



## wwPDB EM Validation Summary Report ⓘ

Dec 12, 2022 – 09:17 PM EST

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 Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

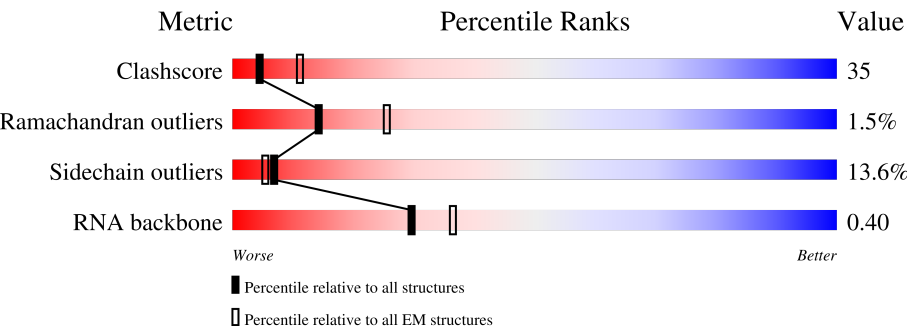
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

# 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.








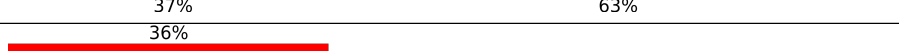
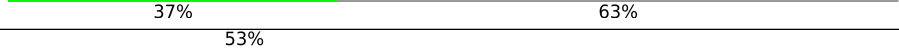









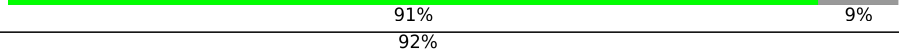
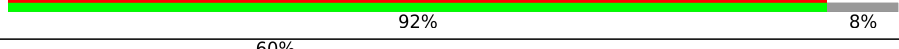

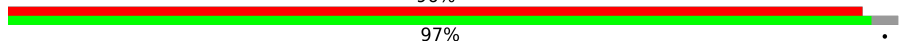




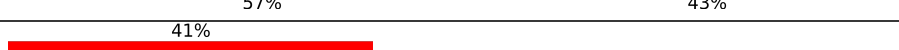
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2413	<div><div>11%</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>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	H	1008	
9	N	2163	
10	J	101	
10	R	101	
11	O	196	
11	S	196	
12	P	146	
12	T	146	
13	Q	110	
13	U	110	
14	V	94	
14	Y	94	
15	W	86	
15	Z	86	
16	X	77	
16	a	77	
17	b	109	
18	c	95	
19	d	89	
20	e	86	
21	f	93	
22	g	115	
23	h	187	
24	C	20	
25	D	112	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
26	E	160	
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

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.

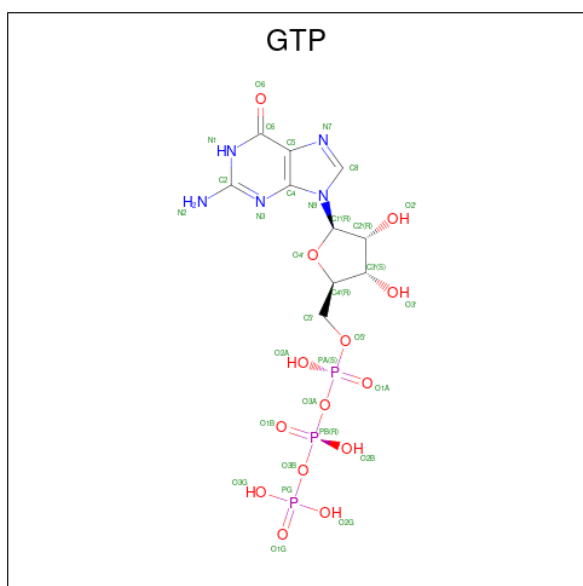


Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	85	Total	C	N	O	P	0	0
			1806	807	309	605	85		

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

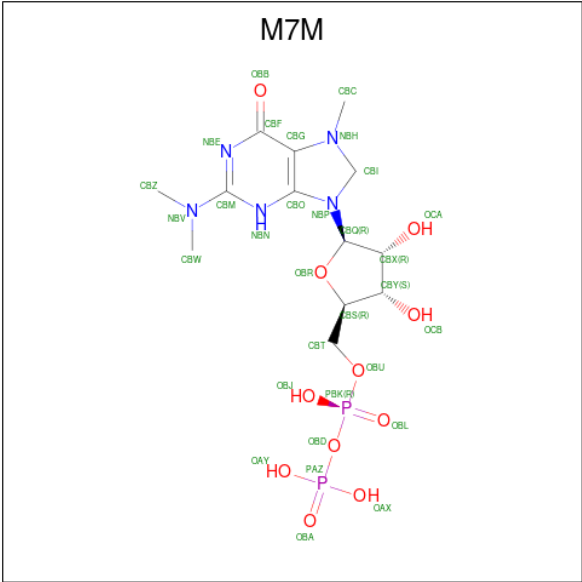
Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	113	Total	C	N	O	P	0	0
			2385	1068	405	799	113		

- 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:  $C_{13}H_{23}N_5O_{11}P_2$ ).

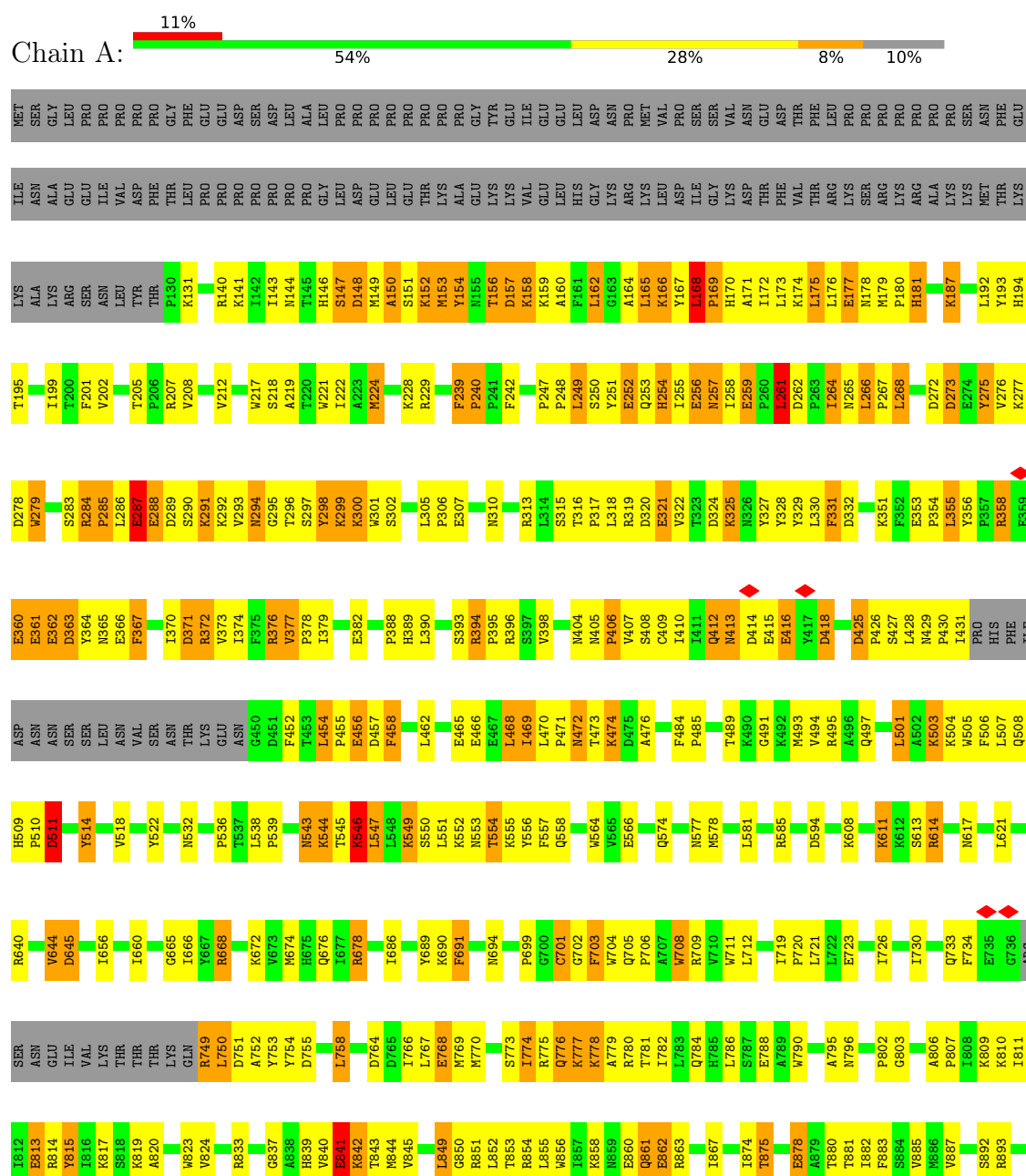


Mol	Chain	Residues	Atoms					AltConf
29	E	1	Total	C	N	O	P	0
			31	13	5	11	2	

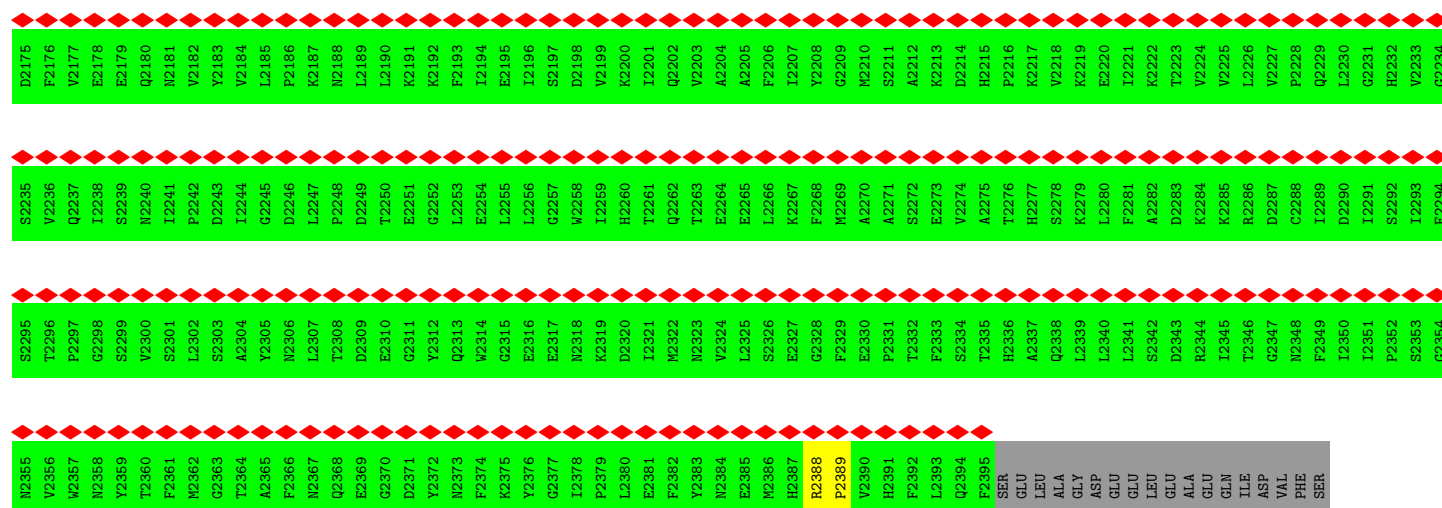
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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

