



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 08:43 AM JST

PDB ID : 6LQR
EMDB ID : EMD-0951
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State C)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 8.60 Å(reported)
Based on initial model : 6LQP

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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:

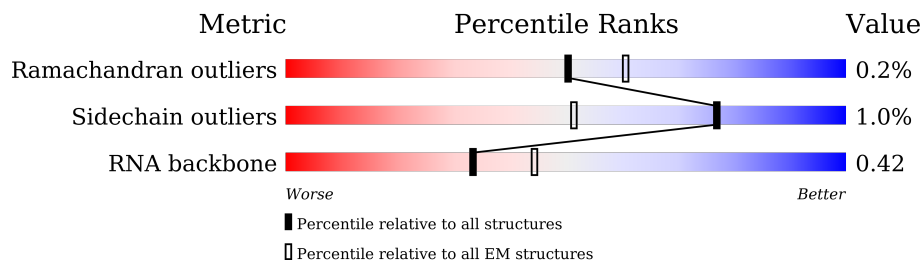
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance

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

The reported resolution of this entry is 8.60 Å.

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



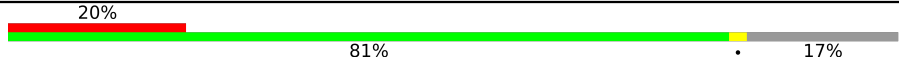

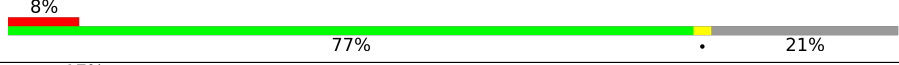

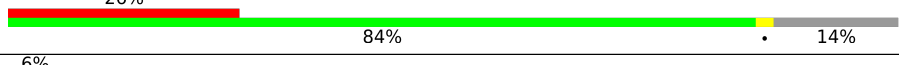
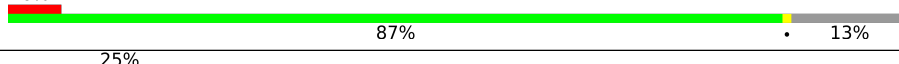
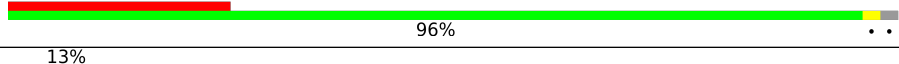

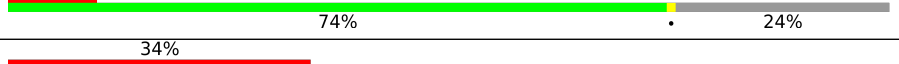
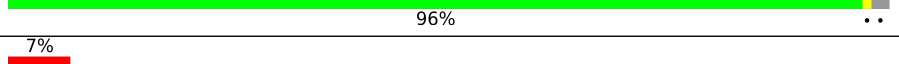
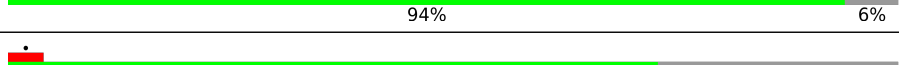
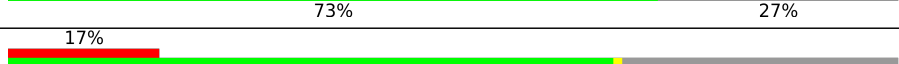
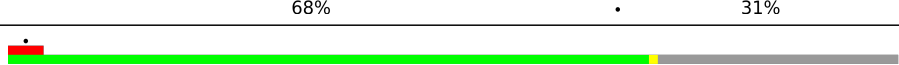
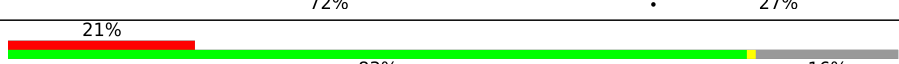

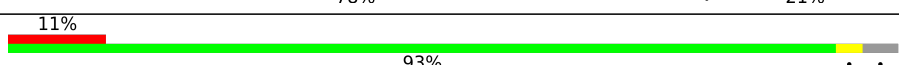
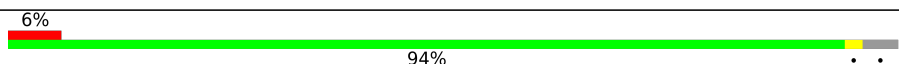
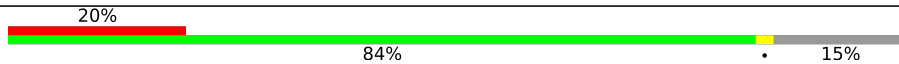
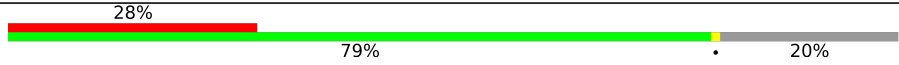


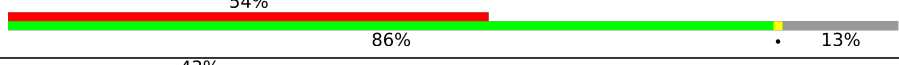
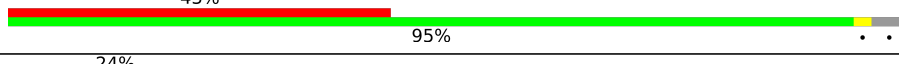
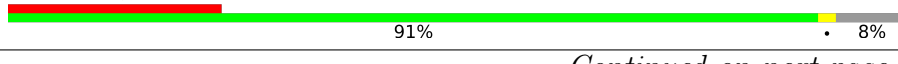

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 ≥ 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	3A	333	
2	5A	700	
3	SA	1809	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	








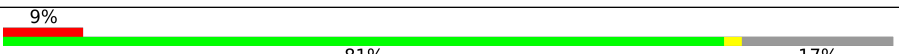



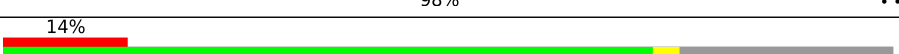

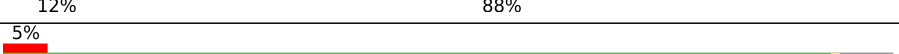
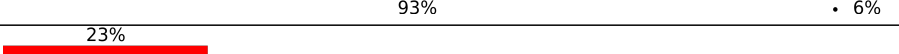
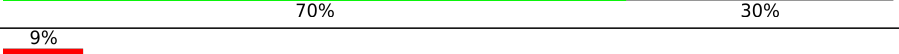
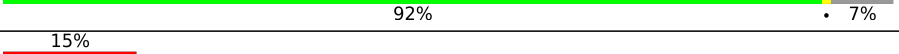








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Mol	Chain	Length	Quality of chain
9	SJ	200	
10	SK	197	
11	SM	156	
12	SO	151	
13	SP	137	
14	SR	143	
15	SX	130	
16	SY	145	
17	SZ	135	
18	Sc	82	
19	Sd	67	
20	3B	327	
20	3C	327	
21	3D	504	
22	3E	511	
23	3F	573	
24	3G	126	
24	3H	126	
25	A4	776	
26	A5	643	
27	A8	713	
28	A9	575	
29	AE	1769	
30	AF	513	
31	AG	896	

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Mol	Chain	Length	Quality of chain
32	B1	923	
33	B2	943	
34	B3	817	
35	B8	594	
36	BE	939	
37	B6	440	
38	5B	214	
39	5C	554	
40	5D	250	
41	5E	593	
42	5F	183	
43	5G	290	
44	5H	610	
45	5I	489	
46	5J	217	
47	5K	189	
48	RA	707	
49	RB	357	
50	RD	1729	
51	RE	1237	
52	RF	297	
53	RG	252	
53	RH	252	
54	RJ	1183	
55	RK	367	

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Mol	Chain	Length	Quality of chain
56	RL	1056	
56	RM	1056	
57	RN	810	
58	RO	552	
59	RP	2493	
60	RQ	899	
61	RS	483	
62	RT	326	
63	RY	534	
64	X1	347	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 215267 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 RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	175	Total	C	N	O	P	0	0
			3711	1661	648	1227	175		

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	192	Total	C	N	O	P	0	0
			4117	1838	746	1341	192		

- Molecule 3 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1283	Total	C	N	O	P	0	0
			27362	12228	4872	8979	1283		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	230	Total	C	N	O	S	0	0
			1830	1156	335	335	4		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	229	Total	C	N	O	S	0	0
			1815	1161	331	320	3		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SG	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	167	Total	C	N	O	S	0	0
			1327	834	256	235	2		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	165	Total	C	N	O	S	0	0
			1321	853	226	242			

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	166	Total	C	N	O	S	0	0
			1324	824	262	236	2		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	123	Total	C	N	O	S	0	0
			997	641	189	164	3		

- Molecule 12 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SO	134	Total	C	N	O	S	0	0
			1087	698	202	186	1		

- Molecule 13 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SP	118	Total	C	N	O	S	0	0
			868	536	164	165	3		

- Molecule 14 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SR	125	Total	C	N	O	0	0
			973	625	174	174		

- Molecule 15 is a protein called 40S ribosomal protein S22-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SX	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SZ	102	Total	C	N	O	0	0
			809	517	148	144		

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 19 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Sd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 20 is a protein called rRNA 2'-O-methyltransferase fibrillar.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
20	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 23 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	10		

- Molecule 24 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
24	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A4	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A5	514	Total	C	N	O	S	0	0
			3976	2520	688	755	13		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A8	532	Total	C	N	O	S	0	0
			3229	2008	592	626	3		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A9	128	Total	C	N	O	S	0	0
			939	594	173	170	2		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AE	1534	Total	C	N	O	S	0	0
			9955	6242	1771	1923	19		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 31 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AG	826	Total	C	N	O	S	0	0
			6570	4181	1111	1259	19		

- Molecule 32 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B1	793	Total	C	N	O	S	0	0
			6331	4046	1085	1182	18		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B2	825	Total	C	N	O	S	0	0
			6502	4156	1096	1223	27		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B3	757	Total	C	N	O	S	0	0
			5919	3769	993	1130	27		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B8	477	Total	C	N	O	S	0	0
			3764	2387	662	705	10		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BE	820	Total	C	N	O	S	0	0
			6450	4090	1114	1225	21		

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B6	374	Total	C	N	O	S	0	0
			2800	1782	501	505	12		

- Molecule 38 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5B	60	Total	C	N	O		0	0
			495	310	101	84			

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5C	458	Total	C	N	O	S	0	0
			3612	2276	636	689	11		

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5D	167	Total	C	N	O	S	0	0
			1396	862	266	263	5		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5E	193	Total	C	N	O	S	0	0
			1564	970	280	310	4		

- Molecule 42 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 43 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5G	219	Total	C	N	O	S	0	0
			1756	1107	325	318	6		

- Molecule 44 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5H	74	Total	C	N	O	S	0	0
			596	373	122	101			

- Molecule 45 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 46 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 47 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 48 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 49 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 50 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RD	316	Total	C	N	O	S	0	0
			2412	1541	414	452	5		

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 52 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 53 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
53	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 54 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 55 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RK	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 56 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
56	RM	766	Total	C	N	O		0	0
			3779	2247	766	766			

- Molecule 57 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RN	607	Total	C	N	O	S	0	0
			4529	2861	820	837	11		

- Molecule 58 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	RO	525	Total	C	N	O	S	0	0
			3766	2412	646	696	12		

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RP	2108	Total	C	N	O	S	0	0
			12171	7483	2291	2381	16		

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 61 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RS	251	Total	C	N	O	S	0	0
			2051	1340	349	359	3		

- Molecule 62 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RT	169	Total	C	N	O	S	0	0
			1334	849	244	237	4		

- Molecule 63 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	RY	37	Total	C	N	O	0	0
			299	191	48	60		

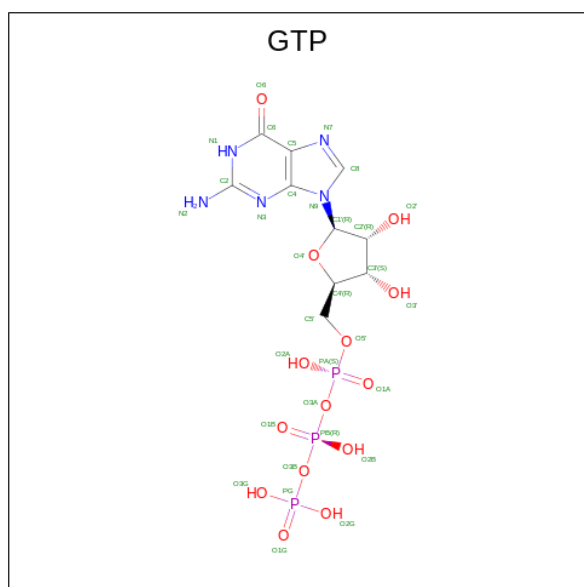
- Molecule 64 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	X1	22	Total	C	N	O	0	0
			110	66	22	22		

- Molecule 65 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	Sc	1	Total	Zn	0
			1	1	
65	5K	1	Total	Zn	0
			1	1	

- Molecule 66 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

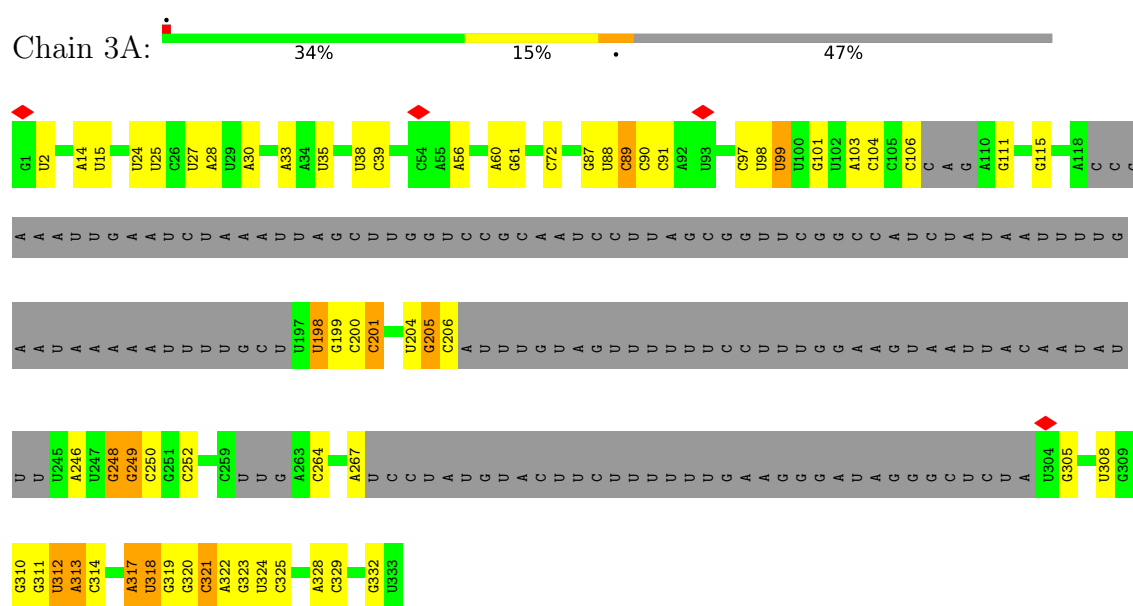
- Molecule 67 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	RJ	1	Total	Mg	0
			1	1	

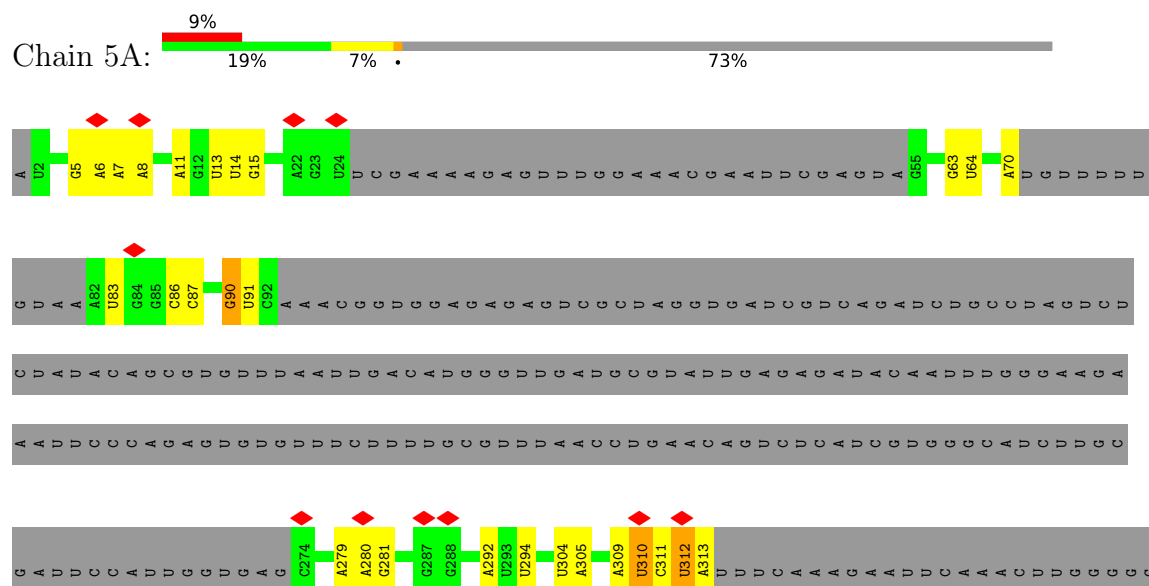
3 Residue-property plots [i](#)

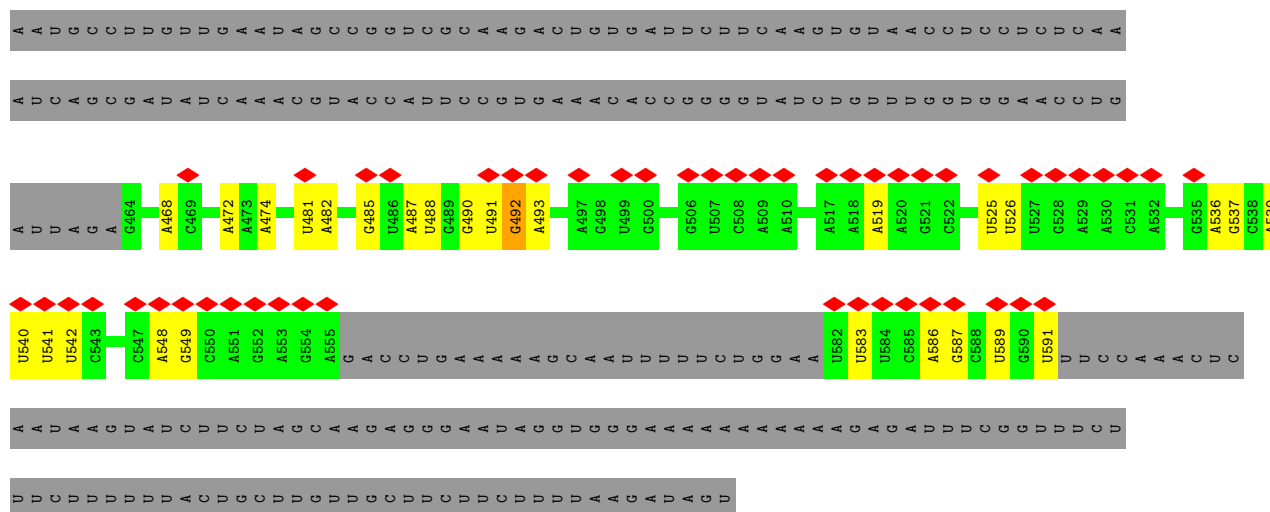
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: U3 snoRNA

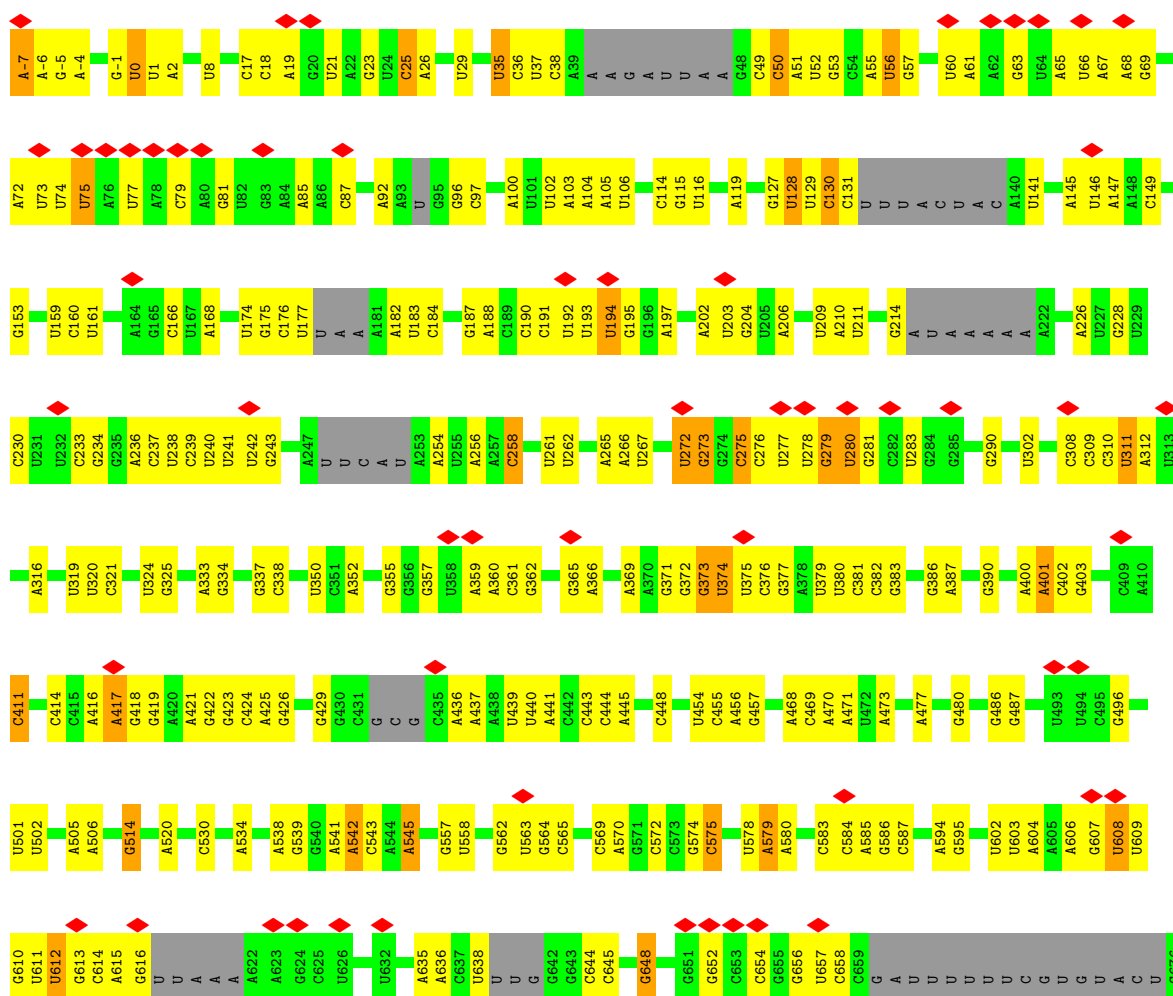
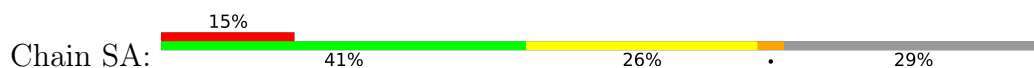


