wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 05:35 PM JST

PDB ID	:	7D5S
EMDB ID	:	EMD-30584
Title	:	Cryo-EM structure of 90S preribosome with inactive Utp24 (state A2)
Authors	:	Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on	:	2020-09-28
Resolution	:	4.60 Å(reported)
Based on initial model	:	6LQU

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

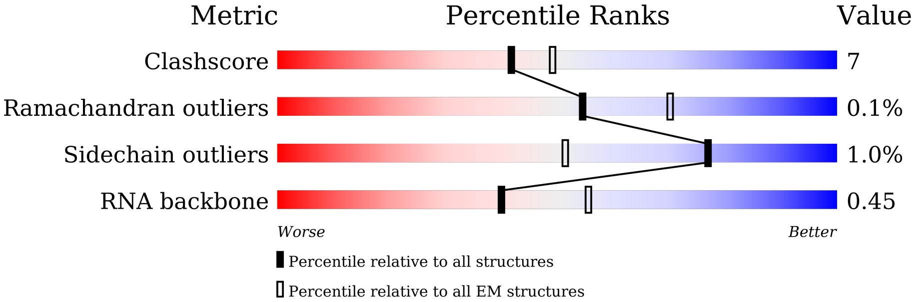
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance ⓘ

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

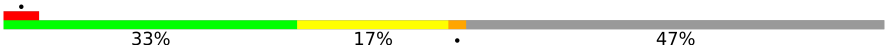
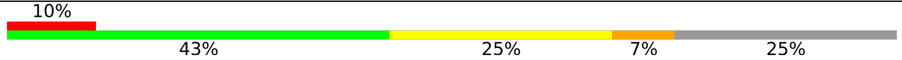
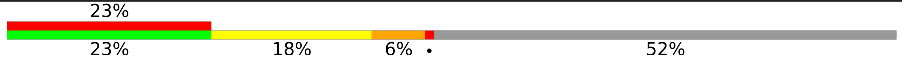
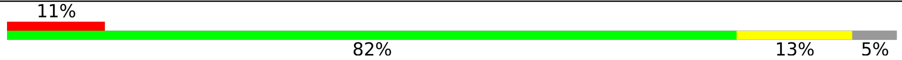
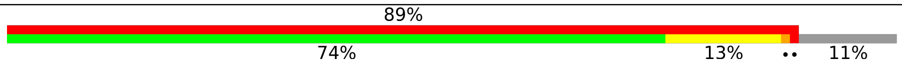
The reported resolution of this entry is 4.60 Å.

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)
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 >=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 <=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	1808	
4	SG	225	
5	SK	197	
6	SN	143	
7	SO	151	

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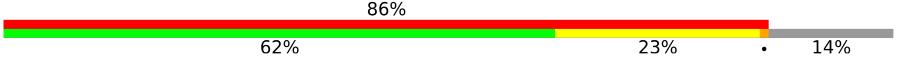
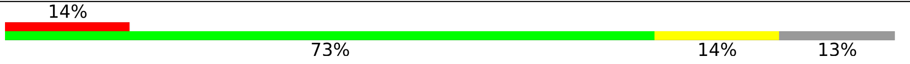
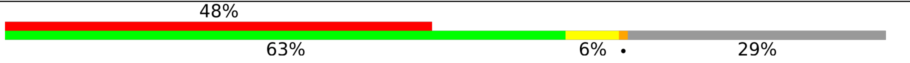
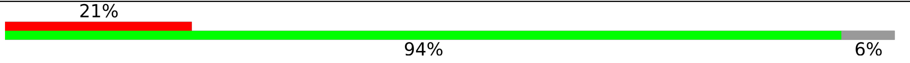
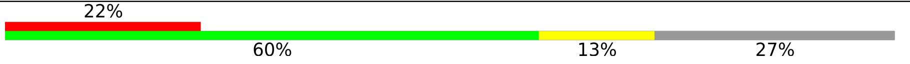
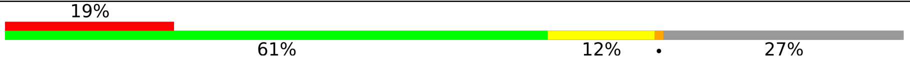
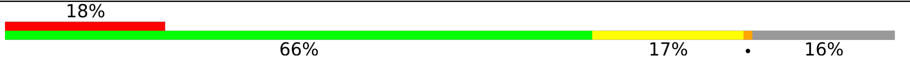
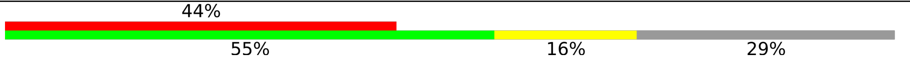
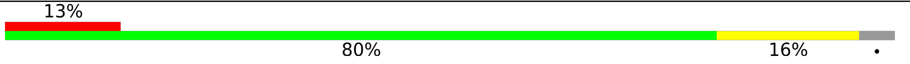
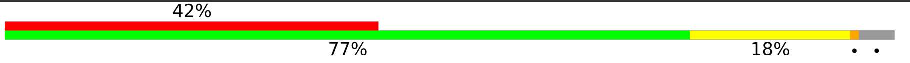
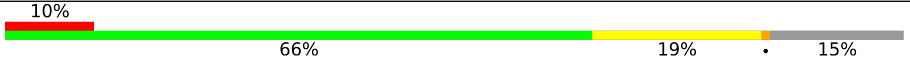
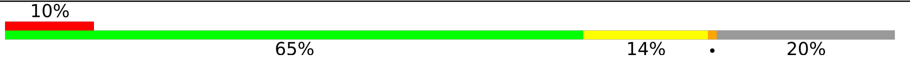
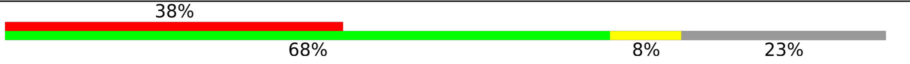
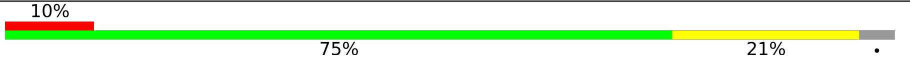
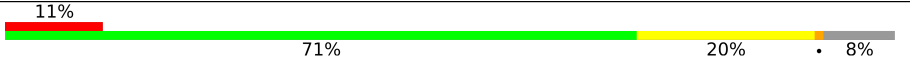
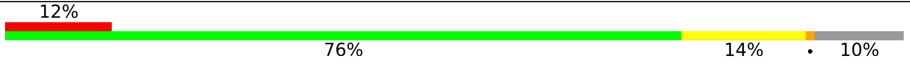
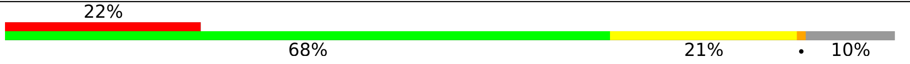
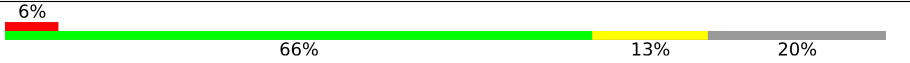
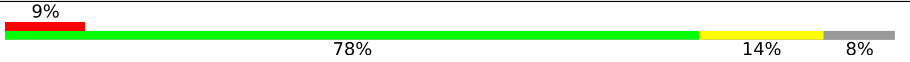
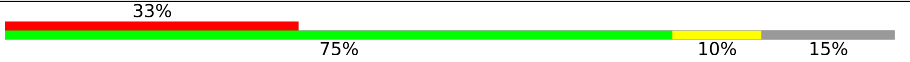
Mol	Chain	Length	Quality of chain
8	SP	137	
9	SR	143	
10	ST	146	
11	SY	145	
12	Sd	67	
13	3B	327	
13	3C	327	
14	3D	504	
15	3E	511	
16	3F	573	
17	3G	126	
17	3H	126	
18	A4	776	
19	A5	643	
20	A8	713	
21	A9	575	
22	AE	1769	
23	AF	513	
24	AG	896	
25	B1	923	
26	B2	943	
27	B3	817	
28	B8	594	
29	BE	939	
30	B6	440	

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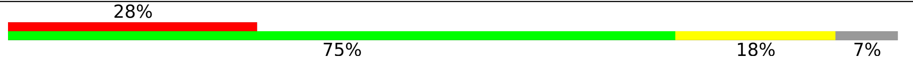
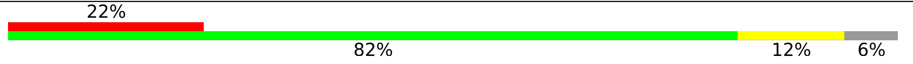
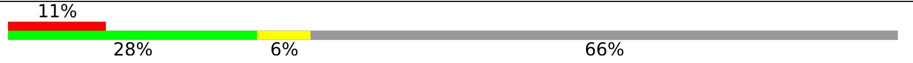
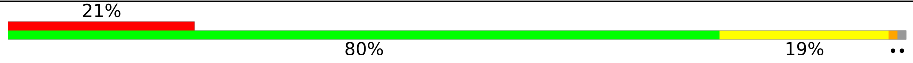
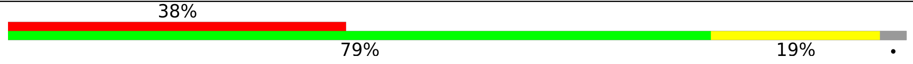
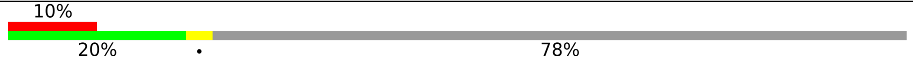
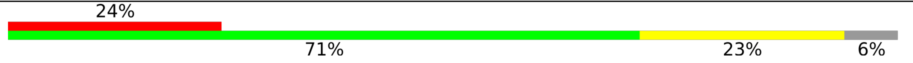
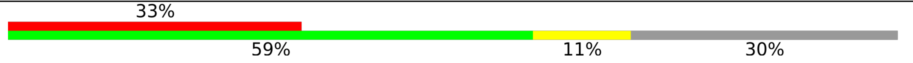
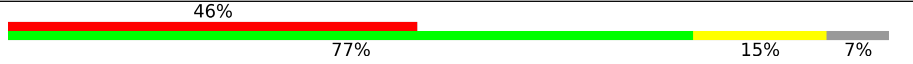
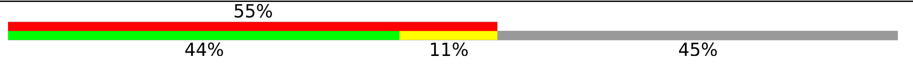
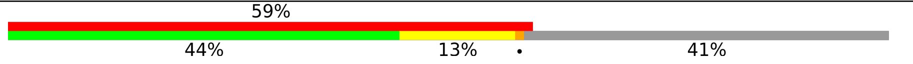
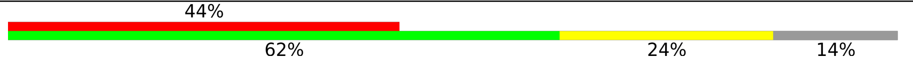
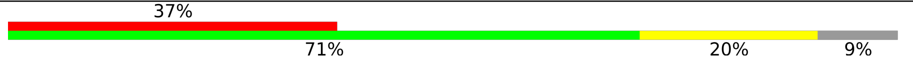
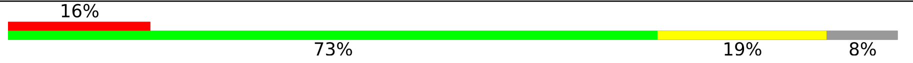
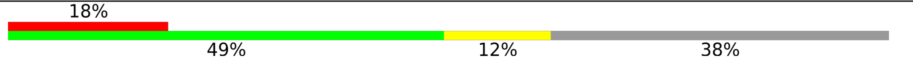
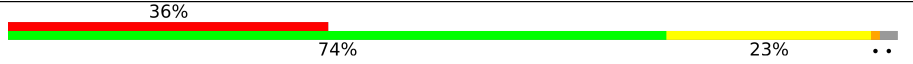
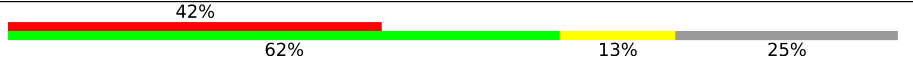
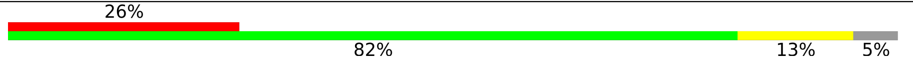
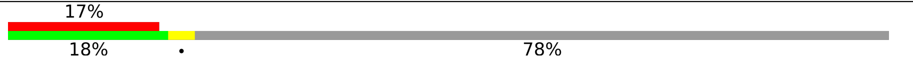
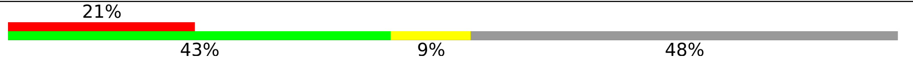
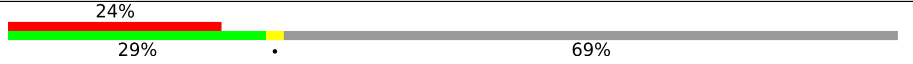
Mol	Chain	Length	Quality of chain
31	5B	214	
32	5C	554	
33	5D	250	
34	5E	593	
35	5F	183	
36	5G	290	
37	5H	610	
38	5I	489	
39	5J	217	
40	5K	189	
41	RC	316	
42	RD	1729	
43	RE	1237	
44	RF	297	
45	RG	252	
45	RH	252	
46	RI	274	
47	RJ	1183	
48	RK	367	
49	RN	810	
50	RO	552	
51	RQ	899	
52	RS	483	
53	RT	326	
54	RW	206	

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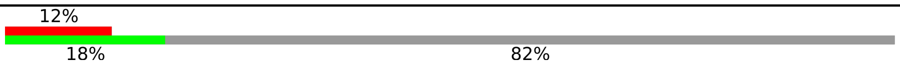
Mol	Chain	Length	Quality of chain
55	X1	347	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 179154 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
			Total	C	N	O	P		
1	3A	175	3711	1661	648	1227	175	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5A	523	11163	4988	1984	3668	523	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	859	18356	8201	3302	5994	859	0	0

- Molecule 4 is a protein called 40S ribosomal protein S5.

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

- Molecule 5 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SN	119	865	545	151	167	2	0	0

- Molecule 7 is a protein called 40S ribosomal protein S13.

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

- Molecule 8 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ST	117	Total 964	C 610	N 184	O 168	S 2	0	0

- Molecule 11 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 13 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	3B	240	Total 1865	C 1184	N 333	O 338	S 10	0	0
13	3C	225	Total 1763	C 1120	N 316	O 317	S 10	0	0

- Molecule 14 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	3D	369	2848	1811	489	540	8	0	0

- Molecule 15 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	3E	431	3028	1888	543	588	9	0	0

- Molecule 16 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	3F	406	3248	2075	566	597	10	0	0

- Molecule 17 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	3G	121	916	583	158	171	4	0	0
			Total	C	N	O	S		
17	3H	121	916	583	158	171	4	0	0

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 4.

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

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 5.

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

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	A8	548	3307	2054	608	642	3	0	0

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 9.

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

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	AE	649	5181	3355	849	960	17	0	0

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 24 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 25 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	B1	834	6635	4223	1140	1253	19	0	0

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	B2	851	6723	4294	1133	1269	27	0	0

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	B3	752	5882	3746	987	1122	27	0	0

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	21		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 31 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5C	516	Total	C	N	O	S	0	0
			4084	2561	736	775	12		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 35 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 36 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 37 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	5H	136	Total	C	N	O	0	0
			1065	658	211	196		

- Molecule 38 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 39 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 40 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 41 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	RC	175	Total	C	N	O	S	0	0
			1410	903	252	245	10		

- Molecule 42 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	RD	265	1314	784	265	265	0	0

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 44 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	RF	174	1404	905	230	261	8	0	0

- Molecule 45 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 46 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	RI	252	2045	1309	362	366	8	0	0

- Molecule 47 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	RJ	732	5953	3829	1057	1041	26	0	0

- Molecule 48 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 49 is a protein called Nucleolar complex protein 14.

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

- Molecule 50 is a protein called Nucleolar complex protein 4.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RQ	194	Total 1436	C 892	N 270	O 272	S 2	0	0

- Molecule 52 is a protein called Essential nuclear protein 1.

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

- Molecule 53 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RT	171	Total 1357	C 864	N 249	O 240	S 4	0	0

- Molecule 54 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	RW	63	Total 381	C 234	N 69	O 78	0	0

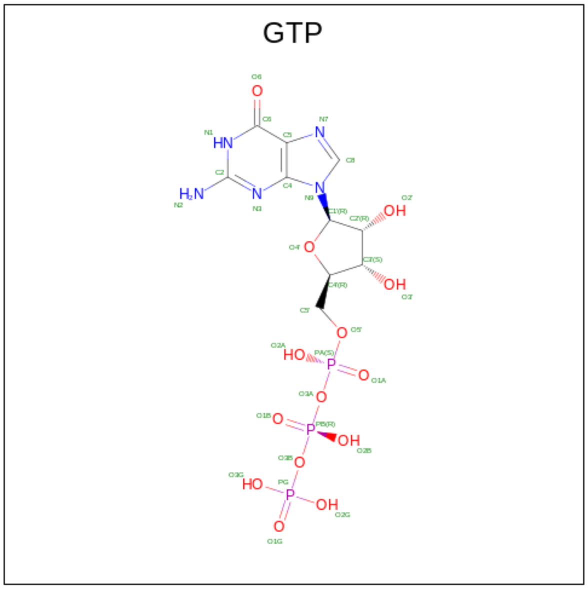
- Molecule 55 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	X1	61	Total 305	C 183	N 61	O 61	0	0

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
56	5K	1	1	1	0

- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

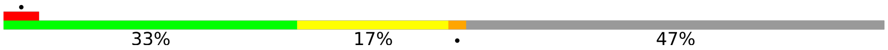
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
58	RJ	1	1	1	0

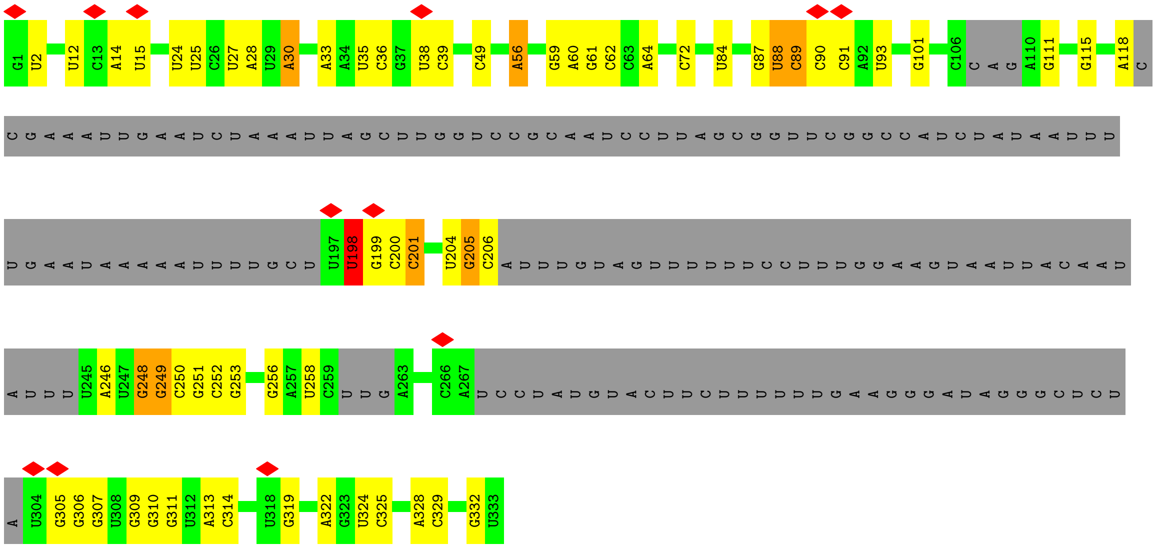
3 Residue-property plots ⓘ

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: U3 snoRNA

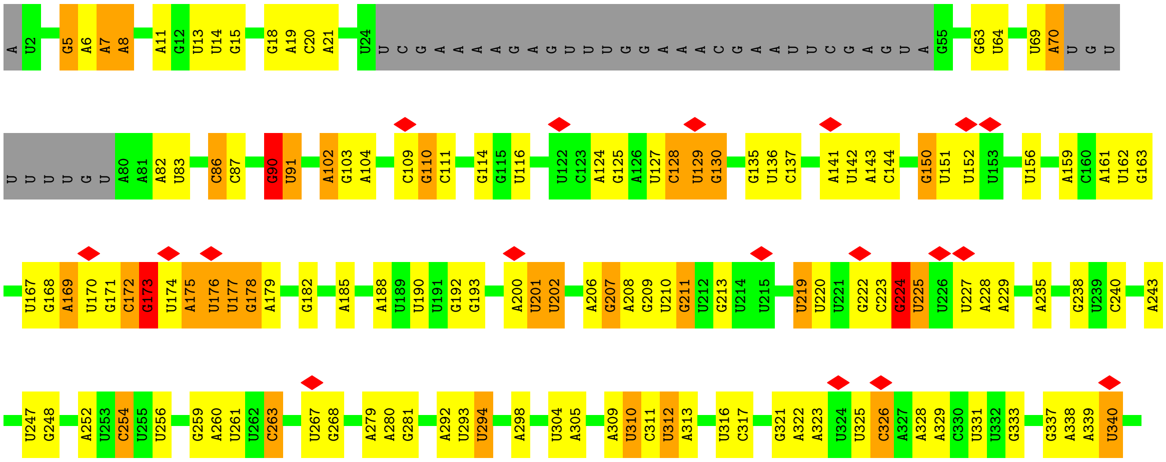
Chain 3A:

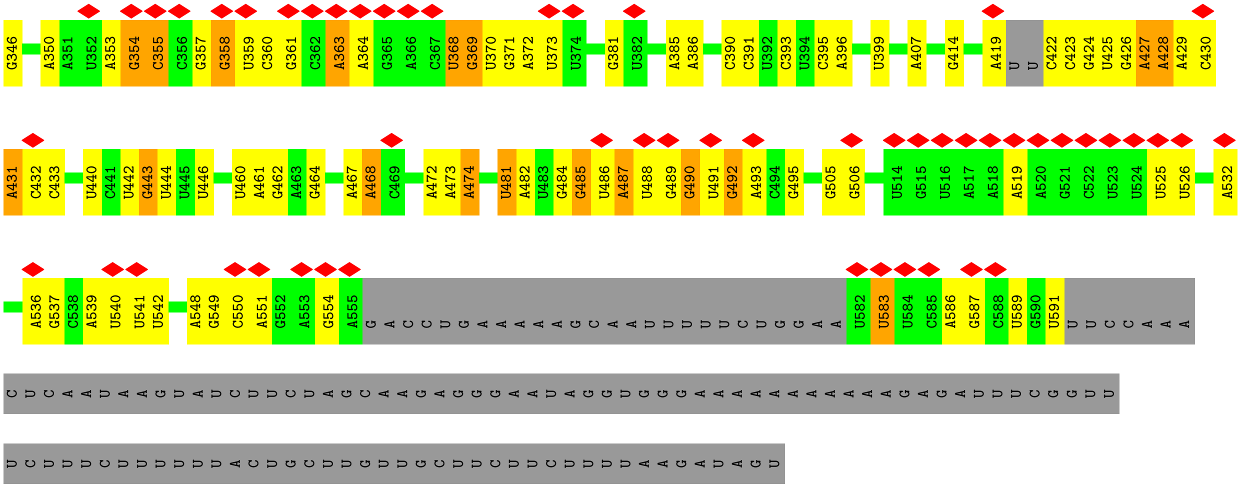




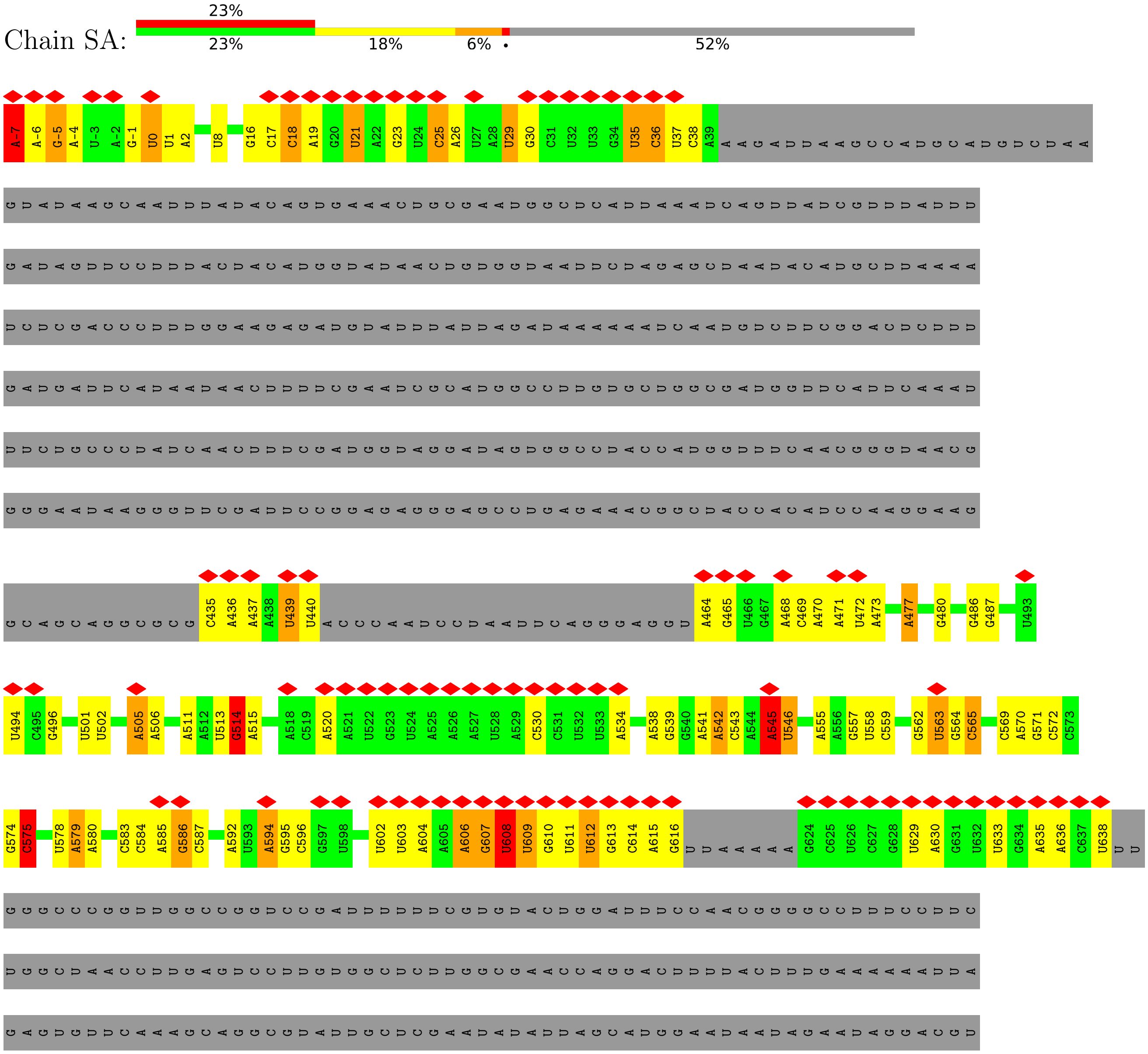
- Molecule 2: 5' ETS

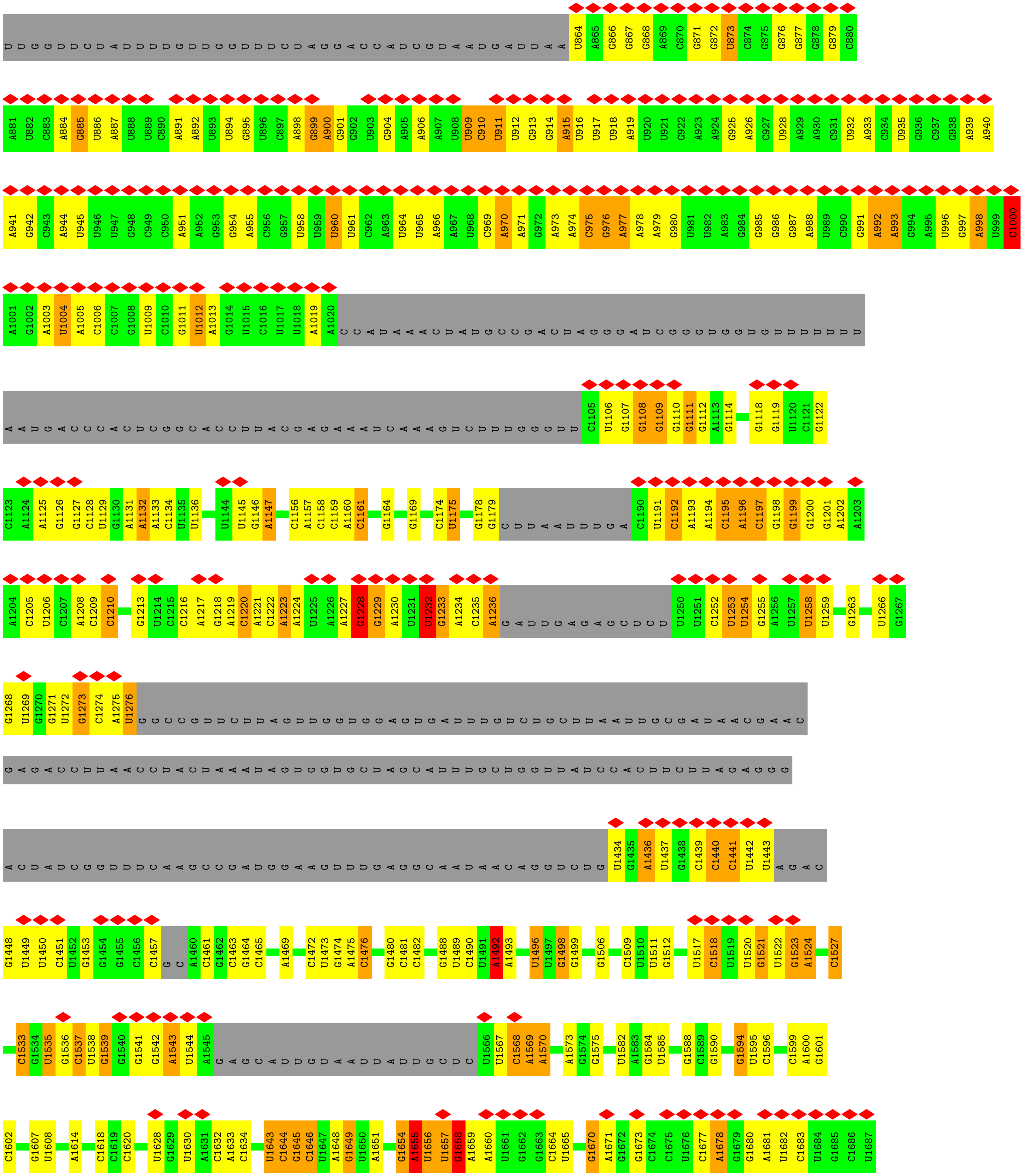
Chain 5A:





