



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:34 PM UTC

PDB ID : 7TNT / pdb_00007tnt
EMDB ID : EMD-26020
Title : The tubulin-based conoid from detergent-extract *Toxoplasma gondii* cells
Authors : Sun, S.Y.; Pintilie, G.D.; Chen, M.; Chiu, W.
Deposited on : 2022-01-21
Resolution : 9.30 Å (reported)
Based on initial model : 7MIZ

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:

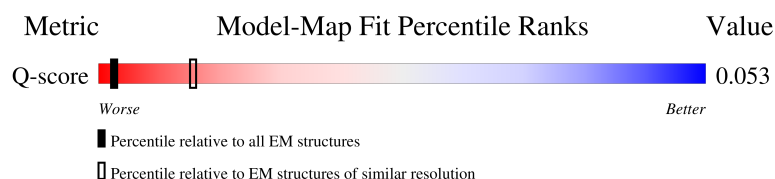
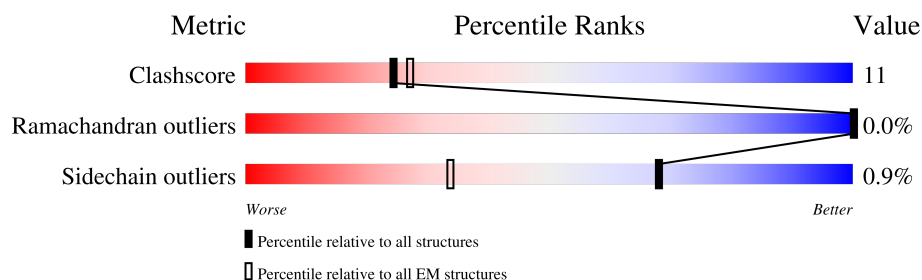
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	228 (8.80 - 9.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	2A	437	22% 71% 24% ..
1	2B	437	27% 74% 22% ..
1	2C	437	27% 81% 16% ..
1	2D	437	33% 75% 21% ..

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Mol	Chain	Length	Quality of chain
1	2E	437	
1	2F	437	
1	2G	437	
1	2H	437	
1	2I	437	
1	4A	437	
1	4B	437	
1	4C	437	
1	4D	437	
1	4E	437	
1	4F	437	
1	4G	437	
1	4H	437	
1	4I	437	
2	3A	426	
2	3B	426	
2	3C	426	
2	3D	426	
2	3E	426	
2	3F	426	
2	3G	426	
2	3H	426	
2	3I	426	
2	5A	426	
2	5B	426	

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Mol	Chain	Length	Quality of chain
2	5C	426	
2	5D	426	
2	5E	426	
2	5F	426	
2	5G	426	
2	5H	426	
2	5I	426	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 119808 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 alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2B	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2D	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2F	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2H	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	2I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4B	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4D	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4F	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
1	4H	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	4I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

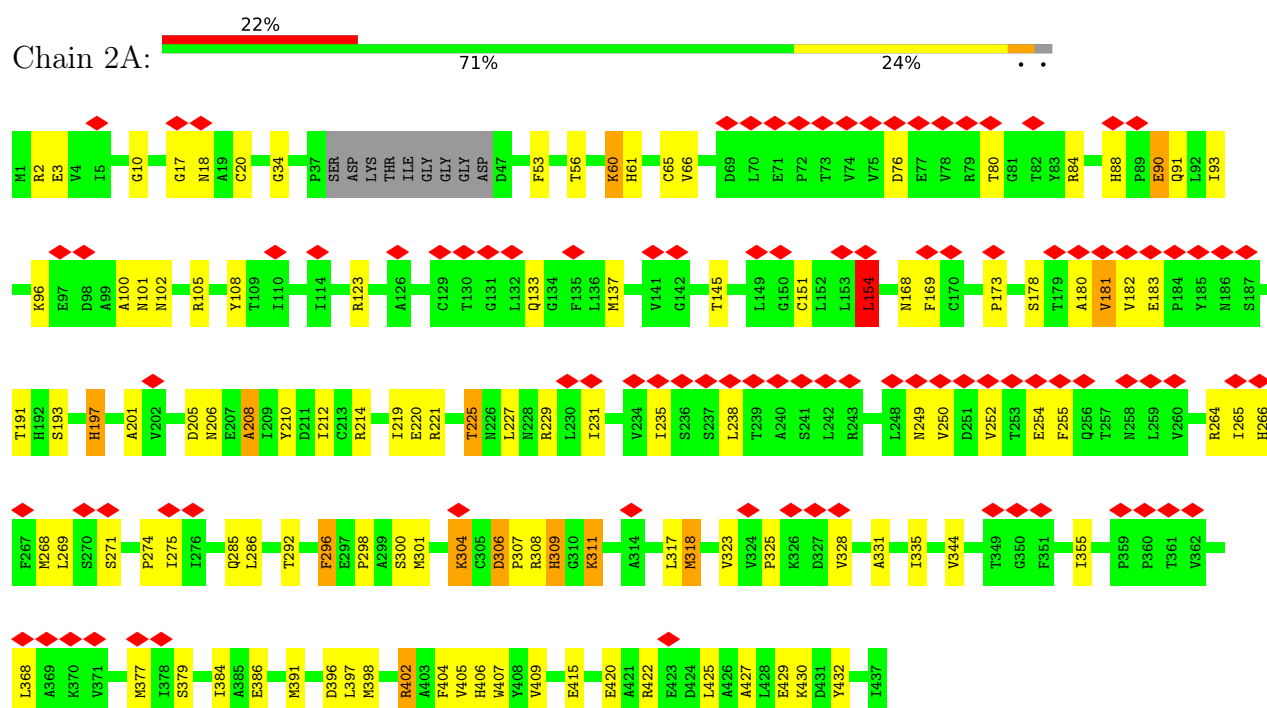
- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3A	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3C	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3E	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3G	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3I	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5A	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5C	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5E	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5G	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5I	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

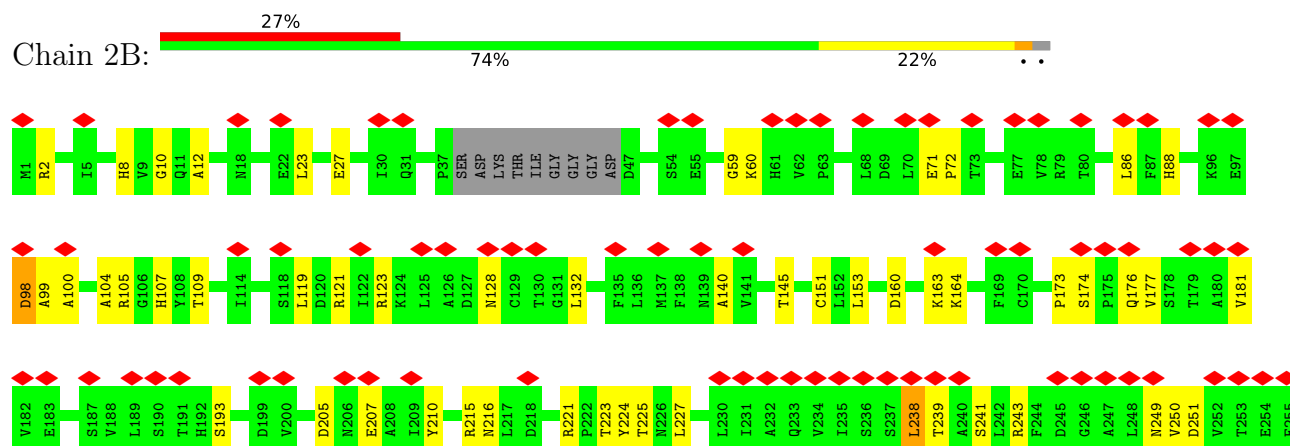
3 Residue-property plots

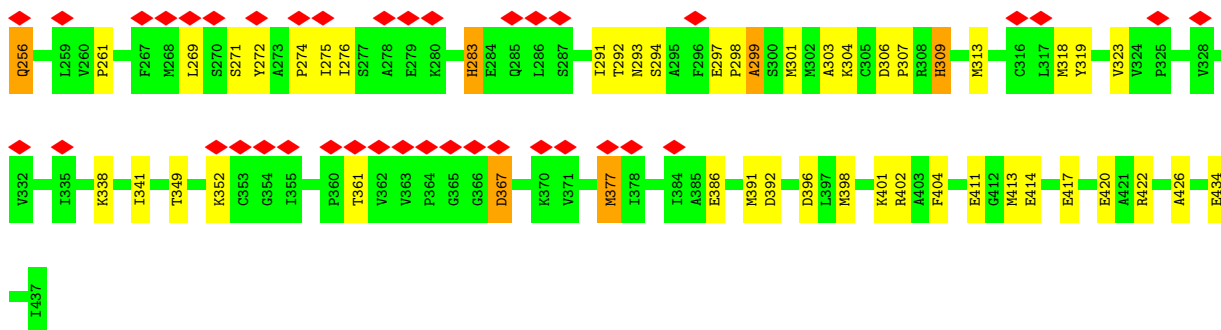
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

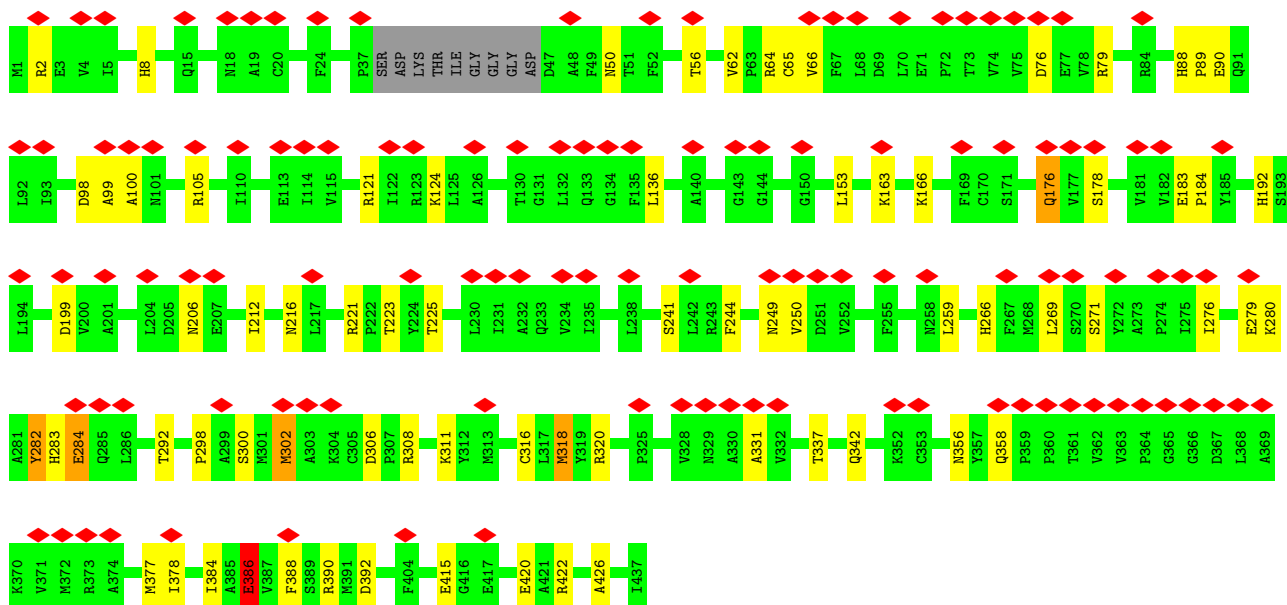
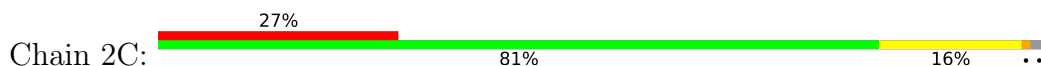


• Molecule 1: Tubulin alpha chain

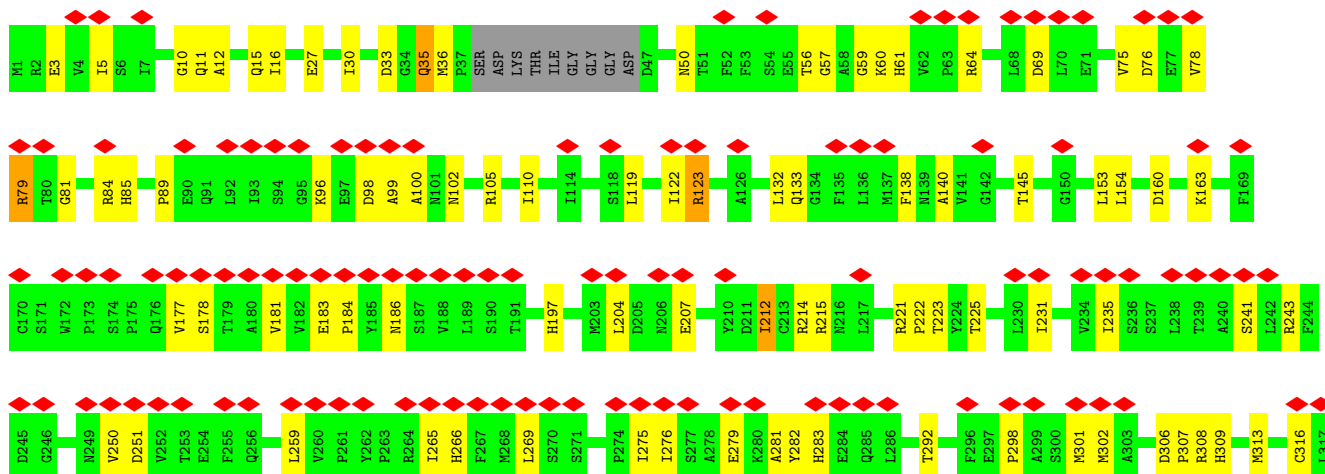
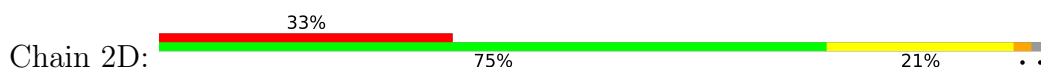


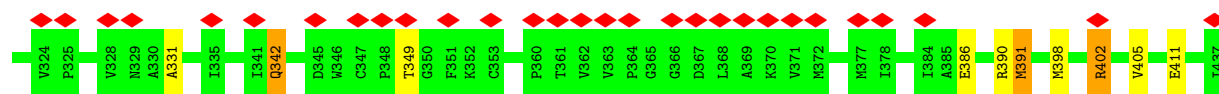


• Molecule 1: Tubulin alpha chain

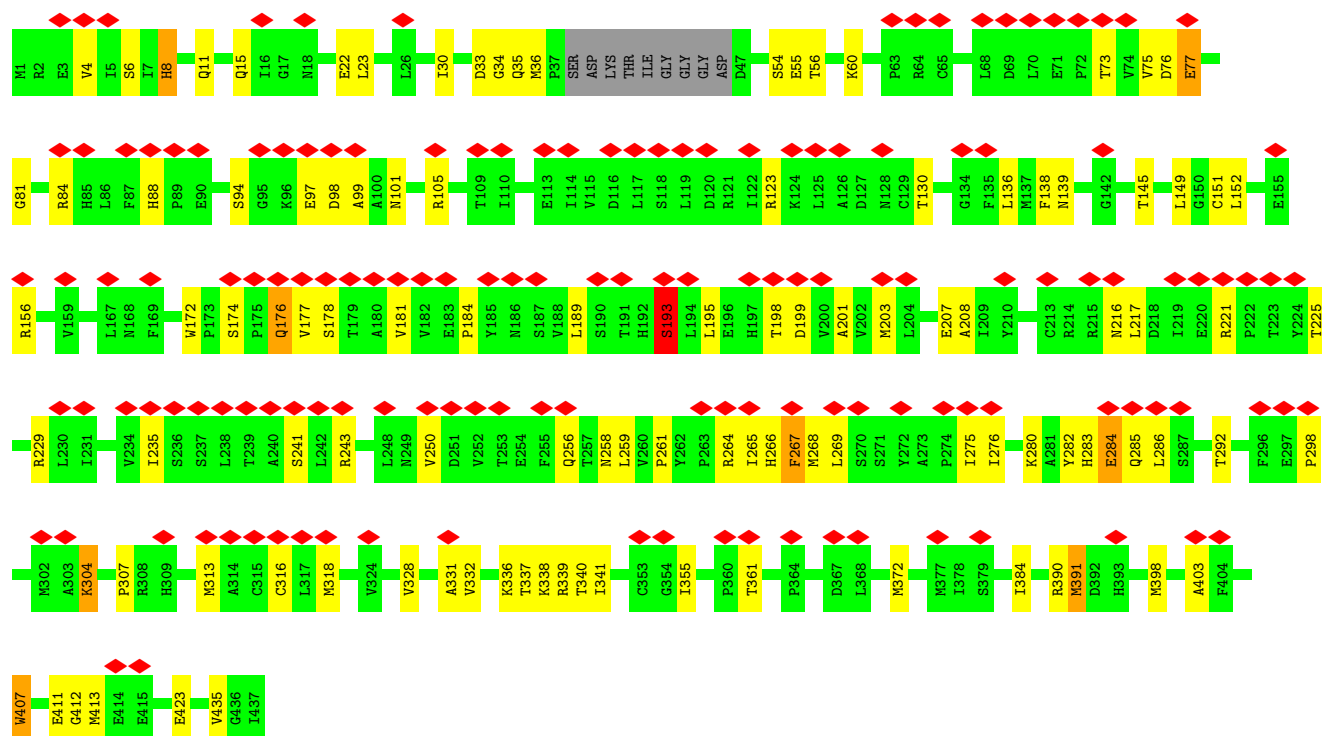
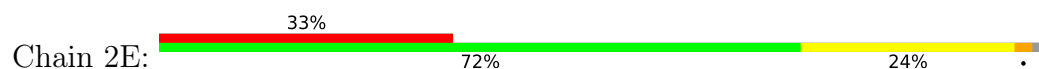


