wwPDB EM Validation Summary Report (i)

Nov 21, 2022 – 05:39 PM JST

PDB ID	:	7D4I
EMDB ID	:	EMD-30574
Title	:	Cryo-EM structure of 90S small ribosomal precursors complex with the DEAH-box RNA helicase Dhr1 (State F)
Authors	:	Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on	:	2020-09-24
Resolution	:	4.00 Å(reported)
Based on initial model	:	6LQS

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

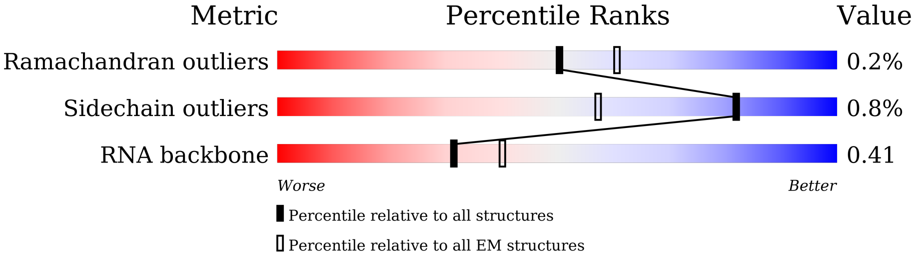
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

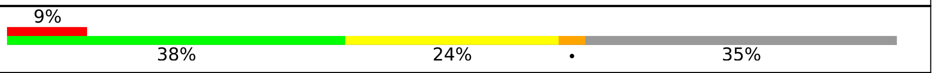
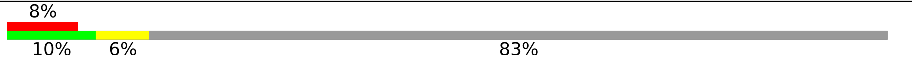
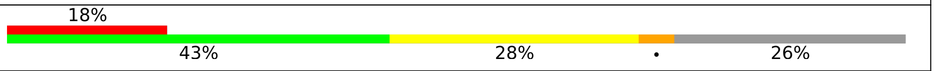
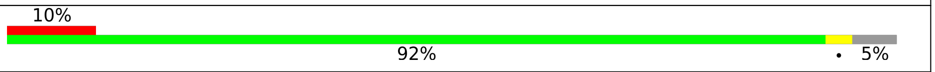
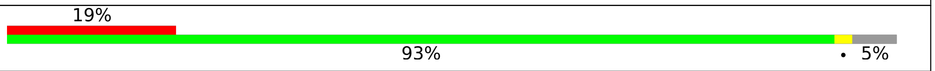
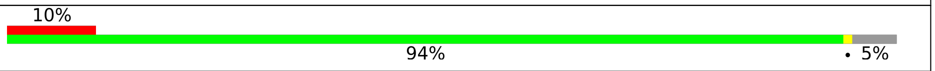
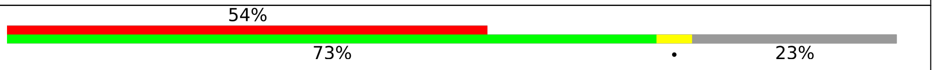
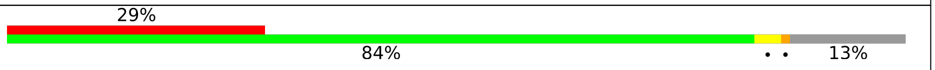
The reported resolution of this entry is 4.00 Å.

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 <=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	1812	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	

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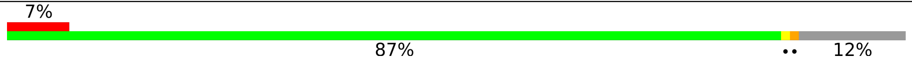
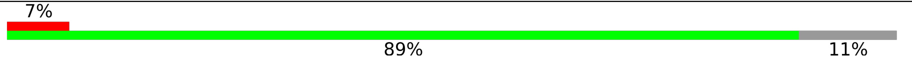
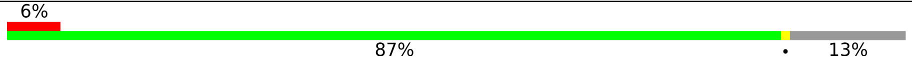
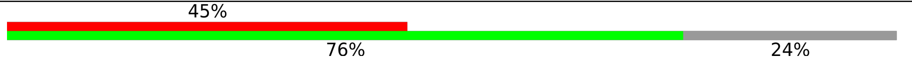
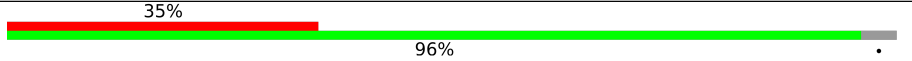
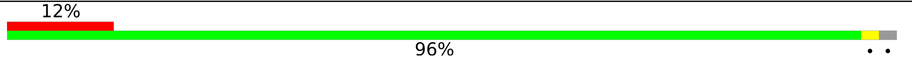
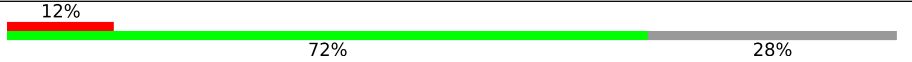
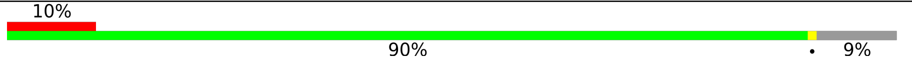
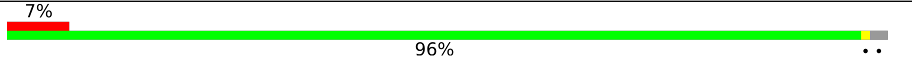
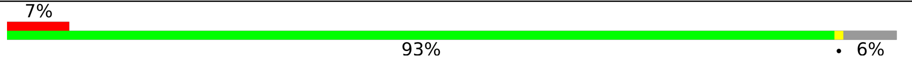
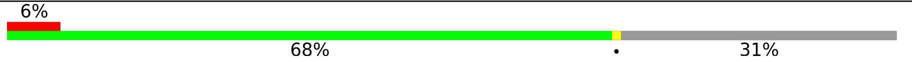
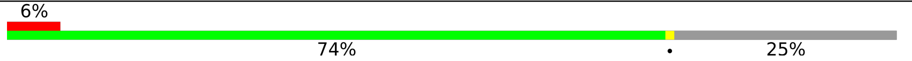
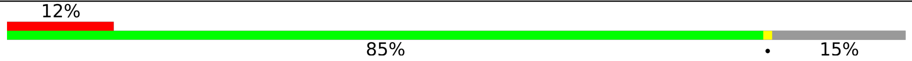
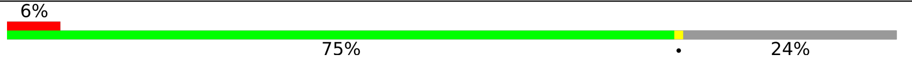
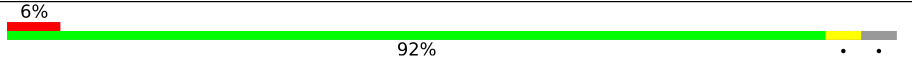
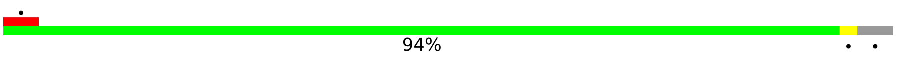
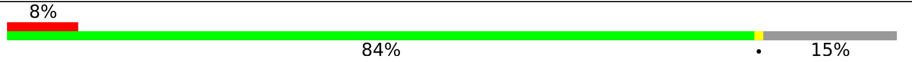
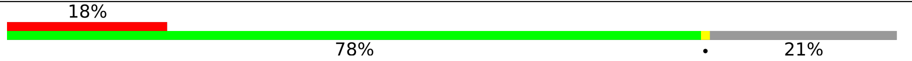
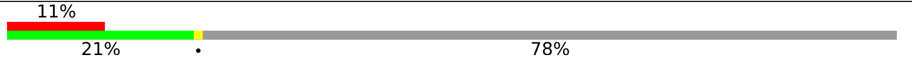
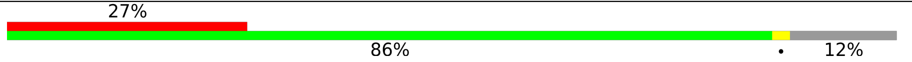
Mol	Chain	Length	Quality of chain
9	SJ	200	 54% 72% • 26%
10	SK	197	 7% 87% •• 12%
11	SM	156	 71% 88% 12%
12	SO	151	 7% 89% 11%
13	SP	137	 • 83% • 15%
14	SR	143	 6% 87% • 13%
15	ST	146	 45% 76% 24%
16	SU	144	 35% 96% •
17	SX	130	 12% 96% • •
18	SY	145	 12% 72% 28%
19	SZ	135	 10% 90% • 9%
20	Sc	82	 7% 96% • •
21	Sd	67	 7% 93% • 6%
22	3B	327	 • 73% • 26%
22	3C	327	 6% 68% • 31%
23	3D	504	 6% 74% • 25%
24	3E	511	 12% 85% • 15%
25	3F	573	 6% 75% • 24%
26	3G	126	 6% 92% • •
26	3H	126	 • 94% • •
27	A4	776	 8% 84% • 15%
28	A5	643	 18% 78% • 21%
29	A8	713	 65% 76% • 23%
30	A9	575	 11% 21% • 78%
31	AE	1769	 27% 86% • 12%

