



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:34 PM UTC

PDB ID : 9EH0 / pdb\_00009eh0  
EMDB ID : EMD-48042  
Title : RNA polymerase II-DSIF-SPT6-PAF1c-TFIIS-IWS1-SETD2-nucleosome, 30 bp upstream  
Authors : Markert, J.; Farnung, L.  
Deposited on : 2024-11-21  
Resolution : 3.60 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

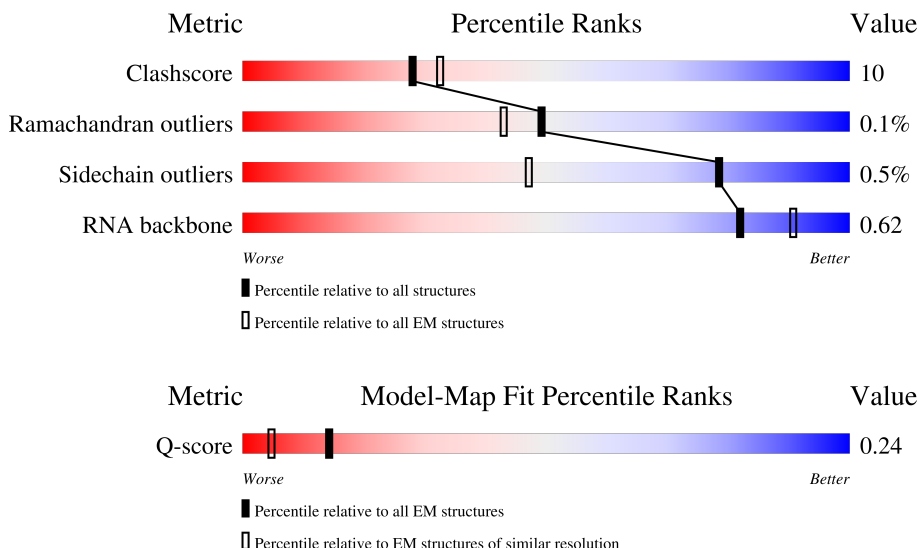
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 ( 3.10 - 4.10 )

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  $\geq 3$ , 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	1984	
2	B	1251	
3	C	275	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	142	
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	1729	
14	N	198	
15	O	821	
16	P	13	
17	Q	1179	
18	R	713	
19	S	304	
20	T	198	
21	U	666	
22	V	531	
23	W	305	
24	X	531	
25	Y	121	
26	Z	1087	
27	a	136	
27	e	136	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
28	b	103	 70%6%24%
28	f	103	 75%0%24%
29	c	130	 76%0%20%
29	g	130	 78%0%21%
30	d	123	 72%0%25%
30	h	123	 71%0%28%
31	l	1133	 32%0%64%

## 2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 73438 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1426	Total	C	N	O	P	S	0	0
			11255	7074	2014	2095	2	70		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1122	Total	C	N	O	S	0	0
			8980	5684	1576	1656	64		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	258	Total	C	N	O	S	0	0
			2072	1300	356	410	6		

- Molecule 4 is a protein called RNA polymerase Rpb4/RPC9 core domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	126	Total	C	N	O	S	0	0
			1004	630	170	200	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	78	Total	C	N	O	S	0	0
			626	401	106	114	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1333	866	214	245	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	149	Total	C	N	O	S	0	0
			1197	759	195	238	5		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	116	Total	C	N	O	S	0	0
			942	582	168	181	11		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	66	Total	C	N	O	S	0	0
			524	339	88	91	6		

- Molecule 11 is a protein called RNA polymerase II subunit J.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	47	Total	C	N	O	S	0	0
			397	246	77	68	6		

- Molecule 13 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	1002	Total	C	N	O	S	0	0
			4883	2708	1072	1096	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q7KZ85
M	-1	ASN	-	expression tag	UNP Q7KZ85
M	0	ALA	-	expression tag	UNP Q7KZ85

- Molecule 14 is a DNA chain called Non-template.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	181	Total	C	N	O	P	0	0
			3695	1757	664	1093	181		

- Molecule 15 is a protein called Protein IWS1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	132	Total	C	N	O	S	0	0
			1046	663	181	196	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-1	SER	-	expression tag	UNP Q96ST2
O	0	ASN	-	expression tag	UNP Q96ST2
O	1	ALA	-	expression tag	UNP Q96ST2

- Molecule 16 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	11	Total	C	N	O	P	0	0
			233	105	42	75	11		

- Molecule 17 is a protein called RNA polymerase-associated protein CTR9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	890	Total	C	N	O	S	0	0
			7226	4579	1264	1352	31		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1174	GLU	-	expression tag	UNP Q6PD62
Q	1175	ASN	-	expression tag	UNP Q6PD62
Q	1176	LEU	-	expression tag	UNP Q6PD62
Q	1177	TYR	-	expression tag	UNP Q6PD62

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1178	PHE	-	expression tag	UNP Q6PD62
Q	1179	GLN	-	expression tag	UNP Q6PD62

- Molecule 18 is a protein called RNA polymerase-associated protein RTF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	244	Total	C	N	O	S	0	0
			1836	1152	340	337	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-2	SER	-	expression tag	UNP Q92541
R	-1	ASN	-	expression tag	UNP Q92541
R	0	ALA	-	expression tag	UNP Q92541

- Molecule 19 is a protein called Transcription elongation factor A protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	161	Total	C	N	O	0	0
			657	334	161	162		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	-2	SER	-	expression tag	UNP P23193
S	-1	ASN	-	expression tag	UNP P23193
S	0	ALA	-	expression tag	UNP P23193

- Molecule 20 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	192	Total	C	N	O	P	0	0
			3955	1874	745	1144	192		

- Molecule 21 is a protein called RNA polymerase-associated protein LEO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	125	Total	C	N	O	S	0	0
			856	538	151	166	1		



- Molecule 22 is a protein called RNA polymerase II-associated factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	244	Total	C	N	O	S	0	0
			1703	1061	305	333	4		

- Molecule 23 is a protein called WDR61.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	300	Total	C	N	O	S	0	0
			2333	1483	392	454	4		

- Molecule 24 is a protein called Parafibromin.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	43	Total	C	N	O	0	0
			353	220	69	64		

- Molecule 25 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	116	Total	C	N	O	S	0	0
			911	570	159	173	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	-3	GLY	-	expression tag	UNP P63272
Y	-2	PRO	-	expression tag	UNP P63272
Y	-1	GLY	-	expression tag	UNP P63272
Y	0	SER	-	expression tag	UNP P63272

- Molecule 26 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	510	Total	C	N	O	P	S	0	0
			4025	2552	709	745	1	18		

- Molecule 27 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	101	Total	C	N	O	S	0	0
			823	520	157	142	4		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	94	Total	C	N	O	S	0	0
			776	491	149	133	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	36	MET	LYS	engineered mutation	UNP A0A310TTQ1
e	36	MET	LYS	engineered mutation	UNP A0A310TTQ1

- Molecule 28 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	78	Total	C	N	O	S	0	0
			622	393	120	108	1		
28	f	78	Total	C	N	O	S	0	0
			622	393	120	108	1		

- Molecule 29 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	104	Total	C	N	O		0	0
			800	504	156	140			
29	g	103	Total	C	N	O		0	0
			795	501	155	139			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	99	ARG	GLY	conflict	UNP P06897
c	123	SER	ALA	conflict	UNP P06897
g	99	ARG	GLY	conflict	UNP P06897
g	123	SER	ALA	conflict	UNP P06897

- Molecule 30 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	92	Total	C	N	O	S	0	0
			721	454	129	136	2		
30	h	89	Total	C	N	O	S	0	0
			694	438	122	132	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	3	MET	-	initiating methionine	UNP P02281
d	32	THR	SER	engineered mutation	UNP P02281
h	3	MET	-	initiating methionine	UNP P02281
h	32	THR	SER	engineered mutation	UNP P02281

- Molecule 31 is a protein called Histone-lysine N-methyltransferase SETD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1	412	Total	C	N	O	S	0	0
			2893	1772	545	555	21		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1432	SER	-	expression tag	UNP Q9BYW2
1	1433	ASN	-	expression tag	UNP Q9BYW2
1	1434	ALA	-	expression tag	UNP Q9BYW2
1	1962	LEU	PRO	conflict	UNP Q9BYW2

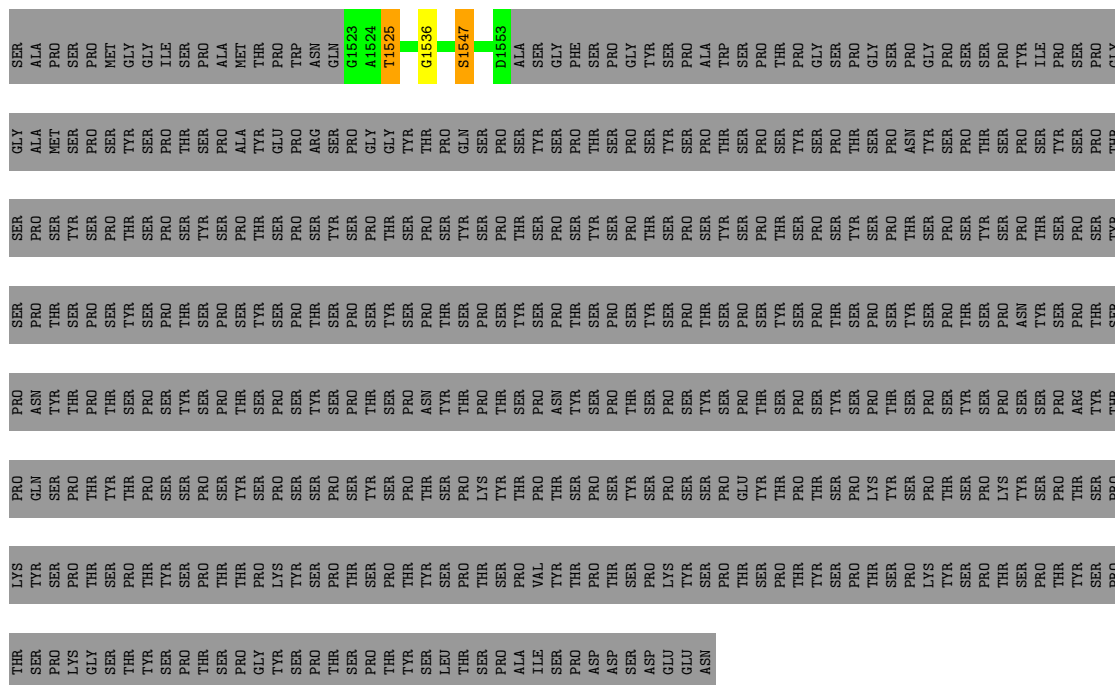
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	A	2	Total	Zn	0
			2	2	
32	B	1	Total	Zn	0
			1	1	
32	C	1	Total	Zn	0
			1	1	
32	I	2	Total	Zn	0
			2	2	
32	J	1	Total	Zn	0
			1	1	
32	L	1	Total	Zn	0
			1	1	
32	Y	1	Total	Zn	0
			1	1	