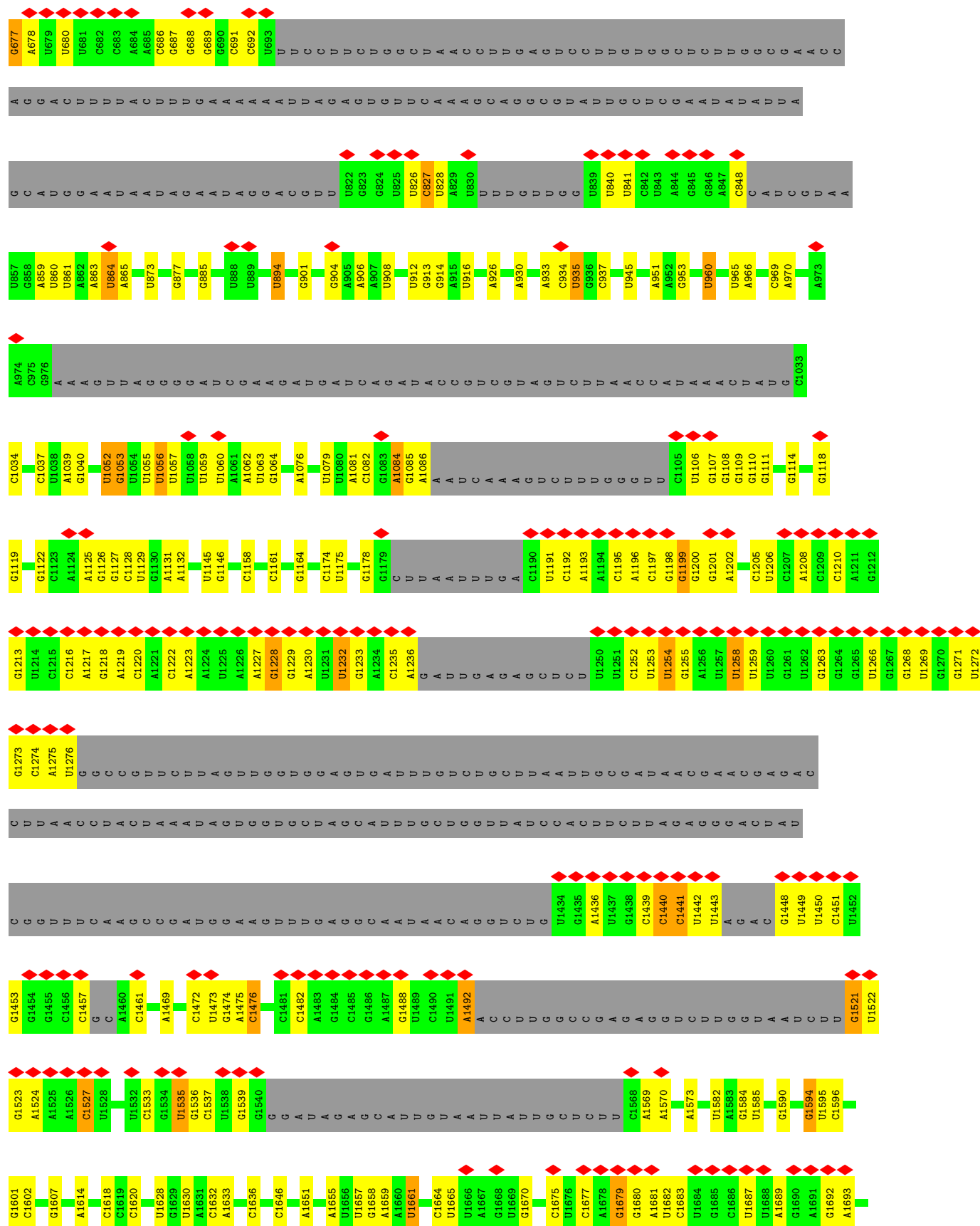
• Molecule 2: 5' ETS

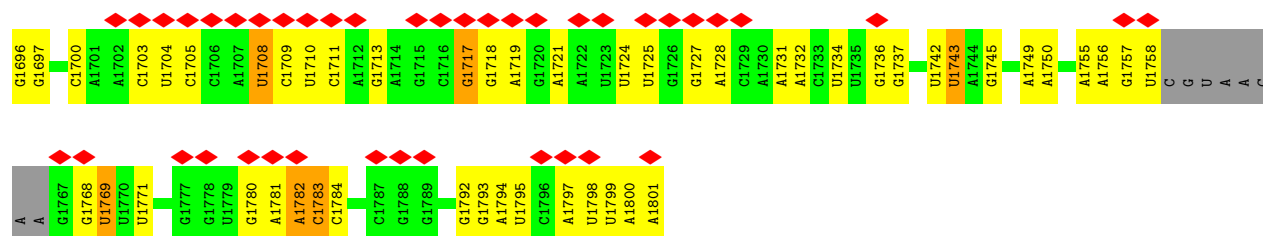




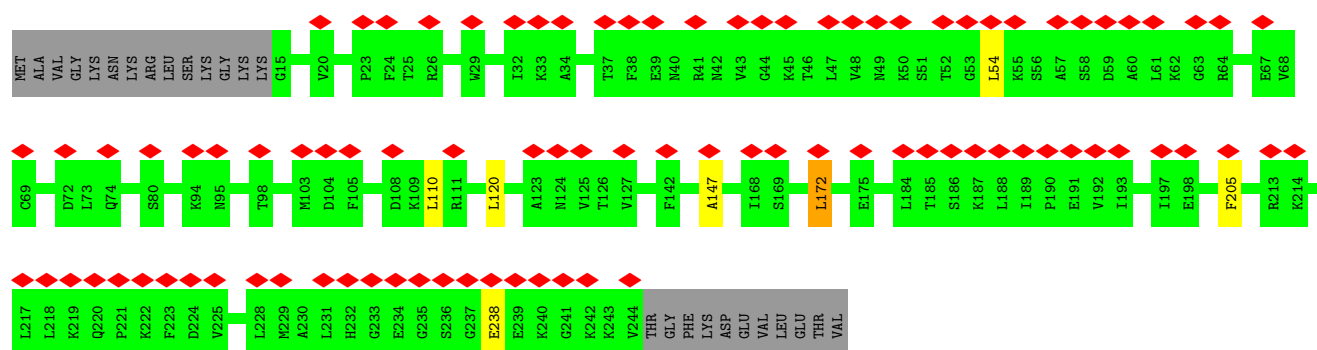
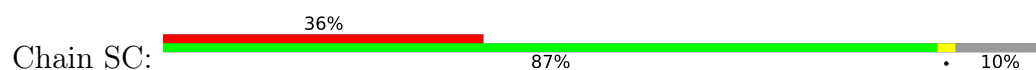
• Molecule 3: 18S pre-rRNA



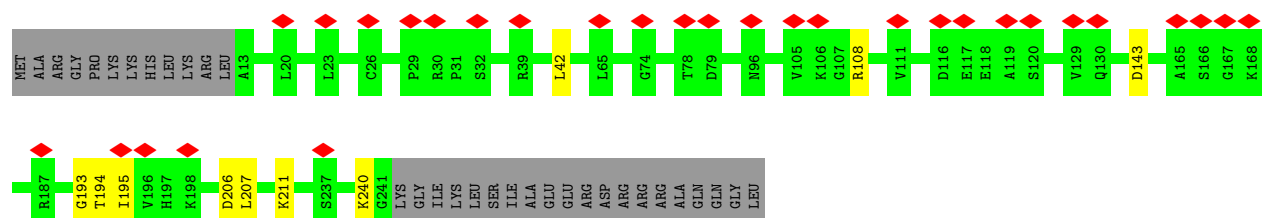
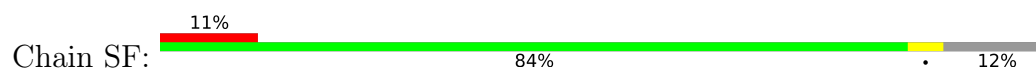




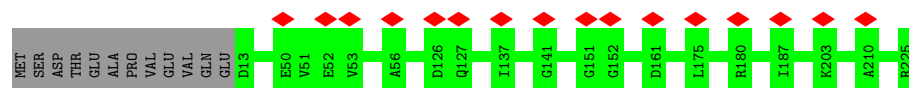
• Molecule 4: 40S ribosomal protein S1-A



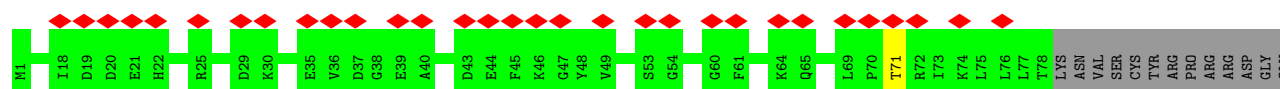
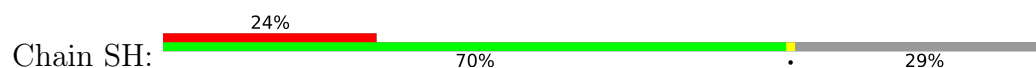
• Molecule 5: 40S ribosomal protein S4-A

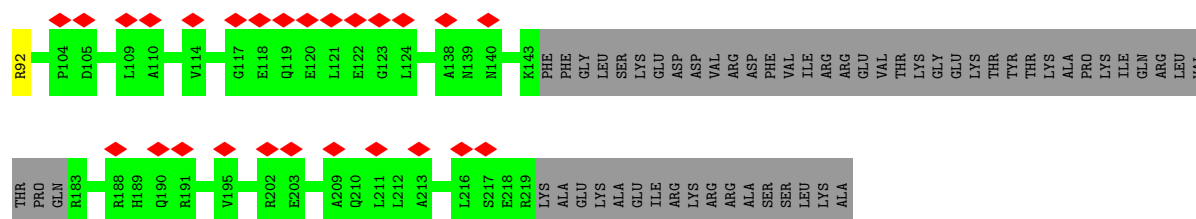


• Molecule 6: 40S ribosomal protein S5

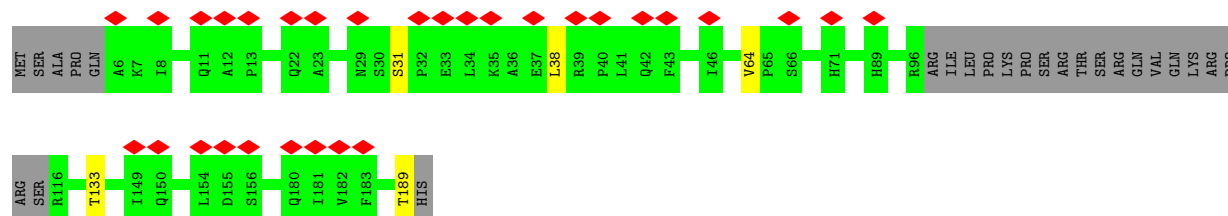
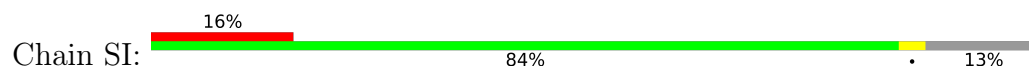


• Molecule 7: 40S ribosomal protein S6-A

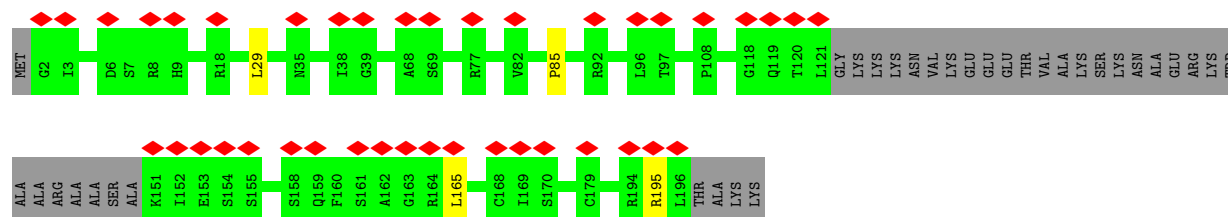
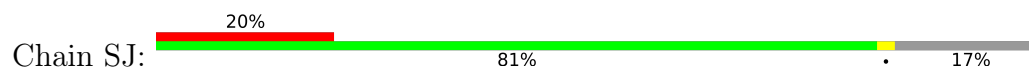




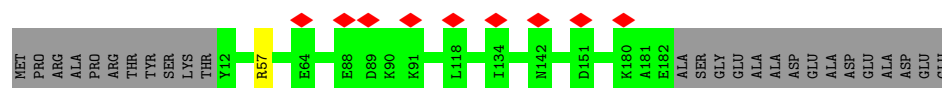
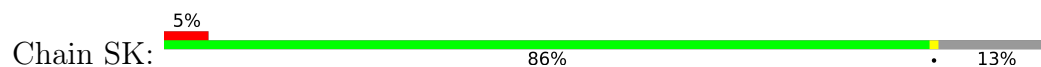
• Molecule 8: 40S ribosomal protein S7-A



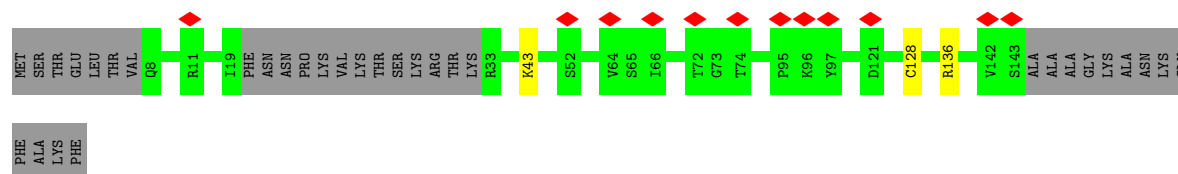
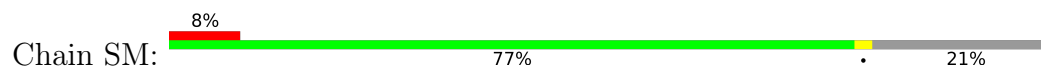
• Molecule 9: 40S ribosomal protein S8-A



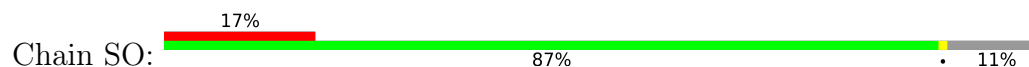
• Molecule 10: 40S ribosomal protein S9-A

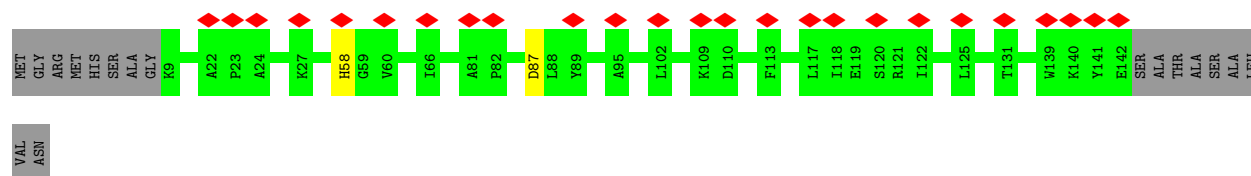


• Molecule 11: 40S ribosomal protein S11-A

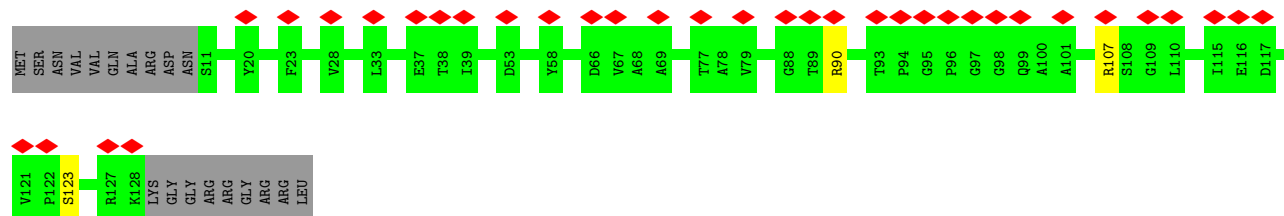
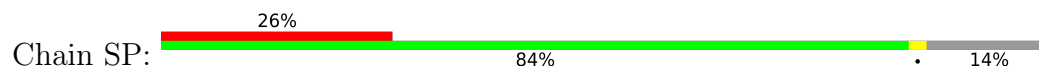


• Molecule 12: 40S ribosomal protein S13

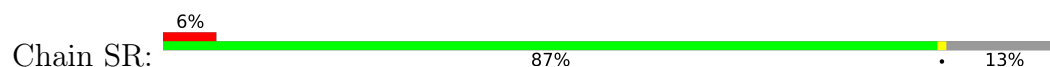




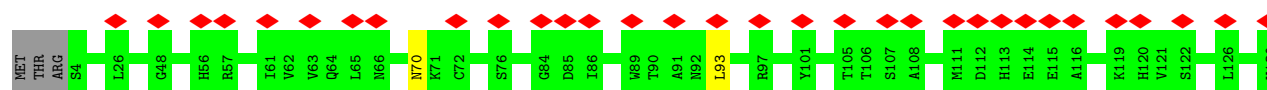
- Molecule 13: 40S ribosomal protein S14-A



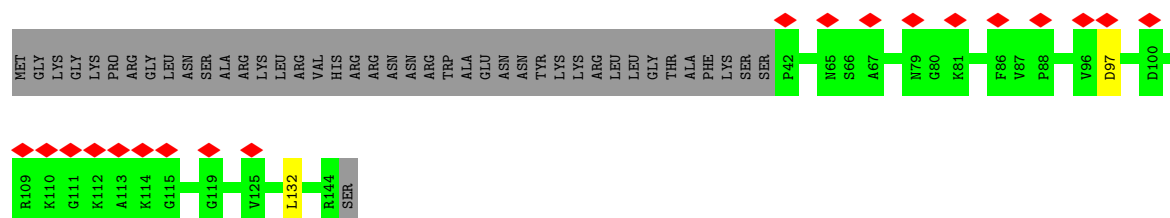
- Molecule 14: 40S ribosomal protein S16-A



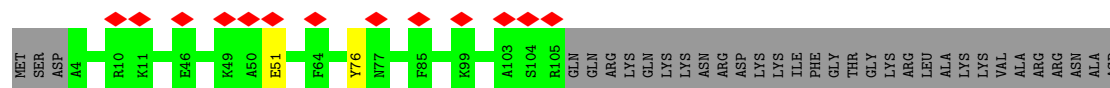
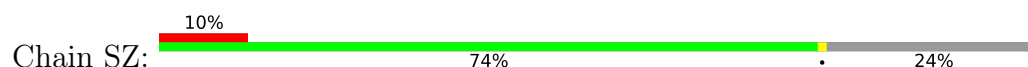
- Molecule 15: 40S ribosomal protein S22-B

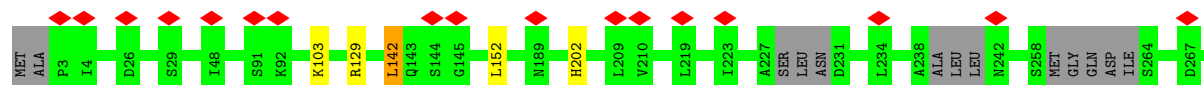
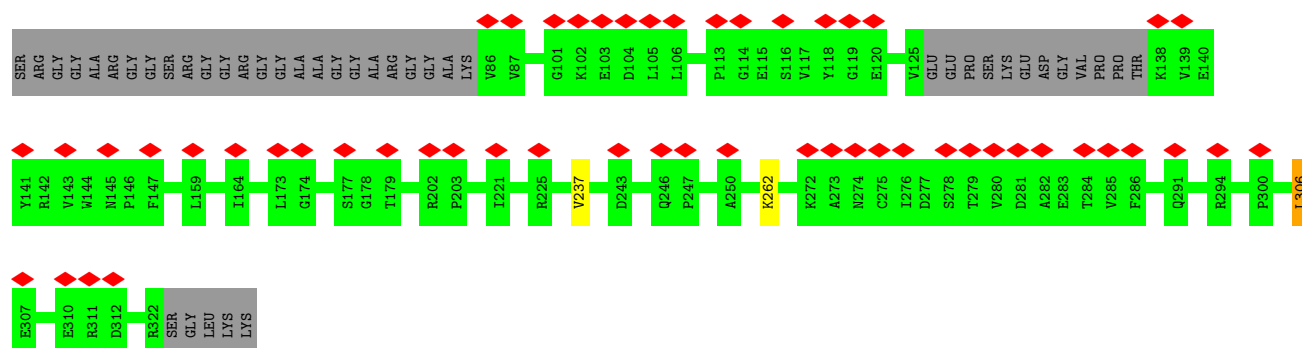
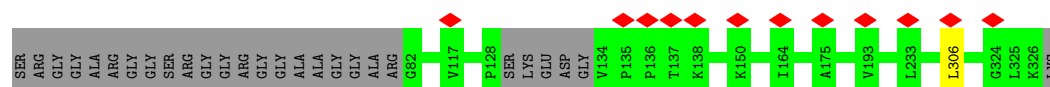
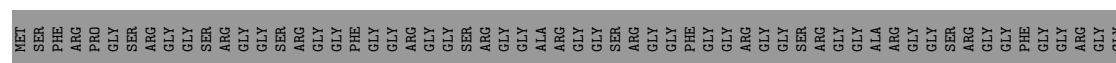
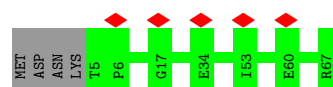
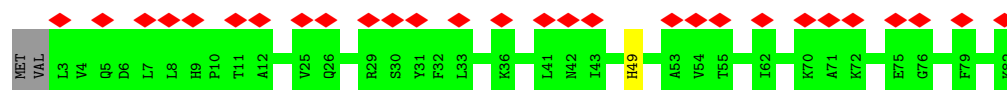