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Mol	Chain	Length	Quality of chain
32	AF	513	21% 94% • 5%
33	AG	896	18% 91% • 8%
34	B1	900	9% 87% • 12%
35	B2	943	11% 86% • 13%
36	B3	817	10% 91% • 7%
37	B8	594	6% 77% • 22%
38	BE	939	11% 93% • 5%
39	B6	440	13% 84% • 14%
40	5B	214	10% 26% • 73%
41	5C	554	14% 86% • 13%
42	5D	250	22% 83% 16%
43	5E	593	8% 36% 64%
44	5F	183	34% 98% • •
45	5G	290	14% 82% • 17%
46	5H	610	• 15% 84%
47	5I	489	5% 93% • 6%
48	5J	217	17% 61% 38%
49	5K	189	5% 78% • 21%
50	RD	1729	18% 18% • 82%
51	RE	1237	24% 87% • 12%
52	RF	297	33% 80% • 19%
53	RG	252	73% 84% • 14%
53	RH	252	64% 90% • 9%
54	RJ	1183	8% 61% • 38%
55	RK	367	9% 97% • •

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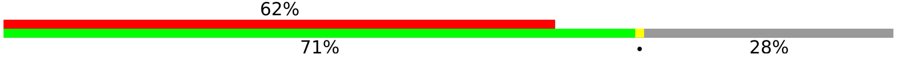
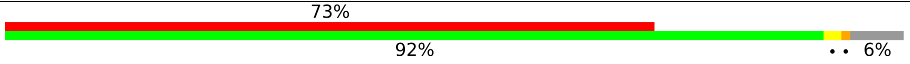
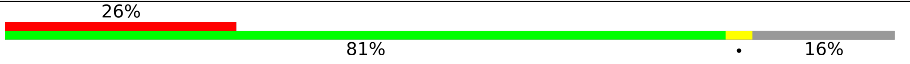
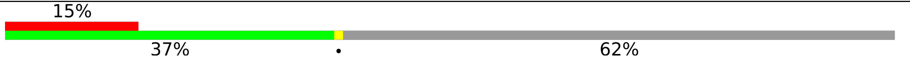
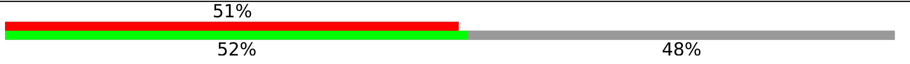
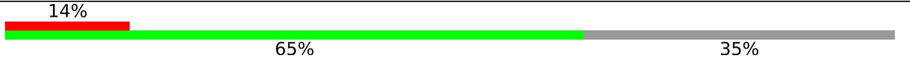
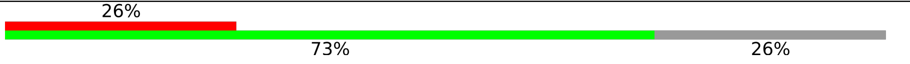
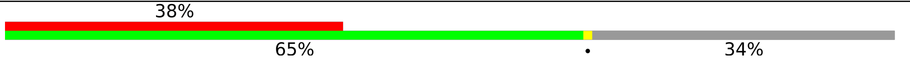
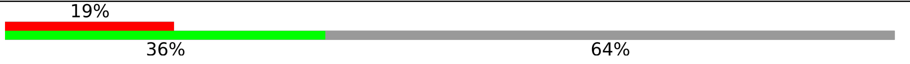
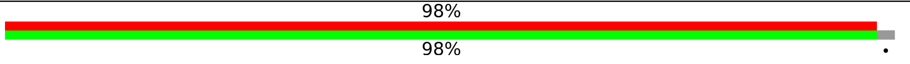
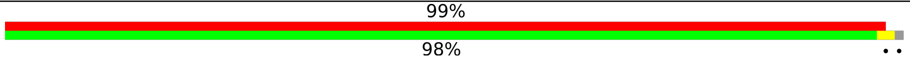
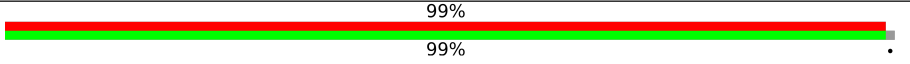
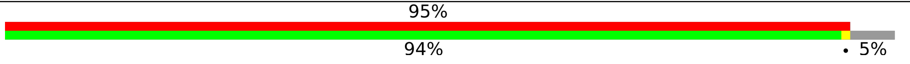
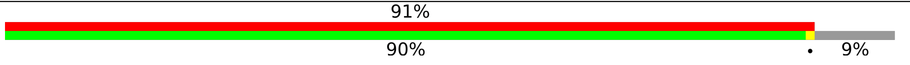
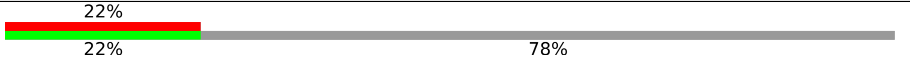
Mol	Chain	Length	Quality of chain
56	RN	810	
57	RO	552	
58	RP	2493	
59	RQ	899	
60	RS	480	
61	RT	326	
62	RW	206	
63	RZ	1267	
64	X1	611	
65	X2	694	
66	R5	305	
67	R1	246	
68	R3	394	
69	R6	223	
70	R2	265	
71	M3	250	
72	R0	240	
73	r4	359	
74	C4	292	
75	R4	1001	
76	r6	733	
77	R7	184	
78	M4	1073	
79	M6	186	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 253642 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	216	4570	2044	784	1526	216	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5A	118	2536	1131	467	820	118	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1337	28478	12732	5036	9373	1337	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SC	242	1923	1214	356	349	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SF	247	1915	1223	351	338	3	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	182	Total	C	N	O	S	0	0
			1456	916	273	266	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	SI	165	Total	C	N	O	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	148	Total	C	N	O	S	0	0
			1181	739	228	212	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	174	Total	C	N	O	S	0	0
			1410	892	272	245	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	137	Total	C	N	O	S	0	0
			1113	715	212	183	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	116	Total	C	N	O	S	0	0
			848	524	158	163	3		

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

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

- Molecule 15 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	111	Total 902	C 568	N 171	O 161	S 2	0	0

- Molecule 16 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	138	Total 1075	C 673	N 203	O 197	S 2	0	0

- Molecule 17 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 18 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SY	104	Total 792	C 506	N 145	O 139	S 2	0	0

- Molecule 19 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	SZ	123	Total 986	C 626	N 188	O 172	0	0

- Molecule 20 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	3B	242	1878	1190	338	340	10	0	0
22	3C	224	1754	1114	314	316	10	0	0

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	3D	378	2974	1886	511	568	9	0	0

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	3E	435	3056	1904	548	595	9	0	0

- Molecule 25 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	3F	437	3498	2227	609	652	10	0	0

- Molecule 26 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	3G	121	916	583	158	171	4	0	0
26	3H	121	916	583	158	171	4	0	0

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	A4	657	5187	3286	902	978	21	0	0

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	A5	511	3953	2507	682	751	13	0	0

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 8.

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

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 9.

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

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AE	1552	10262	6453	1810	1979	20	0	0

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	AF	487	3860	2431	692	725	12	0	0

- Molecule 33 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	AG	825	6565	4178	1110	1258	19	0	0

- Molecule 34 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	B1	791	6316	4037	1082	1179	18	0	0

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	B2	824	6497	4153	1095	1222	27	0	0

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	B3	757	5906	3763	993	1123	27	0	0

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	B8	463	3648	2314	640	684	10	0	0

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	BE	890	6876	4356	1191	1308	21	0	0

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	B6	377	3077	1984	529	549	15	0	0

- Molecule 40 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	5B	58	482	302	98	82	0	0

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	5C	482	3825	2409	684	721	11	0	0

- Molecule 42 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	209	Total 1778	C 1111	N 344	O 317	S 6	0	0

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	213	Total 1728	C 1072	N 304	O 348	S 4	0	0

- Molecule 44 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5F	182	Total 1530	C 967	N 287	O 269	S 7	0	0

- Molecule 45 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	241	Total 1956	C 1228	N 368	O 353	S 7	0	0

- Molecule 46 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	5H	95	Total 700	C 435	N 143	O 122	0	0

- Molecule 47 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5I	461	Total 3765	C 2354	N 686	O 709	S 16	0	0

- Molecule 48 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	134	Total 1127	C 712	N 205	O 207	S 3	0	0

- Molecule 49 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	5K	150	1190	765	212	203	10	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5K	138	ASN	ASP	variant	UNP Q05498

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	RD	316	2413	1541	415	452	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	RE	1090	8805	5720	1452	1609	24	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	RJ	738	5994	3851	1063	1054	26	0	0

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

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

- Molecule 56 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RN	584	Total 4459	C 2819	N 800	O 827	S 13	0	0

- Molecule 57 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RO	520	Total 3741	C 2397	N 641	O 691	S 12	0	0

- Molecule 58 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	RP	2084	Total 12263	C 7556	N 2298	O 2392	S 17	0	0

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RQ	339	Total 2408	C 1484	N 456	O 466	S 2	0	0

- Molecule 60 is a protein called Essential nuclear protein 1.

