



## wwPDB EM Validation Summary Report ⓘ

Nov 5, 2024 – 03:13 AM JST

PDB ID : 5ZWM  
EMDB ID : EMD-6972  
Title : Cryo-EM structure of the yeast pre-B complex at an average resolution of 3.4 4.6 angstrom (tri-snRNP and U2 snRNP Part)  
Authors : Bai, R.; Wan, R.; Yan, C.; Lei, J.; Shi, Y.  
Deposited on : 2018-05-16  
Resolution : 3.40 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>.

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

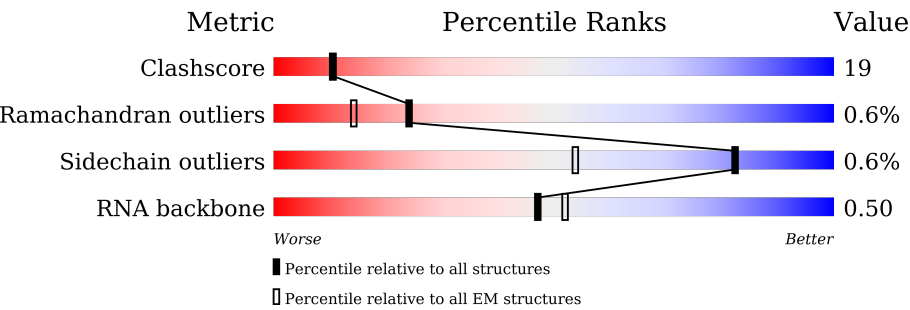


# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191




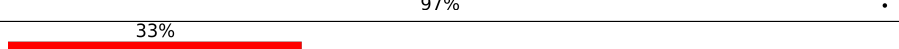
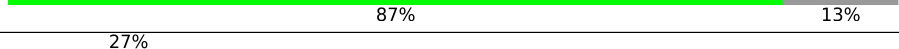
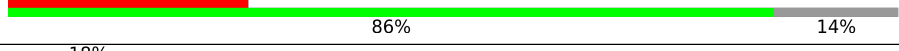


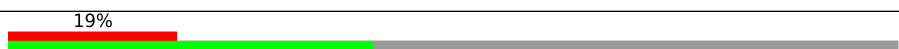
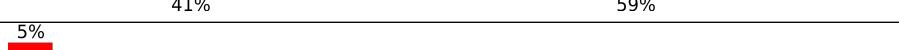
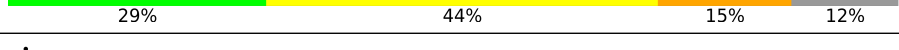




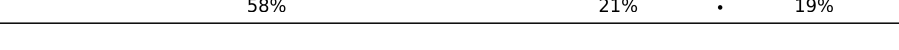





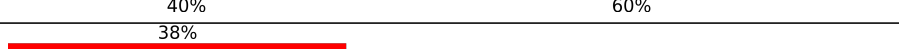
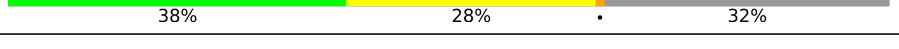
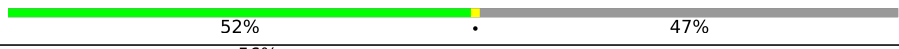

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey 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	2413	<div><div>8%</div><div>60%</div><div>29%</div><div>10%</div></div>
2	K	465	<div><div>53%</div><div>38%</div><div>8%</div></div>
3	L	494	<div><div>58%</div><div>26%</div><div>16%</div></div>
4	N	899	<div><div>65%</div><div>16%</div><div>19%</div></div>
5	J	469	<div><div>50%</div><div>14%</div><div>35%</div></div>
6	E	143	<div><div>71%</div><div>27%</div></div>
7	M	126	<div><div>75%</div><div>25%</div></div>

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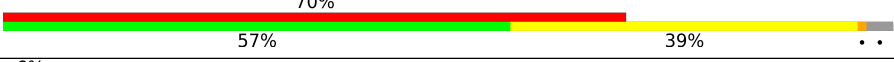
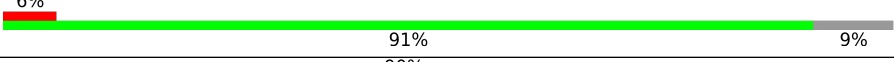
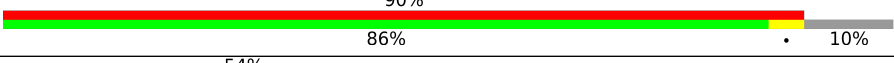
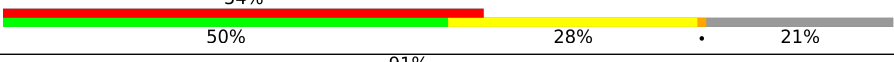
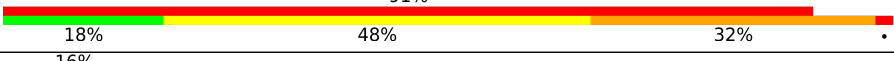

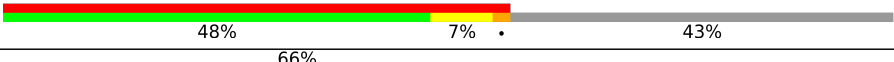


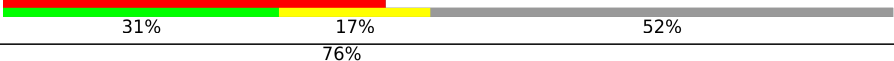






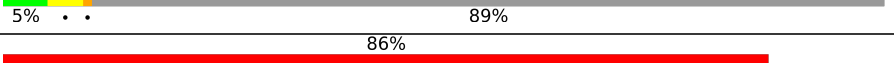


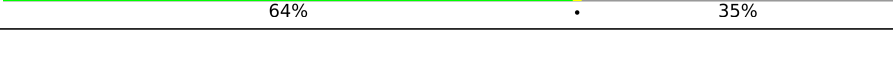
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Mol	Chain	Length	Quality of chain
8	C	1008	
9	z	109	
10	q	95	
11	r	89	
12	x	86	
13	t	93	
14	y	115	
15	s	187	
16	F	112	
17	I	160	
18	B	214	
19	O	587	
20	S	101	
20	d	101	
20	l	101	
21	P	196	
21	a	196	
21	h	196	
22	Q	146	
22	b	146	
22	m	146	
23	R	110	
23	c	110	
23	n	110	
24	T	94	

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Mol	Chain	Length	Quality of chain
24	e	94	
24	i	94	
25	U	86	
25	f	86	
25	j	86	
26	V	77	
26	g	77	
26	k	77	
27	D	2163	
28	G	44	
29	H	1175	
30	o	238	
31	p	111	
32	1	971	
33	2	436	
34	3	1361	
35	4	213	
36	5	107	
37	6	85	
38	X	148	
39	Y	266	
40	Z	204	
41	u	530	
42	w	280	
43	v	266	



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
46	ZN	5	201	-	-	X	-



## 2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 111041 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2177	Total	C	N	O	S	0	0
			17877	11496	3054	3263	64		

- Molecule 2 is a protein called U4/U6 small nuclear ribonucleoprotein PRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	429	Total	C	N	O	S	0	0
			3375	2101	610	650	14		

- Molecule 3 is a protein called Pre-mRNA-processing factor 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	416	Total	C	N	O	S	0	0
			3171	2001	573	585	12		

- Molecule 4 is a protein called Pre-mRNA-splicing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	728	Total	C	N	O	S	0	0
			4897	3045	905	933	14		

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein PRP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	304	Total	C	N	O	S	0	0
			2439	1545	445	435	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	139	Total	C	N	O	S	0	0
			1146	725	199	211	11		



- Molecule 7 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	126	Total	C	N	O	S	0	0
			950	605	163	177	5		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	z	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 10 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	q	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 11 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	r	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 12 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	x	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 13 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	t	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 14 is a protein called U6 snRNA-associated Sm-like protein LSm7.



Mol	Chain	Residues	Atoms				AltConf	Trace
14	y	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 15 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	s	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 16 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	99	Total	C	N	O	P	0	0
			2043	913	341	690	99		

- Molecule 17 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	110	Total	C	N	O	P	0	0
			2334	1044	399	781	110		

- Molecule 18 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B	175	Total	C	N	O	P	0	0
			3715	1663	651	1227	174		

- Molecule 19 is a protein called 66 kDa U4/U6.U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	74	Total	C	N	O	S	0	0
			574	350	103	120	1		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	79	Total	C	N	O		0	0
			316	158	79	79			
20	S	82	Total	C	N	O	S	0	0
			632	402	109	119	2		
20	l	81	Total	C	N	O	S	0	0
			611	390	106	113	2		



- Molecule 21 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	73	Total	C	N	O	0	0
			292	146	73	73		
21	P	70	Total	C	N	O	S	0
			563	360	98	102	3	0
21	h	78	Total	C	N	O	S	0
			610	389	110	108	3	0

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	b	77	Total	C	N	O	0	0
			308	154	77	77		
22	Q	99	Total	C	N	O	S	0
			751	475	137	137	2	0
22	m	82	Total	C	N	O	S	0
			644	409	110	123	2	0

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	c	90	Total	C	N	O	0	0
			360	180	90	90		
23	R	92	Total	C	N	O	S	0
			752	481	136	131	4	0
23	n	65	Total	C	N	O	S	0
			528	340	102	84	2	0

- Molecule 24 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	e	72	Total	C	N	O	0	0
			288	144	72	72		
24	T	77	Total	C	N	O	S	0
			602	396	95	108	3	0
24	i	75	Total	C	N	O	S	0
			575	379	92	101	3	0

- Molecule 25 is a protein called Small nuclear ribonucleoprotein F.



Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	70	Total	C	N	O		0	0
			280	140	70	70			
25	U	73	Total	C	N	O	S	0	0
			585	376	102	106	1		
25	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	70	Total	C	N	O		0	0
			280	140	70	70			
26	V	75	Total	C	N	O	S	0	0
			577	363	100	112	2		
26	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 27 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	1699	Total	C	N	O	S	1	0
			13601	8717	2266	2564	54		

- Molecule 28 is a RNA chain called Pre-mRNA-BPS.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	44	Total	C	N	O	P	0	0
			928	419	161	304	44		

- Molecule 29 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	206	Total	C	N	O	P	0	0
			4345	1940	722	1477	206		

- Molecule 30 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	o	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein B''.



Mol	Chain	Residues	Atoms				AltConf	Trace
31	p	73	Total	C	N	O	0	0
			466	304	81	81		

- Molecule 32 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1	816	Total	C	N	O	S	0	0
			6472	4165	1101	1166	40		

- Molecule 33 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	211	Total	C	N	O	S	0	0
			1726	1121	292	304	9		

- Molecule 34 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	3	1180	Total	C	N	O	S	0	0
			9380	5996	1580	1753	51		

- Molecule 35 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	173	Total	C	N	O	S	0	0
			1429	930	239	258	2		

- Molecule 36 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 37 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	6	84	Total	C	N	O	S	0	0
			693	429	130	132	2		

- Molecule 38 is a protein called U2 snRNP component IST3.