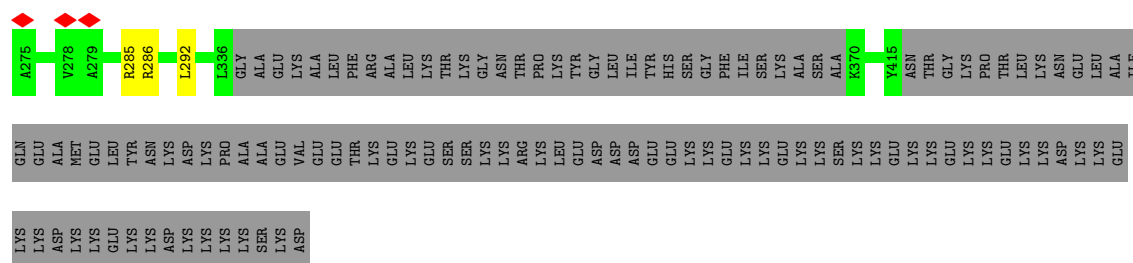
- Molecule 16: 40S ribosomal protein S23-A



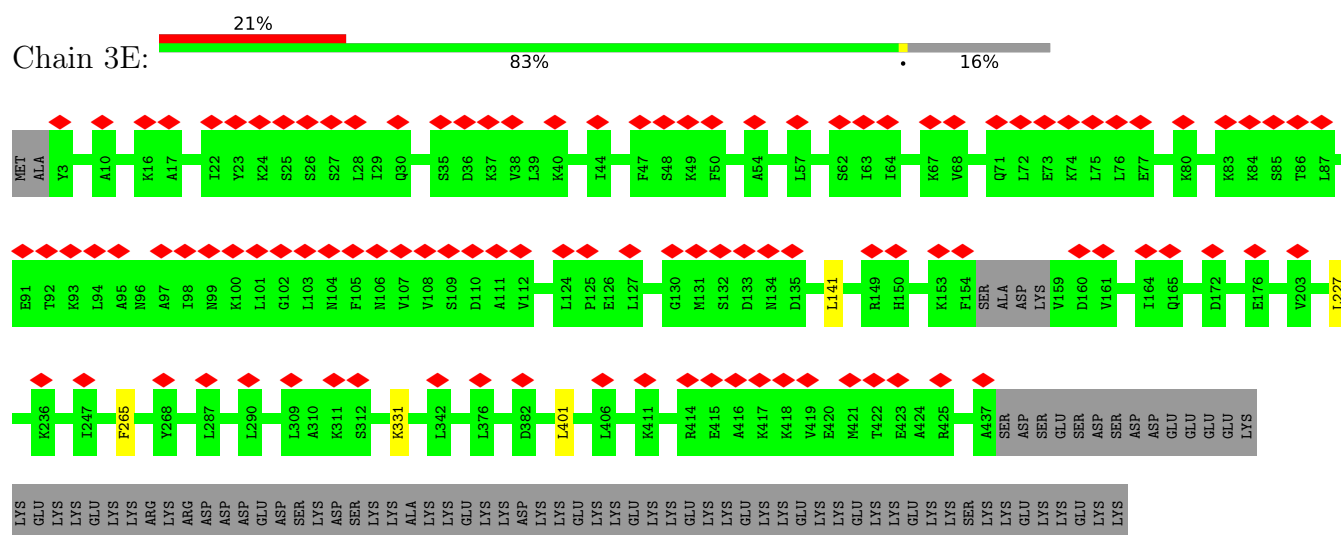
- Molecule 17: 40S ribosomal protein S24-A



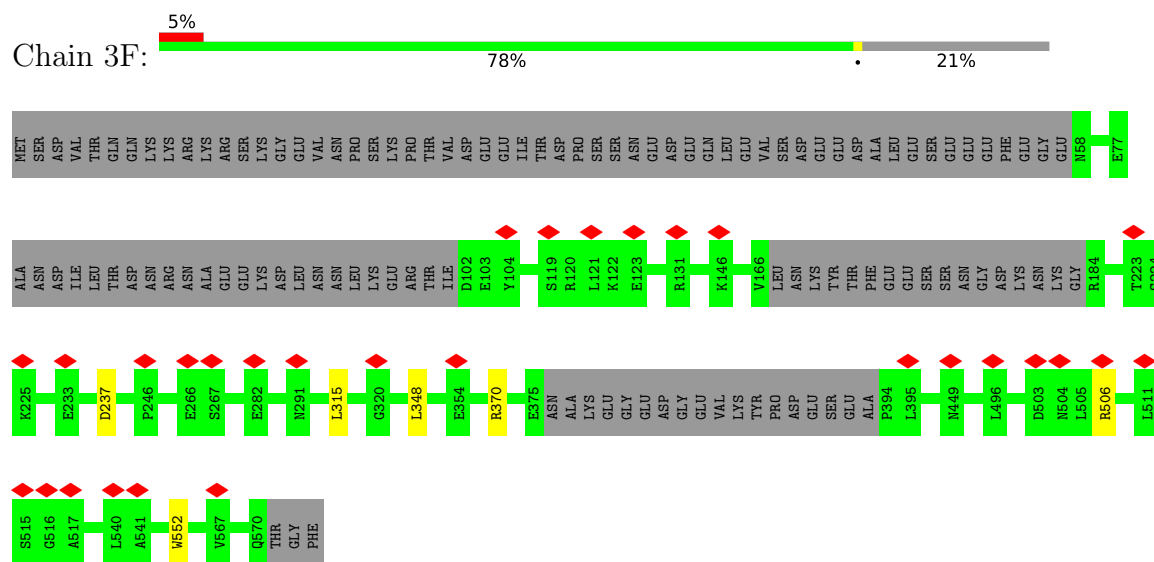




• Molecule 22: Nucleolar protein 58

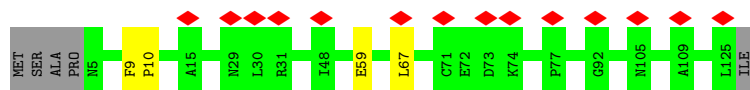


• Molecule 23: Ribosomal RNA-processing protein 9

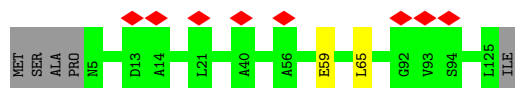


• Molecule 24: 13 kDa ribonucleoprotein-associated protein

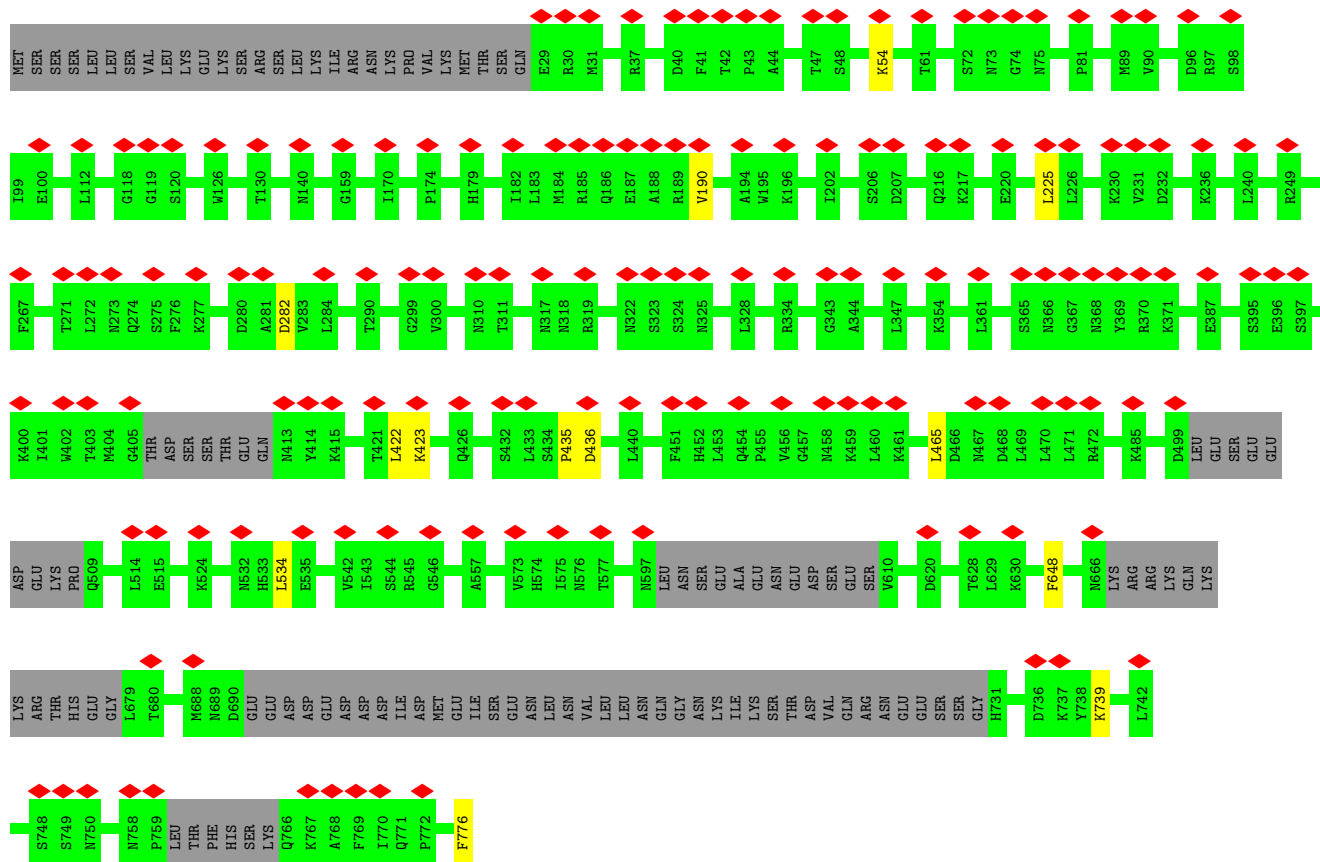
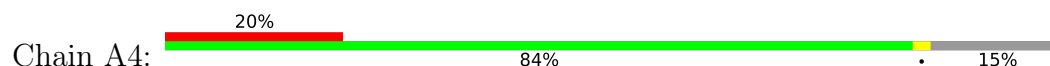




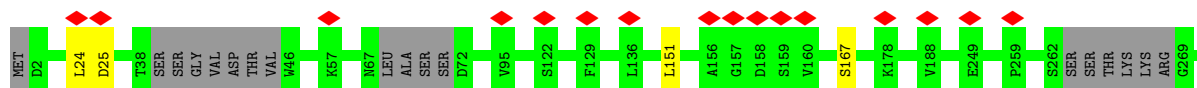
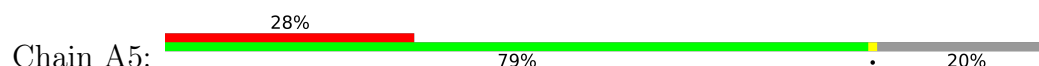
- Molecule 24: 13 kDa ribonucleoprotein-associated protein

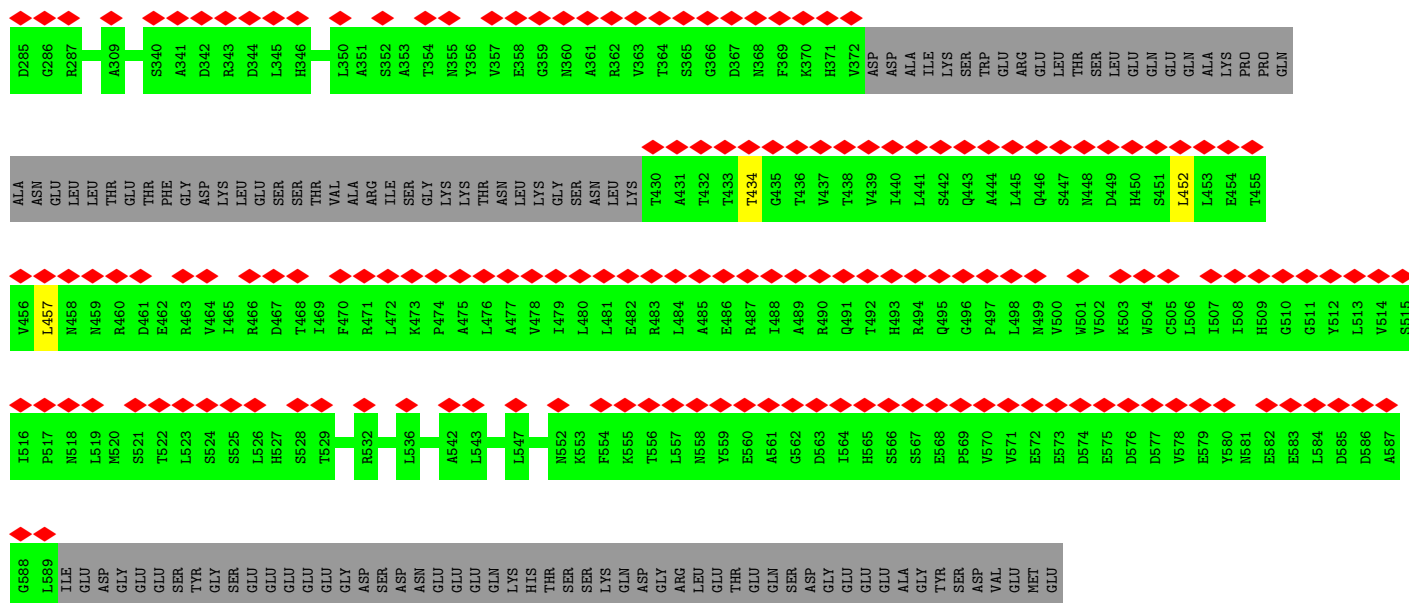


- Molecule 25: U3 small nucleolar RNA-associated protein 4

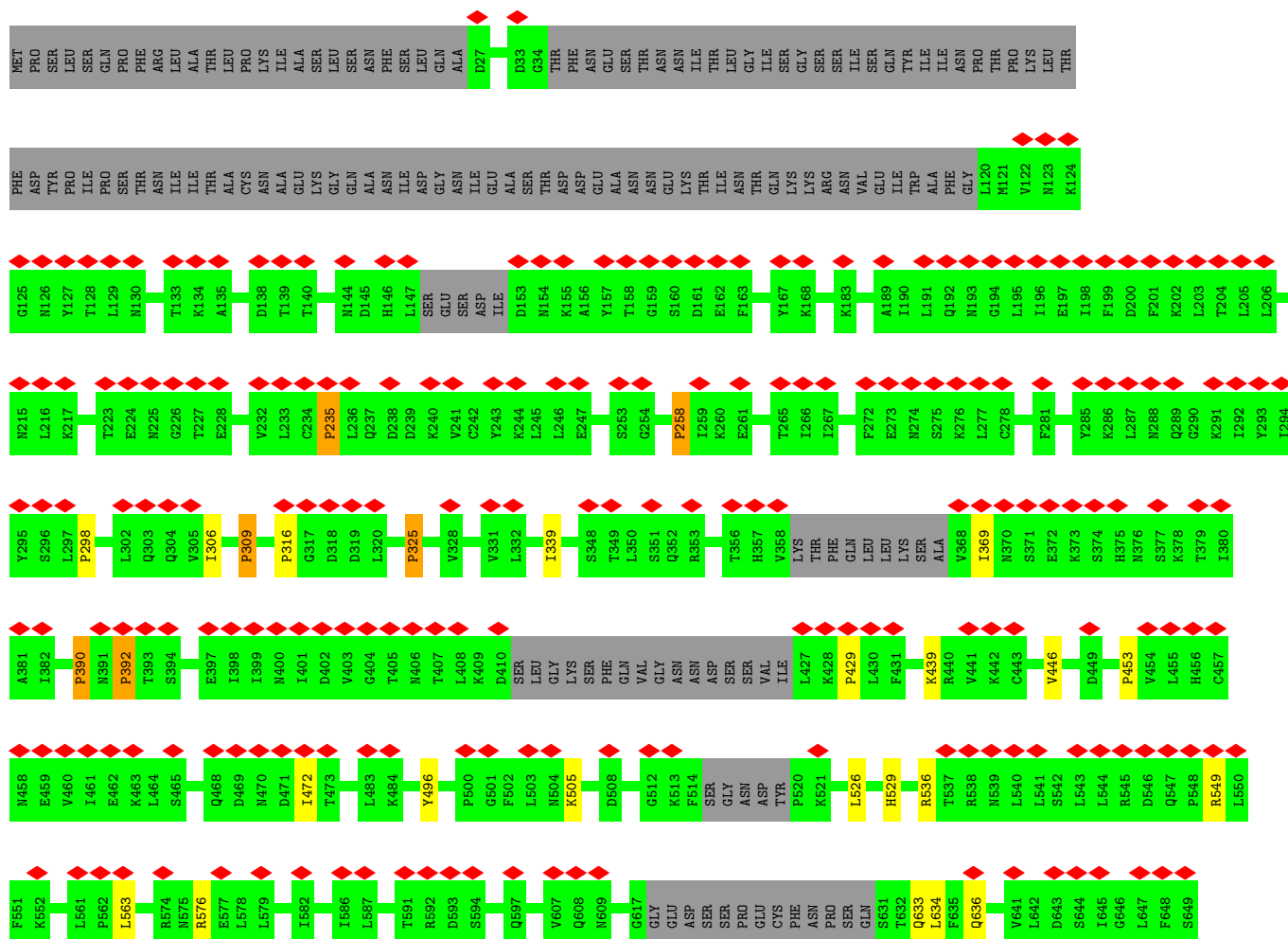
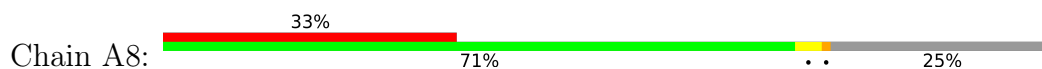


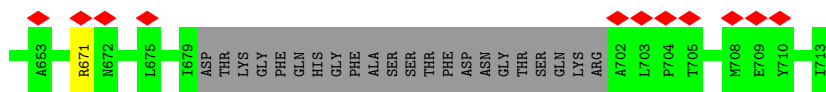
- Molecule 26: U3 small nucleolar RNA-associated protein 5



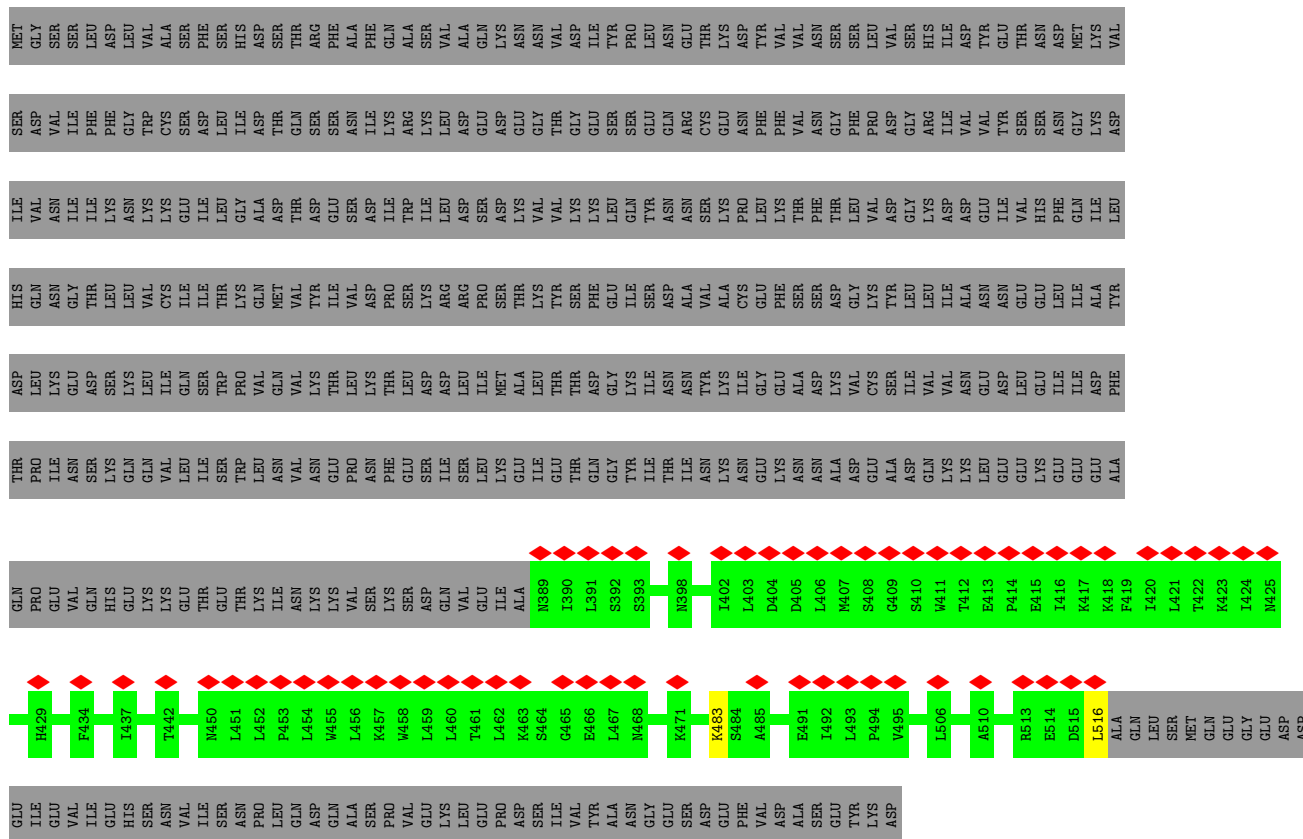


• Molecule 27: U3 small nucleolar RNA-associated protein 8

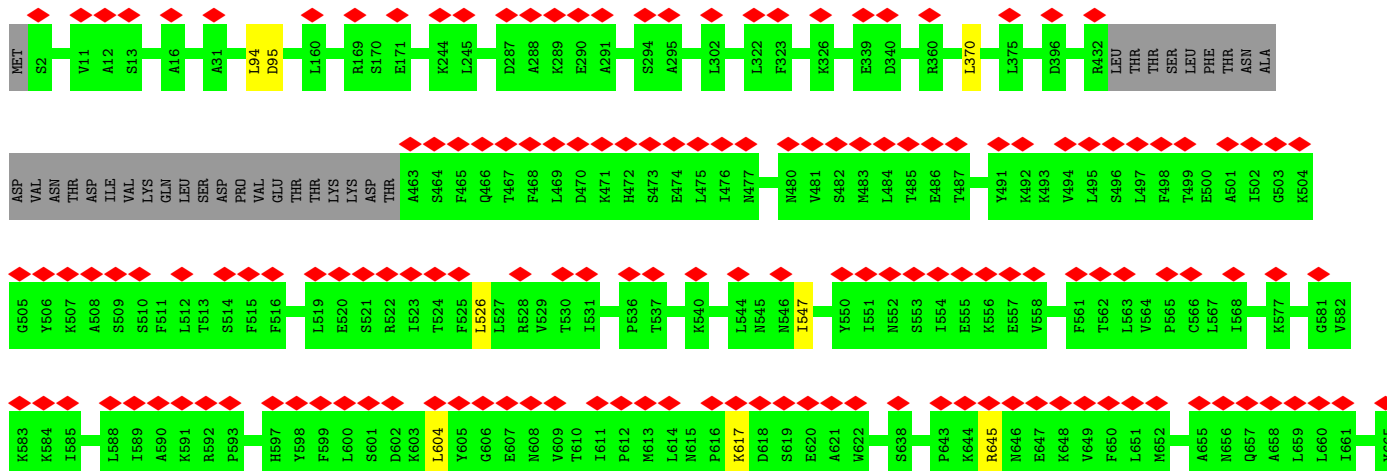
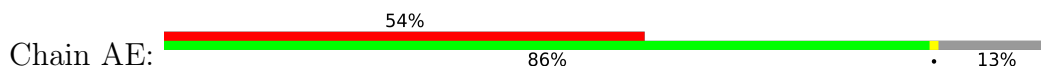