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

- Molecule 61 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RT	213	Total 1652	C 1051	N 300	O 297	S 4	0	0

- Molecule 62 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
62	RW	153	762	456	153	153	0	0

- Molecule 63 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	RZ	838	6598	4212	1145	1206	35	1	0

- Molecule 64 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
64	X1	221	1105	663	221	221	0	0

- Molecule 65 is a protein called Unassigned peptides 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
65	X2	141	705	423	141	141	0	0

- Molecule 66 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	R5	299	2304	1444	393	451	16	0	0

- Molecule 67 is a protein called Exosome complex component SKI6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	R1	244	1886	1177	335	366	8	0	0

- Molecule 68 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	R3	339	2588	1640	441	497	10	1	0

- Molecule 69 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	R6	223	1701	1072	285	334	10	1	0

- Molecule 70 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	R2	265	2035	1299	334	397	5	1	0

- Molecule 71 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	M3	215	1639	1024	273	332	10	0	0

- Molecule 72 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	R0	237	1792	1143	295	344	10	0	0

- Molecule 73 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	r4	293	2236	1393	403	428	12	0	0

- Molecule 74 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	C4	222	1653	1034	287	325	7	0	0

- Molecule 75 is a protein called Exosome complex exonuclease DIS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	R4	948	7430	4693	1308	1394	35	0	0

- Molecule 76 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	r6	414	2517	1544	469	498	6	0	0

- Molecule 77 is a protein called Exosome complex protein LRP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	R7	113	894	565	151	174	4	0	0

- Molecule 78 is a protein called ATP-dependent RNA helicase DOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	M4	978	7626	4871	1294	1419	42	0	0

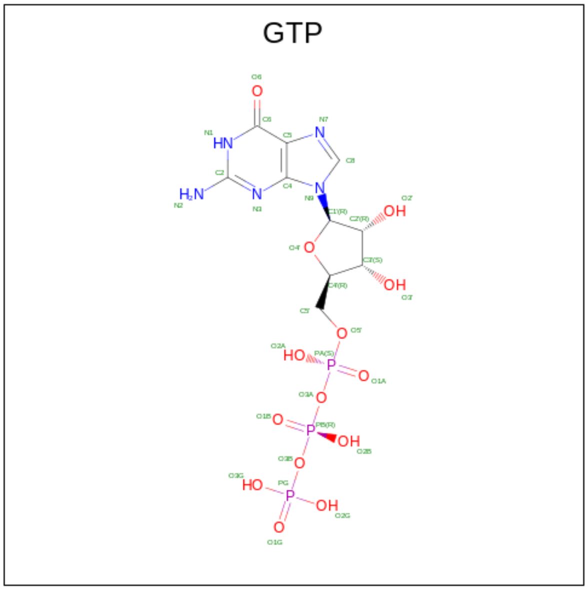
- Molecule 79 is a protein called M-phase phosphoprotein 6 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
79	M6	40	275	170	51	54	0	0

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
80	Sc	1	1	1	0
80	5K	1	1	1	0

- Molecule 81 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

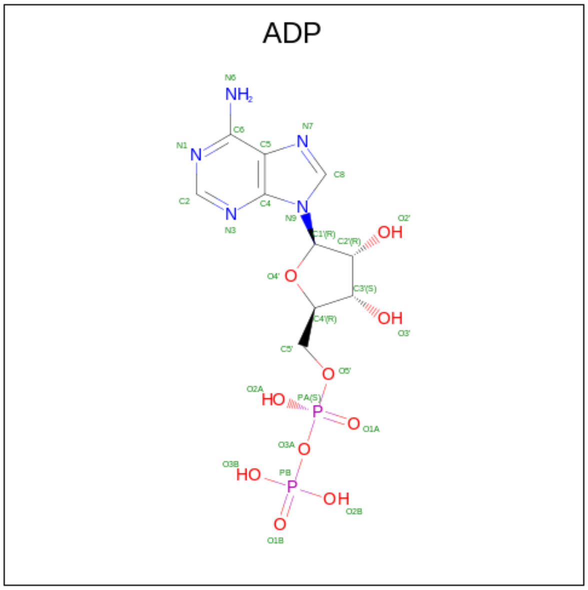


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
81	RJ	1	32	10	5	14	3	0

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 83 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