• Molecule 1: Tubulin alpha chain

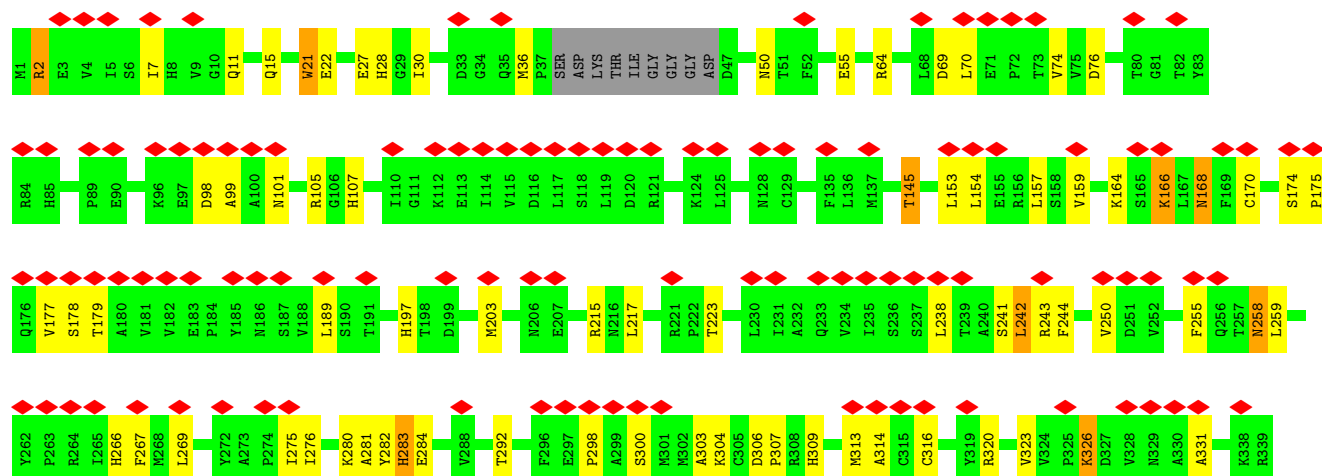
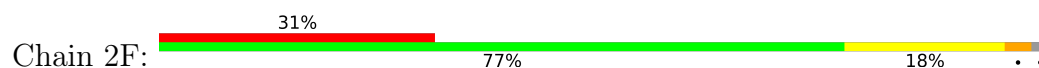




• Molecule 1: Tubulin alpha chain

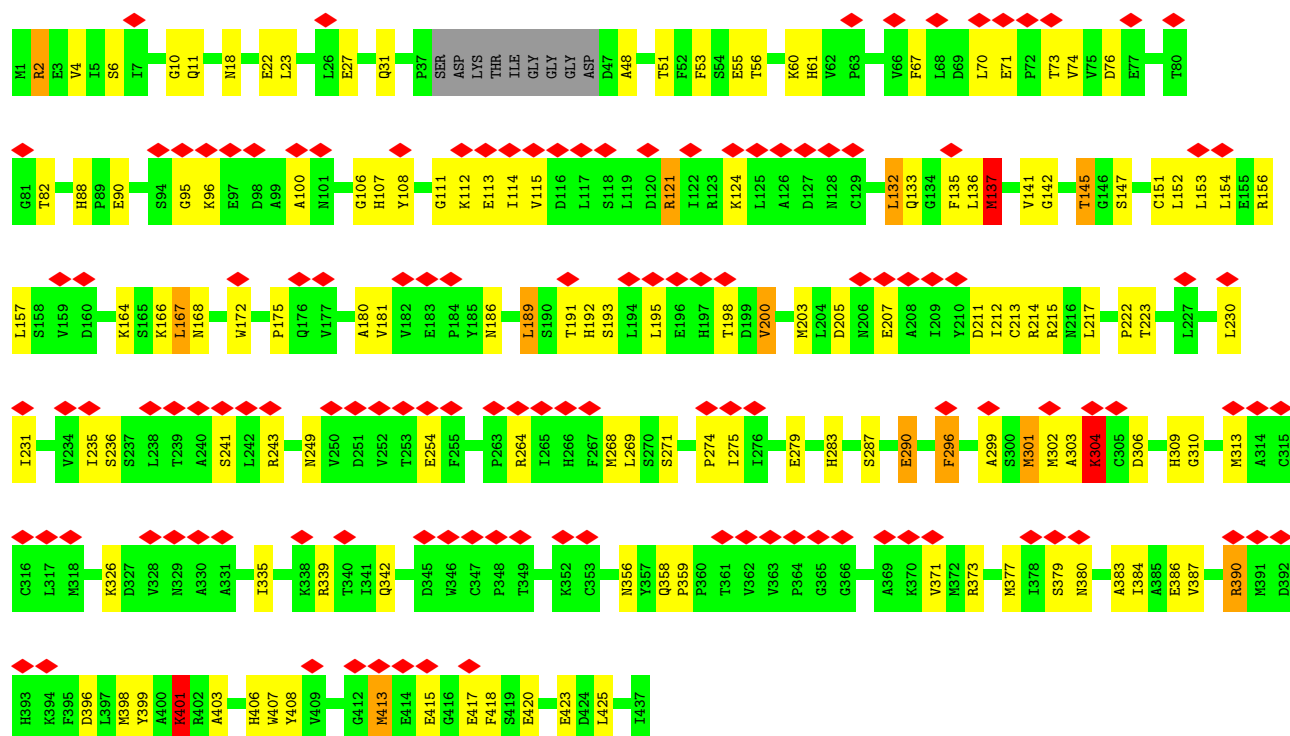


• Molecule 1: Tubulin alpha chain

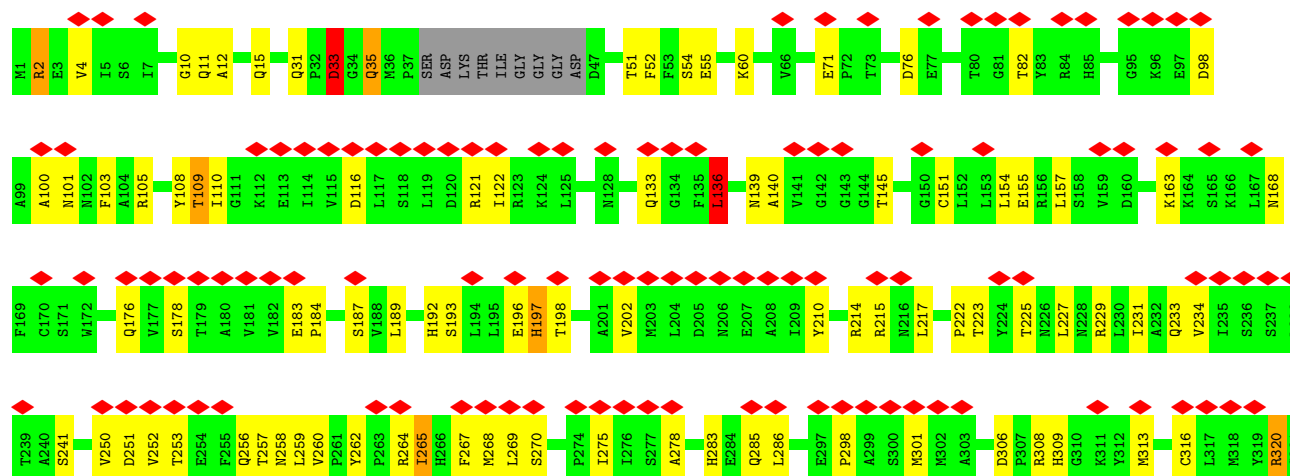


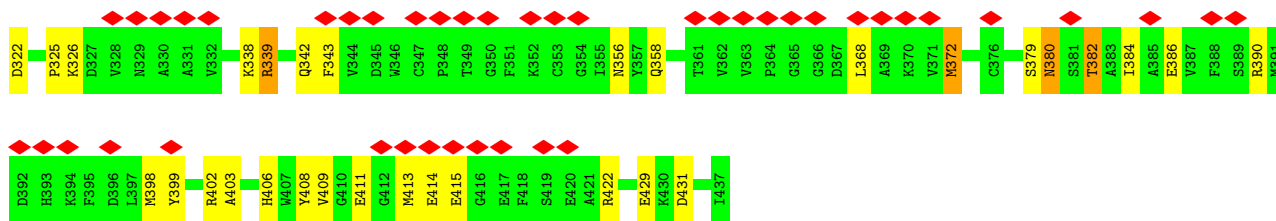


• Molecule 1: Tubulin alpha chain

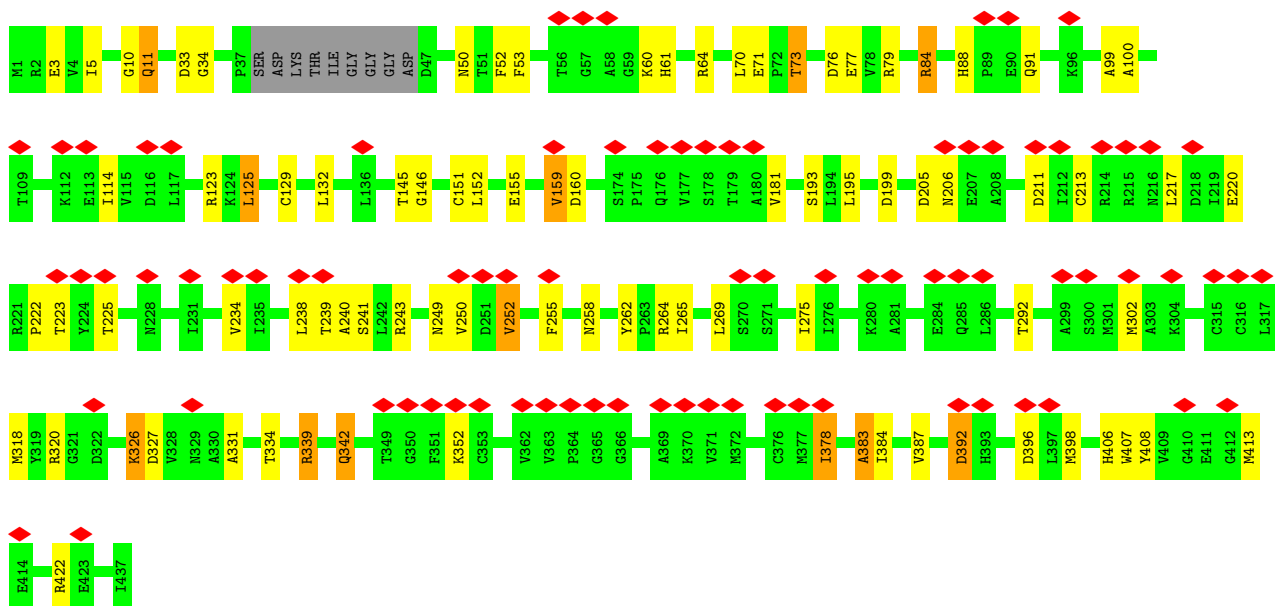
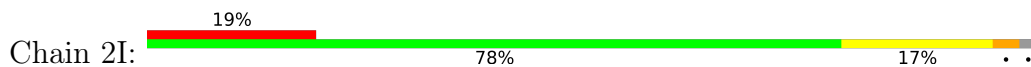


• Molecule 1: Tubulin alpha chain

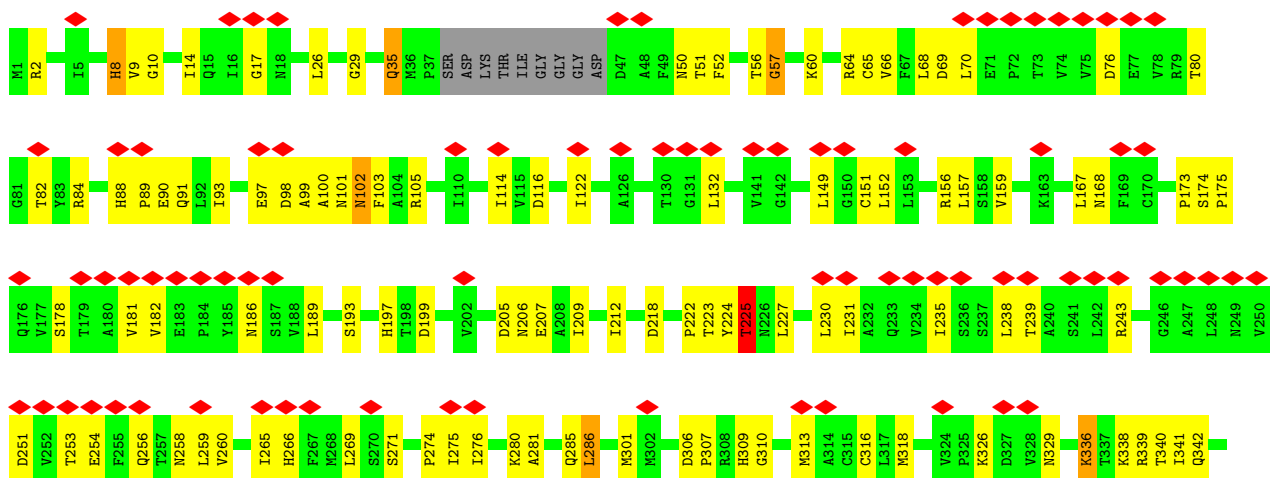


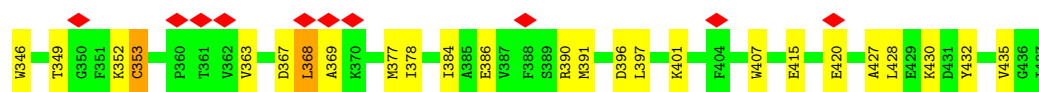


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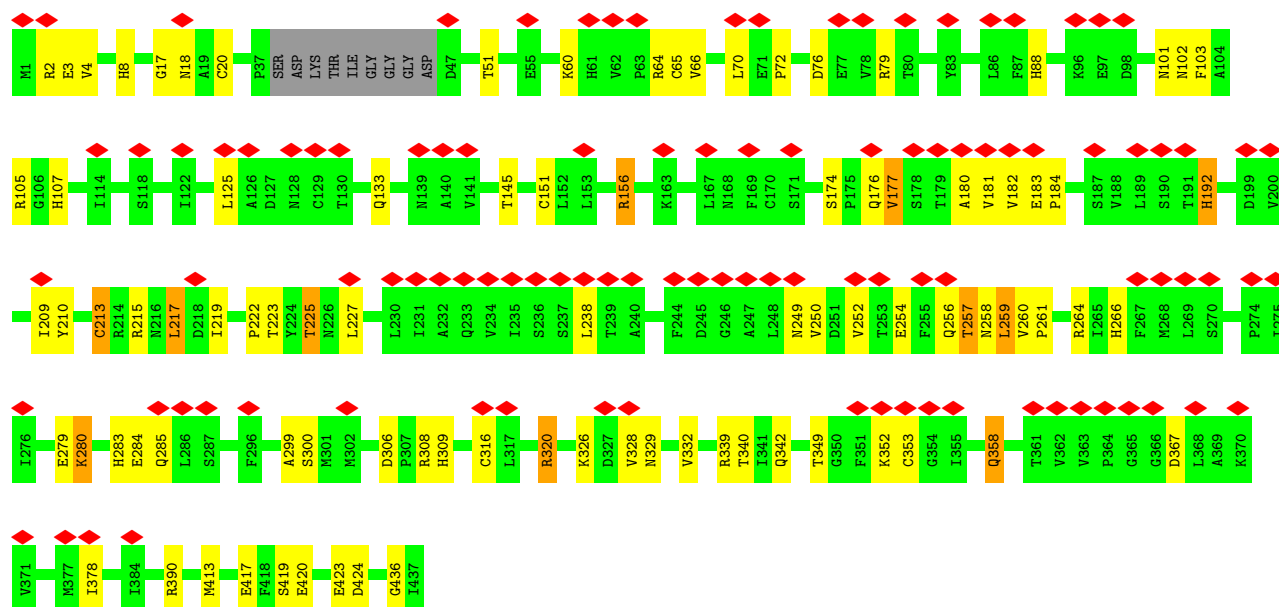
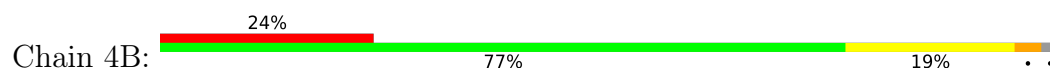


• Molecule 1: Tubulin alpha chain

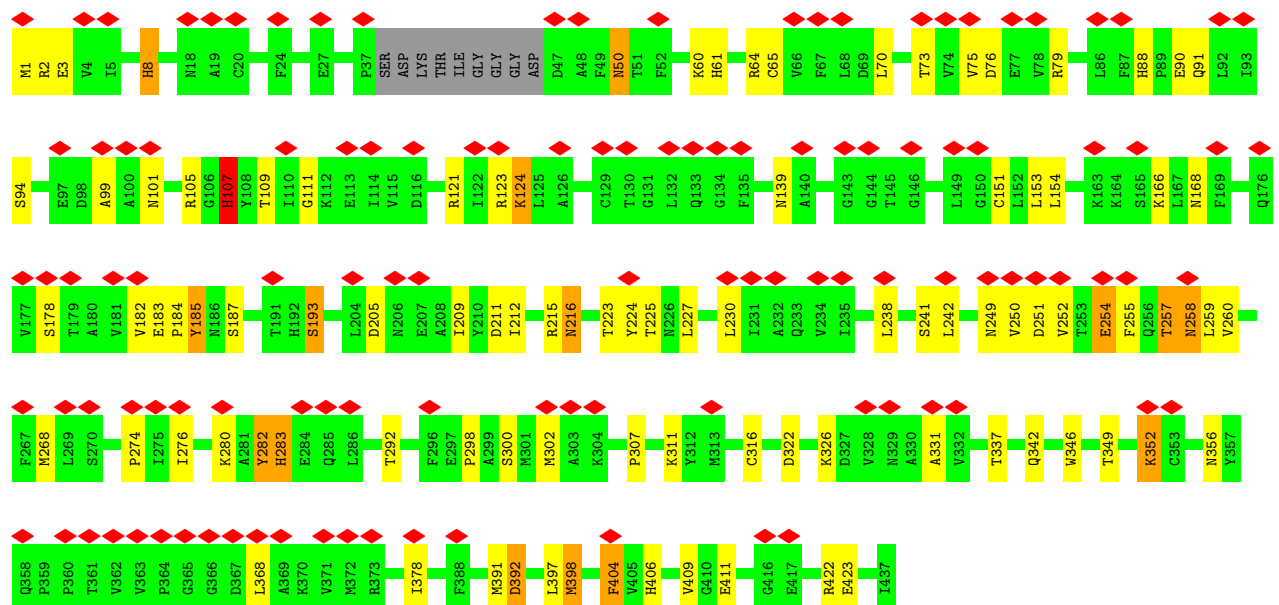
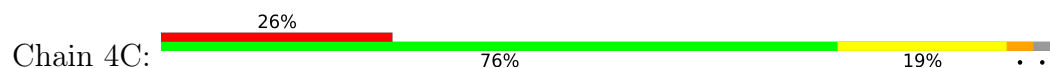