• Molecule 28: U3 small nucleolar RNA-associated protein 9



• Molecule 29: U3 small nucleolar RNA-associated protein 10



D1433	I1373	M1313	L1253	P1071	E1004	L943	LEU	ASN	A666
S1434	V1374	T1314	L1254	ILE	E1005	V944	SER	SER	K667
S1435	P1375	A1315	S1255	LYS	M1006	I945	ASP	ILE	T668
T1436	P1376	L1316	T1256	LEU	PHE	L946	GLU	ASN	T679
R1437	S1377	V1317	S1257	LEU	LEU	ALA	THR	GLU	Y680
S1438	I1378	S1318	T1258	VAL	LEU	THR	THR	MET	A681
S1439	K1379	L1319	M1259	ASP	LEU	LEU	ASP	GLN	S682
V1440	L1380	Y1320	E1260	LEU	SER	SER	THR	THR	S683
I1441	F1381	GLY	D1261	H1080	PHE	E954	ASP	ASP	Y684
S1442	D1382	LYS	I1262	V1081	THR	V955	THR	PHE	S685
L1443	A1383	LYS	E1083	N1082	ALA	I956	SER	SER	S686
I1444	S1384	LEU	E1084	E1084	LEU	L957	LYS	LYS	L687
I1445	L1385	GLU	H1085	L1085	GLN	H958	ARG	ARG	F688
I1446	A1386	G1266	S1086	S1086	ASP	S959	ARG	ARG	E689
I1447	L1387	L1267	G1087	G1087	V1020	V960	ARG	ARG	E690
I1448	S1388	T1267	L1088	L1088	R1024	M961	E896	T830	S693
D1449	S1389	V1269	M1089	M1089	R1025	P962	T897	S631	H694
L1450	M1390	I1270	D1090	D1090	V1026	I963	L898	K632	Y695
K1451	P1391	Q1331	L1091	L1091	K1027	F964	I899	N633	L696
E1452	L1392	S1213	D1092	D1092	L1028	T965	SER	CYS	R699
V1453	K1393	T1334	L1093	L1093	F1029	F966	THR	ASN	S700
E1454	E1394	L1335	I1094	I1094	S1030	M967	LEU	THR	S701
K1455	Q1395	A1336	I1095	I1095	T1031	G968	THR	ASN	W702
V1456	L1396	T1337	K1096	K1096	L1032	ALA	ILE	ILE	E703
L1457	Q1397	E1338	L1097	L1097	LYS	HIS	THR	GLN	K704
F1458	V1398	K1339	L1098	L1098	THR	SER	THR	GLN	T711
R1459	A1399	V1340	T1099	T1099	ILE	ILE	THR	ALA	E714
I1460	I1400	S1341	S1100	S1100	ARG	ARG	GLU	LEU	H715
M1461	L1401	S1342	S1101	S1101	GLN	VAL	LEU	LEU	F716
S1462	L1402	D1343	V1165	V1165	ASP	VAL	LEU	LEU	E717
T1463	L1403	M1344	L1166	L1166	ASP	THR	LEU	LEU	S719
E1464	F1404	T1345	LEU	LEU	A1041	PHE	ASP	GLU	L720
I1465	A1405	E1346	ASP	ASP	L1039	THR	THR	ASP	V721
G1466	G1406	V1347	GLU	GLU	A1042	THR	THR	ASP	W722
L1467	L1407	K1348	THR	THR	I1049	THR	THR	THR	L723
S1468	I1408	I1349	D1172	D1172	ALA	VAL	THR	THR	V724
L1469	K1409	S1350	K1173	K1173	GLN	GLU	VAL	VAL	S725
D1470	R1410	S1351	K1174	K1174	TVR	ARG	ARG	ARG	K727
T1471	I1411	L1352	L1175	L1175	SER	THR	THR	THR	E728
V1472	P1412	A1353	I1176	I1176	ALA	THR	THR	THR	K729
A1473	S1413	L1354	R1177	R1177	L1057	VAL	VAL	VAL	F732
V1474	F1414	I1355	N1178	N1178	V1058	P992	P992	P992	M733
S1475	L1415	T1356	I1179	I1179	N1059	A993	A993	A993	I734
M1476	M1416	N1357	R1180	R1180	F1060	I995	I995	I995	D735
F1477	S1417	C1358	GLU	GLU	K1061	K996	K996	K996	F736
L1478	N1418	V1359	PHE	PHE	I1062	N997	N997	N997	V737
S1479	I1419	Q1360	GLY	GLY	E1063	S998	S998	S998	A740
T1480	L1420	L1361	THR	THR	A1064	K999	K999	K999	L741
L1481	D1421	L1362	LEU	LEU	E1065	G1000	G1000	G1000	N742
E1482	V1422	G1363	ASP	ASP	R1066	E1002	E1002	E1002	S743
S1483	L1423	V1364	PHE	PHE	L1067	I1069	I1069	I1069	Q808
T1484	H1424	K1365	GLU	GLU	L1068	LEU	LEU	LEU	
V1425	V1425	S1366	VAL	VAL	E1070				
I1426	I1426	I1367	LEU	LEU					
N1487	Y1427	A1368							
F1428	F1428	F1369							
S1429	S1429	Y1370							
K1490	K1490	P1371							
K1491	K1491	K1372							
S1492	S1492								





Response	Percentage
Yes	84%
No	14%

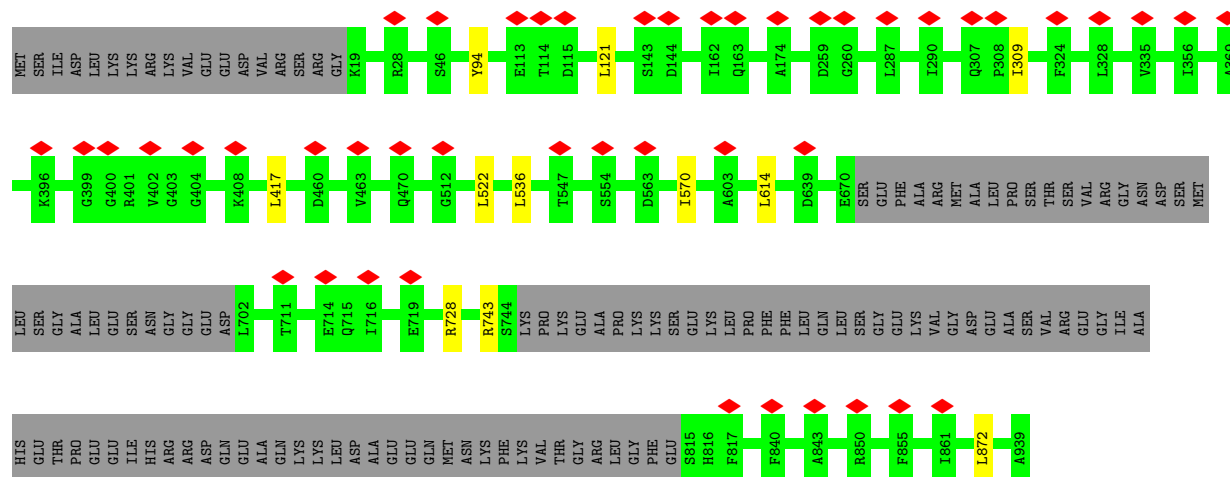
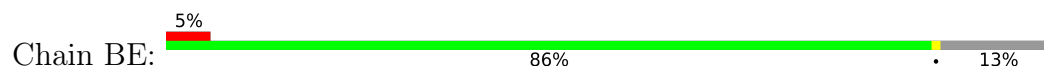


9% 86% 13%

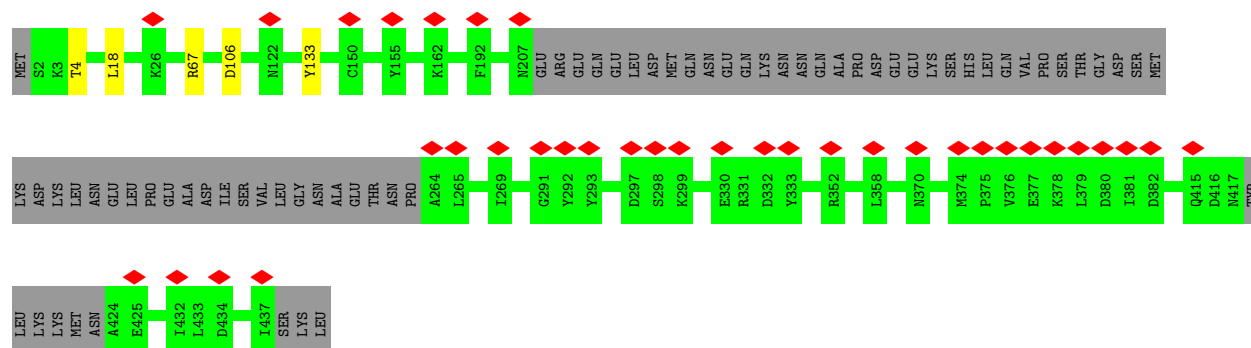
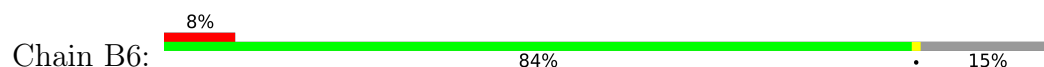




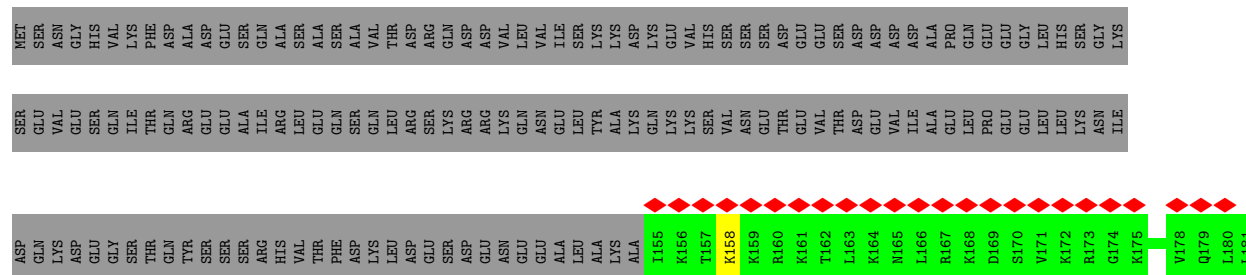
- Molecule 36: U3 small nucleolar RNA-associated protein 21

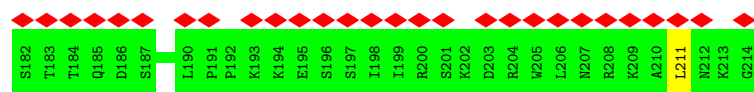


- Molecule 37: U3 small nucleolar RNA-associated protein 6

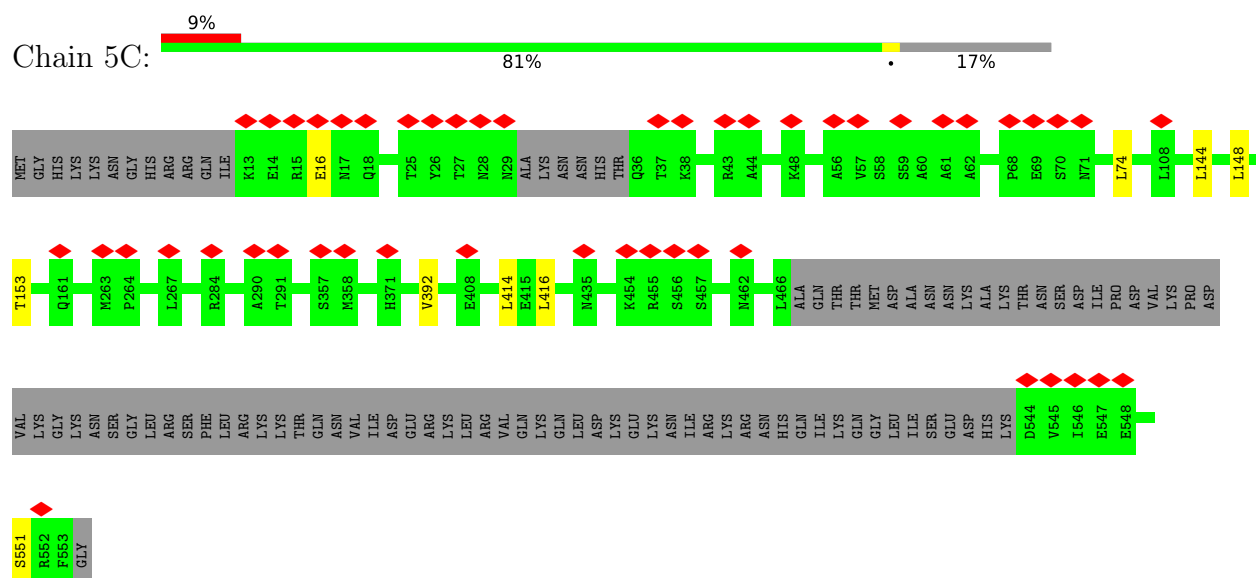


- Molecule 38: Bud site selection protein 21

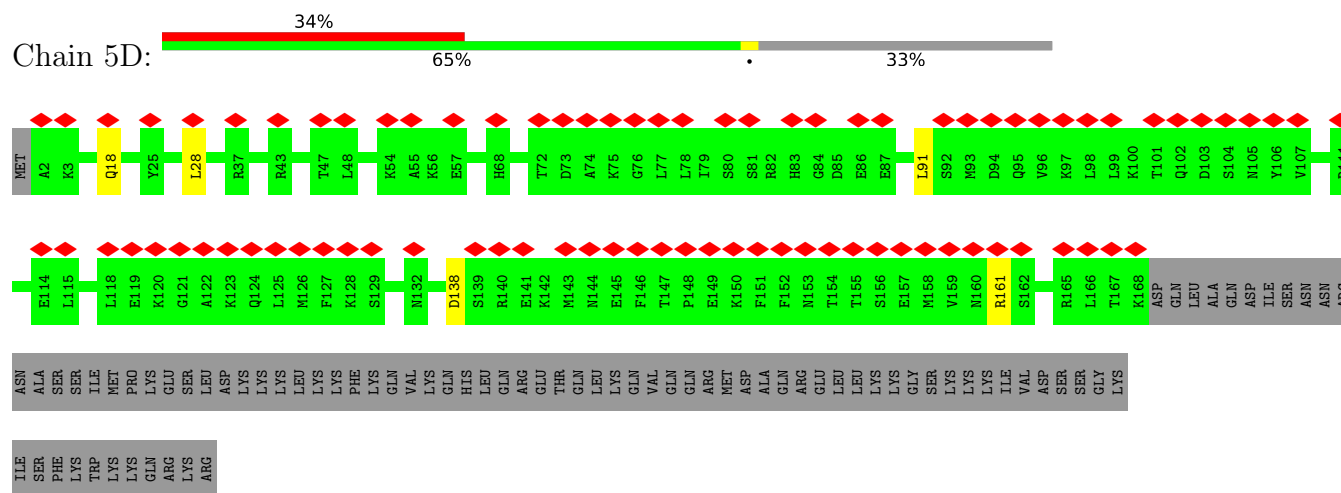




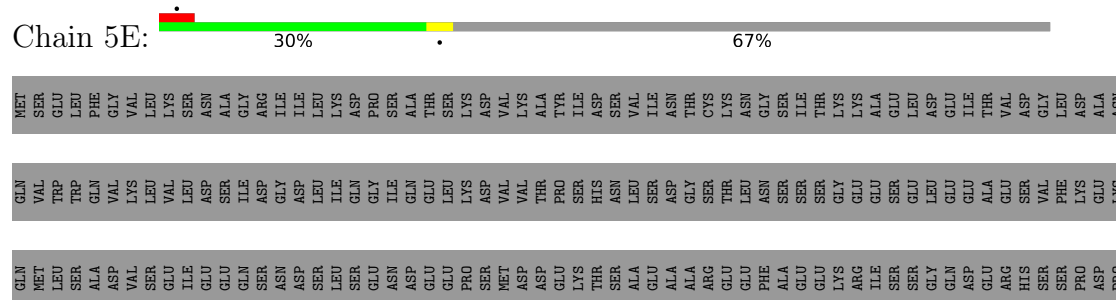
• Molecule 39: U3 small nucleolar RNA-associated protein 7



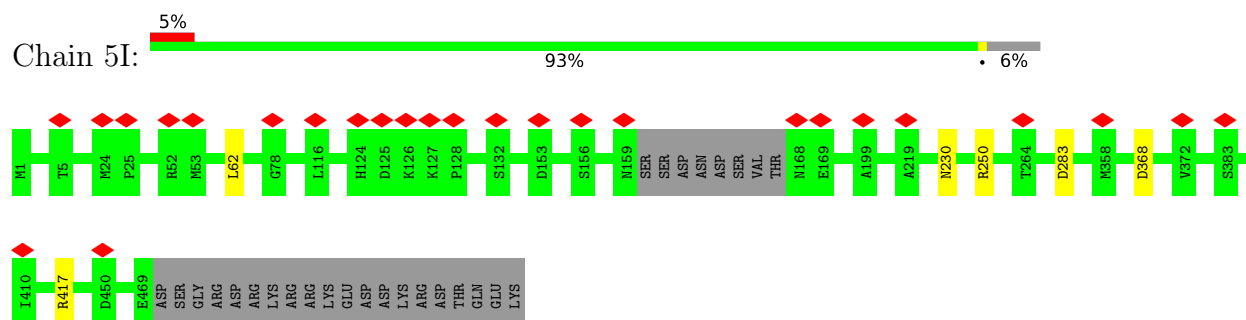
• Molecule 40: U3 small nucleolar RNA-associated protein 11



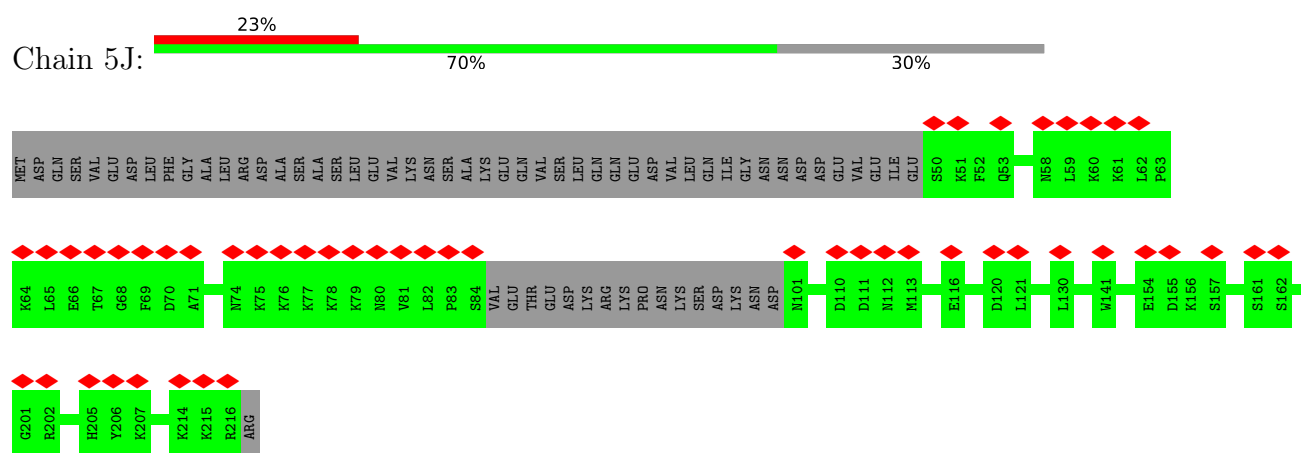
• Molecule 41: U3 small nucleolar RNA-associated protein MPP10



