



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 01:53 AM UTC

PDB ID : 7QJB / pdb_00007qjb
EMDB ID : EMD-14016
Title : Structure of recombinant human gamma-Tubulin Ring Complex 12-spoked assembly intermediate (spokes 3-14, homogeneous dataset)
Authors : Zupa, E.; Pfeffer, S.
Deposited on : 2021-12-16
Resolution : 9.20 Å (reported)
Based on initial models : 6X0U, 6V6S, 7AS4, 6L81

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:

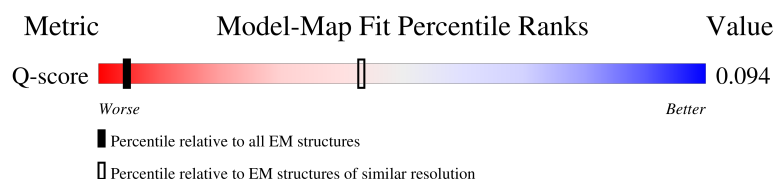
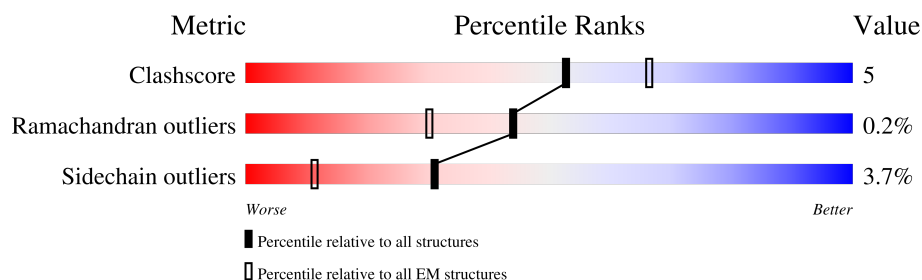
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.20 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	239 (8.70 - 9.70)

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	1	451	7% 69% 21% • 7%
1	2	451	10% 70% 20% • 7%
1	Q	451	36% 71% 19% • 7%
1	R	451	25% 72% 19% • 7%

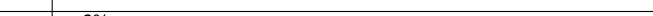
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Mol	Chain	Length	Quality of chain
1	S	451	
1	T	451	
1	U	451	
1	V	451	
1	W	451	
1	X	451	
1	Y	451	
1	Z	451	
2	e	375	
3	D	907	
3	F	907	
3	H	907	
3	N	907	
3	a	907	
3	h	907	
3	j	907	
4	C	902	
4	E	902	
4	G	902	
4	M	902	
5	I	667	
5	K	667	
6	J	1024	
6	l	1024	
7	L	1819	

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Mol	Chain	Length	Quality of chain
7	c	1819	 8% 91%
8	b	82	 6% 61% 17% 21%
8	d	82	 45% 61% 10% 28%
8	i	82	 20% 68% 11% 21%
8	k	82	 74% 5% 21%
8	m	82	 68% 11% 21%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 108374 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
1	1	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	2	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	Q	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	R	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	S	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	T	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	U	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	V	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	W	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	X	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	Y	420	Total 3373	C 2134	N 586	O 638	S 15	0	0
1	Z	420	Total 3373	C 2134	N 586	O 638	S 15	0	0

- Molecule 2 is a protein called actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	364	Total 2847	C 1803	N 476	O 548	S 20	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	116	Total	C	N	O	S	0	0
			933	591	171	169	2		
3	D	581	Total	C	N	O	S	0	0
			4796	3061	842	868	25		
3	F	599	Total	C	N	O	S	0	0
			4941	3151	871	894	25		
3	H	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
3	N	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
3	h	99	Total	C	N	O	S	0	0
			803	509	148	144	2		
3	j	107	Total	C	N	O	S	0	0
			843	533	156	152	2		

- Molecule 4 is a protein called Gamma-tubulin complex component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	620	Total	C	N	O	S	0	0
			5044	3257	845	910	32		
4	E	638	Total	C	N	O	S	0	0
			5202	3354	873	942	33		
4	G	640	Total	C	N	O	S	0	0
			5206	3354	875	944	33		
4	M	636	Total	C	N	O	S	0	0
			5186	3342	871	940	33		

- Molecule 5 is a protein called Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	521	Total	C	N	O	S	0	0
			4225	2737	720	750	18		
5	K	562	Total	C	N	O	S	0	0
			4579	2964	781	816	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	534	Total	C	N	O	S	0	0
			4429	2893	737	776	23		
6	l	108	Total	C	N	O	S	0	0
			847	539	150	157	1		

- Molecule 7 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	566	Total	C	N	O	S	0	0
			4587	3000	773	789	25		
7	c	158	Total	C	N	O	S	0	0
			1220	771	209	232	8		

- Molecule 8 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
8	k	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
8	m	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
8	b	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
8	d	59	Total	C	N	O	S	0	0
			454	281	79	90	4		

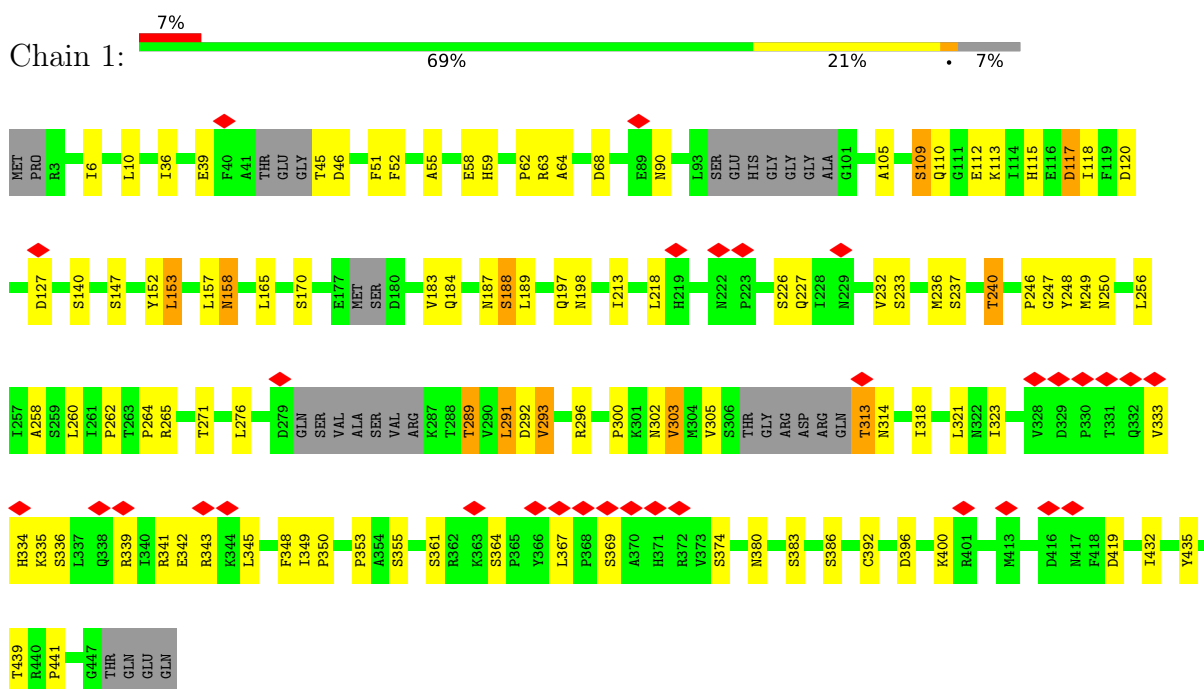
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		AltConf
9	l	6	Total	O	0
			6	6	

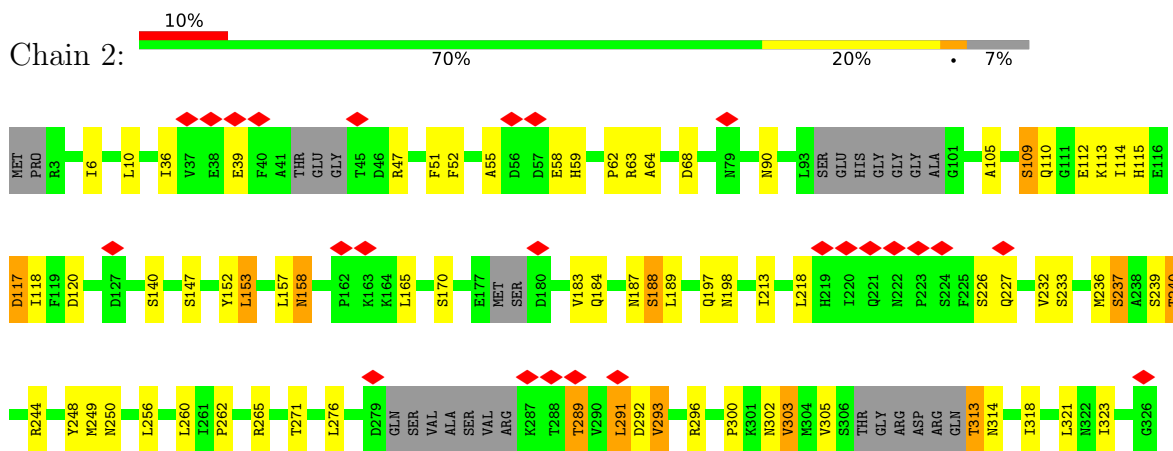
3 Residue-property plots

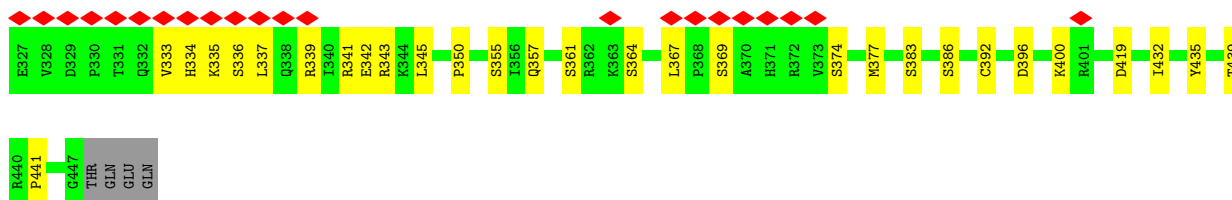
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

