



wwPDB EM Map/Model Validation Report ⓘ

Sep 28, 2016 – 11:07 AM EDT

PDB ID : 5LQW
EMDB ID: : EMD-4099
Title : yeast activated spliceosome
Authors : Rauhut, R.; Luehrmann, R.
Deposited on : 2016-08-17
Resolution : 5.80 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

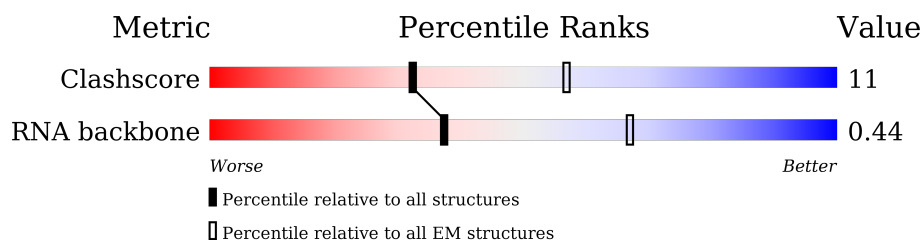
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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.











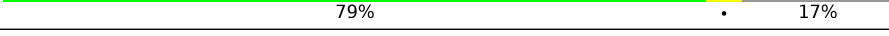
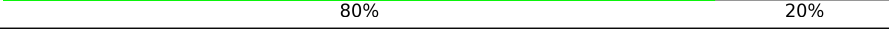
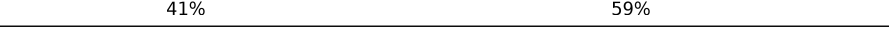

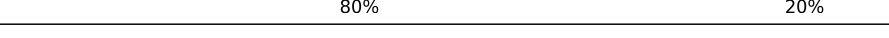
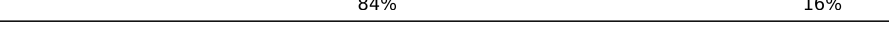
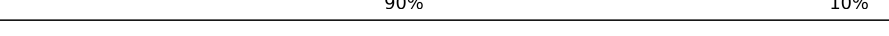


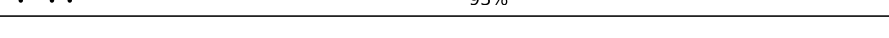
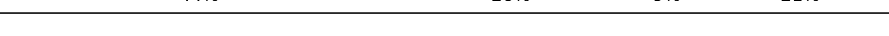


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	2413	87% 12%
2	B	1008	82% 16%
3	C	2163	83% 16%
4	D	364	51% 49%
5	E	157	83% 12%
6	F	339	60% 36%
7	H	577	75% 24%
8	J	148	69% 30%
9	K	451	73% 25%
10	L	266	12% 88%

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Mol	Chain	Length	Quality of chain
11	M	379	
12	N	204	
13	O	876	
14	P	859	
15	Q	971	
16	R	687	
17	W	590	
18	X	1361	
19	Y	107	
20	Z	85	
21	b	196	
22	d	101	
23	e	94	
24	f	86	
25	g	77	
26	h	146	
27	j	110	
28	2	1175	
29	5	179	
30	6	112	
31	9	572	

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 18351 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	2130	Total	C	0	2130
			2130	2130		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	ASN	MET	conflict	UNP P33334

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

Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	843	Total	C	0	843
			843	843		

- Molecule 3 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	C	1811	Total	C	0	1811
			1811	1811		

- Molecule 4 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	D	187	Total	C	0	187
			187	187		

- Molecule 5 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	E	138	Total	C	0	138
			138	138		

- Molecule 6 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	F	218	Total	C	0	218
			218	218		

- Molecule 7 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	H	437	Total	C	0	437
			437	437		

- Molecule 8 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	J	104	Total	C	0	104
			104	104		

- Molecule 9 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	K	338	Total	C	0	338
			338	338		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms		AltConf	Trace
10	L	32	Total	C	0	32
			32	32		

- Molecule 11 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	M	169	Total	C	0	169
			169	169		

- Molecule 12 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	N	159	Total	C	0	159
			159	159		

- Molecule 13 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	O	628	Total	C	0	628
			628	628		

- Molecule 14 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	P	202	Total	C	0	202
			202	202		

- Molecule 15 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	Q	791	Total	C	0	791
			791	791		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms		AltConf	Trace
16	R	219	Total	C	0	219
			219	219		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms		AltConf	Trace
17	W	128	Total	C	0	128
			128	128		

- Molecule 18 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms		AltConf	Trace
18	X	1095	Total	C	0	1095
			1095	1095		

- Molecule 19 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms		AltConf	Trace
19	Y	89	Total	C	0	89
			89	89		

- Molecule 20 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms	AltConf	Trace
20	Z	68	Total C 68 68	0	68

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

Mol	Chain	Residues	Atoms	AltConf	Trace
21	b	80	Total C 80 80	0	80

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms	AltConf	Trace
22	d	82	Total C 82 82	0	82

- Molecule 23 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms	AltConf	Trace
23	e	75	Total C 75 75	0	75

