



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:45 PM UTC

PDB ID : 9H9R / pdb_00009h9r
EMDB ID : EMD-51972
Title : Full gamma-tubulin ring complex composed of the Candida albicans gamma-tubulin small complex in complex with Spc72 CM1
Authors : Vermeulen, B.J.A.; Pfeffer, S.
Deposited on : 2024-10-31
Resolution : 8.20 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

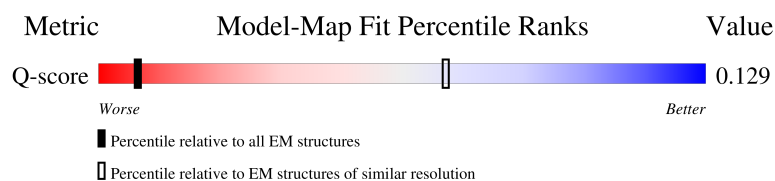
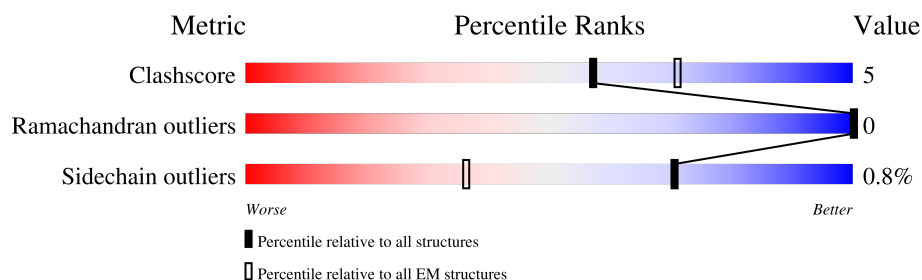
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 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.



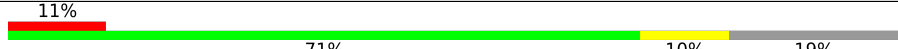
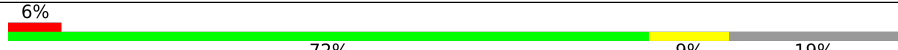
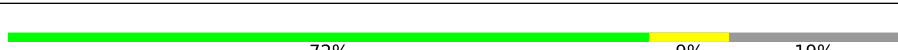
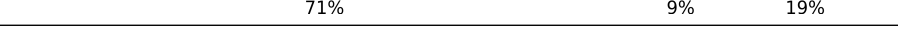
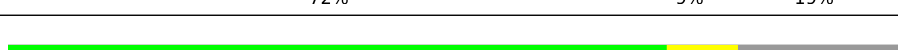
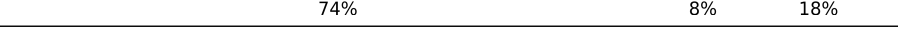
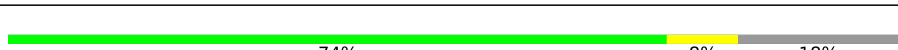
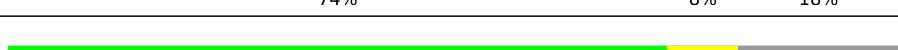
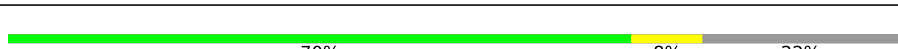
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	337 (7.70 - 8.70)

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	A	498	 71% 9% 19%
1	B	498	 71% 10% 19%
1	G	498	 72% 9% 19%
1	H	498	 71% 10% 19%

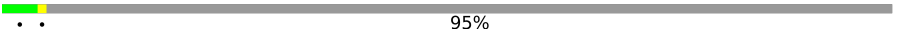
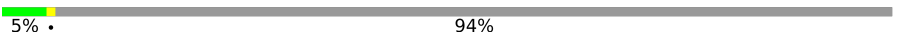
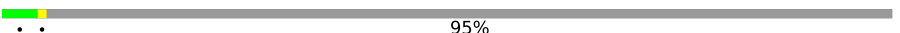
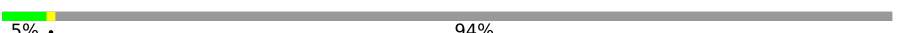
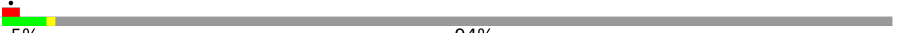
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Mol	Chain	Length	Quality of chain
1	M	498	
1	N	498	
1	S	498	
1	T	498	
1	Y	498	
1	Z	498	
1	e	498	
1	f	498	
1	k	498	
1	l	498	
2	C	896	
2	I	896	
2	O	896	
2	U	896	
2	a	896	
2	g	896	
2	m	896	
3	D	810	
3	J	810	
3	P	810	
3	V	810	
3	b	810	
3	h	810	
3	n	810	
4	E	615	

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Mol	Chain	Length	Quality of chain
4	F	615	 95%
4	K	615	 94%
4	L	615	 95%
4	Q	615	 94%
4	R	615	 95%
4	W	615	 94%
4	X	615	 95%
4	c	615	 94%
4	d	615	 95%
4	i	615	 94%
4	j	615	 95%
4	o	615	 94%
4	p	615	 95%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 128163 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 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	B	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		
1	G	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	H	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		
1	M	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	N	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		
1	S	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	T	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		
1	Y	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	Z	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		
1	e	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	f	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		
1	k	401	Total	C	N	O	S	0	0
			3188	2016	535	624	13		
1	l	404	Total	C	N	O	S	0	0
			3220	2039	541	627	13		

- Molecule 2 is a protein called Spindle pole body component.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	735	Total	C	N	O	S	0	0
			6001	3869	993	1119	20		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	735	Total 6001	C 3869	N 993	O 1119	S 20	0	0
2	O	735	Total 6001	C 3869	N 993	O 1119	S 20	0	0
2	U	735	Total 6001	C 3869	N 993	O 1119	S 20	0	0
2	a	735	Total 6001	C 3869	N 993	O 1119	S 20	0	0
2	g	735	Total 6001	C 3869	N 993	O 1119	S 20	0	0
2	m	735	Total 6001	C 3869	N 993	O 1119	S 20	0	0

There are 175 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-24	MET	-	initiating methionine	UNP Q59PZ2
C	-23	HIS	-	expression tag	UNP Q59PZ2
C	-22	HIS	-	expression tag	UNP Q59PZ2
C	-21	HIS	-	expression tag	UNP Q59PZ2
C	-20	HIS	-	expression tag	UNP Q59PZ2
C	-19	HIS	-	expression tag	UNP Q59PZ2
C	-18	HIS	-	expression tag	UNP Q59PZ2
C	-17	ASP	-	expression tag	UNP Q59PZ2
C	-16	TYR	-	expression tag	UNP Q59PZ2
C	-15	ASP	-	expression tag	UNP Q59PZ2
C	-14	ILE	-	expression tag	UNP Q59PZ2
C	-13	PRO	-	expression tag	UNP Q59PZ2
C	-12	THR	-	expression tag	UNP Q59PZ2
C	-11	THR	-	expression tag	UNP Q59PZ2
C	-10	GLU	-	expression tag	UNP Q59PZ2
C	-9	ASN	-	expression tag	UNP Q59PZ2
C	-8	LEU	-	expression tag	UNP Q59PZ2
C	-7	TYR	-	expression tag	UNP Q59PZ2
C	-6	PHE	-	expression tag	UNP Q59PZ2
C	-5	GLN	-	expression tag	UNP Q59PZ2
C	-4	GLY	-	expression tag	UNP Q59PZ2
C	-3	ALA	-	expression tag	UNP Q59PZ2
C	-2	MET	-	expression tag	UNP Q59PZ2
C	-1	ASP	-	expression tag	UNP Q59PZ2
C	0	PRO	-	expression tag	UNP Q59PZ2
I	-24	MET	-	initiating methionine	UNP Q59PZ2
I	-23	HIS	-	expression tag	UNP Q59PZ2

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-22	HIS	-	expression tag	UNP Q59PZ2
I	-21	HIS	-	expression tag	UNP Q59PZ2
I	-20	HIS	-	expression tag	UNP Q59PZ2
I	-19	HIS	-	expression tag	UNP Q59PZ2
I	-18	HIS	-	expression tag	UNP Q59PZ2
I	-17	ASP	-	expression tag	UNP Q59PZ2
I	-16	TYR	-	expression tag	UNP Q59PZ2
I	-15	ASP	-	expression tag	UNP Q59PZ2
I	-14	ILE	-	expression tag	UNP Q59PZ2
I	-13	PRO	-	expression tag	UNP Q59PZ2
I	-12	THR	-	expression tag	UNP Q59PZ2
I	-11	THR	-	expression tag	UNP Q59PZ2
I	-10	GLU	-	expression tag	UNP Q59PZ2
I	-9	ASN	-	expression tag	UNP Q59PZ2
I	-8	LEU	-	expression tag	UNP Q59PZ2
I	-7	TYR	-	expression tag	UNP Q59PZ2
I	-6	PHE	-	expression tag	UNP Q59PZ2
I	-5	GLN	-	expression tag	UNP Q59PZ2
I	-4	GLY	-	expression tag	UNP Q59PZ2
I	-3	ALA	-	expression tag	UNP Q59PZ2
I	-2	MET	-	expression tag	UNP Q59PZ2
I	-1	ASP	-	expression tag	UNP Q59PZ2
I	0	PRO	-	expression tag	UNP Q59PZ2
O	-24	MET	-	initiating methionine	UNP Q59PZ2
O	-23	HIS	-	expression tag	UNP Q59PZ2
O	-22	HIS	-	expression tag	UNP Q59PZ2
O	-21	HIS	-	expression tag	UNP Q59PZ2
O	-20	HIS	-	expression tag	UNP Q59PZ2
O	-19	HIS	-	expression tag	UNP Q59PZ2
O	-18	HIS	-	expression tag	UNP Q59PZ2
O	-17	ASP	-	expression tag	UNP Q59PZ2
O	-16	TYR	-	expression tag	UNP Q59PZ2
O	-15	ASP	-	expression tag	UNP Q59PZ2
O	-14	ILE	-	expression tag	UNP Q59PZ2
O	-13	PRO	-	expression tag	UNP Q59PZ2
O	-12	THR	-	expression tag	UNP Q59PZ2
O	-11	THR	-	expression tag	UNP Q59PZ2
O	-10	GLU	-	expression tag	UNP Q59PZ2
O	-9	ASN	-	expression tag	UNP Q59PZ2
O	-8	LEU	-	expression tag	UNP Q59PZ2
O	-7	TYR	-	expression tag	UNP Q59PZ2
O	-6	PHE	-	expression tag	UNP Q59PZ2

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-5	GLN	-	expression tag	UNP Q59PZ2
O	-4	GLY	-	expression tag	UNP Q59PZ2
O	-3	ALA	-	expression tag	UNP Q59PZ2
O	-2	MET	-	expression tag	UNP Q59PZ2
O	-1	ASP	-	expression tag	UNP Q59PZ2
O	0	PRO	-	expression tag	UNP Q59PZ2
U	-24	MET	-	initiating methionine	UNP Q59PZ2
U	-23	HIS	-	expression tag	UNP Q59PZ2
U	-22	HIS	-	expression tag	UNP Q59PZ2
U	-21	HIS	-	expression tag	UNP Q59PZ2
U	-20	HIS	-	expression tag	UNP Q59PZ2
U	-19	HIS	-	expression tag	UNP Q59PZ2
U	-18	HIS	-	expression tag	UNP Q59PZ2
U	-17	ASP	-	expression tag	UNP Q59PZ2
U	-16	TYR	-	expression tag	UNP Q59PZ2
U	-15	ASP	-	expression tag	UNP Q59PZ2
U	-14	ILE	-	expression tag	UNP Q59PZ2
U	-13	PRO	-	expression tag	UNP Q59PZ2
U	-12	THR	-	expression tag	UNP Q59PZ2
U	-11	THR	-	expression tag	UNP Q59PZ2
U	-10	GLU	-	expression tag	UNP Q59PZ2
U	-9	ASN	-	expression tag	UNP Q59PZ2
U	-8	LEU	-	expression tag	UNP Q59PZ2
U	-7	TYR	-	expression tag	UNP Q59PZ2
U	-6	PHE	-	expression tag	UNP Q59PZ2
U	-5	GLN	-	expression tag	UNP Q59PZ2
U	-4	GLY	-	expression tag	UNP Q59PZ2
U	-3	ALA	-	expression tag	UNP Q59PZ2
U	-2	MET	-	expression tag	UNP Q59PZ2
U	-1	ASP	-	expression tag	UNP Q59PZ2
U	0	PRO	-	expression tag	UNP Q59PZ2
a	-24	MET	-	initiating methionine	UNP Q59PZ2
a	-23	HIS	-	expression tag	UNP Q59PZ2
a	-22	HIS	-	expression tag	UNP Q59PZ2
a	-21	HIS	-	expression tag	UNP Q59PZ2
a	-20	HIS	-	expression tag	UNP Q59PZ2
a	-19	HIS	-	expression tag	UNP Q59PZ2
a	-18	HIS	-	expression tag	UNP Q59PZ2
a	-17	ASP	-	expression tag	UNP Q59PZ2
a	-16	TYR	-	expression tag	UNP Q59PZ2
a	-15	ASP	-	expression tag	UNP Q59PZ2
a	-14	ILE	-	expression tag	UNP Q59PZ2

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Chain	Residue	Modelled	Actual	Comment	Reference
a	-13	PRO	-	expression tag	UNP Q59PZ2
a	-12	THR	-	expression tag	UNP Q59PZ2
a	-11	THR	-	expression tag	UNP Q59PZ2
a	-10	GLU	-	expression tag	UNP Q59PZ2
a	-9	ASN	-	expression tag	UNP Q59PZ2
a	-8	LEU	-	expression tag	UNP Q59PZ2
a	-7	TYR	-	expression tag	UNP Q59PZ2
a	-6	PHE	-	expression tag	UNP Q59PZ2
a	-5	GLN	-	expression tag	UNP Q59PZ2
a	-4	GLY	-	expression tag	UNP Q59PZ2
a	-3	ALA	-	expression tag	UNP Q59PZ2
a	-2	MET	-	expression tag	UNP Q59PZ2
a	-1	ASP	-	expression tag	UNP Q59PZ2
a	0	PRO	-	expression tag	UNP Q59PZ2
g	-24	MET	-	initiating methionine	UNP Q59PZ2
g	-23	HIS	-	expression tag	UNP Q59PZ2
g	-22	HIS	-	expression tag	UNP Q59PZ2
g	-21	HIS	-	expression tag	UNP Q59PZ2
g	-20	HIS	-	expression tag	UNP Q59PZ2
g	-19	HIS	-	expression tag	UNP Q59PZ2
g	-18	HIS	-	expression tag	UNP Q59PZ2
g	-17	ASP	-	expression tag	UNP Q59PZ2
g	-16	TYR	-	expression tag	UNP Q59PZ2
g	-15	ASP	-	expression tag	UNP Q59PZ2
g	-14	ILE	-	expression tag	UNP Q59PZ2
g	-13	PRO	-	expression tag	UNP Q59PZ2
g	-12	THR	-	expression tag	UNP Q59PZ2
g	-11	THR	-	expression tag	UNP Q59PZ2
g	-10	GLU	-	expression tag	UNP Q59PZ2
g	-9	ASN	-	expression tag	UNP Q59PZ2
g	-8	LEU	-	expression tag	UNP Q59PZ2
g	-7	TYR	-	expression tag	UNP Q59PZ2
g	-6	PHE	-	expression tag	UNP Q59PZ2
g	-5	GLN	-	expression tag	UNP Q59PZ2
g	-4	GLY	-	expression tag	UNP Q59PZ2
g	-3	ALA	-	expression tag	UNP Q59PZ2
g	-2	MET	-	expression tag	UNP Q59PZ2
g	-1	ASP	-	expression tag	UNP Q59PZ2
g	0	PRO	-	expression tag	UNP Q59PZ2
m	-24	MET	-	initiating methionine	UNP Q59PZ2
m	-23	HIS	-	expression tag	UNP Q59PZ2
m	-22	HIS	-	expression tag	UNP Q59PZ2

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Chain	Residue	Modelled	Actual	Comment	Reference
m	-21	HIS	-	expression tag	UNP Q59PZ2
m	-20	HIS	-	expression tag	UNP Q59PZ2
m	-19	HIS	-	expression tag	UNP Q59PZ2
m	-18	HIS	-	expression tag	UNP Q59PZ2
m	-17	ASP	-	expression tag	UNP Q59PZ2
m	-16	TYR	-	expression tag	UNP Q59PZ2
m	-15	ASP	-	expression tag	UNP Q59PZ2
m	-14	ILE	-	expression tag	UNP Q59PZ2
m	-13	PRO	-	expression tag	UNP Q59PZ2
m	-12	THR	-	expression tag	UNP Q59PZ2
m	-11	THR	-	expression tag	UNP Q59PZ2
m	-10	GLU	-	expression tag	UNP Q59PZ2
m	-9	ASN	-	expression tag	UNP Q59PZ2
m	-8	LEU	-	expression tag	UNP Q59PZ2
m	-7	TYR	-	expression tag	UNP Q59PZ2
m	-6	PHE	-	expression tag	UNP Q59PZ2
m	-5	GLN	-	expression tag	UNP Q59PZ2
m	-4	GLY	-	expression tag	UNP Q59PZ2
m	-3	ALA	-	expression tag	UNP Q59PZ2
m	-2	MET	-	expression tag	UNP Q59PZ2
m	-1	ASP	-	expression tag	UNP Q59PZ2
m	0	PRO	-	expression tag	UNP Q59PZ2

- Molecule 3 is a protein called Spc98p.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		
3	J	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		
3	P	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		
3	V	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		
3	b	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		
3	h	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		
3	n	635	Total	C	N	O	S	0	0
			5313	3463	873	966	11		

There are 189 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-24	MET	-	initiating methionine	UNP A0A1D8PS42
D	-23	HIS	-	expression tag	UNP A0A1D8PS42
D	-22	HIS	-	expression tag	UNP A0A1D8PS42
D	-21	HIS	-	expression tag	UNP A0A1D8PS42
D	-20	HIS	-	expression tag	UNP A0A1D8PS42
D	-19	HIS	-	expression tag	UNP A0A1D8PS42
D	-18	HIS	-	expression tag	UNP A0A1D8PS42
D	-17	ASP	-	expression tag	UNP A0A1D8PS42
D	-16	TYR	-	expression tag	UNP A0A1D8PS42
D	-15	ASP	-	expression tag	UNP A0A1D8PS42
D	-14	ILE	-	expression tag	UNP A0A1D8PS42
D	-13	PRO	-	expression tag	UNP A0A1D8PS42
D	-12	THR	-	expression tag	UNP A0A1D8PS42
D	-11	THR	-	expression tag	UNP A0A1D8PS42
D	-10	GLU	-	expression tag	UNP A0A1D8PS42
D	-9	ASN	-	expression tag	UNP A0A1D8PS42
D	-8	LEU	-	expression tag	UNP A0A1D8PS42
D	-7	TYR	-	expression tag	UNP A0A1D8PS42
D	-6	PHE	-	expression tag	UNP A0A1D8PS42
D	-5	GLN	-	expression tag	UNP A0A1D8PS42
D	-4	GLY	-	expression tag	UNP A0A1D8PS42
D	-3	ALA	-	expression tag	UNP A0A1D8PS42
D	-2	MET	-	expression tag	UNP A0A1D8PS42
D	-1	ASP	-	expression tag	UNP A0A1D8PS42
D	0	PRO	-	expression tag	UNP A0A1D8PS42
D	123	VAL	LEU	conflict	UNP A0A1D8PS42
D	717	CYS	VAL	conflict	UNP A0A1D8PS42
J	-24	MET	-	initiating methionine	UNP A0A1D8PS42
J	-23	HIS	-	expression tag	UNP A0A1D8PS42
J	-22	HIS	-	expression tag	UNP A0A1D8PS42
J	-21	HIS	-	expression tag	UNP A0A1D8PS42
J	-20	HIS	-	expression tag	UNP A0A1D8PS42
J	-19	HIS	-	expression tag	UNP A0A1D8PS42
J	-18	HIS	-	expression tag	UNP A0A1D8PS42
J	-17	ASP	-	expression tag	UNP A0A1D8PS42
J	-16	TYR	-	expression tag	UNP A0A1D8PS42
J	-15	ASP	-	expression tag	UNP A0A1D8PS42
J	-14	ILE	-	expression tag	UNP A0A1D8PS42
J	-13	PRO	-	expression tag	UNP A0A1D8PS42
J	-12	THR	-	expression tag	UNP A0A1D8PS42
J	-11	THR	-	expression tag	UNP A0A1D8PS42
J	-10	GLU	-	expression tag	UNP A0A1D8PS42
J	-9	ASN	-	expression tag	UNP A0A1D8PS42