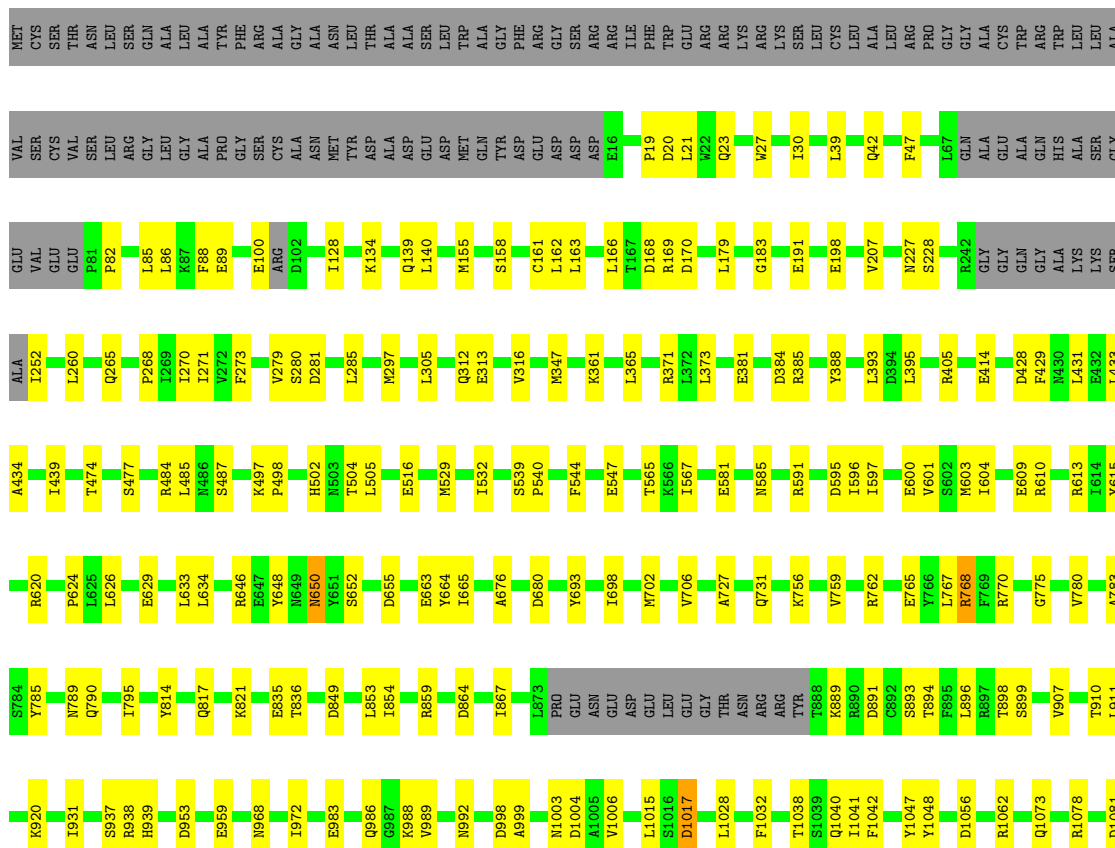
- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	1	Total	Mg	0
			1	1	





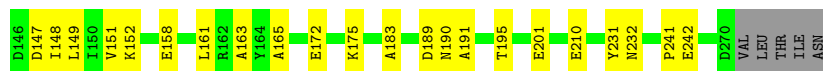
- Molecule 2: DNA-directed RNA polymerase subunit beta





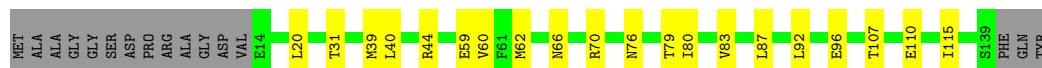
- Molecule 3: DNA-directed RNA polymerase II subunit RPB3

Chain C: 77% 16% 6%



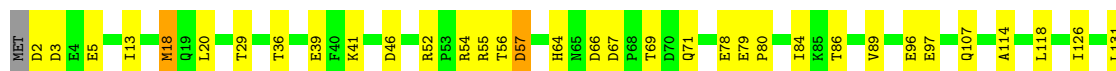
- Molecule 4: RNA polymerase Rpb4/RPC9 core domain-containing protein

Chain D: 75% 14% 11%



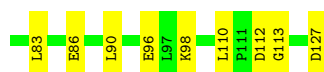
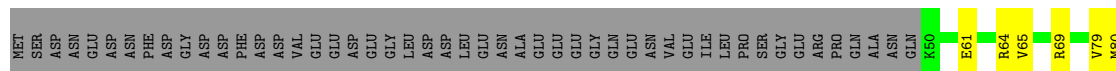
- Molecule 5: DNA-directed RNA polymerase II subunit E

Chain E: 78% 20% .



- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F: 50% 12% 39%



- Molecule 7: DNA-directed RNA polymerase II subunit RPB7

Chain G: 82% 17% .



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Met	A2	E7	D8	T9	D14	I15	E18	R27	L28	S32	K37	D38	L39	I40	L41	D42	L52	L58	V59	I60	E66	D72	G73	E74	V75	N76	R84	V91	V96	T110	R111	L112	V116	M123	A129	L132	E136	V137	D138	F144	F150
-----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------

- 
- | Amino Acid | Mutation Count |
|------------|----------------|
| MET        | 125            |
| GLU        | 125            |
| PRO        | 125            |
| ASP        | 125            |
| GLY        | 125            |
| THR        | 125            |
| TYR        | 125            |
| GLU        | 125            |
| PRO        | 125            |
| G10        | 125            |
| I14        | 125            |
| C17        | 125            |
| Q18        | 125            |
| E19        | 125            |
| N22        | 125            |
| M23        | 125            |
| D29        | 125            |
| K30        | 125            |
| E31        | 125            |
| R32        | 125            |
| I34        | 125            |
| L35        | 125            |
| L36        | 125            |
| C42        | 125            |
| D43        | 125            |
| N56        | 125            |
| K57        | 125            |
| I58        | 125            |
| T59        | 125            |
| H60        | 125            |
| Q67        | 125            |
| D71        | 125            |
| Q74        | 125            |
| D75        | 125            |
| P76        | 125            |
| T77        | 125            |
| L78        | 125            |
| P79        | 125            |
| E82        | 125            |
| D83        | 125            |
| C86        | 125            |
| Q87        | 125            |
| R103       | 125            |
| A104       | 125            |
| E105       | 125            |
| D106       | 125            |

- |    |    |    |    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| M1 | C7 | F8 | T9 | C10 | I13 | V14 | W18 | Y21 | L22 | L25 | E31 | R42 | Y43 | C44 | C45 | R46 | R47 | M48 | A51 | L59 | E66 | LYS |
|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

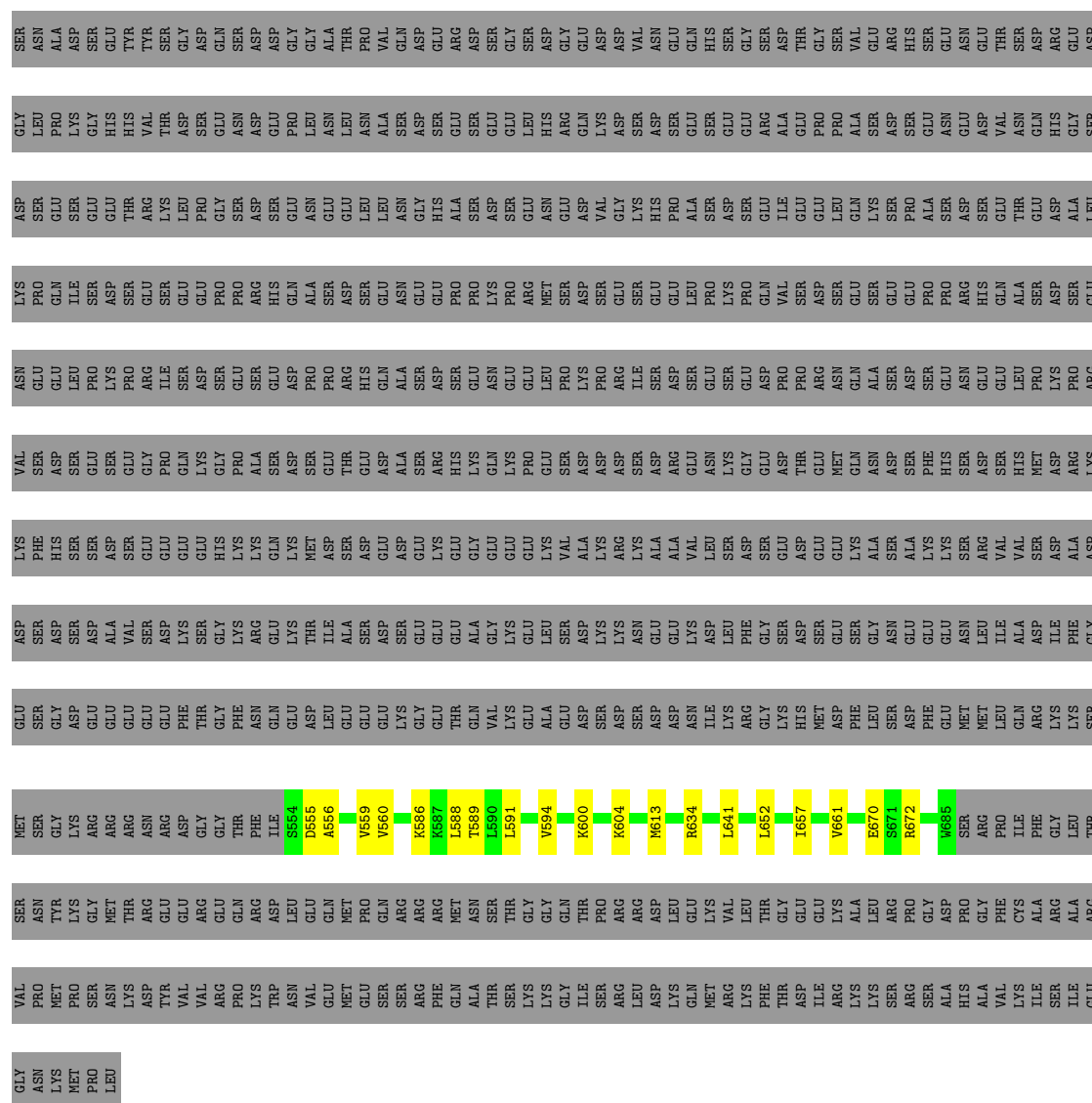
- |    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|-----|-----|
| #1 | L11 | K17 | D24 | T25 | K26 | V27 | L32 | N36 | K37 | T41 | Q49 | K70 | T77 | T78 | P79 | D80 | Y81 | Q84 | D93 | L94 | L100 | R104 | V107 | G115 | T1E | GUI |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|-----|-----|