- Molecule 1: Tubulin alpha chain

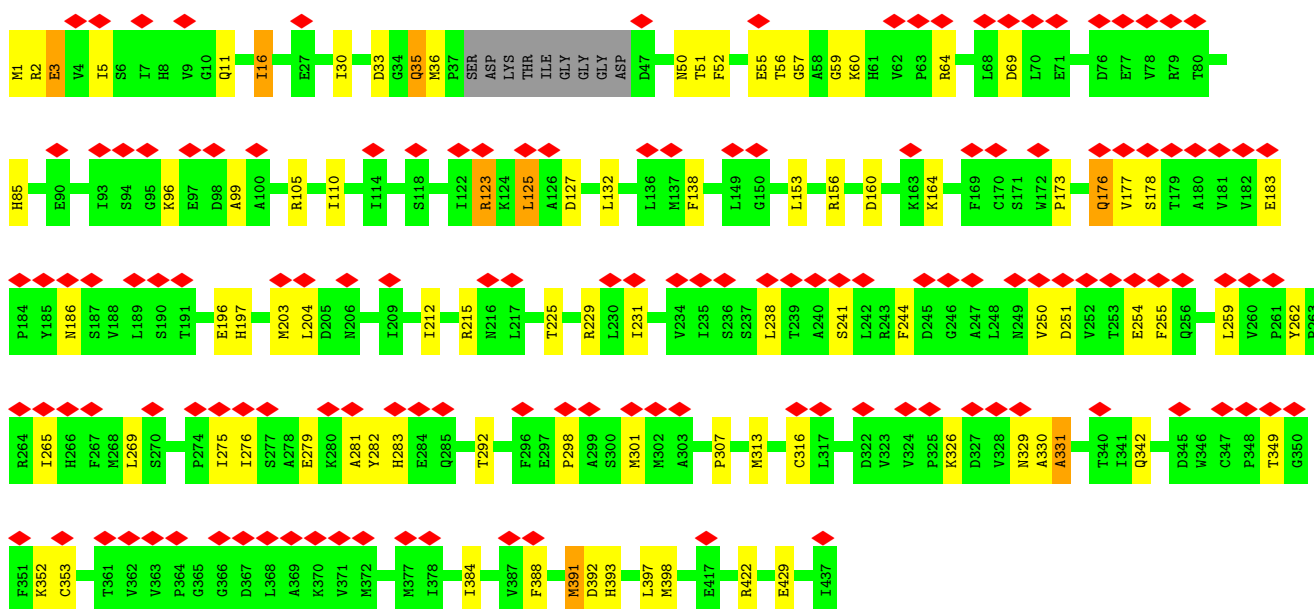


- Molecule 1: Tubulin alpha chain



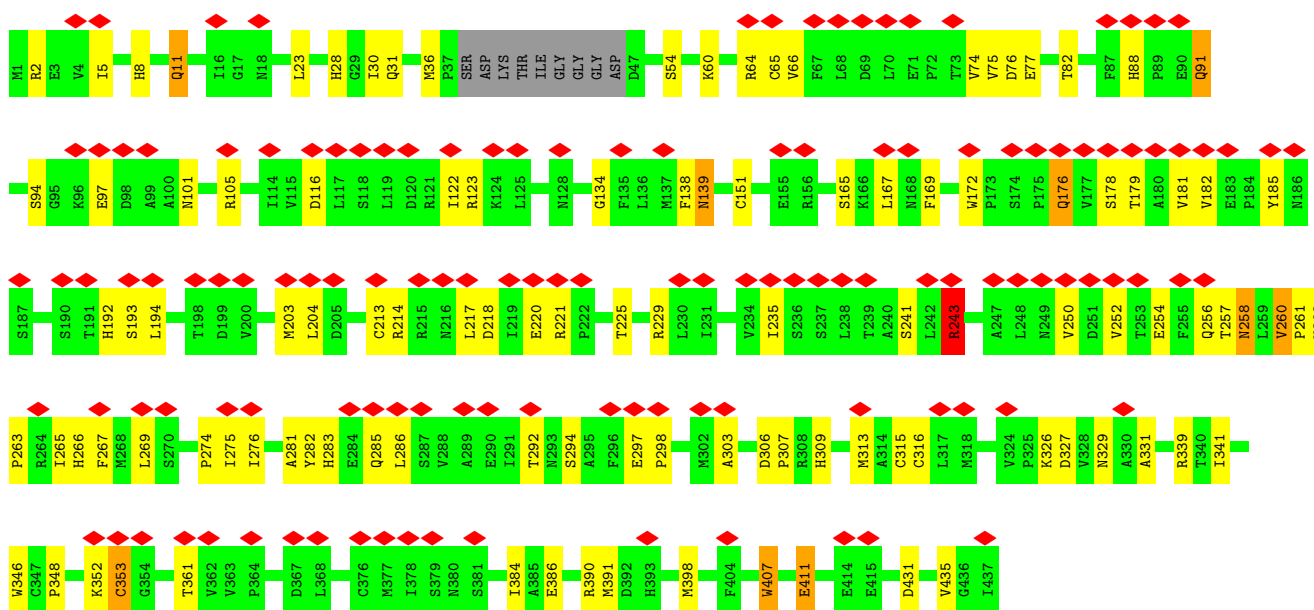
- Molecule 1: Tubulin alpha chain

Chain 4D: 



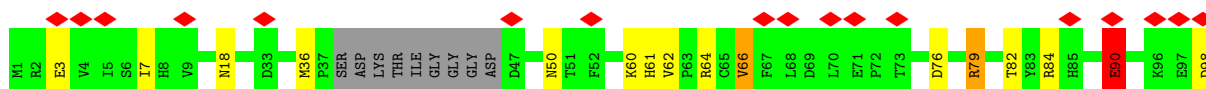
• Molecule 1: Tubulin alpha chain

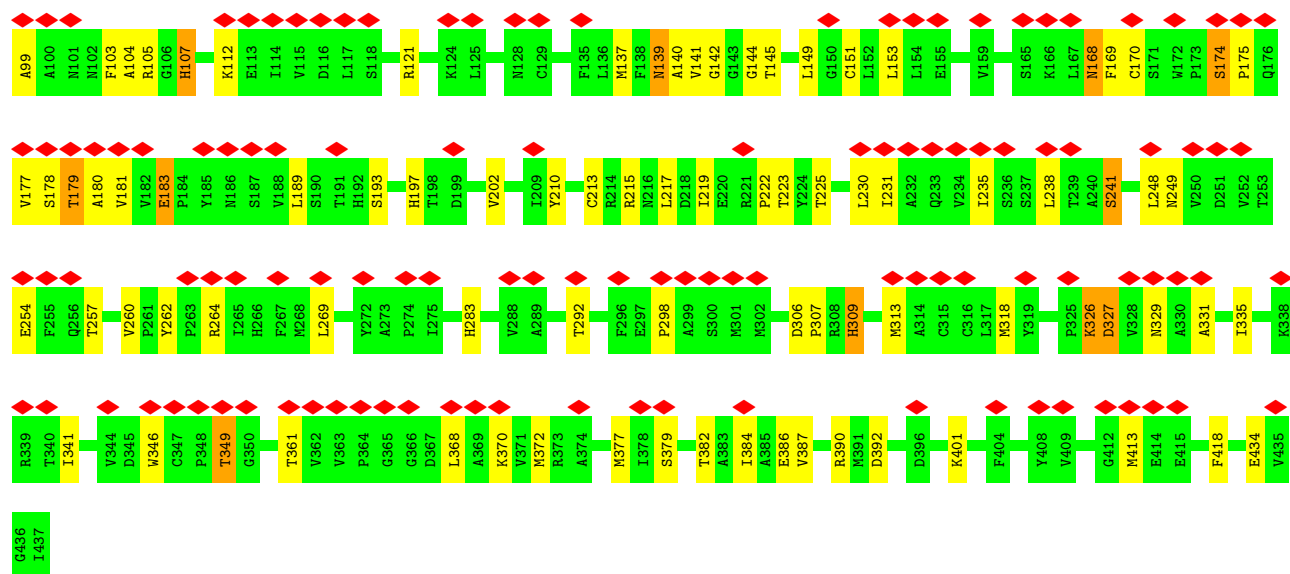
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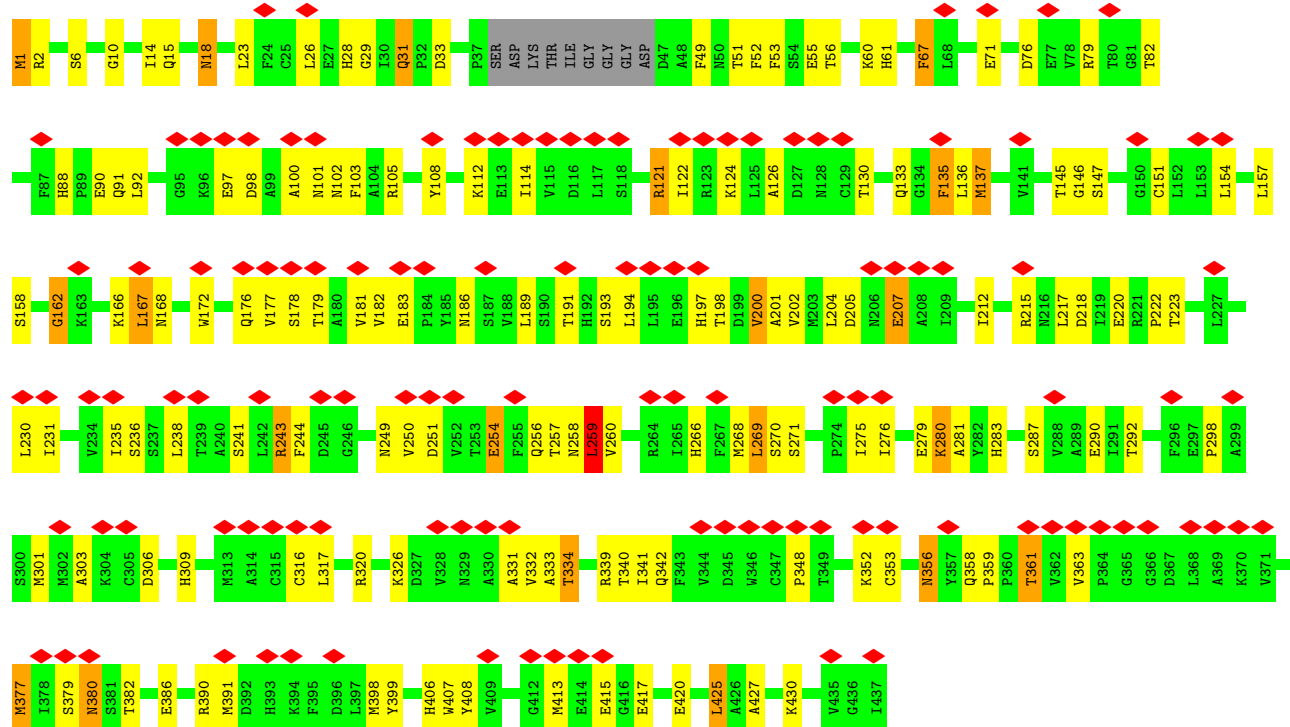
• Molecule 1: Tubulin alpha chain

Chain 4F: 



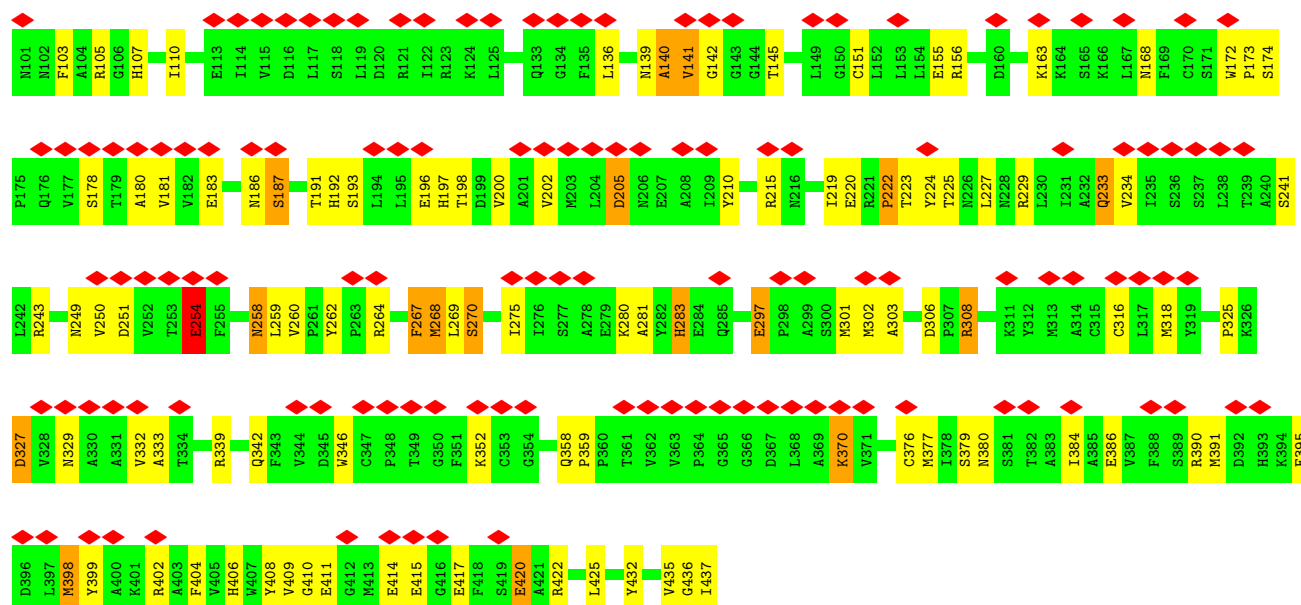


• Molecule 1: Tubulin alpha chain

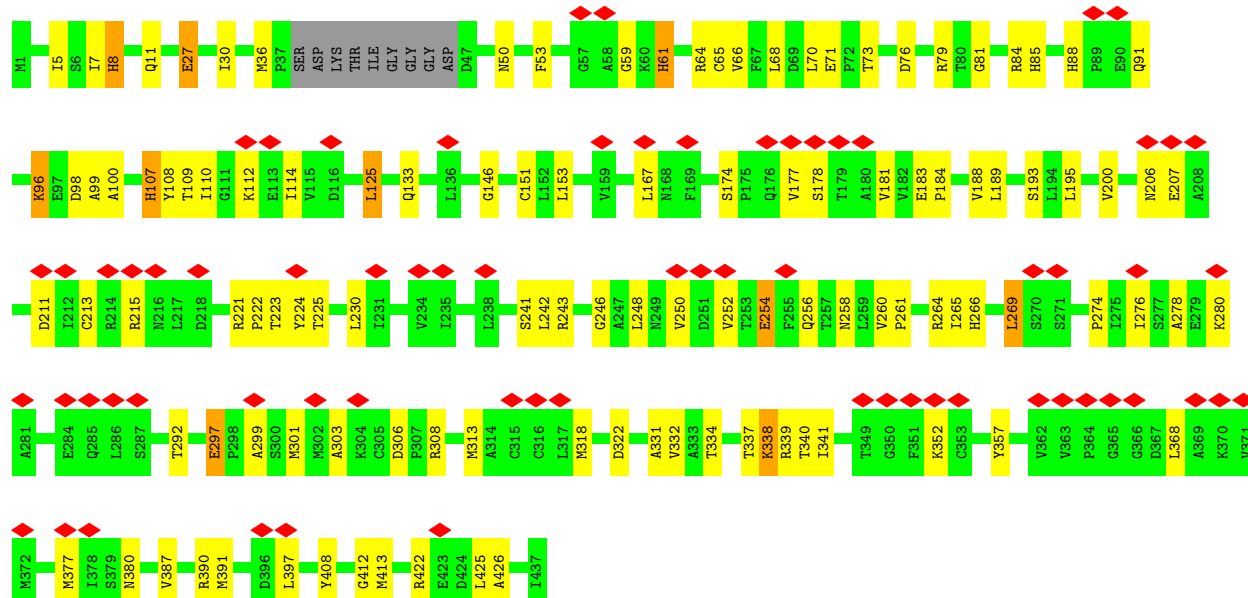
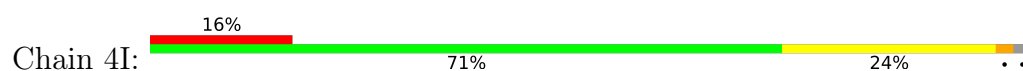