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-8	LEU	-	expression tag	UNP A0A1D8PS42
J	-7	TYR	-	expression tag	UNP A0A1D8PS42
J	-6	PHE	-	expression tag	UNP A0A1D8PS42
J	-5	GLN	-	expression tag	UNP A0A1D8PS42
J	-4	GLY	-	expression tag	UNP A0A1D8PS42
J	-3	ALA	-	expression tag	UNP A0A1D8PS42
J	-2	MET	-	expression tag	UNP A0A1D8PS42
J	-1	ASP	-	expression tag	UNP A0A1D8PS42
J	0	PRO	-	expression tag	UNP A0A1D8PS42
J	123	VAL	LEU	conflict	UNP A0A1D8PS42
J	717	CYS	VAL	conflict	UNP A0A1D8PS42
P	-24	MET	-	initiating methionine	UNP A0A1D8PS42
P	-23	HIS	-	expression tag	UNP A0A1D8PS42
P	-22	HIS	-	expression tag	UNP A0A1D8PS42
P	-21	HIS	-	expression tag	UNP A0A1D8PS42
P	-20	HIS	-	expression tag	UNP A0A1D8PS42
P	-19	HIS	-	expression tag	UNP A0A1D8PS42
P	-18	HIS	-	expression tag	UNP A0A1D8PS42
P	-17	ASP	-	expression tag	UNP A0A1D8PS42
P	-16	TYR	-	expression tag	UNP A0A1D8PS42
P	-15	ASP	-	expression tag	UNP A0A1D8PS42
P	-14	ILE	-	expression tag	UNP A0A1D8PS42
P	-13	PRO	-	expression tag	UNP A0A1D8PS42
P	-12	THR	-	expression tag	UNP A0A1D8PS42
P	-11	THR	-	expression tag	UNP A0A1D8PS42
P	-10	GLU	-	expression tag	UNP A0A1D8PS42
P	-9	ASN	-	expression tag	UNP A0A1D8PS42
P	-8	LEU	-	expression tag	UNP A0A1D8PS42
P	-7	TYR	-	expression tag	UNP A0A1D8PS42
P	-6	PHE	-	expression tag	UNP A0A1D8PS42
P	-5	GLN	-	expression tag	UNP A0A1D8PS42
P	-4	GLY	-	expression tag	UNP A0A1D8PS42
P	-3	ALA	-	expression tag	UNP A0A1D8PS42
P	-2	MET	-	expression tag	UNP A0A1D8PS42
P	-1	ASP	-	expression tag	UNP A0A1D8PS42
P	0	PRO	-	expression tag	UNP A0A1D8PS42
P	123	VAL	LEU	conflict	UNP A0A1D8PS42
P	717	CYS	VAL	conflict	UNP A0A1D8PS42
V	-24	MET	-	initiating methionine	UNP A0A1D8PS42
V	-23	HIS	-	expression tag	UNP A0A1D8PS42
V	-22	HIS	-	expression tag	UNP A0A1D8PS42
V	-21	HIS	-	expression tag	UNP A0A1D8PS42

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Chain	Residue	Modelled	Actual	Comment	Reference
V	-20	HIS	-	expression tag	UNP A0A1D8PS42
V	-19	HIS	-	expression tag	UNP A0A1D8PS42
V	-18	HIS	-	expression tag	UNP A0A1D8PS42
V	-17	ASP	-	expression tag	UNP A0A1D8PS42
V	-16	TYR	-	expression tag	UNP A0A1D8PS42
V	-15	ASP	-	expression tag	UNP A0A1D8PS42
V	-14	ILE	-	expression tag	UNP A0A1D8PS42
V	-13	PRO	-	expression tag	UNP A0A1D8PS42
V	-12	THR	-	expression tag	UNP A0A1D8PS42
V	-11	THR	-	expression tag	UNP A0A1D8PS42
V	-10	GLU	-	expression tag	UNP A0A1D8PS42
V	-9	ASN	-	expression tag	UNP A0A1D8PS42
V	-8	LEU	-	expression tag	UNP A0A1D8PS42
V	-7	TYR	-	expression tag	UNP A0A1D8PS42
V	-6	PHE	-	expression tag	UNP A0A1D8PS42
V	-5	GLN	-	expression tag	UNP A0A1D8PS42
V	-4	GLY	-	expression tag	UNP A0A1D8PS42
V	-3	ALA	-	expression tag	UNP A0A1D8PS42
V	-2	MET	-	expression tag	UNP A0A1D8PS42
V	-1	ASP	-	expression tag	UNP A0A1D8PS42
V	0	PRO	-	expression tag	UNP A0A1D8PS42
V	123	VAL	LEU	conflict	UNP A0A1D8PS42
V	717	CYS	VAL	conflict	UNP A0A1D8PS42
b	-24	MET	-	initiating methionine	UNP A0A1D8PS42
b	-23	HIS	-	expression tag	UNP A0A1D8PS42
b	-22	HIS	-	expression tag	UNP A0A1D8PS42
b	-21	HIS	-	expression tag	UNP A0A1D8PS42
b	-20	HIS	-	expression tag	UNP A0A1D8PS42
b	-19	HIS	-	expression tag	UNP A0A1D8PS42
b	-18	HIS	-	expression tag	UNP A0A1D8PS42
b	-17	ASP	-	expression tag	UNP A0A1D8PS42
b	-16	TYR	-	expression tag	UNP A0A1D8PS42
b	-15	ASP	-	expression tag	UNP A0A1D8PS42
b	-14	ILE	-	expression tag	UNP A0A1D8PS42
b	-13	PRO	-	expression tag	UNP A0A1D8PS42
b	-12	THR	-	expression tag	UNP A0A1D8PS42
b	-11	THR	-	expression tag	UNP A0A1D8PS42
b	-10	GLU	-	expression tag	UNP A0A1D8PS42
b	-9	ASN	-	expression tag	UNP A0A1D8PS42
b	-8	LEU	-	expression tag	UNP A0A1D8PS42
b	-7	TYR	-	expression tag	UNP A0A1D8PS42
b	-6	PHE	-	expression tag	UNP A0A1D8PS42

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Chain	Residue	Modelled	Actual	Comment	Reference
b	-5	GLN	-	expression tag	UNP A0A1D8PS42
b	-4	GLY	-	expression tag	UNP A0A1D8PS42
b	-3	ALA	-	expression tag	UNP A0A1D8PS42
b	-2	MET	-	expression tag	UNP A0A1D8PS42
b	-1	ASP	-	expression tag	UNP A0A1D8PS42
b	0	PRO	-	expression tag	UNP A0A1D8PS42
b	123	VAL	LEU	conflict	UNP A0A1D8PS42
b	717	CYS	VAL	conflict	UNP A0A1D8PS42
h	-24	MET	-	initiating methionine	UNP A0A1D8PS42
h	-23	HIS	-	expression tag	UNP A0A1D8PS42
h	-22	HIS	-	expression tag	UNP A0A1D8PS42
h	-21	HIS	-	expression tag	UNP A0A1D8PS42
h	-20	HIS	-	expression tag	UNP A0A1D8PS42
h	-19	HIS	-	expression tag	UNP A0A1D8PS42
h	-18	HIS	-	expression tag	UNP A0A1D8PS42
h	-17	ASP	-	expression tag	UNP A0A1D8PS42
h	-16	TYR	-	expression tag	UNP A0A1D8PS42
h	-15	ASP	-	expression tag	UNP A0A1D8PS42
h	-14	ILE	-	expression tag	UNP A0A1D8PS42
h	-13	PRO	-	expression tag	UNP A0A1D8PS42
h	-12	THR	-	expression tag	UNP A0A1D8PS42
h	-11	THR	-	expression tag	UNP A0A1D8PS42
h	-10	GLU	-	expression tag	UNP A0A1D8PS42
h	-9	ASN	-	expression tag	UNP A0A1D8PS42
h	-8	LEU	-	expression tag	UNP A0A1D8PS42
h	-7	TYR	-	expression tag	UNP A0A1D8PS42
h	-6	PHE	-	expression tag	UNP A0A1D8PS42
h	-5	GLN	-	expression tag	UNP A0A1D8PS42
h	-4	GLY	-	expression tag	UNP A0A1D8PS42
h	-3	ALA	-	expression tag	UNP A0A1D8PS42
h	-2	MET	-	expression tag	UNP A0A1D8PS42
h	-1	ASP	-	expression tag	UNP A0A1D8PS42
h	0	PRO	-	expression tag	UNP A0A1D8PS42
h	123	VAL	LEU	conflict	UNP A0A1D8PS42
h	717	CYS	VAL	conflict	UNP A0A1D8PS42
n	-24	MET	-	initiating methionine	UNP A0A1D8PS42
n	-23	HIS	-	expression tag	UNP A0A1D8PS42
n	-22	HIS	-	expression tag	UNP A0A1D8PS42
n	-21	HIS	-	expression tag	UNP A0A1D8PS42
n	-20	HIS	-	expression tag	UNP A0A1D8PS42
n	-19	HIS	-	expression tag	UNP A0A1D8PS42
n	-18	HIS	-	expression tag	UNP A0A1D8PS42

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Chain	Residue	Modelled	Actual	Comment	Reference
n	-17	ASP	-	expression tag	UNP A0A1D8PS42
n	-16	TYR	-	expression tag	UNP A0A1D8PS42
n	-15	ASP	-	expression tag	UNP A0A1D8PS42
n	-14	ILE	-	expression tag	UNP A0A1D8PS42
n	-13	PRO	-	expression tag	UNP A0A1D8PS42
n	-12	THR	-	expression tag	UNP A0A1D8PS42
n	-11	THR	-	expression tag	UNP A0A1D8PS42
n	-10	GLU	-	expression tag	UNP A0A1D8PS42
n	-9	ASN	-	expression tag	UNP A0A1D8PS42
n	-8	LEU	-	expression tag	UNP A0A1D8PS42
n	-7	TYR	-	expression tag	UNP A0A1D8PS42
n	-6	PHE	-	expression tag	UNP A0A1D8PS42
n	-5	GLN	-	expression tag	UNP A0A1D8PS42
n	-4	GLY	-	expression tag	UNP A0A1D8PS42
n	-3	ALA	-	expression tag	UNP A0A1D8PS42
n	-2	MET	-	expression tag	UNP A0A1D8PS42
n	-1	ASP	-	expression tag	UNP A0A1D8PS42
n	0	PRO	-	expression tag	UNP A0A1D8PS42
n	123	VAL	LEU	conflict	UNP A0A1D8PS42
n	717	CYS	VAL	conflict	UNP A0A1D8PS42

- Molecule 4 is a protein called Mto2p-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	37	Total	C	N	O	S	0	0
			314	198	57	58	1		
4	F	31	Total	C	N	O	S	0	0
			273	172	51	49	1		
4	K	37	Total	C	N	O	S	0	0
			314	198	57	58	1		
4	L	31	Total	C	N	O	S	0	0
			273	172	51	49	1		
4	Q	37	Total	C	N	O	S	0	0
			314	198	57	58	1		
4	R	31	Total	C	N	O	S	0	0
			273	172	51	49	1		
4	W	37	Total	C	N	O	S	0	0
			314	198	57	58	1		
4	X	31	Total	C	N	O	S	0	0
			273	172	51	49	1		
4	c	37	Total	C	N	O	S	0	0
			314	198	57	58	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	31	Total	C	N	O	S	0	0
			273	172	51	49	1		
4	i	37	Total	C	N	O	S	0	0
			314	198	57	58	1		
4	j	31	Total	C	N	O	S	0	0
			273	172	51	49	1		
4	o	37	Total	C	N	O	S	0	0
			314	198	57	58	1		
4	p	31	Total	C	N	O	S	0	0
			273	172	51	49	1		

There are 224 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	600	GLY	-	expression tag	UNP Q5AGV5
E	601	SER	-	expression tag	UNP Q5AGV5
E	602	GLY	-	expression tag	UNP Q5AGV5
E	603	SER	-	expression tag	UNP Q5AGV5
E	604	GLY	-	expression tag	UNP Q5AGV5
E	605	SER	-	expression tag	UNP Q5AGV5
E	606	GLU	-	expression tag	UNP Q5AGV5
E	607	GLN	-	expression tag	UNP Q5AGV5
E	608	LYS	-	expression tag	UNP Q5AGV5
E	609	LEU	-	expression tag	UNP Q5AGV5
E	610	ILE	-	expression tag	UNP Q5AGV5
E	611	SER	-	expression tag	UNP Q5AGV5
E	612	GLU	-	expression tag	UNP Q5AGV5
E	613	GLU	-	expression tag	UNP Q5AGV5
E	614	ASP	-	expression tag	UNP Q5AGV5
E	615	LEU	-	expression tag	UNP Q5AGV5
F	600	GLY	-	expression tag	UNP Q5AGV5
F	601	SER	-	expression tag	UNP Q5AGV5
F	602	GLY	-	expression tag	UNP Q5AGV5
F	603	SER	-	expression tag	UNP Q5AGV5
F	604	GLY	-	expression tag	UNP Q5AGV5
F	605	SER	-	expression tag	UNP Q5AGV5
F	606	GLU	-	expression tag	UNP Q5AGV5
F	607	GLN	-	expression tag	UNP Q5AGV5
F	608	LYS	-	expression tag	UNP Q5AGV5
F	609	LEU	-	expression tag	UNP Q5AGV5
F	610	ILE	-	expression tag	UNP Q5AGV5
F	611	SER	-	expression tag	UNP Q5AGV5
F	612	GLU	-	expression tag	UNP Q5AGV5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	613	GLU	-	expression tag	UNP Q5AGV5
F	614	ASP	-	expression tag	UNP Q5AGV5
F	615	LEU	-	expression tag	UNP Q5AGV5
K	600	GLY	-	expression tag	UNP Q5AGV5
K	601	SER	-	expression tag	UNP Q5AGV5
K	602	GLY	-	expression tag	UNP Q5AGV5
K	603	SER	-	expression tag	UNP Q5AGV5
K	604	GLY	-	expression tag	UNP Q5AGV5
K	605	SER	-	expression tag	UNP Q5AGV5
K	606	GLU	-	expression tag	UNP Q5AGV5
K	607	GLN	-	expression tag	UNP Q5AGV5
K	608	LYS	-	expression tag	UNP Q5AGV5
K	609	LEU	-	expression tag	UNP Q5AGV5
K	610	ILE	-	expression tag	UNP Q5AGV5
K	611	SER	-	expression tag	UNP Q5AGV5
K	612	GLU	-	expression tag	UNP Q5AGV5
K	613	GLU	-	expression tag	UNP Q5AGV5
K	614	ASP	-	expression tag	UNP Q5AGV5
K	615	LEU	-	expression tag	UNP Q5AGV5
L	600	GLY	-	expression tag	UNP Q5AGV5
L	601	SER	-	expression tag	UNP Q5AGV5
L	602	GLY	-	expression tag	UNP Q5AGV5
L	603	SER	-	expression tag	UNP Q5AGV5
L	604	GLY	-	expression tag	UNP Q5AGV5
L	605	SER	-	expression tag	UNP Q5AGV5
L	606	GLU	-	expression tag	UNP Q5AGV5
L	607	GLN	-	expression tag	UNP Q5AGV5
L	608	LYS	-	expression tag	UNP Q5AGV5
L	609	LEU	-	expression tag	UNP Q5AGV5
L	610	ILE	-	expression tag	UNP Q5AGV5
L	611	SER	-	expression tag	UNP Q5AGV5
L	612	GLU	-	expression tag	UNP Q5AGV5
L	613	GLU	-	expression tag	UNP Q5AGV5
L	614	ASP	-	expression tag	UNP Q5AGV5
L	615	LEU	-	expression tag	UNP Q5AGV5
Q	600	GLY	-	expression tag	UNP Q5AGV5
Q	601	SER	-	expression tag	UNP Q5AGV5
Q	602	GLY	-	expression tag	UNP Q5AGV5
Q	603	SER	-	expression tag	UNP Q5AGV5
Q	604	GLY	-	expression tag	UNP Q5AGV5
Q	605	SER	-	expression tag	UNP Q5AGV5
Q	606	GLU	-	expression tag	UNP Q5AGV5

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	607	GLN	-	expression tag	UNP Q5AGV5
Q	608	LYS	-	expression tag	UNP Q5AGV5
Q	609	LEU	-	expression tag	UNP Q5AGV5
Q	610	ILE	-	expression tag	UNP Q5AGV5
Q	611	SER	-	expression tag	UNP Q5AGV5
Q	612	GLU	-	expression tag	UNP Q5AGV5
Q	613	GLU	-	expression tag	UNP Q5AGV5
Q	614	ASP	-	expression tag	UNP Q5AGV5
Q	615	LEU	-	expression tag	UNP Q5AGV5
R	600	GLY	-	expression tag	UNP Q5AGV5
R	601	SER	-	expression tag	UNP Q5AGV5
R	602	GLY	-	expression tag	UNP Q5AGV5
R	603	SER	-	expression tag	UNP Q5AGV5
R	604	GLY	-	expression tag	UNP Q5AGV5
R	605	SER	-	expression tag	UNP Q5AGV5
R	606	GLU	-	expression tag	UNP Q5AGV5
R	607	GLN	-	expression tag	UNP Q5AGV5
R	608	LYS	-	expression tag	UNP Q5AGV5
R	609	LEU	-	expression tag	UNP Q5AGV5
R	610	ILE	-	expression tag	UNP Q5AGV5
R	611	SER	-	expression tag	UNP Q5AGV5
R	612	GLU	-	expression tag	UNP Q5AGV5
R	613	GLU	-	expression tag	UNP Q5AGV5
R	614	ASP	-	expression tag	UNP Q5AGV5
R	615	LEU	-	expression tag	UNP Q5AGV5
W	600	GLY	-	expression tag	UNP Q5AGV5
W	601	SER	-	expression tag	UNP Q5AGV5
W	602	GLY	-	expression tag	UNP Q5AGV5
W	603	SER	-	expression tag	UNP Q5AGV5
W	604	GLY	-	expression tag	UNP Q5AGV5
W	605	SER	-	expression tag	UNP Q5AGV5
W	606	GLU	-	expression tag	UNP Q5AGV5
W	607	GLN	-	expression tag	UNP Q5AGV5
W	608	LYS	-	expression tag	UNP Q5AGV5
W	609	LEU	-	expression tag	UNP Q5AGV5
W	610	ILE	-	expression tag	UNP Q5AGV5
W	611	SER	-	expression tag	UNP Q5AGV5
W	612	GLU	-	expression tag	UNP Q5AGV5
W	613	GLU	-	expression tag	UNP Q5AGV5
W	614	ASP	-	expression tag	UNP Q5AGV5
W	615	LEU	-	expression tag	UNP Q5AGV5
X	600	GLY	-	expression tag	UNP Q5AGV5

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Chain	Residue	Modelled	Actual	Comment	Reference
X	601	SER	-	expression tag	UNP Q5AGV5
X	602	GLY	-	expression tag	UNP Q5AGV5
X	603	SER	-	expression tag	UNP Q5AGV5
X	604	GLY	-	expression tag	UNP Q5AGV5
X	605	SER	-	expression tag	UNP Q5AGV5
X	606	GLU	-	expression tag	UNP Q5AGV5
X	607	GLN	-	expression tag	UNP Q5AGV5
X	608	LYS	-	expression tag	UNP Q5AGV5
X	609	LEU	-	expression tag	UNP Q5AGV5
X	610	ILE	-	expression tag	UNP Q5AGV5
X	611	SER	-	expression tag	UNP Q5AGV5
X	612	GLU	-	expression tag	UNP Q5AGV5
X	613	GLU	-	expression tag	UNP Q5AGV5
X	614	ASP	-	expression tag	UNP Q5AGV5
X	615	LEU	-	expression tag	UNP Q5AGV5
c	600	GLY	-	expression tag	UNP Q5AGV5
c	601	SER	-	expression tag	UNP Q5AGV5
c	602	GLY	-	expression tag	UNP Q5AGV5
c	603	SER	-	expression tag	UNP Q5AGV5
c	604	GLY	-	expression tag	UNP Q5AGV5
c	605	SER	-	expression tag	UNP Q5AGV5
c	606	GLU	-	expression tag	UNP Q5AGV5
c	607	GLN	-	expression tag	UNP Q5AGV5
c	608	LYS	-	expression tag	UNP Q5AGV5
c	609	LEU	-	expression tag	UNP Q5AGV5
c	610	ILE	-	expression tag	UNP Q5AGV5
c	611	SER	-	expression tag	UNP Q5AGV5
c	612	GLU	-	expression tag	UNP Q5AGV5
c	613	GLU	-	expression tag	UNP Q5AGV5
c	614	ASP	-	expression tag	UNP Q5AGV5
c	615	LEU	-	expression tag	UNP Q5AGV5
d	600	GLY	-	expression tag	UNP Q5AGV5
d	601	SER	-	expression tag	UNP Q5AGV5
d	602	GLY	-	expression tag	UNP Q5AGV5
d	603	SER	-	expression tag	UNP Q5AGV5
d	604	GLY	-	expression tag	UNP Q5AGV5
d	605	SER	-	expression tag	UNP Q5AGV5
d	606	GLU	-	expression tag	UNP Q5AGV5
d	607	GLN	-	expression tag	UNP Q5AGV5
d	608	LYS	-	expression tag	UNP Q5AGV5
d	609	LEU	-	expression tag	UNP Q5AGV5
d	610	ILE	-	expression tag	UNP Q5AGV5

