



## wwPDB EM Validation Summary Report i

Apr 23, 2024 – 08:43 am BST

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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 i symbol.

The types of validation reports are described at  
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

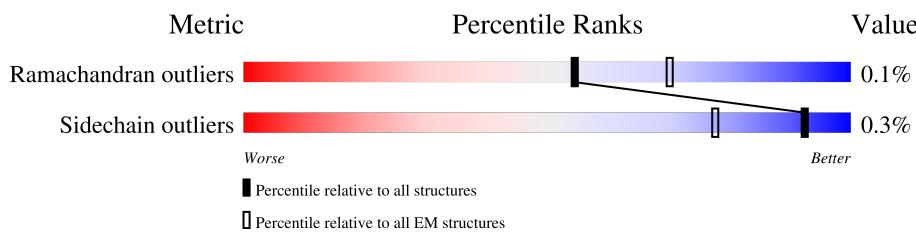
EMDB validation analysis : 0.0.1.dev92  
MolProbit : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 1 Overall quality at a glance

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

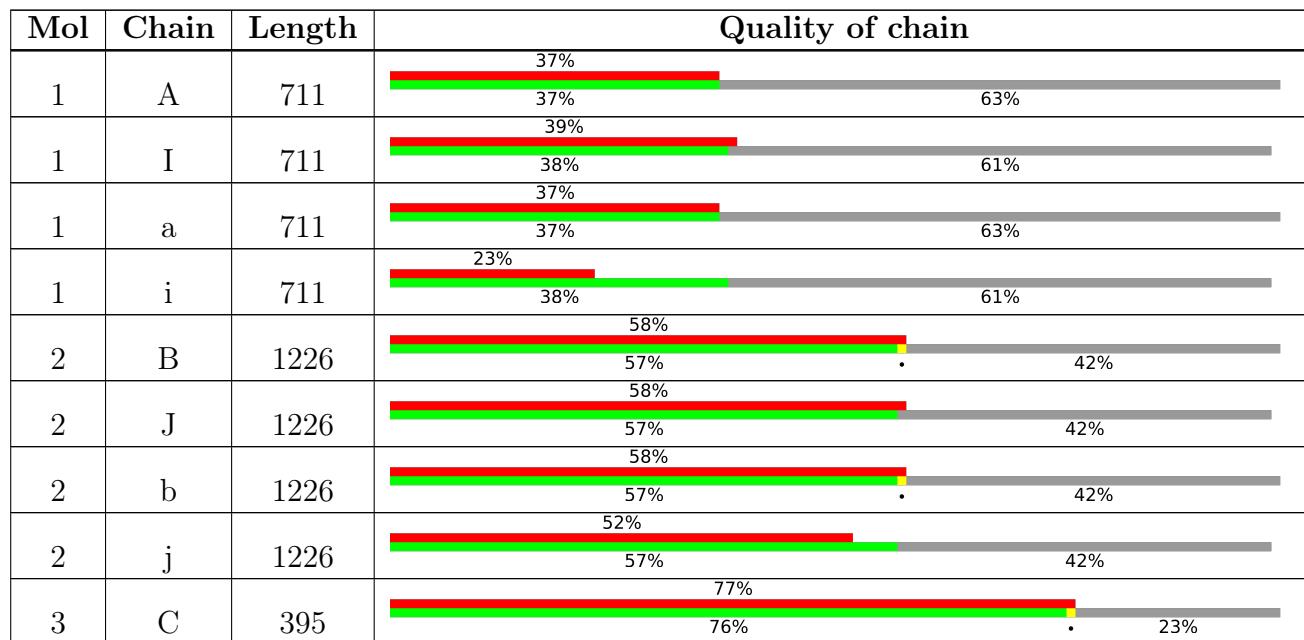
The reported resolution of this entry is 3.30 Å.

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 <=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.



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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%	38%	62%
7	P	451	38%	38%	62%
7	h	451	38%	38%	62%
7	p	451	38%	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 2165	N 1402	O 357	S 397	9	0
1	I	275	Total	C 2228	N 1441	O 368	S 410	9	0
1	a	266	Total	C 2165	N 1402	O 357	S 397	9	0
1	i	275	Total	C 2229	N 1441	O 368	S 411	9	0

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		
			2349	1482	407	446	14	0	0
3	K	304	Total	C	N	O	S		
			2349	1482	407	446	14	0	0
3	c	304	Total	C	N	O	S		
			2349	1482	407	446	14	0	0
3	k	304	Total	C	N	O	S		
			2349	1482	407	446	14	0	0

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
			Total	C	N	O	S		
7	H	170	1398	888	245	261	4	0	0
7	P	170	1398	888	245	261	4	0	0
7	h	170	1398	888	245	261	4	0	0
7	p	170	1398	888	245	261	4	0	0

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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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

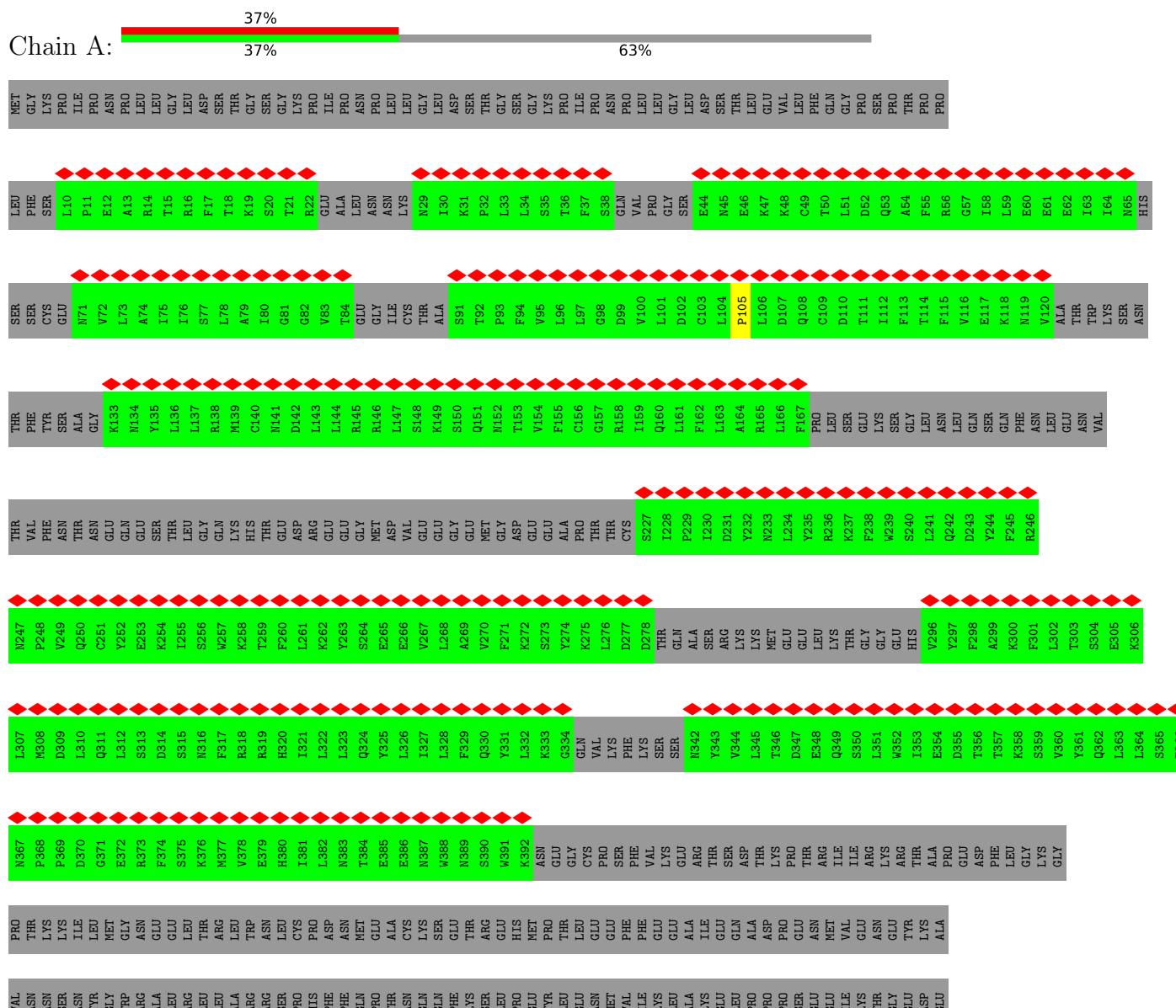
- Molecule 8 is a protein called THOC2 anchor (putative).

