



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:12 PM BST

PDB ID : 3JCM  
EMDB ID: : EMD-6561  
Title : Cryo-EM structure of the spliceosomal U4/U6.U5 tri-snRNP  
Authors : Wan, R.; Yan, C.; Bai, R.; Wang, L.; Huang, M.; Wong, C.C.; Shi, Y.  
Deposited on : 2015-12-23  
Resolution : 3.80 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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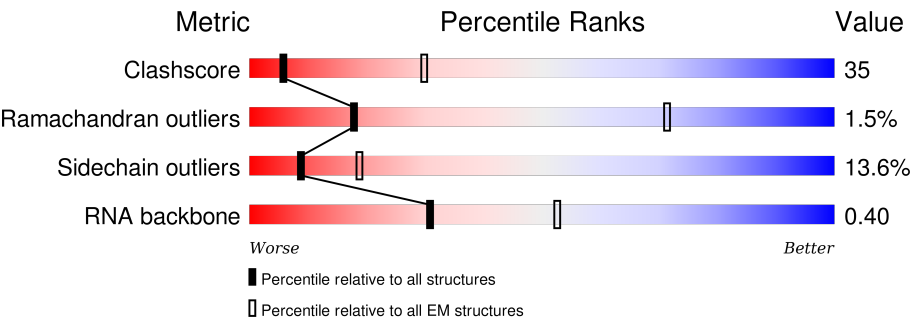
MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 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 3.80 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.














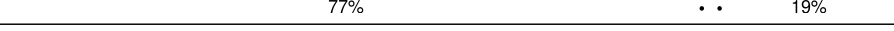




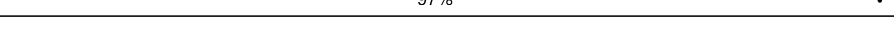


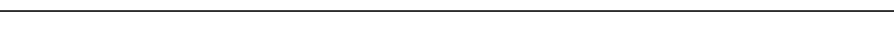

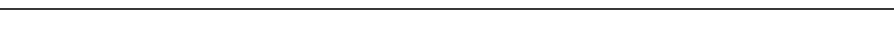
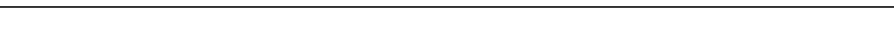


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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  $\geq 3$ , 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	<div><div>54%</div><div>28%</div><div>8%</div><div>10%</div></div>
2	B	465	<div><div>40%</div><div>43%</div><div>9%</div><div>8%</div></div>
3	I	494	<div><div>42%</div><div>31%</div><div>10%</div><div>16%</div></div>
4	G	899	<div><div>53%</div><div>22%</div><div>7%</div><div>18%</div></div>
5	K	469	<div><div>35%</div><div>20%</div><div>41%</div></div>
6	L	143	<div><div>50%</div><div>38%</div><div>8%</div></div>
7	M	126	<div><div>75%</div><div>21%</div><div>5%</div></div>
8	H	1008	<div><div>41%</div><div>32%</div><div>10%</div><div>16%</div></div>


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Mol	Chain	Length	Quality of chain
9	N	2163	 76% 22%
10	J	101	 76% 22%
10	R	101	 75% 22%
11	O	196	 37% 63%
11	S	196	 37% 63%
12	P	146	 52% 47%
12	T	146	 52% 47%
13	Q	110	 81% 19%
13	U	110	 82% 18%
14	V	94	 77% 23%
14	Y	94	 77% 23%
15	W	86	 77% 19%
15	Z	86	 77% 19%
16	X	77	 91% 9%
16	a	77	 92% 8%
17	b	109	 60% 40%
18	c	95	 97%
19	d	89	 87% 13%
20	e	86	 86% 14%
21	f	93	 82% 17%
22	g	115	 57% 43%
23	h	187	 41% 59%
24	C	20	 10% 10% 80%
25	D	112	 13% 13% 15% 60%
26	E	160	 23% 18% 11% 47%

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Mol	Chain	Length	Quality of chain
27	F	214	

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
28	GTP	H	1500	-	-	X	-

## 2 Entry composition [i](#)

There are 29 unique types of molecules in this entry. The entry contains 58253 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	2174	Total	C	N	O	S	0	0
			16889	10715	2978	3138	58		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3378	2102	610	652	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	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	G	734	Total	C	N	O	S	0	0
			4927	3063	911	939	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	279	Total	C	N	O	S	0	0
			2328	1476	422	416	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

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

- Molecule 9 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	1686	Total	C	N	O	0	0
			6744	3372	1686	1686		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	R	79	Total	C	N	O	0	0
			316	158	79	79		
10	J	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	S	73	Total	C	N	O	0	0
			292	146	73	73		
11	O	73	Total	C	N	O	0	0
			292	146	73	73		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	T	77	Total	C	N	O	0	0
			308	154	77	77		
12	P	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	90	Total	C	N	O	0	0
			360	180	90	90		
13	Q	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	72	Total	C	N	O	0	0
			288	144	72	72		
14	Y	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	70	Total	C	N	O	0	0
			280	140	70	70		
15	Z	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	X	70	Total	C	N	O	0	0
			280	140	70	70		
16	a	71	Total	C	N	O	0	0
			284	142	71	71		

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	f	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	g	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	h	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 24 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	20	Total	C	N	O	P	0	0
			429	193	79	137	20		

- Molecule 25 is a RNA chain called SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	45	Total	C	N	O	P	0	0
			945	422	170	308	45		

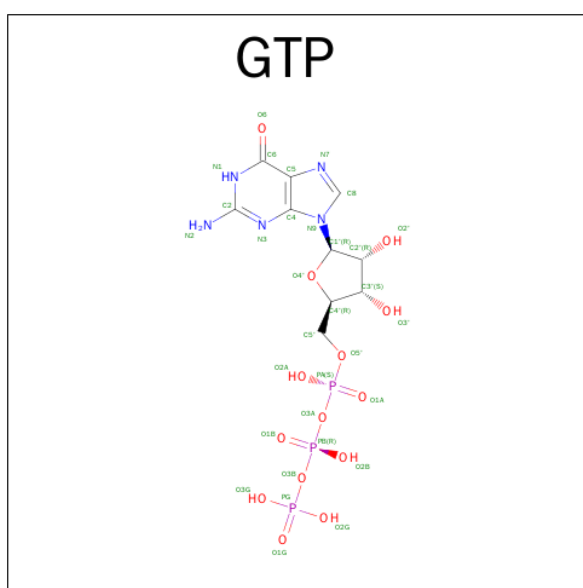
- Molecule 26 is a RNA chain called SNR14 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	85	Total	C	N	O	P	0	0
			1806	807	309	605	85		

- Molecule 27 is a RNA chain called SNR7-L snRNA.

