



Full wwPDB EM Validation Report ⓘ

Dec 17, 2022 – 08:30 pm GMT

PDB ID : 7APK
EMDB ID : EMD-11857
Title : Structure of the human THO - UAP56 complex
Authors : Hohmann, U.; Puehringer, T.; Plaschka, C.
Deposited on : 2020-10-17
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation 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:

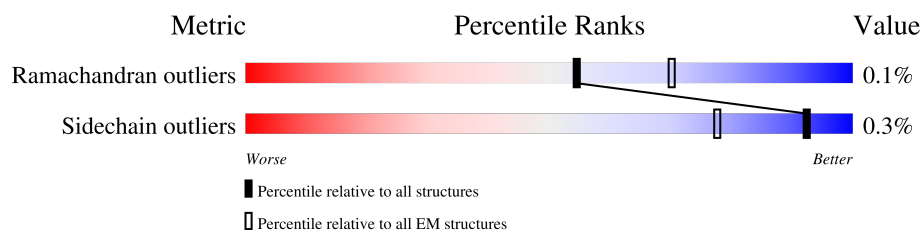
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	711	<div> <div>37%</div> <div>37%</div> <div>63%</div> </div>
1	I	711	<div> <div>39%</div> <div>38%</div> <div>61%</div> </div>
1	a	711	<div> <div>37%</div> <div>37%</div> <div>63%</div> </div>
1	i	711	<div> <div>23%</div> <div>38%</div> <div>61%</div> </div>
2	B	1226	<div> <div>58%</div> <div>57%</div> <div>42%</div> </div>
2	J	1226	<div> <div>58%</div> <div>57%</div> <div>42%</div> </div>
2	b	1226	<div> <div>58%</div> <div>57%</div> <div>42%</div> </div>
2	j	1226	<div> <div>52%</div> <div>57%</div> <div>42%</div> </div>
3	C	395	<div> <div>77%</div> <div>76%</div> <div>23%</div> </div>

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Mol	Chain	Length	Quality of chain
3	K	395	77% 76% 23%
3	c	395	77% 76% 23%
3	k	395	77% 76% 23%
4	E	683	37% 76% 23%
4	M	683	67% 80% 20%
4	e	683	75% 75% 25%
4	m	683	71% 80% 20%
5	F	341	21% 98% ..
5	N	341	97% 98% ..
5	f	341	96% 96% . .
5	n	341	99% 98% ..
6	G	204	71% 75% 25%
6	O	204	68% 76% 24%
6	g	204	75% 75% 25%
6	o	204	45% 76% 24%
7	H	451	38% 62%
7	P	451	38% 62%
7	h	451	38% 62%
7	p	451	38% 62%
8	X	37	100% 100%
8	x	37	97% 100%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 72697 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 THO complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	266	Total	C	N	O	S	0	0
			2165	1402	357	397	9		
1	I	275	Total	C	N	O	S	0	0
			2228	1441	368	410	9		
1	a	266	Total	C	N	O	S	0	0
			2165	1402	357	397	9		
1	i	275	Total	C	N	O	S	0	0
			2229	1441	368	411	9		

There are 220 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-53	MET	-	initiating methionine	UNP Q96FV9
A	-52	GLY	-	expression tag	UNP Q96FV9
A	-51	LYS	-	expression tag	UNP Q96FV9
A	-50	PRO	-	expression tag	UNP Q96FV9
A	-49	ILE	-	expression tag	UNP Q96FV9
A	-48	PRO	-	expression tag	UNP Q96FV9
A	-47	ASN	-	expression tag	UNP Q96FV9
A	-46	PRO	-	expression tag	UNP Q96FV9
A	-45	LEU	-	expression tag	UNP Q96FV9
A	-44	LEU	-	expression tag	UNP Q96FV9
A	-43	GLY	-	expression tag	UNP Q96FV9
A	-42	LEU	-	expression tag	UNP Q96FV9
A	-41	ASP	-	expression tag	UNP Q96FV9
A	-40	SER	-	expression tag	UNP Q96FV9
A	-39	THR	-	expression tag	UNP Q96FV9
A	-38	GLY	-	expression tag	UNP Q96FV9
A	-37	SER	-	expression tag	UNP Q96FV9
A	-36	GLY	-	expression tag	UNP Q96FV9
A	-35	LYS	-	expression tag	UNP Q96FV9
A	-34	PRO	-	expression tag	UNP Q96FV9
A	-33	ILE	-	expression tag	UNP Q96FV9
A	-32	PRO	-	expression tag	UNP Q96FV9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-31	ASN	-	expression tag	UNP Q96FV9
A	-30	PRO	-	expression tag	UNP Q96FV9
A	-29	LEU	-	expression tag	UNP Q96FV9
A	-28	LEU	-	expression tag	UNP Q96FV9
A	-27	GLY	-	expression tag	UNP Q96FV9
A	-26	LEU	-	expression tag	UNP Q96FV9
A	-25	ASP	-	expression tag	UNP Q96FV9
A	-24	SER	-	expression tag	UNP Q96FV9
A	-23	THR	-	expression tag	UNP Q96FV9
A	-22	GLY	-	expression tag	UNP Q96FV9
A	-21	SER	-	expression tag	UNP Q96FV9
A	-20	GLY	-	expression tag	UNP Q96FV9
A	-19	LYS	-	expression tag	UNP Q96FV9
A	-18	PRO	-	expression tag	UNP Q96FV9
A	-17	ILE	-	expression tag	UNP Q96FV9
A	-16	PRO	-	expression tag	UNP Q96FV9
A	-15	ASN	-	expression tag	UNP Q96FV9
A	-14	PRO	-	expression tag	UNP Q96FV9
A	-13	LEU	-	expression tag	UNP Q96FV9
A	-12	LEU	-	expression tag	UNP Q96FV9
A	-11	GLY	-	expression tag	UNP Q96FV9
A	-10	LEU	-	expression tag	UNP Q96FV9
A	-9	ASP	-	expression tag	UNP Q96FV9
A	-8	SER	-	expression tag	UNP Q96FV9
A	-7	THR	-	expression tag	UNP Q96FV9
A	-6	LEU	-	expression tag	UNP Q96FV9
A	-5	GLU	-	expression tag	UNP Q96FV9
A	-4	VAL	-	expression tag	UNP Q96FV9
A	-3	LEU	-	expression tag	UNP Q96FV9
A	-2	PHE	-	expression tag	UNP Q96FV9
A	-1	GLN	-	expression tag	UNP Q96FV9
A	0	GLY	-	expression tag	UNP Q96FV9
A	1	PRO	-	expression tag	UNP Q96FV9
I	-53	MET	-	initiating methionine	UNP Q96FV9
I	-52	GLY	-	expression tag	UNP Q96FV9
I	-51	LYS	-	expression tag	UNP Q96FV9
I	-50	PRO	-	expression tag	UNP Q96FV9
I	-49	ILE	-	expression tag	UNP Q96FV9
I	-48	PRO	-	expression tag	UNP Q96FV9
I	-47	ASN	-	expression tag	UNP Q96FV9
I	-46	PRO	-	expression tag	UNP Q96FV9
I	-45	LEU	-	expression tag	UNP Q96FV9

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-44	LEU	-	expression tag	UNP Q96FV9
I	-43	GLY	-	expression tag	UNP Q96FV9
I	-42	LEU	-	expression tag	UNP Q96FV9
I	-41	ASP	-	expression tag	UNP Q96FV9
I	-40	SER	-	expression tag	UNP Q96FV9
I	-39	THR	-	expression tag	UNP Q96FV9
I	-38	GLY	-	expression tag	UNP Q96FV9
I	-37	SER	-	expression tag	UNP Q96FV9
I	-36	GLY	-	expression tag	UNP Q96FV9
I	-35	LYS	-	expression tag	UNP Q96FV9
I	-34	PRO	-	expression tag	UNP Q96FV9
I	-33	ILE	-	expression tag	UNP Q96FV9
I	-32	PRO	-	expression tag	UNP Q96FV9
I	-31	ASN	-	expression tag	UNP Q96FV9
I	-30	PRO	-	expression tag	UNP Q96FV9
I	-29	LEU	-	expression tag	UNP Q96FV9
I	-28	LEU	-	expression tag	UNP Q96FV9
I	-27	GLY	-	expression tag	UNP Q96FV9
I	-26	LEU	-	expression tag	UNP Q96FV9
I	-25	ASP	-	expression tag	UNP Q96FV9
I	-24	SER	-	expression tag	UNP Q96FV9
I	-23	THR	-	expression tag	UNP Q96FV9
I	-22	GLY	-	expression tag	UNP Q96FV9
I	-21	SER	-	expression tag	UNP Q96FV9
I	-20	GLY	-	expression tag	UNP Q96FV9
I	-19	LYS	-	expression tag	UNP Q96FV9
I	-18	PRO	-	expression tag	UNP Q96FV9
I	-17	ILE	-	expression tag	UNP Q96FV9
I	-16	PRO	-	expression tag	UNP Q96FV9
I	-15	ASN	-	expression tag	UNP Q96FV9
I	-14	PRO	-	expression tag	UNP Q96FV9
I	-13	LEU	-	expression tag	UNP Q96FV9
I	-12	LEU	-	expression tag	UNP Q96FV9
I	-11	GLY	-	expression tag	UNP Q96FV9
I	-10	LEU	-	expression tag	UNP Q96FV9
I	-9	ASP	-	expression tag	UNP Q96FV9
I	-8	SER	-	expression tag	UNP Q96FV9
I	-7	THR	-	expression tag	UNP Q96FV9
I	-6	LEU	-	expression tag	UNP Q96FV9
I	-5	GLU	-	expression tag	UNP Q96FV9
I	-4	VAL	-	expression tag	UNP Q96FV9
I	-3	LEU	-	expression tag	UNP Q96FV9

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-2	PHE	-	expression tag	UNP Q96FV9
I	-1	GLN	-	expression tag	UNP Q96FV9
I	0	GLY	-	expression tag	UNP Q96FV9
I	1	PRO	-	expression tag	UNP Q96FV9
a	-53	MET	-	initiating methionine	UNP Q96FV9
a	-52	GLY	-	expression tag	UNP Q96FV9
a	-51	LYS	-	expression tag	UNP Q96FV9
a	-50	PRO	-	expression tag	UNP Q96FV9
a	-49	ILE	-	expression tag	UNP Q96FV9
a	-48	PRO	-	expression tag	UNP Q96FV9
a	-47	ASN	-	expression tag	UNP Q96FV9
a	-46	PRO	-	expression tag	UNP Q96FV9
a	-45	LEU	-	expression tag	UNP Q96FV9
a	-44	LEU	-	expression tag	UNP Q96FV9
a	-43	GLY	-	expression tag	UNP Q96FV9
a	-42	LEU	-	expression tag	UNP Q96FV9
a	-41	ASP	-	expression tag	UNP Q96FV9
a	-40	SER	-	expression tag	UNP Q96FV9
a	-39	THR	-	expression tag	UNP Q96FV9
a	-38	GLY	-	expression tag	UNP Q96FV9
a	-37	SER	-	expression tag	UNP Q96FV9
a	-36	GLY	-	expression tag	UNP Q96FV9
a	-35	LYS	-	expression tag	UNP Q96FV9
a	-34	PRO	-	expression tag	UNP Q96FV9
a	-33	ILE	-	expression tag	UNP Q96FV9
a	-32	PRO	-	expression tag	UNP Q96FV9
a	-31	ASN	-	expression tag	UNP Q96FV9
a	-30	PRO	-	expression tag	UNP Q96FV9
a	-29	LEU	-	expression tag	UNP Q96FV9
a	-28	LEU	-	expression tag	UNP Q96FV9
a	-27	GLY	-	expression tag	UNP Q96FV9
a	-26	LEU	-	expression tag	UNP Q96FV9
a	-25	ASP	-	expression tag	UNP Q96FV9
a	-24	SER	-	expression tag	UNP Q96FV9
a	-23	THR	-	expression tag	UNP Q96FV9
a	-22	GLY	-	expression tag	UNP Q96FV9
a	-21	SER	-	expression tag	UNP Q96FV9
a	-20	GLY	-	expression tag	UNP Q96FV9
a	-19	LYS	-	expression tag	UNP Q96FV9
a	-18	PRO	-	expression tag	UNP Q96FV9
a	-17	ILE	-	expression tag	UNP Q96FV9
a	-16	PRO	-	expression tag	UNP Q96FV9

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Chain	Residue	Modelled	Actual	Comment	Reference
a	-15	ASN	-	expression tag	UNP Q96FV9
a	-14	PRO	-	expression tag	UNP Q96FV9
a	-13	LEU	-	expression tag	UNP Q96FV9
a	-12	LEU	-	expression tag	UNP Q96FV9
a	-11	GLY	-	expression tag	UNP Q96FV9
a	-10	LEU	-	expression tag	UNP Q96FV9
a	-9	ASP	-	expression tag	UNP Q96FV9
a	-8	SER	-	expression tag	UNP Q96FV9
a	-7	THR	-	expression tag	UNP Q96FV9
a	-6	LEU	-	expression tag	UNP Q96FV9
a	-5	GLU	-	expression tag	UNP Q96FV9
a	-4	VAL	-	expression tag	UNP Q96FV9
a	-3	LEU	-	expression tag	UNP Q96FV9
a	-2	PHE	-	expression tag	UNP Q96FV9
a	-1	GLN	-	expression tag	UNP Q96FV9
a	0	GLY	-	expression tag	UNP Q96FV9
a	1	PRO	-	expression tag	UNP Q96FV9
i	-53	MET	-	initiating methionine	UNP Q96FV9
i	-52	GLY	-	expression tag	UNP Q96FV9
i	-51	LYS	-	expression tag	UNP Q96FV9
i	-50	PRO	-	expression tag	UNP Q96FV9
i	-49	ILE	-	expression tag	UNP Q96FV9
i	-48	PRO	-	expression tag	UNP Q96FV9
i	-47	ASN	-	expression tag	UNP Q96FV9
i	-46	PRO	-	expression tag	UNP Q96FV9
i	-45	LEU	-	expression tag	UNP Q96FV9
i	-44	LEU	-	expression tag	UNP Q96FV9
i	-43	GLY	-	expression tag	UNP Q96FV9
i	-42	LEU	-	expression tag	UNP Q96FV9
i	-41	ASP	-	expression tag	UNP Q96FV9
i	-40	SER	-	expression tag	UNP Q96FV9
i	-39	THR	-	expression tag	UNP Q96FV9
i	-38	GLY	-	expression tag	UNP Q96FV9
i	-37	SER	-	expression tag	UNP Q96FV9
i	-36	GLY	-	expression tag	UNP Q96FV9
i	-35	LYS	-	expression tag	UNP Q96FV9
i	-34	PRO	-	expression tag	UNP Q96FV9
i	-33	ILE	-	expression tag	UNP Q96FV9
i	-32	PRO	-	expression tag	UNP Q96FV9
i	-31	ASN	-	expression tag	UNP Q96FV9
i	-30	PRO	-	expression tag	UNP Q96FV9
i	-29	LEU	-	expression tag	UNP Q96FV9

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Chain	Residue	Modelled	Actual	Comment	Reference
i	-28	LEU	-	expression tag	UNP Q96FV9
i	-27	GLY	-	expression tag	UNP Q96FV9
i	-26	LEU	-	expression tag	UNP Q96FV9
i	-25	ASP	-	expression tag	UNP Q96FV9
i	-24	SER	-	expression tag	UNP Q96FV9
i	-23	THR	-	expression tag	UNP Q96FV9
i	-22	GLY	-	expression tag	UNP Q96FV9
i	-21	SER	-	expression tag	UNP Q96FV9
i	-20	GLY	-	expression tag	UNP Q96FV9
i	-19	LYS	-	expression tag	UNP Q96FV9
i	-18	PRO	-	expression tag	UNP Q96FV9
i	-17	ILE	-	expression tag	UNP Q96FV9
i	-16	PRO	-	expression tag	UNP Q96FV9
i	-15	ASN	-	expression tag	UNP Q96FV9
i	-14	PRO	-	expression tag	UNP Q96FV9
i	-13	LEU	-	expression tag	UNP Q96FV9
i	-12	LEU	-	expression tag	UNP Q96FV9
i	-11	GLY	-	expression tag	UNP Q96FV9
i	-10	LEU	-	expression tag	UNP Q96FV9
i	-9	ASP	-	expression tag	UNP Q96FV9
i	-8	SER	-	expression tag	UNP Q96FV9
i	-7	THR	-	expression tag	UNP Q96FV9
i	-6	LEU	-	expression tag	UNP Q96FV9
i	-5	GLU	-	expression tag	UNP Q96FV9
i	-4	VAL	-	expression tag	UNP Q96FV9
i	-3	LEU	-	expression tag	UNP Q96FV9
i	-2	PHE	-	expression tag	UNP Q96FV9
i	-1	GLN	-	expression tag	UNP Q96FV9
i	0	GLY	-	expression tag	UNP Q96FV9
i	1	PRO	-	expression tag	UNP Q96FV9