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

### 3 Residue-property plots

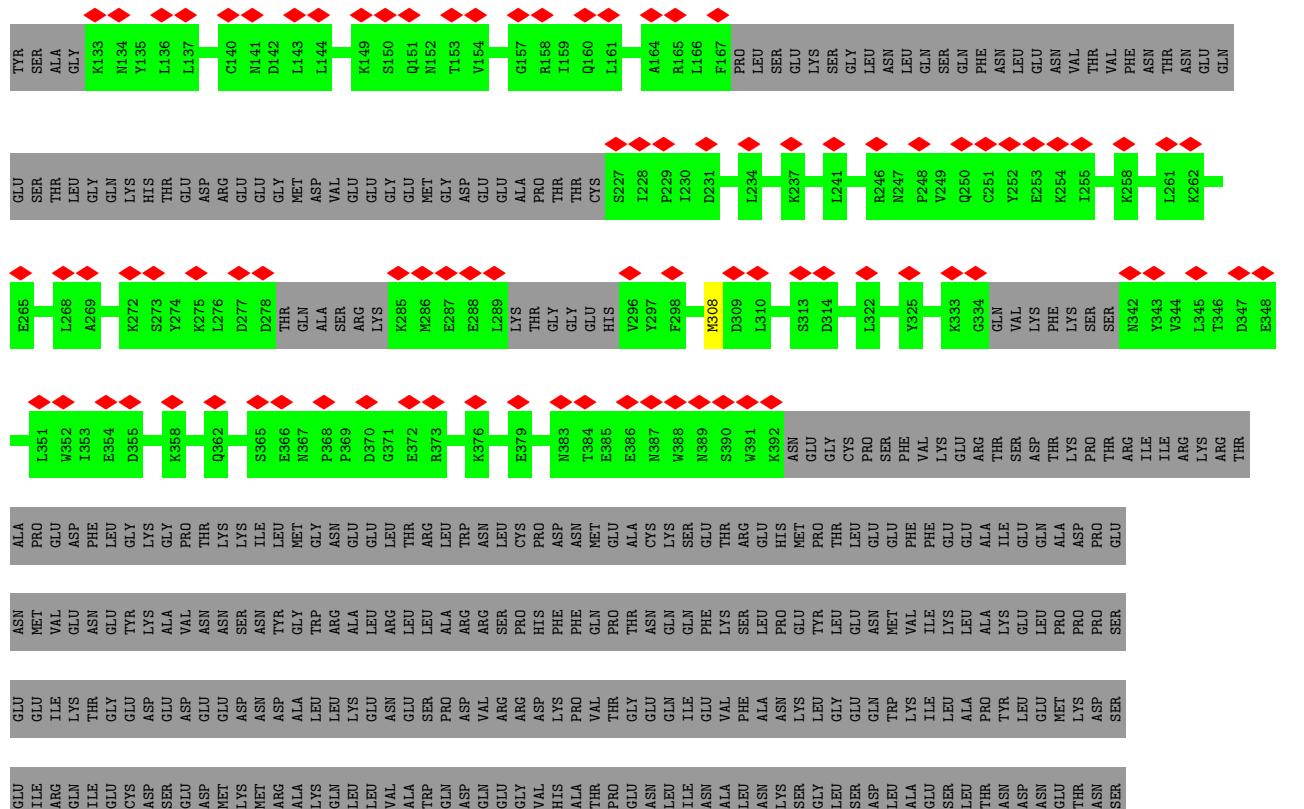
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: THO complex subunit 1

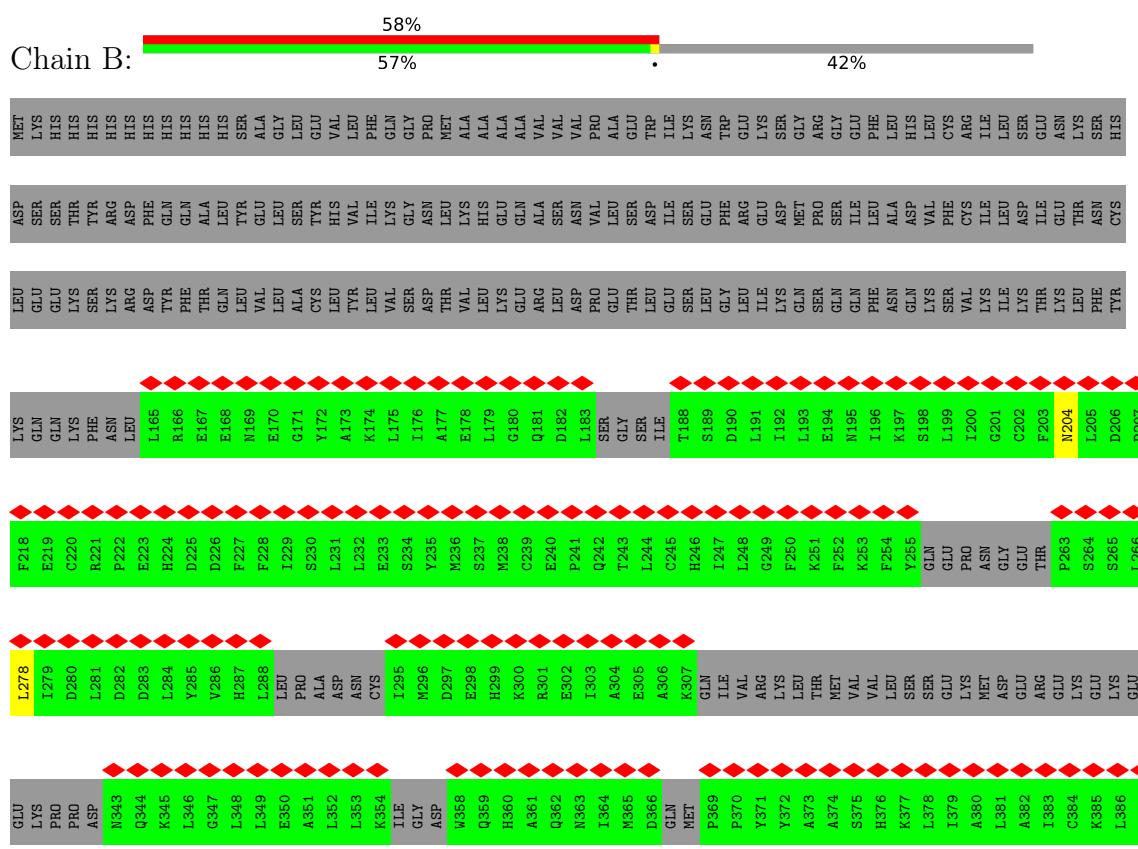






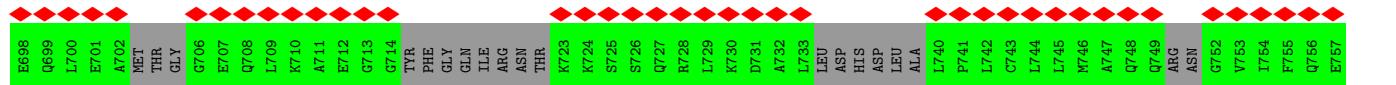
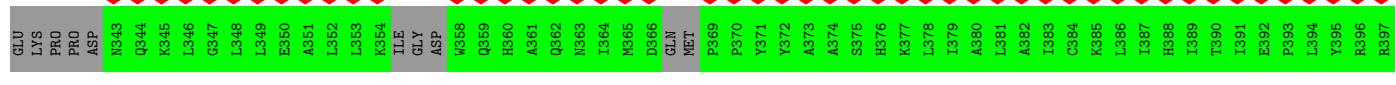
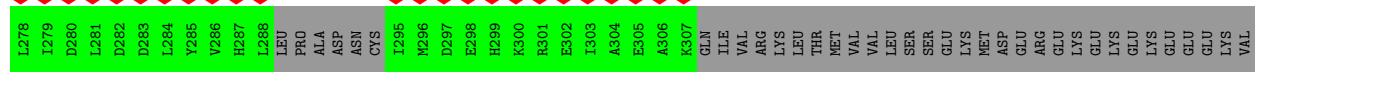
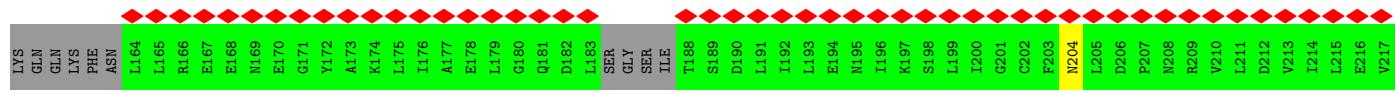
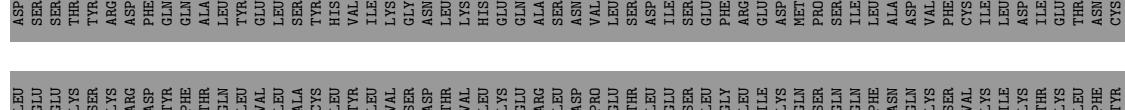