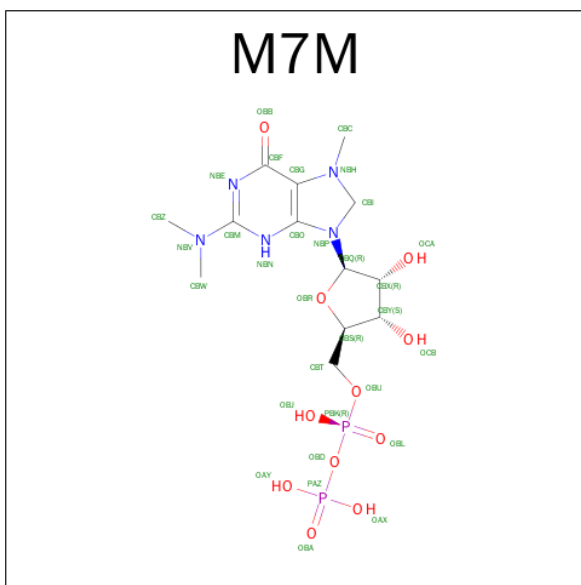
Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	113	Total	C	N	O	P	0	0
			2385	1068	405	799	113		

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



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

- Molecule 29 is N,N,7-TRIMETHYLGUANOSINE 5'-(TRIHYDROGEN DIPHOSPHATE) (three-letter code: M7M) (formula:  $C_{13}H_{23}N_5O_{11}P_2$ ).