- Molecule 3: 18S rRNA

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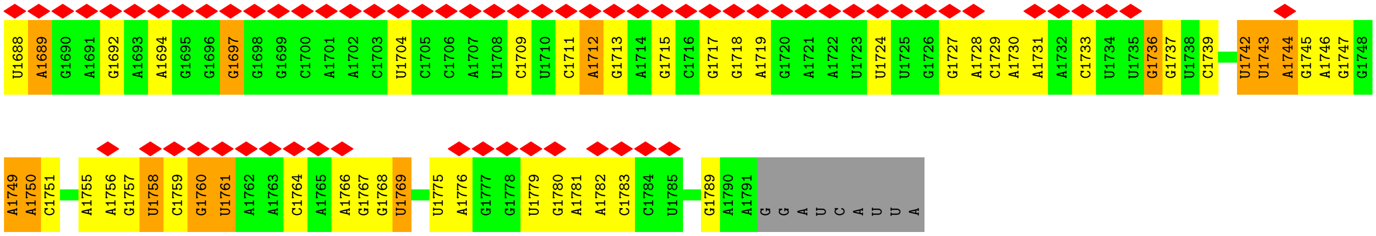
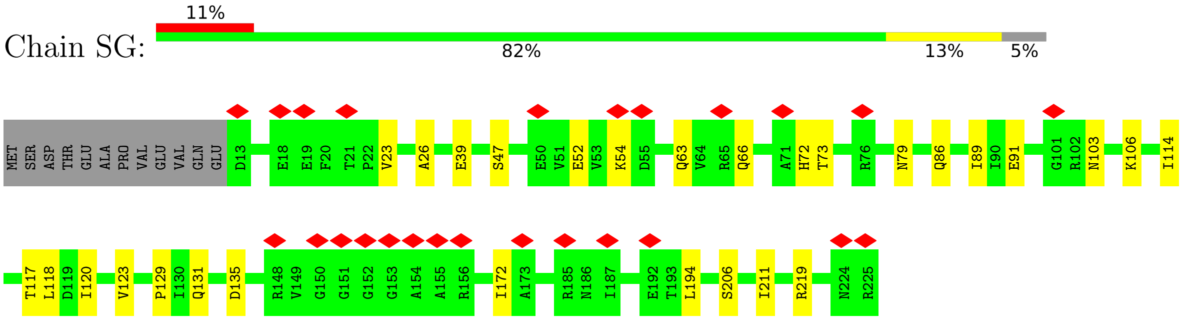
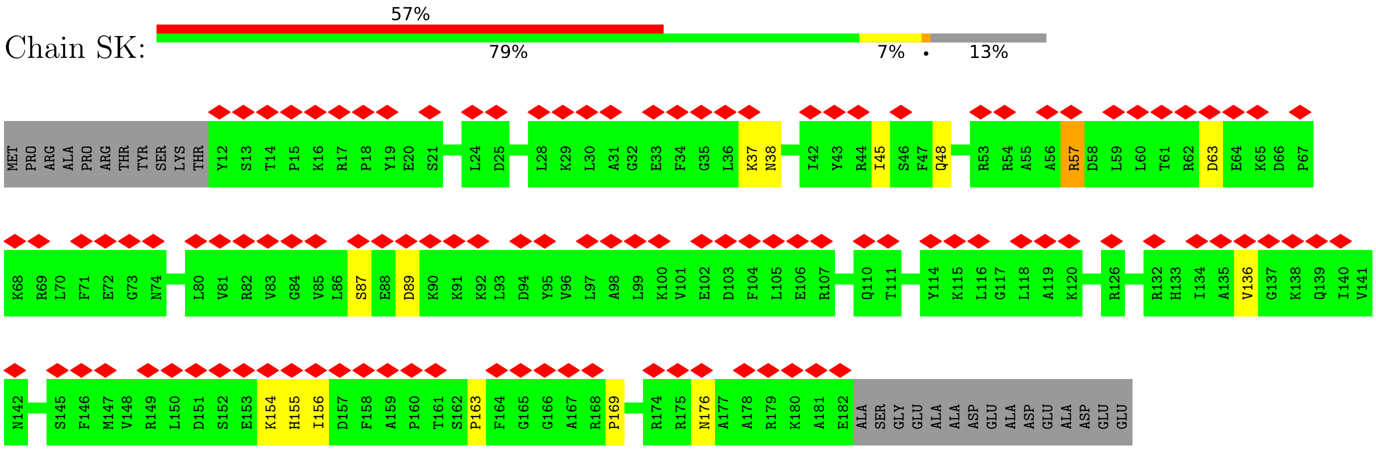
A881 U882 C883 A884 G885 U886 A887 U888 U889 C890 A891 A892 U893 U894 G895 U896 C897 A898 G899 A900 G901 G902 U903 G904 A905 A906 A907 U908 U909 C910 U911 U912 G913 G914 A915 U916 U917 U918 A919 U920 U921 G922 A923 A924 G925 A926 C927 U928 A929 A930 C931 U932 A933 C934 U935 G936 C937 G938 A939 A940
A941 G942 C943 A944 U945 U946 U947 G948 C949 C950 A951 A952 G953 G954 A955 C956 G957 U958 U959 U960 U961 C962 A963 U964 U965 A966 A967 U968 C969 A970 A971 G972 A973 A974 C975 G976 A977 A978 A979 G980 U981 U982 A983 G984 G985 G986 G987 A988 U989 C990 G991 A992 A993 G994 A995 U996 G997 A998 U999 C1000
A1001 G1002 A1003 U1004 A1005 C1006 C1007 G1008 U1009 C1010 G1011 U1012 A1013 G1014 U1015 C1016 U1017 U1018 A1019 A1020 C C A U A A A C U A U G C C G A C U A G G G A U C G G G U G G U G U U U U U U
A A U G A C C C A C U C G G C A C C U U A C G A G A A A U C A A A G U C U U U G G G U U C1105 U1106 G1107 G1108 G1109 G1110 G1111 G1112 A1113 G1114 G1118 G1119 U1120 C1121 G1122
C1123 A1124 A1125 G1126 G1127 C1128 U1129 G1130 A1131 A1132 A1133 C1134 U1135 U1136 U1144 U1145 G1146 A1147 C1156 A1157 C1158 C1159 A1160 C1161 G1164 G1169 C1174 U1175 G1178 G1179 C U U A A U U U G A C1190 U1191 C1192 A1193 A1194 C1195 A1196 C1197 G1198 G1199 G1200 G1201 A1202 A1203
A1204 C1205 U1206 C1207 A1208 C1209 C1210 G1213 U1214 C1215 C1216 A1217 G1218 A1219 C1220 A1221 C1222 A1223 A1224 U1225 A1226 A1227 G1228 G1229 A1230 U1231 U1232 G1233 A1234 C1235 A1236 G A U U G A G A G C U C U U1250 U1251 C1252 U1253 U1254 G1255 A1256 U1257 U1258 U1259 G1263 U1266 G1267
G1268 U1269 G1270 G1271 U1272 G1273 C1274 A1275 U1276 G G C C G U U C U U A G U U G G U G G A G U G A U U U G U C U G C U U A A U U G C G A U A A C G A A C
G A G A C C U U A A C C U A C U A A A U A G U G G U G C U A G C A U U U G C U G G U U A U C C A C U U C U U A G A G G G
A C U A U C G G G U U U C A A G C C G A U G G A A G U U U G A G G C A A U A A C A G G U C U G U1434 G1435 A1436 U1437 G1438 C1439 C1440 C1441 U1442 U1443 A G A C
G1448 U1449 U1450 C1451 U1452 G1453 G1454 G1455 C1456 C1457 G C A1460 C1461 G1462 C1463 G1464 C1465 A1469 C1472 U1473 G1474 A1475 C1476 G1480 C1481 C1482 G1488 U1489 C1490 U1491 A1492 A1493 U1496 U1497 G1498 G1499 G1506 C1509 U1510 U1511 G1512 U1517 C1518 U1519 U1520 G1521 U1522 G1523 A1524 C1527
C1533 G1534 U1535 G1536 C1537 U1538 G1539 G1540 G1541 G1542 A1543 U1544 A1545 G A G C A U G G U A A A U U A U U G C U C U1566 U1567 C1568 A1569 A1570 A1573 G1574 C1575 U1582 A1583 G1584 U1585 G1588 C1589 G1590 G1594 U1595 C1596 C1599 A1600 G1601
C1602 G1607 U1608 A1614 C1618 C1619 C1620 U1628 G1629 U1630 A1631 C1632 A1633 C1634 U1643 C1644 G1645 C1646 U1647 A1648 G1649 U1650 A1651 G1654 A1655 U1656 U1657 G1658 A1659 A1660 U1661 G1662 G1663 C1664 U1665 G1670 A1671 G1672 G1673 C1674 C1675 U1676 C1677 A1678 G1679 G1680 A1681 U1682 C1683 U1684 G1685 C1686 U1687



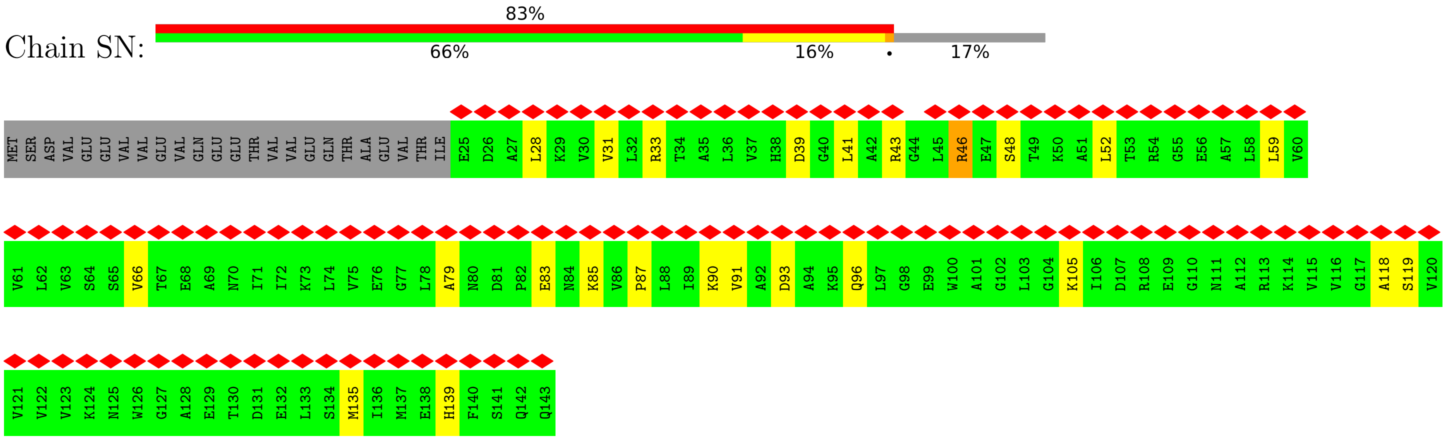
- Molecule 4: 40S ribosomal protein S5



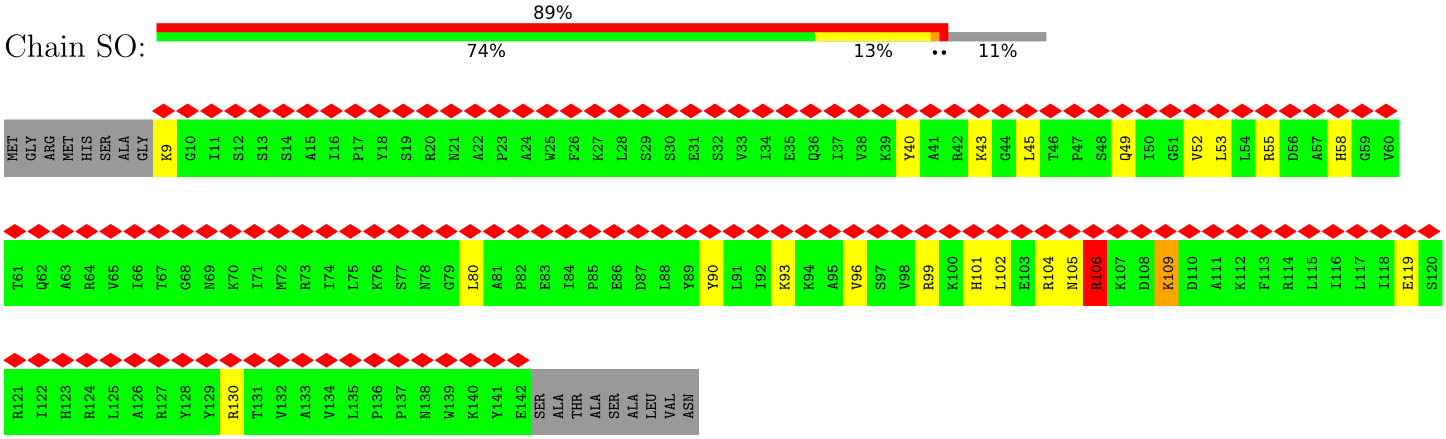
- Molecule 5: 40S ribosomal protein S9-A



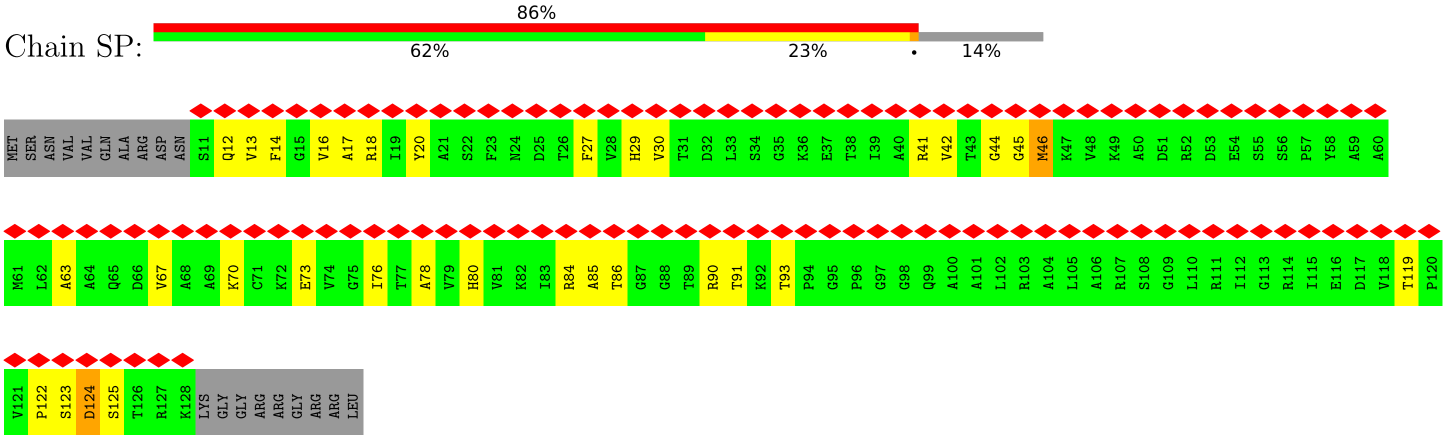
- Molecule 6: 40S ribosomal protein S12



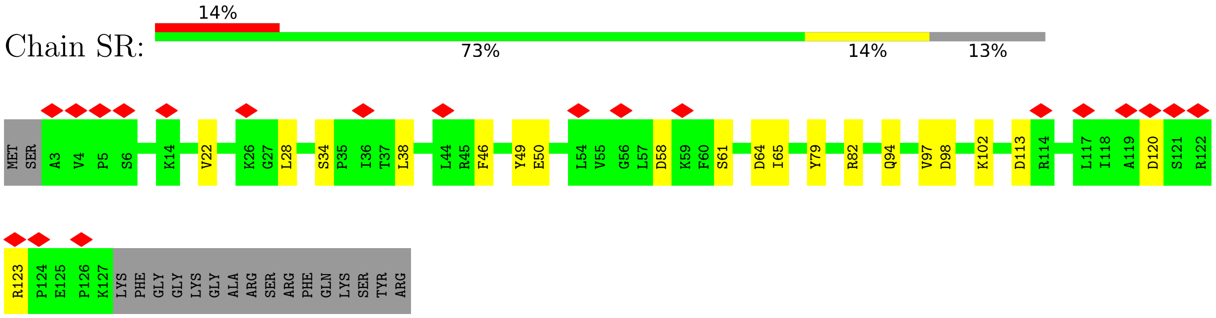
- Molecule 7: 40S ribosomal protein S13



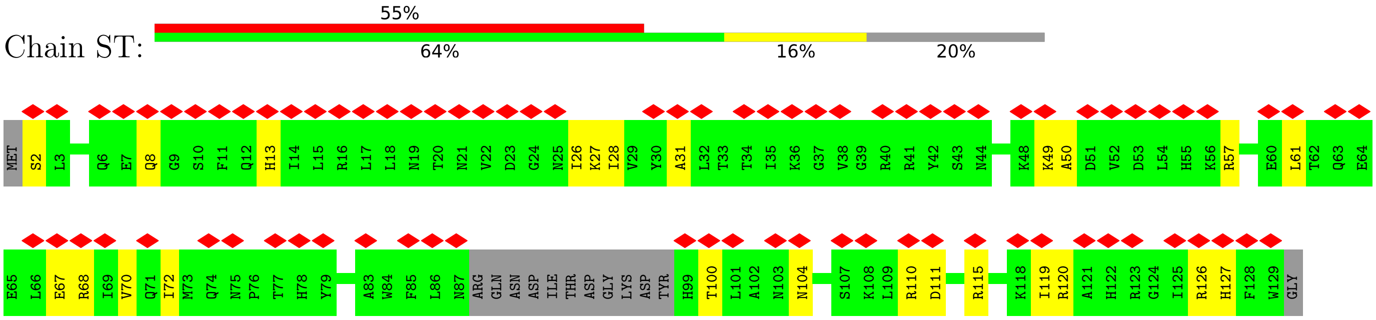
- Molecule 8: 40S ribosomal protein S14-A



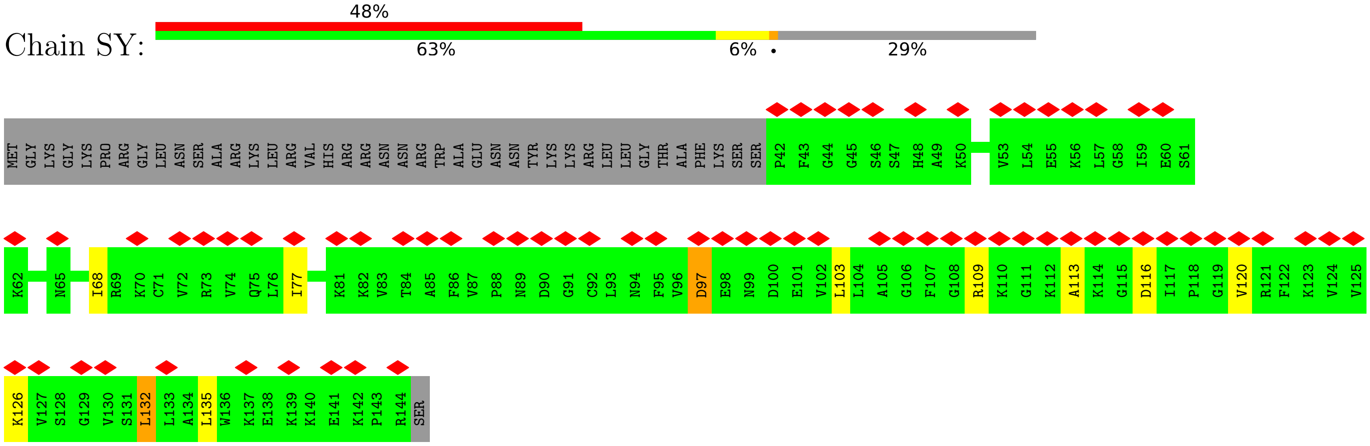
- Molecule 9: 40S ribosomal protein S16-A



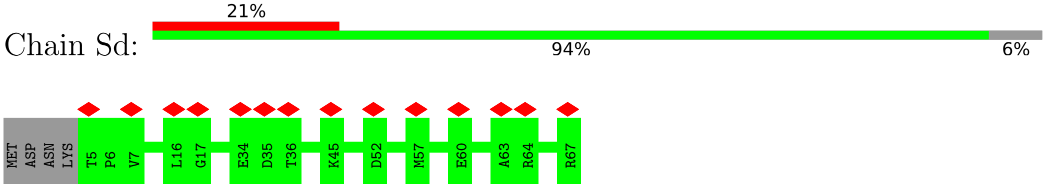
- Molecule 10: 40S ribosomal protein S18-A



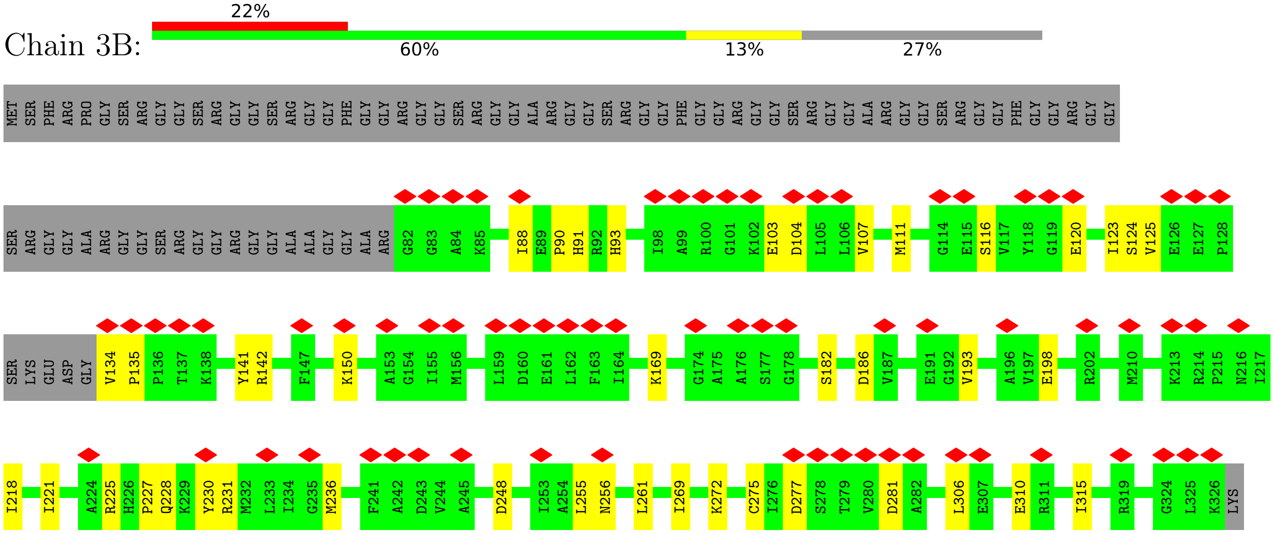
- Molecule 11: 40S ribosomal protein S23-A



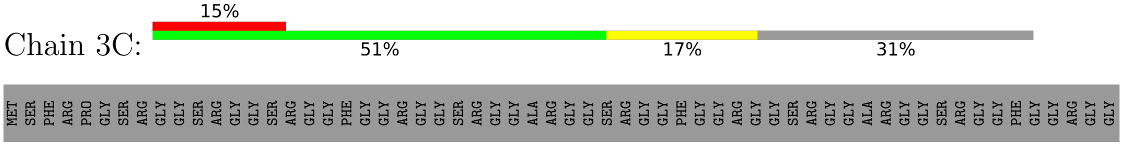
- Molecule 12: 40S ribosomal protein S28-A

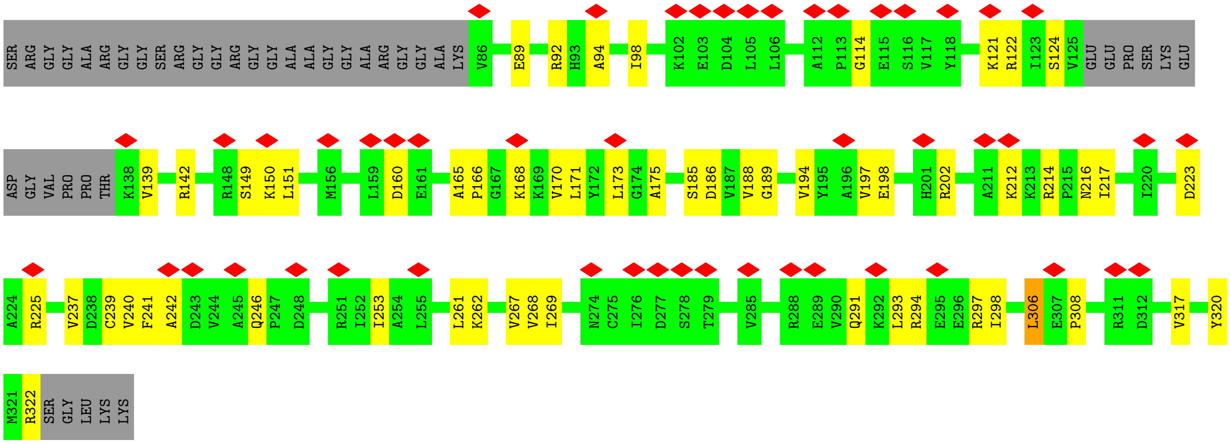


- Molecule 13: rRNA 2’-O-methyltransferase fibrillarin



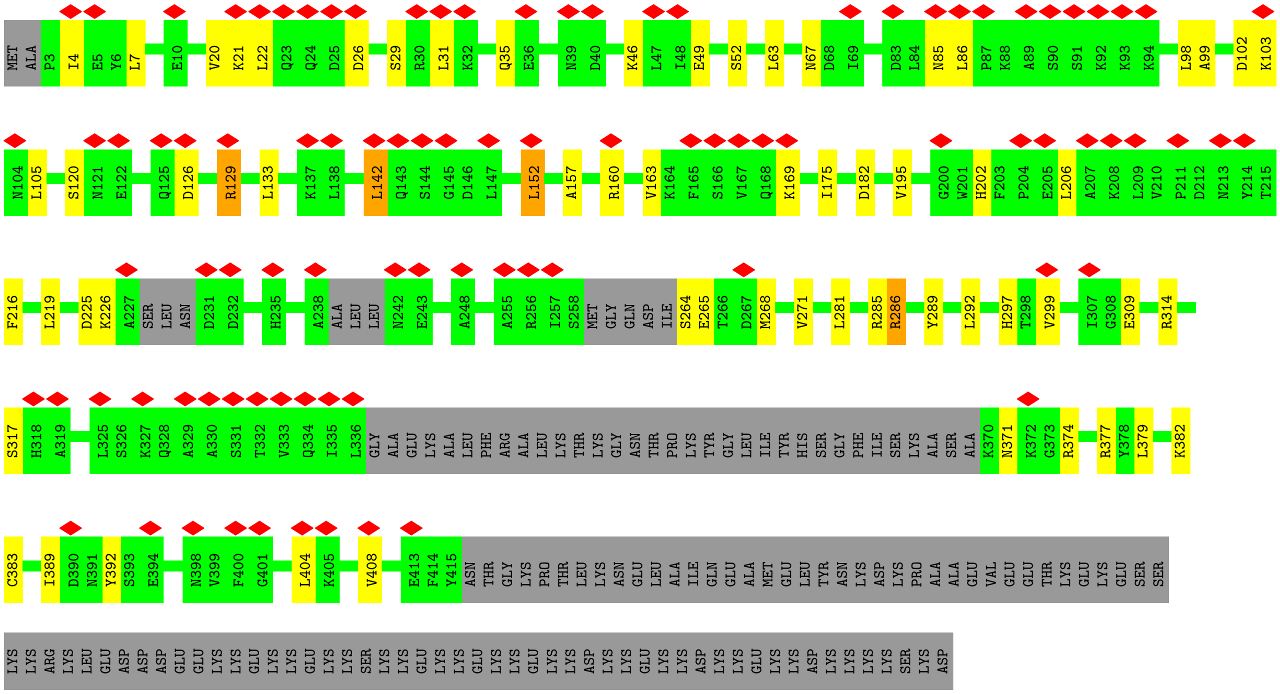
- Molecule 13: rRNA 2’-O-methyltransferase fibrillarin





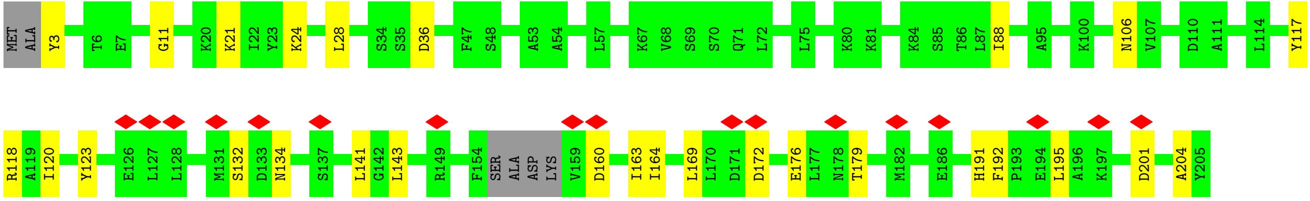
- Molecule 14: Nucleolar protein 56

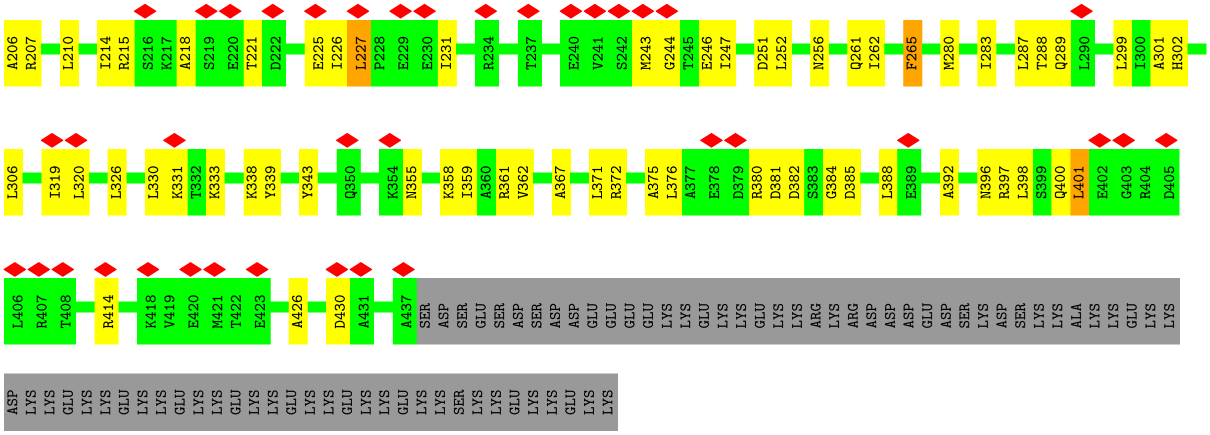
Chain 3D:



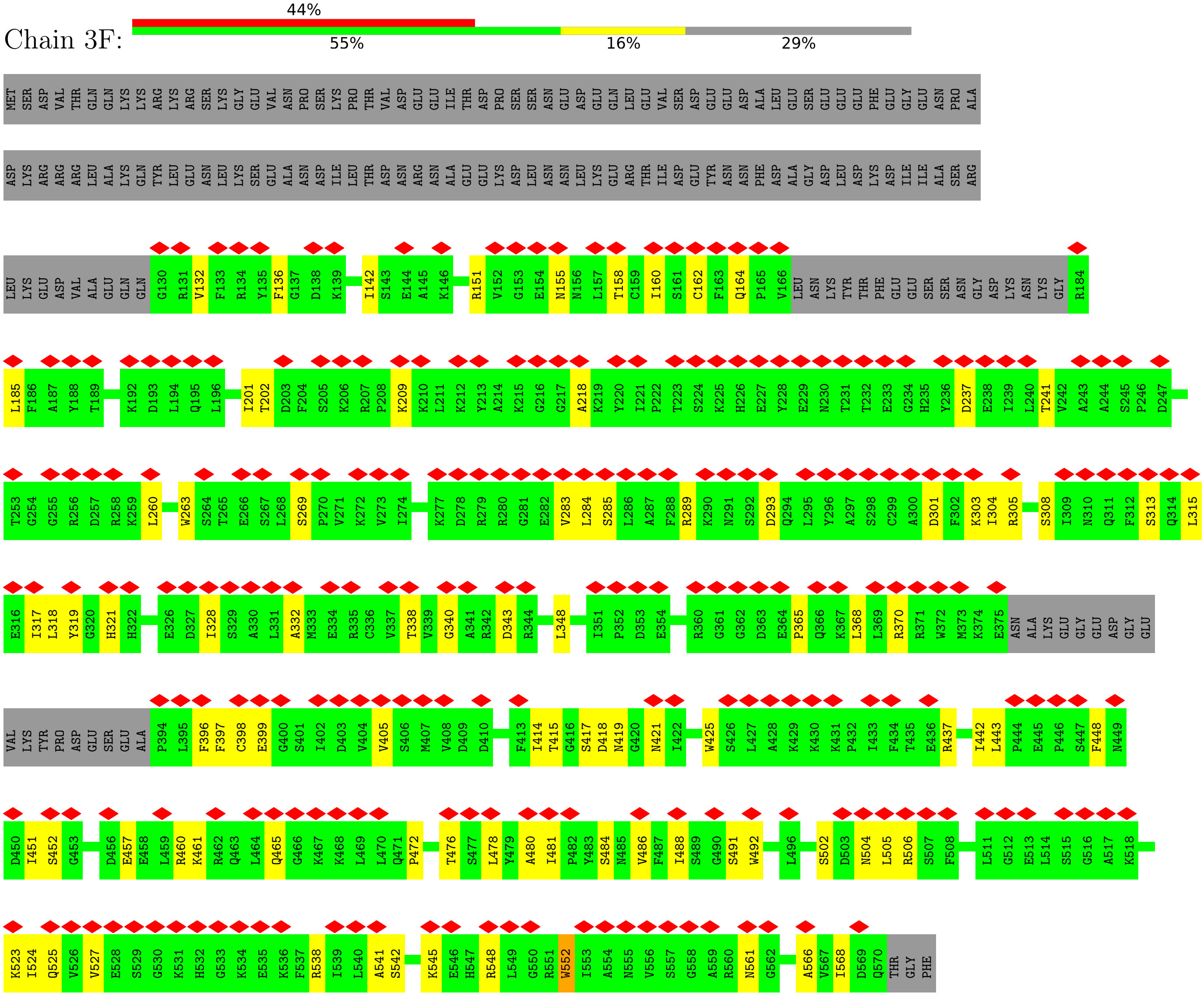
- Molecule 15: Nucleolar protein 58

Chain 3E:



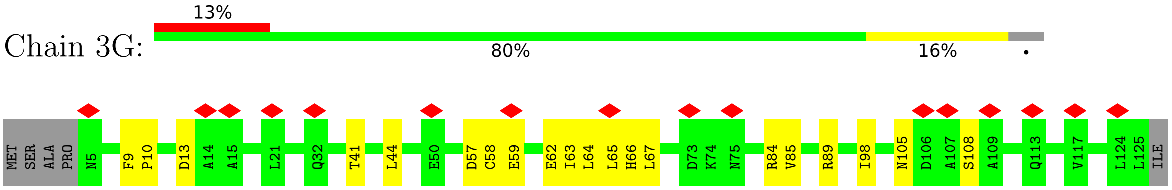


- Molecule 16: Ribosomal RNA-processing protein 9



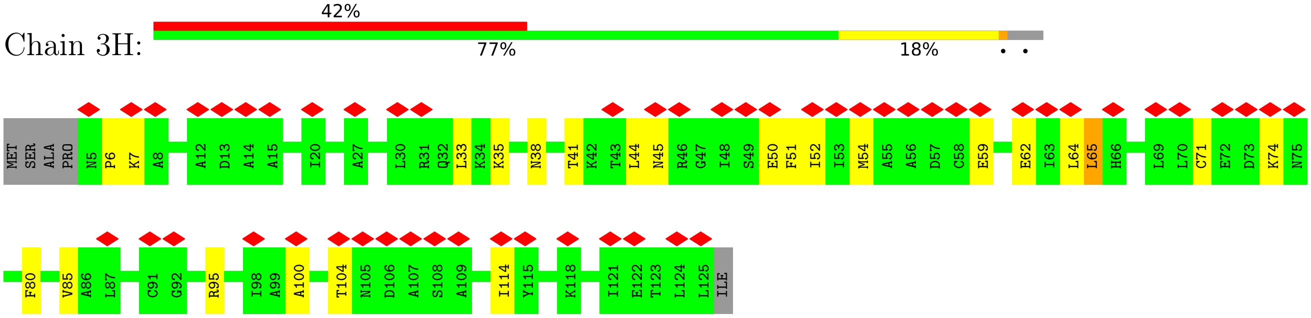
- Molecule 17: 13 kDa ribonucleoprotein-associated protein

Chain 3G:



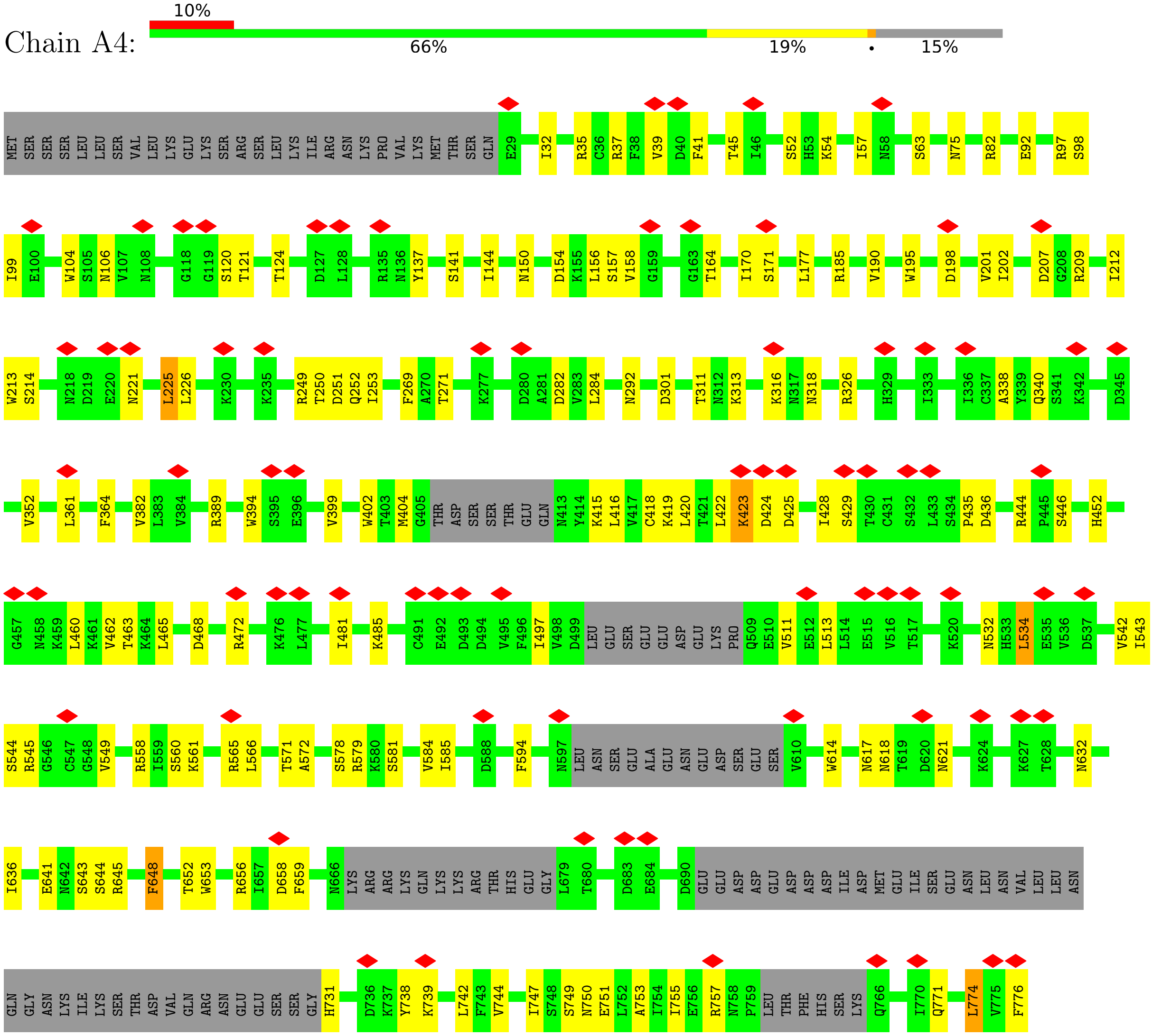
- Molecule 17: 13 kDa ribonucleoprotein-associated protein

Chain 3H:



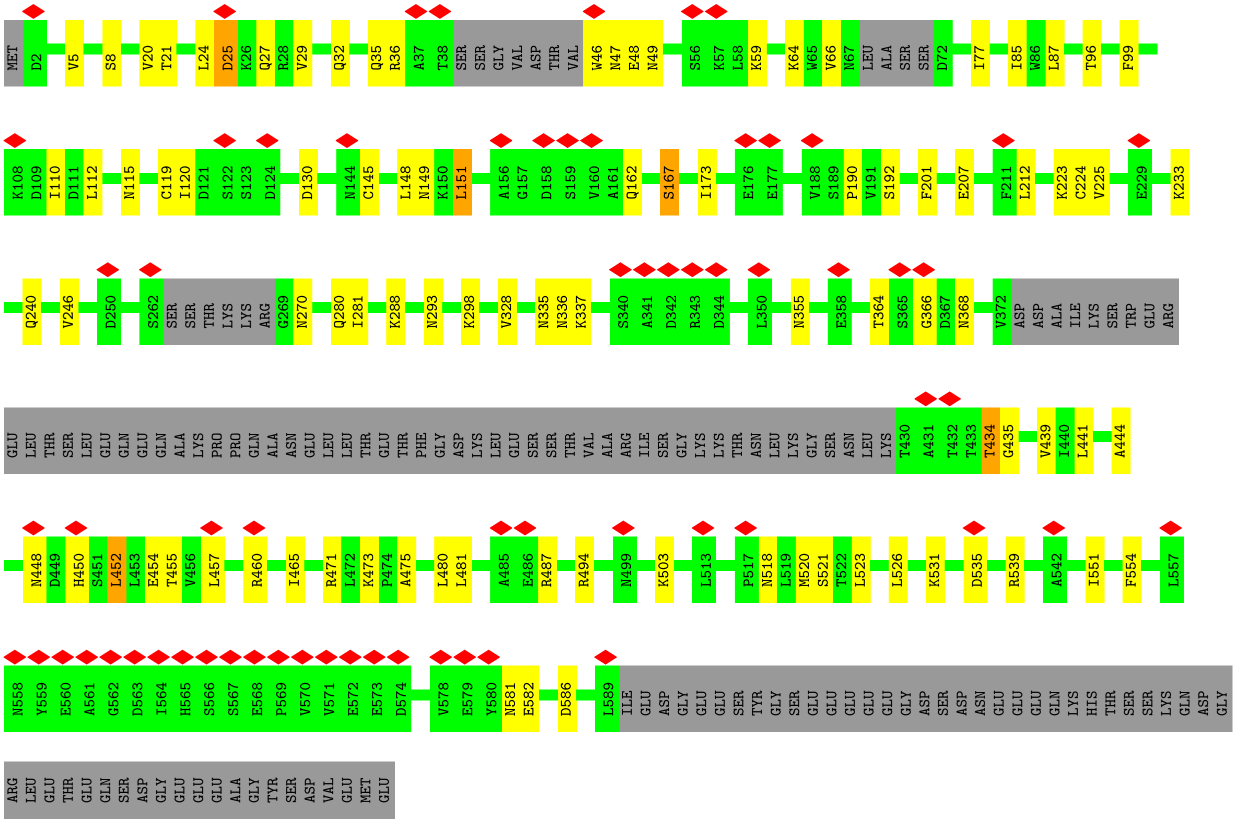
- Molecule 18: U3 small nucleolar RNA-associated protein 4

Chain A4:



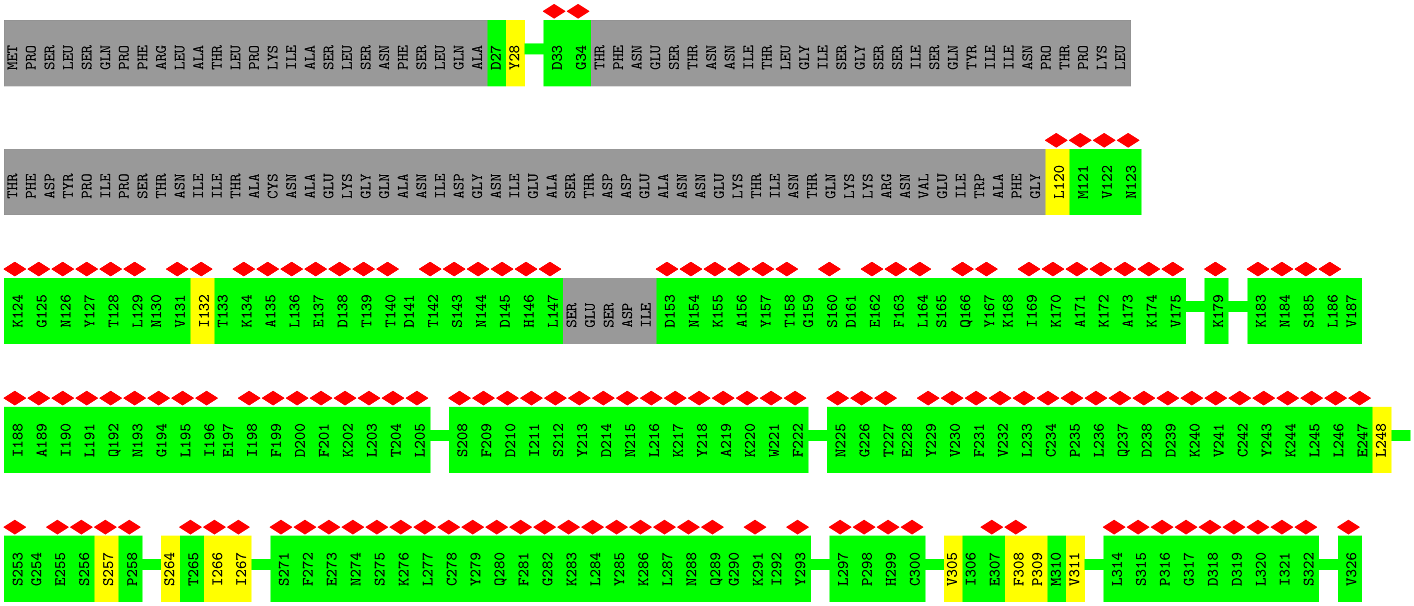
- Molecule 19: U3 small nucleolar RNA-associated protein 5

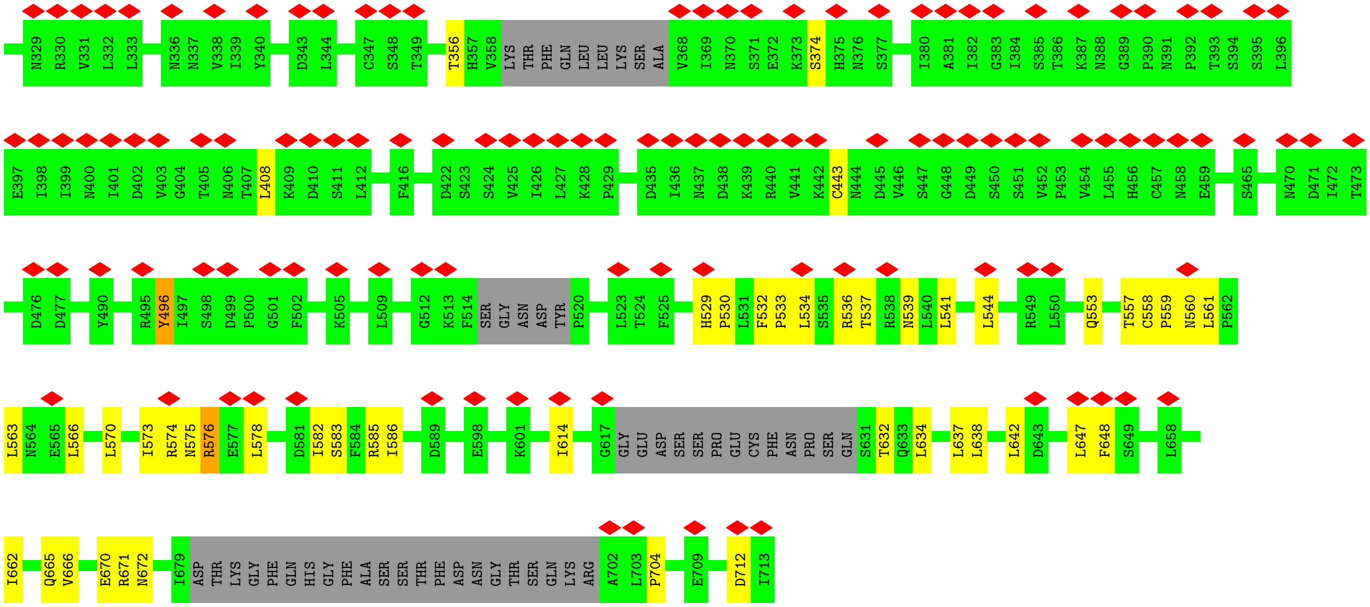
Chain A5:



- Molecule 20: U3 small nucleolar RNA-associated protein 8

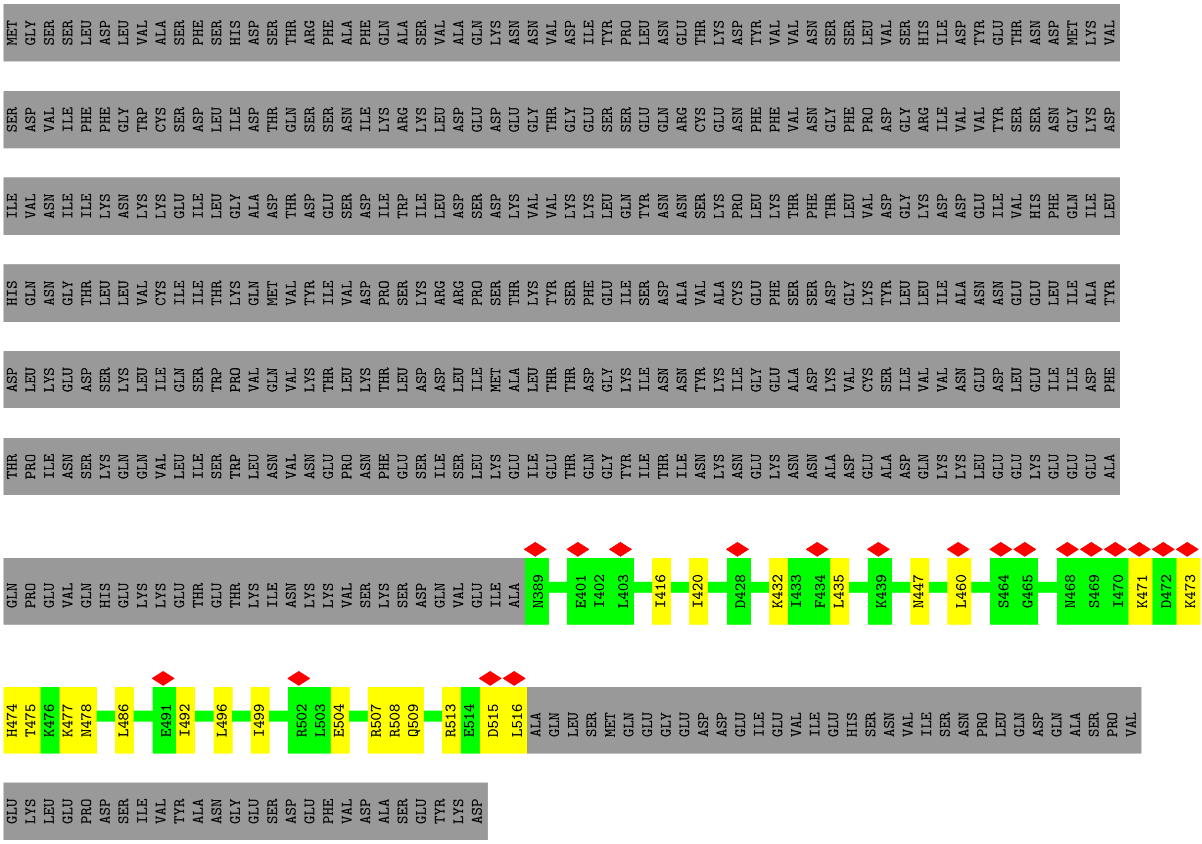
Chain A8:





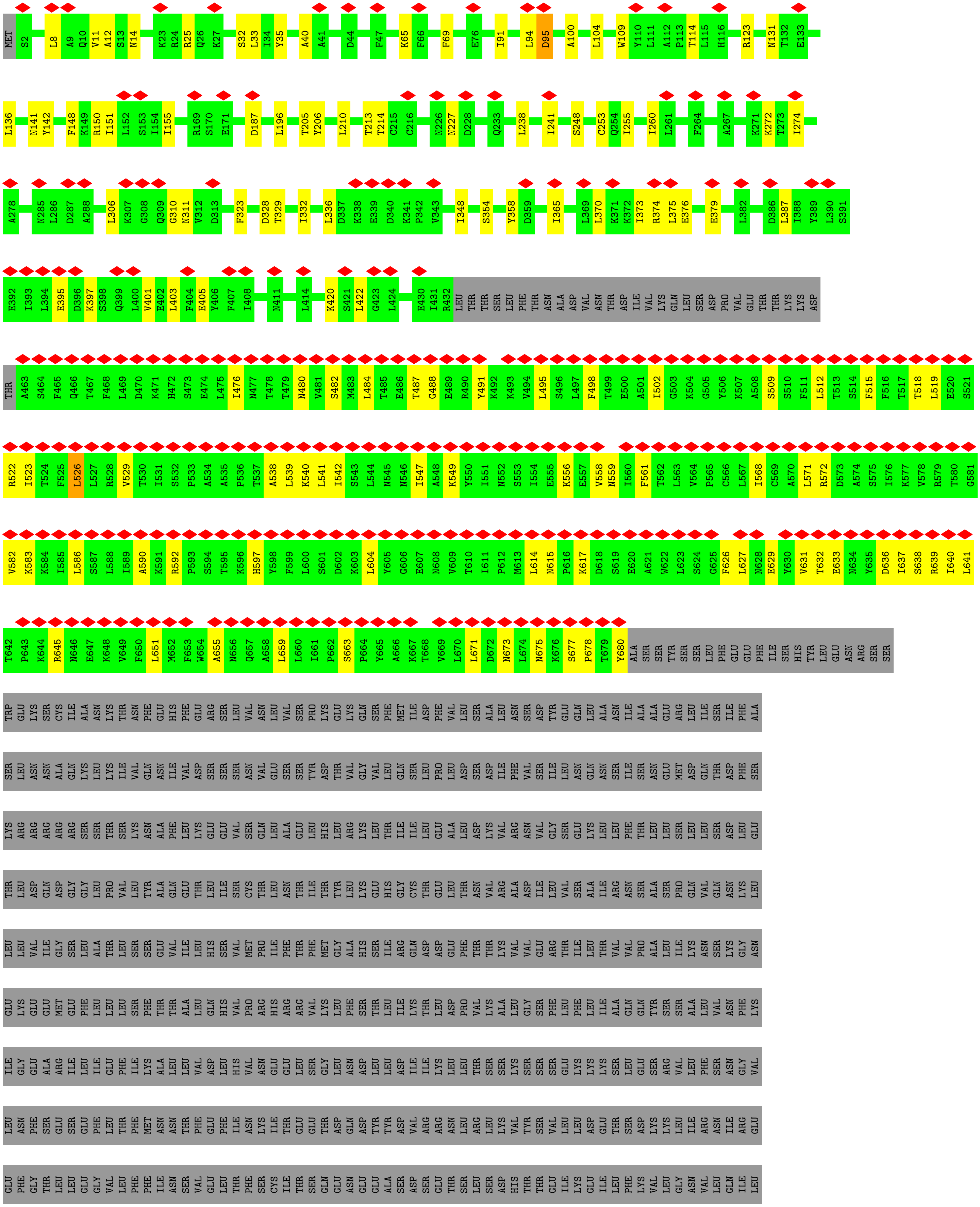
- Molecule 21: U3 small nucleolar RNA-associated protein 9

Chain A9:



- Molecule 22: U3 small nucleolar RNA-associated protein 10

Chain AE: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L136 N141 Y142 F148 K149 R150 I151 L152 S153 I154 I155 R169 S170 E171 D187 L196 T205 Y206 L210 T213 T214 C215 C216 N226 N227 D228 Q233 L238 I241 S248 C253 Q254 I255 I260 L261 F264 A267 K271 K272 T273 I274
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E392 I393 L394 E395 D396 K397 S398 Q399 L400 V401 E402 L403 F404 E405 Y406 F407 I408 N411 L414 K420 S421 L422 G423 L424 E430 I431 R432 LEU THR THR SER LEU PHE THR ASN ALA ASP VAL ASN THR ASP ILE VAL LYS GLN LEU SER ASP PRO VAL GLU THR THR LYS LYS ASP
THR A463 S464 F465 Q466 T467 F468 L469 D470 K471 H472 S473 E474 L475 I476 N477 T478 T479 N480 V481 S482 M483 L484 T485 E486 T487 G488 E489 R490 Y491 K492 K493 V494 L495 S496 L497 F498 T499 E500 A501 I502 G503 K504 G505 Y506 K507 A508 S509 S510 F511 L512 T513 S514 F515 F516 T517 T518 L519 E520 S521
R522 I523 T524 F525 L526 L527 R528 V529 T530 I531 S532 P533 A534 A535 P536 T537 A538 L539 K540 L541 I542 S543 L544 N545 N546 I547 A548 K549 Y550 I551 N552 S553 I554 E555 K556 E557 V558 N559 I560 F561 T562 L563 V564 P565 C566 L567 I568 C569 A570 L571 R572 D573 A574 S575 I576 K577 V578 R579 T580 G581
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TRP GLU LYS SER CYS ILE ALA ASN LYS THR ASN PHE GLU HIS PHE GLU ARG SER LEU VAL ASN LEU VAL SER PRO LYS GLU LYS GLN SER PHE MET ILE ASP PHE VAL LEU SER ALA LEU ASN SER ASP TYR GLU GLN LEU ALA ASN ILE ALA ALA GLU ARG LEU ILE SER ILE PHE ALA
SER LEU ASN ASN ALA GLN LYS LEU LYS ILE VAL GLN ASN ILE VAL ASP SER SER SER ASN VAL GLU SER SER TYR ASP THR VAL GLY VAL LEU GLN SER LEU PRO LEU ASP SER SER ASP ILE PHE VAL SER ILE LEU ASN GLN ASN SER ILE SER ASN GLU MET ASP GLN THR ASP PHE SER
LYS ARG ARG ARG ARG SER SER THR SER LYS ASN ALA PHE LEU LYS GLU GLU VAL SER GLN LEU ALA GLU LEU HIS LEU ARG LYS LEU THR ILE LEU GLU ALA LEU ASP LYS VAL ARG ASN VAL GLY SER GLU LYS LEU LEU PHE THR LEU LEU SER LEU LEU SER ASP LEU GLU
THR LEU ASP GLN ASP GLY GLY LEU PRO VAL LEU TYR ALA GLN GLU THR LEU ILE SER CYS THR LEU ASN THR ILE THR TYR LEU LYS GLU HIS GLY CYS THR GLU LEU THR ASN VAL ARG ALA ASP ILE LEU VAL SER ALA ILE ARG ASN SER ALA SER PRO GLN VAL GLN ASN LYS LEU
LEU LEU VAL ILE GLY SER LEU ALA THR LEU SER SER GLU VAL ILE LEU HIS SER VAL MET PRO ILE PHE THR PHE MET GLY ALA HIS SER ILE ARG GLN ASP ASP GLU PHE THR THR LYS VAL VAL GLU ARG THR ILE LEU THR VAL VAL PRO ALA LEU ILE LYS ASN SER LYS GLY ASN
GLU LYS GLU GLU MET GLU PHE LEU LEU LEU SER PHE THR THR ALA LEU GLN HIS VAL PRO ARG HIS ARG ARG VAL LYS LEU PHE SER THR LEU ILE LYS THR LEU ASP PRO VAL LYS ALA LEU GLY SER PHE LEU PHE LEU ILE ALA GLN GLN TYR SER SER ALA LEU VAL ASN PHE LYS
ILE GLY GLU ALA ARG ILE LEU ILE GLU PHE ILE LYS ALA LEU LEU VAL ASP LEU HIS VAL ASN GLU GLU LEU SER GLY LEU ASN ASP LEU LEU ASP ILE ILE LYS LEU LEU THR SER SER LYS SER SER GLU LYS LYS SER LEU GLU SER ARG VAL LEU PHE SER ASN GLY VAL
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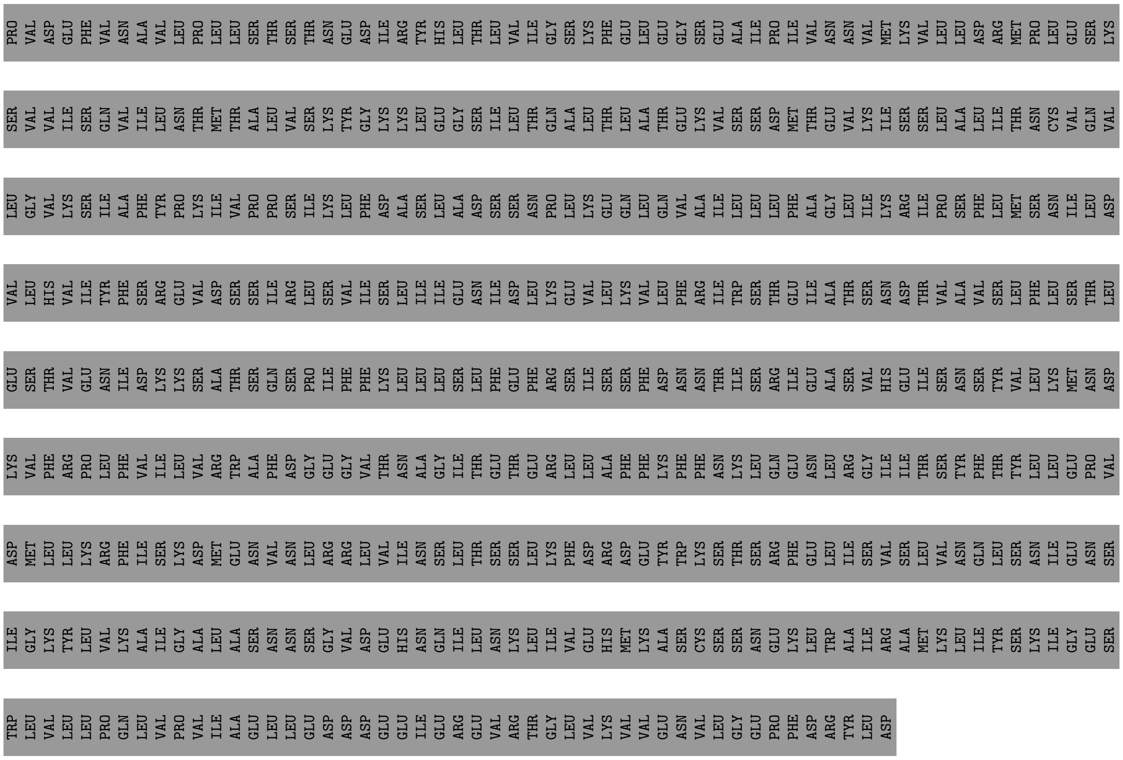
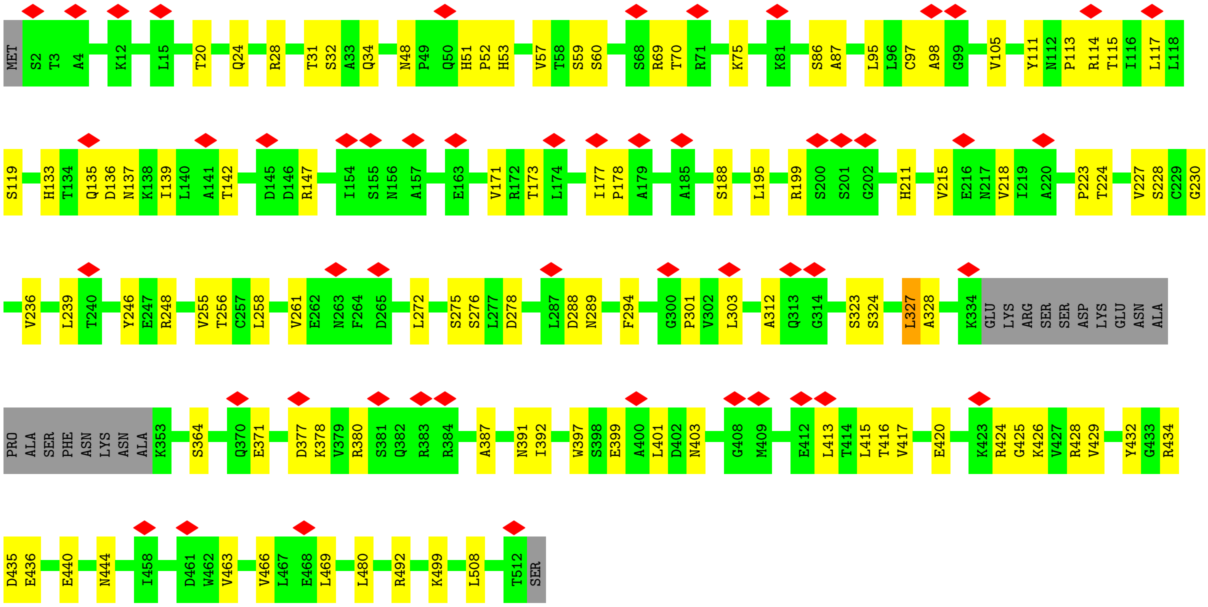
GLU PHE GLY THR LEU LEU GLU GLY VAL LEU PHE PHE ILE ASN SER VAL GLU LEU THR PHE SER CYS ILE THR SER GLN GLN ASN GLU GLU ALA SER ASP SER GLU THR SER LEU SER ASP HIS THR THR GLU ILE LYS GLU ILE LEU PHE LYS VAL LEU GLY ASN VAL LEU GLN ILE LEU



- Molecule 23: U3 small nucleolar RNA-associated protein 15

Chain AF:



- Molecule 24: NET1-associated nuclear protein 1

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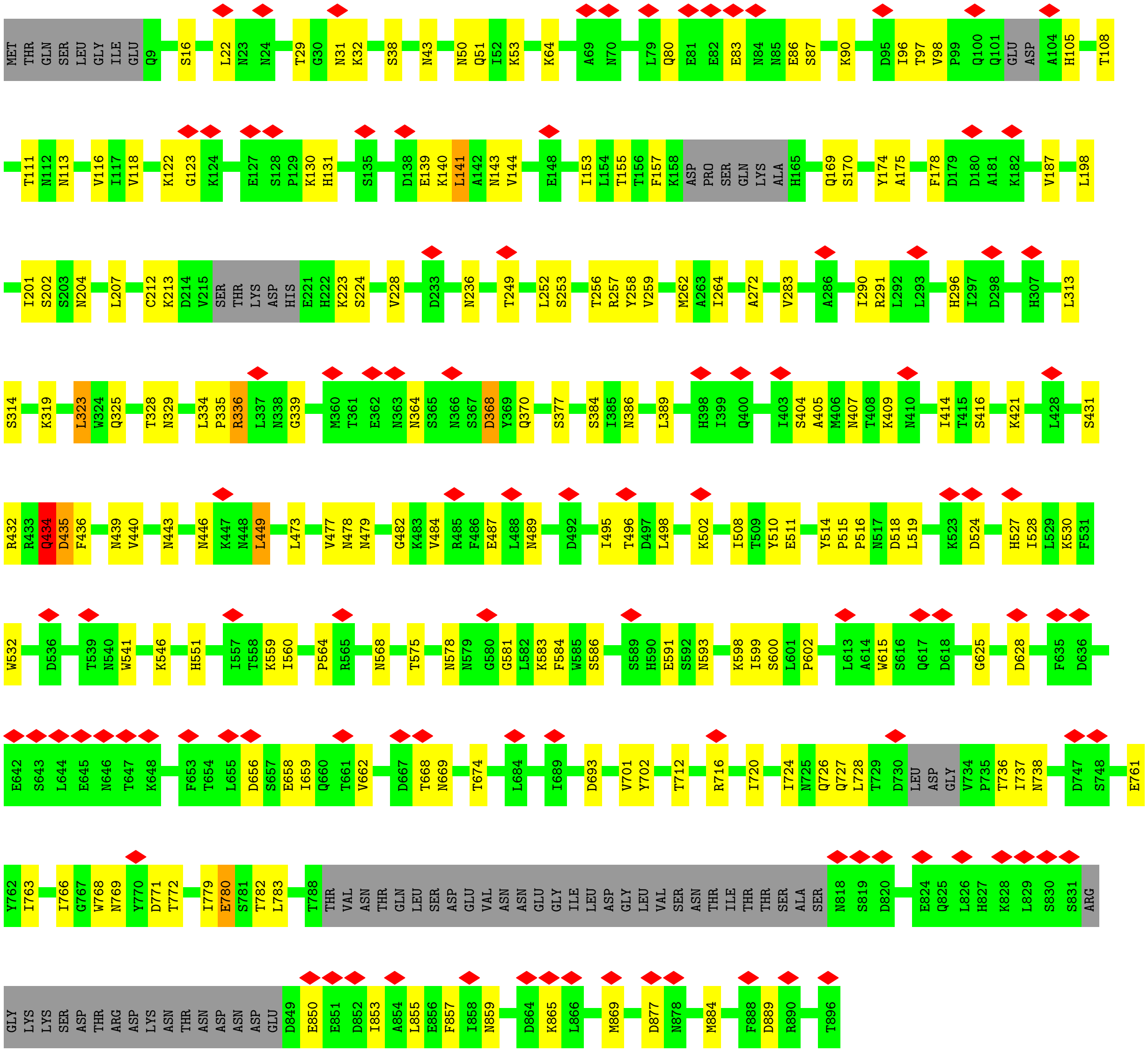
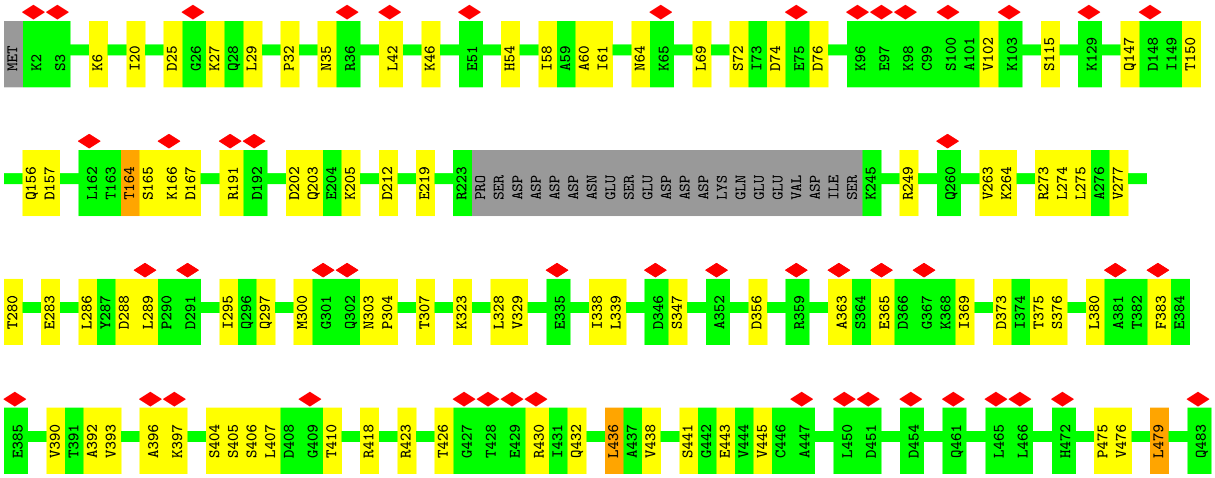
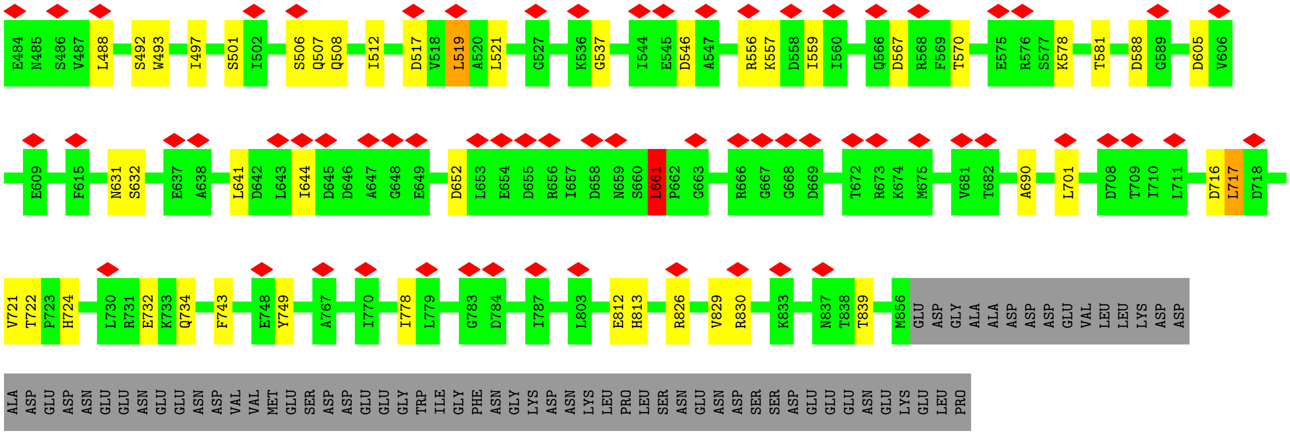


- Molecule 25: Periodic tryptophan protein 2

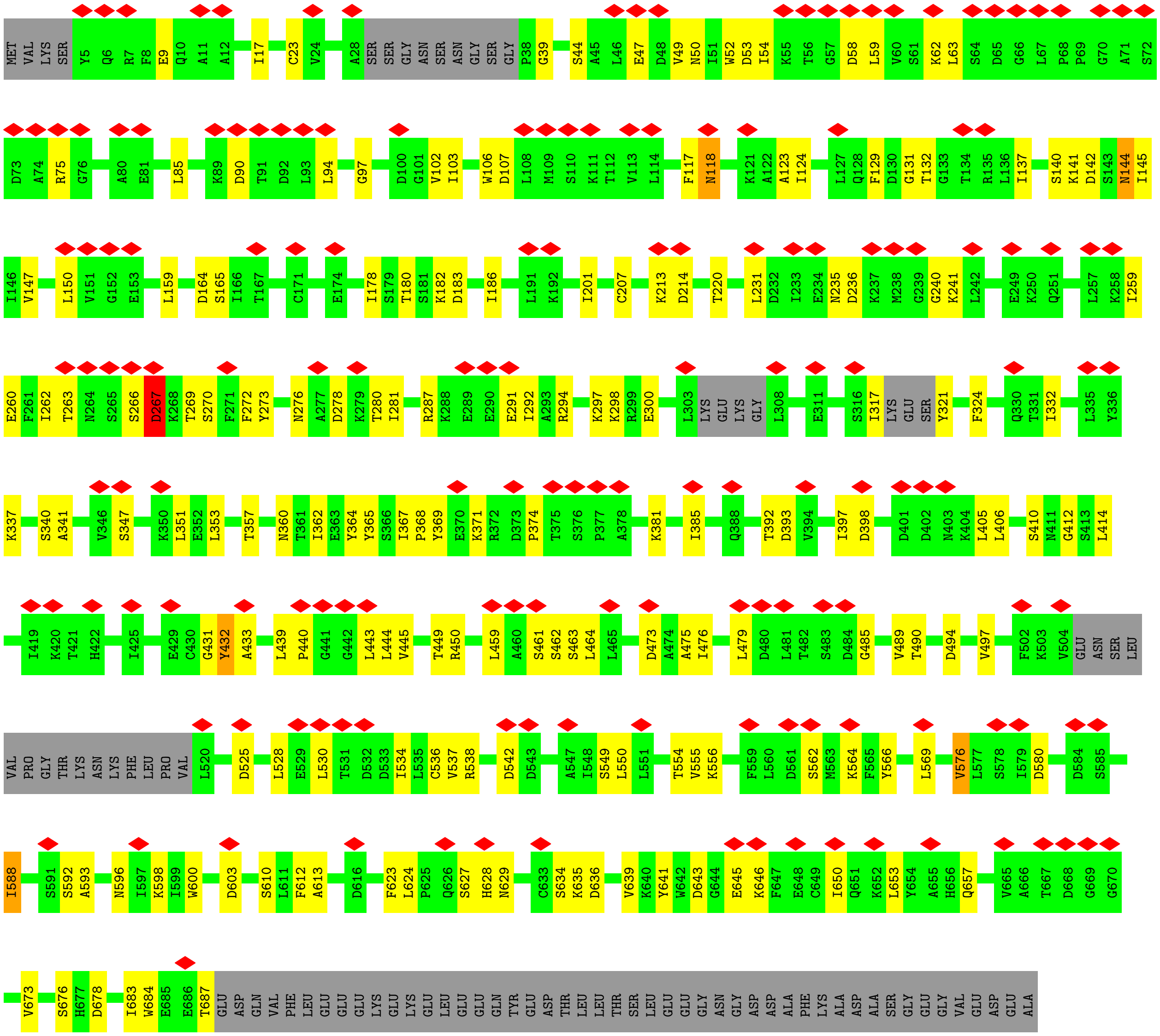
Chain B1:

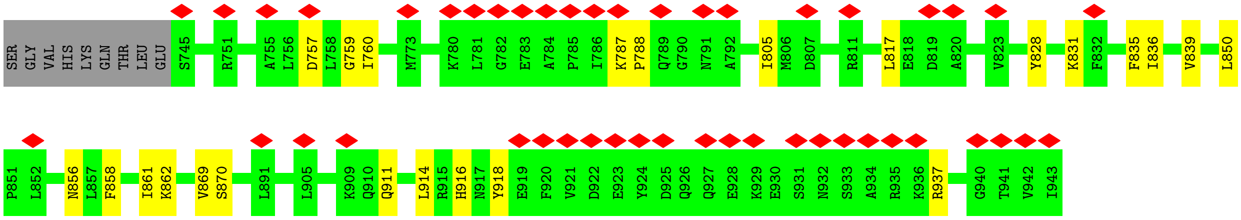




- Molecule 26: U3 small nucleolar RNA-associated protein 12

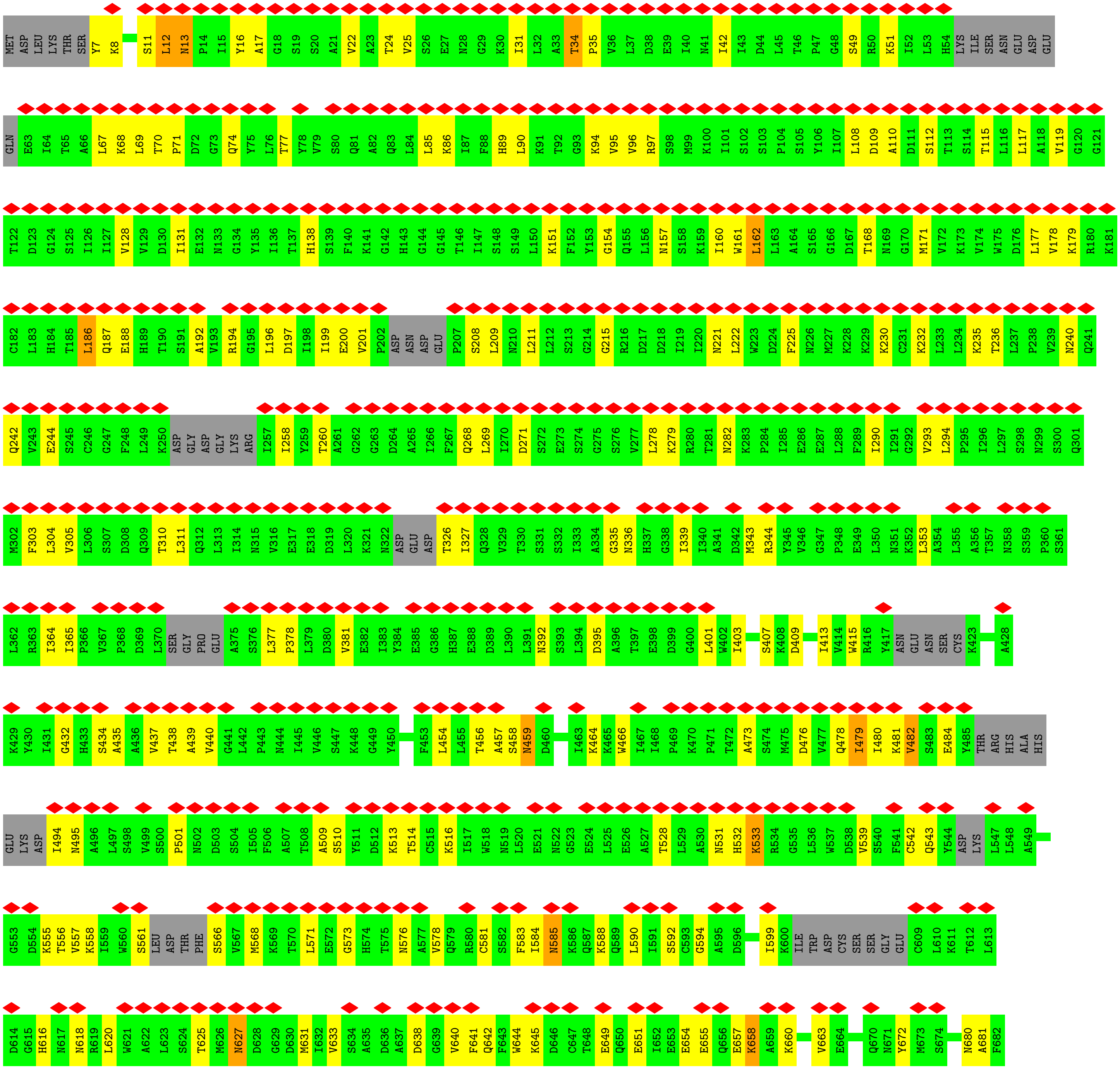
Chain B2:

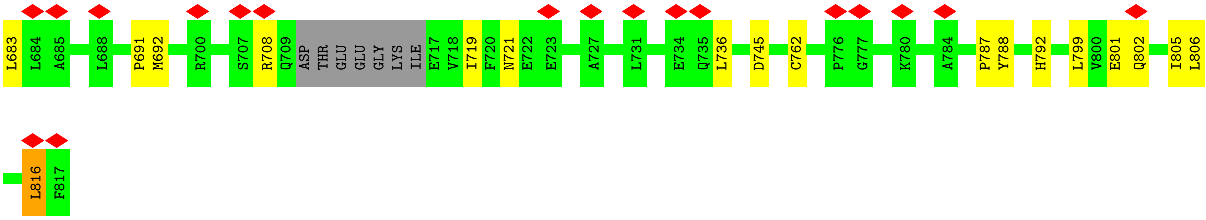




- Molecule 27: U3 small nucleolar RNA-associated protein 13

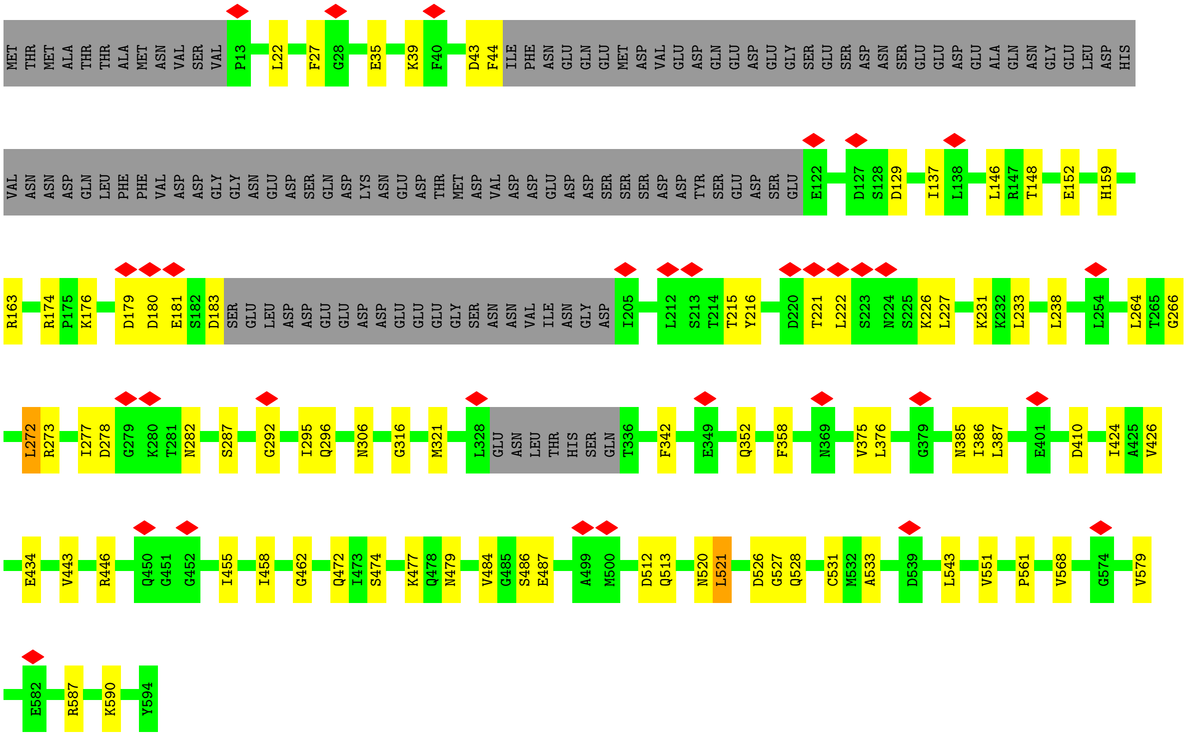
Chain B3:





- Molecule 28: U3 small nucleolar RNA-associated protein 18

Chain B8:



- Molecule 29: U3 small nucleolar RNA-associated protein 21

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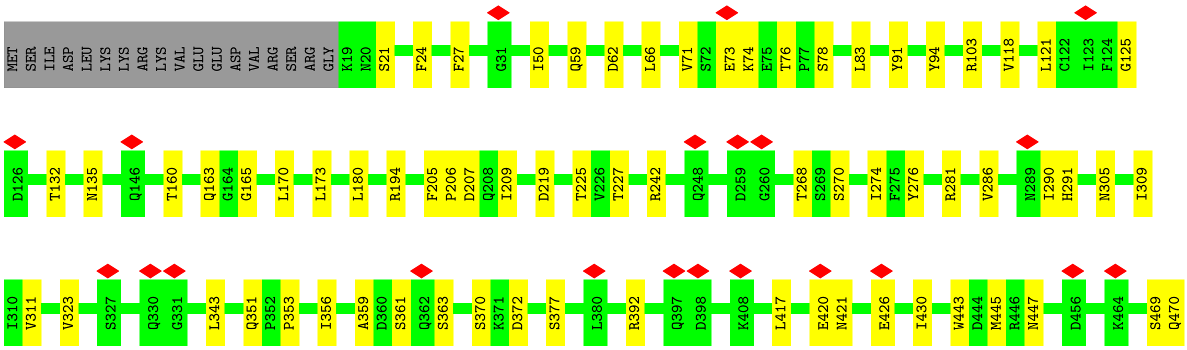

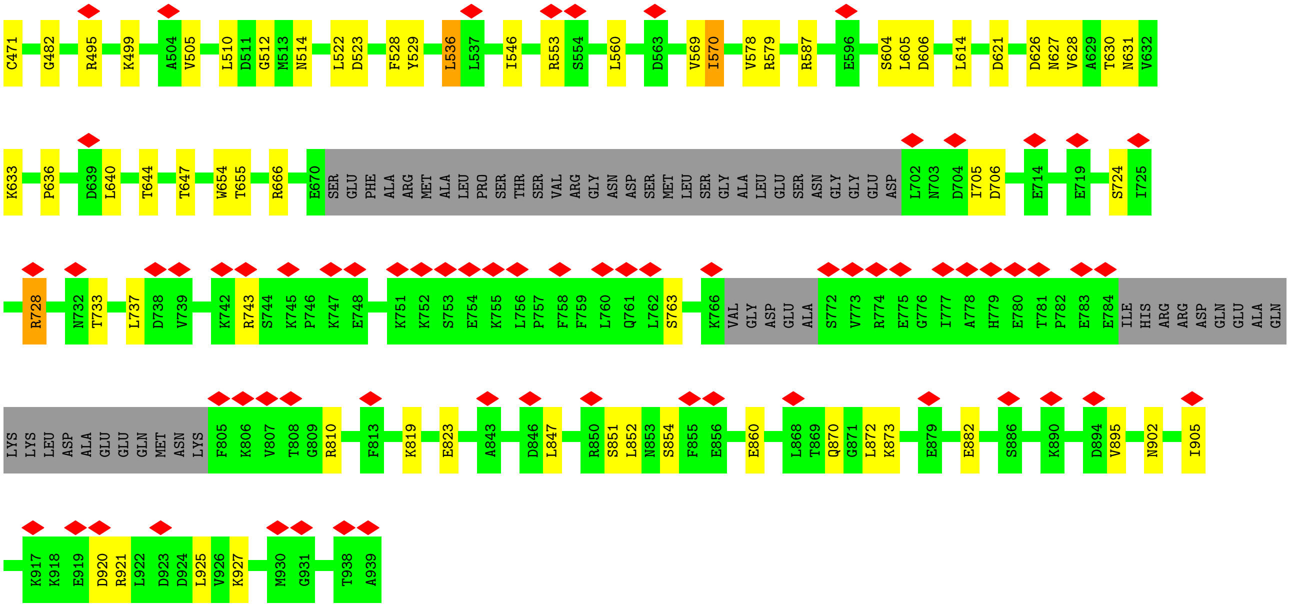

- Molecule 30: U3 small nucleolar RNA-associated protein 6

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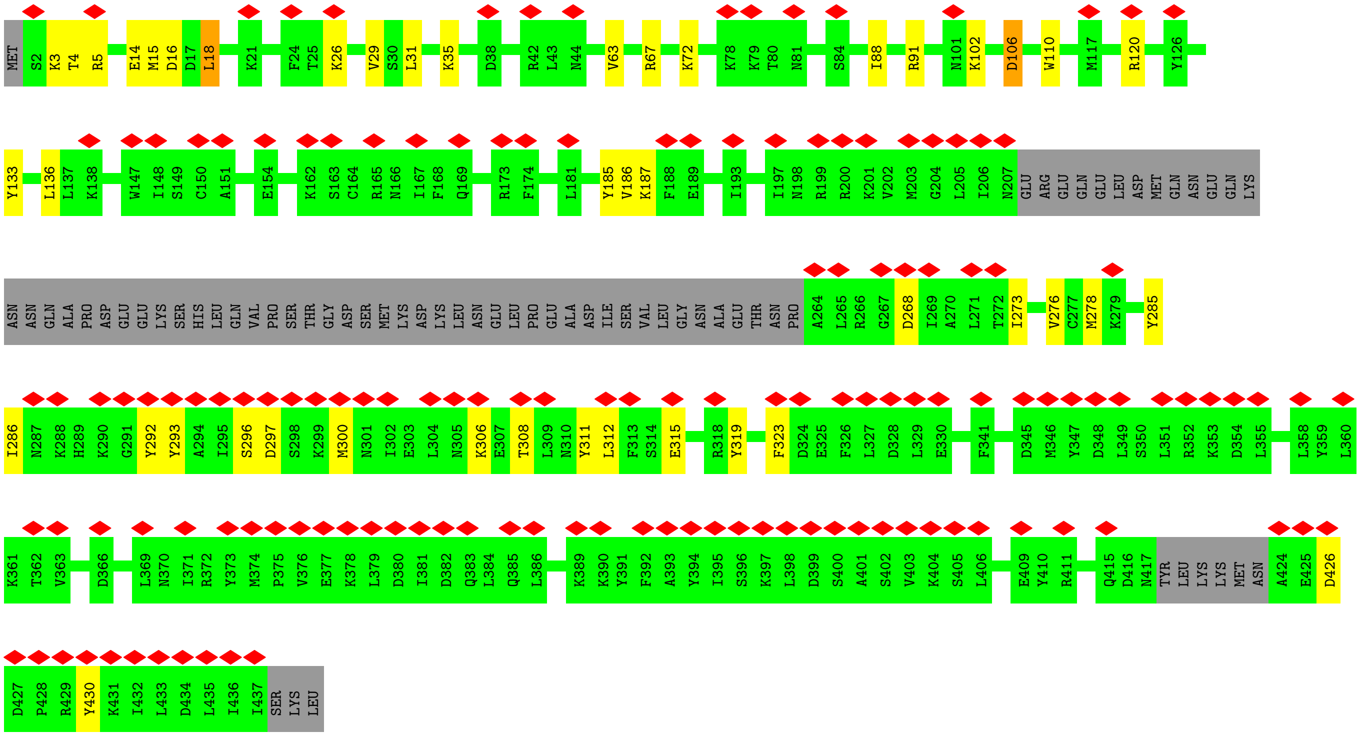
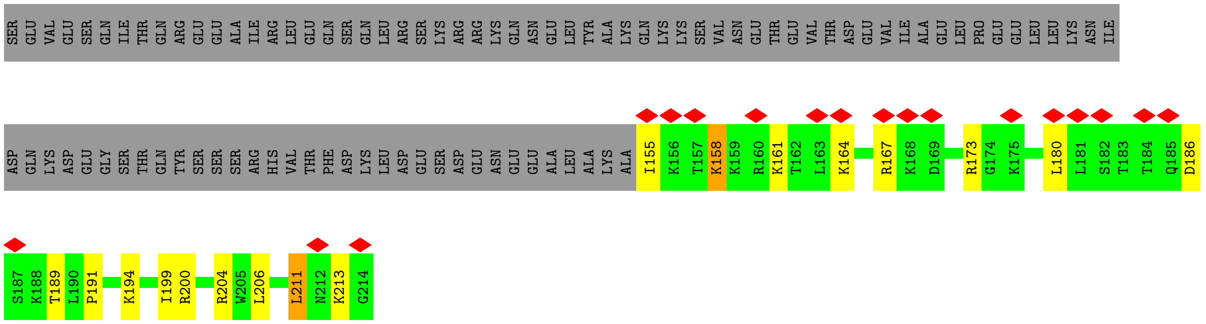


- Molecule 31: Bud site selection protein 21

Chain 5B:



- Molecule 32: U3 small nucleolar RNA-associated protein 7

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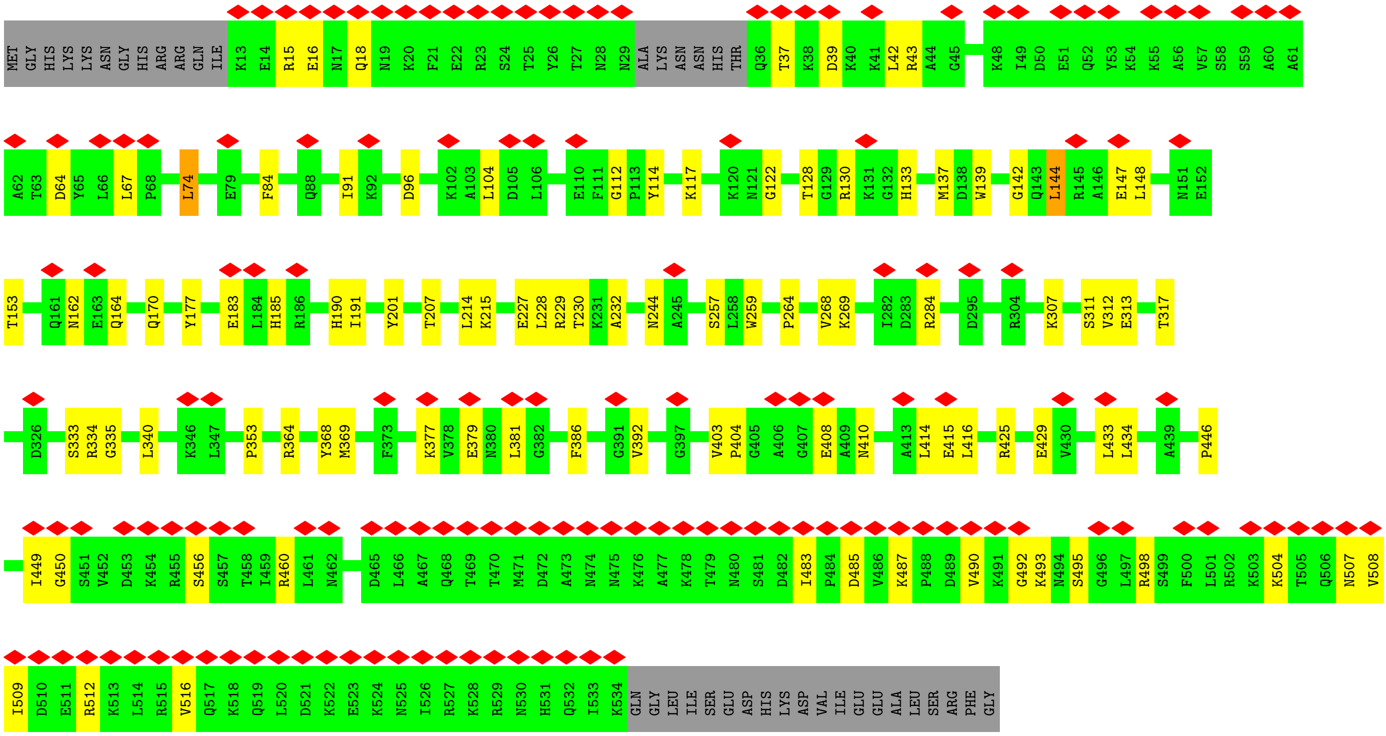

