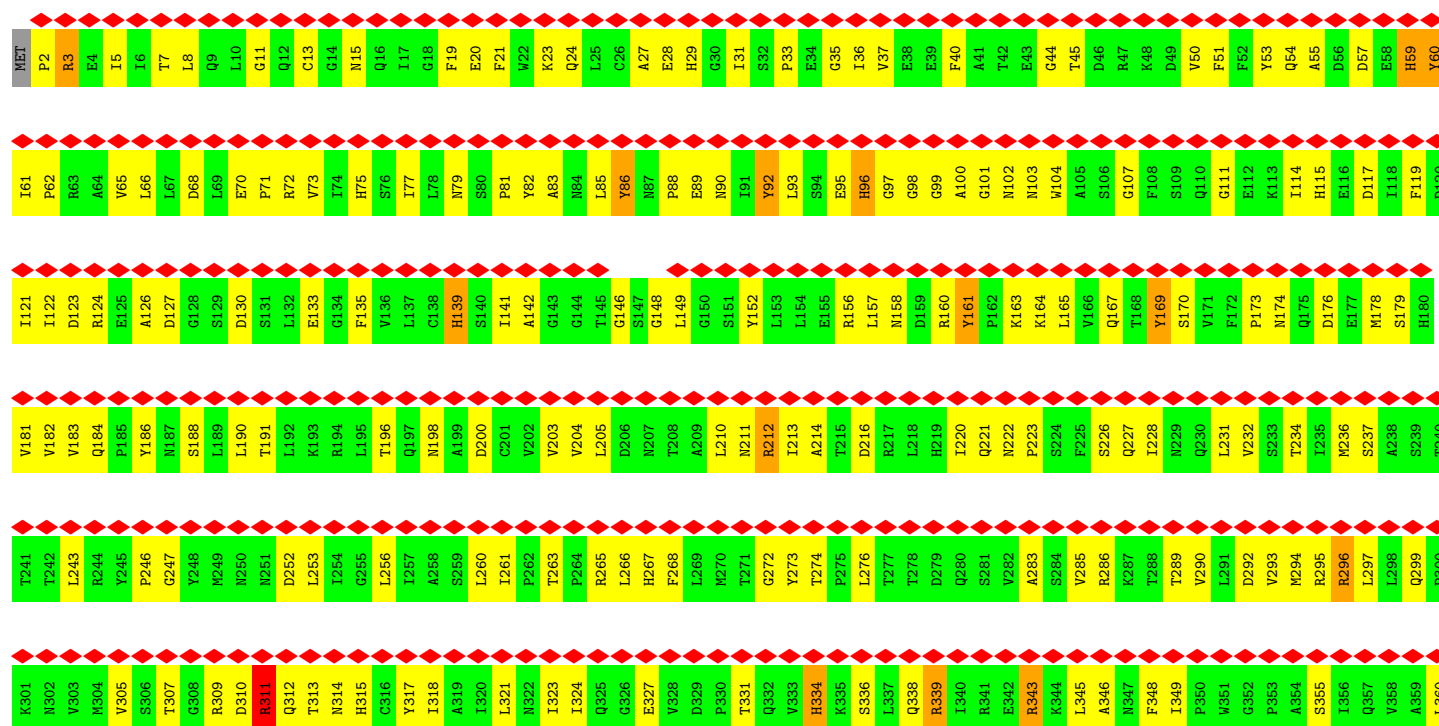


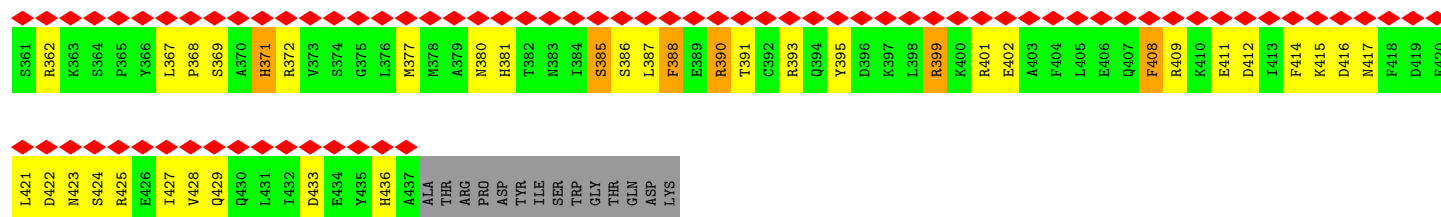
• Molecule 8: Tubulin gamma-1 chain





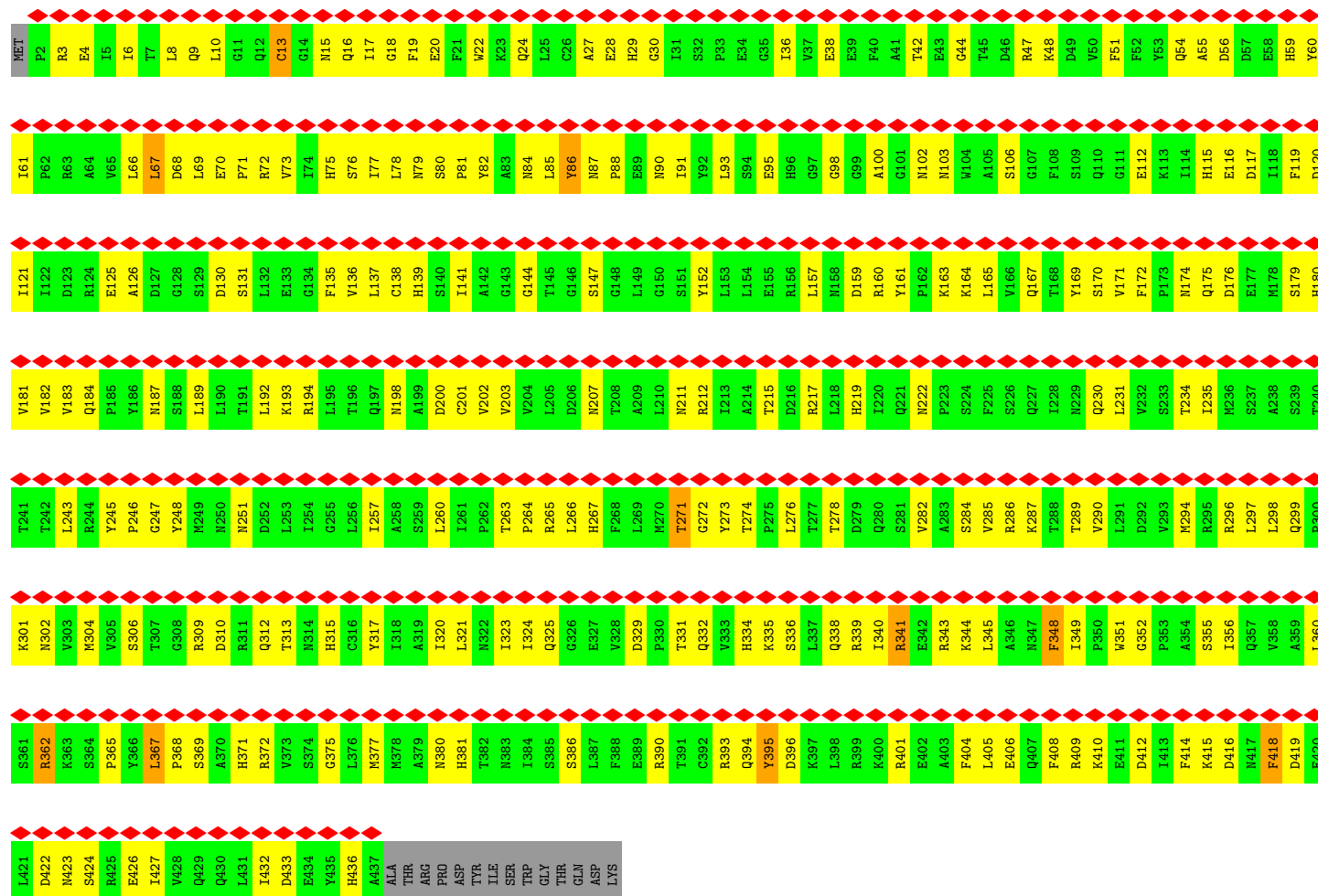
• Molecule 8: Tubulin gamma-1 chain





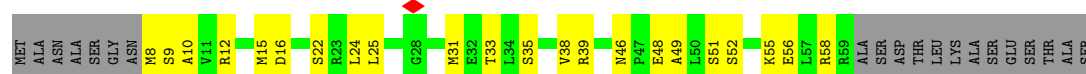
• Molecule 8: Tubulin gamma-1 chain

Chain n: . .