- Molecule 2 is a protein called THO complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	706	Total	C	N	O	S	0	0
			4700	2972	834	874	20		
2	J	707	Total	C	N	O	S	0	0
			4702	2975	832	875	20		
2	b	706	Total	C	N	O	S	0	0
			4700	2972	834	874	20		
2	j	707	Total	C	N	O	S	0	0
			4696	2969	832	875	20		

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	MET	-	initiating methionine	UNP Q8NI27
B	-21	LYS	-	expression tag	UNP Q8NI27
B	-20	HIS	-	expression tag	UNP Q8NI27
B	-19	HIS	-	expression tag	UNP Q8NI27
B	-18	HIS	-	expression tag	UNP Q8NI27
B	-17	HIS	-	expression tag	UNP Q8NI27
B	-16	HIS	-	expression tag	UNP Q8NI27
B	-15	HIS	-	expression tag	UNP Q8NI27
B	-14	HIS	-	expression tag	UNP Q8NI27
B	-13	HIS	-	expression tag	UNP Q8NI27
B	-12	HIS	-	expression tag	UNP Q8NI27
B	-11	HIS	-	expression tag	UNP Q8NI27
B	-10	SER	-	expression tag	UNP Q8NI27
B	-9	ALA	-	expression tag	UNP Q8NI27
B	-8	GLY	-	expression tag	UNP Q8NI27
B	-7	LEU	-	expression tag	UNP Q8NI27
B	-6	GLU	-	expression tag	UNP Q8NI27
B	-5	VAL	-	expression tag	UNP Q8NI27
B	-4	LEU	-	expression tag	UNP Q8NI27
B	-3	PHE	-	expression tag	UNP Q8NI27
B	-2	GLN	-	expression tag	UNP Q8NI27
B	-1	GLY	-	expression tag	UNP Q8NI27
B	0	PRO	-	expression tag	UNP Q8NI27
J	-22	MET	-	initiating methionine	UNP Q8NI27
J	-21	LYS	-	expression tag	UNP Q8NI27
J	-20	HIS	-	expression tag	UNP Q8NI27
J	-19	HIS	-	expression tag	UNP Q8NI27
J	-18	HIS	-	expression tag	UNP Q8NI27
J	-17	HIS	-	expression tag	UNP Q8NI27
J	-16	HIS	-	expression tag	UNP Q8NI27
J	-15	HIS	-	expression tag	UNP Q8NI27
J	-14	HIS	-	expression tag	UNP Q8NI27
J	-13	HIS	-	expression tag	UNP Q8NI27
J	-12	HIS	-	expression tag	UNP Q8NI27
J	-11	HIS	-	expression tag	UNP Q8NI27
J	-10	SER	-	expression tag	UNP Q8NI27
J	-9	ALA	-	expression tag	UNP Q8NI27
J	-8	GLY	-	expression tag	UNP Q8NI27
J	-7	LEU	-	expression tag	UNP Q8NI27
J	-6	GLU	-	expression tag	UNP Q8NI27
J	-5	VAL	-	expression tag	UNP Q8NI27
J	-4	LEU	-	expression tag	UNP Q8NI27

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	PHE	-	expression tag	UNP Q8NI27
J	-2	GLN	-	expression tag	UNP Q8NI27
J	-1	GLY	-	expression tag	UNP Q8NI27
J	0	PRO	-	expression tag	UNP Q8NI27
b	-22	MET	-	initiating methionine	UNP Q8NI27
b	-21	LYS	-	expression tag	UNP Q8NI27
b	-20	HIS	-	expression tag	UNP Q8NI27
b	-19	HIS	-	expression tag	UNP Q8NI27
b	-18	HIS	-	expression tag	UNP Q8NI27
b	-17	HIS	-	expression tag	UNP Q8NI27
b	-16	HIS	-	expression tag	UNP Q8NI27
b	-15	HIS	-	expression tag	UNP Q8NI27
b	-14	HIS	-	expression tag	UNP Q8NI27
b	-13	HIS	-	expression tag	UNP Q8NI27
b	-12	HIS	-	expression tag	UNP Q8NI27
b	-11	HIS	-	expression tag	UNP Q8NI27
b	-10	SER	-	expression tag	UNP Q8NI27
b	-9	ALA	-	expression tag	UNP Q8NI27
b	-8	GLY	-	expression tag	UNP Q8NI27
b	-7	LEU	-	expression tag	UNP Q8NI27
b	-6	GLU	-	expression tag	UNP Q8NI27
b	-5	VAL	-	expression tag	UNP Q8NI27
b	-4	LEU	-	expression tag	UNP Q8NI27
b	-3	PHE	-	expression tag	UNP Q8NI27
b	-2	GLN	-	expression tag	UNP Q8NI27
b	-1	GLY	-	expression tag	UNP Q8NI27
b	0	PRO	-	expression tag	UNP Q8NI27
j	-22	MET	-	initiating methionine	UNP Q8NI27
j	-21	LYS	-	expression tag	UNP Q8NI27
j	-20	HIS	-	expression tag	UNP Q8NI27
j	-19	HIS	-	expression tag	UNP Q8NI27
j	-18	HIS	-	expression tag	UNP Q8NI27
j	-17	HIS	-	expression tag	UNP Q8NI27
j	-16	HIS	-	expression tag	UNP Q8NI27
j	-15	HIS	-	expression tag	UNP Q8NI27
j	-14	HIS	-	expression tag	UNP Q8NI27
j	-13	HIS	-	expression tag	UNP Q8NI27
j	-12	HIS	-	expression tag	UNP Q8NI27
j	-11	HIS	-	expression tag	UNP Q8NI27
j	-10	SER	-	expression tag	UNP Q8NI27
j	-9	ALA	-	expression tag	UNP Q8NI27
j	-8	GLY	-	expression tag	UNP Q8NI27

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Chain	Residue	Modelled	Actual	Comment	Reference
j	-7	LEU	-	expression tag	UNP Q8NI27
j	-6	GLU	-	expression tag	UNP Q8NI27
j	-5	VAL	-	expression tag	UNP Q8NI27
j	-4	LEU	-	expression tag	UNP Q8NI27
j	-3	PHE	-	expression tag	UNP Q8NI27
j	-2	GLN	-	expression tag	UNP Q8NI27
j	-1	GLY	-	expression tag	UNP Q8NI27
j	0	PRO	-	expression tag	UNP Q8NI27

- Molecule 3 is a protein called THO complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	304	Total	C	N	O	S	0	0
			2349	1482	407	446	14		
3	K	304	Total	C	N	O	S	0	0
			2349	1482	407	446	14		
3	c	304	Total	C	N	O	S	0	0
			2349	1482	407	446	14		
3	k	304	Total	C	N	O	S	0	0
			2349	1482	407	446	14		

There are 176 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-43	MET	-	initiating methionine	UNP Q96J01
C	-42	LYS	-	expression tag	UNP Q96J01
C	-41	GLY	-	expression tag	UNP Q96J01
C	-40	SER	-	expression tag	UNP Q96J01
C	-39	ALA	-	expression tag	UNP Q96J01
C	-38	TRP	-	expression tag	UNP Q96J01
C	-37	SER	-	expression tag	UNP Q96J01
C	-36	HIS	-	expression tag	UNP Q96J01
C	-35	PRO	-	expression tag	UNP Q96J01
C	-34	GLN	-	expression tag	UNP Q96J01
C	-33	PHE	-	expression tag	UNP Q96J01
C	-32	GLU	-	expression tag	UNP Q96J01
C	-31	LYS	-	expression tag	UNP Q96J01
C	-30	GLY	-	expression tag	UNP Q96J01
C	-29	GLY	-	expression tag	UNP Q96J01
C	-28	GLY	-	expression tag	UNP Q96J01
C	-27	SER	-	expression tag	UNP Q96J01
C	-26	GLY	-	expression tag	UNP Q96J01

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-25	GLY	-	expression tag	UNP Q96J01
C	-24	GLY	-	expression tag	UNP Q96J01
C	-23	SER	-	expression tag	UNP Q96J01
C	-22	GLY	-	expression tag	UNP Q96J01
C	-21	GLY	-	expression tag	UNP Q96J01
C	-20	SER	-	expression tag	UNP Q96J01
C	-19	ALA	-	expression tag	UNP Q96J01
C	-18	TRP	-	expression tag	UNP Q96J01
C	-17	SER	-	expression tag	UNP Q96J01
C	-16	HIS	-	expression tag	UNP Q96J01
C	-15	PRO	-	expression tag	UNP Q96J01
C	-14	GLN	-	expression tag	UNP Q96J01
C	-13	PHE	-	expression tag	UNP Q96J01
C	-12	GLU	-	expression tag	UNP Q96J01
C	-11	LYS	-	expression tag	UNP Q96J01
C	-10	THR	-	expression tag	UNP Q96J01
C	-9	ALA	-	expression tag	UNP Q96J01
C	-8	GLY	-	expression tag	UNP Q96J01
C	-7	LEU	-	expression tag	UNP Q96J01
C	-6	GLU	-	expression tag	UNP Q96J01
C	-5	VAL	-	expression tag	UNP Q96J01
C	-4	LEU	-	expression tag	UNP Q96J01
C	-3	PHE	-	expression tag	UNP Q96J01
C	-2	GLN	-	expression tag	UNP Q96J01
C	-1	GLY	-	expression tag	UNP Q96J01
C	0	PRO	-	expression tag	UNP Q96J01
K	-43	MET	-	initiating methionine	UNP Q96J01
K	-42	LYS	-	expression tag	UNP Q96J01
K	-41	GLY	-	expression tag	UNP Q96J01
K	-40	SER	-	expression tag	UNP Q96J01
K	-39	ALA	-	expression tag	UNP Q96J01
K	-38	TRP	-	expression tag	UNP Q96J01
K	-37	SER	-	expression tag	UNP Q96J01
K	-36	HIS	-	expression tag	UNP Q96J01
K	-35	PRO	-	expression tag	UNP Q96J01
K	-34	GLN	-	expression tag	UNP Q96J01
K	-33	PHE	-	expression tag	UNP Q96J01
K	-32	GLU	-	expression tag	UNP Q96J01
K	-31	LYS	-	expression tag	UNP Q96J01
K	-30	GLY	-	expression tag	UNP Q96J01
K	-29	GLY	-	expression tag	UNP Q96J01
K	-28	GLY	-	expression tag	UNP Q96J01

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-27	SER	-	expression tag	UNP Q96J01
K	-26	GLY	-	expression tag	UNP Q96J01
K	-25	GLY	-	expression tag	UNP Q96J01
K	-24	GLY	-	expression tag	UNP Q96J01
K	-23	SER	-	expression tag	UNP Q96J01
K	-22	GLY	-	expression tag	UNP Q96J01
K	-21	GLY	-	expression tag	UNP Q96J01
K	-20	SER	-	expression tag	UNP Q96J01
K	-19	ALA	-	expression tag	UNP Q96J01
K	-18	TRP	-	expression tag	UNP Q96J01
K	-17	SER	-	expression tag	UNP Q96J01
K	-16	HIS	-	expression tag	UNP Q96J01
K	-15	PRO	-	expression tag	UNP Q96J01
K	-14	GLN	-	expression tag	UNP Q96J01
K	-13	PHE	-	expression tag	UNP Q96J01
K	-12	GLU	-	expression tag	UNP Q96J01
K	-11	LYS	-	expression tag	UNP Q96J01
K	-10	THR	-	expression tag	UNP Q96J01
K	-9	ALA	-	expression tag	UNP Q96J01
K	-8	GLY	-	expression tag	UNP Q96J01
K	-7	LEU	-	expression tag	UNP Q96J01
K	-6	GLU	-	expression tag	UNP Q96J01
K	-5	VAL	-	expression tag	UNP Q96J01
K	-4	LEU	-	expression tag	UNP Q96J01
K	-3	PHE	-	expression tag	UNP Q96J01
K	-2	GLN	-	expression tag	UNP Q96J01
K	-1	GLY	-	expression tag	UNP Q96J01
K	0	PRO	-	expression tag	UNP Q96J01
c	-43	MET	-	initiating methionine	UNP Q96J01
c	-42	LYS	-	expression tag	UNP Q96J01
c	-41	GLY	-	expression tag	UNP Q96J01
c	-40	SER	-	expression tag	UNP Q96J01
c	-39	ALA	-	expression tag	UNP Q96J01
c	-38	TRP	-	expression tag	UNP Q96J01
c	-37	SER	-	expression tag	UNP Q96J01
c	-36	HIS	-	expression tag	UNP Q96J01
c	-35	PRO	-	expression tag	UNP Q96J01
c	-34	GLN	-	expression tag	UNP Q96J01
c	-33	PHE	-	expression tag	UNP Q96J01
c	-32	GLU	-	expression tag	UNP Q96J01
c	-31	LYS	-	expression tag	UNP Q96J01
c	-30	GLY	-	expression tag	UNP Q96J01

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Chain	Residue	Modelled	Actual	Comment	Reference
c	-29	GLY	-	expression tag	UNP Q96J01
c	-28	GLY	-	expression tag	UNP Q96J01
c	-27	SER	-	expression tag	UNP Q96J01
c	-26	GLY	-	expression tag	UNP Q96J01
c	-25	GLY	-	expression tag	UNP Q96J01
c	-24	GLY	-	expression tag	UNP Q96J01
c	-23	SER	-	expression tag	UNP Q96J01
c	-22	GLY	-	expression tag	UNP Q96J01
c	-21	GLY	-	expression tag	UNP Q96J01
c	-20	SER	-	expression tag	UNP Q96J01
c	-19	ALA	-	expression tag	UNP Q96J01
c	-18	TRP	-	expression tag	UNP Q96J01
c	-17	SER	-	expression tag	UNP Q96J01
c	-16	HIS	-	expression tag	UNP Q96J01
c	-15	PRO	-	expression tag	UNP Q96J01
c	-14	GLN	-	expression tag	UNP Q96J01
c	-13	PHE	-	expression tag	UNP Q96J01
c	-12	GLU	-	expression tag	UNP Q96J01
c	-11	LYS	-	expression tag	UNP Q96J01
c	-10	THR	-	expression tag	UNP Q96J01
c	-9	ALA	-	expression tag	UNP Q96J01
c	-8	GLY	-	expression tag	UNP Q96J01
c	-7	LEU	-	expression tag	UNP Q96J01
c	-6	GLU	-	expression tag	UNP Q96J01
c	-5	VAL	-	expression tag	UNP Q96J01
c	-4	LEU	-	expression tag	UNP Q96J01
c	-3	PHE	-	expression tag	UNP Q96J01
c	-2	GLN	-	expression tag	UNP Q96J01
c	-1	GLY	-	expression tag	UNP Q96J01
c	0	PRO	-	expression tag	UNP Q96J01
k	-43	MET	-	initiating methionine	UNP Q96J01
k	-42	LYS	-	expression tag	UNP Q96J01
k	-41	GLY	-	expression tag	UNP Q96J01
k	-40	SER	-	expression tag	UNP Q96J01
k	-39	ALA	-	expression tag	UNP Q96J01
k	-38	TRP	-	expression tag	UNP Q96J01
k	-37	SER	-	expression tag	UNP Q96J01
k	-36	HIS	-	expression tag	UNP Q96J01
k	-35	PRO	-	expression tag	UNP Q96J01
k	-34	GLN	-	expression tag	UNP Q96J01
k	-33	PHE	-	expression tag	UNP Q96J01
k	-32	GLU	-	expression tag	UNP Q96J01

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Chain	Residue	Modelled	Actual	Comment	Reference
k	-31	LYS	-	expression tag	UNP Q96J01
k	-30	GLY	-	expression tag	UNP Q96J01
k	-29	GLY	-	expression tag	UNP Q96J01
k	-28	GLY	-	expression tag	UNP Q96J01
k	-27	SER	-	expression tag	UNP Q96J01
k	-26	GLY	-	expression tag	UNP Q96J01
k	-25	GLY	-	expression tag	UNP Q96J01
k	-24	GLY	-	expression tag	UNP Q96J01
k	-23	SER	-	expression tag	UNP Q96J01
k	-22	GLY	-	expression tag	UNP Q96J01
k	-21	GLY	-	expression tag	UNP Q96J01
k	-20	SER	-	expression tag	UNP Q96J01
k	-19	ALA	-	expression tag	UNP Q96J01
k	-18	TRP	-	expression tag	UNP Q96J01
k	-17	SER	-	expression tag	UNP Q96J01
k	-16	HIS	-	expression tag	UNP Q96J01
k	-15	PRO	-	expression tag	UNP Q96J01
k	-14	GLN	-	expression tag	UNP Q96J01
k	-13	PHE	-	expression tag	UNP Q96J01
k	-12	GLU	-	expression tag	UNP Q96J01
k	-11	LYS	-	expression tag	UNP Q96J01
k	-10	THR	-	expression tag	UNP Q96J01
k	-9	ALA	-	expression tag	UNP Q96J01
k	-8	GLY	-	expression tag	UNP Q96J01
k	-7	LEU	-	expression tag	UNP Q96J01
k	-6	GLU	-	expression tag	UNP Q96J01
k	-5	VAL	-	expression tag	UNP Q96J01
k	-4	LEU	-	expression tag	UNP Q96J01
k	-3	PHE	-	expression tag	UNP Q96J01
k	-2	GLN	-	expression tag	UNP Q96J01
k	-1	GLY	-	expression tag	UNP Q96J01
k	0	PRO	-	expression tag	UNP Q96J01