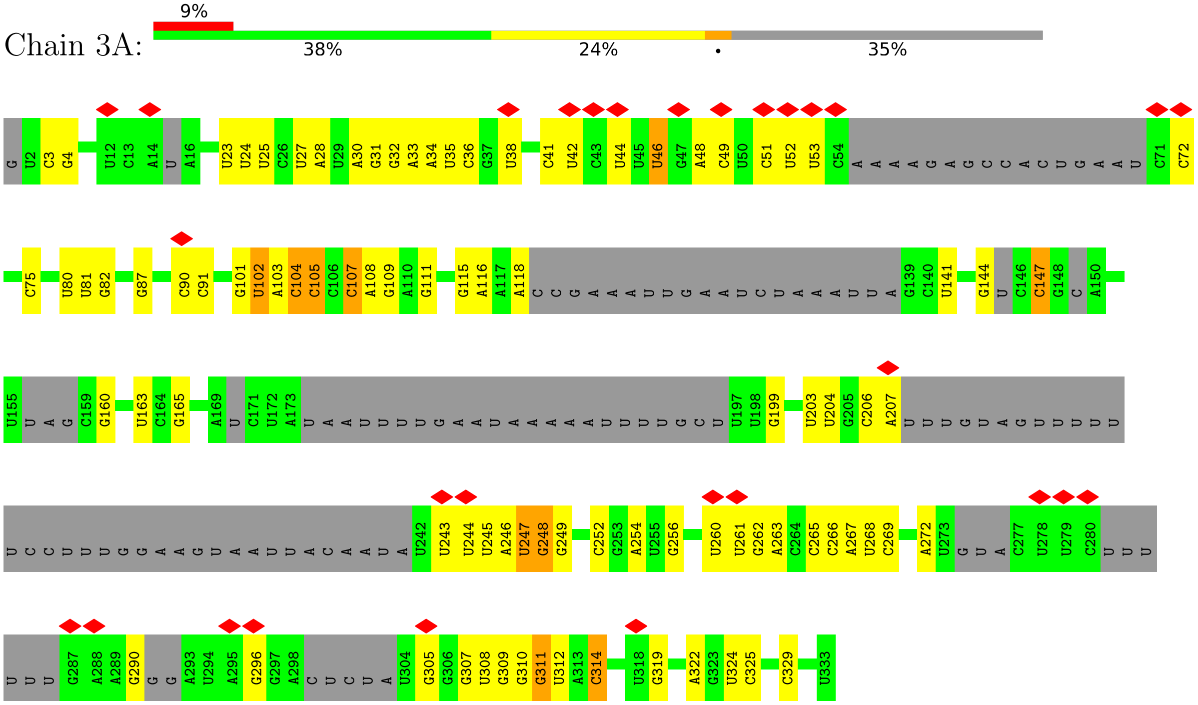


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
83	RZ	1	27	10	5	10	2	0

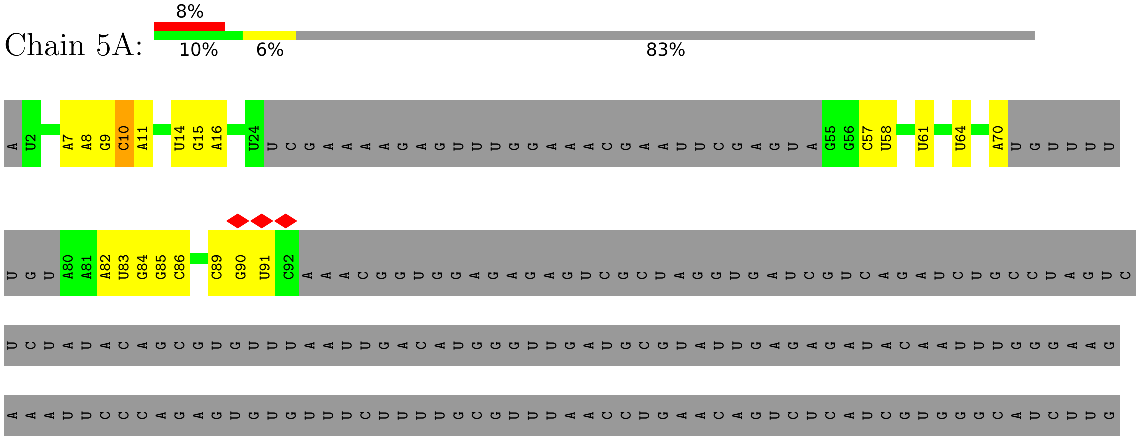
3 Residue-property plots ⓘ

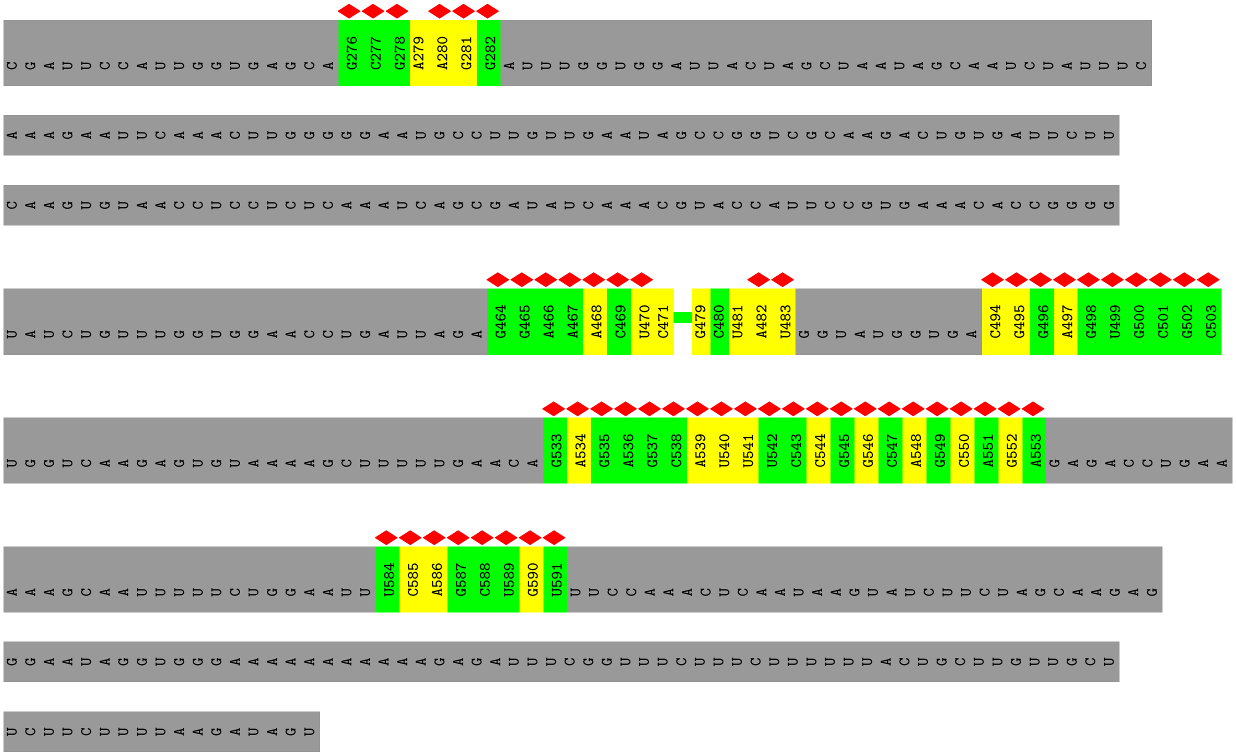
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



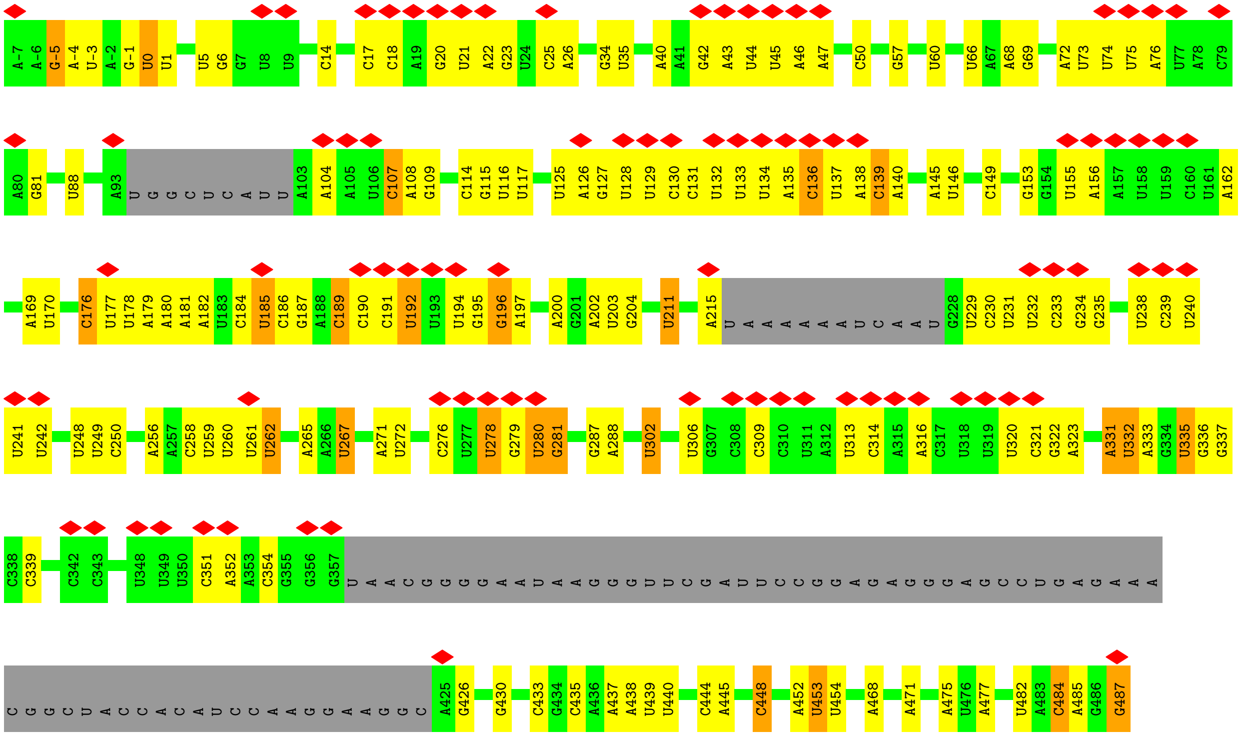
- Molecule 2: 5' ETS

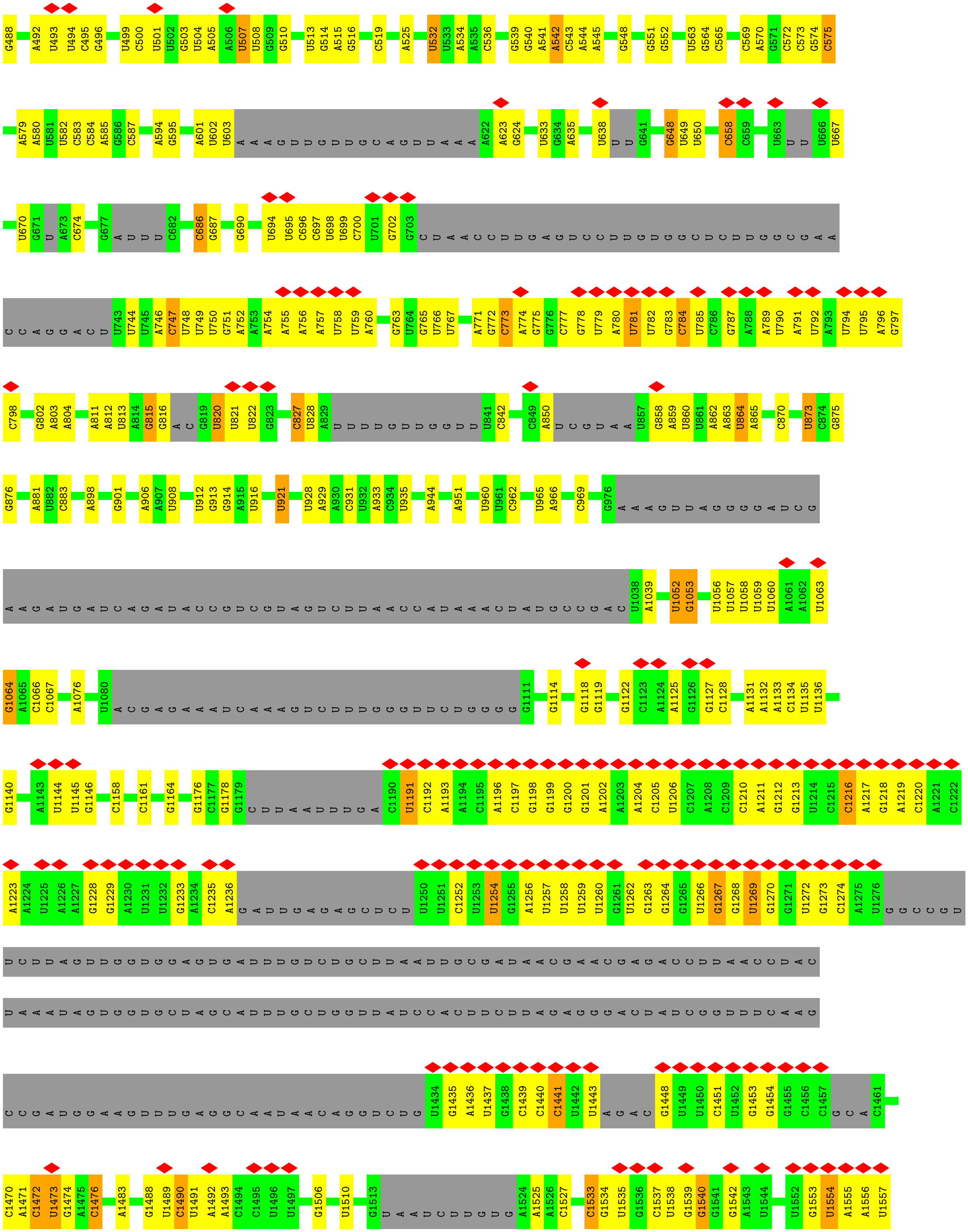




- Molecule 3: 18S rRNA

Chain SA:

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A579 A580 U581 U582 C583 C584 A585 G586 C587 A594 G595 A601 U602 U603 A A A G U U G U U G C A G U U A A A A622 A623 G624 U633 G634 A635 U638 U U G641 G648 U649 U650 C658 C659 U663 U U U666 U667
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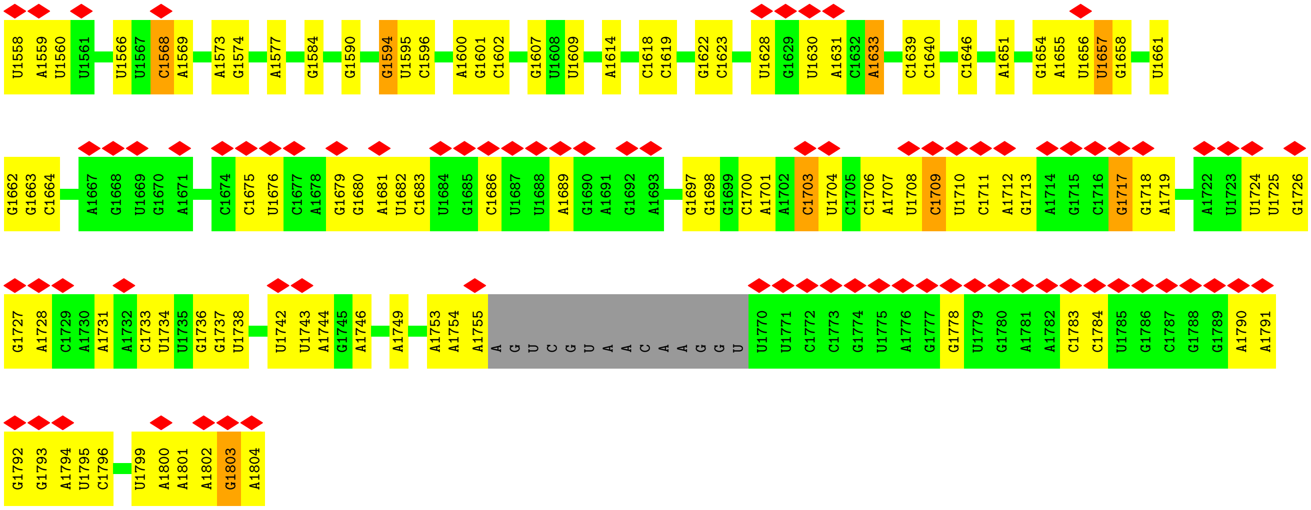
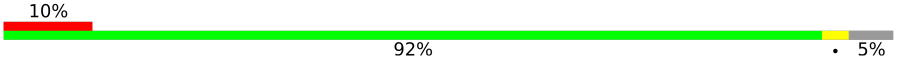
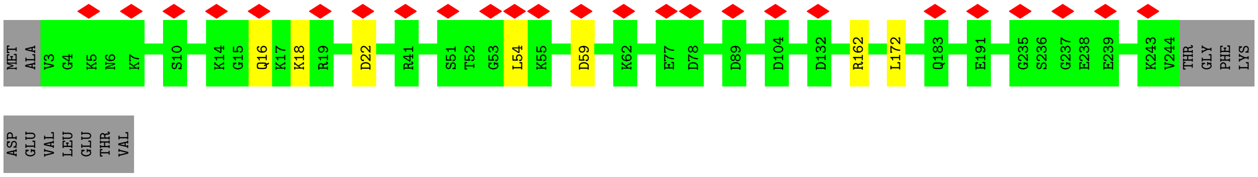
G1140 A1143 U1144 U1145 G1146 C1158 C1161 G1164 G1176 C1177 G1178 G1179 C U U A A U U U G A C1190 U1191 C1192 A1193 A1194 C1195 A1196 C1197 G1198 G1199 G1200 G1201 A1202 A1203 A1204 C1205 U1206 C1207 A1208 C1209 C1210 A1211 G1212 G1213 U1214 C1215 C1216 A1217 G1218 A1219 C1220 A1221 C1222
A1223 A1224 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 U1260 G1261 U1262 G1263 G1264 G1265 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 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 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 A C1461
C1470 A1471 C1472 U1473 G1474 A1475 C1476 A1483 G1488 U1489 C1490 U1491 A1492 A1493 C1494 C1495 U1496 U1497 G1506 U1510 G1513 U A A U C U U G U G A1524 A1525 A1526 C1527 C1533 G1534 U1535 G1536 C1537 U1538 G1539 G1540 G1541 G1542 A1543 U1544 U1552 G1553 U1554 A1555 A1556 U1557



- Molecule 4: 40S ribosomal protein S1-A

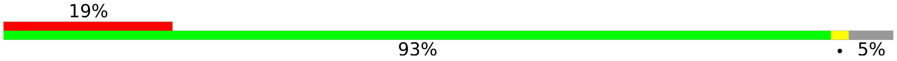
Chain SC:

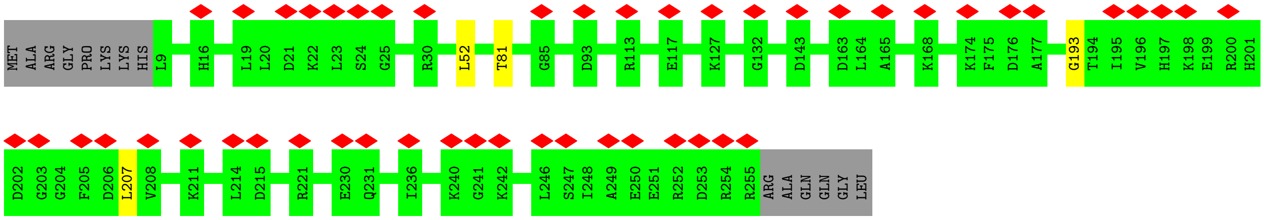




- Molecule 5: 40S ribosomal protein S4-A

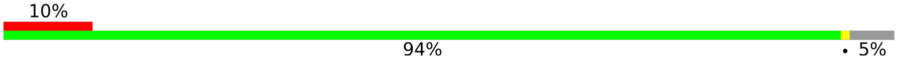
Chain SF:

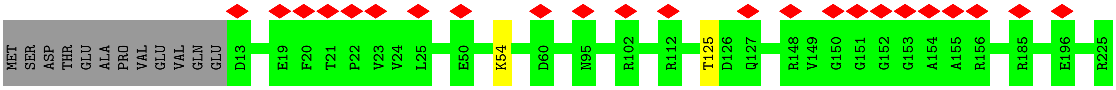




- Molecule 6: 40S ribosomal protein S5

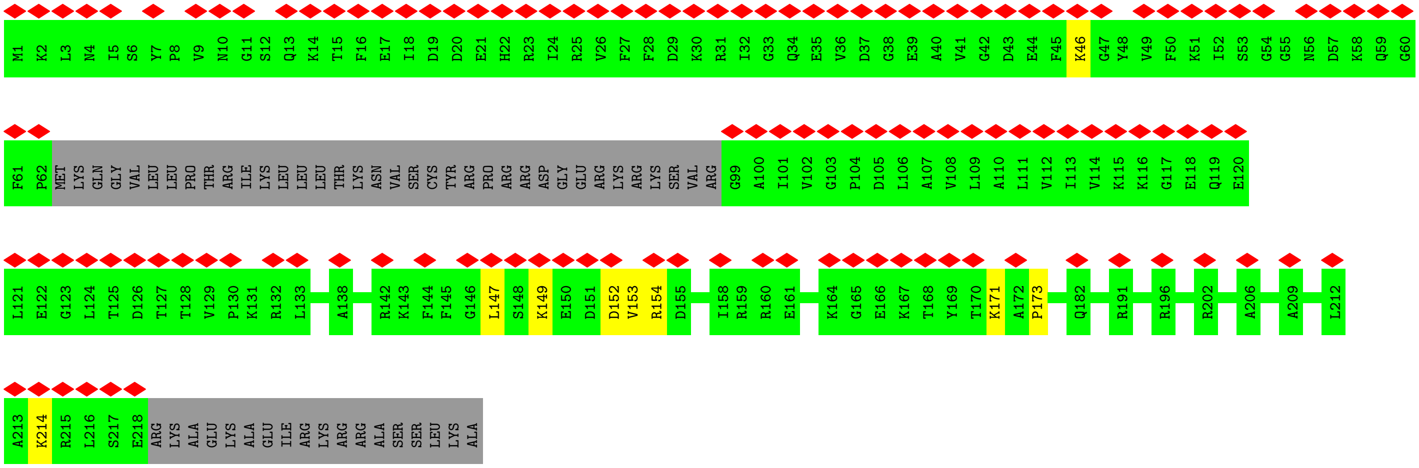
Chain SG:



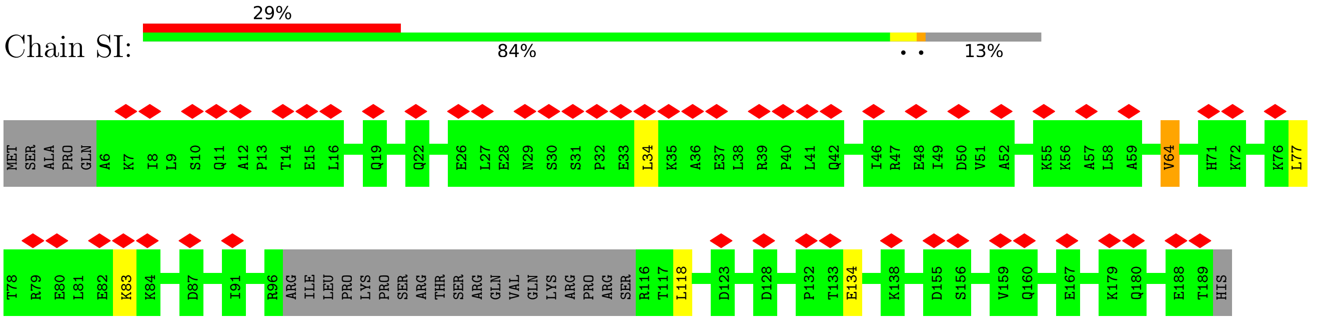


- Molecule 7: 40S ribosomal protein S6-A

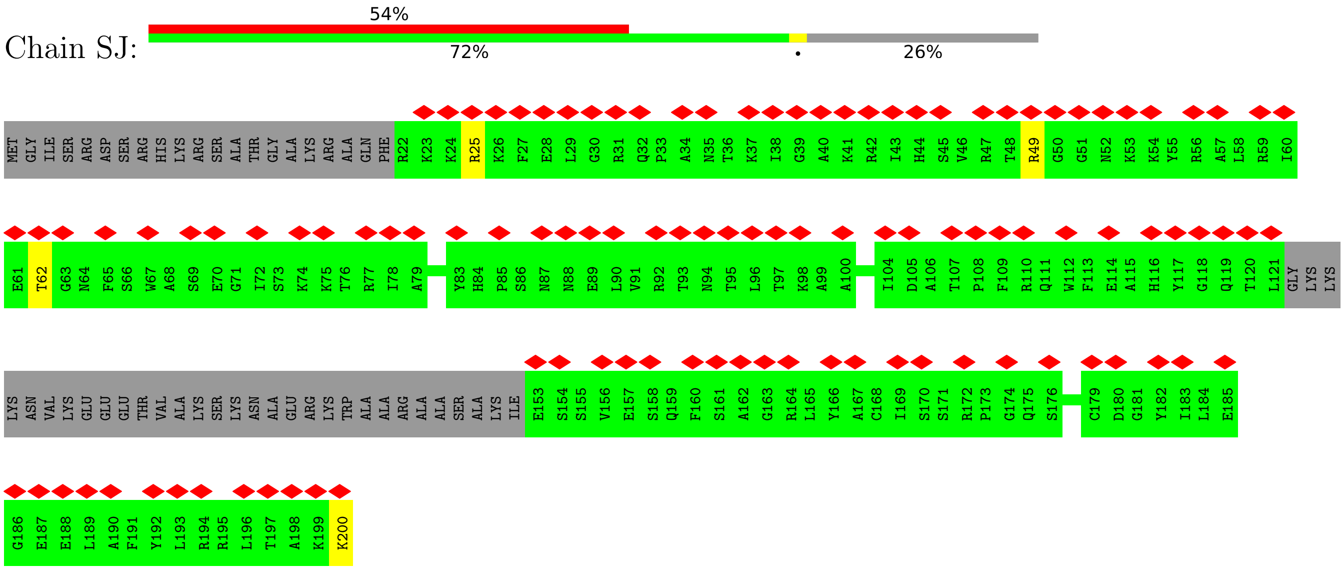
Chain SH:



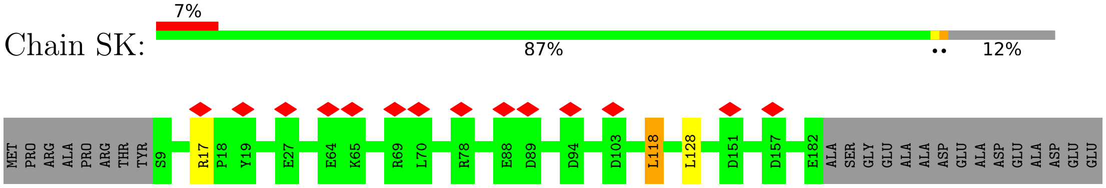
- Molecule 8: 40S ribosomal protein S7-A



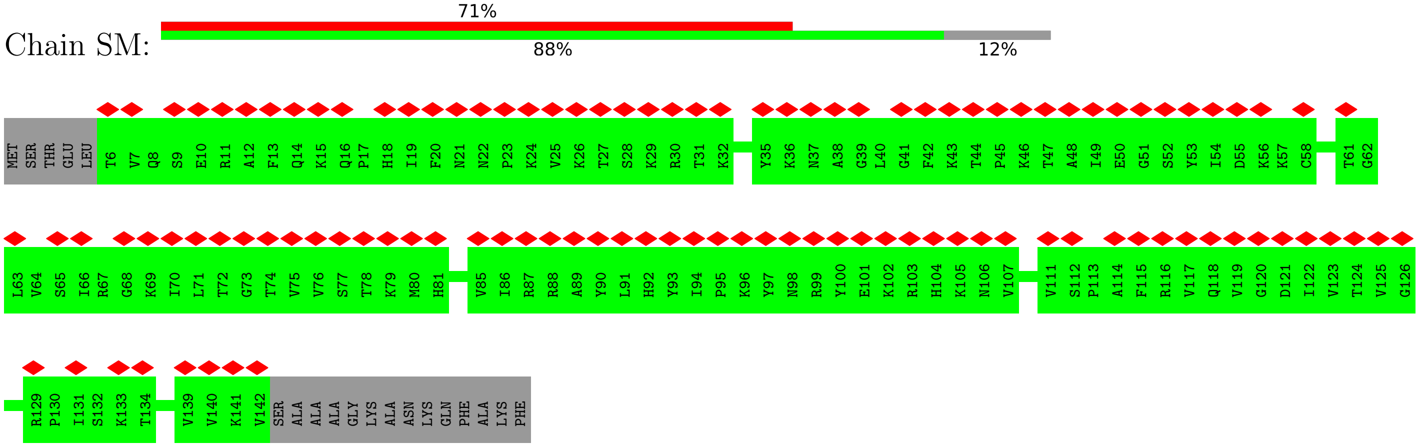
- Molecule 9: 40S ribosomal protein S8-A



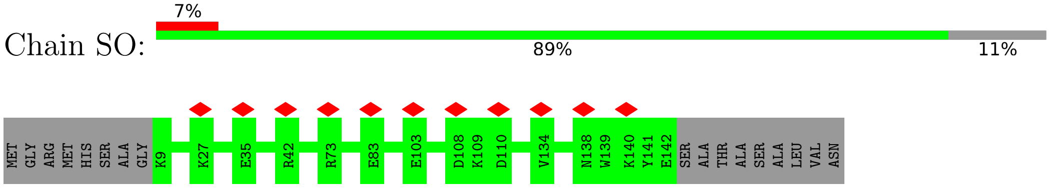
- Molecule 10: 40S ribosomal protein S9-A



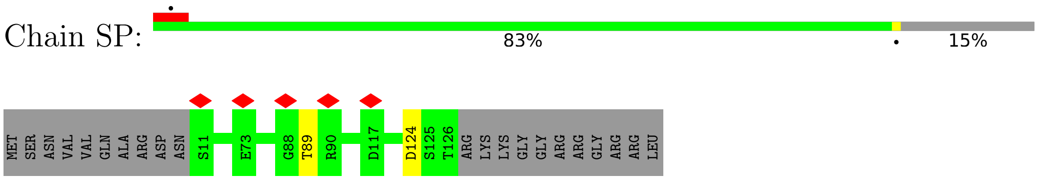
- Molecule 11: 40S ribosomal protein S11-A



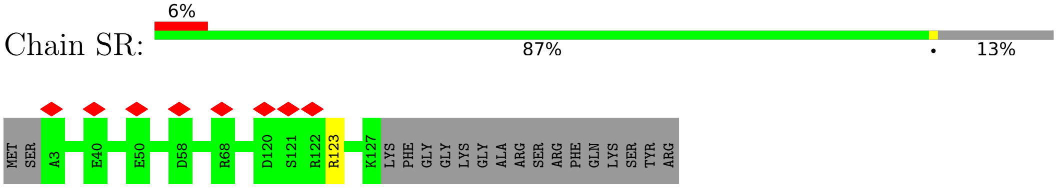
- Molecule 12: 40S ribosomal protein S13



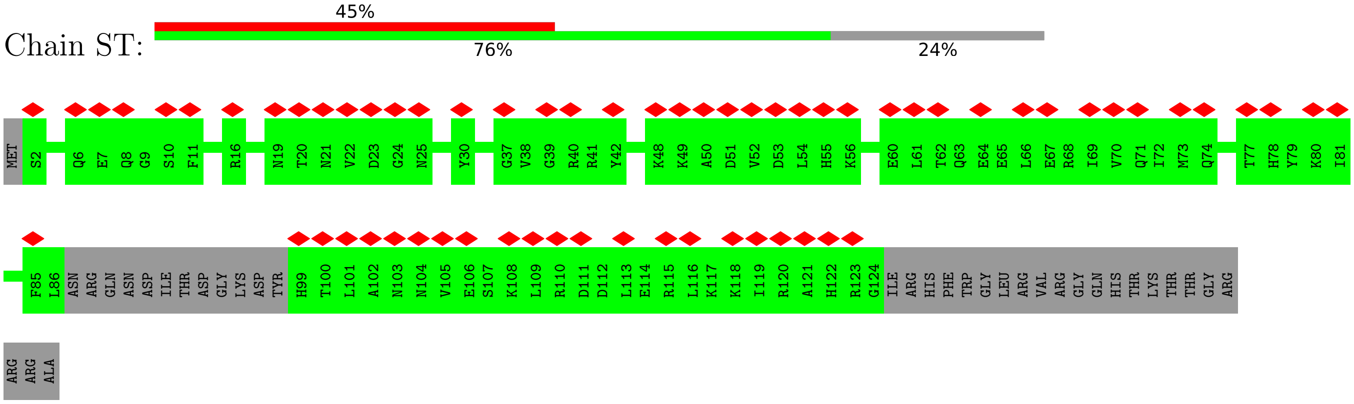
- Molecule 13: 40S ribosomal protein S14-A