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | THR | ASP | GLN | LYS | ASP | VAL | GLN | PRO | PRO | LYS | Q12 | I16 | I17 | I18 | C19 | G20 | E21 | E25 | N26 | I34 | E38 | C39 | G40 | K46 | D56 | A57 | R58 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- [illegible]



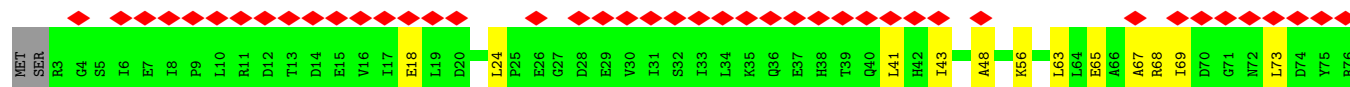


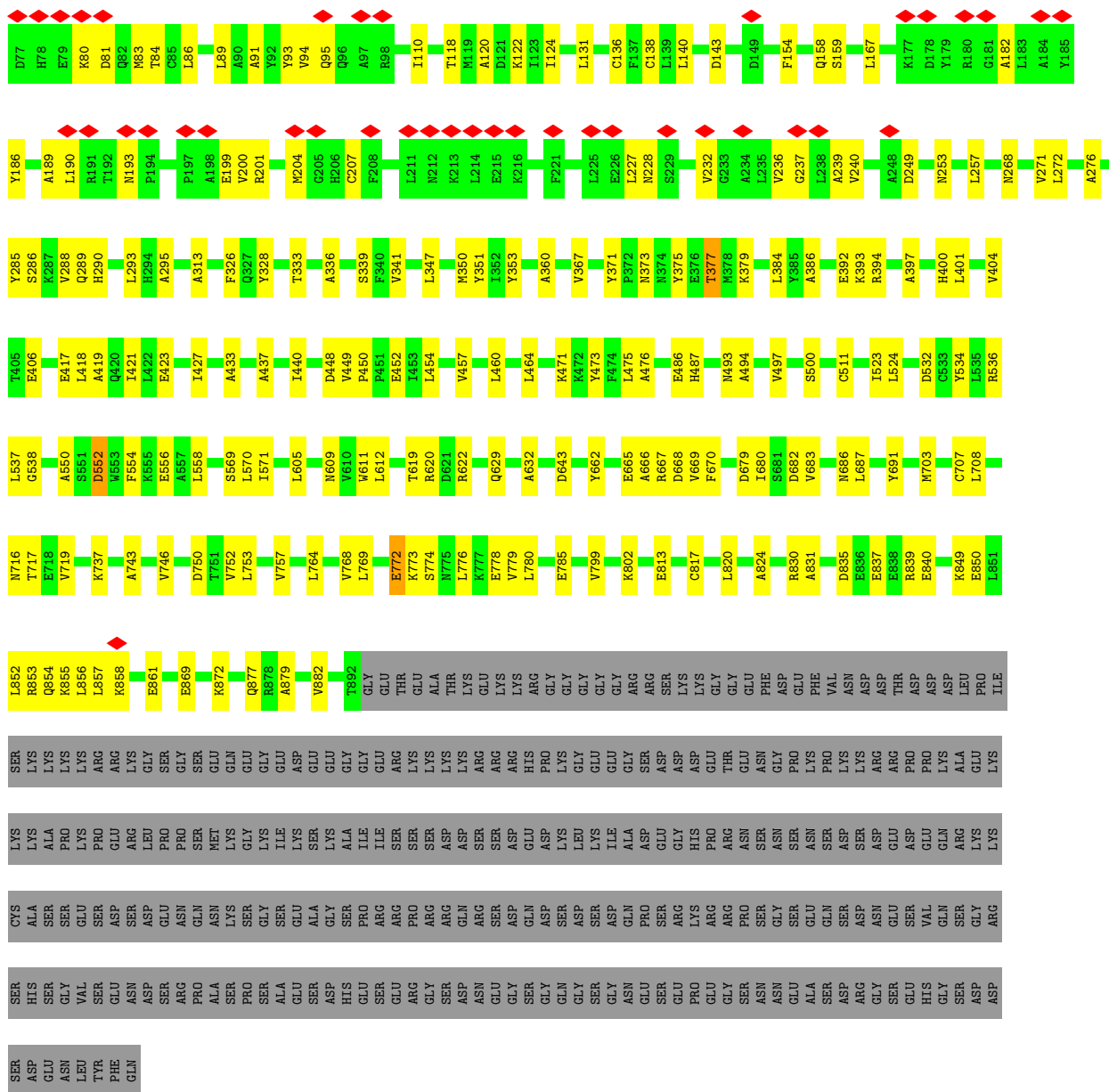


- Molecule 16: RNA

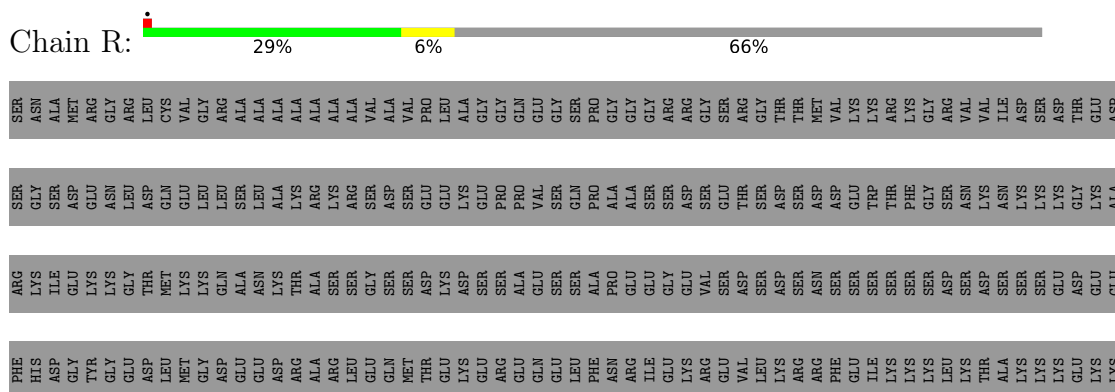


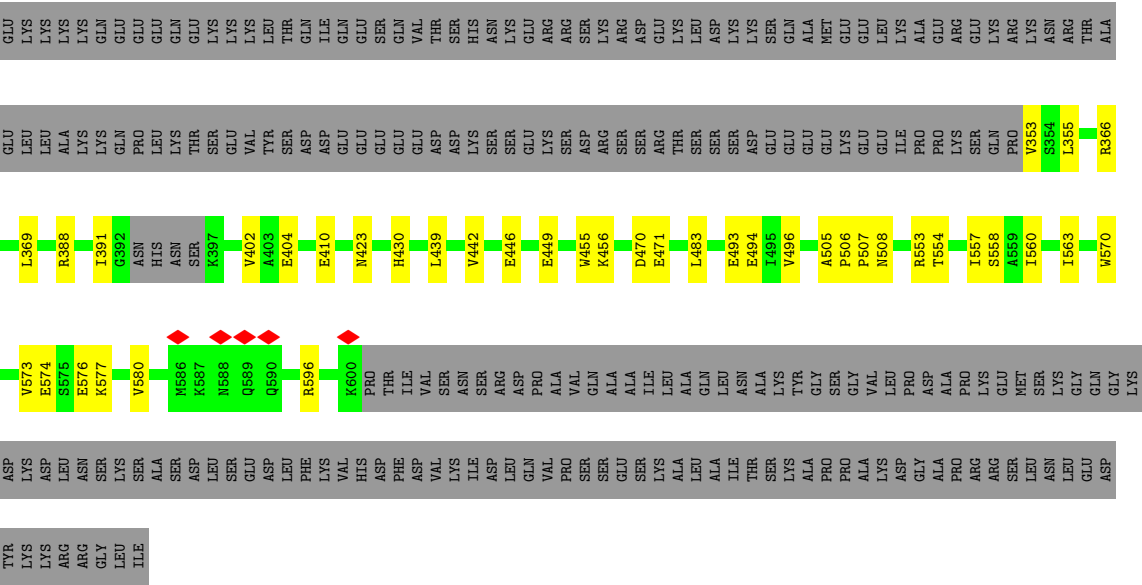
- Molecule 17: RNA polymerase-associated protein CTR9 homolog



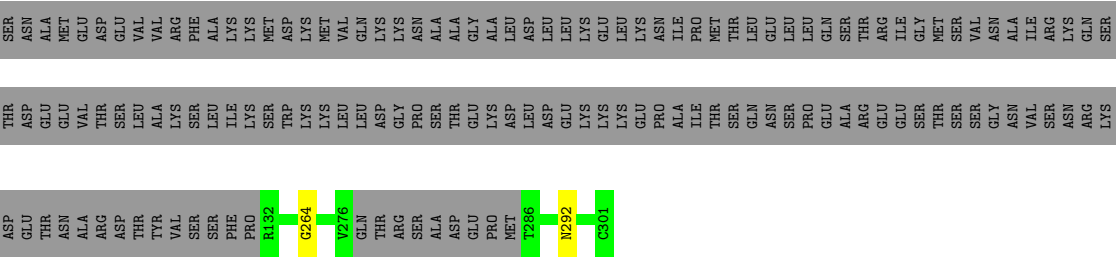


- Molecule 18: RNA polymerase-associated protein RTF1 homolog

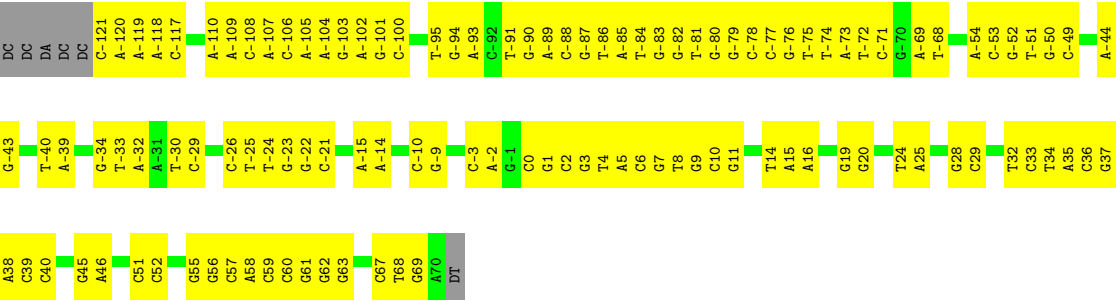
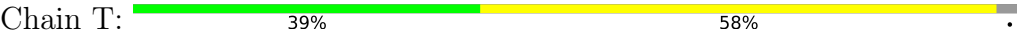