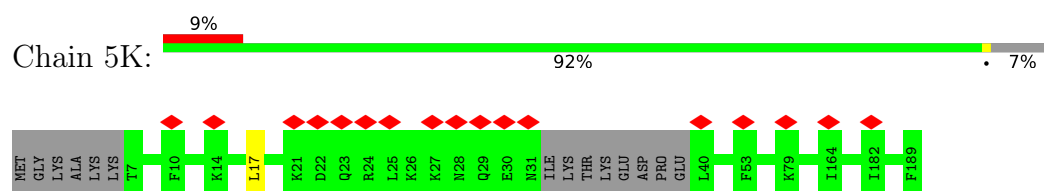
- Molecule 45: Protein SOF1



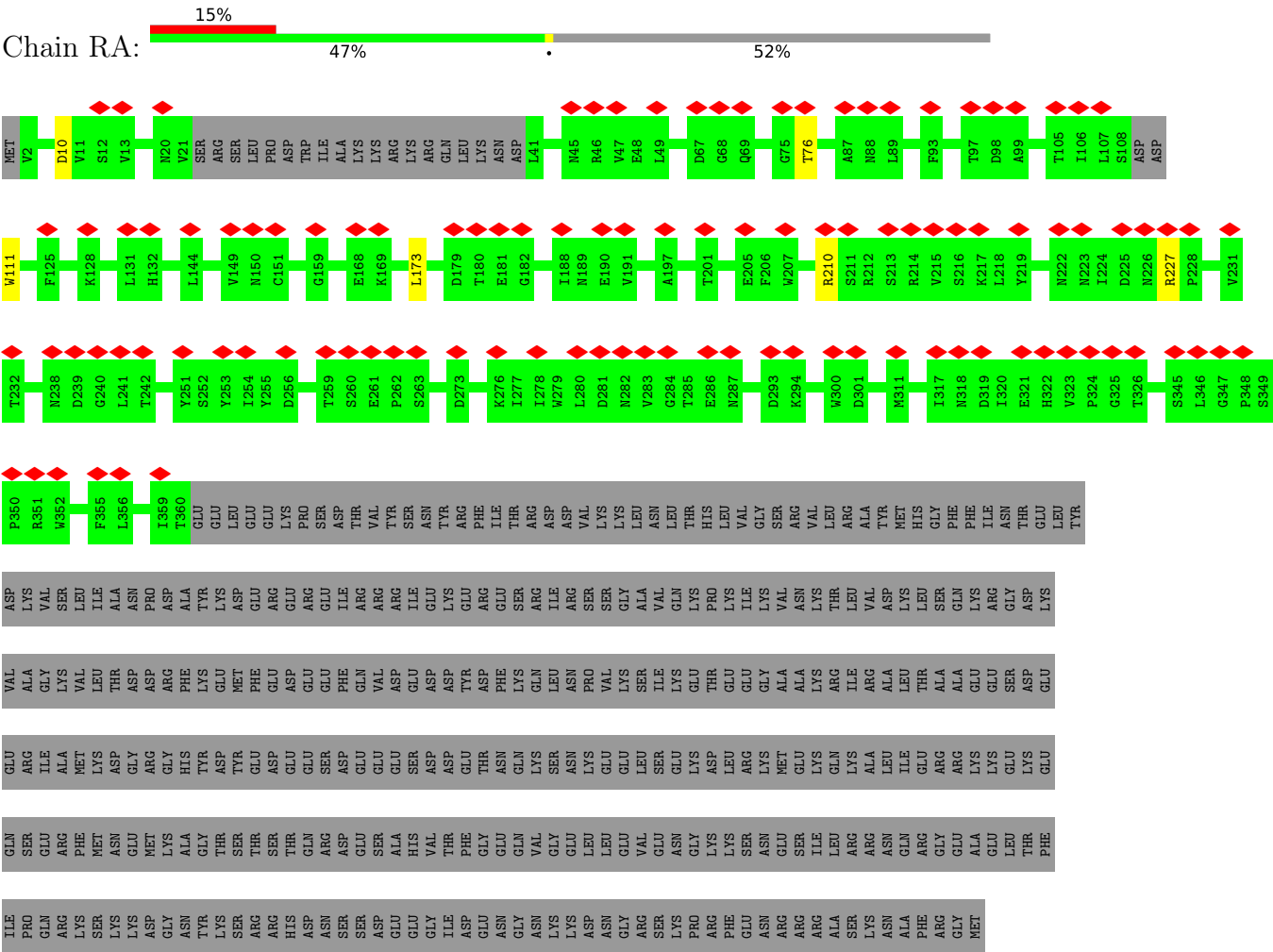
- Molecule 46: rRNA-processing protein FCF2



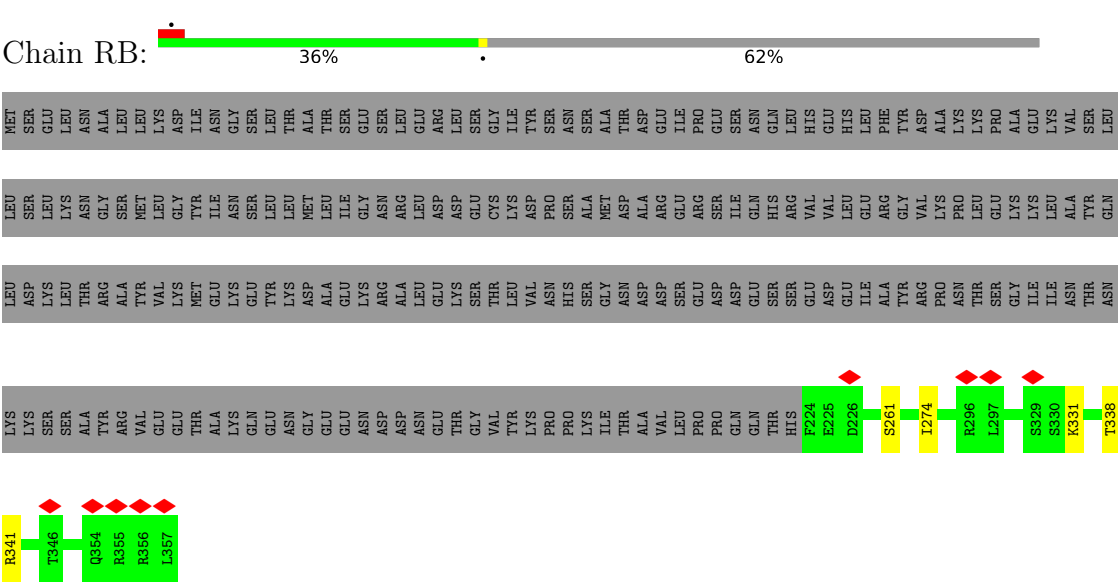
- Molecule 47: rRNA-processing protein FCF1



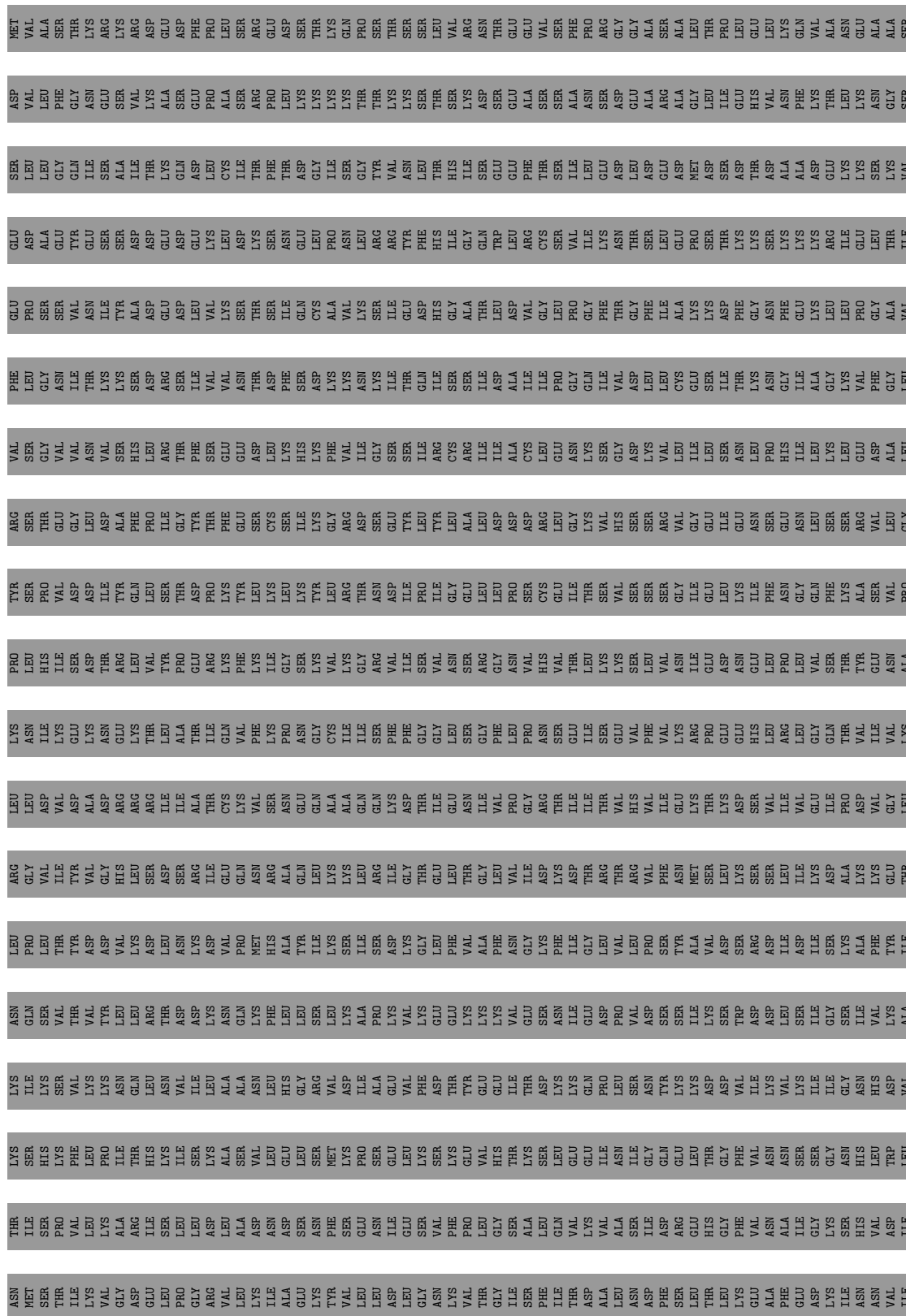
● Molecule 48: Ribosome biogenesis protein ENP2

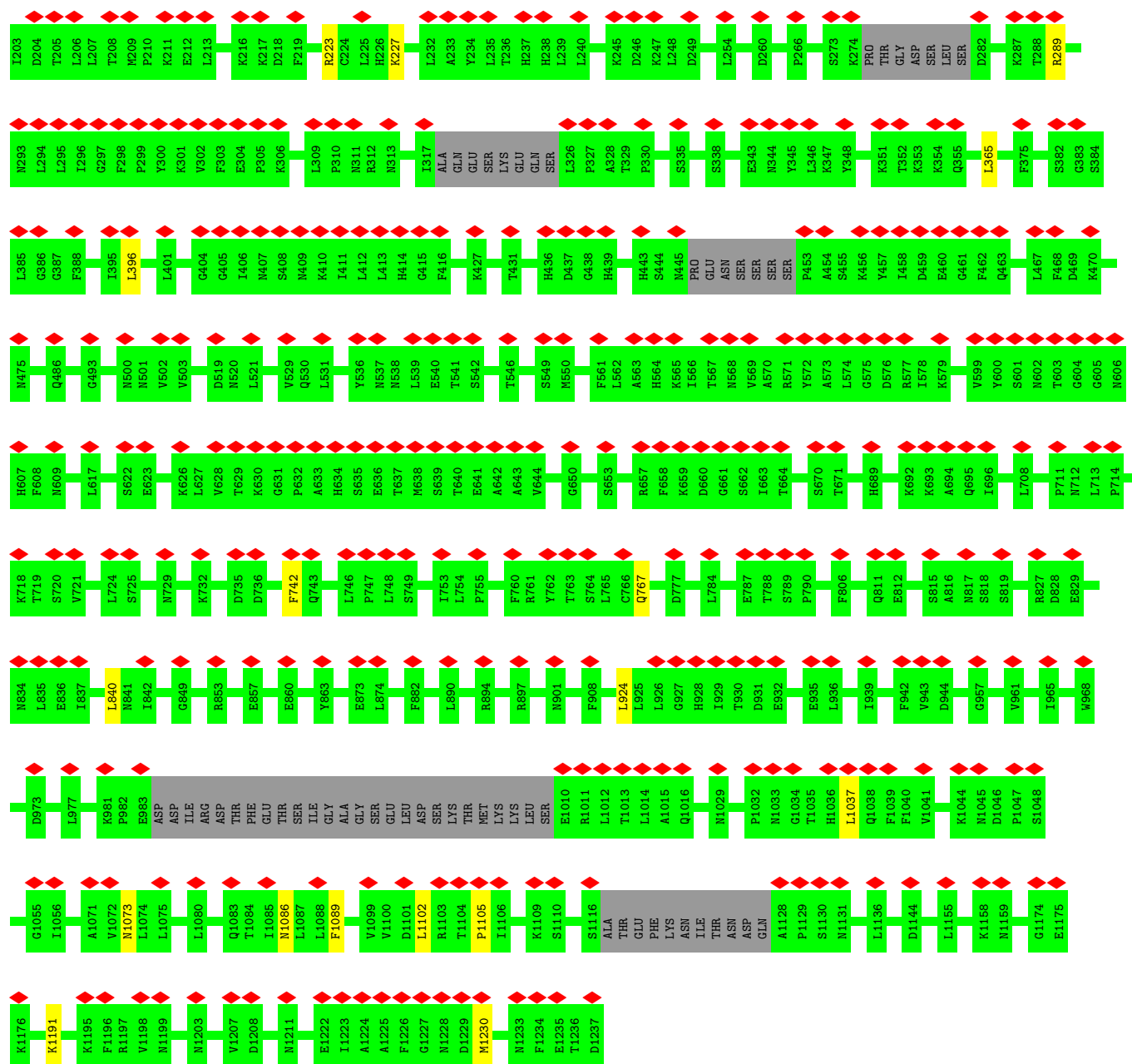


● Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

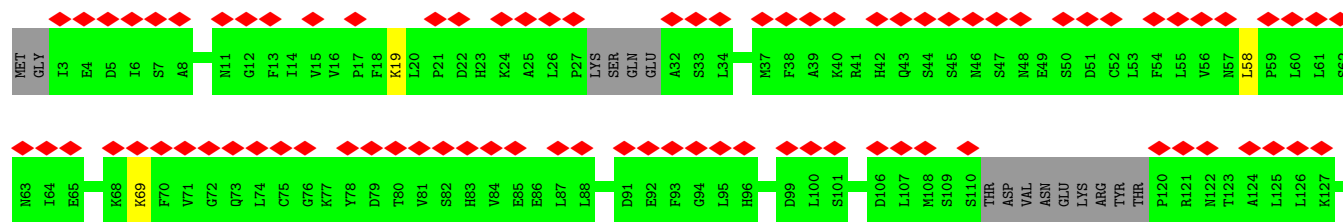
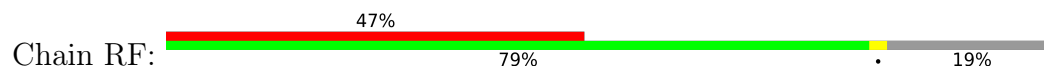


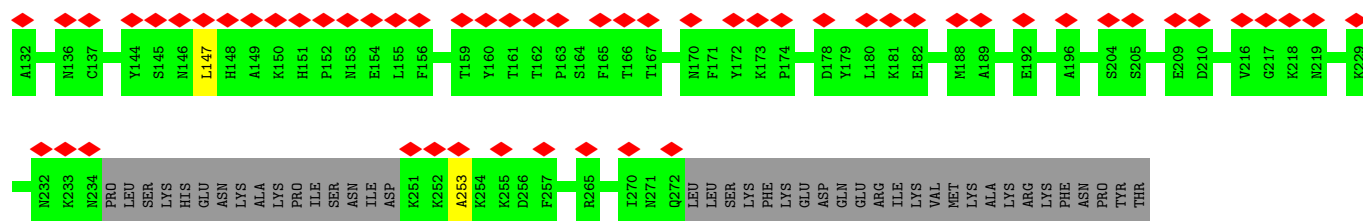
● Molecule 50: rRNA biogenesis protein RRP5





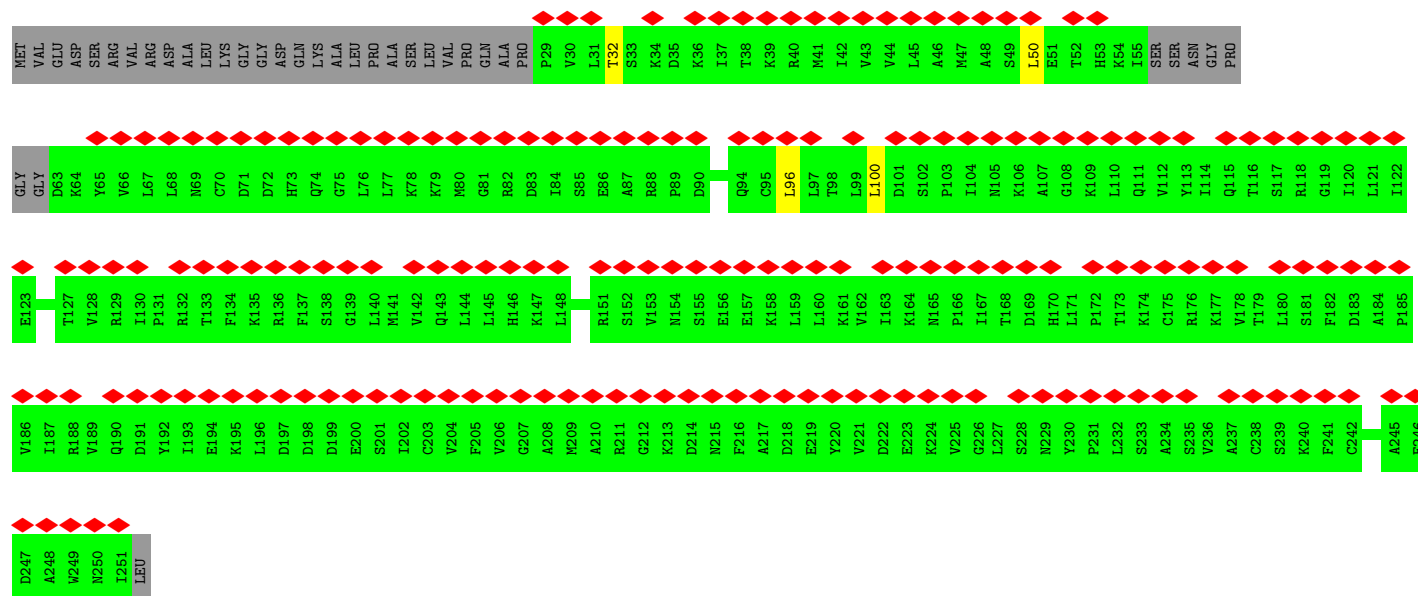
• Molecule 52: Ribosomal RNA-processing protein 7





• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

Chain RG: 74% 84% 14%

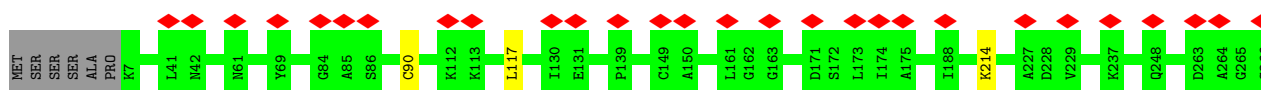


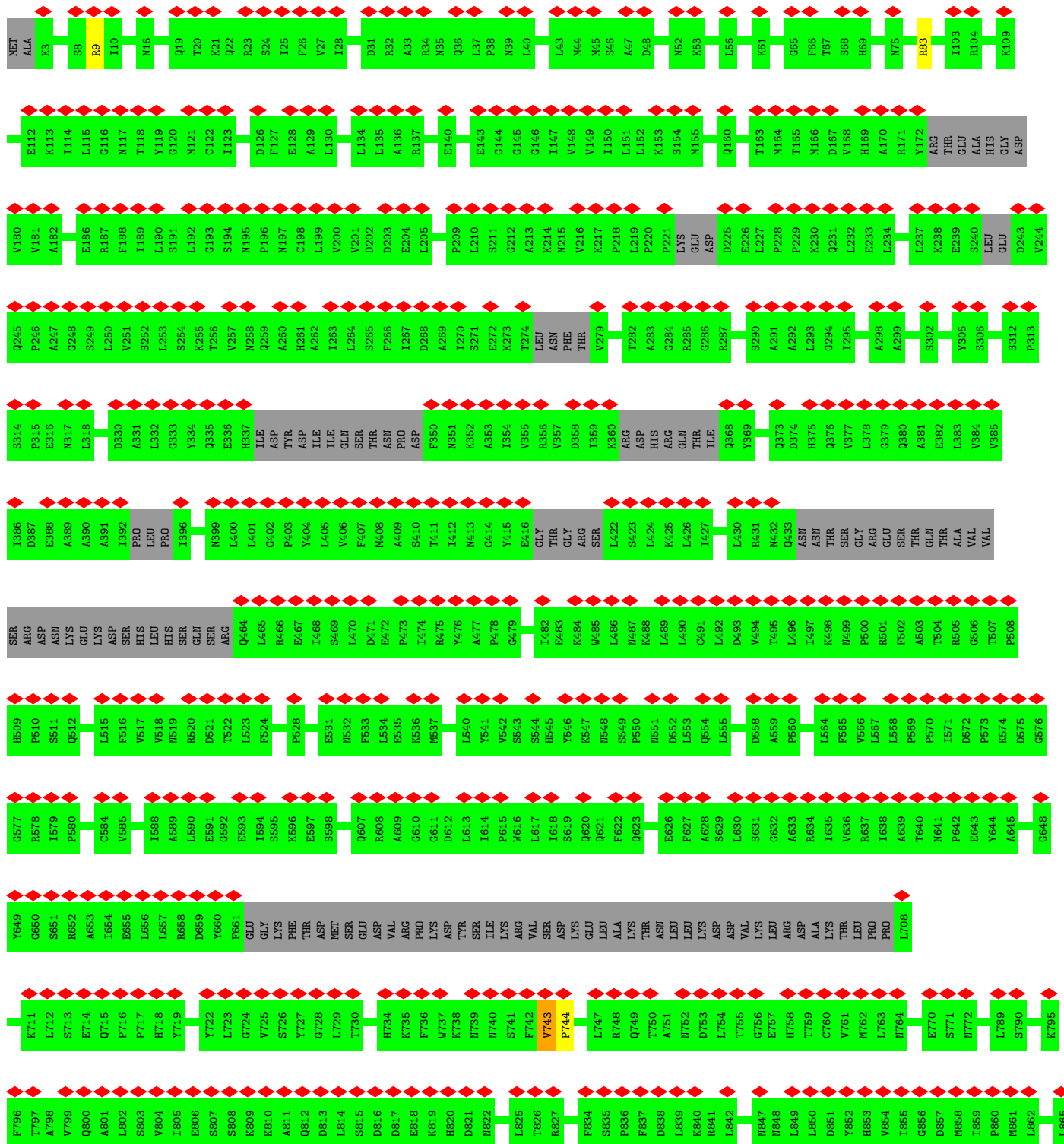
• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

