



## wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 12:55 PM JST

PDB ID : 6J6N  
EMDB ID : EMD-0691  
Title : Cryo-EM structure of the yeast B\*-b1 complex at an average resolution of 3.86 angstrom  
Authors : Wan, R.; Bai, R.; Yan, C.; Lei, J.; Shi, Y.  
Deposited on : 2019-01-15  
Resolution : 3.86 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

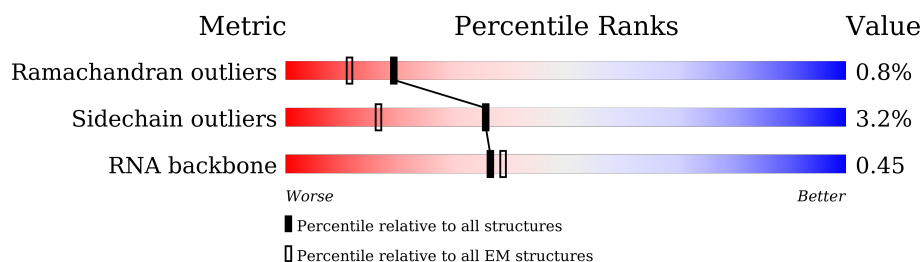
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.86 Å.

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



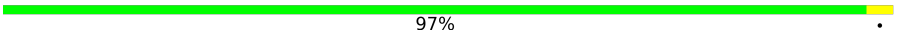

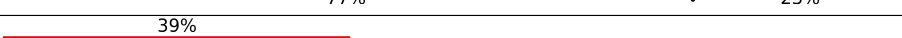
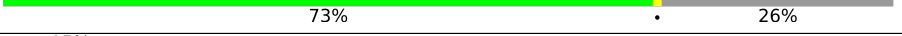

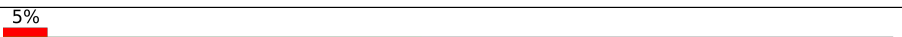
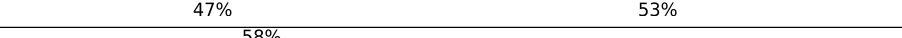


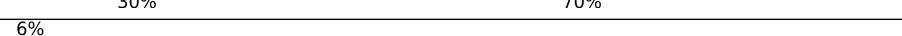


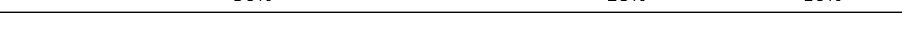



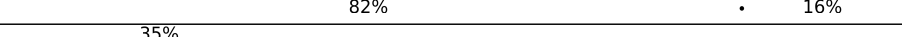


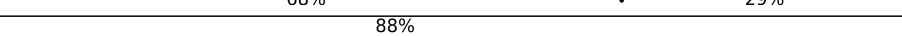



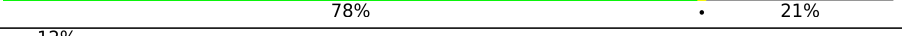

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	
2	C	1008	
3	J	135	
4	O	451	
5	P	379	
6	Q	364	
7	R	339	
8	S	175	

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Mol	Chain	Length	Quality of chain
9	T	157	
10	Z	577	
11	c	590	
12	d	687	
13	I	215	
14	n	455	
15	H	235	
16	B	246	
17	D	214	
18	E	112	
19	L	1175	
20	v	859	
21	a	111	
22	b	238	
23	t	175	
24	i	94	
24	u	94	
25	m	146	
25	z	146	
26	j	77	
26	x	77	
27	h	86	
27	w	86	
28	e	110	
28	g	110	

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Mol	Chain	Length	Quality of chain
29	k	196	
29	s	196	
30	l	101	
30	y	101	
31	o	503	
31	p	503	
31	q	503	
31	r	503	

## 2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 78937 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	1913	Total	C	N	O	S	0	0
			15793	10154	2714	2868	57		

- Molecule 2 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	920	Total	C	N	O	S	0	0
			7348	4733	1223	1362	30		

- Molecule 3 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 4 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	357	Total	C	N	O	S	0	0
			2810	1777	493	530	10		

- Molecule 5 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	205	Total	C	N	O	S	0	0
			1608	1003	294	304	7		

- Molecule 6 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	292	Total	C	N	O	S	0	0
			2301	1461	399	426	15		

- Molecule 7 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 8 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	70	Total	C	N	O	S	0	0
			567	355	113	98	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Z	447	Total	C	N	O	S	0	0
			3651	2343	602	688	18		

- Molecule 11 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	436	Total	C	N	O	S	0	0
			2978	1843	552	575	8		

- Molecule 12 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	566	Total	C	N	O	S	0	0
			3881	2433	707	732	9		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 14 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	n	299	Total	C	N	O	P	S	0	0
			1894	1175	340	372	1	6		

- Molecule 15 is a protein called Pre-mRNA-splicing factor ISY1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	71	Total	C	N	O	S	0	0
			629	399	116	113	1		

- Molecule 16 is a RNA chain called UBC4 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	57	Total	C	N	O	P	0	0
			1206	542	209	398	57		

- Molecule 17 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	179	Total	C	N	O	P	0	0
			3795	1699	660	1258	178		

- Molecule 18 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 19 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	205	Total	C	N	O	P	0	0
			4325	1936	728	1456	205		

- Molecule 20 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	722	Total	C	N	O	S	0	0
			4625	2893	825	895	12		

- Molecule 21 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	84	Total	C	N	O	0	0
			416	248	84	84		

- Molecule 22 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	b	169	Total	C	N	O	0	0
			841	503	169	169		

- Molecule 23 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	156	Total	C	N	O	S	0	0
			926	585	160	180	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	74	Total	C	N	O	S	0	0
			526	346	87	90	3		
24	i	74	Total	C	N	O	S	0	0
			541	358	90	90	3		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	m	119	Total	C	N	O	S	0	0
			917	575	163	176	3		
25	z	108	Total	C	N	O	S	0	0
			824	521	142	158	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	75	Total	C	N	O	S	0	0
			552	350	98	103	1		
26	x	75	Total	C	N	O	S	0	0
			552	350	98	103	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein F.



Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	68	Total	C	N	O	S	0	0
			518	337	96	84	1		
27	w	68	Total	C	N	O	S	0	0
			518	337	96	84	1		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	101	Total	C	N	O	S	0	0
			785	504	149	128	4		
28	e	101	Total	C	N	O	S	0	0
			785	504	149	128	4		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	100	Total	C	N	O	S	0	0
			809	514	150	142	3		
29	s	93	Total	C	N	O	S	0	0
			749	476	138	132	3		

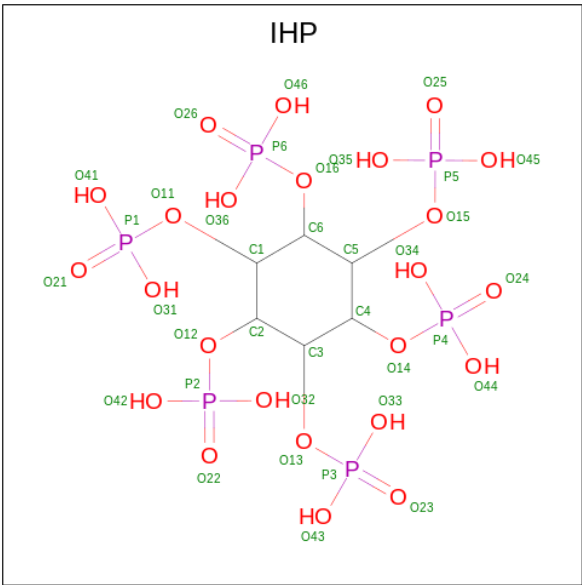
- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	83	Total	C	N	O	S	0	0
			641	408	111	120	2		
30	y	81	Total	C	N	O	S	0	0
			616	394	107	113	2		

- Molecule 31 is a protein called Pre-mRNA-processing factor 19.

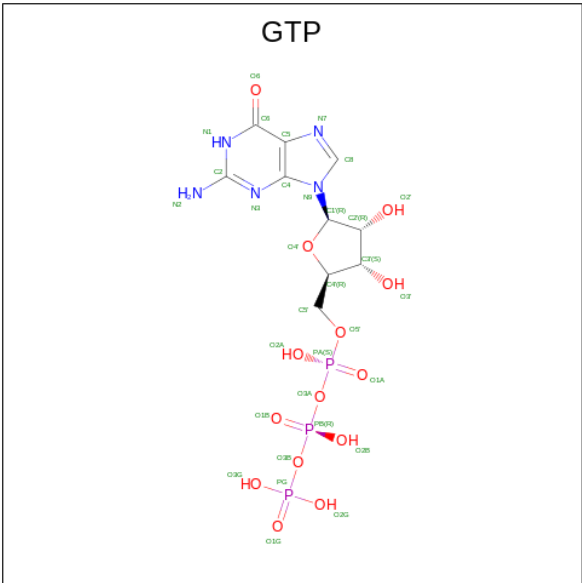
Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		
31	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
31	q	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
31	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		

- Molecule 32 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: C<sub>6</sub>H<sub>18</sub>O<sub>24</sub>P<sub>6</sub>).



Mol	Chain	Residues	Atoms				AltConf
32	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 33 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



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

- Molecule 34 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	C	1	Total 1	Mg 1	0
34	E	5	Total 5	Mg 5	0

- Molecule 35 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	Q	2	Total 2	Zn 2	0
35	R	1	Total 1	Zn 1	0
35	T	3	Total 3	Zn 3	0



THR	PHE	MET	GLY	THR	ALA	PHE	ASN	ASN	GLN	GLU	GLY	ASP	TYR	TYR	PHE	PHE	LYS	LYS	GLY	GLY	ILE	PRO	PRO	LEU	LEU	PHE	PHE	TYR	ASN	ASN	GLU	GLU	MET	HIS	ARG	PRO	PRO	VAL	VAL	HIS	PHE	PHE	GLN	LEU	GLY	GLY	ASP	ASP	GLU	GLU	GLY	LEU	LEU	GLN	ALA	ALA	GLU	GLN	ILE	ASP	VAL	PHE	PHE	THR
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Chain C:  90% 9%

MET	GLU	GLY	ASP	ASP	LEU	PHE	ASP	GLU	PHE	GLY	ASN	LEU	ILE	GLY	VAL	ASP	PRO	PHE	ASP	SER	ASP	GLU	GLU	GLU	SER	VAL	GLN	GLN	THR	THR	PHE	GLY	SER	ASN	ASN	ASN	ASN	GLN	ILE	GLU	GLU	ARG	ARG	LEU	LEU	THR	SER	GLY	GLY	LYS
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Protein	Number of Residues
GLU	10
LEU	10
GLY	10
ILE	10
SER	10
LEU	10
E67	10
G71	10
E96	10
L234	10
N289	10
N294	10
K300	10
K362	10
N366	10
K461	10
D517	10
SER	10
LYS	10
THR	10
GLU	10
THR	10
ASN	10
ASN	10
GLU	10
ASP	10
ASP	10
GLU	10
ASP	10
E530	10
D531	10
D532	10
S685	10
PHE	10
ALA	10
SER	10
ILE	10
PRO	10
VAL	10
SER	10
ASN	10
SER	10
ILE	10
S696	10
L703	10
P704	10
N700	10

Chain J:  20% 80%

MET	S2	ARG	ARG	ARG	ARG	PRO	GLN	GLN	GLY	SER	GLN	GLN	GLN	GLN	GLN	GLN	GLN	ASN	ALA	ALA	ILE	ALA	LYS	LYS	LYS	ASP	ASP	ALA	ALA	SER	ARG	PRO	LEU	ALA	VAL	VAL	LYS	GLN	GLN	ILE	GLU	THR	MET	HIS	GLU	LYS	ARG	GLU	ILE	GLU	VAL	GLN	VAL	SER	LEU	LEU	ARG	ASP	ARG
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GLU	GLU	GLU	GLU	THR	LEU	SER	GLU	GLU	GLN	ILE	ASP	LYS	LYS	CYS	GLU	ALA	LEU	ARG	ALA	LYS	THR	ASN	TRP	GLU	GLN	GLN	GLN	ARG	MET	SER	SER	LEU	TYR	THR	PRO	ARG	LYS	ALA	ALA	ARG	LEU	THR	THR	GLU	GLN	HIS	HIS	ARG	HIS
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Chain 0:  76% . 21%