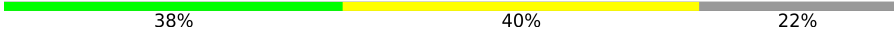


• Molecule 9: Mitotic-spindle organizing protein 1

Chain o: . .

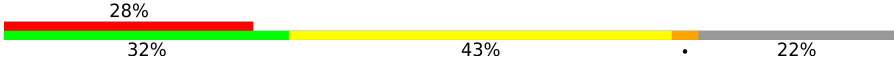


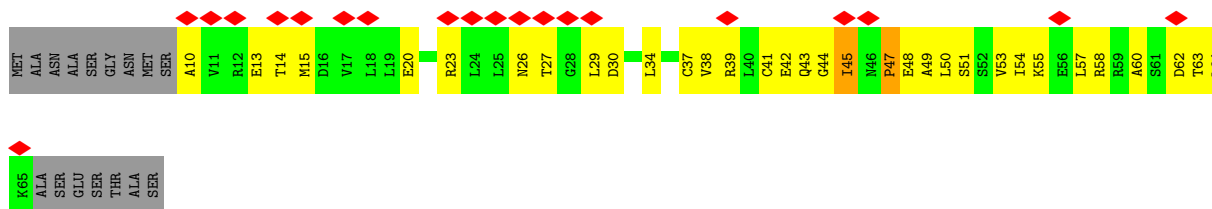
• Molecule 9: Mitotic-spindle organizing protein 1

Chain p: 



• Molecule 9: Mitotic-spindle organizing protein 1

Chain q: 



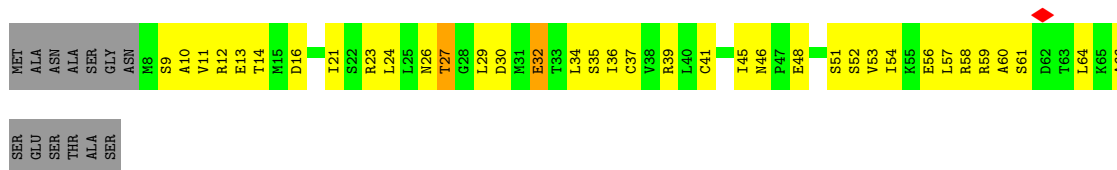
• Molecule 9: Mitotic-spindle organizing protein 1

Chain r: 



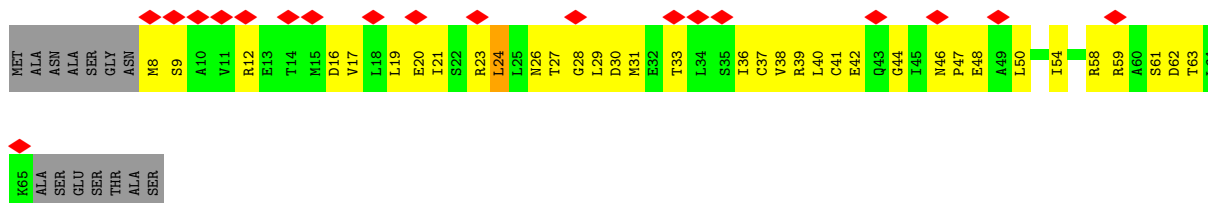
• Molecule 9: Mitotic-spindle organizing protein 1

Chain s: 



• Molecule 9: Mitotic-spindle organizing protein 1

Chain t: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	299022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.276	Depositor
Minimum map value	-0.152	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0217	Depositor
Map size (Å)	547.8528, 547.8528, 547.8528	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4267, 1.4267, 1.4267	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	A	2.23	151/4614 (3.3%)	2.38	288/6236 (4.6%)
1	C	2.20	165/4614 (3.6%)	2.30	241/6236 (3.9%)
1	E	2.21	139/4603 (3.0%)	2.31	230/6221 (3.7%)
1	G	2.26	166/4614 (3.6%)	2.30	240/6236 (3.8%)
1	M	2.22	169/4598 (3.7%)	2.27	203/6215 (3.3%)
2	B	2.24	168/5227 (3.2%)	2.36	280/7060 (4.0%)
2	D	2.21	172/5227 (3.3%)	2.34	298/7060 (4.2%)
2	F	2.23	181/5227 (3.5%)	2.33	272/7060 (3.9%)
2	H	2.23	170/5227 (3.3%)	2.27	251/7060 (3.6%)
2	N	2.23	156/5227 (3.0%)	2.32	263/7060 (3.7%)
2	O	2.30	27/764 (3.5%)	2.42	48/1026 (4.7%)
2	Q	2.23	26/892 (2.9%)	2.51	68/1199 (5.7%)
2	R	2.30	24/805 (3.0%)	2.64	79/1081 (7.3%)
2	S	2.31	37/892 (4.1%)	2.62	82/1199 (6.8%)
2	T	2.27	25/764 (3.3%)	2.59	72/1026 (7.0%)
3	I	2.26	164/4738 (3.5%)	2.32	277/6416 (4.3%)
3	K	2.41	169/4738 (3.6%)	2.36	268/6416 (4.2%)
4	J	2.34	170/5372 (3.2%)	2.36	313/7271 (4.3%)
5	L	2.20	195/6435 (3.0%)	2.37	356/8710 (4.1%)
6	P	2.25	104/2954 (3.5%)	2.28	138/4003 (3.4%)
7	U	2.23	19/640 (3.0%)	2.58	47/854 (5.5%)
7	V	2.15	18/640 (2.8%)	2.60	55/854 (6.4%)
7	W	2.31	26/640 (4.1%)	2.65	61/854 (7.1%)
7	X	2.19	20/640 (3.1%)	2.56	49/854 (5.7%)
8	a	2.23	115/3551 (3.2%)	2.37	200/4815 (4.2%)
8	b	2.25	121/3551 (3.4%)	2.35	213/4815 (4.4%)
8	c	2.35	152/3551 (4.3%)	2.35	205/4815 (4.3%)
8	d	2.31	140/3551 (3.9%)	2.32	168/4815 (3.5%)
8	e	2.25	116/3551 (3.3%)	2.41	219/4815 (4.5%)
8	f	2.28	128/3551 (3.6%)	2.36	196/4815 (4.1%)
8	g	2.22	106/3551 (3.0%)	2.33	198/4815 (4.1%)
8	h	2.27	128/3551 (3.6%)	2.35	208/4815 (4.3%)
8	i	2.28	142/3551 (4.0%)	2.39	208/4815 (4.3%)
8	j	2.29	134/3551 (3.8%)	2.36	199/4815 (4.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	k	2.51	139/3551 (3.9%)	2.37	219/4815 (4.5%)
8	l	2.25	124/3551 (3.5%)	2.39	214/4815 (4.4%)
8	m	2.27	144/3551 (4.1%)	2.34	187/4815 (3.9%)
8	n	2.30	140/3551 (3.9%)	2.31	189/4815 (3.9%)
9	o	2.27	12/403 (3.0%)	2.51	26/541 (4.8%)
9	p	2.25	10/429 (2.3%)	2.65	37/577 (6.4%)
9	q	2.33	14/432 (3.2%)	2.69	43/581 (7.4%)
9	r	2.27	12/454 (2.6%)	2.56	36/610 (5.9%)
9	s	2.30	18/451 (4.0%)	2.65	48/606 (7.9%)
9	t	2.33	25/446 (5.6%)	2.68	40/599 (6.7%)
All	All	2.27	4581/132421 (3.5%)	2.36	7532/179131 (4.2%)