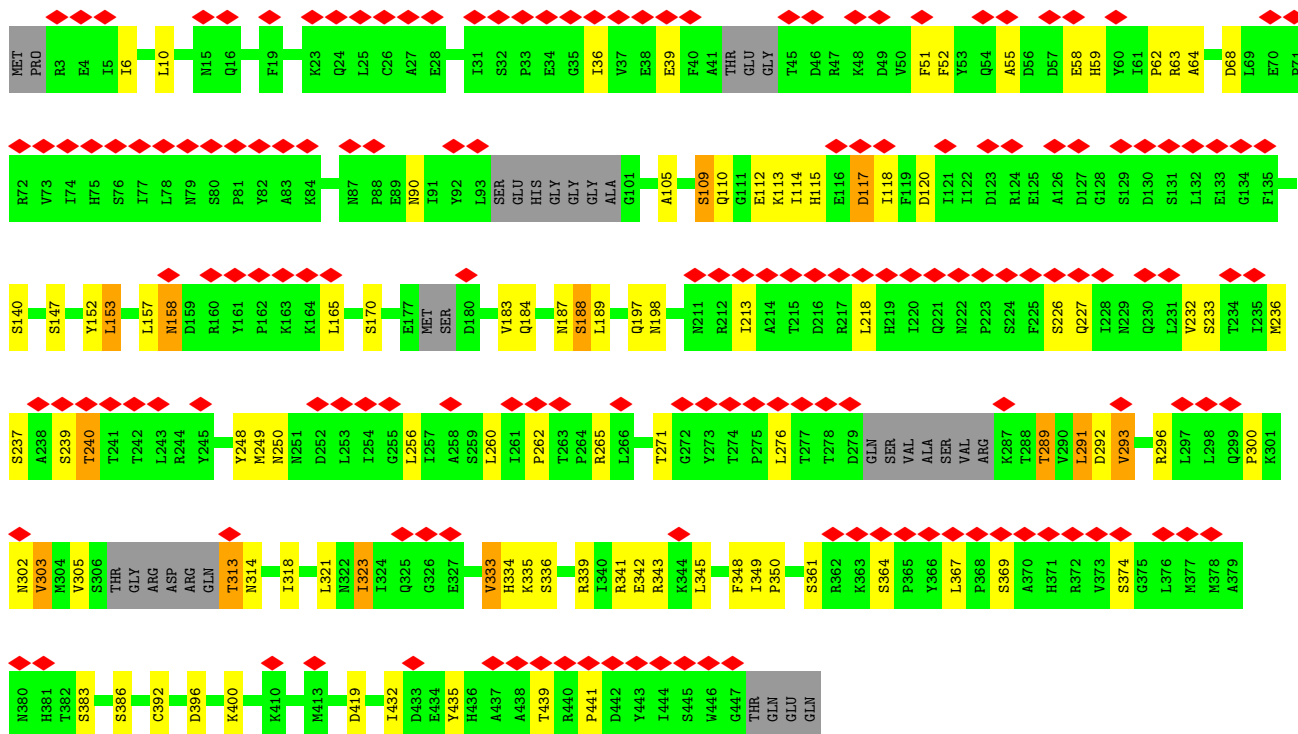


- Molecule 1: Tubulin gamma-1 chain

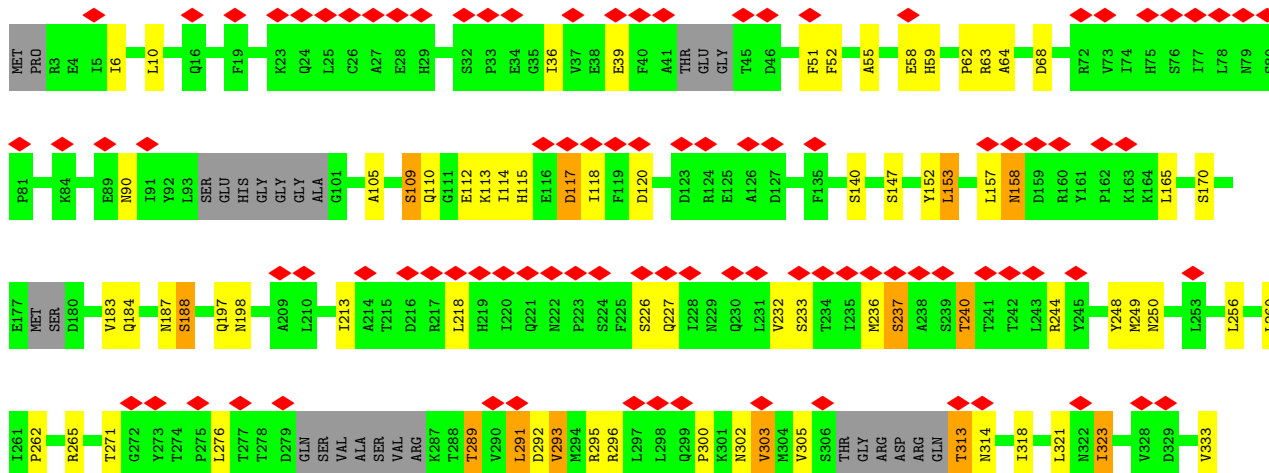


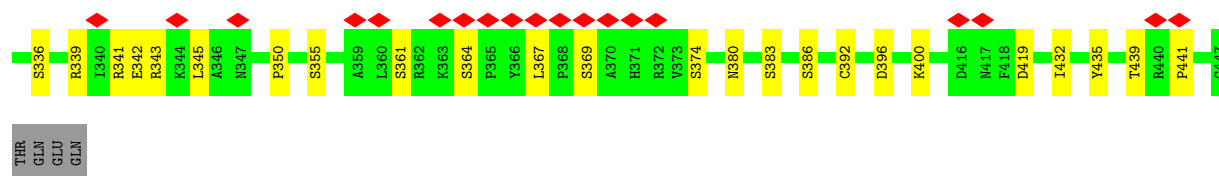


• Molecule 1: Tubulin gamma-1 chain

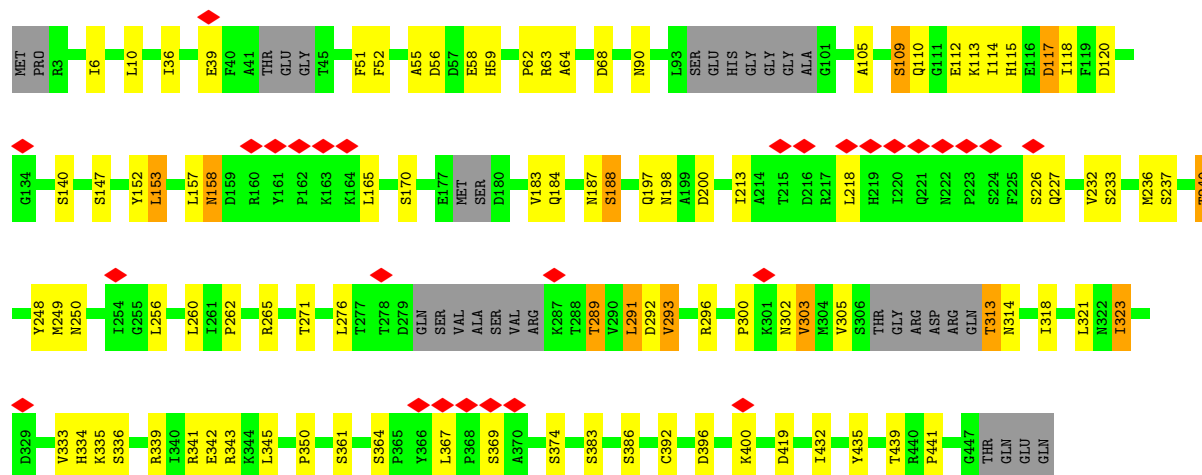


• Molecule 1: Tubulin gamma-1 chain

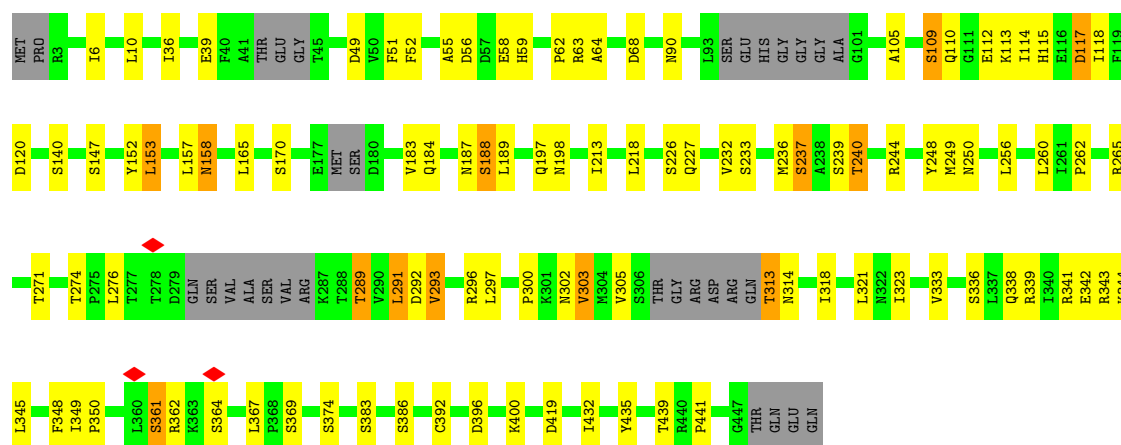




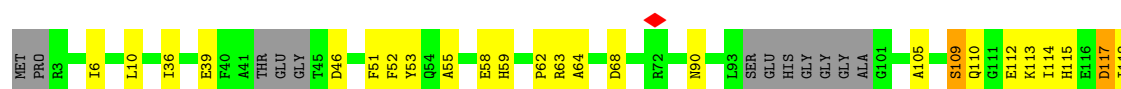
• Molecule 1: Tubulin gamma-1 chain

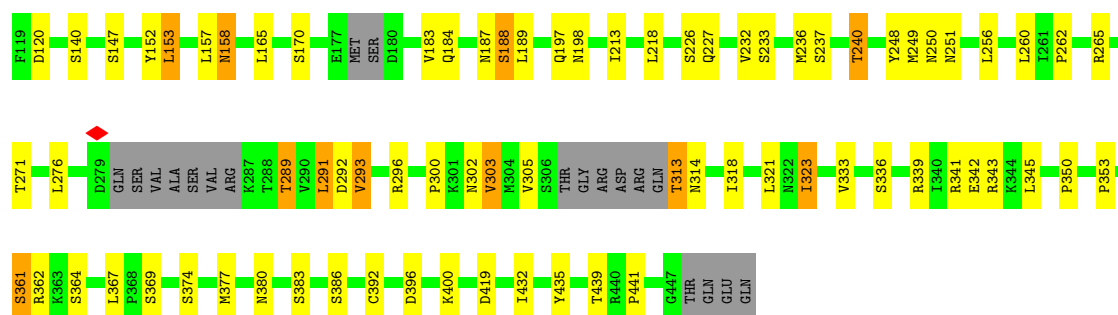