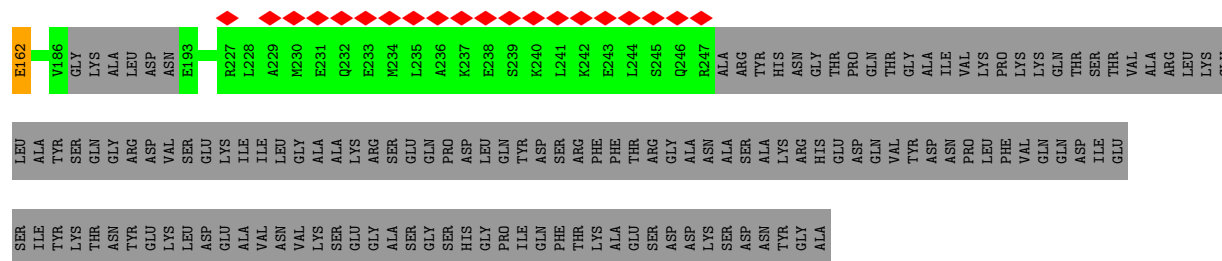
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PHE	GLY	GLY	GLU	GLY	LVS	LVS	VAL	THR	LEU	GLN	HIS	VAL	PRO	THR	ASP	PHE	SER	GLU	ALA	SER	GLN	VAL	ILE	SER	LVS	LVS	ASP	HIS	ASP	ASP	HIS	ALA	SER	S95	M113	P149	V150	D151	R218	D219	C327	E346	S347	E348	K349	T350	G351	L352	T333	K334	E335	S336
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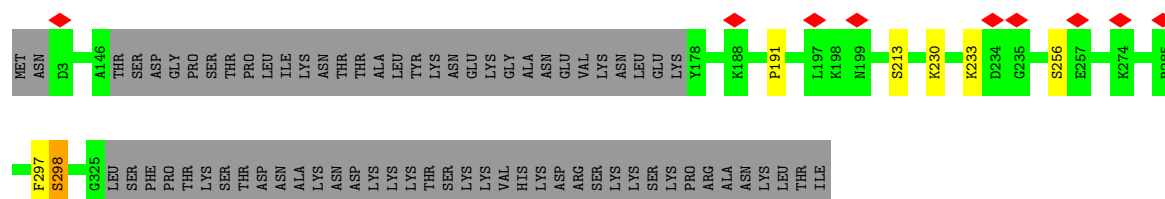
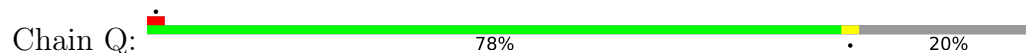
F451

Chain P: 

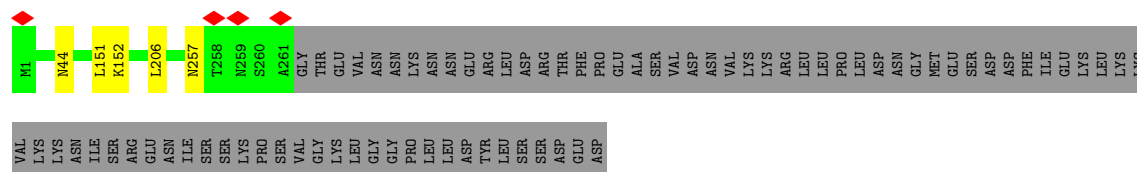
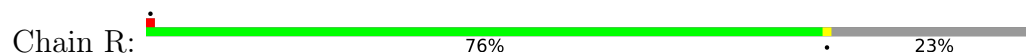
MET	PHE	SER	ASN	ARG	LEU	PRO	PRO	PRO	LYS	HIS	SER	SER	GLN	GLY	ARG	VAL	SER	THR	ALA	LEU	SER	SER	ASP	ARG	VAL	GLU	PRO	A28	N87	V94	THR	GLU	THR	HIS	HIS	GLN	A100	P101	A102	N103	L104	L105	L106	N107	N108	S109	D141	D150	G151	SER	ASN	ASP	ARG	G156	E157	N160
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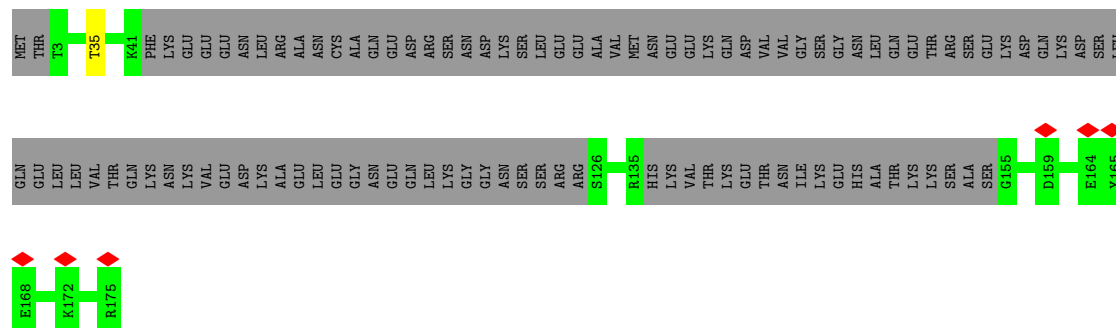
• Molecule 6: Pre-mRNA-splicing factor SLT11



• Molecule 7: Pre-mRNA-splicing factor CWC2



• Molecule 8: Pre-mRNA-splicing factor CWC15

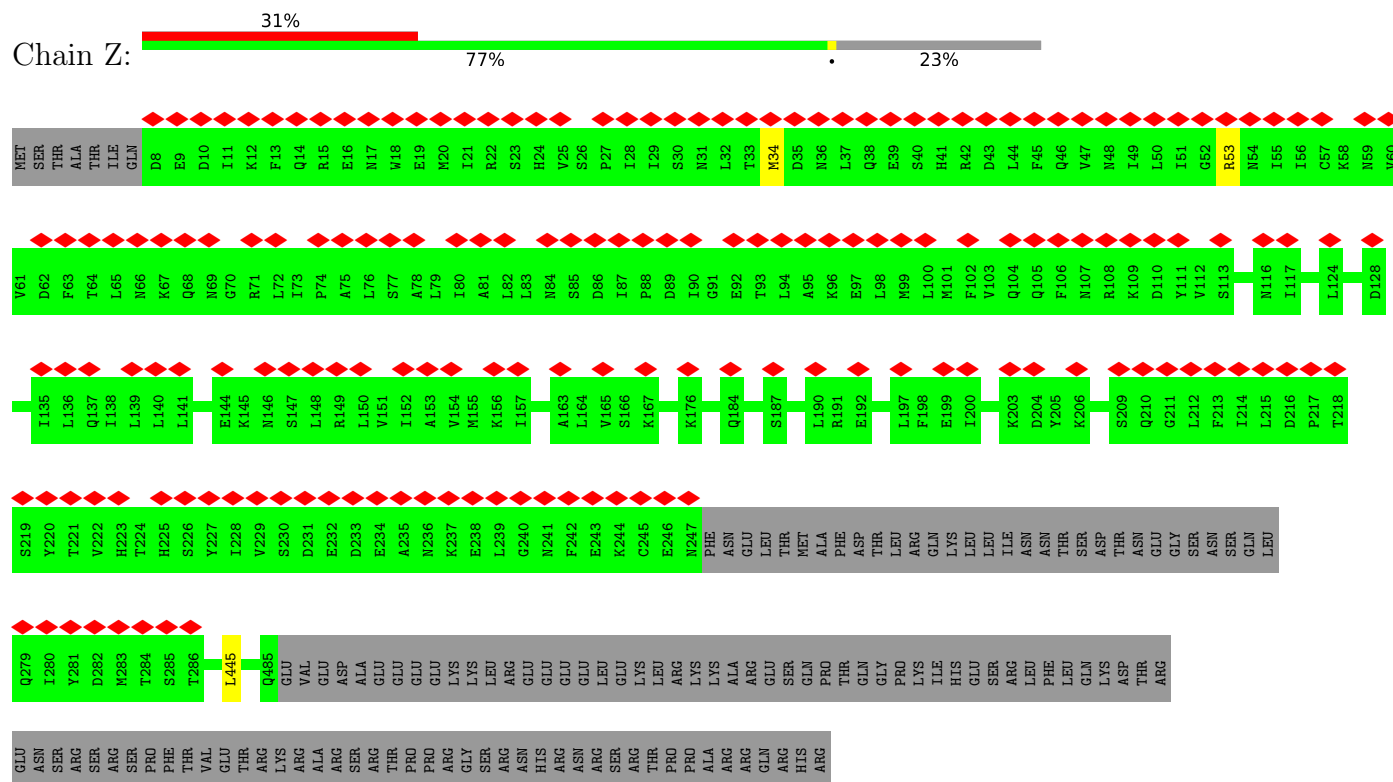


• Molecule 9: Pre-mRNA-splicing factor BUD31



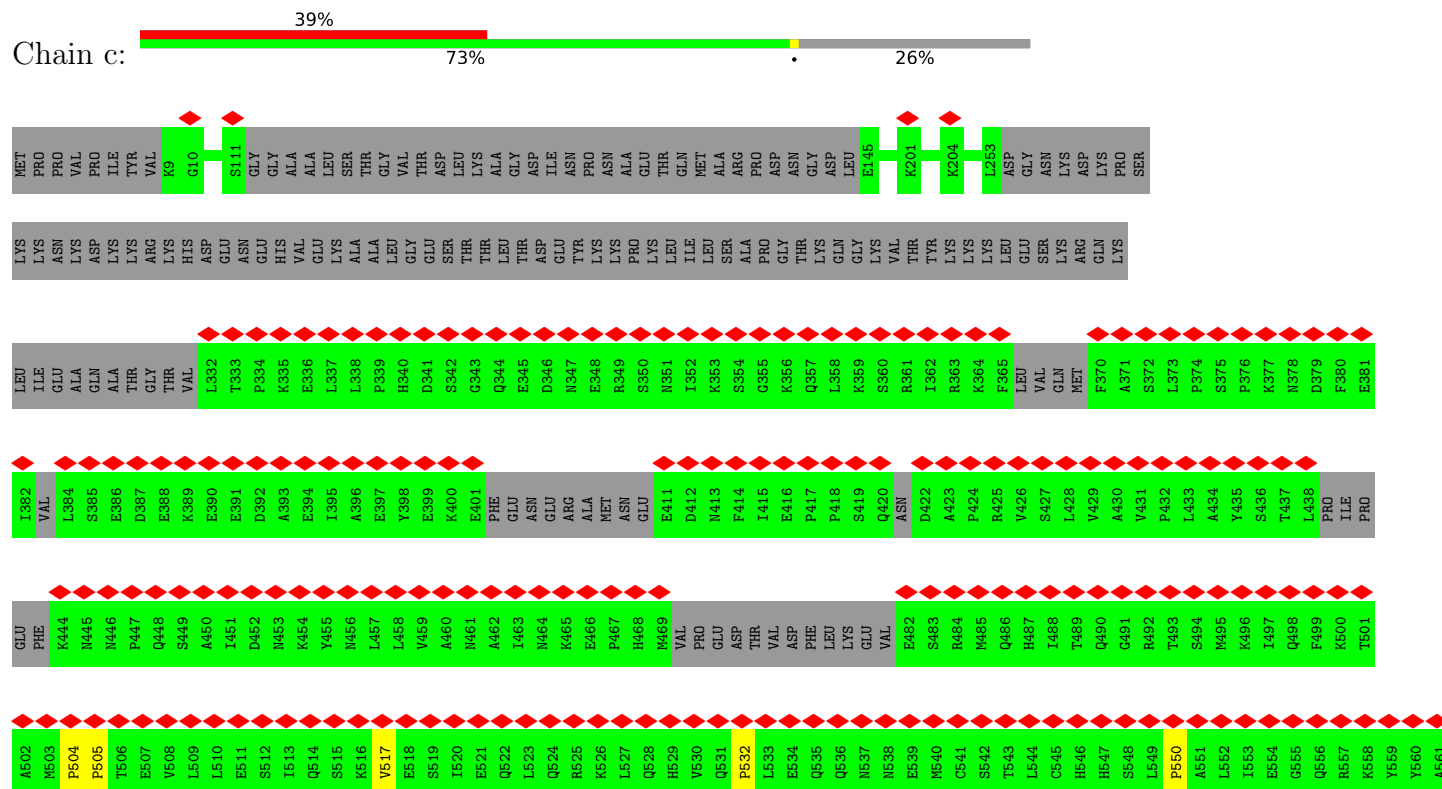
● Molecule 10: Pre-mRNA-splicing factor CWC22

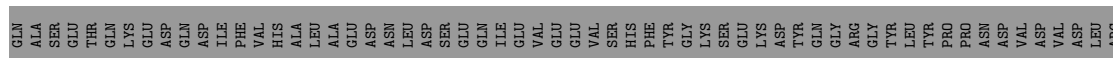
Chain Z:



● Molecule 11: Pre-mRNA-splicing factor CEF1

Chain c:

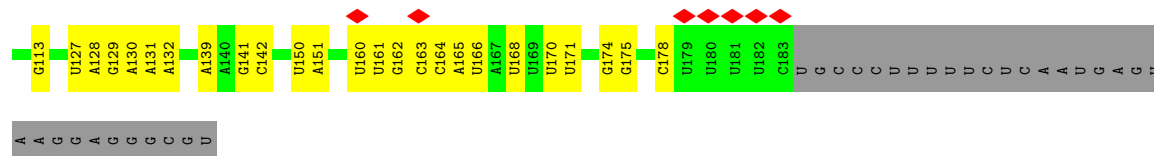
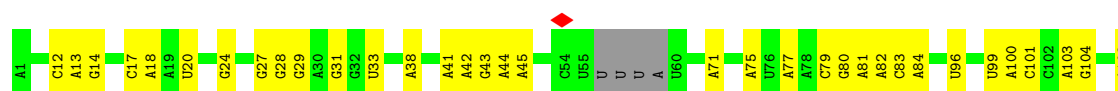




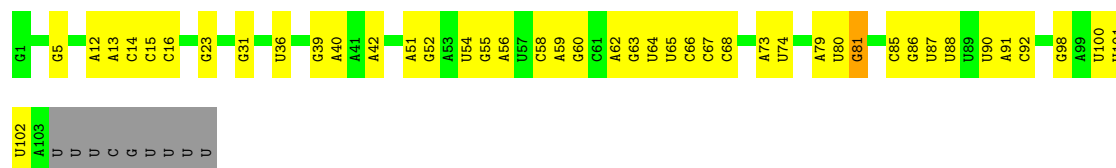




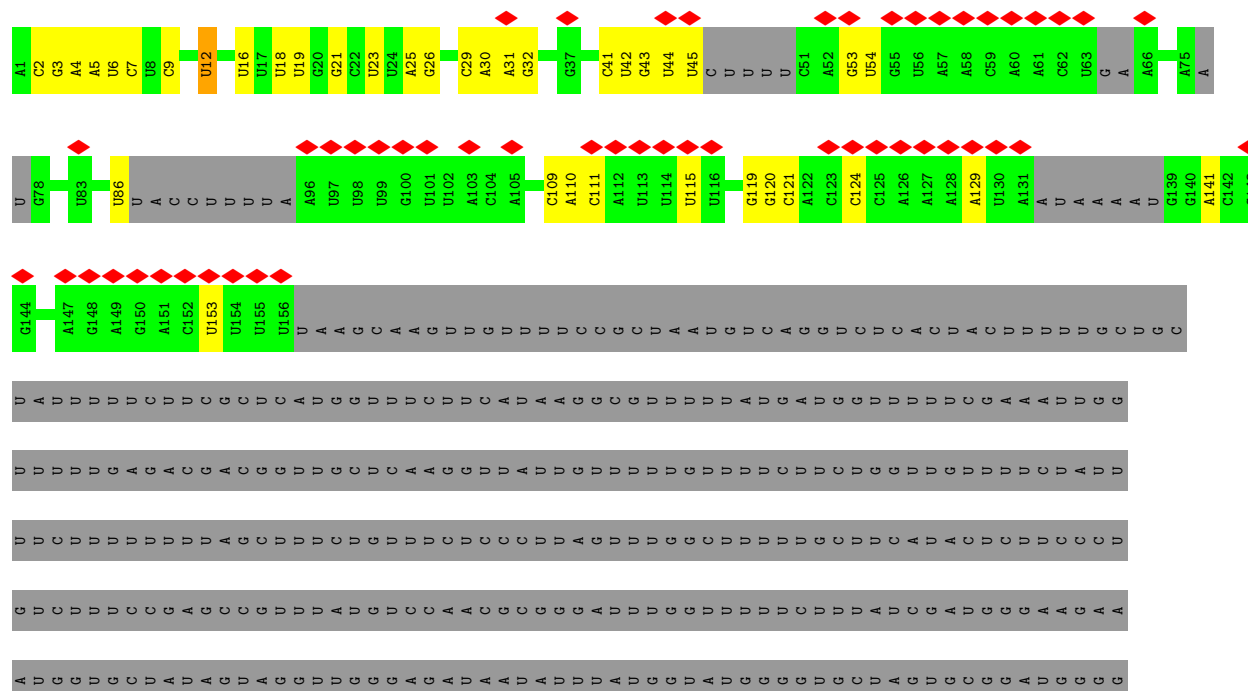
- Molecule 17: U5 snRNA

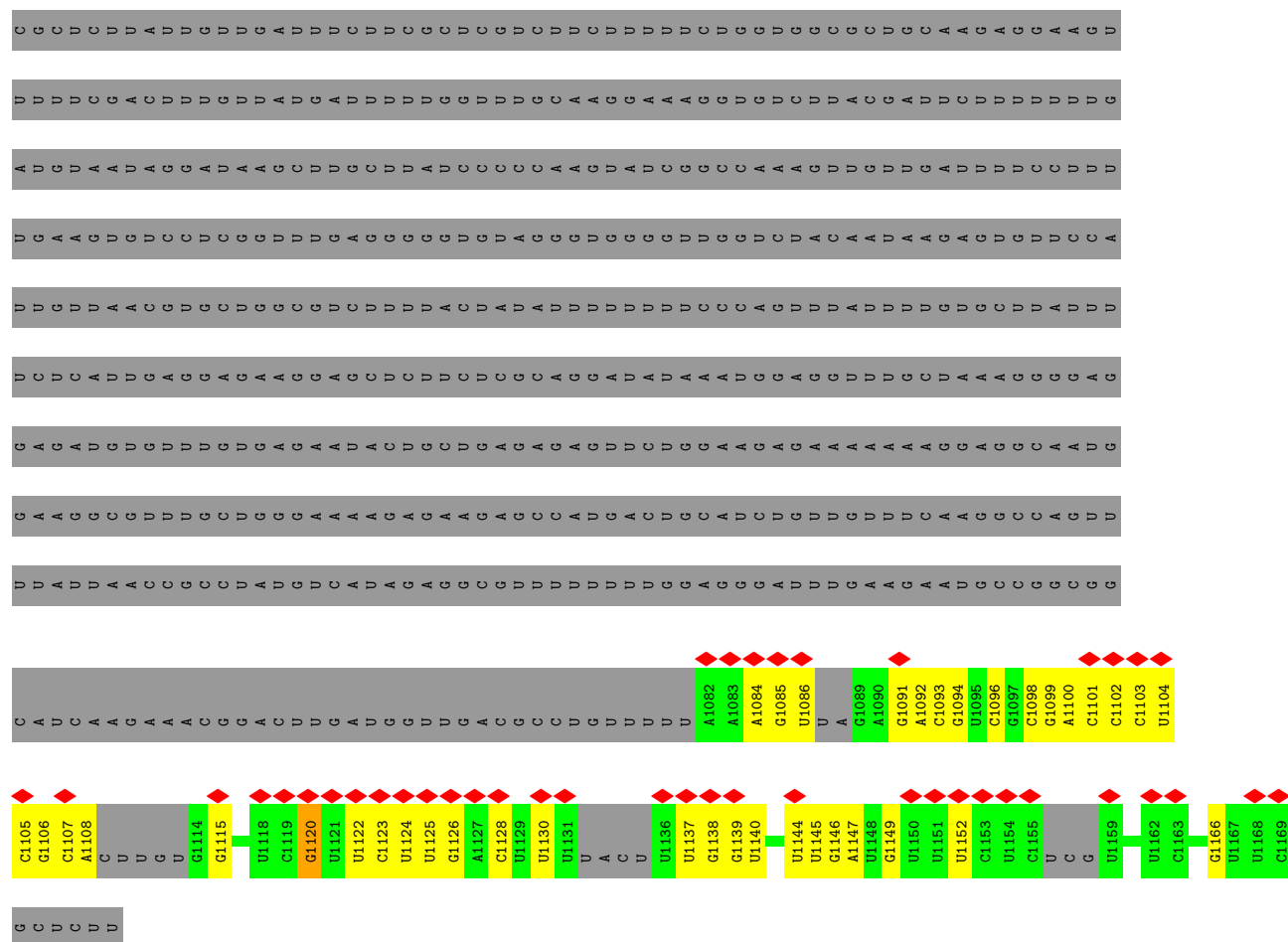


- Molecule 18: U6 snRNA

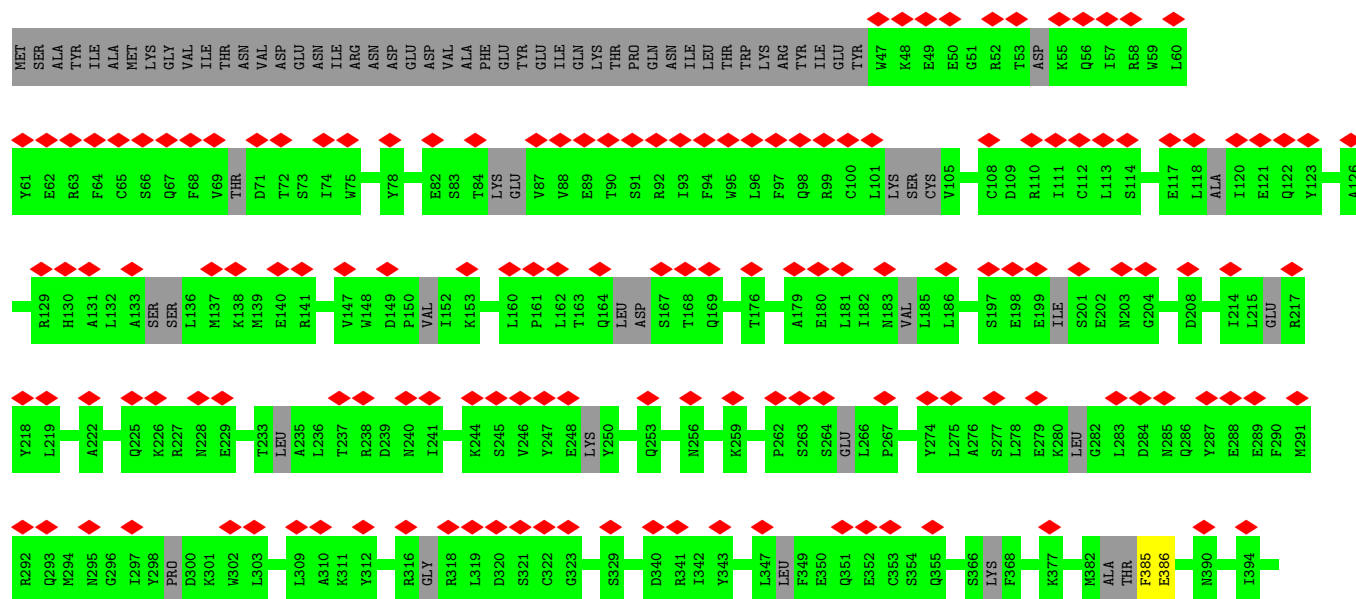
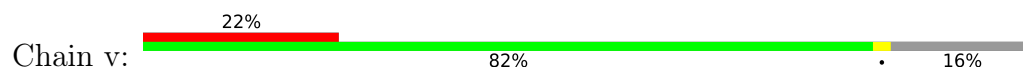


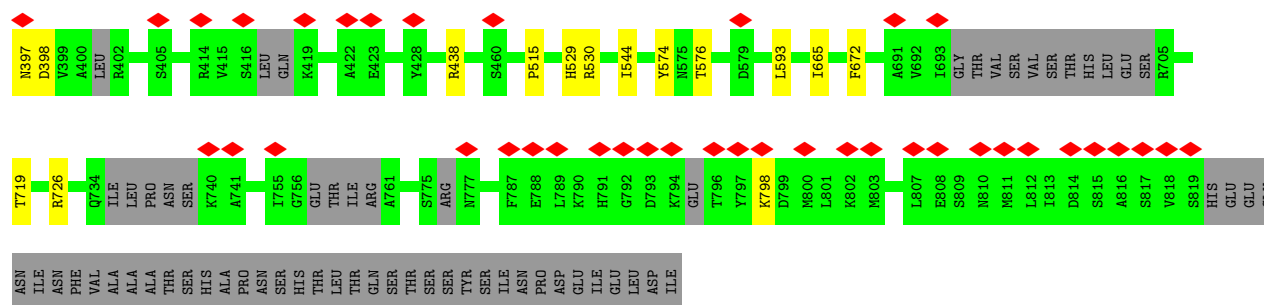
- Molecule 19: U2 snRNA



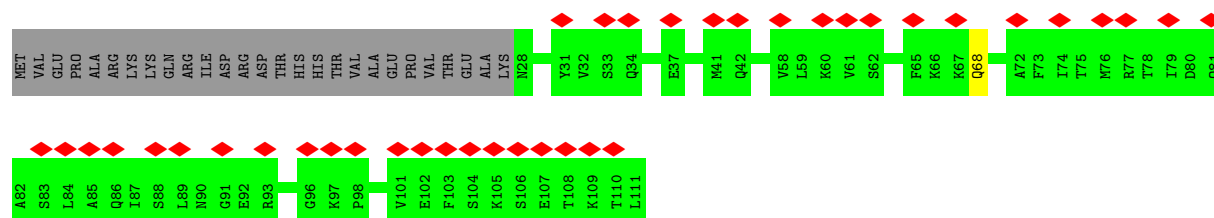
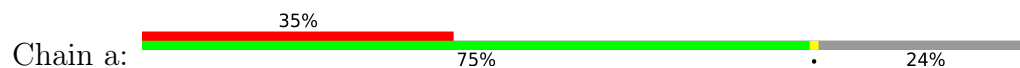