- Molecule 4 is a protein called THO complex subunit 5 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	523	Total	C	N	O	S	0	0
			3687	2337	648	681	21		
4	M	549	Total	C	N	O	S	0	0
			4216	2689	734	768	25		
4	e	512	Total	C	N	O	S	0	0
			3598	2281	634	664	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	m	549	Total	C	N	O	S	0	0
			4216	2689	734	768	25		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	525	ILE	VAL	conflict	UNP Q13769
E	579	ILE	VAL	conflict	UNP Q13769
M	525	ILE	VAL	conflict	UNP Q13769
M	579	ILE	VAL	conflict	UNP Q13769
e	525	ILE	VAL	conflict	UNP Q13769
e	579	ILE	VAL	conflict	UNP Q13769
m	525	ILE	VAL	conflict	UNP Q13769
m	579	ILE	VAL	conflict	UNP Q13769

- Molecule 5 is a protein called THO complex subunit 6 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	337	Total	C	N	O	S	0	0
			2604	1647	459	483	15		
5	N	337	Total	C	N	O	S	0	0
			2604	1647	459	483	15		
5	f	329	Total	C	N	O	S	0	0
			2537	1604	448	470	15		
5	n	337	Total	C	N	O	S	0	0
			2604	1647	459	483	15		

- Molecule 6 is a protein called THO complex subunit 7 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	153	Total	C	N	O		0	0
			760	454	153	153			
6	O	155	Total	C	N	O	S	0	0
			1084	669	201	207	7		
6	g	153	Total	C	N	O		0	0
			760	454	153	153			
6	o	155	Total	C	N	O	S	0	0
			1084	669	201	207	7		

- Molecule 7 is a protein called Spliceosome RNA helicase DDX39B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	170	Total	C	N	O	S	0	0
			1398	888	245	261	4		
7	P	170	Total	C	N	O	S	0	0
			1398	888	245	261	4		
7	h	170	Total	C	N	O	S	0	0
			1398	888	245	261	4		
7	p	170	Total	C	N	O	S	0	0
			1398	888	245	261	4		

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-22	GLY	-	expression tag	UNP Q13838
H	-21	PRO	-	expression tag	UNP Q13838
H	-20	MET	-	expression tag	UNP Q13838
H	-19	LYS	-	expression tag	UNP Q13838
H	-18	GLY	-	expression tag	UNP Q13838
H	-17	SER	-	expression tag	UNP Q13838
H	-16	ALA	-	expression tag	UNP Q13838
H	-15	TRP	-	expression tag	UNP Q13838
H	-14	SER	-	expression tag	UNP Q13838
H	-13	HIS	-	expression tag	UNP Q13838
H	-12	PRO	-	expression tag	UNP Q13838
H	-11	GLN	-	expression tag	UNP Q13838
H	-10	PHE	-	expression tag	UNP Q13838
H	-9	GLU	-	expression tag	UNP Q13838
H	-8	LYS	-	expression tag	UNP Q13838
H	-7	LEU	-	expression tag	UNP Q13838
H	-6	GLU	-	expression tag	UNP Q13838
H	-5	VAL	-	expression tag	UNP Q13838
H	-4	LEU	-	expression tag	UNP Q13838
H	-3	PHE	-	expression tag	UNP Q13838
H	-2	GLN	-	expression tag	UNP Q13838
H	-1	GLY	-	expression tag	UNP Q13838
H	0	PRO	-	expression tag	UNP Q13838
P	-22	GLY	-	expression tag	UNP Q13838
P	-21	PRO	-	expression tag	UNP Q13838
P	-20	MET	-	expression tag	UNP Q13838
P	-19	LYS	-	expression tag	UNP Q13838
P	-18	GLY	-	expression tag	UNP Q13838
P	-17	SER	-	expression tag	UNP Q13838
P	-16	ALA	-	expression tag	UNP Q13838
P	-15	TRP	-	expression tag	UNP Q13838

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-14	SER	-	expression tag	UNP Q13838
P	-13	HIS	-	expression tag	UNP Q13838
P	-12	PRO	-	expression tag	UNP Q13838
P	-11	GLN	-	expression tag	UNP Q13838
P	-10	PHE	-	expression tag	UNP Q13838
P	-9	GLU	-	expression tag	UNP Q13838
P	-8	LYS	-	expression tag	UNP Q13838
P	-7	LEU	-	expression tag	UNP Q13838
P	-6	GLU	-	expression tag	UNP Q13838
P	-5	VAL	-	expression tag	UNP Q13838
P	-4	LEU	-	expression tag	UNP Q13838
P	-3	PHE	-	expression tag	UNP Q13838
P	-2	GLN	-	expression tag	UNP Q13838
P	-1	GLY	-	expression tag	UNP Q13838
P	0	PRO	-	expression tag	UNP Q13838
h	-22	GLY	-	expression tag	UNP Q13838
h	-21	PRO	-	expression tag	UNP Q13838
h	-20	MET	-	expression tag	UNP Q13838
h	-19	LYS	-	expression tag	UNP Q13838
h	-18	GLY	-	expression tag	UNP Q13838
h	-17	SER	-	expression tag	UNP Q13838
h	-16	ALA	-	expression tag	UNP Q13838
h	-15	TRP	-	expression tag	UNP Q13838
h	-14	SER	-	expression tag	UNP Q13838
h	-13	HIS	-	expression tag	UNP Q13838
h	-12	PRO	-	expression tag	UNP Q13838
h	-11	GLN	-	expression tag	UNP Q13838
h	-10	PHE	-	expression tag	UNP Q13838
h	-9	GLU	-	expression tag	UNP Q13838
h	-8	LYS	-	expression tag	UNP Q13838
h	-7	LEU	-	expression tag	UNP Q13838
h	-6	GLU	-	expression tag	UNP Q13838
h	-5	VAL	-	expression tag	UNP Q13838
h	-4	LEU	-	expression tag	UNP Q13838
h	-3	PHE	-	expression tag	UNP Q13838
h	-2	GLN	-	expression tag	UNP Q13838
h	-1	GLY	-	expression tag	UNP Q13838
h	0	PRO	-	expression tag	UNP Q13838
p	-22	GLY	-	expression tag	UNP Q13838
p	-21	PRO	-	expression tag	UNP Q13838
p	-20	MET	-	expression tag	UNP Q13838
p	-19	LYS	-	expression tag	UNP Q13838

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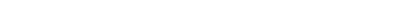
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Chain	Residue	Modelled	Actual	Comment	Reference
p	-18	GLY	-	expression tag	UNP Q13838
p	-17	SER	-	expression tag	UNP Q13838
p	-16	ALA	-	expression tag	UNP Q13838
p	-15	TRP	-	expression tag	UNP Q13838
p	-14	SER	-	expression tag	UNP Q13838
p	-13	HIS	-	expression tag	UNP Q13838
p	-12	PRO	-	expression tag	UNP Q13838
p	-11	GLN	-	expression tag	UNP Q13838
p	-10	PHE	-	expression tag	UNP Q13838
p	-9	GLU	-	expression tag	UNP Q13838
p	-8	LYS	-	expression tag	UNP Q13838
p	-7	LEU	-	expression tag	UNP Q13838
p	-6	GLU	-	expression tag	UNP Q13838
p	-5	VAL	-	expression tag	UNP Q13838
p	-4	LEU	-	expression tag	UNP Q13838
p	-3	PHE	-	expression tag	UNP Q13838
p	-2	GLN	-	expression tag	UNP Q13838
p	-1	GLY	-	expression tag	UNP Q13838
p	0	PRO	-	expression tag	UNP Q13838

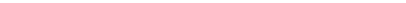
- Molecule 8 is a protein called THOC2 anchor (putative).

Mol	Chain	Residues	Atoms				AltConf	Trace
8	X	37	Total	C	N	O	0	0
			185	111	37	37		
8	x	37	Total	C	N	O	0	0
			185	111	37	37		

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

Chain I: 

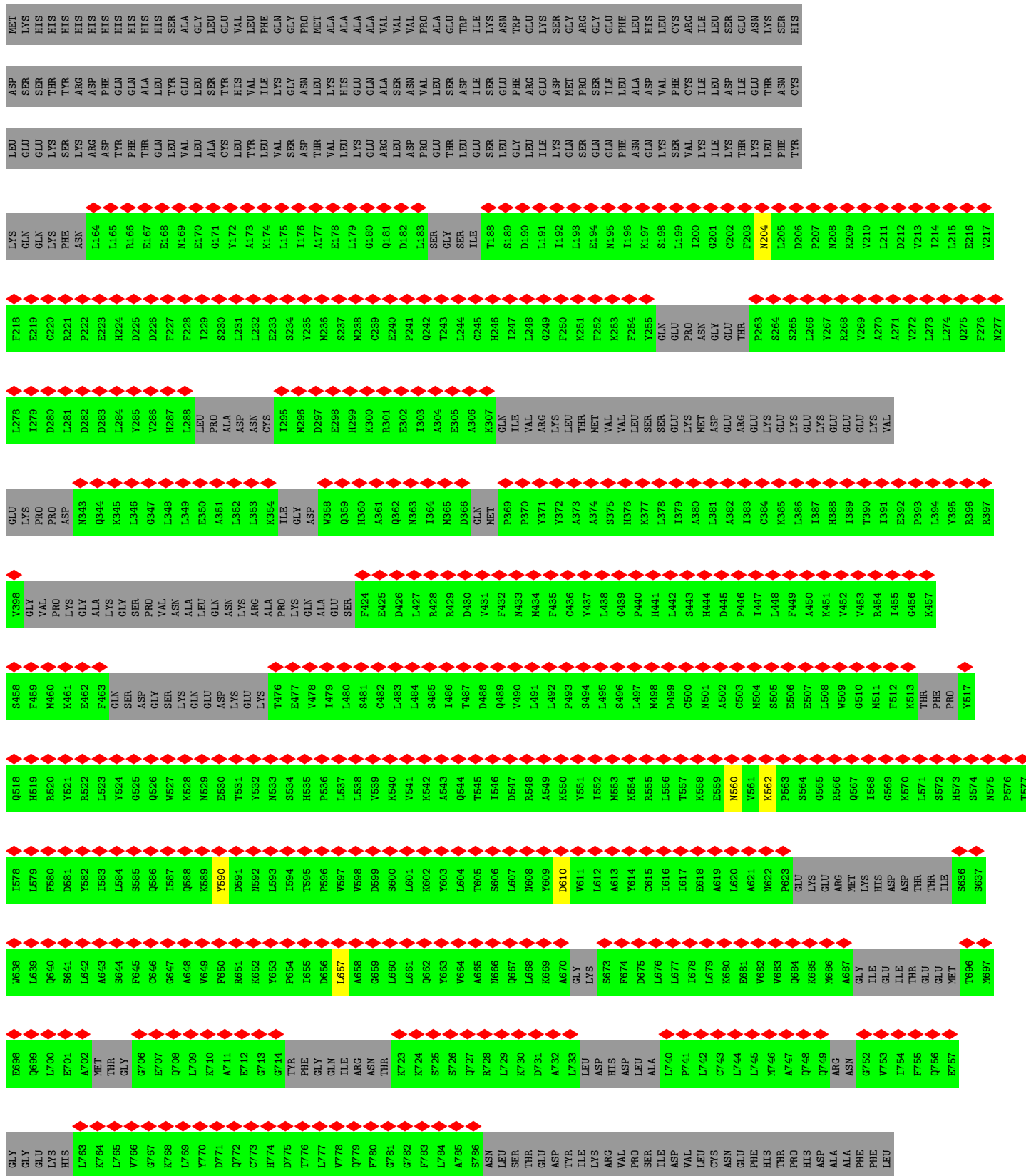
GLU ASP MET LYS MET ARG ALA LYS GLN GLN LEU VAL ALA ALA TRP GLN ASP GLN GLU GLY VAL HIS ALA THR PRO GLU ASN ASN ILE ASN LEU ALA LEU ASN LYS SER SER GLY LEU LEU ASP LEU ALA GLU SER THR THR ASP ASN ASN GLU THR ASN SER

Chain a:  37% 63%



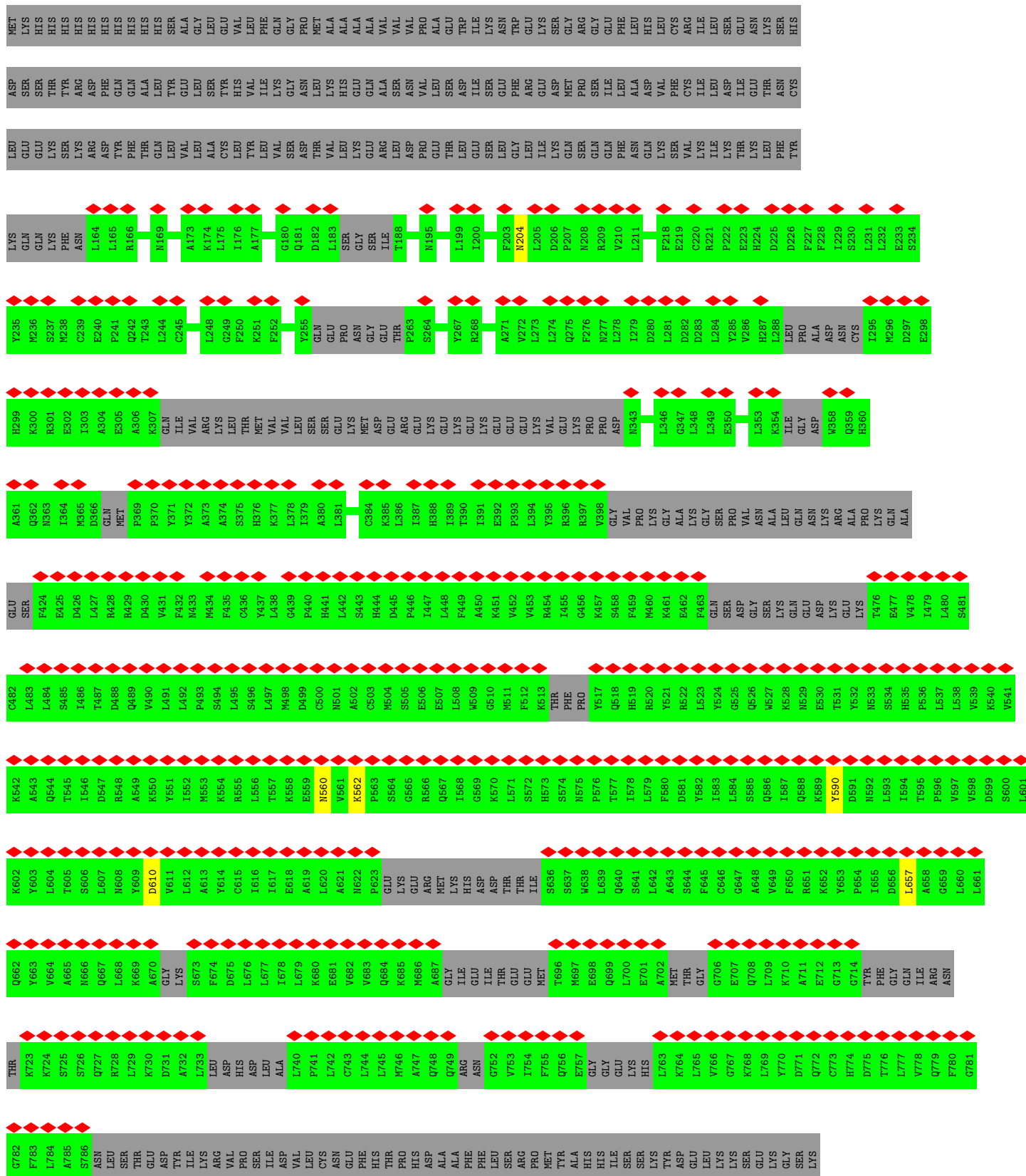
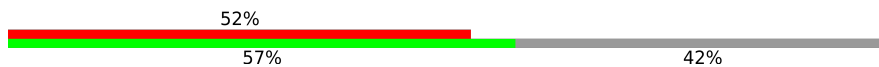


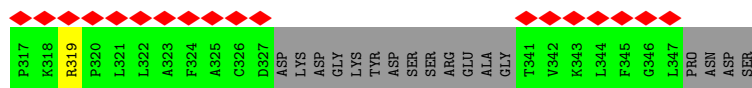
Chain J:



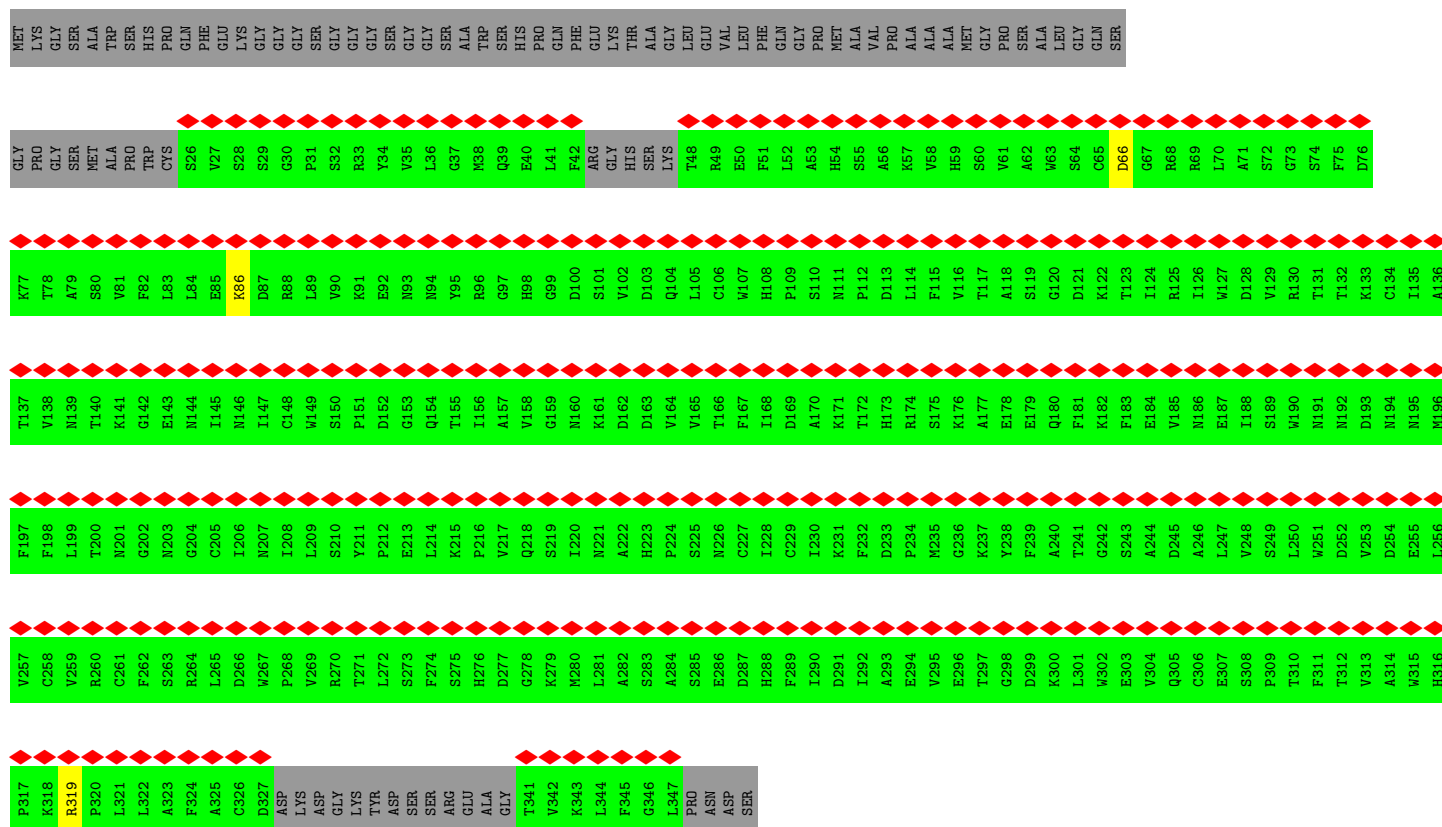
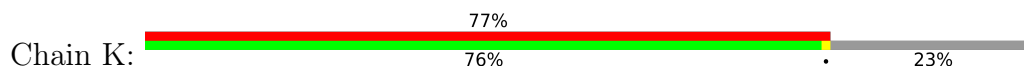


Chain j:

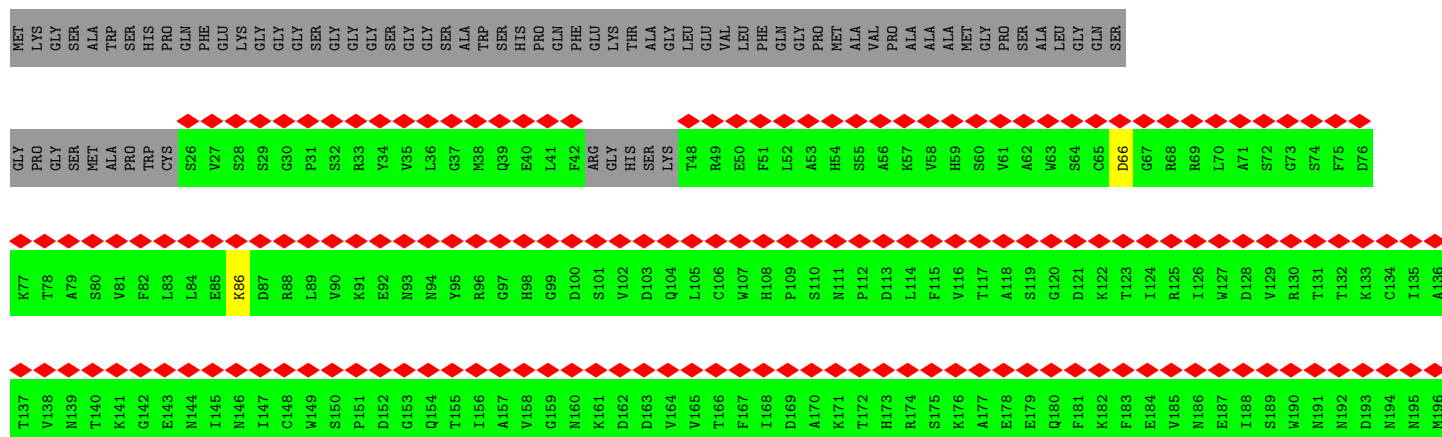
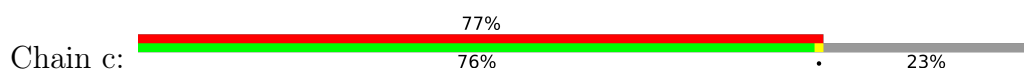


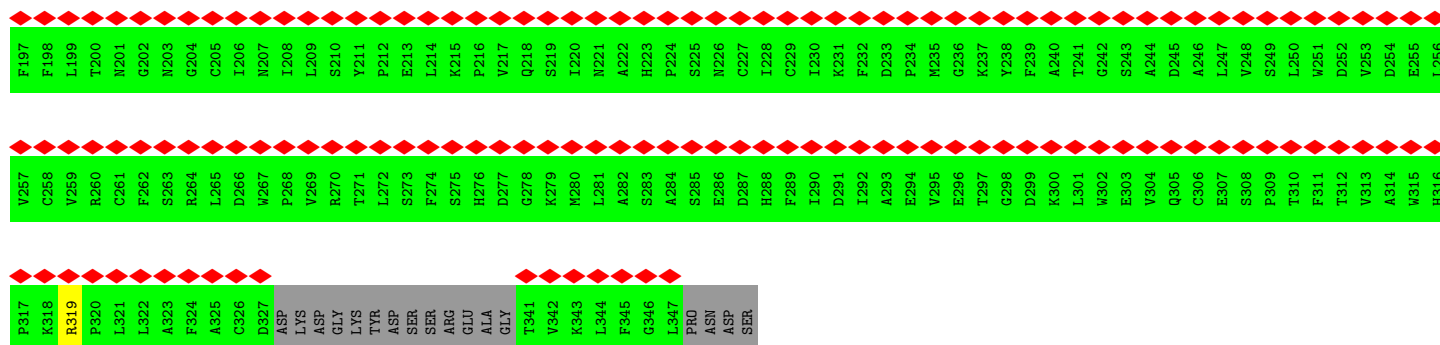


• Molecule 3: THO complex subunit 3

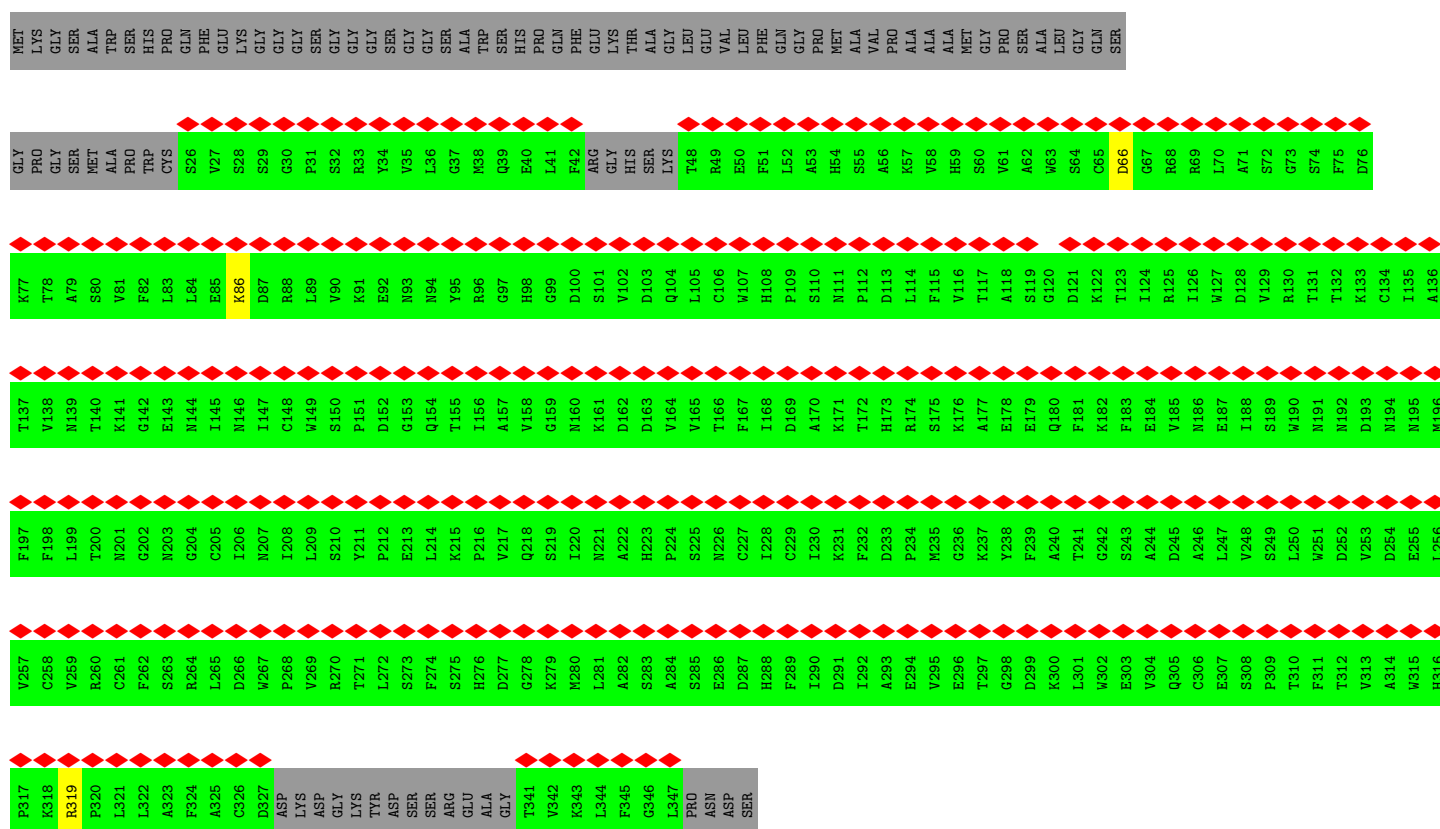
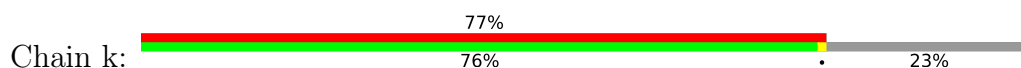


• Molecule 3: THO complex subunit 3

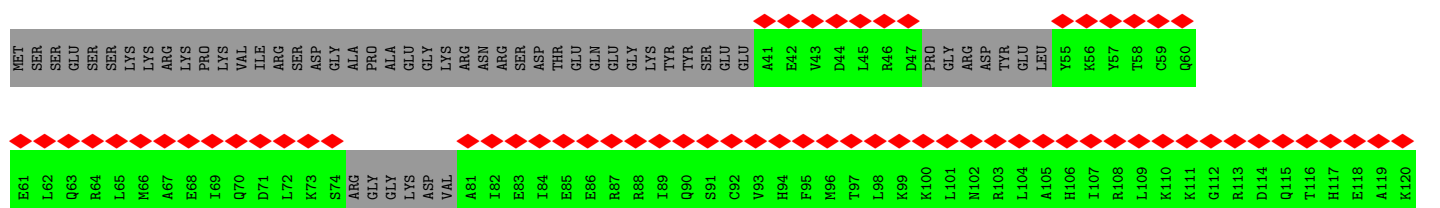
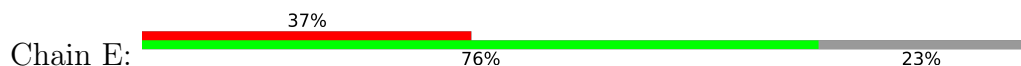