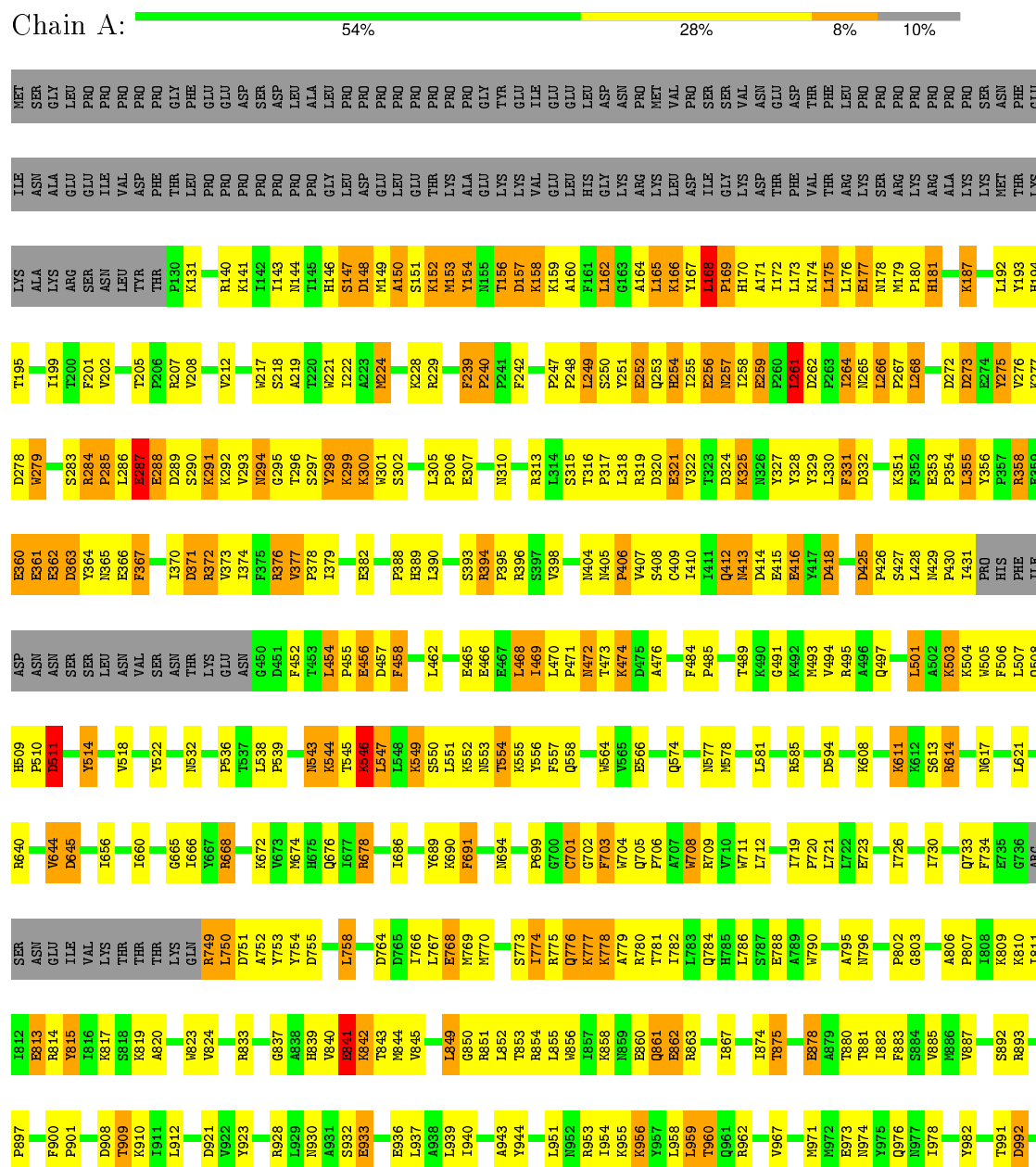


Mol	Chain	Residues	Atoms					AltConf
29	E	1	Total	C	N	O	P	0
			31	13	5	11	2	

### 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

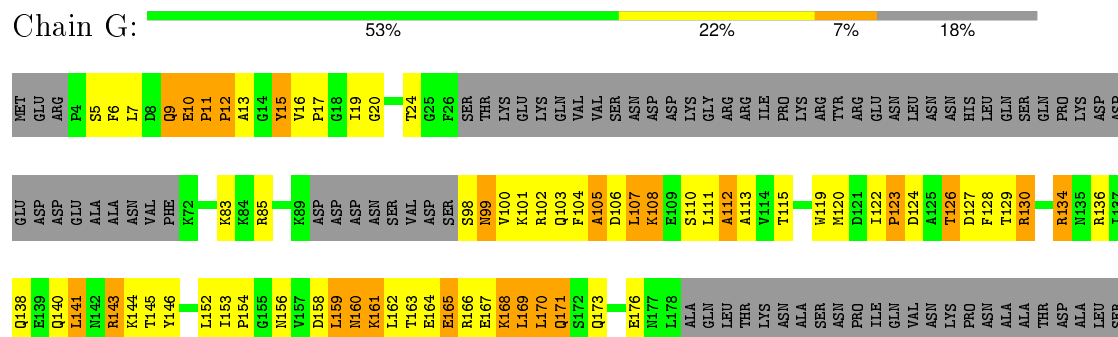


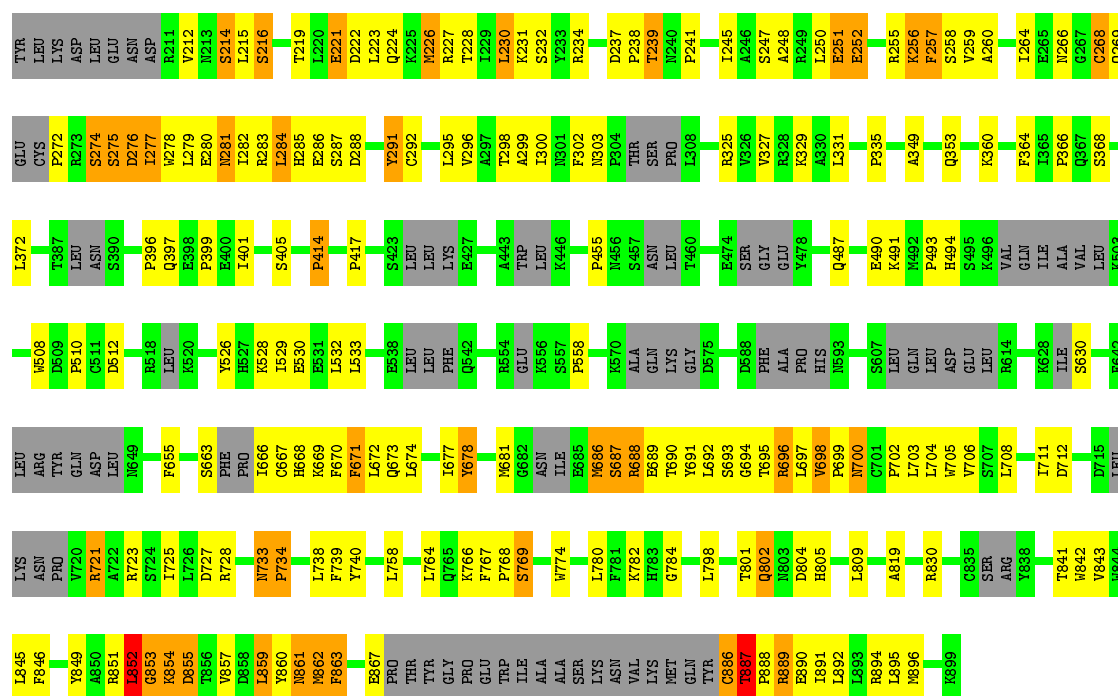
THR	L2049	E1916	E1842	H1746	I1632	Y1542	W1468	L1357	R1274	M1170	I1073	L995
VAL	L2050	L1920	N1846	D1747	F1633	L1557	A1469	D1358	M1275	L1171	I1074	Y998
MET	L2053	V1921	N1846	I1748	H1635	E1558	E1460	I1359	E1276	H1172	D1075	I999
THR	L2060	R1922	L1850	Y1751	Q1647	H1559	A1461	E1364	E1277	F1174	P1076	E1002
LEU	L2064	V1935	F1851	Y1752	I1649	T1463	K1464	T1365	V1278	E1175	M1077	R1006
ASN	R2065	T1936	D1854	K1755	F1649	I1649	R1465	I1367	V1279	G1179	A1078	K1007
ALA	K2066	R1937	T1855	F1756	R1650	R1650	Q1468	Q1368	D1282	L1182	D1080	L1008
ASP	Y2067	M1940	N1856	D1758	H1652	A1651	A1468	N1369	E1283	L1183	I1081	F1009
VAL	N2068	V1857	V1857	Y1759	L1653	Q1470	Q1470	L1373	G1284	T1183	I1082	P1010
ASP		F1951	H1863	T1761	W1654	F1574	A1578	L1373	V1285	D1184	T1083	N1011
LEU	I2071	P1958	K1863	D1762	I1657	S1579	R1473	K1378	D1287	F1195	M1087	W1012
ILE	L2074	P1958	K1864	D1762	I1658	G1580	R1474	M1379	R1296	E1196	V1088	I1013
ASN	T2075	K1973	T1865	Y1767	H1658	F1581	R1475	P1380	L1297	N1197	V1089	K1014
GLY	Q2076	L1974	F1867	Y1767	I1661	E1582	A1476	T1381	T1297	L1297	P1015	P1015
ALA	T2077	F1867	G1868	T1771	V1662	M1585	F1477	R1382	K1299	M1202	M1095	S1016
SER	E2078	V1978	N1869	G1772	F1663	Q1586	E1478	F1383	K1299	N1203	S1096	D1017
ALA	I2079	P1984	V1870	G1773	D1664	Q1586	E1479	P1385	A1300	R1204	H1097	S1016
ASP	K2080	P1984	A1871	M1774	I1668	K1589	E1481	A1386	I1301	K1205	Y1101	E1019
TYR	D2081	P1984	A1871	I1775	I1668	K1589	E1481	A1386	L1302	W1207	I1021	I1021
GLU	I2082	N1990	I1875	G1776	I1668	T1591	W1484	Y1389	E1306	P1208	R1105	P1022
SER	I2083	I1981	N1876	I1777	I1678	H1592	K1390	T1390	E1307	K1209	G1106	L1023
GLN	L2084	Y1982	G1877	D1778	K1690	A1593	I1488	P1391	E1308	D1210	L1107	L1024
THR	G2085	W1995	C1878	L1779	K1690	R1594	P1469	K1392	I1309	S1211	K1108	V1025
PHE	G2085	W1995	C1878	L1779	K1690	R1594	P1469	K1392	I1309	S1211	F1109	
SER	S2148	R1998	F1880	M1783	M1694	L1598	L1494	T1400	K1311	R1214	F1114	T1029
GLU	P2389	R1998	N1881	Y1787	S1697	I1601	F1495	S1415	E1307	L1215	Q1115	M1033
LEU	F2395	A2004	N1883	G1788	A1698	P1602	Q1496	A1401	E1308	L1216	Y1116	H1034
ALA	R2013	R2007	K1885	W1790	A1699	P1602	R1497	S1403	I1309	R1217	Y1117	L1034
GLY	N2018	L2011	K1886	F1791	M1703	R1605	D1498	H1404	R1317	M1221	G1118	I1038
ASP	E2019	L2011	K1887	K1795	E1704	F1606	H1500	L1406	M1321	L1222	L1125	W1039
GLU	E2020	L2011	H1888	P1796	S1705	T1607	T1501	I1407	T1329	V1234	Q1128	D1040
LEU	S2021	L2011	L1889	P1796	S1705	L1608	L1502	I1407	T1329	V1234	Q1128	V1041
GLU	A2022	L2011	K1892	S1801	W1709	W1609	H1508	W1414	W1335	L1238	E1143	G1044
ALA	K2023	L2026	I1893	S1801	E1710	W1610	S1415	S1415	W1335	L1238	E1143	G1044
ALA	L2026	L2026	I1894	I1805	V1711	P1611	R1509	K1416	N1336	A1246	F1144	A1047
ILE	L2026	L2026	H1895	I1805	S1712	P1612	I1510	Q1417	N1336	A1246	F1144	A1047
ASP	L2026	L2026	K1896	N1809	K1713	T1613	R1511	T1418	L1339	V1248	Q1146	V1048
VAL	D2029	L2026	L1896	N1809	P1714	M1614	R1512	T1418	L1339	V1248	Q1146	V1048
PHE	I2032	L2026	S1906	L1815	S1715	M1615	L1519	I1422	I1340	K1253	E1153	E1051
SER	W2040	L2026	Q1907	L1815	S1715	M1615	L1519	I1422	S1341	M1254	E1153	E1051
ASN	P2041	L2026	L1908	R1818	E1719	N1618	R1521	I1437	L1342	M1254	E1153	E1051
GLU	S2042	L2026	A1909	R1818	E1719	N1618	R1521	I1437	L1342	M1254	E1153	E1051
ALA	F2043	L2026	K1910	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLY	E2046	L2026	K1911	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ALA	E2046	L2026	K1912	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1913	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
SER	E2046	L2026	K1914	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1915	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1916	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1917	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1918	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1919	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1920	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1921	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1922	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1923	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1924	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1925	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1926	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1927	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1928	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1929	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1930	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1931	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1932	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1933	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1934	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1935	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1936	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1937	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1938	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1939	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1940	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1941	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1942	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1943	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1944	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1945	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1946	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1947	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1948	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1949	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1950	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1951	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1952	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1953	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1954	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1955	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1956	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
THR	E2046	L2026	K1957	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
GLU	E2046	L2026	K1958	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054
ASN	E2046	L2026	K1959	N1836	S1735	G1622	F1525	I1440	Y1345	N1256	H1156	L1054