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Chain	Residue	Modelled	Actual	Comment	Reference
d	611	SER	-	expression tag	UNP Q5AGV5
d	612	GLU	-	expression tag	UNP Q5AGV5
d	613	GLU	-	expression tag	UNP Q5AGV5
d	614	ASP	-	expression tag	UNP Q5AGV5
d	615	LEU	-	expression tag	UNP Q5AGV5
i	600	GLY	-	expression tag	UNP Q5AGV5
i	601	SER	-	expression tag	UNP Q5AGV5
i	602	GLY	-	expression tag	UNP Q5AGV5
i	603	SER	-	expression tag	UNP Q5AGV5
i	604	GLY	-	expression tag	UNP Q5AGV5
i	605	SER	-	expression tag	UNP Q5AGV5
i	606	GLU	-	expression tag	UNP Q5AGV5
i	607	GLN	-	expression tag	UNP Q5AGV5
i	608	LYS	-	expression tag	UNP Q5AGV5
i	609	LEU	-	expression tag	UNP Q5AGV5
i	610	ILE	-	expression tag	UNP Q5AGV5
i	611	SER	-	expression tag	UNP Q5AGV5
i	612	GLU	-	expression tag	UNP Q5AGV5
i	613	GLU	-	expression tag	UNP Q5AGV5
i	614	ASP	-	expression tag	UNP Q5AGV5
i	615	LEU	-	expression tag	UNP Q5AGV5
j	600	GLY	-	expression tag	UNP Q5AGV5
j	601	SER	-	expression tag	UNP Q5AGV5
j	602	GLY	-	expression tag	UNP Q5AGV5
j	603	SER	-	expression tag	UNP Q5AGV5
j	604	GLY	-	expression tag	UNP Q5AGV5
j	605	SER	-	expression tag	UNP Q5AGV5
j	606	GLU	-	expression tag	UNP Q5AGV5
j	607	GLN	-	expression tag	UNP Q5AGV5
j	608	LYS	-	expression tag	UNP Q5AGV5
j	609	LEU	-	expression tag	UNP Q5AGV5
j	610	ILE	-	expression tag	UNP Q5AGV5
j	611	SER	-	expression tag	UNP Q5AGV5
j	612	GLU	-	expression tag	UNP Q5AGV5
j	613	GLU	-	expression tag	UNP Q5AGV5
j	614	ASP	-	expression tag	UNP Q5AGV5
j	615	LEU	-	expression tag	UNP Q5AGV5
o	600	GLY	-	expression tag	UNP Q5AGV5
o	601	SER	-	expression tag	UNP Q5AGV5
o	602	GLY	-	expression tag	UNP Q5AGV5
o	603	SER	-	expression tag	UNP Q5AGV5
o	604	GLY	-	expression tag	UNP Q5AGV5

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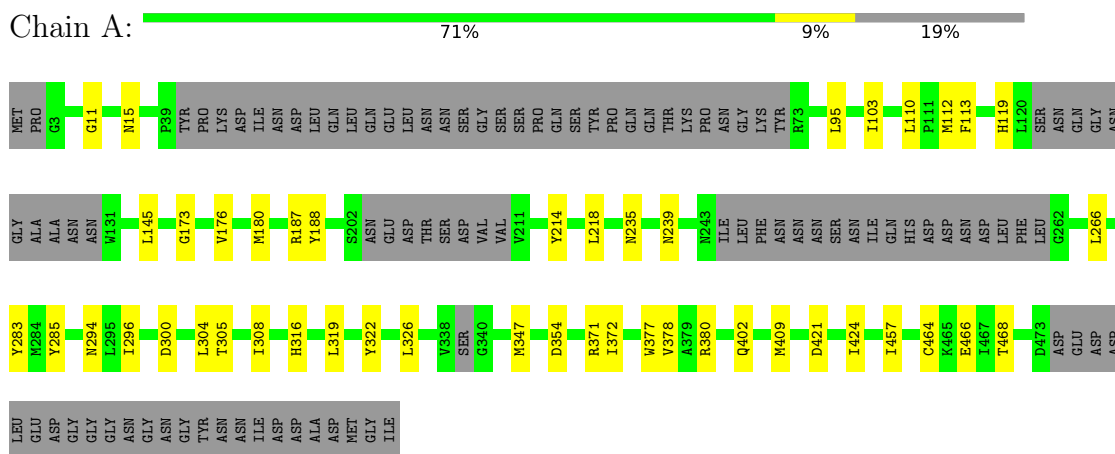
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
o	605	SER	-	expression tag	UNP Q5AGV5
o	606	GLU	-	expression tag	UNP Q5AGV5
o	607	GLN	-	expression tag	UNP Q5AGV5
o	608	LYS	-	expression tag	UNP Q5AGV5
o	609	LEU	-	expression tag	UNP Q5AGV5
o	610	ILE	-	expression tag	UNP Q5AGV5
o	611	SER	-	expression tag	UNP Q5AGV5
o	612	GLU	-	expression tag	UNP Q5AGV5
o	613	GLU	-	expression tag	UNP Q5AGV5
o	614	ASP	-	expression tag	UNP Q5AGV5
o	615	LEU	-	expression tag	UNP Q5AGV5
p	600	GLY	-	expression tag	UNP Q5AGV5
p	601	SER	-	expression tag	UNP Q5AGV5
p	602	GLY	-	expression tag	UNP Q5AGV5
p	603	SER	-	expression tag	UNP Q5AGV5
p	604	GLY	-	expression tag	UNP Q5AGV5
p	605	SER	-	expression tag	UNP Q5AGV5
p	606	GLU	-	expression tag	UNP Q5AGV5
p	607	GLN	-	expression tag	UNP Q5AGV5
p	608	LYS	-	expression tag	UNP Q5AGV5
p	609	LEU	-	expression tag	UNP Q5AGV5
p	610	ILE	-	expression tag	UNP Q5AGV5
p	611	SER	-	expression tag	UNP Q5AGV5
p	612	GLU	-	expression tag	UNP Q5AGV5
p	613	GLU	-	expression tag	UNP Q5AGV5
p	614	ASP	-	expression tag	UNP Q5AGV5
p	615	LEU	-	expression tag	UNP Q5AGV5

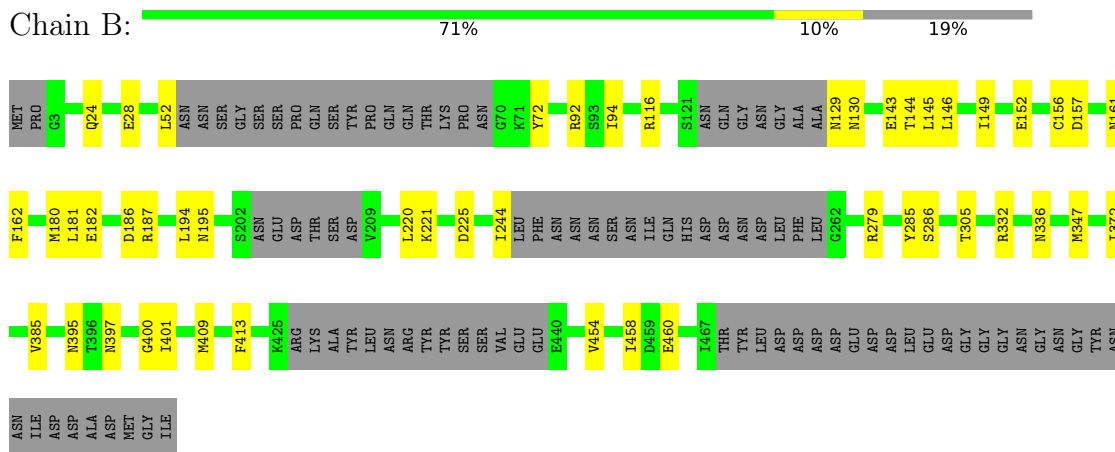
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Tubulin gamma chain