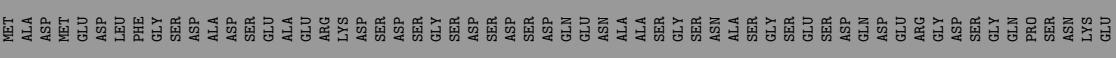
• Molecule 19: Transcription elongation factor A protein 1



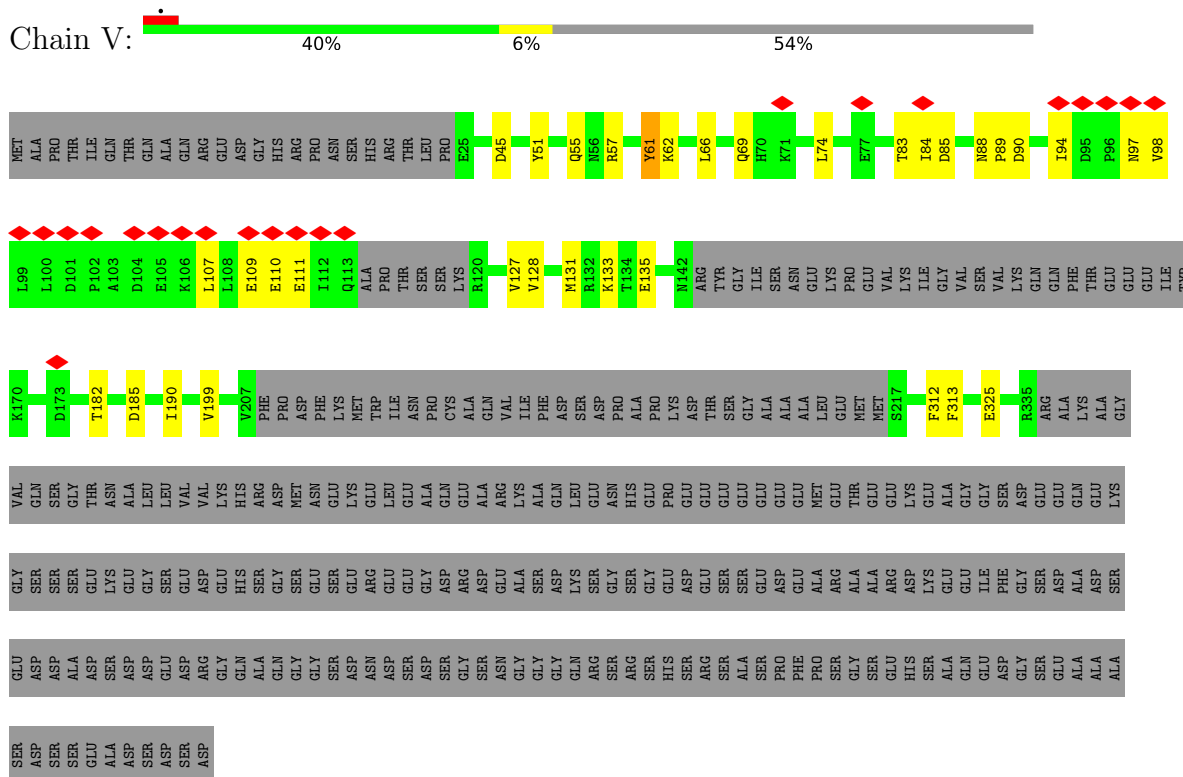
• Molecule 20: Template DNA



• Molecule 21: RNA polymerase-associated protein LEO1



- Molecule 22: RNA polymerase II-associated factor 1 homolog



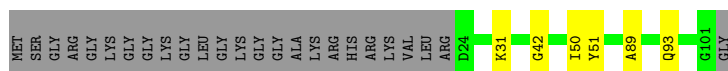
- Molecule 23: WDR61

[illegible][illegible]

GLY	PRO	GLY	SER	MET	A2	L13	L18	D26	Q27	A38	T39	L40	Q41	N42	E47	N48	V49	C52	T53	S56	Q75	K81	Y85	A86	T90	R111	D112	T113	K116	T117
-----	-----	-----	-----	-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------

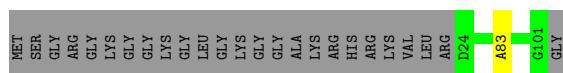


Chain b:  70% 6% 24%




- Molecule 28: Histone H4

Chain f:  75% 0% 24%




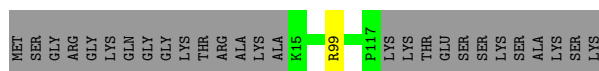
- Molecule 29: Histone H2A type 1

Chain c:  76% 0% 20%



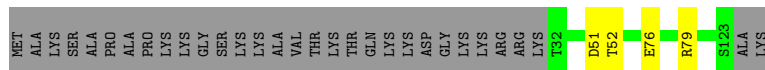
- Molecule 29: Histone H2A type 1

Chain g:  78% 0% 21%



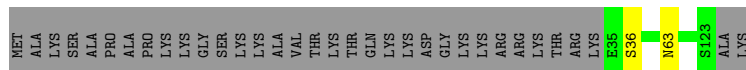
- Molecule 30: Histone H2B 1.1

Chain d:  72% 0% 25%



- Molecule 30: Histone H2B 1.1

Chain h:  71% 0% 28%



- Molecule 31: Histone-lysine N-methyltransferase SETD2

Chain i:  32% 0% 64%



LYS	GLU	TRP	ALA	TYR	SER	VAL	SER	PRO	GLU	ASN	PRO	GLU	ASN	THR	PRO	ASN	R1670
HIS	MET	ASP	PRO	GLN	SER	ASP	THR	ASP	THR	THR	ASP	THR	THR	GLU	VAL	THR	Y1671
LYS	THR	PRO	GLN	GLN	TYR	PRO	GLU	SER	ARG	GLU	ARG	THR	ASP	PRO	GLU	PRO	E1674
LYS	PHE	THR	PRO	THR	VAL	ASN	ARG	ASN	ARG	GLU	ARG	GLU	SER	PRO	GLU	ASP	A1675
GLU	TLE	TRP	GLN	CYS	ALA	PRO	ARG	PRO	ARG	GLU	GLU	GLN	SER	GLU	GLU	SER	A1676
TYR	VAL	GLU	PRO	PRO	GLN	ASN	LYS	ARG	LYS	ARG	GLU	GLU	THR	ASP	GLU	THR	A1677
LYS	CYS	SER	GLN	THR	SER	GLY	LEU	ALA	PHE	ASP	ASP	GLU	LEU	LYS	GLN	LEU	C1678
TYR	LEU	GLY	PRO	TYR	GLY	VAL	GLU	GLY	GLU	ASP	GLU	GLY	SER	SER	SER	SER	F1679
MET	PRO	ASP	SER	GLY	VAL	VAL	GLN	VAL	GLN	LYS	VAL	GLN	THR	THR	GLN	THR	G1681
GLN	TYR	ALA	MET	THR	HIS	LEU	VAL	LEU	VAL	THR	THR	SER	LEU	LEU	GLN	GLU	M1684
LYS	ARG	SER	VAL	SER	GLN	PRO	ALA	PRO	GLN	GLN	GLN	ASP	THR	LEU	LEU	ALA	C1685
PHE	VAL	LEU	VAL	PRO	ASP	THR	GLN	PRO	GLN	ASN	VAL	VAL	PRO	THR	PRO	THR	R1686
GLY	PRO	GLU	THR	TYR	SER	PRO	ARG	PRO	ARG	LYS	GLU	GLN	ASP	GLN	GLN	ASP	G1687
ALA	ASP	HIS	ASN	SER	SER	MET	ALA	SER	GLU	GLU	SER	SER	THR	THR	THR	THR	Y1688
VAL	CYS	GLU	ASN	GLN	VAL	VAL	VAL	VAL	VAL	LYS	GLU	LEU	PRO	LEU	LEU	PRO	L1689
TYR	LYS	ALA	LEU	GLN	ALA	ASP	GLN	ARG	ARG	LYS	ARG	ARG	THR	PRO	PRO	LYS	G1690
LYS	VAL	GLU	LEU	THR	VAL	PRO	VAL	PRO	LYS	LYS	SER	SER	LYS	GLN	GLN	LYS	
PRO	GLY	MET	ASP	PRO	LEU	CYS	GLN	ARG	GLN	ARG	GLN	GLN	MET	CYS	GLN	LEU	I1697
GLU	TLE	LEU	PRO	TLE	VAL	SER	GLN	SER	GLN	SER	GLN	GLN	PHE	VAL	VAL	PHE	R1698
ASP	THR	GLY	PRO	VAL	PRO	PRO	GLN	PRO	GLN	SER	PRO	ASP	ARG	ASP	ASP	ARG	A1699
THR	THR	PRO	SER	SER	PRO	PRO	GLN	PRO	GLN	SER	GLN	ASP	SER	THR	THR	ARG	A1700
LEU	GLU	THR	PRO	TYR	GLY	TYR	ASN	TYR	THR	THR	THR	THR	LYS	GLU	GLU	LEU	K1703
LEU	LEU	ASP	PRO	ALA	PRO	ASP	LEU	PRO	PRO	PRO	ASN	ASN	ILE	ASN	ASN	ILE	E1707
GLU	PHE	ASP	LYS	GLN	VAL	HIS	GLY	HIS	ASP	SER	ASP	ASP	ILE	TLE	GLU	ILE	R1708
LYS	LYS	GLU	PRO	PRO	GLN	ALA	MET	ALA	SER	SER	T2005	THR	SER	GLU	GLU	SER	S1709
HIS	HIS	ASN	LYS	SER	GLY	PRO	THR	THR	THR	ALA			ALA	ALA	GLU	GLU	R1709
ALA	ALA	MET	ILE	GLN	ASN	PRO	SER	SER	PRO	TYR	D2018		SER	SER	SER	ASN	
ARG	ARG	LYS	VAL	TYR	THR	VAL	LEU	ARG	GLY	GLU	E2021		LYS	LEU	LEU	MET	
LYS	LEU	ALA	LEU	TLE	SER	GLY	PRO	GLY	THR	GLY	V2022		PRO	THR	THR	ASP	
LEU	THR	SER	PRO	GLN	TRP	HIS	THR	HIS	THR	THR	Y2023		SER	THR	SER	SER	
VAL	VAL	GLN	TRP	GLN	SER	THR	SER	THR	ARG	ASP	R2024		ILE	GLU	GLU	ILE	
MET	MET	LYS	LYS	TLE	SER	GLU	LEU	PRO	LEU	PRO	T2025		SER	PRO	PRO	SER	
ASN	ASN	THR	THR	PHE	GLN	PRO	GLY	ASP	THR	ASP	T2031		ALA	GLU	GLU	ASP	
LYS	LYS	ALA	ALA	THR	GLN	SER	ASN	SER	ASN	ARG			ALA	ALA	ALA	ALA	
GLU	GLU	ALA	ASP	H													