● Molecule 20: Pre-mRNA-splicing factor SYF1

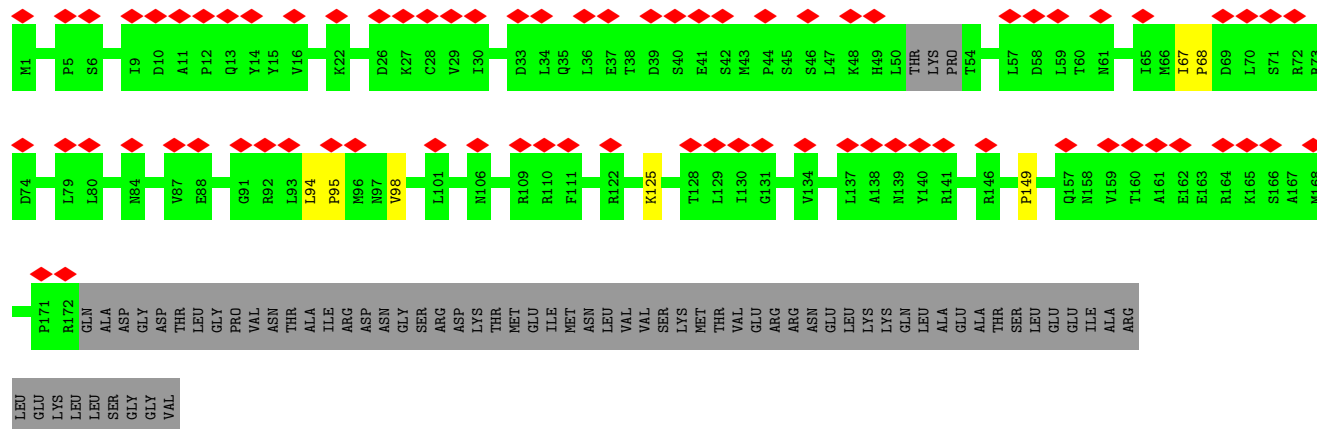




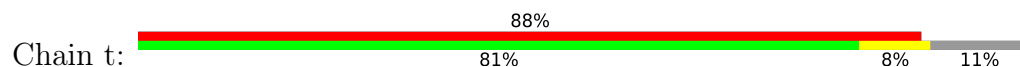
• Molecule 21: U2 small nuclear ribonucleoprotein B''

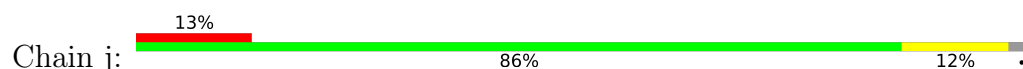


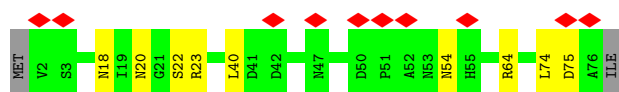
• Molecule 22: U2 small nuclear ribonucleoprotein A'



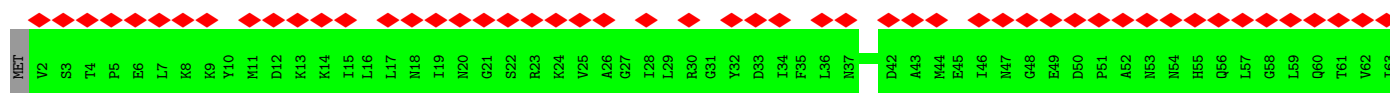
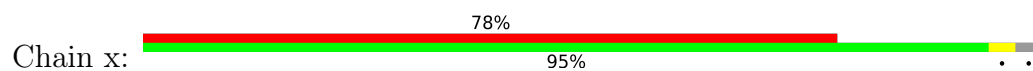
• Molecule 23: Pre-mRNA-splicing factor SNT309



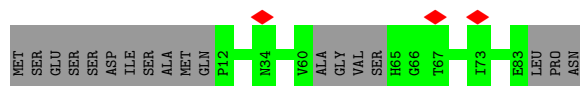
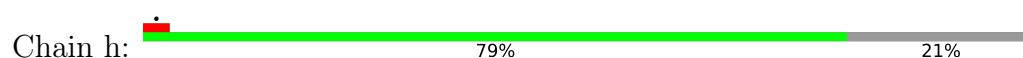




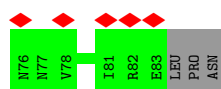
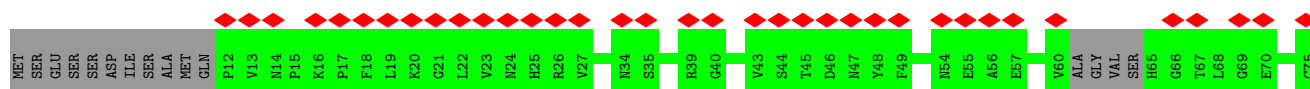
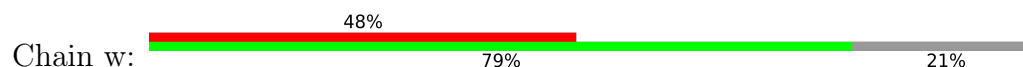
- Molecule 26: Small nuclear ribonucleoprotein G



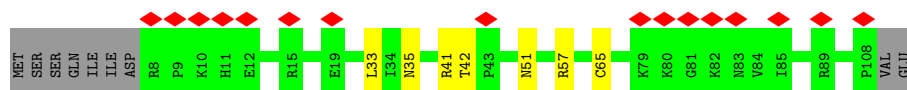
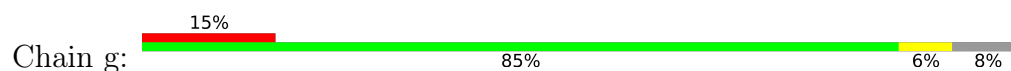
- Molecule 27: Small nuclear ribonucleoprotein F



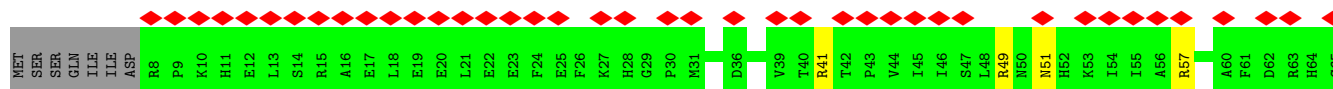
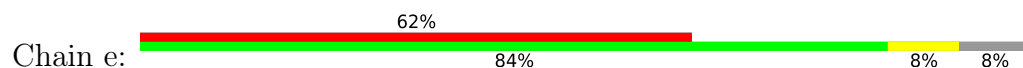
- Molecule 27: Small nuclear ribonucleoprotein F



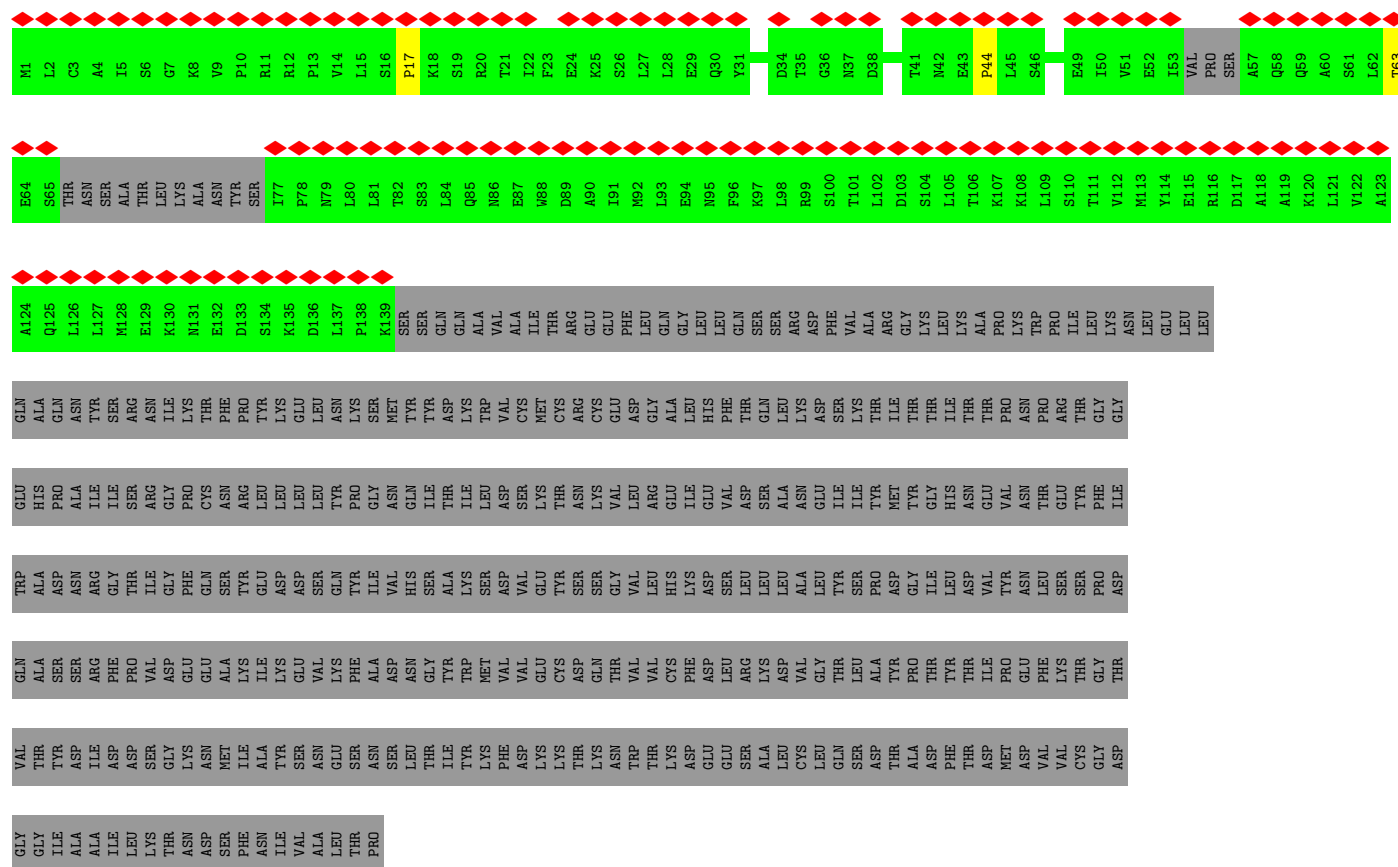
- Molecule 28: Small nuclear ribonucleoprotein Sm D2



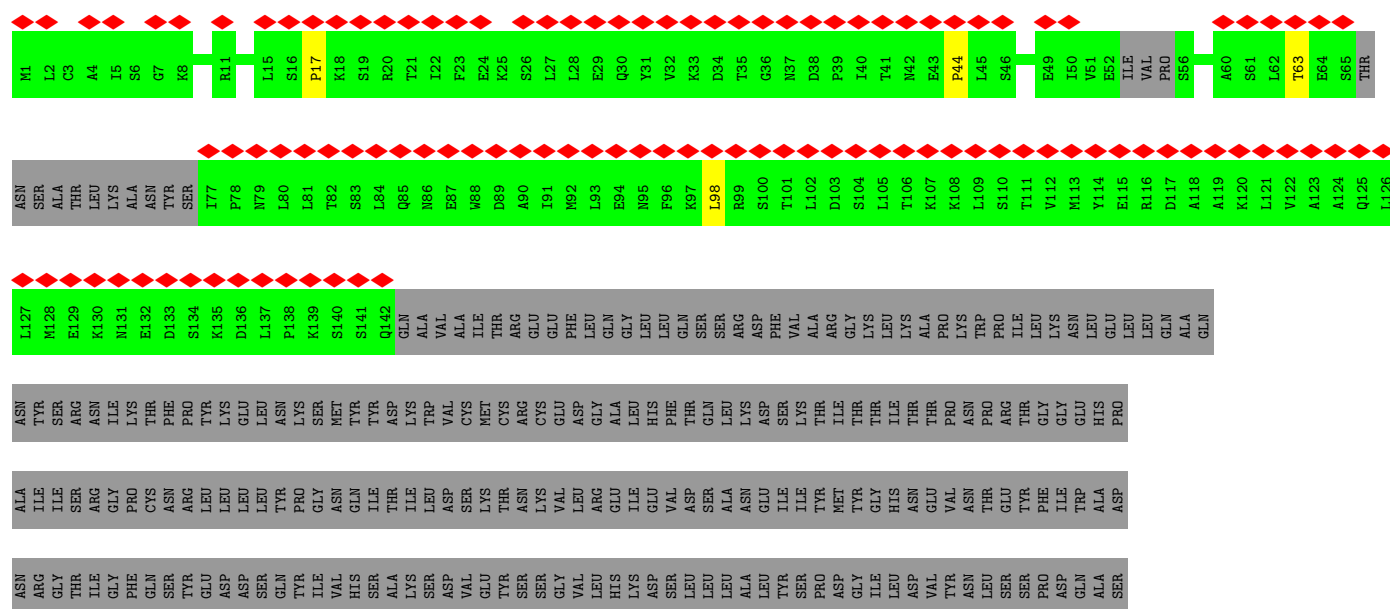
- Molecule 28: Small nuclear ribonucleoprotein Sm D2