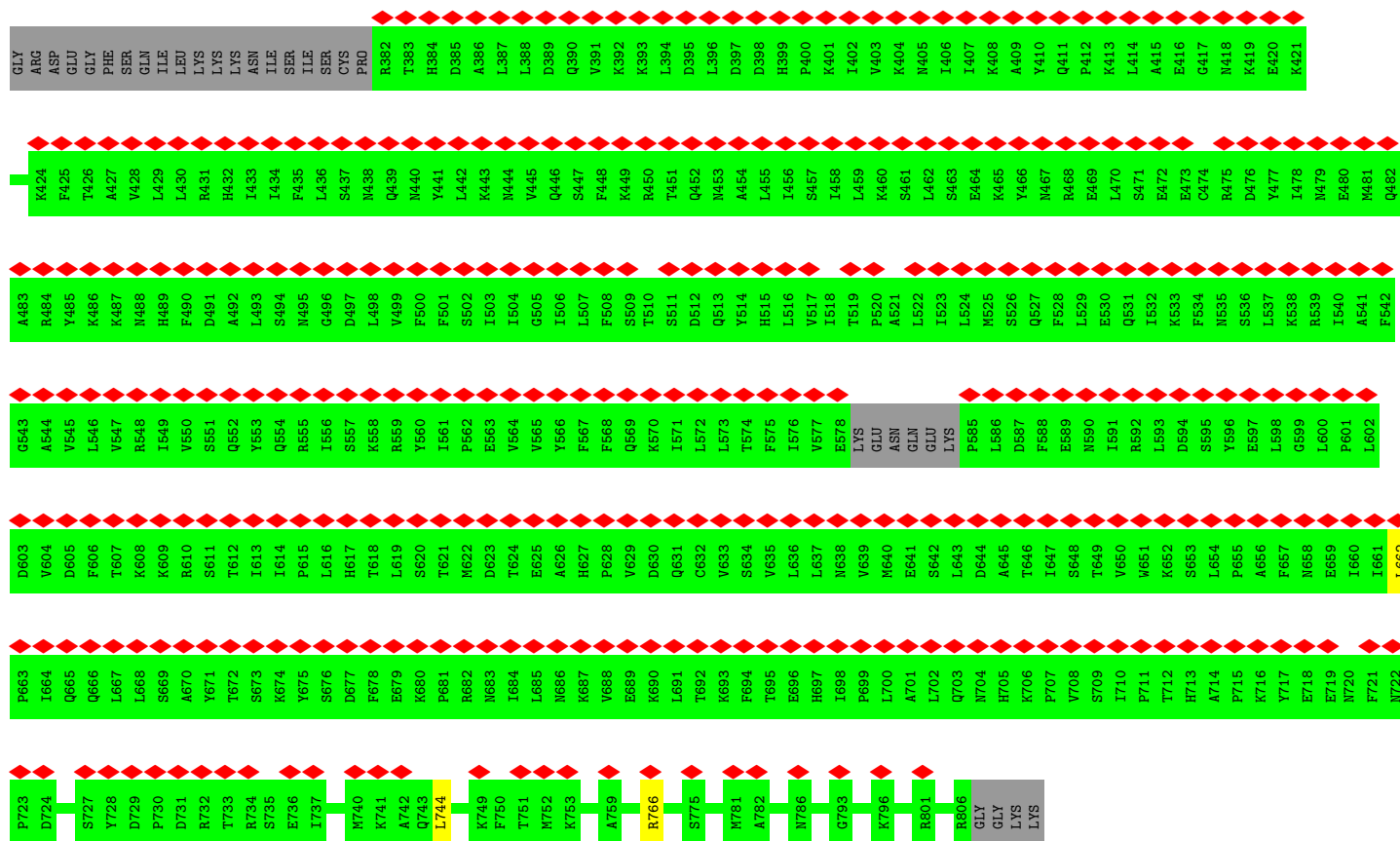
Chain RH: 76% 90% 9%



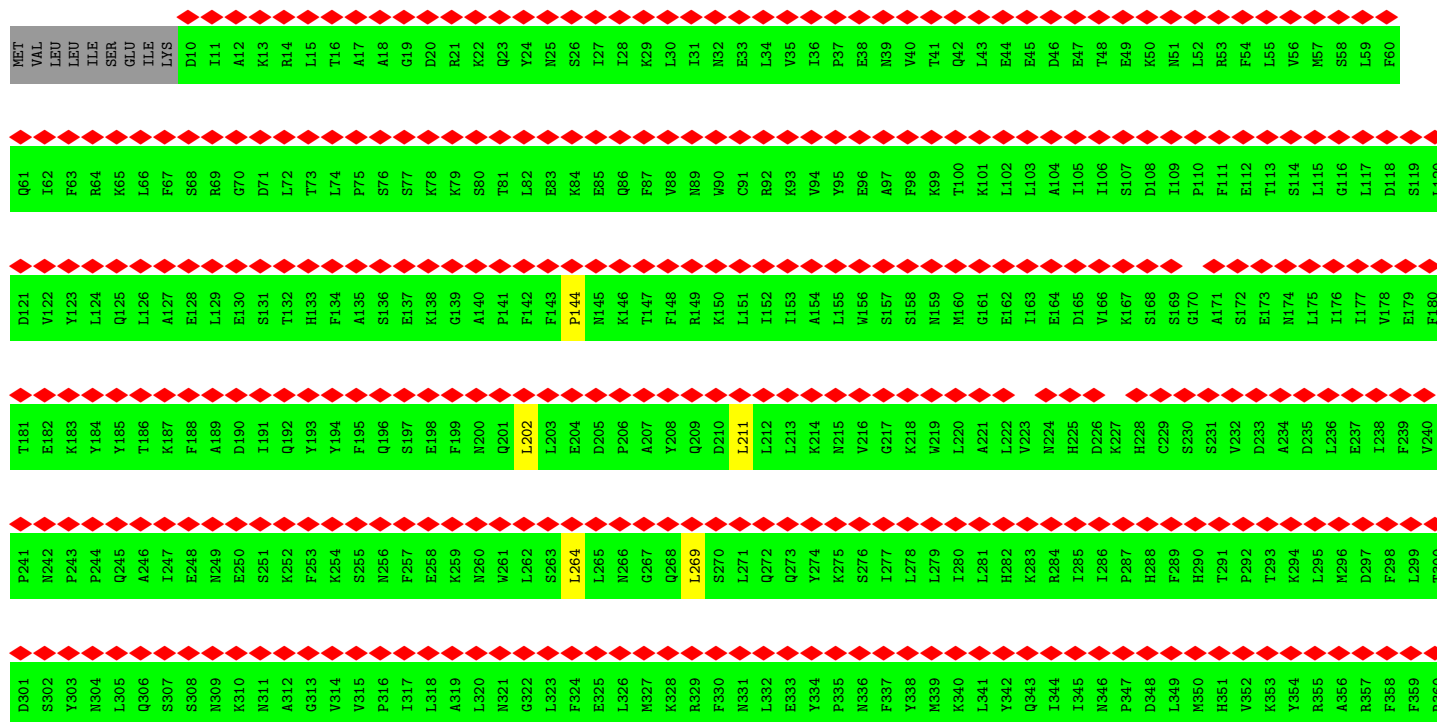
Chain RJ:



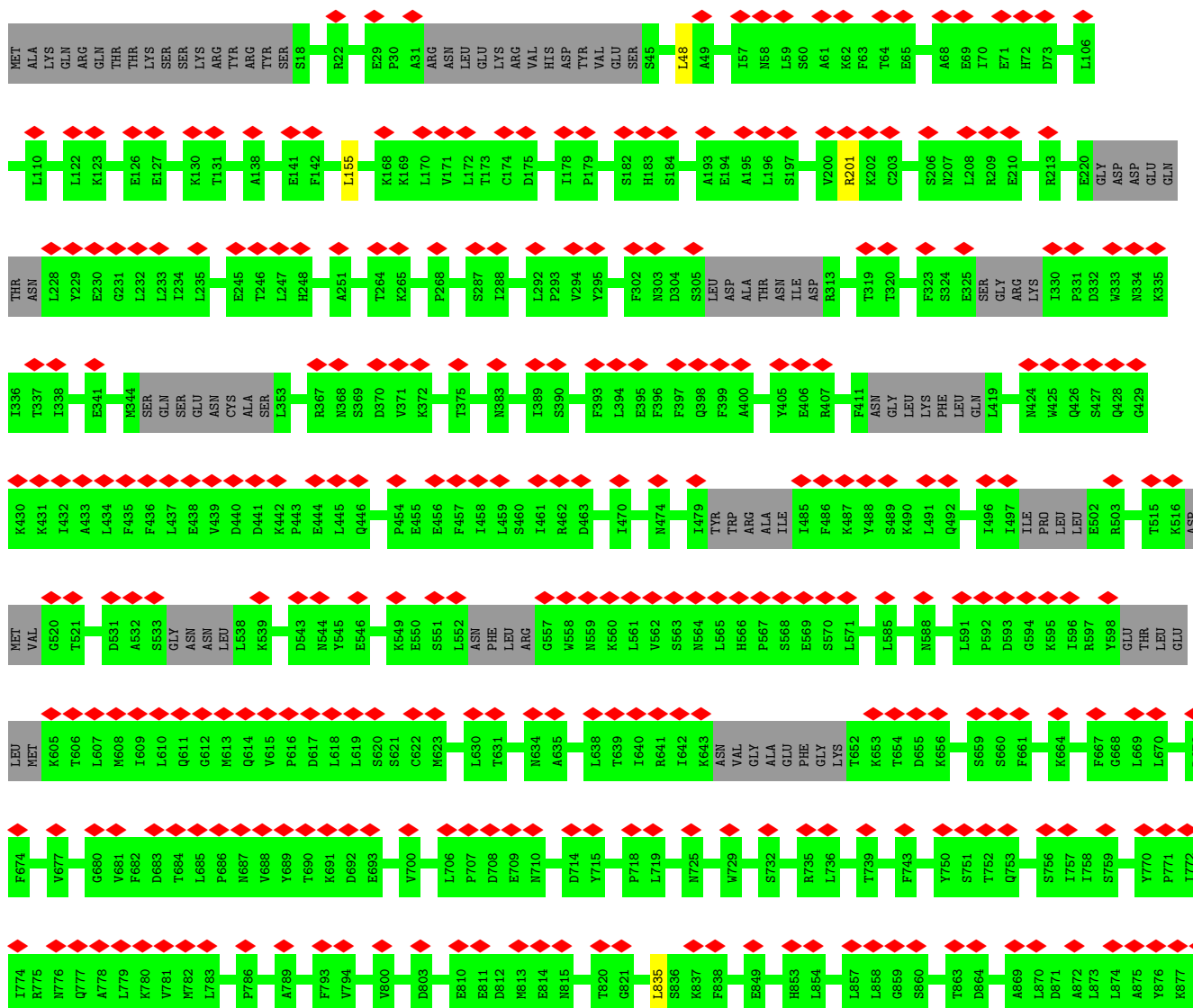
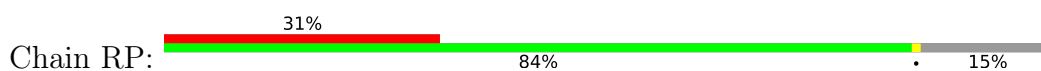


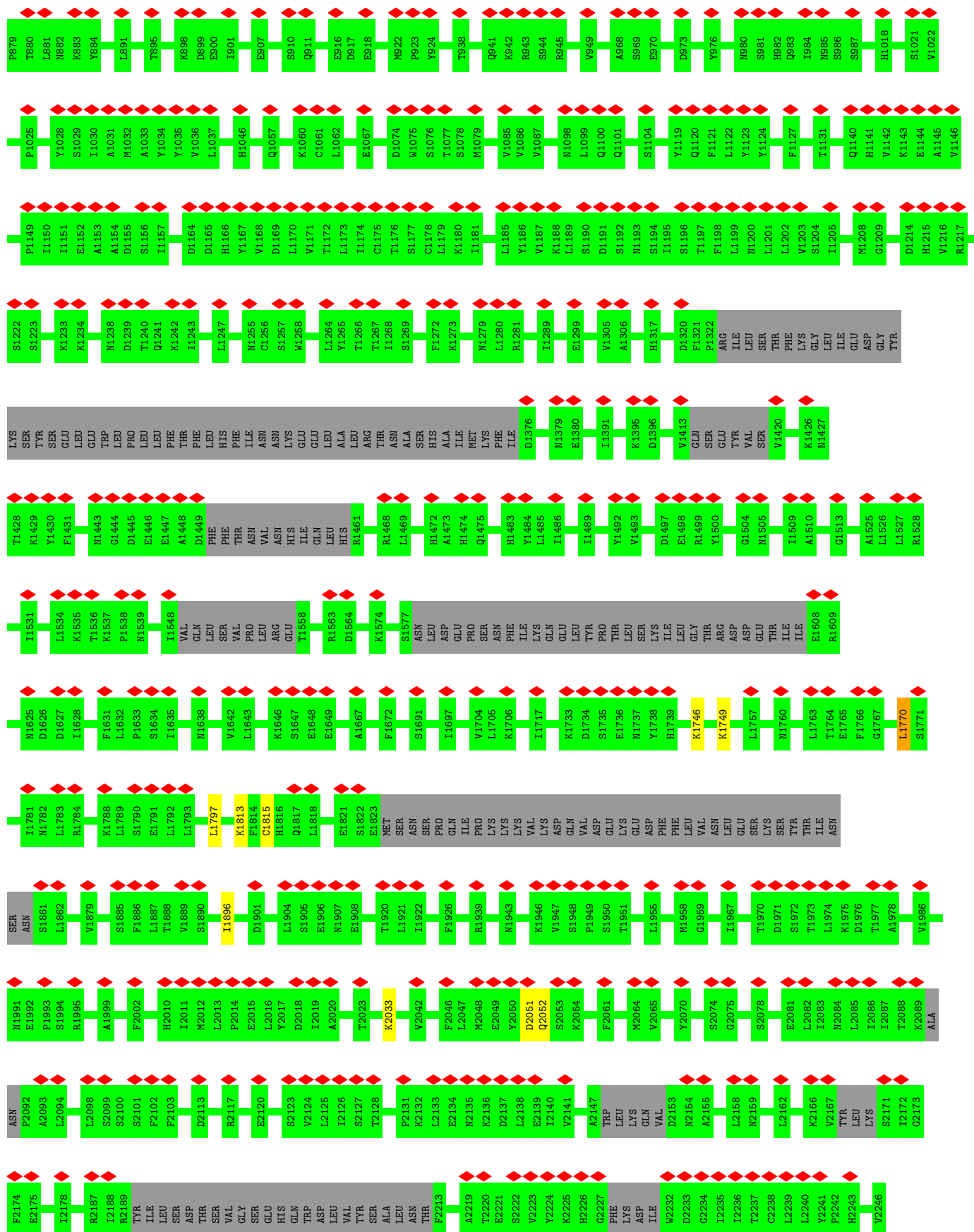


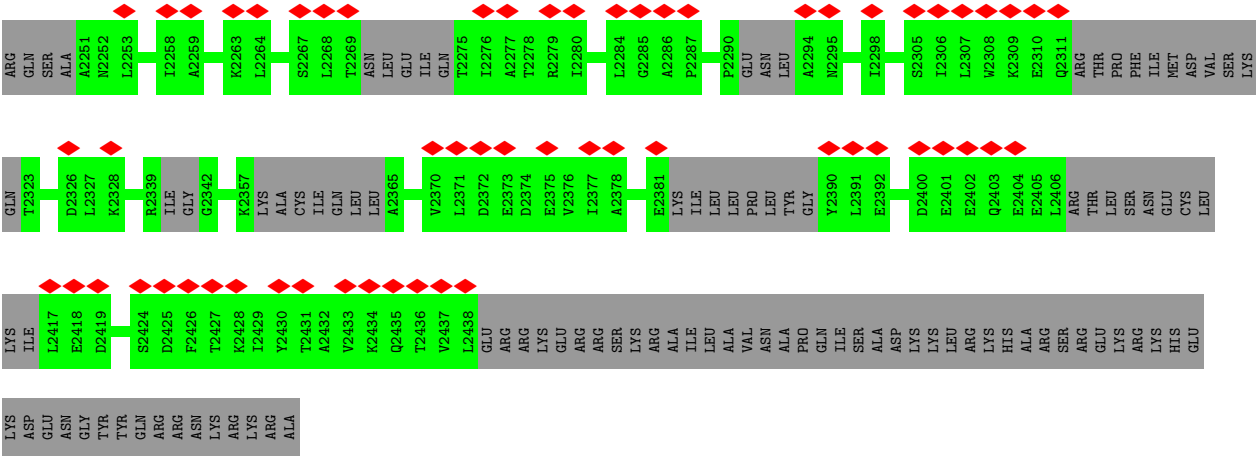
• Molecule 58: Nucleolar complex protein 4

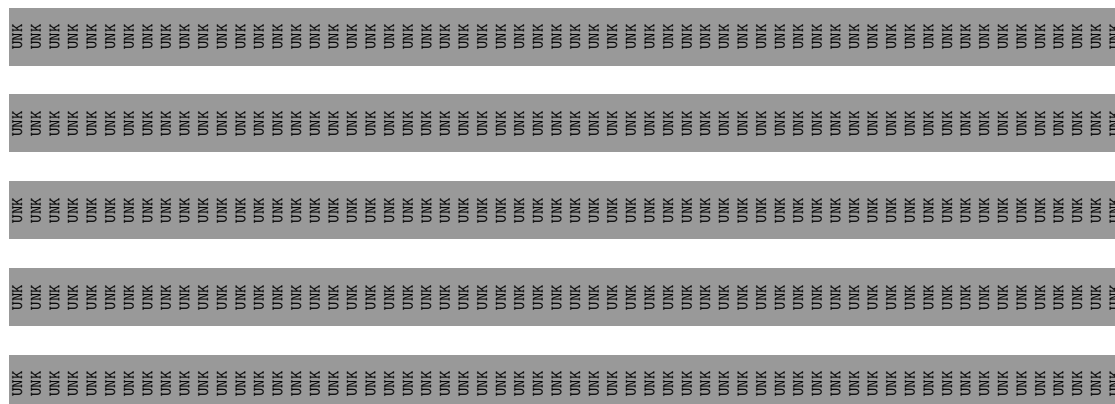
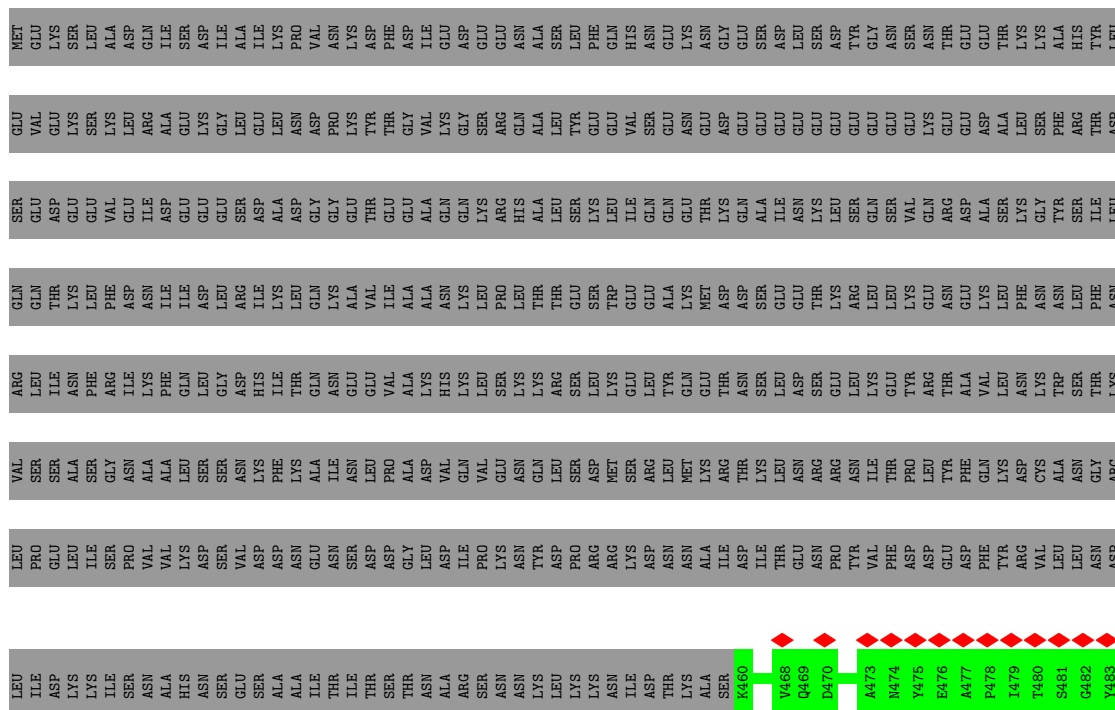


- Molecule 59: U3 small nucleolar RNA-associated protein 20











4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3050	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	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, ZN, MG