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	17
1	C	0	20
1	E	0	17
1	G	0	18
1	M	0	19
2	B	0	24
2	D	0	12
2	F	0	19
2	H	0	27
2	N	0	23
2	O	0	2
2	Q	0	5
2	R	0	3
2	S	0	3
2	T	0	1
3	I	0	16
3	K	0	19
4	J	0	21
5	L	0	31
6	P	0	8
7	U	0	1
7	V	0	2
7	W	0	1
7	X	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	a	0	12
8	b	0	13
8	c	0	10
8	d	0	9
8	e	0	13
8	f	0	12
8	g	0	12
8	h	0	13
8	i	0	7
8	j	0	15
8	k	0	13
8	l	0	10
8	m	0	14
8	n	0	8
All	All	0	473

The worst 5 of 4581 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	515	ARG	CZ-NH2	63.18	2.15	1.33
3	I	16	ILE	CG1-CD1	35.98	2.92	1.51
8	k	435	TYR	CG-CD2	33.11	2.08	1.39
4	J	242	TRP	CD2-CE3	31.39	1.90	1.40
8	k	435	TYR	CG-CD1	30.15	2.02	1.39

The worst 5 of 7532 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	515	ARG	NE-CZ-NH1	-27.59	93.91	121.50
5	L	1469	VAL	N-CA-C	-15.33	96.72	113.43
8	f	139	HIS	CA-CB-CG	14.37	128.17	113.80
8	k	187	ASN	CA-CB-CG	14.11	126.71	112.60
3	K	515	ARG	NE-CZ-NH2	13.77	131.59	119.20

There are no chirality outliers.

5 of 473 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	ARG	Sidechain
1	A	326	TYR	Sidechain
1	A	361	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	377	TYR	Sidechain
1	A	386	TYR	Sidechain

5.2 Too-close contacts

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	4519	0	4476	17	0
1	C	4519	0	4476	11	0
1	E	4508	0	4466	16	0
1	G	4519	0	4476	16	0
1	M	4503	0	4456	20	0
2	B	5118	0	5103	11	0
2	D	5118	0	5103	17	0
2	F	5118	0	5103	18	0
2	H	5118	0	5103	14	0
2	N	5118	0	5103	17	0
2	O	753	0	779	5	0
2	Q	878	0	903	2	0
2	R	794	0	814	1	0
2	S	878	0	903	8	0
2	T	753	0	779	0	0
3	I	4635	0	4670	41	0
3	K	4635	0	4670	35	0
4	J	5252	0	5318	49	0
5	L	6303	0	6356	18	0
6	P	2892	0	2854	4	0
7	U	634	0	635	4	0
7	V	634	0	635	1	0
7	W	634	0	635	2	0
7	X	634	0	635	2	0
8	a	3479	0	3428	6	0
8	b	3479	0	3428	8	0
8	c	3479	0	3428	13	0
8	d	3479	0	3428	10	0
8	e	3479	0	3428	7	0
8	f	3479	0	3428	9	0
8	g	3479	0	3428	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	h	3479	0	3428	18	0
8	i	3479	0	3428	14	0
8	j	3479	0	3428	18	0
8	k	3479	0	3428	33	0
8	l	3479	0	3428	16	0
8	m	3479	0	3428	10	0
8	n	3479	0	3428	10	0
9	o	403	0	426	1	0
9	p	429	0	446	1	0
9	q	432	0	457	2	0
9	r	454	0	477	1	0
9	s	451	0	476	2	0
9	t	446	0	471	1	0
All	All	129788	0	129196	437	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 437 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:242:TRP:CZ3	4:J:242:TRP:CH2	1.79	1.66
4:J:242:TRP:CH2	4:J:242:TRP:CZ2	1.81	1.63
4:J:242:TRP:CZ3	4:J:242:TRP:CE3	1.77	1.62
4:J:242:TRP:CE3	4:J:242:TRP:CD2	1.90	1.58
4:J:242:TRP:CZ2	4:J:242:TRP:CE2	1.95	1.54

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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.

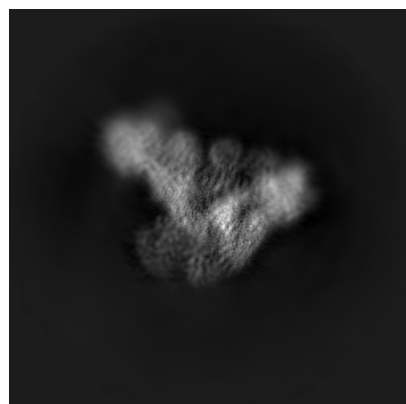
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52730. These allow visual inspection of the internal detail of the map and identification of artifacts.

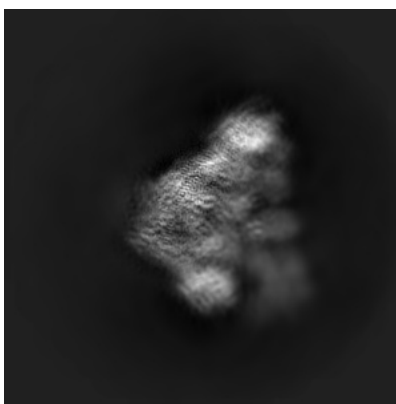
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