• Molecule 1: Tubulin gamma-1 chain



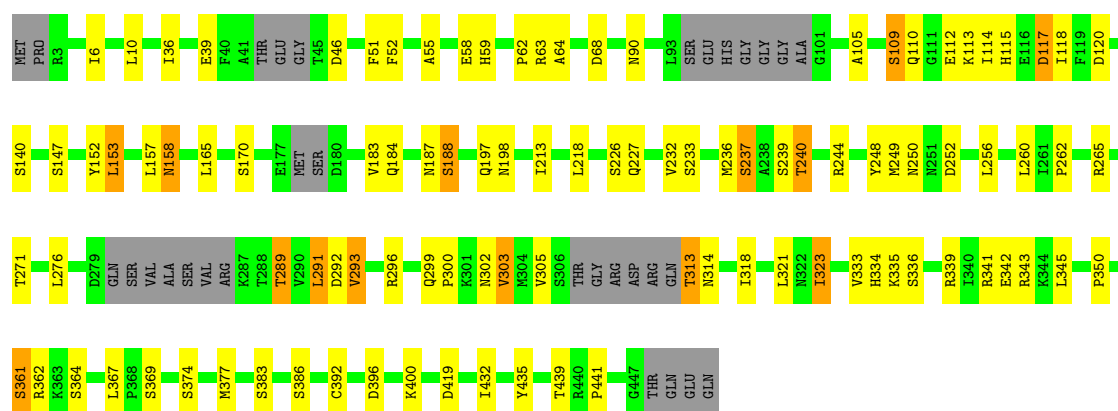
• Molecule 1: Tubulin gamma-1 chain





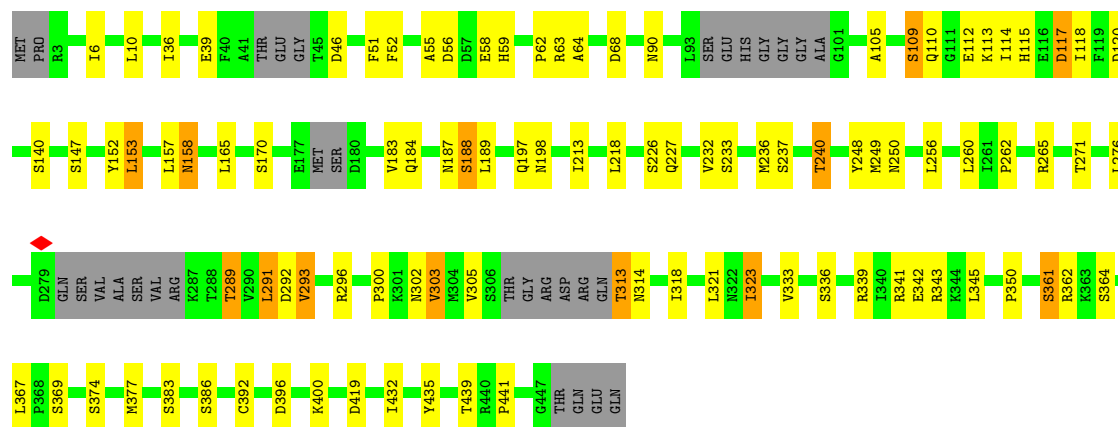
- Molecule 1: Tubulin gamma-1 chain

Chain V: 71% 20% 7%



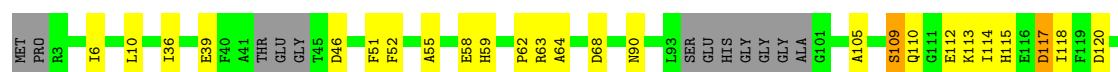
- Molecule 1: Tubulin gamma-1 chain

Chain W: 71% 19% 7%

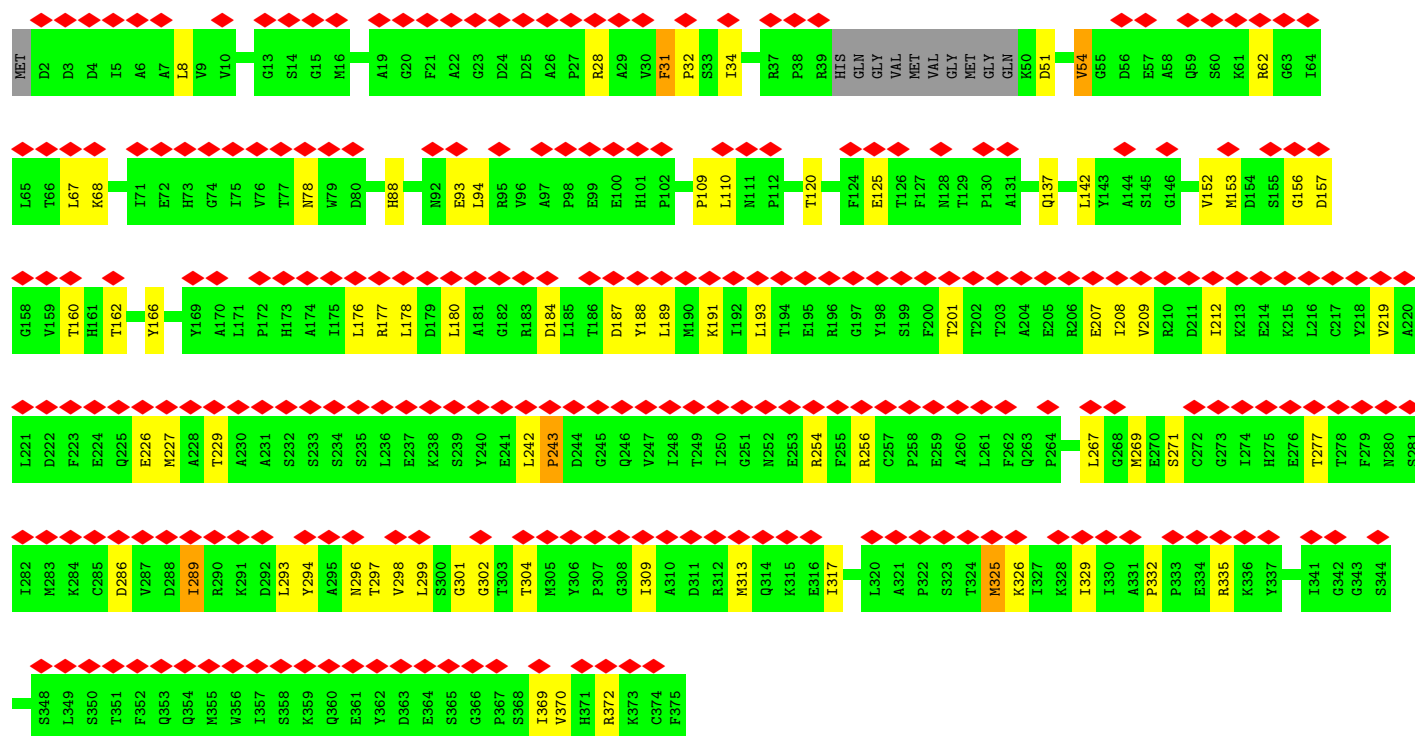


- Molecule 1: Tubulin gamma-1 chain

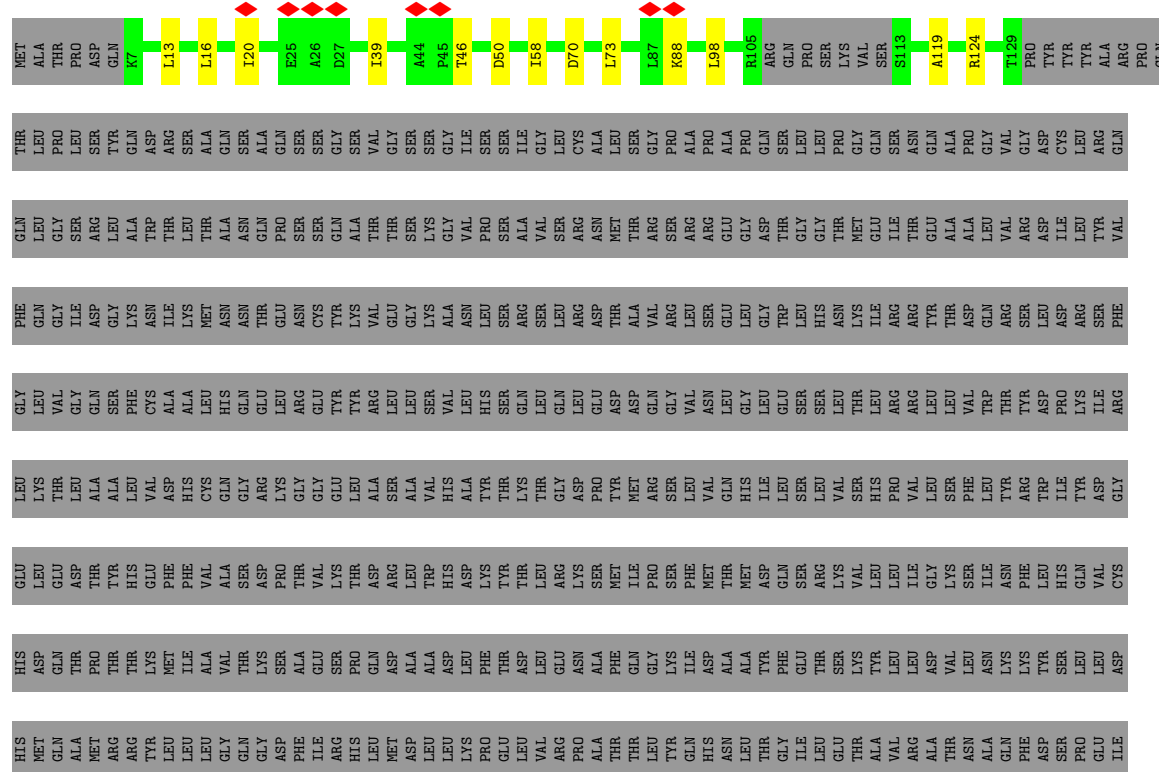
Chain X: 70% 20% 7%