• Molecule 2: U4/U6 small nuclear ribonucleoprotein PRP4

Chain B:  40% 43% 9% 8%

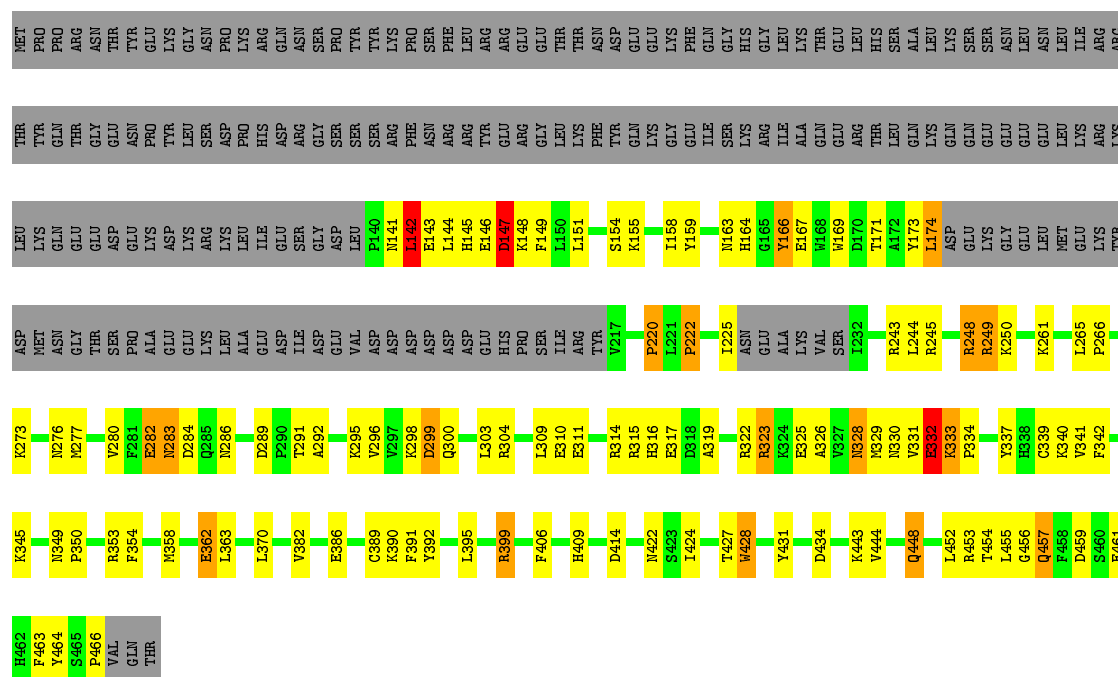
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• Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3