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

Mol	Chain	Residues	Atoms	AltConf	Trace
24	f	72	Total C 72 72	0	72

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

Mol	Chain	Residues	Atoms	AltConf	Trace
25	g	69	Total C 69 69	0	69

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms	AltConf	Trace
26	h	82	Total C 82 82	0	82

- Molecule 27 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms	AltConf	Trace
27	j	94	Total C 94 94	0	94

- Molecule 28 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
28	2	81	Total C N O P 1707 764 285 577 81	0	0

- Molecule 29 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
29	5	141	Total C N O P 2999 1342 530 986 141	0	0

- Molecule 30 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
30	6	102	Total C N O P 2170 972 386 710 102	0	0

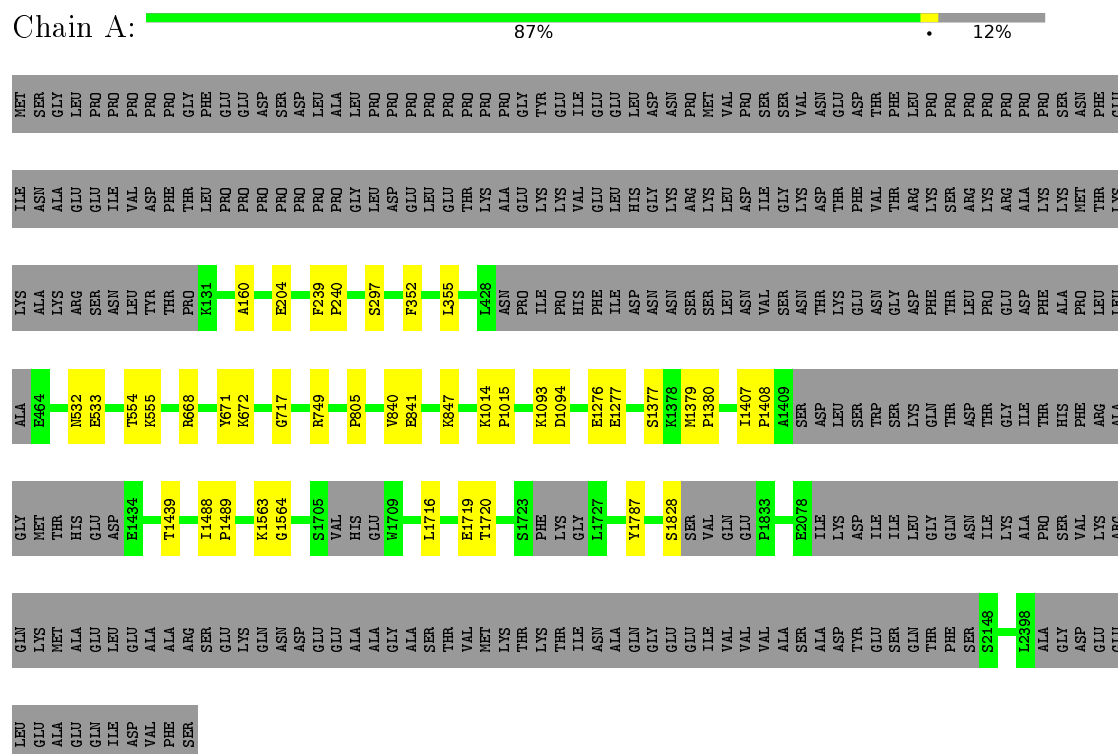
- Molecule 31 is a RNA chain called actin pre-mRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
31	9	54	Total C N O P 1135 509 187 385 54	0	0

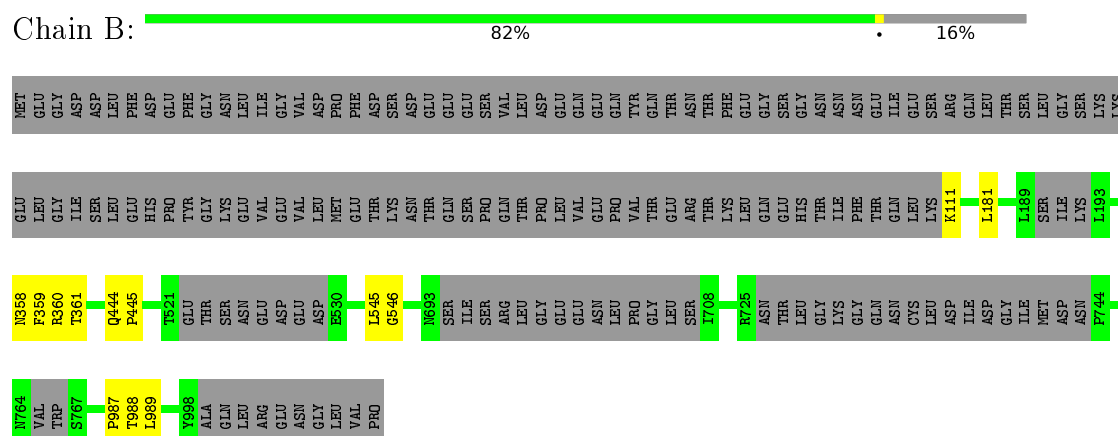
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