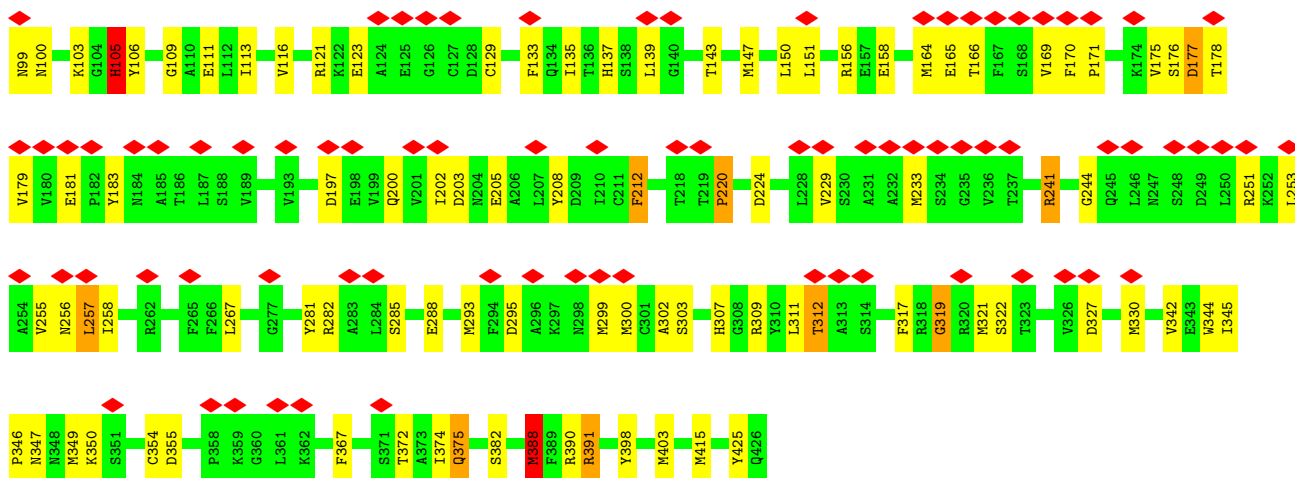
• Molecule 1: Tubulin alpha chain



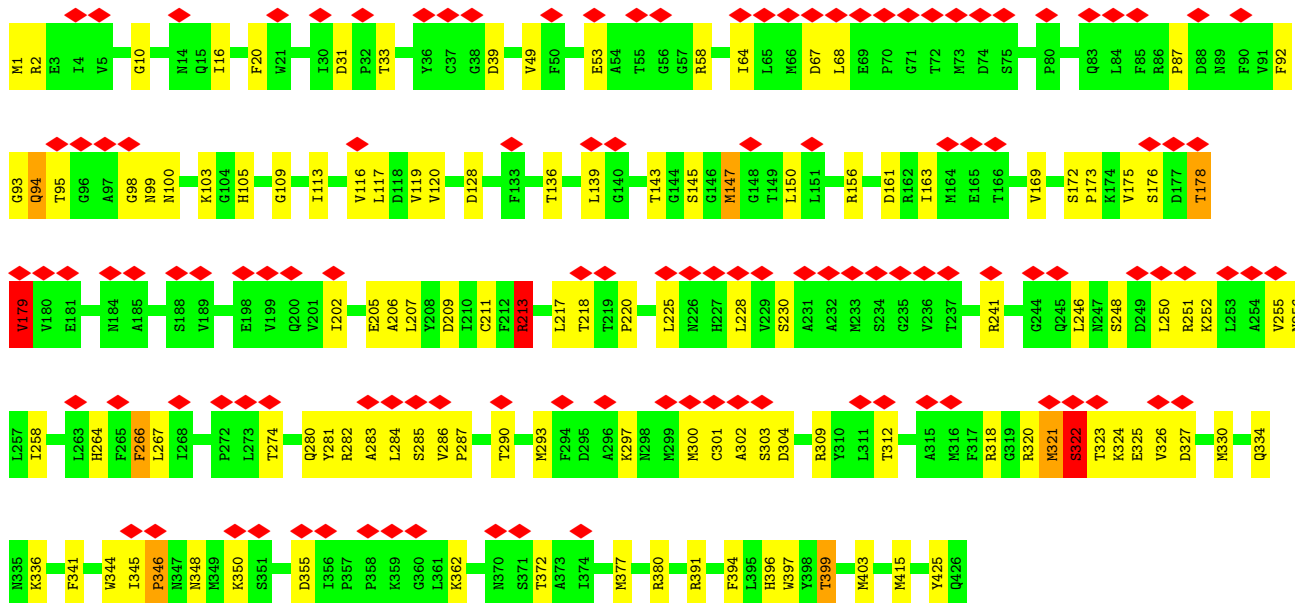


• Molecule 1: Tubulin alpha chain

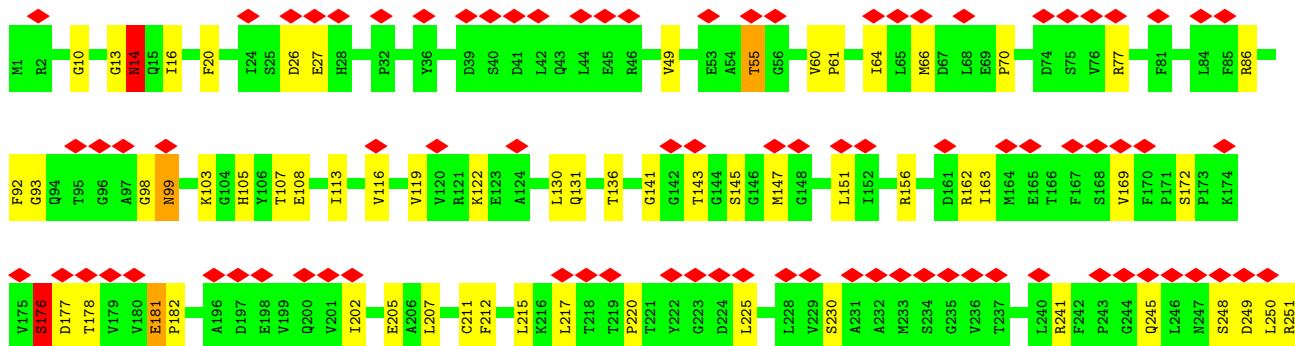
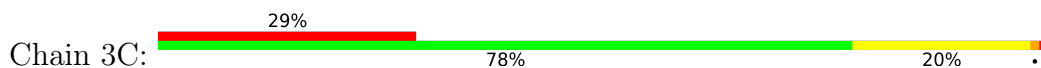


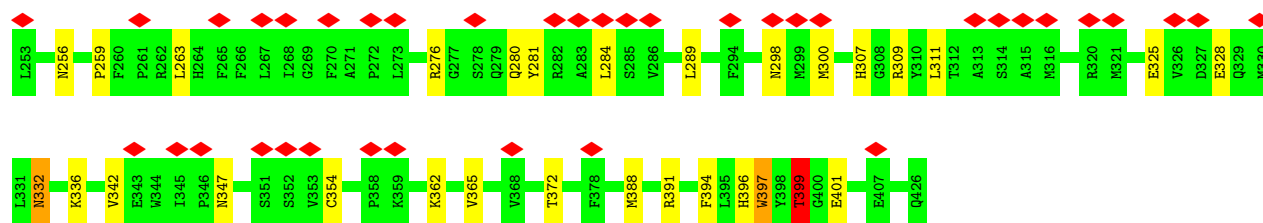


• Molecule 2: Tubulin beta chain

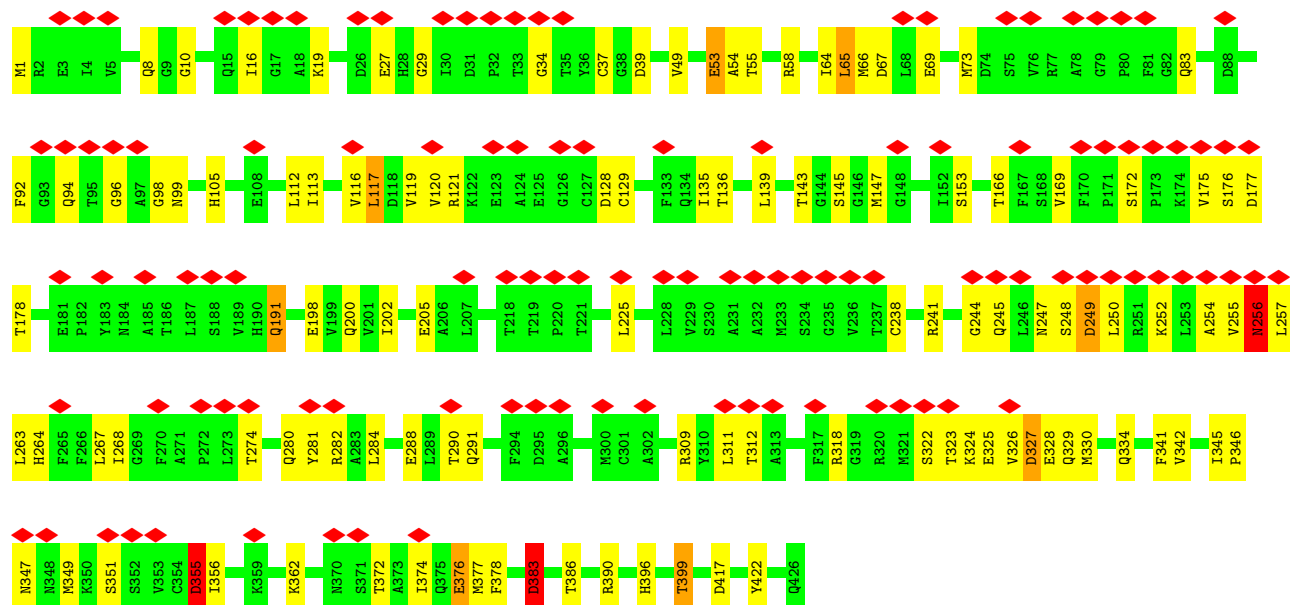
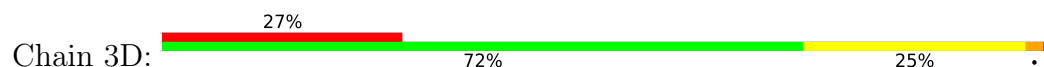


• Molecule 2: Tubulin beta chain

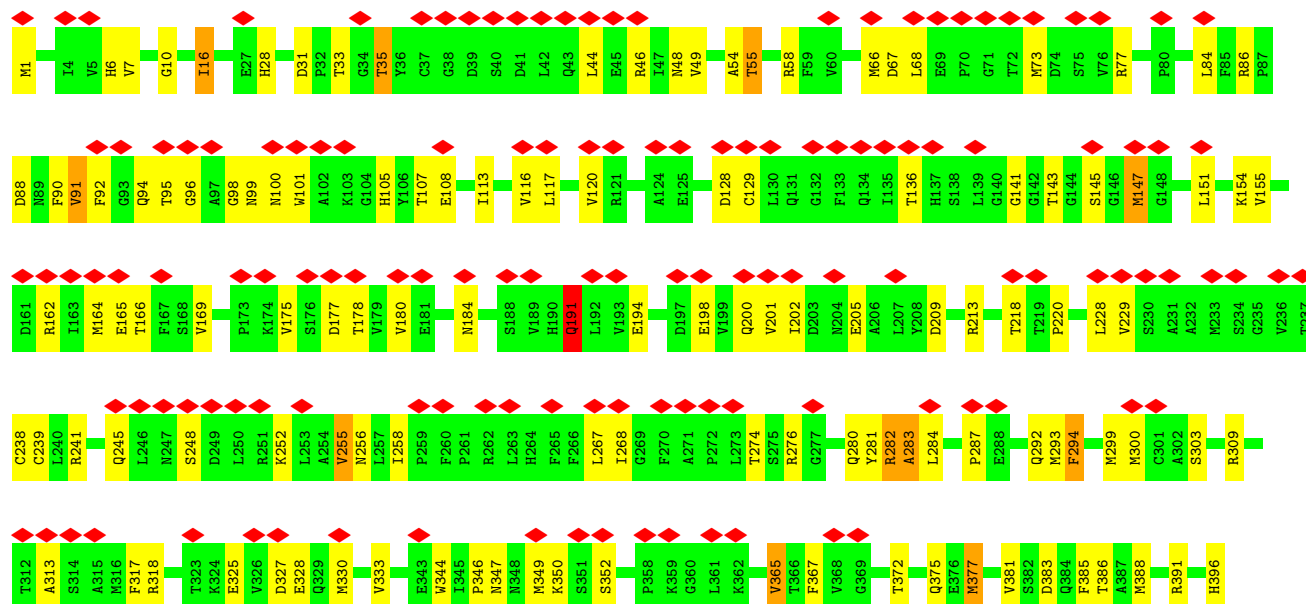


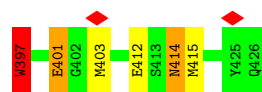


• Molecule 2: Tubulin beta chain

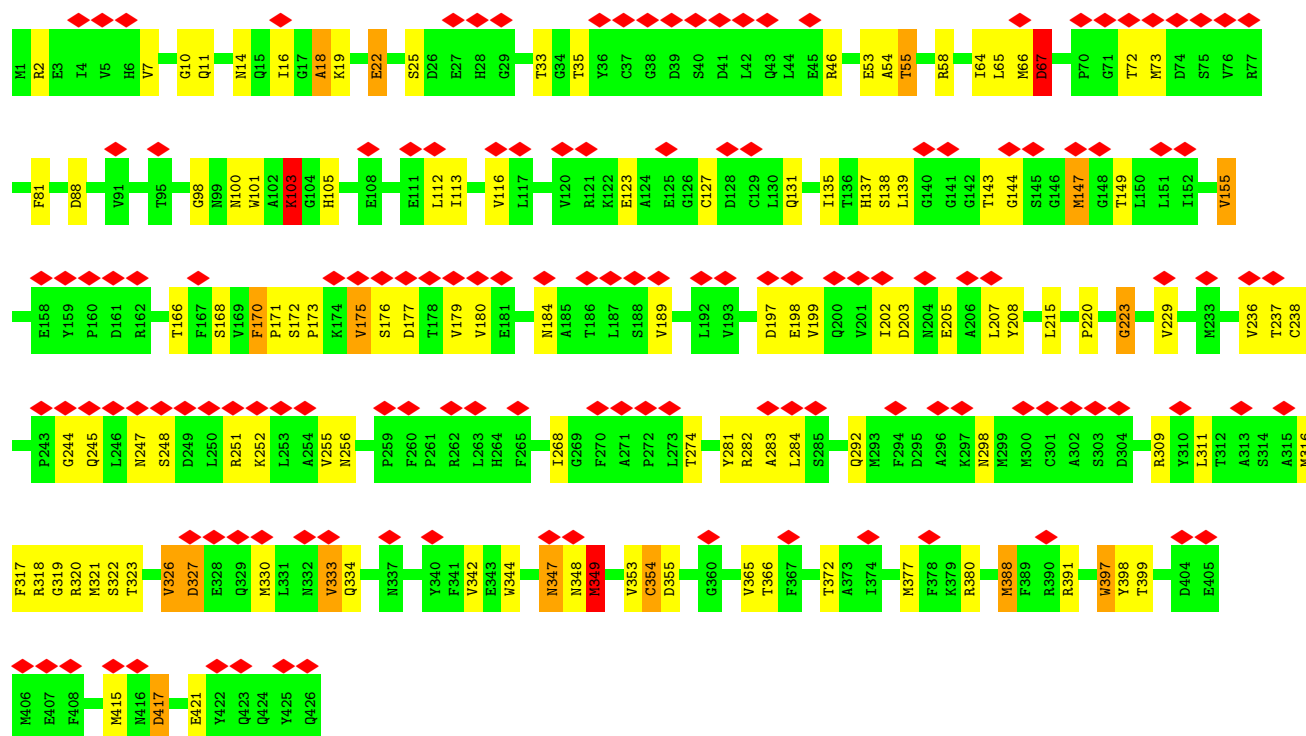
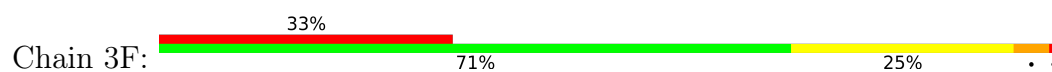


• Molecule 2: Tubulin beta chain

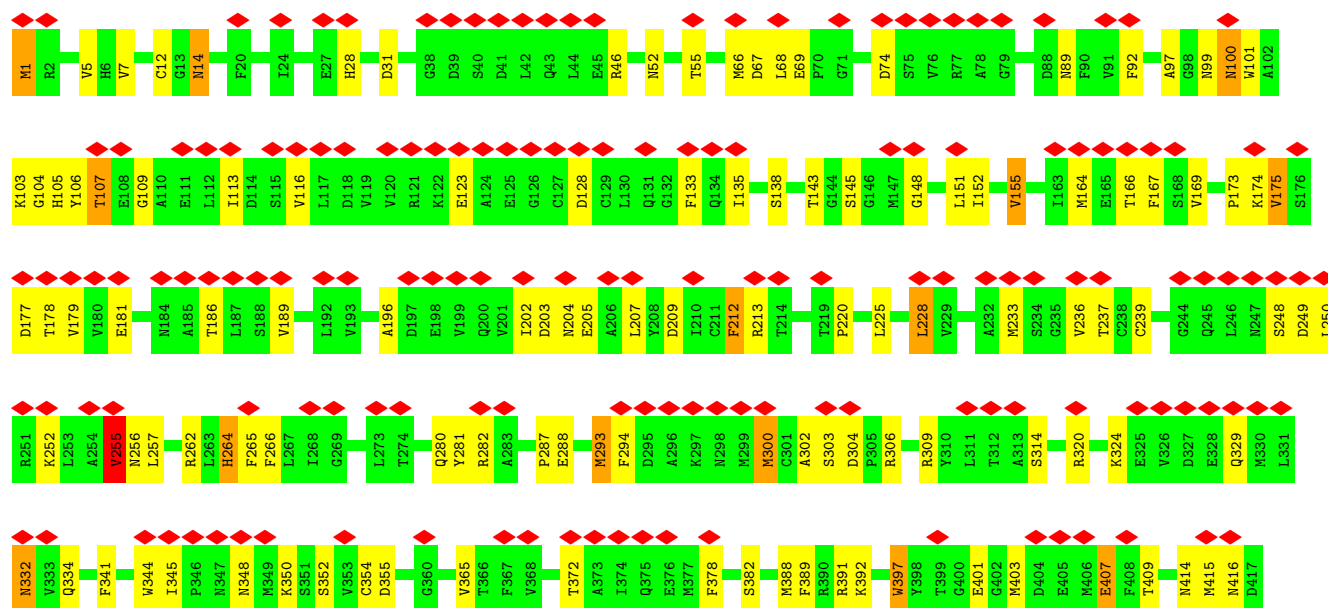
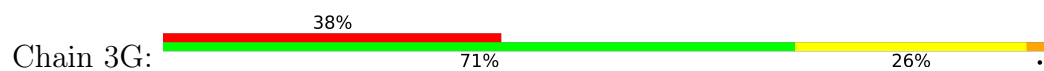