Chain K: 35% 20% 41%



• Molecule 6: Spliceosomal protein DIB1

Chain L: 50% 38% 8%





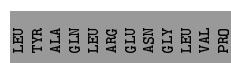
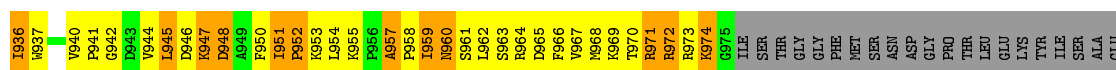
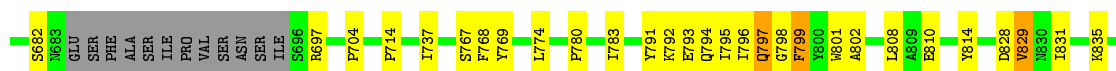
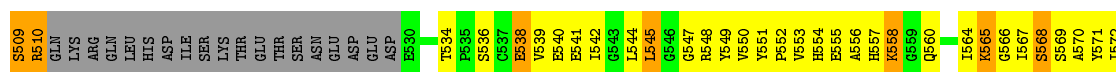
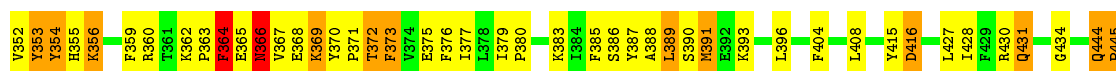
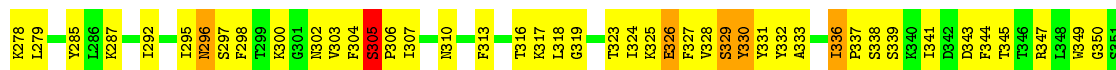
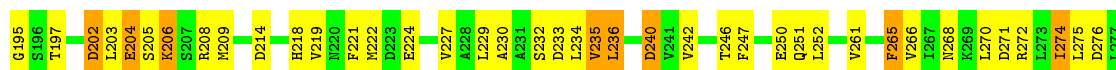
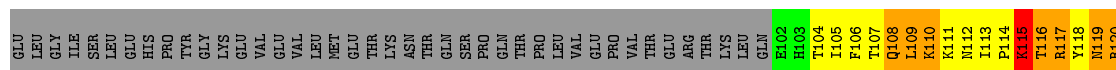
- Molecule 7: 13 kDa ribonucleoprotein-associated protein

Chain M:  75% 21% 5%




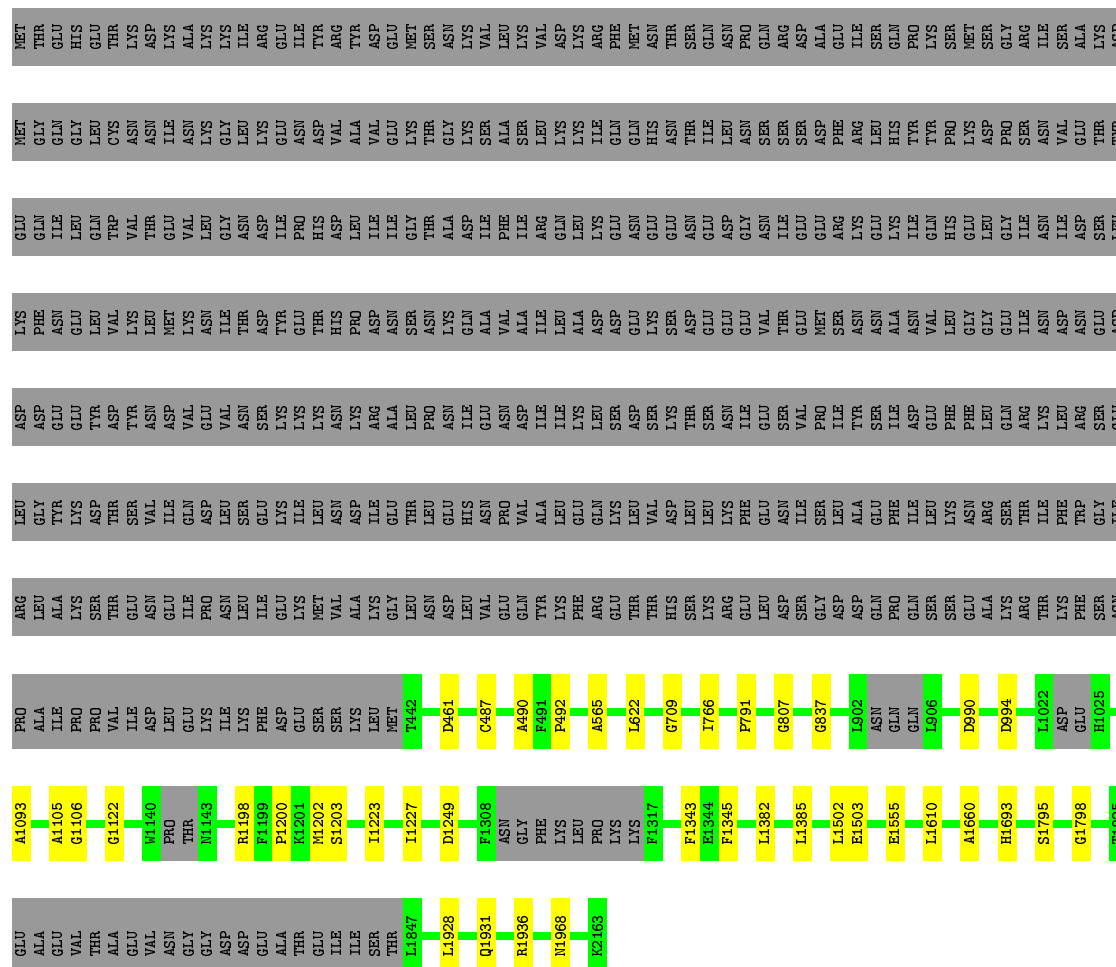
- Molecule 8: Pre-mRNA-splicing factor SNU114