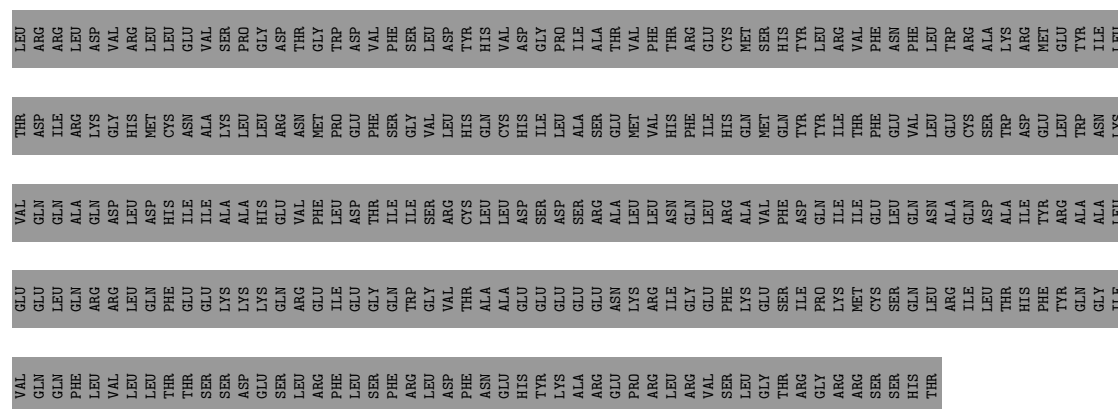




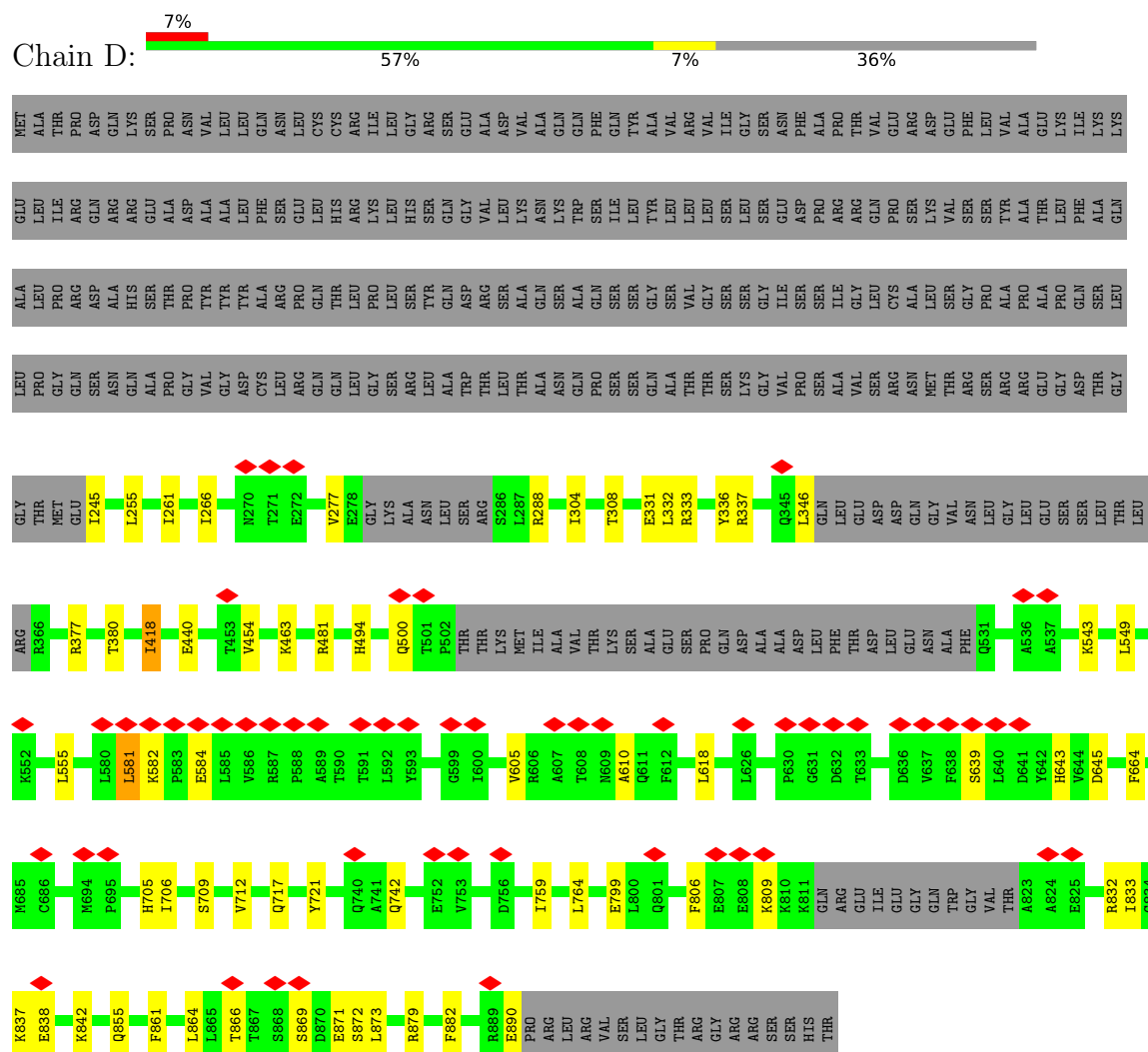


• Molecule 3: Gamma-tubulin complex component 3

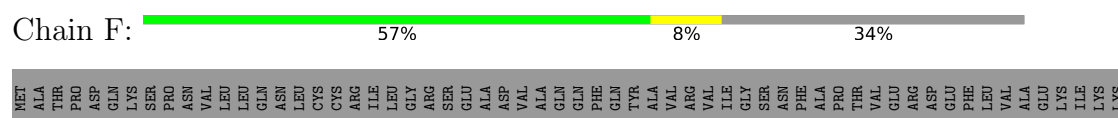


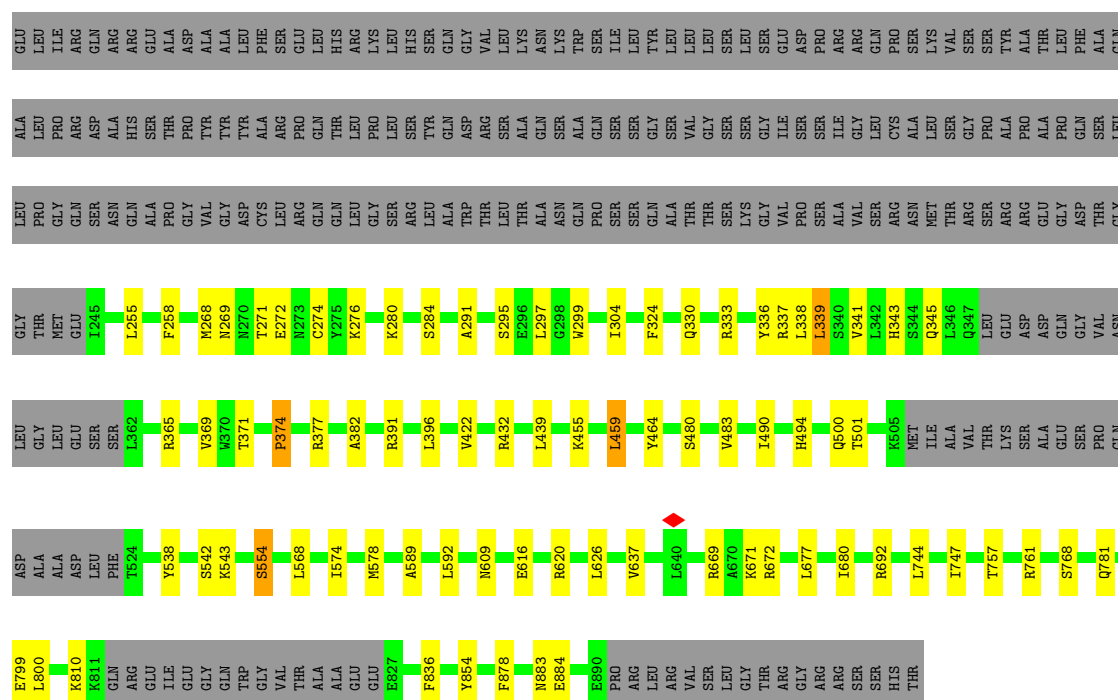


- Molecule 3: Gamma-tubulin complex component 3



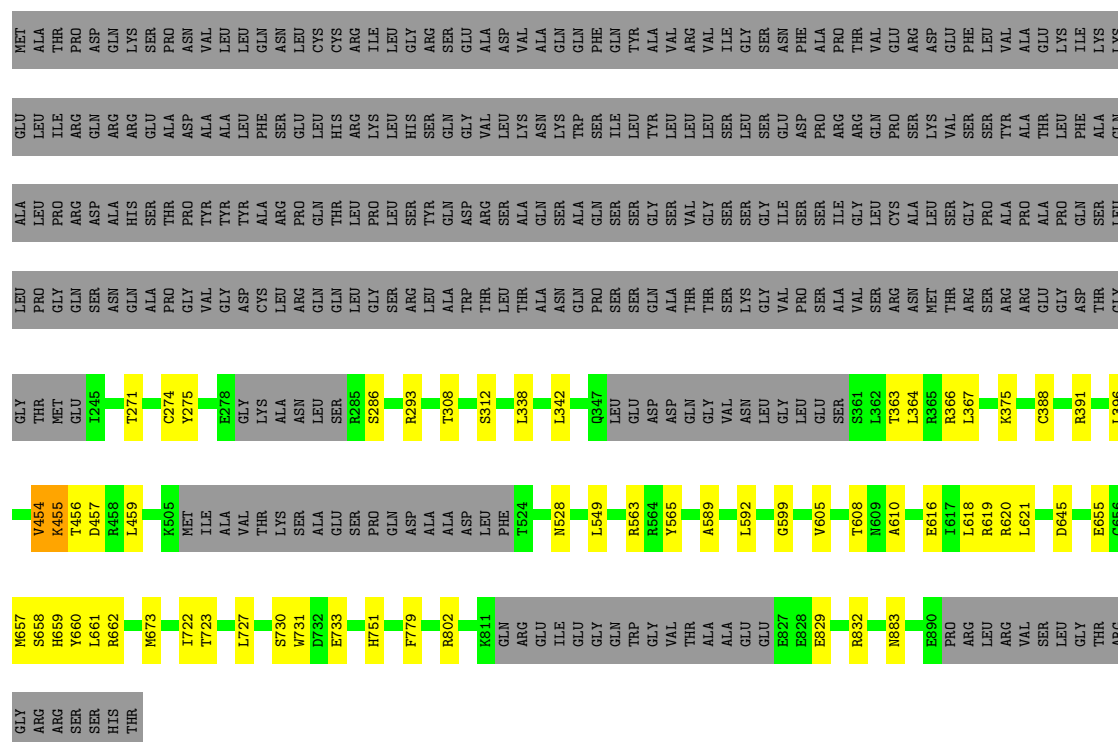
- Molecule 3: Gamma-tubulin complex component 3





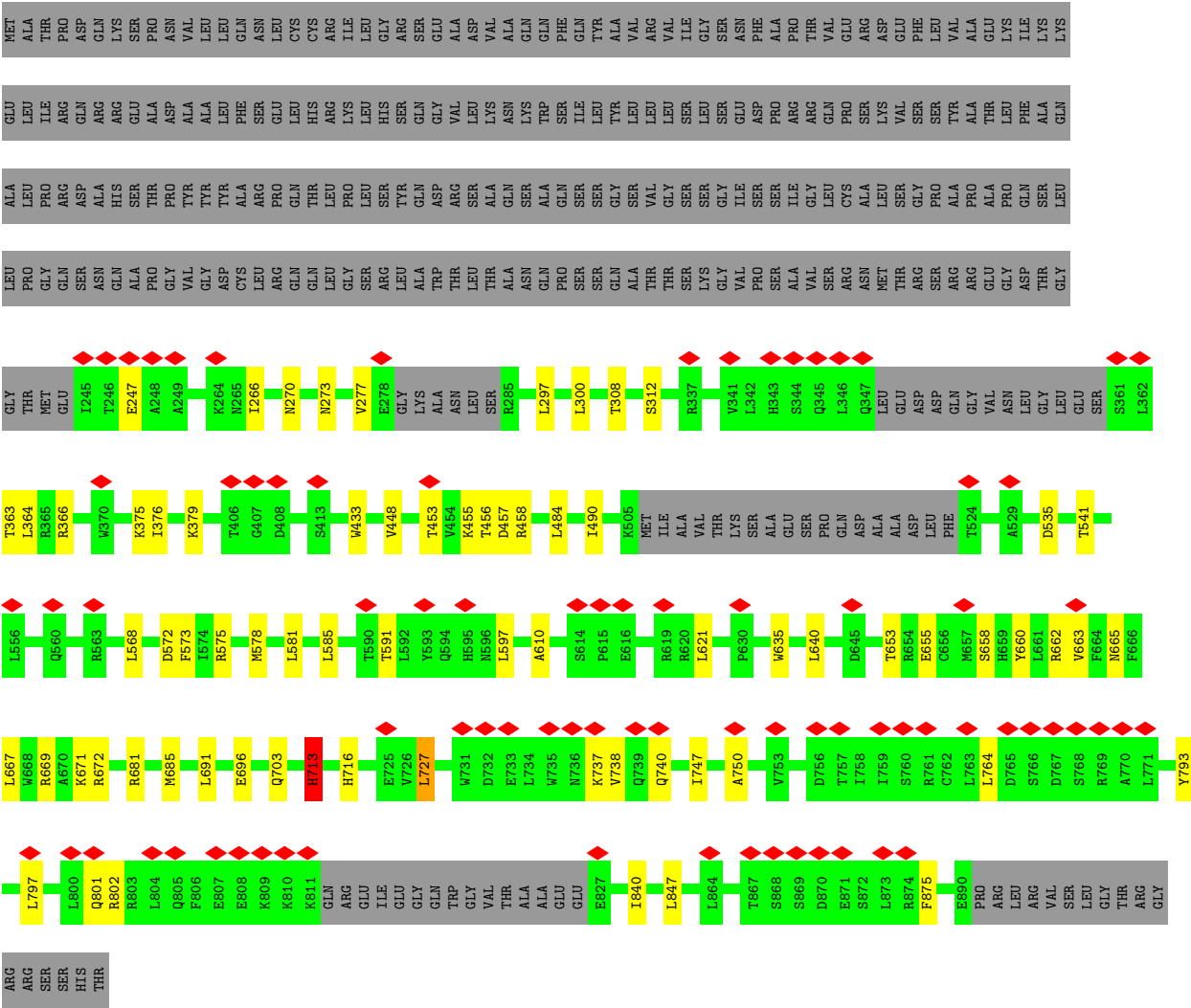
• Molecule 3: Gamma-tubulin complex component 3