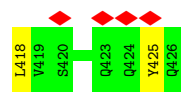


• Molecule 2: Tubulin beta chain

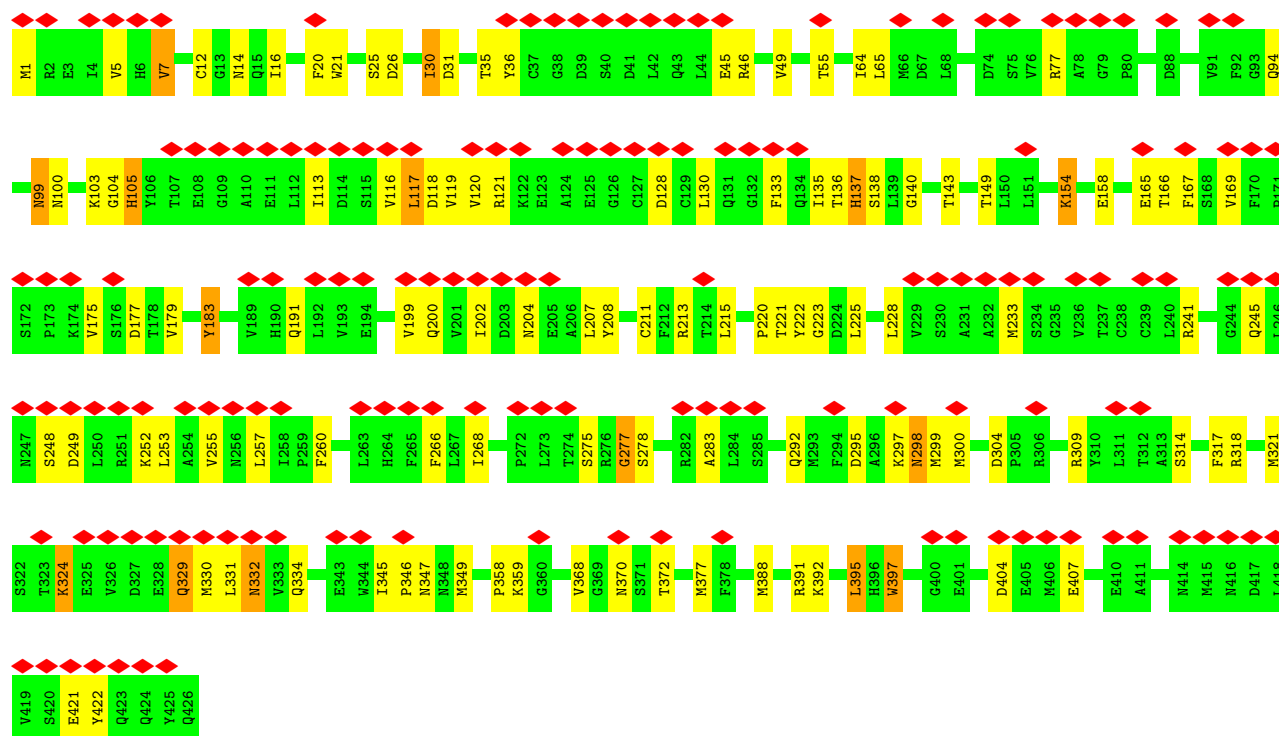
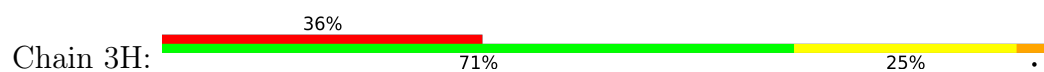


• Molecule 2: Tubulin beta chain

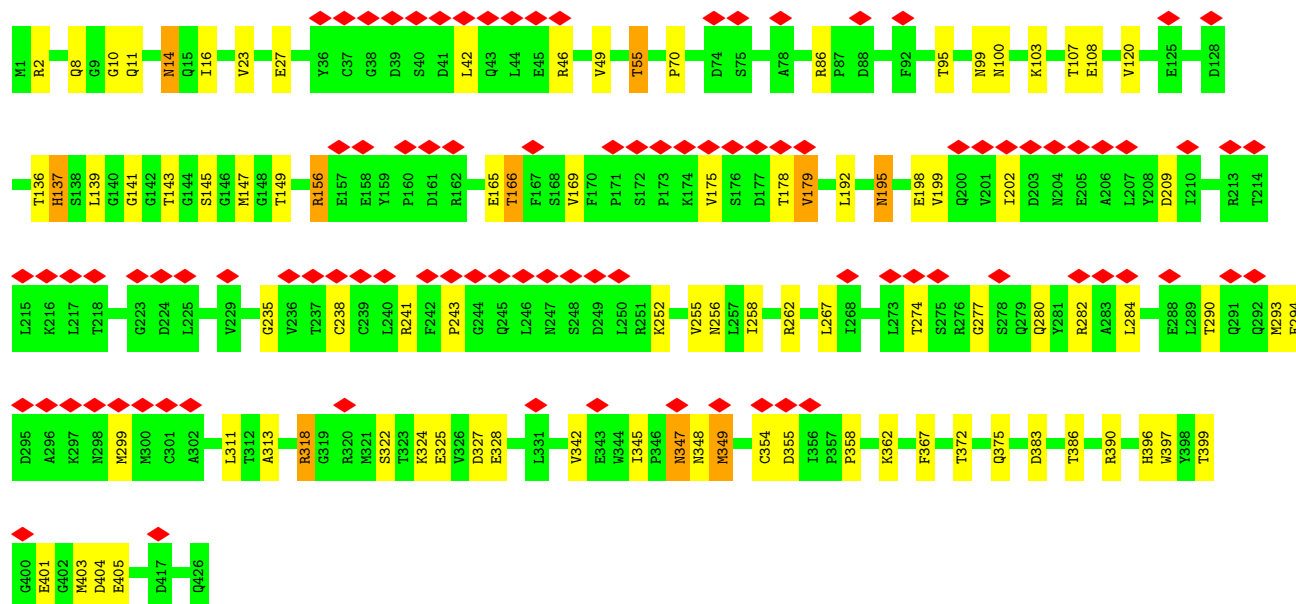
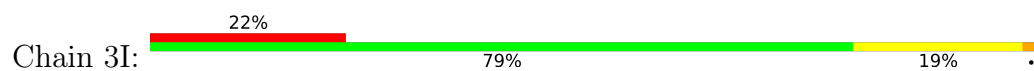




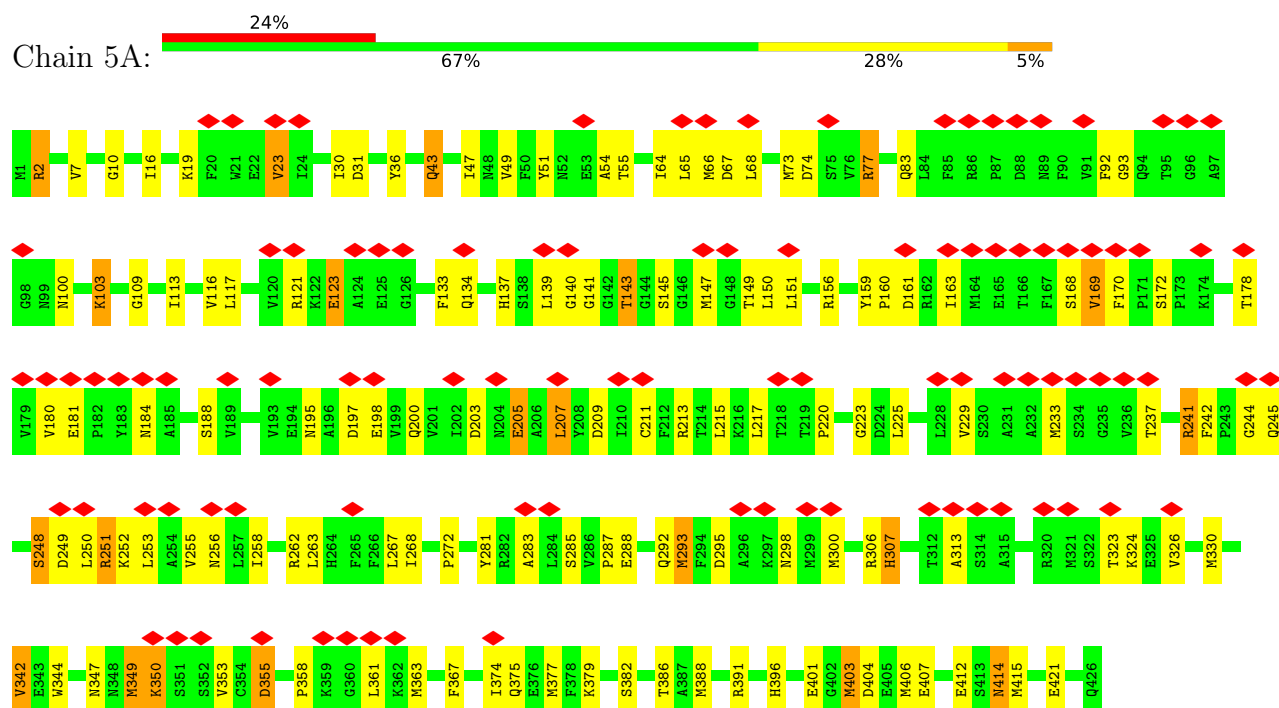
• Molecule 2: Tubulin beta chain



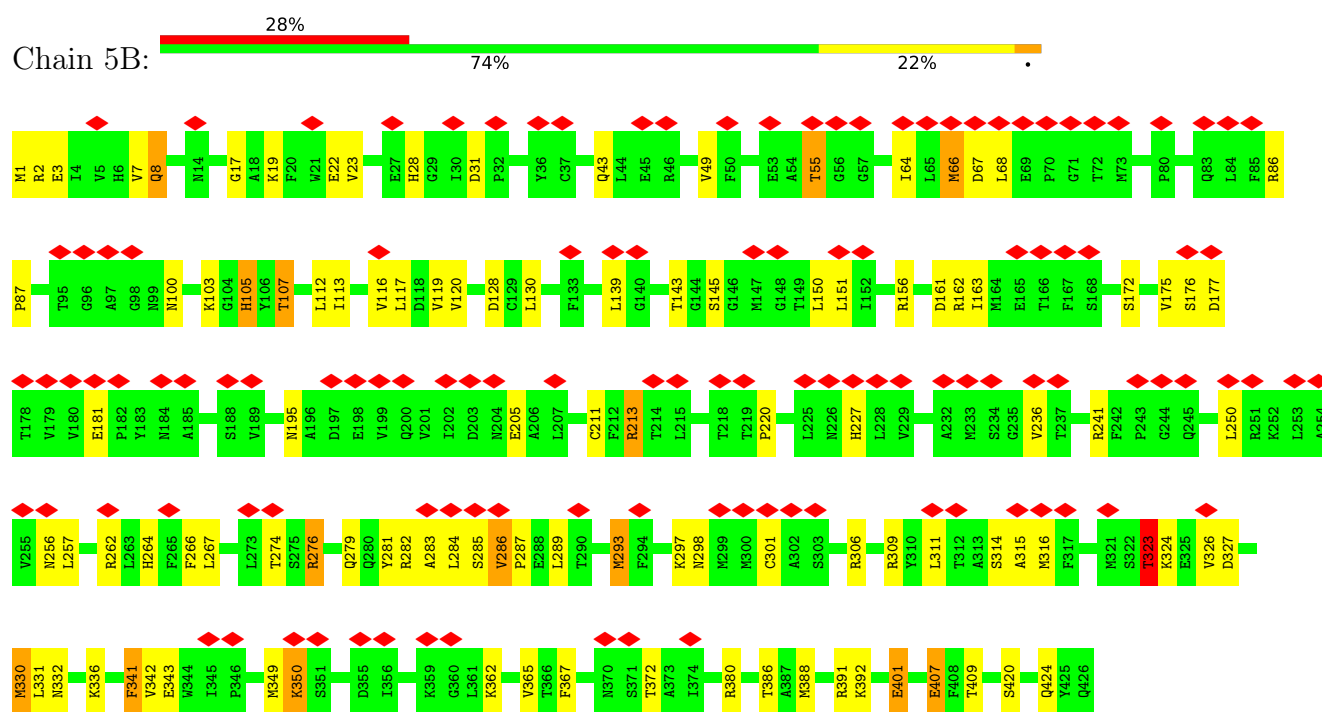
• Molecule 2: Tubulin beta chain



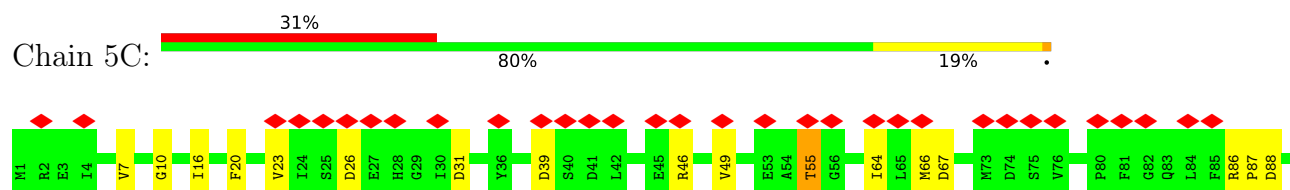
- Molecule 2: Tubulin beta chain

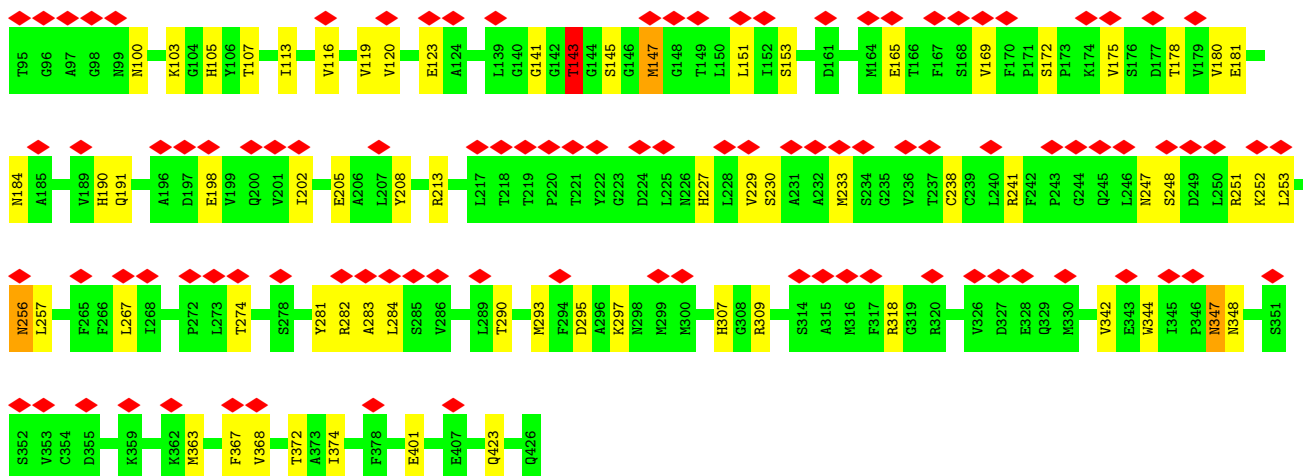


- Molecule 2: Tubulin beta chain

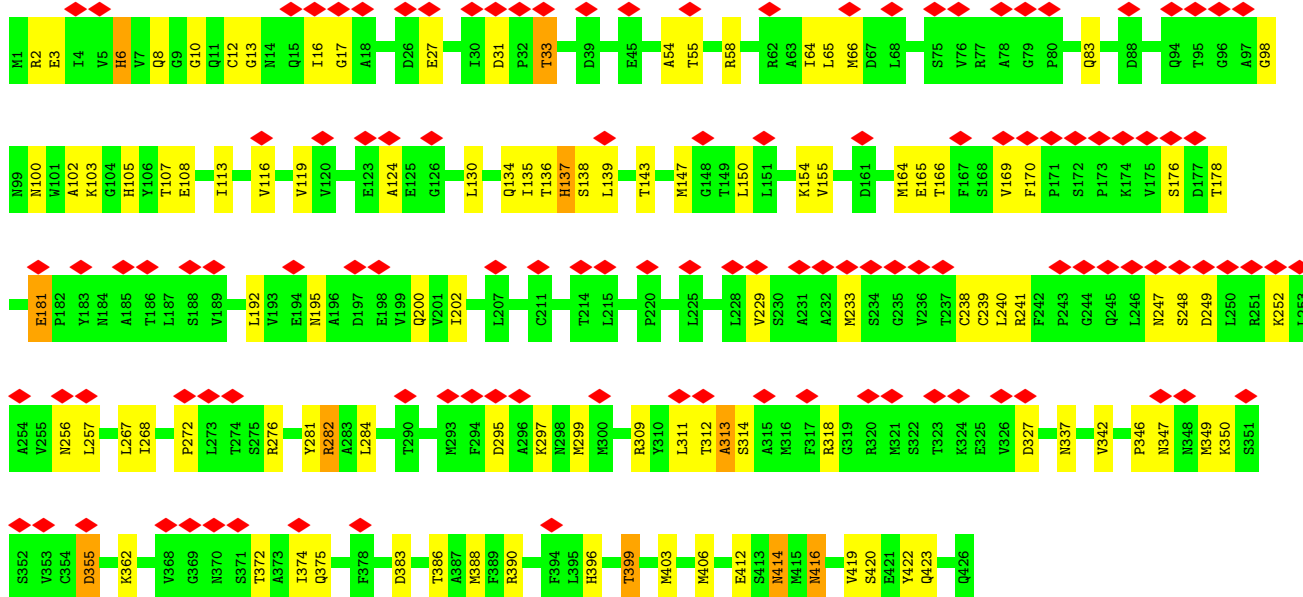
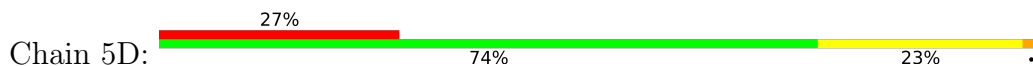


- Molecule 2: Tubulin beta chain

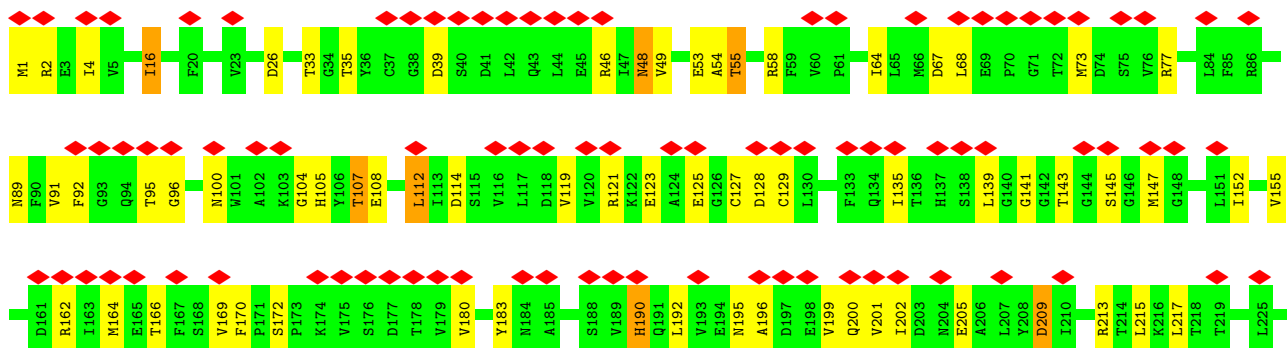
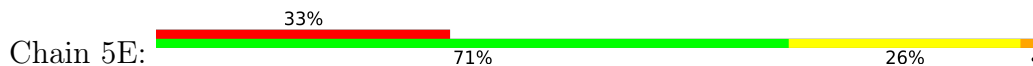