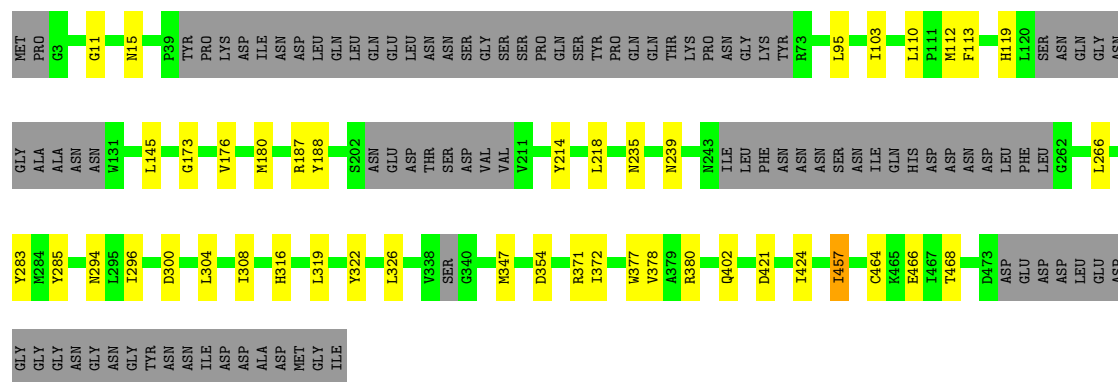


- Molecule 1: Tubulin gamma chain

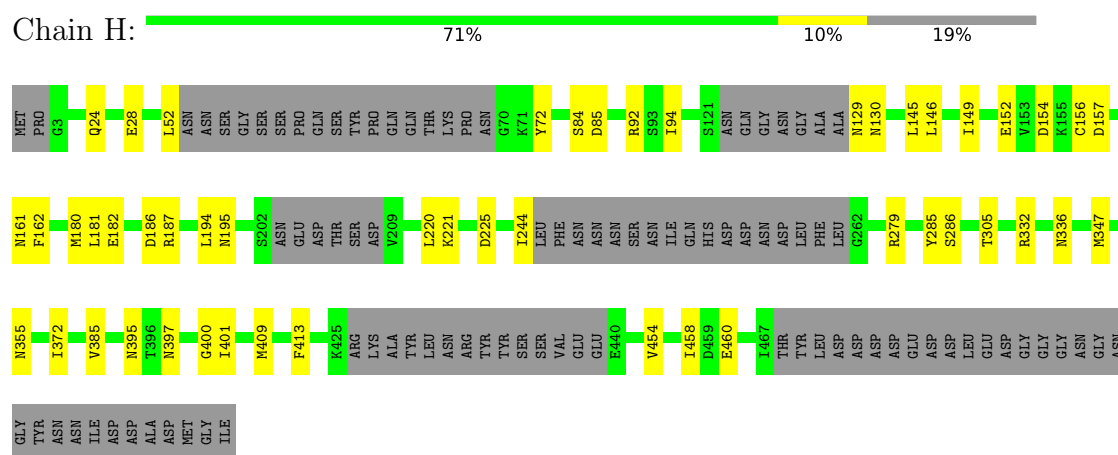


- Molecule 1: Tubulin gamma chain

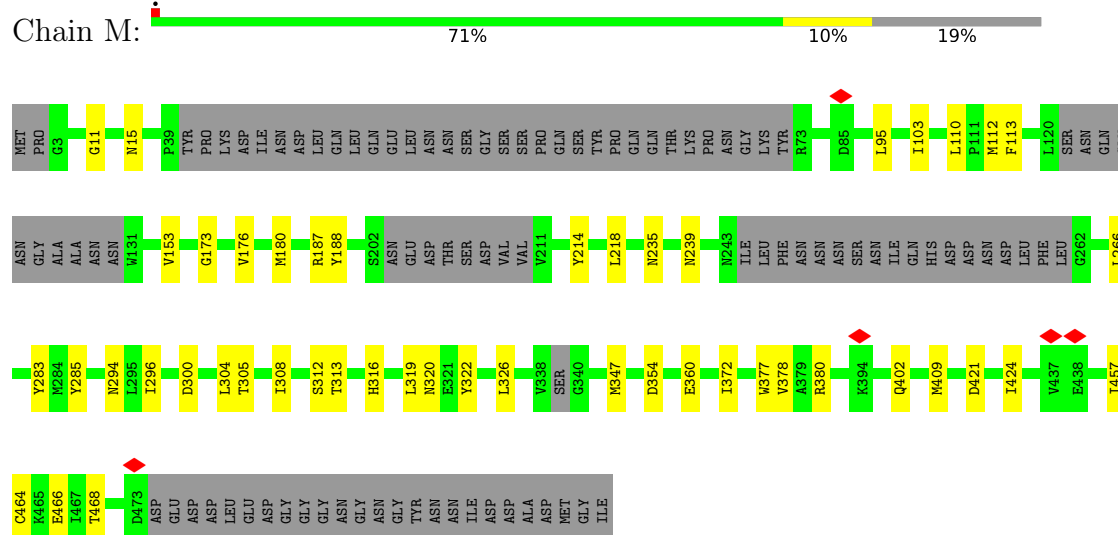




- Molecule 1: Tubulin gamma chain

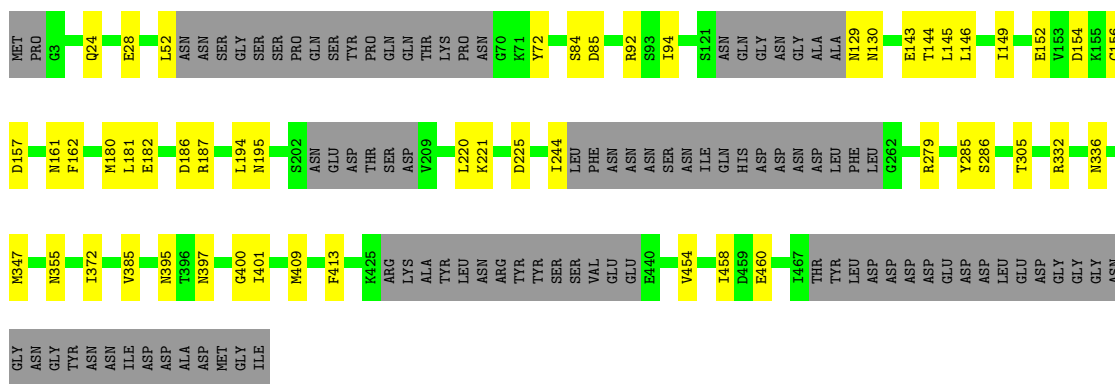


- Molecule 1: Tubulin gamma chain

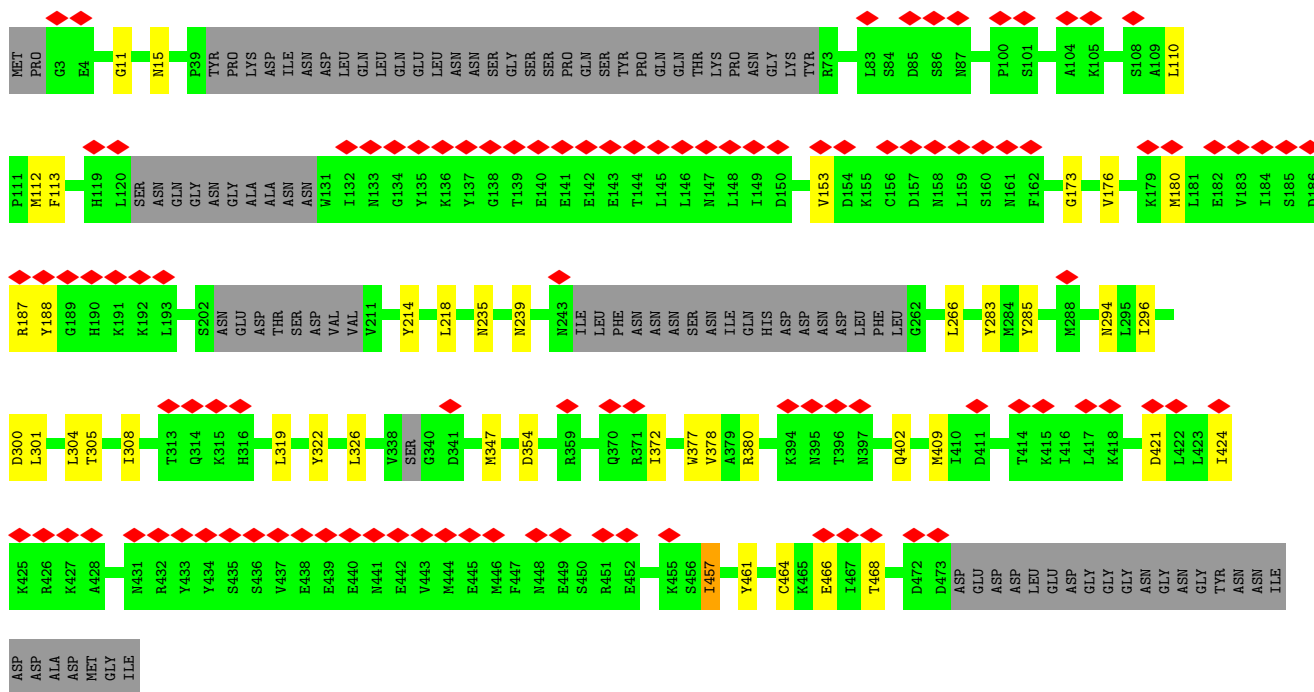


- Molecule 1: Tubulin gamma chain

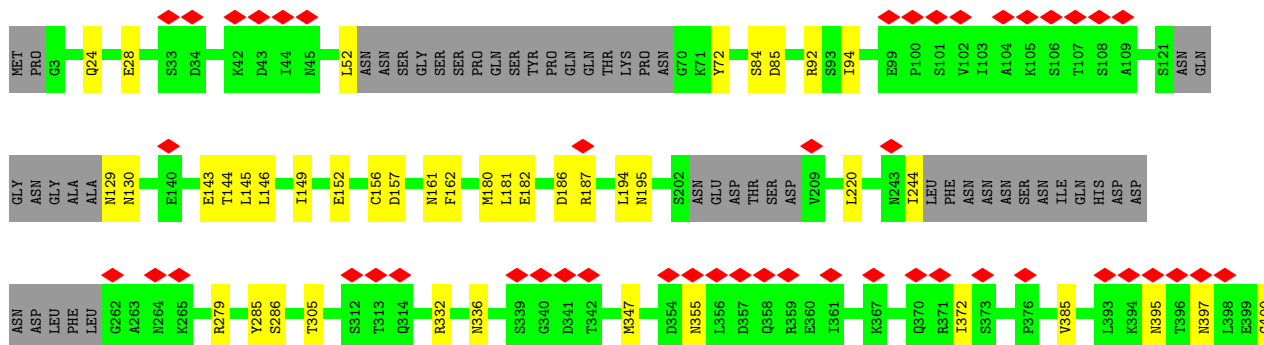




- Molecule 1: Tubulin gamma chain

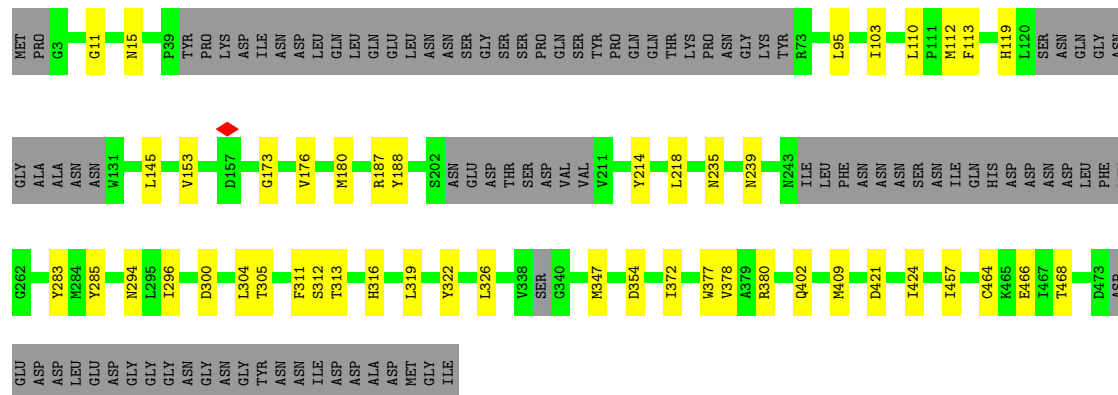


- Molecule 1: Tubulin gamma chain

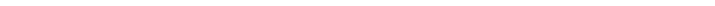


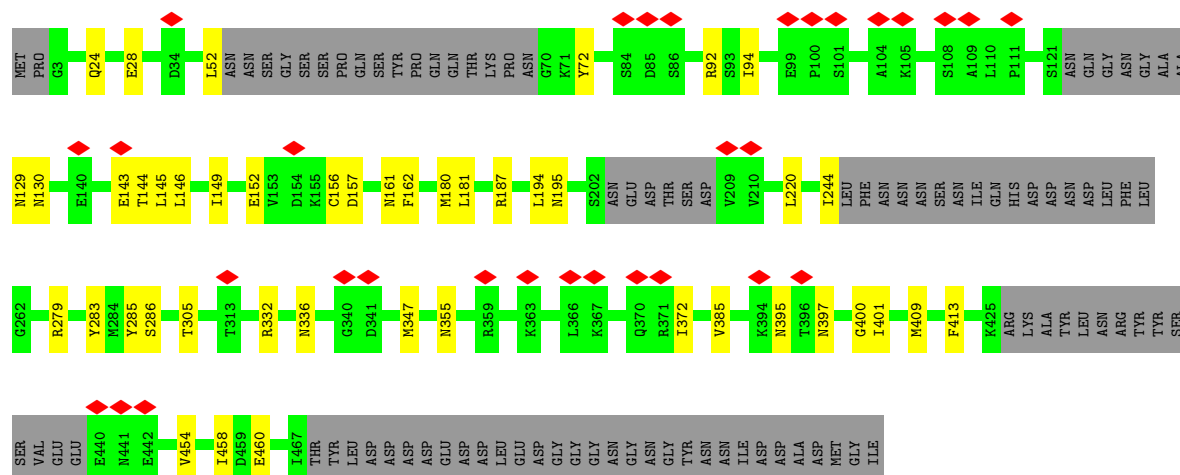
- Molecule 1: Tubulin gamma chain

Chain Y: 71% 9% 19%



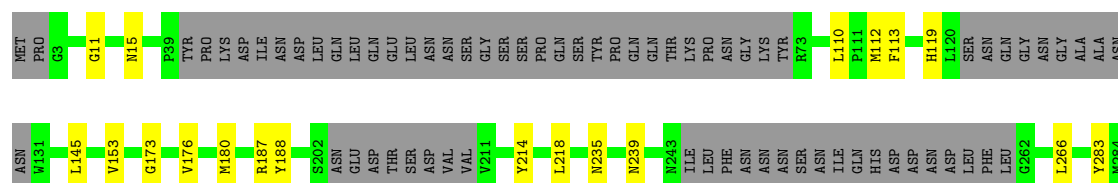
- Molecule 1: Tubulin gamma chain

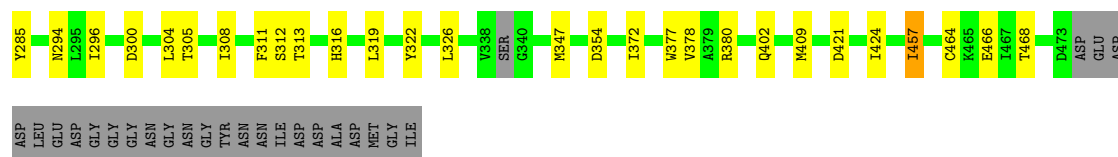
Chain Z:  6% 72% 9% 13%



- Molecule 1: Tubulin gamma chain

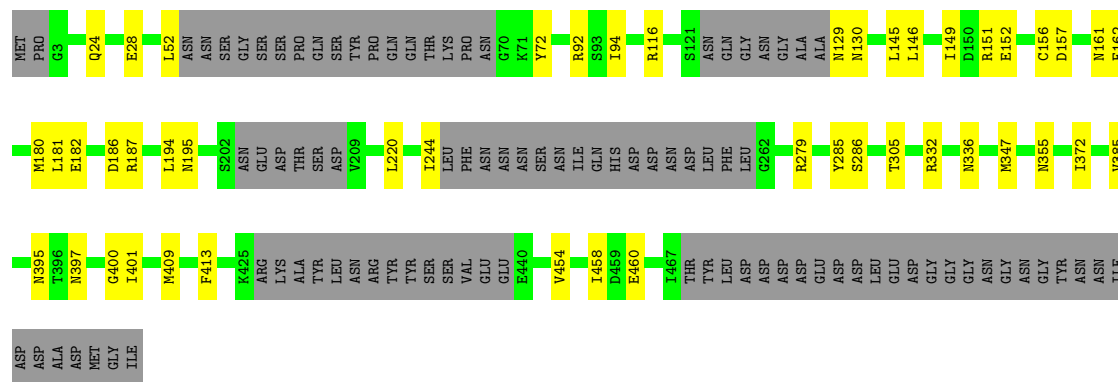
Chain e: 71% 9% 19%





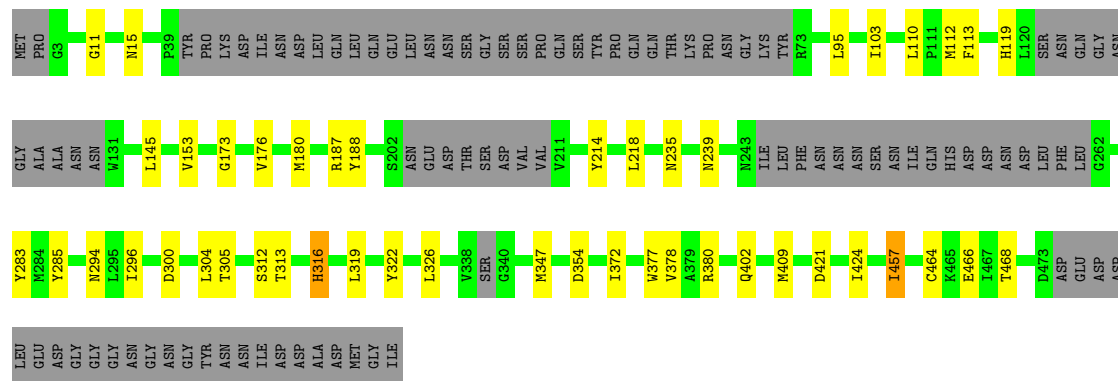
- Molecule 1: Tubulin gamma chain

Chain f: 72% 9% 19%



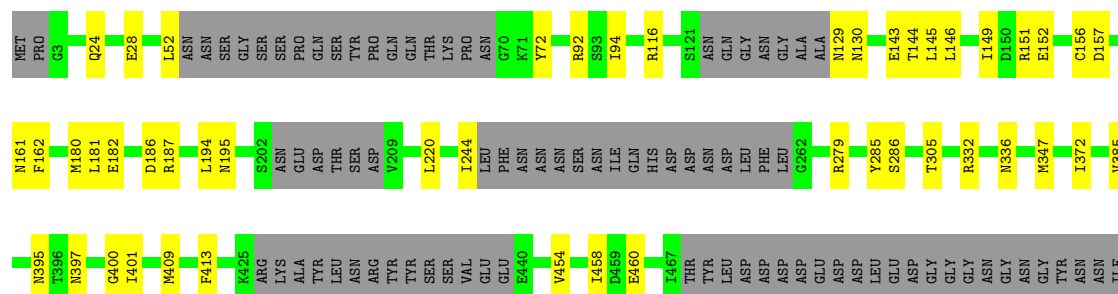
- Molecule 1: Tubulin gamma chain

Chain k: 71% 9% 19%



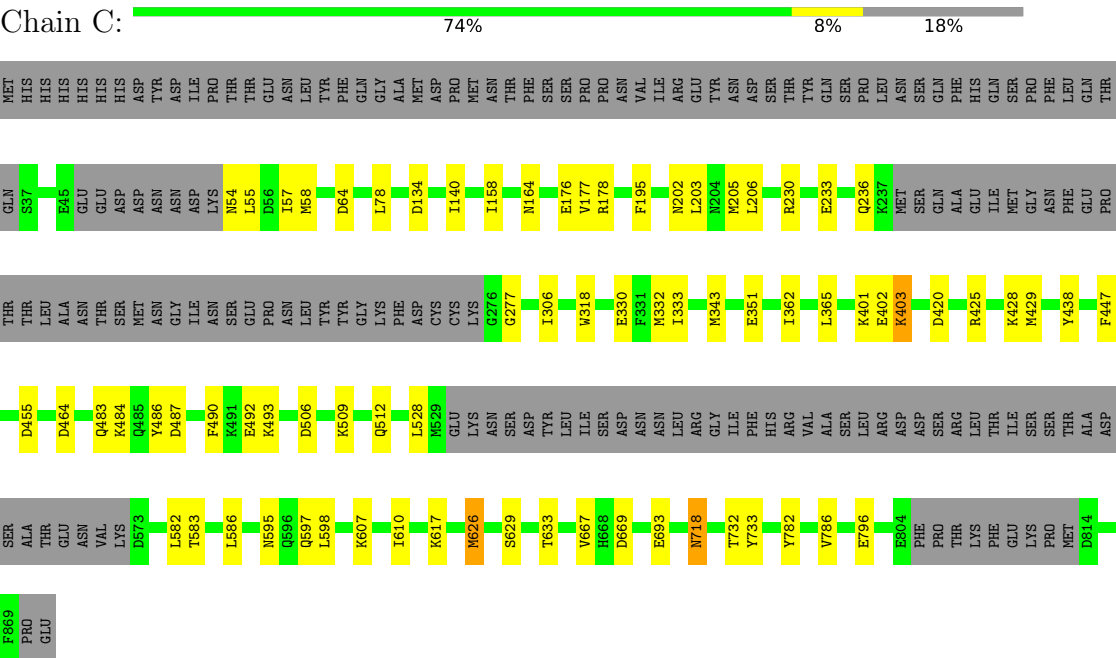
- Molecule 1: Tubulin gamma chain

Chain l: 72% 9% 19%

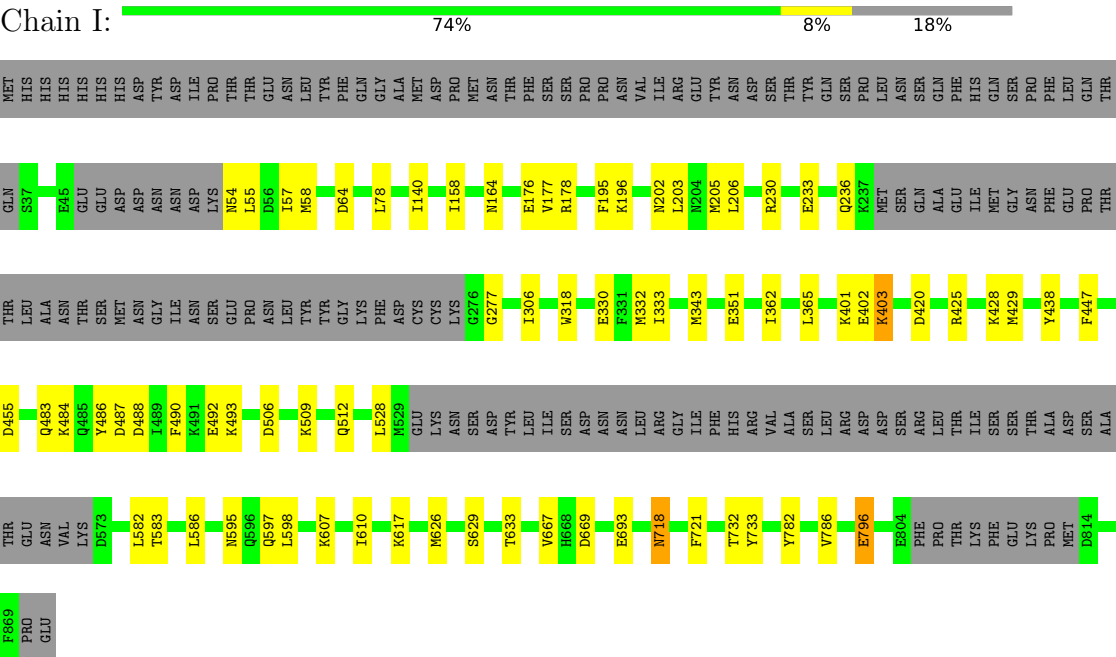


ASP
ASP
ALA
ASP
MET
GLY
ILE

• Molecule 2: Spindle pole body component

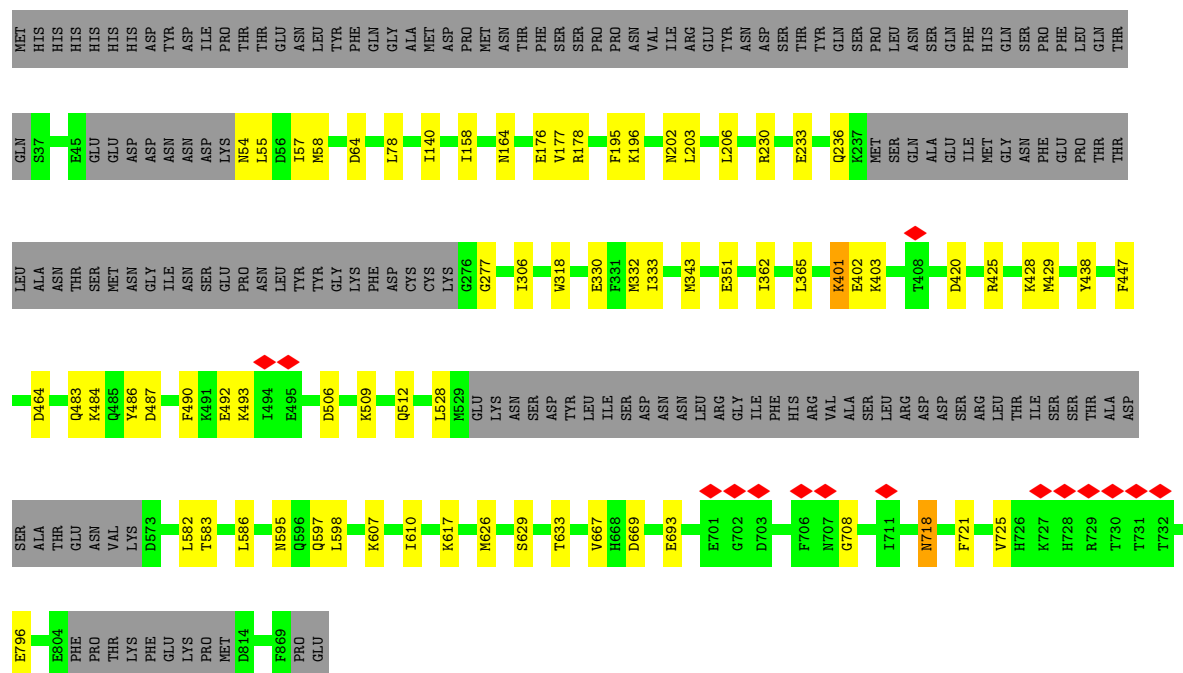


• Molecule 2: Spindle pole body component

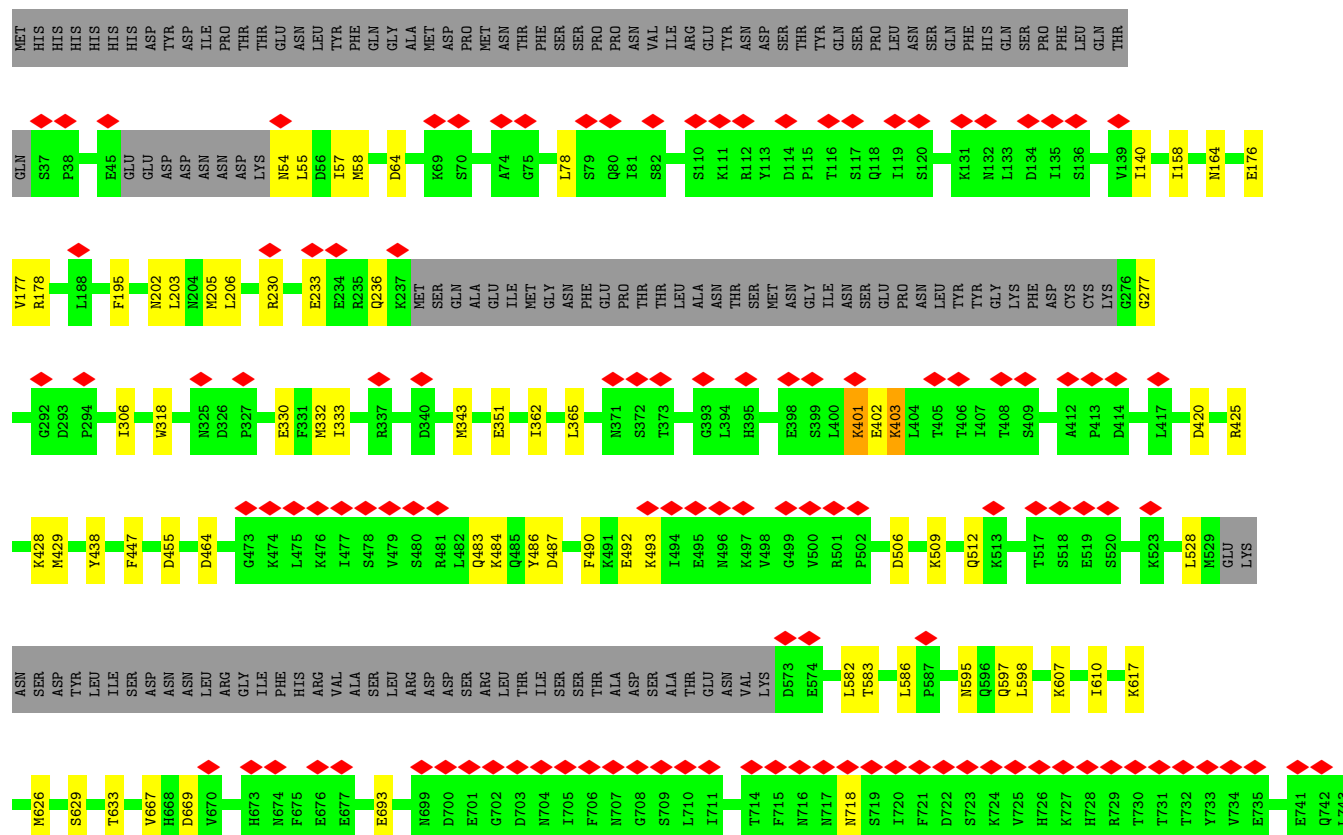
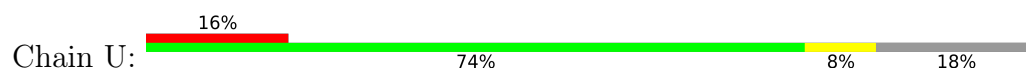


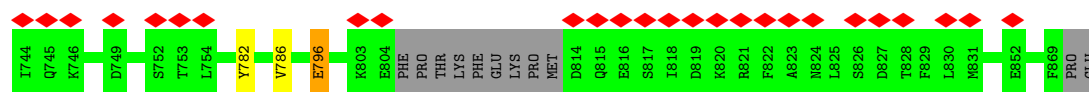
• Molecule 2: Spindle pole body component





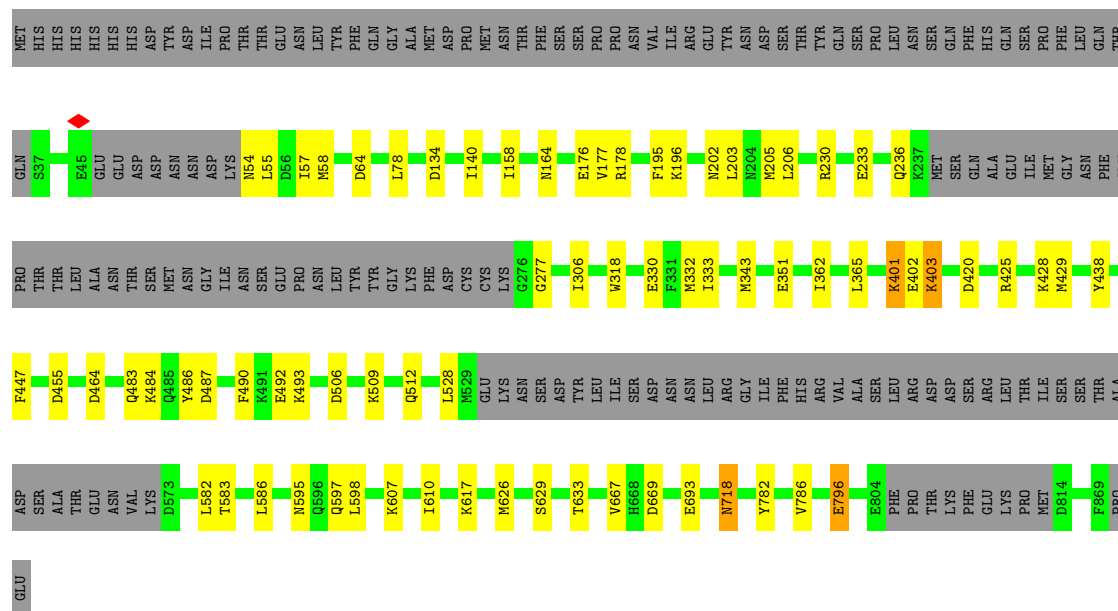
• Molecule 2: Spindle pole body component





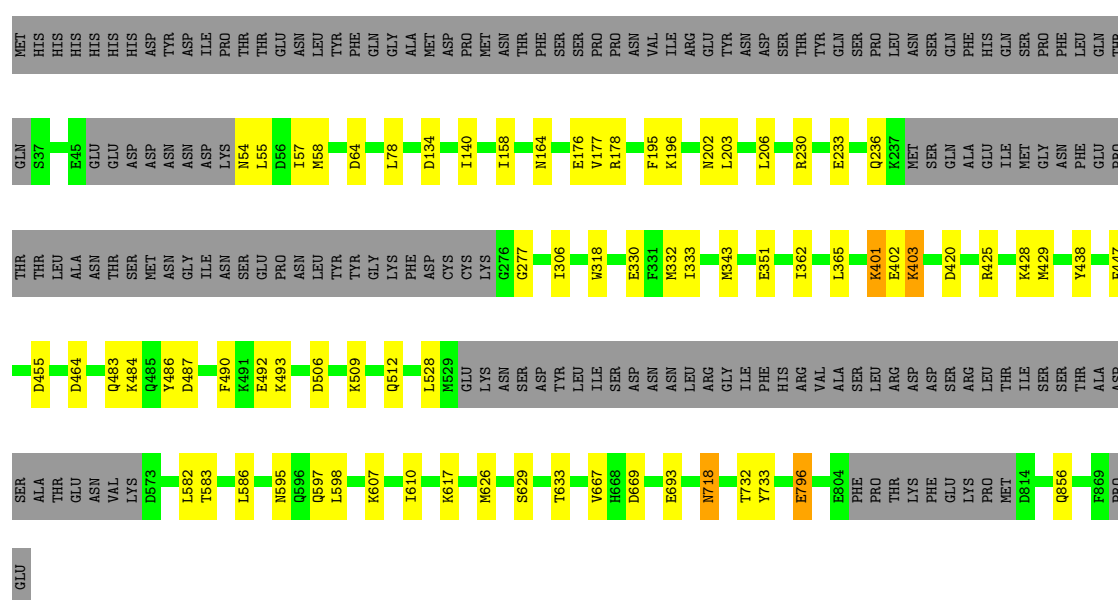
- Molecule 2: Spindle pole body component