Chain H: 59% 6% 35%

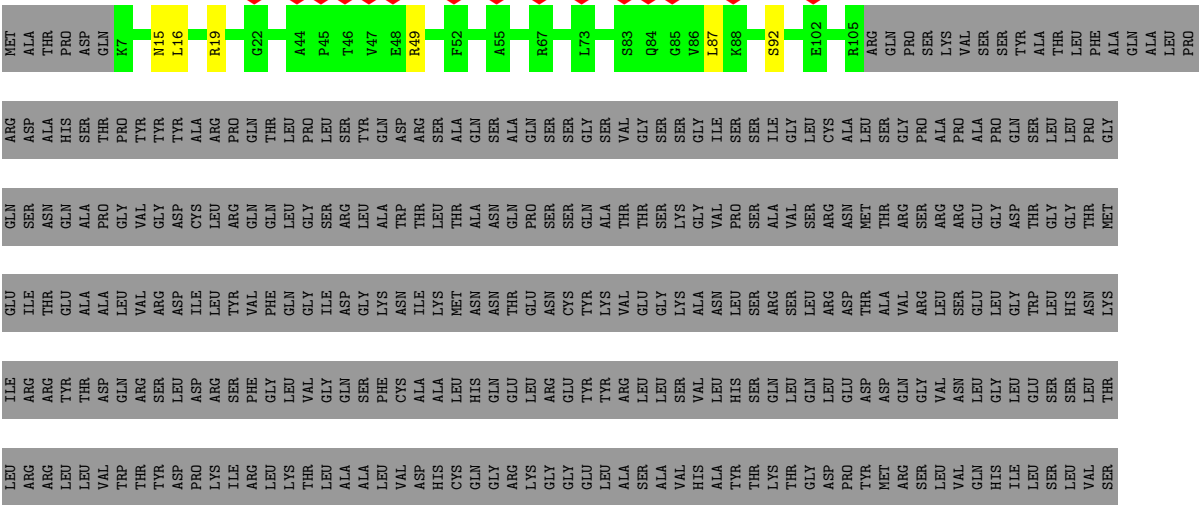


• Molecule 3: Gamma-tubulin complex component 3

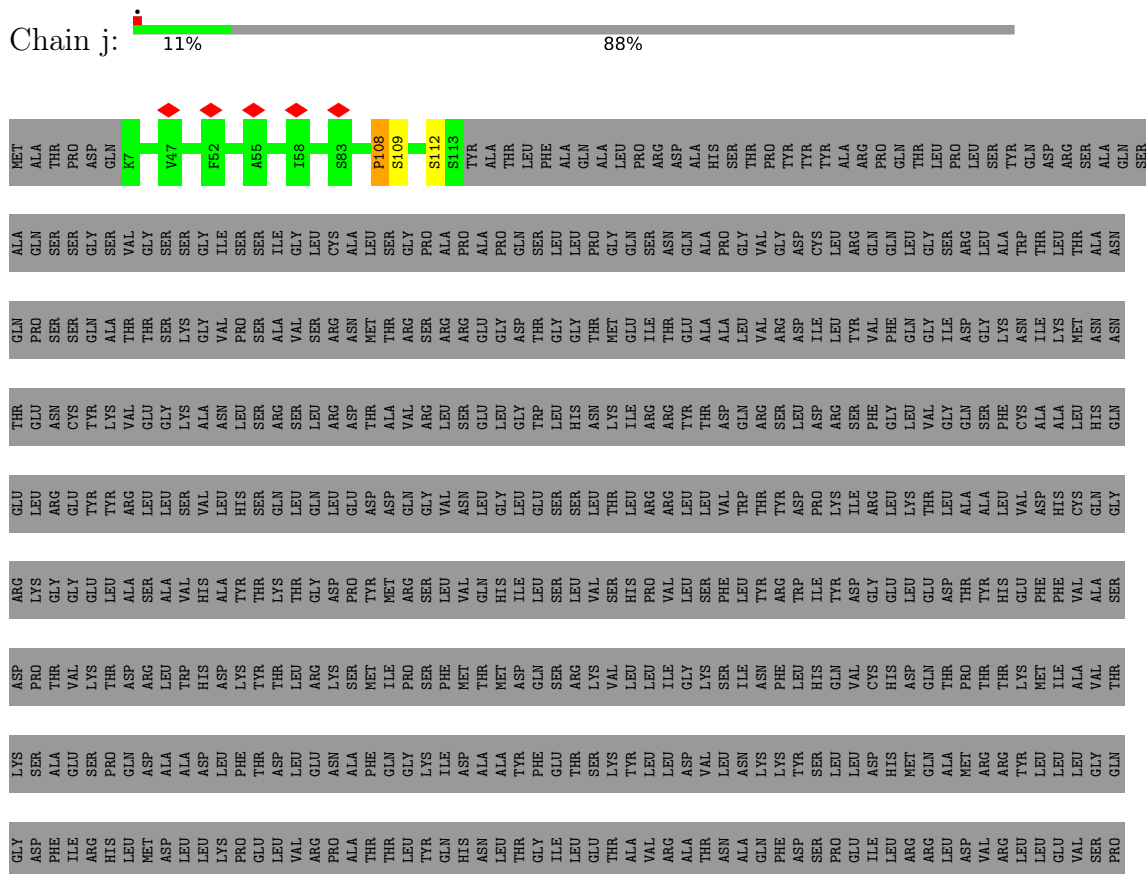
Chain N: 9% 58% 8% 35%

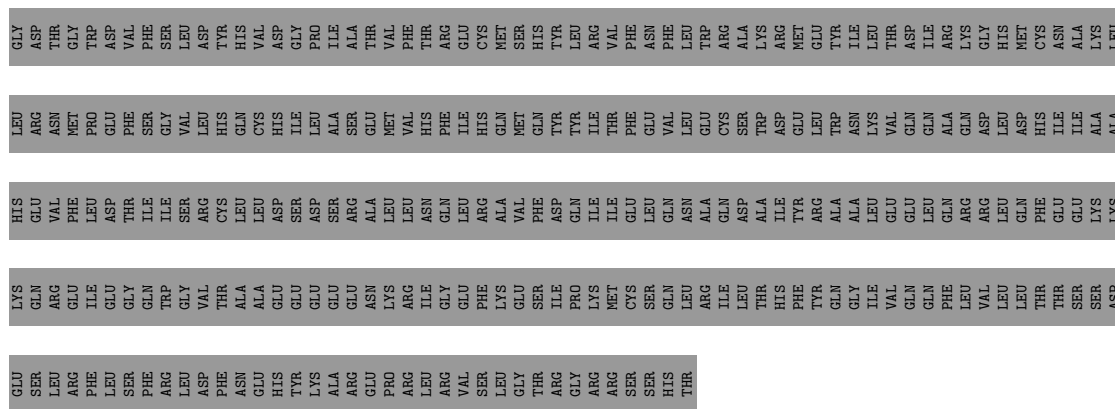


• Molecule 3: Gamma-tubulin complex component 3

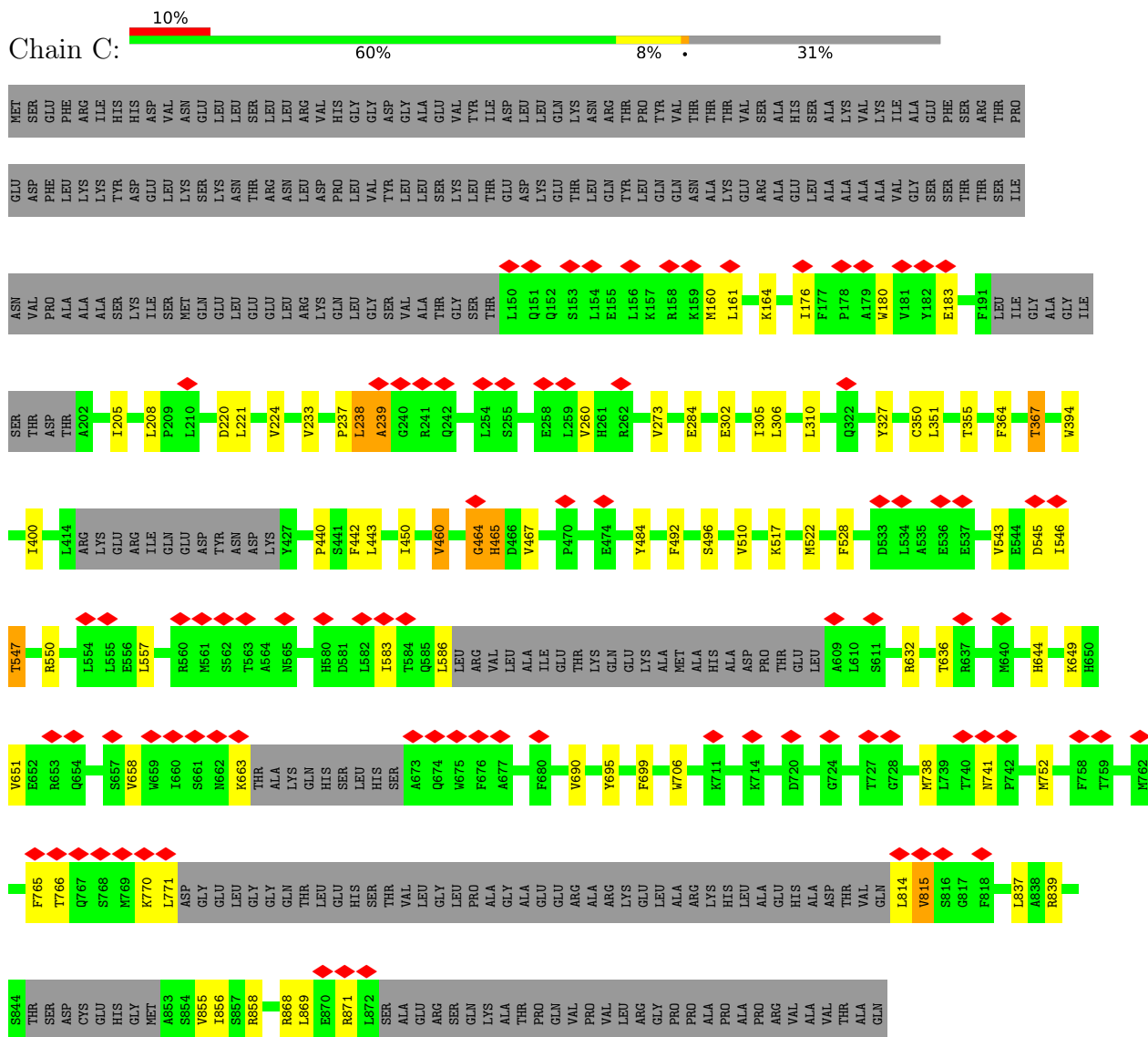


- Molecule 3: Gamma-tubulin complex component 3



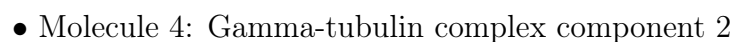


- Molecule 4: Gamma-tubulin complex component 2



- Molecule 4: Gamma-tubulin complex component 2

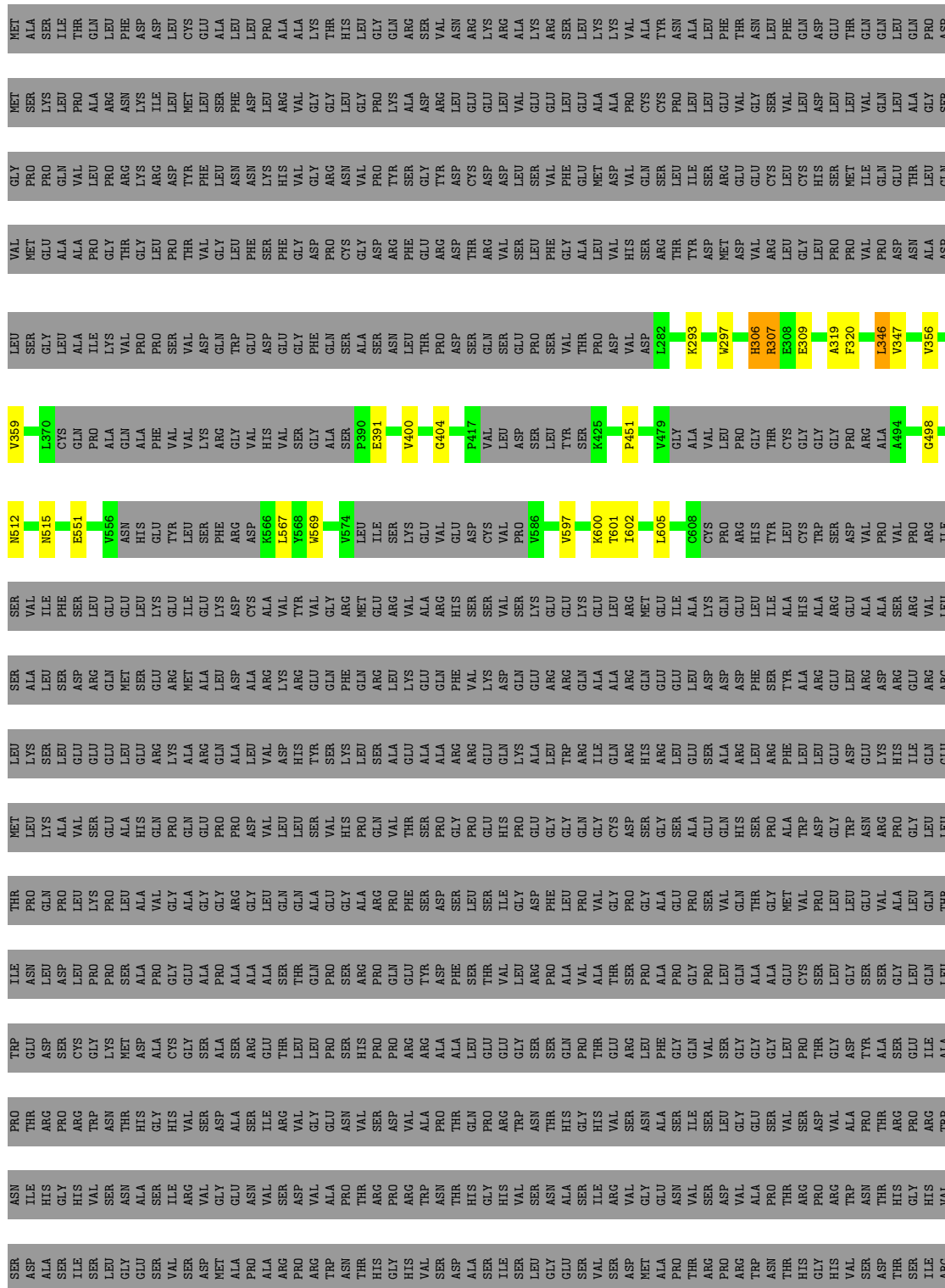




GLU	ARG	A615	P403	SER	ASN	GLU	MET
ALA	ARG	R637	M408	THR	VAL	ASP	SER
LYS	GLU	F642	V435	ASP	ALA	PHE	ARG
LEU	LEU				LYS	LYS	ILE
ARG	ALA	M645	I439	G227	SER	TYR	HIS
ARG	ALA	P440	P440	G227	LYS	ASP	HIS
HIS	LYS	M662	S441	V233	ILE	GLU	ASP
LEU	THR	K663	F442		MET	LYS	ASN
LEU	THR		L443	R241	GLN	SER	GLU
GLU	ALA	Q444	Q444	Q242	GLU	LYS	LEU
GLU	GLN	K445	K445		LEU	ASN	LEU
HIS	GLN	M446	M446	H261	GLU	THR	SER
ALA	HIS	A447	A447		GLU	ARG	LEU
ASP	SER			L264	LEU	ASN	LEU
THR	LEU	I450	I450		ARG	LEU	ARG
VAL	HIS	R514	R514	T274	LYS	ASP	VAL
GLN	SER				PRO	PRO	HIS
L1814	ALA			I277	GLY	LEU	GLY
	Q674	K517	K517		VAL	VAL	GLY
F818	R683	R518	R518	S281	SER	TYR	ASP
I822	Q684	M522	M522	S282	VAL	LEU	GLY
S844	R685	D523	D523	F283	ALA	LEU	ALA
THR	Y696	Q524	Q524	E284	THR	SER	GLU
THR		G525	G525	T298	GLY	LYS	VAL
SER					SER	LEU	TYR
ASP	E700	P548	P548	K301	THR	THR	ILE
GLU	I719	P549	P549		L150	GLU	ASP
GLU	H15	R550	R550	I305	LYS	ASP	LEU
G851	V722	M578	M578	S308	S153	LYS	LEU
V855	L734	P579	P579		L154	GLU	GLN
		H580	H580	H314	E155	THR	LYS
F864	L771				L156	LEU	ASN
R876	GLY	L586	L586	L319	K157	GLN	ARG
SER	GLU	ARG	ARG		R158	TYR	THR
GLN	LEU	VAL	VAL	L324	K159	LEU	PRO
LYS	GLY	LEU	LEU		M160	GLN	TYR
ALA	GLY	ALA	ALA	L328	L161	GLN	VAL
THR	GLN	GLU	ILE	T334	K164	ASN	THR
PRO	THR	THR	GLU		K167	LYS	THR
GLN	LEU	LYS	LYS	L338	K168	ARG	VAL
VAL	GLU	GLN	GLN		L174	ALA	ALA
PRO	HIS	GLU	GLU	T343		GLU	HIS
VAL	THR	THR	THR			LEU	SER
LEU	SER	THR	THR	G353	A186	ALA	ALA
ARG	VAL	THR	THR		L187	ALA	LYS
GLY	LEU	VAL	ALA	L356	I188	ALA	VAL
PRO	GLY	LEU	ALA		G189	VAL	LYS
PRO	LEU	HIS	ALA	H360	D190	VAL	ILE
PRO	LEU	ALA	HIS		F191	GLY	ALA
ALA	PRO	ASP	ALA		LEU	SER	GLU
PRO	ALA	PRO	ASP	S363	ILE	SER	PHE
ALA	GLY	THR	THR		GLY	THR	SER
PRO	ALA	THR	THR	L375	ALA	THR	ARG
PRO	ALA	E607	E607		GLY	THR	THR
PRO	ALA				ILE	SER	PRO



Chain L: 28% 1% 69%





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

• Molecule 8: Mitotic-spindle organizing protein 1



MET ALA SER SER SER GLY ALA GLY ALA ALA A11 A12 A13 A14 A15 A16 A20 V21 R22 D40 M41 E42 I46 C47 V48 C51 K65 E66 L67 R68 K69 A70 T71 E72 A73 L74 K75 ALA ALA GLU ASN MET THR SER

• Molecule 8: Mitotic-spindle organizing protein 1



MET ALA SER SER SER GLY ALA GLY ALA ALA A11 V21 T24 V27 I34 K75 ALA ALA GLU ASN MET THR SER

• Molecule 8: Mitotic-spindle organizing protein 1



MET ALA SER SER SER GLY ALA GLY ALA ALA A11 A12 M25 L39 D40 M41 L44 P57 S61 I64 K65 E66 L67 K75 ALA ALA GLU ASN MET THR SER