Mol	Chain	Residues	Atoms				AltConf	Trace
38	X	128	Total	C	N	O	0	0
			1051	662	181	208		

- Molecule 39 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	89	Total	C	N	O	S	0	0
			730	458	130	140	2		

- Molecule 40 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	22	Total	C	N	O	S	0	0
			173	110	25	37	1		

- Molecule 41 is a protein called Pre-mRNA-splicing factor PRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	u	461	Total	C	N	O	S	0	0
			3895	2475	675	730	15		

- Molecule 42 is a protein called Pre-mRNA-splicing factor PRP21.

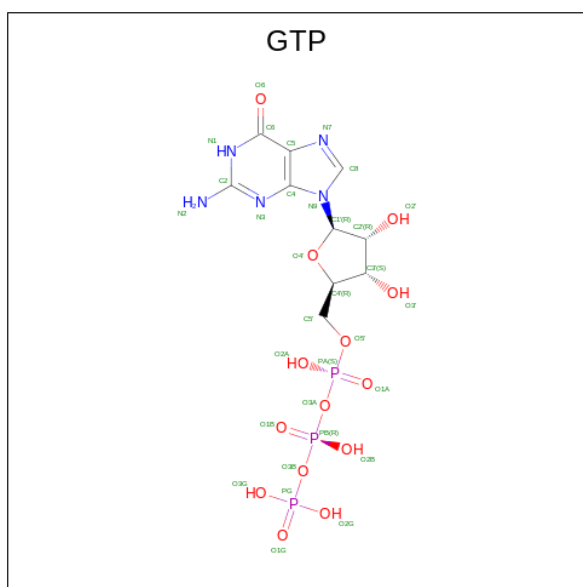
Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	127	Total	C	N	O	S	0	0
			1084	689	193	196	6		

- Molecule 43 is a protein called Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	174	Total	C	N	O	S	0	0
			1372	862	235	269	6		

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).





Mol	Chain	Residues	Atoms					AltConf
44	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 45 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
45	C	1	Total	Mg	0
			1	1	

- Molecule 46 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	5	3	Total	Zn	0
			3	3	
46	u	2	Total	Zn	0
			2	2	
46	v	1	Total	Zn	0
			1	1	





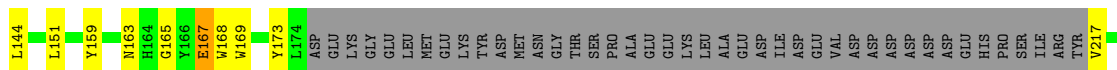








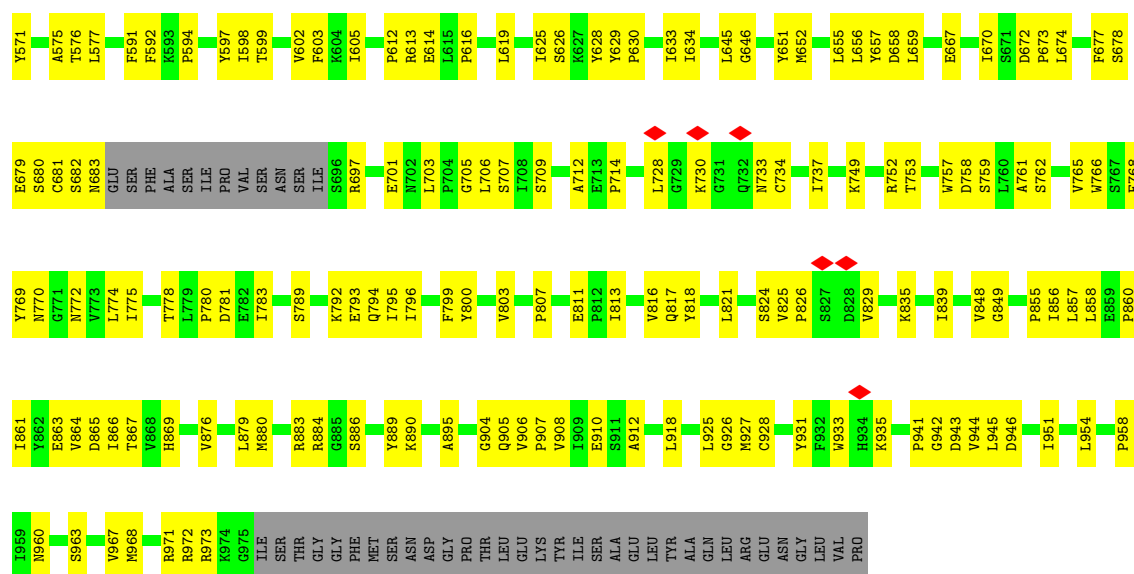














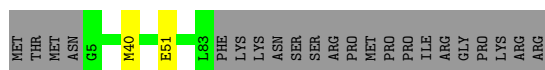
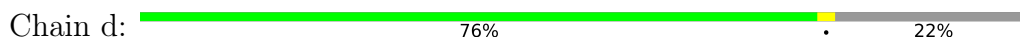




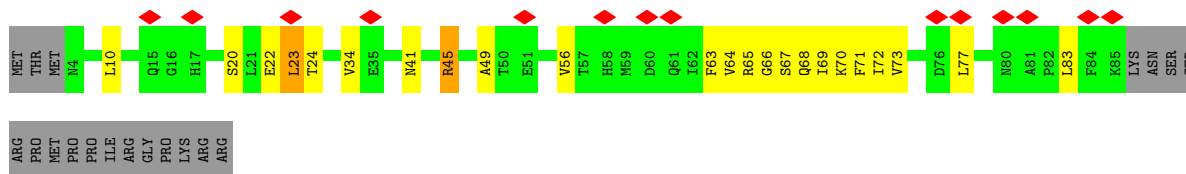




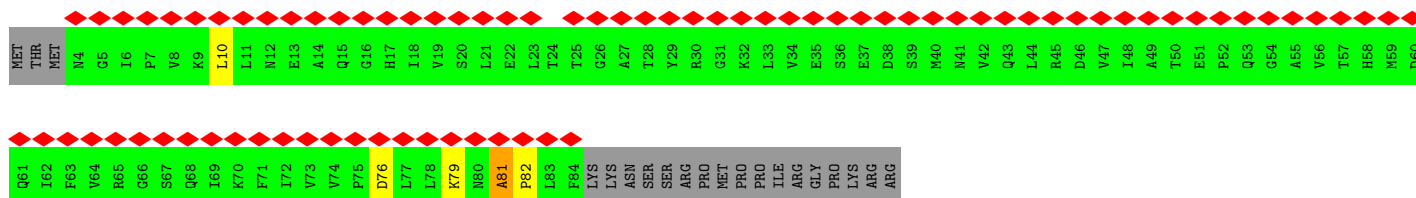
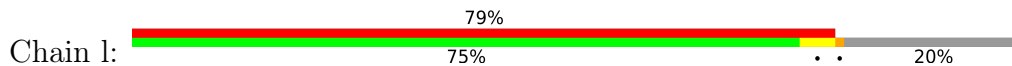
- Molecule 20: Small nuclear ribonucleoprotein Sm D3



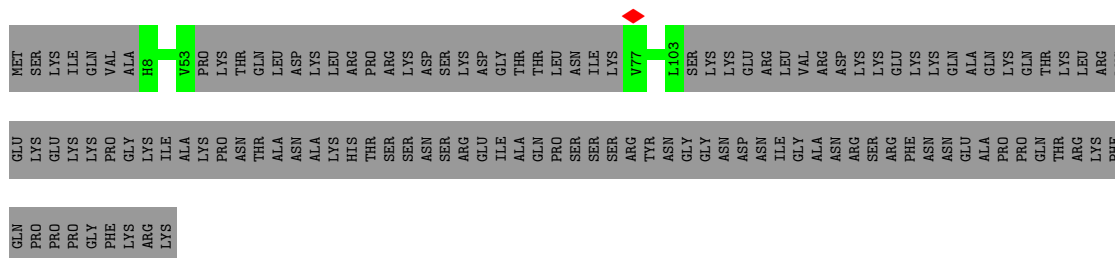
- Molecule 20: Small nuclear ribonucleoprotein Sm D3



- Molecule 20: Small nuclear ribonucleoprotein Sm D3



- Molecule 21: Small nuclear ribonucleoprotein-associated protein B



- Molecule 21: Small nuclear ribonucleoprotein-associated protein B

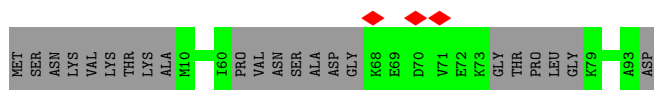




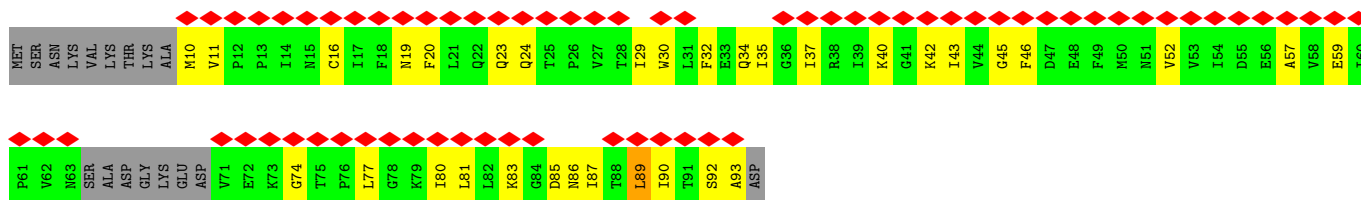
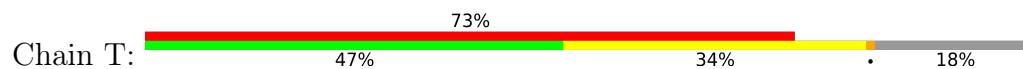




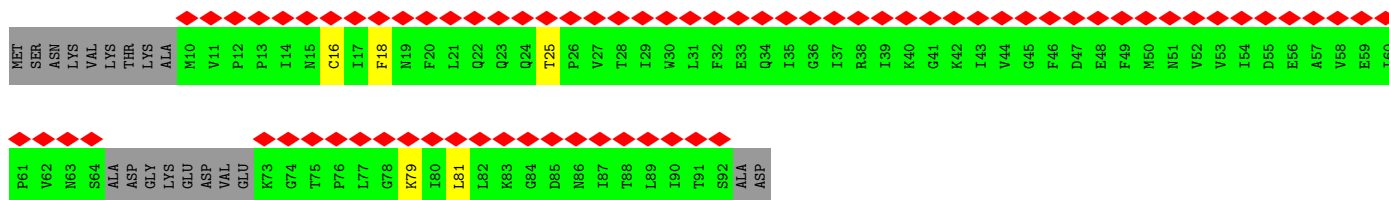
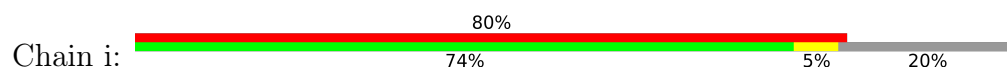




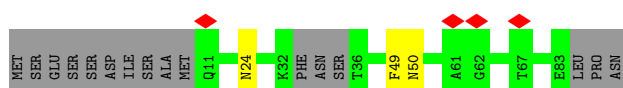
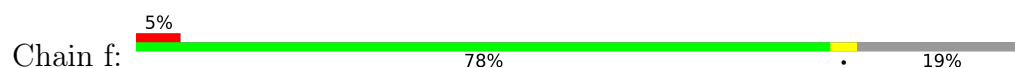
- Molecule 24: Small nuclear ribonucleoprotein E