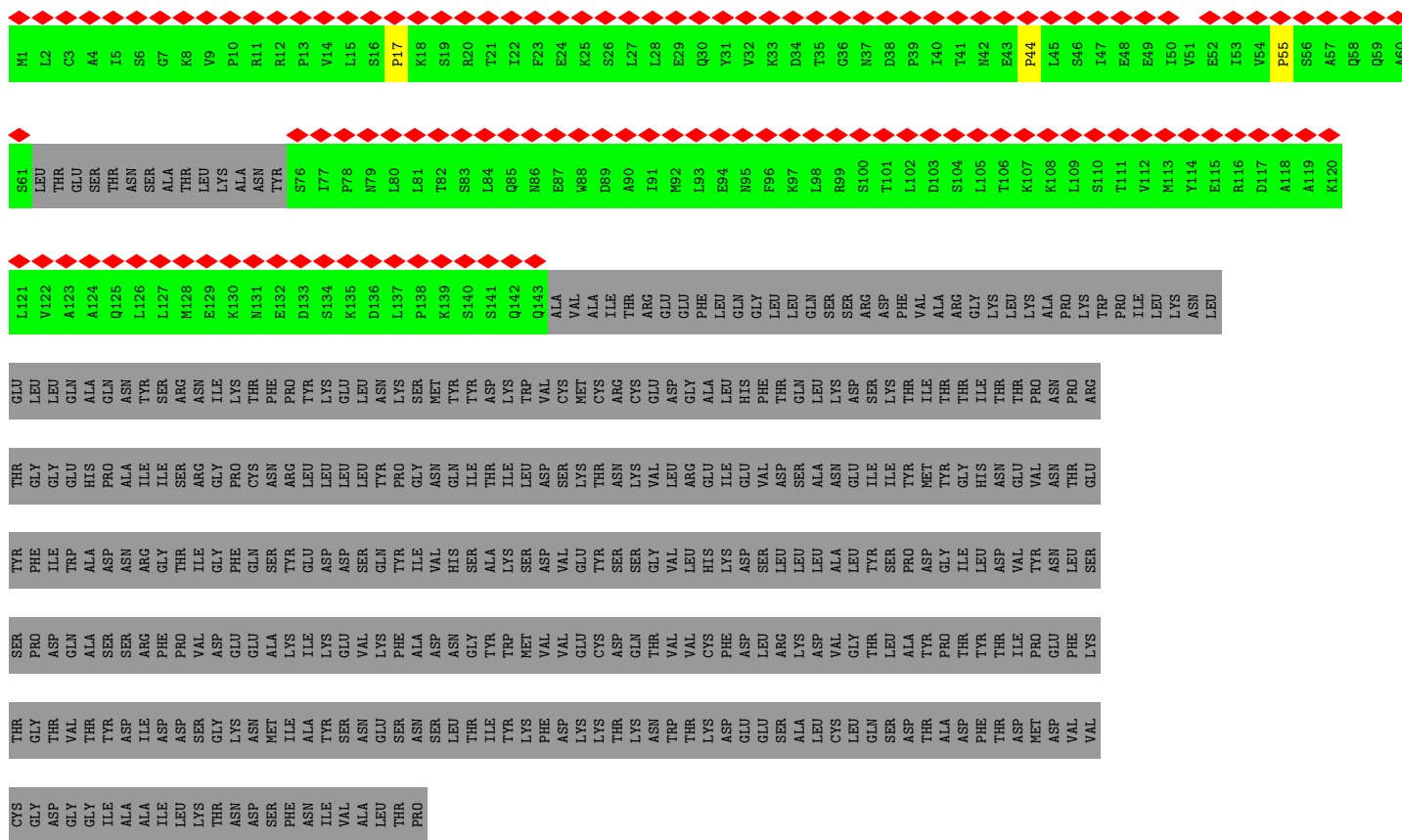


- Molecule 31: Pre-mRNA-processing factor 19





- Molecule 31: Pre-mRNA-processing factor 19



- Molecule 31: Pre-mRNA-processing factor 19



[illegible]

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	395458	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	49.3	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	0.209	Depositor
Minimum map value	-0.095	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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: IHP, MG, SEP, 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	0.45	0/16198	0.61	0/21958
2	C	0.44	0/7503	0.62	0/10159
3	J	0.40	0/191	0.67	0/254
4	O	0.52	0/2872	0.65	0/3902
5	P	0.38	0/1629	0.55	0/2194
6	Q	0.38	0/2339	0.62	0/3154
7	R	0.41	0/2135	0.58	0/2871
8	S	0.33	0/581	0.56	0/776
9	T	0.49	0/1315	0.59	0/1759
10	Z	0.35	0/3712	0.56	0/5004
11	c	0.32	0/2996	0.48	0/4033
12	d	0.36	0/3931	0.50	0/5356
13	I	0.36	0/826	0.51	0/1097
14	n	0.34	0/1894	0.58	0/2529
15	H	0.37	0/644	0.70	0/864
16	B	0.49	0/1347	0.92	0/2091
17	D	0.56	0/4239	0.96	0/6598
18	E	0.80	1/2452 (0.0%)	0.95	0/3817
19	L	0.37	2/4815 (0.0%)	0.79	0/7467
20	v	0.42	0/4662	0.51	0/6358
21	a	0.42	0/415	0.57	0/577
22	b	0.69	0/839	0.70	0/1169
23	t	0.29	0/924	0.42	0/1244
24	i	0.29	0/551	0.50	0/750
24	u	0.29	0/535	0.48	0/730
25	m	0.35	0/926	0.55	0/1257
25	z	0.30	0/833	0.54	0/1134
26	j	0.45	0/557	0.54	0/756
26	x	0.34	0/557	0.51	0/756
27	h	0.28	0/529	0.50	0/715
27	w	0.28	0/529	0.50	0/715
28	e	0.38	0/799	0.52	0/1078

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
28	g	0.40	0/799	0.55	0/1078
29	k	0.41	0/815	0.60	0/1092
29	s	0.36	0/755	0.59	0/1014
30	l	0.49	0/650	0.57	0/879
30	y	0.31	0/625	0.50	0/847
31	o	0.28	0/835	0.50	0/1126
31	p	0.25	0/848	0.51	0/1143
31	q	0.30	0/856	0.52	0/1155
31	r	0.29	0/828	0.54	0/1117
All	All	0.43	3/81286 (0.0%)	0.64	0/112573

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	L	12	U	O3'-P	7.07	1.69	1.61
19	L	1120	G	O3'-P	-5.48	1.54	1.61
18	E	81	G	O3'-P	-5.11	1.55	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1905/2413 (79%)	1793 (94%)	95 (5%)	17 (1%)	14 48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	914/1008 (91%)	872 (95%)	41 (4%)	1 (0%)	48	80
3	J	25/135 (18%)	23 (92%)	2 (8%)	0	100	100
4	O	355/451 (79%)	316 (89%)	33 (9%)	6 (2%)	7	36
5	P	197/379 (52%)	183 (93%)	6 (3%)	8 (4%)	2	22
6	Q	288/364 (79%)	263 (91%)	20 (7%)	5 (2%)	7	36
7	R	259/339 (76%)	247 (95%)	10 (4%)	2 (1%)	16	51
8	S	64/175 (37%)	60 (94%)	4 (6%)	0	100	100
9	T	155/157 (99%)	146 (94%)	6 (4%)	3 (2%)	6	35
10	Z	443/577 (77%)	422 (95%)	21 (5%)	0	100	100
11	c	418/590 (71%)	398 (95%)	20 (5%)	0	100	100
12	d	534/687 (78%)	520 (97%)	13 (2%)	1 (0%)	44	75
13	I	98/215 (46%)	94 (96%)	4 (4%)	0	100	100
14	n	279/455 (61%)	249 (89%)	25 (9%)	5 (2%)	7	35
15	H	69/235 (29%)	61 (88%)	8 (12%)	0	100	100
20	v	666/859 (78%)	642 (96%)	22 (3%)	2 (0%)	37	70
21	a	82/111 (74%)	78 (95%)	3 (4%)	1 (1%)	11	43
22	b	165/238 (69%)	138 (84%)	20 (12%)	7 (4%)	2	22
23	t	150/175 (86%)	145 (97%)	4 (3%)	1 (1%)	19	54
24	i	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
24	u	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
25	m	117/146 (80%)	111 (95%)	6 (5%)	0	100	100
25	z	106/146 (73%)	100 (94%)	6 (6%)	0	100	100
26	j	73/77 (95%)	67 (92%)	5 (7%)	1 (1%)	9	39
26	x	73/77 (95%)	65 (89%)	7 (10%)	1 (1%)	9	39
27	h	64/86 (74%)	60 (94%)	4 (6%)	0	100	100
27	w	64/86 (74%)	61 (95%)	3 (5%)	0	100	100
28	e	99/110 (90%)	95 (96%)	3 (3%)	1 (1%)	13	46
28	g	99/110 (90%)	93 (94%)	4 (4%)	2 (2%)	6	34
29	k	96/196 (49%)	90 (94%)	5 (5%)	1 (1%)	13	46
29	s	89/196 (45%)	83 (93%)	6 (7%)	0	100	100
30	l	81/101 (80%)	79 (98%)	0	2 (2%)	4	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	y	79/101 (78%)	75 (95%)	4 (5%)	0	100	100
31	o	120/503 (24%)	115 (96%)	5 (4%)	0	100	100
31	p	122/503 (24%)	118 (97%)	4 (3%)	0	100	100
31	q	125/503 (25%)	116 (93%)	9 (7%)	0	100	100
31	r	119/503 (24%)	112 (94%)	7 (6%)	0	100	100
All	All	8732/13195 (66%)	8224 (94%)	441 (5%)	67 (1%)	19	51

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	260	PRO
1	A	403	TYR
1	A	773	SER
1	A	1575	TRP

### 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	1737/2182 (80%)	1700 (98%)	37 (2%)	48	67
2	C	830/910 (91%)	820 (99%)	10 (1%)	67	78
3	J	21/121 (17%)	21 (100%)	0	100	100
4	O	312/397 (79%)	304 (97%)	8 (3%)	41	62
5	P	175/328 (53%)	169 (97%)	6 (3%)	32	55
6	Q	265/332 (80%)	262 (99%)	3 (1%)	70	79
7	R	224/296 (76%)	221 (99%)	3 (1%)	65	76
8	S	57/151 (38%)	56 (98%)	1 (2%)	54	71
9	T	141/141 (100%)	139 (99%)	2 (1%)	62	75
10	Z	417/538 (78%)	414 (99%)	3 (1%)	81	86
11	c	214/525 (41%)	209 (98%)	5 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	d	274/633 (43%)	269 (98%)	5 (2%)	54	71
13	I	92/193 (48%)	92 (100%)	0	100	100
14	n	122/412 (30%)	108 (88%)	14 (12%)	4	20
15	H	69/216 (32%)	69 (100%)	0	100	100
20	v	294/786 (37%)	279 (95%)	15 (5%)	20	46
23	t	39/165 (24%)	26 (67%)	13 (33%)	0	1
24	i	55/83 (66%)	52 (94%)	3 (6%)	18	44
24	u	52/83 (63%)	51 (98%)	1 (2%)	52	70
25	m	106/129 (82%)	97 (92%)	9 (8%)	8	32
25	z	95/129 (74%)	95 (100%)	0	100	100
26	j	56/66 (85%)	48 (86%)	8 (14%)	2	16
26	x	56/66 (85%)	55 (98%)	1 (2%)	54	71
27	h	51/77 (66%)	51 (100%)	0	100	100
27	w	51/77 (66%)	51 (100%)	0	100	100
28	e	82/103 (80%)	74 (90%)	8 (10%)	6	24
28	g	82/103 (80%)	77 (94%)	5 (6%)	15	41
29	k	92/176 (52%)	79 (86%)	13 (14%)	3	16
29	s	85/176 (48%)	82 (96%)	3 (4%)	31	55
30	l	72/89 (81%)	53 (74%)	19 (26%)	0	3
30	y	68/89 (76%)	68 (100%)	0	100	100
31	o	60/451 (13%)	57 (95%)	3 (5%)	20	46
31	p	62/451 (14%)	58 (94%)	4 (6%)	14	39
31	q	62/451 (14%)	59 (95%)	3 (5%)	21	47
31	r	60/451 (13%)	57 (95%)	3 (5%)	20	46
All	All	6530/11576 (56%)	6322 (97%)	208 (3%)	36	57

5 of 208 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	t	85	THR
28	g	33	LEU
31	p	44	PRO
23	t	108	SER
25	m	47	LEU



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
9	T	112	ASN
20	v	643	HIS
25	z	30	GLN
10	Z	84	ASN
12	d	123	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	B	55/246 (22%)	33 (60%)	5 (9%)
17	D	177/214 (82%)	56 (31%)	8 (4%)
18	E	102/112 (91%)	43 (42%)	5 (4%)
19	L	194/1175 (16%)	75 (38%)	13 (6%)
All	All	528/1747 (30%)	207 (39%)	31 (5%)

5 of 207 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	B	-11	U
16	B	-10	G
16	B	-9	A
16	B	-8	U
16	B	-6	U

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	E	55	G
19	L	1093	C
18	E	100	U
19	L	1107	C
19	L	120	G

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	$\# Z  > 2$
14	SEP	n	73	14	8,9,10	1.51	1 (12%)	8,12,14	0.99	0

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
14	SEP	n	73	14	-	3/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	n	73	SEP	P-O1P	3.29	1.61	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	n	73	SEP	CB-OG-P-O2P
14	n	73	SEP	CB-OG-P-O3P
14	n	73	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 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
32	IHP	A	3000	-	36,36,36	0.76	0	54,60,60	0.57	0
33	GTP	C	1500	34	26,34,34	0.95	2 (7%)	32,54,54	0.68	0

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
32	IHP	A	3000	-	-	6/30/54/54	0/1/1/1
33	GTP	C	1500	34	-	9/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	C	1500	GTP	C5-C6	-2.56	1.42	1.47
33	C	1500	GTP	C8-N7	-2.10	1.31	1.35

There are no bond angle outliers.