• Molecule 8: Mitotic-spindle organizing protein 1



MET ALA SER SER SER GLY ALA GLY ALA ALA A11 E23 T24 L28 L35 L39 E42 S45 I46 C47 V48 R49 D26 L50 C51 E52 Q53 Q54 I55 S61 S62 V63 I64 L67 R68 K75 ALA ALA GLU ASN MET THR SER

• Molecule 8: Mitotic-spindle organizing protein 1



MET ALA SER SER SER GLY ALA GLY ALA ALA ALA ALA ALA ALA N17 L18 N19 A20 V21 R22 E23 T24 M25 D26 V27 L28 I31 I34 L35 G38 L39 D40 M41 E42 T43 L44 S45 I46 C47 V48 R49 L50 C51 E52 Q53 Q54 I55 N56 P57 E58 A59 L60 V63 I64 K65 E66 L67 R68 T71 E72 A73 L74 K75 ALA ALA GLU ASN MET THR SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6456	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.170	Depositor
Minimum map value	-0.034	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0318	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.66, 2.66, 2.66	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	0.24	0/3441	0.60	0/4661
1	2	0.25	0/3441	0.60	0/4661
1	Q	0.24	0/3441	0.60	0/4661
1	R	0.24	0/3441	0.60	0/4661
1	S	0.24	0/3441	0.59	0/4661
1	T	0.25	0/3441	0.59	0/4661
1	U	0.24	0/3441	0.60	0/4661
1	V	0.24	0/3441	0.59	0/4661
1	W	0.24	0/3441	0.60	0/4661
1	X	0.24	0/3441	0.60	0/4661
1	Y	0.24	0/3441	0.59	0/4661
1	Z	0.24	0/3441	0.60	0/4661
2	e	0.55	1/2908 (0.0%)	0.84	4/3938 (0.1%)
3	D	0.35	1/4897 (0.0%)	0.73	5/6610 (0.1%)
3	F	0.38	1/5044 (0.0%)	0.78	6/6809 (0.1%)
3	H	0.32	0/5009	0.71	4/6761 (0.1%)
3	N	0.34	0/5009	0.76	6/6761 (0.1%)
3	a	0.31	0/948	0.76	1/1277 (0.1%)
3	h	0.30	0/815	0.65	0/1096
3	j	0.28	0/855	0.76	1/1152 (0.1%)
4	C	0.35	0/5151	0.77	7/6955 (0.1%)
4	E	0.41	2/5311 (0.0%)	0.75	7/7169 (0.1%)
4	G	0.34	1/5315 (0.0%)	0.71	4/7175 (0.1%)
4	M	0.38	0/5295	0.78	11/7147 (0.2%)
5	I	0.34	0/4322	0.77	7/5853 (0.1%)
5	K	0.42	2/4683 (0.0%)	0.76	10/6338 (0.2%)
6	J	0.36	0/4525	0.81	9/6119 (0.1%)
6	l	0.33	0/863	0.76	2/1166 (0.2%)
7	L	0.37	0/4697	0.79	8/6348 (0.1%)
7	c	0.40	0/1235	0.79	2/1664 (0.1%)
8	b	0.36	0/484	0.76	0/653
8	d	0.34	0/454	0.73	0/611
8	i	0.33	0/484	0.69	0/653
8	k	0.25	0/484	0.61	0/653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	m	0.33	0/484	0.74	0/653
All	All	0.33	8/110564 (0.0%)	0.70	94/149493 (0.1%)

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	D	0	2
3	F	0	2
3	H	0	2
3	N	0	1
3	h	0	1
3	j	0	2
4	C	0	3
4	E	0	2
4	G	0	2
4	M	0	1
5	I	0	3
5	K	0	2
6	J	0	4
7	L	0	2
All	All	0	29

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	e	243	PRO	N-CD	20.77	1.76	1.47
4	E	184	ARG	CD-NE	7.35	1.56	1.46
4	E	184	ARG	NE-CZ	7.10	1.40	1.33
5	K	166	PRO	C-N	6.23	1.42	1.34
3	F	299	TRP	CZ3-CH2	5.61	1.54	1.40

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	727	LEU	CB-CG-CD2	-9.48	82.25	110.70
4	M	464	GLY	CA-C-O	-8.43	116.74	122.22
3	H	456	THR	N-CA-C	-8.10	97.86	109.29
6	l	121	PRO	N-CA-CB	7.76	111.40	103.25
4	C	460	VAL	CG1-CB-CG2	-7.68	93.91	110.80

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	C	237	PRO	Peptide
4	C	239	ALA	Peptide
4	C	464	GLY	Peptide
3	D	440	GLU	Peptide
3	D	481	ARG	Peptide

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	1	3373	0	3325	55	0
1	2	3373	0	3325	59	0
1	Q	3373	0	3325	50	0
1	R	3373	0	3325	48	0
1	S	3373	0	3325	48	0
1	T	3373	0	3325	53	0
1	U	3373	0	3325	55	0
1	V	3373	0	3325	51	0
1	W	3373	0	3325	52	0
1	X	3373	0	3325	55	0
1	Y	3373	0	3325	53	0
1	Z	3373	0	3325	55	0
2	e	2847	0	2810	64	0
3	D	4796	0	4775	37	0
3	F	4941	0	4935	52	0
3	H	4907	0	4896	29	0
3	N	4907	0	4896	47	0
3	a	933	0	953	11	0
3	h	803	0	831	5	0
3	j	843	0	846	0	0
4	C	5044	0	5081	45	0
4	E	5202	0	5241	48	0
4	G	5206	0	5230	48	0
4	M	5186	0	5219	58	0
5	I	4225	0	4259	30	0
5	K	4579	0	4586	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	J	4429	0	4482	24	0
6	l	847	0	789	6	0
7	L	4587	0	4636	34	0
7	c	1220	0	1231	16	0
8	b	484	0	512	13	0
8	d	454	0	482	6	0
8	i	484	0	512	7	0
8	k	484	0	512	2	0
8	m	484	0	512	6	0
9	l	6	0	0	0	0
All	All	108374	0	108126	1150	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 5.

The worst 5 of 1150 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:e:243:PRO:CD	2:e:243:PRO:N	1.76	1.37
2:e:242:LEU:HD12	2:e:243:PRO:CD	1.68	1.24
2:e:242:LEU:CD1	2:e:243:PRO:HD2	1.75	1.15
2:e:160:THR:HG22	2:e:178:LEU:O	1.50	1.10
2:e:160:THR:HG23	2:e:178:LEU:CB	1.92	0.99

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	1	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	2	408/451 (90%)	386 (95%)	22 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	R	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	S	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	T	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	U	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	V	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	W	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	X	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	Y	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
1	Z	408/451 (90%)	386 (95%)	22 (5%)	0	100	100
2	e	360/375 (96%)	345 (96%)	15 (4%)	0	100	100
3	D	571/907 (63%)	546 (96%)	25 (4%)	0	100	100
3	F	591/907 (65%)	556 (94%)	35 (6%)	0	100	100
3	H	584/907 (64%)	557 (95%)	25 (4%)	2 (0%)	36	72
3	N	584/907 (64%)	568 (97%)	16 (3%)	0	100	100
3	a	112/907 (12%)	108 (96%)	4 (4%)	0	100	100
3	h	97/907 (11%)	93 (96%)	4 (4%)	0	100	100
3	j	105/907 (12%)	94 (90%)	10 (10%)	1 (1%)	12	49
4	C	606/902 (67%)	571 (94%)	32 (5%)	3 (0%)	24	63
4	E	626/902 (69%)	577 (92%)	48 (8%)	1 (0%)	43	78
4	G	628/902 (70%)	585 (93%)	43 (7%)	0	100	100
4	M	624/902 (69%)	591 (95%)	31 (5%)	2 (0%)	36	72
5	I	511/667 (77%)	482 (94%)	27 (5%)	2 (0%)	30	67
5	K	548/667 (82%)	525 (96%)	20 (4%)	3 (0%)	24	63
6	J	506/1024 (49%)	472 (93%)	31 (6%)	3 (1%)	21	59
6	l	104/1024 (10%)	96 (92%)	7 (7%)	1 (1%)	12	49
7	L	540/1819 (30%)	501 (93%)	36 (7%)	3 (1%)	21	59
7	c	148/1819 (8%)	139 (94%)	9 (6%)	0	100	100
8	b	63/82 (77%)	63 (100%)	0	0	100	100
8	d	57/82 (70%)	55 (96%)	2 (4%)	0	100	100
8	i	63/82 (77%)	62 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	k	63/82 (77%)	60 (95%)	3 (5%)	0	100	100
8	m	63/82 (77%)	63 (100%)	0	0	100	100
All	All	13050/23174 (56%)	12341 (95%)	688 (5%)	21 (0%)	44	78

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	239	ALA
4	C	465	HIS
4	E	581	ASP
3	H	455	LYS
5	I	601	LEU

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	376/400 (94%)	342 (91%)	34 (9%)	9	27
1	2	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	Q	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	R	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	S	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	T	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	U	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	V	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	W	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	X	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	Y	376/400 (94%)	343 (91%)	33 (9%)	9	28
1	Z	376/400 (94%)	343 (91%)	33 (9%)	9	28
2	e	310/318 (98%)	303 (98%)	7 (2%)	44	64
3	D	525/798 (66%)	524 (100%)	1 (0%)	87	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	542/798 (68%)	535 (99%)	7 (1%)	61	74
3	H	539/798 (68%)	537 (100%)	2 (0%)	84	84
3	N	539/798 (68%)	538 (100%)	1 (0%)	87	87
3	a	101/798 (13%)	101 (100%)	0	100	100
3	h	88/798 (11%)	88 (100%)	0	100	100
3	j	88/798 (11%)	88 (100%)	0	100	100
4	C	556/791 (70%)	551 (99%)	5 (1%)	70	79
4	E	574/791 (73%)	572 (100%)	2 (0%)	86	86
4	G	572/791 (72%)	567 (99%)	5 (1%)	70	79
4	M	572/791 (72%)	567 (99%)	5 (1%)	70	79
5	I	472/594 (80%)	472 (100%)	0	100	100
5	K	509/594 (86%)	507 (100%)	2 (0%)	84	84
6	J	498/933 (53%)	497 (100%)	1 (0%)	87	87
6	l	84/933 (9%)	84 (100%)	0	100	100
7	L	501/1546 (32%)	501 (100%)	0	100	100
7	c	135/1546 (9%)	133 (98%)	2 (2%)	57	72
8	b	53/62 (86%)	52 (98%)	1 (2%)	50	67
8	d	53/62 (86%)	52 (98%)	1 (2%)	50	67
8	i	53/62 (86%)	53 (100%)	0	100	100
8	k	53/62 (86%)	52 (98%)	1 (2%)	50	67
8	m	53/62 (86%)	53 (100%)	0	100	100
All	All	11982/20324 (59%)	11542 (96%)	440 (4%)	31	51

5 of 440 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T	364	SER
1	V	237	SER
7	c	47	THR
1	Y	374	SER
1	U	10	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 281 such sidechains are listed below:

Mol	Chain	Res	Type
1	V	430	GLN
1	W	267	HIS
1	Y	315	HIS
3	H	860	GLN
3	H	705	HIS

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.

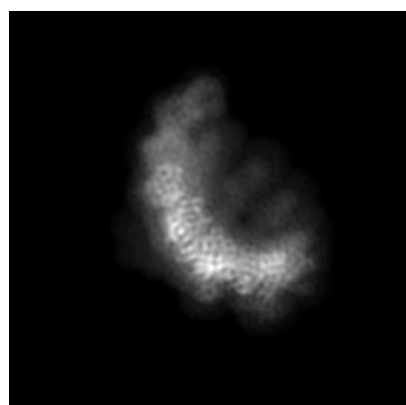
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14016. These allow visual inspection of the internal detail of the map and identification of artifacts.