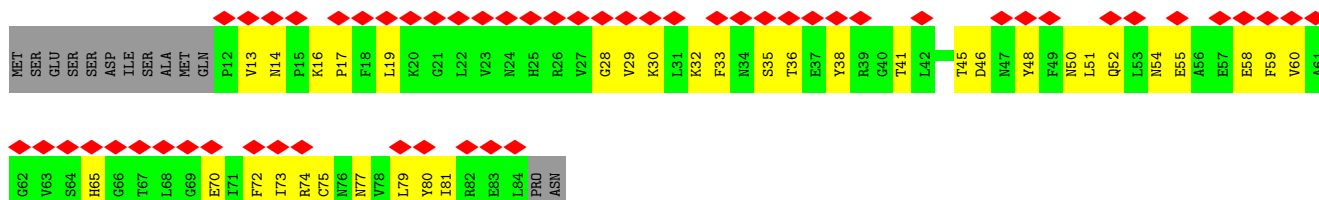
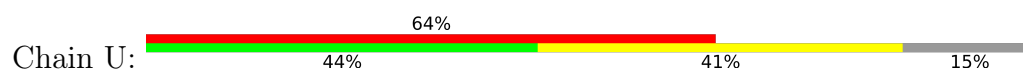
- Molecule 24: Small nuclear ribonucleoprotein E



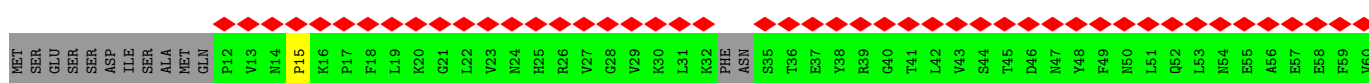
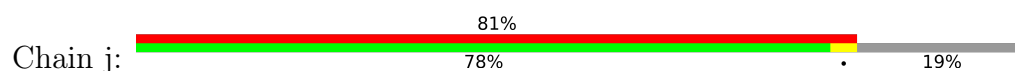
- Molecule 25: Small nuclear ribonucleoprotein F



- Molecule 25: Small nuclear ribonucleoprotein F



- Molecule 25: Small nuclear ribonucleoprotein F







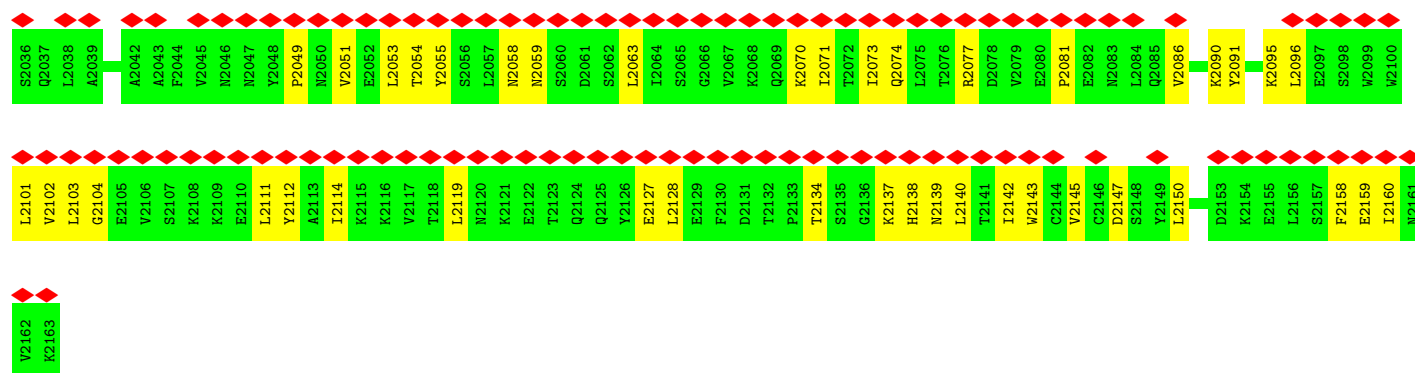




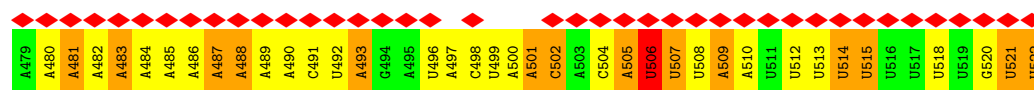
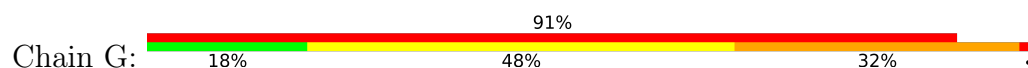


WORLDWIDE  
**PDB**  
PROTEIN DATA BANK

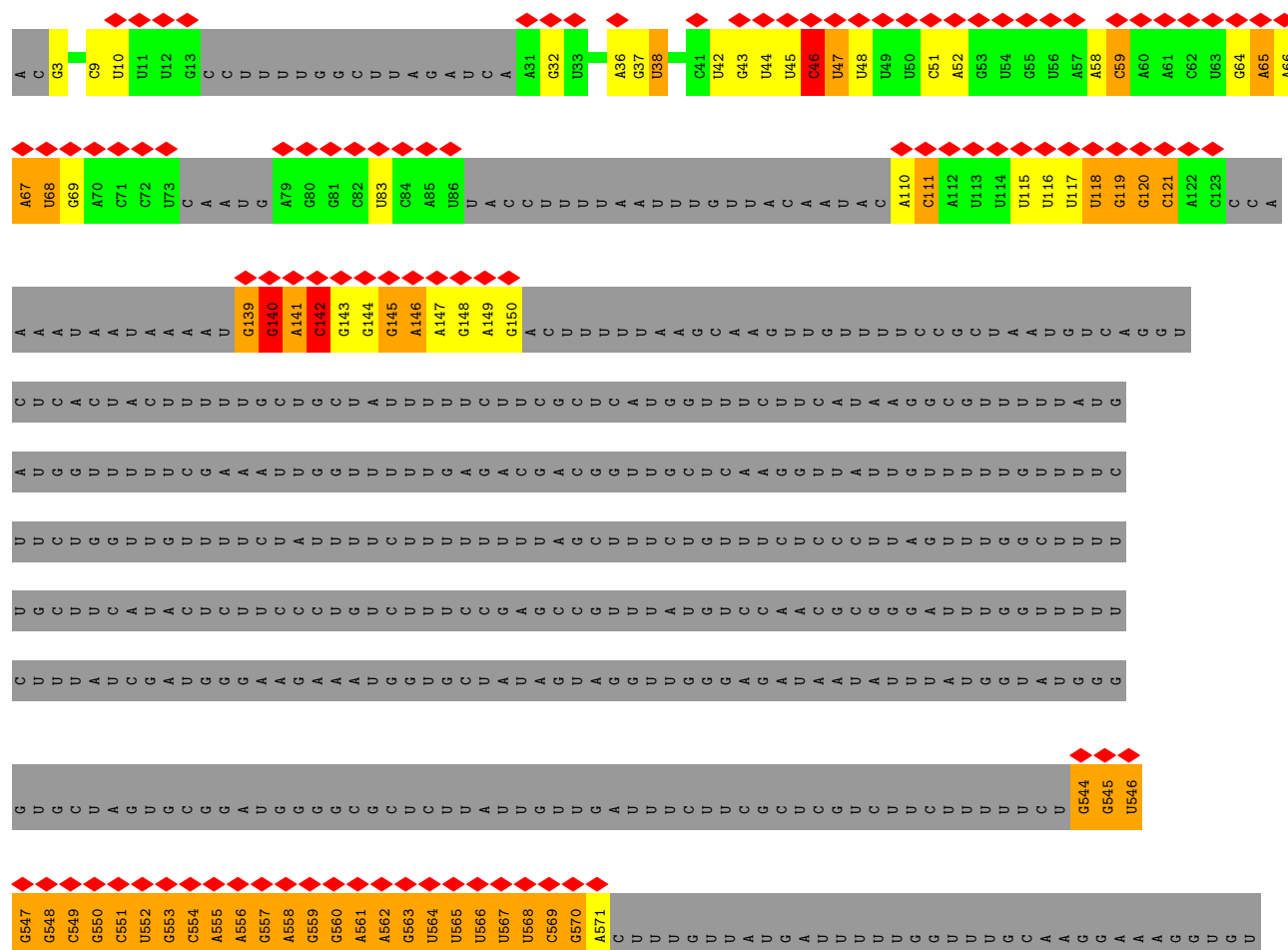




• Molecule 28: Pre-mRNA-BPS



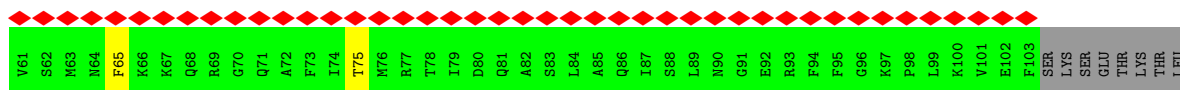
• Molecule 29: U2 snRNA



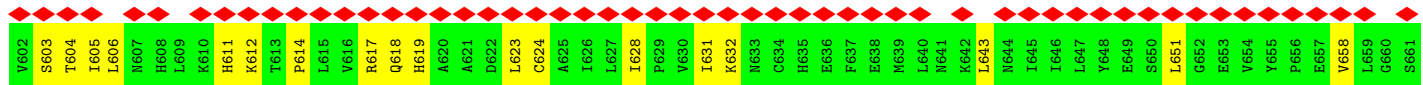
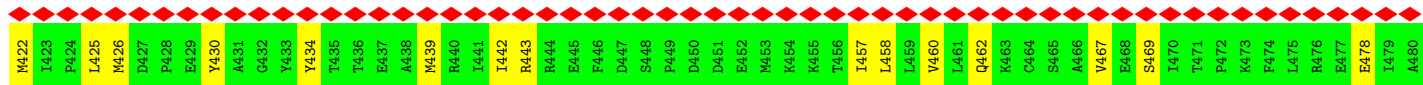
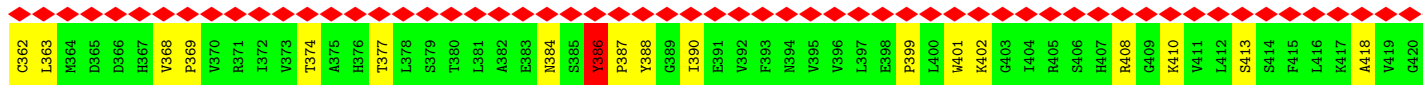
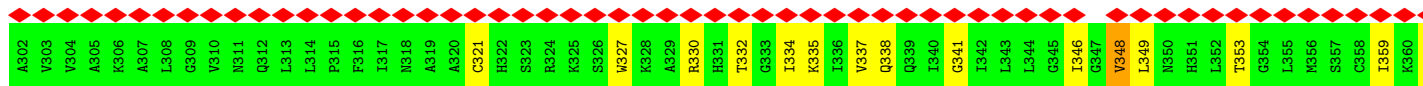
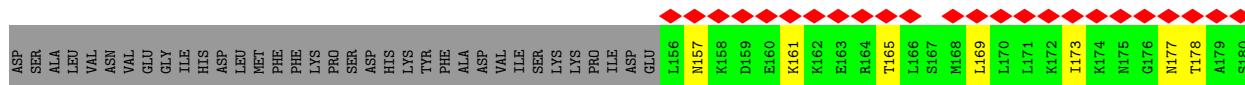
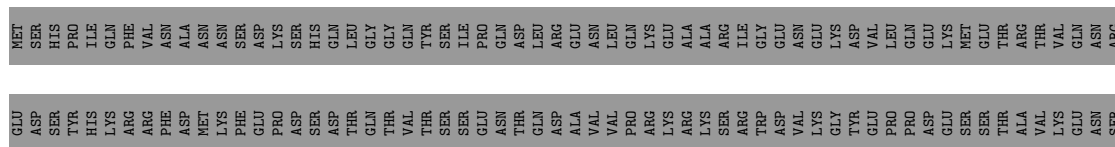
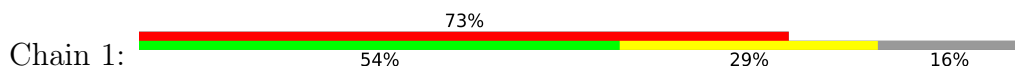