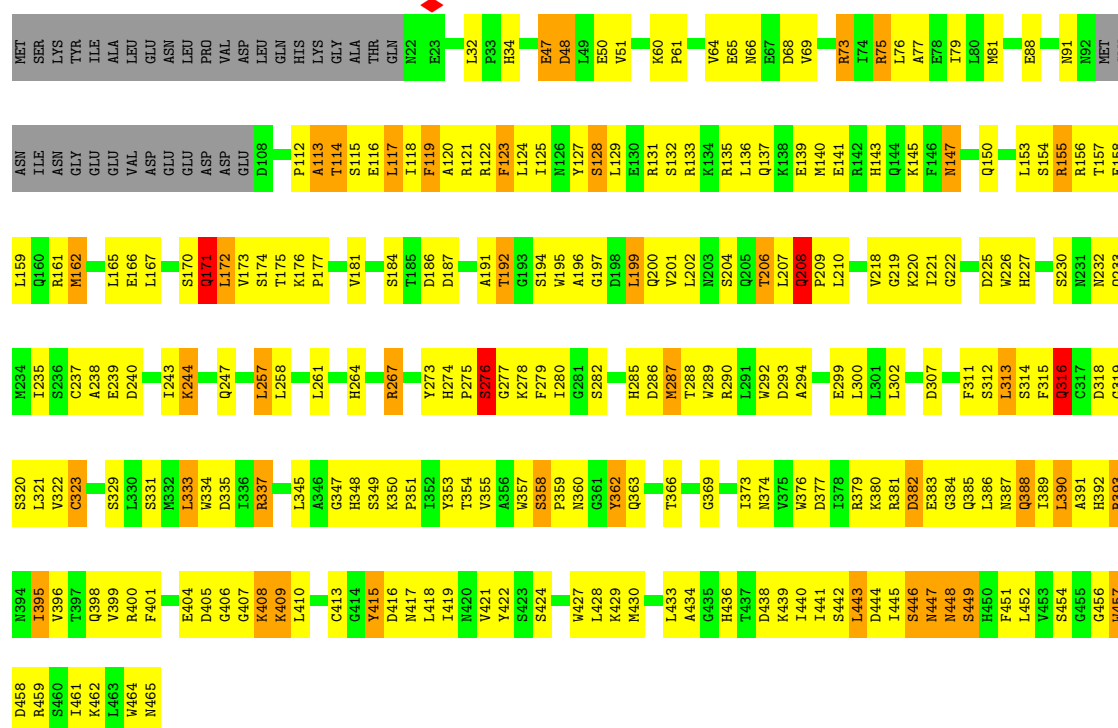






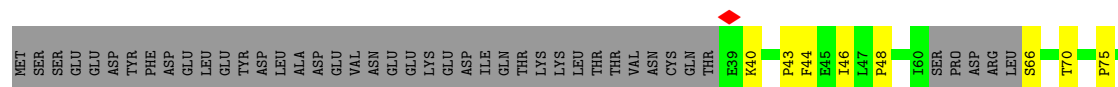
• Molecule 2: U4/U6 small nuclear ribonucleoprotein PRP4

Chain B: 40% 43% 9% 8%

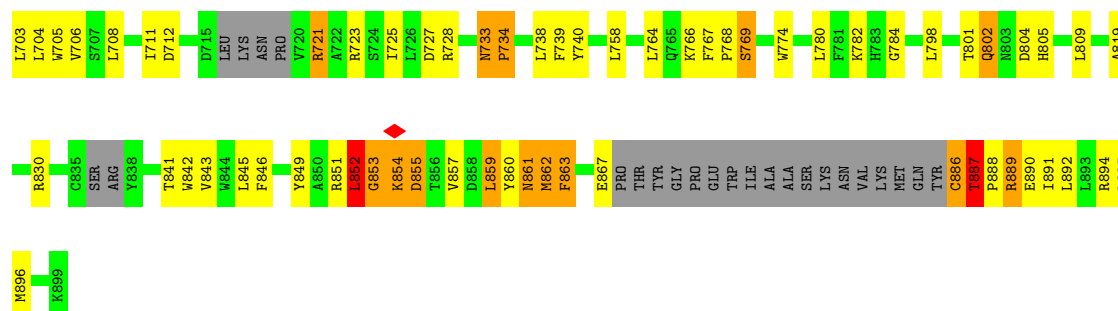


• Molecule 3: Pre-mRNA-processing factor 31

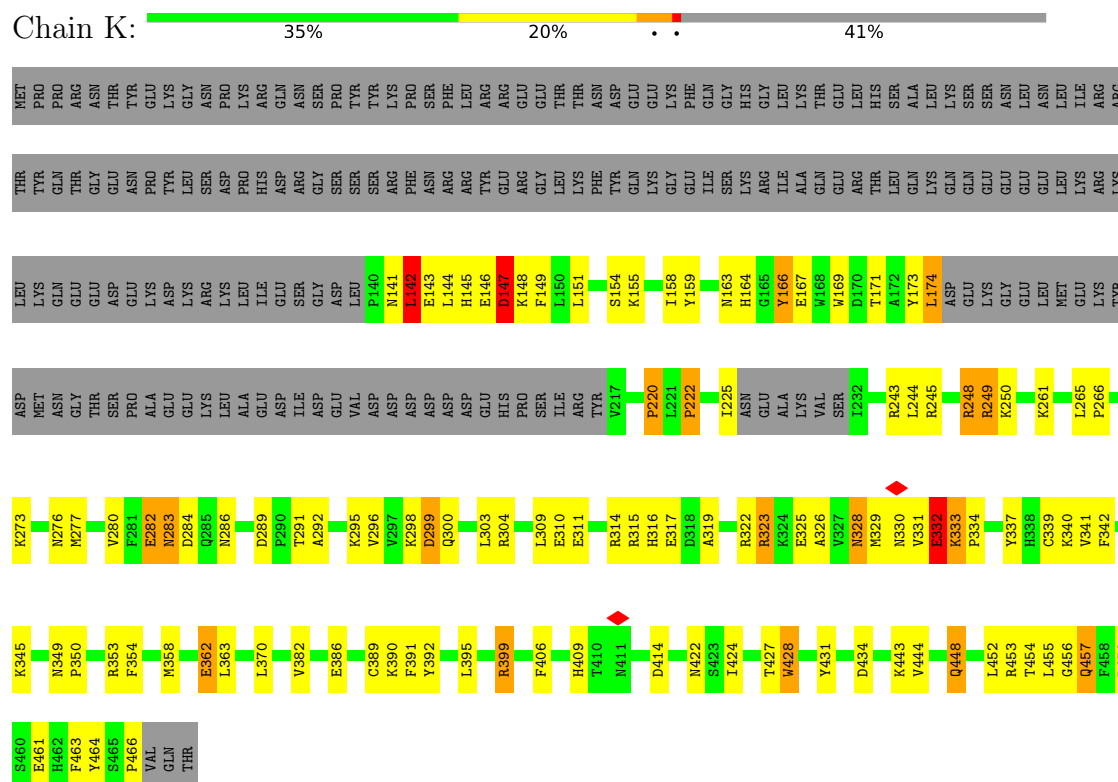
Chain I: 42% 31% 10% 16%



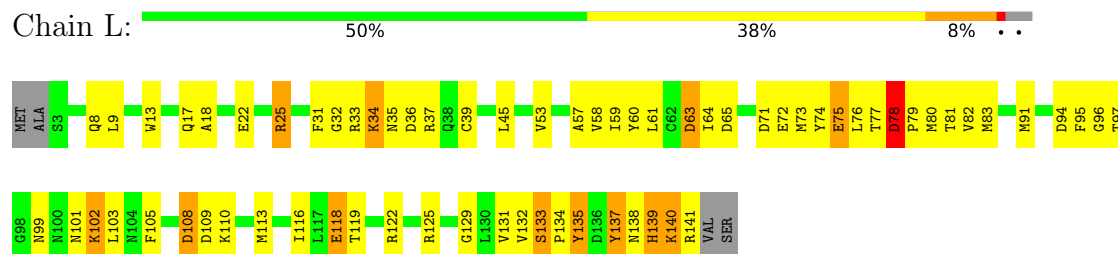




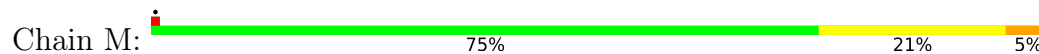
- Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3