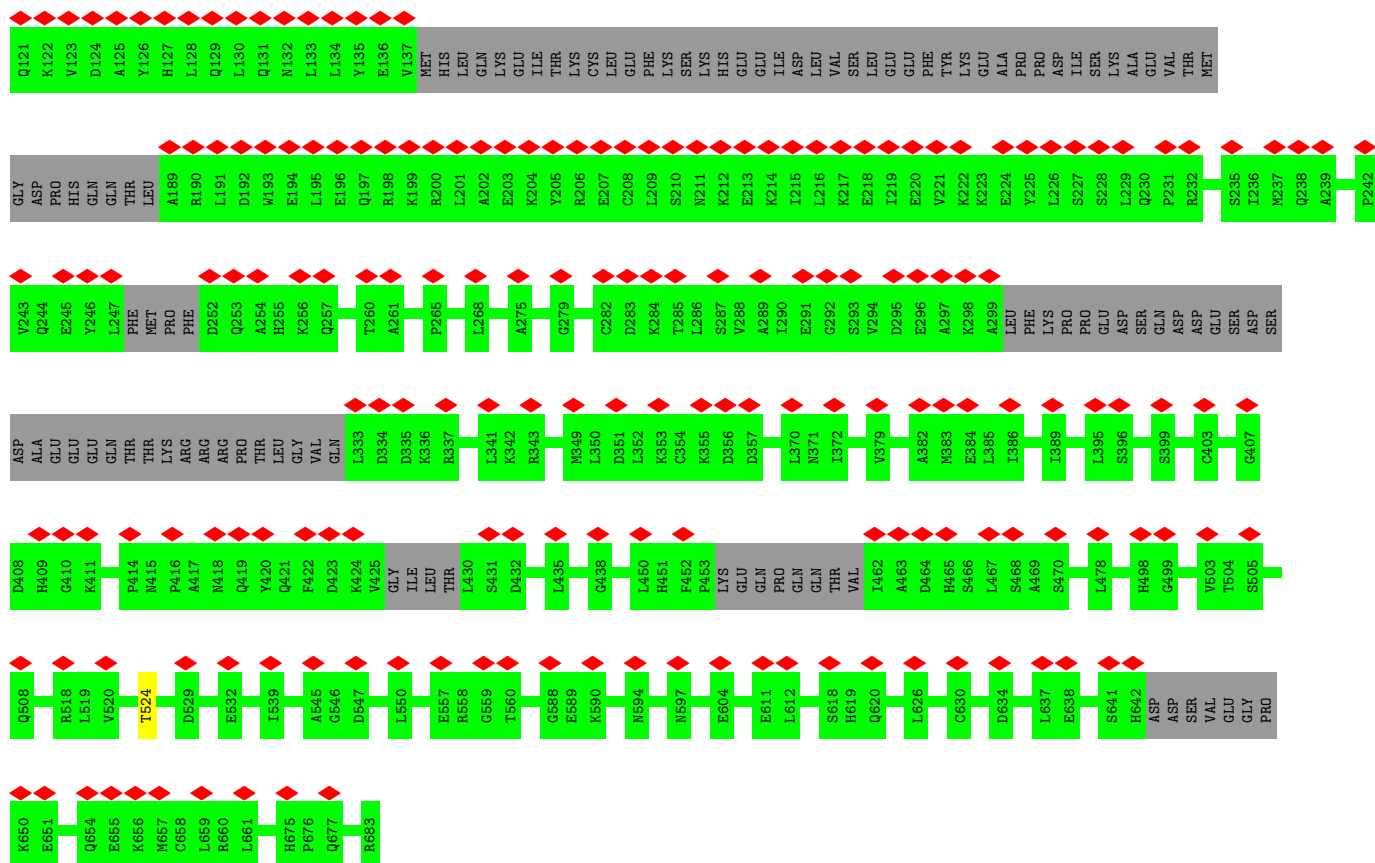


• Molecule 3: THO complex subunit 3

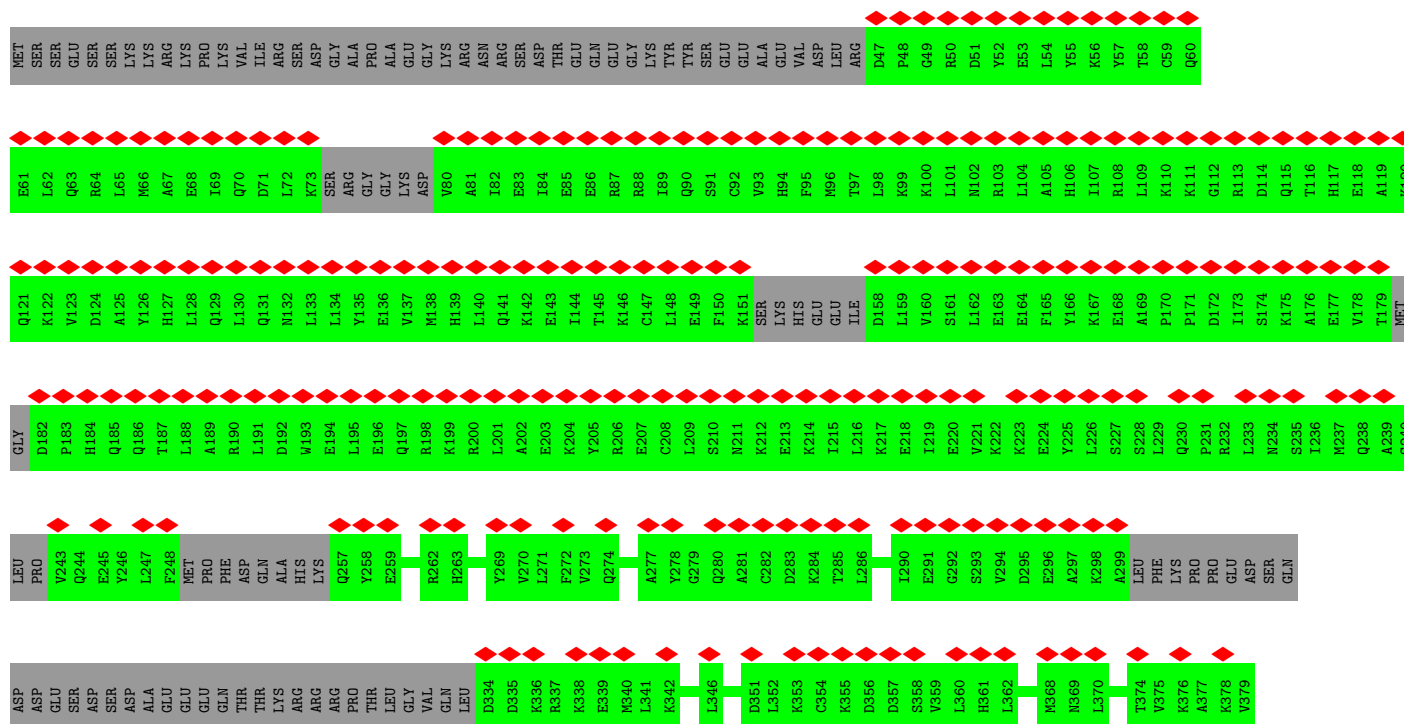
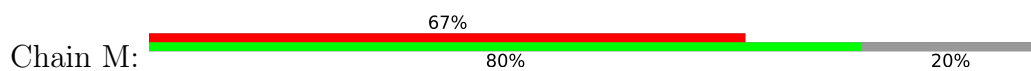


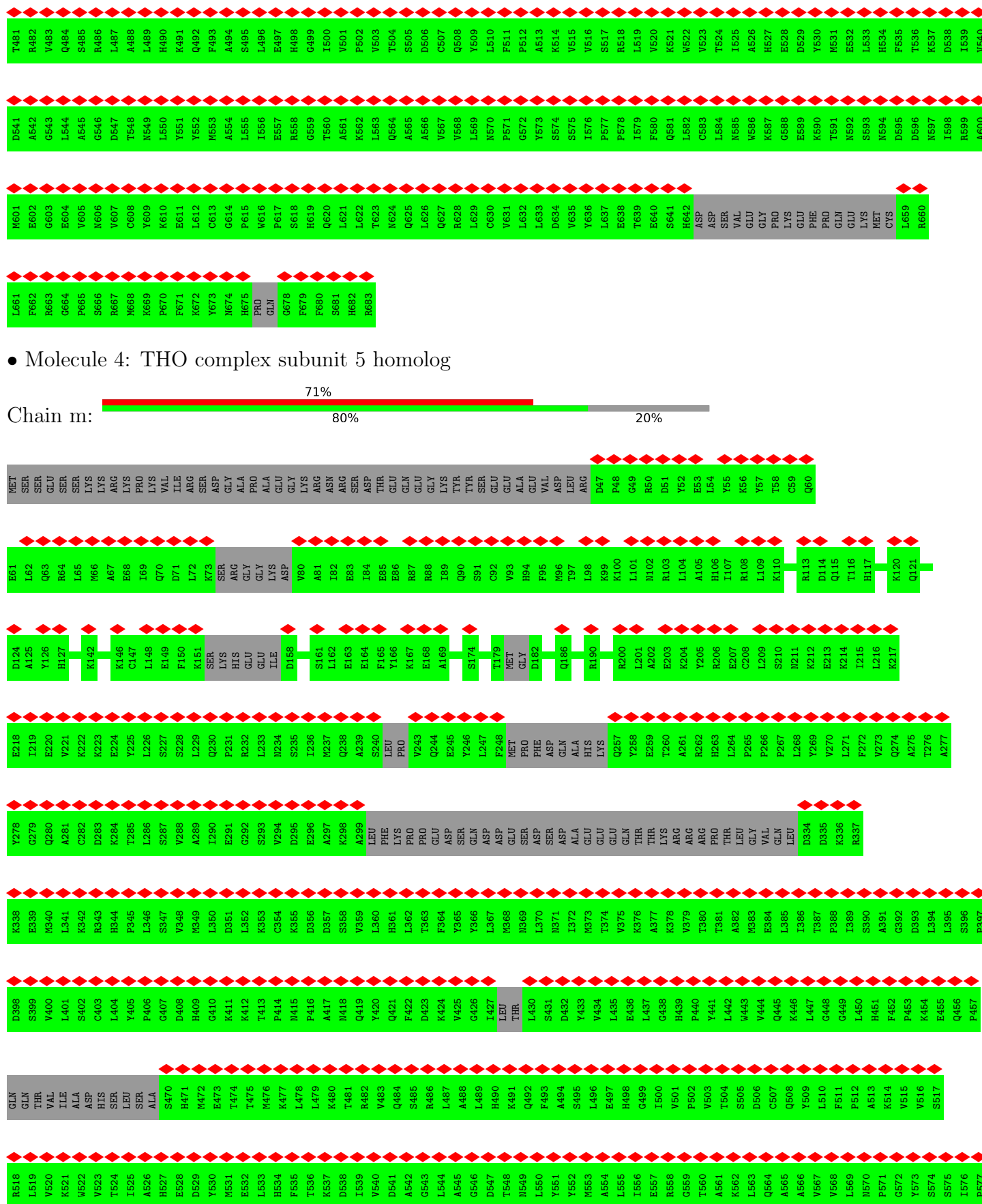
• Molecule 4: THO complex subunit 5 homolog





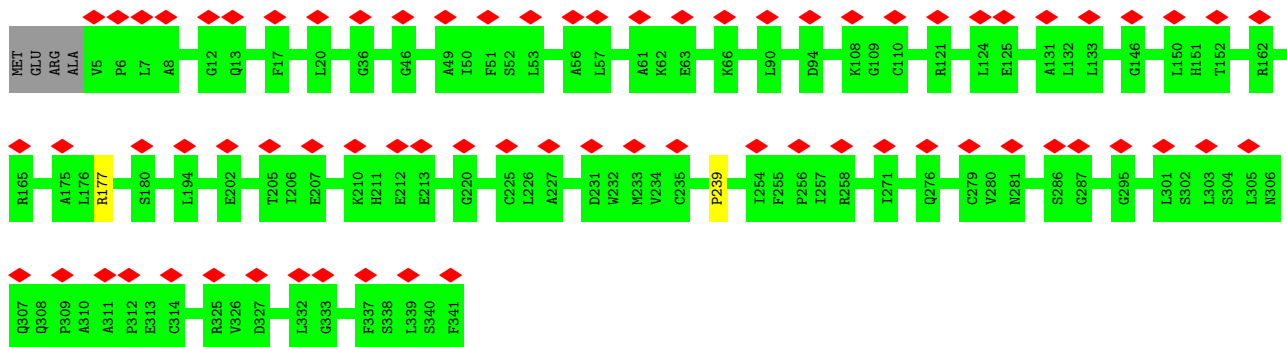
• Molecule 4: THO complex subunit 5 homolog







• Molecule 5: THO complex subunit 6 homolog

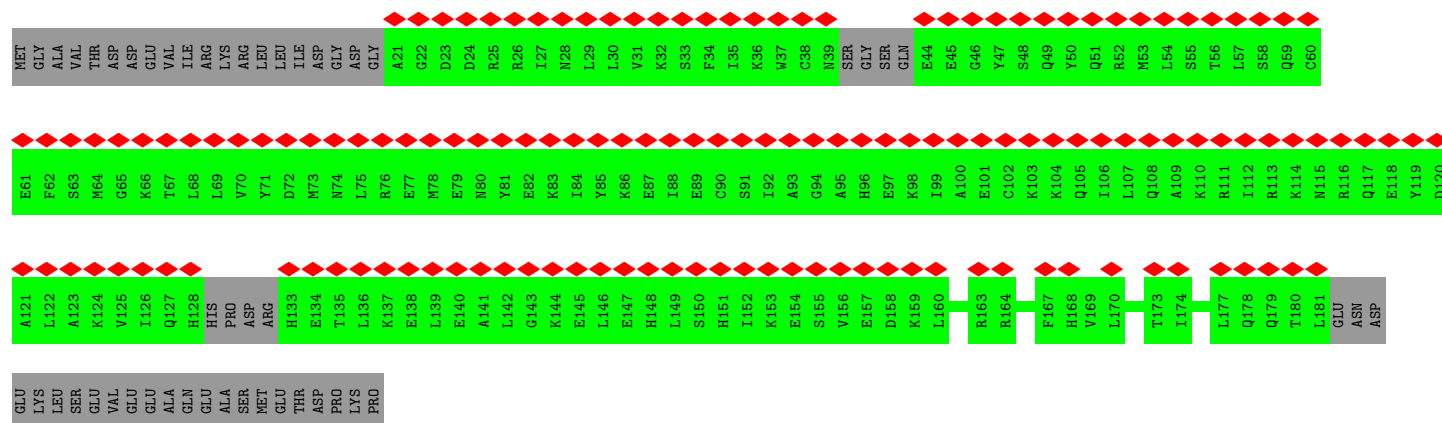
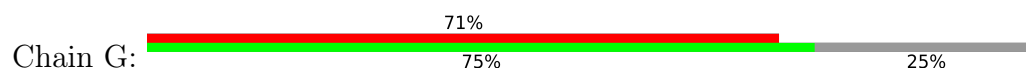


• Molecule 5: THO complex subunit 6 homolog

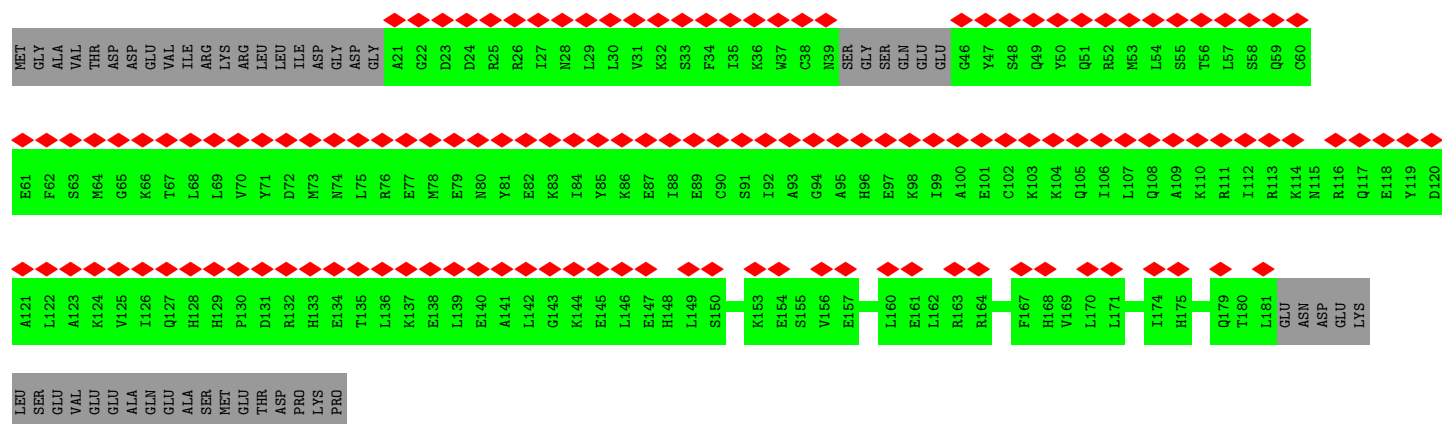
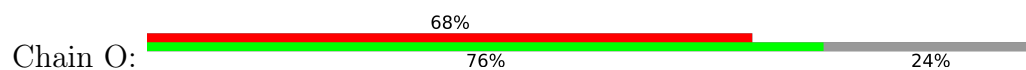


• Molecule 5: THO complex subunit 6 homolog

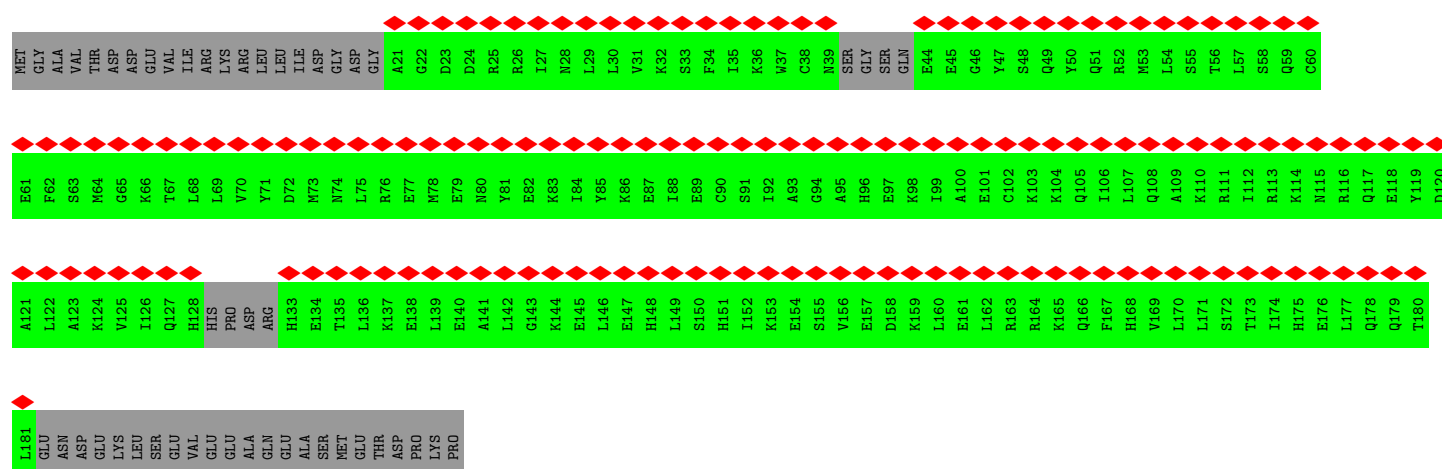
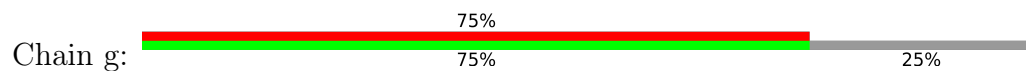