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	3A	0.91	0/4141	1.25	38/6433 (0.6%)
2	5A	0.80	0/4605	1.08	13/7168 (0.2%)
3	SA	0.70	0/30585	1.16	235/47611 (0.5%)
4	SC	0.47	0/1856	0.73	5/2490 (0.2%)
5	SF	0.35	0/1854	0.66	1/2504 (0.0%)
6	SG	0.53	0/1690	0.64	0/2285
7	SH	0.31	0/1341	0.60	0/1789
8	SI	0.38	0/1341	0.67	1/1806 (0.1%)
9	SJ	0.31	0/1347	0.59	1/1801 (0.1%)
10	SK	0.47	0/1410	0.60	0/1888
11	SM	0.31	0/1020	0.58	0/1374
12	SO	0.45	0/1109	0.62	0/1495
13	SP	0.49	0/879	0.68	0/1186
14	SR	0.58	0/990	0.73	1/1335 (0.1%)
15	SX	0.51	0/1020	0.66	1/1371 (0.1%)
16	SY	0.54	0/798	0.67	1/1065 (0.1%)
17	SZ	0.43	0/822	0.64	0/1103
18	Sc	0.44	0/613	0.65	0/828
19	Sd	0.54	0/499	0.66	0/670
20	3B	0.59	0/1901	0.66	1/2567 (0.0%)
20	3C	0.44	0/1796	0.62	1/2424 (0.0%)
21	3D	0.44	0/2891	0.63	3/3895 (0.1%)
22	3E	0.41	0/3059	0.62	3/4153 (0.1%)
23	3F	0.42	0/3715	0.64	2/5001 (0.0%)
24	3G	0.52	0/928	0.76	1/1262 (0.1%)
24	3H	0.47	0/928	0.69	2/1262 (0.2%)
25	A4	0.47	0/5321	0.66	5/7207 (0.1%)
26	A5	0.48	0/4044	0.68	5/5493 (0.1%)
27	A8	0.34	0/3249	0.71	10/4454 (0.2%)
28	A9	0.31	0/951	0.58	1/1287 (0.1%)
29	AE	0.37	0/10049	0.56	6/13737 (0.0%)
30	AF	0.53	0/3993	0.67	4/5413 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AG	0.47	0/6699	0.65	3/9077 (0.0%)
32	B1	0.64	0/6474	0.68	7/8763 (0.1%)
33	B2	0.43	0/6628	0.67	3/8954 (0.0%)
34	B3	0.39	0/6014	0.69	7/8137 (0.1%)
35	B8	0.58	0/3848	0.66	4/5218 (0.1%)
36	BE	0.58	0/6580	0.66	7/8901 (0.1%)
37	B6	0.45	0/2849	0.58	1/3853 (0.0%)
38	5B	0.34	0/499	0.62	0/659
39	5C	0.61	0/3690	0.69	5/4991 (0.1%)
40	5D	0.51	0/1417	0.67	2/1885 (0.1%)
41	5E	0.39	0/1580	0.73	3/2115 (0.1%)
42	5F	0.38	0/1559	0.69	1/2097 (0.0%)
43	5G	0.39	0/1792	0.72	2/2425 (0.1%)
44	5H	0.52	0/601	0.57	0/789
45	5I	0.61	0/3844	0.66	2/5174 (0.0%)
46	5J	0.42	0/1302	0.55	0/1728
47	5K	0.56	0/1426	0.66	1/1917 (0.1%)
48	RA	0.34	0/2769	0.67	1/3753 (0.0%)
49	RB	0.38	0/1121	0.62	0/1487
50	RD	0.31	0/2453	0.63	3/3308 (0.1%)
51	RE	0.38	0/8924	0.63	8/12070 (0.1%)
52	RF	0.34	0/2004	0.63	2/2697 (0.1%)
53	RG	0.39	0/1727	0.68	2/2329 (0.1%)
53	RH	0.42	0/1828	0.61	0/2470
54	RJ	0.50	0/6514	0.61	1/8768 (0.0%)
55	RK	0.44	0/2832	0.65	3/3825 (0.1%)
56	RL	0.29	0/4549	0.50	0/6241
56	RM	0.25	0/3765	0.47	0/5218
57	RN	0.36	0/4591	0.58	2/6187 (0.0%)
58	RO	0.38	0/3849	0.62	5/5261 (0.1%)
59	RP	0.28	0/12225	0.51	5/16812 (0.0%)
60	RQ	0.46	0/1678	0.58	0/2282
61	RS	0.33	0/2104	0.67	1/2854 (0.0%)
62	RT	0.33	0/1355	0.65	1/1821 (0.1%)
63	RY	0.29	0/307	0.51	0/415
All	All	0.51	0/222142	0.77	423/308838 (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
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	2
31	AG	0	2
32	B1	0	2
33	B2	0	8
34	B3	0	11
36	BE	0	1
39	5C	0	1
40	5D	0	1
43	5G	0	2
45	5I	0	2
48	RA	0	2
49	RB	0	1
51	RE	0	1
52	RF	0	1
54	RJ	0	2
55	RK	0	1
56	RL	0	1
56	RM	0	1
57	RN	0	1
58	RO	0	1
59	RP	0	3
60	RQ	0	1
62	RT	0	1
All	All	0	71

There are no bond length outliers.

The worst 5 of 423 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3A	321	C	N1-C1'-C2'	-10.80	99.96	114.00
3	SA	861	U	C2-N1-C1'	10.60	130.42	117.70
3	SA	376	C	N1-C2-O2	10.43	125.16	118.90
3	SA	1174	C	N1-C2-O2	10.35	125.11	118.90
3	SA	1034	C	C5-C6-N1	10.00	126.00	121.00

There are no chirality outliers.

5 of 71 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	34	72
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	17	57
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
17	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	15	55
18	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
19	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
21	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
22	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
23	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	47	81
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	19	60
24	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
26	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
27	A8	516/713 (72%)	397 (77%)	107 (21%)	12 (2%)	6	34
28	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
29	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
30	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
31	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	51	86
32	B1	787/923 (85%)	732 (93%)	55 (7%)	0	100	100
33	B2	813/943 (86%)	724 (89%)	87 (11%)	2 (0%)	47	81
34	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	41	77
35	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
36	BE	814/939 (87%)	765 (94%)	49 (6%)	0	100	100
37	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
38	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
39	5C	452/554 (82%)	419 (93%)	32 (7%)	1 (0%)	47	81

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	5D	165/250 (66%)	145 (88%)	20 (12%)	0	100	100
41	5E	187/593 (32%)	175 (94%)	10 (5%)	2 (1%)	14	52
42	5F	180/183 (98%)	164 (91%)	16 (9%)	0	100	100
43	5G	217/290 (75%)	203 (94%)	14 (6%)	0	100	100
44	5H	72/610 (12%)	65 (90%)	7 (10%)	0	100	100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
46	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
47	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
48	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
49	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	19	60
50	RD	310/1729 (18%)	284 (92%)	23 (7%)	3 (1%)	15	55
51	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
52	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
53	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
53	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
54	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	51	86
55	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
56	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	41	77
56	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	29	69
57	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	47	81
58	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
59	RP	2042/2493 (82%)	1815 (89%)	226 (11%)	1 (0%)	100	100
60	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100
61	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
62	RT	163/326 (50%)	147 (90%)	16 (10%)	0	100	100
63	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	23878/33924 (70%)	21529 (90%)	2311 (10%)	38 (0%)	50	81

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	A8	258	PRO
27	A8	309	PRO

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Mol	Chain	Res	Type
27	A8	325	PRO
27	A8	390	PRO
27	A8	392	PRO

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	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	76	86
5	SF	196/222 (88%)	190 (97%)	6 (3%)	40	62
6	SG	180/191 (94%)	180 (100%)	0	100	100
7	SH	139/201 (69%)	137 (99%)	2 (1%)	67	80
8	SI	146/170 (86%)	145 (99%)	1 (1%)	84	90
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	65	80
10	SK	147/166 (89%)	146 (99%)	1 (1%)	84	90
11	SM	110/137 (80%)	108 (98%)	2 (2%)	59	77
12	SO	117/128 (91%)	116 (99%)	1 (1%)	78	87
13	SP	90/105 (86%)	89 (99%)	1 (1%)	73	84
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	107 (99%)	1 (1%)	78	87
16	SY	85/120 (71%)	84 (99%)	1 (1%)	71	83
17	SZ	85/113 (75%)	85 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	201 (100%)	0	100	100
20	3C	190/240 (79%)	187 (98%)	3 (2%)	62	79
21	3D	296/435 (68%)	293 (99%)	3 (1%)	76	86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	91	94
23	3F	396/503 (79%)	394 (100%)	2 (0%)	88	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	3G	100/104 (96%)	100 (100%)	0	100	100
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	591/713 (83%)	584 (99%)	7 (1%)	71	83
26	A5	433/574 (75%)	432 (100%)	1 (0%)	93	96
27	A8	174/657 (26%)	164 (94%)	10 (6%)	20	45
28	A9	89/533 (17%)	88 (99%)	1 (1%)	73	84
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	91	94
30	AF	437/454 (96%)	433 (99%)	4 (1%)	78	87
31	AG	750/826 (91%)	740 (99%)	10 (1%)	69	81
32	B1	696/812 (86%)	691 (99%)	5 (1%)	84	90
33	B2	712/832 (86%)	707 (99%)	5 (1%)	84	90
34	B3	665/719 (92%)	655 (98%)	10 (2%)	65	80
35	B8	421/529 (80%)	420 (100%)	1 (0%)	93	96
36	BE	718/819 (88%)	714 (99%)	4 (1%)	86	92
37	B6	251/414 (61%)	247 (98%)	4 (2%)	62	79
38	5B	57/196 (29%)	55 (96%)	2 (4%)	36	59
39	5C	394/480 (82%)	392 (100%)	2 (0%)	88	93
40	5D	156/234 (67%)	154 (99%)	2 (1%)	69	81
41	5E	175/535 (33%)	162 (93%)	13 (7%)	13	38
42	5F	171/172 (99%)	169 (99%)	2 (1%)	71	83
43	5G	194/258 (75%)	190 (98%)	4 (2%)	53	72
44	5H	63/538 (12%)	63 (100%)	0	100	100
45	5I	416/443 (94%)	414 (100%)	2 (0%)	88	93
46	5J	140/200 (70%)	140 (100%)	0	100	100
47	5K	157/169 (93%)	157 (100%)	0	100	100
48	RA	303/636 (48%)	300 (99%)	3 (1%)	76	86
49	RB	117/315 (37%)	114 (97%)	3 (3%)	46	66
50	RD	226/1544 (15%)	220 (97%)	6 (3%)	44	65
51	RE	984/1125 (88%)	975 (99%)	9 (1%)	78	87
52	RF	221/274 (81%)	219 (99%)	2 (1%)	78	87
53	RG	195/222 (88%)	193 (99%)	2 (1%)	76	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	RH	206/222 (93%)	204 (99%)	2 (1%)	76	86
54	RJ	683/1039 (66%)	676 (99%)	7 (1%)	76	86
55	RK	307/312 (98%)	303 (99%)	4 (1%)	69	81
56	RL	164/934 (18%)	162 (99%)	2 (1%)	71	83
57	RN	422/732 (58%)	421 (100%)	1 (0%)	93	96
58	RO	329/506 (65%)	328 (100%)	1 (0%)	92	95
59	RP	499/2307 (22%)	493 (99%)	6 (1%)	71	83
60	RQ	148/808 (18%)	145 (98%)	3 (2%)	55	74
61	RS	225/424 (53%)	225 (100%)	0	100	100
62	RT	146/282 (52%)	144 (99%)	2 (1%)	67	80
63	RY	31/482 (6%)	30 (97%)	1 (3%)	39	61
All	All	17291/29262 (59%)	17116 (99%)	175 (1%)	77	86

5 of 175 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	5G	211	ASN
52	RF	69	LYS
45	5I	250	ARG
50	RD	1670	LYS
54	RJ	869	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 298 such sidechains are listed below:

Mol	Chain	Res	Type
51	RE	841	ASN
59	RP	1702	HIS
51	RE	1086	ASN
54	RJ	778	GLN
31	AG	453	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	55 (32%)	8 (4%)
2	5A	186/700 (26%)	54 (29%)	4 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	SA	1261/1809 (69%)	482 (38%)	19 (1%)
All	All	1616/2842 (56%)	591 (36%)	31 (1%)

5 of 591 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	56	U
3	SA	1521	G
3	SA	372	G
3	SA	1632	C
3	SA	1052	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
66	GTP	RJ	1201	67	26,34,34	0.94	2 (7%)	32,54,54	0.92	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
66	GTP	RJ	1201	67	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	RJ	1201	GTP	C5-C6	-2.47	1.42	1.47
66	RJ	1201	GTP	C8-N7	-2.05	1.31	1.35

There are no bond angle outliers.

There are no chirality outliers.

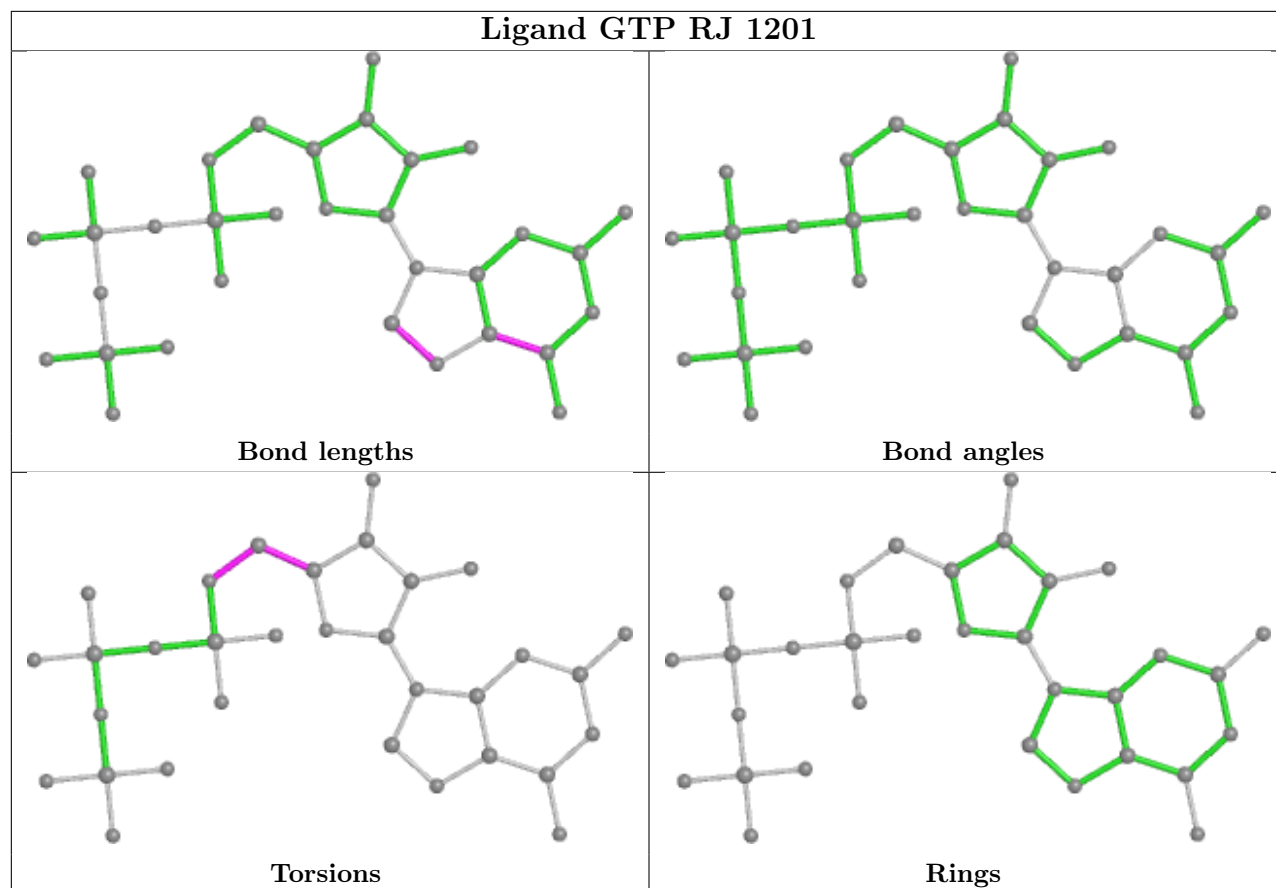
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
66	RJ	1201	GTP	O4'-C4'-C5'-O5'
66	RJ	1201	GTP	C3'-C4'-C5'-O5'
66	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

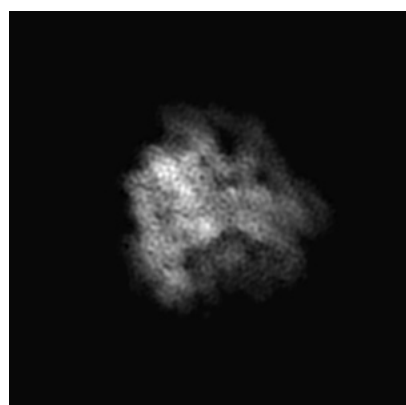
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0951. These allow visual inspection of the internal detail of the map and identification of artifacts.

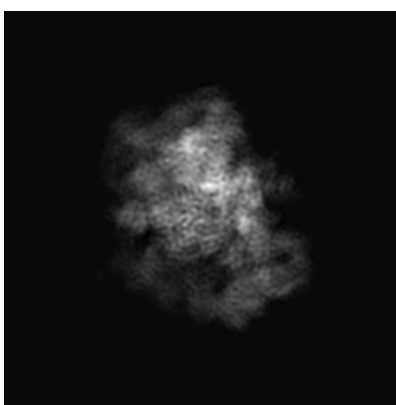
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

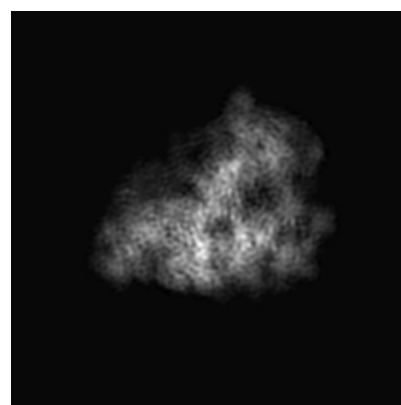
6.1.1 Primary map



X



Y

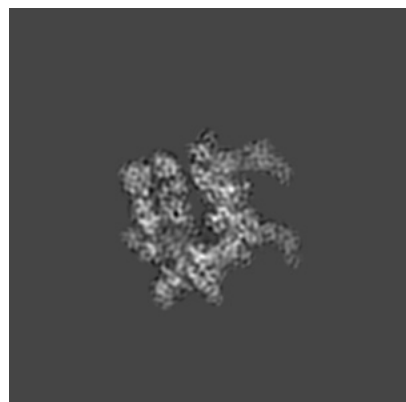


Z

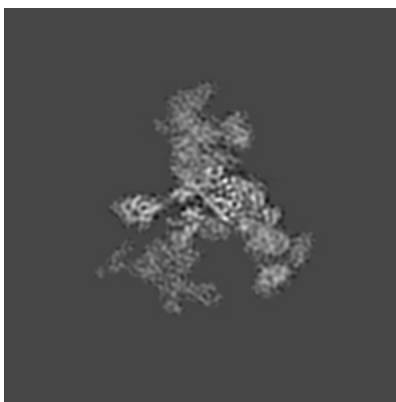
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

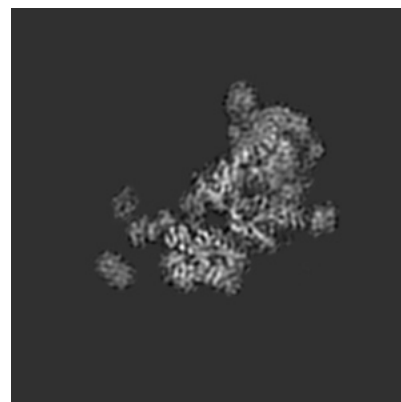
6.2.1 Primary map



X Index: 224



Y Index: 224

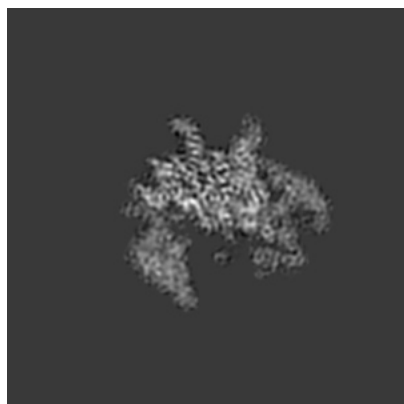


Z Index: 224

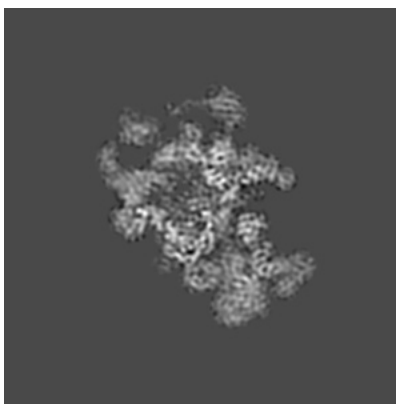
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