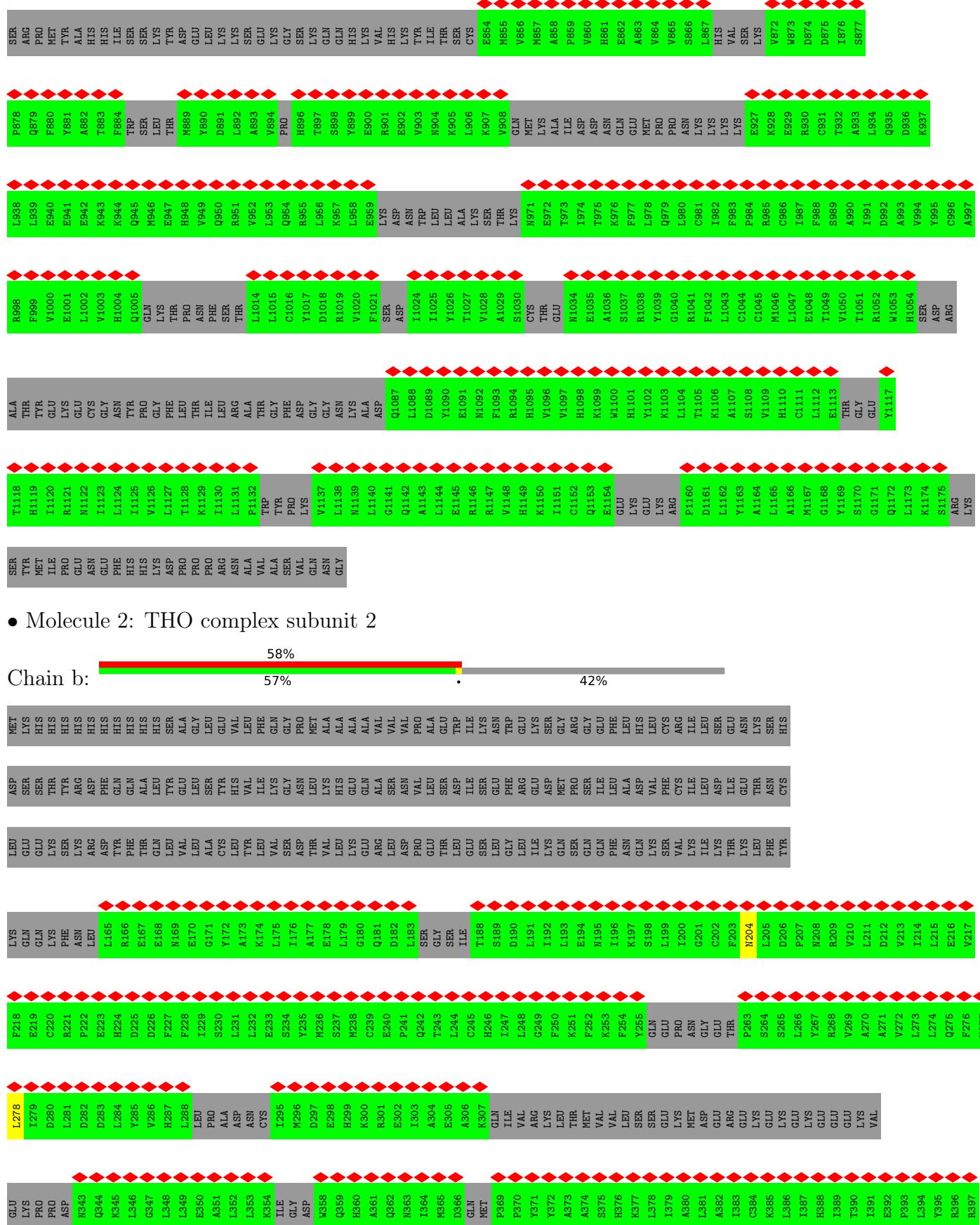
### • Molecule 2: THO complex subunit 2





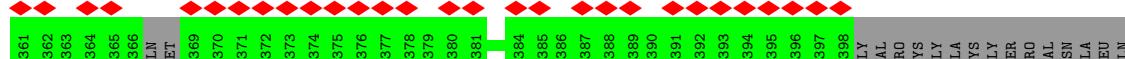
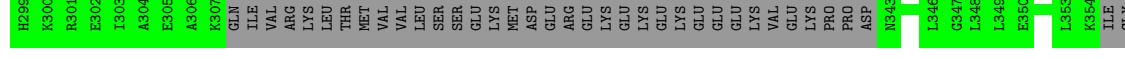
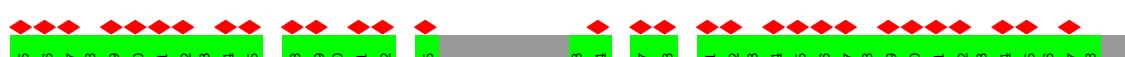
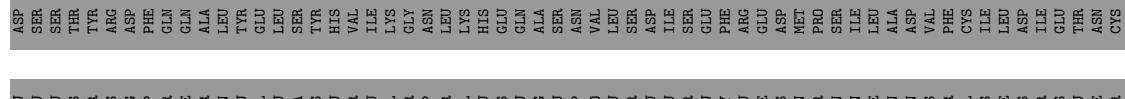
- Molecule 2: THO complex subunit 2