Chain H:  41% 32% 10% 16%



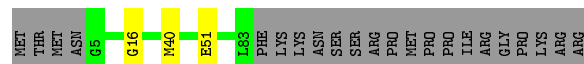
- Molecule 9: Pre-mRNA-splicing helicase BRR2

Chain N:  76% 22%



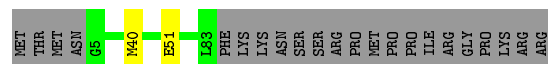
- Molecule 10: Small nuclear ribonucleoprotein Sm D3

Chain R:  75% 22%



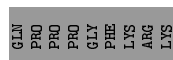
- Molecule 10: Small nuclear ribonucleoprotein Sm D3

Chain J:  76% 22%

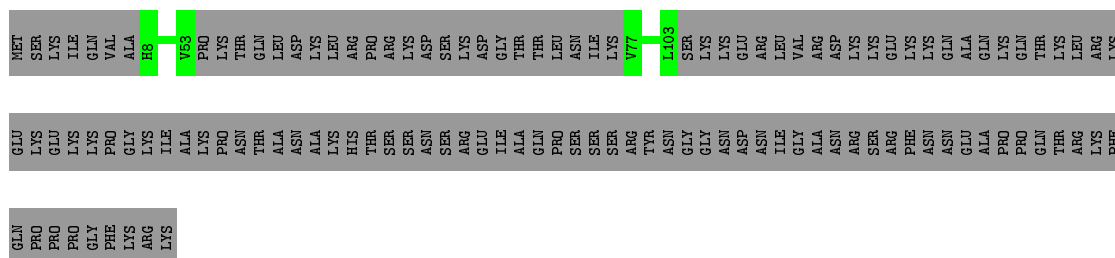


- Molecule 11: Small nuclear ribonucleoprotein-associated protein B

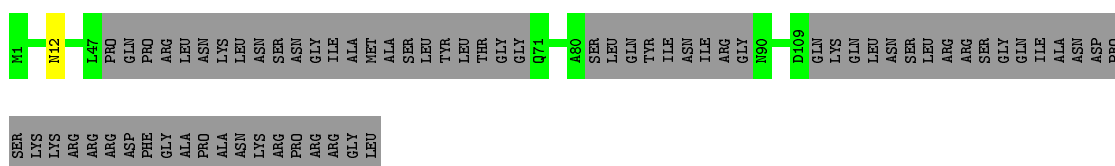
Chain S:  37% 63%



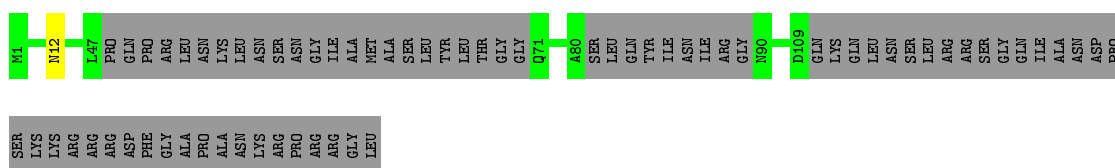
- Chain 0:  37% 63%

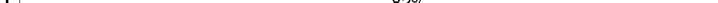


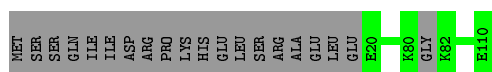
- Chain T:  52% . 47%

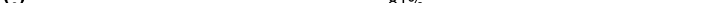


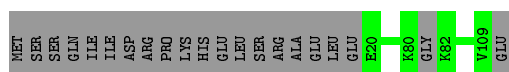
- Chain P:  52% . 47%



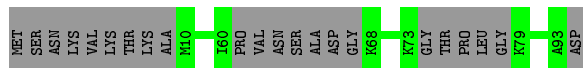
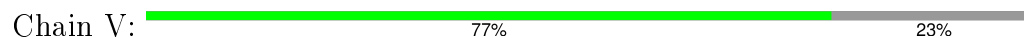
- Chain U:  82% 18%



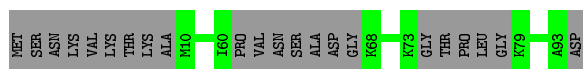
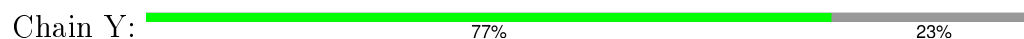
- Chain Q:  81% 19%



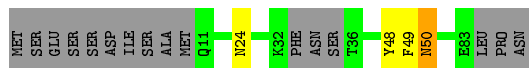
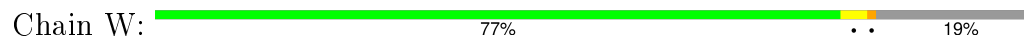
- Molecule 14: Small nuclear ribonucleoprotein E



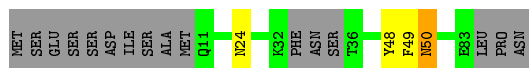
- Molecule 14: Small nuclear ribonucleoprotein E



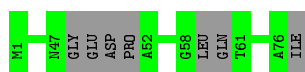
- Molecule 15: Small nuclear ribonucleoprotein F



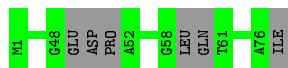
- Molecule 15: Small nuclear ribonucleoprotein F



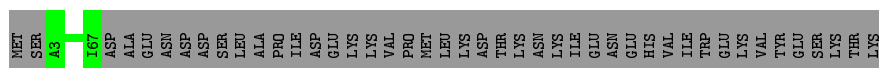
- Molecule 16: Small nuclear ribonucleoprotein G



- Molecule 16: Small nuclear ribonucleoprotein G



- Molecule 17: U6 snRNA-associated Sm-like protein LSm8



- |     |
|-----|
| A-6 |
| A-5 |
| A-4 |
| A-3 |
| A-2 |
| A-1 |
| U0  |
| U1  |
| A2  |
| A3  |
| G4  |
| G5  |
| U6  |
| A7  |
| U8  |
| G9  |
| U10 |
| A11 |
| U12 |
| U13 |