- Molecule 6: Spliceosomal protein DIB1



- Molecule 7: 13 kDa ribonucleoprotein-associated protein





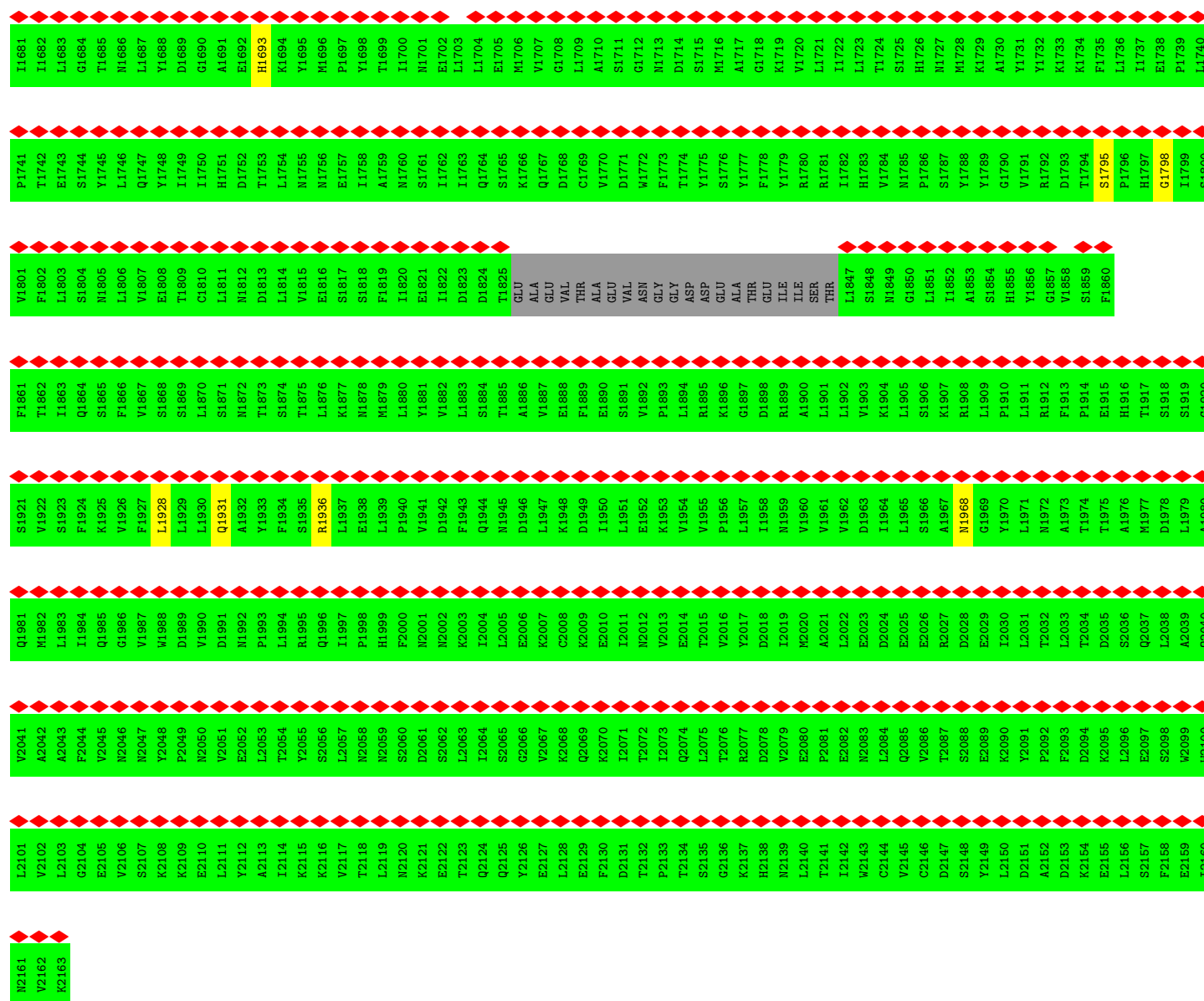


## Chain N:

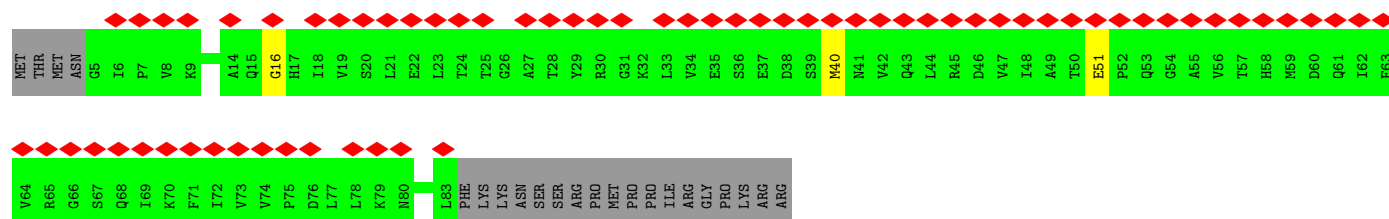
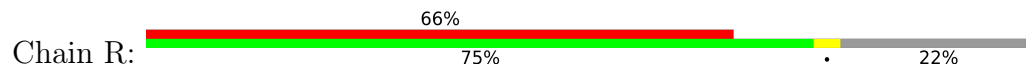


P841	L781	A721	G661	E601	H541	T481	PRO	ARG	LEU	ASP	LYS	GLU	GLY	THR	MET
A842	K782	M722	Q662	T602	H542	S482	ALA	LEU	ASP	GLU	PHE	GLN	GLY	THR	MET
H843	T783	N723	E663	Q603	H543	L483	PRO	LYS	GLY	ASN	ASN	ILE	GLN	GLY	GLN
T844	E784	D724	Y664	V604	H544	P484	VAL	THR	ASP	LEU	VAL	THR	GLN	THR	CYS
V845	A785	A725	P665	V606	H546	D485	ILE	GLU	THR	THR	LYS	VAL	CYS	ASN	ASN
I846	A786	C726	R666	V606	H546	W486	ASP	ASN	VAL	ASP	LYS	VAL	ASN	ASN	ASN
L847	N787	T727	I667	S607	T547	C487	ILE	GLU	THR	THR	ILE	GLY	GLY	LEU	LEU
K848	N788	E728	I668	T608	H548	Q488	LYS	PRO	ASN	GLU	VAL	GLY	GLY	LEU	LEU
G849	L789	K729	G669	P609	H549	E489	GLU	GLY	GLY	VAL	THR	ILE	GLY	GLY	GLY
T850	D790	V730	L670	E610	L550	A490	ILE	ASN	PRO	GLU	ASN	ASN	ASN	LEU	LEU
D851	P791	L731	S671	K611	N551	F491	LYS	LEU	LEU	ASN	THR	ASN	ASN	ASN	ASN
V852	S792	E732	A672	W612	L552	P492	PHE	ILE	ILE	SER	THR	ASN	GLY	LEU	LEU
Y853	L793	S733	T673	D613	S553	S493	ASP	GLY	GLY	LYS	TYR	ILE	GLY	GLY	GLY
S854	K794	I734	L674	I614	A554	S494	GLU	GLY	GLY	GLU	GLU	PRO	ASN	ASN	ASN
R855	K795	N735	P675	T615	F555	E495	SER	MET	VAL	LYS	HIS	ASP	VAL	VAL	VAL
E856	L796	E736	N676	T616	K556	T496	LEU	GLY	LEU	ASN	THR	THR	GLY	GLY	GLY
K857	T797	G737	Y677	R617	L557	T497	MET	ASN	ASP	ASN	ASN	ASP	VAL	VAL	VAL
G858	E798	N738	E678	M618	V558	S498	LEU	ASN	LEU	PRO	LYS	THR	GLY	GLY	GLY
S859	N799	Q739	D679	S619	Y559	L499	GLU	GLY	THR	ASN	ASN	THR	GLY	GLY	GLY
W860	G800	I740	V680	M620	I560	N500	ASN	VAL	ASN	GLU	GLN	ALA	SER	LEU	LEU
E861	I801	I741	G681	N621	A561	P501	ILE	ASN	ASN	ILE	GLN	ALA	GLY	LYS	LYS
K862	G802	V742	R682	L622	P562	I502	T442	ASP	ASN	ILE	GLN	ALA	GLY	LYS	LYS
L863	T803	F743	F683	A623	L563	Q503	V443	GLY	LEU	ASN	ASN	VAL	THR	THR	THR
S864	H804	V744	L684	I624	K564	S504	T444	VAL	LEU	ASN	GLN	ALA	THR	GLY	GLY
P865	H805	H745	R685	V625	A565	K505	V446	ARG	GLU	ASN	ASN	VAL	ASP	LEU	LEU
Q866	A806	S746	V686	V626	L566	V506	E450	PHE	LEU	LEU	ALA	PHE	ASP	LEU	LEU
D867	G807	R747	P687	E626	L566	V506	G451	THR	THR	ASP	GLY	ASN	GLN	GLY	GLY
V868	L808	K748	K688	L627	V567	F507	S452	HIS	VAL	LYS	LYS	GLY	GLY	GLY	GLY
L869	T809	E749	E689	R629	Q568	H508	F453	THR	ASN	SER	ASP	GLY	GLY	THR	THR
K870	R810	T750	G690	L630	E569	A509	K454	LYS	LEU	THR	ASP	GLY	GLY	THR	THR
M871	S811	S751	L691	L631	Q570	A510	R455	ARG	LEU	ASN	GLY	GLY	GLY	ASN	ASN
L872	R812	R752	F692	L632	V571	F511	V456	GLU	PHE	GLY	VAL	ASN	ASN	GLN	GLN
G873	D813	T753	Y693	I633	E573	E512	K457	LEU	GLY	THR	THR	ASN	ASN	GLN	GLN
A874	S814	A754	F694	D634	F574	D514	P458	ASP	GLY	GLY	GLY	ASN	GLY	GLY	GLY
R875	L815	T755	D695	E635											

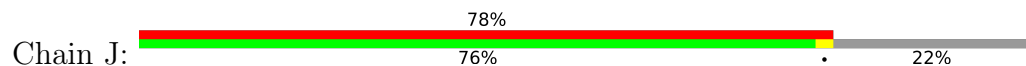
I1621	F1561	Q1501	K1441	E1381	T1321	P1261	K1201	PRO THR	Q1081	E1021	S961	V901
E1622	S1562	L1502	S1442	L1382	P1322	D1262	M1202	M1143	S1082	L1022	S962	L902
K1623	M1563	E1503	H1443	A1383	L1323	I1263	S1203	CL144	Y1083	ASP	D963	ASN
L1624	L1564	K1504	V1444	L1384	L1324	V1264	V1204	CL144	F1084	GLU	G964	GLN
T1625	Q1565	K1505	L1445	L1385	M1326	G1265	T1205	P1145	S1085	L1025	Q965	L906
D1626	Q1566	I1506	L1446	L1386	T1206	G1266	T1206	LI146	Q1086	T1027	L966	P907
G1627	A1567	R1507	A1447	M1387	N1207	E1267	N1207	R1147	L1087	Q1028	K967	I908
H1628	F1568	F1508	T1448	W1388	A1208	F1268	A1208	Q1148	K1088	I1029	K968	E909
L1629	E1569	P1449	P1449	R1389	I1329	T1269	Q1209	K1150	F1089	D1030	F969	S910
R1630	A1570	C1510	V1450	Q1390	P1210	L1270	P1210	LI151	E1090	L1031	R970	Q911
A1631	Q1571	L1511	Q1451	M1391	I1211	S1271	I1211	CL152	G1091	F1032	E971	F912
P1632	A1572	S1512	F1452	K1392	T1212	F1272	T1212	PI153	F1092	R1033	S972	V913
L1633	E1573	C1513	E1453	G1393	R1213	T1273	R1213	VI154	A1093	I1034	L974	S914
K1634	A1574	R1394	L1454	R1394	S1214	V1274	S1214	E1155	L1094	F1035	V974	K915
H1635	A1575	A1395	L1455	A1395	V1215	E1275	V1215	VI156	M1095	S1036	H975	L916
G1636	G1576	V1396	S1456	V1396	M1216	L1276	M1216	LI157	S1096	M1037	S976	V917
V1637	R1457	I1397	R1457	L1397	R1217	K1277	R1217	KL158	D1097	A977	A977	D918
G1638	R1458	T1398	R1458	T1398	F1218	Q1278	F1218	R1159	I1098	S1038	L978	N919
I1639	W1459	M1399	W1459	M1399	N1219	H1279	N1219	LI160	V1099	E1039	C979	L920
L1640	R1460	P1400	R1460	P1400	I1220	H1279	I1220	E1161	F1100	E1040	T980	N921
Y1641	Q1461	S1401	Q1461	S1401	E1221	Q1281	E1221	AL162	H1101	F1041	L981	A922
K1642	R1462	G1402	V1342	V1342	I1222	Q1281	I1222	S1163	H1102	K1042	K982	E923
G1643	K1463	E1403	F1343	F1343	I1223	M1283	I1223	TI164	Q1103	V1044	E983	V924
M1644	N1464	K1404	E1344	E1344	A1224	L1284	A1224	VI165	Q1103	S1045	Q984	V925
A1645	L1465	I1405	F1345	F1345	D1225	P1285	D1225	PI166	A1105	V1046	E985	A926
S1646	Q1466	D1406	K1346	K1346	W1226	P1286	W1226	LI167	G1106	R1047	L986	G927
N1647	S1467	F1407	T1347	T1347	I1227	M1287	I1227	GL168	R1107	E1048	V987	N928
D1648	L1468	L1408	F1348	F1348	W1228	F1288	W1228	DI169	L1108	E1049	L988	I929
E1649	E1469	L1409	N1349	N1349	D1229	F1289	D1229	Y1170	L1109	E1050	Y989	K930
R1650	D1590	S1530	K1350	K1350	M1230	L1290	M1230	LI171	R1110	K1051	D990	C931
I1651	C1591	M1531	M1471	M1471	N1231	T1291	N1231	LI172	A1111	R1052	A991	R932
V1652	M1592	I1532	I1472	I1472	V1232	L1292	V1232	LI173	M1112	E1053	E992	N933
K1653	E1593	Y1533	Y1473	Y1473	H1233	L1293	H1233	EL174	F1113	L1054	Y993	D934
R1654	M1594	M1534	D1474	K1414	G1234	S1294	G1234	TI175	E1114	K1055	D994	A935
L1655	A1595	F1535	D1475	A1415	S1235	E1295	S1235	PI176	I1115	Q1056	Y995	V936
Y1656	S1596	S1536	A1476	F1416	L1236	N1296	L1236	LI177	C1116	L1057	I996	N937
E1657	A1597	I1537	H1477	S1417	E1237	W1297	E1237	PI178	L1117	L1058	E997	W938
V1658	F1598	P1538	E1478	H1418	P1238	W1298	P1238	EL178	K1118	E1059	A998	L939
G1659	M1599	E1539	I1479	L1419	F1239	H1299	F1239	VI179	R1119	K1060	T999	A940
A1660	K1600	R1540	S1480	A1420	L1240	S1300	L1240	GL180	G1120	A1061	D1000	Y941
V1661	F1601	I1541	Q1481	G1421	L1241	L1301	L1241	R1181	W1121	P1062	L1001	T942
S1662	E1602	E1542	G1482	G1422	M1242	F1302	M1242	AL182	G1122	I1063	G1002	Y943
V1663	K1603	P1543	V1483	K1423	L1243	E1303	L1243	LI183	H1123	P1064	M1003	L944
L1664	A1604	L1544	Y1484	I1424	E1244	L1304	E1244	RI184	P1124	I1065	I1004	Y945
L1665	I1605	E1545	G1485	I1425	D1245	P1305	D1245	S1185	T1125	R1066	A1005	V946
I1666	E1606	LI546	A1486	M1426	T1246	V1306	T1246	EL186	F1126	E1067	S1006	R947
S1667	W1607	M1547	V1487	K1427	D1247	S1307	D1247	K1187	M1127	D1068	S1007	M948
K1668	D1608	LI548	Y1488	L1428	G1248	F1308	G1248	VI188	L1128	I1069	F1008	L949
D1669	M1609	Q1549	E1489	G1429	Y1248	ASN	Y1248	GL189	L1129	D1070	Y1009	A950
S1671	L1610	S1550	T1490	M1430	S1250	GLY	S1250	K1190	M1130	D1071	I1010	S951
A1672	M1611	F1551	L1491	D1431	I1251	PHE	I1251	Q1191	L1131	P1072	M1011	P952
F1673	V1612	K1552	I1492	P1432	L1252	LEU	L1252	Y1192	C1132	L1073	H1012	M953
A1674	E1613	D1553	S1493	S1433	Y1253	PRO	Y1253	Y1193	K1133	A1074	A1013	L954
L1675	E1614	V1554	R1494	L1434	Y1254	LYS	Y1254	DI194	S1134	K1075	S1014	Y955
C1675	E1615	E1555	M1495	M1435	D1255	F1317	D1255	L1195	A1135	V1076	M1015	K956
K1676	Q1616	HI556	T1496	L1436	V1256	P1318	V1256	LI196	T1136	N1077	D1016	P957
T1677	I1617	I1557	F1497	K1437	T1257	P1319	T1257	L1197	F1137	L1078	V1017	P958
D1678	V1618	S1558	K1437	L1438	F1258	P1320	F1258	R1198	K1138	L1079	Y1018	P959
E1679	P1619	F1559	A1499	L1439	I1259		I1259	F1199	M1139	L1080	M1019	L960
V1680	Y1620	N1560	T1500	A1440	T1260			P1200	W1140		R1020	