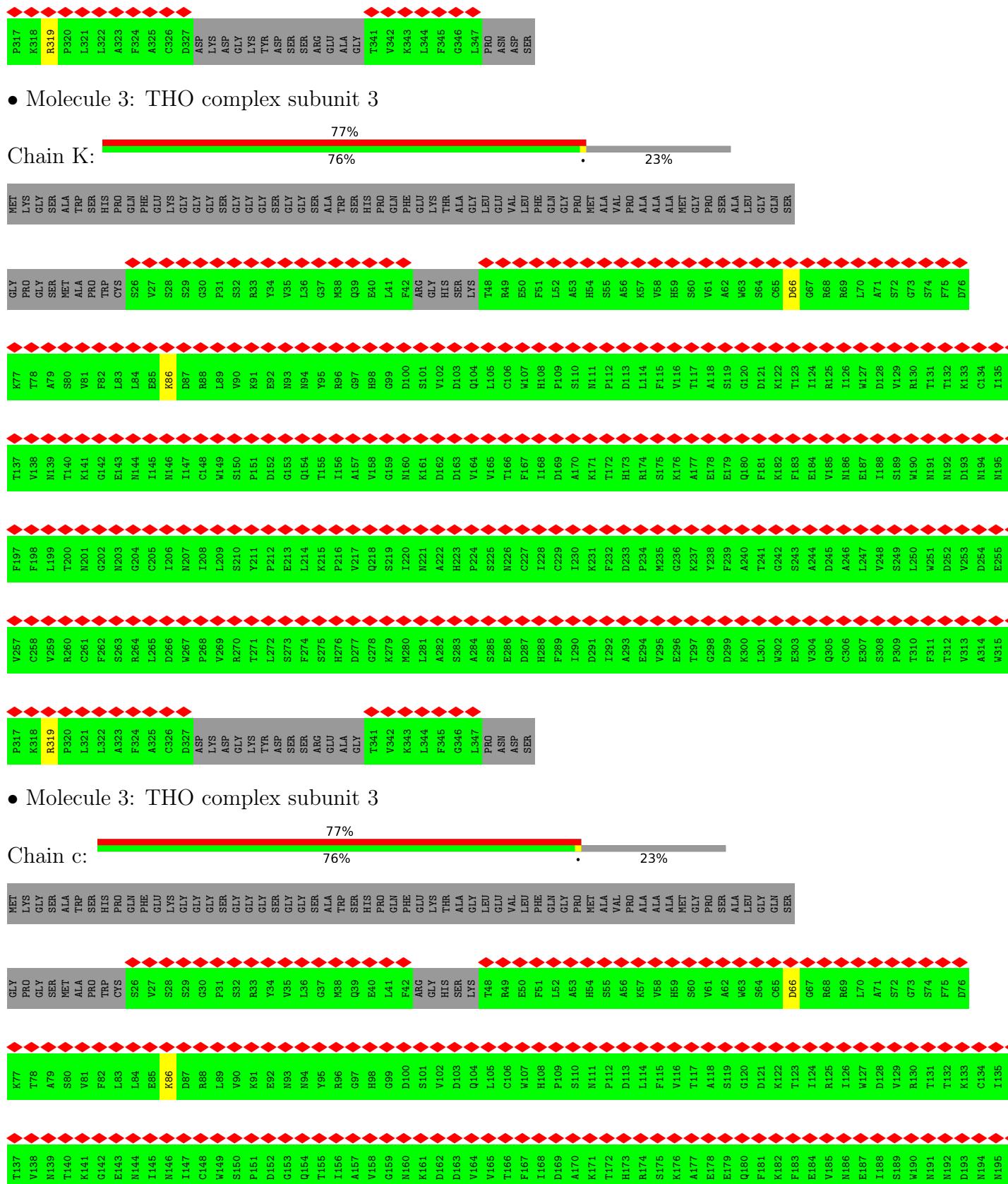




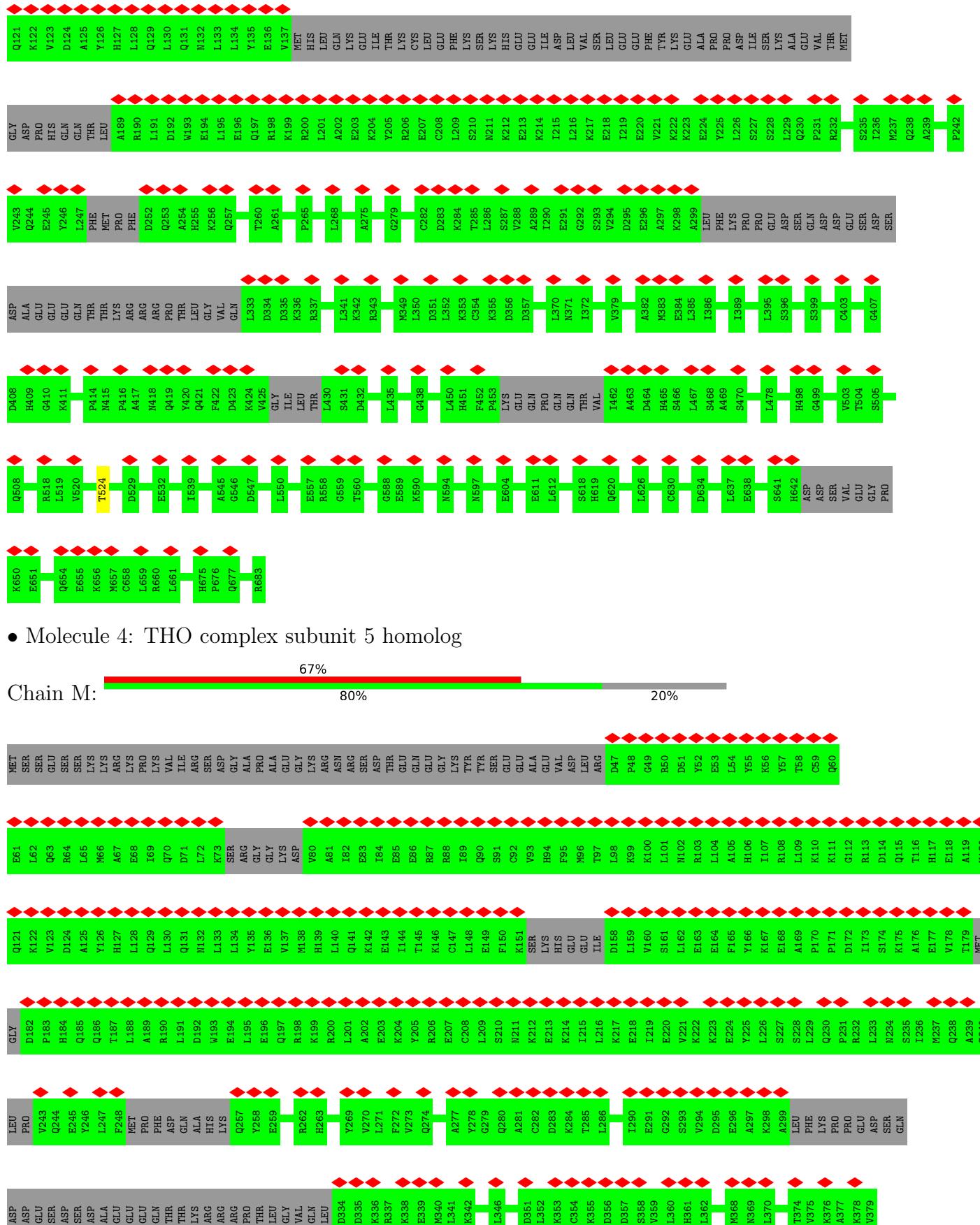
- Molecule 2: THO complex subunit 2



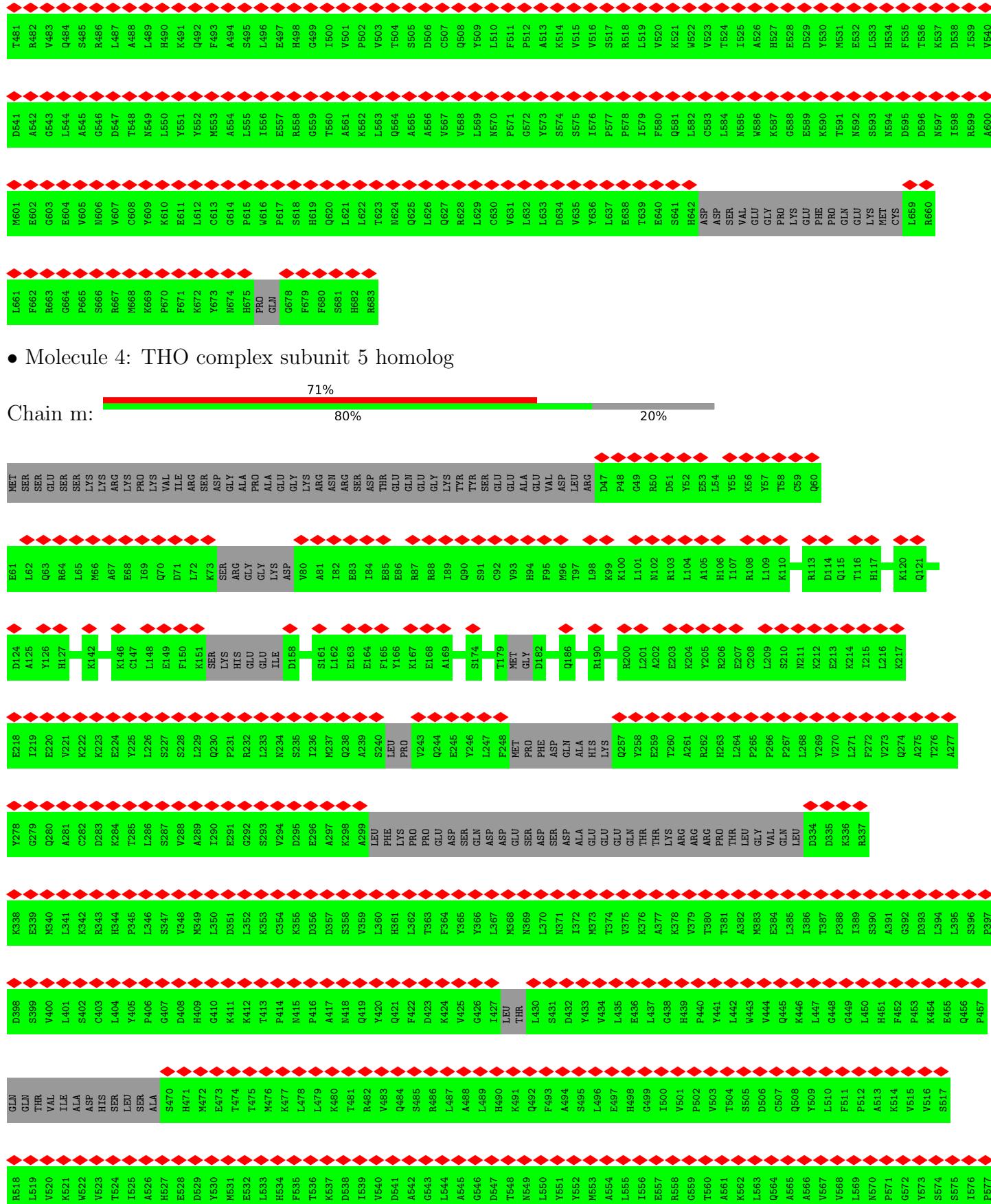






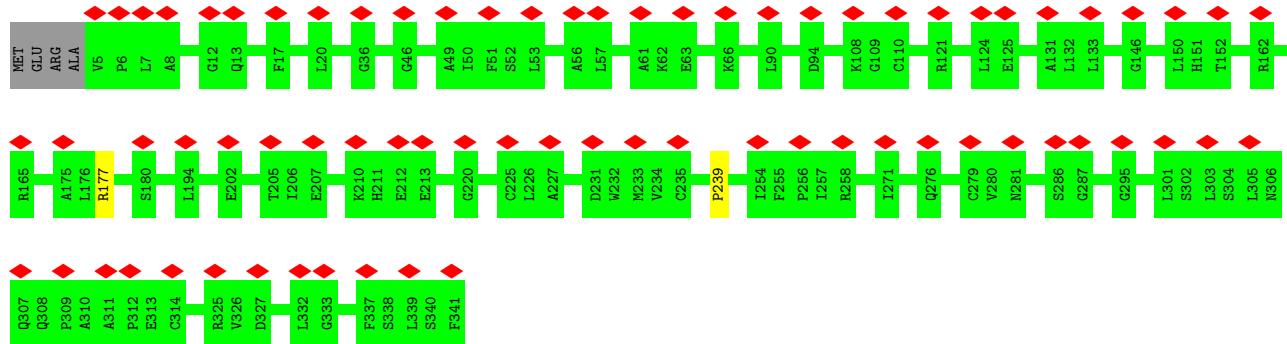




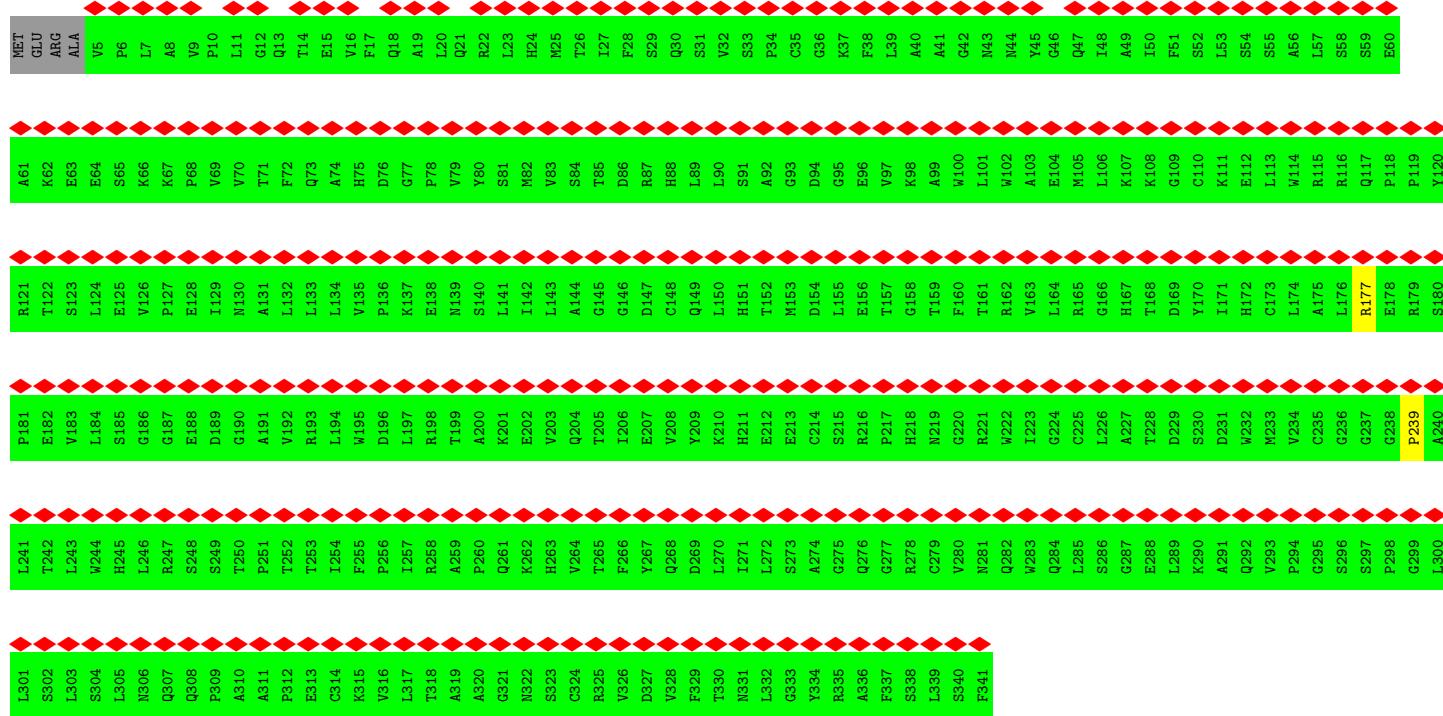


P578	E638	V5	E64	E64	S641	Q581
S302	E182	V6	P6	P6	H642	A59
L303	T122	P6	P6	ASP	ASP	
L243	T123	P7	P7	ASP	ASP	
L241	R121	P8	P8	SER	SER	
L301	R175	P9	P9	VAL	VAL	
	L176	P10	P10	GLU	GLU	
	R177	P11	P11	ARG	GLY	
		P12	P12	PRO	PRO	
		P13	P13	LYS	LYS	
		P14	P14	GLU	GLU	
		P15	P15	MET	MET	
		P16	P16	PHE	PHE	
		P17	P17	PRO	PRO	
		P18	P18	K586	K586	
		P19	P19	T591	T591	
		P20	P20	N592	N592	
		P21	P21	G588	G588	
		P22	P22	E589	E589	
		P23	P23	N584	N584	
		P24	P24	D585	D585	
		P25	P25	D586	D586	
		P26	P26	R660	R660	
		P27	P27	R661	R661	
		P28	P28	I588	I588	
		P29	P29	F682	F682	
		P30	P30	R667	R667	
		P31	P31	E604	E604	
		P32	P32	G664	G664	
		P33	P33	P665	P665	
		P34	P34	E602	E602	
		P35	P35	S666	S666	
		P36	P36	G603	G603	
		P37	P37	R668	R668	
		P38	P38	V605	V605	
		P39	P39	N674	N674	
		P40	P40	E611	E611	
		P41	P41	H675	H675	
		P42	P42	P670	P670	
		P43	P43	P677	P677	
		P44	P44	C608	C608	
		P45	P45	K672	K672	
		P46	P46	Y609	Y609	
		P47	P47	Y673	Y673	
		P48	P48	K614	K614	
		P49	P49	G578	G578	
		P50	P50	P615	P615	
		P51	P51	F679	F679	
		P52	P52	W616	W616	
		P53	P53	F680	F680	
		P54	P54	P676	P676	
		P55	P55	S681	S681	
		P56	P56	H682	H682	
		P57	P57	R683	R683	
		P58	P58	T623	T623	
		P59	P59	N694	N694	
		P60	P60	Q625	Q625	
		P61	P61	L626	L626	
		P62	P62	V631	V631	
		P63	P63	L632	L632	
		P64	P64	R638	R638	
		P65	P65	L639	L639	
		P66	P66	C630	C630	
		P67	P67	V631	V631	
		P68	P68	L632	L632	
		P69	P69	R638	R638	
		P70	P70	L639	L639	
		P71	P71	C646	C646	
		P72	P72	Y120	Y120	
		P73	P73	P239	P239	
		P74	P74			
		P75	P75			
		P76	P76			
		P77	P77			
		P78	P78			
		P79	P79			
		P80	P80			
		P81	P81			
		P82	P82			
		P83	P83			
		P84	P84			
		P85	P85			
		P86	P86			
		P87	P87			
		P88	P88			
		P89	P89			
		P90	P90			
		P91	P91			
		P92	P92			
		P93	P93			
		P94	P94			
		P95	P95			
		P96	P96			
		P97	P97			
		P98	P98			
		P99	P99			
		P100	P100			
		P101	P101			
		P102	P102			
		P103	P103			
		P104	P104			
		P105	P105			
		P106	P106			
		P107	P107			
		P108	P108			
		P109	P109			
		P110	P110			
		P111	P111			
		P112	P112			
		P113	P113			
		P114	P114			
		P115	P115			
		P116	P116			
		P117	P117			
		P118	P118			
		P119	P119			
		P120	P120			