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	301837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.683	Depositor
Minimum map value	-0.193	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.01	Depositor
Map size ( $\text{\AA}$ )	550.0, 550.0, 550.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, ZN, MG, SEP

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	0.18	0/11437	0.32	0/15433
2	B	0.20	0/9158	0.32	0/12360
3	C	0.21	0/2115	0.33	0/2873
4	D	0.15	0/1017	0.27	0/1368
5	E	0.18	0/1751	0.31	0/2366
6	F	0.19	0/636	0.29	0/859
7	G	0.15	0/1364	0.32	0/1853
8	H	0.22	0/1219	0.34	0/1644
9	I	0.18	0/964	0.28	0/1305
10	J	0.25	0/533	0.33	0/719
11	K	0.20	0/939	0.33	0/1271
12	L	0.19	0/403	0.28	0/536
13	M	0.13	0/4944	0.27	0/6387
14	N	0.23	0/4138	0.50	0/6379
15	O	0.12	0/1062	0.23	0/1428
16	P	0.12	0/260	0.42	0/402
17	Q	0.19	1/7365 (0.0%)	0.33	3/9927 (0.0%)
18	R	0.12	0/1866	0.28	0/2519
19	S	0.14	0/659	0.19	0/827
20	T	0.26	0/4443	0.45	0/6859
21	U	0.15	0/870	0.28	0/1183
22	V	0.13	0/1728	0.33	2/2357 (0.1%)
23	W	0.15	0/2392	0.32	0/3257
24	X	0.18	0/356	0.35	0/478
25	Y	0.13	0/927	0.25	0/1250
26	Z	0.11	0/4084	0.23	0/5498
27	a	0.27	0/835	0.40	0/1120
27	e	0.24	0/786	0.37	0/1053
28	b	0.23	0/629	0.35	0/843
28	f	0.23	0/629	0.34	0/843
29	c	0.23	0/810	0.34	0/1095
29	g	0.22	0/805	0.33	0/1088

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
30	d	0.24	0/732	0.34	0/986
30	h	0.24	0/705	0.35	0/951
31	l	0.18	0/2932	0.40	0/3963
All	All	0.19	1/75493 (0.0%)	0.34	5/103280 (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
31	l	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Q	450	PRO	CA-C	9.63	1.57	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	450	PRO	O-C-N	7.54	124.78	121.31
17	Q	772	GLU	CA-C-N	5.84	132.21	121.70
17	Q	772	GLU	C-N-CA	5.84	132.21	121.70
22	V	61	TYR	CA-C-N	5.34	131.31	121.70
22	V	61	TYR	C-N-CA	5.34	131.31	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	l	2018	ASP	Peptide
31	l	2021	GLU	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11255	0	11374	199	0
2	B	8980	0	9019	162	0
3	C	2072	0	2020	40	0
4	D	1004	0	980	16	0
5	E	1720	0	1737	36	0
6	F	626	0	657	10	0
7	G	1333	0	1321	23	0
8	H	1197	0	1156	30	0
9	I	942	0	872	25	0
10	J	524	0	541	14	0
11	K	920	0	942	17	0
12	L	397	0	405	15	0
13	M	4883	0	2550	14	0
14	N	3695	0	2038	226	0
15	O	1046	0	1096	12	0
16	P	233	0	118	16	0
17	Q	7226	0	7169	159	0
18	R	1836	0	1699	27	0
19	S	657	0	199	2	0
20	T	3955	0	2154	145	0
21	U	856	0	680	14	0
22	V	1703	0	1426	30	0
23	W	2333	0	2246	47	0
24	X	353	0	371	9	0
25	Y	911	0	907	15	0
26	Z	4025	0	4041	59	0
27	a	823	0	864	8	0
27	e	776	0	815	3	0
28	b	622	0	660	4	0
28	f	622	0	660	1	0
29	c	800	0	851	4	0
29	g	795	0	846	1	0
30	d	721	0	742	2	0
30	h	694	0	709	1	0
31	l	2893	0	2422	38	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	C	1	0	0	0	0
32	I	2	0	0	0	0
32	J	1	0	0	0	0
32	L	1	0	0	0	0
32	Y	1	0	0	0	0
33	A	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	73438	0	66287	1328	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 1328 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:276:ALA:HB1	17:Q:288:VAL:HG23	1.31	1.12
1:A:1172:ASN:N	1:A:1215:GLU:OE2	1.99	0.95
20:T:9:DG:H2''	20:T:10:DC:H5'	1.50	0.94
20:T:67:DC:H2'	20:T:68:DT:H71	1.49	0.93
2:B:790:GLN:O	2:B:968:ASN:ND2	2.01	0.93

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1408/1984 (71%)	1319 (94%)	88 (6%)	1 (0%)	48	79
2	B	1112/1251 (89%)	1024 (92%)	88 (8%)	0	100	100
3	C	254/275 (92%)	229 (90%)	25 (10%)	0	100	100
4	D	124/142 (87%)	120 (97%)	4 (3%)	0	100	100
5	E	207/210 (99%)	198 (96%)	9 (4%)	0	100	100
6	F	76/127 (60%)	74 (97%)	2 (3%)	0	100	100
7	G	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
8	H	147/150 (98%)	134 (91%)	13 (9%)	0	100	100
9	I	114/125 (91%)	103 (90%)	11 (10%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	64/67 (96%)	57 (89%)	7 (11%)	0	100	100
11	K	113/117 (97%)	110 (97%)	3 (3%)	0	100	100
12	L	45/58 (78%)	41 (91%)	3 (7%)	1 (2%)	5	30
13	M	976/1729 (56%)	920 (94%)	55 (6%)	1 (0%)	48	79
15	O	130/821 (16%)	127 (98%)	3 (2%)	0	100	100
17	Q	888/1179 (75%)	847 (95%)	41 (5%)	0	100	100
18	R	240/713 (34%)	231 (96%)	9 (4%)	0	100	100
19	S	157/304 (52%)	154 (98%)	3 (2%)	0	100	100
21	U	117/666 (18%)	106 (91%)	10 (8%)	1 (1%)	14	46
22	V	234/531 (44%)	216 (92%)	18 (8%)	0	100	100
23	W	298/305 (98%)	288 (97%)	10 (3%)	0	100	100
24	X	41/531 (8%)	41 (100%)	0	0	100	100
25	Y	114/121 (94%)	108 (95%)	6 (5%)	0	100	100
26	Z	497/1087 (46%)	479 (96%)	18 (4%)	0	100	100
27	a	99/136 (73%)	96 (97%)	3 (3%)	0	100	100
27	e	90/136 (66%)	89 (99%)	1 (1%)	0	100	100
28	b	76/103 (74%)	76 (100%)	0	0	100	100
28	f	76/103 (74%)	75 (99%)	1 (1%)	0	100	100
29	c	102/130 (78%)	101 (99%)	1 (1%)	0	100	100
29	g	101/130 (78%)	100 (99%)	1 (1%)	0	100	100
30	d	90/123 (73%)	89 (99%)	1 (1%)	0	100	100
30	h	87/123 (71%)	83 (95%)	4 (5%)	0	100	100
31	l	406/1133 (36%)	374 (92%)	30 (7%)	2 (0%)	24	57
All	All	8652/14782 (58%)	8170 (94%)	476 (6%)	6 (0%)	49	79

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	39	CYS
13	M	700	HIS
31	l	2018	ASP
31	l	2022	VAL
1	A	1343	LEU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1245/1761 (71%)	1241 (100%)	4 (0%)	86	83
2	B	986/1084 (91%)	983 (100%)	3 (0%)	86	83
3	C	235/252 (93%)	234 (100%)	1 (0%)	84	81
4	D	109/126 (86%)	109 (100%)	0	100	100
5	E	191/192 (100%)	189 (99%)	2 (1%)	68	75
6	F	68/111 (61%)	68 (100%)	0	100	100
7	G	146/153 (95%)	146 (100%)	0	100	100
8	H	130/131 (99%)	130 (100%)	0	100	100
9	I	104/112 (93%)	102 (98%)	2 (2%)	50	67
10	J	55/56 (98%)	55 (100%)	0	100	100
11	K	104/106 (98%)	104 (100%)	0	100	100
12	L	44/55 (80%)	44 (100%)	0	100	100
13	M	196/1524 (13%)	196 (100%)	0	100	100
15	O	118/737 (16%)	116 (98%)	2 (2%)	53	69
17	Q	761/1011 (75%)	753 (99%)	8 (1%)	65	74
18	R	170/625 (27%)	169 (99%)	1 (1%)	78	79
19	S	4/268 (2%)	4 (100%)	0	100	100
21	U	65/590 (11%)	65 (100%)	0	100	100
22	V	144/462 (31%)	143 (99%)	1 (1%)	76	78
23	W	255/260 (98%)	250 (98%)	5 (2%)	48	66
24	X	40/467 (9%)	40 (100%)	0	100	100
25	Y	102/105 (97%)	102 (100%)	0	100	100
26	Z	435/939 (46%)	435 (100%)	0	100	100
27	a	87/111 (78%)	87 (100%)	0	100	100
27	e	82/111 (74%)	82 (100%)	0	100	100
28	b	64/79 (81%)	64 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	f	64/79 (81%)	64 (100%)	0	100	100
29	c	82/102 (80%)	82 (100%)	0	100	100
29	g	82/102 (80%)	82 (100%)	0	100	100
30	d	79/103 (77%)	79 (100%)	0	100	100
30	h	76/103 (74%)	76 (100%)	0	100	100
31	l	237/1017 (23%)	234 (99%)	3 (1%)	61	72
All	All	6560/12934 (51%)	6528 (100%)	32 (0%)	78	80

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	W	272	ASP
31	l	1489	LYS
15	O	604	LYS
9	I	83	ASP
31	l	2031	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
12	L	26	ASN
26	Z	244	ASN
17	Q	373	ASN
25	Y	12	HIS
30	d	49	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	P	11/13 (84%)	2 (18%)	2 (18%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	P	17	A
16	P	19	A