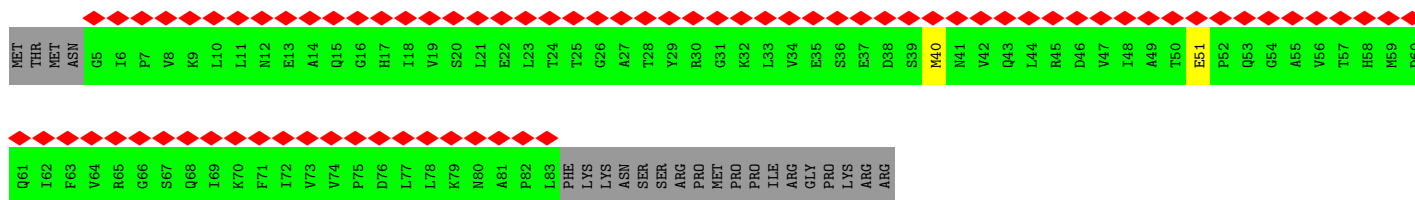


• Molecule 10: Small nuclear ribonucleoprotein Sm D3

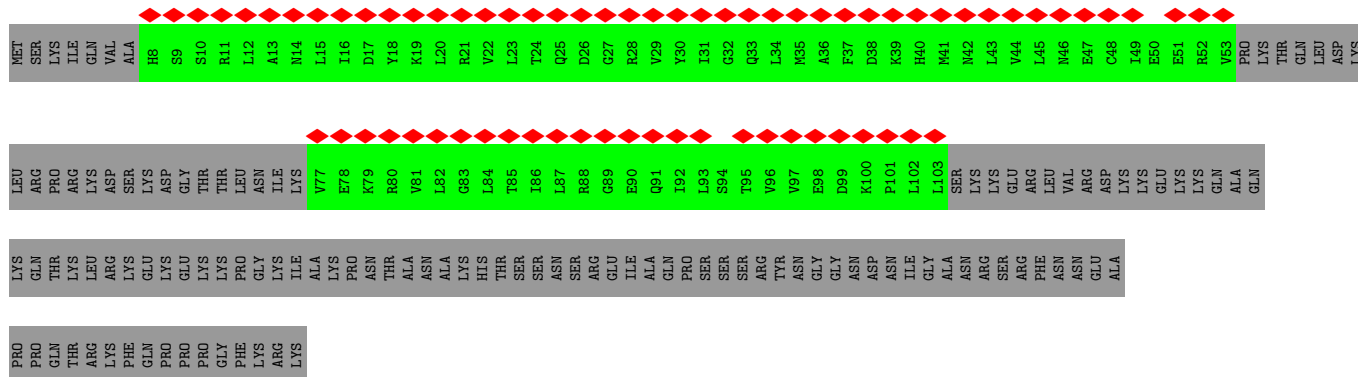


• Molecule 10: Small nuclear ribonucleoprotein Sm D3

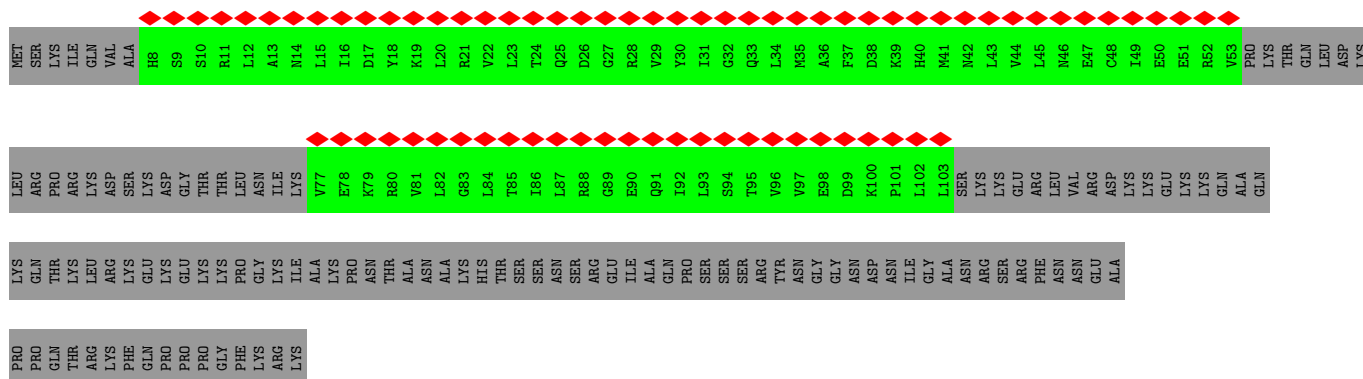




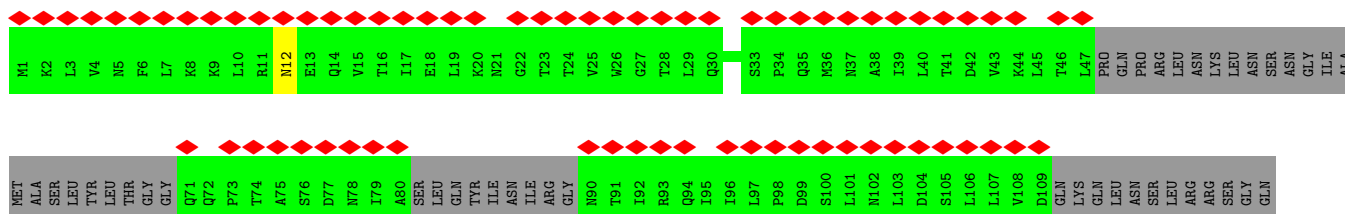
• Molecule 11: Small nuclear ribonucleoprotein-associated protein B



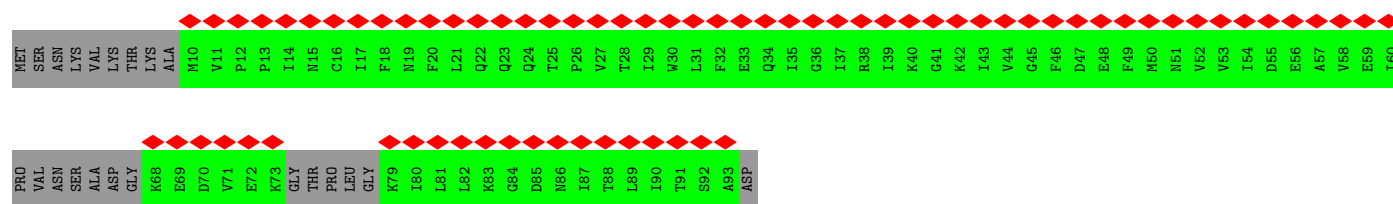
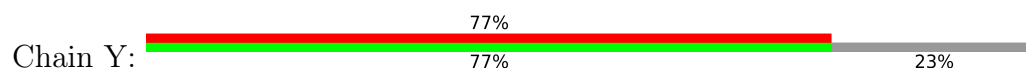
• Molecule 11: Small nuclear ribonucleoprotein-associated protein B



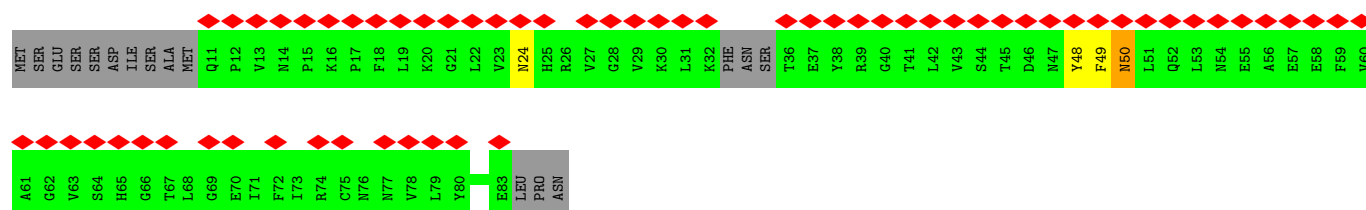
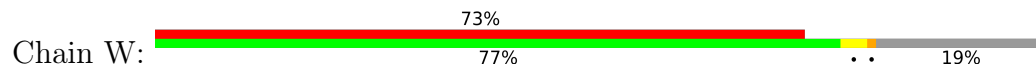
• Molecule 12: Small nuclear ribonucleoprotein Sm D1



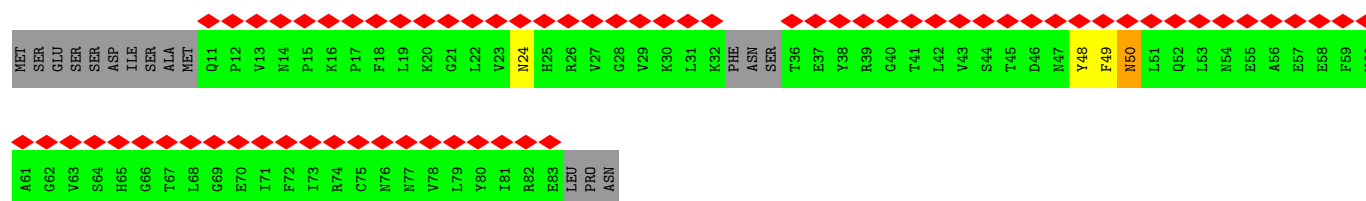
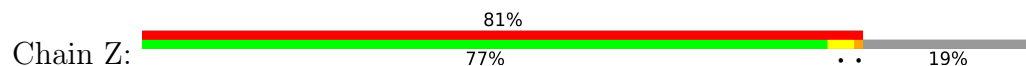