There are no chirality outliers.

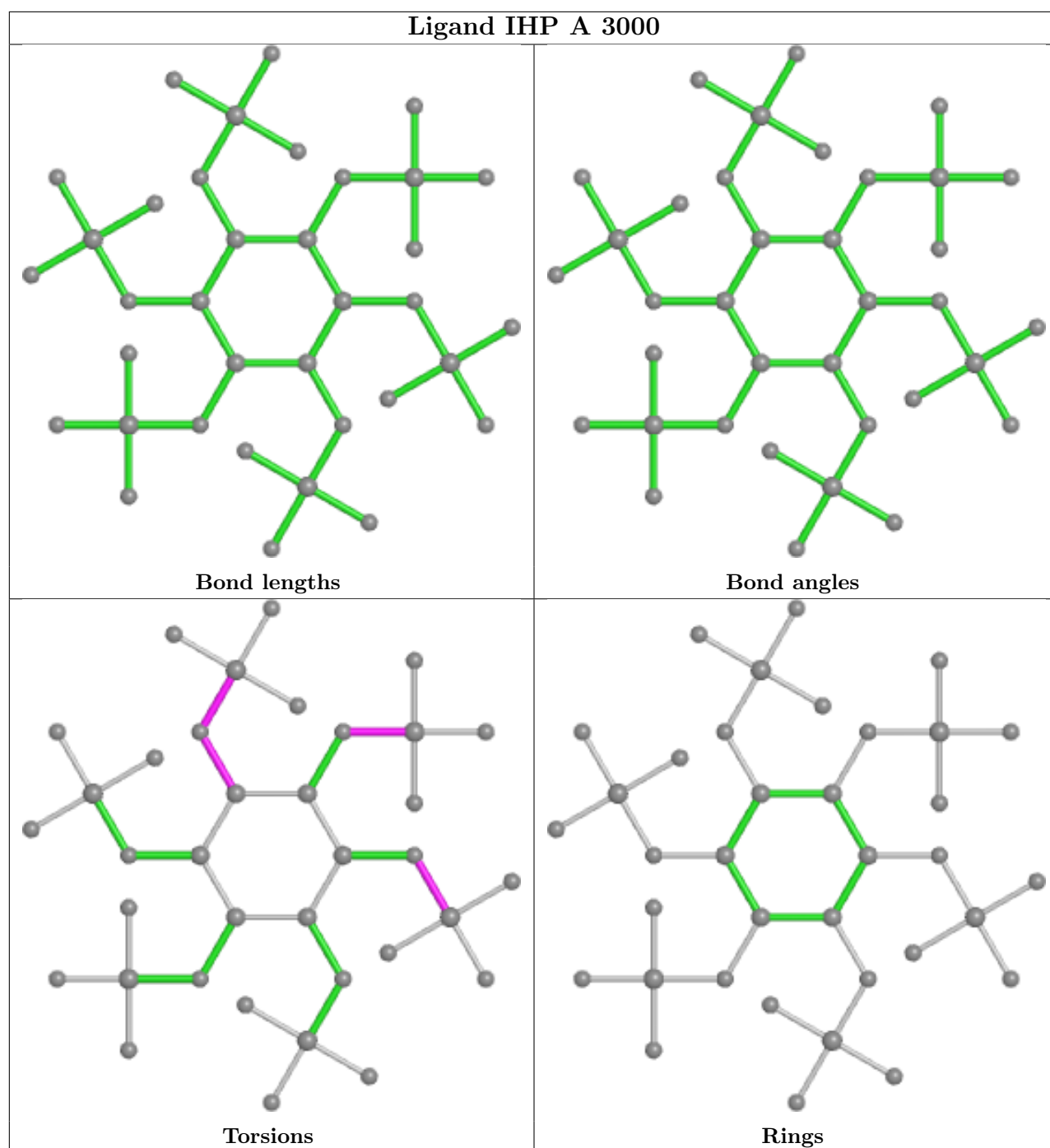
5 of 15 torsion outliers are listed below:

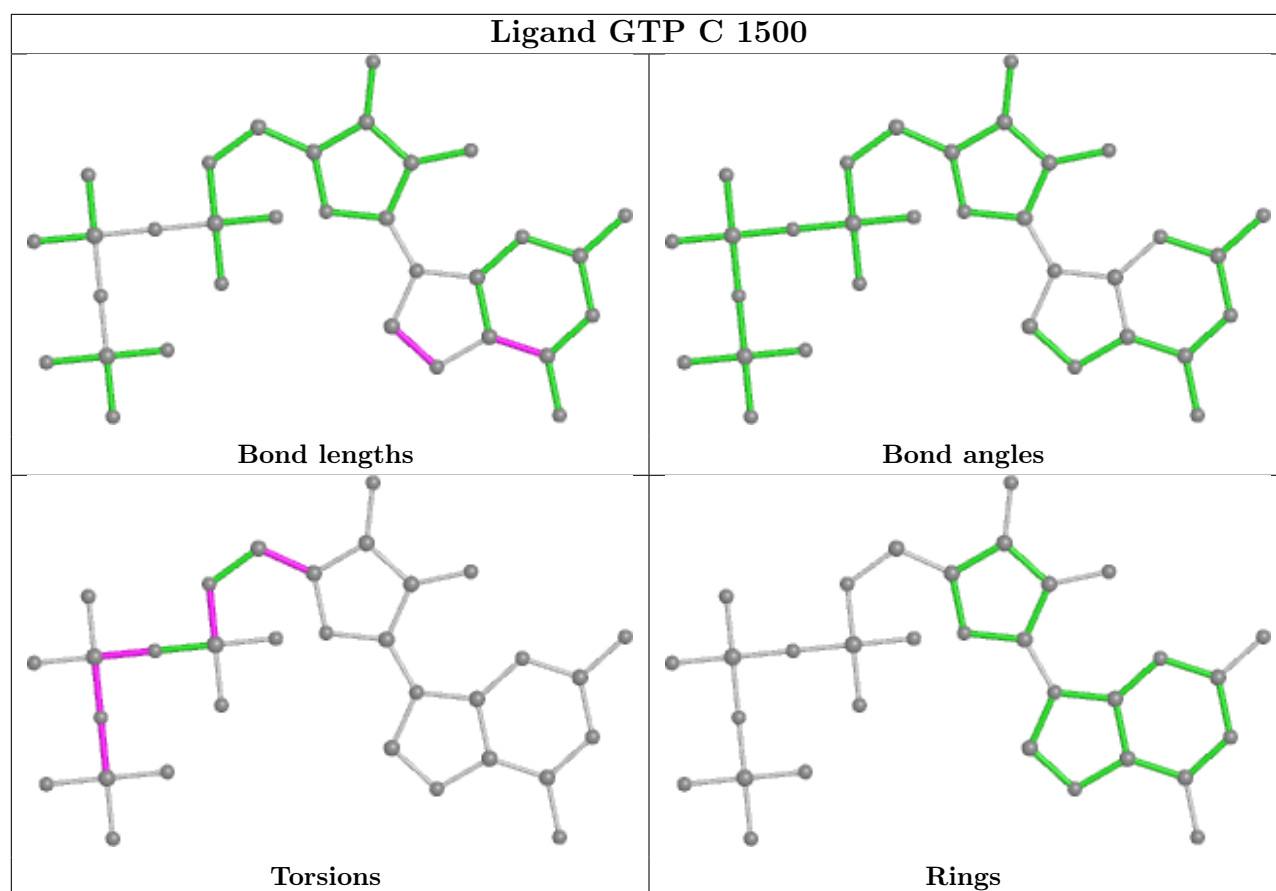
Mol	Chain	Res	Type	Atoms
32	A	3000	IHP	C2-C3-O13-P3
32	A	3000	IHP	C5-O15-P5-O25
33	C	1500	GTP	C5'-O5'-PA-O3A
33	C	1500	GTP	C5'-O5'-PA-O1A
33	C	1500	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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.

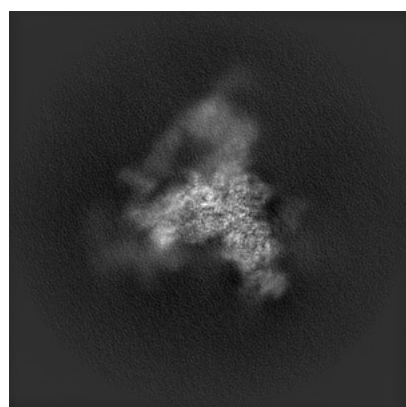
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0691. These allow visual inspection of the internal detail of the map and identification of artifacts.

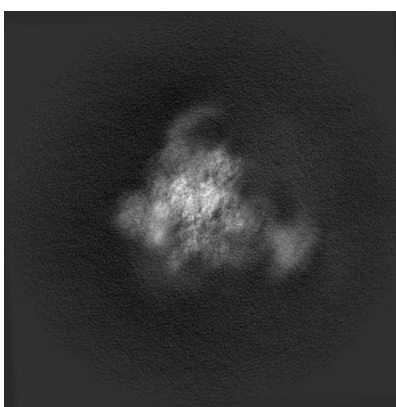
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

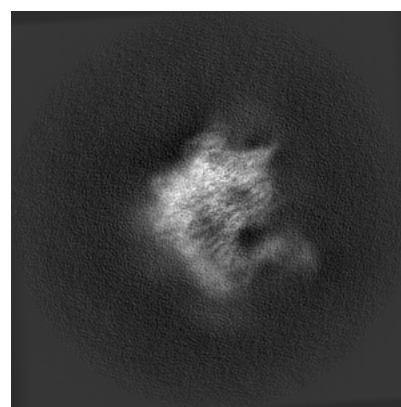
#### 6.1.1 Primary map



X



Y

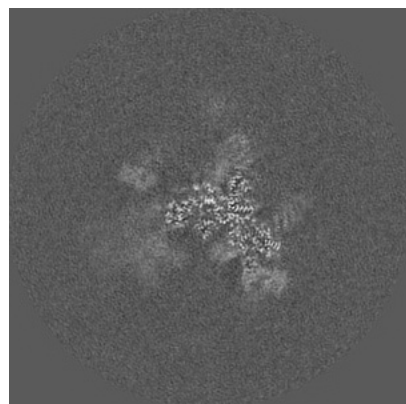


Z

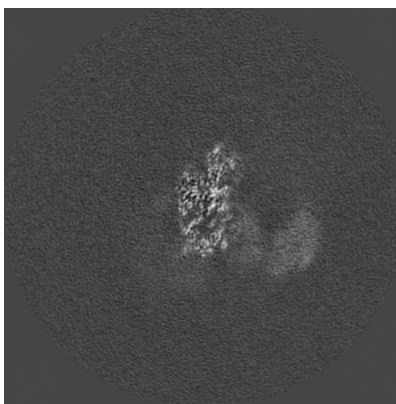
The images above show the map projected in three orthogonal directions.