All (2) RNA pucker outliers are listed below:



Mol	Chain	Res	Type
16	P	16	A
16	P	18	A

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	SEP	A	1547	1	8,9,10	1.61	1 (12%)	7,12,14	1.28	1 (14%)
26	TPO	Z	775	26	8,10,11	1.13	0	10,14,16	1.90	1 (10%)
1	TPO	A	1525	1	8,10,11	1.12	0	10,14,16	2.13	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	1547	1	-	0/6/8/10	-
26	TPO	Z	775	26	-	2/9/11/13	-
1	TPO	A	1525	1	-	0/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1547	SEP	P-O1P	3.51	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1525	TPO	P-OG1-CB	-6.08	106.81	123.33
26	Z	775	TPO	P-OG1-CB	-5.19	109.22	123.33
1	A	1547	SEP	OG-CB-CA	2.76	110.83	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
26	Z	775	TPO	C-CA-CB-CG2
26	Z	775	TPO	CB-OG1-P-O2P

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1547	SEP	1	0
26	Z	775	TPO	2	0
1	A	1525	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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
21	U	1
22	V	1
13	M	1
31	l	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U	497:ASP	C	505:SER	N	27.02
1	V	299:GLU	C	310:ASN	N	12.71
1	M	1334:ASN	C	1338:ILE	N	5.60
1	l	1709:SER	C	1710:ARG	N	4.41

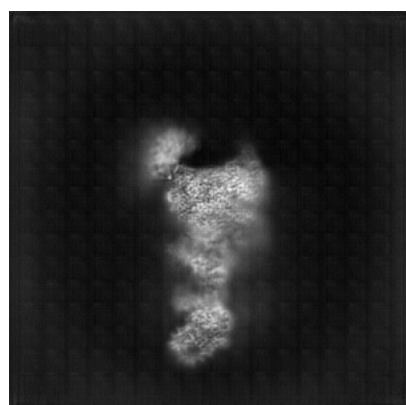
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48042. These allow visual inspection of the internal detail of the map and identification of artifacts.

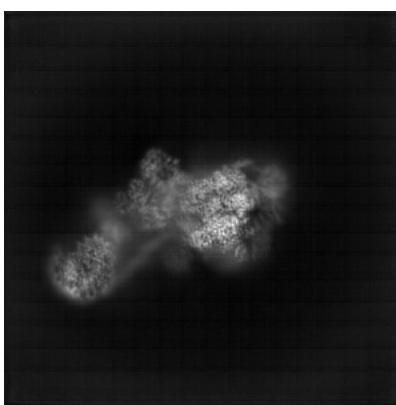
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

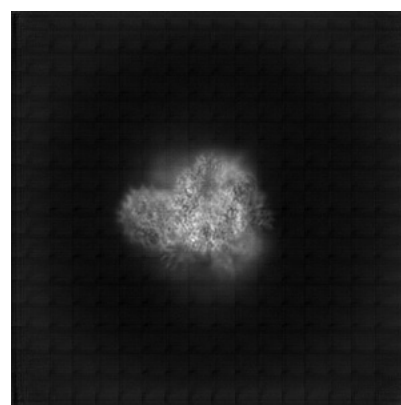
#### 6.1.1 Primary map



X



Y

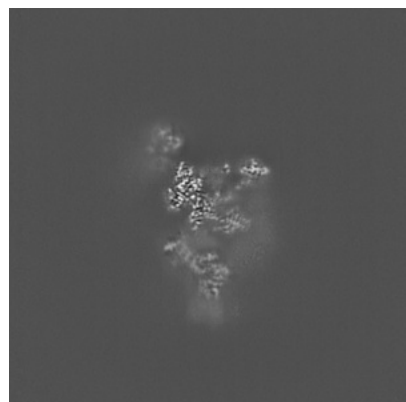


Z

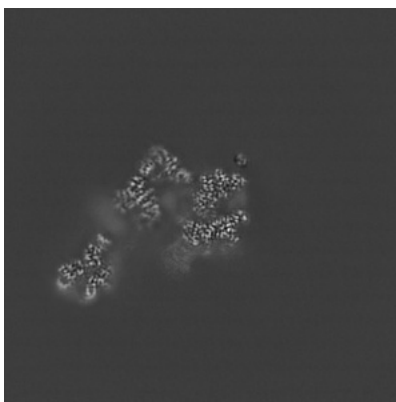
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

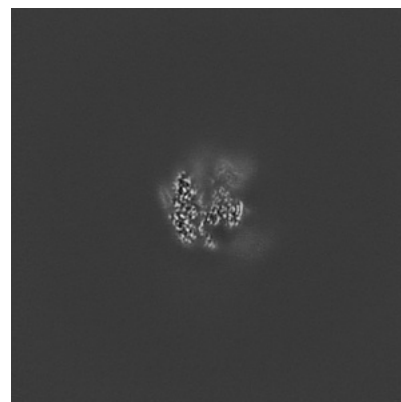
#### 6.2.1 Primary map



X Index: 250



Y Index: 250

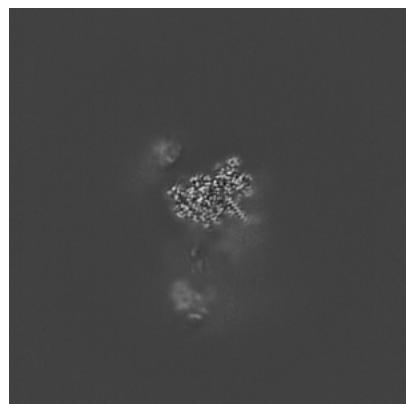


Z Index: 250

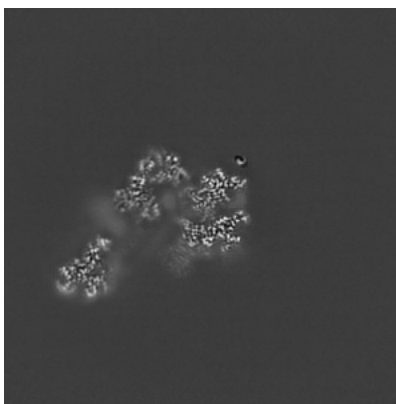
The images above show central slices of the map in three orthogonal directions.

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

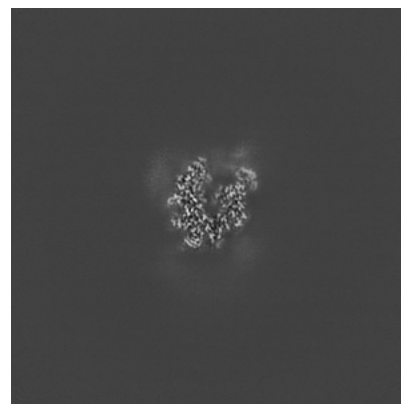
### 6.3.1 Primary map



X Index: 221



Y Index: 253



Z Index: 275

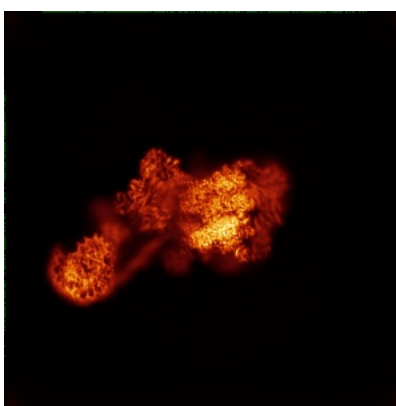
The images above show the largest variance slices of the map in three orthogonal directions.