- Molecule 33: U3 small nucleolar RNA-associated protein 11

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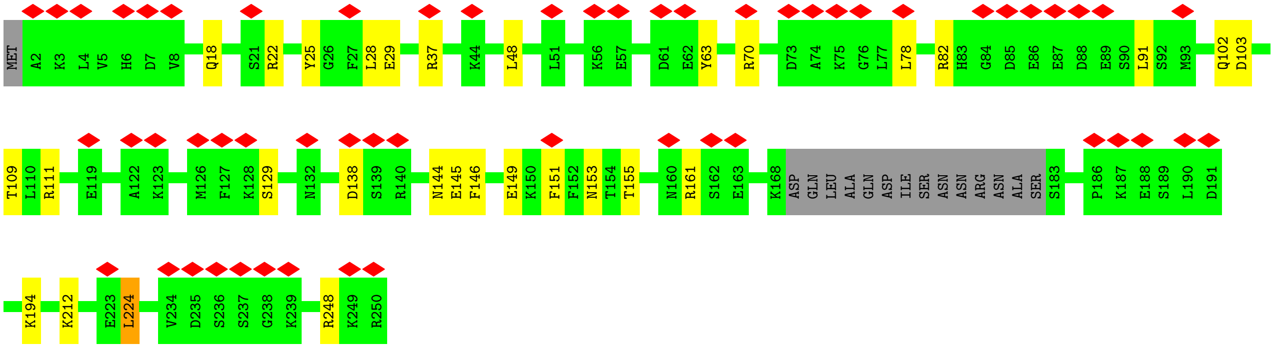
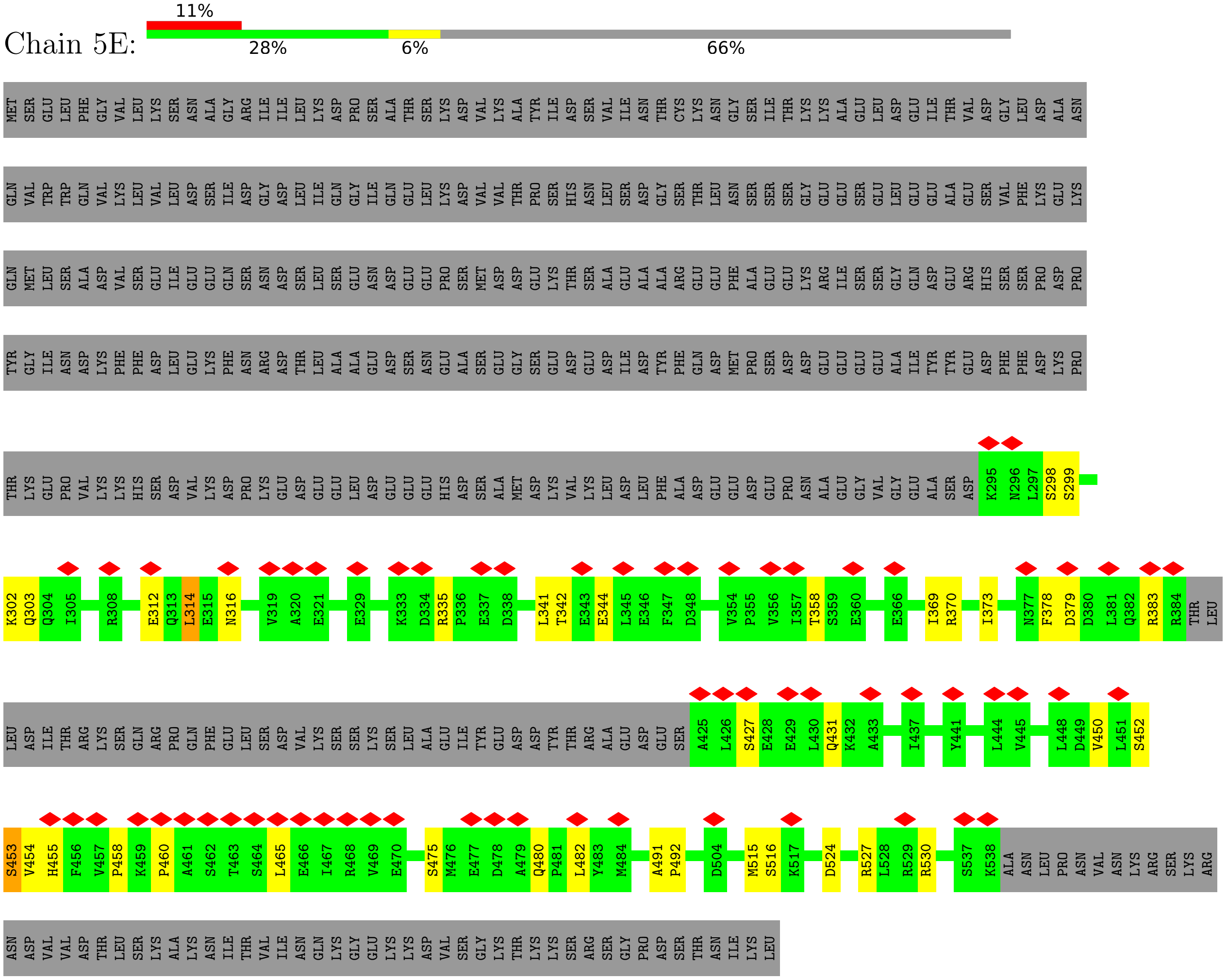


- Molecule 34: U3 small nucleolar RNA-associated protein MPP10

Chain 5E:



- Molecule 35: U3 small nucleolar ribonucleoprotein protein IMP3

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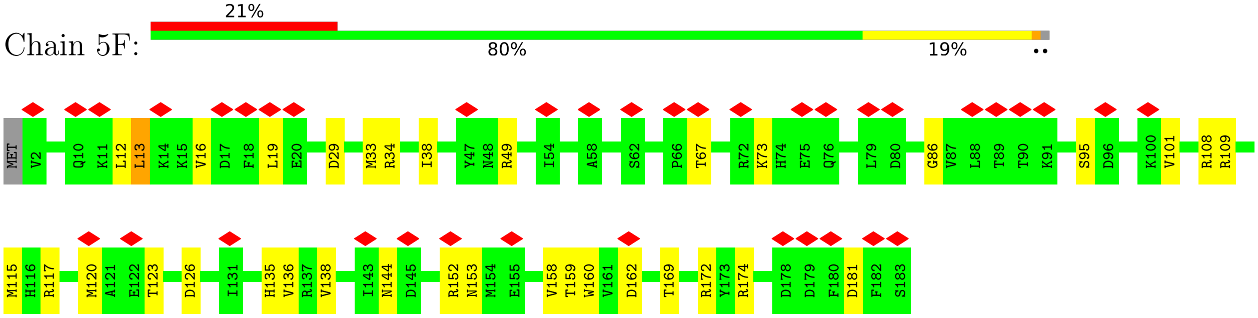

- Molecule 36: U3 small nucleolar ribonucleoprotein protein IMP4

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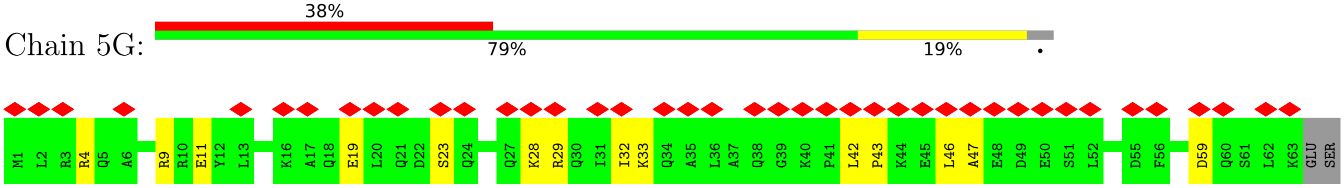
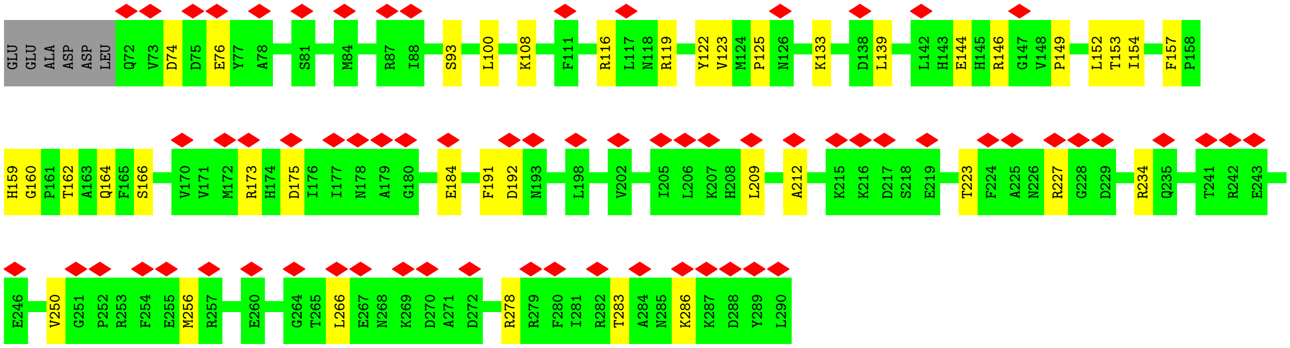
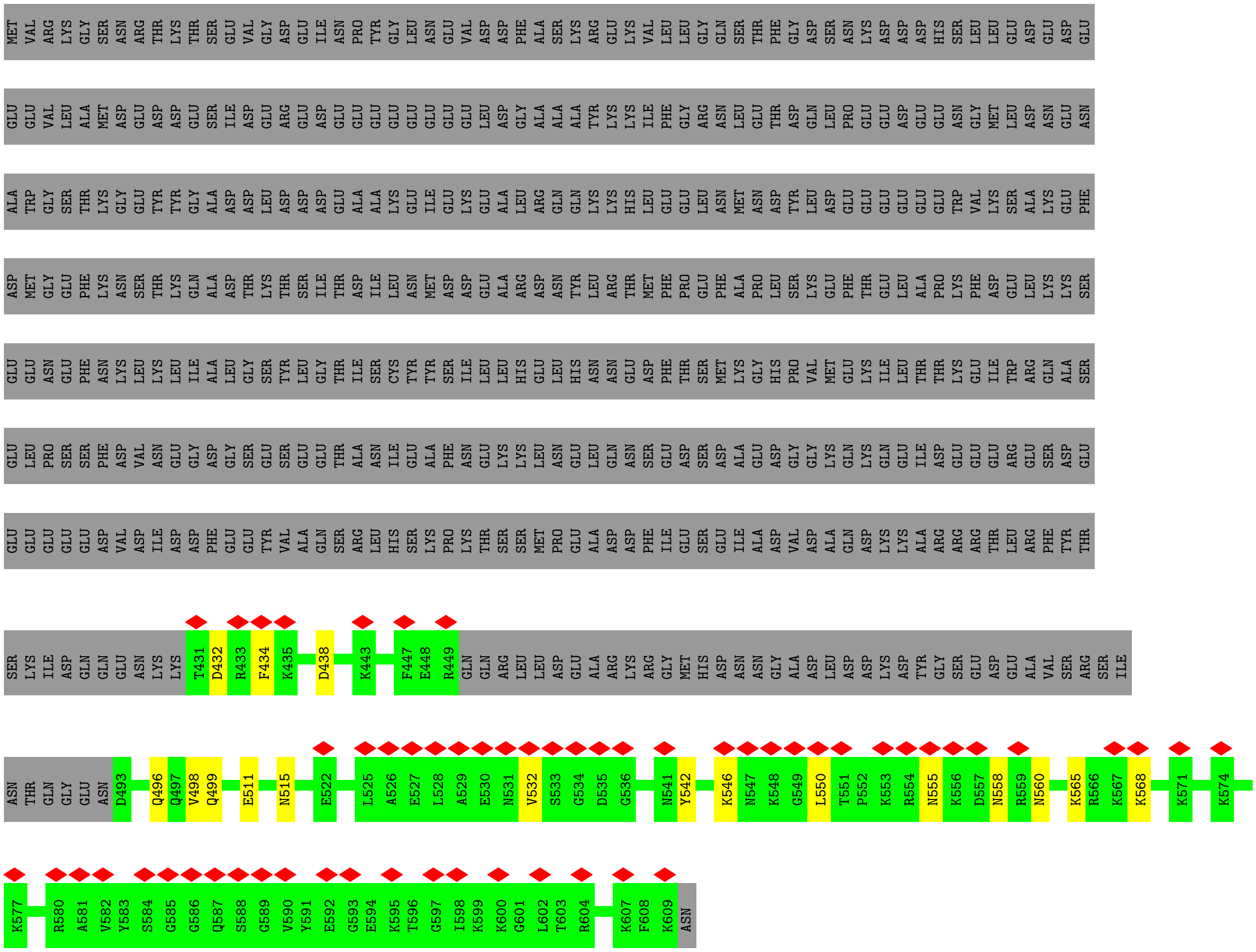




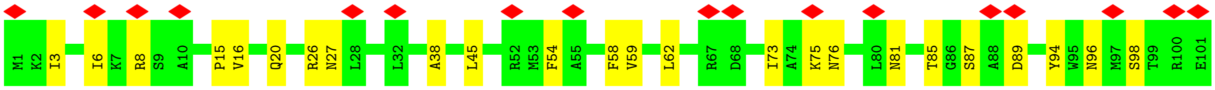
- Molecule 37: Something about silencing protein 10

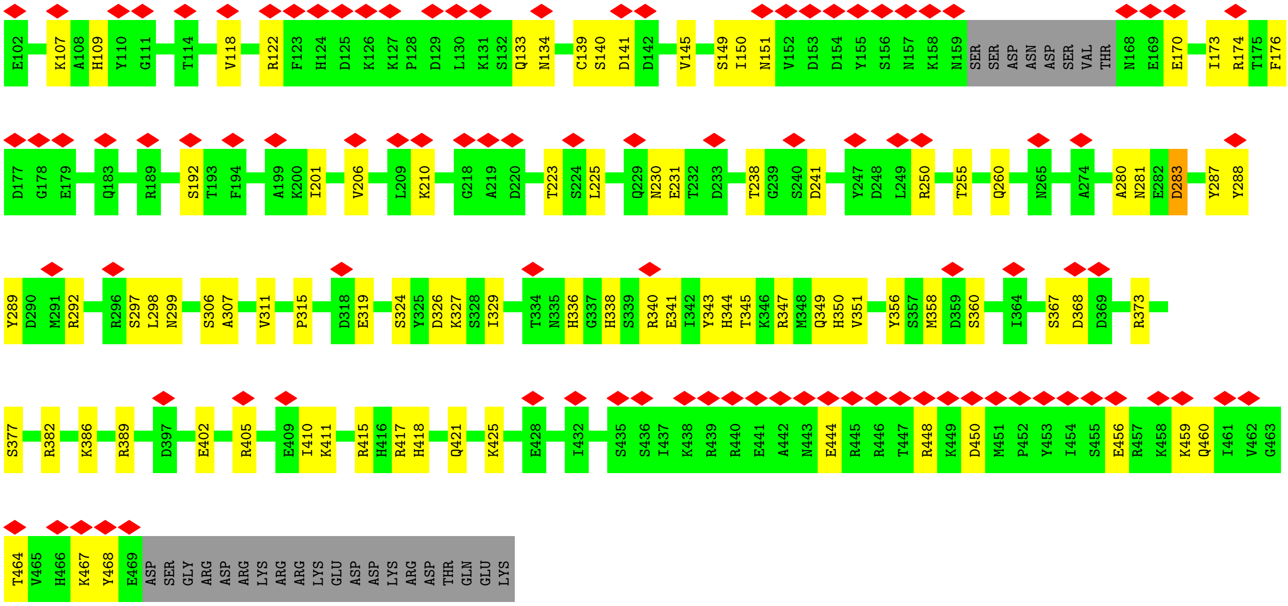
Chain 5H:



- Molecule 38: Protein SOF1

Chain 5I:





- Molecule 39: rRNA-processing protein FCF2

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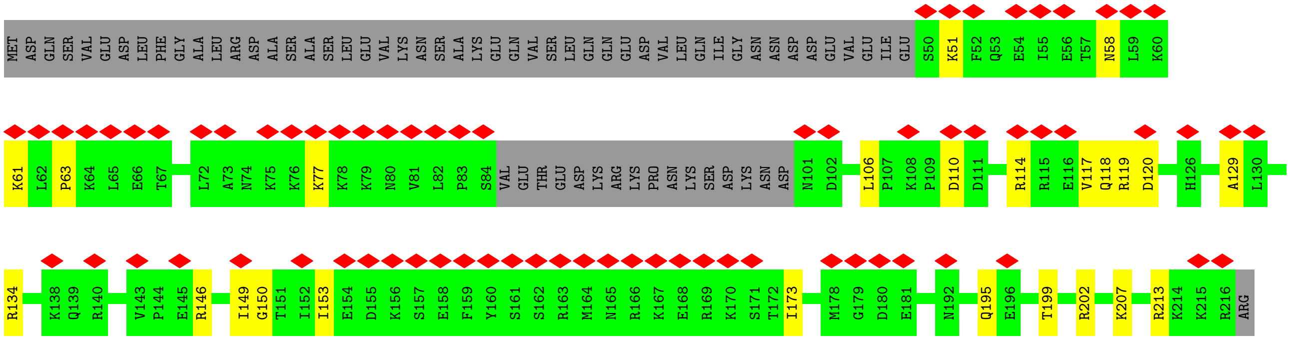
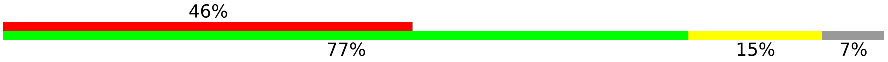
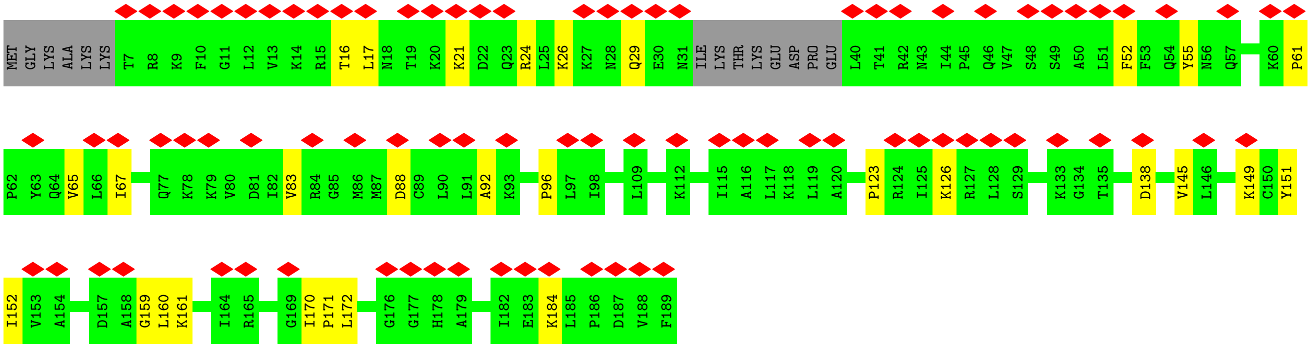


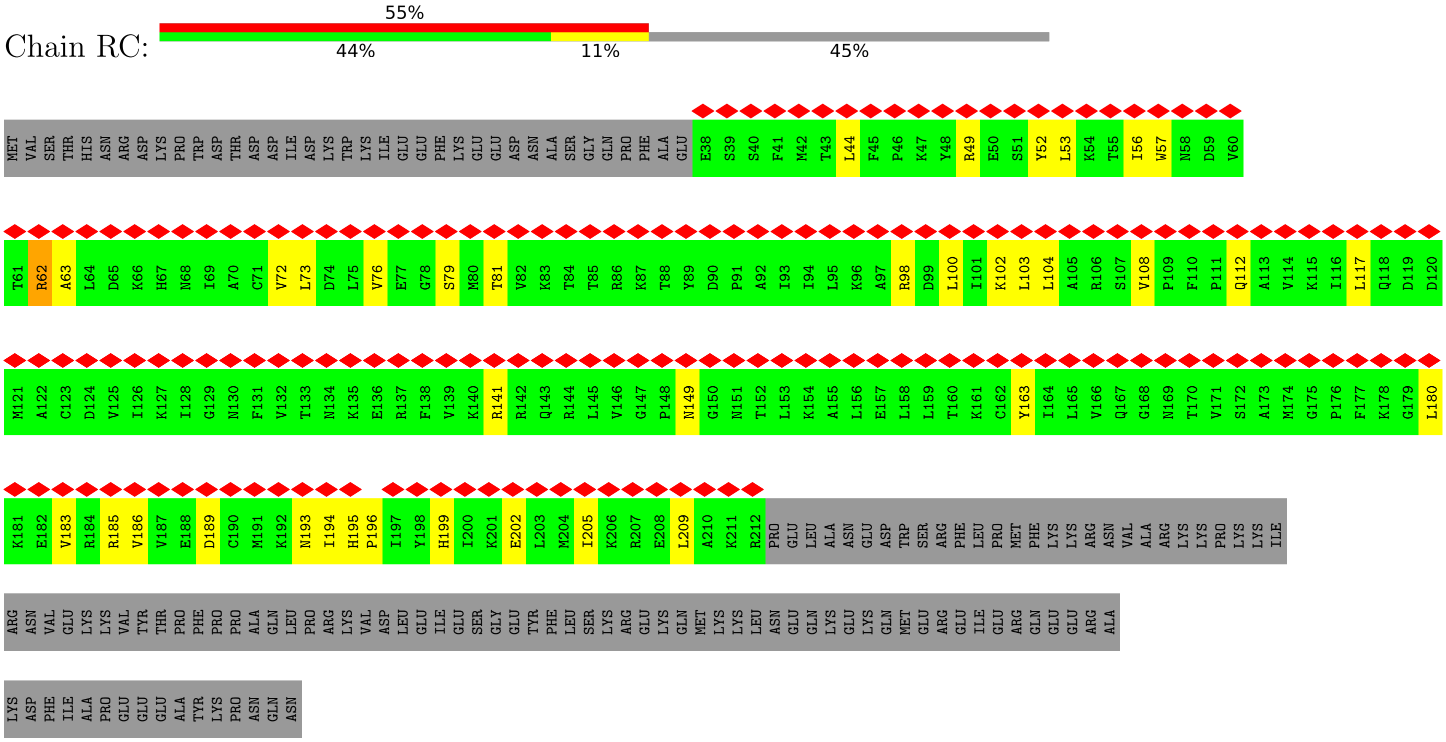
- Molecule 40: rRNA-processing protein FCF1

Chain 5K:





- Molecule 41: KRR1 small subunit processome component



MET VAL SER THR HIS ASN ARG ASP LYS PRO TRP ASP THR ASP ASP ILE ASP LYS TRP LYS ILE GLU GLU PHE LYS GLU GLU ASP ASN ALA SER GLY GLN PRO PHE ALA GLU E38 S39 S40 F41 M42 T43 L44 F45 P46 K47 Y48 R49 E50 S51 Y52 L53 K54 T55 I56 W57 N58 D59 V60

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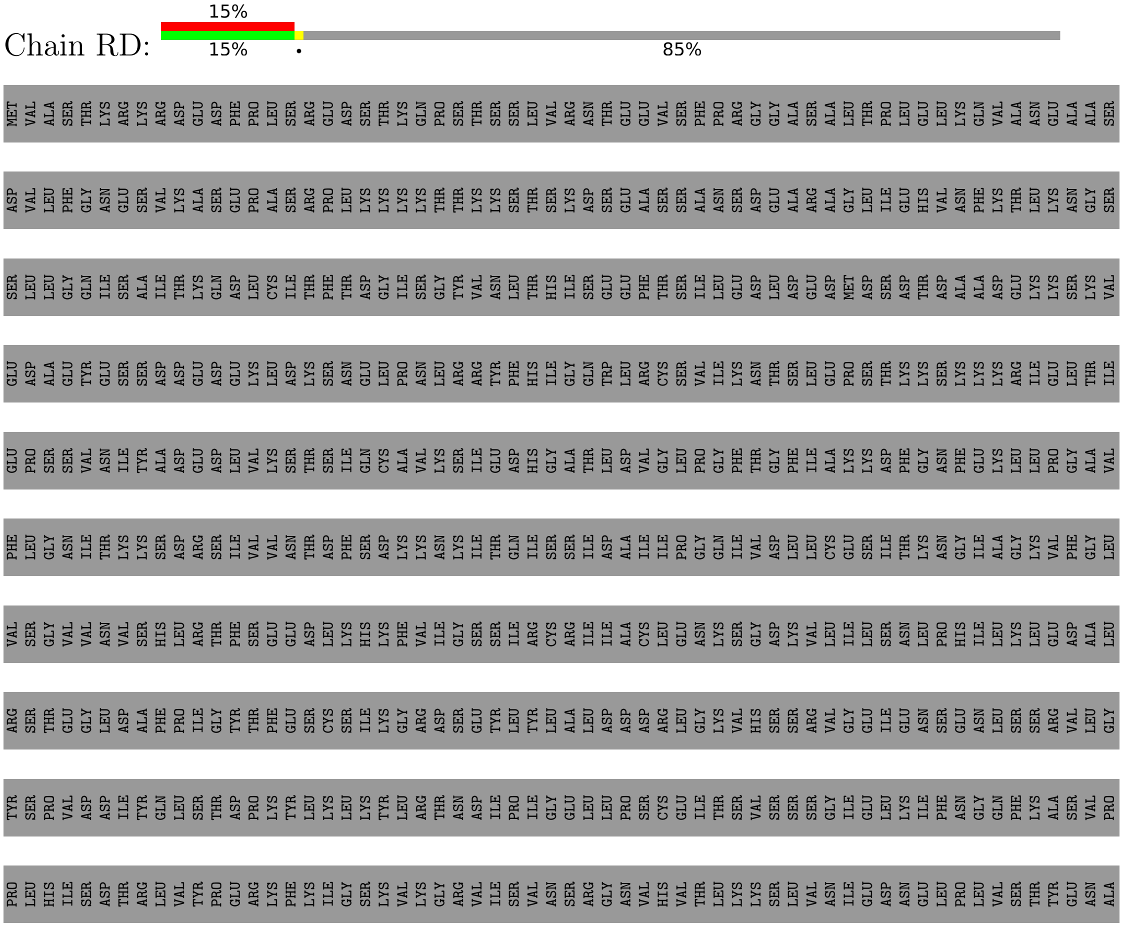
M121 A122 C123 D124 V125 I126 K127 I128 G129 N130 F131 V132 T133 N134 K135 E136 R137 F138 V139 K140 R141 R142 Q143 R144 L145 V146 G147 P148 N149 G150 N151 T152 L153 K154 A155 L156 E157 L158 L159 T160 K161 C162 Y163 I164 L165 V166 Q167 G168 N169 T170 V171 S172 A173 M174 G175 P176 F177 K178 G179 L180

K181 E182 V183 R184 R185 V186 V187 E188 D189 C190 M191 K192 N193 I194 H195 P196 I197 Y198 H199 I200 K201 E202 L203 M204 I205 K206 R207 E208 L209 A210 K211 R212 PRO GLU LEU ALA ASN GLU ASP TRP SER ARG PHE LEU PRO MET PHE LYS LYS ARG ASN VAL ALA ARG LYS LYS PRO LYS ILE

ARG ASN VAL GLU LYS LYS VAL TYR THR PRO PHE PRO PRO ALA GLN LEU PRO ARG LYS VAL ASP LEU GLU ILE GLU SER GLY GLU TYR PHE LEU SER LYS ARG GLU LYS GLN MET LYS LYS LEU ASN GLU GLN LYS GLU LYS GLN MET GLU ARG GLU ILE GLU ARG GLN GLU GLU ARG ALA

LYS ASP PHE ILE ALA PRO GLU GLU GLU ALA TYR LYS PRO ASN GLN ASN

- Molecule 42: rRNA biogenesis protein RRP5



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ASP VAL LEU PHE GLY ASN GLU SER VAL LYS ALA SER GLU PRO ALA SER ARG PRO LEU LYS LYS LYS LYS THR THR LYS LYS SER THR SER LYS ASP SER GLU ALA SER SER ALA ASN SER ASP GLU ALA ARG ALA GLY LEU ILE GLU HIS VAL ASN PHE LYS THR LEU LYS ASN GLY SER

SER LEU LEU GLY GLN ILE SER ALA ILE THR LYS GLN ASP LEU CYS ILE THR PHE THR ASP GLY ILE SER GLY TYR VAL ASN LEU THR HIS ILE SER GLU GLU PHE THR SER ILE LEU GLU ASP LEU ASP GLU ASP MET ASP SER ASP THR ASP ALA ALA ASP GLU LYS LYS SER LYS VAL

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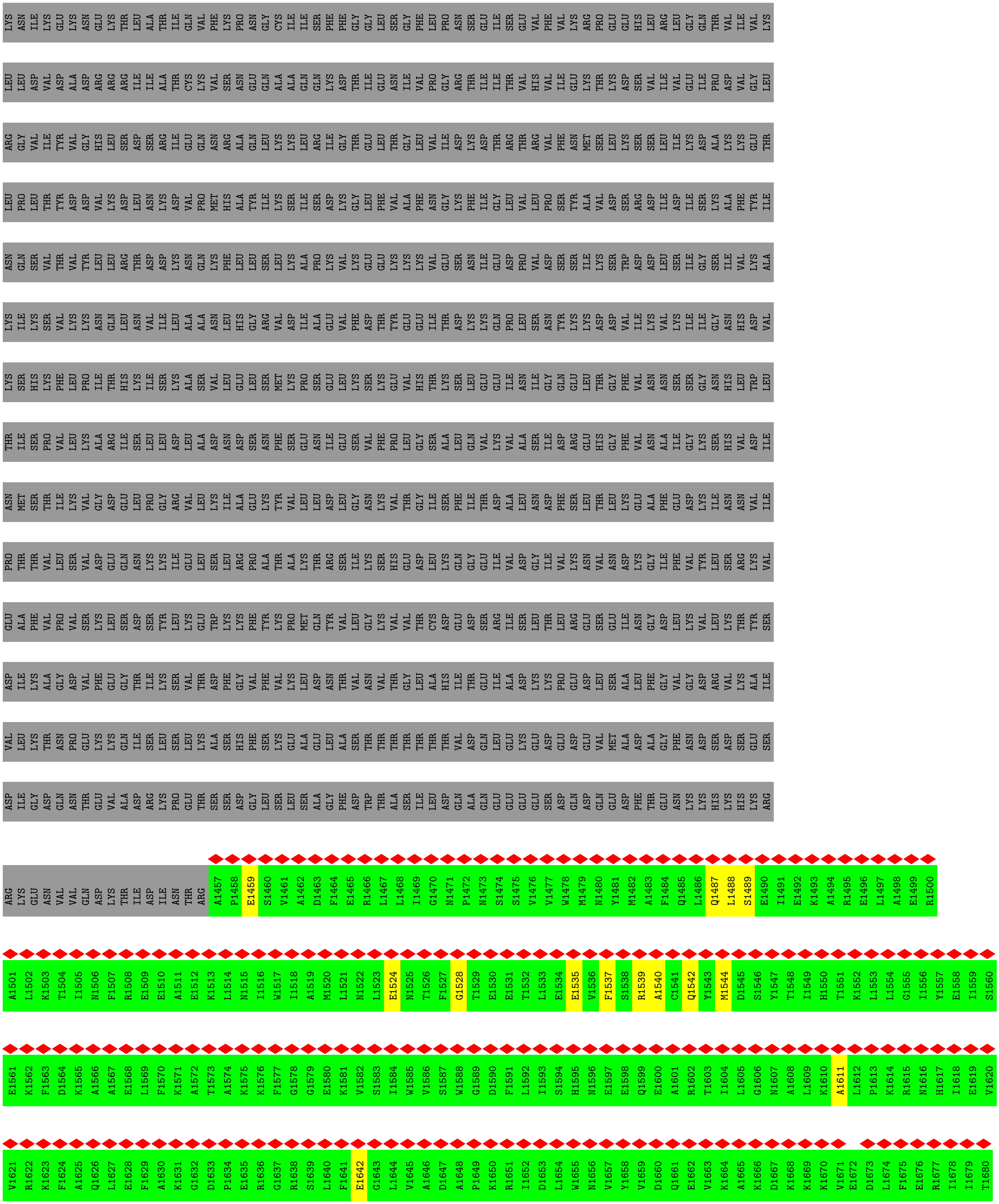
VAL SER GLY VAL VAL ASN VAL SER HIS LEU ARG THR PHE SER GLU GLU ASP LEU LYS HIS LYS PHE VAL ILE GLY SER SER ILE ARG CYS ARG ILE ILE ALA CYS LEU GLU ASN LYS SER GLY ASP LYS VAL LEU ILE LEU SER ASN LEU PRO HIS ILE LEU LYS LEU GLU ASP ALA LEU

ARG SER THR GLU GLY LEU ASP ALA PHE PRO ILE GLY TYR THR PHE GLU SER CYS SER ILE LYS GLY ARG ASP SER GLU TYR LEU TYR ALA LEU ASP ASP ASP ARG LEU GLY LYS VAL HIS SER SER ARG VAL GLY GLU ILE GLU ASN SER GLU ASN LEU SER SER ARG VAL LEU GLY

TYR SER PRO VAL ASP ASP ILE TYR GLN LEU SER THR ASP PRO LYS TYR LEU LYS LEU LYS TYR LEU ARG THR ASN ASP ILE PRO ILE GLY GLU LEU LEU PRO SER CYS GLU ILE THR SER VAL SER SER SER GLY ILE GLU LEU LYS ILE PHE ASN GLY GLN PHE LYS ALA SER VAL PRO

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



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GLU ALA PHE VAL PRO VAL SER LYS LEU SER ASP SER TYR LEU LYS GLU TRP LYS LYS PHE TYR LYS PRO MET GLN TYR VAL LEU GLY LYS VAL VAL THR CYS ASP GLU ASP SER ARG ILE SER LEU THR LEU ARG GLU SER GLU ILE ASN GLY ASP LEU LYS VAL LEU LYS THR TYR SER

ASP ILE LYS ALA GLY ASP VAL PHE GLU GLY THR ILE LYS SER VAL THR ASP PHE GLY VAL PHE VAL LYS LEU ASP ASN THR VAL ASN VAL THR GLY LEU ALA HIS ILE THR GLU ILE ALA ASP LYS LYS PRO GLU ASP LEU SER ALA LEU PHE GLY VAL GLY ASP ARG VAL LYS ALA ILE