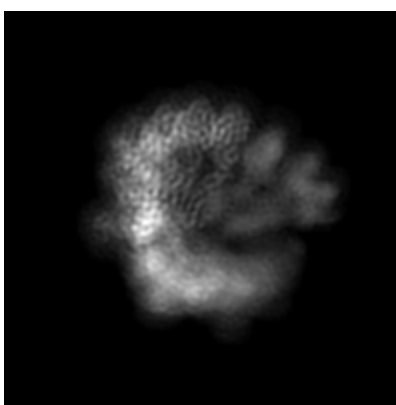
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

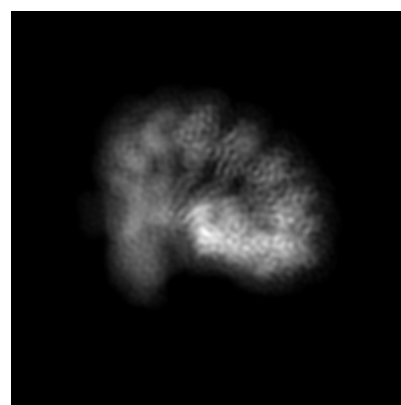
6.1.1 Primary map



X



Y



Z

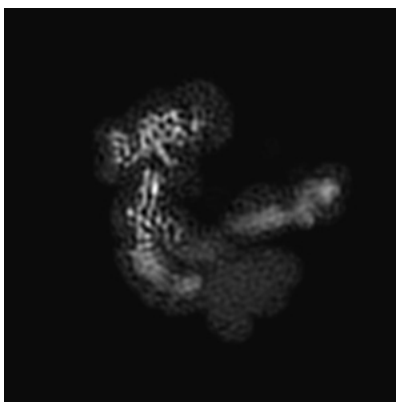
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

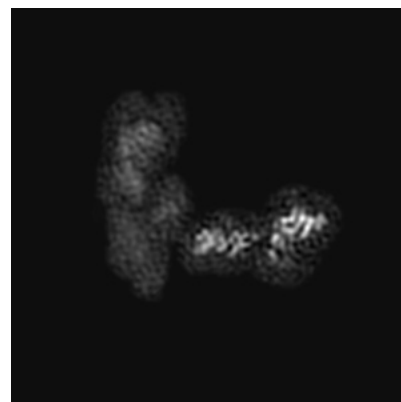
6.2.1 Primary map



X Index: 100



Y Index: 100



Z Index: 100

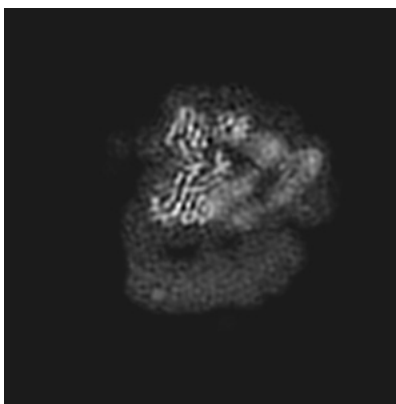
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

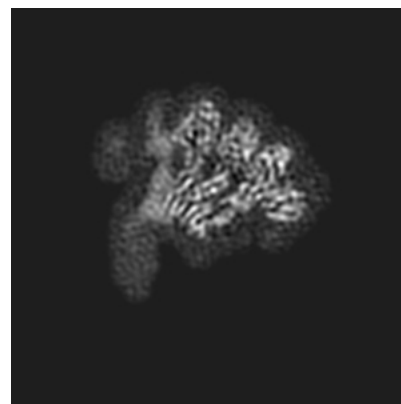
6.3.1 Primary map



X Index: 134



Y Index: 84

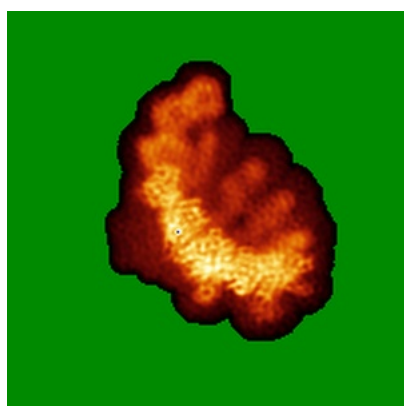


Z Index: 72

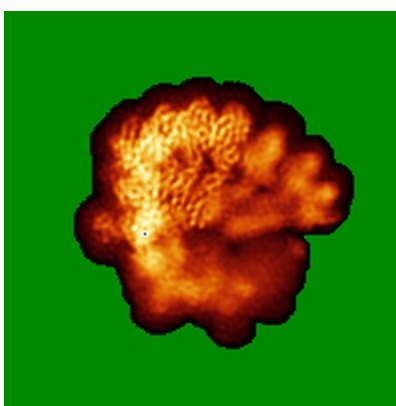
The images above show the largest variance slices of the map in three orthogonal directions.

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

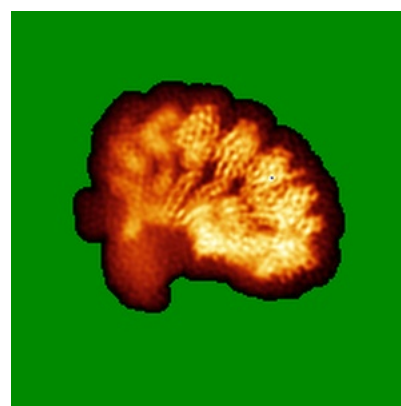
6.4.1 Primary map



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 0.0318. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

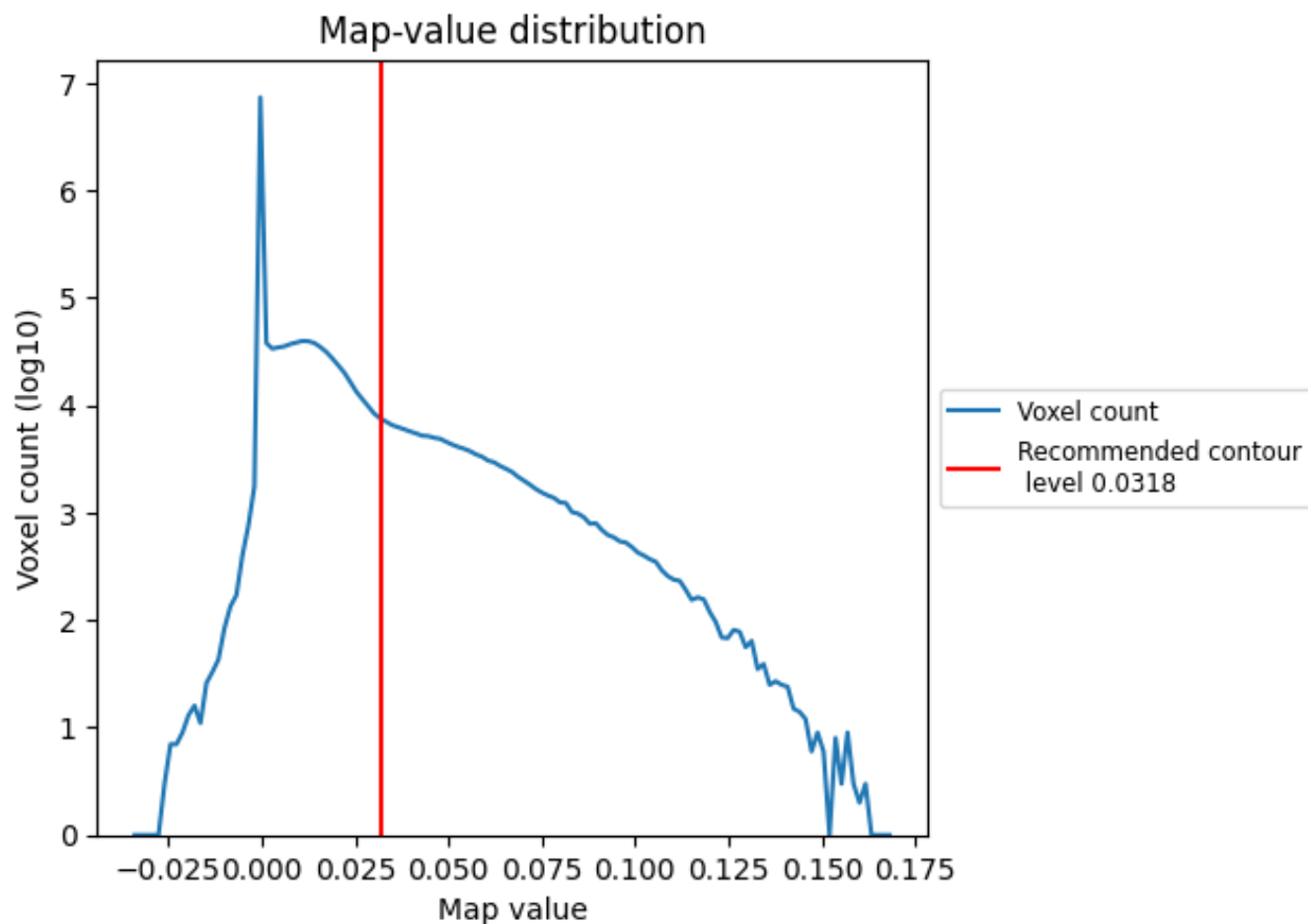
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

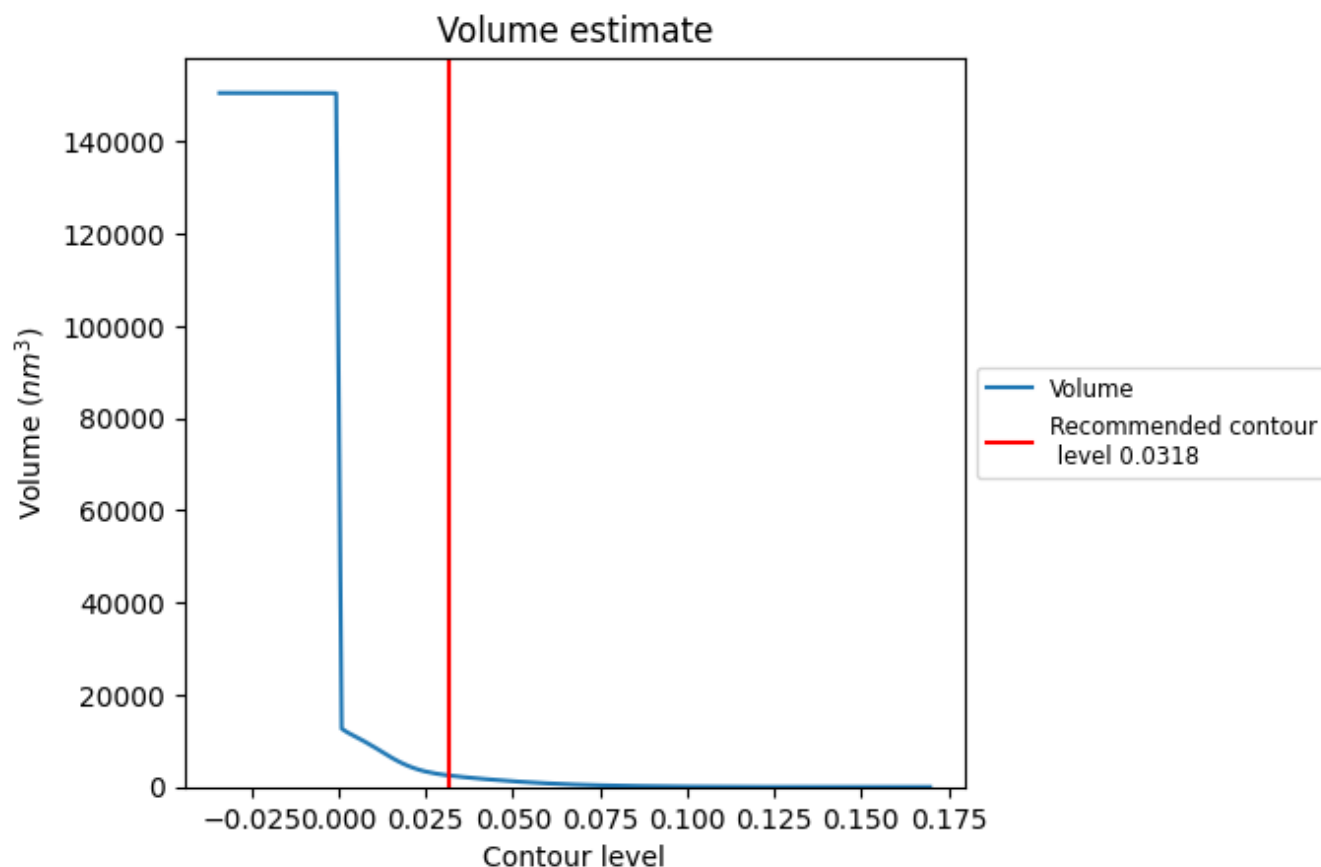
This section contains the results of statistical analysis of the map.

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.