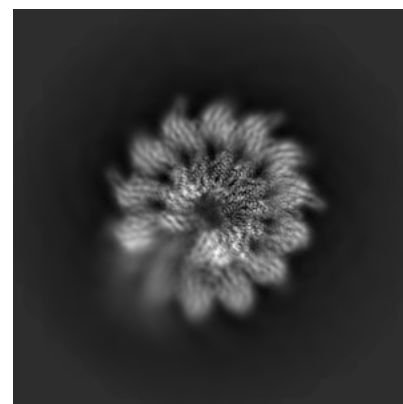
6.1.1 Primary map



X

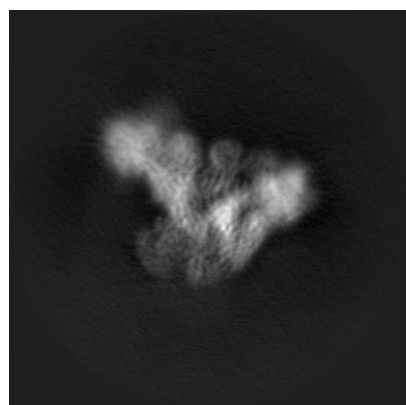


Y

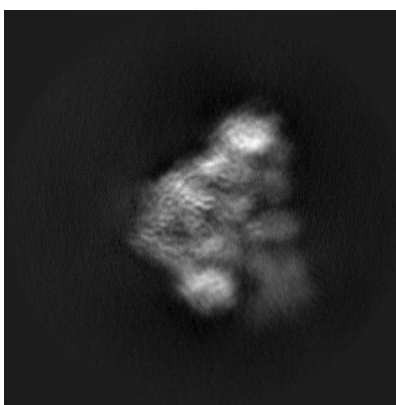


Z

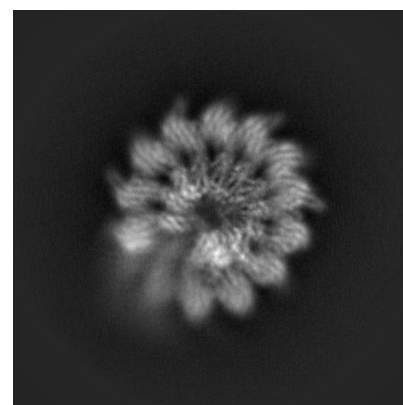
6.1.2 Raw map



X



Y

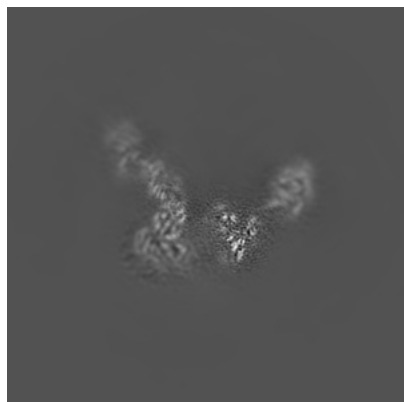


Z

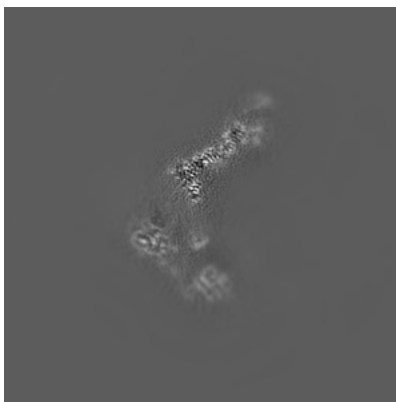
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