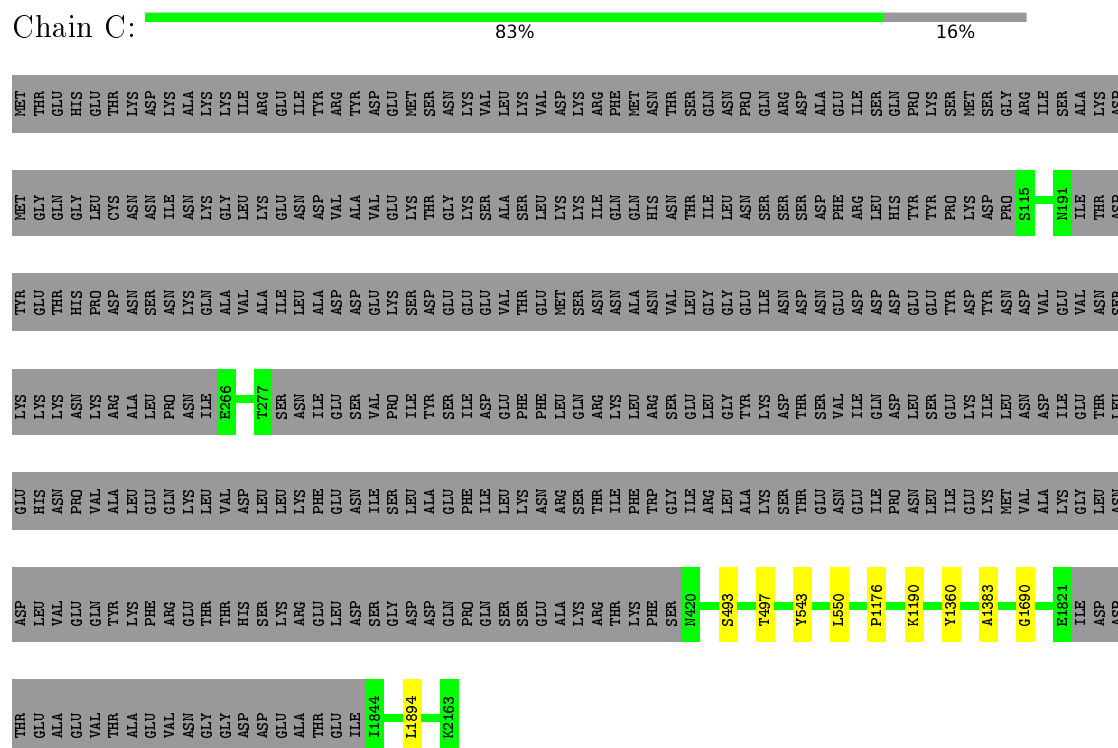
- Molecule 1: Pre-mRNA-splicing factor 8



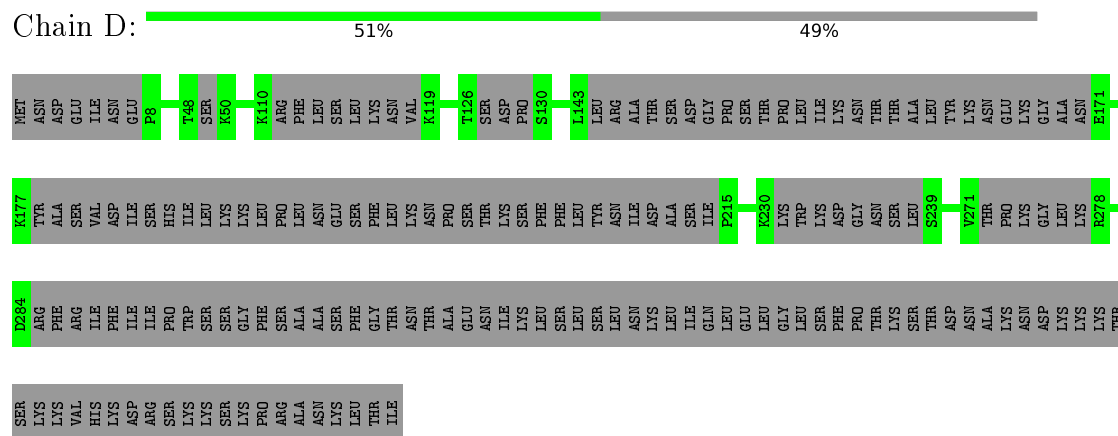
- Molecule 2: Pre-mRNA-splicing factor SNU114



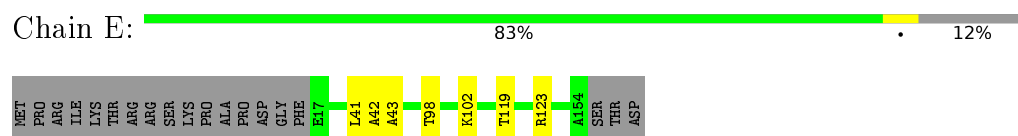
- Molecule 3: Pre-mRNA-splicing helicase BRR2