• Molecule 5: THO complex subunit 6 homolog



• Molecule 5: THO complex subunit 6 homolog



• Molecule 5: THO complex subunit 6 homolog

Chain f:

MET	A61	L241	V5	E64	E64	V6
GLU	K62	T242	S65	S65	S65	P6
ARG	E63	L243	V183	V183	V183	L7
ALA						

ARG	P181	L241	V5	E64	E64	V6
THR	E182	T242	S65	S65	S65	P6
SER	E183	L243	V183	V183	V183	L7
LEU						

P189	S249	D189	I129	V69	P10	E64	V6
P309							
A310	T250	G190	N330	V70	L11	K67	A8
A311	P251	A191	A131	T71	G12	E247	G18
P312	T252	V192	L132	F72	Q13	Q307	L129

P181	L241	V5	E64	E64	E64	V6
C314	I254	L194	L334	A74	E15	E15
K315	F255	W195	V135	H75	V16	V16
V316	P256	D196	P336	D76	F17	F17
L317	I257	L197	K337	G77	Q18	Q18
T318	R258	R193	L133	Q73	T14	T14
A319	A259	T199	M339	V79	L20	L20
A320	P260	A200	S340	Y80	Q21	Q21
G321	Q261	K201	L141	S81	R22	R22
N322	K262	E202	I142	M82	L23	L23

P181	L241	V5	E64	E64	E64	V6
C323	H263	V203	L143	V83	H24	H24
C324	V264	Q204	A144	S94	M25	M25
R325	T265	T205	G145	T85	T26	T26
V326	F266	I206	G146	D86	F266	F266
D327	Y267	E207	D47	R87	D267	D267
V328	Q268	V208	C148	H88	S29	S29
F329	D269	Y209	Q149	L89	Q30	Q30
T330	L270	K210	L550	L90	S31	S31
N331	I271	H551	S91	V32	N331	N331

P181	L241	V5	E64	E64	E64	V6
C323	S273	E213	M553	G93	P34	P34
Y334	A274	C214	D554	D94	D94	C35
R335	G275	S215	L555	G95	G95	G36
A336	Q276	R216	E156	E96	A336	E96
F337	G277	P217	T157	V97	F337	V97
S338	R278	H218	G158	K98	S338	S338
L339	C279	I219	T159	A99	L339	L339

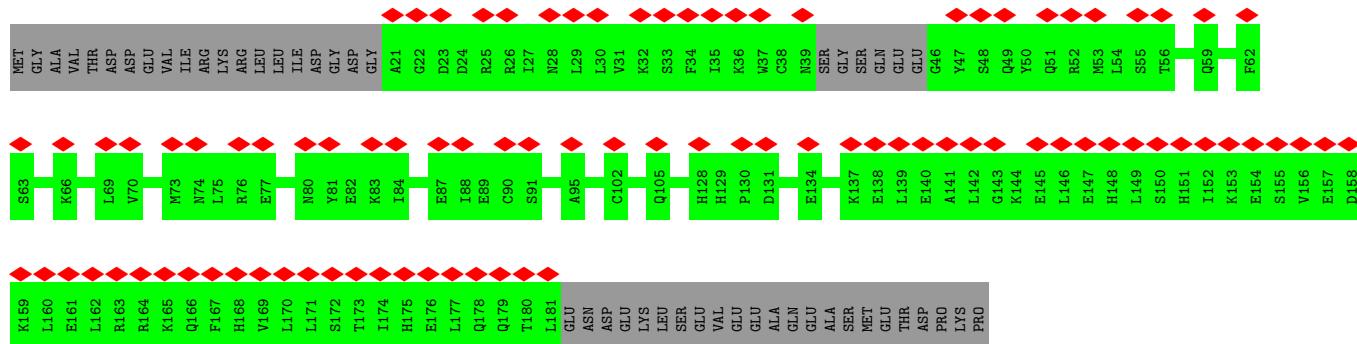
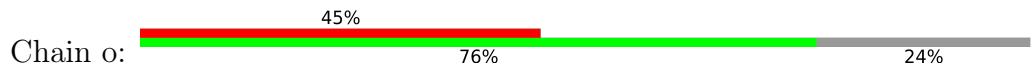
P181	L241	V5	E64	E64	E64	V6
C323	A291	D231	I171	K111	S52	S52
W283	Q292	W232	H172	C173	E112	L53
L289	E288	T223	T168	K108	A103	N44

- Molecule 5: THO complex subunit 6 homolog

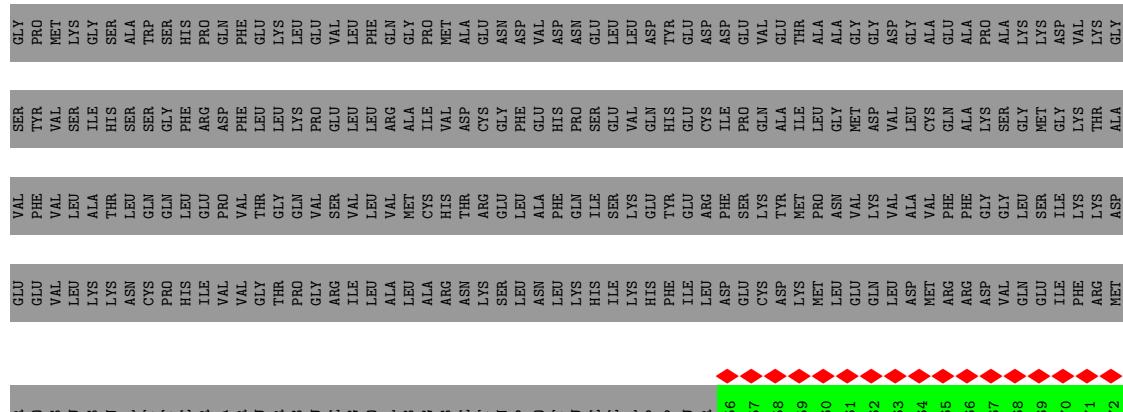
PRO	P239	R177	G237	Q117	E178	Y120
TYR	A240	P118	C238	P119	P118	E60



- Molecule 6: THO complex subunit 7 homolog



- Molecule 7: Spliceosome RNA helicase DDX39B

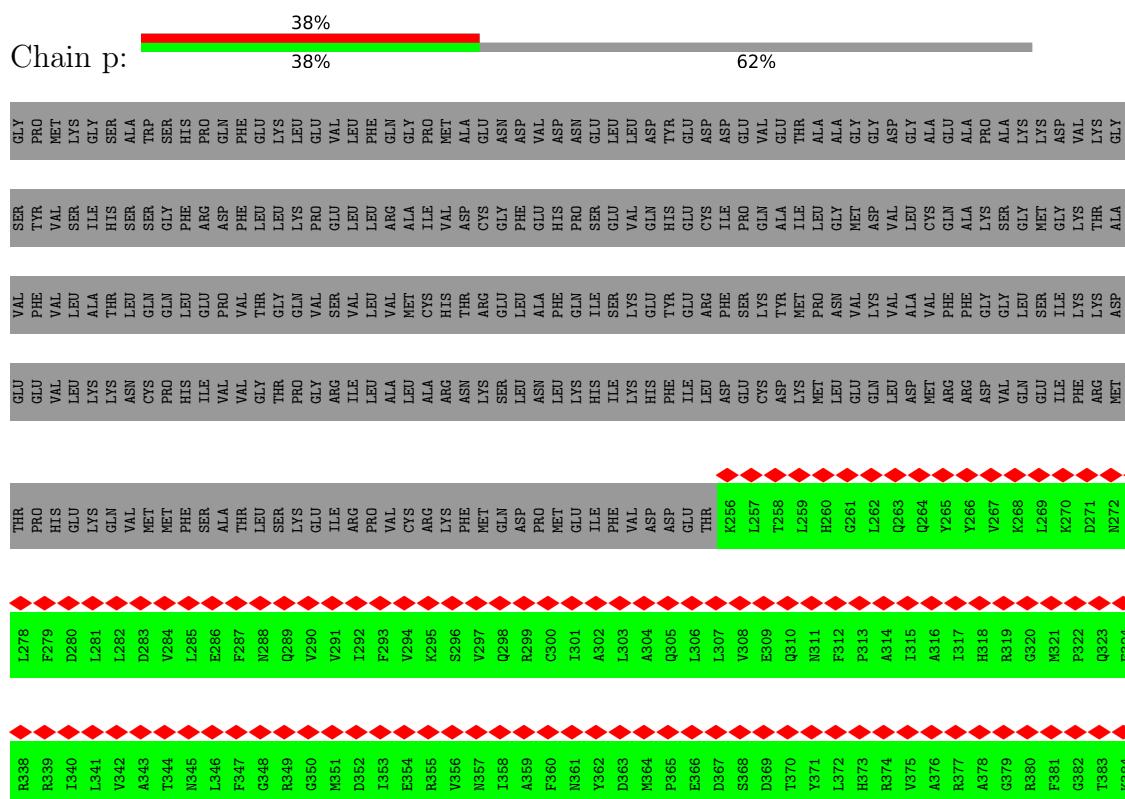


- Molecule 7: Spliceosome RNA helicase DDX39B





- Molecule 7: Spliceosome RNA helicase DDX39B



- Molecule 8: THOC2 anchor (putative)



- Molecule 8: THOC2 anchor (putative)



## 4 Experimental information (i)

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 (Å)	589.60004, 589.60004, 589.60004	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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.