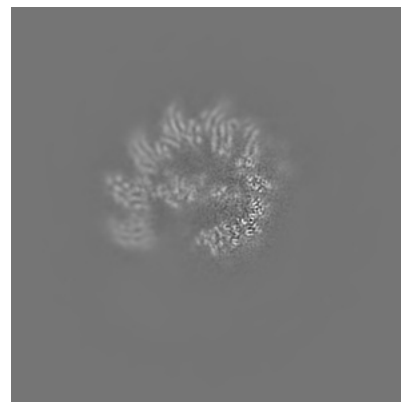
6.2.1 Primary map



X Index: 192

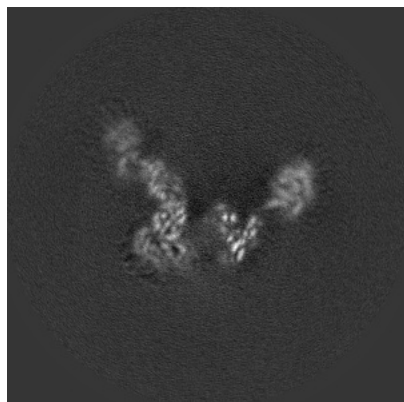


Y Index: 192

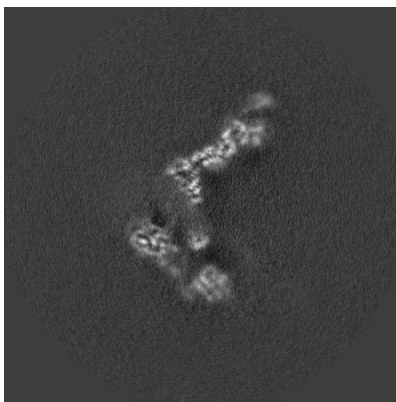


Z Index: 192

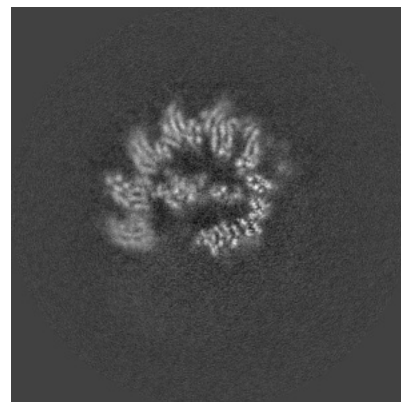
6.2.2 Raw map



X Index: 192



Y Index: 192

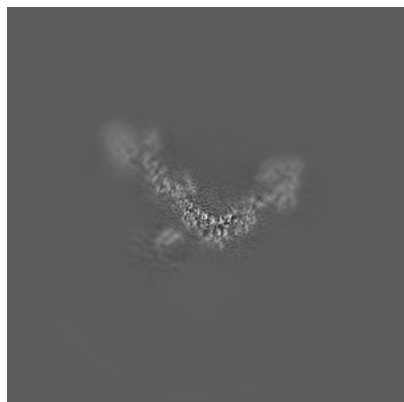


Z Index: 192

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

6.3 Largest variance slices [i](#)

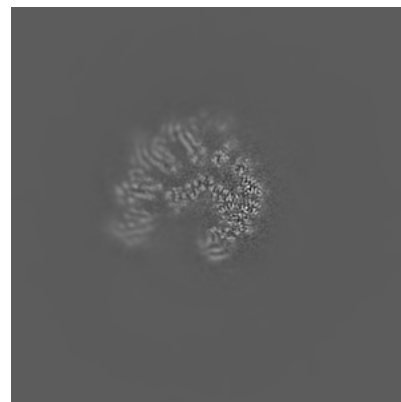
6.3.1 Primary map



X Index: 225

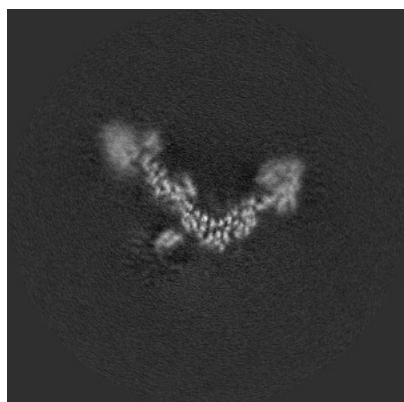


Y Index: 212

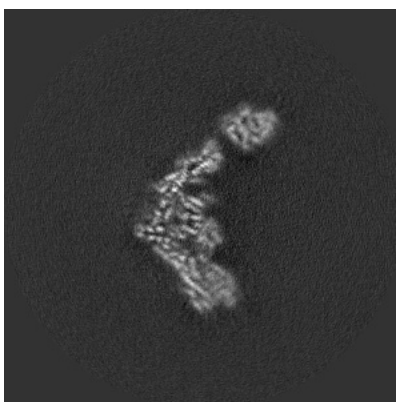


Z Index: 181

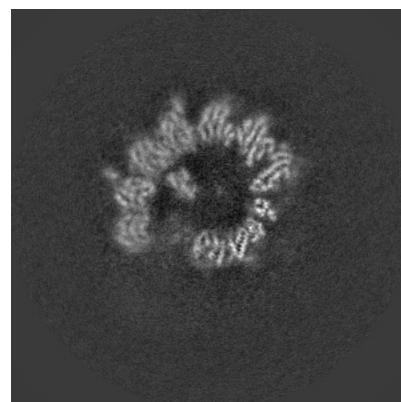
6.3.2 Raw map



X Index: 225



Y Index: 211

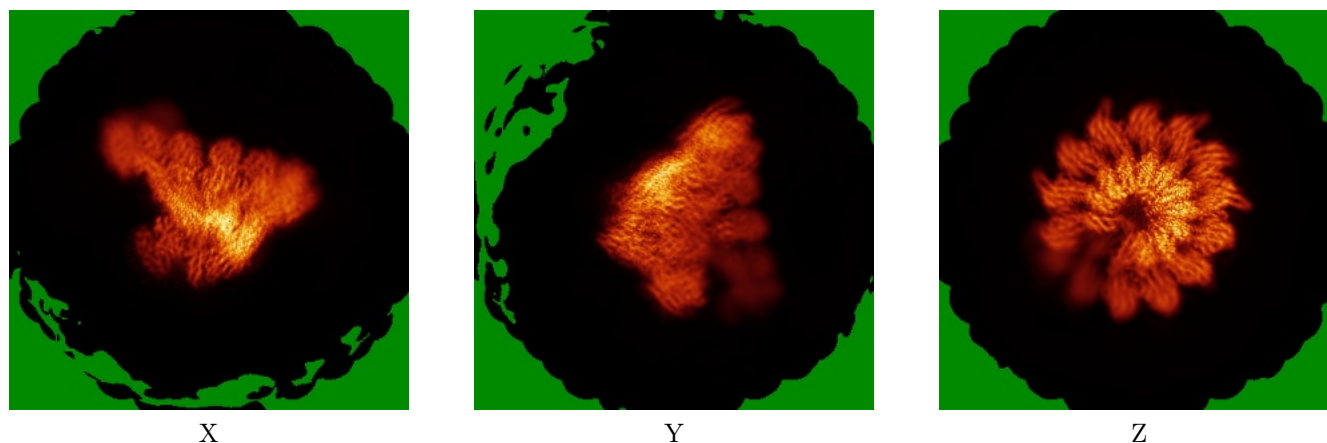


Z Index: 203

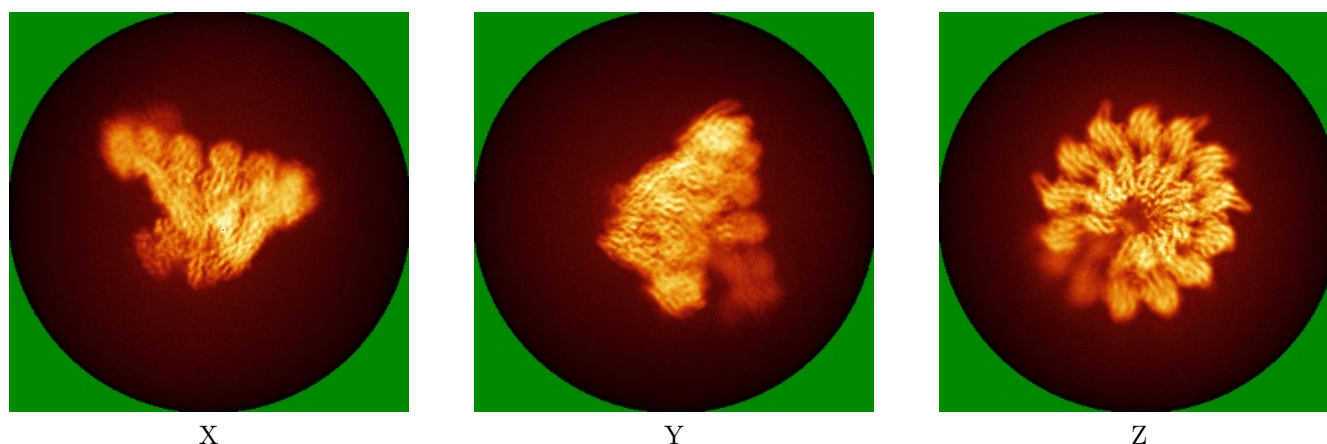
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

6.4.1 Primary map



6.4.2 Raw map



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.

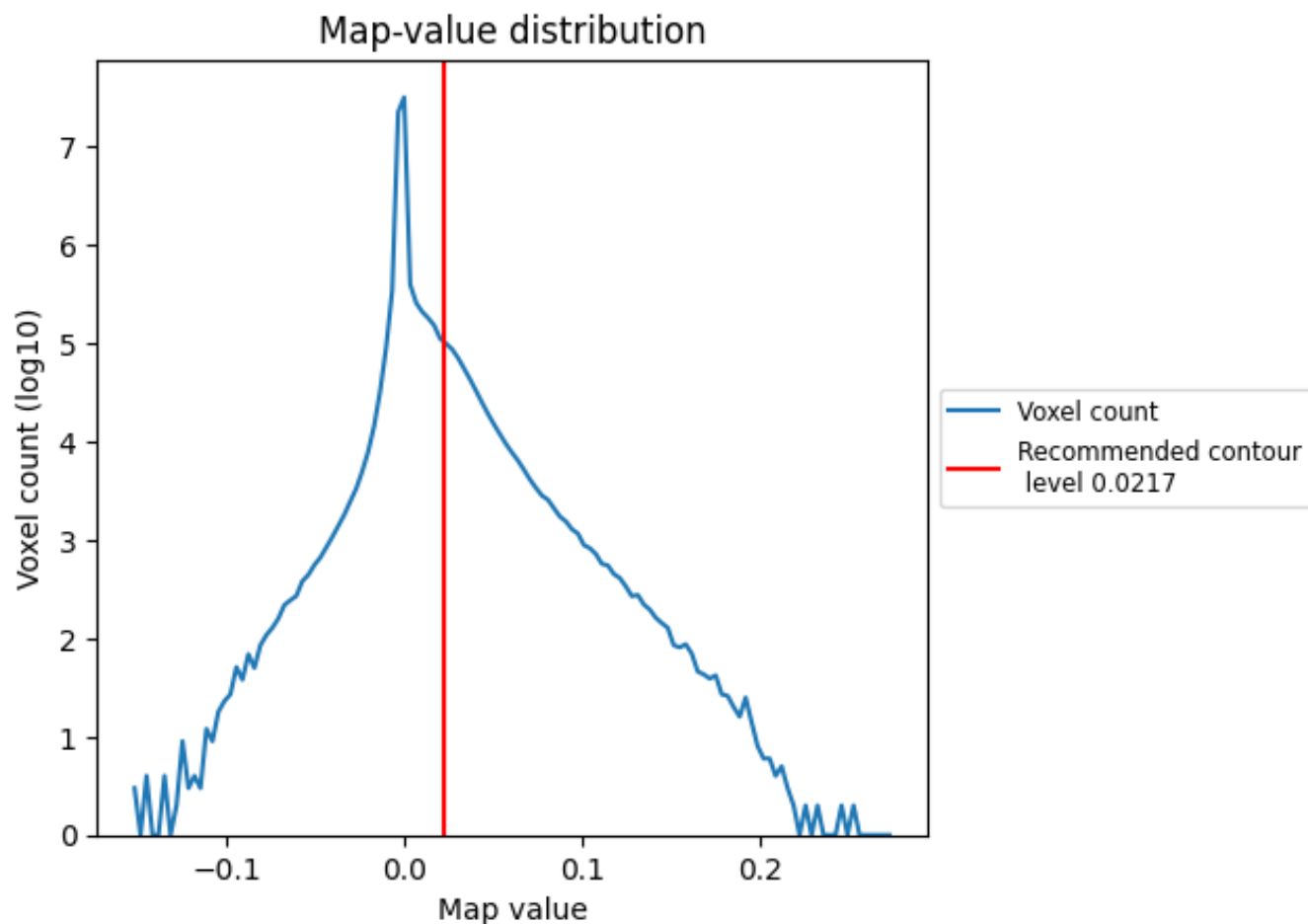
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