- Molecule 4: Pre-mRNA-splicing factor SLT11

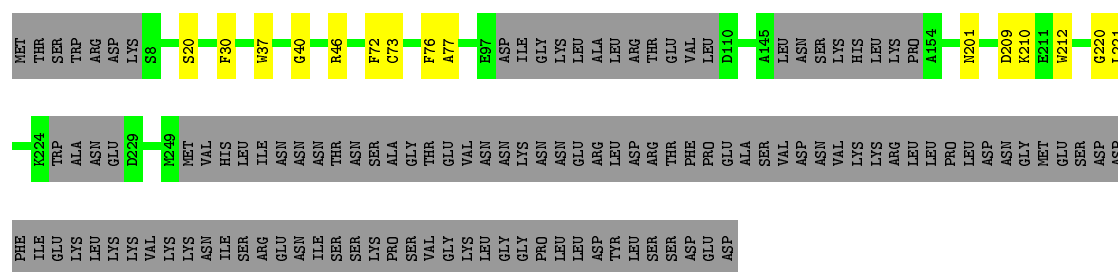


- Molecule 5: Pre-mRNA-splicing factor BUD31

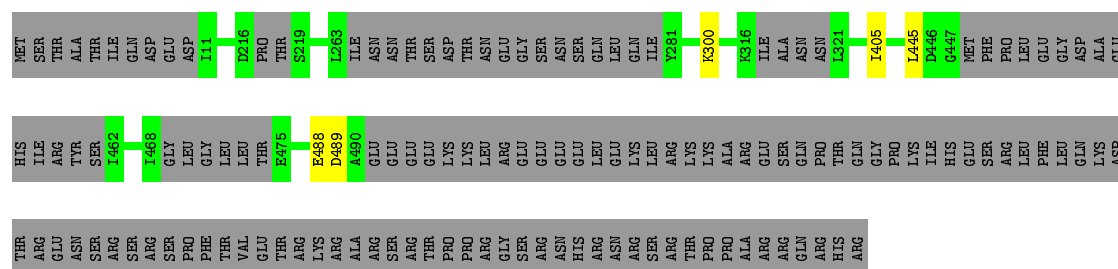


- Molecule 6: Pre-mRNA-splicing factor CWC2

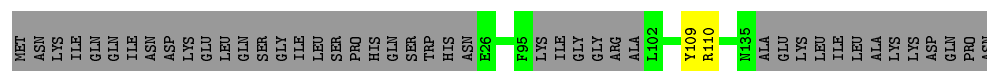




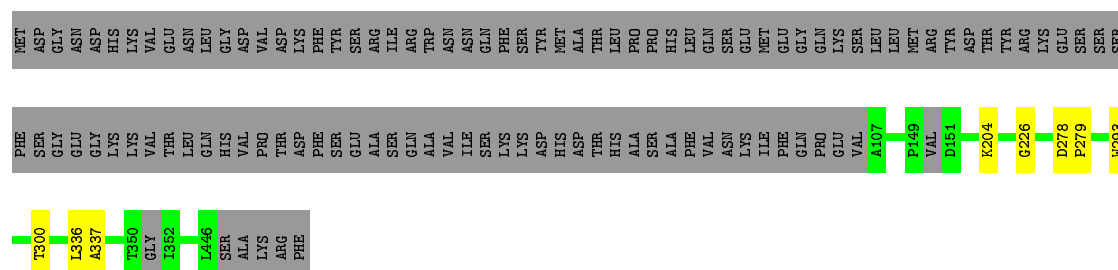
- Molecule 7: Pre-mRNA-splicing factor CWC22



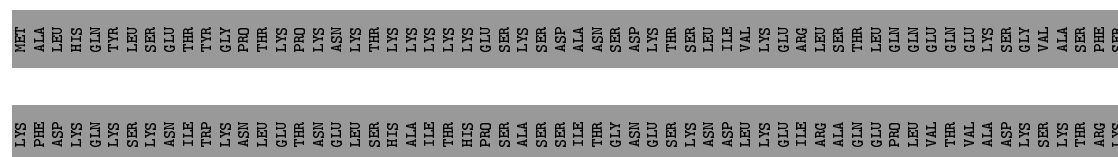
- Molecule 8: U2 snRNP component IST3



- Molecule 9: Pre-mRNA-splicing factor PRP46



- Molecule 10: Pre-mRNA-splicing factor CWC26



LYS	ASN	GLN	THR	ALA	SER	SER	LEU	THR	ILE	GLU	ASP	PRO	ALA	ILE	THR	PHE	THR	THR	HIS	ASP	GLY	LEU	ARG	LYS	THR	SER	LEU	LEU	TYR	ASP	LYS	PRO	ALA	PRO	PRO	GLU	GLU	ASN	ARG	PHE	ALA	ILE	MET	PRO	GLY	SER	ARG	TRP	ASP	GLY	V2345	V236
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- Molecule 11: Pre-mRNA-processing protein 45