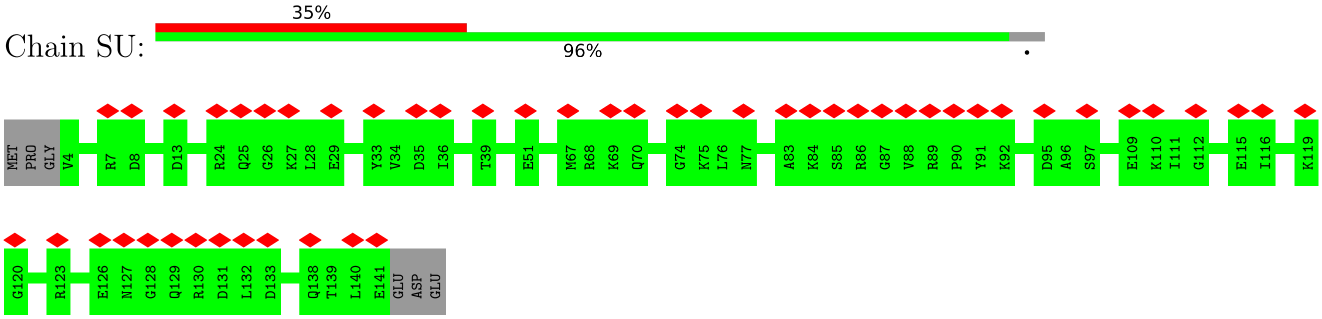
- Molecule 14: 40S ribosomal protein S16-A



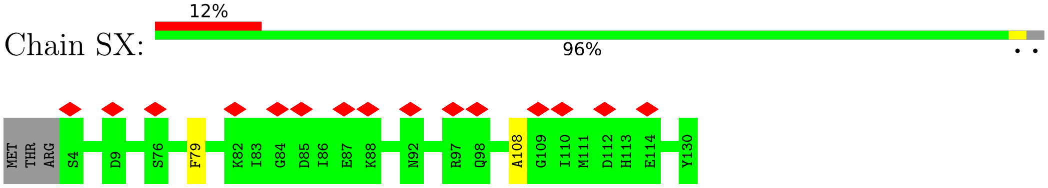
- Molecule 15: 40S ribosomal protein S18-A



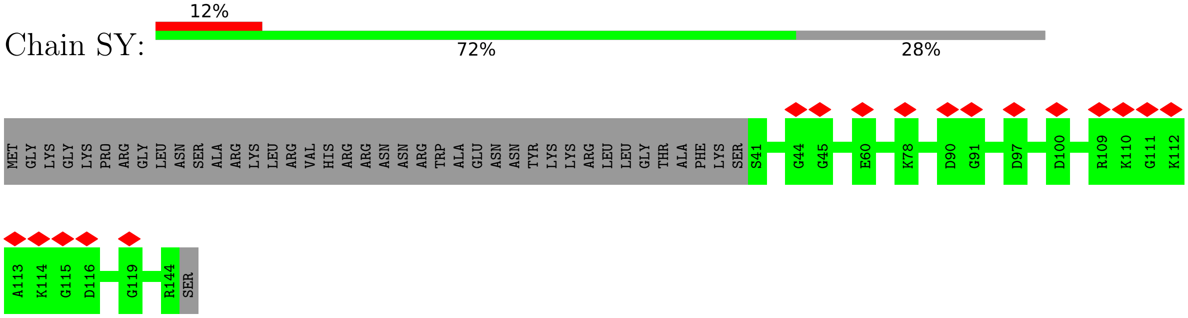
- Molecule 16: 40S ribosomal protein S19-A



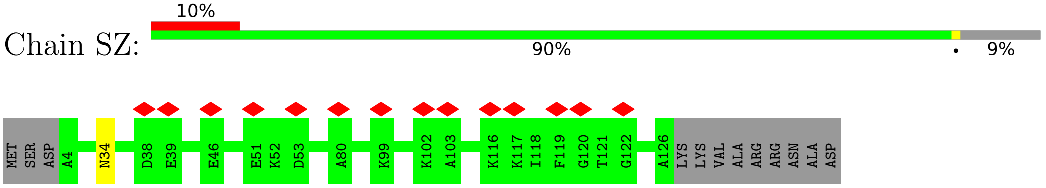
- Molecule 17: 40S ribosomal protein S22-B



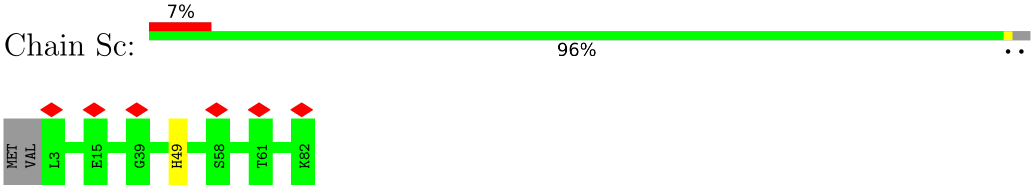
- Molecule 18: 40S ribosomal protein S23-A



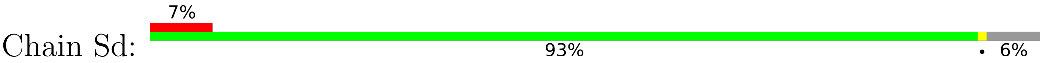
- Molecule 19: 40S ribosomal protein S24-A

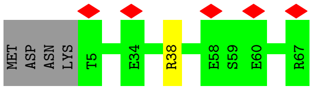


- Molecule 20: 40S ribosomal protein S27-A

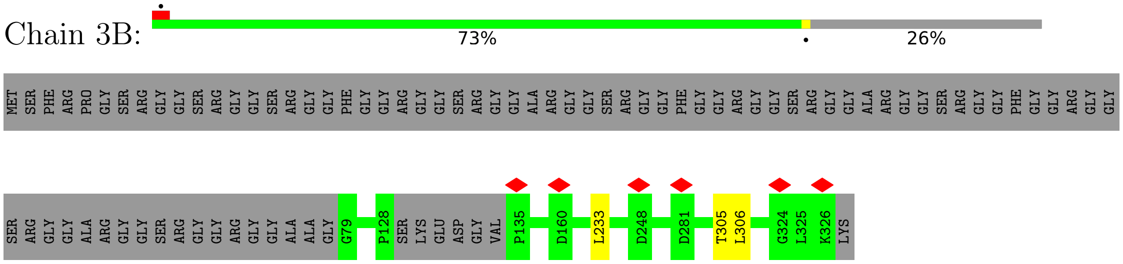


- Molecule 21: 40S ribosomal protein S28-A

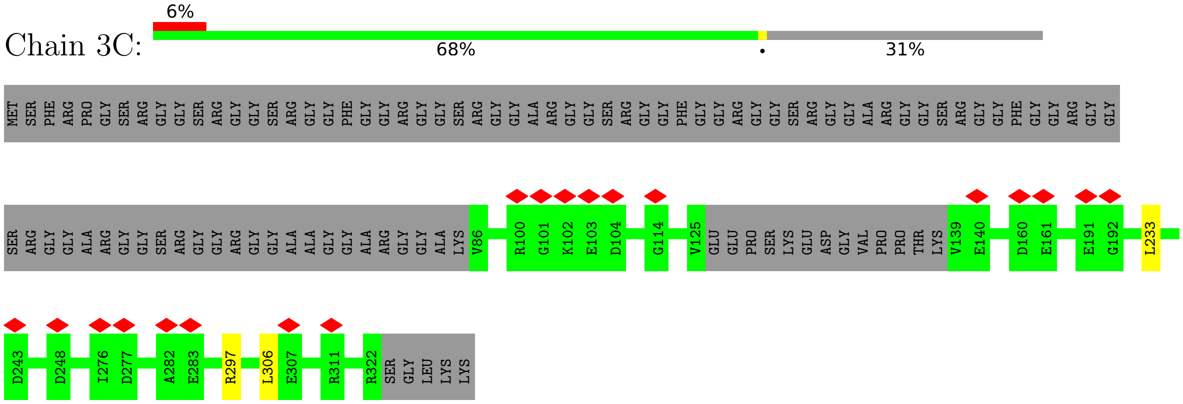




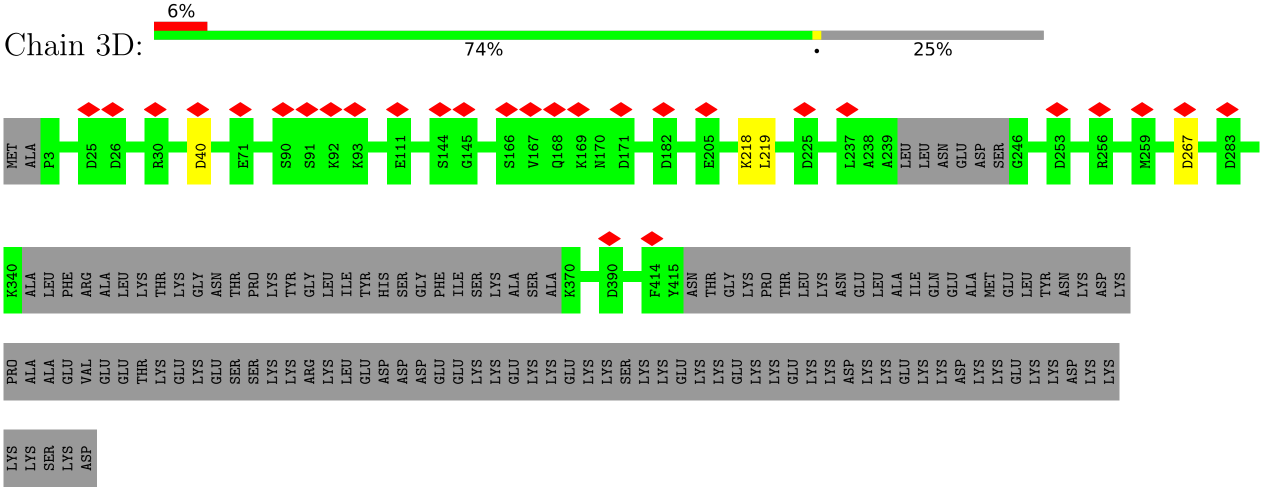
- Molecule 22: rRNA 2’-O-methyltransferase fibrillarin