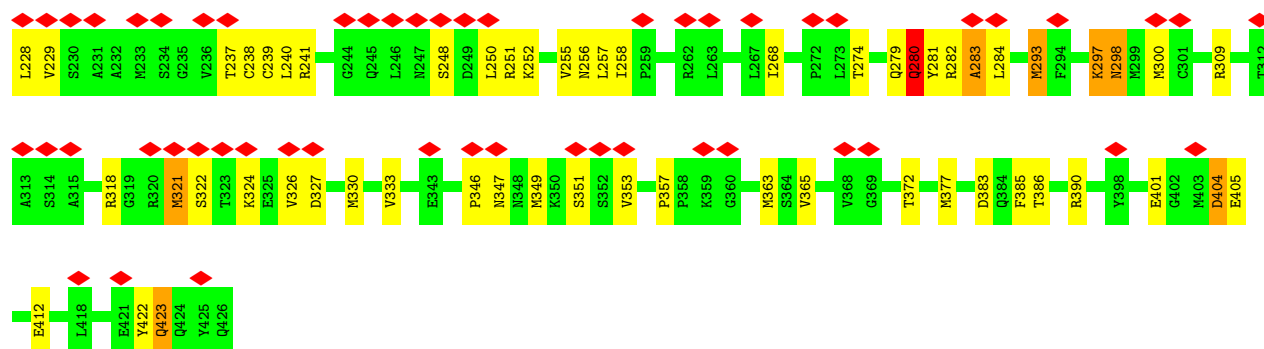


• Molecule 2: Tubulin beta chain

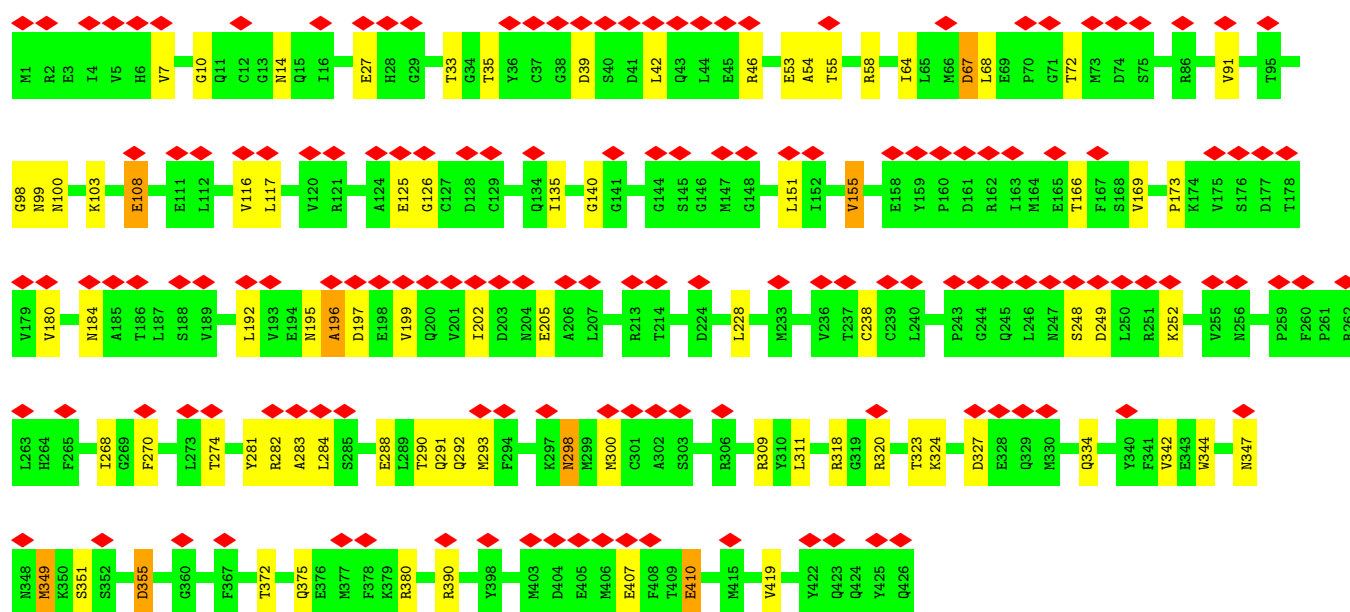
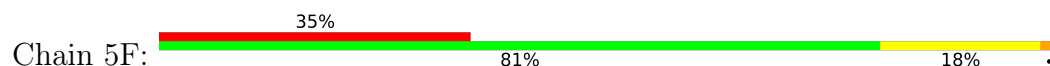


• Molecule 2: Tubulin beta chain

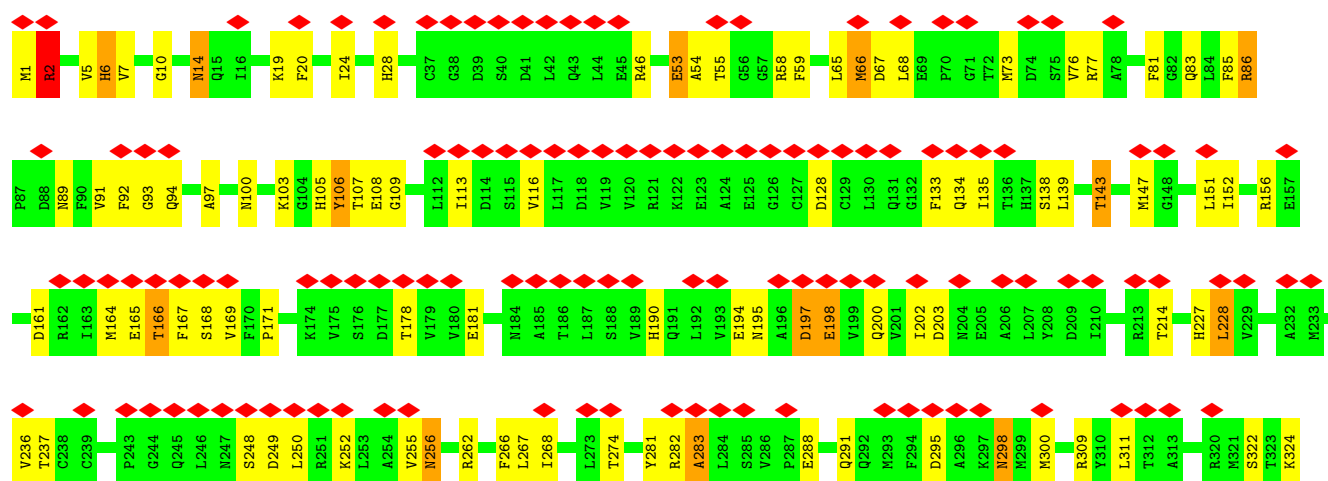


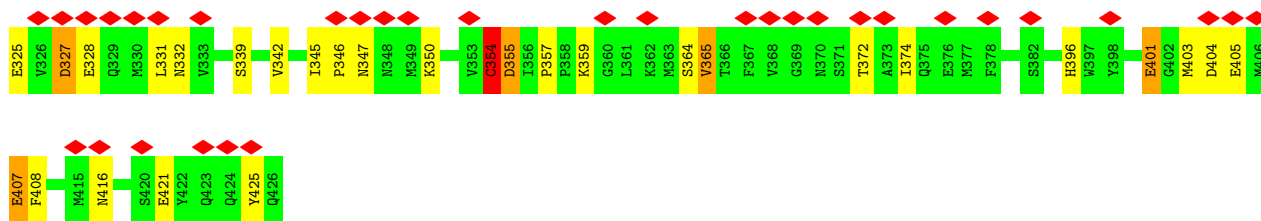


• Molecule 2: Tubulin beta chain

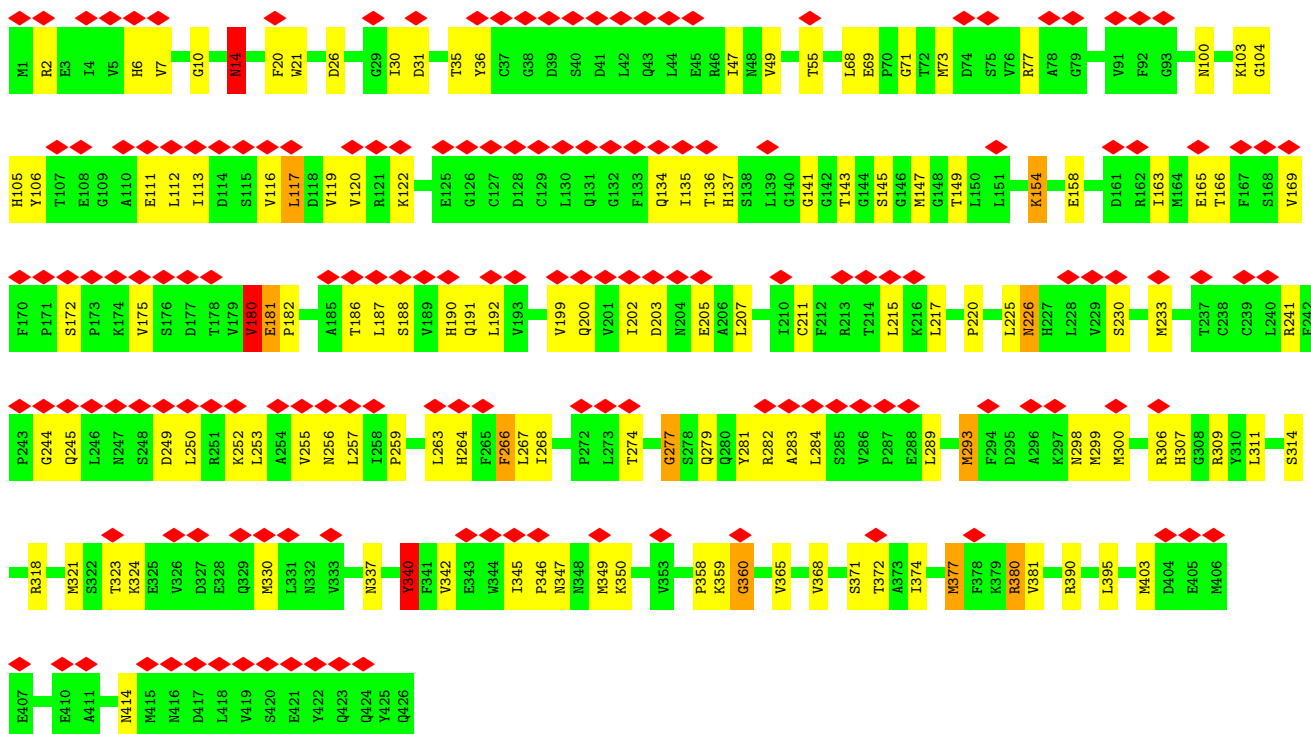


• Molecule 2: Tubulin beta chain

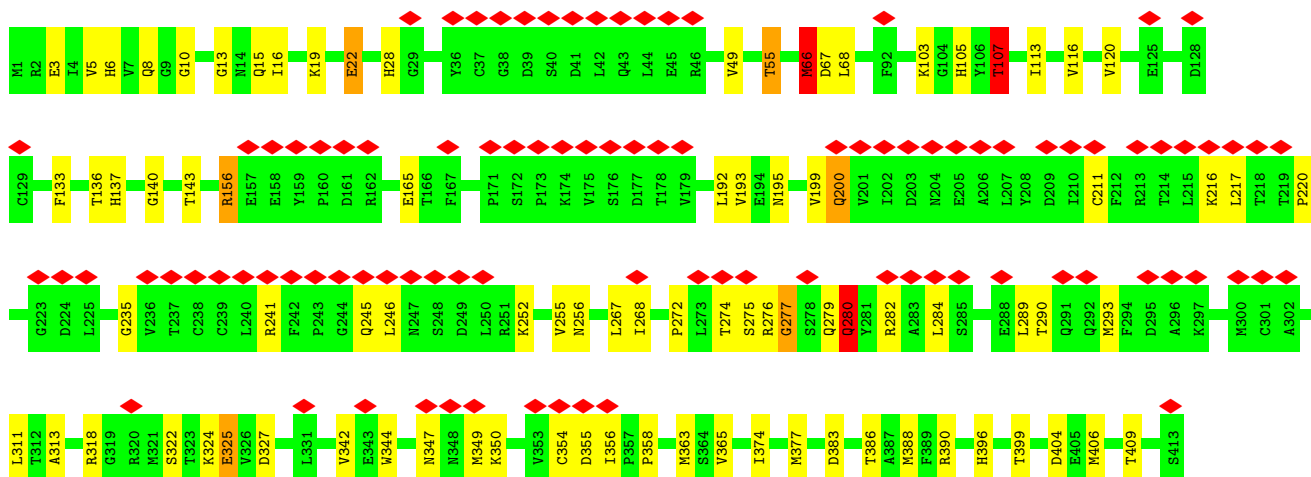
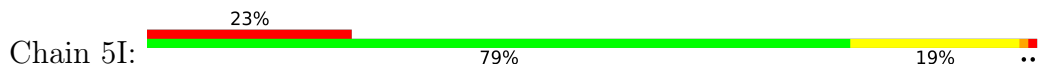




• Molecule 2: Tubulin beta chain



• Molecule 2: Tubulin beta chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	29524	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	96	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.463	Depositor
Minimum map value	-3.203	Depositor
Average map value	0.053	Depositor
Map value standard deviation	0.287	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	452.352, 452.352, 452.352	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.534, 3.534, 3.534	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	2A	1.13	7/3398 (0.2%)	1.42	28/4606 (0.6%)
1	2B	1.08	8/3398 (0.2%)	1.31	21/4606 (0.5%)
1	2C	1.03	6/3398 (0.2%)	1.23	16/4606 (0.3%)
1	2D	1.00	4/3398 (0.1%)	1.26	14/4606 (0.3%)
1	2E	1.07	9/3398 (0.3%)	1.32	24/4606 (0.5%)
1	2F	1.12	3/3398 (0.1%)	1.42	32/4606 (0.7%)
1	2G	1.21	13/3398 (0.4%)	1.49	33/4606 (0.7%)
1	2H	1.19	10/3398 (0.3%)	1.46	29/4606 (0.6%)
1	2I	1.04	3/3398 (0.1%)	1.31	23/4606 (0.5%)
1	4A	1.22	10/3398 (0.3%)	1.47	25/4606 (0.5%)
1	4B	1.09	9/3398 (0.3%)	1.30	20/4606 (0.4%)
1	4C	1.07	7/3398 (0.2%)	1.33	19/4606 (0.4%)
1	4D	1.05	5/3398 (0.1%)	1.31	19/4606 (0.4%)
1	4E	1.08	7/3398 (0.2%)	1.31	19/4606 (0.4%)
1	4F	1.11	10/3398 (0.3%)	1.35	20/4606 (0.4%)
1	4G	1.21	10/3398 (0.3%)	1.54	45/4606 (1.0%)
1	4H	1.20	9/3398 (0.3%)	1.46	30/4606 (0.7%)
1	4I	1.08	11/3398 (0.3%)	1.30	20/4606 (0.4%)
2	3A	1.15	7/3404 (0.2%)	1.42	30/4606 (0.7%)
2	3B	1.07	9/3404 (0.3%)	1.37	20/4606 (0.4%)
2	3C	1.02	4/3404 (0.1%)	1.26	18/4606 (0.4%)
2	3D	1.09	6/3404 (0.2%)	1.32	22/4606 (0.5%)
2	3E	1.04	5/3404 (0.1%)	1.33	24/4606 (0.5%)
2	3F	1.12	6/3404 (0.2%)	1.39	31/4606 (0.7%)
2	3G	1.24	12/3404 (0.4%)	1.49	39/4606 (0.8%)
2	3H	1.13	10/3404 (0.3%)	1.44	23/4606 (0.5%)
2	3I	1.02	1/3404 (0.0%)	1.30	22/4606 (0.5%)
2	5A	1.15	9/3404 (0.3%)	1.47	41/4606 (0.9%)
2	5B	1.07	5/3404 (0.1%)	1.35	28/4606 (0.6%)
2	5C	1.00	3/3404 (0.1%)	1.27	14/4606 (0.3%)
2	5D	1.06	4/3404 (0.1%)	1.31	21/4606 (0.5%)
2	5E	1.07	3/3404 (0.1%)	1.35	23/4606 (0.5%)
2	5F	1.10	4/3404 (0.1%)	1.30	14/4606 (0.3%)
2	5G	1.17	7/3404 (0.2%)	1.51	36/4606 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	5H	1.16	13/3404 (0.4%)	1.43	19/4606 (0.4%)
2	5I	1.05	2/3404 (0.1%)	1.33	23/4606 (0.5%)
All	All	1.10	251/122436 (0.2%)	1.37	885/165816 (0.5%)

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	2A	0	7
1	2B	0	5
1	2C	0	6
1	2D	0	3
1	2E	0	7
1	2F	0	7
1	2G	0	12
1	2H	0	8
1	2I	0	6
1	4A	0	10
1	4B	0	5
1	4C	0	6
1	4D	0	5
1	4E	0	8
1	4F	0	7
1	4G	0	7
1	4H	0	9
1	4I	0	5
2	3A	0	11
2	3B	0	7
2	3C	0	8
2	3D	0	8
2	3E	0	8
2	3F	0	8
2	3G	0	5
2	3H	0	9
2	3I	0	4
2	5A	0	14
2	5B	0	4
2	5C	0	6
2	5D	0	6
2	5E	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	5F	0	4
2	5G	0	12
2	5H	0	8
2	5I	0	5
All	All	0	259

The worst 5 of 251 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2E	8	HIS	CE1-NE2	-11.47	1.21	1.32
1	2F	107	HIS	CE1-NE2	11.16	1.43	1.32
2	3A	137	HIS	CE1-NE2	10.33	1.42	1.32
2	5B	264	HIS	CE1-NE2	-9.29	1.23	1.32
1	4C	8	HIS	CE1-NE2	-9.16	1.23	1.32

The worst 5 of 885 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3I	375	GLN	CB-CG-CD	-13.58	89.52	112.60
1	2F	386	GLU	CB-CG-CD	10.86	131.06	112.60
1	2F	358	GLN	CB-CA-C	10.83	126.84	109.51
2	3F	298	ASN	OD1-CG-ND2	-10.40	112.20	122.60
2	5I	325	GLU	N-CA-CB	10.17	126.00	110.44

There are no chirality outliers.