Chain M:  41% 1% 55%

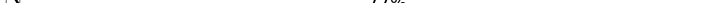
AS1	AS19	L123	G128	K129	N153	D154	E162	S170	N171	N176	G177	TYR	THR	VAL	ALA	ALA	LEU	GLU	ARG	ARG	VAL	GLY	LYS	ALA	LEU	LEU	ASP	ASN	ASN	GLU	N194	L235	L236	LVS	GLU	GLU	SER	LEU	LEU	GLU	LEU	SER	GLN	ARG	ALA	ALA	ARG	THR	VAL	GLY	THR	PRO	GLN	THR
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GLY ILE VAL LYS PRO LYS LYS GLN THR SER SER THR VAL ALA ARG LEU LYS GIJ LEU ALA TYR SER SER GLN GLY ARG ASP VAL VAL SER GLU LYS ILE ILE LEU LEU GLY GLY ALA ALA LYS ARG ARG SER GLN GLN PRO ASP LEU TYR THR ASP SER ARG PHE THR ARG GLY ALA ASN SER SER LYS

ARG	HIS	GLU	GLN	ASP	GLN	VAL	TYR	ASP	ASN	PRO	LEU	PHE	VAL	GLN	GLN	ASP	ILE	LEU	GLU	SER	ILE	TYR	LYS	THR	ASN	TYR	GLU	GLY	LYS	ASP	GLY	ALA	VAL	ASN	VAL	VAL	LYS	SER	SER	GLY	SER	HIS	GLY	PRO	ILE	GLN	PHE	THR	LYS	ALA	GLU	SER	ASP	ASP	LYS	SER	ASP	ASN	TYR
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	GLY	ALA
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6	1	1
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95	1	1
96	1	1
97	1	1
98	1	1
99	1	1
100	1	1

- Molecule 12: Pre-mRNA leakage protein 1

Chain N:  77% • 22%

MET	PHE	HIS	ARG	ARG	LYS	ARG	PRO	TYR	ASN	THR	THR	ARG	ARG	ASN	THR	GLY	HIS	HIS	ASP	ASP	LYS	LYS	PHE	LYS	LYS	GLN	GLN	TYR	TYR	ILE	ILE	ASP	I28	S42	ASN	ASN	GLU	GLU	GLY	GLY	ILE	ILE	ALA	ALA	R51	H112	SER	LEU	LEU	ASP	ASP	THR	THR	ASP	ASP	ASP	ASP	ARG	ARG	E123	G130	I131	P134
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- Molecule 13: Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2