## • Molecule 32: U2 snRNP component HSH155











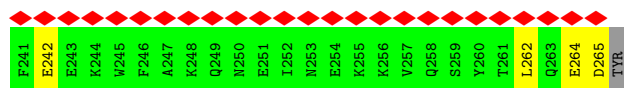




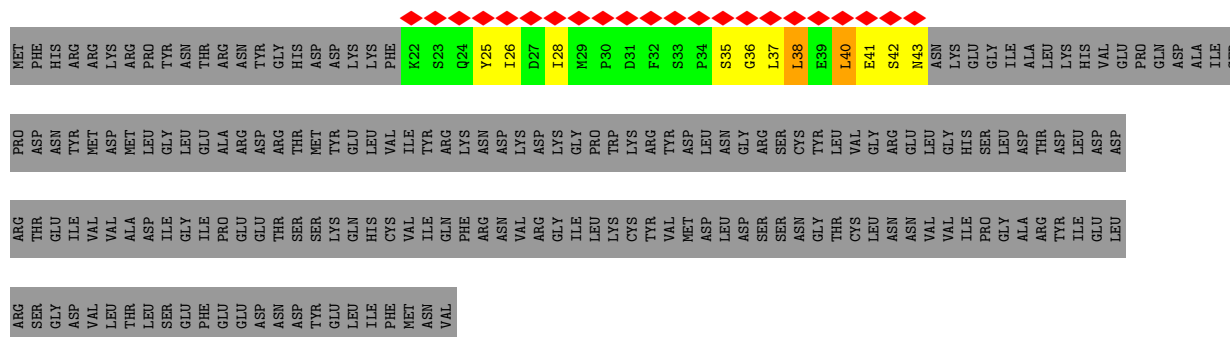




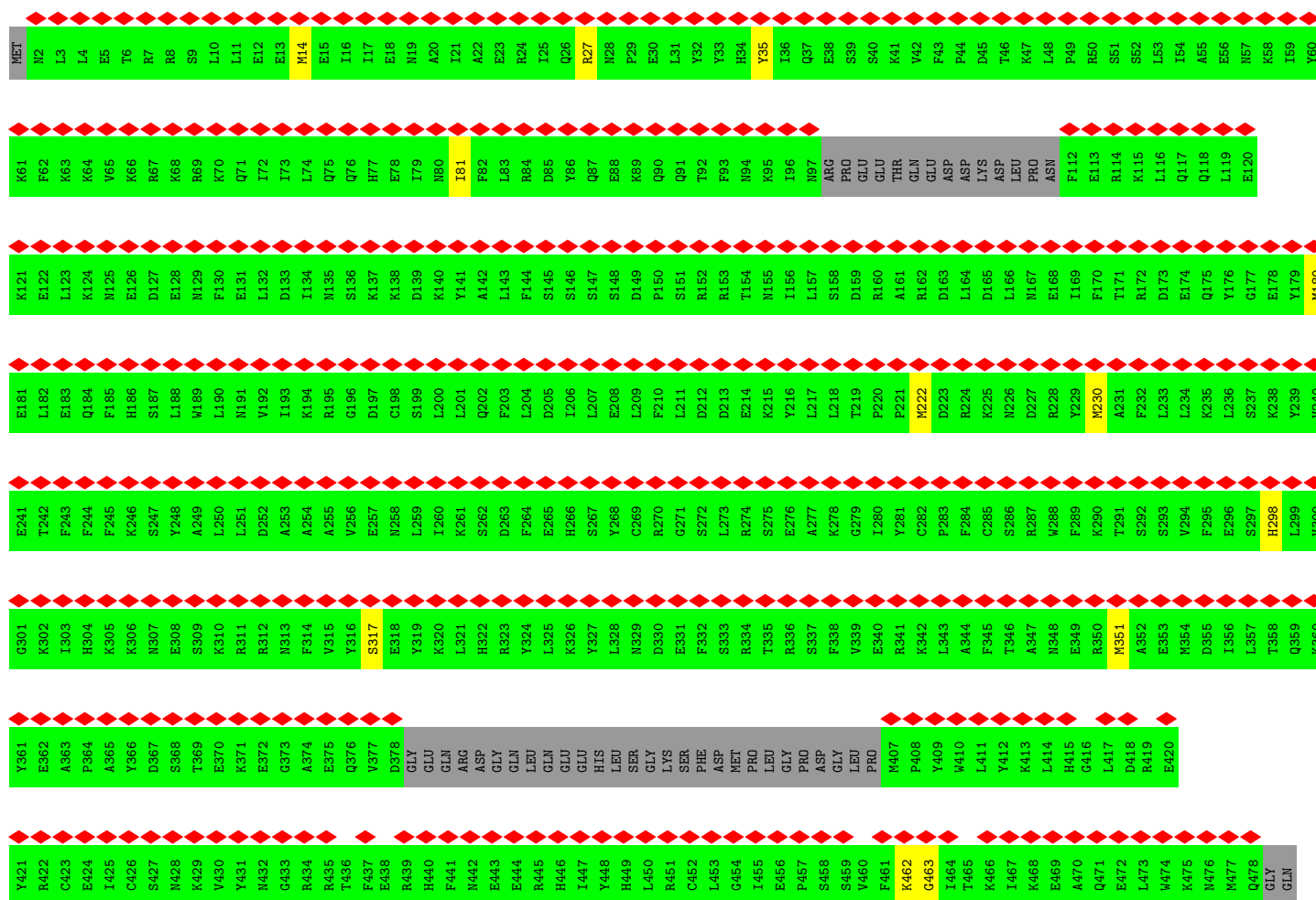
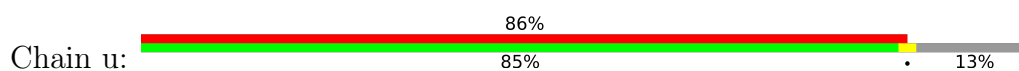




• Molecule 40: Pre-mRNA leakage protein 1



• Molecule 41: Pre-mRNA-splicing factor PRP9









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	500657	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 K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.386	Depositor
Minimum map value	-0.170	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.023	Depositor
Map size ( $\text{\AA}$ )	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.338, 1.338, 1.338	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.33	2/18332 (0.0%)	0.51	1/24851 (0.0%)
2	K	0.33	0/3431	0.59	0/4631
3	L	0.31	0/3219	0.48	0/4332
4	N	0.28	0/4937	0.47	0/6704
5	J	0.30	0/2485	0.46	0/3333
6	E	0.34	0/1167	0.50	0/1571
7	M	0.31	0/963	0.51	0/1310
8	C	0.32	0/6874	0.52	0/9305
9	z	0.49	0/259	0.70	0/322
10	q	0.49	0/367	0.65	0/457
11	r	0.59	0/307	0.75	0/382
12	x	0.48	0/295	0.68	0/367
13	t	0.50	0/306	0.71	0/379
14	y	0.49	0/262	0.71	0/324
15	s	0.47	0/306	0.68	0/379
16	F	0.38	0/2277	0.90	0/3534
17	I	0.53	4/2604 (0.2%)	0.99	10/4046 (0.2%)
18	B	0.36	1/4151 (0.0%)	0.97	18/6462 (0.3%)
19	O	0.25	0/573	0.42	0/763
20	S	0.41	0/641	0.65	2/868 (0.2%)
20	d	0.29	0/315	0.46	0/392
20	l	0.45	1/620 (0.2%)	0.68	1/841 (0.1%)
21	P	0.41	0/567	0.61	0/762
21	a	0.28	0/290	0.46	0/359
21	h	0.37	0/615	0.61	0/829
22	Q	0.39	0/756	0.69	1/1023 (0.1%)
22	b	0.27	0/305	0.47	0/376
22	m	0.42	0/649	0.61	0/880
23	R	0.38	0/764	0.57	0/1026
23	c	0.25	0/358	0.45	0/444
23	n	0.41	0/535	0.57	0/717
24	T	0.38	0/612	0.59	1/830 (0.1%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
24	e	0.29	0/285	0.43	0/351
24	i	0.43	0/585	0.62	0/795
25	U	0.39	0/597	0.62	0/807
25	f	0.30	0/278	0.45	0/344
25	j	0.44	0/564	0.66	2/761 (0.3%)
26	V	0.41	0/582	0.67	1/785 (0.1%)
26	g	0.25	0/277	0.46	0/341
26	k	0.37	0/532	0.60	0/715
27	D	0.40	1/13899 (0.0%)	0.62	6/18845 (0.0%)
28	G	0.26	0/1038	0.87	3/1611 (0.2%)
29	H	1.10	61/4835 (1.3%)	1.70	185/7502 (2.5%)
30	o	1.03	9/839 (1.1%)	1.65	11/1127 (1.0%)
31	p	0.81	3/467 (0.6%)	1.35	2/623 (0.3%)
32	1	0.28	0/6600	0.48	1/8962 (0.0%)
33	2	0.26	0/1775	0.45	0/2402
34	3	0.30	0/9564	0.57	1/12963 (0.0%)
35	4	0.26	0/1453	0.43	0/1954
36	5	0.28	0/827	0.46	0/1105
37	6	0.28	0/702	0.44	0/939
38	X	0.49	0/1071	0.65	0/1445
39	Y	0.52	0/743	0.70	0/994
40	Z	0.51	0/176	0.59	0/237
41	u	0.35	5/3972 (0.1%)	0.41	0/5322
42	w	0.45	4/1105 (0.4%)	0.37	0/1475
43	v	0.29	1/1396 (0.1%)	0.41	0/1881
All	All	0.42	92/114304 (0.1%)	0.71	246/157085 (0.2%)

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
1	A	0	1
2	K	0	2
3	L	0	1
4	N	0	2
8	C	0	2
27	D	0	4
32	1	0	4
34	3	0	1
41	u	0	2
All	All	0	19



The worst 5 of 92 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	H	1161	U	O3'-P	-15.59	1.42	1.61
29	H	1092	A	O3'-P	-14.82	1.43	1.61
29	H	1116	A	O3'-P	-11.52	1.47	1.61
29	H	1163	C	O5'-C5'	9.10	1.59	1.44
29	H	1116	A	C3'-O3'	-8.99	1.29	1.42