Chain a: 74% 8% 18%



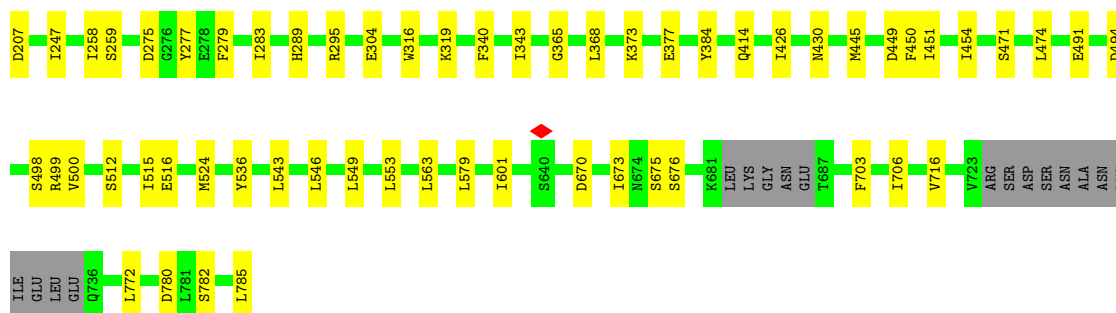
- Molecule 2: Spindle pole body component

Chain g: 74% 8% 18%



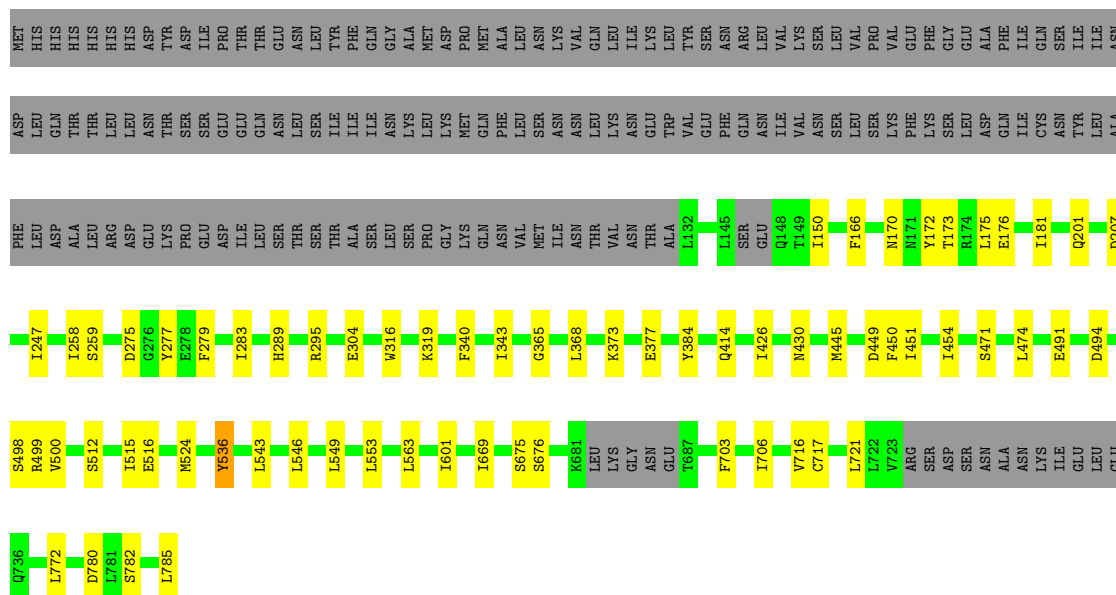
- Molecule 2: Spindle pole body component

Chain m: 74% 8% 18%



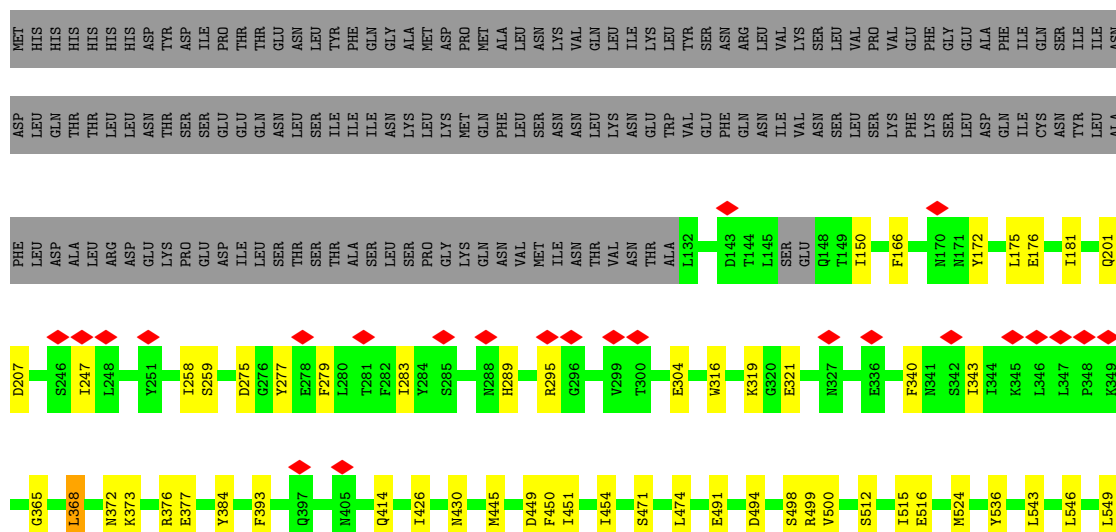
• Molecule 3: Spc98p

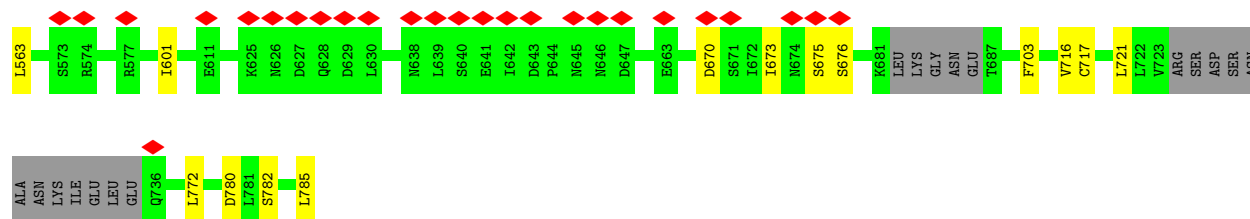
Chain P: 70% 8% 22%



• Molecule 3: Spc98p

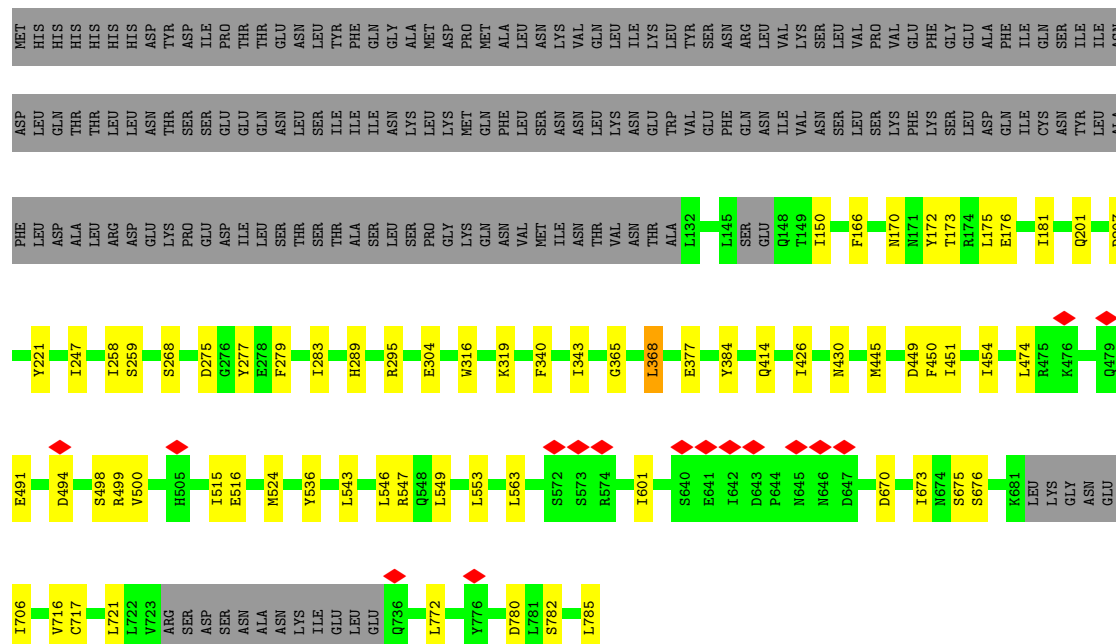
Chain V: 7% 70% 8% 22%





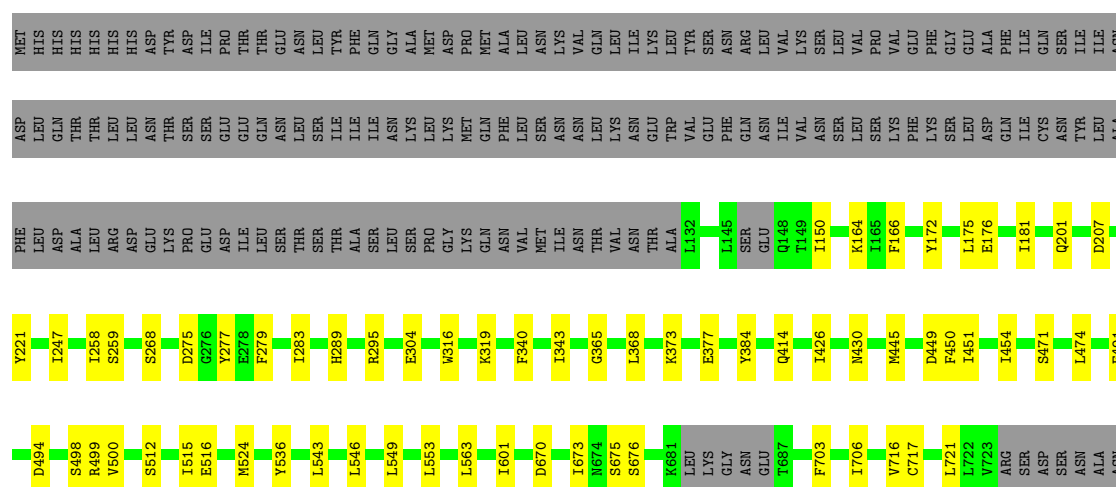
• Molecule 3: Spc98p

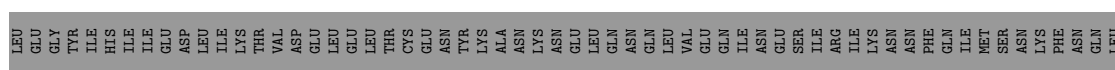
Chain b: 70% 8% 22%



• Molecule 3: Spc98p

Chain h: 70% 9% 22%





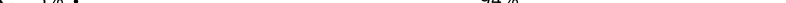
[illegible]

- Molecule 4: Mto2p-binding domain-containing protein

Chain F: 95%

LEU	GLU	ASN	GLY	HIS	LEU	E242	PRO	SER	GLU	MET
LEU	ASP	PHE	VAL	GLY	ASP	L243	LYS	GLN	GLU	SER
ASP	SER	GLN	SER	GLY	GLU	R244	ASN	VAL	GLU	GLU
GLN	THR	ILE	THR	SER	ALA	R245	ILE	ASP	GLU	LEU
TYR	ASN	MET	ASN	ASN	LEU		SER	ILE	SER	GLY
LYS	SER	SER	ASN	THR	GLU	V248	PRO	ASN	GLU	ILE
ASN	VAL	ASN	VAL	THR	LEU		TRP	ILE	GLU	ASN
PRO	LYS	ASN	ALA	THR	ASN			SER	GLU	GLN
LYS	ASN	PHE	ASN	SER	LEU	I252	ARG	GLN	GLU	GLU
SER	SER	ASN	LYS	PRO	GLY		PHE	ASN	MET	ASN
THR	THR	GLN	ASN	LYS	GLN	M257	ARG	HIS	GLN	ASN
THR	ASN	ASN	ASP	GLU	TYR		PRO	LYS	ILE	ASN
ASN	LEU	LEU	LEU	THR	ASN	L261	THR	SER	THR	SER
ASN	ARG	ARG	LEU	THR	ASN	Q262		ASN	GLN	ASN
GLN	GLN	GLN	GLU	LEU	LYS		ARG	LEU	ASN	VAL
THR	THR	LEU	GLY	GLN	ILE	R269	GLY	GLU	SER	GLU
ASN	ASN	LEU	TYR	GLN	GLU		ASP	GLU	VAL	ILE
ASN	ASN	SER	ILE	SER	THR		PRO	ARG	GLN	LEU
ASN	LYS	GLY	ILE	SER	ASN	HIS	GLU	LEU	GLN	SER
ASN	GLY	LYS	ILE	ALA	LYS	GLU	THR	SER	GLN	ASN
ASN	ASN	ASN	GLU	GLN	GLU	PHE	PRO	THR	GLU	ASN
ASN	ASN	ASN	GLU	ILE	GLU	ASN	ASP	THR	GLU	SER
ASN	ASN	LYS	LEU	LEU	VAL	LEU	ARG	PRO	GLY	ALA
ASN	ASN	ASN	ILE	VAL	ASP	LEU	SER	ASN	THR	GLN
ASN	ASN	LEU	LYS	LYS	LYS	LEU	LEU	ASP	THR	ASN
ASN	THR	ASN	THR	LEU	ASP	ARG	PHE	ASN	LEU	SER
ARG	ARG	GLU	VAL	ASN	ASN	ARG	GLN	ASN	SER	SER
GLU	GLU	GLU	ASN	VAL	GLM	ASN	ASN	ASN	SER	ASN
SER	SER	PHE	GLU	LEU	ILE	ASN	LYS	ASN	SER	THR
SER	TYR	LYS	LEU	LYS	SER	ASN	PRO	ASN	PRO	SER
SER	SER	ASN	GLU	LEU	GLU	ASN	ASN	ASN	PHE	SER
TYR	SER	ASN	GLU	LEU	TYR	ILE	LEU	LYS	ILE	SER
ASN	ASN	ASN	THR	GLU	GLU	MET	LEU	VAL	SER	ASN
ASN	ASN	GLN	GLN	THR	ARG	ASN	PHE	ASN	ARG	LEU
HIS	ASN	GLN	ASN	ARG	ILE	ASN	ASN	LYS	PRO	ILE
ARG	ARG	GLN	TYR	LEU	ILE	GLU	ASN	ASN	ASN	PHE
ASN	ASN	GLN	LYS	ASN	LEU	ASN	GLY	ASN	SER	ASN
ASN	ASN	GLN	ALA	ASN	LEU	ASN	LEU	PRO	PRO	GLN
SER	SER	GLN	GLN	GLN	ILE	PRO	SER	THR	LEU	GLN
SER	SER	GLN	ALA	ASN	ILE	ASN	ASN	THR	GLN	GLN
SER	SER	GLN	GLN	SER	GLU	GLN	ARG	ASN	GLN	GLN
SER	SER	GLN	ASN	LYS	ILE	THR	MET	ASP	GLY	GLN
GLY	SER	LYS	GLN	PRO	ILE	SER	VAL	ILE	THR	GLN
SER	GLY	LEU	LEU	HIS	TYR	SER	THR	THR	SER	GLN
SER	SER	ILE	VAL	ASP	ILE	THR	THR	ILE	THR	GLN
GLY	GLU	TYR	GLU	LEU	LEU	LEU	GLY	ILE	ARG	GLN
GLY	GLU	TYR	GLN	PHE	ILE	GLU	ASN	THR	PRO	GLN
GLU	GLU	GLY	ILE	THR	ASN	ILE	ASN	ILE	ASN	GLN
GLN	GLN	LYS	GLN	PRO	ILE	GLN	ASN	ASN	SER	GLN
LYS	LYS	CYS	ASN	PRO	GLU	GLN	ALA	ASN	LEU	GLY
LEU	LEU	ILE	GLU	PRO	TYR	HIS	THR	LEU	THR	THR
ILE	ILE	ILE	SER	TYR	ASP	GLN	THR	THR	THR	GLN
THR	THR	THR	SER	THR	LYS	ASN	LYS	THR	ARG	THR
SER	SER	ILE	ILE	SER	ASN	GLN	GLN	SER	ASP	ASN
GLU	GLU	GLN	GLN	TYR	TYR	ILE	ILE	THR	THR	GLU
ASP	ASP	ASN	ASN	TYR	SER	GLU	R249	ILE	TYR	PRO

- Molecule 4: Mto2p-binding domain-containing protein

Chain K:  5% 94%

[illegible]

PRO	LYS	ASN	ILE	ASN	PRO	TRP	ARG	GLN	PHE	ARG	PRO	THR	LEU	ARG	GLY	ASN	R231	R235	E242	L254	M257	R258
LEU	TYR	ASN	LYS	GLN	ILE	ASN	ASP	PRO	HIS	GLU	PHE	HIS	LEU	LEU	GLY	ASP	GLN	ALA	LEU	LEU	ASN	GLN
LEU	TYR	ASN	LYS	GLN	ILE	ASN	ASP	PRO	HIS	GLU	PHE	HIS	LEU	LEU	GLY	ASP	GLN	ALA	LEU	LEU	ASN	GLN
LYS	GLU	THR	ASN	GLN	GLN	SER	ILE	ILE	ASN	VAL	ASP	GLN	VAL	LEU	GLY	VAL	VAL	THR	THR	ALA	ASN	LYS
ASN	ASP	LEU	GLU	TYR	ILE	HIS	GLU	ASN	ASP	VAL	ASP	GLN	GLU	LEU	VAL	ASN	ASN	GLN	THR	ASN	LYS	ASN
LEU	ARG	GLN	GLU	ASN	ASN	ASN	GLU	ASN	ASP	PHE	GLU	GLU	LEU	ASN	GLU	ASN	PHE	GLN	ILE	TYR	GLN	ASP
GLN	LEU	ARG	GLN	ASN	ASN	ASN	GLU	ASN	ASP	PHE	GLU	GLU	LEU	ASN	GLU	ASN	PHE	GLN	ILE	TYR	GLN	ASP
THR	THR	ASN	THR	THR	ASN	ASN	ASN	ASN	ASN	THR	TYR	HIS	ASN	ASN	GLN	GLN	ARG	ASN	THR	ASN	PRO	ASN
THR	THR	ASN	THR	THR	ASN	ASN	ASN	ASN	ASN	THR	TYR	HIS	ASN	ASN	GLN	GLN	ARG	ASN	THR	ASN	PRO	ASN

● Molecule 4: Mto2p-binding domain-containing protein

Chain L: . . 95%																					
MET	SER	ASN	LEU	SER	ASN	ASN	GLU	ILE	ASN	GLU	GLY	ASN	VAL	ILE	ASN	GLN	GLN	GLN	GLY	THR	THR
GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
SER	GLN	VAL	ASN	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
PRO	LYS	ASN	ILE	SER	TRP	ARG	GLN	ARG	PRO	THR	LEU	ARG	GLY	ASN	THR	LEU	PRO	GLU	GLY	ASN	R239
E242	L243	R244	K245	V248	I252	M257	L261	Q262	R269	LEU	ASP	PRO	HIS	GLU	PHE	ASN	ASN	ASN	ASN	ASN	ASN
LEU	ASP	GLU	ALA	LEU	ASN	LYS	TYR	ASN	LYS	ILE	ASN	THR	ASN	ALA	LYS	GLU	PHE	ASN	ASN	ASN	ASN
HIS	GLY	GLY	SER	ASN	THR	SER	PRO	GLY	LYS	GLN	LEU	THR	GLN	GLN	ALA	SER	ILE	ILE	ILE	ILE	ILE
GLY	VAL	THR	ASN	ASN	VAL	ALA	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
ASN	PHE	GLN	ILE	SER	LYS	PHE	ASN	GLN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
GLU	LEU	ASP	TYR	GLN	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN

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

- Molecule 4: Mto2p-binding domain-containing protein

[illegible]

- Molecule 4: Mto2p-binding domain-containing protein





[illegible]