• Molecule 6: THO complex subunit 7 homolog

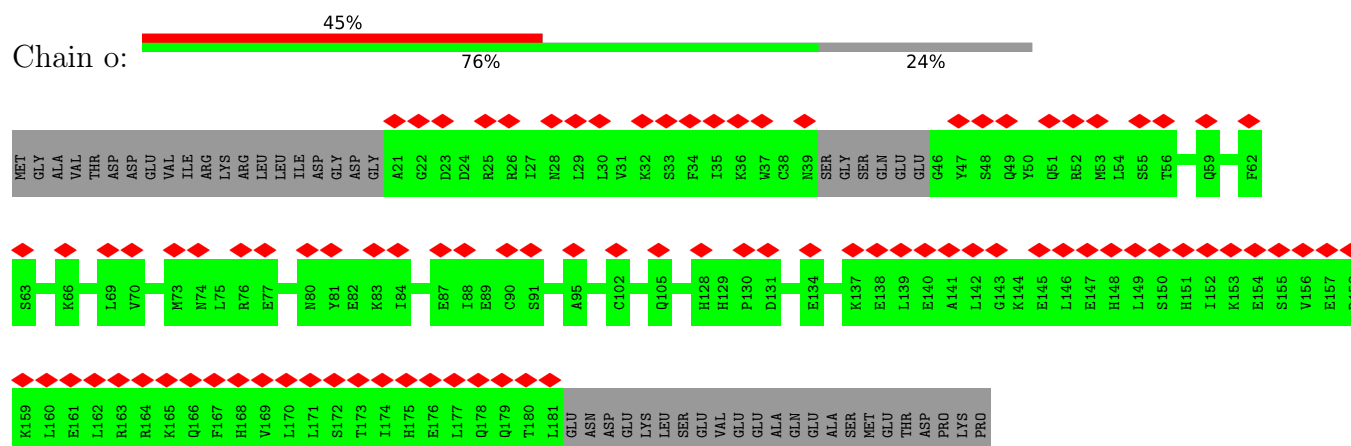


• Molecule 6: THO complex subunit 7 homolog



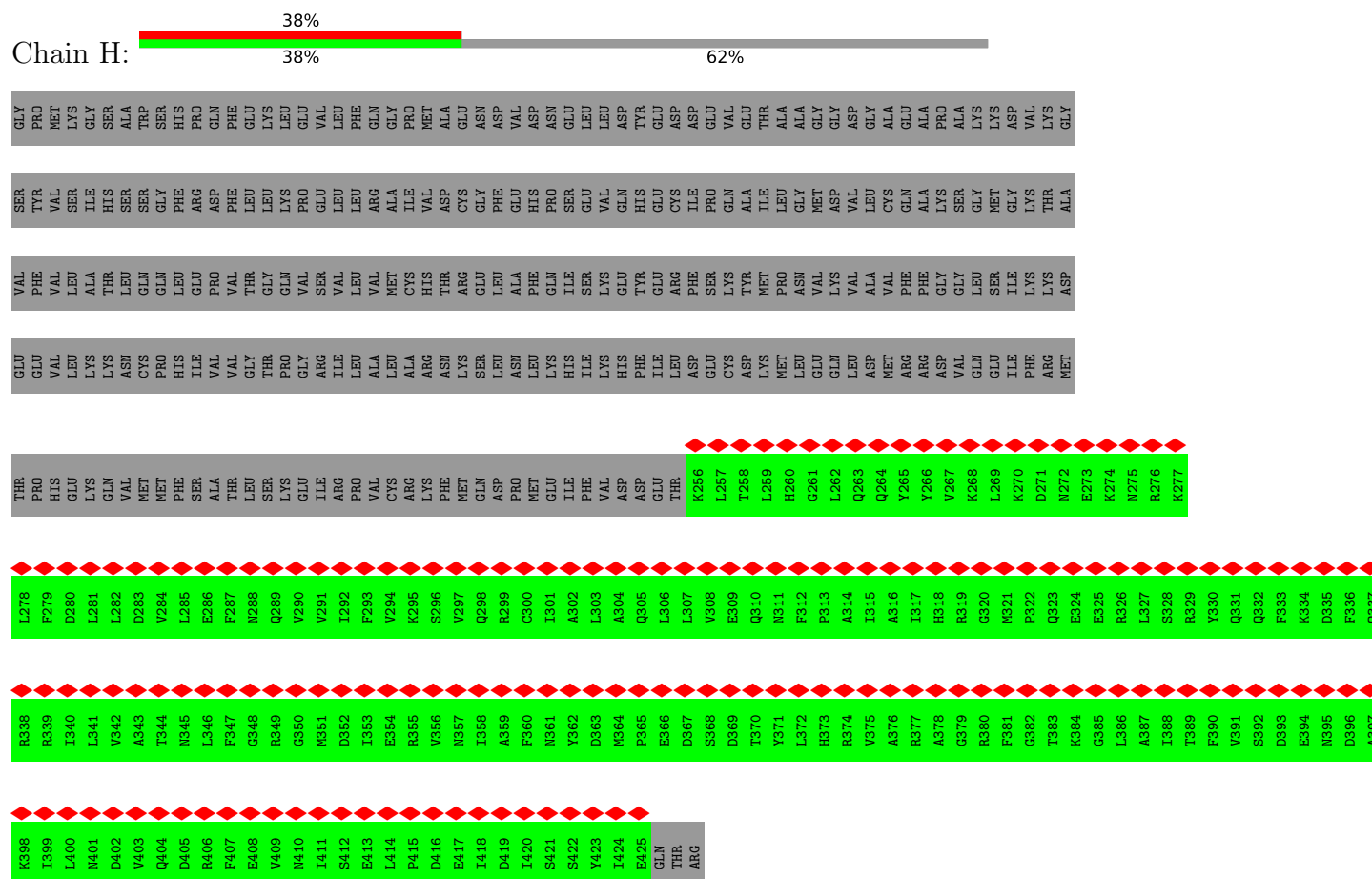
- Molecule 6: THO complex subunit 7 homolog

Chain o:



- Molecule 7: Spliceosome RNA helicase DDX39B

Chain H:



K398	R338	L278	THR	GLU	VAL	SER
I399	R339	F279	PRO	GLU	PHE	TYR
L400	R340	D280	HIS	VAL	VAL	VAL
M401	L341	L281	GLU	LEU	LEU	SER
D402	L342	L282	GLN	LYS	ALA	ILE
V403	A343	D283	VAL	ASN	THR	HIS
Q404	L344	V284	MET	CYS	LEU	SER
D405	N345	L285	MET	PRO	GLN	GLY
R406	L346	E286	PHE	HIS	LEU	ARG
F407	F347	F287	SER	ILE	GLU	ASP
E408	G348	D288	ALA	VAL	PRO	ASP
V409	R349	Q289	THR	VAL	VAL	PHE
M410	G350	Q290	LEU	GLY	THR	LEU
I411	N351	V291	LYS	THR	GLY	LEU
S412	D352	I292	ARG	ILE	THR	LEU
E413	L353	F293	PRO	LEU	GLY	LEU
L414	E354	V294	VAL	ALA	VAL	ARG
P415	R355	K295	CYS	LEU	MET	ALA
D416	V356	K296	ARG	ALA	CYS	ILE
E417	V357	V297	LYS	ARG	VAL	VAL
I418	N358	V298	ASN	ASN	THR	ASP
D419	A359	Q298	MET	LYS	ARG	CYS
I420	F360	R299	GLN	SER	GLY	GLY
S421	N361	C300	ASP	LEU	LEU	PHE
S422	F362	I301	PRO	LEU	ALA	GLU
Y423	D363	A302	MET	LEU	PHE	HIS
I424	M364	L303	GLU	LYS	GLN	PRO
E425	P365	Q305	ILE	HIS	ILE	SER
GLN	E366	L306	VAL	ILE	SER	GLU
ARG	D367	L307	ASP	GLU	VAL	GLN
	S368	V308	THR	ASP	PHE	ILE
	D369	E309	K256	GLU	GLN	PRO
	T370	Q310	L257	CYS	LYS	ALA
	Y371	N311	T258	ASP	TYR	ALA
	L372	F312	L259	LYS	MET	ILE
	H373	P313	H260	MET	PRO	LEU
	R374	A314	G261	LEU	ASN	GLY
	V375	I315	L262	GLU	VAL	MET
	A376	A316	Q263	GLN	LYS	ASP
	R377	I317	Q264	LEU	VAL	VAL
	A378	H318	Q265	ASP	ALA	LEU
	G379	R319	Y266	MET	VAL	CYS
	F380	G320	Y267	ARG	PHE	GLN
	R381	M321	L269	ASP	PHE	LYS
	G382	P322	K268	VAL	GLY	SER
	T383	Q323	D270	GLN	LEU	GLY
	K384	E324	K271	ILE	ILE	MET
	G385	E325	N272	PHE	LYS	GLY
	L386	R326	E273	ARG	THR	LYS
	A387	L327	K274	GLU	ASP	ALA
	I388	S328	N275	GLN	LEU	ASP
	T389	R329	R276	LEU	SER	
	F390	Y330	K277	GLU	GLY	
	V391	Q331		ILE	ILE	
	S392	F332		GLY	LYS	
	D393	K334		PHE	LYS	
	E394	D335		ARG	THR	
	N395	D336		MET	ASP	
	D396	Q337				
	A397					

- Molecule 7: Spliceosome RNA helicase DDX39B



K398	R338	L278	THR	GLU	VAL	ASP	ALA	GLY	THR	GLY
I399	R339	F279	PRO	GLU	PHE	GLN	THR	GLY	PRO	PRO
L400	I340	D280	GLU	VAL	VAL	GLN	VAL	VAL	TYR	GLY
N401	L341	L281	LYS	LYS	ALA	ALA	THR	ILE	SER	LYS
D402	V342	L282	GLN	ASN	THR	LEU	LEU	HIS	SER	GLY
V403	A343	D283	VAL	CYS	GLN	GLN	GLN	SER	ALA	ALA
Q404	T344	V284	MET	PRO	GLN	GLN	GLN	GLY	SER	TRP
D405	N345	L285	PHE	HIS	LEU	LEU	PHE	PHE	HIS	HIS
R406	L346	E286	SER	ILE	GLU	ARG	ASP	ARG	PRO	PRO
F407	F347	F287	ALA	VAL	VAL	VAL	VAL	ASP	GLN	GLN
E408	G348	N288	THR	VAL	THR	THR	PHE	PHE	PHE	PHE
V409	R349	Q289	SER	GLY	THR	GLY	GLY	LEU	GLY	GLY
N410	G350	V290	LYS	PRO	PRO	PRO	VAL	LYS	LEU	LEU
I411	M351	V291	ILE	ARG	ILE	ARG	SER	GLU	VAL	VAL
S412	D352	I292	PRO	PRO	LEU	LEU	VAL	LEU	LEU	LEU
E413	I353	F293	VAL	VAL	ALA	ALA	VAL	ARG	GLN	PHE
L414	E354	V294	CYS	CYS	LEU	LEU	MET	VAL	ARG	GLY
P415	R355	K295	ARG	ARG	ALA	ALA	CYS	ILE	ILE	PRO
D416	V356	S296	LYS	LYS	ARG	ASN	HIS	VAL	VAL	MET
E417	N357	V297	PHE	PHE	ASN	THR	THR	ASP	ALA	ALA
I418	I358	Q298	MET	GLN	LYS	ARG	ARG	CYS	GLY	GLY
D419	A359	R299	ASN	ASN	LEU	LEU	GLU	GLY	ASN	ASN
I420	F360	C300	PRO	ASN	ALA	ALA	ALA	GLU	VAL	VAL
S421	N361	I301	MET	LEU	PHE	PHE	GLN	PRO	ASN	ASN
S422	Y362	A302	ILE	HIS	ILE	HIS	ILE	SER	GLU	GLU
Y423	D363	L303	PHE	ILE	SER	LYS	VAL	VAL	LEU	LEU
I424	M364	A304	ASN	HIS	GLU	GLU	GLN	GLN	ASP	ASP
E425	P365	Q305	ASP	PHE	TYR	TYR	GLU	HIS	TYR	TYR
GLN	E366	L306	GLU	ILE	GLU	GLU	ARG	CYS	GLU	ASP
THR	D367	L307	THR	LEU	ARG	ARG	VAL	ILE	ASP	ASP
ARG	S368	V308	K256	ASP	PHE	PHE	ALA	ILE	ASP	ASP
	D369	E309	L257	GLU	SER	SER	SER	GLN	PRO	GLU
	T370	Q310	T258	CYS	LYS	LYS	TYR	GLU	GLU	VAL
	Y371	N311	H260	LYS	MET	LYS	MET	ILE	ALA	THR
	L372	F312	L259	MET	PRO	PRO	PRO	LEU	ALA	ALA
	H373	P313	G261	LEU	ASN	ASN	ASN	GLY	GLY	ALA
	R374	A314	L262	GLN	VAL	VAL	VAL	MET	ASP	GLY
	V375	I315	Q263	LEU	VAL	VAL	VAL	VAL	VAL	GLY
	A376	A316	Q264	ASP	ALA	ALA	ALA	LEU	LEU	GLY
	R377	I317	Y265	MET	VAL	VAL	VAL	CYS	ALA	ALA
	A378	H318	Y266	ARG	PHE	PHE	PHE	GLN	GLU	GLU
	G379	R319	V267	ARG	ARG	ARG	ALA	LYS	LYS	LYS
	R380	G320	K268	VAL	VAL	VAL	GLY	GLY	GLY	LYS
	F381	M321	L269	GLU	SER	SER	SER	MET	ASP	LYS
	G382	F322	K270	ILE	ILE	ILE	ILE	GLY	GLY	VAL
	T383	Q323	D271	PHE	PHE	PHE	LYS	LYS	THR	LYS
	K384	E324	N272	ARG	MET	MET	LYS	THR	ALA	GLY
	G385	E325	E273	GLN	GLY	GLY	GLY	GLY	GLY	GLY
	L386	R326	K274	LEU	LEU	LEU	SER	MET	ASP	VAL
	A387	L327	N275	GLU	GLU	GLU	SER	GLY	GLY	VAL
	I388	S328	R276	ILE	ILE	ILE	ILE	ILE	ILE	VAL
	T389	R329	K277	MET	MET	MET	ASP	LYS	THR	LYS
	F390	Y330		ARG	ARG	ARG	ASP	LYS	ALA	GLY
	V391	Q331								
	S392	Q332								
	D393	F333								
	E394	K334								
	N395	D335								
	D396	F336								
	A397	Q337								

X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19	X20	X21	X22	X23	X24	X25	X26	X27	X28	X29	X30	X31	X32	X33	X34	X35	X36	X37	X38	X39	X40	X41	X42	X43	X44	X45	X46	X47	X48	X49	X50	X51	X52	X53	X54	X55	X56	X57	X58	X59	X60	X61	X62	X63	X64	X65	X66	X67	X68	X69	X70	X71	X72	X73	X74	X75	X76	X77	X78	X79	X80	X81	X82	X83	X84	X85	X86	X87	X88	X89	X90	X91	X92	X93	X94	X95	X96	X97	X98	X99	X100
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	195098	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.274	Depositor
Minimum map value	-0.103	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.05257	Depositor
Map size (\AA)	589.60004, 589.60004, 589.60004	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	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	0.27	0/2204	0.45	0/2974
1	I	0.29	0/2268	0.48	0/3062
1	a	0.27	0/2204	0.45	0/2974
1	i	0.29	0/2269	0.48	0/3063
2	B	0.27	0/4741	0.45	2/6440 (0.0%)
2	J	0.28	0/4743	0.44	1/6444 (0.0%)
2	b	0.28	0/4741	0.45	2/6440 (0.0%)
2	j	0.27	0/4736	0.44	1/6435 (0.0%)
3	C	0.29	0/2404	0.56	0/3265
3	K	0.29	0/2404	0.56	0/3265
3	c	0.29	0/2404	0.56	0/3265
3	k	0.29	0/2404	0.56	0/3265
4	E	0.30	0/3754	0.49	0/5118
4	M	0.29	0/4301	0.49	0/5827
4	e	0.30	0/3661	0.48	0/4991
4	m	0.29	0/4301	0.49	0/5827
5	F	0.32	0/2666	0.57	0/3623
5	N	0.32	0/2666	0.56	0/3623
5	f	0.32	0/2596	0.57	0/3524
5	n	0.32	0/2666	0.57	0/3623
6	G	0.24	0/757	0.27	0/1052
6	O	0.27	0/1094	0.39	0/1476
6	g	0.24	0/757	0.27	0/1052
6	o	0.27	0/1094	0.39	0/1476
7	H	0.26	0/1421	0.44	0/1915
7	P	0.26	0/1421	0.44	0/1915
7	h	0.26	0/1421	0.44	0/1915
7	p	0.26	0/1421	0.44	0/1915
All	All	0.29	0/73519	0.49	6/99764 (0.0%)

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
2	B	0	2
2	J	0	2
2	b	0	2
2	j	0	2
3	C	0	2
3	K	0	2
3	c	0	2
3	k	0	2
4	M	0	1
4	m	0	1
All	All	0	18

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	278	LEU	CA-CB-CG	6.95	131.29	115.30
2	B	278	LEU	CA-CB-CG	6.92	131.21	115.30
2	J	610	ASP	CB-CG-OD2	5.33	123.09	118.30
2	B	610	ASP	CB-CG-OD2	5.17	122.96	118.30
2	b	610	ASP	CB-CG-OD2	5.17	122.96	118.30
2	j	610	ASP	CB-CG-OD2	5.16	122.95	118.30

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	562	LYS	Peptide
2	B	590	TYR	Peptide
3	C	319	ARG	Peptide
3	C	86	LYS	Peptide
2	J	562	LYS	Peptide
2	J	590	TYR	Peptide
3	K	319	ARG	Peptide
3	K	86	LYS	Peptide
4	M	660	ARG	Peptide
2	b	562	LYS	Peptide
2	b	590	TYR	Peptide
3	c	319	ARG	Peptide
3	c	86	LYS	Peptide
2	j	562	LYS	Peptide
2	j	590	TYR	Peptide