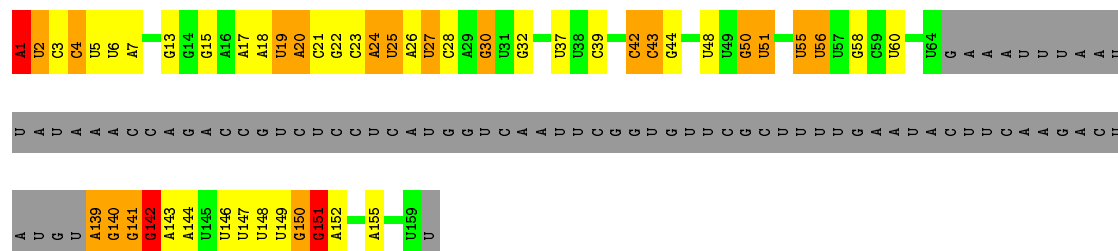
- Molecule 25: SNR6 snRNA

Chain D:  13% 13% 15% 60%

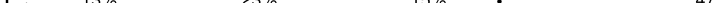


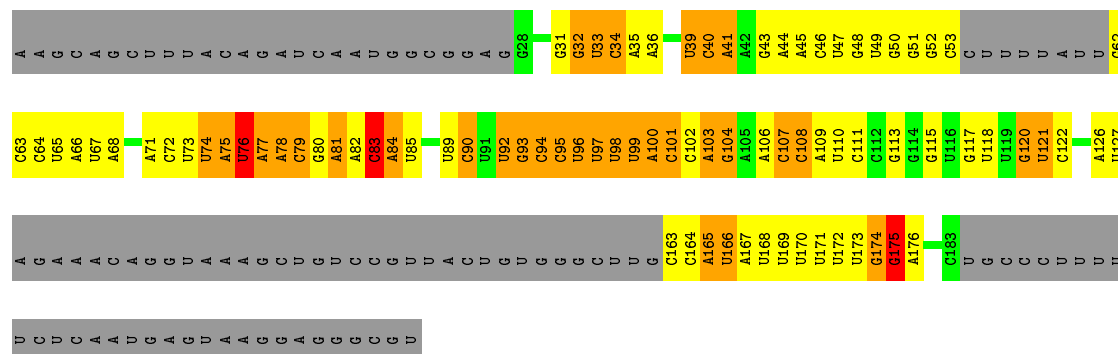
- Molecule 26: SNR14 snRNA

Chain E:  23% 18% 11% • 47%



- Molecule 27: SNR7-L snRNA

Chain F:  13% 23% 15% . 47%



## 4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN	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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, M7M

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	$\# Z  > 2$
1	A	0.86	22/17296 (0.1%)	0.91	24/23336 (0.1%)
10	J	0.29	0/315	0.46	0/392
10	R	0.29	0/315	0.46	0/392
11	O	0.28	0/290	0.46	0/359
11	S	0.28	0/290	0.46	0/359
12	P	0.27	0/305	0.47	0/376
12	T	0.27	0/305	0.46	0/376
13	Q	0.25	0/354	0.45	0/439
13	U	0.25	0/358	0.45	0/444
14	V	0.29	0/285	0.43	0/351
14	Y	0.29	0/285	0.43	0/351
15	W	0.30	0/278	0.45	0/344
15	Z	0.30	0/278	0.45	0/344
16	X	0.24	0/277	0.46	0/341
16	a	0.27	0/281	0.46	0/346
17	b	0.48	0/259	0.70	0/322
18	c	0.49	0/367	0.66	0/457
19	d	0.58	0/307	0.74	0/382
2	B	0.72	2/3434 (0.1%)	0.86	0/4635
20	e	0.48	0/295	0.68	0/367
21	f	0.50	0/306	0.71	0/379
22	g	0.48	0/262	0.71	0/324
23	h	0.47	0/306	0.68	0/379
24	C	0.34	0/481	0.71	0/747
25	D	0.81	0/1054	0.93	3/1634 (0.2%)
26	E	0.94	8/2016 (0.4%)	1.12	17/3136 (0.5%)
27	F	0.44	2/2659 (0.1%)	0.80	1/4131 (0.0%)
3	I	0.84	1/3219 (0.0%)	0.99	13/4332 (0.3%)
4	G	0.62	3/4967 (0.1%)	0.79	14/6746 (0.2%)
5	K	0.67	1/2376 (0.0%)	0.83	3/3183 (0.1%)
6	L	0.73	0/1167	0.87	0/1571
7	M	0.95	0/963	1.02	2/1310 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
8	H	0.55	2/6874 (0.0%)	0.78	8/9305 (0.1%)
9	N	0.52	0/6738	0.65	0/8412
All	All	0.70	41/59562 (0.1%)	0.84	85/80302 (0.1%)

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	3
2	B	0	2
3	I	0	1
4	G	0	7
5	K	0	1
7	M	0	4
8	H	0	2
All	All	0	20

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	E	1	A	C5-C4	10.58	1.46	1.38
26	E	1	A	N7-C5	-8.64	1.34	1.39
1	A	1335	TRP	CG-CD2	-8.36	1.29	1.43
26	E	1	A	N9-C4	-8.09	1.32	1.37
26	E	1	A	C5-C6	7.52	1.47	1.41

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	E	1	A	C2-N3-C4	20.61	120.90	110.60
4	G	853	GLY	N-CA-C	12.86	145.25	113.10
26	E	1	A	N3-C4-C5	-11.57	118.70	126.80
8	H	951	ILE	C-N-CD	-10.75	96.95	120.60
1	A	1616	ARG	NE-CZ-NH1	10.12	125.36	120.30