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

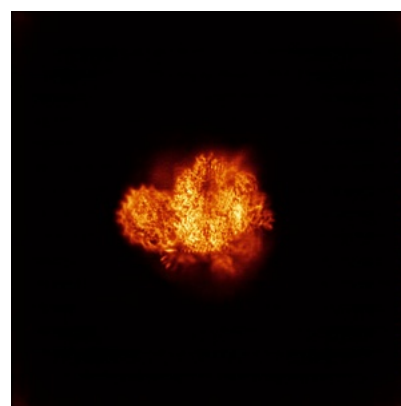
### 6.4.1 Primary map



X



Y

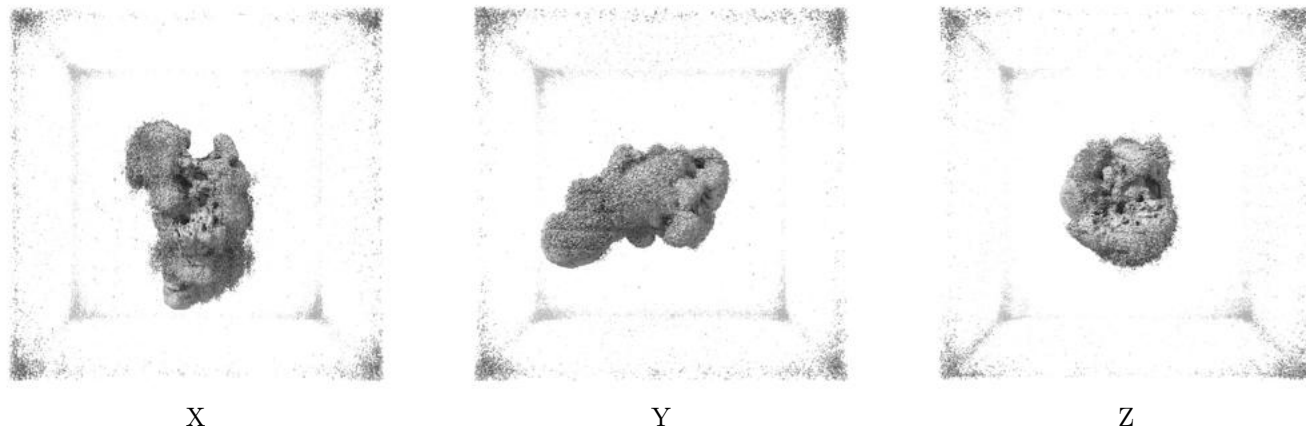


Z

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

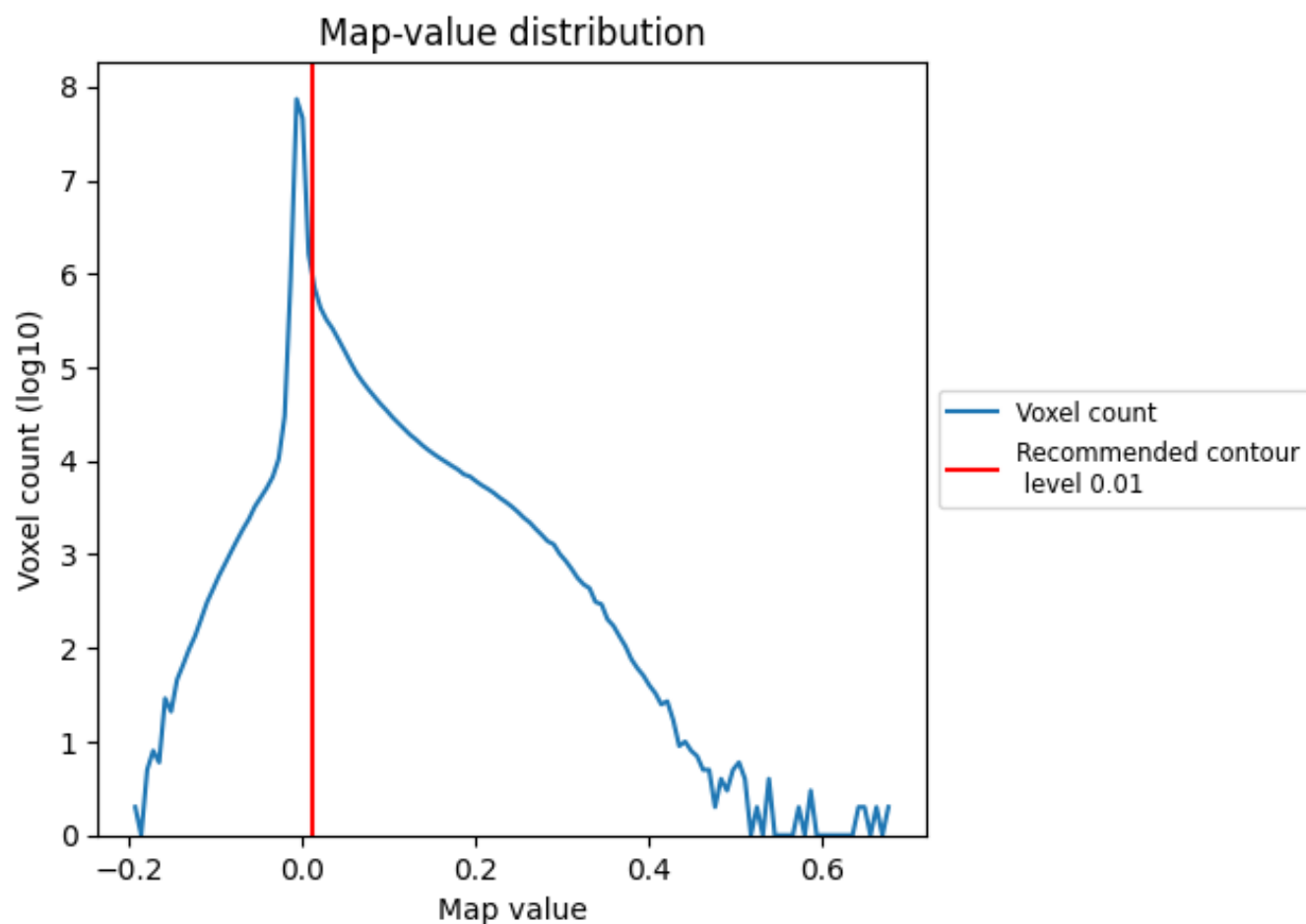
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

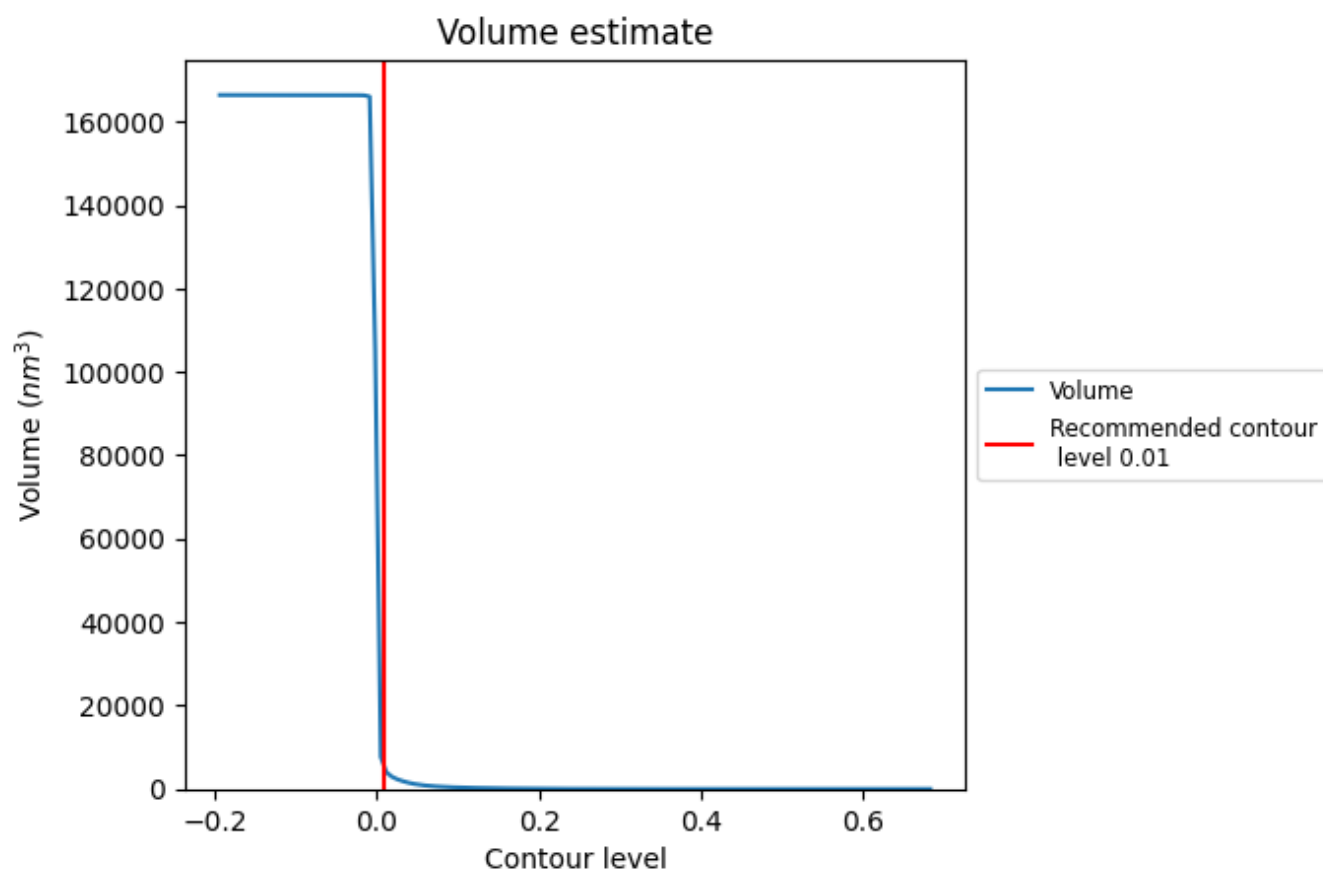
This section contains the results of statistical analysis of the map.

### 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](#)

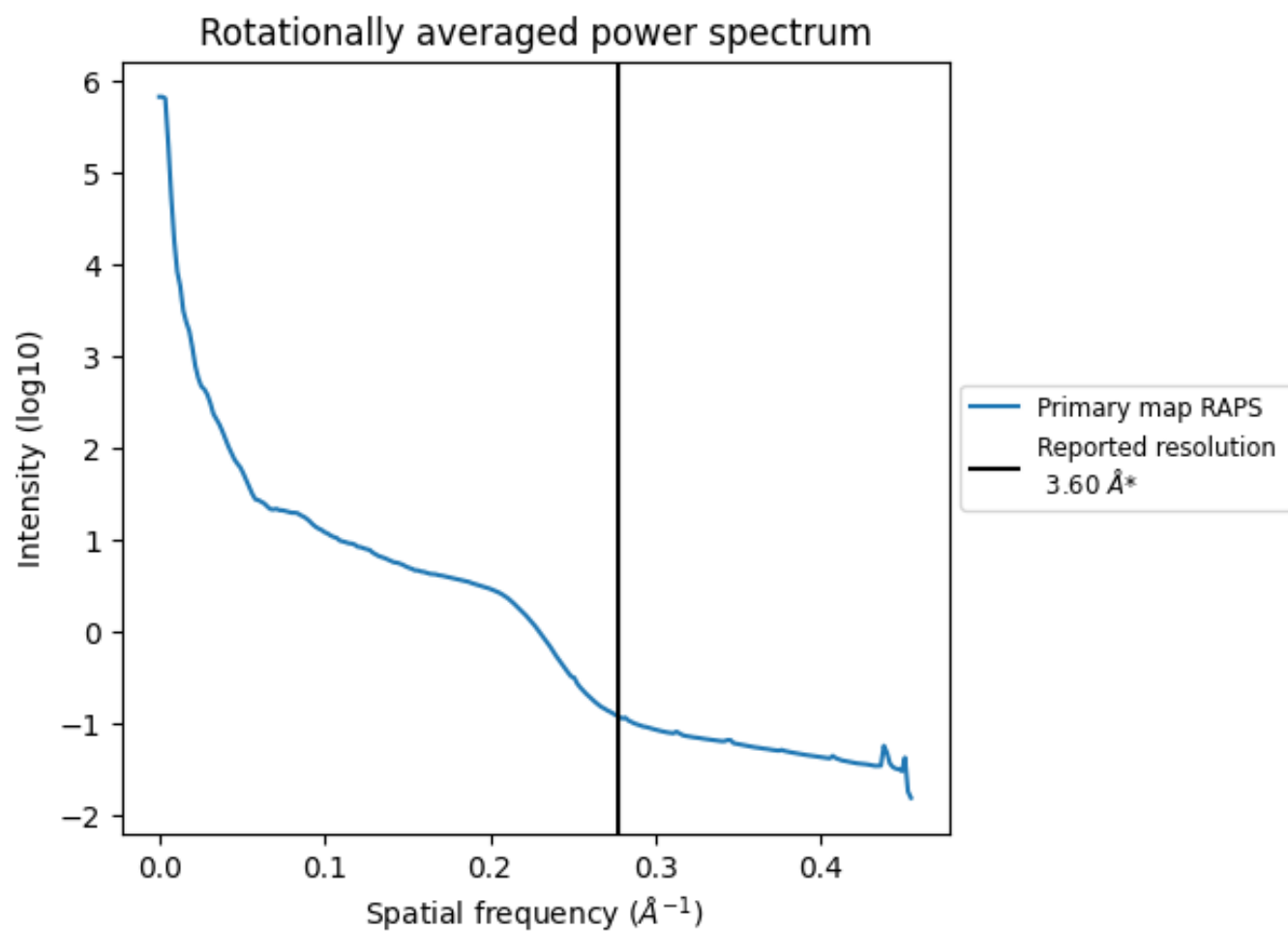


The volume at the recommended contour level is 5148 nm<sup>3</sup>; this corresponds to an approximate mass of 4651 kDa.