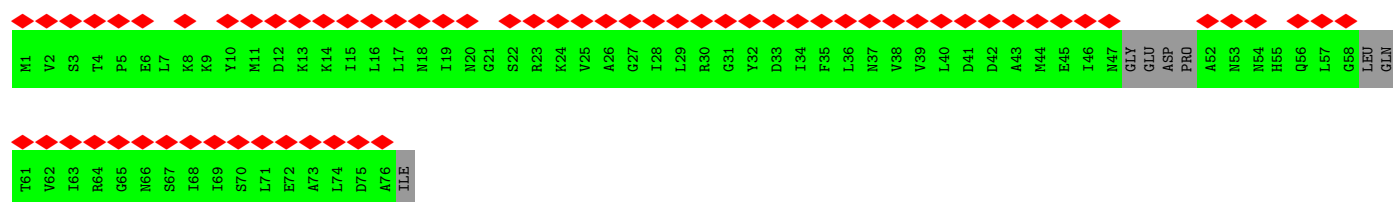
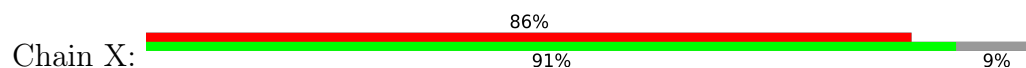
• Molecule 15: Small nuclear ribonucleoprotein F



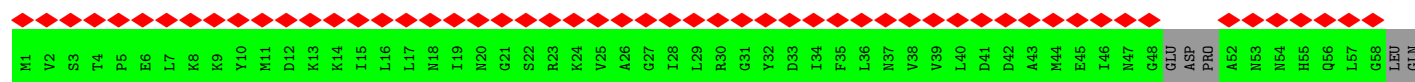
• Molecule 15: Small nuclear ribonucleoprotein F



• Molecule 16: Small nuclear ribonucleoprotein G

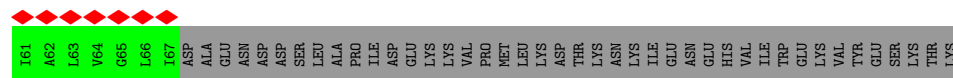


• Molecule 16: Small nuclear ribonucleoprotein G

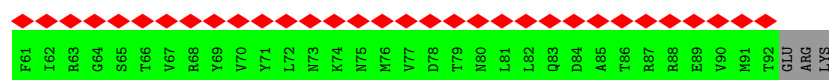
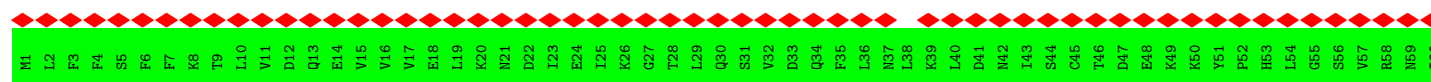




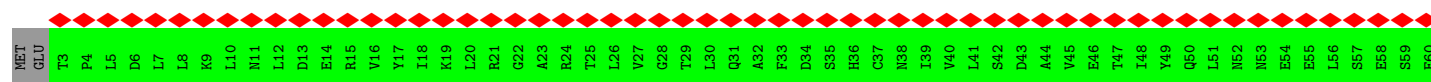
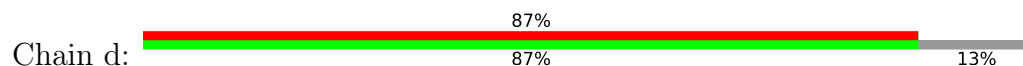
- Molecule 17: U6 snRNA-associated Sm-like protein LSm8



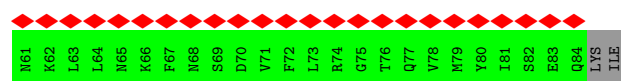
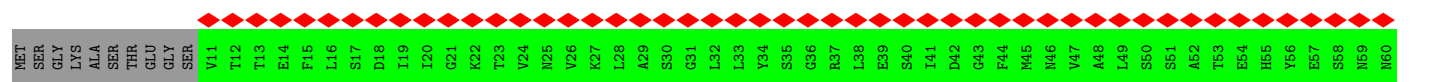
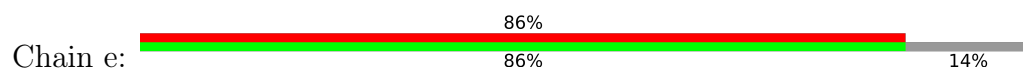
- Molecule 18: U6 snRNA-associated Sm-like protein LSm2



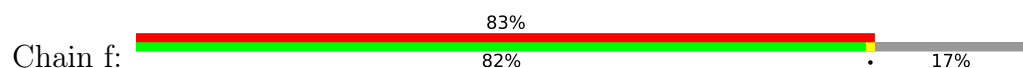
- Molecule 19: U6 snRNA-associated Sm-like protein LSm3



- Molecule 20: U6 snRNA-associated Sm-like protein LSm6



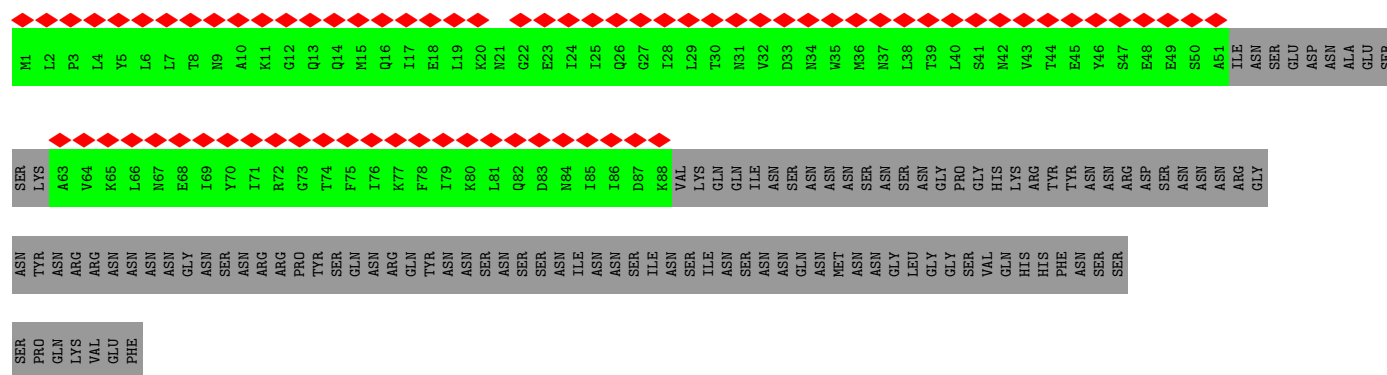
- Molecule 21: U6 snRNA-associated Sm-like protein LSm5



- Molecule 22: U6 snRNA-associated Sm-like protein LSm7



- Molecule 23: U6 snRNA-associated Sm-like protein LSm4



- Molecule 24: pre-mRNA



- Molecule 25: SNR6 snRNA







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	172134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	
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	0.204	Depositor
Minimum map value	-0.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0147	Depositor
Map size ( $\text{\AA}$ )	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.32, 1.32, 1.32	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.86	22/17296 (0.1%)	0.91	24/23336 (0.1%)
2	B	0.72	2/3434 (0.1%)	0.86	0/4635
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%)
8	H	0.55	2/6874 (0.0%)	0.78	8/9305 (0.1%)
9	N	0.52	0/6738	0.65	0/8412
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
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
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%)
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%)	9	43
2	B	425/465 (91%)	380 (89%)	36 (8%)	9 (2%)	7	40
3	I	410/494 (83%)	380 (93%)	24 (6%)	6 (2%)	10	46
4	G	684/899 (76%)	604 (88%)	64 (9%)	16 (2%)	6	38

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	K	273/469 (58%)	247 (90%)	21 (8%)	5 (2%)	8	42
6	L	137/143 (96%)	129 (94%)	6 (4%)	2 (2%)	10	46
7	M	124/126 (98%)	118 (95%)	4 (3%)	2 (2%)	9	44
8	H	837/1008 (83%)	770 (92%)	47 (6%)	20 (2%)	6	37
9	N	1674/2163 (77%)	1555 (93%)	109 (6%)	10 (1%)	25	62
10	J	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	5	36
10	R	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	5	36
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%)	11	46
12	T	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	11	46
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%)	2	25
15	Z	66/86 (77%)	60 (91%)	3 (4%)	3 (4%)	2	25
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%)	11	46
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%)	14	46

5 of 120 Ramachandran outliers are listed below:

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

Continued on next page...

*Continued from previous page...*

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%)	5	26
2	B	374/410 (91%)	321 (86%)	53 (14%)	3	21
3	I	327/445 (74%)	264 (81%)	63 (19%)	1	10
4	G	361/813 (44%)	295 (82%)	66 (18%)	1	11
5	K	253/436 (58%)	228 (90%)	25 (10%)	8	32
6	L	129/132 (98%)	113 (88%)	16 (12%)	4	24
7	M	104/104 (100%)	98 (94%)	6 (6%)	20	51
8	H	757/910 (83%)	639 (84%)	118 (16%)	2	17
All	All	4054/5432 (75%)	3501 (86%)	553 (14%)	7	22

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

Mol	Chain	Res	Type
8	H	208	ARG
8	H	329	SER
8	H	206	LYS
8	H	582	SER
1	A	1920	LEU

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

Mol	Chain	Res	Type
4	G	285	HIS
8	H	158	HIS

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
4	G	700	ASN
6	L	17	GLN
8	H	334	HIS

### 5.3.3 RNA [i](#)

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
27	F	33	U
27	F	81	A
27	F	166	U
27	F	77	A
27	F	83	C

## 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 monosaccharides 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
28	GTP	H	1500	-	26,34,34	0.93	1 (3%)	32,54,54	1.62	4 (12%)
29	M7M	E	201	26	29,33,33	1.50	5 (17%)	39,52,52	2.02	7 (17%)

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
28	GTP	H	1500	-	-	4/18/38/38	0/3/3/3
29	M7M	E	201	26	-	6/20/48/48	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	E	201	M7M	CBG-CBO	4.47	1.46	1.37
29	E	201	M7M	CBG-NBH	-3.22	1.32	1.35
29	E	201	M7M	CBF-NBE	-2.80	1.33	1.38
28	H	1500	GTP	C6-N1	-2.41	1.34	1.37
29	E	201	M7M	CBO-NBP	-2.12	1.32	1.35

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	E	201	M7M	NBP-CBI-NBH	-5.79	95.09	103.38
29	E	201	M7M	PBK-OB-PAZ	-5.05	115.50	132.83
28	H	1500	GTP	PB-O3B-PG	-4.56	117.19	132.83
29	E	201	M7M	PBK-OB-UBT	4.44	147.72	121.68
28	H	1500	GTP	PA-O3A-PB	-4.06	118.89	132.83

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
29	E	201	M7M	NBE-CBM-NBV-CBW
29	E	201	M7M	NBE-CBM-NBV-CBZ
29	E	201	M7M	NBN-CBM-NBV-CBZ
29	E	201	M7M	CBS-CBT-OBUPBK
28	H	1500	GTP	O4'-C4'-C5'-O5'