The worst 5 of 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

There are no chirality outliers.

5 of 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

## 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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

5 of 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

### 5.3.2 Protein sidechains [\(i\)](#)

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	j	560	ASN
5	n	177	ARG
2	J	657	LEU
5	N	177	ARG
2	b	204	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
5	f	172	HIS
4	m	369	ASN
7	h	288	ASN
2	j	518	GLN
5	n	172	HIS

### 5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [\(i\)](#)

There are no 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 [\(i\)](#)

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

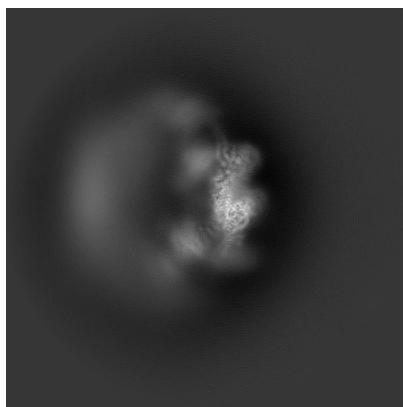
## 6 Map visualisation (i)

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.

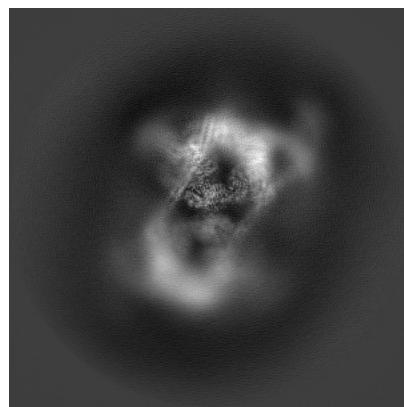
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections (i)

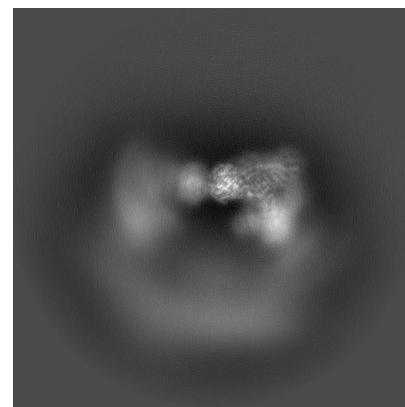
#### 6.1.1 Primary map



X



Y

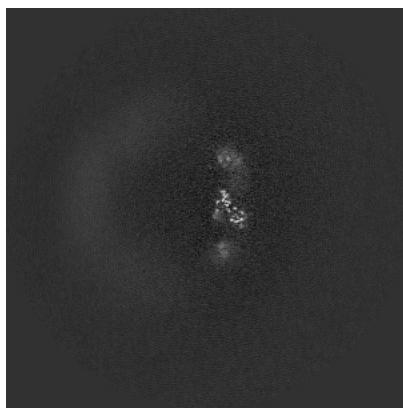


Z

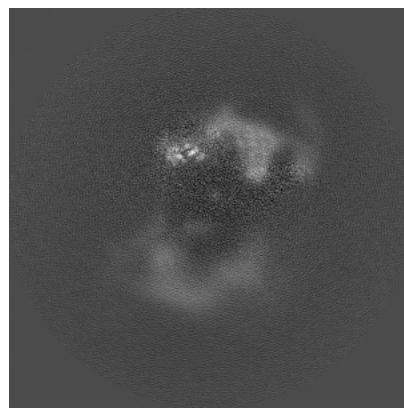
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices (i)

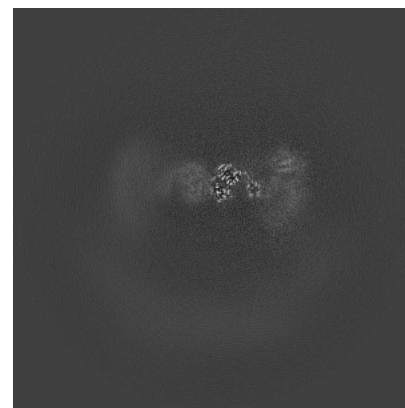
#### 6.2.1 Primary map



X Index: 220



Y Index: 220

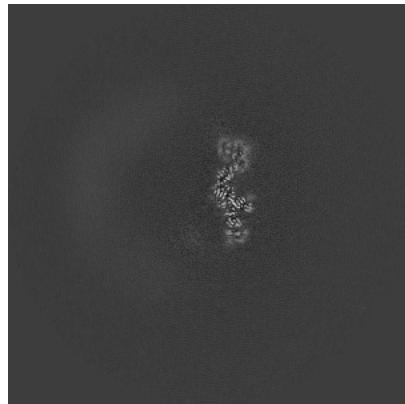


Z Index: 220

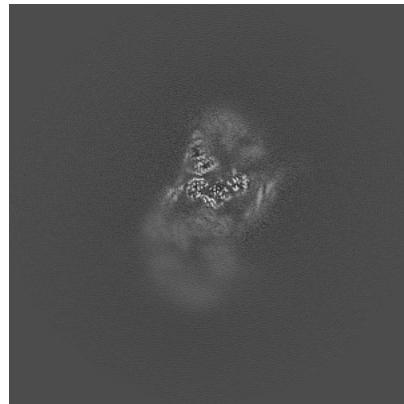
The images above show central slices of the map in three orthogonal directions.

### 6.3 Largest variance slices [\(i\)](#)

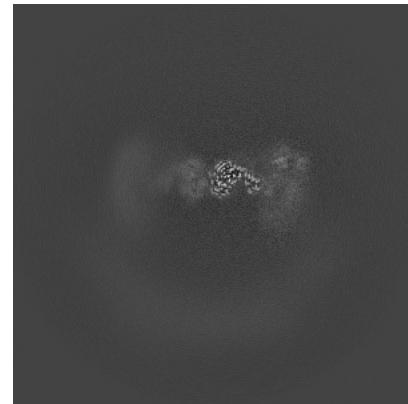
#### 6.3.1 Primary map



X Index: 236



Y Index: 243

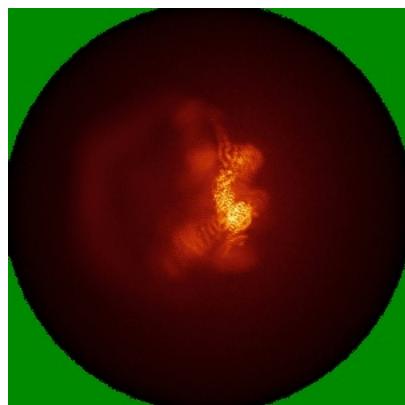


Z Index: 218

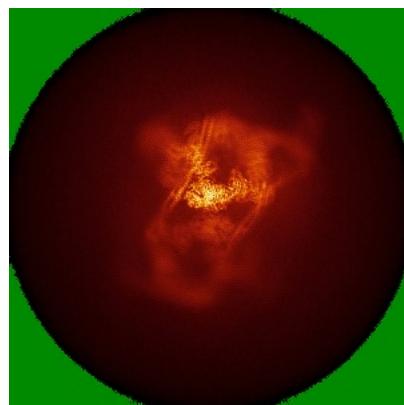
The images above show the largest variance slices of the map in three orthogonal directions.