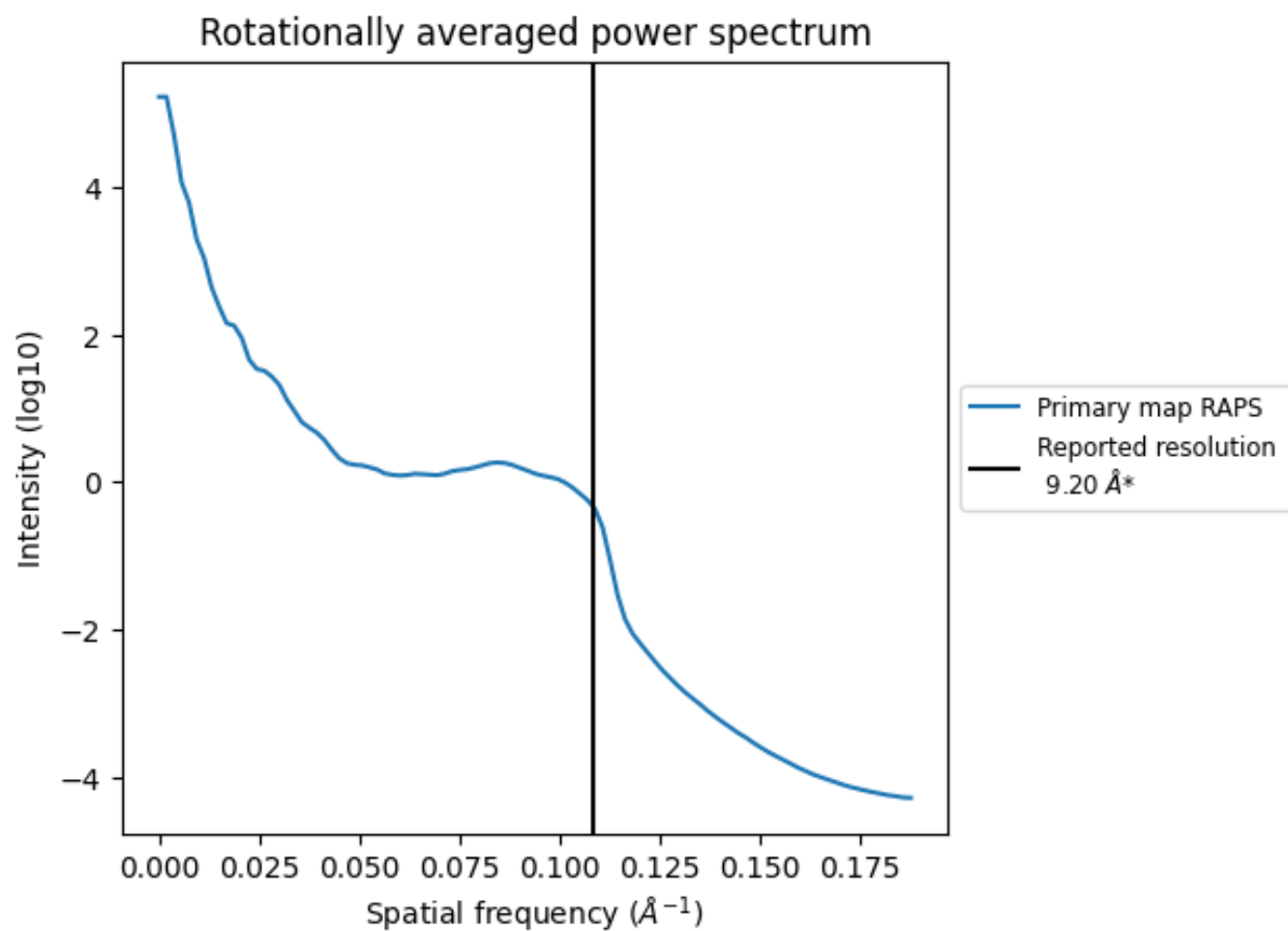
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2484 nm³; this corresponds to an approximate mass of 2244 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 0.109 Å⁻¹

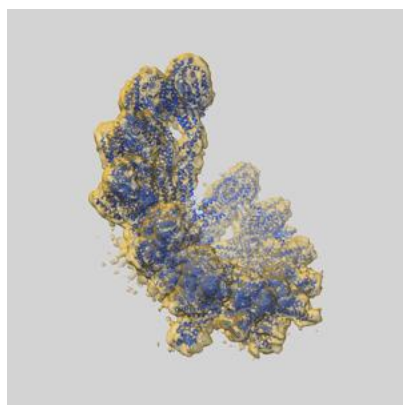
8 Fourier-Shell correlation

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

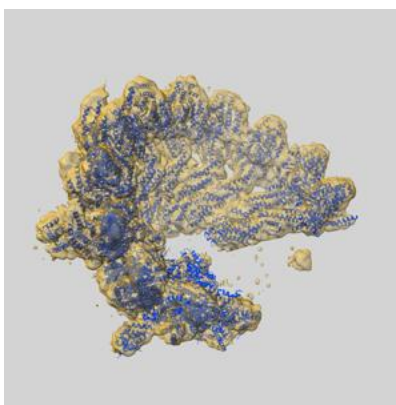
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14016 and PDB model 7QJB. Per-residue inclusion information can be found in section [3](#) on page [8](#).

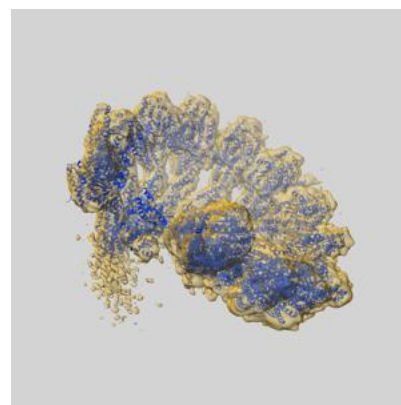
9.1 Map-model overlay [i](#)



X



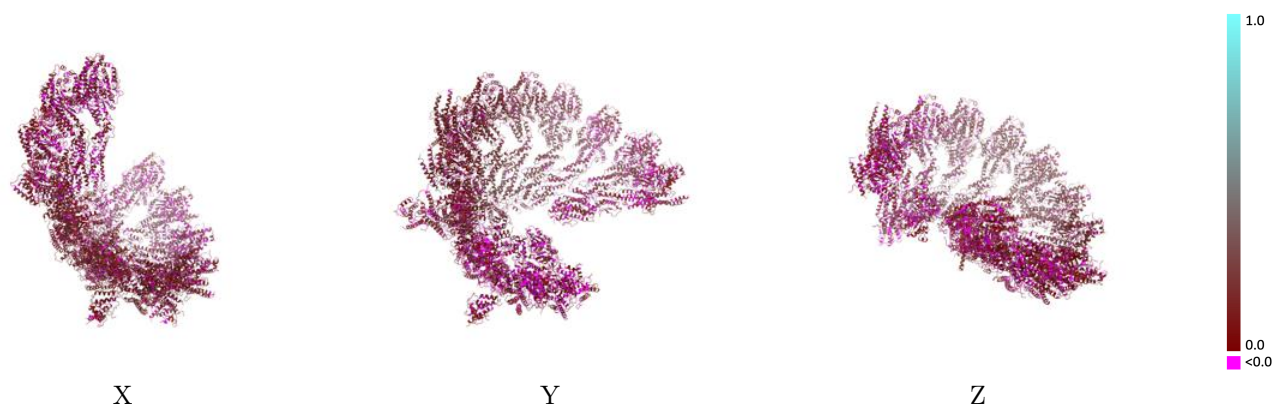
Y



Z

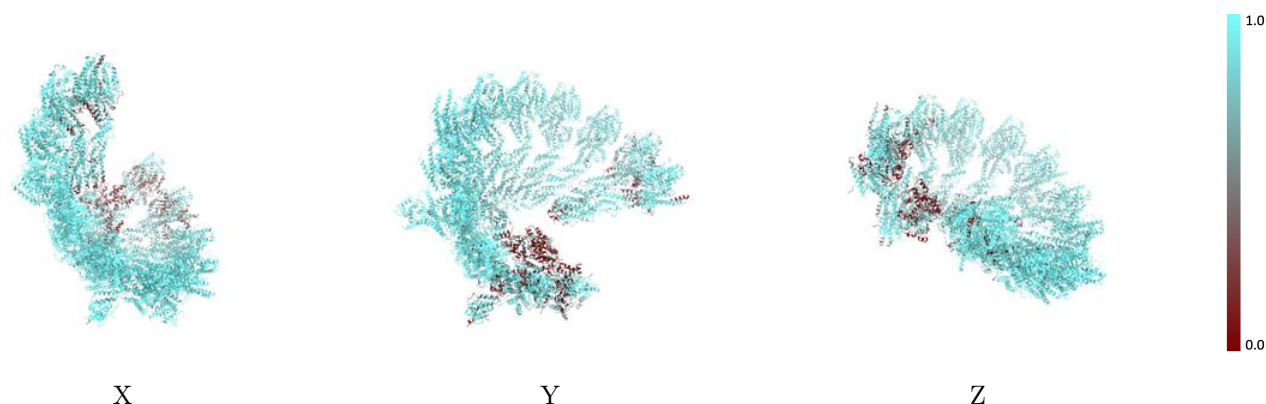
The images above show the 3D surface view of the map at the recommended contour level 0.0318 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



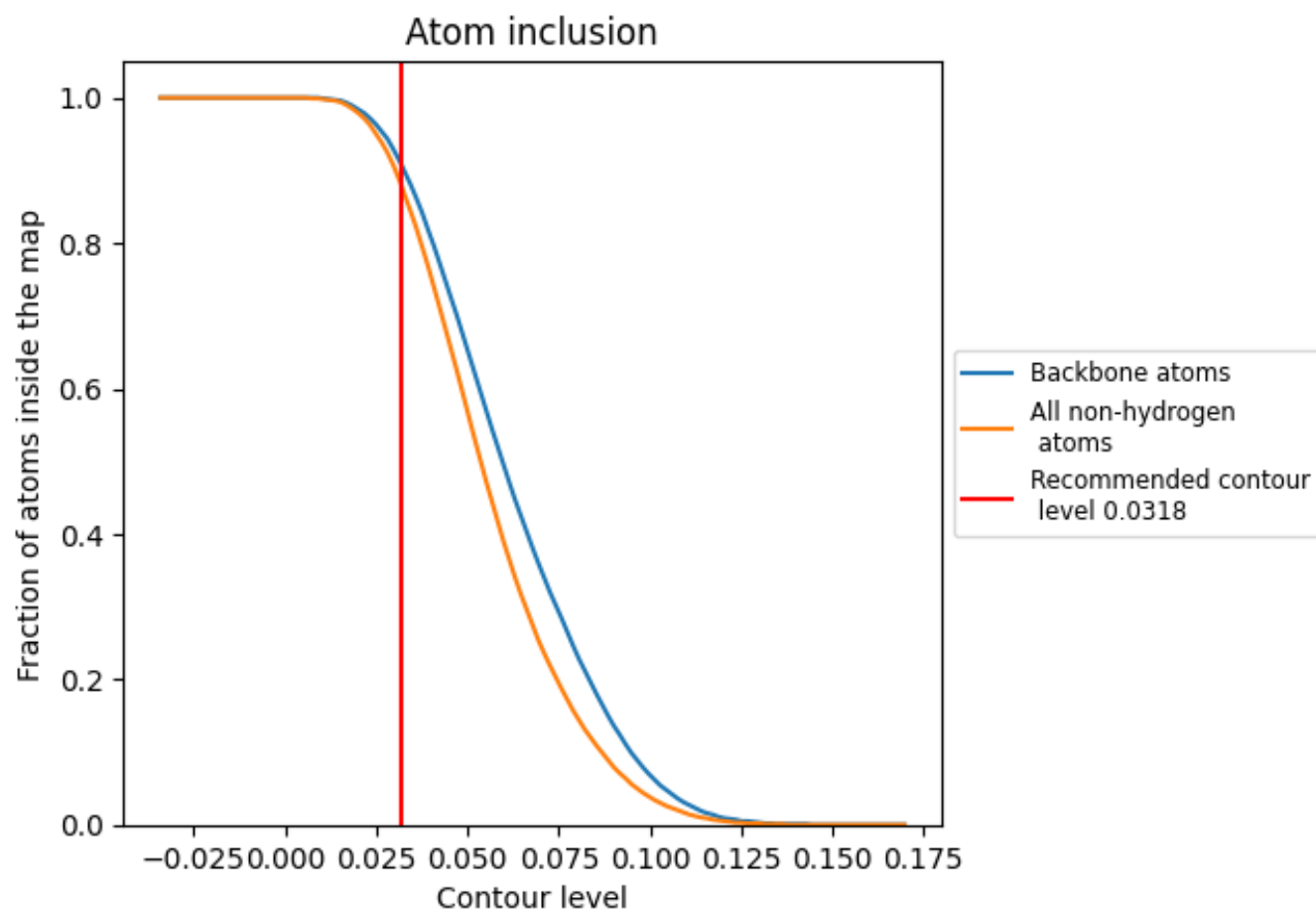
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0318).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.0318) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8810	 0.0940
1	 0.8850	 0.0630
2	 0.8610	 0.0530
C	 0.8160	 0.0630
D	 0.8430	 0.0730
E	 0.9700	 0.0760
F	 0.9610	 0.1220
G	 0.9630	 0.1340
H	 0.9690	 0.1370
I	 0.9610	 0.1390
J	 0.9630	 0.1440
K	 0.9630	 0.1360
L	 0.9830	 0.0860
M	 0.8480	 0.0670
N	 0.8220	 0.0630
Q	 0.5840	 0.0400
R	 0.6810	 0.0380
S	 0.9050	 0.0460
T	 0.9680	 0.1100
U	 0.9700	 0.1220
V	 0.9760	 0.1260
W	 0.9680	 0.1180
X	 0.9690	 0.1300
Y	 0.9600	 0.1060
Z	 0.9450	 0.0400
a	 0.8020	 0.1210
b	 0.7960	 0.1370
c	 0.4660	 0.0670
d	 0.3210	 0.0920
e	 0.2530	 0.0500
h	 0.7670	 0.0760
i	 0.7290	 0.1030
j	 0.9150	 0.0860
k	 0.9430	 0.1250
l	 0.9630	 0.1320
m	 0.9480	 0.1580