Chain O:  68% . 28%

NET	SER	SER	SER	ILE	THR	THR	SER	GLU	THR	GLY	LYS	ARG	ARG	ARG	VAL	LYS	ARG	ARG	THR	THR	TYR	GLU	VAL	THR	THR	ARG	GLN	ASN	ASP	ASN	ALA	VAL	ARG	ILE	GLU	PRO	GLU	SER	SER	SER	LEU	LEU	GLY	GLU	ALA	LYS	ASP	LYS	ASN	SER	SER	ARG	LEU	GLN	LEU	LYS	ARG	SER	TYR	PRO	ASN	LYS
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VAL	PHE	SER	ASN	ASN	GLN	GLY	GLU	LYS	ASN	ASN	LEU	LYS	GLY	GLN	LEU	GLY	SER	GLN	LYS	LYS	SER	SER	LYS	TYR	ASP	GLU	LYS	ILE	THR	SER	ASN	ASN	GLU	GLY	LEU	LEU	THR	THR	LYS	LYS	TYR	ALA	SER	SER	ASN	ASN	LYS	TYR	VAL
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PHE	ASN	VAL	GLU	THR	HIS	LYS	ILE	LYS	ASN	ALA	LYS	GLU	GLU	ILE	ASP	LYS	ILE	ASN	ARG	GLN	ARG	ARG	TRP	THR	GLU	GLU	GLN	GLN	LEU	ARG	ASN	ALA	ALA	MET	GLY	GLY	GLN	SER	SER	ASP	HIS	LYS	PRO	ASP	ASP	ASP	ILE	THR	THR	GLU	GLY	GLY	SER	ASP	ASP	LYS	TYR	ASP	ASP	THR	THR	ASP	ALA	MET
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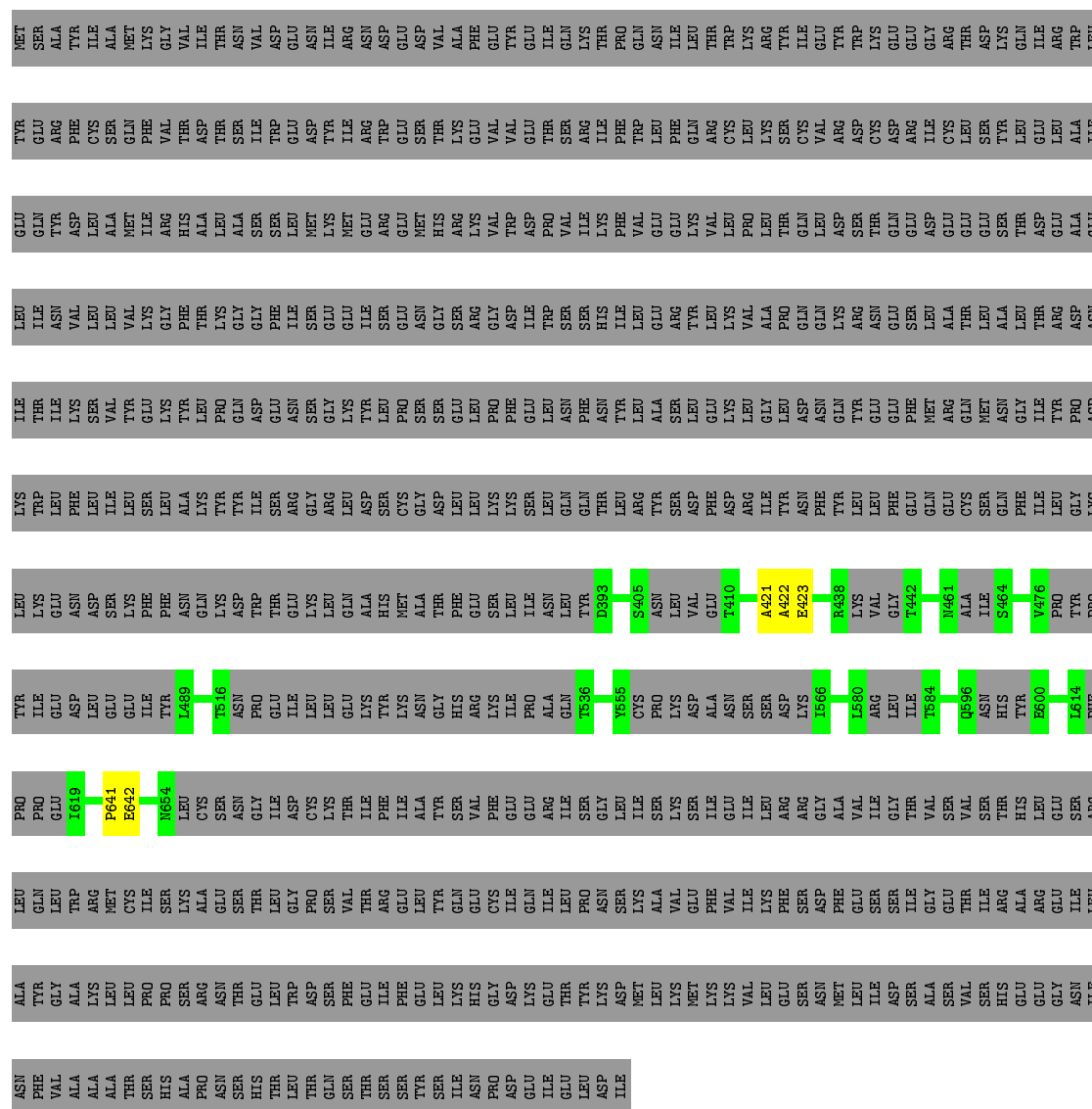
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D601	D602	I603	K604	P605	P606	D609	K610	G627	A628	L629	I635	G637	GLN	LYS	R690	L697	GLU	GLY	VAL	S702	W714	S720	W754	E755	K756	W757	D758	Q759	A760	R761	W762	K763	I764	A768	GLY	TYR	ILE	ASN	ALA	ALA	ARG	I775	G799	R800	S801	S802	S803	C804	C805
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H810	I814	L815	F816	VAL	ASN	HTS	LYS	GLU	LYS	A823	K864	ASP	LEU	ILE	ASP	ASP	LYS	THR	ASN	ARG	GLY	ARG	ARG
P811	L815	F816	VAL	ASN	HTS	LYS	GLU	LYS	A823	K864	ASP	LEU	ILE	ASP	ASP	LYS	THR	ASN	ARG	GLY	ARG	ARG	

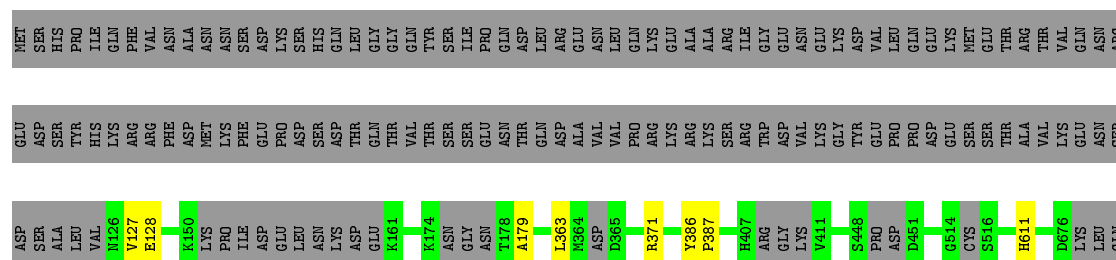
- Molecule 14: Pre-mRNA-splicing factor SYF1