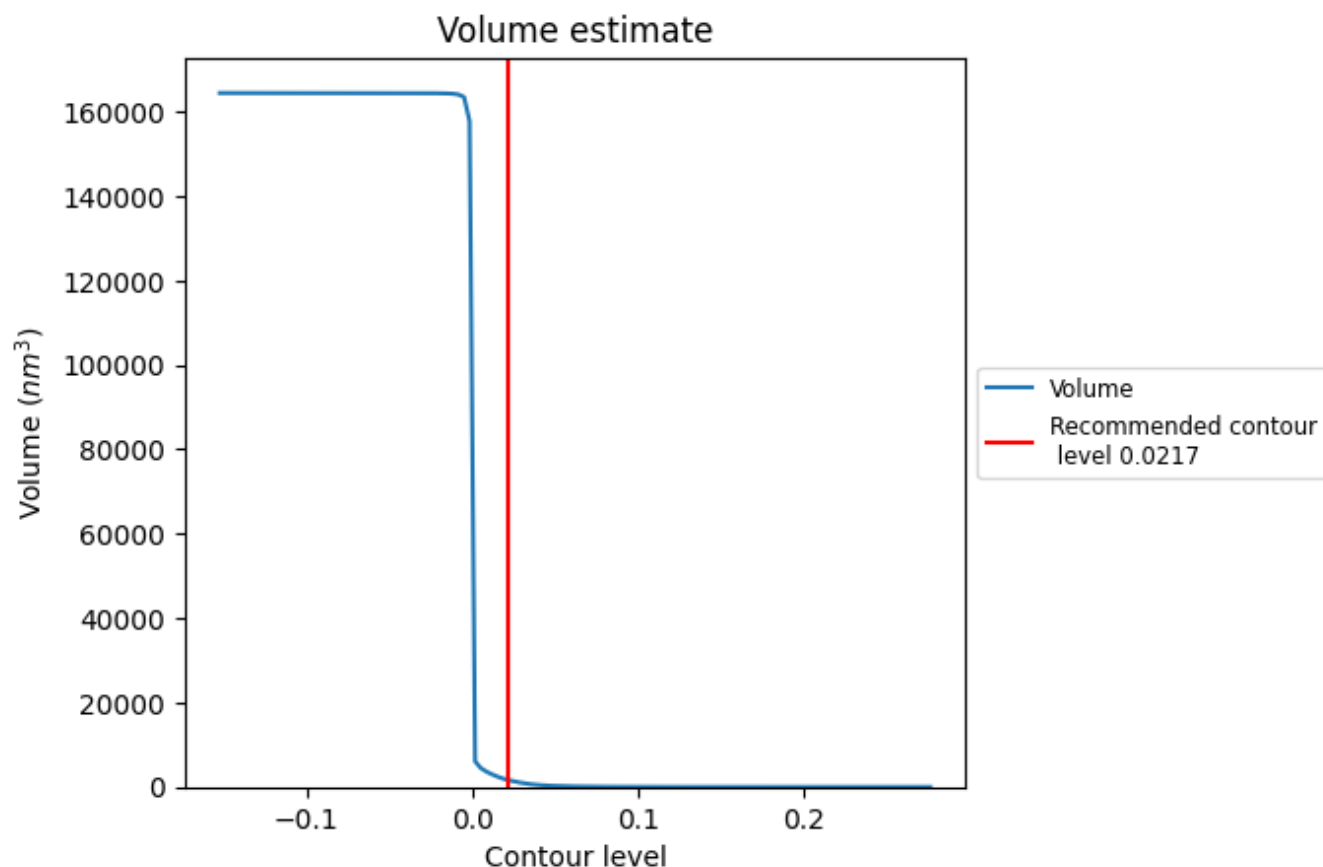
This section contains the results of statistical analysis of the map.

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.

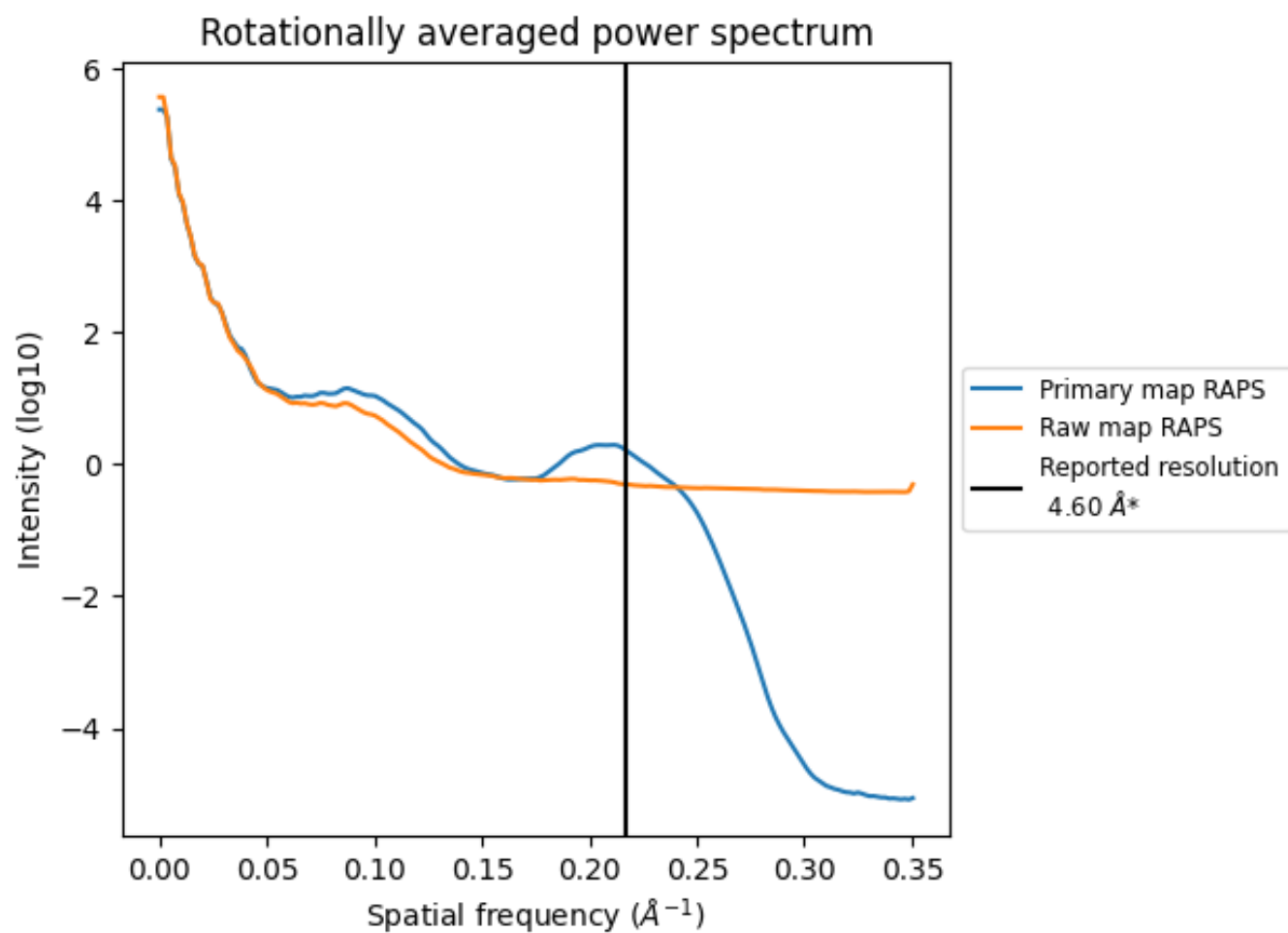
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1642 nm^3 ; this corresponds to an approximate mass of 1483 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 ⓘ