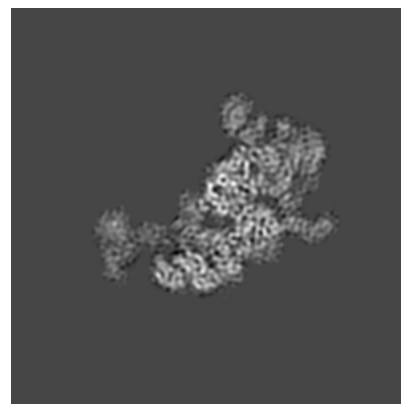
6.3.1 Primary map



X Index: 252



Y Index: 194

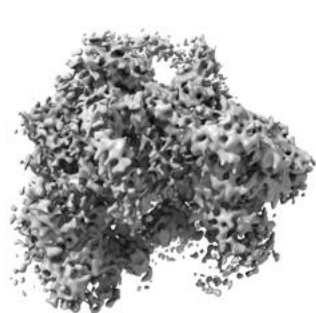


Z Index: 243

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

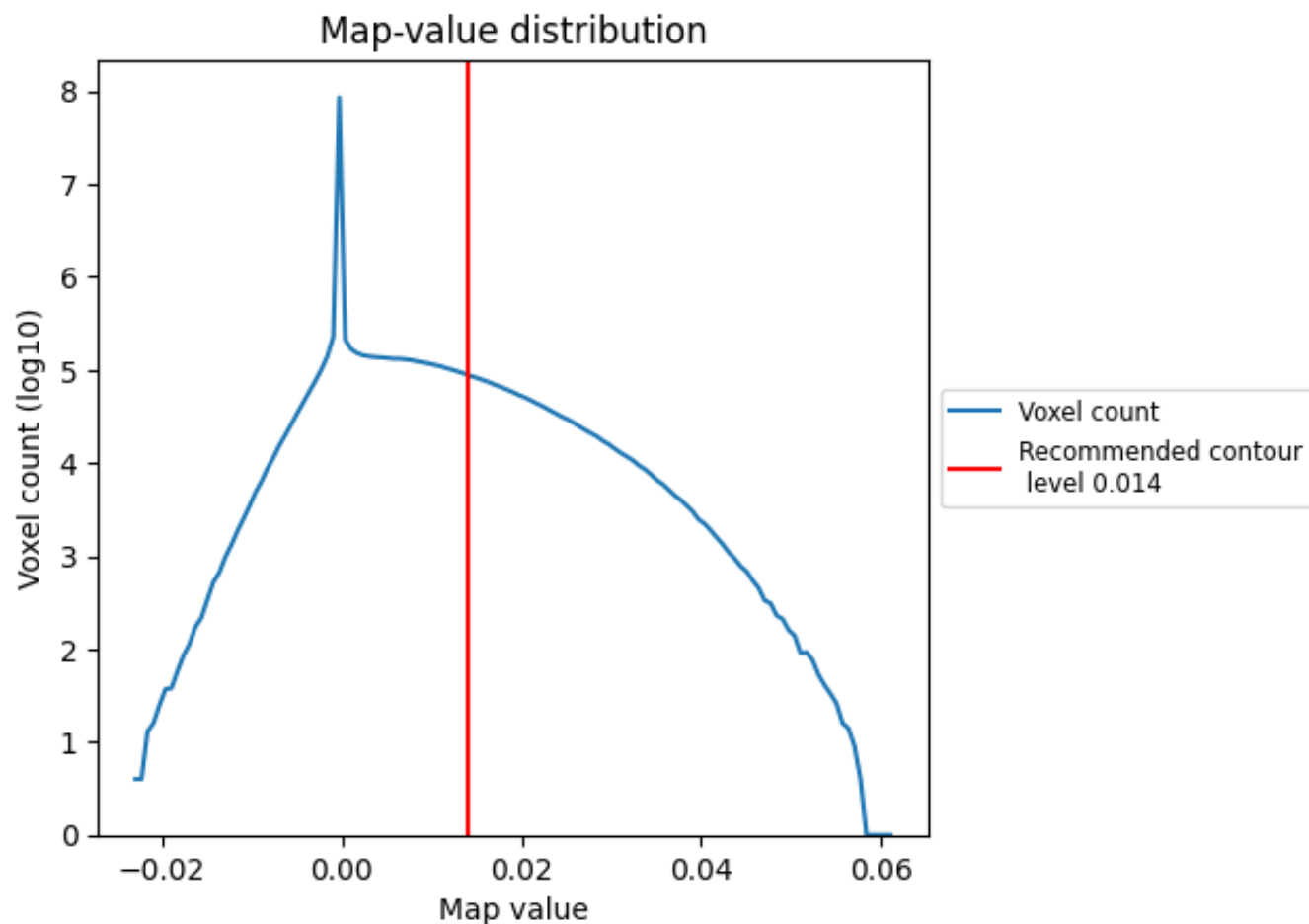
6.5 Mask visualisation

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

7 Map analysis [i](#)

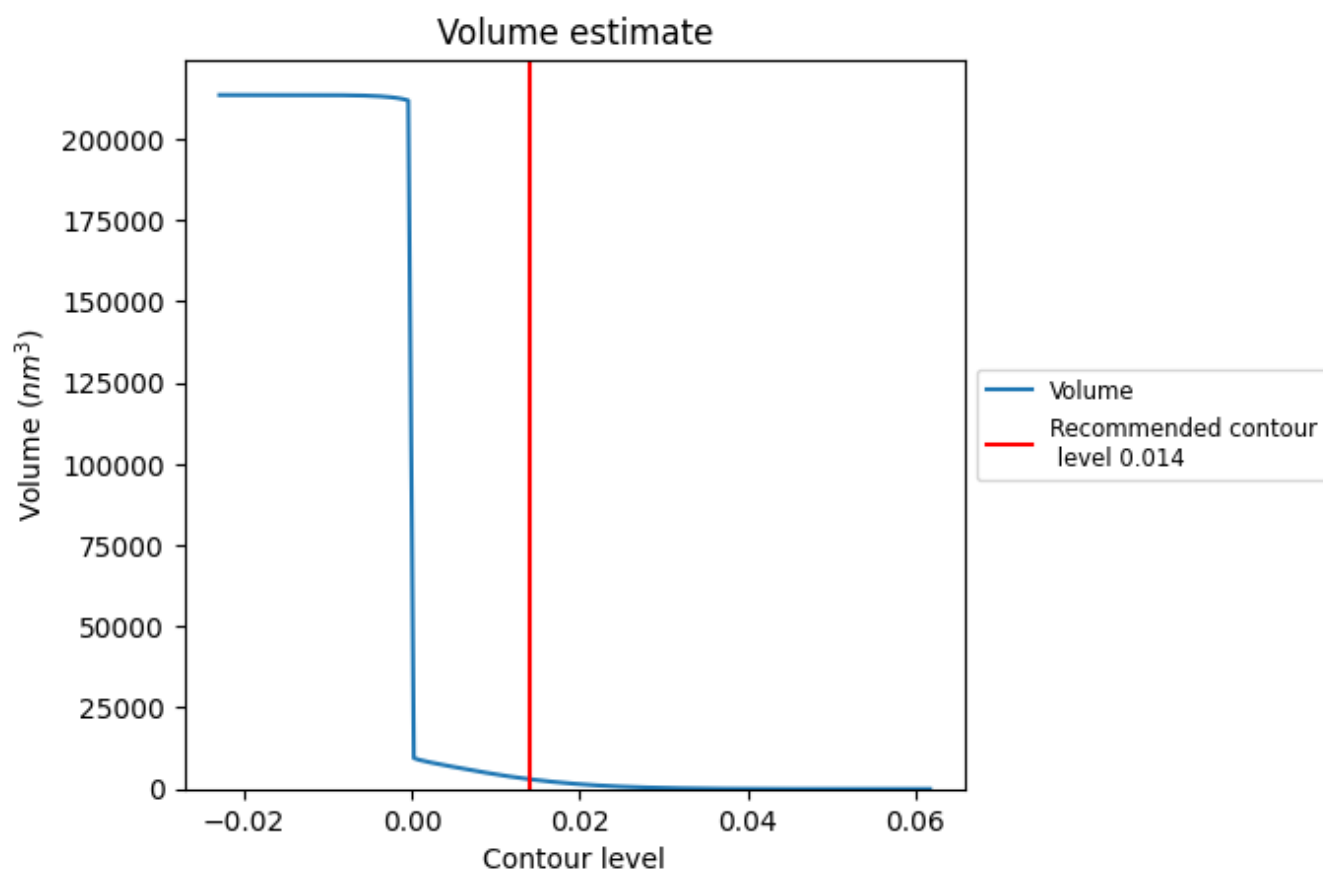
This section contains the results of statistical analysis of the map.

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.

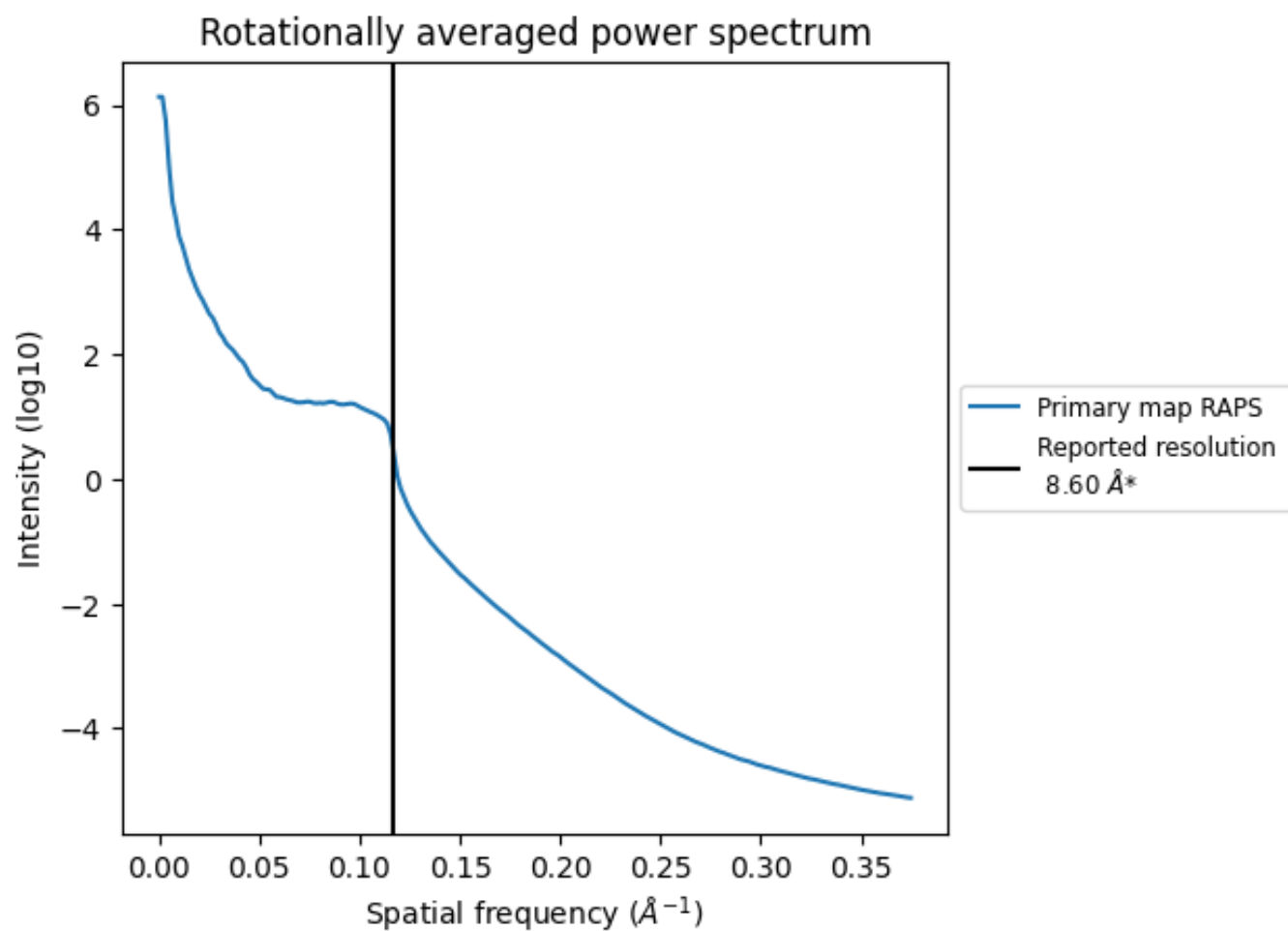
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3008 nm³; this corresponds to an approximate mass of 2717 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 0.116 Å⁻¹

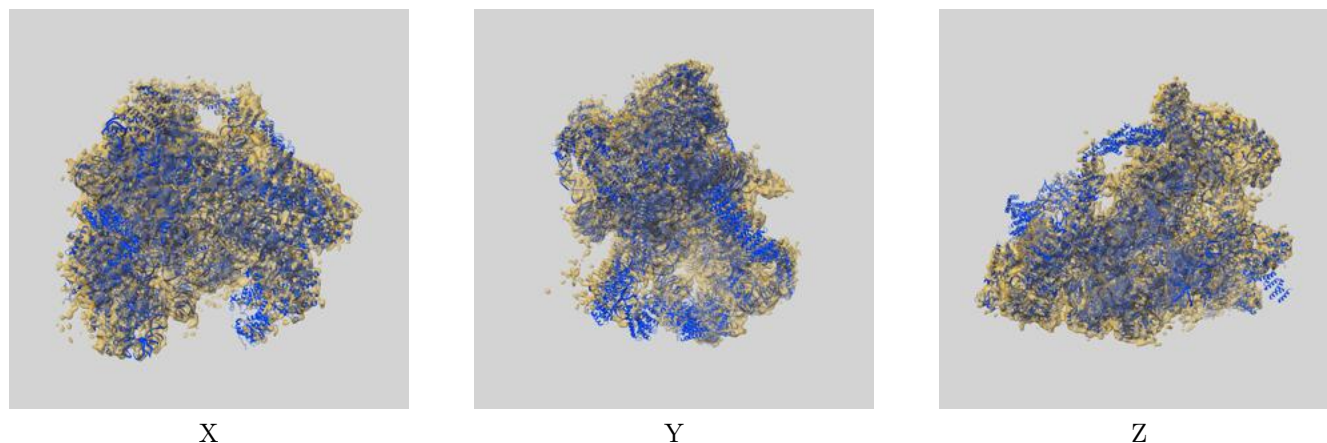
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

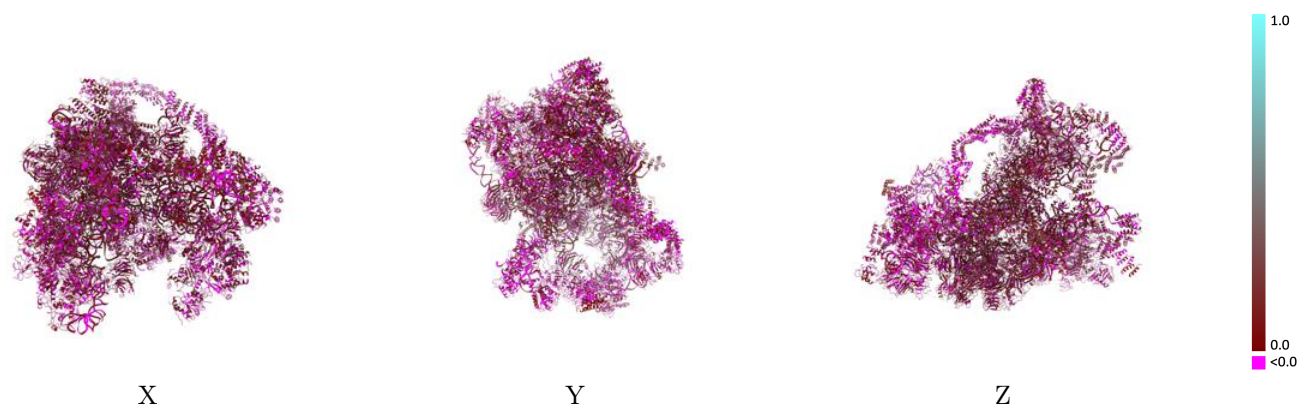
This section contains information regarding the fit between EMDB map EMD-0951 and PDB model 6LQR. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



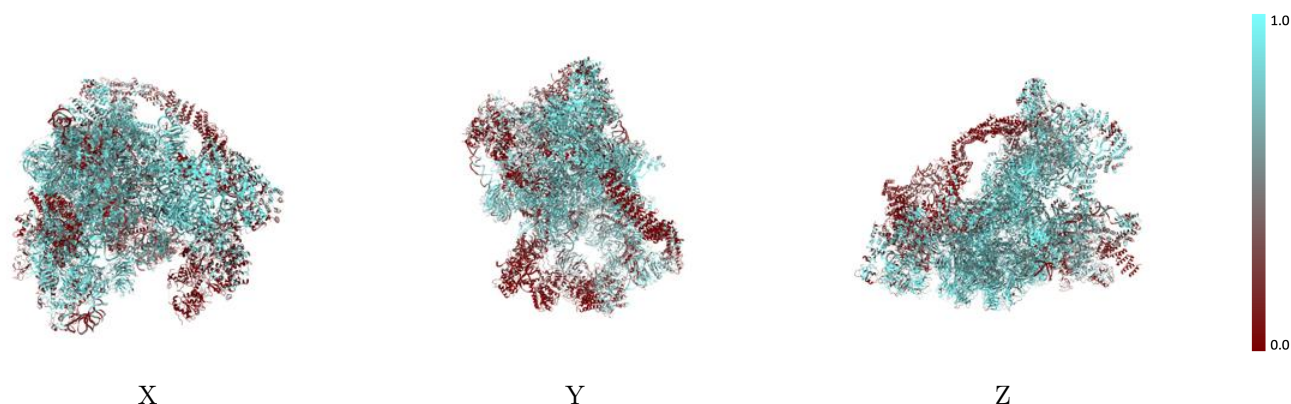
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



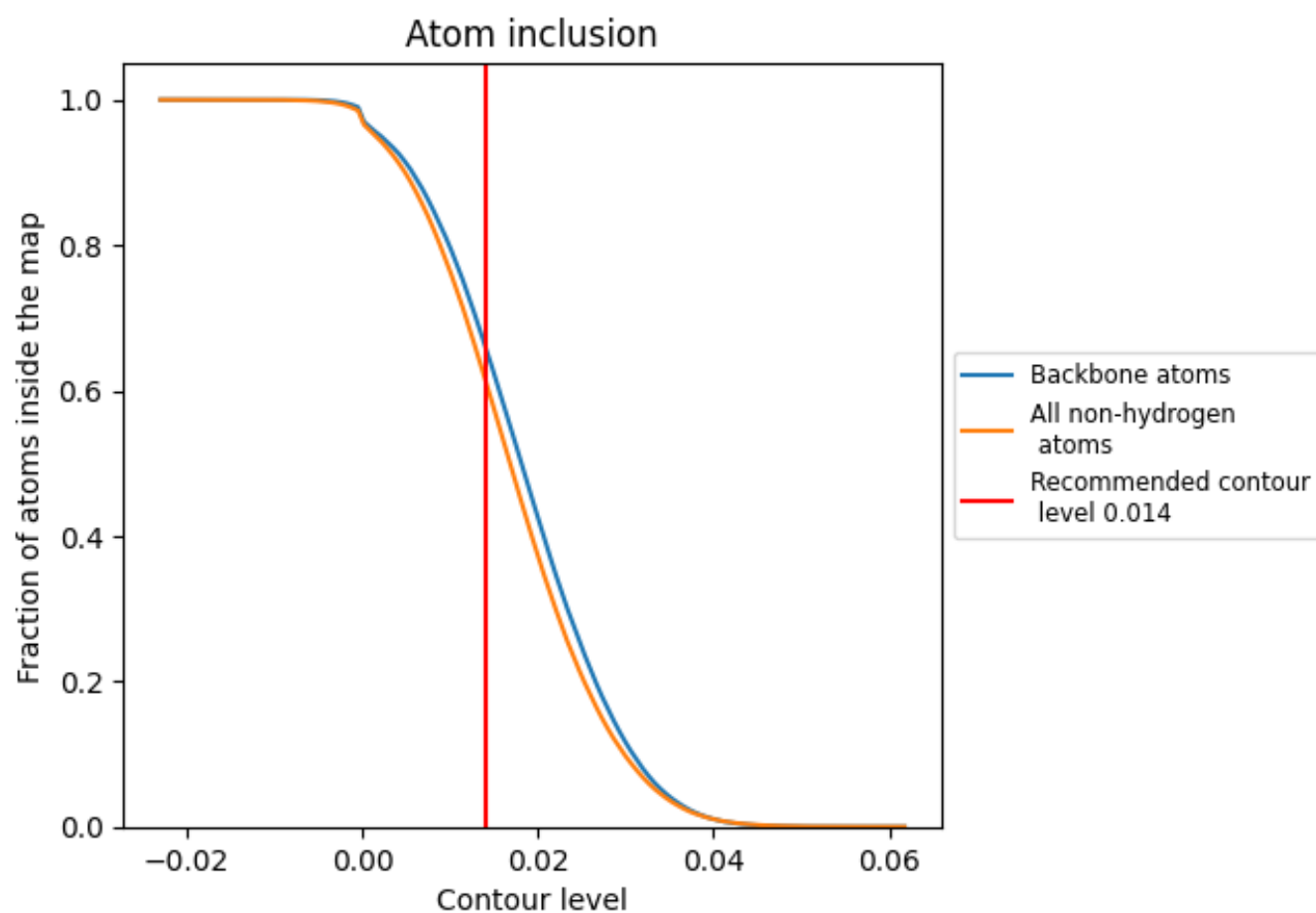
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 62% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6162	 0.0800
3A	 0.9097	 0.1510
3B	 0.7969	 0.1140
3C	 0.6797	 0.0660
3D	 0.8065	 0.1300
3E	 0.6940	 0.0930
3F	 0.8072	 0.1120
3G	 0.7633	 0.1090
3H	 0.7876	 0.1290
5A	 0.5880	 0.0630
5B	 0.1208	 0.0310
5C	 0.7704	 0.1040
5D	 0.4063	 0.0490
5E	 0.7423	 0.1350
5F	 0.7364	 0.1260
5G	 0.6731	 0.0950
5H	 0.7543	 0.1070
5I	 0.8407	 0.1040
5J	 0.5671	 0.0960
5K	 0.7416	 0.1100
A4	 0.6848	 0.0470
A5	 0.6059	 0.0740
A8	 0.5478	 0.0590
A9	 0.4816	 0.0400
AE	 0.3844	 0.0540
AF	 0.4860	 0.0490
AG	 0.6675	 0.0340
B1	 0.8254	 0.1060
B2	 0.7952	 0.0960
B3	 0.7848	 0.0710
B6	 0.7683	 0.1260
B8	 0.7800	 0.0970
BE	 0.8308	 0.1070
RA	 0.5967	 0.0600
RB	 0.7441	 0.1240



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Chain	Atom inclusion	Q-score
RD	 0.0796	 0.0120
RE	 0.5562	 0.0610
RF	 0.3928	 0.0800
RG	 0.1279	 0.0160
RH	 0.1389	 0.0120
RJ	 0.7031	 0.1020
RK	 0.7463	 0.1140
RL	 0.3282	 0.0860
RM	 0.1559	 0.0450
RN	 0.1106	 0.0080
RO	 0.0220	 -0.0030
RP	 0.6093	 0.0830
RQ	 0.5521	 0.0900
RS	 0.0454	 -0.0100
RT	 0.4823	 0.0510
RY	 0.3754	 0.0560
SA	 0.7138	 0.1010
SC	 0.5150	 0.0690
SF	 0.7693	 0.0950
SG	 0.7891	 0.1220
SH	 0.5729	 0.0710
SI	 0.6505	 0.1140
SJ	 0.7194	 0.0430
SK	 0.7949	 0.1150
SM	 0.8202	 0.0610
SO	 0.6930	 0.0860
SP	 0.6229	 0.0520
SR	 0.7914	 0.1080
SX	 0.5927	 0.1030
SY	 0.6426	 0.0990
SZ	 0.7611	 0.1050
Sc	 0.5462	 0.0810
Sd	 0.7757	 0.1250
X1	 0.5364	 0.0930