- Molecule 4: Mto2p-binding domain-containing protein

Chain d: 95%

LEU	GLU	ASN	GLY	HIS	LEU	E242	PRO	SER	GLU	MET
LEU	ASP	PHE	VAL	GLY	LEU	L243	LYS	GLN	GLU	SER
ASN	GLN	GLN	SER	GLY	GLU	M244	ASN	VAL	GLU	ASN
GLN	ILE	ILE	THR	SER	ALA	R245	SER	ASP	GLU	LEU
LYS	SER	MET	ASN	ASN	LEU		PRO	ASN	GLU	ASN
GLN	ASN	SER	VAL	THR	LEU	V248	TRP	ILE	GLU	ILE
PRO	LYS	ASN	ALA	SER	ASN		ARG	SER	GLU	ASN
ASN	PHE	ASN	ASN	PRO	LYS	I252	GLN	LEU	MET	GLU
ASP	ASN	ASN	LYS	GLY	GLN	M257	PHE	LEU	GLU	ASN
THR	GLN	ASN	ASN	LYS	THR		ARG	HIS	GLN	ASP
THR	LEU	LEU	ASP	GLU	TYR	L261	PRO	LYS	ILE	ASN
ASN	ASN	ARG	LEU	THR	ASN	Q262	THR	SER	THR	SER
THR	THR	GLN	GLU	LEU	LYS		LEU	LEU	GLN	ASN
ASN	ASN	SER	GLY	GLN	ILE	M269	GLY	ASN	GLU	VAL
ASN	ASN	LEU	TYR	GLN	GLN		SER	MET	VAL	ILE
ASN	ASN	GLU	HIS	ILE	ALA	PRO	PRO	ARG	GLN	LEU
ASN	LYS	LYS	ILE	SER	ASN	HIS	GLU	LEU	GLN	SER
ASN	ASN	GLU	ILE	ALA	LYS		SER	SER	ASN	ASN
ASN	ASN	ASN	GLU	GLN	GLU	PHE	THR	THR	GLN	LYS
ASN	ASN	ASN	ASP	LEU	ILE	HIS	PRO	ASP	GLN	ASN
ASN	ASN	LYS	ASP	GLU	SER	THR	ARG	PRO	PRO	GLY
ASN	ASN	ASN	ILE	VAL	ASP	LEU	SER	VAL	THR	ALA
ASN	ASN	LEU	LYS	LYS	LYS	LEU	LEU	ASP	LEU	THR
ASN	ASN	ASP	THR	LEU	ASP	ARG	PHE	ASN	LEU	THR
ARG	ARG	GLU	VAL	ASN	LEU	GLN	GLN	ASN	ASN	GLN
SER	SER	PHE	SER	VAL	GLN	ASN	ASN	ASN	SER	SER
SER	SER	SER	GLU	LEU	ILE	ASN	LYS	ASN	SER	THR
TYR	TYR	LYS	LEU	LYS	SER	ASN	PRO	ASN	PRO	SER
SER	SER	ASN	GLU	LEU	GLU	ASN	ASN	ASN	PHE	SER
SER	SER	ASN	LEU	GLU	TYR	ILE	LEU	LYS	ILE	PRO
ASN	TYR	HIS	THR	LEU	GLU	MET	PHE	VAL	SER	ASN
ASN	ASN	GLN	CYS	MET	SER	ASN	LYS	ASN	GLN	GLN
ASN	ASN	GLN	GLU	THR	ARG	ASN	ASN	LYS	ASN	LEU
HIS	HIS	GLN	ASN	ARG	ILE	GLU	ASN	ASN	ASN	VAL
ASN	ASN	TYR	TYR	LEU	ILE	ASN	GLY	ASN	PHE	SER
ASN	ASN	GLN	LYS	ASP	LEU	ASN	GLN	ASN	PRO	LYS
SER	SER	GLN	ALA	GLN	LEU	PRO	SER	THR	THR	GLN
SER	SER	GLN	ASN	SER	ASN	LEU	PRO	ASN	ASN	GLN
SER	SER	GLN	ASN	LYS	LEU	GLN	ASP	ASP	GLN	GLN
SER	SER	LYS	GLN	PRO	ILE	THR	MET	ASP	GLY	GLY
GLY	GLY	LEU	LEU	HIS	TYR	SER	VAL	ILE	THR	GLN
SER	SER	ILE	VAL	ASP	ILE	THR	THR	ILE	SER	GLN
GLY	GLY	GLU	GLU	LEU	LEU	LEU	GLY	SER	ARG	ASN
SER	SER	TYR	GLN	PHE	ILE	GLU	ASN	THR	PRO	GLN
GLU	GLU	TYR	GLN	THR	THR	GLN	ASN	THR	GLN	GLN
GLN	GLN	LYS	ASN	PRO	GLU	GLN	ALA	ASN	LEU	GLY
LYS	LYS	CYS	GLU	PRO	TYR	HIS	THR	LEU	THR	THR
LEU	LEU	ILE	SER	TYR	ASP	GLN	THR	THR	ILE	GLN
ILE	ILE	THR	ILE	THR	LYS	ASN	LYS	PRO	ARG	GLN
GLU	GLU	ILE	GLN	THR	ASN	LEU	THR	ASN	ASP	THR
GLY	GLY	GLN	ILE	THR	ASN	GLN	ASN	ARG	SER	ASN
SER	SER	GLN	GLN	GLN	GLN	GLN	LYS	THR	ASP	GLU
ASN	ASN	ASN	ASN	ASN	TYR	ASN	R239	ILE	TYR	PRO
GLU	GLU	ASN	ASN	TYR	SER	GLN		GLN	SER	GLU

- Molecule 4: Mto2p-binding domain-containing protein

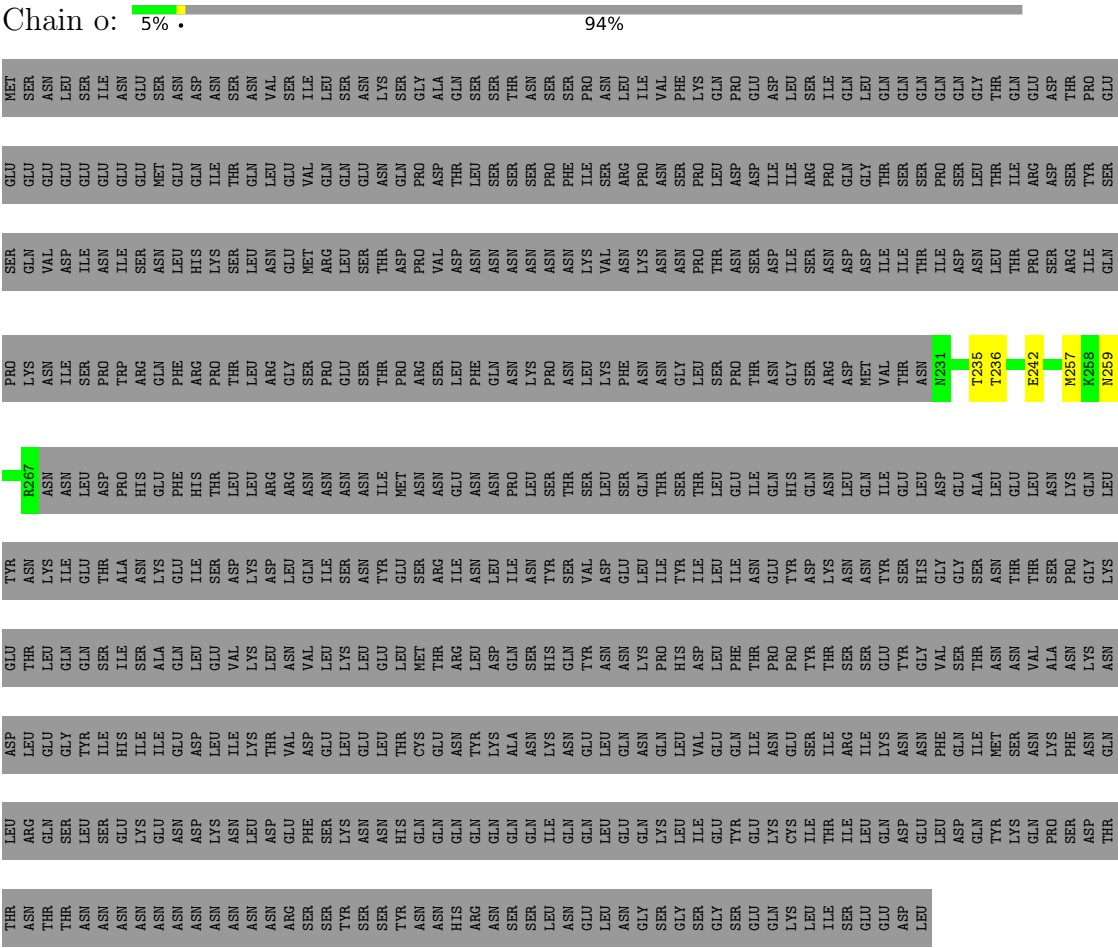
Chain i: 5% • 94%

[illegible]

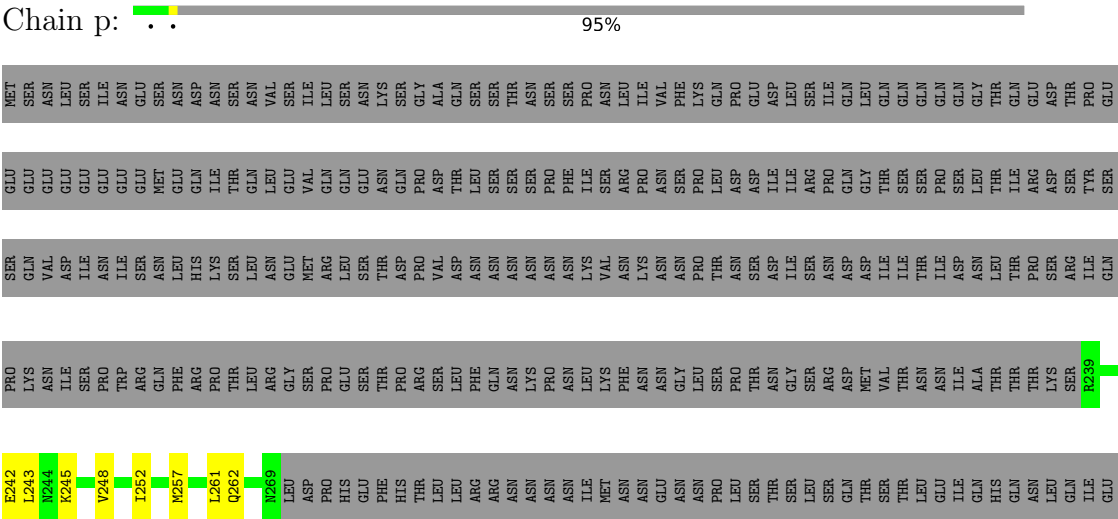


LEU

• Molecule 4: Mto2p-binding domain-containing protein



• Molecule 4: Mto2p-binding domain-containing protein



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8261	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 ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00502	Depositor
Map size (Å)	547.84, 547.84, 547.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.20	1/3245 (0.0%)	0.35	0/4388
1	B	0.19	0/3278	0.33	0/4432
1	G	0.20	1/3245 (0.0%)	0.35	0/4388
1	H	0.19	0/3278	0.33	0/4432
1	M	0.20	1/3245 (0.0%)	0.35	0/4388
1	N	0.19	0/3278	0.33	0/4432
1	S	0.20	0/3245	0.35	0/4388
1	T	0.19	0/3278	0.33	0/4432
1	Y	0.20	1/3245 (0.0%)	0.35	0/4388
1	Z	0.19	0/3278	0.33	0/4432
1	e	0.20	1/3245 (0.0%)	0.35	0/4388
1	f	0.19	0/3278	0.33	0/4432
1	k	0.20	1/3245 (0.0%)	0.35	0/4388
1	l	0.19	0/3278	0.33	0/4432
2	C	0.24	0/6114	0.43	1/8238 (0.0%)
2	I	0.24	0/6114	0.43	2/8238 (0.0%)
2	O	0.24	0/6114	0.43	2/8238 (0.0%)
2	U	0.24	0/6114	0.43	1/8238 (0.0%)
2	a	0.24	0/6114	0.43	2/8238 (0.0%)
2	g	0.24	0/6114	0.43	2/8238 (0.0%)
2	m	0.24	0/6114	0.43	2/8238 (0.0%)
3	D	0.22	0/5433	0.41	0/7353
3	J	0.22	0/5433	0.41	0/7353
3	P	0.22	0/5433	0.41	0/7353
3	V	0.22	0/5433	0.41	0/7353
3	b	0.22	0/5433	0.41	0/7353
3	h	0.22	0/5433	0.41	0/7353
3	n	0.22	0/5433	0.41	0/7353
4	E	0.36	0/315	0.67	0/419
4	F	0.20	0/274	0.39	0/363
4	K	0.37	0/315	0.66	0/419
4	L	0.20	0/274	0.40	0/363
4	Q	0.37	0/315	0.67	0/419
4	R	0.20	0/274	0.39	0/363

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	W	0.37	0/315	0.66	0/419
4	X	0.20	0/274	0.40	0/363
4	c	0.36	0/315	0.67	0/419
4	d	0.20	0/274	0.40	0/363
4	i	0.37	0/315	0.66	0/419
4	j	0.20	0/274	0.39	0/363
4	o	0.37	0/315	0.66	0/419
4	p	0.20	0/274	0.39	0/363
All	All	0.22	6/130613 (0.0%)	0.40	12/176351 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	316	HIS	C-O	-5.04	1.15	1.23
1	M	316	HIS	C-O	-5.03	1.15	1.23
1	Y	316	HIS	C-O	-5.03	1.15	1.23
1	k	316	HIS	C-O	-5.03	1.15	1.23
1	G	316	HIS	C-O	-5.03	1.15	1.23

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	m	597	GLN	CA-C-O	-5.31	114.92	120.55
2	O	597	GLN	CA-C-O	-5.30	114.93	120.55
2	U	597	GLN	CA-C-O	-5.29	114.94	120.55
2	g	597	GLN	CA-C-O	-5.29	114.95	120.55
2	I	597	GLN	CA-C-O	-5.28	114.96	120.55

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3188	0	3133	30	0
1	B	3220	0	3188	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	3188	0	3133	30	0
1	H	3220	0	3188	36	0
1	M	3188	0	3133	58	0
1	N	3220	0	3188	37	0
1	S	3188	0	3133	29	0
1	T	3220	0	3188	53	0
1	Y	3188	0	3133	37	0
1	Z	3220	0	3188	33	0
1	e	3188	0	3133	35	0
1	f	3220	0	3188	41	0
1	k	3188	0	3133	29	0
1	l	3220	0	3188	41	0
2	C	6001	0	5981	53	0
2	I	6001	0	5981	56	0
2	O	6001	0	5981	52	0
2	U	6001	0	5981	46	0
2	a	6001	0	5981	52	0
2	g	6001	0	5981	51	0
2	m	6001	0	5981	49	0
3	D	5313	0	5293	53	0
3	J	5313	0	5293	52	0
3	P	5313	0	5293	58	0
3	V	5313	0	5293	61	0
3	b	5313	0	5293	48	0
3	h	5313	0	5293	56	0
3	n	5313	0	5293	60	0
4	E	314	0	337	6	0
4	F	273	0	288	7	0
4	K	314	0	337	6	0
4	L	273	0	288	7	0
4	Q	314	0	337	9	0
4	R	273	0	288	7	0
4	W	314	0	337	4	0
4	X	273	0	288	7	0
4	c	314	0	337	9	0
4	d	273	0	288	7	0
4	i	314	0	337	8	0
4	j	273	0	288	7	0
4	o	314	0	337	8	0
4	p	273	0	288	7	0
All	All	128163	0	127540	1232	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 1232 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:M:319:LEU:O	1:T:85:ASP:HB3	1.12	1.27
4:Q:234:THR:CG2	3:V:471:SER:HB3	1.66	1.24
1:M:319:LEU:HD22	1:T:84:SER:CA	1.74	1.16
1:e:311:PHE:HB3	1:l:116:ARG:HH22	1.05	1.16
1:M:319:LEU:O	1:T:85:ASP:CB	1.94	1.16

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	389/498 (78%)	385 (99%)	4 (1%)	0	100	100
1	B	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
1	G	389/498 (78%)	385 (99%)	4 (1%)	0	100	100
1	H	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
1	M	389/498 (78%)	385 (99%)	4 (1%)	0	100	100
1	N	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
1	S	389/498 (78%)	385 (99%)	4 (1%)	0	100	100
1	T	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
1	Y	389/498 (78%)	385 (99%)	4 (1%)	0	100	100
1	Z	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
1	e	389/498 (78%)	385 (99%)	4 (1%)	0	100	100
1	f	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
1	k	389/498 (78%)	385 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	l	392/498 (79%)	382 (97%)	10 (3%)	0	100	100
2	C	725/896 (81%)	711 (98%)	14 (2%)	0	100	100
2	I	725/896 (81%)	712 (98%)	13 (2%)	0	100	100
2	O	725/896 (81%)	711 (98%)	14 (2%)	0	100	100
2	U	725/896 (81%)	712 (98%)	13 (2%)	0	100	100
2	a	725/896 (81%)	712 (98%)	13 (2%)	0	100	100
2	g	725/896 (81%)	712 (98%)	13 (2%)	0	100	100
2	m	725/896 (81%)	712 (98%)	13 (2%)	0	100	100
3	D	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
3	J	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
3	P	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
3	V	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
3	b	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
3	h	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
3	n	627/810 (77%)	610 (97%)	17 (3%)	0	100	100
4	E	35/615 (6%)	35 (100%)	0	0	100	100
4	F	29/615 (5%)	29 (100%)	0	0	100	100
4	K	35/615 (6%)	35 (100%)	0	0	100	100
4	L	29/615 (5%)	29 (100%)	0	0	100	100
4	Q	35/615 (6%)	35 (100%)	0	0	100	100
4	R	29/615 (5%)	29 (100%)	0	0	100	100
4	W	35/615 (6%)	35 (100%)	0	0	100	100
4	X	29/615 (5%)	29 (100%)	0	0	100	100
4	c	35/615 (6%)	35 (100%)	0	0	100	100
4	d	29/615 (5%)	29 (100%)	0	0	100	100
4	i	35/615 (6%)	35 (100%)	0	0	100	100
4	j	29/615 (5%)	29 (100%)	0	0	100	100
4	o	35/615 (6%)	35 (100%)	0	0	100	100
4	p	29/615 (5%)	29 (100%)	0	0	100	100
All	All	15379/27524 (56%)	15069 (98%)	310 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	A	363/452 (80%)	362 (100%)	1 (0%)	86	86
1	B	370/452 (82%)	370 (100%)	0	100	100
1	G	363/452 (80%)	361 (99%)	2 (1%)	78	83
1	H	370/452 (82%)	370 (100%)	0	100	100
1	M	363/452 (80%)	362 (100%)	1 (0%)	86	86
1	N	370/452 (82%)	370 (100%)	0	100	100
1	S	363/452 (80%)	361 (99%)	2 (1%)	78	83
1	T	370/452 (82%)	370 (100%)	0	100	100
1	Y	363/452 (80%)	362 (100%)	1 (0%)	86	86
1	Z	370/452 (82%)	370 (100%)	0	100	100
1	e	363/452 (80%)	361 (99%)	2 (1%)	78	83
1	f	370/452 (82%)	370 (100%)	0	100	100
1	k	363/452 (80%)	361 (99%)	2 (1%)	78	83
1	l	370/452 (82%)	370 (100%)	0	100	100
2	C	676/847 (80%)	666 (98%)	10 (2%)	57	72
2	I	676/847 (80%)	665 (98%)	11 (2%)	55	70
2	O	676/847 (80%)	665 (98%)	11 (2%)	55	70
2	U	676/847 (80%)	665 (98%)	11 (2%)	55	70
2	a	676/847 (80%)	665 (98%)	11 (2%)	55	70
2	g	676/847 (80%)	665 (98%)	11 (2%)	55	70
2	m	676/847 (80%)	665 (98%)	11 (2%)	55	70
3	D	598/768 (78%)	595 (100%)	3 (0%)	81	83
3	J	598/768 (78%)	595 (100%)	3 (0%)	81	83
3	P	598/768 (78%)	595 (100%)	3 (0%)	81	83
3	V	598/768 (78%)	595 (100%)	3 (0%)	81	83
3	b	598/768 (78%)	595 (100%)	3 (0%)	81	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	h	598/768 (78%)	595 (100%)	3 (0%)	81	83
3	n	598/768 (78%)	595 (100%)	3 (0%)	81	83
4	E	36/594 (6%)	36 (100%)	0	100	100
4	F	31/594 (5%)	31 (100%)	0	100	100
4	K	36/594 (6%)	35 (97%)	1 (3%)	38	60
4	L	31/594 (5%)	31 (100%)	0	100	100
4	Q	36/594 (6%)	36 (100%)	0	100	100
4	R	31/594 (5%)	31 (100%)	0	100	100
4	W	36/594 (6%)	35 (97%)	1 (3%)	38	60
4	X	31/594 (5%)	31 (100%)	0	100	100
4	c	36/594 (6%)	35 (97%)	1 (3%)	38	60
4	d	31/594 (5%)	31 (100%)	0	100	100
4	i	36/594 (6%)	36 (100%)	0	100	100
4	j	31/594 (5%)	31 (100%)	0	100	100
4	o	36/594 (6%)	36 (100%)	0	100	100
4	p	31/594 (5%)	31 (100%)	0	100	100
All	All	14518/25949 (56%)	14407 (99%)	111 (1%)	70	80

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	U	718	ASN
3	n	536	TYR
2	a	617	LYS
3	n	524	MET
2	m	362	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 189 such sidechains are listed below:

Mol	Chain	Res	Type
2	a	105	HIS
1	f	243	ASN
2	a	619	ASN
3	b	633	ASN
2	g	716	ASN

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.