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

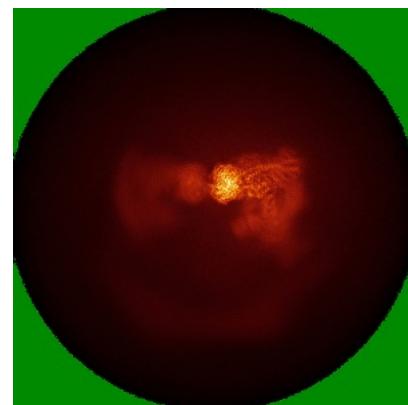
#### 6.4.1 Primary map



X



Y



Z

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

## 6.5 Orthogonal surface views [\(i\)](#)

### 6.5.1 Primary map



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

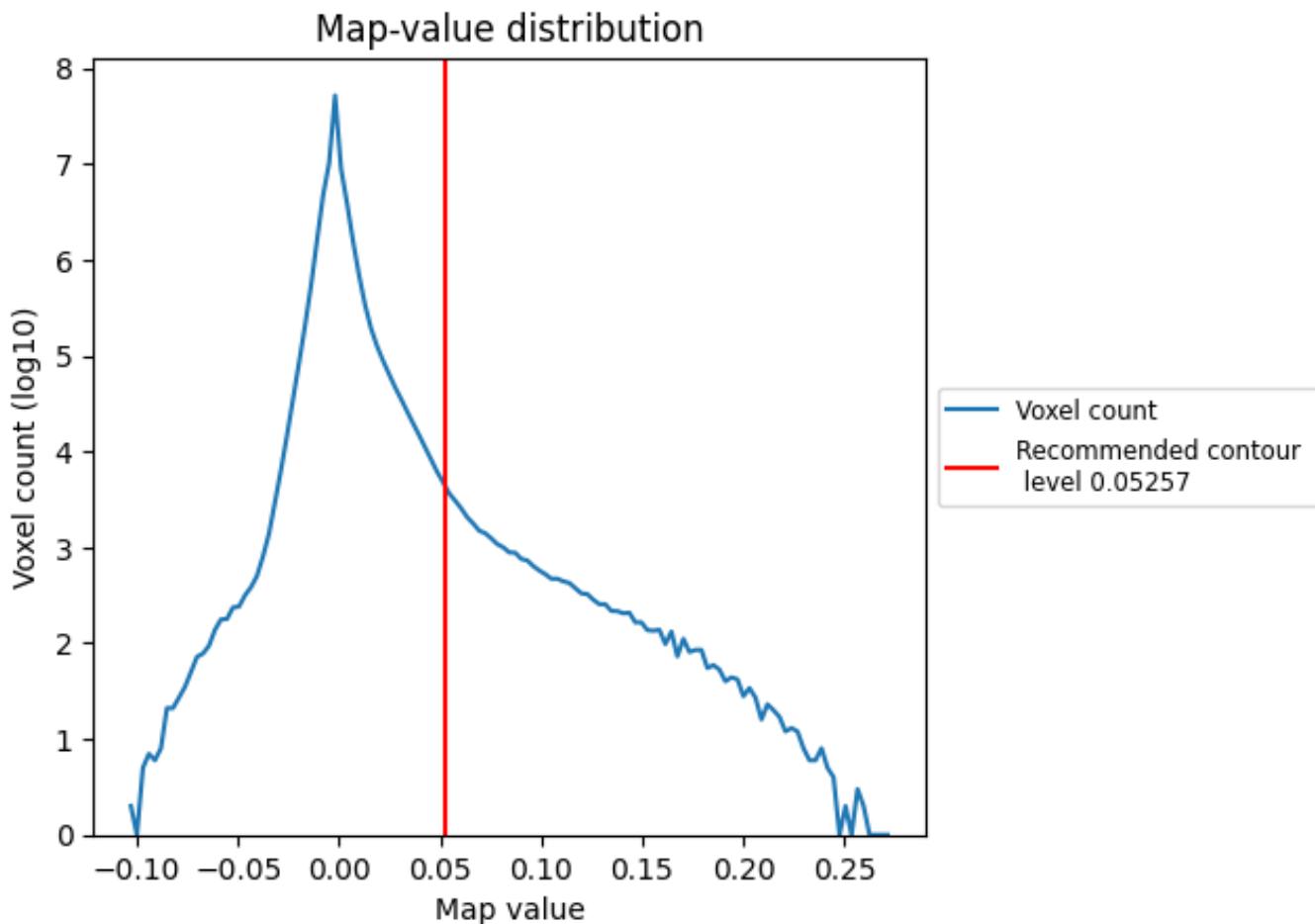
## 6.6 Mask visualisation [\(i\)](#)

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

## 7 Map analysis (i)

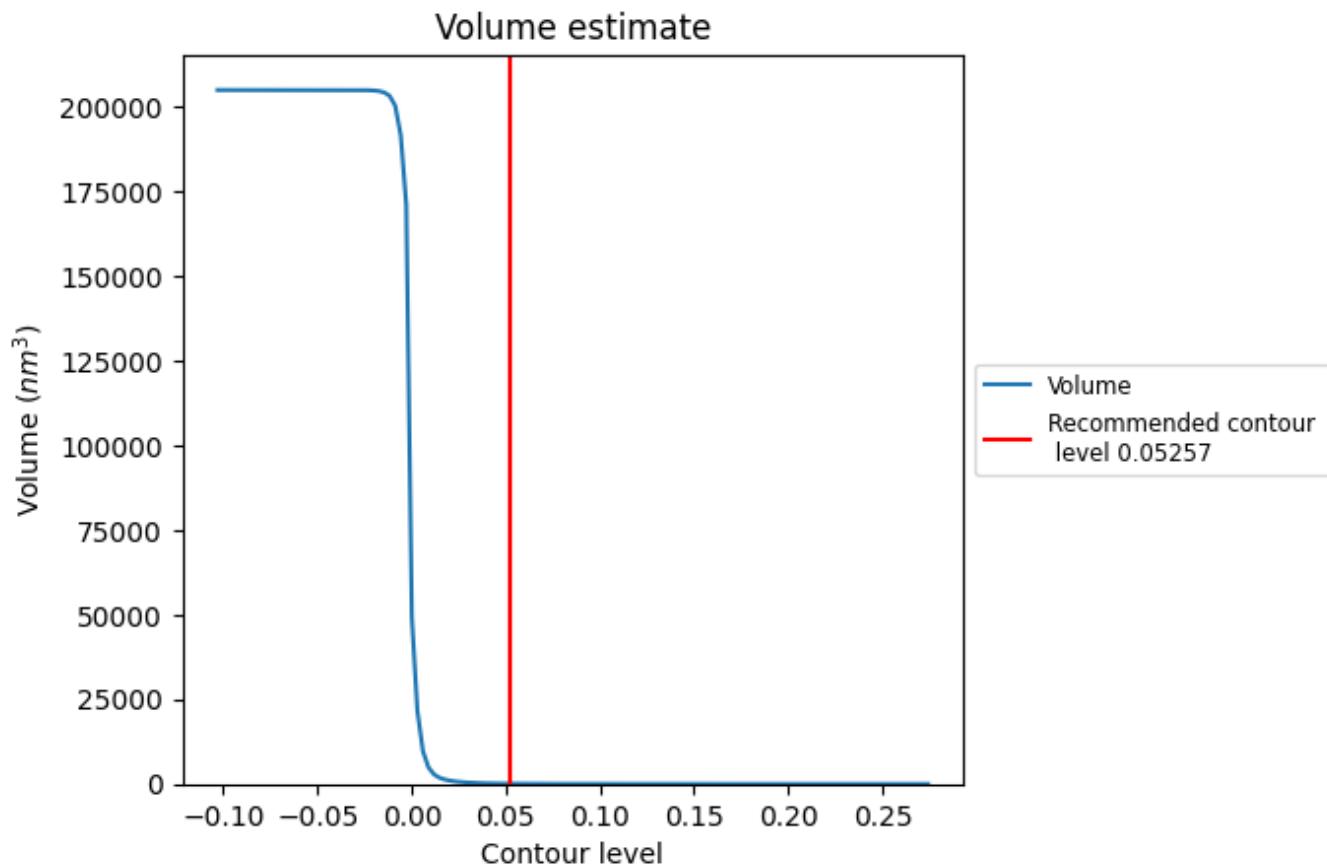
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

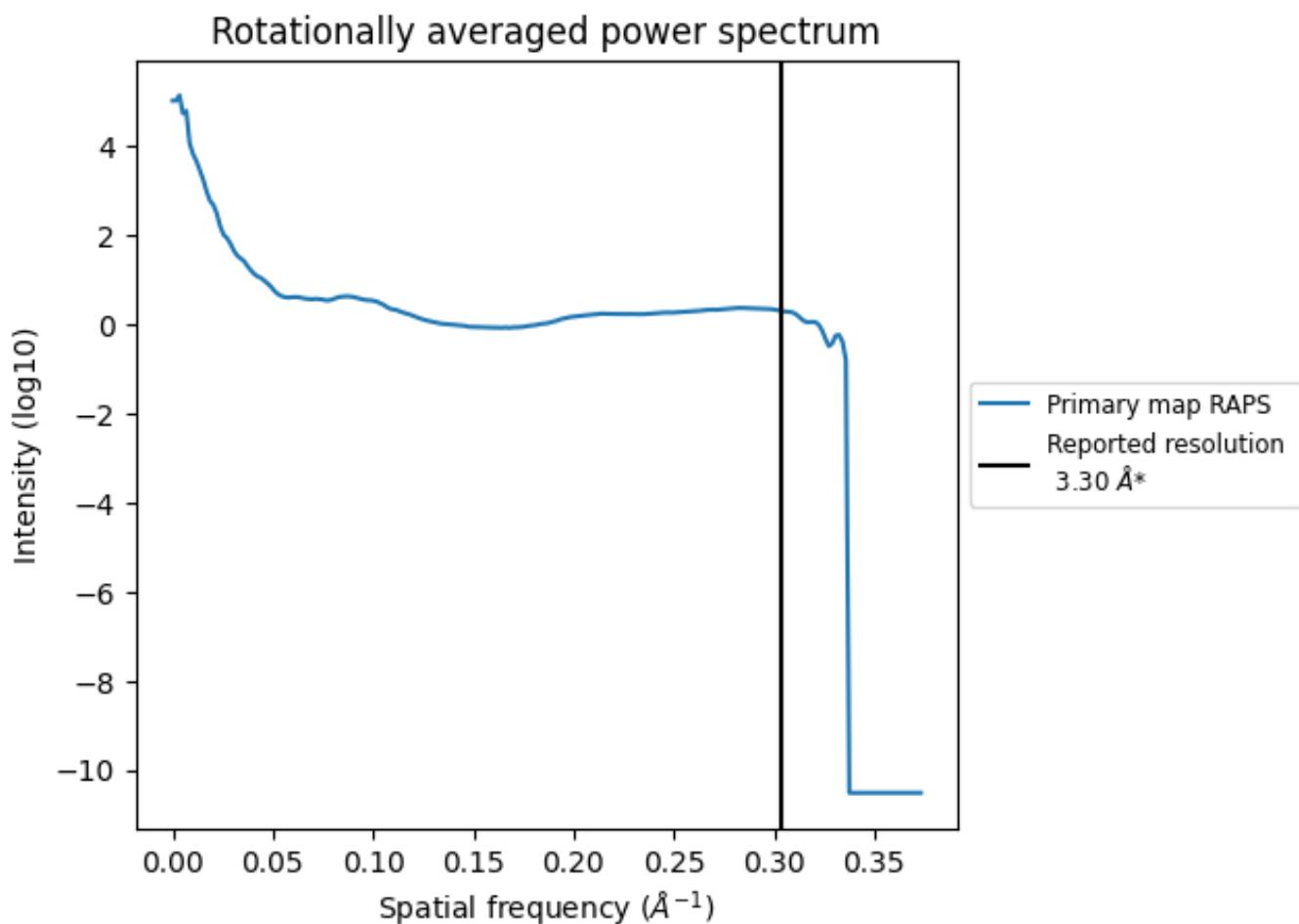
## 7.2 Volume estimate (i)



The volume at the recommended contour level is  $81 \text{ nm}^3$ ; 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 [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of  $0.303 \text{ \AA}^{-1}$