The worst 5 of 246 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1162	U	C5'-C4'-O4'	14.85	126.92	109.10
29	H	1093	C	P-O5'-C5'	14.77	144.53	120.90
29	H	1147	A	C5'-C4'-C3'	-14.16	93.34	116.00
29	H	1092	A	C2'-C3'-O3'	14.09	140.49	109.50
29	H	1098	C	N1-C1'-C2'	-13.36	96.64	114.00

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	239	PHE	Peptide
2	K	208	GLN	Peptide
2	K	383	GLU	Peptide
3	L	397	GLU	Peptide
4	N	11	PRO	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17877	0	17800	639	0
2	K	3375	0	3343	176	0
3	L	3171	0	3140	127	0
4	N	4897	0	3994	115	0
5	J	2439	0	2341	62	0
6	E	1146	0	1133	29	0
7	M	950	0	1004	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	6732	0	6904	274	0
9	z	260	0	72	0	0
10	q	368	0	99	0	0
11	r	308	0	80	0	0
12	x	296	0	83	0	0
13	t	308	0	85	0	0
14	y	264	0	76	0	0
15	s	308	0	85	0	0
16	F	2043	0	1033	49	0
17	I	2334	0	1173	108	0
18	B	3715	0	1878	150	0
19	O	574	0	552	31	0
20	S	632	0	653	26	0
20	d	316	0	86	0	0
20	l	611	0	627	0	0
21	P	563	0	600	40	0
21	a	292	0	78	0	0
21	h	610	0	640	0	0
22	Q	751	0	776	65	0
22	b	308	0	78	0	0
22	m	644	0	686	0	0
23	R	752	0	786	50	0
23	c	360	0	89	0	0
23	n	528	0	573	0	0
24	T	602	0	631	37	0
24	e	288	0	74	0	0
24	i	575	0	597	0	0
25	U	585	0	587	39	0
25	f	280	0	77	0	0
25	j	554	0	556	0	0
26	V	577	0	595	37	0
26	g	280	0	79	0	0
26	k	529	0	557	0	0
27	D	13601	0	13596	641	0
28	G	928	0	468	48	0
29	H	4345	0	2199	249	0
30	o	841	0	614	0	0
31	p	466	0	373	0	0
32	1	6472	0	6702	243	0
33	2	1726	0	1734	62	0
34	3	9380	0	9482	399	0
35	4	1429	0	1458	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	5	814	0	811	30	0
37	6	693	0	705	25	0
38	X	1051	0	1015	100	0
39	Y	730	0	710	52	0
40	Z	173	0	165	7	0
41	u	3895	0	3824	0	0
42	w	1084	0	1081	0	0
43	v	1372	0	1345	0	0
44	C	32	0	12	6	0
45	C	1	0	0	0	0
46	5	3	0	0	3	0
46	u	2	0	0	0	0
46	v	1	0	0	0	0
All	All	111041	0	100594	3508	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 19.

The worst 5 of 3508 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2310:GLU:CB	1:A:2333:PHE:CZ	1.85	1.52
1:A:2398:LEU:HD13	27:D:1060:LYS:CD	1.36	1.51
1:A:2310:GLU:CB	1:A:2333:PHE:HZ	1.19	1.44
1:A:2398:LEU:HD13	27:D:1060:LYS:CE	1.48	1.42
1:A:2310:GLU:HB2	1:A:2333:PHE:CZ	0.89	1.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	2169/2413 (90%)	2040 (94%)	115 (5%)	14 (1%)	22	50
2	K	425/465 (91%)	388 (91%)	34 (8%)	3 (1%)	19	47
3	L	410/494 (83%)	392 (96%)	15 (4%)	3 (1%)	19	47
4	N	678/899 (75%)	626 (92%)	51 (8%)	1 (0%)	48	78
5	J	294/469 (63%)	281 (96%)	10 (3%)	3 (1%)	13	39
6	E	137/143 (96%)	128 (93%)	9 (7%)	0	100	100
7	M	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
8	C	837/1008 (83%)	779 (93%)	53 (6%)	5 (1%)	22	50
9	z	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
10	q	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
11	r	75/89 (84%)	70 (93%)	5 (7%)	0	100	100
12	x	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
13	t	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	9	31
14	y	62/115 (54%)	62 (100%)	0	0	100	100
15	s	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
19	O	68/587 (12%)	64 (94%)	3 (4%)	1 (2%)	8	30
20	S	80/101 (79%)	77 (96%)	3 (4%)	0	100	100
20	d	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	4	22
20	l	79/101 (78%)	70 (89%)	8 (10%)	1 (1%)	10	33
21	P	66/196 (34%)	62 (94%)	4 (6%)	0	100	100
21	a	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
21	h	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
22	Q	93/146 (64%)	89 (96%)	3 (3%)	1 (1%)	12	37
22	b	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	9	31
22	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
23	R	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
23	c	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
23	n	63/110 (57%)	60 (95%)	3 (5%)	0	100	100
24	T	73/94 (78%)	72 (99%)	1 (1%)	0	100	100
24	e	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
24	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	U	71/86 (83%)	68 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	f	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	2	13
25	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
26	V	73/77 (95%)	66 (90%)	6 (8%)	1 (1%)	9	31
26	g	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
26	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	D	1694/2163 (78%)	1631 (96%)	60 (4%)	3 (0%)	44	72
30	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	8	29
31	p	69/111 (62%)	67 (97%)	2 (3%)	0	100	100
32	1	814/971 (84%)	762 (94%)	46 (6%)	6 (1%)	19	47
33	2	205/436 (47%)	192 (94%)	11 (5%)	2 (1%)	13	39
34	3	1164/1361 (86%)	1046 (90%)	109 (9%)	9 (1%)	16	44
35	4	165/213 (78%)	164 (99%)	1 (1%)	0	100	100
36	5	101/107 (94%)	87 (86%)	13 (13%)	1 (1%)	13	39
37	6	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	11	35
38	X	126/148 (85%)	117 (93%)	7 (6%)	2 (2%)	8	29
39	Y	85/266 (32%)	80 (94%)	3 (4%)	2 (2%)	5	23
40	Z	20/204 (10%)	14 (70%)	6 (30%)	0	100	100
41	u	453/530 (86%)	415 (92%)	38 (8%)	0	100	100
42	w	123/280 (44%)	112 (91%)	11 (9%)	0	100	100
43	v	168/266 (63%)	142 (84%)	25 (15%)	1 (1%)	22	50
All	All	12585/17187 (73%)	11769 (94%)	746 (6%)	70 (1%)	24	50

5 of 70 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	PRO
2	K	395	ILE
3	L	328	VAL
8	C	364	PHE
8	C	602	VAL

### 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	1964/2182 (90%)	1962 (100%)	2 (0%)	92	97
2	K	373/410 (91%)	371 (100%)	2 (0%)	86	91
3	L	327/445 (74%)	327 (100%)	0	100	100
4	N	361/813 (44%)	361 (100%)	0	100	100
5	J	248/436 (57%)	248 (100%)	0	100	100
6	E	129/132 (98%)	129 (100%)	0	100	100
7	M	104/104 (100%)	104 (100%)	0	100	100
8	C	757/910 (83%)	757 (100%)	0	100	100
19	O	60/534 (11%)	60 (100%)	0	100	100
20	S	71/89 (80%)	71 (100%)	0	100	100
20	l	67/89 (75%)	64 (96%)	3 (4%)	23	50
21	P	64/176 (36%)	64 (100%)	0	100	100
21	h	67/176 (38%)	67 (100%)	0	100	100
22	Q	81/129 (63%)	81 (100%)	0	100	100
22	m	77/129 (60%)	71 (92%)	6 (8%)	10	33
23	R	85/103 (82%)	85 (100%)	0	100	100
23	n	59/103 (57%)	52 (88%)	7 (12%)	4	16
24	T	69/83 (83%)	69 (100%)	0	100	100
24	i	65/83 (78%)	60 (92%)	5 (8%)	10	33
25	U	65/77 (84%)	65 (100%)	0	100	100
25	j	61/77 (79%)	60 (98%)	1 (2%)	58	75
26	V	64/66 (97%)	64 (100%)	0	100	100
26	k	58/66 (88%)	55 (95%)	3 (5%)	19	45
27	D	1524/1955 (78%)	1522 (100%)	2 (0%)	92	97
30	o	46/219 (21%)	43 (94%)	3 (6%)	14	39
31	p	23/100 (23%)	22 (96%)	1 (4%)	25	50
32	1	724/867 (84%)	724 (100%)	0	100	100
33	2	190/392 (48%)	190 (100%)	0	100	100
34	3	1088/1244 (88%)	1087 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	4	154/189 (82%)	154 (100%)	0	100	100
36	5	93/97 (96%)	92 (99%)	1 (1%)	70	81
37	6	76/77 (99%)	76 (100%)	0	100	100
38	X	114/132 (86%)	112 (98%)	2 (2%)	54	73
39	Y	77/240 (32%)	67 (87%)	10 (13%)	3	13
40	Z	21/186 (11%)	18 (86%)	3 (14%)	2	10
41	u	425/492 (86%)	420 (99%)	5 (1%)	67	80
42	w	118/259 (46%)	115 (98%)	3 (2%)	42	65
43	v	156/236 (66%)	154 (99%)	2 (1%)	65	78
All	All	10105/14097 (72%)	10043 (99%)	62 (1%)	82	90

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	n	82	LYS
41	u	298	HIS
34	3	147	PHE
41	u	81	ILE
42	w	158	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 141 such sidechains are listed below:

Mol	Chain	Res	Type
34	3	641	GLN
34	3	920	GLN
38	X	25	ASN
8	C	817	GLN
8	C	776	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	F	95/112 (84%)	38 (40%)	1 (1%)
17	I	106/160 (66%)	31 (29%)	6 (5%)
18	B	173/214 (80%)	64 (36%)	13 (7%)
28	G	43/44 (97%)	22 (51%)	2 (4%)
29	H	196/1175 (16%)	52 (26%)	23 (11%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	613/1705 (35%)	207 (33%)	45 (7%)

5 of 207 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	F	2	U
16	F	12	U
16	F	13	U
16	F	14	U
16	F	17	U

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	H	1100	A
29	H	1122	U
29	H	1101	C
29	H	1119	C
29	H	1124	U

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

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
44	GTP	C	1500	45	26,34,34	0.94	1 (3%)	32,54,54	1.61	4 (12%)

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
44	GTP	C	1500	45	-	4/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C	1500	GTP	C6-N1	-2.42	1.34	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	PB-O3B-PG	-4.54	117.24	132.83
44	C	1500	GTP	PA-O3A-PB	-4.03	119.00	132.83
44	C	1500	GTP	C3'-C2'-C1'	3.35	106.02	100.98
44	C	1500	GTP	C8-N7-C5	2.49	107.74	102.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	O4'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'
44	C	1500	GTP	PB-O3A-PA-O2A
44	C	1500	GTP	PB-O3A-PA-O1A

There are no ring outliers.