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Mol	Chain	Res	Type	Group
3	k	319	ARG	Peptide
3	k	86	LYS	Peptide
4	m	660	ARG	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [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	248/711 (35%)	239 (96%)	8 (3%)	1 (0%)	34	66
1	I	255/711 (36%)	241 (94%)	12 (5%)	2 (1%)	19	51
1	a	248/711 (35%)	240 (97%)	7 (3%)	1 (0%)	34	66
1	i	255/711 (36%)	241 (94%)	12 (5%)	2 (1%)	19	51
2	B	644/1226 (52%)	625 (97%)	19 (3%)	0	100	100
2	J	645/1226 (53%)	623 (97%)	22 (3%)	0	100	100
2	b	644/1226 (52%)	625 (97%)	19 (3%)	0	100	100
2	j	645/1226 (53%)	623 (97%)	22 (3%)	0	100	100
3	C	298/395 (75%)	273 (92%)	24 (8%)	1 (0%)	41	71
3	K	298/395 (75%)	273 (92%)	24 (8%)	1 (0%)	41	71
3	c	298/395 (75%)	273 (92%)	24 (8%)	1 (0%)	41	71
3	k	298/395 (75%)	273 (92%)	24 (8%)	1 (0%)	41	71
4	E	505/683 (74%)	479 (95%)	26 (5%)	0	100	100
4	M	529/683 (78%)	503 (95%)	26 (5%)	0	100	100
4	e	492/683 (72%)	470 (96%)	22 (4%)	0	100	100
4	m	529/683 (78%)	503 (95%)	26 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	F	335/341 (98%)	305 (91%)	29 (9%)	1 (0%)	41	71
5	N	335/341 (98%)	307 (92%)	27 (8%)	1 (0%)	41	71
5	f	325/341 (95%)	298 (92%)	26 (8%)	1 (0%)	41	71
5	n	335/341 (98%)	305 (91%)	29 (9%)	1 (0%)	41	71
6	G	147/204 (72%)	147 (100%)	0	0	100	100
6	O	151/204 (74%)	151 (100%)	0	0	100	100
6	g	147/204 (72%)	147 (100%)	0	0	100	100
6	o	151/204 (74%)	151 (100%)	0	0	100	100
7	H	168/451 (37%)	165 (98%)	3 (2%)	0	100	100
7	P	168/451 (37%)	165 (98%)	3 (2%)	0	100	100
7	h	168/451 (37%)	165 (98%)	3 (2%)	0	100	100
7	p	168/451 (37%)	165 (98%)	3 (2%)	0	100	100
All	All	9429/16044 (59%)	8975 (95%)	440 (5%)	14 (0%)	54	81

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	66	ASP
1	I	308	MET
3	K	66	ASP
3	c	66	ASP
1	i	308	MET
3	k	66	ASP
1	I	105	PRO
1	i	105	PRO
1	A	105	PRO
1	a	105	PRO
5	F	239	PRO
5	N	239	PRO
5	f	239	PRO
5	n	239	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	236/646 (36%)	236 (100%)	0	100	100
1	I	240/646 (37%)	240 (100%)	0	100	100
1	a	236/646 (36%)	236 (100%)	0	100	100
1	i	241/646 (37%)	241 (100%)	0	100	100
2	B	345/1105 (31%)	342 (99%)	3 (1%)	78	87
2	J	345/1105 (31%)	342 (99%)	3 (1%)	78	87
2	b	345/1105 (31%)	342 (99%)	3 (1%)	78	87
2	j	344/1105 (31%)	341 (99%)	3 (1%)	78	87
3	C	252/330 (76%)	252 (100%)	0	100	100
3	K	252/330 (76%)	252 (100%)	0	100	100
3	c	252/330 (76%)	252 (100%)	0	100	100
3	k	252/330 (76%)	252 (100%)	0	100	100
4	E	321/615 (52%)	320 (100%)	1 (0%)	92	96
4	M	424/615 (69%)	424 (100%)	0	100	100
4	e	311/615 (51%)	311 (100%)	0	100	100
4	m	424/615 (69%)	424 (100%)	0	100	100
5	F	284/287 (99%)	283 (100%)	1 (0%)	91	95
5	N	284/287 (99%)	283 (100%)	1 (0%)	91	95
5	f	276/287 (96%)	275 (100%)	1 (0%)	91	95
5	n	284/287 (99%)	283 (100%)	1 (0%)	91	95
6	O	85/184 (46%)	85 (100%)	0	100	100
6	o	85/184 (46%)	85 (100%)	0	100	100
7	H	153/400 (38%)	153 (100%)	0	100	100
7	P	153/400 (38%)	153 (100%)	0	100	100
7	h	153/400 (38%)	153 (100%)	0	100	100
7	p	153/400 (38%)	153 (100%)	0	100	100
All	All	6730/13900 (48%)	6713 (100%)	17 (0%)	92	96

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	204	ASN
2	B	560	ASN
2	B	657	LEU
4	E	524	THR
5	F	177	ARG
2	J	204	ASN
2	J	560	ASN
2	J	657	LEU
5	N	177	ARG
2	b	204	ASN
2	b	560	ASN
2	b	657	LEU
5	f	177	ARG
2	j	204	ASN
2	j	560	ASN
2	j	657	LEU
5	n	177	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	GLN
1	A	320	HIS
1	A	380	HIS
2	B	204	ASN
2	B	224	HIS
2	B	518	GLN
2	B	560	ASN
2	B	588	GLN
2	B	608	ASN
2	B	667	GLN
3	C	316	HIS
4	E	274	GLN
4	E	369	ASN
4	E	465	HIS
4	E	492	GLN
4	E	675	HIS
5	F	130	ASN
5	F	149	GLN
5	F	172	HIS
5	F	261	GLN
7	H	288	ASN
7	H	357	ASN

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Mol	Chain	Res	Type
7	H	404	GLN
1	I	242	GLN
2	J	204	ASN
2	J	224	HIS
2	J	518	GLN
2	J	560	ASN
2	J	588	GLN
2	J	608	ASN
2	J	667	GLN
3	K	316	HIS
4	M	369	ASN
4	M	492	GLN
4	M	675	HIS
5	N	149	GLN
5	N	172	HIS
5	N	261	GLN
7	P	288	ASN
7	P	357	ASN
7	P	404	GLN
1	a	242	GLN
1	a	320	HIS
1	a	380	HIS
2	b	204	ASN
2	b	224	HIS
2	b	518	GLN
2	b	560	ASN
2	b	588	GLN
2	b	608	ASN
2	b	667	GLN
3	c	316	HIS
4	e	274	GLN
4	e	369	ASN
4	e	492	GLN
4	e	675	HIS
5	f	130	ASN
5	f	172	HIS
5	f	261	GLN
7	h	288	ASN
7	h	357	ASN
7	h	404	GLN
1	i	242	GLN
2	j	204	ASN

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Mol	Chain	Res	Type
2	j	224	HIS
2	j	518	GLN
2	j	560	ASN
2	j	588	GLN
2	j	608	ASN
2	j	667	GLN
3	k	316	HIS
4	m	369	ASN
4	m	492	GLN
4	m	675	HIS
5	n	149	GLN
5	n	172	HIS
5	n	261	GLN
7	p	288	ASN
7	p	357	ASN
7	p	404	GLN

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 monosaccharides 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	X	1
8	x	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	20:UNK	C	50:UNK	N	23.23
1	x	20:UNK	C	50:UNK	N	23.23

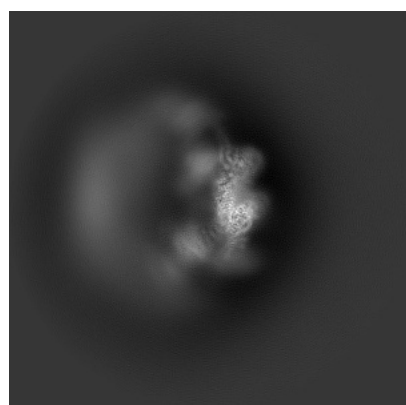
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11857. These allow visual inspection of the internal detail of the map and identification of artifacts.

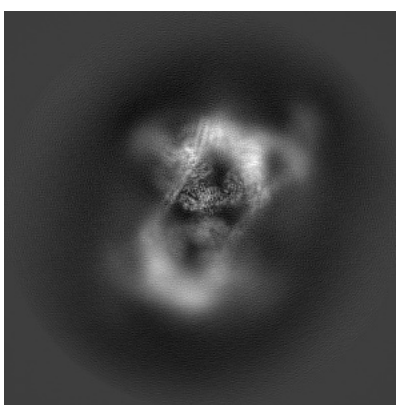
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

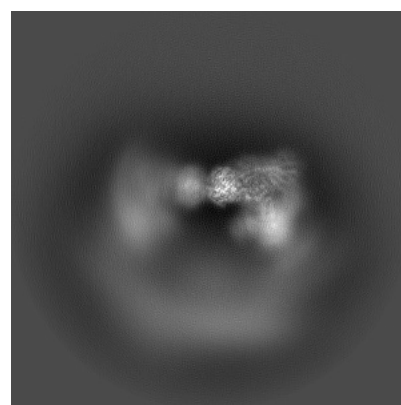
6.1.1 Primary map



X



Y

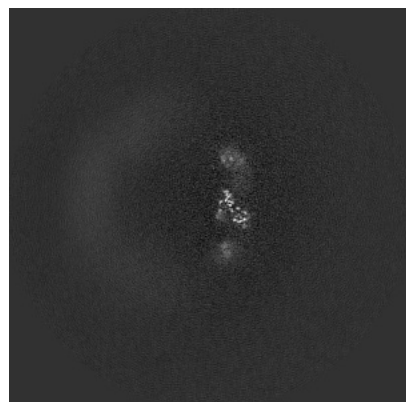


Z

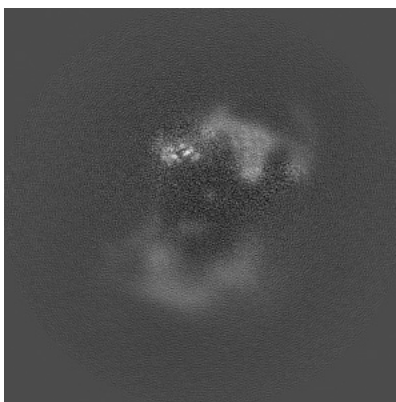
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

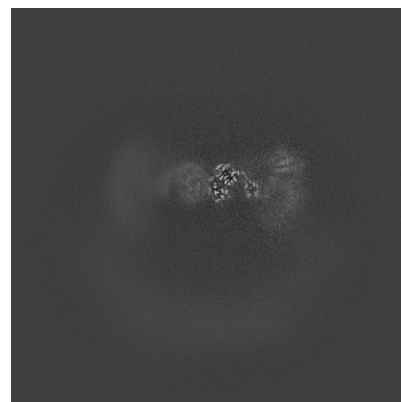
6.2.1 Primary map



X Index: 220



Y Index: 220

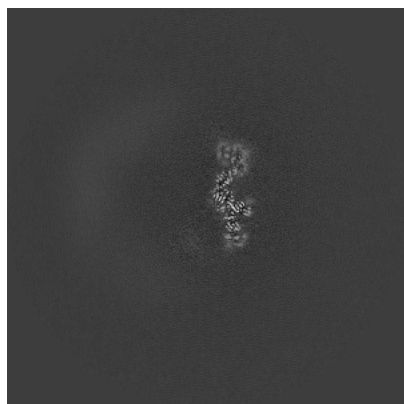


Z Index: 220

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

6.3 Largest variance slices [i](#)

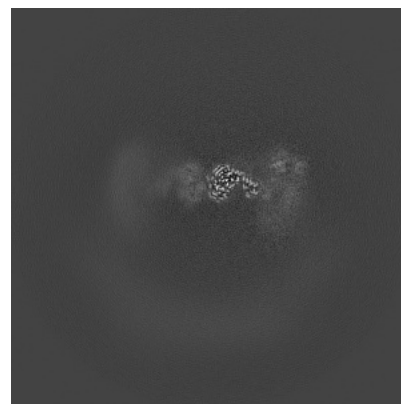
6.3.1 Primary map



X Index: 236



Y Index: 243



Z Index: 218

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05257. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