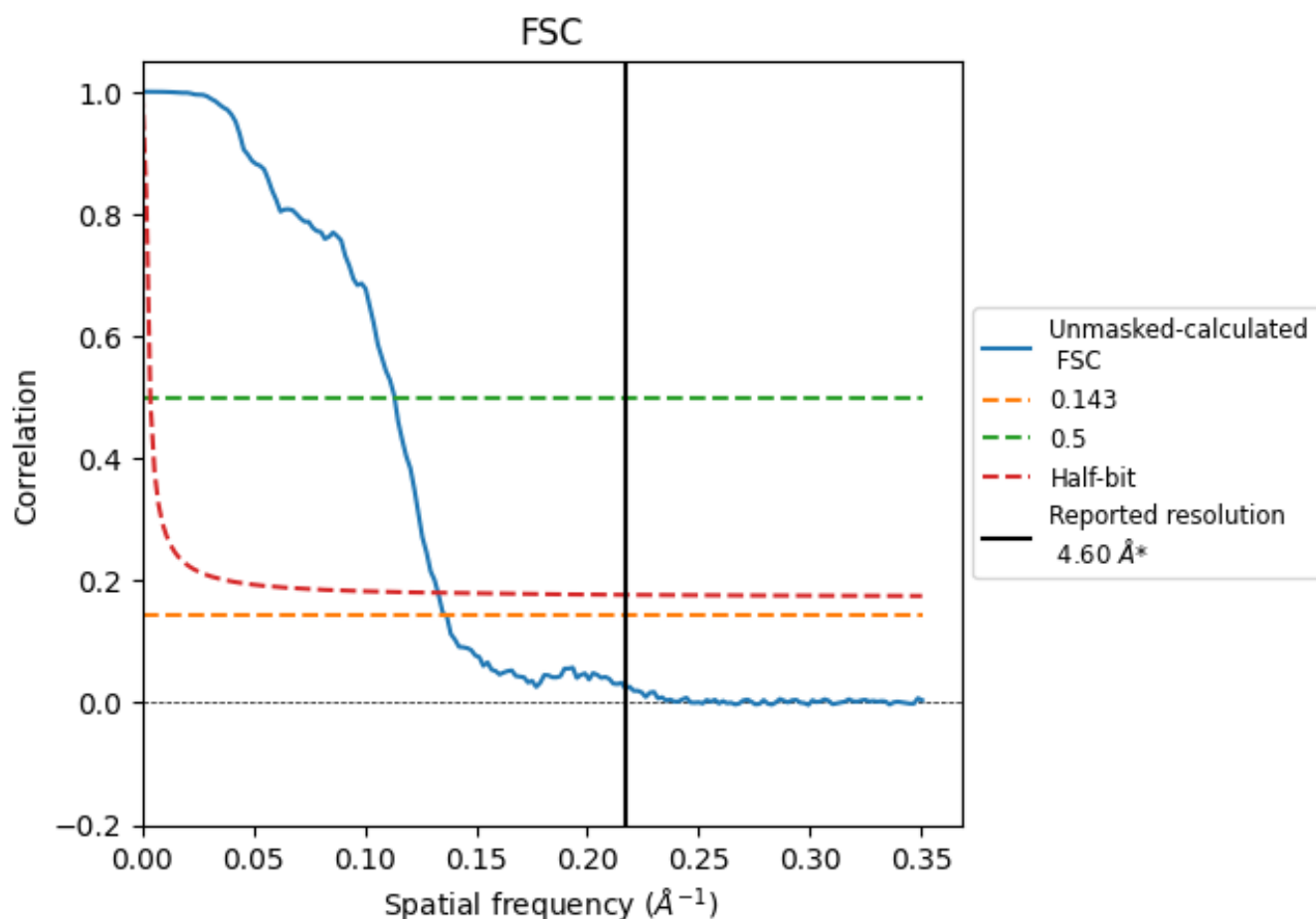


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

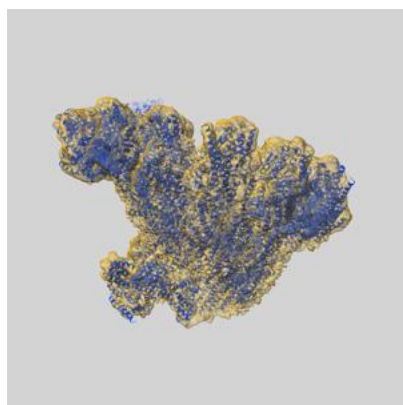
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.34	8.83	7.52

*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 7.34 differs from the reported value 4.6 by more than 10 %

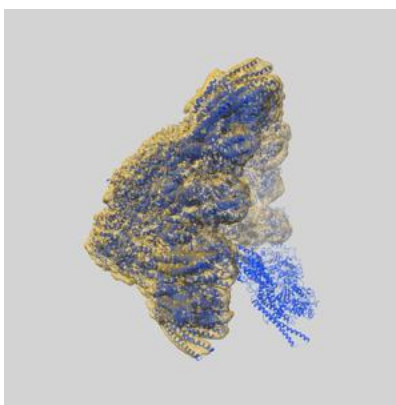
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52730 and PDB model 9I8N. Per-residue inclusion information can be found in section 3 on page 9.

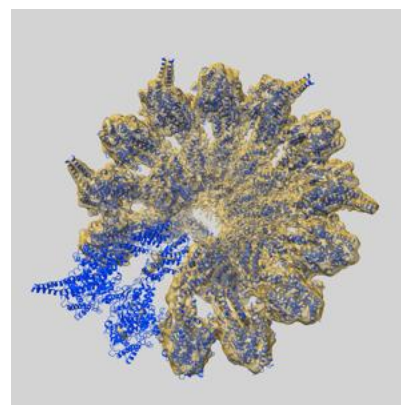
9.1 Map-model overlay [i](#)