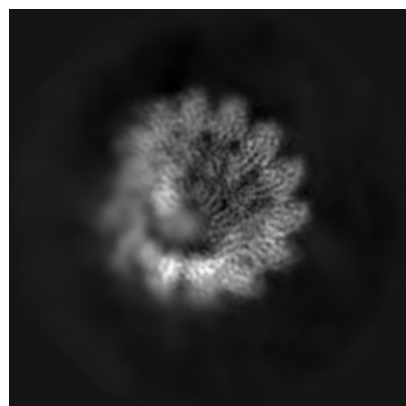
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51972. These allow visual inspection of the internal detail of the map and identification of artifacts.

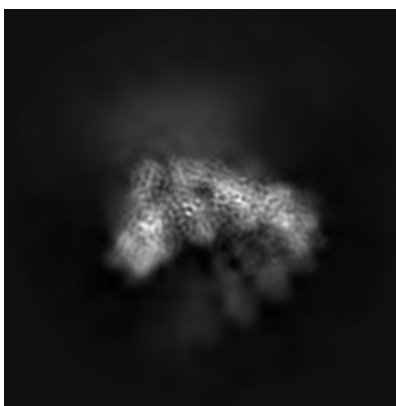
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

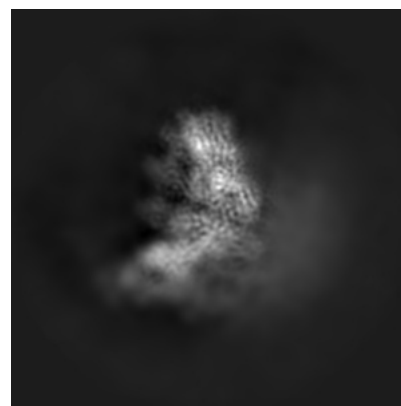
6.1.1 Primary map



X

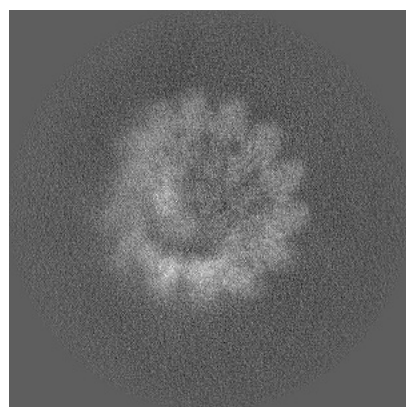


Y

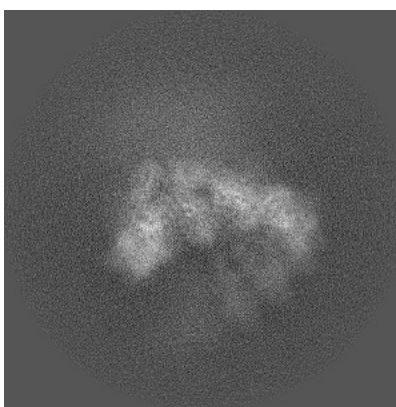


Z

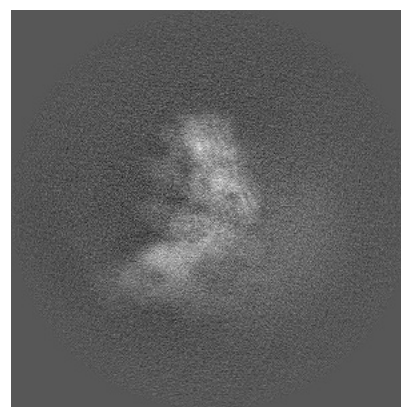
6.1.2 Raw map



X



Y

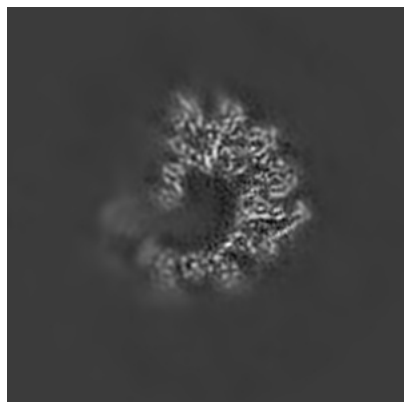


Z

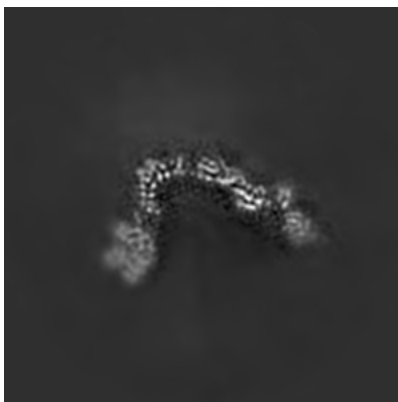
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

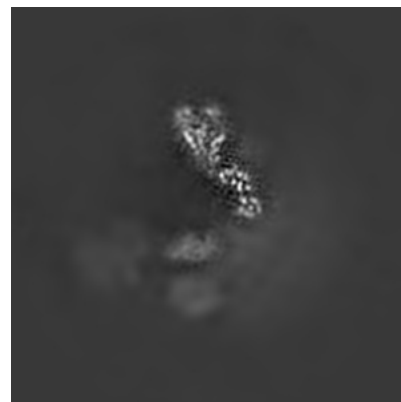
6.2.1 Primary map



X Index: 256

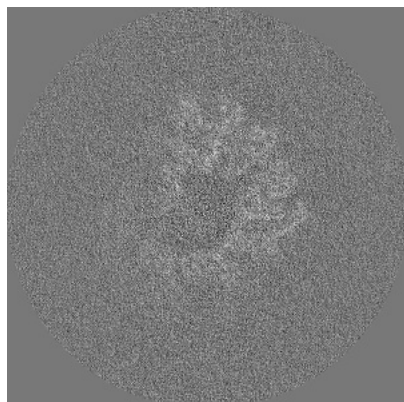


Y Index: 256

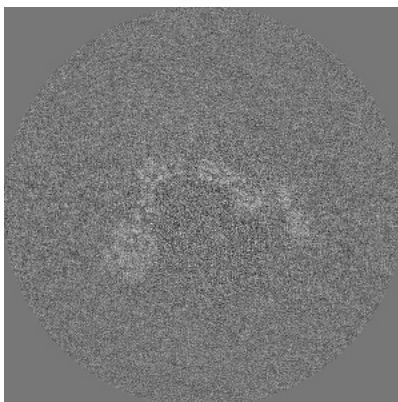


Z Index: 256

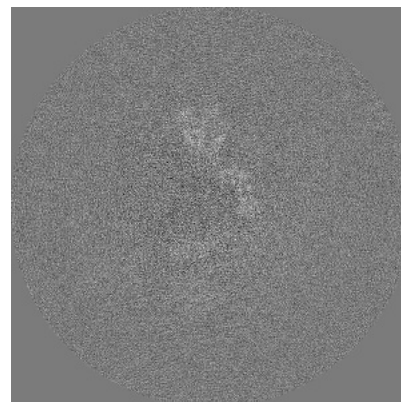
6.2.2 Raw map



X Index: 256



Y Index: 256

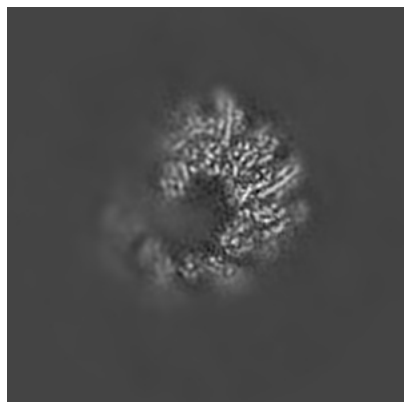


Z Index: 256

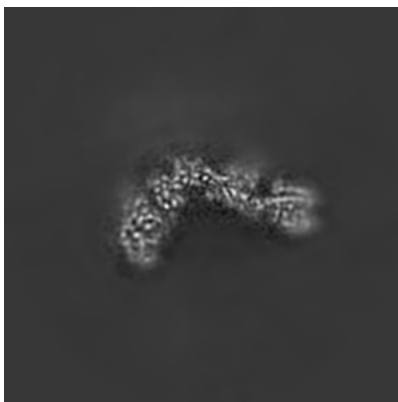
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 265

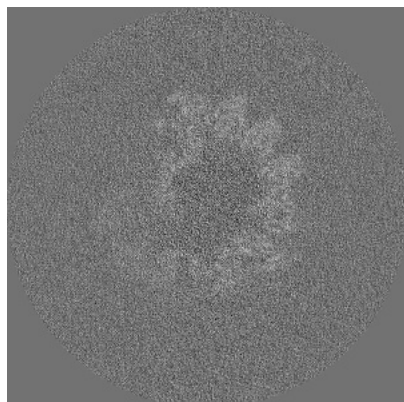


Y Index: 283

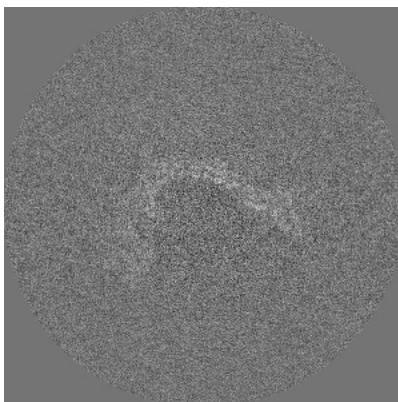


Z Index: 182

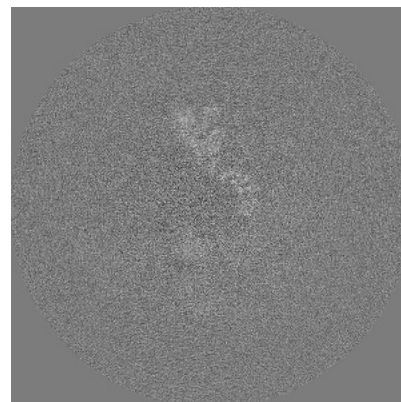
6.3.2 Raw map



X Index: 239



Y Index: 265

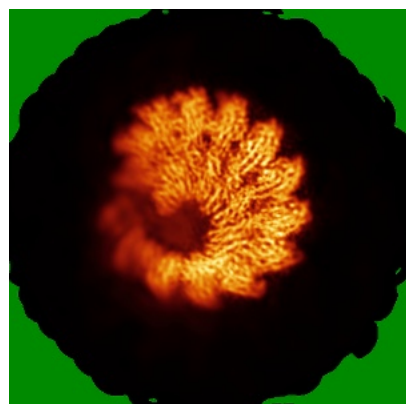


Z Index: 253

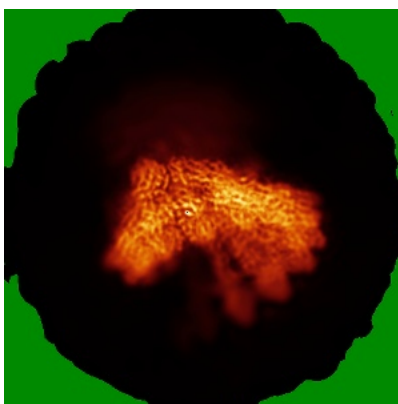
The images above show the largest variance slices of the map in three orthogonal directions.

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

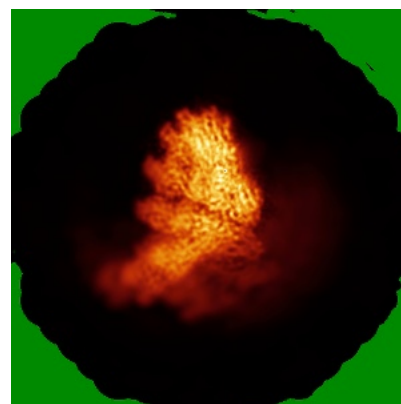
6.4.1 Primary map



X

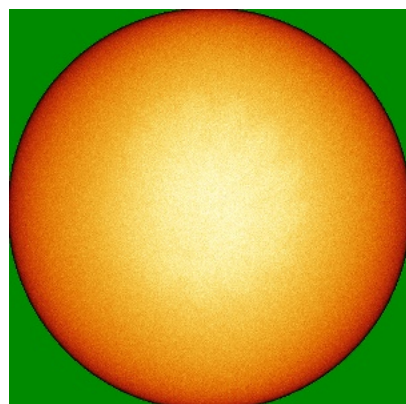


Y

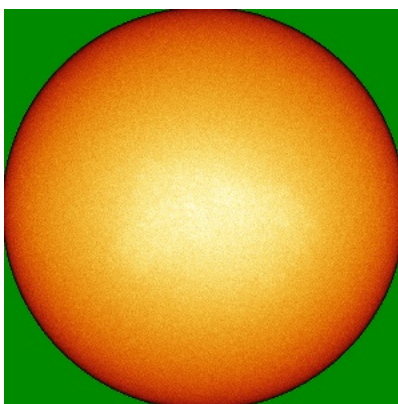


Z

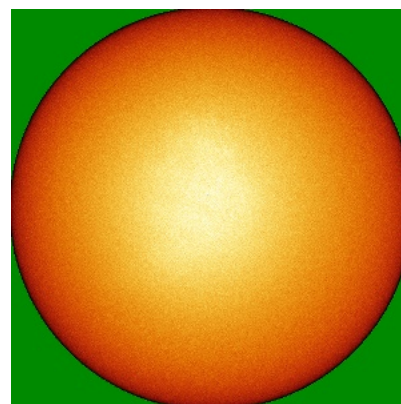
6.4.2 Raw map



X



Y

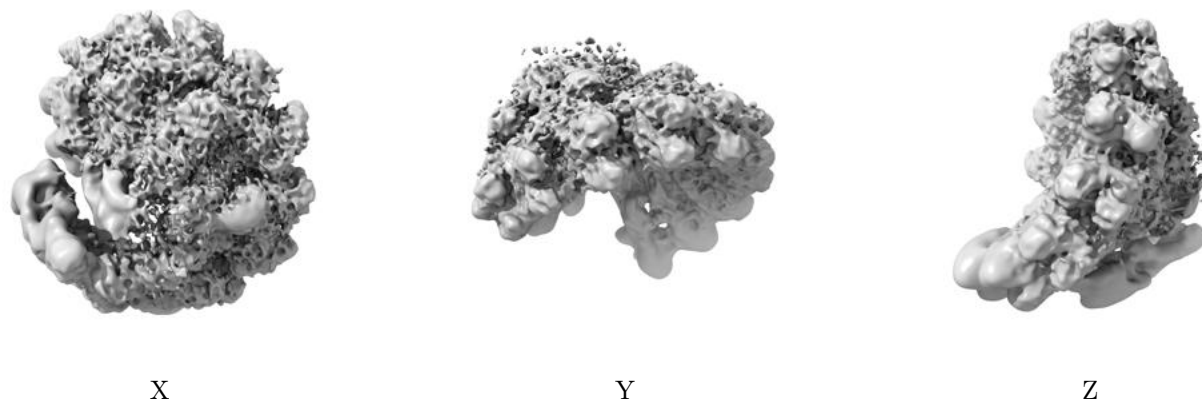


Z

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

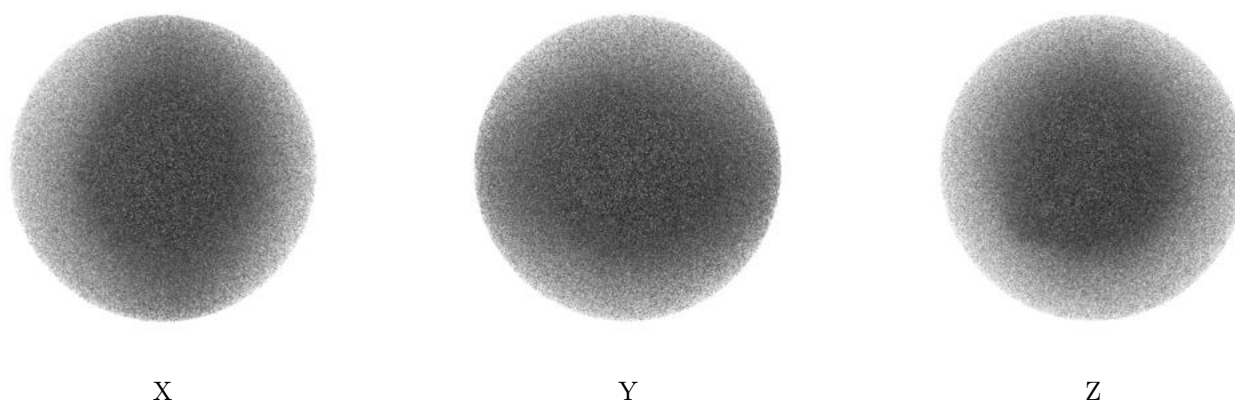
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00502. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

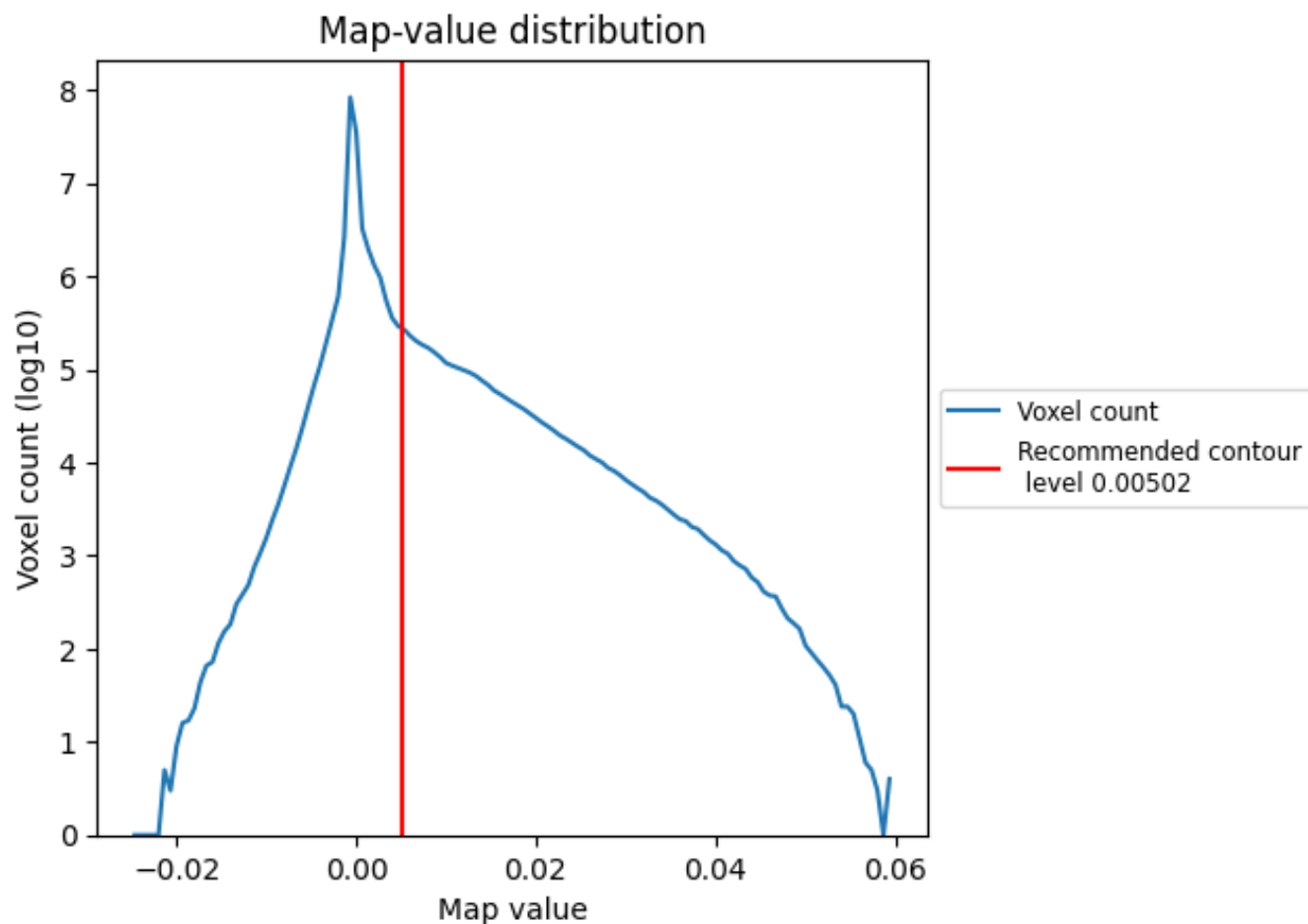
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

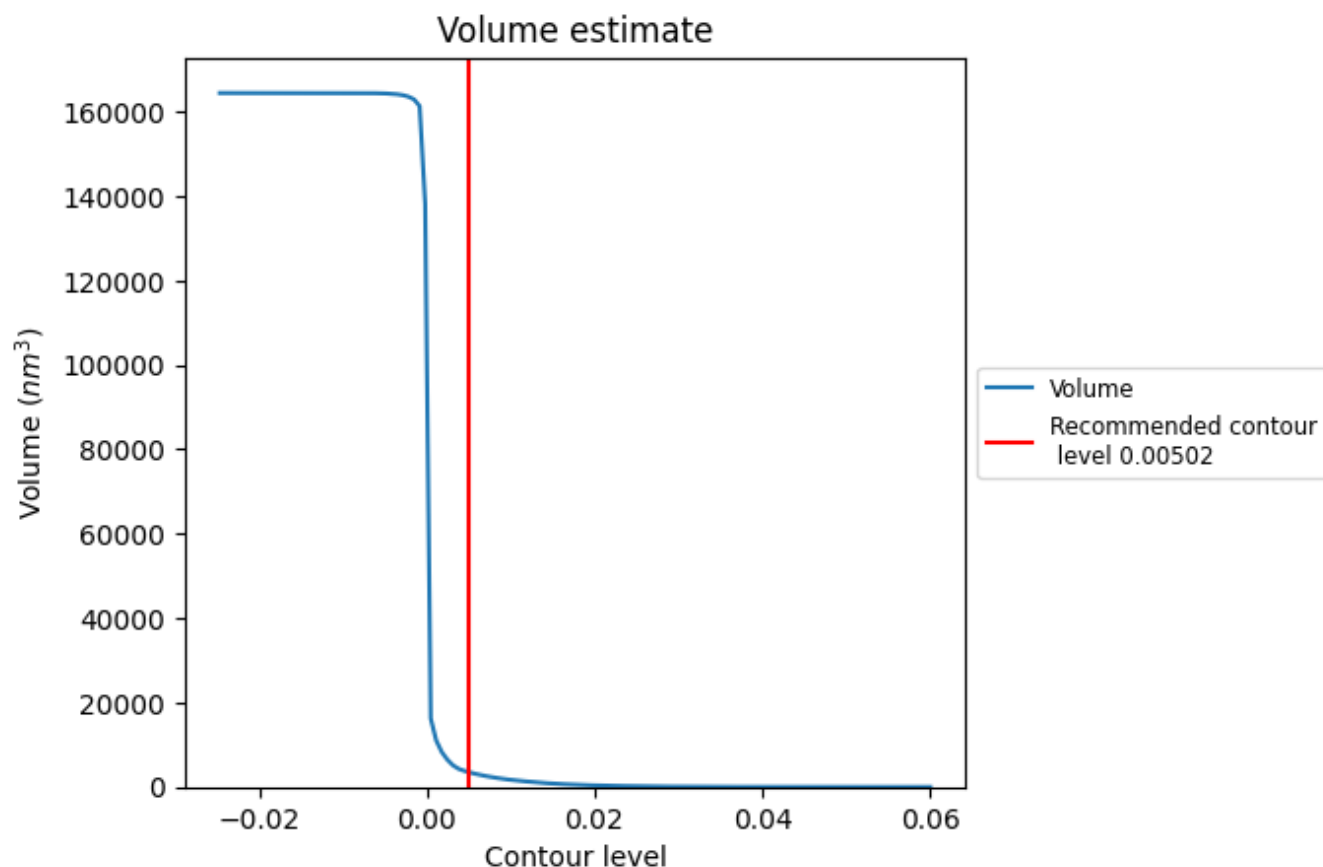
This section contains the results of statistical analysis of the map.