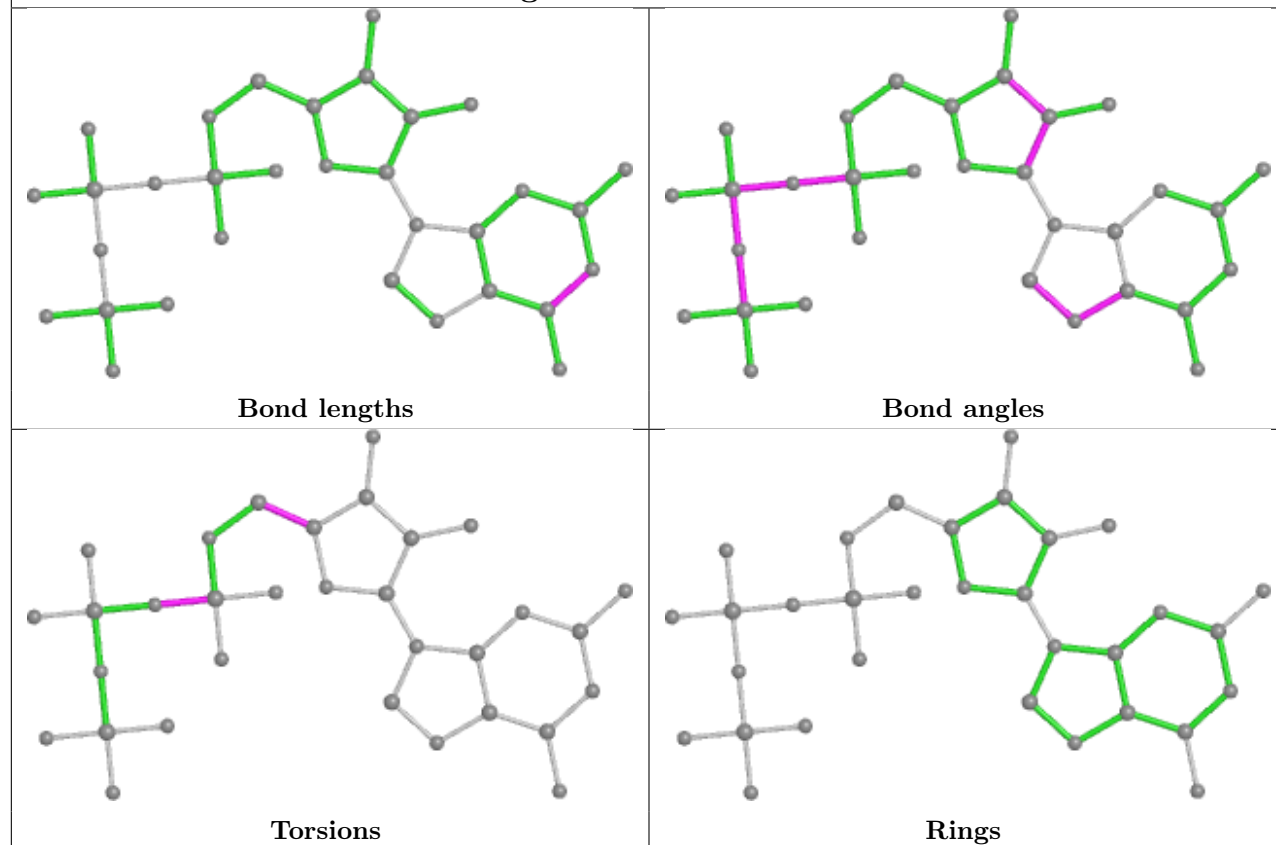
There are no ring outliers.

2 monomers are involved in 16 short contacts:

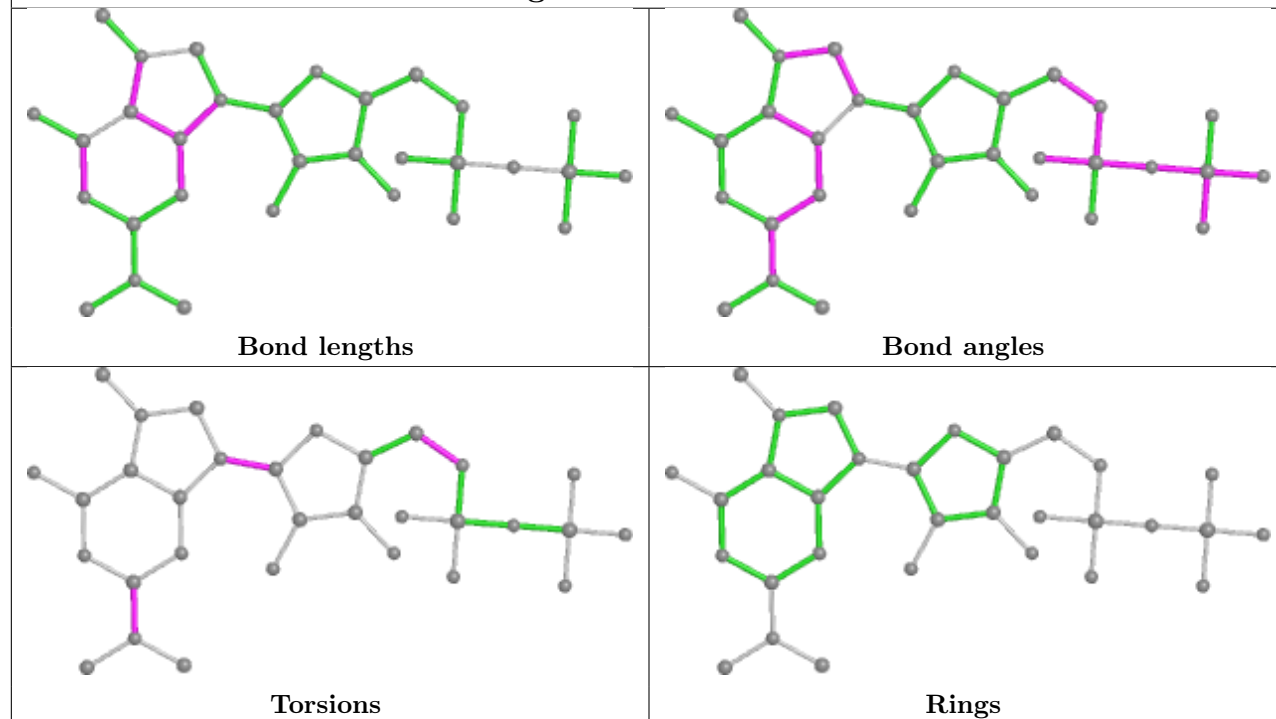
Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	H	1500	GTP	10	0
29	E	201	M7M	6	0

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

## Ligand GTP H 1500



## Ligand M7M E 201



## 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.

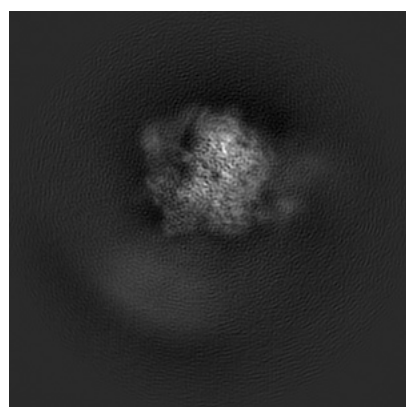
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6561. These allow visual inspection of the internal detail of the map and identification of artifacts.

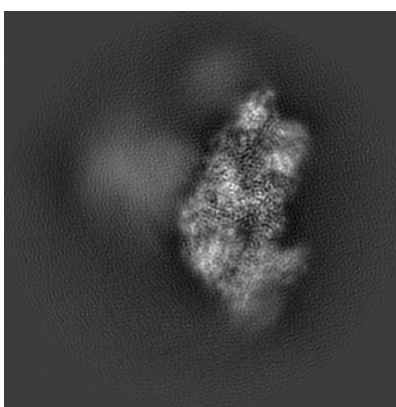
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

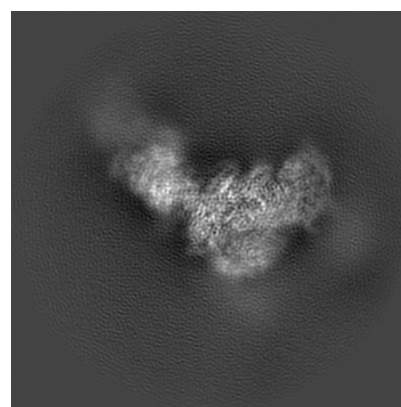
#### 6.1.1 Primary map



X



Y

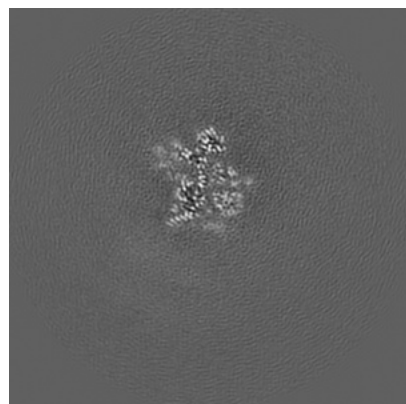


Z

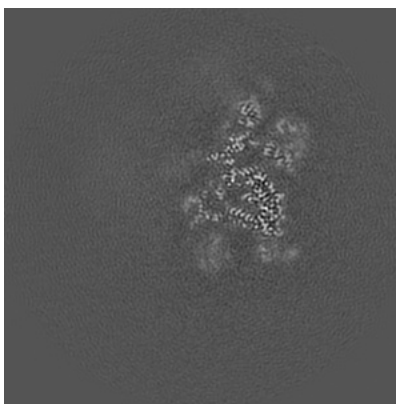
The images above show the map projected in three orthogonal directions.

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

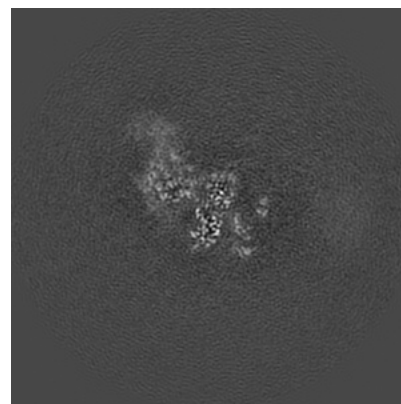
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

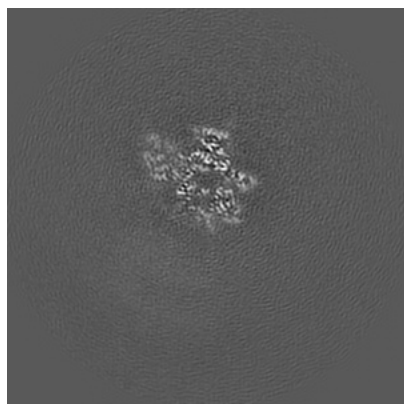


Z Index: 160

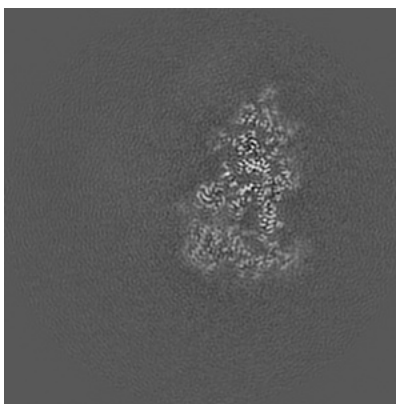
The images above show central slices of the map in three orthogonal directions.