VAL LEU LYS THR ASN PRO GLU LYS LYS GLN ILE SER LEU SER LEU LYS ALA SER HIS PHE SER LYS GLU ALA GLU LEU ALA SER THR THR THR THR THR THR THR VAL ASP GLN LEU GLU LYS GLU ASP GLU ASP GLU VAL MET ALA ASP ALA GLY PHE ASN ASP SER ASP SER GLU SER

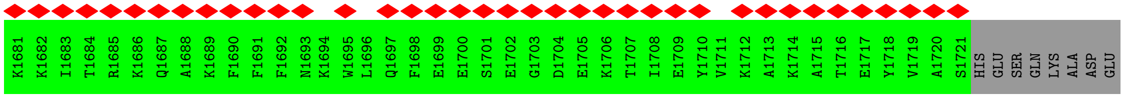
ASP ILE GLY ASP GLN ASN THR GLU VAL ALA ASP ARG LYS PRO GLU THR SER SER ASP GLY LEU SER LEU SER ALA GLY PHE ASP TRP THR ALA SER ILE LEU ASP GLN ALA GLN GLU GLU GLU GLU SER ASP GLN ASP GLN GLU ASP PHE THR GLU ASN LYS LYS HIS LYS HIS LYS ARG

ARG LYS GLU ASN VAL VAL GLN ASP LYS THR ILE ASP ILE ASN THR ARG A1457 P1458 E1459 S1460 V1461 A1462 D1463 F1464 E1465 R1466 L1467 L1468 I1469 G1470 N1471 P1472 N1473 S1474 S1475 V1476 V1477 W1478 M1479 N1480 Y1481 M1482 A1483 F1484 Q1485 L1486 Q1487 L1488 S1489 E1490 I1491 E1492 K1493 A1494 R1495 E1496 L1497 A1498 E1499 R1500

A1501 L1502 K1503 T1504 I1505 N1506 F1507 R1508 E1509 E1510 A1511 E1512 K1513 L1514 N1515 I1516 W1517 I1518 A1519 M1520 L1521 N1522 L1523 E1524 N1525 T1526 F1527 G1528 T1529 E1530 E1531 T1532 L1533 E1534 E1535 V1536 F1537 S1538 R1539 A1540 C1541 Q1542 Y1543 M1544 D1545 S1546 Y1547 T1548 I1549 H1550 T1551 K1552 L1553 L1554 G1555 I1556 Y1557 E1558 I1559 S1560

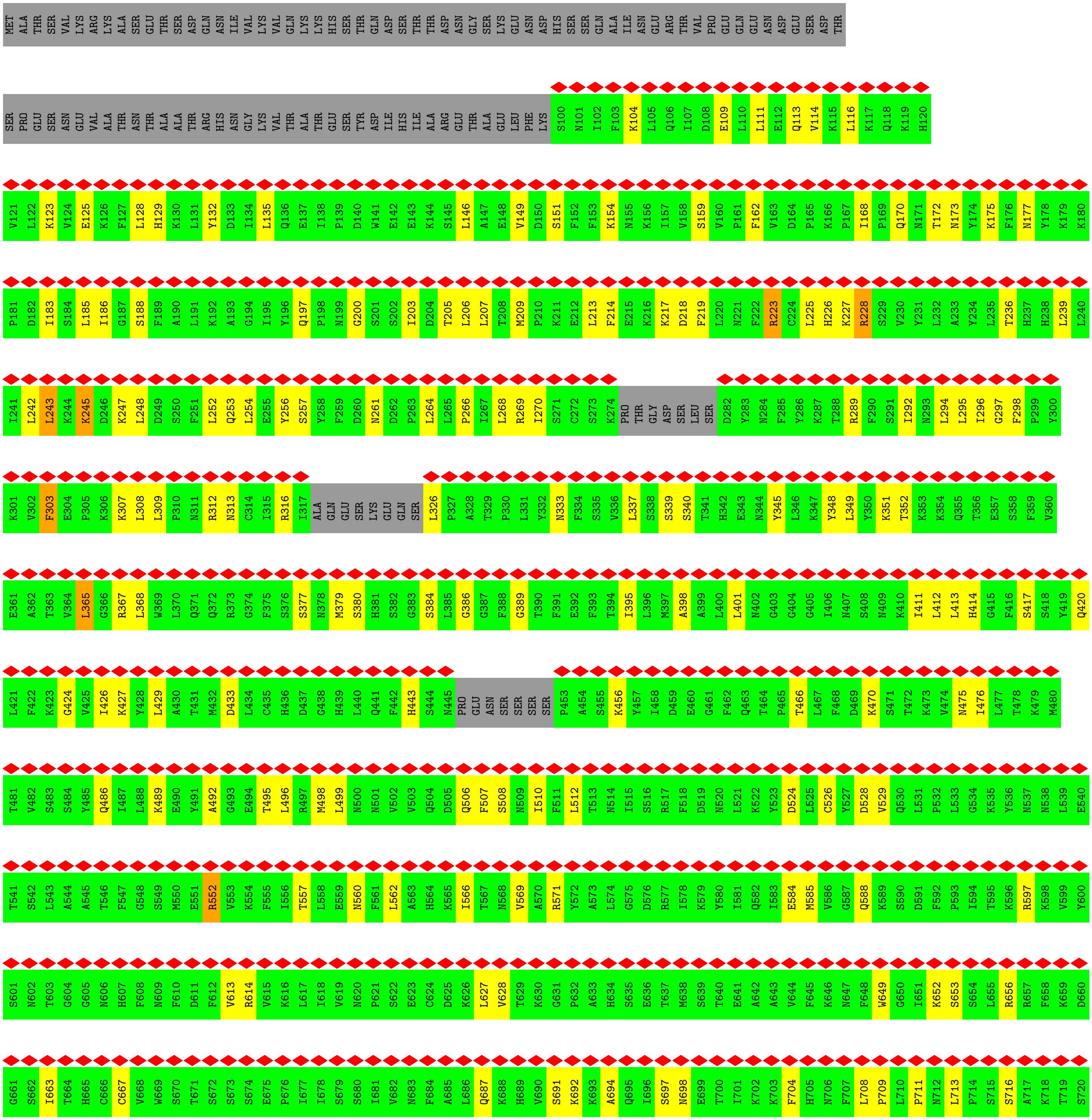
E1561 K1562 F1563 D1564 K1565 A1566 A1567 E1568 L1569 F1570 K1571 A1572 T1573 A1574 K1575 K1576 F1577 G1578 G1579 E1580 K1581 V1582 S1583 I1584 W1585 V1586 S1587 W1588 G1589 D1590 F1591 L1592 I1593 S1594 H1595 N1596 E1597 E1598 Q1599 E1600 A1601 R1602 T1603 I1604 L1605 G1606 N1607 A1608 L1609 K1610 A1611 L1612 P1613 K1614 R1615 N1616 H1617 I1618 E1619 V1620

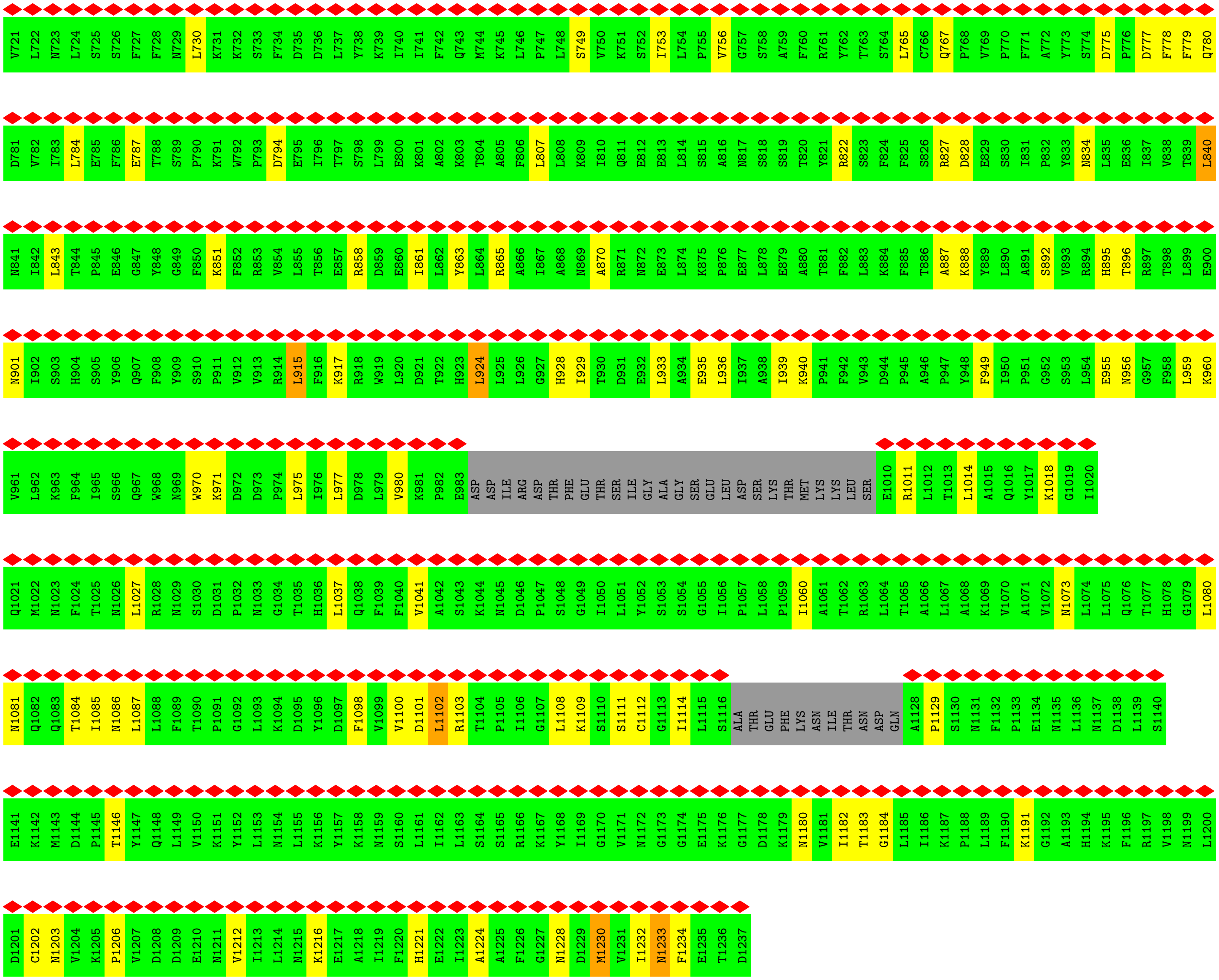
V1621 R1622 K1623 F1624 A1625 Q1626 L1627 E1628 F1629 A1630 K1631 G1632 D1633 P1634 E1635 R1636 G1637 R1638 S1639 L1640 F1641 E1642 G1643 L1644 V1645 A1646 D1647 A1648 P1649 K1650 R1651 I1652 D1653 L1654 W1655 N1656 V1657 Y1658 V1659 D1660 Q1661 E1662 V1663 K1664 A1665 K1666 D1667 K1668 K1669 K1670 V1671 E1672 D1673 L1674 F1675 E1676 R1677 I1678 I1679 T1680



- Molecule 43: U3 small nucleolar RNA-associated protein 22

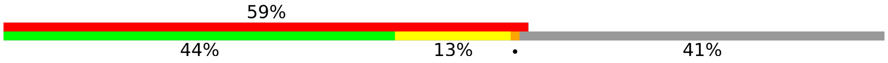
Chain RE:

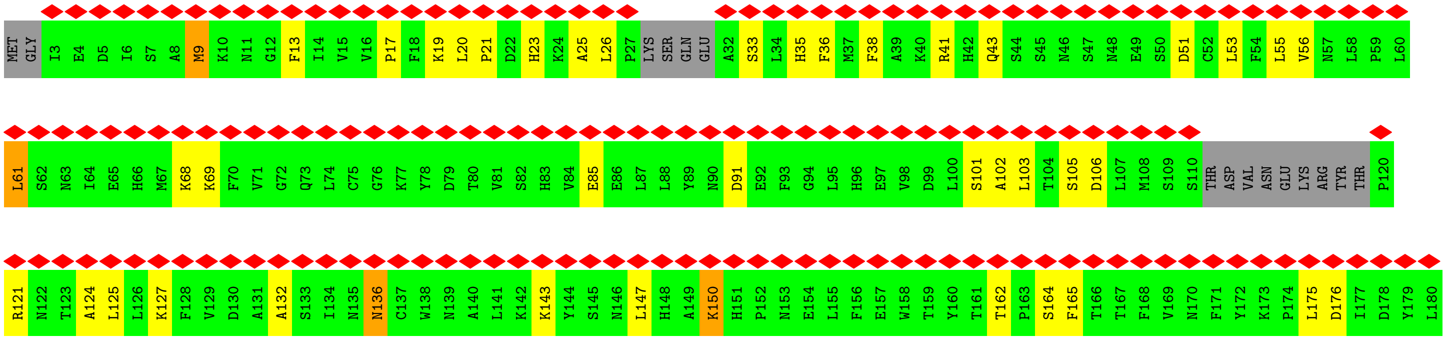


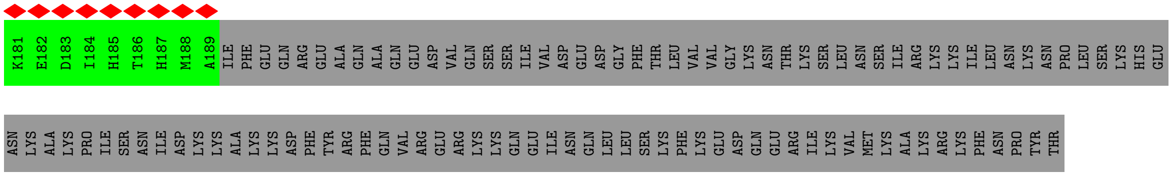


- Molecule 44: Ribosomal RNA-processing protein 7

Chain RF:

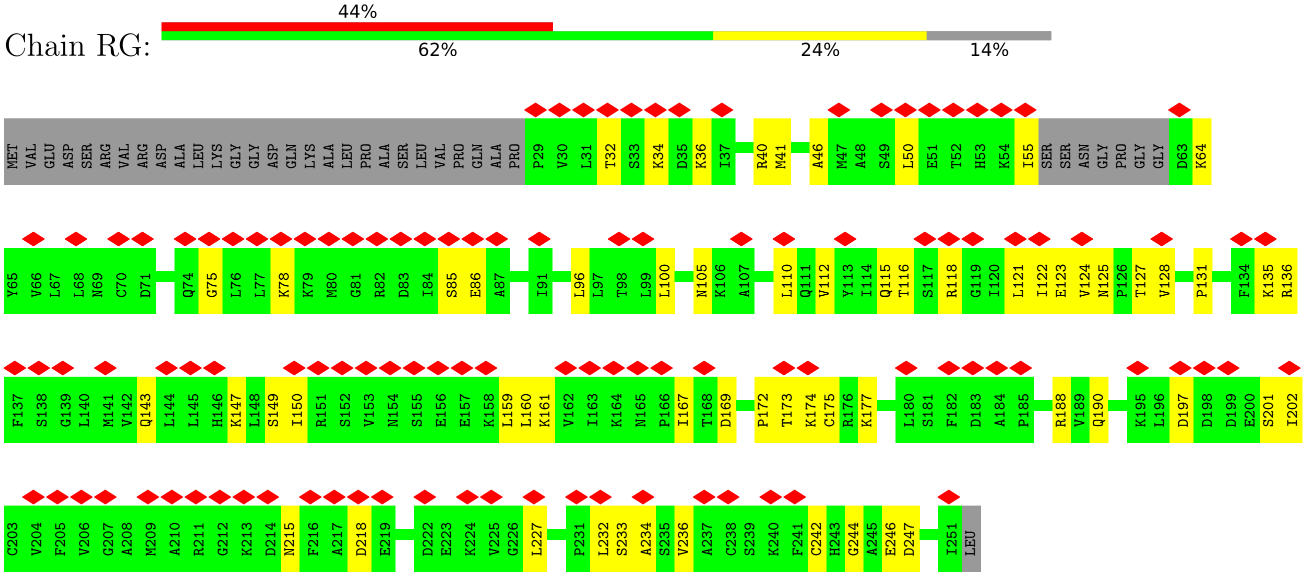






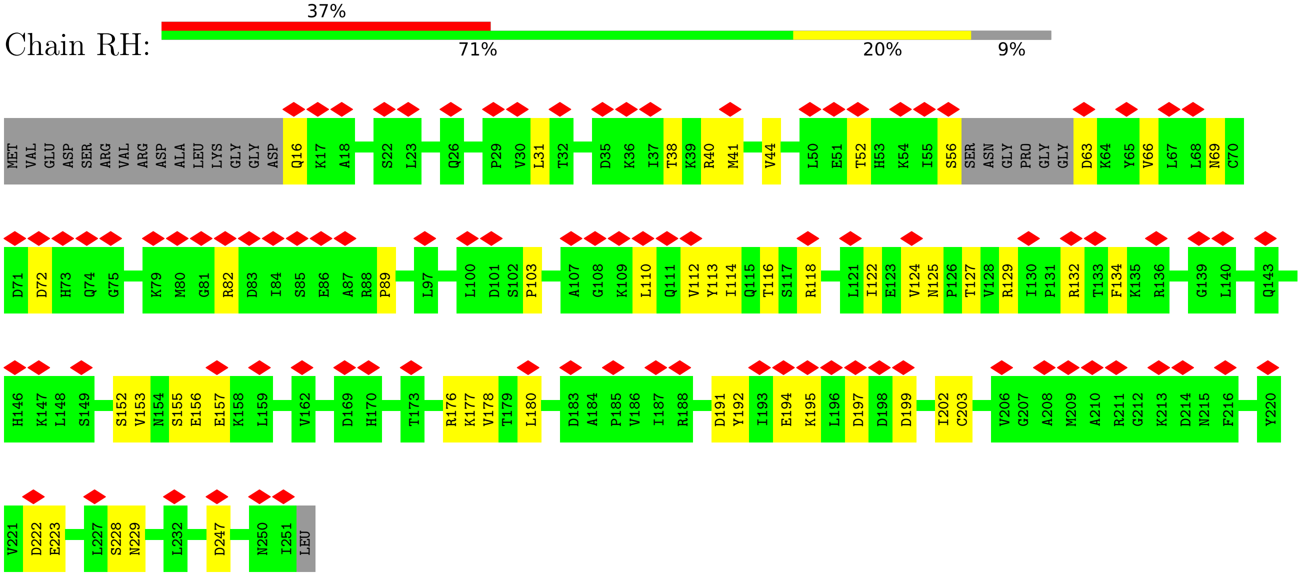
- Molecule 45: Ribosomal RNA small subunit methyltransferase NEP1

Chain RG:



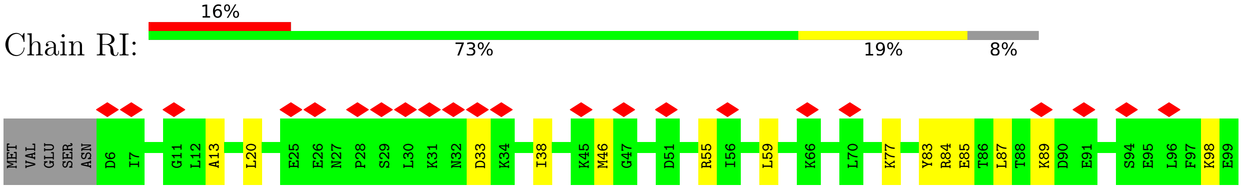
- Molecule 45: Ribosomal RNA small subunit methyltransferase NEP1

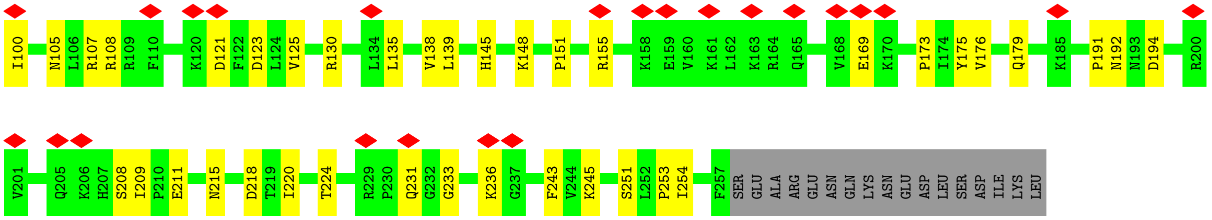
Chain RH:



- Molecule 46: Ribosome biogenesis protein UTP30

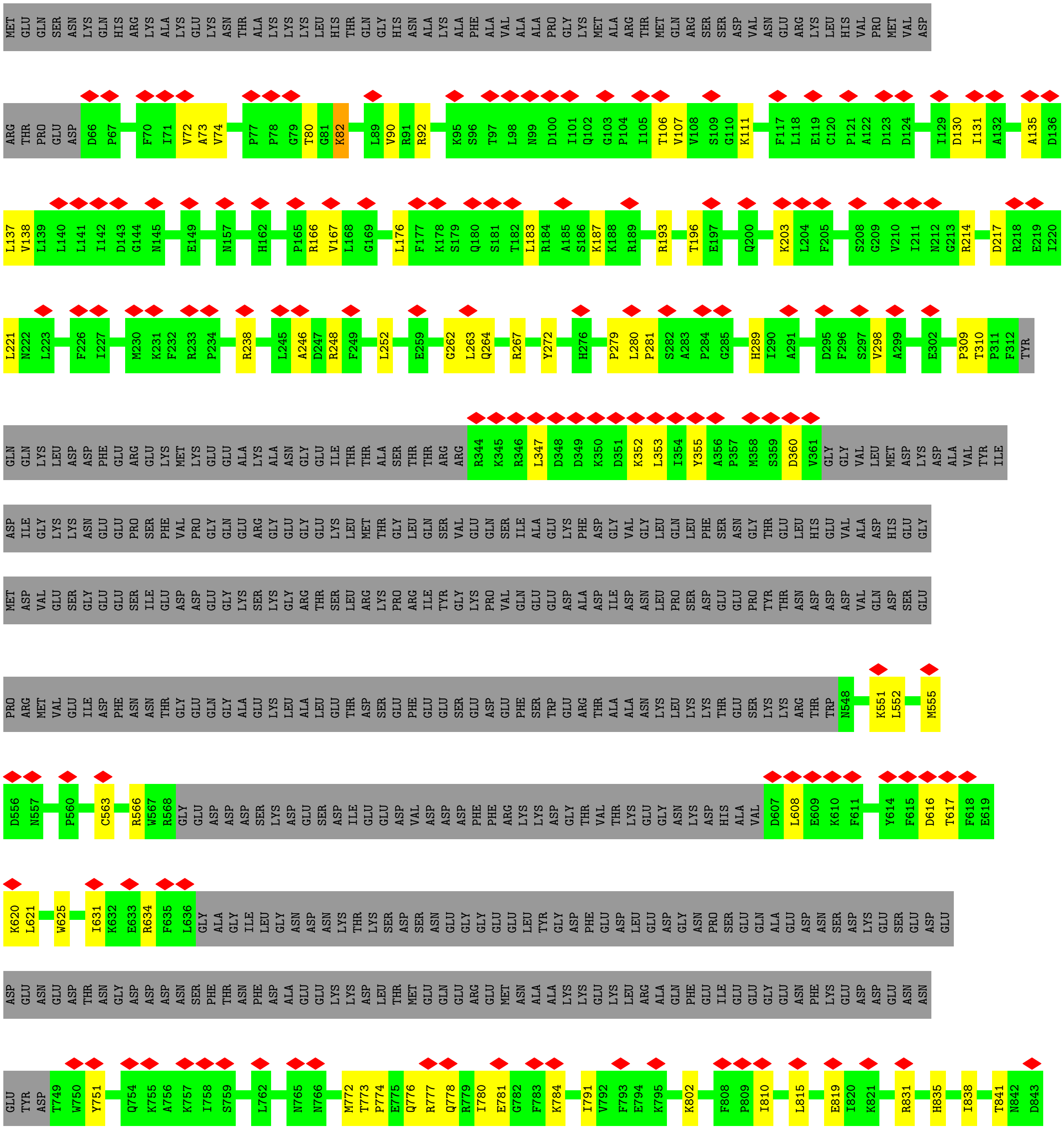
Chain RI:

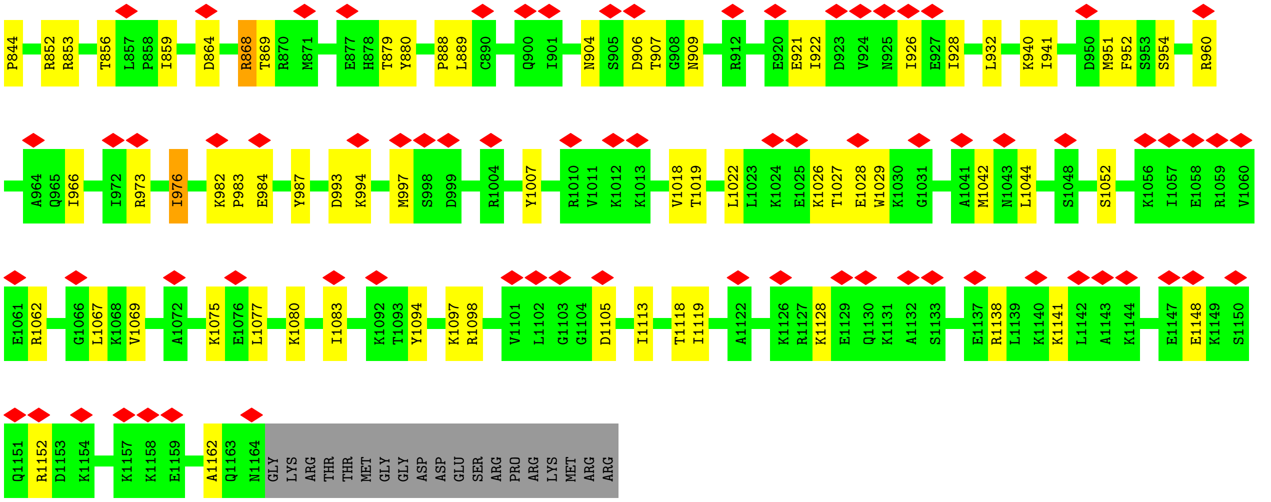




- Molecule 47: Ribosome biogenesis protein BMS1

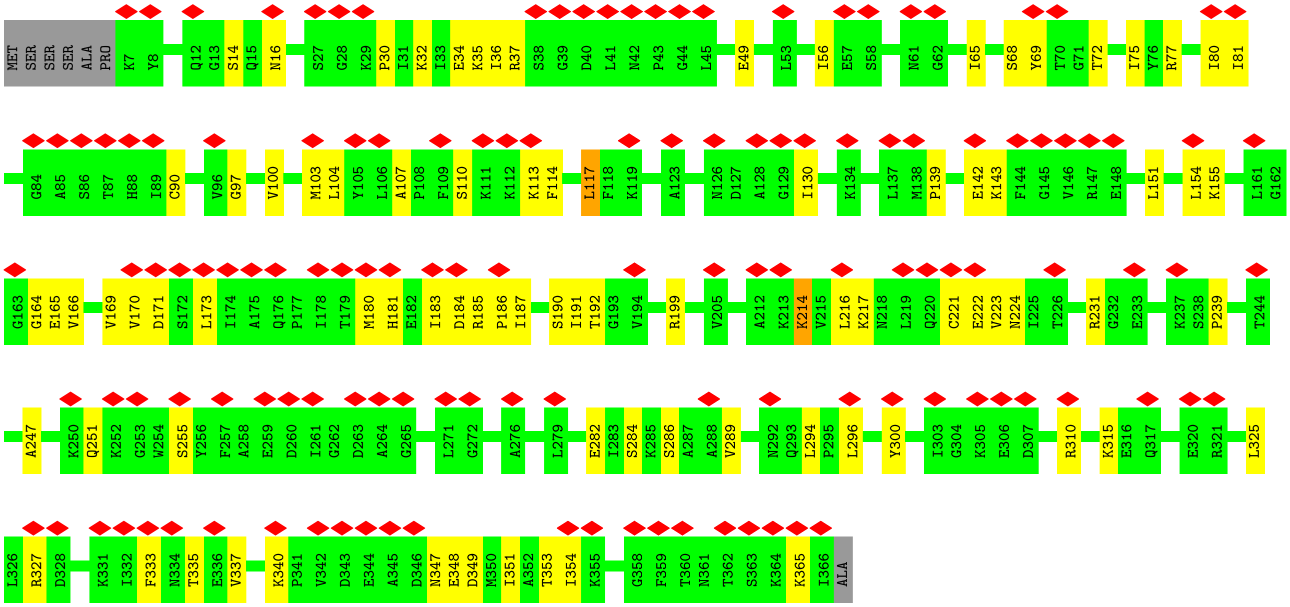
Chain RJ:





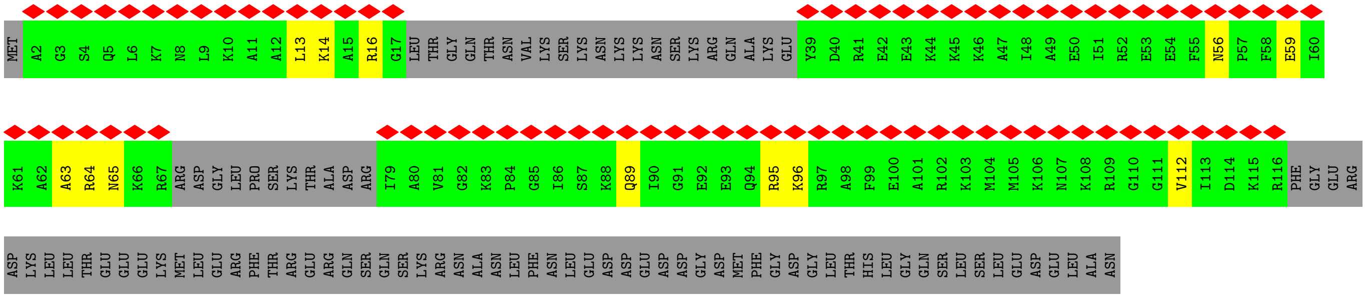
- Molecule 48: RNA 3'-terminal phosphate cyclase-like protein

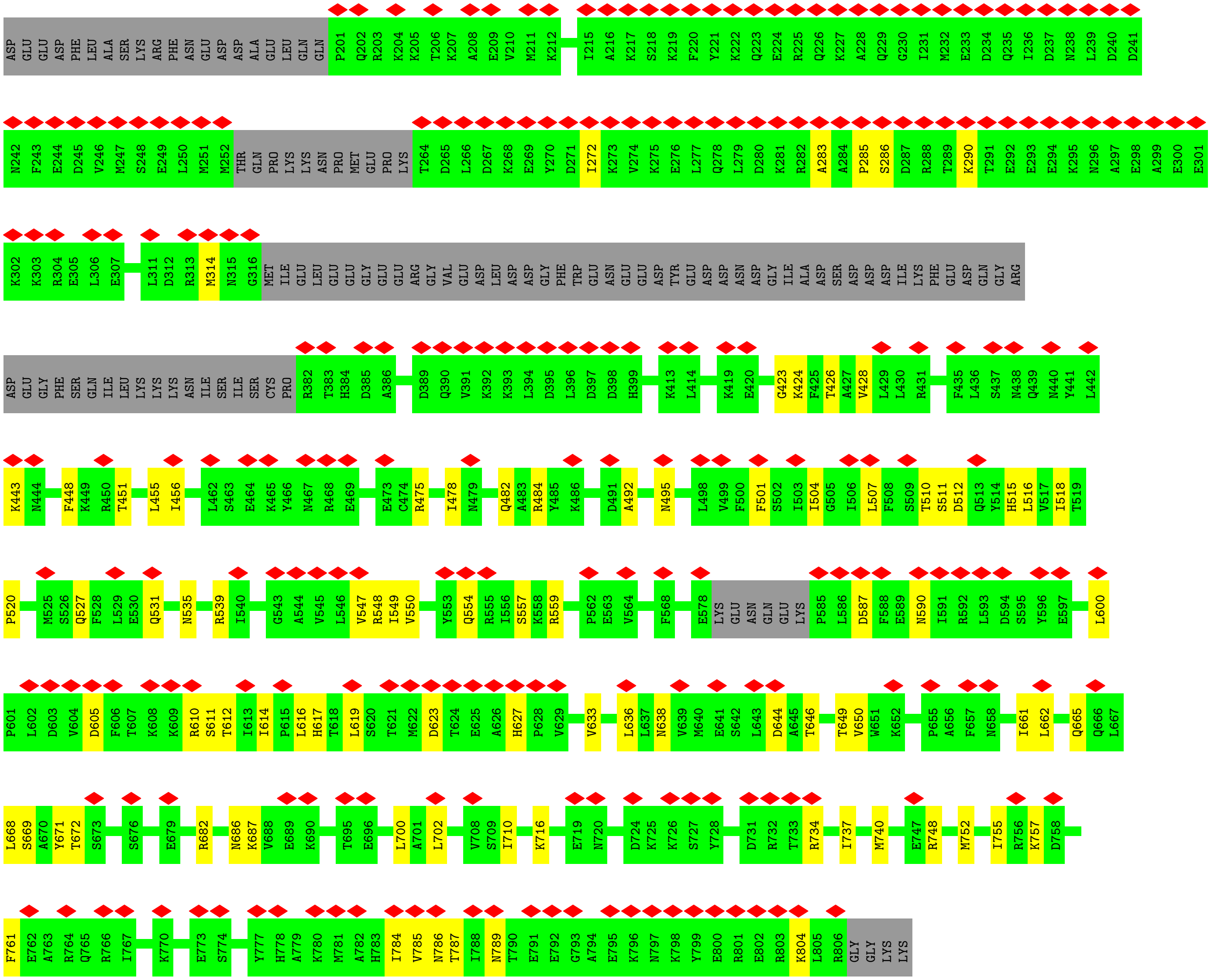
Chain RK:



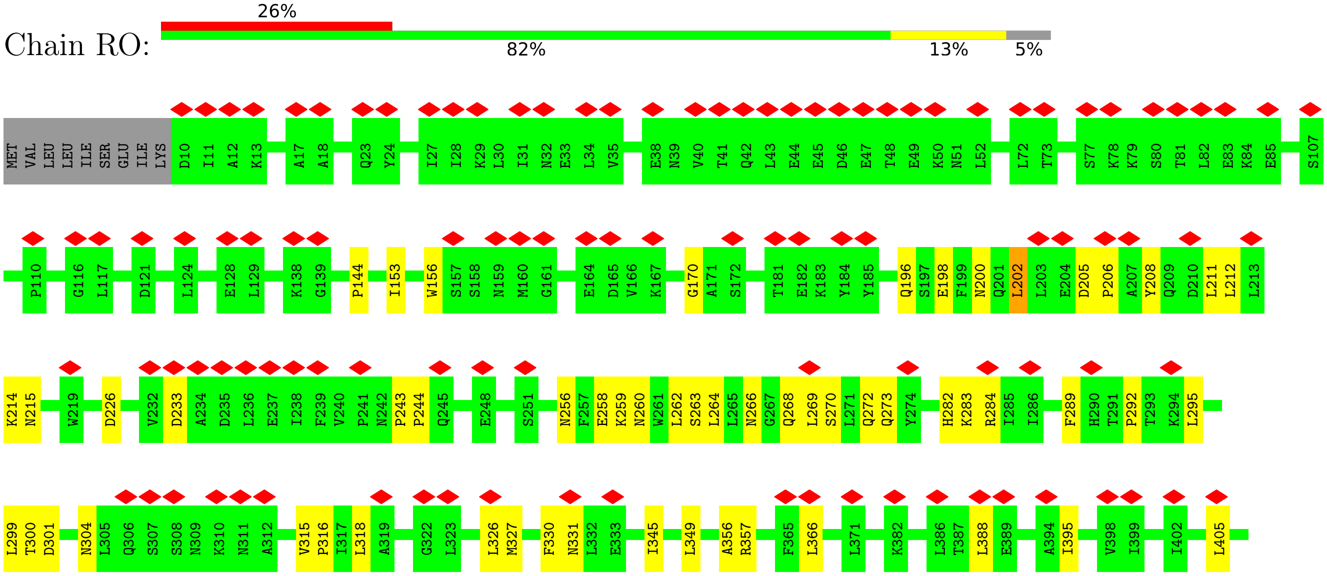
- Molecule 49: Nucleolar complex protein 14

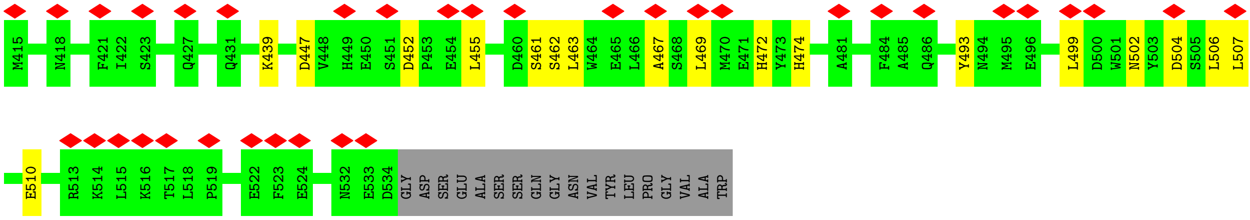
Chain RN:





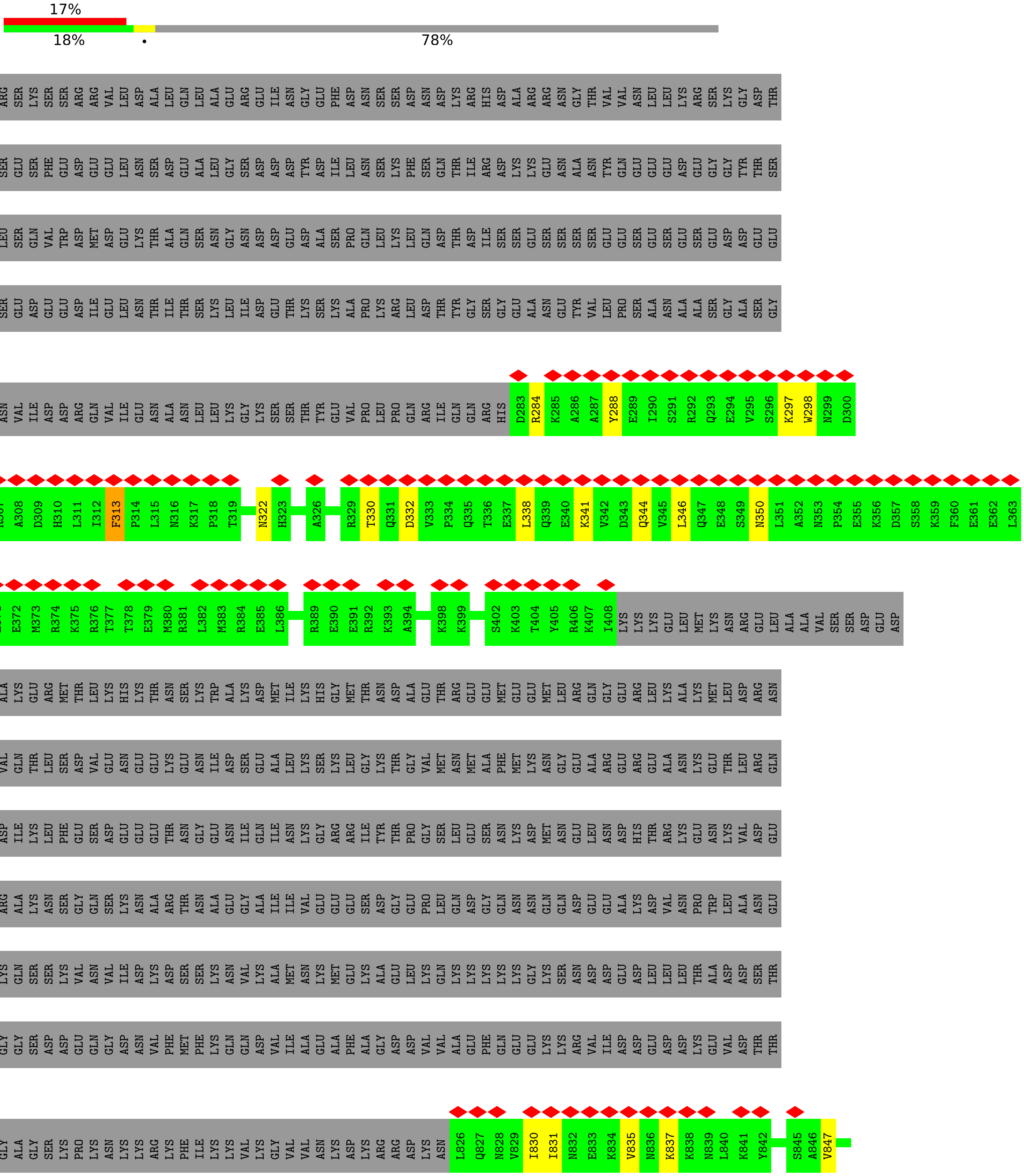
- Molecule 50: Nucleolar complex protein 4

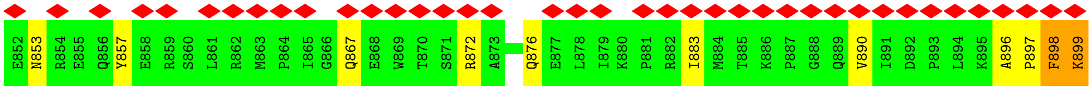




- Molecule 51: U3 small nucleolar RNA-associated protein 14

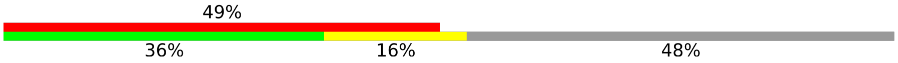
Chain RQ:

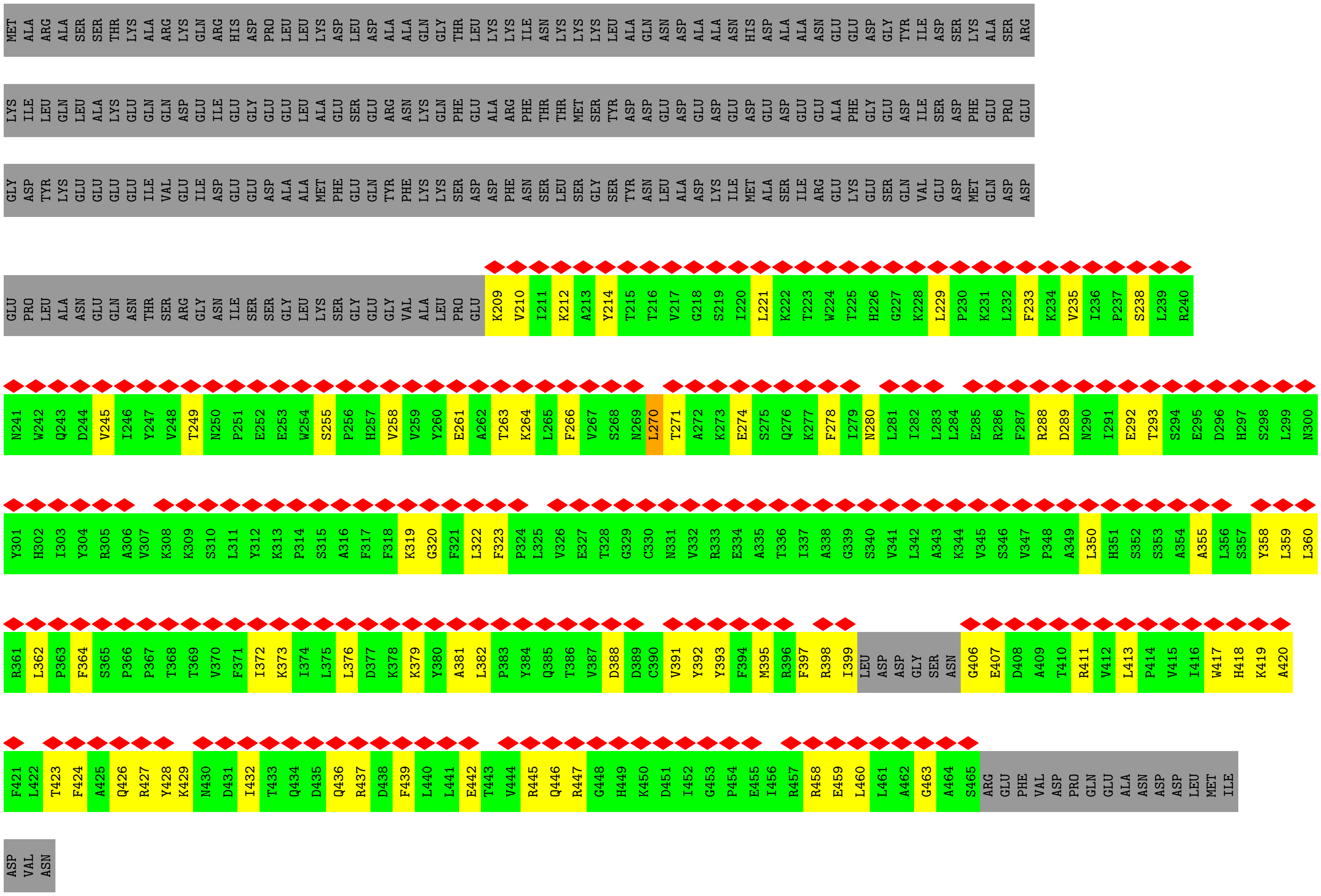




- Molecule 52: Essential nuclear protein 1

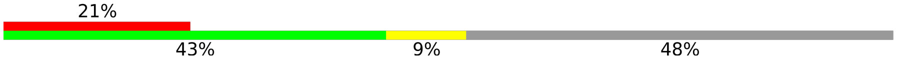
Chain RS:

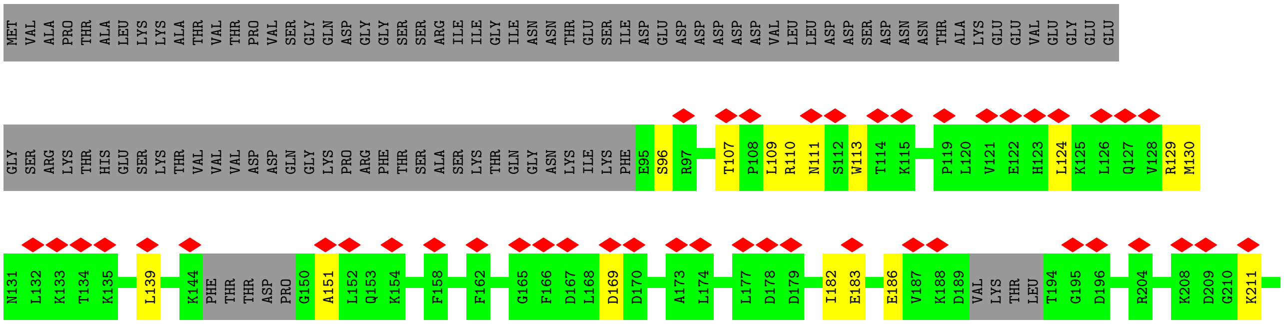


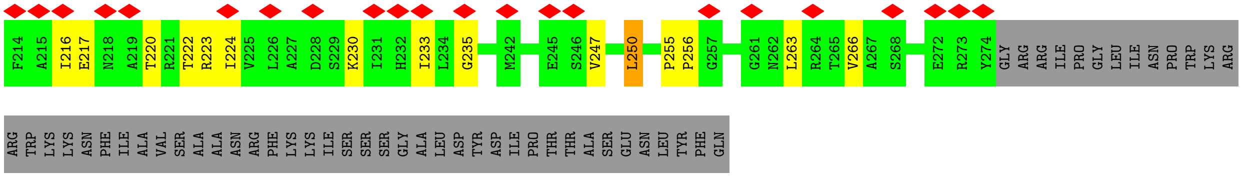


- Molecule 53: Pno1

Chain RT:

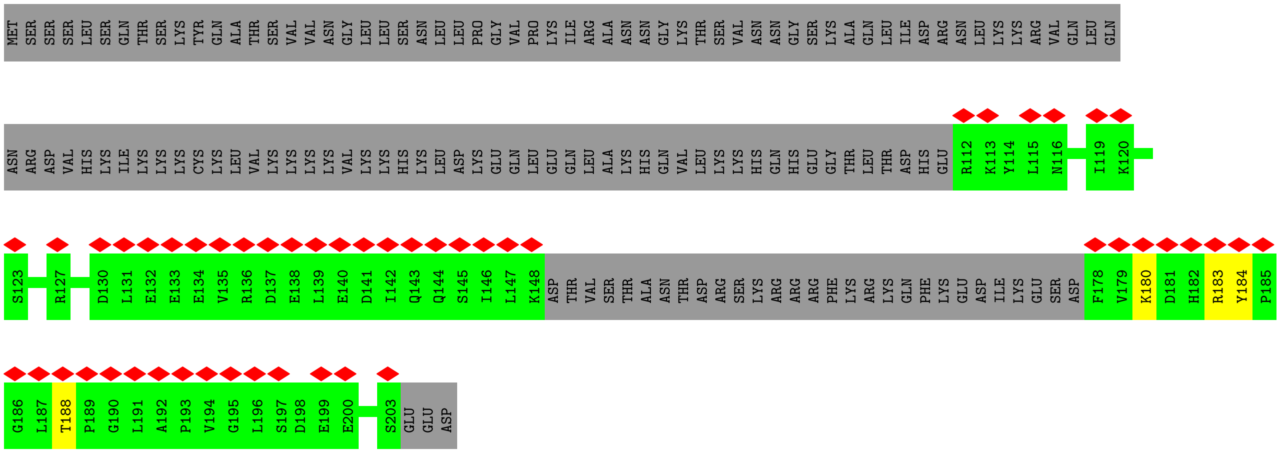






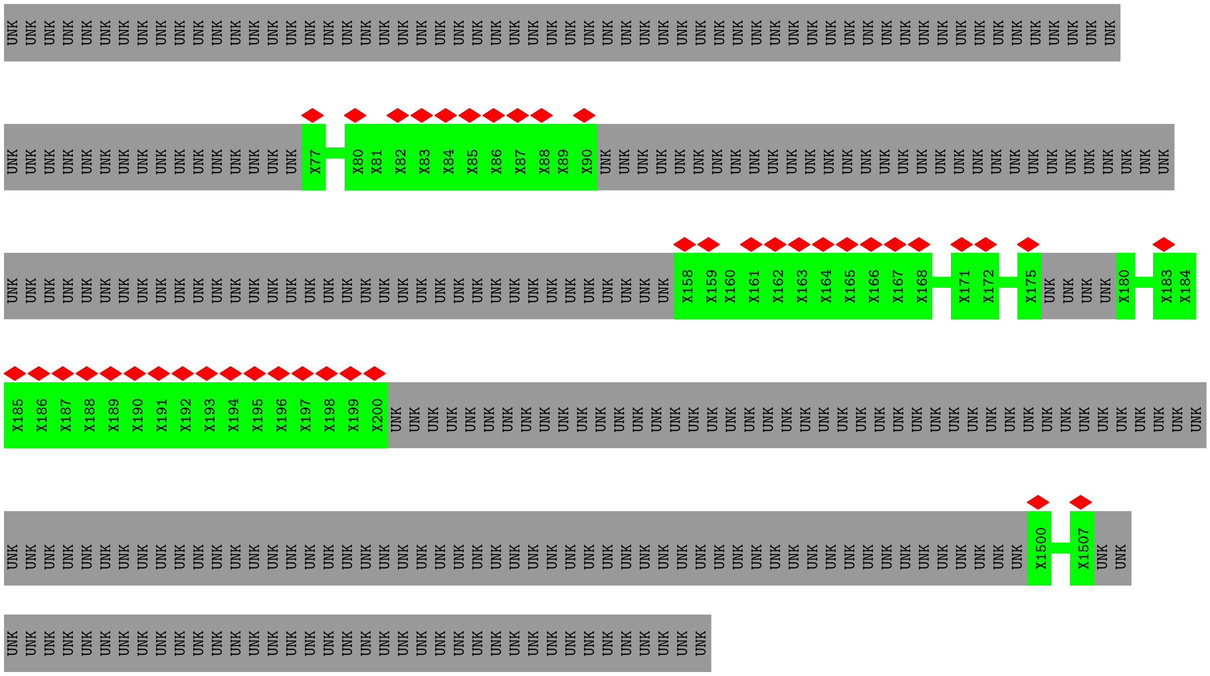
- Molecule 54: Regulator of rDNA transcription protein 14

Chain RW:



- Molecule 55: Unassigned peptides 1

Chain X1:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40111	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 ($e^-/\text{Å}^2$)	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	0.055	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	531.19995, 531.19995, 531.19995	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3279998, 1.3279998, 1.3279998	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 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	3A	0.92	0/4141	1.17	24/6433 (0.4%)
2	5A	0.84	0/12485	1.11	50/19449 (0.3%)
3	SA	0.71	0/20532	1.15	138/31980 (0.4%)
4	SG	0.53	0/1690	0.64	0/2285
5	SK	0.47	0/1410	0.60	0/1888
6	SN	0.32	0/873	0.73	1/1185 (0.1%)
7	SO	0.35	0/1109	0.66	1/1495 (0.1%)
8	SP	0.36	0/879	0.75	1/1186 (0.1%)
9	SR	0.58	0/990	0.73	1/1335 (0.1%)
10	ST	0.38	0/980	0.63	0/1319
11	SY	0.54	0/798	0.67	1/1065 (0.1%)
12	Sd	0.54	0/499	0.66	0/670
13	3B	0.59	0/1901	0.66	1/2567 (0.0%)
13	3C	0.44	0/1796	0.62	1/2424 (0.0%)
14	3D	0.44	0/2891	0.63	3/3895 (0.1%)
15	3E	0.41	0/3059	0.62	3/4153 (0.1%)
16	3F	0.43	0/3317	0.64	2/4469 (0.0%)
17	3G	0.52	0/928	0.76	1/1262 (0.1%)
17	3H	0.47	0/928	0.69	2/1262 (0.2%)
18	A4	0.47	0/5321	0.66	5/7207 (0.1%)
19	A5	0.48	0/4044	0.68	5/5493 (0.1%)
20	A8	0.30	0/3328	0.61	0/4565
21	A9	0.31	0/951	0.58	1/1287 (0.1%)
22	AE	0.45	0/5274	0.64	6/7142 (0.1%)
23	AF	0.53	0/3993	0.67	4/5413 (0.1%)
24	AG	0.47	0/6699	0.65	3/9077 (0.0%)
25	B1	0.64	0/6780	0.68	7/9175 (0.1%)
26	B2	0.43	0/6853	0.67	3/9256 (0.0%)
27	B3	0.34	0/5977	0.73	7/8087 (0.1%)
28	B8	0.58	0/3848	0.66	4/5218 (0.1%)
29	BE	0.57	0/6948	0.66	7/9391 (0.1%)
30	B6	0.45	0/2849	0.58	1/3853 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	5B	0.34	0/499	0.62	0/659
32	5C	0.59	0/4166	0.68	5/5624 (0.1%)
33	5D	0.50	0/1998	0.66	3/2644 (0.1%)
34	5E	0.48	0/1665	0.64	1/2233 (0.0%)
35	5F	0.67	0/1559	0.73	2/2097 (0.1%)
36	5G	0.57	0/2337	0.66	1/3148 (0.0%)
37	5H	0.45	0/1074	0.56	0/1422
38	5I	0.61	0/3844	0.67	2/5174 (0.0%)
39	5J	0.42	0/1302	0.54	0/1728
40	5K	0.56	0/1426	0.67	1/1917 (0.1%)
41	RC	0.36	0/1432	0.64	0/1926
42	RD	0.27	0/1313	0.41	0/1830
43	RE	0.32	0/8924	0.67	9/12070 (0.1%)
44	RF	0.32	0/1441	0.69	2/1951 (0.1%)
45	RG	0.39	0/1727	0.68	2/2329 (0.1%)
45	RH	0.42	0/1828	0.61	0/2470
46	RI	0.46	0/2080	0.65	0/2797
47	RJ	0.51	0/6085	0.61	1/8186 (0.0%)
48	RK	0.44	0/2832	0.65	3/3825 (0.1%)
49	RN	0.36	0/4591	0.58	1/6187 (0.0%)
50	RO	0.38	0/3849	0.62	5/5261 (0.1%)
51	RQ	0.48	0/1459	0.58	0/1981
52	RS	0.33	0/2104	0.67	1/2854 (0.0%)
53	RT	0.42	0/1379	0.63	1/1853 (0.1%)
54	RW	0.34	0/385	0.50	0/529
All	All	0.55	0/185370	0.79	323/258181 (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
7	SO	0	1
10	ST	0	1
14	3D	0	3
15	3E	0	1
16	3F	0	1
17	3G	0	2
17	3H	0	1
18	A4	0	2
19	A5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
20	A8	0	4
24	AG	0	2
25	B1	0	3
26	B2	0	9
27	B3	0	7
29	BE	0	1
33	5D	0	1
34	5E	0	1
35	5F	0	1
36	5G	0	1
38	5I	0	2
43	RE	0	2
47	RJ	0	2
48	RK	0	1
49	RN	0	1
50	RO	0	1
51	RQ	0	1
All	All	0	53

There are no bond length outliers.

The worst 5 of 323 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	SA	1174	C	N1-C2-O2	10.37	125.12	118.90
35	5F	13	LEU	CA-CB-CG	10.29	138.97	115.30
19	A5	25	ASP	CB-CG-OD1	9.52	126.86	118.30
17	3G	67	LEU	CA-CB-CG	9.35	136.81	115.30
3	SA	1000	C	N1-C2-O2	9.32	124.49	118.90

There are no chirality outliers.

5 of 53 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	3D	142	LEU	Peptide
14	3D	202	HIS	Peptide
14	3D	286	ARG	Peptide
7	SO	58	HIS	Peptide
10	ST	13	HIS	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	3A	3711	0	1882	19	0
2	5A	11163	0	5611	80	0
3	SA	18356	0	9246	200	0
4	SG	1669	0	1724	18	0
5	SK	1388	0	1467	12	0
6	SN	865	0	874	15	0
7	SO	1087	0	1152	23	0
8	SP	868	0	894	26	0
9	SR	973	0	1029	13	0
10	ST	964	0	991	17	0
11	SY	786	0	843	7	0
12	Sd	497	0	535	0	0
13	3B	1865	0	1910	29	0
13	3C	1763	0	1805	35	0
14	3D	2848	0	2815	42	0
15	3E	3028	0	2813	60	0
16	3F	3248	0	3274	56	0
17	3G	916	0	964	11	0
17	3H	916	0	964	23	0
18	A4	5226	0	5199	94	0
19	A5	3976	0	3919	57	0
20	A8	3307	0	2316	40	0
21	A9	939	0	898	17	0
22	AE	5181	0	5373	84	0
23	AF	3911	0	3906	71	0
24	AG	6570	0	6473	125	0
25	B1	6635	0	6525	93	0
26	B2	6723	0	6698	131	0
27	B3	5882	0	5964	143	0
28	B8	3764	0	3757	58	0
29	BE	6810	0	6787	89	0
30	B6	2800	0	2517	30	0
31	5B	495	0	561	14	0
32	5C	4084	0	4092	73	0
33	5D	1972	0	2054	25	0
34	5E	1647	0	1678	31	0
35	5F	1530	0	1572	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	5G	2296	0	2325	38	0
37	5H	1065	0	1097	16	0
38	5I	3765	0	3714	71	0
39	5J	1280	0	1331	20	0
40	5K	1403	0	1484	19	0
41	RC	1410	0	1503	40	0
42	RD	1314	0	610	21	0
43	RE	8716	0	8828	159	0
44	RF	1404	0	1364	25	0
45	RG	1701	0	1767	39	0
45	RH	1799	0	1872	33	0
46	RI	2045	0	2162	36	0
47	RJ	5953	0	6152	95	0
48	RK	2781	0	2878	52	0
49	RN	4529	0	4262	65	0
50	RO	3766	0	3269	48	0
51	RQ	1436	0	1280	28	0
52	RS	2051	0	2096	54	0
53	RT	1357	0	1426	17	0
54	RW	381	0	255	4	0
55	X1	305	0	73	0	0
56	5K	1	0	0	0	0
57	RJ	32	0	12	1	0
58	RJ	1	0	0	0	0
All	All	179154	0	160842	2432	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 7.

The worst 5 of 2432 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)
42:RD:1487:GLN:O	43:RE:411:ILE:HG23	1.40	1.18
27:B3:12:LEU:HD23	27:B3:377:LEU:HB2	1.23	1.17
8:SP:42:VAL:HG12	8:SP:67:VAL:HG23	1.31	1.12
8:SP:42:VAL:CG1	8:SP:67:VAL:HG23	1.82	1.09
27:B3:12:LEU:CB	27:B3:377:LEU:HD12	1.84	1.07

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
5	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
6	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
7	SO	132/151 (87%)	121 (92%)	10 (8%)	1 (1%)	19	60
8	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	17	56
9	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
10	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
11	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
12	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
13	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
13	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
14	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
15	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
16	3F	400/573 (70%)	362 (90%)	37 (9%)	1 (0%)	41	76
17	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	19	60
17	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
18	A4	648/776 (84%)	591 (91%)	57 (9%)	0	100	100
19	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
20	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	34	72
21	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
22	AE	645/1769 (36%)	595 (92%)	50 (8%)	0	100	100
23	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
24	AG	812/896 (91%)	732 (90%)	79 (10%)	1 (0%)	51	85
25	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
26	B2	839/943 (89%)	748 (89%)	89 (11%)	2 (0%)	47	81

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	B3	728/817 (89%)	595 (82%)	131 (18%)	2 (0%)	41	76
28	B8	469/594 (79%)	438 (93%)	31 (7%)	0	100	100
29	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
30	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
31	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
32	5C	512/554 (92%)	474 (93%)	37 (7%)	1 (0%)	47	81
33	5D	231/250 (92%)	205 (89%)	26 (11%)	0	100	100
34	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	29	68
35	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
36	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
37	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
38	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
39	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
40	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
41	RC	173/316 (55%)	169 (98%)	4 (2%)	0	100	100
42	RD	263/1729 (15%)	254 (97%)	9 (3%)	0	100	100
43	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100	100
44	RF	168/297 (57%)	145 (86%)	23 (14%)	0	100	100
45	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
45	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
46	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
47	RJ	722/1183 (61%)	670 (93%)	51 (7%)	1 (0%)	51	85
48	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
49	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	47	81
50	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
51	RQ	188/899 (21%)	177 (94%)	11 (6%)	0	100	100
52	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
53	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
54	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
All	All	18453/27161 (68%)	16810 (91%)	1628 (9%)	15 (0%)	54	85

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	5E	454	VAL
7	SO	106	ARG
8	SP	45	GLY
47	RJ	82	LYS
20	A8	309	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	SG	180/191 (94%)	180 (100%)	0	100	100
5	SK	147/166 (89%)	146 (99%)	1 (1%)	84	90
6	SN	88/119 (74%)	86 (98%)	2 (2%)	50	70
7	SO	117/128 (91%)	114 (97%)	3 (3%)	46	67
8	SP	90/105 (86%)	89 (99%)	1 (1%)	73	85
9	SR	105/119 (88%)	105 (100%)	0	100	100
10	ST	105/129 (81%)	104 (99%)	1 (1%)	76	86
11	SY	85/120 (71%)	84 (99%)	1 (1%)	71	84
12	Sd	56/60 (93%)	56 (100%)	0	100	100
13	3B	201/240 (84%)	201 (100%)	0	100	100
13	3C	190/240 (79%)	187 (98%)	3 (2%)	62	79
14	3D	296/435 (68%)	293 (99%)	3 (1%)	76	86
15	3E	262/433 (60%)	261 (100%)	1 (0%)	91	94
16	3F	354/503 (70%)	352 (99%)	2 (1%)	86	92
17	3G	100/104 (96%)	100 (100%)	0	100	100
17	3H	100/104 (96%)	100 (100%)	0	100	100
18	A4	591/713 (83%)	584 (99%)	7 (1%)	71	84
19	A5	433/574 (75%)	432 (100%)	1 (0%)	93	96
20	A8	174/657 (26%)	173 (99%)	1 (1%)	86	92
21	A9	89/533 (17%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	AE	589/1633 (36%)	587 (100%)	2 (0%)	92	95
23	AF	437/454 (96%)	433 (99%)	4 (1%)	78	87
24	AG	750/826 (91%)	740 (99%)	10 (1%)	69	82
25	B1	730/812 (90%)	726 (100%)	4 (0%)	88	93
26	B2	736/832 (88%)	730 (99%)	6 (1%)	81	89
27	B3	660/719 (92%)	640 (97%)	20 (3%)	41	63
28	B8	421/529 (80%)	420 (100%)	1 (0%)	93	96
29	BE	757/819 (92%)	754 (100%)	3 (0%)	91	94
30	B6	251/414 (61%)	247 (98%)	4 (2%)	62	79
31	5B	57/196 (29%)	55 (96%)	2 (4%)	36	60
32	5C	448/480 (93%)	445 (99%)	3 (1%)	84	90
33	5D	221/234 (94%)	219 (99%)	2 (1%)	78	87
34	5E	185/535 (35%)	184 (100%)	1 (0%)	88	93
35	5F	171/172 (99%)	170 (99%)	1 (1%)	86	92
36	5G	251/258 (97%)	249 (99%)	2 (1%)	81	89
37	5H	107/538 (20%)	107 (100%)	0	100	100
38	5I	416/443 (94%)	414 (100%)	2 (0%)	88	93
39	5J	140/200 (70%)	140 (100%)	0	100	100
40	5K	157/169 (93%)	157 (100%)	0	100	100
41	RC	158/289 (55%)	156 (99%)	2 (1%)	69	82
43	RE	984/1125 (88%)	960 (98%)	24 (2%)	49	69
44	RF	159/274 (58%)	153 (96%)	6 (4%)	33	58
45	RG	195/222 (88%)	193 (99%)	2 (1%)	76	86
45	RH	206/222 (93%)	204 (99%)	2 (1%)	76	86
46	RI	235/256 (92%)	235 (100%)	0	100	100
47	RJ	648/1039 (62%)	641 (99%)	7 (1%)	73	85
48	RK	307/312 (98%)	303 (99%)	4 (1%)	69	82
49	RN	422/732 (58%)	422 (100%)	0	100	100
50	RO	329/506 (65%)	328 (100%)	1 (0%)	92	95
51	RQ	132/808 (16%)	129 (98%)	3 (2%)	50	70
52	RS	225/424 (53%)	225 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	RT	148/282 (52%)	146 (99%)	2 (1%)	67	81
54	RW	22/192 (12%)	22 (100%)	0	100	100
All	All	15417/22619 (68%)	15270 (99%)	147 (1%)	77	86