5 of 259 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2A	201	ALA	Mainchain
1	2A	205	ASP	Mainchain
1	2A	208	ALA	Mainchain
1	2A	249	ASN	Sidechain
1	2A	285	GLN	Mainchain

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	2A	3325	0	3252	84	0
1	2B	3325	0	3252	79	0
1	2C	3325	0	3252	61	0
1	2D	3325	0	3252	105	0
1	2E	3325	0	3252	98	0
1	2F	3325	0	3252	61	0
1	2G	3325	0	3252	95	0
1	2H	3325	0	3252	86	0
1	2I	3325	0	3252	57	0
1	4A	3325	0	3252	94	0
1	4B	3325	0	3252	96	0
1	4C	3325	0	3252	84	0
1	4D	3325	0	3251	87	0
1	4E	3325	0	3252	124	0
1	4F	3325	0	3252	89	0
1	4G	3325	0	3252	107	0
1	4H	3325	0	3252	104	0
1	4I	3325	0	3252	74	0
2	3A	3331	0	3207	104	0
2	3B	3331	0	3207	118	0
2	3C	3331	0	3207	75	0
2	3D	3331	0	3207	106	0
2	3E	3331	0	3207	143	0
2	3F	3331	0	3209	116	0
2	3G	3331	0	3209	102	0
2	3H	3331	0	3209	98	0
2	3I	3331	0	3209	60	0
2	5A	3331	0	3207	89	0
2	5B	3331	0	3207	84	0
2	5C	3331	0	3208	65	0
2	5D	3331	0	3206	116	0
2	5E	3331	0	3207	128	0
2	5F	3331	0	3209	74	0
2	5G	3331	0	3209	104	0
2	5H	3331	0	3209	88	0
2	5I	3331	0	3209	57	0
All	All	119808	0	116277	2526	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 11.

The worst 5 of 2526 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)
1:4E:60:LYS:HZ2	1:4F:283:HIS:CD2	1.09	1.60
2:3E:58:ARG:NH1	2:3F:281:TYR:HE1	0.98	1.44
1:4C:121:ARG:HH12	1:4D:283:HIS:CE1	1.35	1.40
1:4E:60:LYS:NZ	1:4F:283:HIS:HD2	0.94	1.40
2:3E:58:ARG:NH1	2:3F:281:TYR:CE1	1.89	1.39

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2A	424/437 (97%)	416 (98%)	7 (2%)	1 (0%)	43	78
1	2B	424/437 (97%)	416 (98%)	8 (2%)	0	100	100
1	2C	424/437 (97%)	419 (99%)	5 (1%)	0	100	100
1	2D	424/437 (97%)	418 (99%)	6 (1%)	0	100	100
1	2E	424/437 (97%)	417 (98%)	7 (2%)	0	100	100
1	2F	424/437 (97%)	415 (98%)	9 (2%)	0	100	100
1	2G	424/437 (97%)	411 (97%)	13 (3%)	0	100	100
1	2H	424/437 (97%)	414 (98%)	10 (2%)	0	100	100
1	2I	424/437 (97%)	418 (99%)	6 (1%)	0	100	100
1	4A	424/437 (97%)	414 (98%)	10 (2%)	0	100	100
1	4B	424/437 (97%)	413 (97%)	11 (3%)	0	100	100
1	4C	424/437 (97%)	416 (98%)	8 (2%)	0	100	100
1	4D	424/437 (97%)	417 (98%)	7 (2%)	0	100	100
1	4E	424/437 (97%)	414 (98%)	10 (2%)	0	100	100
1	4F	424/437 (97%)	417 (98%)	7 (2%)	0	100	100
1	4G	424/437 (97%)	415 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	4H	424/437 (97%)	411 (97%)	13 (3%)	0	100	100
1	4I	424/437 (97%)	419 (99%)	5 (1%)	0	100	100
2	3A	424/426 (100%)	411 (97%)	13 (3%)	0	100	100
2	3B	424/426 (100%)	408 (96%)	16 (4%)	0	100	100
2	3C	424/426 (100%)	409 (96%)	15 (4%)	0	100	100
2	3D	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	3E	424/426 (100%)	406 (96%)	18 (4%)	0	100	100
2	3F	424/426 (100%)	406 (96%)	18 (4%)	0	100	100
2	3G	424/426 (100%)	413 (97%)	11 (3%)	0	100	100
2	3H	424/426 (100%)	411 (97%)	13 (3%)	0	100	100
2	3I	424/426 (100%)	411 (97%)	13 (3%)	0	100	100
2	5A	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	5B	424/426 (100%)	406 (96%)	18 (4%)	0	100	100
2	5C	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	5D	424/426 (100%)	409 (96%)	15 (4%)	0	100	100
2	5E	424/426 (100%)	405 (96%)	19 (4%)	0	100	100
2	5F	424/426 (100%)	407 (96%)	17 (4%)	0	100	100
2	5G	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	5H	424/426 (100%)	411 (97%)	12 (3%)	1 (0%)	43	78
2	5I	424/426 (100%)	412 (97%)	12 (3%)	0	100	100
All	All	15264/15534 (98%)	14845 (97%)	417 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2A	304	LYS
2	5H	180	VAL

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	2A	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2B	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	2C	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2D	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2E	359/368 (98%)	359 (100%)	0	100	100
1	2F	359/368 (98%)	358 (100%)	1 (0%)	86	86
1	2G	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2H	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	2I	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	4A	359/368 (98%)	353 (98%)	6 (2%)	53	69
1	4B	359/368 (98%)	356 (99%)	3 (1%)	73	80
1	4C	359/368 (98%)	356 (99%)	3 (1%)	73	80
1	4D	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	4E	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	4F	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	4G	359/368 (98%)	352 (98%)	7 (2%)	50	67
1	4H	359/368 (98%)	356 (99%)	3 (1%)	73	80
1	4I	359/368 (98%)	354 (99%)	5 (1%)	59	72
2	3A	364/366 (100%)	362 (100%)	2 (0%)	81	83
2	3B	364/366 (100%)	363 (100%)	1 (0%)	86	86
2	3C	364/366 (100%)	363 (100%)	1 (0%)	86	86
2	3D	364/366 (100%)	362 (100%)	2 (0%)	81	83
2	3E	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	3F	364/366 (100%)	357 (98%)	7 (2%)	50	67
2	3G	364/366 (100%)	361 (99%)	3 (1%)	73	80
2	3H	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	3I	364/366 (100%)	361 (99%)	3 (1%)	73	80
2	5A	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5B	364/366 (100%)	362 (100%)	2 (0%)	81	83
2	5C	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5D	364/366 (100%)	363 (100%)	1 (0%)	86	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	5E	364/366 (100%)	357 (98%)	7 (2%)	50	67
2	5F	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5G	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5H	364/366 (100%)	361 (99%)	3 (1%)	73	80
2	5I	364/366 (100%)	361 (99%)	3 (1%)	73	80
All	All	13014/13212 (98%)	12899 (99%)	115 (1%)	68	79

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	4C	107	HIS
2	5H	117	LEU
1	4G	238	LEU
2	5H	112	LEU
2	5E	297	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 207 such sidechains are listed below:

Mol	Chain	Res	Type
1	4B	216	ASN
1	4I	176	GLN
2	5H	195	ASN
1	4C	258	ASN
1	4F	139	ASN

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.

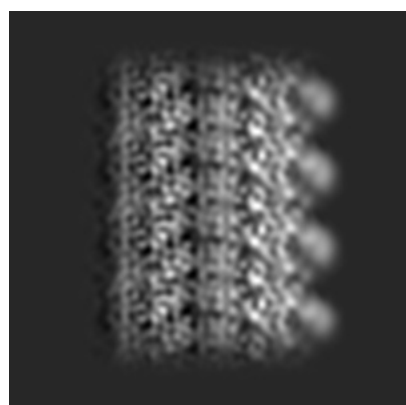
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26020. These allow visual inspection of the internal detail of the map and identification of artifacts.

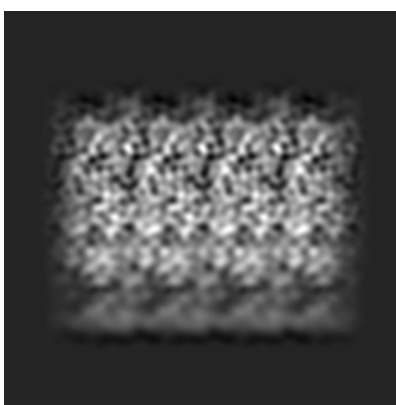
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

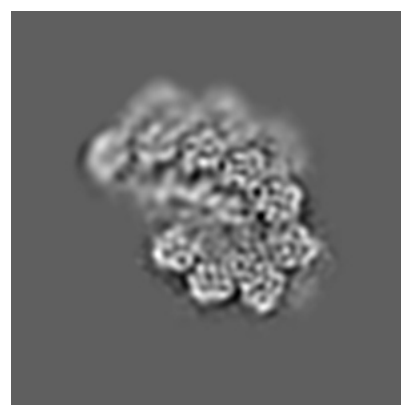
6.1.1 Primary map



X



Y

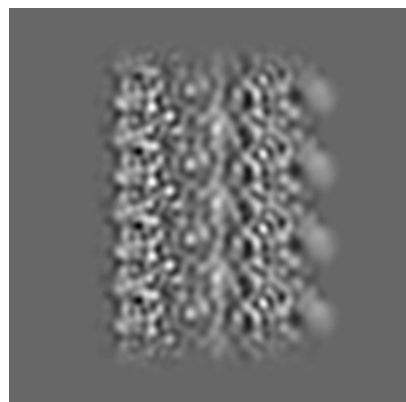


Z

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

6.2 Central slices [i](#)

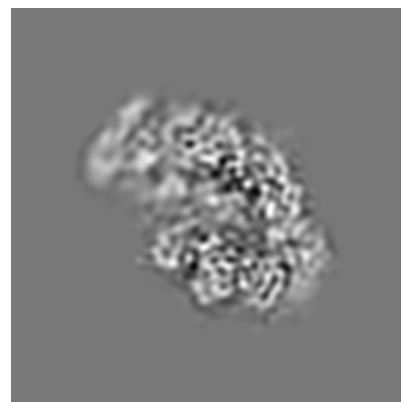
6.2.1 Primary map



X Index: 64



Y Index: 64

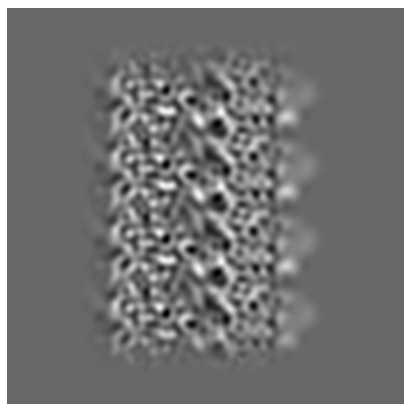


Z Index: 64

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

6.3 Largest variance slices [i](#)

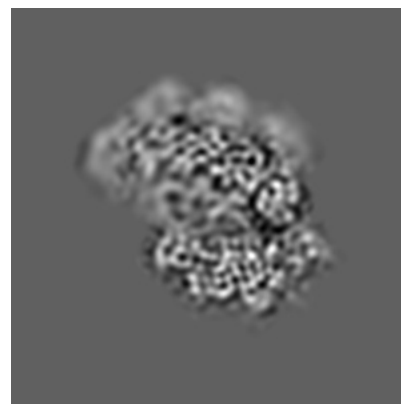
6.3.1 Primary map



X Index: 76



Y Index: 79

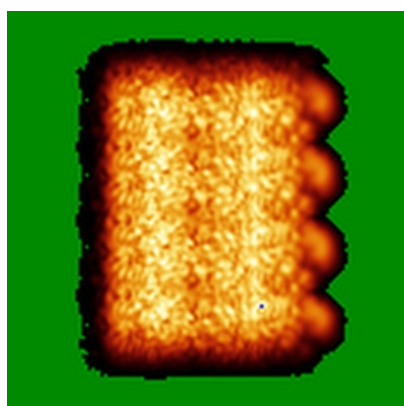


Z Index: 32

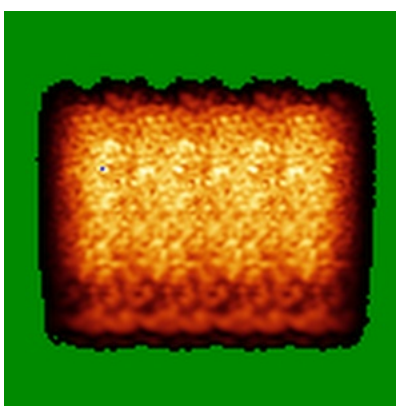
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

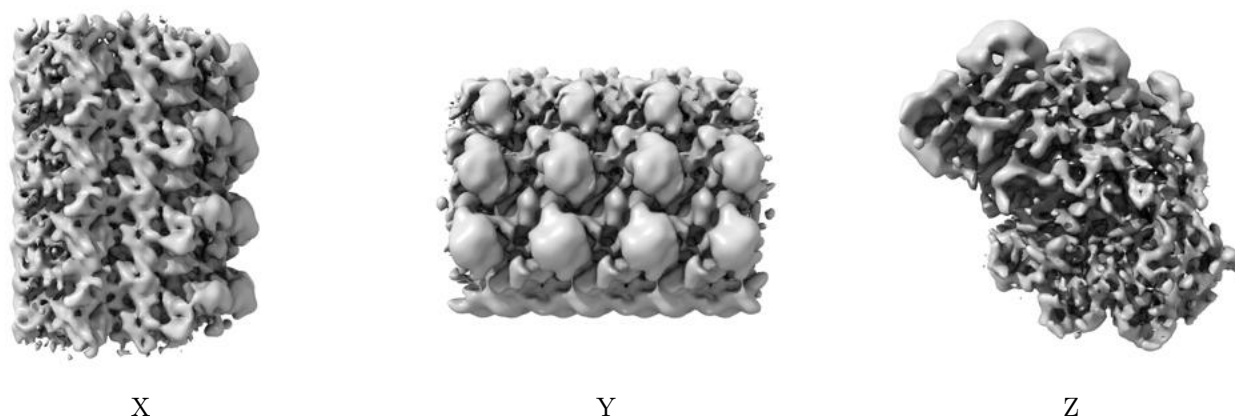


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

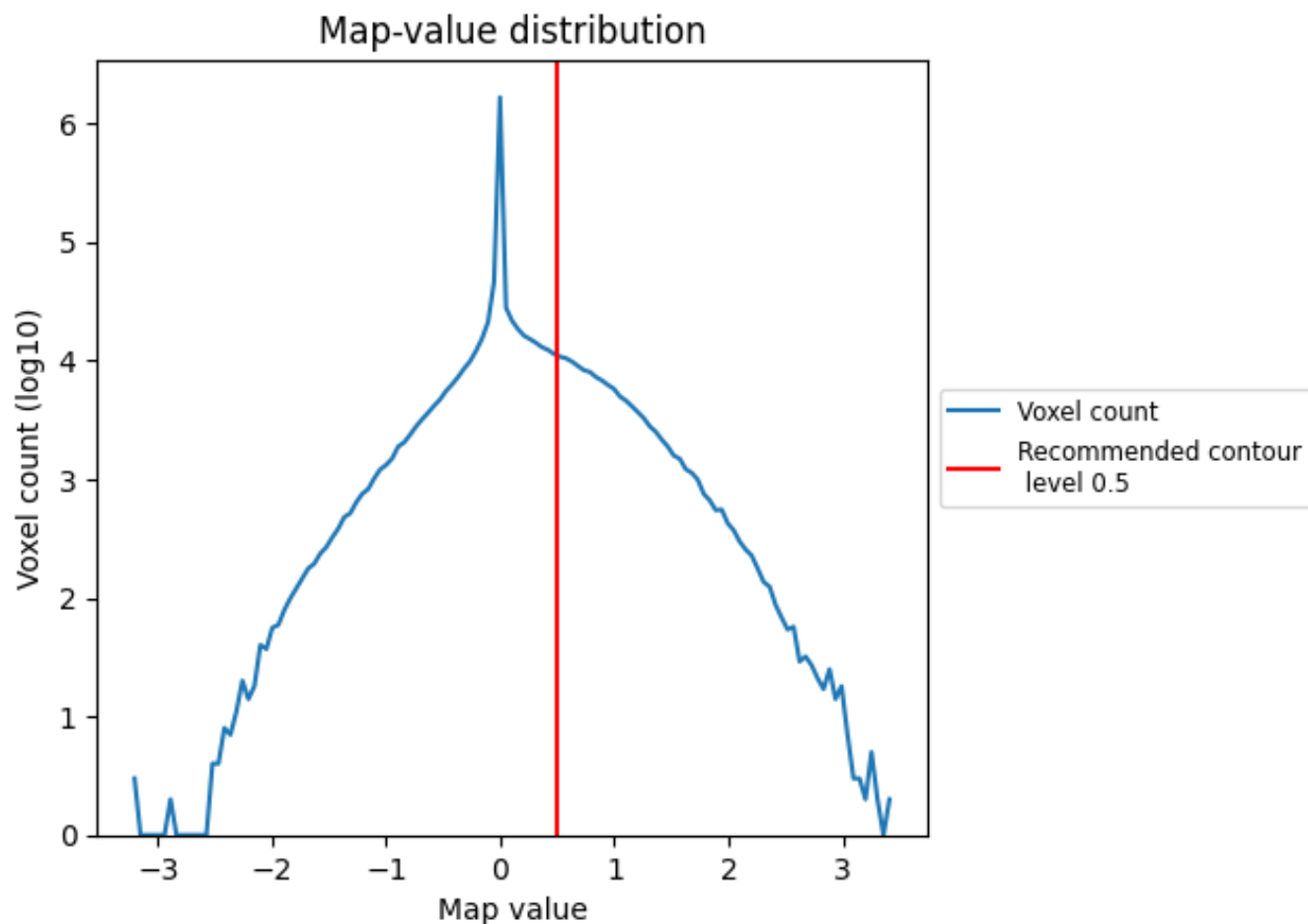
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