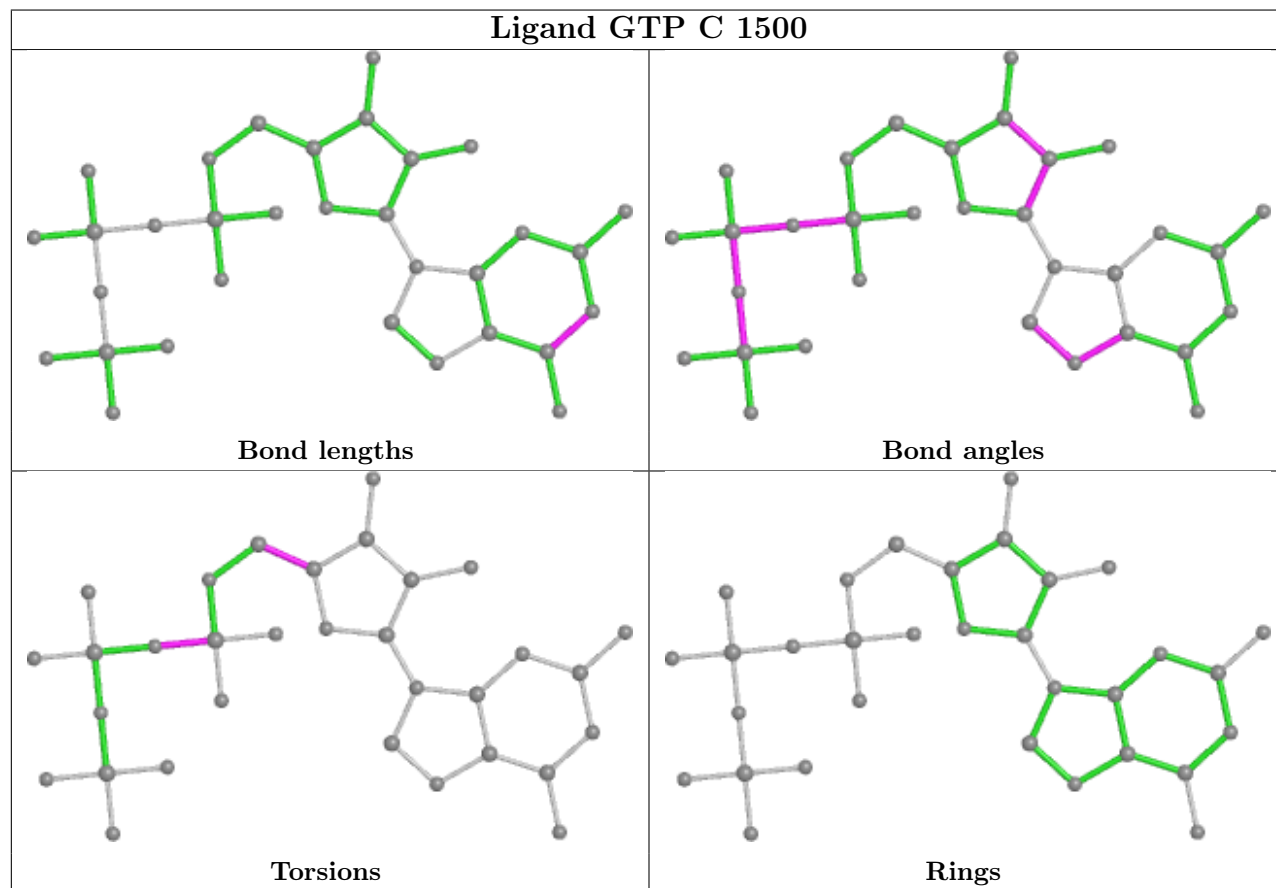
1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	C	1500	GTP	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In



addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



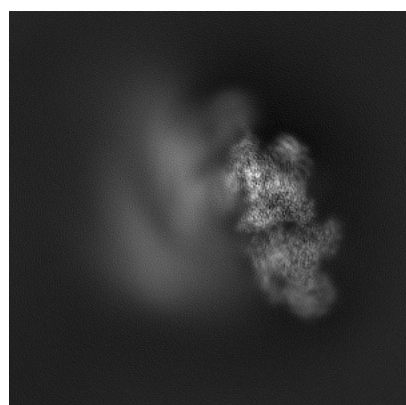
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6972. These allow visual inspection of the internal detail of the map and identification of artifacts.

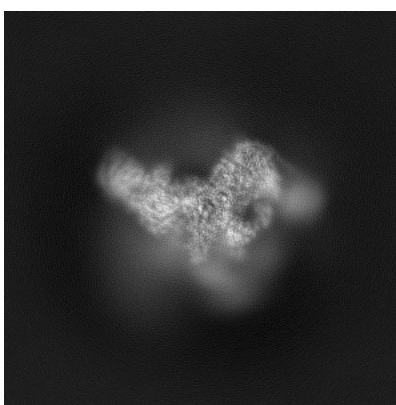
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

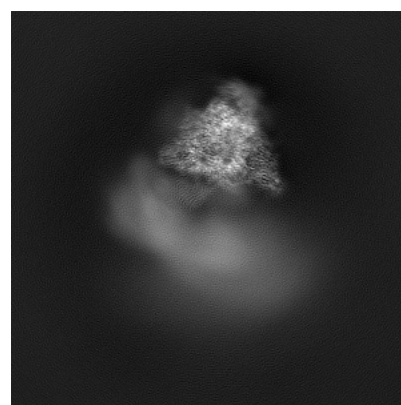
#### 6.1.1 Primary map



X



Y

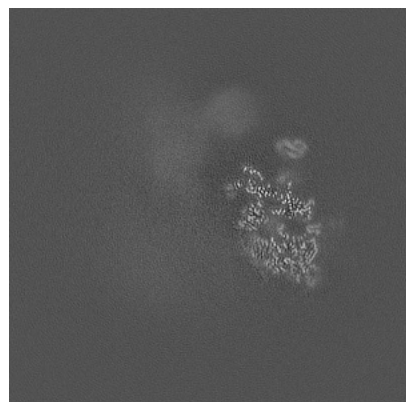


Z

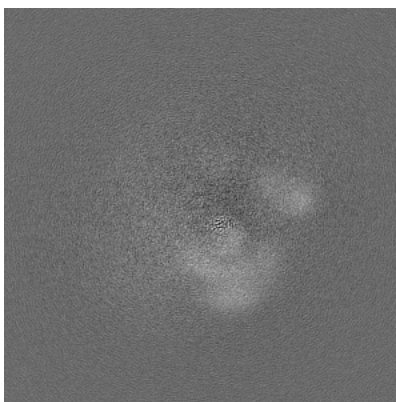
The images above show the map projected in three orthogonal directions.

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

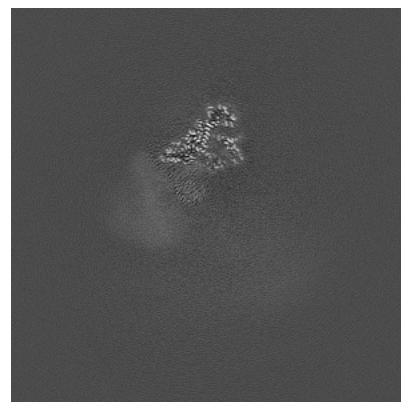
#### 6.2.1 Primary map



X Index: 200



Y Index: 200



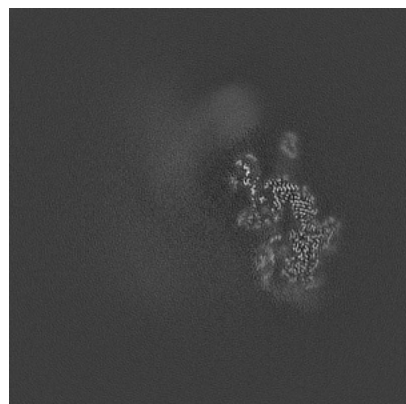
Z Index: 200



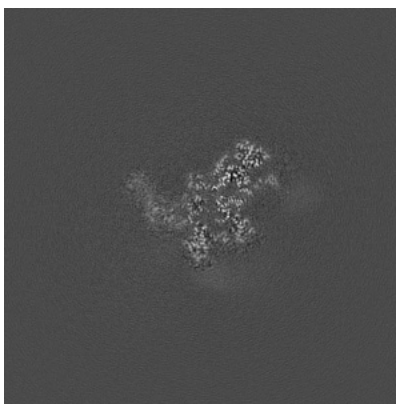
The images above show central slices of the map in three orthogonal directions.

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

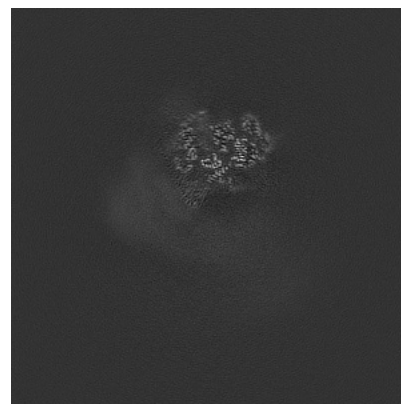
### 6.3.1 Primary map



X Index: 212



Y Index: 247

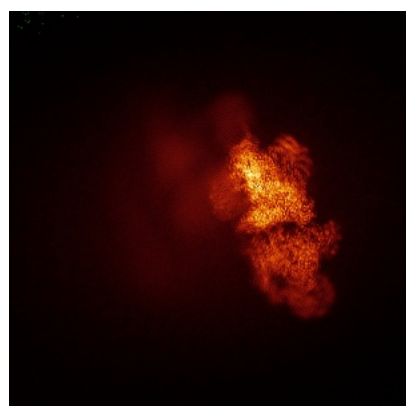


Z Index: 224

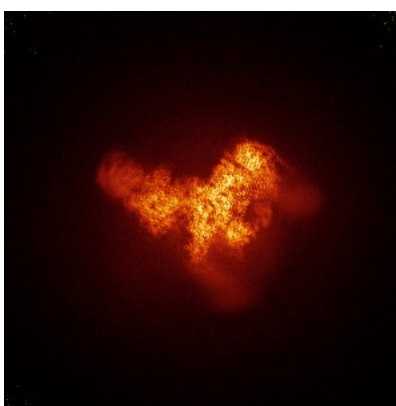
The images above show the largest variance slices of the map in three orthogonal directions.

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

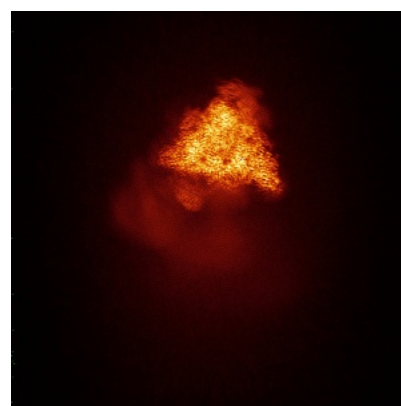
### 6.4.1 Primary map



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.