5 of 147 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	RE	1086	ASN
51	RQ	898	PHE
43	RE	1233	ASN
47	RJ	214	ARG
26	B2	75	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 263 such sidechains are listed below:

Mol	Chain	Res	Type
47	RJ	157	ASN
48	RK	334	ASN
53	RT	127	GLN
25	B1	201	HIS
25	B1	92	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	848/1808 (46%)	299 (35%)	20 (2%)
All	All	1535/2841 (54%)	504 (32%)	33 (2%)

5 of 504 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 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1632	C
3	SA	1654	G
3	SA	1749	A
2	5A	536	A
2	5A	492	G

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
57	GTP	RJ	1201	58	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
57	GTP	RJ	1201	58	-	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)
57	RJ	1201	GTP	C5-C6	-2.46	1.42	1.47
57	RJ	1201	GTP	C8-N7	-2.02	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
57	RJ	1201	GTP	O4'-C4'-C5'-O5'
57	RJ	1201	GTP	C3'-C4'-C5'-O5'
57	RJ	1201	GTP	C4'-C5'-O5'-PA

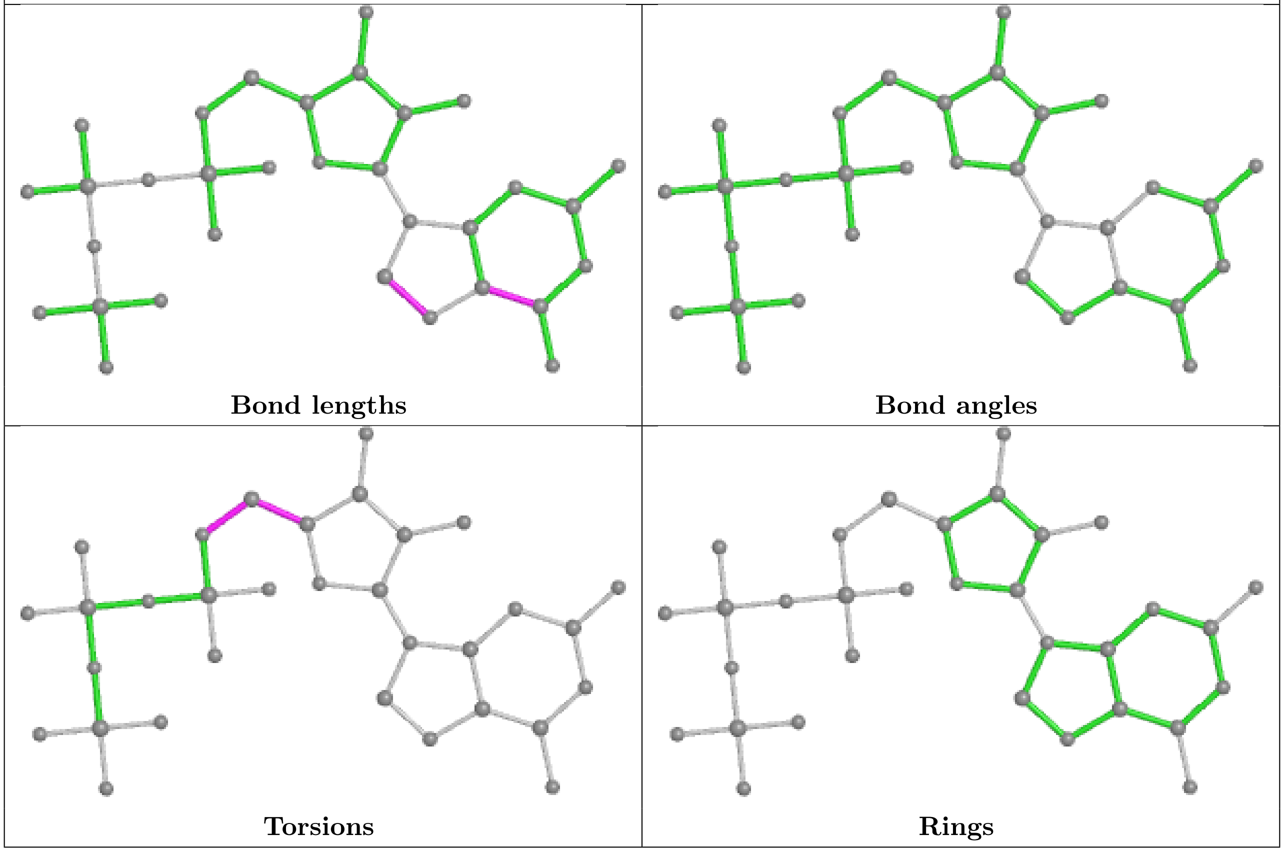
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	RJ	1201	GTP	1	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 then 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 RJ 1201



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

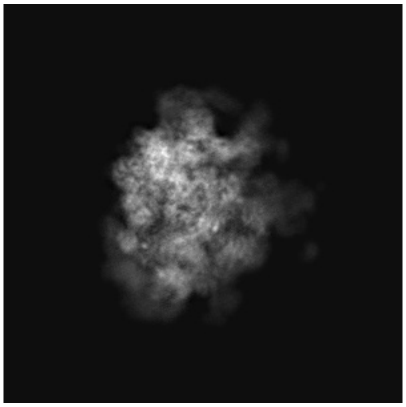
6 Map visualisation

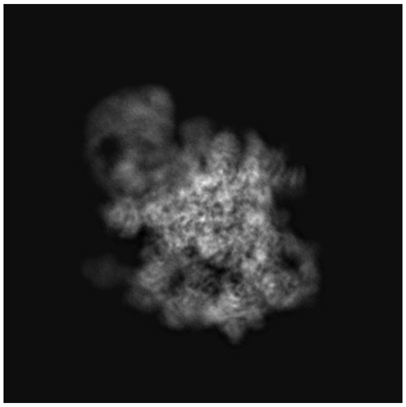
This section contains visualisations of the EMDB entry EMD-30584. These allow visual inspection of the internal detail of the map and identification of artifacts.

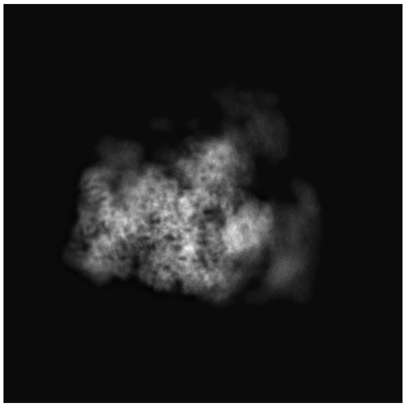
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

6.1.1 Primary map


X

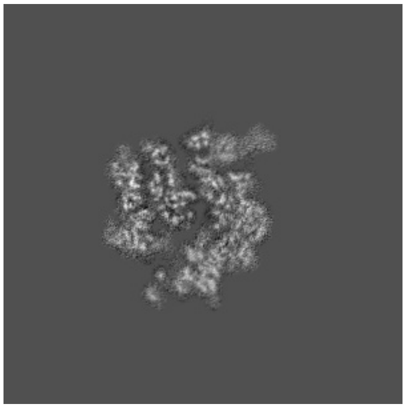

Y

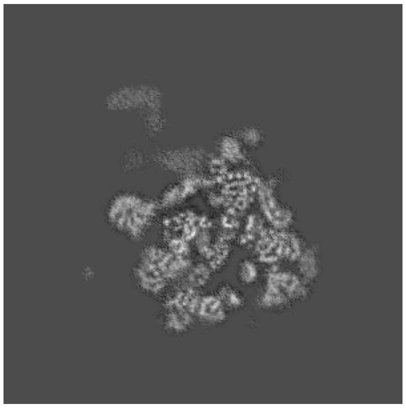

Z

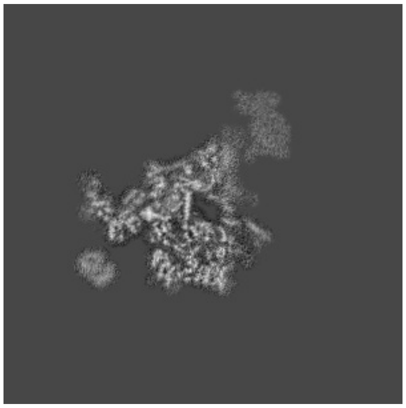
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map


X Index: 200

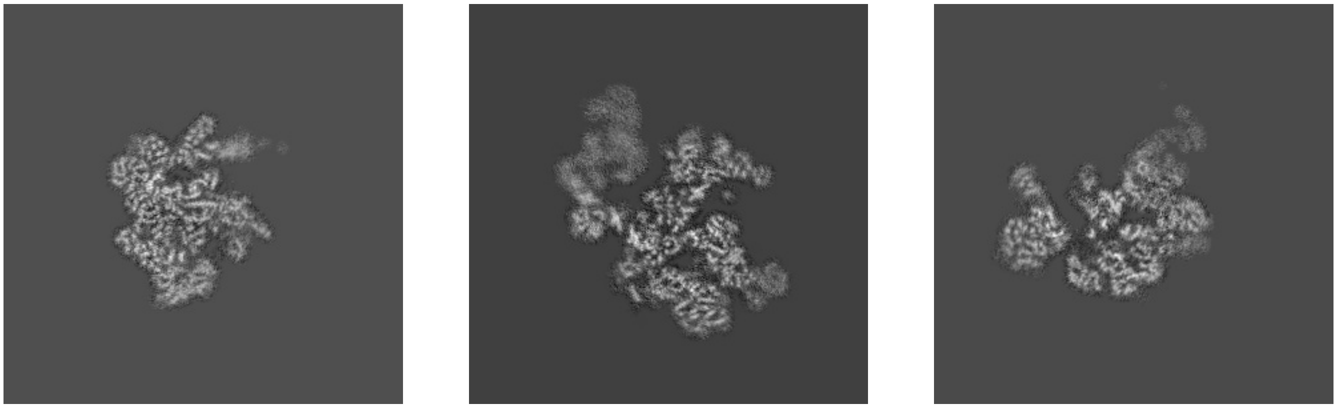

Y Index: 200


Z Index: 200

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

6.3 Largest variance slices ⓘ

6.3.1 Primary map



X Index: 184 Y Index: 177 Z Index: 222

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

6.4 Orthogonal surface views ⓘ

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

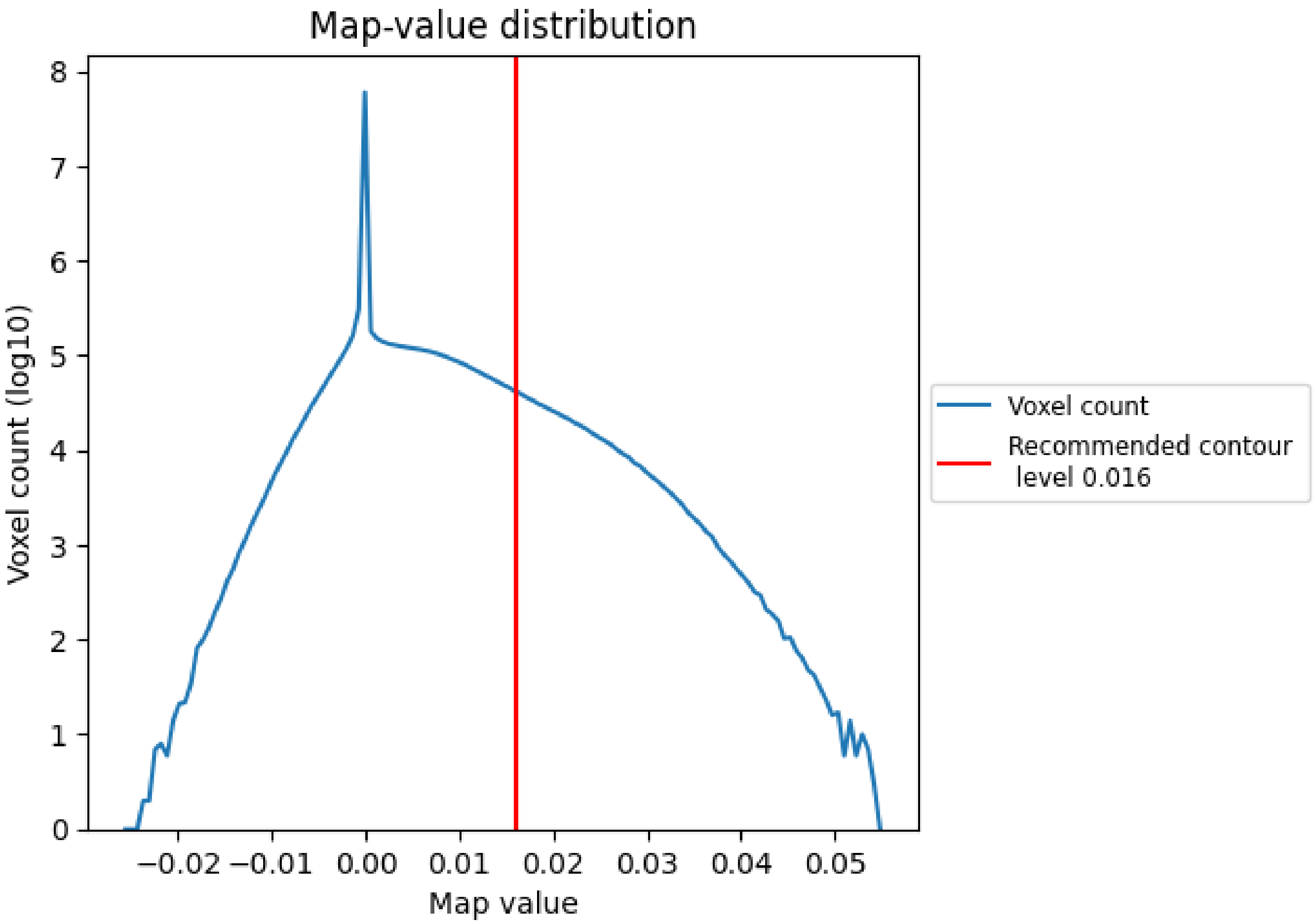
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

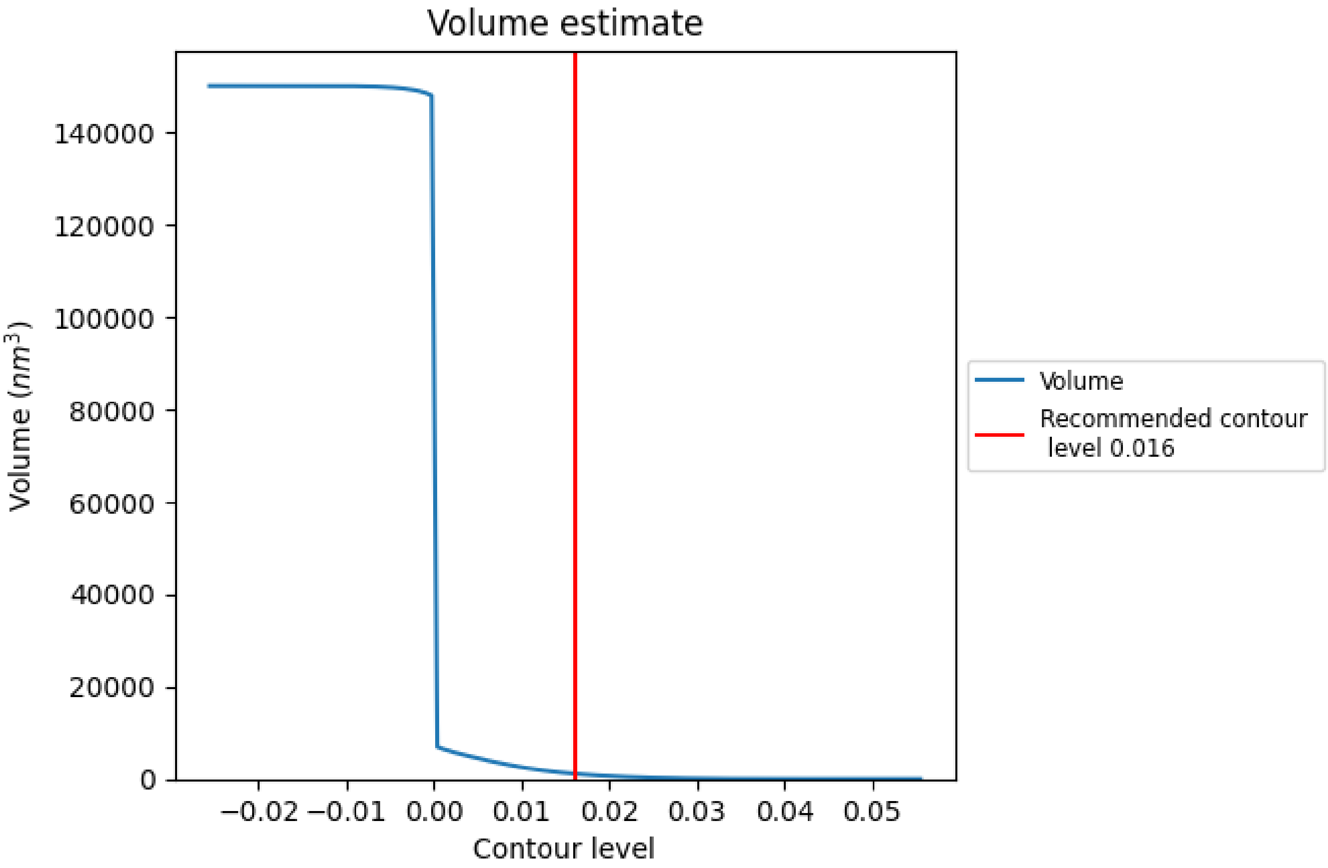
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

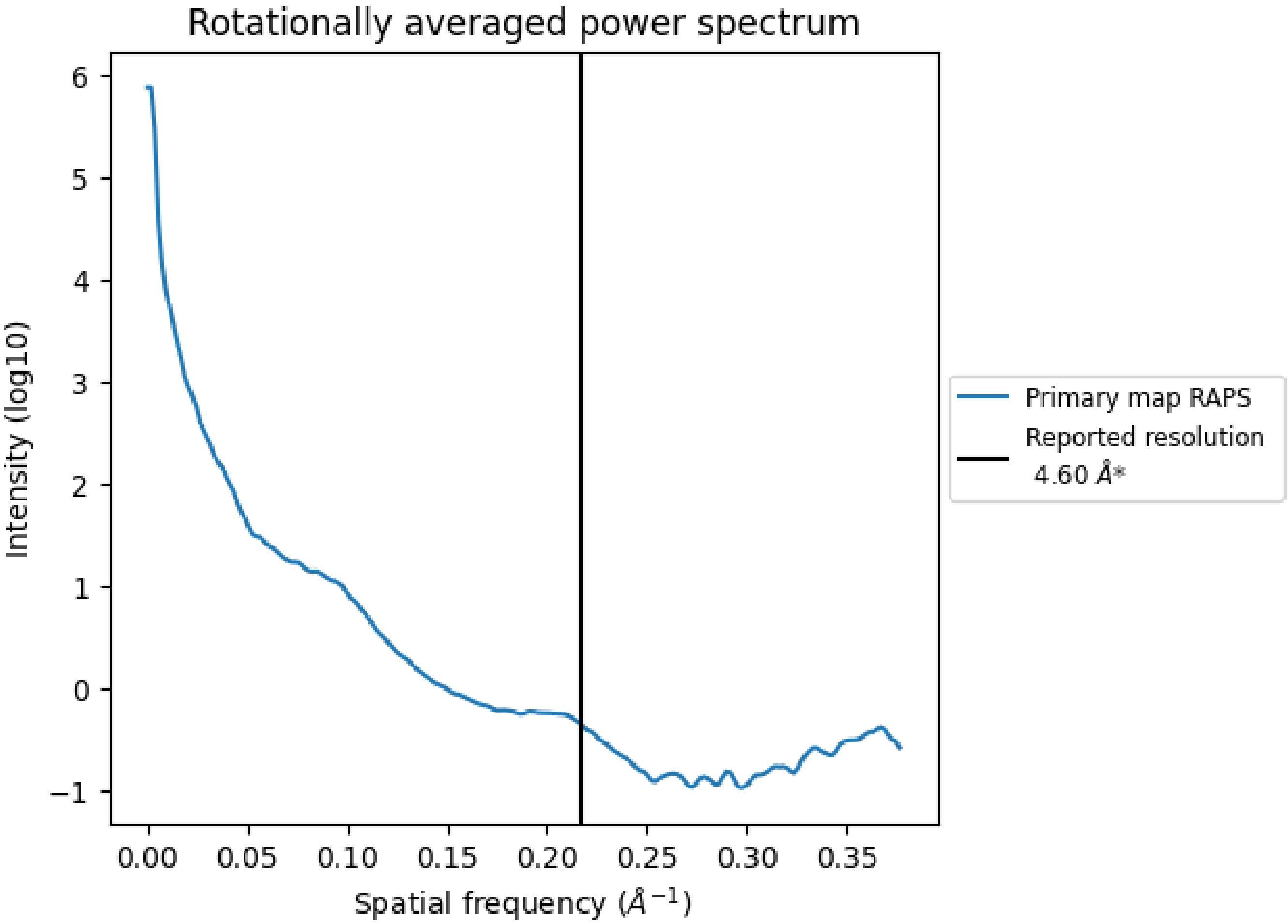
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1155 nm^3; this corresponds to an approximate mass of 1044 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 (i)



*Reported resolution corresponds to spatial frequency of 0.217 Å^{-1}

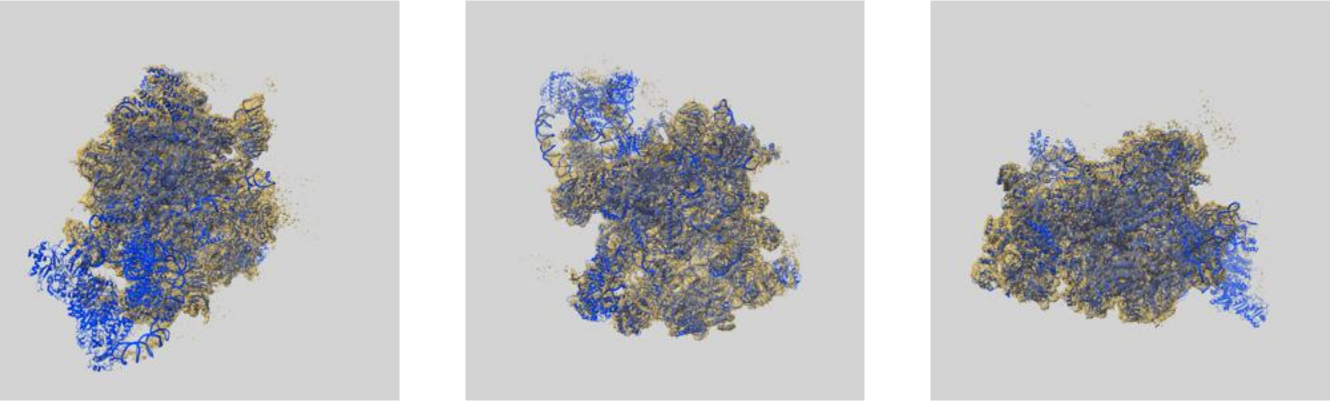
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-30584 and PDB model 7D5S. Per-residue inclusion information can be found in section 3 on page 15.

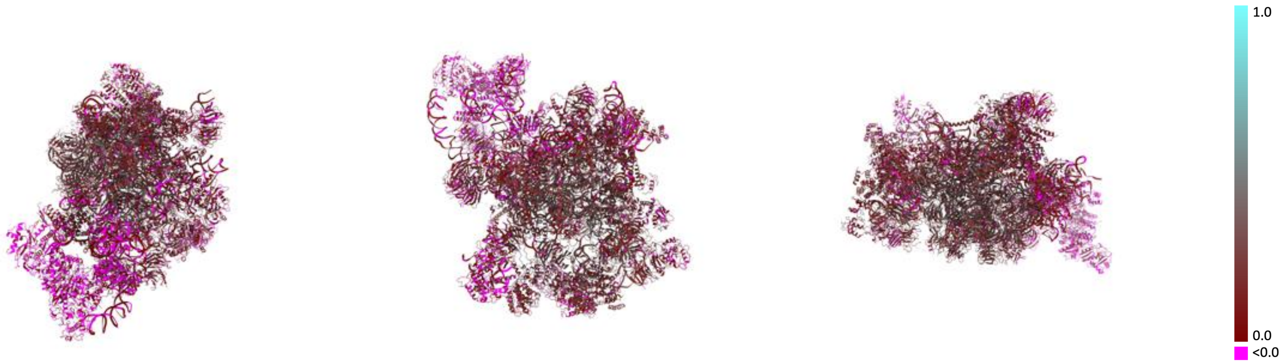
9.1 Map-model overlay ⓘ



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.016 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.

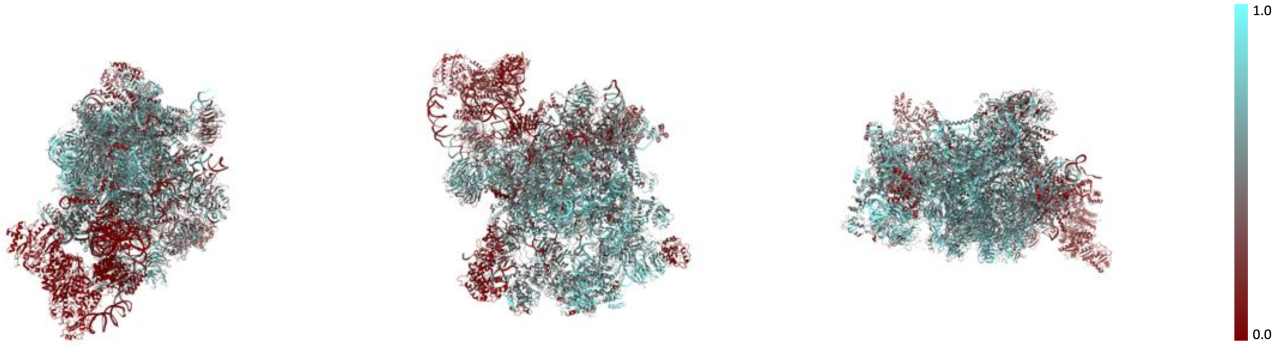
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

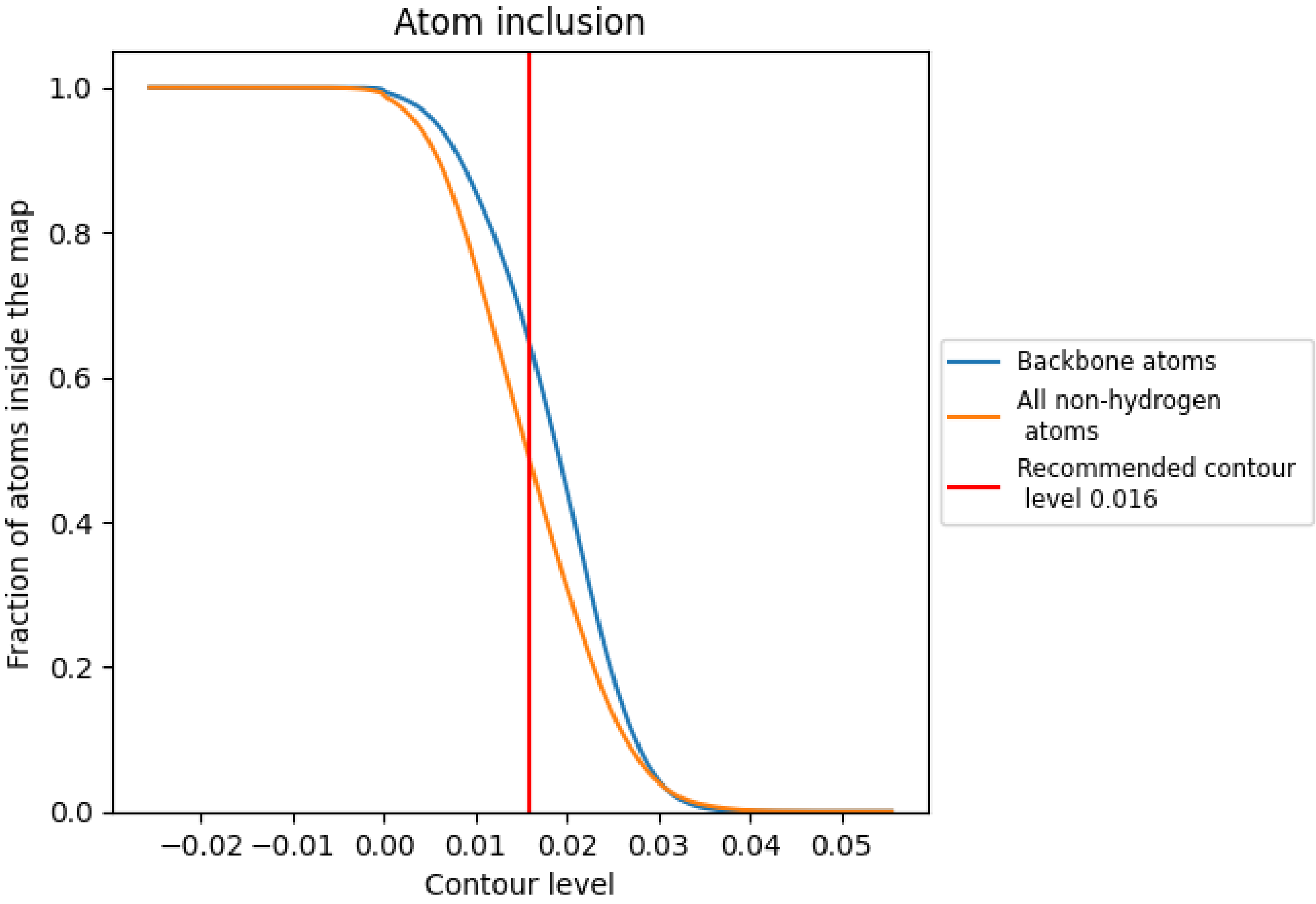
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.016).

9.4 Atom inclusion ⓘ



At the recommended contour level, 64% of all backbone atoms, 48% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4821	0.1810
3A	0.7747	0.2400
3B	0.5187	0.2300
3C	0.5634	0.2000
3D	0.5417	0.1850
3E	0.5949	0.2150
3F	0.3598	0.1270
3G	0.6173	0.2850
3H	0.4436	0.2030
5A	0.7377	0.2250
5B	0.5021	0.1960
5C	0.5186	0.2300
5D	0.5618	0.2480
5E	0.4919	0.2040
5F	0.5777	0.2600
5G	0.4709	0.2230
5H	0.4359	0.1930
5I	0.5635	0.1830
5J	0.3767	0.1950
5K	0.4330	0.1940
A4	0.6488	0.2330
A5	0.6404	0.2520
A8	0.4595	0.1310
A9	0.6134	0.2000
AE	0.3960	0.1900
AF	0.6418	0.2690
AG	0.6369	0.2400
B1	0.6166	0.2730
B2	0.5789	0.1620
B3	0.2622	0.0760
B6	0.4860	0.1650
B8	0.6632	0.2900
BE	0.6515	0.2670
RC	0.0181	0.0130
RD	0.0381	0.0320

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Chain	Atom inclusion	Q-score
RE	0.0027	0.0090
RF	0.0000	-0.0220
RG	0.3784	0.1680
RH	0.4416	0.2090
RI	0.5756	0.2190
RJ	0.5173	0.1940
RK	0.4682	0.1600
RN	0.3658	0.1580
RO	0.5489	0.1940
RQ	0.2303	0.1500
RS	0.1147	0.0550
RT	0.4887	0.1240
RW	0.2090	0.1480
SA	0.4455	0.1350
SG	0.5978	0.2850
SK	0.3333	0.1550
SN	0.0094	0.0370
SO	0.0057	-0.0100
SP	0.0106	0.0160
SR	0.5681	0.3000
ST	0.2812	0.1720
SY	0.2994	0.1390
Sd	0.5744	0.2920
X1	0.3115	0.1720