Chain P:  23% . 76%



- Molecule 15: U2 snRNP component HSH155


Chain Q: 80% 19%



LYS ILE ALA LYS LYS PRO ASN THR ALA ASN LYS HIS THR SER SER ASN SER ARG ARG ILE ALA GLN PRO SER SER SER ARG TYR ASN GLY GLY ASP ASN ILE GLY ALA ASN ARG SER ARG PHE ASN GLU ALA PRO PRO GLN THR ARG LYS PHE GLN PRO PRO GLY PHE LYS


ARG
LYS

- Molecule 22: Small nuclear ribonucleoprotein Sm D3

Chain d:  81% 19%


MET THR MET MET N4 K85 LYS ASN SER SER PRO MET PRO PRO ILE ARG GLU VAL LYS ARG ARG

- Molecule 23: Small nuclear ribonucleoprotein E

Chain e:  80% 20%


MET SER ASN LYS VAL LYS THR ALA M10 S64 ALA ASP GLY LYS GLU ASP VAL GLU R73 S92 ALA ASP

- Molecule 24: Small nuclear ribonucleoprotein F

Chain f:  84% 16%

MET SER GLU SER SER ASP ILE SER ALA MET GLN P12 E83 LEU PRO ASN

- Molecule 25: Small nuclear ribonucleoprotein G

Chain g:  90% 10%

MET Y2 I46 ASN GLY GLU ASP PRO ALA M53 A76 ILE


- Molecule 26: Small nuclear ribonucleoprotein Sm D1

Chain h:  56% 44%

M1 P48 GLN PRO ARG ILE ASN ASN LYS ASN ASN SER ASN GLY ILE ALA MET MET SER LEU TYR THR THR GLY GLY GLN GLN PRO PRO THR ALA S76 D109 GLN LYS GLN LEU ASN SER LEU ARG ARG SER SER GLY GLN ILE ALA ASP PRO SER LYS LYS ARG ARG ASP PHE GLY ALA

PRO ALA ASN LYS ARG PRO ARG ARG GLY LEU

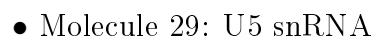
- Molecule 27: Small nuclear ribonucleoprotein Sm D2