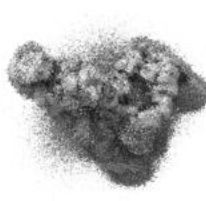


## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.023. 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](#)

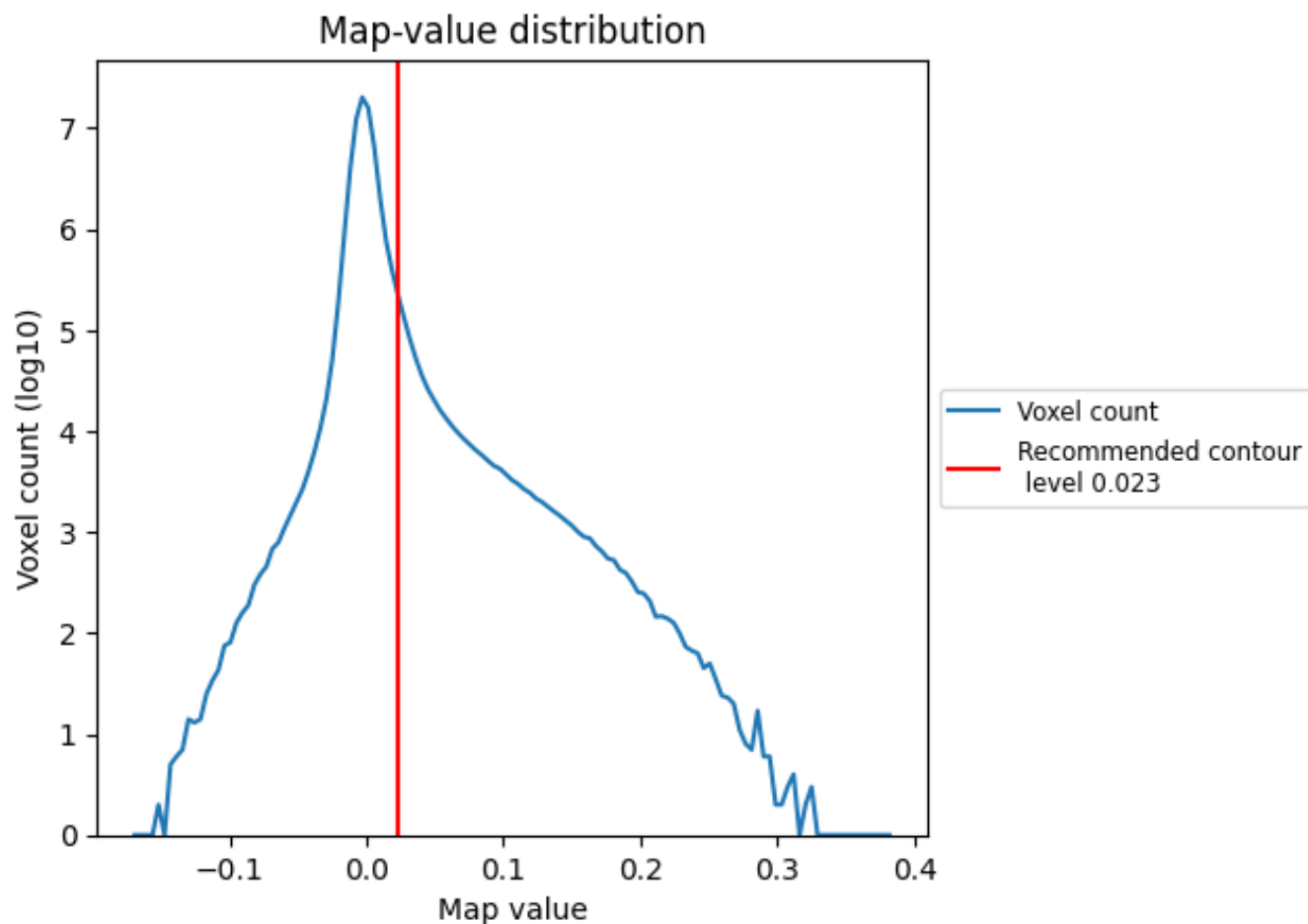
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

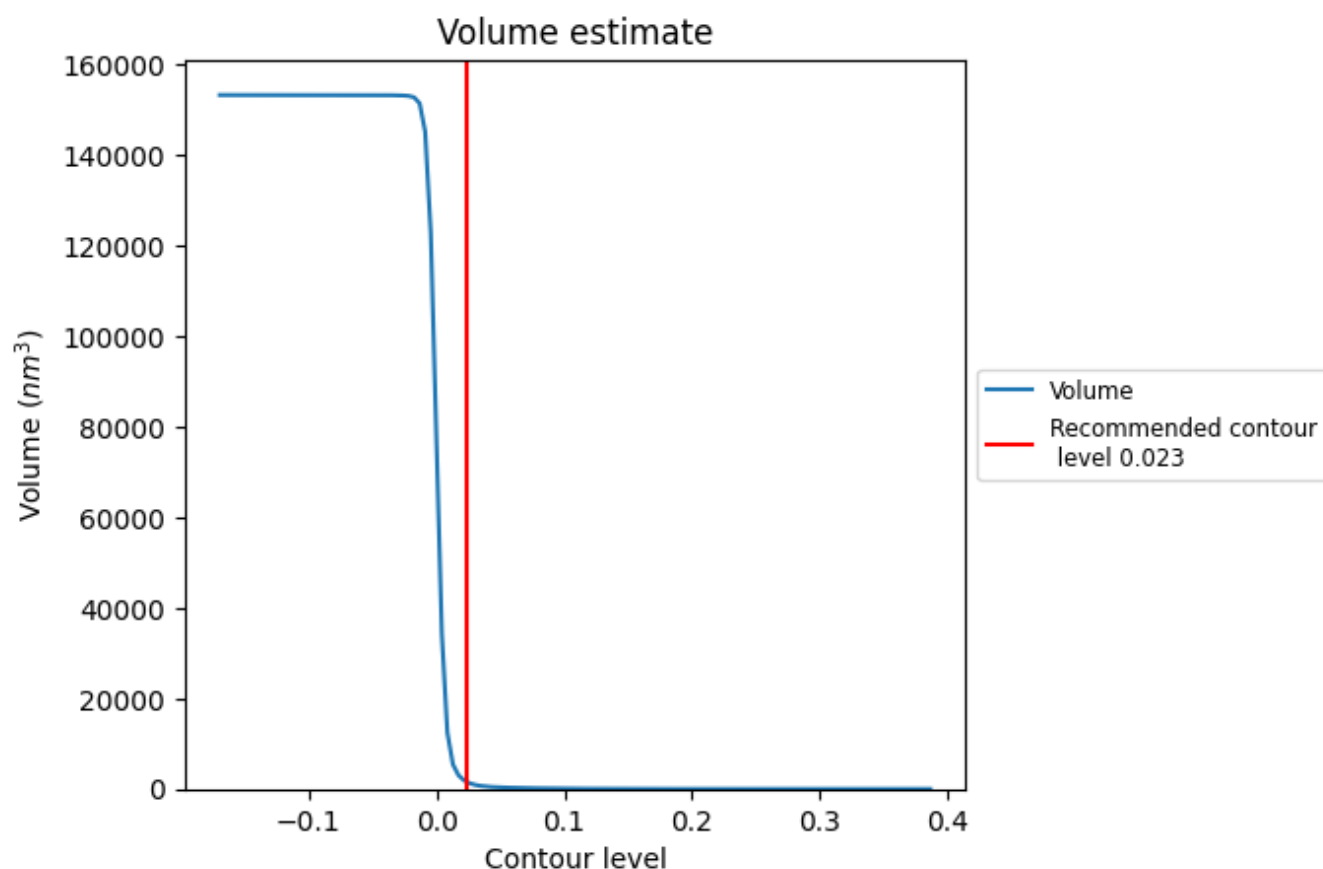
### 7.1 Map-value distribution [i](#)



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](#)

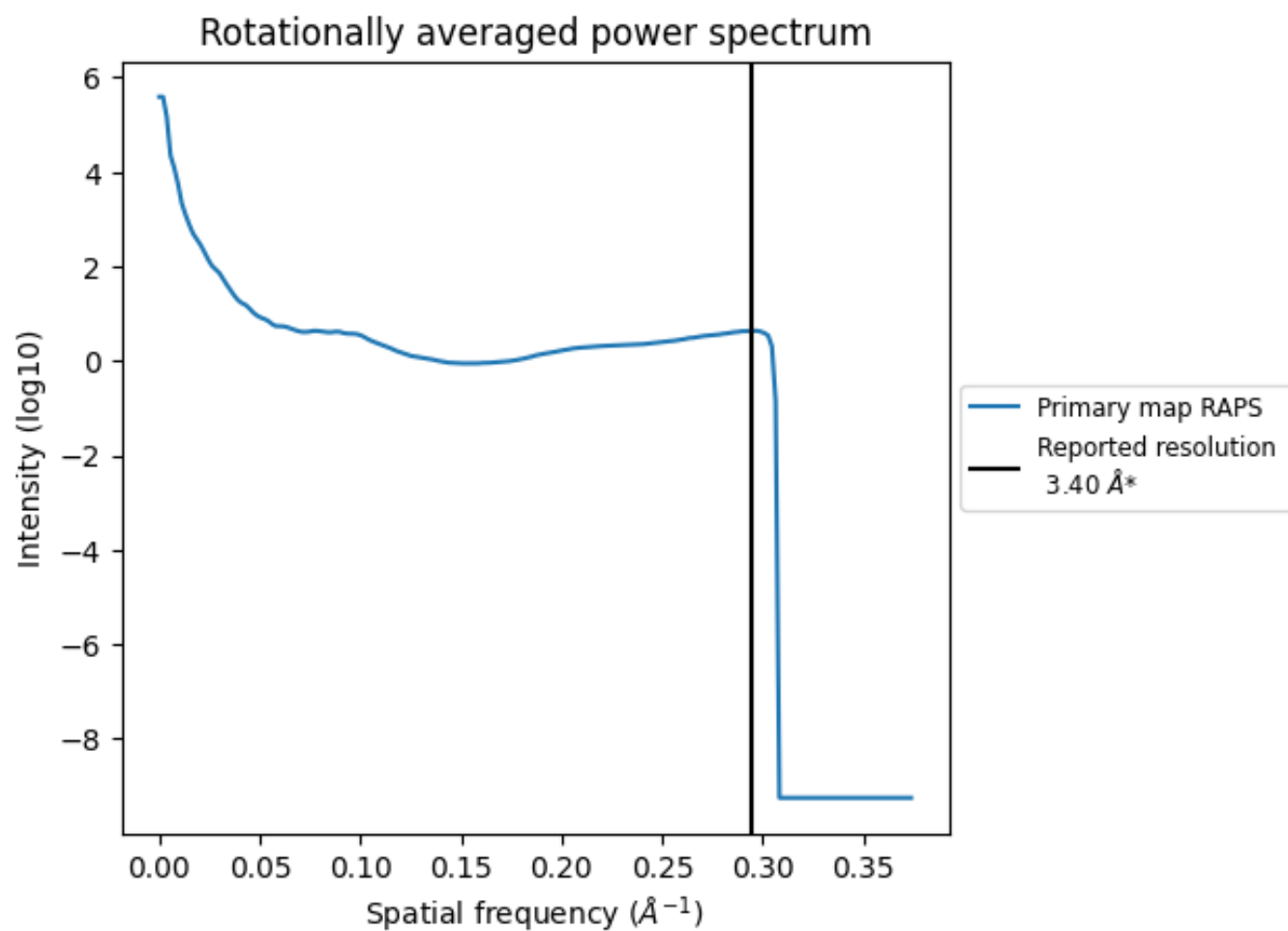


The volume at the recommended contour level is 1701  $\text{nm}^3$ ; this corresponds to an approximate mass of 1536 kDa.