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

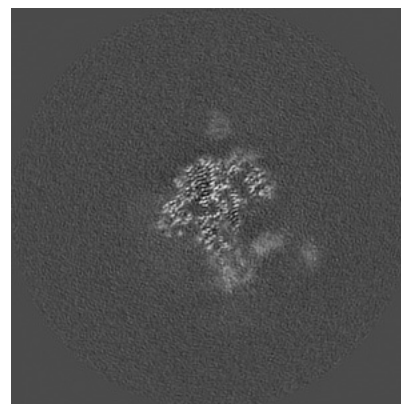
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

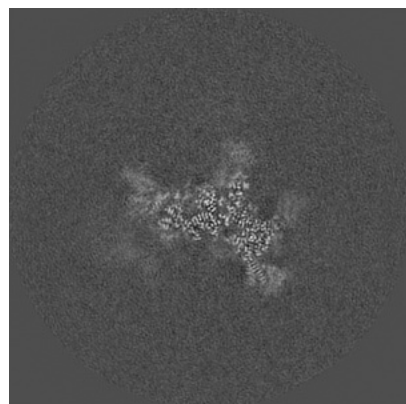


Z Index: 200

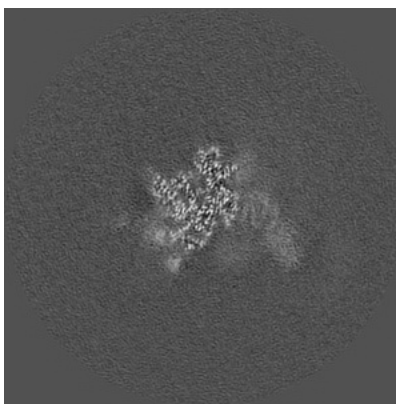
The images above show central slices of the map in three orthogonal directions.

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

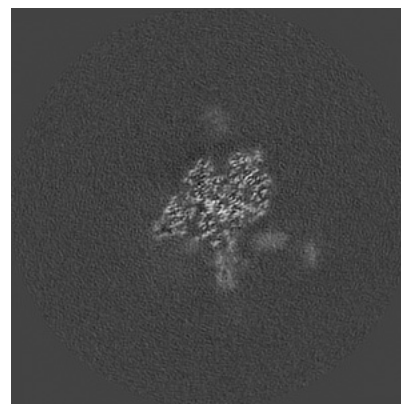
### 6.3.1 Primary map



X Index: 210



Y Index: 228

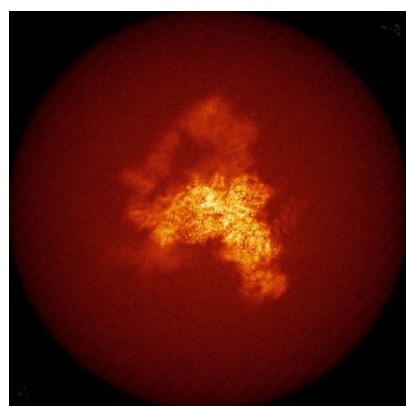


Z Index: 206

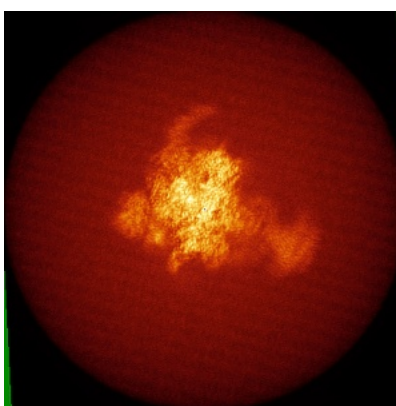
The images above show the largest variance slices of the map in three orthogonal directions.

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

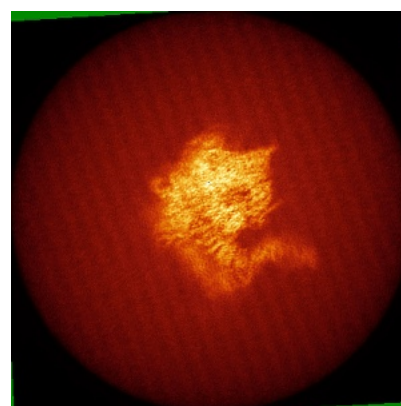
### 6.4.1 Primary map



X



Y



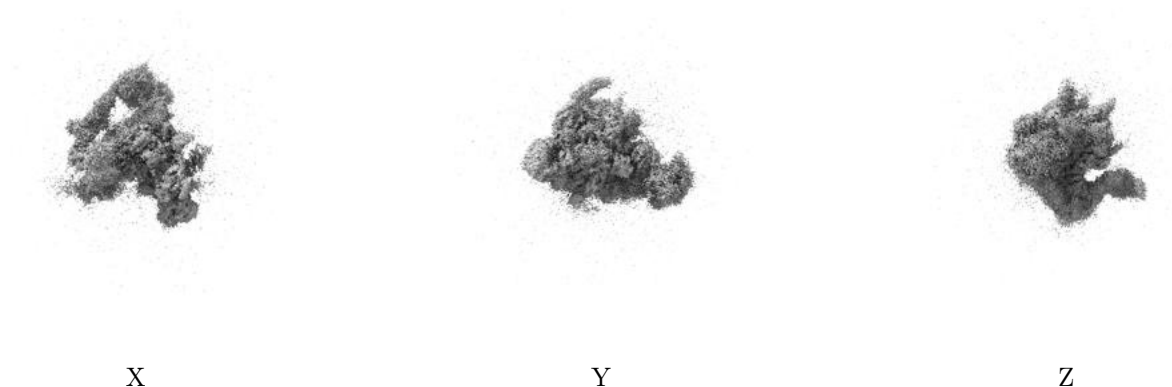
Z

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

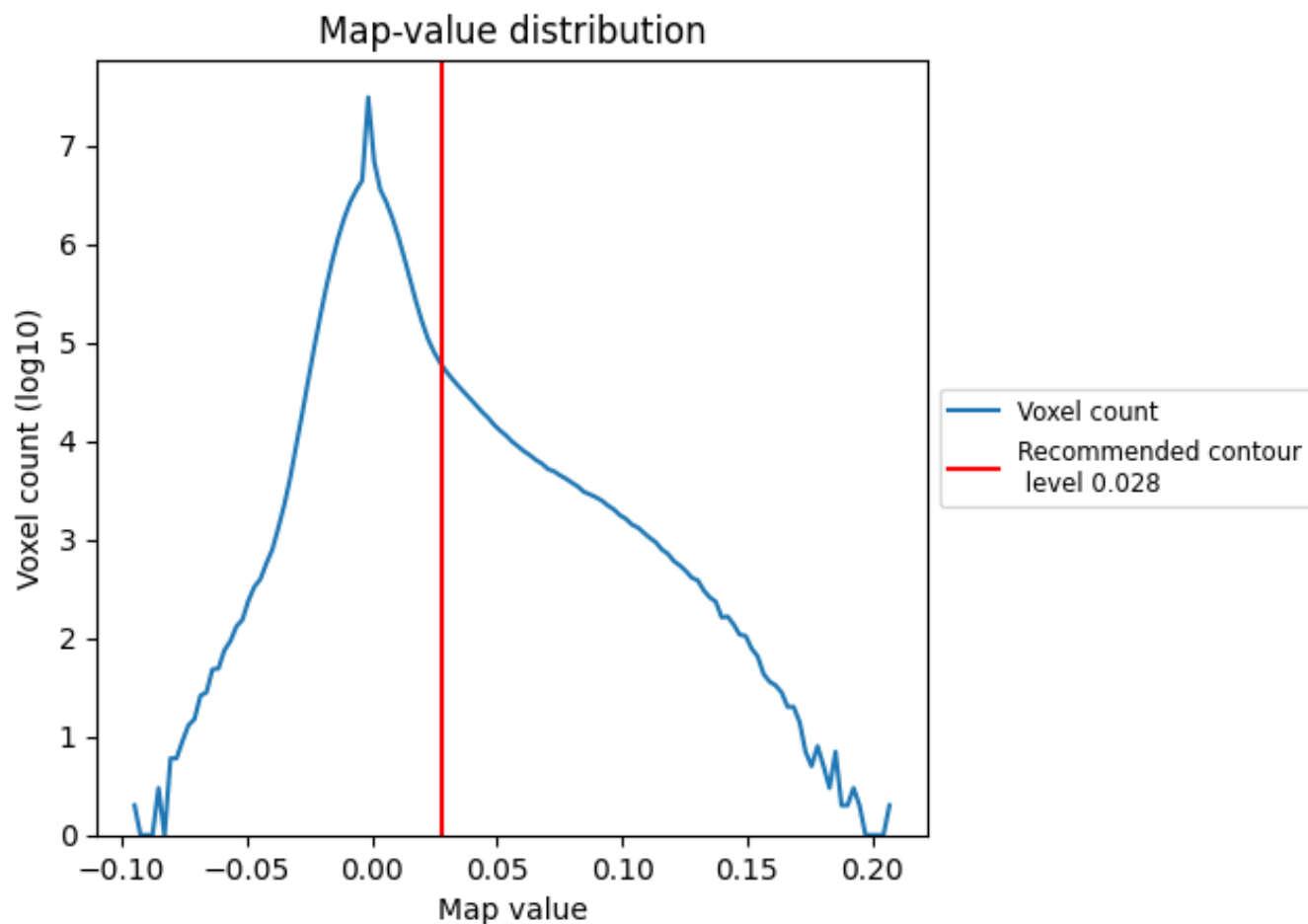
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

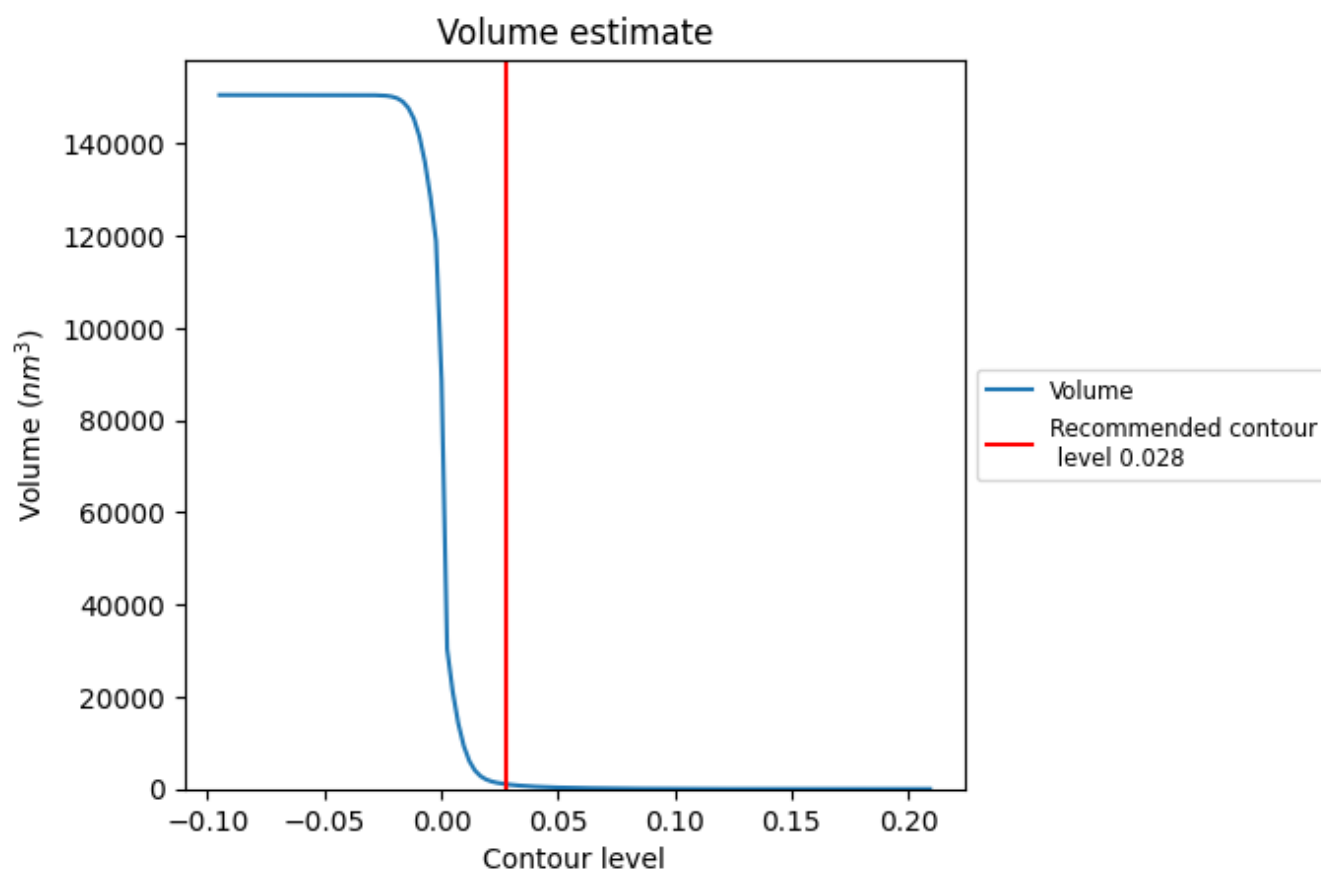
This section contains the results of statistical analysis of the map.