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.

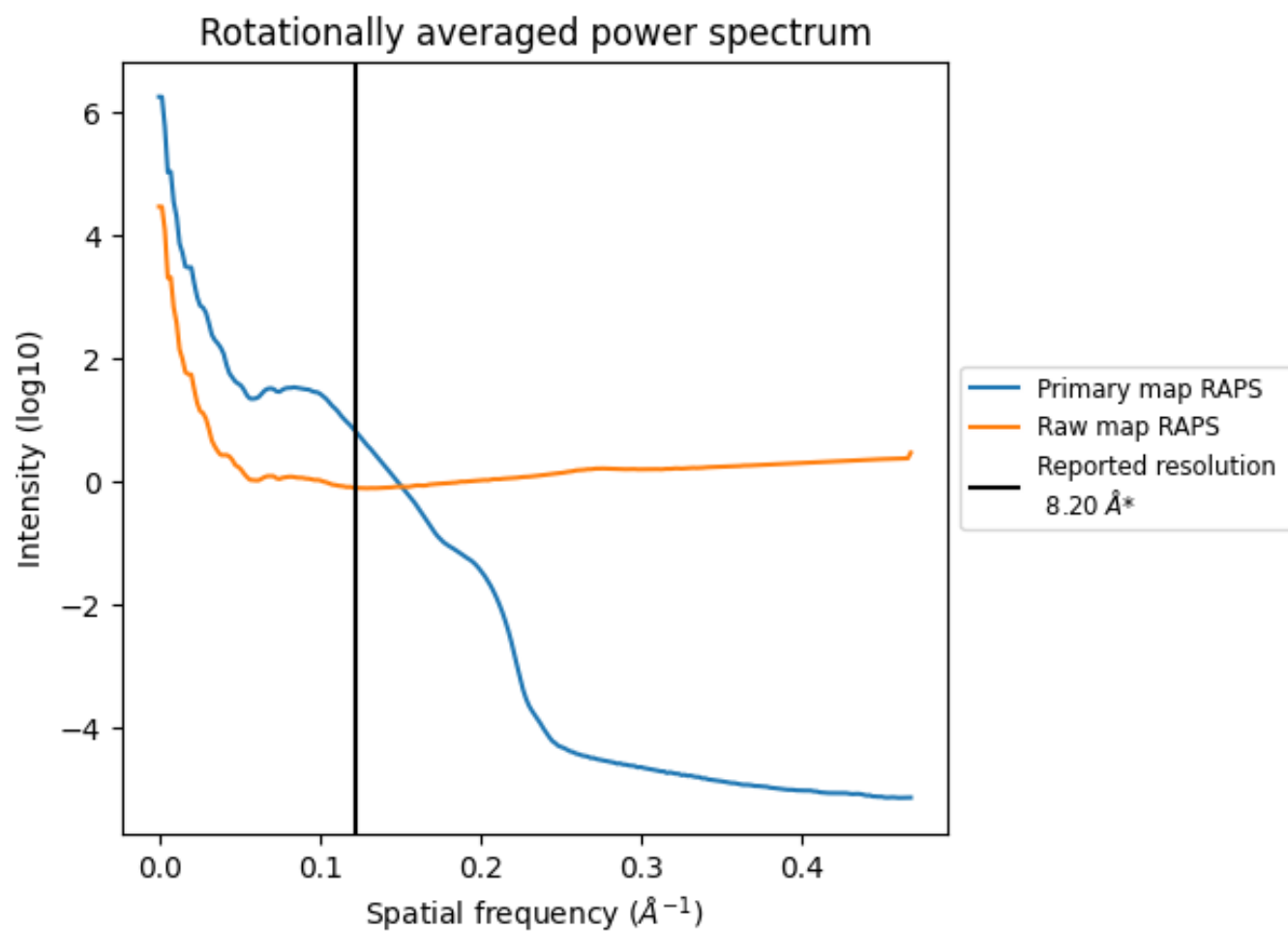
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3504 nm^3 ; this corresponds to an approximate mass of 3166 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 ⓘ

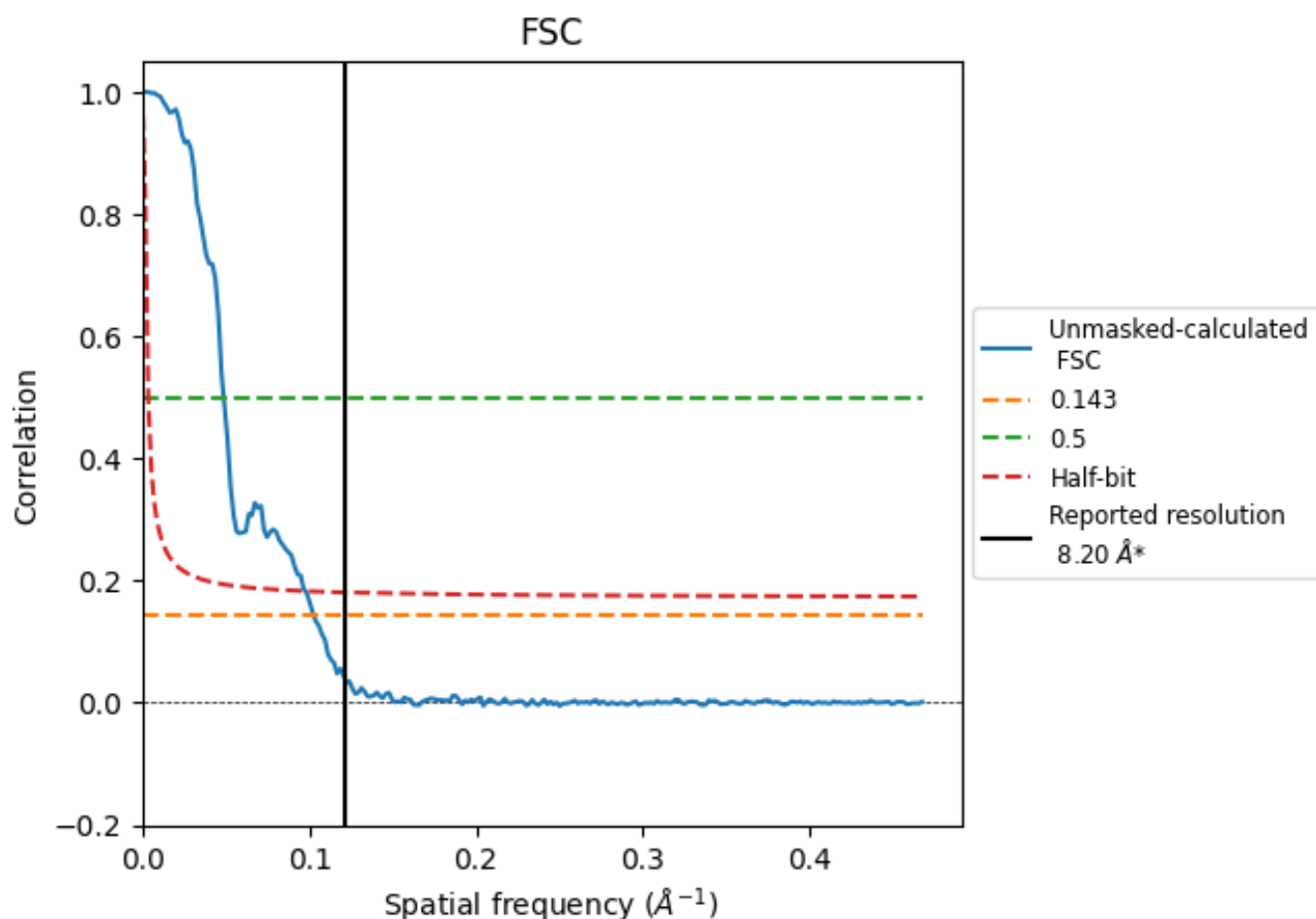


*Reported resolution corresponds to spatial frequency of 0.122 $\text{\AA}^{-1}$

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 0.122 Å⁻¹

8.2 Resolution estimates [i](#)

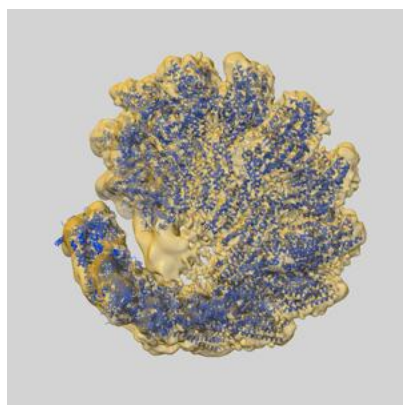
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.74	20.49	10.24

*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 9.74 differs from the reported value 8.2 by more than 10 %

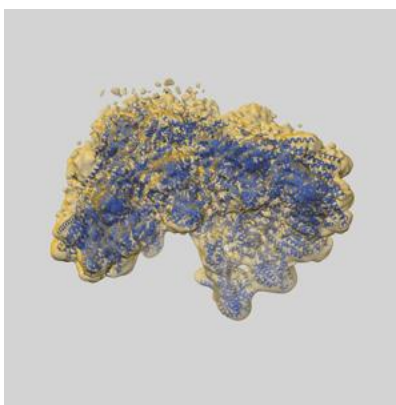
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51972 and PDB model 9H9R. Per-residue inclusion information can be found in section [3](#) on page [22](#).

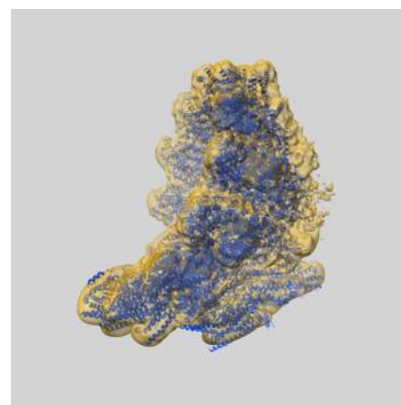
9.1 Map-model overlay [i](#)



X



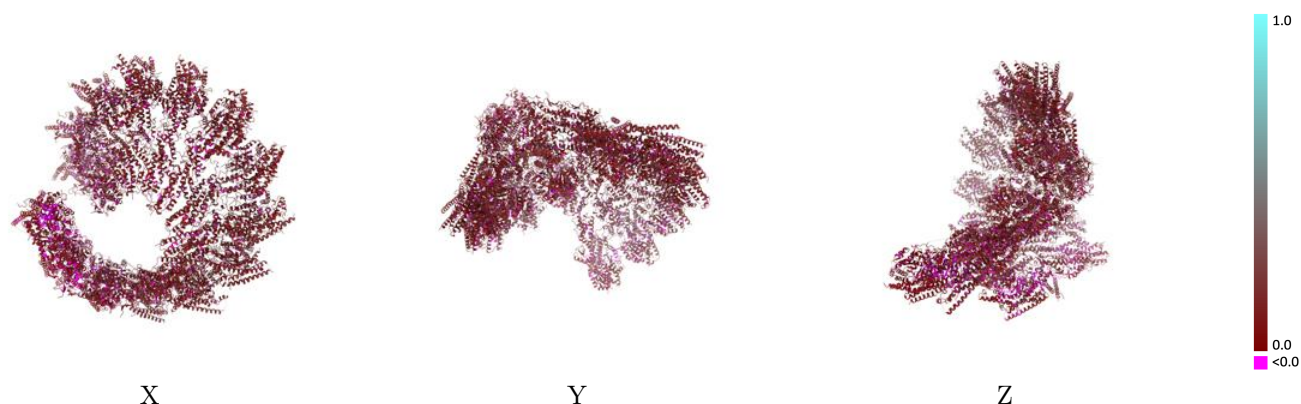
Y



Z

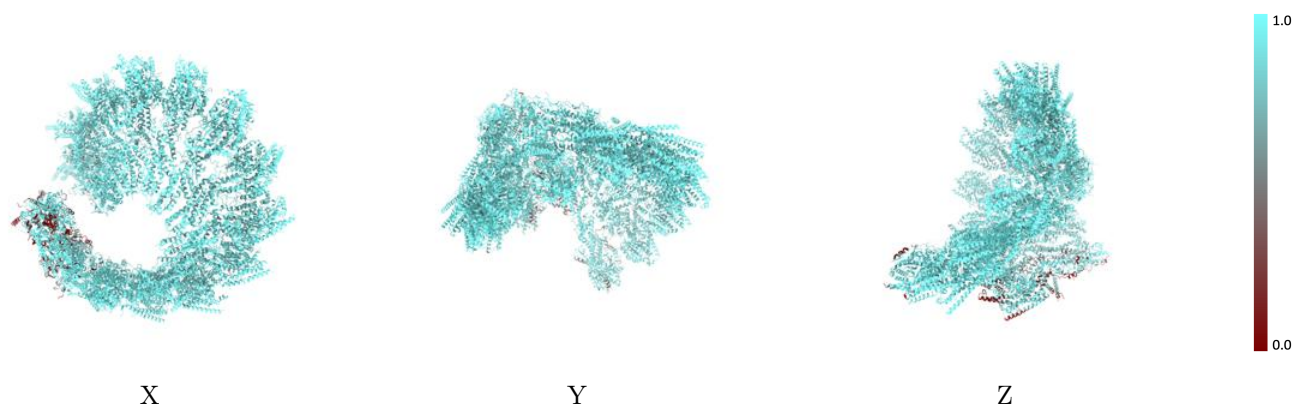
The images above show the 3D surface view of the map at the recommended contour level 0.00502 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



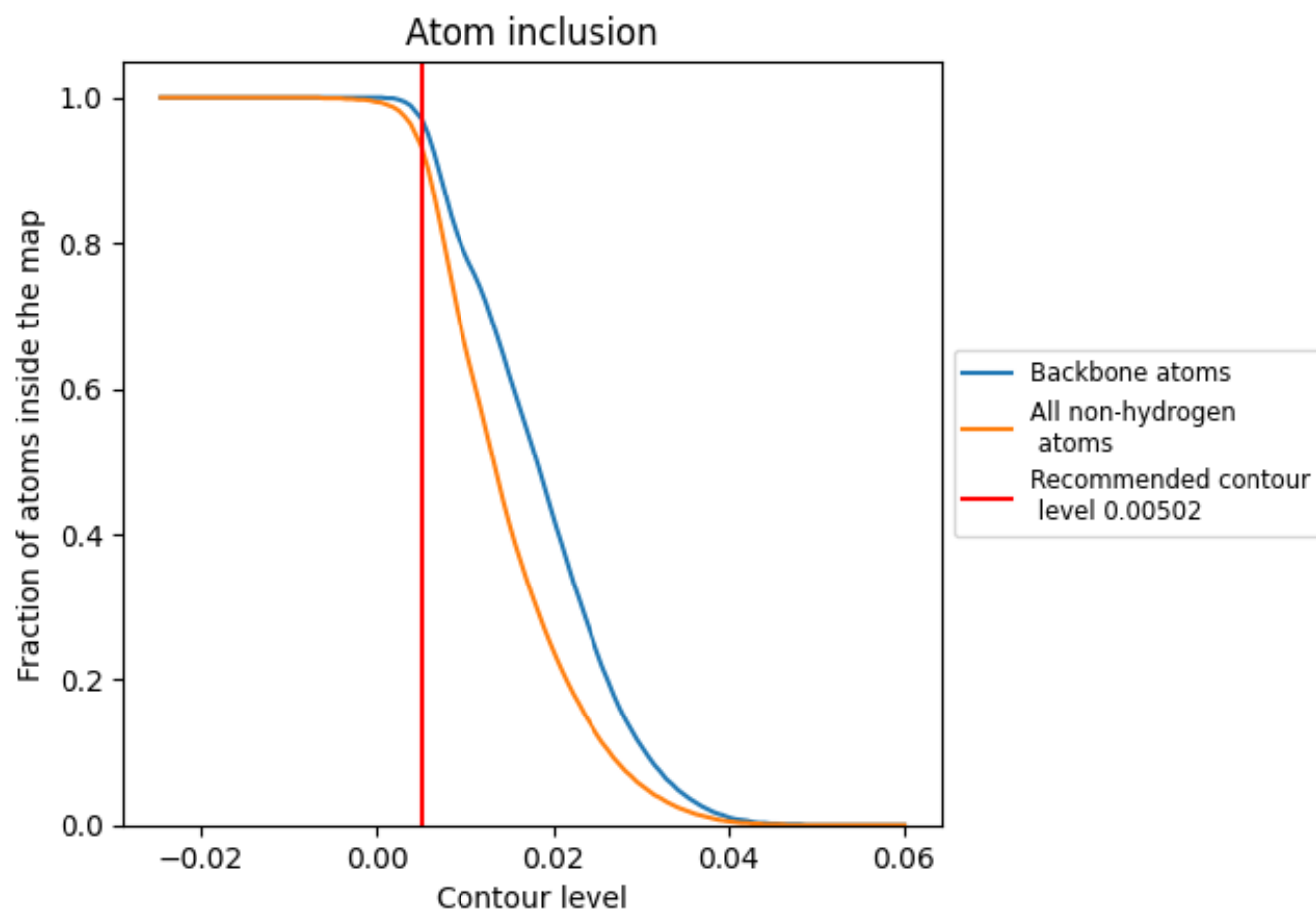
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00502).

9.4 Atom inclusion ⓘ



At the recommended contour level, 97% of all backbone atoms, 93% 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 (0.00502) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.1290
A	 0.9510	 0.1730
B	 0.9610	 0.1690
C	 0.9310	 0.1730
D	 0.9270	 0.1720
E	 0.9540	 0.1420
F	 0.9700	 0.1640
G	 0.9760	 0.1510
H	 0.9650	 0.1590
I	 0.9330	 0.1520
J	 0.9330	 0.1550
K	 0.9610	 0.1290
L	 0.9660	 0.1510
M	 0.9810	 0.0790
N	 0.9850	 0.1250
O	 0.9520	 0.1230
P	 0.9600	 0.1360
Q	 0.9900	 0.0930
R	 0.9960	 0.1510
S	 0.7090	 0.0460
T	 0.8190	 0.0520
U	 0.7770	 0.0600
V	 0.8890	 0.0780
W	 0.6420	 0.0930
X	 0.7290	 0.0610
Y	 0.9840	 0.0860
Z	 0.8860	 0.0590
a	 0.9750	 0.1200
b	 0.9510	 0.1020
c	 0.9900	 0.1080
d	 1.0000	 0.1240
e	 0.9870	 0.1470
f	 0.9850	 0.1340
g	 0.9560	 0.1460
h	 0.9770	 0.1420



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Chain	Atom inclusion	Q-score
i	 0.9350	 0.1200
j	 0.9810	 0.1530
k	 0.9570	 0.1690
l	 0.9780	 0.1540
m	 0.9270	 0.1570
n	 0.9410	 0.1500
o	 0.9480	 0.1620
p	 0.9660	 0.1400