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 0.278  $\text{\AA}^{-1}$

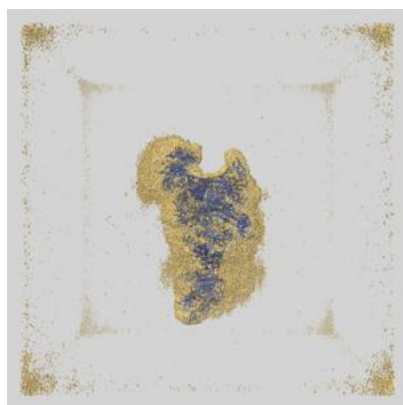
## 8 Fourier-Shell correlation

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

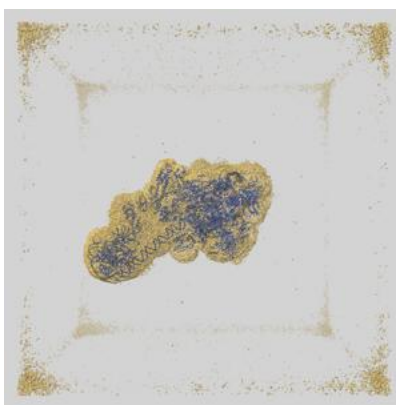
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48042 and PDB model 9EH0. Per-residue inclusion information can be found in section [3](#) on page [12](#).

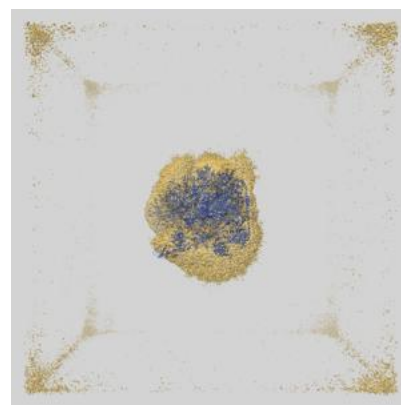
### 9.1 Map-model overlay [i](#)



X



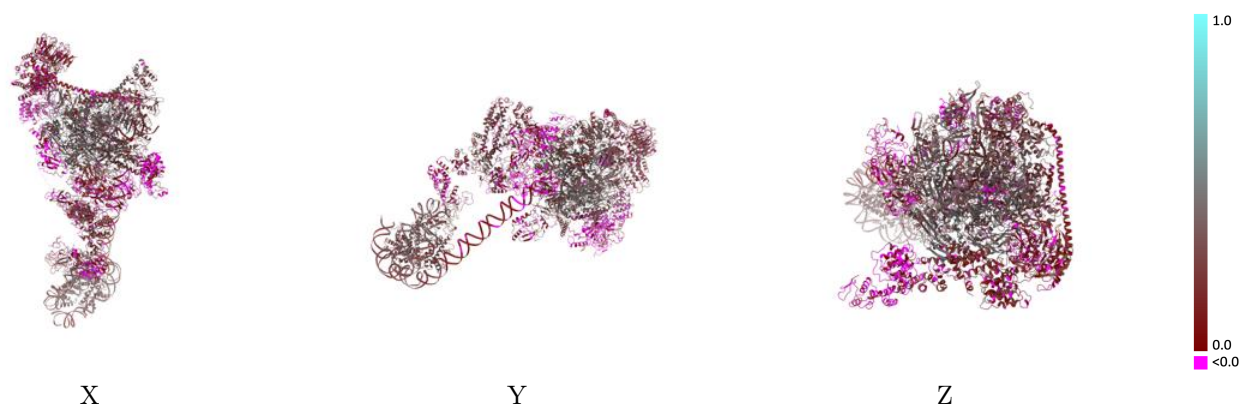
Y



Z

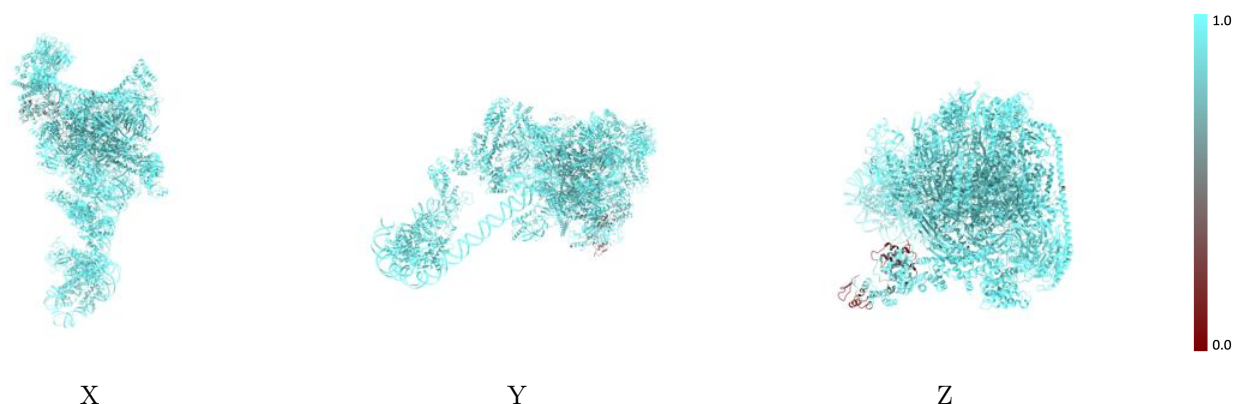
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



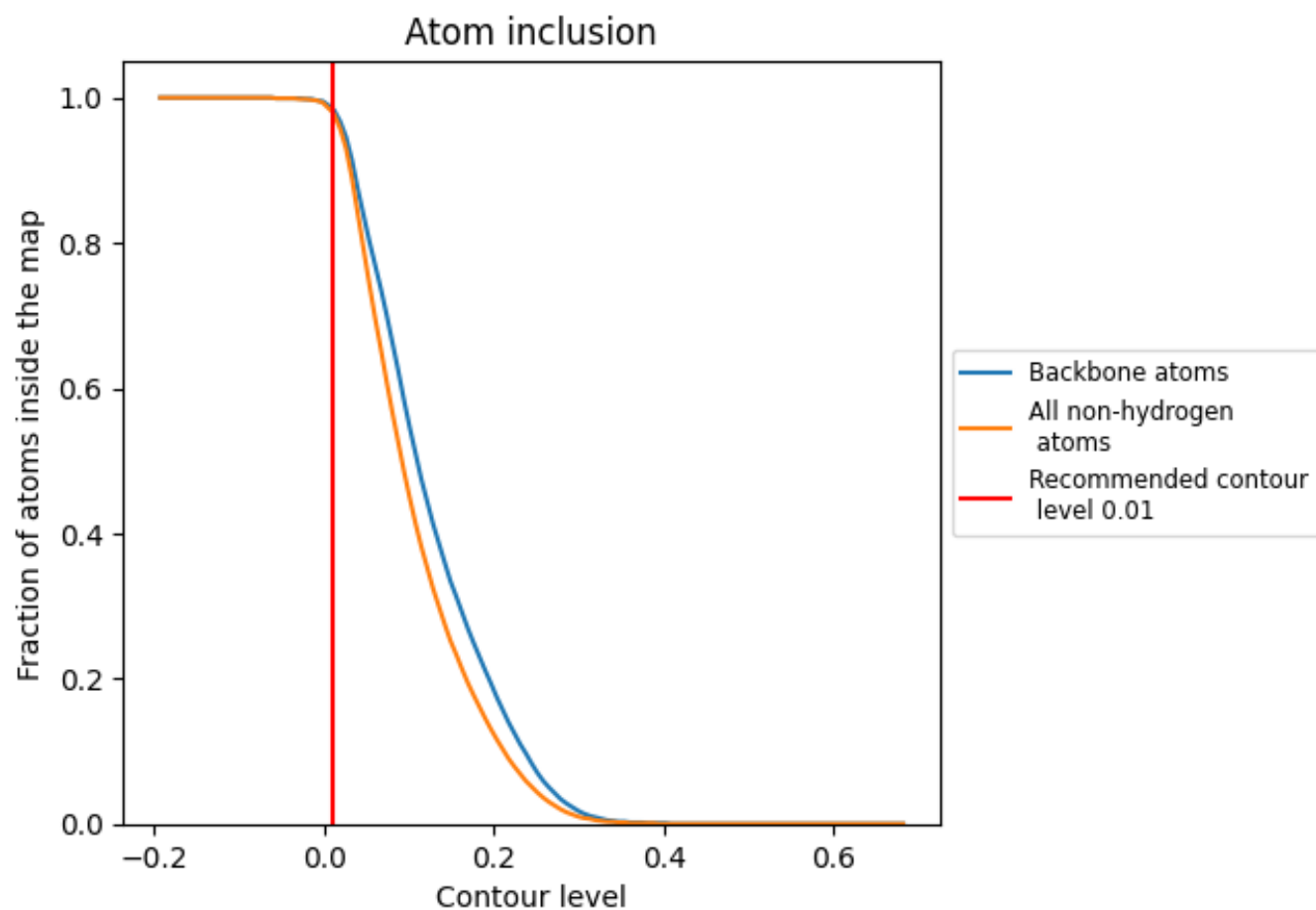
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9800	 0.2400
A	 0.9930	 0.3520
B	 0.9910	 0.3820
C	 0.9970	 0.4190
D	 0.9880	 0.1880
E	 0.9940	 0.3350
F	 0.9870	 0.3930
G	 0.9890	 0.2060
H	 0.9840	 0.3950
I	 0.9890	 0.3460
J	 0.9900	 0.3930
K	 0.9970	 0.4010
L	 1.0000	 0.3580
M	 0.9950	 0.1470
N	 1.0000	 0.2300
O	 1.0000	 0.0150
P	 1.0000	 0.2090
Q	 0.8850	 0.0790
R	 0.9670	 0.0920
S	 1.0000	 0.2400
T	 1.0000	 0.2210
U	 0.9930	 0.0160
V	 0.8710	 0.0570
W	 1.0000	 0.1550
X	 0.9940	 0.1760
Y	 0.9970	 -0.0020
Z	 0.9990	 0.0700
a	 0.9870	 0.3390
b	 0.9980	 0.3680
c	 0.9870	 0.3220
d	 0.9890	 0.3130
e	 0.9810	 0.3320
f	 0.9800	 0.3550
g	 0.9920	 0.3260
h	 0.9880	 0.3260
l	 0.9970	 0.1220