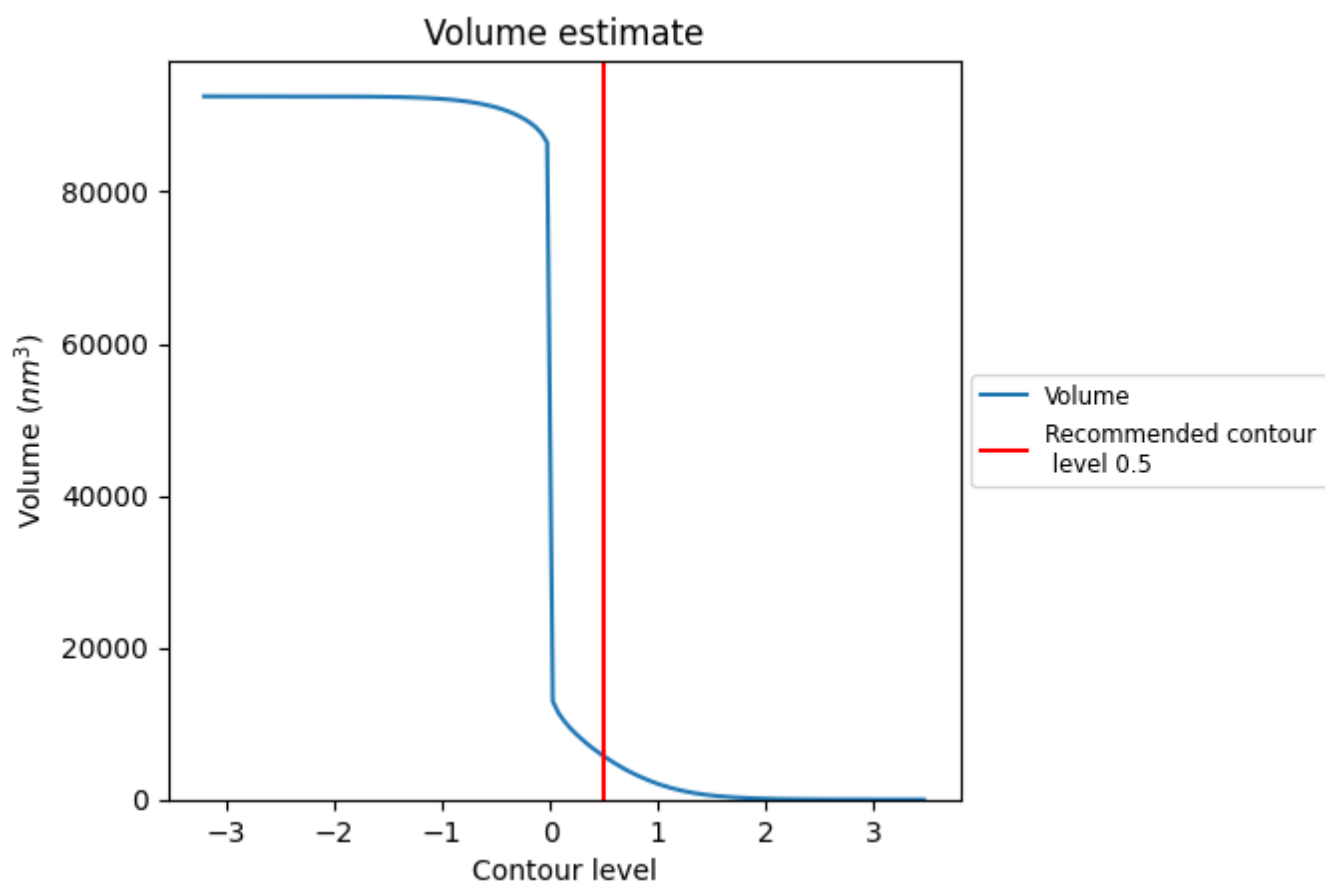
This section contains the results of statistical analysis of the map.

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.

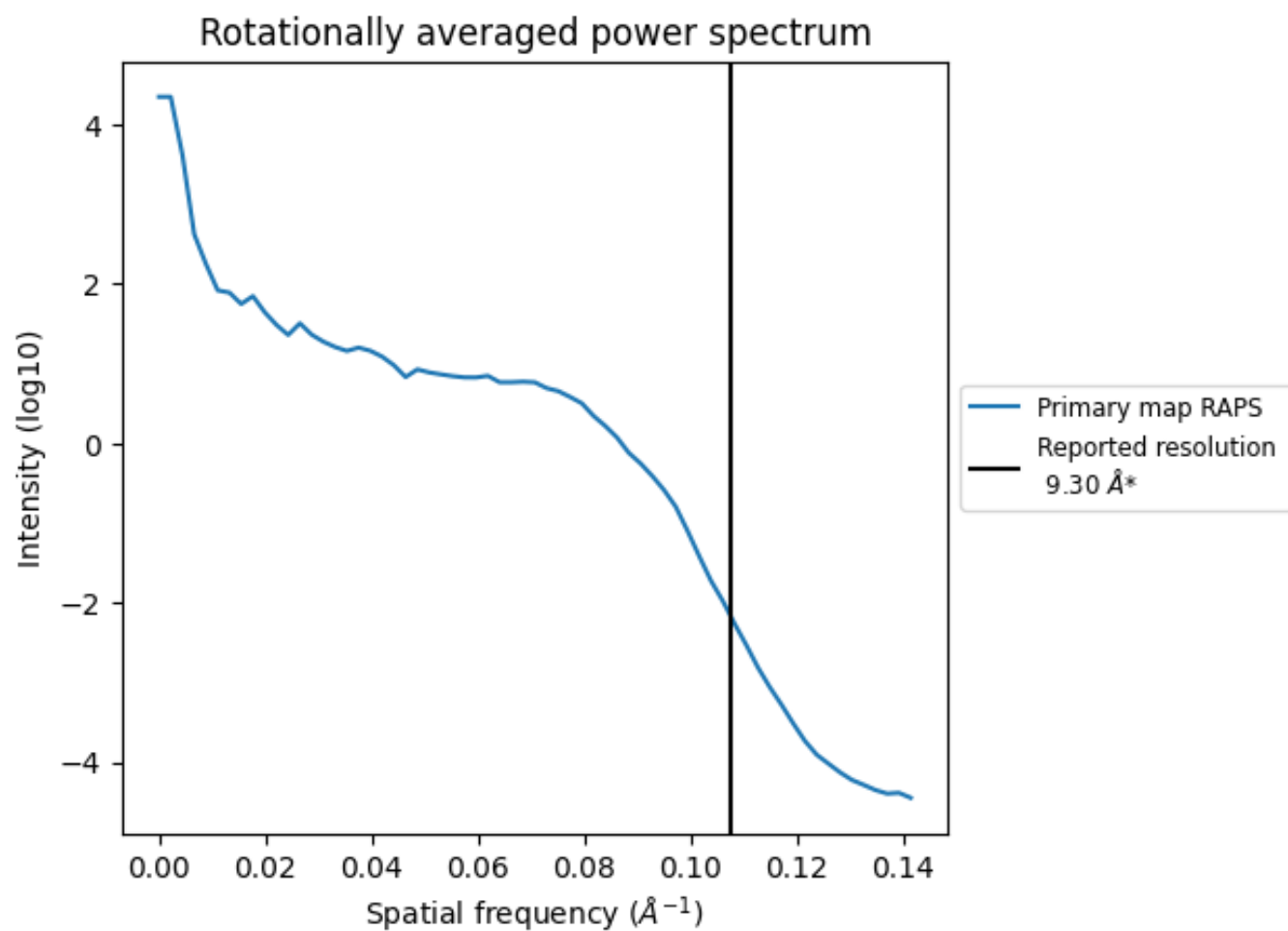
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5688 nm³; this corresponds to an approximate mass of 5138 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 0.108 Å⁻¹

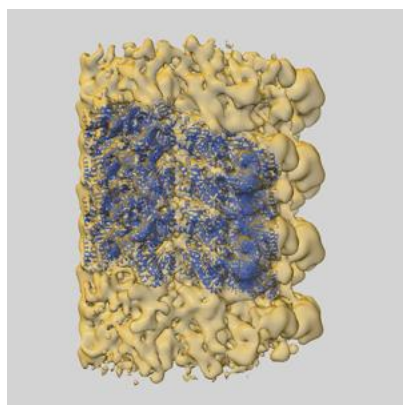
8 Fourier-Shell correlation ⓘ

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

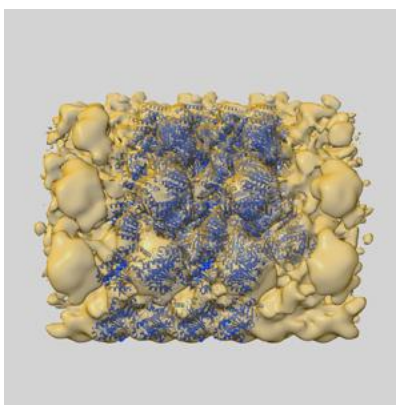
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26020 and PDB model 7TNT. Per-residue inclusion information can be found in section [3](#) on page [7](#).

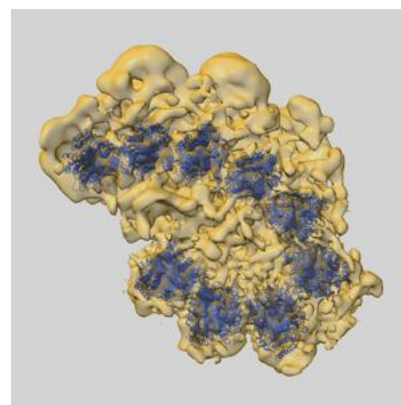
9.1 Map-model overlay [i](#)



X



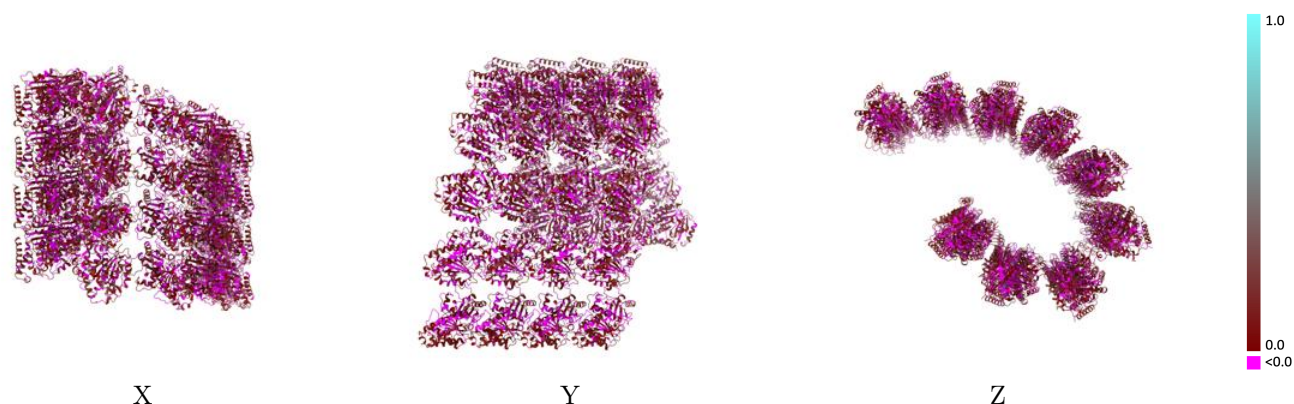
Y



Z

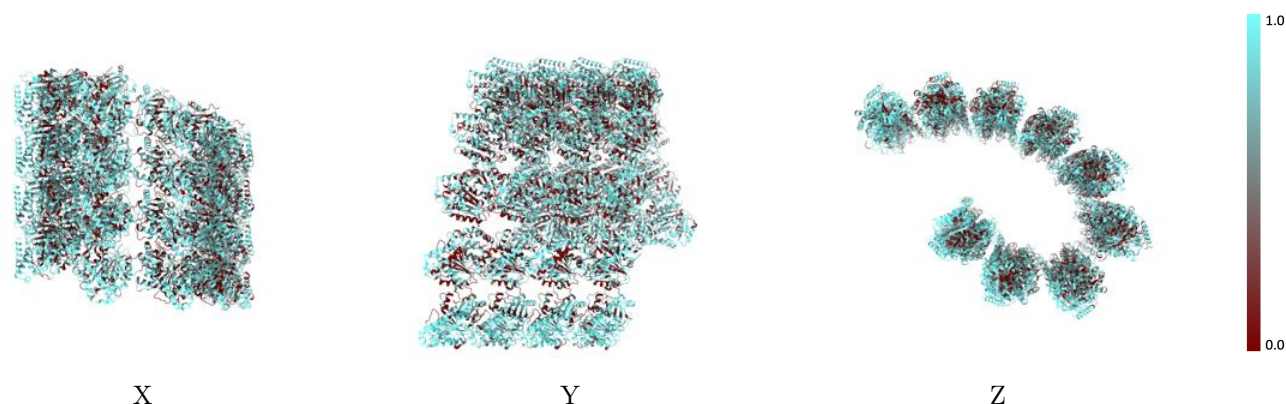
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



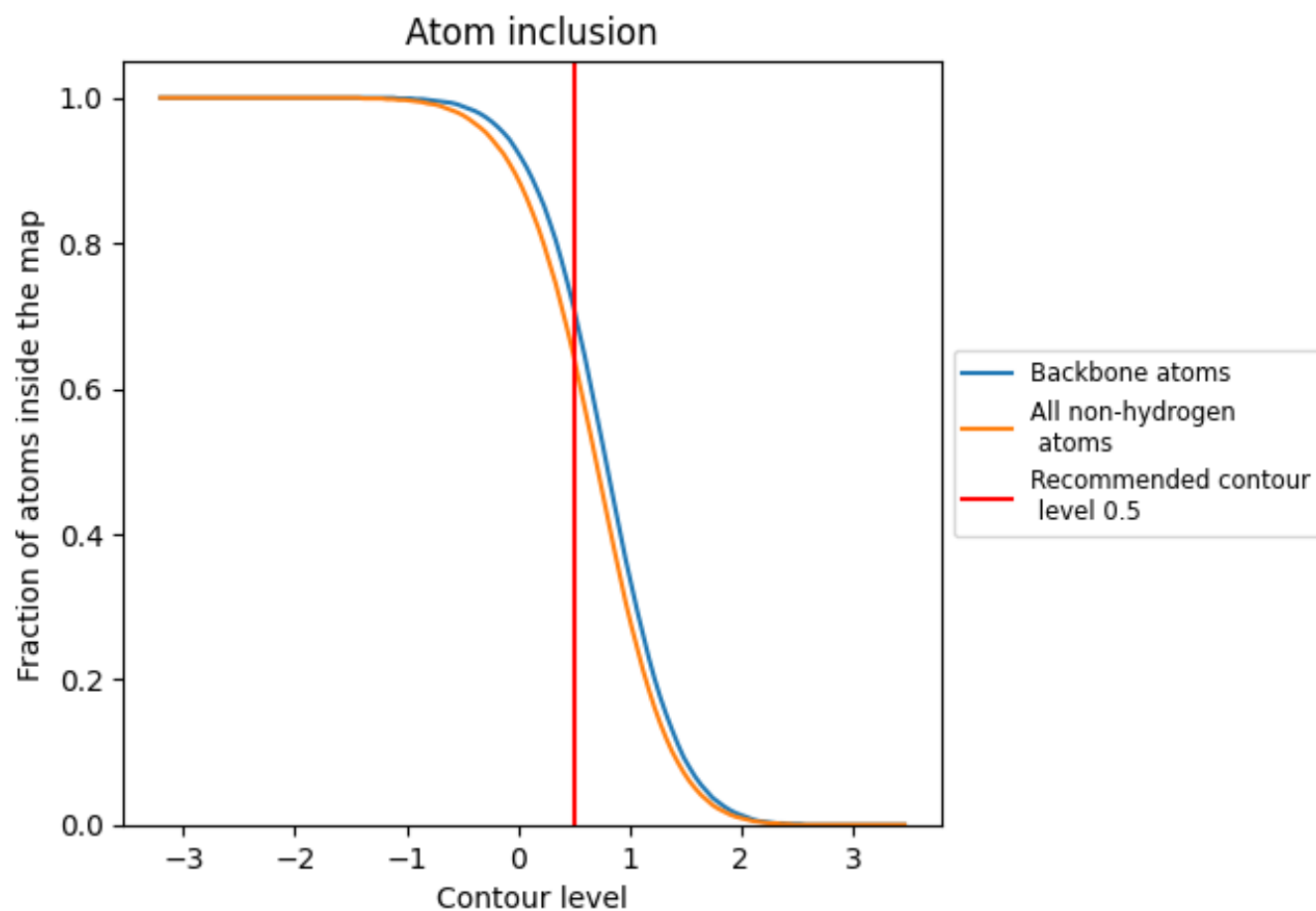
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6440	 0.0530
2A	 0.7180	 0.0590
2B	 0.6580	 0.0530
2C	 0.6420	 0.0620
2D	 0.5940	 0.0530
2E	 0.5920	 0.0500
2F	 0.5900	 0.0480
2G	 0.6300	 0.0580
2H	 0.6000	 0.0350
2I	 0.7640	 0.0390
3A	 0.7140	 0.0620
3B	 0.6630	 0.0700
3C	 0.6540	 0.0620
3D	 0.6530	 0.0650
3E	 0.6030	 0.0510
3F	 0.5930	 0.0610
3G	 0.5680	 0.0410
3H	 0.5900	 0.0380
3I	 0.7520	 0.0330
4A	 0.7220	 0.0590
4B	 0.6720	 0.0680
4C	 0.6470	 0.0650
4D	 0.6030	 0.0540
4E	 0.6060	 0.0530
4F	 0.6110	 0.0610
4G	 0.6360	 0.0590
4H	 0.6160	 0.0390
4I	 0.7810	 0.0400
5A	 0.7070	 0.0650
5B	 0.6580	 0.0640
5C	 0.6430	 0.0630
5D	 0.6500	 0.0700
5E	 0.5900	 0.0470
5F	 0.5820	 0.0490
5G	 0.5630	 0.0350



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Chain	Atom inclusion	Q-score
5H	 0.5740	 0.0330
5I	 0.7390	 0.0260