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

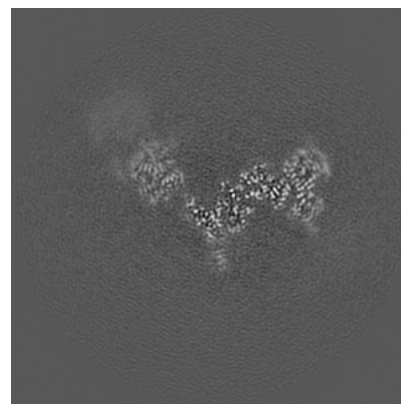
### 6.3.1 Primary map



X Index: 167



Y Index: 171



Z Index: 199

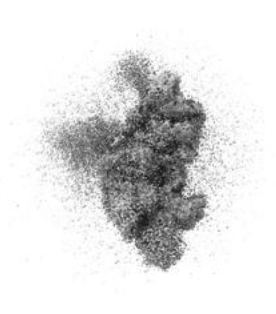
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

## 6.5 Mask visualisation

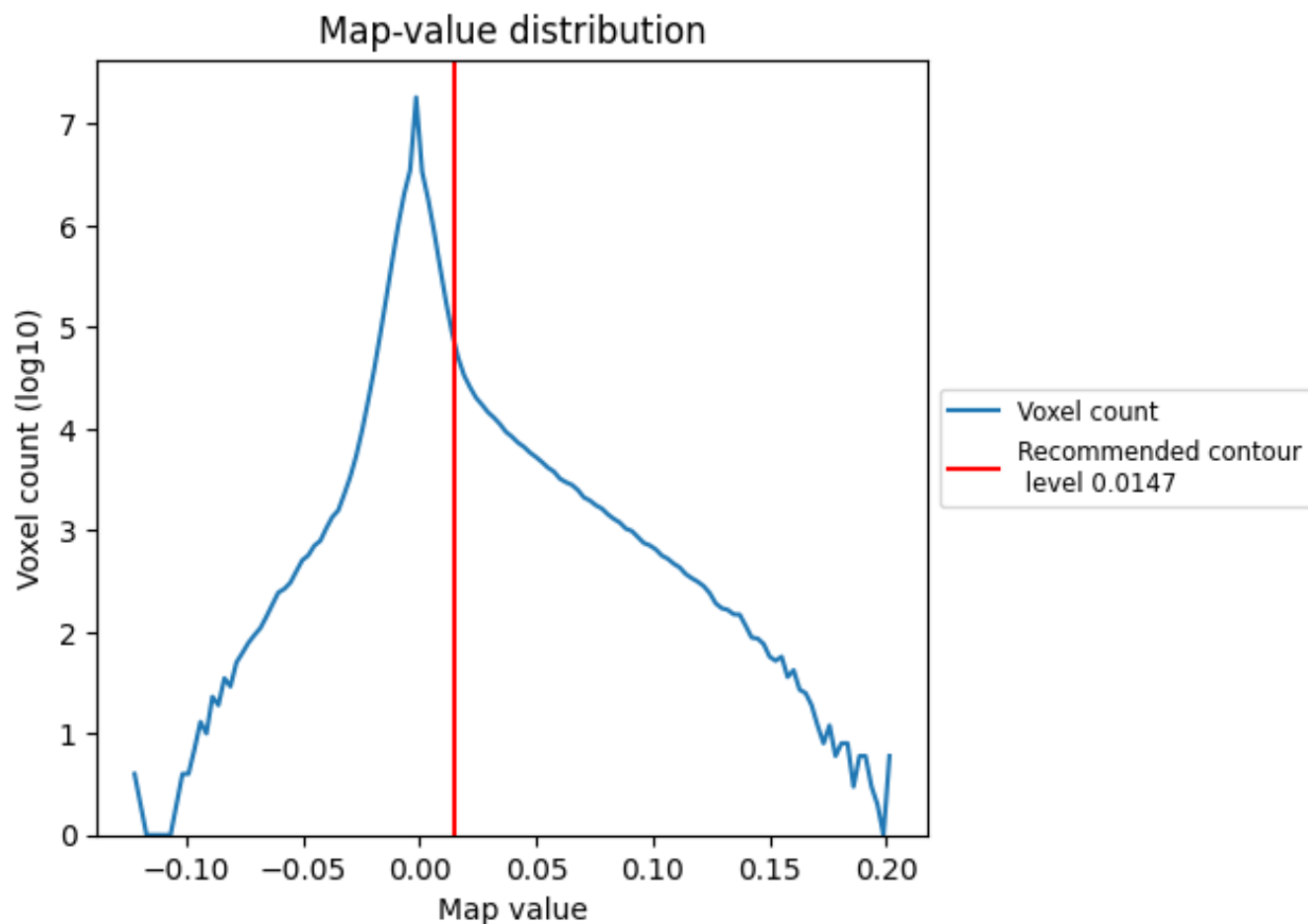
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

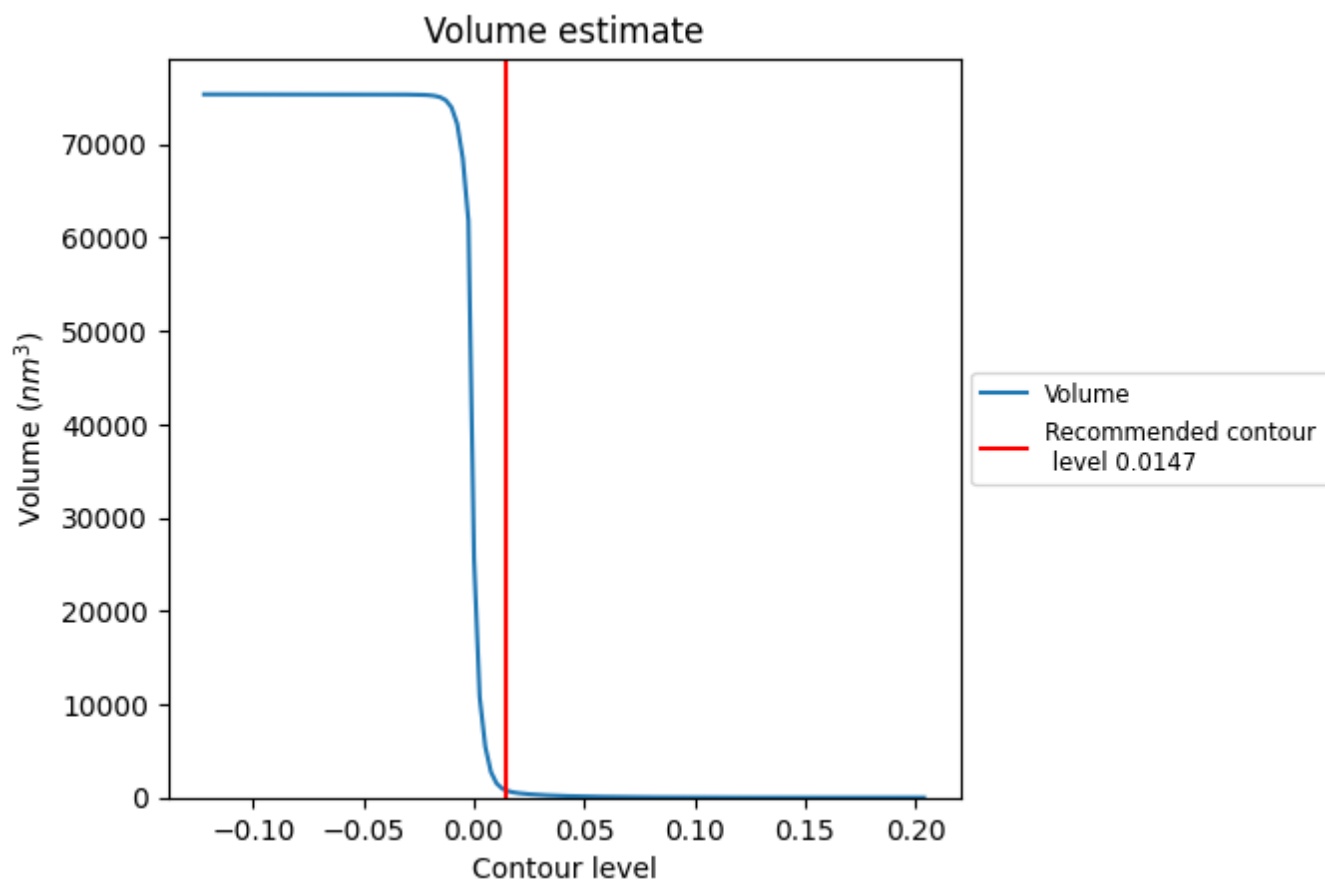
This section contains the results of statistical analysis of the map.

### 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.

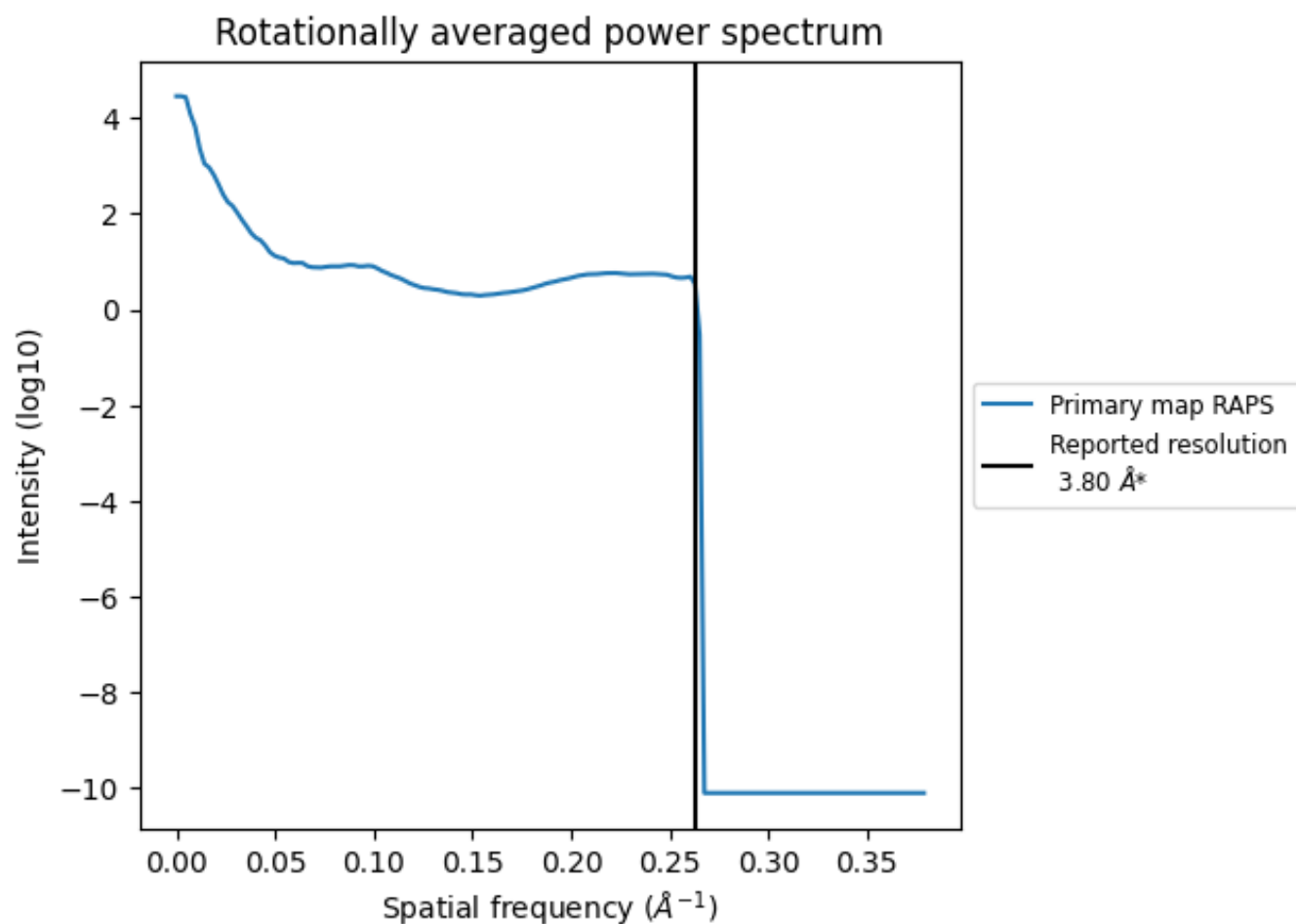
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 773 nm<sup>3</sup>; this corresponds to an approximate mass of 699 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 0.263  $\text{\AA}^{-1}$