### 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.

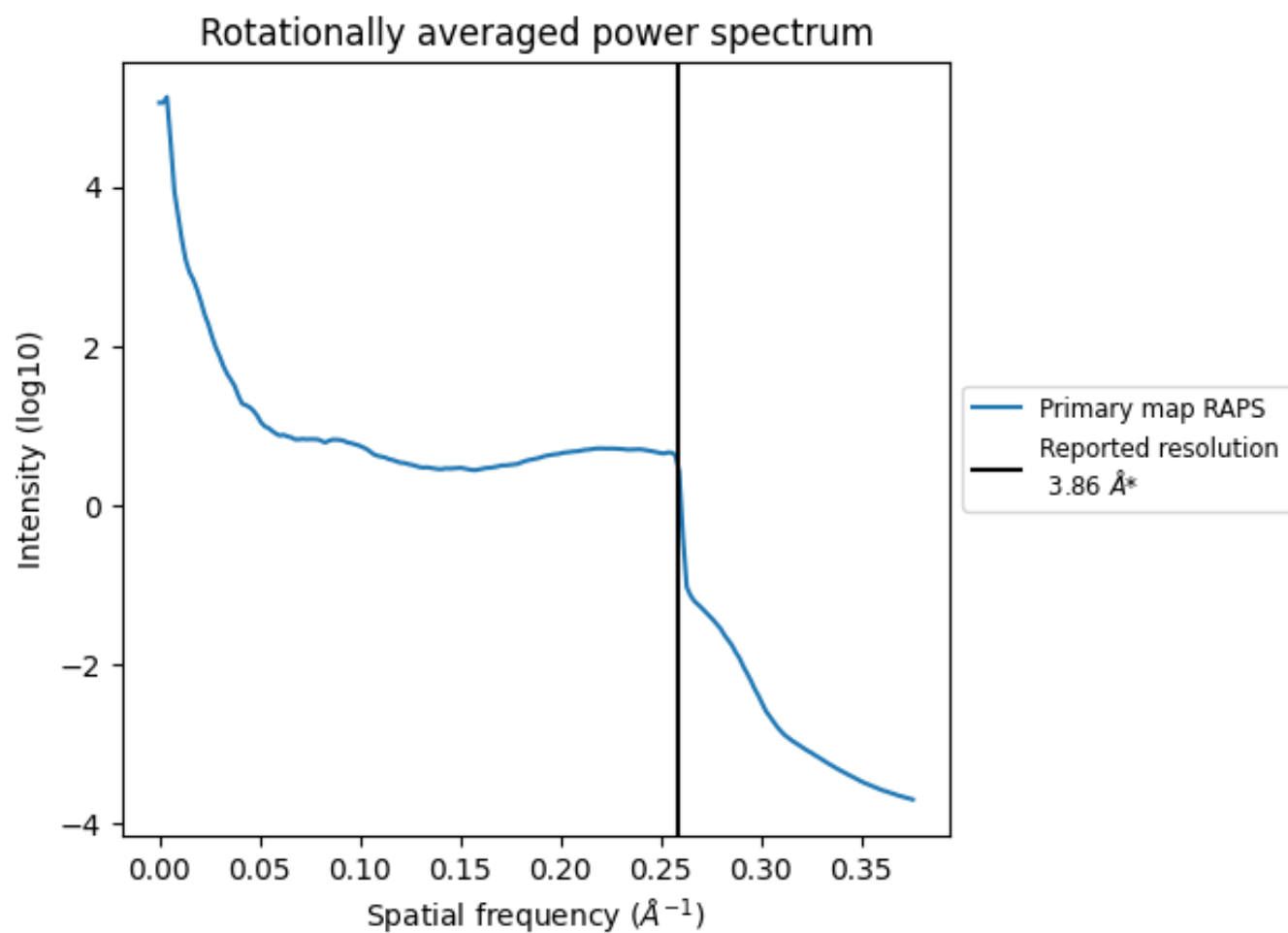
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1021 nm<sup>3</sup>; this corresponds to an approximate mass of 922 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 0.259 Å<sup>-1</sup>

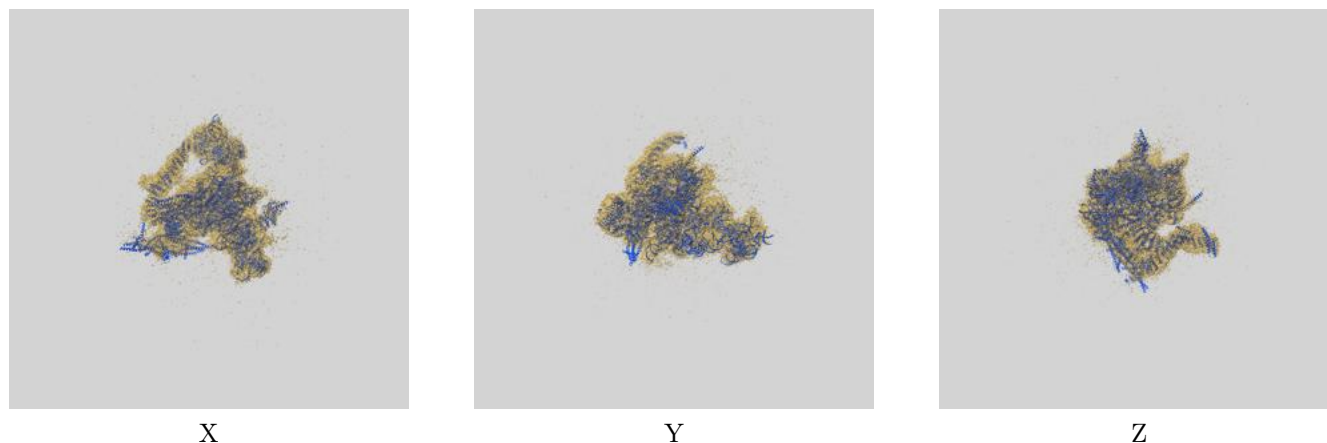
## 8 Fourier-Shell correlation

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-0691 and PDB model 6J6N. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

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



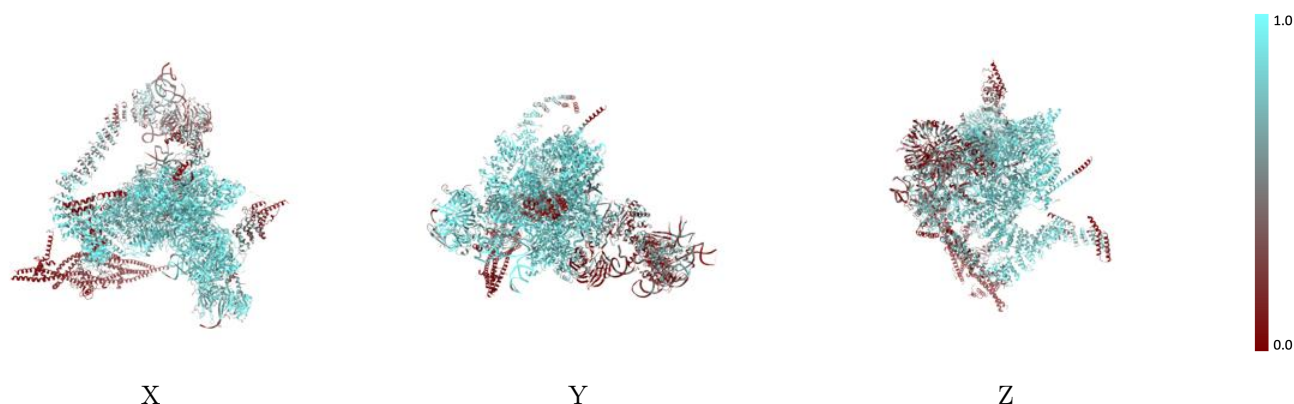
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



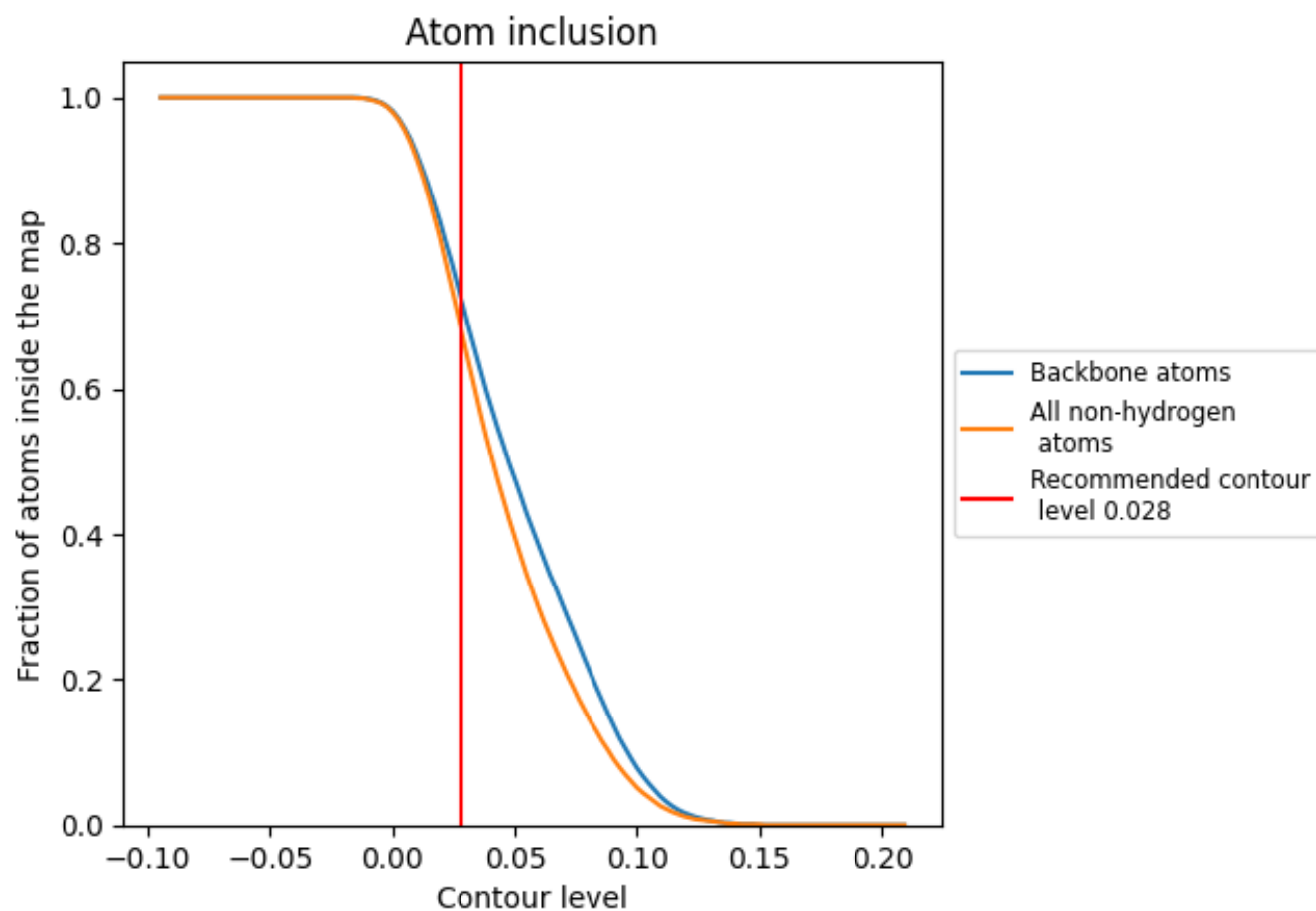
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.028).

## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 72% of all backbone atoms, 68% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6830	 0.2480
A	 0.8210	 0.3620
B	 0.6890	 0.2110
C	 0.8760	 0.3900
D	 0.9030	 0.2580
E	 0.9600	 0.3630
H	 0.4020	 0.0970
I	 0.7530	 0.2890
J	 0.8720	 0.3970
L	 0.4980	 0.0780
O	 0.8800	 0.4260
P	 0.7560	 0.3360
Q	 0.8190	 0.3290
R	 0.8720	 0.3760
S	 0.7630	 0.3950
T	 0.9030	 0.4020
Z	 0.5320	 0.2310
a	 0.5070	 0.0430
b	 0.5120	 0.0450
c	 0.4810	 0.2030
d	 0.7700	 0.2460
e	 0.3070	 0.0600
g	 0.7020	 0.1280
h	 0.8600	 0.1290
i	 0.8350	 0.1430
j	 0.7430	 0.2110
k	 0.7340	 0.2230
l	 0.8200	 0.3080
m	 0.6640	 0.1580
n	 0.1440	 0.0390
o	 0.1020	 -0.0100
p	 0.1200	 0.0050
q	 0.0150	 -0.0080
r	 0.0920	 -0.0100
s	 0.4600	 0.0150



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Chain	Atom inclusion	Q-score
t	 0.0320	 0.0250
u	 0.3050	 0.0300
v	 0.6840	 0.1200
w	 0.3610	 0.0580
x	 0.2390	 0.0380
y	 0.3240	 0.0380
z	 0.3880	 0.0460