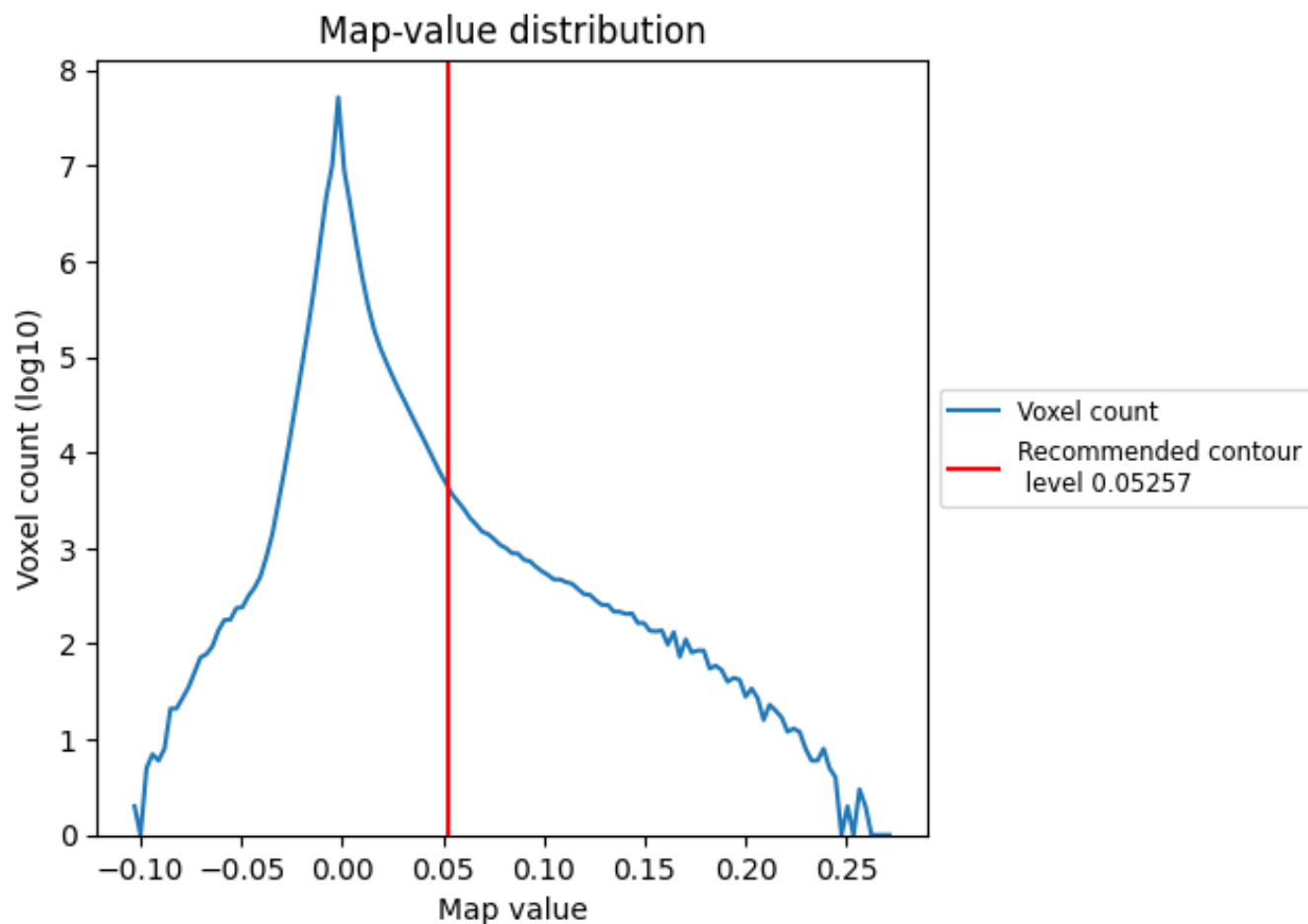
6.5 Mask visualisation

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

7 Map analysis [i](#)

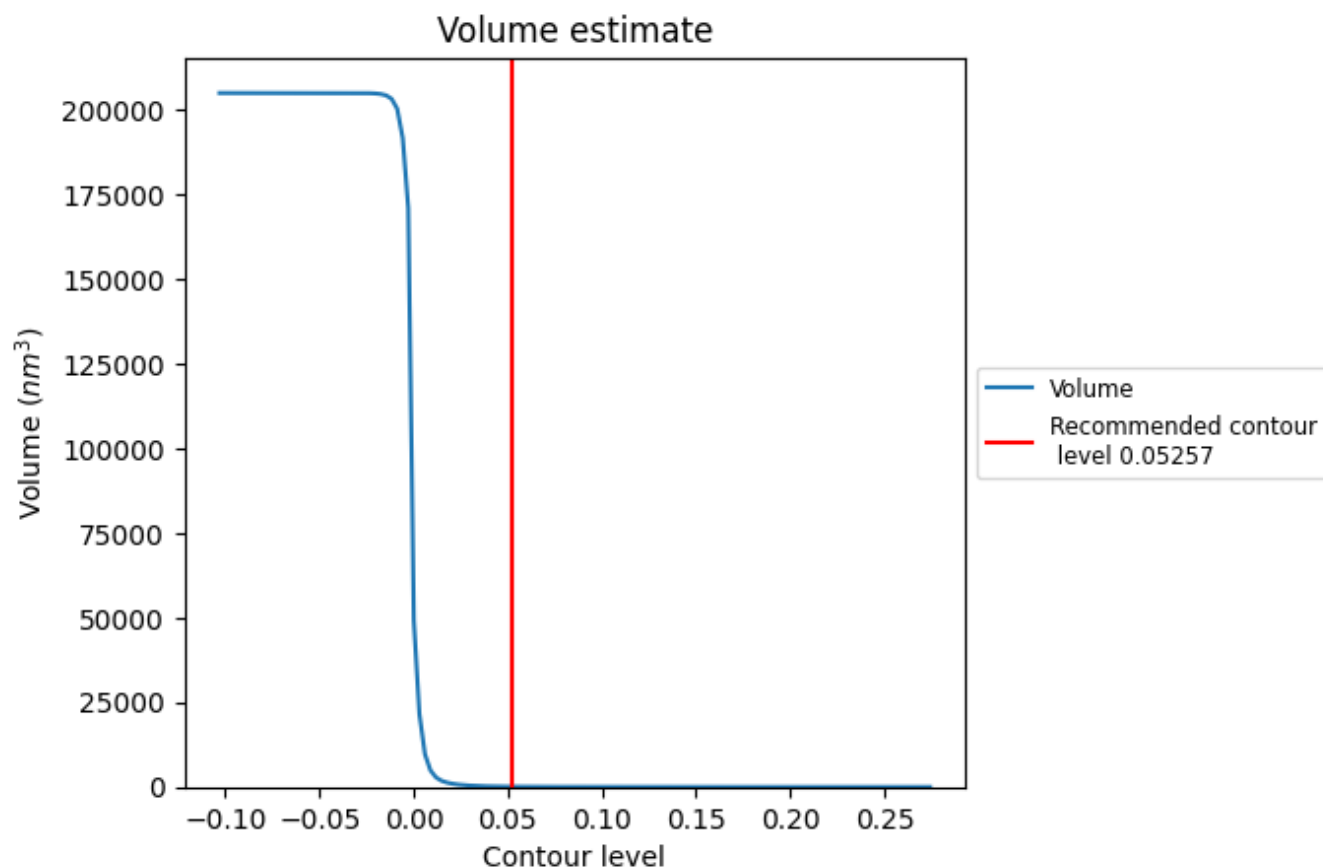
This section contains the results of statistical analysis of the map.

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.

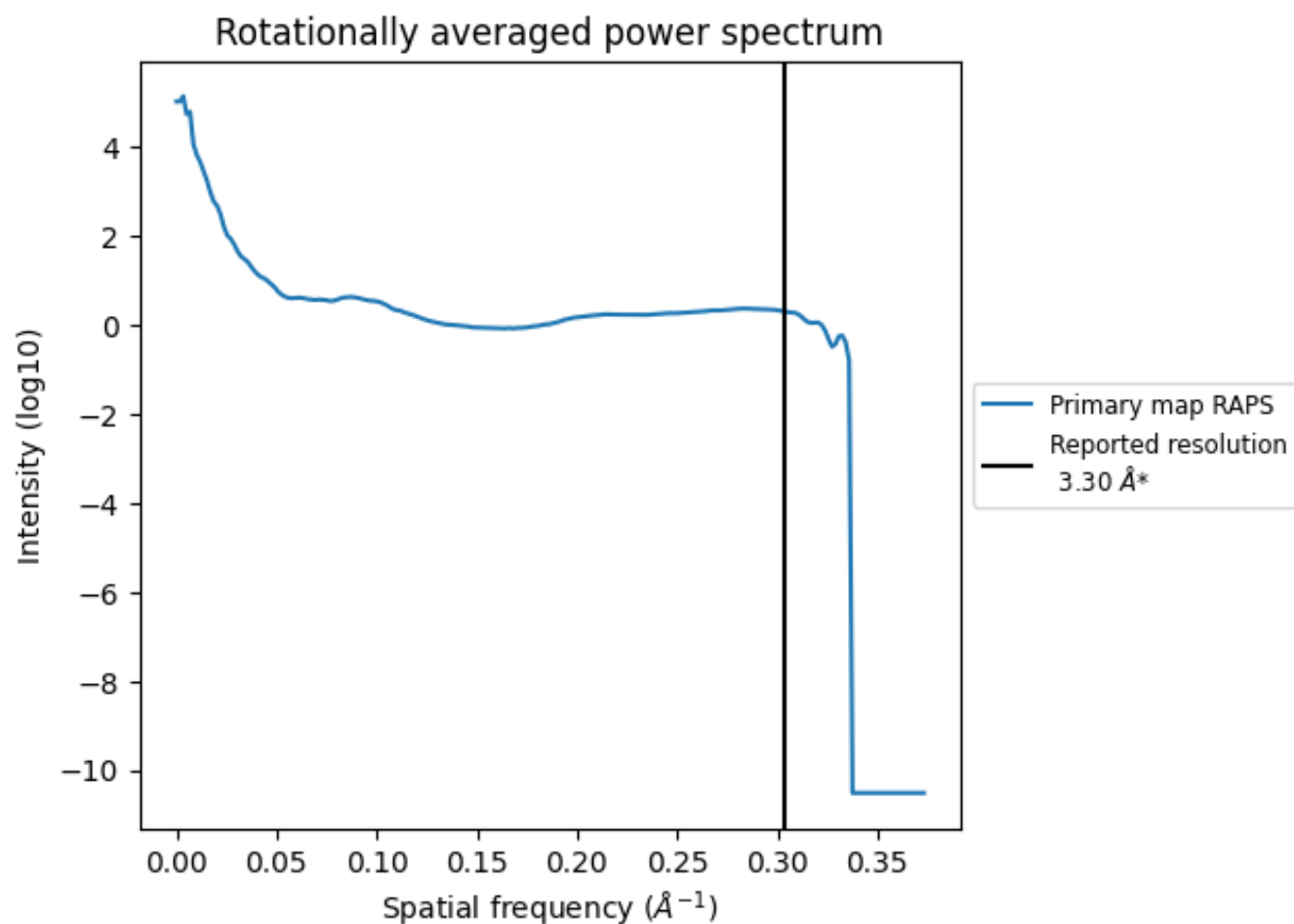
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 81 nm^3 ; this corresponds to an approximate mass of 73 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 0.303 Å⁻¹

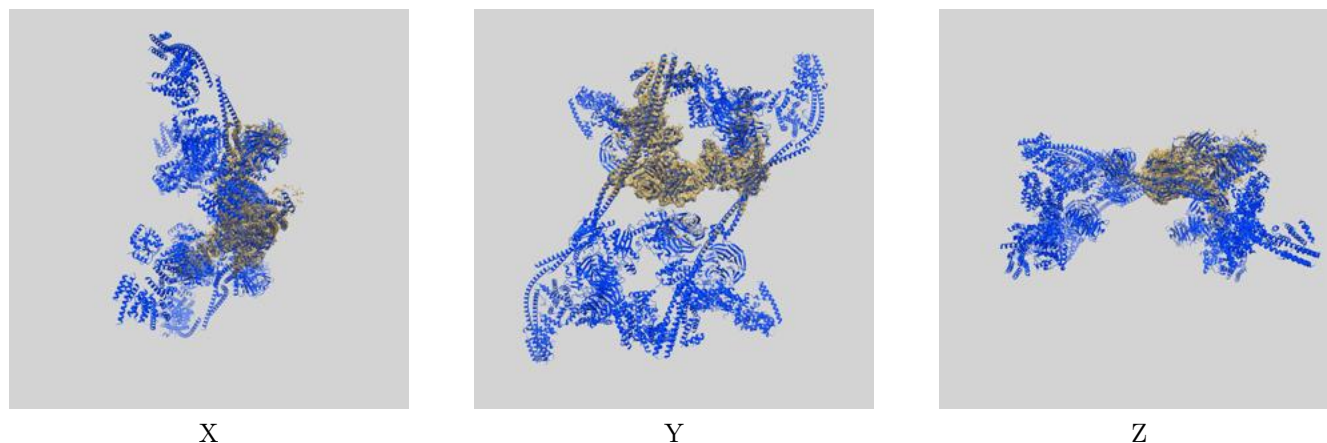
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

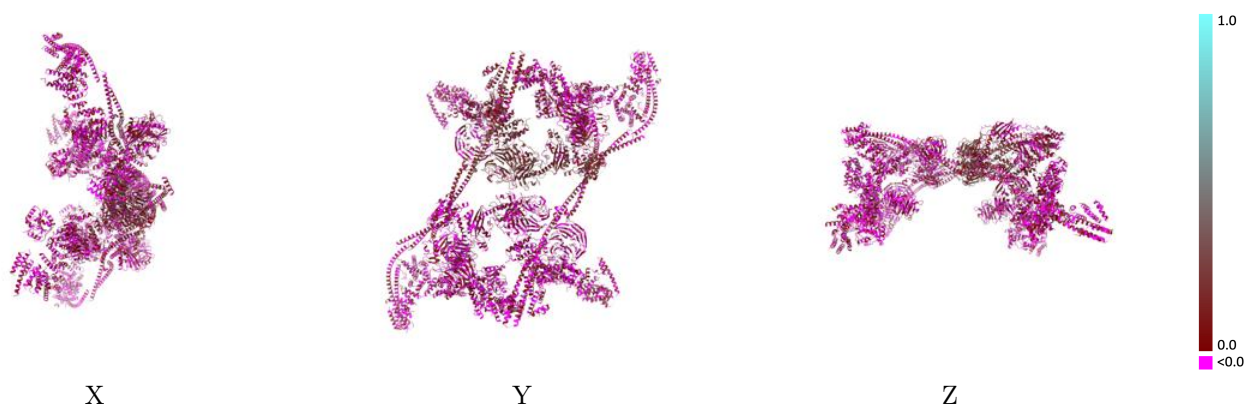
This section contains information regarding the fit between EMDB map EMD-11857 and PDB model 7APK. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



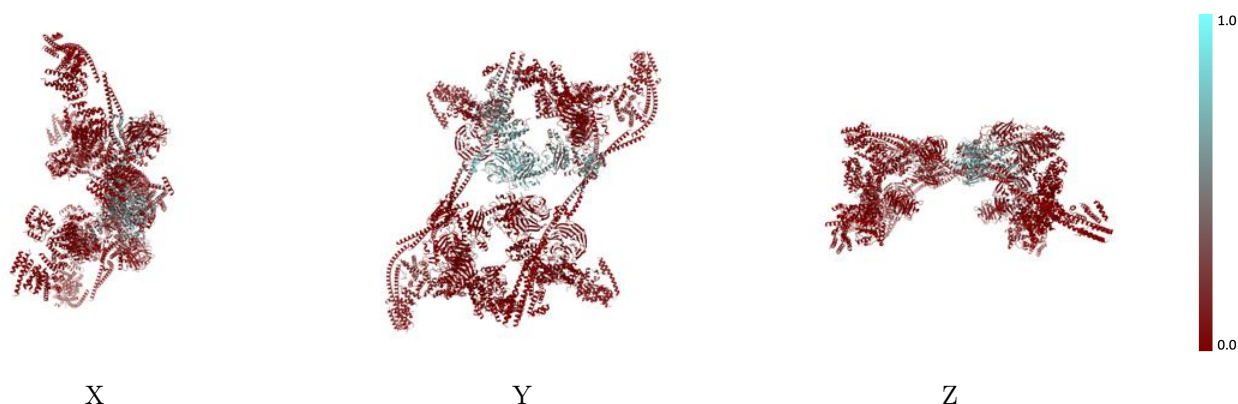
The images above show the 3D surface view of the map at the recommended contour level 0.05257 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



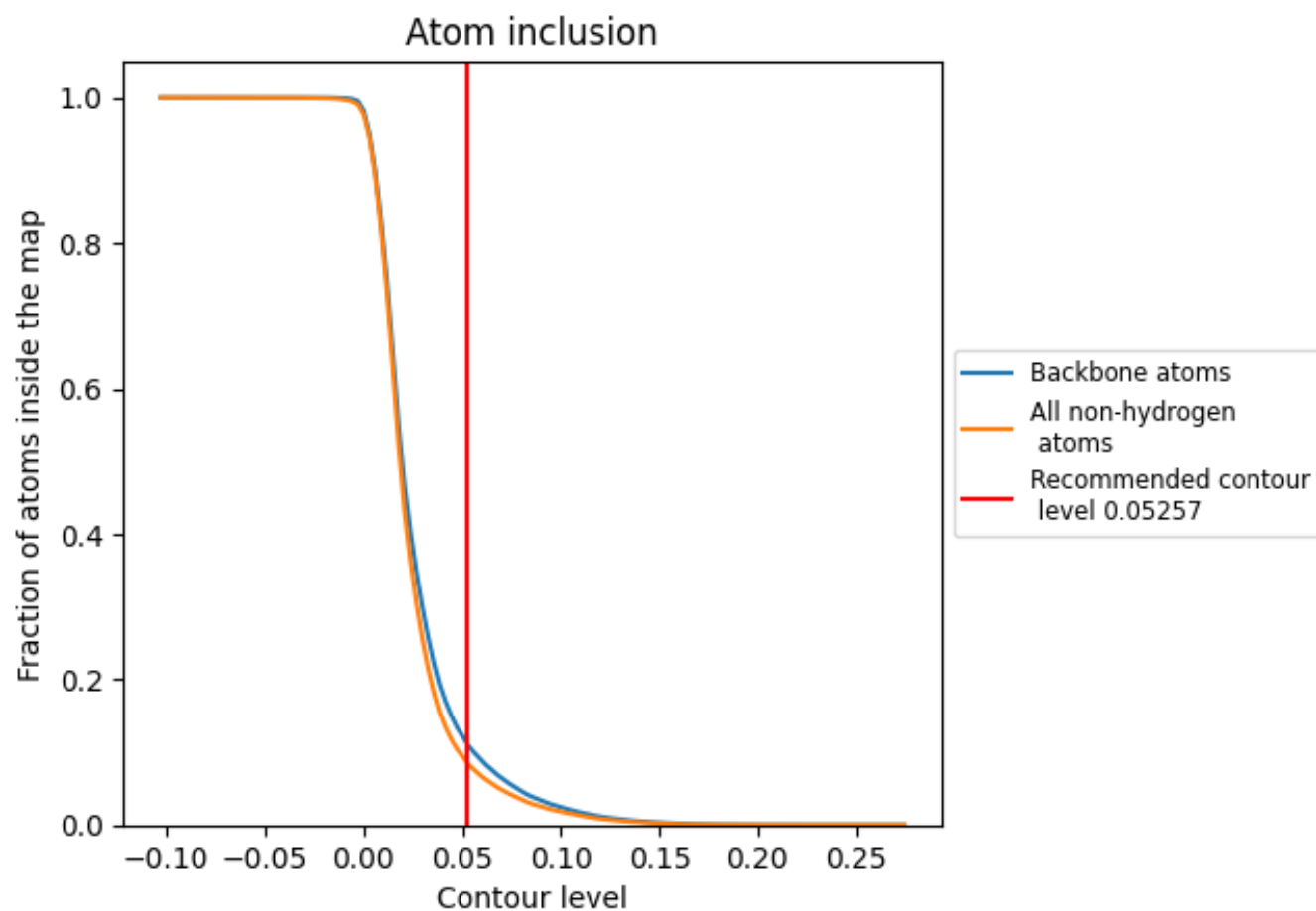
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05257).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 11% of all backbone atoms, 9% 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 (0.05257) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0856	 0.0510
A	 0.0000	 0.0080
B	 0.0015	 0.0250
C	 0.0009	 0.0280
E	 0.4377	 0.1750
F	 0.5723	 0.2190
G	 0.0724	 0.0750
H	 0.0000	 0.0090
I	 0.0000	 0.0160
J	 0.0000	 0.0050
K	 0.0000	 0.0090
M	 0.1568	 0.0950
N	 0.0235	 0.0450
O	 0.0901	 0.0620
P	 0.0000	 -0.0090
X	 0.0000	 0.0070
a	 0.0000	 0.0080
b	 0.0000	 0.0090
c	 0.0000	 0.0010
e	 0.0025	 0.0340
f	 0.0137	 0.0160
g	 0.0000	 0.0560
h	 0.0000	 0.0210
i	 0.3651	 0.1810
j	 0.1096	 0.0780
k	 0.0086	 0.0270
m	 0.1064	 0.0600
n	 0.0000	 0.0190
o	 0.3593	 0.1470
p	 0.0000	 -0.0050
x	 0.0541	 0.0840