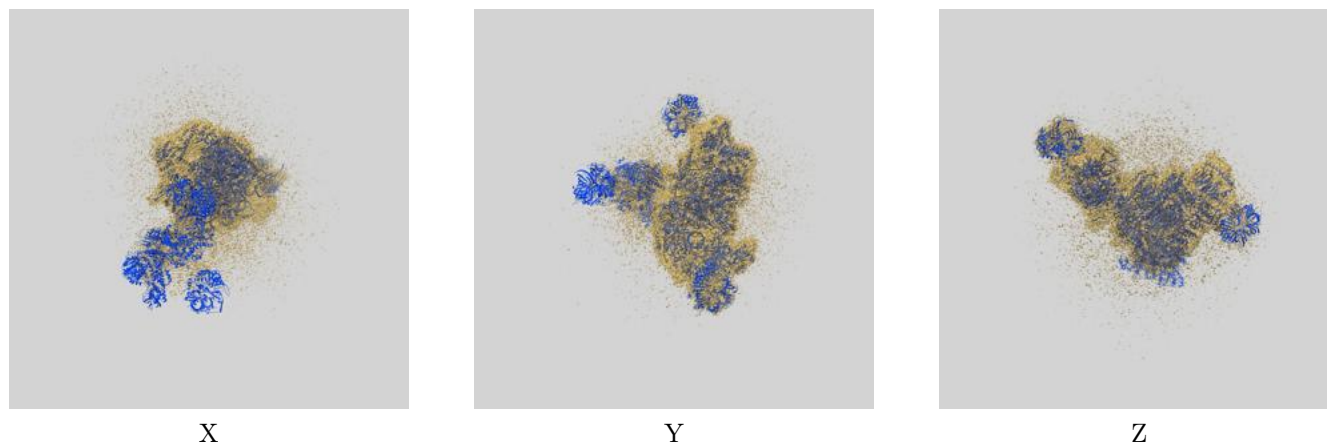
## 8 Fourier-Shell correlation ⓘ

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

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

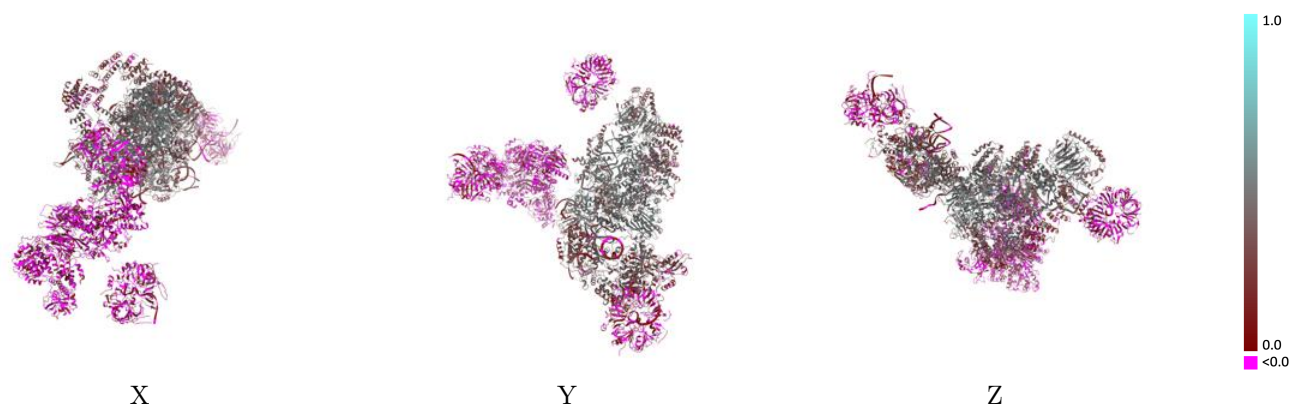
This section contains information regarding the fit between EMDB map EMD-6561 and PDB model 3JCM. Per-residue inclusion information can be found in section 3 on page 11.

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



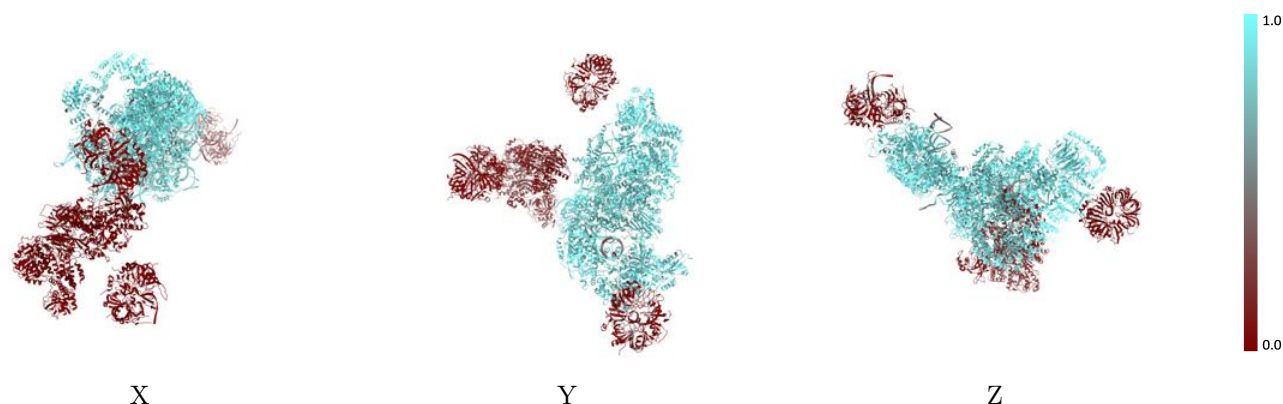
The images above show the 3D surface view of the map at the recommended contour level 0.0147 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



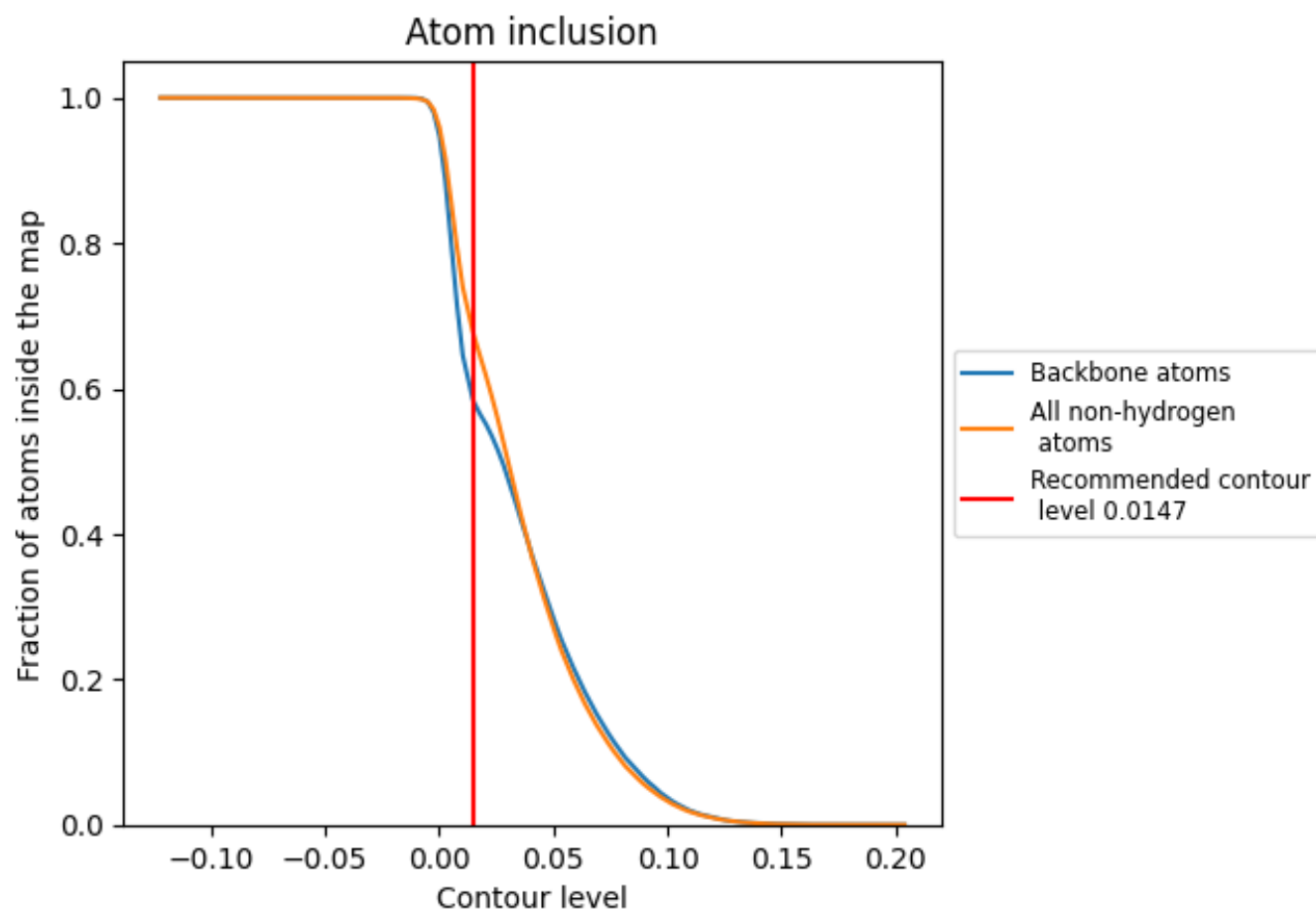
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0147).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 58% 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 (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6783	 0.2940
A	 0.8564	 0.3990
B	 0.9063	 0.4200
C	 0.8695	 0.2880
D	 0.8910	 0.3730
E	 0.7473	 0.3630
F	 0.7107	 0.2090
G	 0.9070	 0.3400
H	 0.8914	 0.3210
I	 0.9216	 0.4400
J	 0.0000	 -0.0190
K	 0.9073	 0.4070
L	 0.9241	 0.4570
M	 0.9275	 0.4890
N	 0.0233	 0.0020
O	 0.0000	 0.0160
P	 0.0032	 0.0440
Q	 0.0000	 0.0460
R	 0.1487	 0.0620
S	 0.0514	 0.0240
T	 0.0909	 0.0940
U	 0.1222	 0.0370
V	 0.0486	 -0.0010
W	 0.1321	 0.0400
X	 0.0500	 0.0310
Y	 0.0000	 -0.0070
Z	 0.0036	 0.0190
a	 0.0000	 0.0320
b	 0.0115	 0.0180
c	 0.0109	 0.0280
d	 0.0097	 0.0140
e	 0.0270	 0.0190
f	 0.0130	 0.0250
g	 0.0114	 0.0220
h	 0.0162	 -0.0580