Chain j:  85% 15%

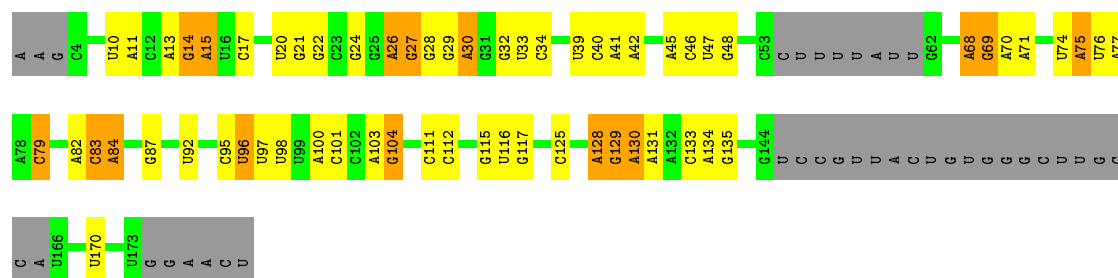
MET SER SER GLN ILE ILE ASP ARG PRO HIS HIS GLU LEU SER R15 P108 VAL GLU

- Molecule 28: U2 snRNA

93%

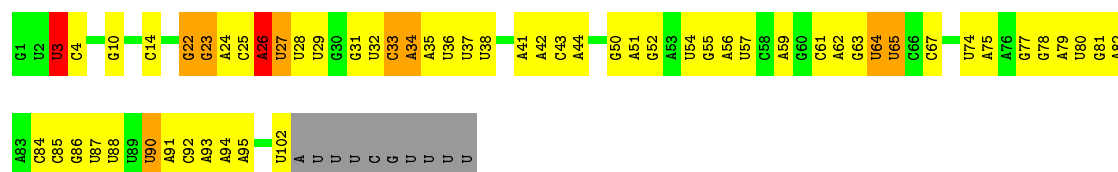


21%



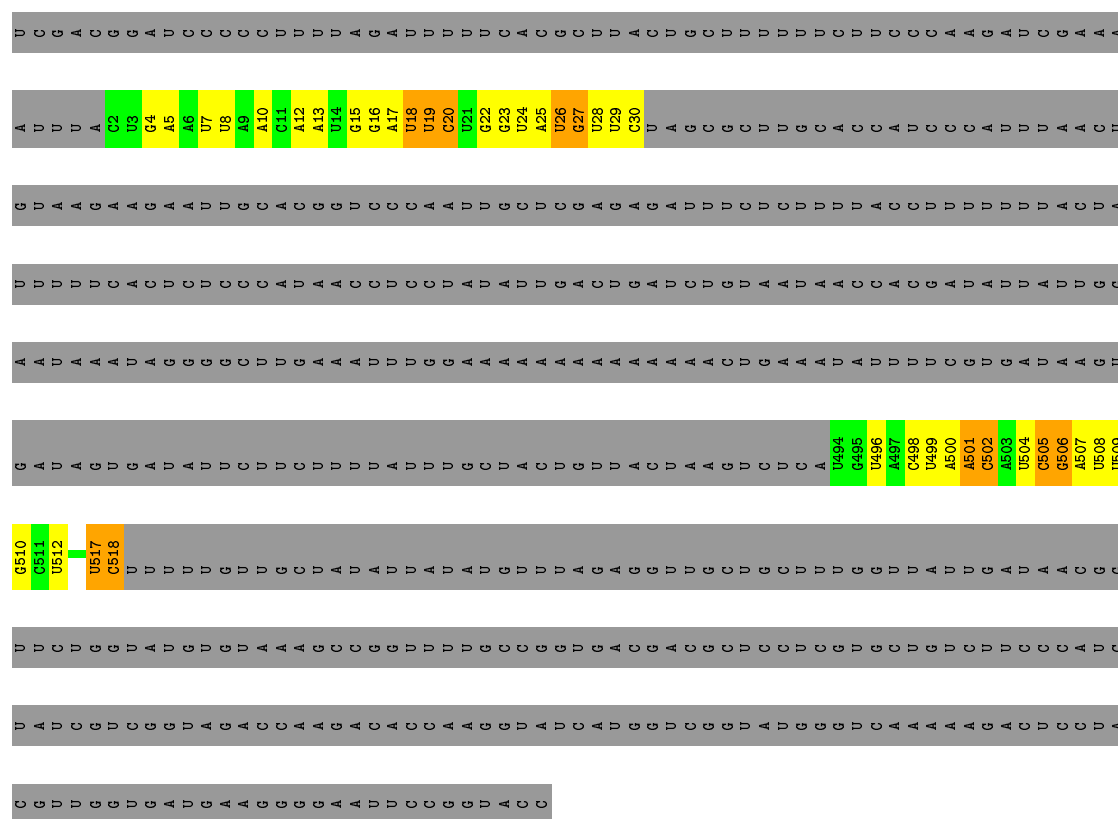
• Molecule 30: U6 snRNA

Chain 6: 39% 43% 7% 9%



• Molecule 31: actin pre-mRNA

Chain 9: 5% 91%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	122000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
28	2	0.13	0/1902	0.79	2/2956 (0.1%)
29	5	0.12	0/3350	0.68	0/5209
30	6	0.16	0/2427	0.76	4/3778 (0.1%)
31	9	0.17	0/1264	0.65	0/1961
All	All	0.14	0/8943	0.72	6/13904 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	2	76	A	C2-N3-C4	15.59	118.39	110.60
28	2	76	A	N1-C2-N3	10.07	134.34	129.30
30	6	3	U	C2-N1-C1'	7.71	126.95	117.70
30	6	3	U	N1-C2-O2	7.28	127.90	122.80
30	6	3	U	N3-C2-O2	-6.56	117.61	122.20

There are no chirality outliers.

There are no planarity outliers.

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	2130	0	0	48	0
2	B	843	0	0	8	0
3	C	1811	0	0	5	0
4	D	187	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	138	0	0	17	0
6	F	218	0	0	22	0
7	H	437	0	0	3	0
8	J	104	0	0	1	0
9	K	338	0	0	4	0
10	L	32	0	0	0	0
11	M	169	0	0	10	0
12	N	159	0	0	1	0
13	O	628	0	0	19	0
14	P	202	0	0	3	0
15	Q	791	0	0	13	0
16	R	219	0	0	4	0
17	W	128	0	0	3	0
18	X	1095	0	0	13	0
19	Y	89	0	0	7	0
20	Z	68	0	0	0	0
21	b	80	0	0	0	0
22	d	82	0	0	0	0
23	e	75	0	0	0	0
24	f	72	0	0	0	0
25	g	69	0	0	0	0
26	h	82	0	0	0	0
27	j	94	0	0	0	0
28	2	1707	0	860	31	0
29	5	2999	0	1515	50	0
30	6	2170	0	1094	53	0
31	9	1135	0	575	32	0
All	All	18351	0	4044	247	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 11.

The worst 5 of 247 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:1377:SER:CA	31:9:18:U:C5	1.87	1.56
5:E:98:THR:CA	30:6:4:C:C2	1.88	1.52
15:Q:927:ALA:CA	28:2:57:A:H1'	1.05	1.51
6:F:72:PHE:CA	30:6:34:A:C2	1.94	1.50
6:F:72:PHE:CA	30:6:34:A:H2	1.20	1.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	2	80/1175 (6%)	21 (26%)	2 (2%)
29	5	137/179 (76%)	31 (22%)	4 (2%)
30	6	101/112 (90%)	41 (40%)	6 (5%)
31	9	52/572 (9%)	27 (51%)	1 (1%)
All	All	370/2038 (18%)	120 (32%)	13 (3%)

5 of 120 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	2	12	U
28	2	14	C
28	2	15	C
28	2	18	U
28	2	20	G

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	5	129	G
30	6	22	G
30	6	64	U
29	5	128	A
30	6	62	A

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
29	5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	166:U	O3'	167:A	P	3.66