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1867	GLU	Peptide
1	A	694	ASN	Peptide
2	B	208	GLN	Peptide
2	B	316	GLN	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16889	0	16134	1106	0
2	B	3378	0	3342	372	0
3	I	3171	0	3140	274	0
4	G	4927	0	4006	390	0
5	K	2328	0	2314	156	0
6	L	1146	0	1133	126	0
7	M	950	0	1004	27	0
8	H	6732	0	6904	868	0
9	N	6744	0	1759	27	0
10	J	316	0	86	0	0
10	R	316	0	86	2	0
11	O	292	0	78	0	0
11	S	292	0	78	0	0
12	P	308	0	78	0	0
12	T	308	0	78	0	0
13	Q	356	0	88	0	0
13	U	360	0	89	0	0
14	V	288	0	74	0	0
14	Y	288	0	74	0	0
15	W	280	0	77	1	0
15	Z	280	0	77	1	0
16	X	280	0	79	0	0
16	a	284	0	82	0	0
17	b	260	0	72	0	0
18	c	368	0	99	0	0
19	d	308	0	80	0	0
20	e	296	0	83	0	0
21	f	308	0	85	0	0
22	g	264	0	76	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	h	308	0	85	0	0
24	C	429	0	214	48	0
25	D	945	0	478	73	0
26	E	1806	0	907	49	0
27	F	2385	0	1209	210	0
28	H	32	0	12	10	0
29	E	31	0	20	6	0
All	All	58253	0	44280	3557	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 35.

The worst 5 of 3557 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)
8:H:856:ILE:HA	8:H:944:VAL:CG1	1.17	1.58
4:G:672:LEU:HD21	4:G:704:LEU:CD2	1.29	1.58
8:H:168:VAL:HG13	8:H:173:LYS:CD	1.09	1.56
8:H:364:PHE:CB	8:H:369:LYS:HG3	1.34	1.54
4:G:672:LEU:CD2	4:G:704:LEU:CD2	1.82	1.52

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	2166/2413 (90%)	2019 (93%)	110 (5%)	37 (2%)	<b>11</b> 56
2	B	425/465 (91%)	380 (89%)	36 (8%)	9 (2%)	<b>9</b> 53
3	I	410/494 (83%)	380 (93%)	24 (6%)	6 (2%)	<b>13</b> 59
4	G	684/899 (76%)	604 (88%)	64 (9%)	16 (2%)	<b>8</b> 51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	K	273/469 (58%)	247 (90%)	21 (8%)	5 (2%)	11	55
6	L	137/143 (96%)	129 (94%)	6 (4%)	2 (2%)	13	59
7	M	124/126 (98%)	118 (95%)	4 (3%)	2 (2%)	12	58
8	H	837/1008 (83%)	770 (92%)	47 (6%)	20 (2%)	7	50
9	N	1674/2163 (77%)	1555 (93%)	109 (6%)	10 (1%)	30	74
10	J	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	7	48
10	R	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	7	48
11	O	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
11	S	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
12	P	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	14	59
12	T	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	14	59
13	Q	85/110 (77%)	82 (96%)	3 (4%)	0	100	100
13	U	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
14	V	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
14	Y	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
15	W	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	3	34
15	Z	66/86 (77%)	60 (91%)	3 (4%)	3 (4%)	3	34
16	X	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
16	a	65/77 (84%)	59 (91%)	6 (9%)	0	100	100
17	b	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
18	c	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
19	d	75/89 (84%)	71 (95%)	4 (5%)	0	100	100
20	e	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
21	f	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	14	59
22	g	62/115 (54%)	62 (100%)	0	0	100	100
23	h	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
All	All	8236/10574 (78%)	7611 (92%)	505 (6%)	120 (2%)	18	59

5 of 120 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ALA
1	A	157	ASP

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Mol	Chain	Res	Type
1	A	239	PHE
1	A	240	PRO
1	A	259	GLU

### 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	1749/2182 (80%)	1543 (88%)	206 (12%)	6	35
2	B	374/410 (91%)	321 (86%)	53 (14%)	4	29
3	I	327/445 (74%)	264 (81%)	63 (19%)	2	13
4	G	361/813 (44%)	295 (82%)	66 (18%)	2	15
5	K	253/436 (58%)	228 (90%)	25 (10%)	10	44
6	L	129/132 (98%)	113 (88%)	16 (12%)	6	33
7	M	104/104 (100%)	98 (94%)	6 (6%)	25	66
8	H	757/910 (83%)	639 (84%)	118 (16%)	3	24
All	All	4054/5432 (75%)	3501 (86%)	553 (14%)	9	30

5 of 553 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	400	ARG
3	I	380	ARG
8	H	538	GLU
2	B	448	ASN
3	I	210	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	450	HIS
3	I	398	GLN

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Mol	Chain	Res	Type
8	H	418	GLN
3	I	146	ASN
3	I	196	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	C	19/20 (95%)	17 (89%)	2 (10%)
25	D	41/112 (36%)	22 (53%)	4 (9%)
26	E	85/160 (53%)	28 (32%)	7 (8%)
27	F	111/214 (51%)	51 (45%)	14 (12%)
All	All	256/506 (50%)	118 (46%)	27 (10%)

5 of 118 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	C	-5	A
24	C	-4	A
24	C	-3	A
24	C	-2	A
24	C	-1	A

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	E	148	U
27	F	75	A
27	F	166	U
27	F	32	G
25	D	83	A

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
29	M7M	E	201	26	29,33,33	1.13	2 (6%)	32,52,52	3.02	8 (25%)
28	GTP	H	1500	-	26,34,34	1.13	2 (7%)	29,54,54	1.80	4 (13%)

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
29	M7M	E	201	26	-	1/20/48/48	0/3/3/3
28	GTP	H	1500	-	-	0/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	E	201	M7M	CBG-CBO	2.72	1.46	1.39
28	H	1500	GTP	C5-C4	3.06	1.47	1.40
29	E	201	M7M	CBF-CBG	3.39	1.46	1.41
28	H	1500	GTP	C6-C5	3.71	1.48	1.41

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	E	201	M7M	CBG-CBO-NBN	-8.85	117.72	126.74
29	E	201	M7M	CBG-CBF-NBE	-5.56	115.11	123.39
28	H	1500	GTP	C5-C6-N1	-4.77	117.29	123.52
29	E	201	M7M	CBW-NBV-CBM	-4.06	117.26	121.34
29	E	201	M7M	CBI-NBP-CBQ	-3.96	110.53	122.43

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
29	E	201	M7M	PBK-OBU-CBT-CBS

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	E	201	M7M	6	0
28	H	1500	GTP	10	0

## 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.