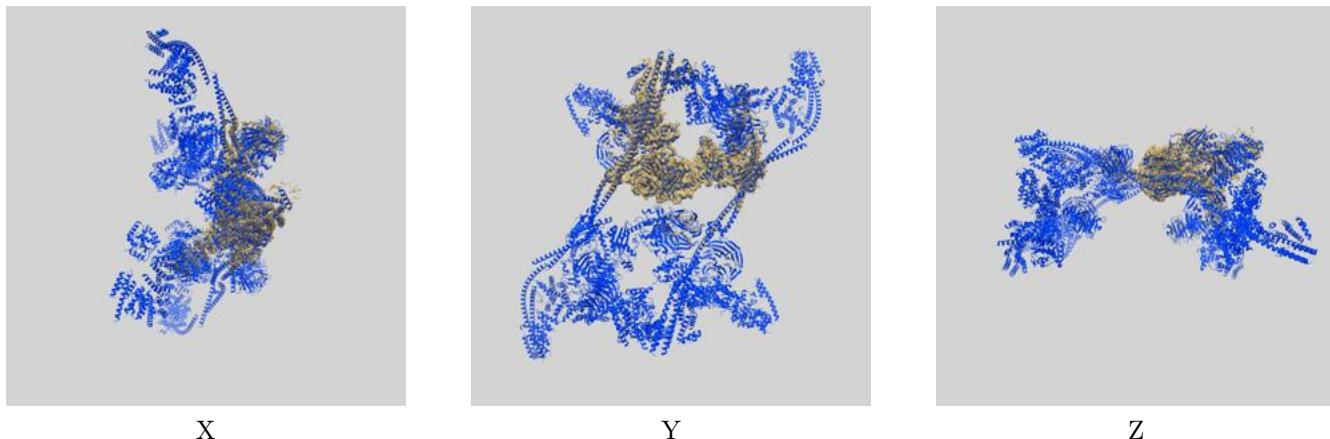
## 8 Fourier-Shell correlation

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

## 9 Map-model fit i

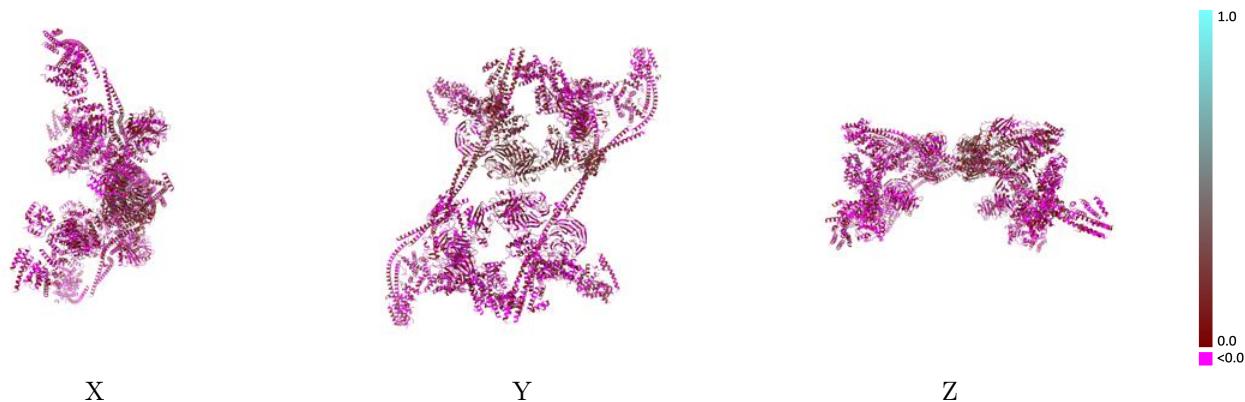
This section contains information regarding the fit between EMDB map EMD-11857 and PDB model 7APK. Per-residue inclusion information can be found in section 3 on page 21.

### 9.1 Map-model overlay i



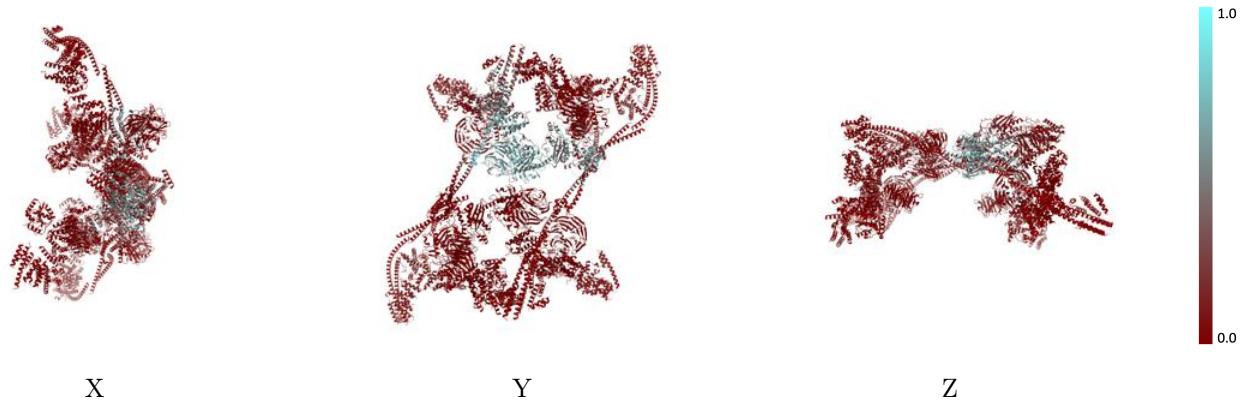
The images above show the 3D surface view of the map at the recommended contour level 0.05257 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



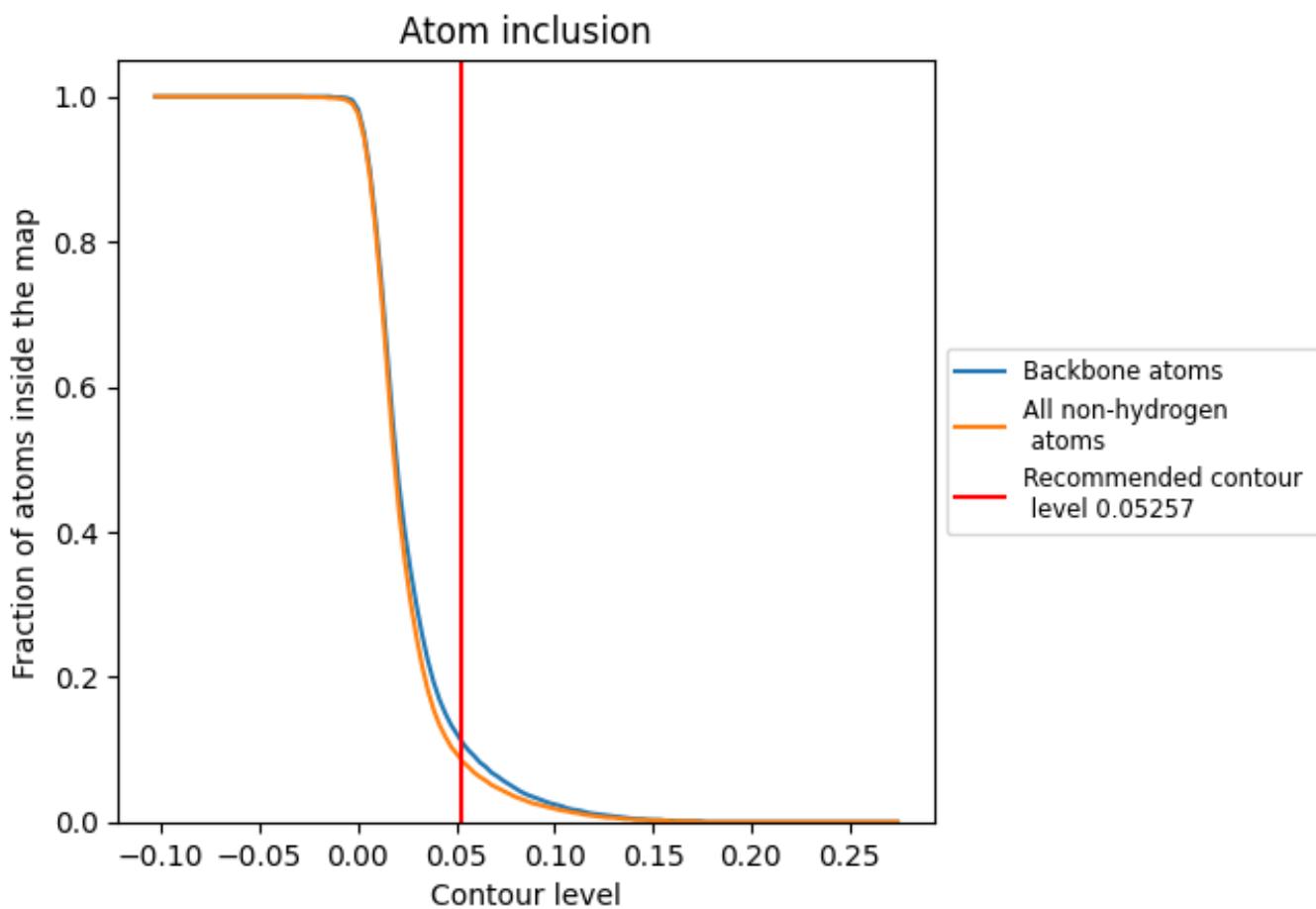
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.0860	0.0510
A	0.0000	0.0080
B	0.0020	0.0250
C	0.0010	0.0280
E	0.4380	0.1750
F	0.5720	0.2190
G	0.0720	0.0750
H	0.0000	0.0090
I	0.0000	0.0160
J	0.0000	0.0050
K	0.0000	0.0090
M	0.1570	0.0950
N	0.0240	0.0450
O	0.0900	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	0.0030	0.0340
f	0.0140	0.0160
g	0.0000	0.0560
h	0.0000	0.0210
i	0.3650	0.1810
j	0.1100	0.0780
k	0.0090	0.0270
m	0.1060	0.0600
n	0.0000	0.0190
o	0.3590	0.1470
p	0.0000	-0.0050
x	0.0540	0.0840