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 0.294 Å<sup>-1</sup>



## 8 Fourier-Shell correlation

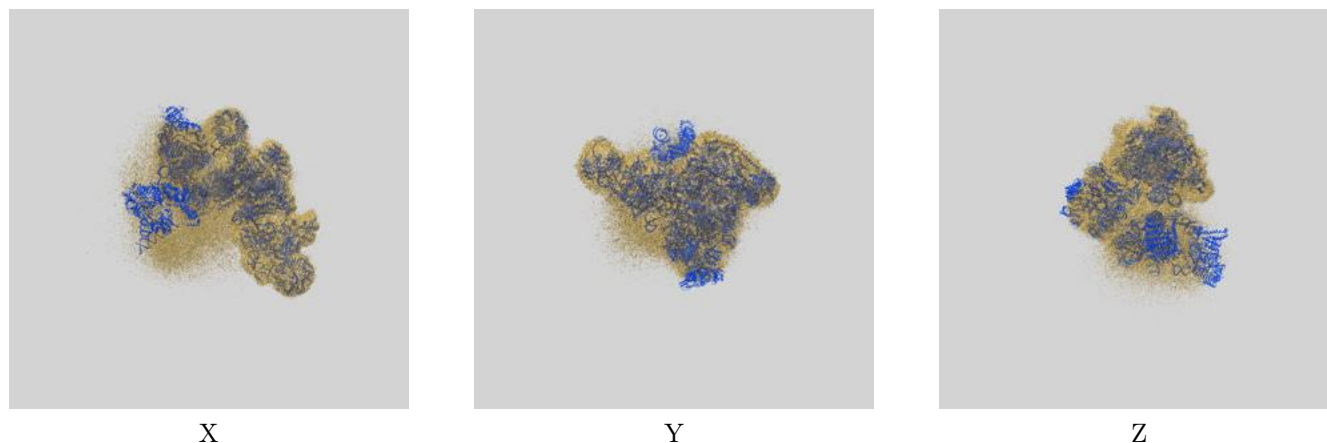
This section was not generated. No FSC curve or half-maps provided.



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

This section contains information regarding the fit between EMDB map EMD-6972 and PDB model 5ZWM. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

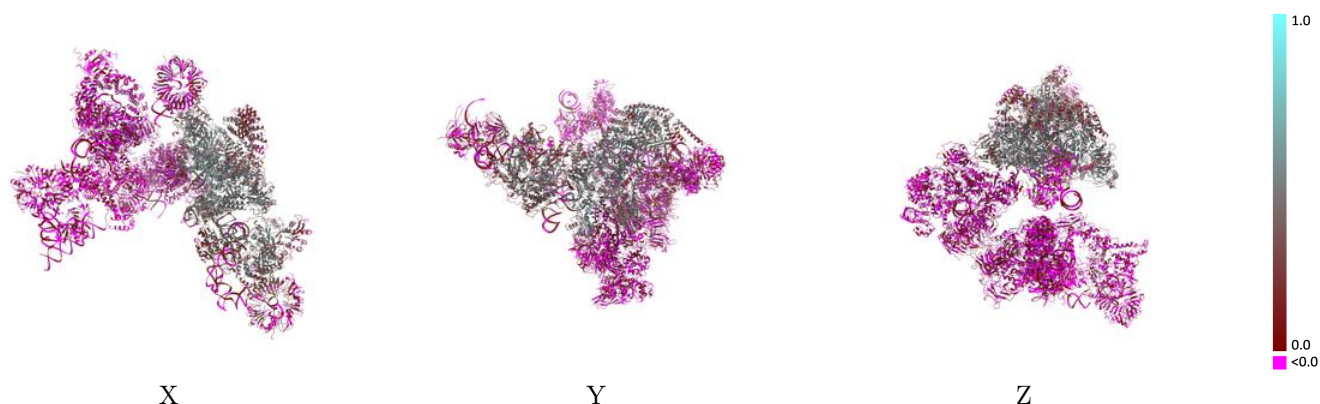
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.023 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.

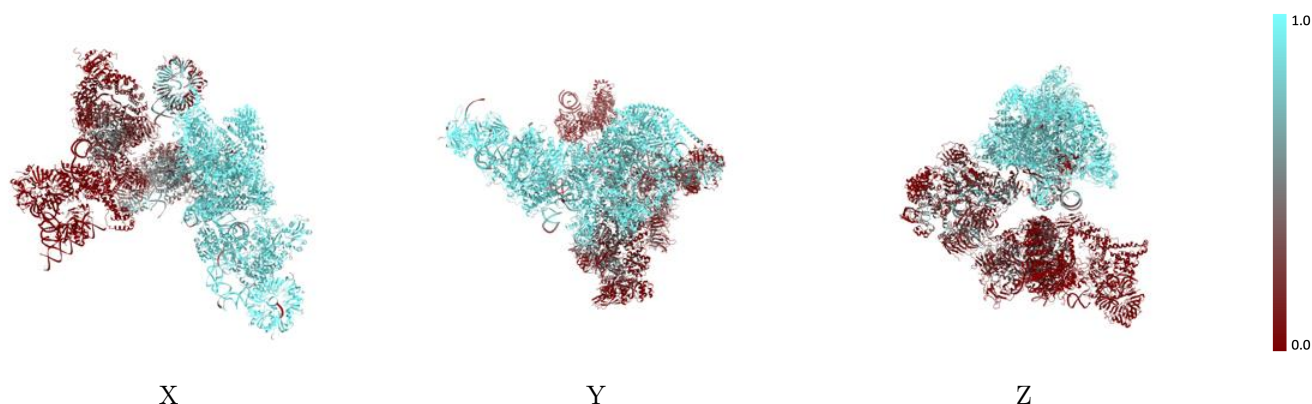


## 9.2 Q-score mapped to coordinate model [i](#)



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.

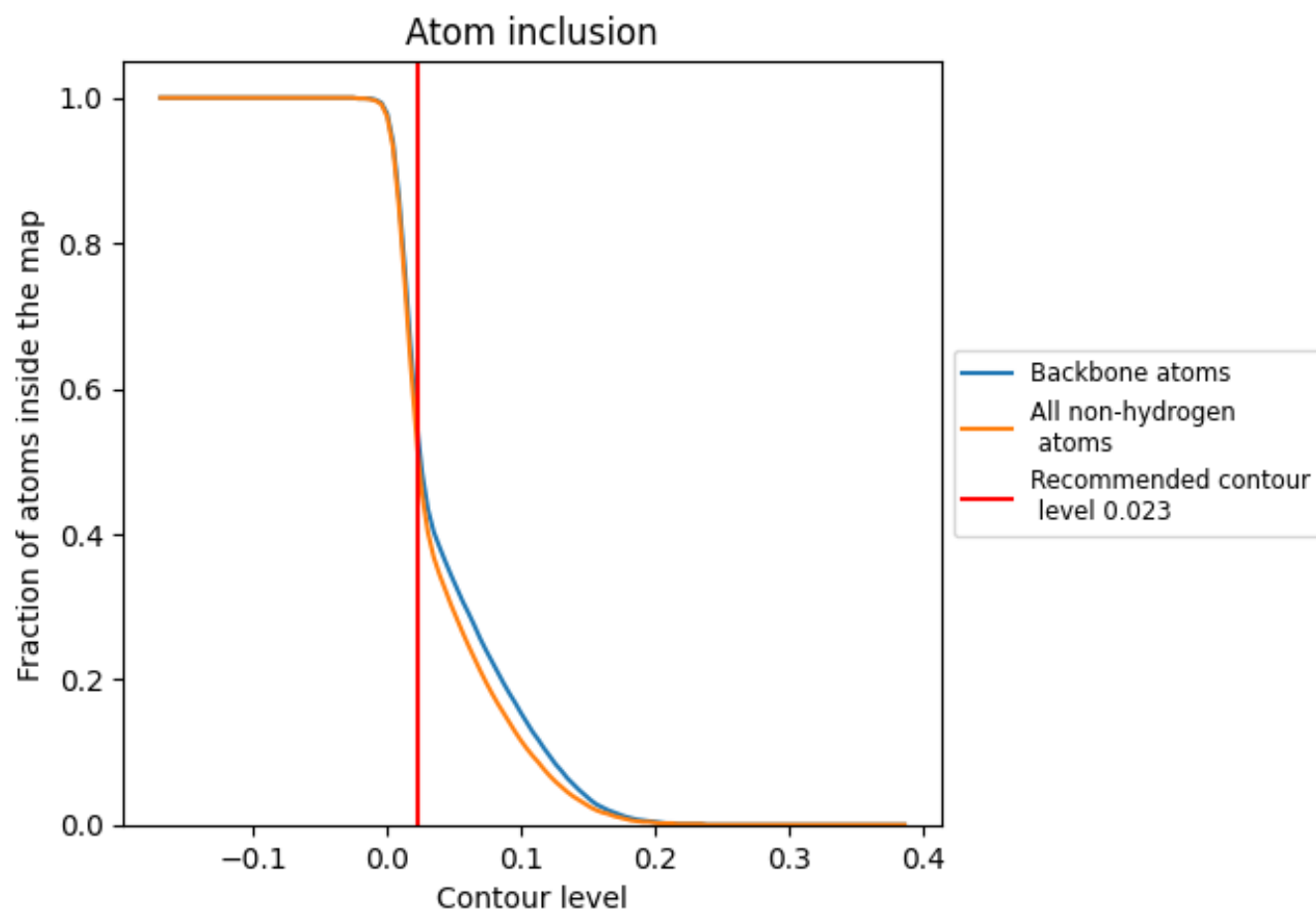
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.023).



## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 53% of all backbone atoms, 50% 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 (0.023) and Q-score for the entire model and for each chain.















































Chain	Atom inclusion	Q-score
All	 0.5050	 0.1620
1	 0.1700	 0.0010
2	 0.1600	 0.0170
3	 0.1710	 0.0070
4	 0.0560	 -0.0180
5	 0.2770	 0.0070
6	 0.3170	 -0.0020
A	 0.8430	 0.3780
B	 0.8820	 0.1520
C	 0.9060	 0.3540
D	 0.2770	 -0.0020
E	 0.9180	 0.4420
F	 0.8230	 0.2670
G	 0.2000	 -0.0050
H	 0.0740	 0.0020
I	 0.8240	 0.3140
J	 0.9240	 0.4150
K	 0.9220	 0.4350
L	 0.9290	 0.4290
M	 0.9550	 0.5200
N	 0.9200	 0.3230
O	 0.7580	 0.2720
P	 0.5390	 -0.0080
Q	 0.3850	 -0.0020
R	 0.4290	 -0.0110
S	 0.5940	 0.0110
T	 0.1550	 -0.0060
U	 0.2720	 -0.0290
V	 0.2620	 0.0160
X	 0.0050	 0.0070
Y	 0.0010	 -0.0100
Z	 0.0060	 -0.0350
a	 0.9490	 0.2050
b	 0.9380	 0.1490
c	 0.9310	 0.0690



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Chain	Atom inclusion	Q-score
d	 0.9810	 0.2910
e	 0.9510	 0.0850
f	 0.9210	 0.1000
g	 0.8570	 0.0540
h	 0.0070	 0.0250
i	 0.0020	 0.0280
j	 0.0040	 -0.0190
k	 0.0040	 -0.0070
l	 0.0150	 0.0050
m	 0.0080	 0.0080
n	 0.0020	 0.0010
o	 0.0080	 0.0140
p	 0.0060	 0.0150
q	 0.4430	 0.0150
r	 0.5030	 0.0150
s	 0.4160	 0.0280
t	 0.6400	 0.0210
u	 0.0320	 -0.0030
v	 0.0980	 -0.0010
w	 0.0060	 -0.0230
x	 0.5510	 0.0480
y	 0.6170	 0.0200
z	 0.2920	 -0.0110