X



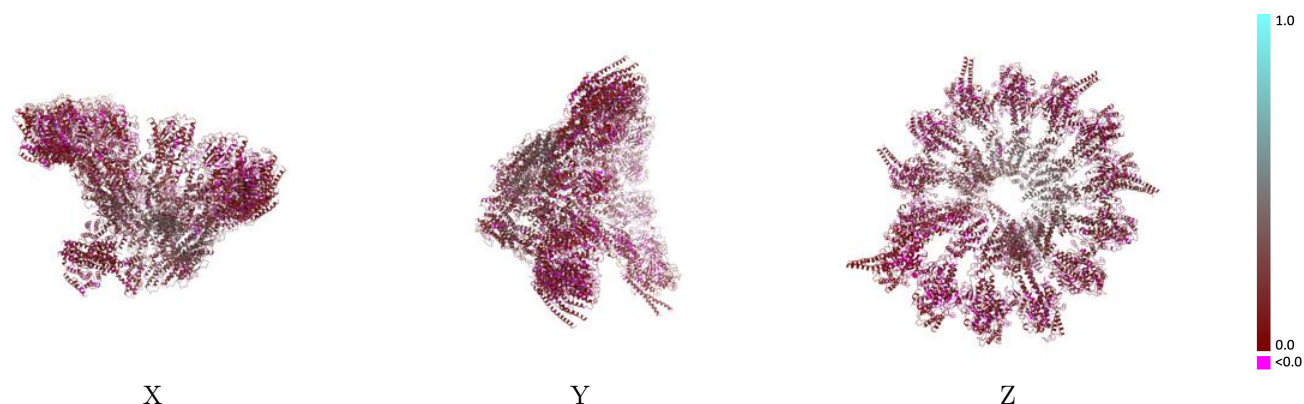
Y



Z

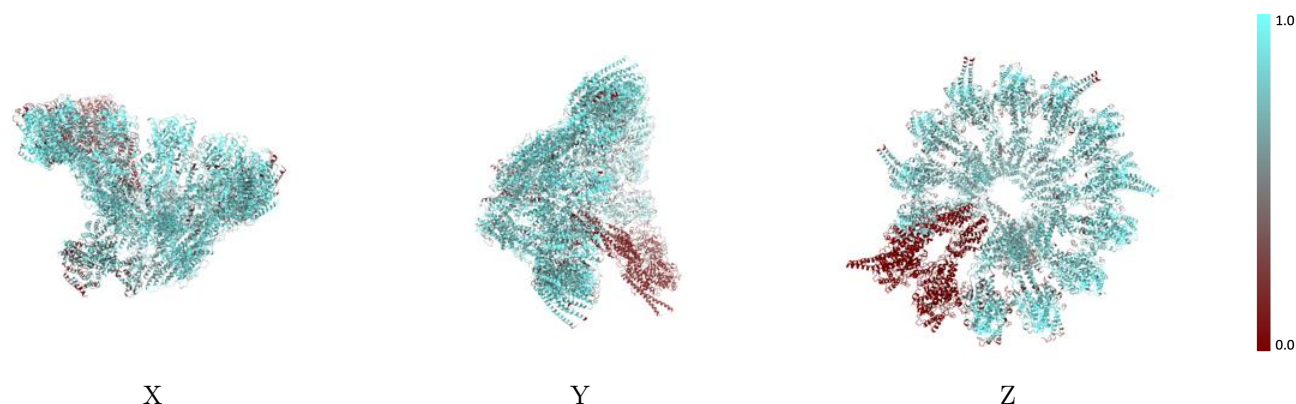
The images above show the 3D surface view of the map at the recommended contour level 0.0217 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



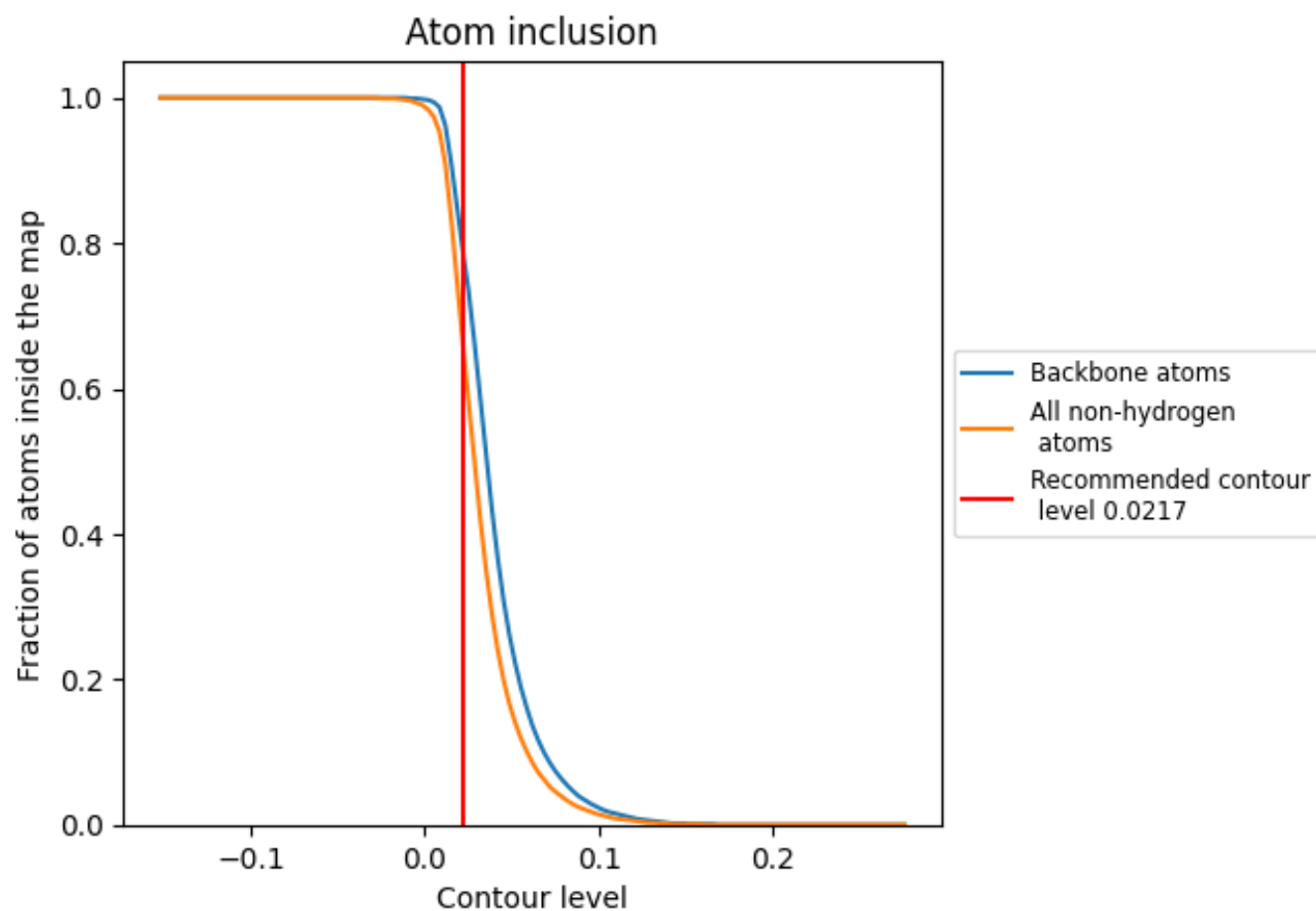
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0217).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0217) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6660	 0.1430
A	 0.7740	 0.1290
B	 0.7540	 0.1560
C	 0.7870	 0.1650
D	 0.7590	 0.1680
E	 0.8060	 0.1940
F	 0.7670	 0.1810
G	 0.8140	 0.2150
H	 0.8140	 0.2320
I	 0.8130	 0.2260
J	 0.7910	 0.1900
K	 0.7840	 0.1600
L	 0.7370	 0.1550
M	 0.0290	 0.0880
N	 0.0000	 0.0740
O	 0.8520	 0.3430
P	 0.7540	 0.2000
Q	 0.5180	 0.1330
R	 0.6590	 0.1460
S	 0.7170	 0.1400
T	 0.4200	 0.1080
U	 0.6280	 0.1310
V	 0.5880	 0.1160
W	 0.5800	 0.1340
X	 0.5700	 0.1220
a	 0.7340	 0.0960
b	 0.7730	 0.1170
c	 0.7230	 0.0790
d	 0.7610	 0.1110
e	 0.7380	 0.0950
f	 0.7420	 0.0980
g	 0.7940	 0.1220
h	 0.8270	 0.1600
i	 0.8150	 0.1450
j	 0.8150	 0.1260



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Chain	Atom inclusion	Q-score
k	 0.7680	 0.0960
l	 0.6540	 0.0830
m	 0.0050	 0.0440
n	 0.0000	 0.0440
o	 0.8400	 0.3530
p	 0.8430	 0.3180
q	 0.4740	 0.1220
r	 0.7050	 0.1580
s	 0.7480	 0.1700
t	 0.5090	 0.1410