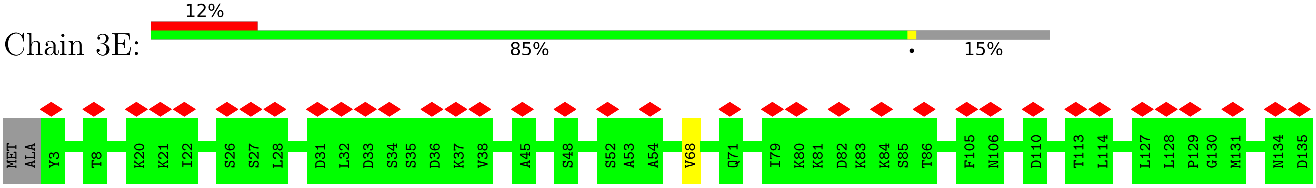
- Molecule 22: rRNA 2’-O-methyltransferase fibrillarin

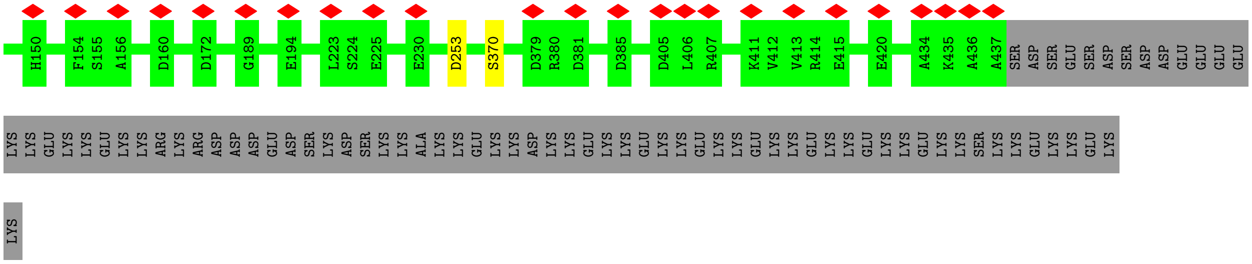


- Molecule 23: Nucleolar protein 56

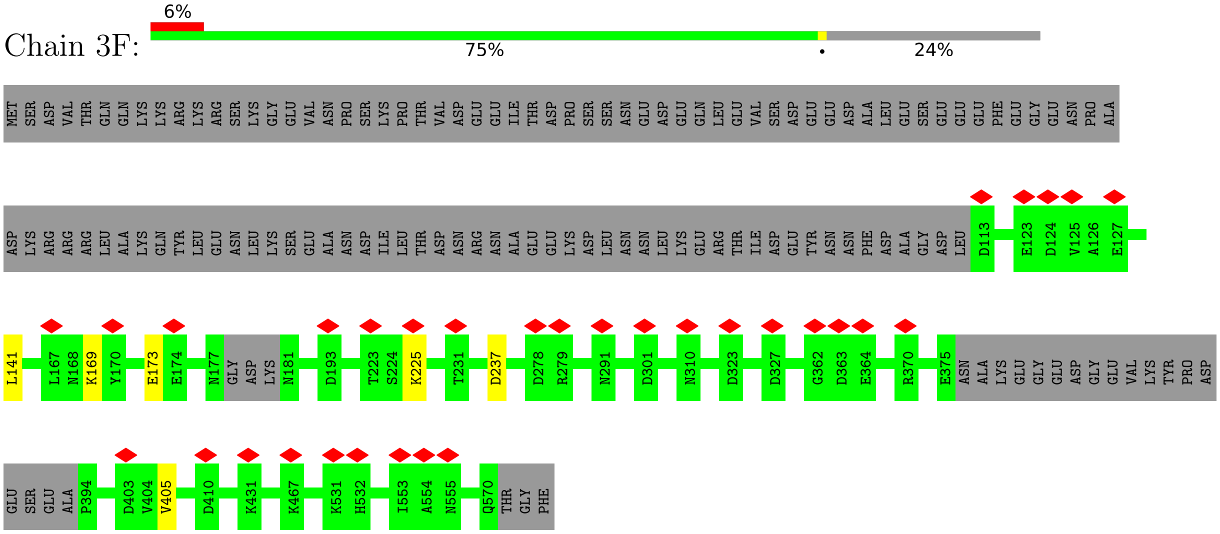


- Molecule 24: Nucleolar protein 58

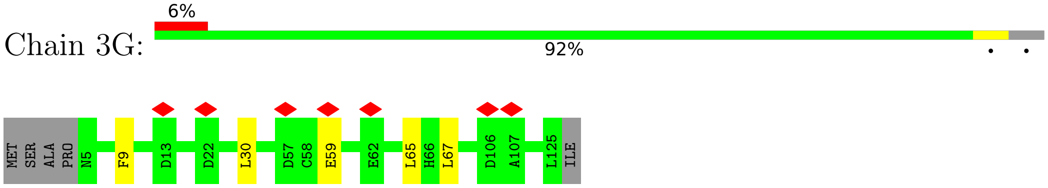




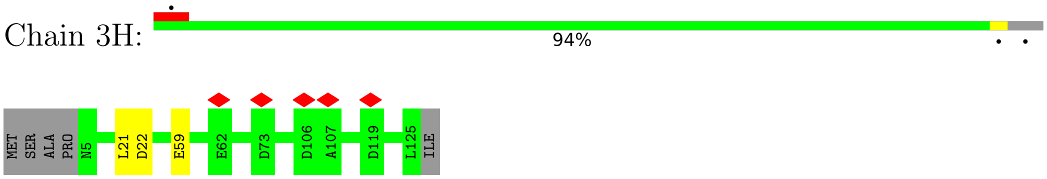
- Molecule 25: Ribosomal RNA-processing protein 9



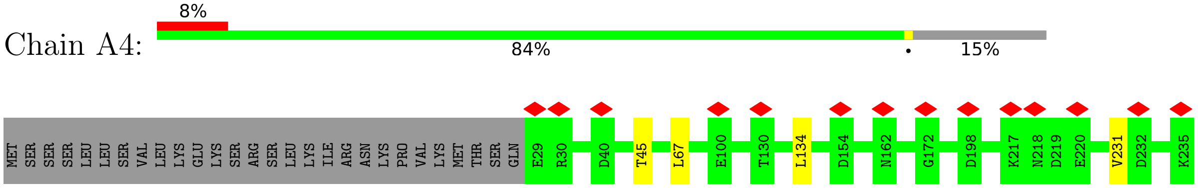
- Molecule 26: 13 kDa ribonucleoprotein-associated protein

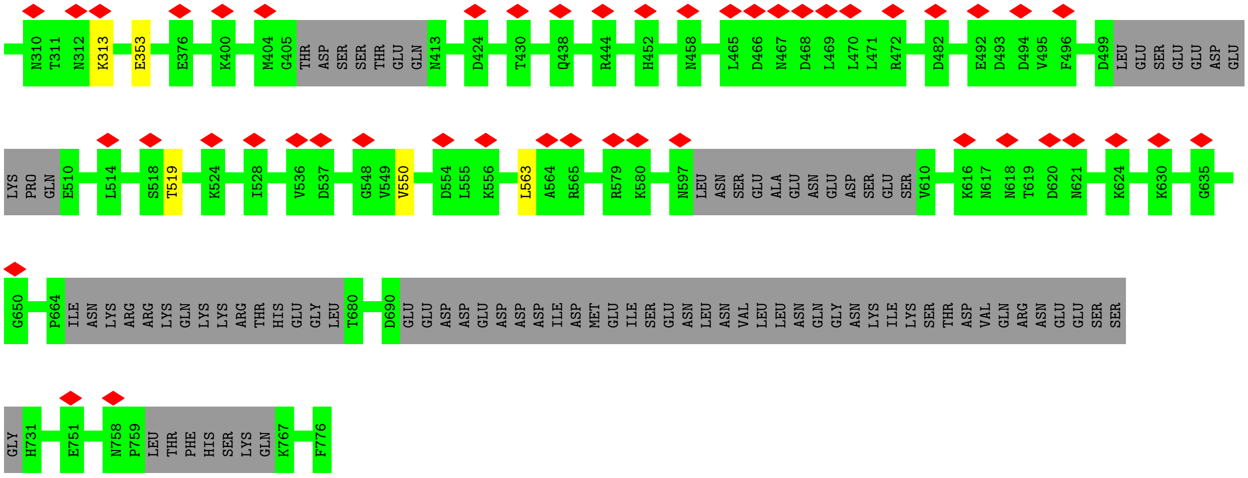


- Molecule 26: 13 kDa ribonucleoprotein-associated protein



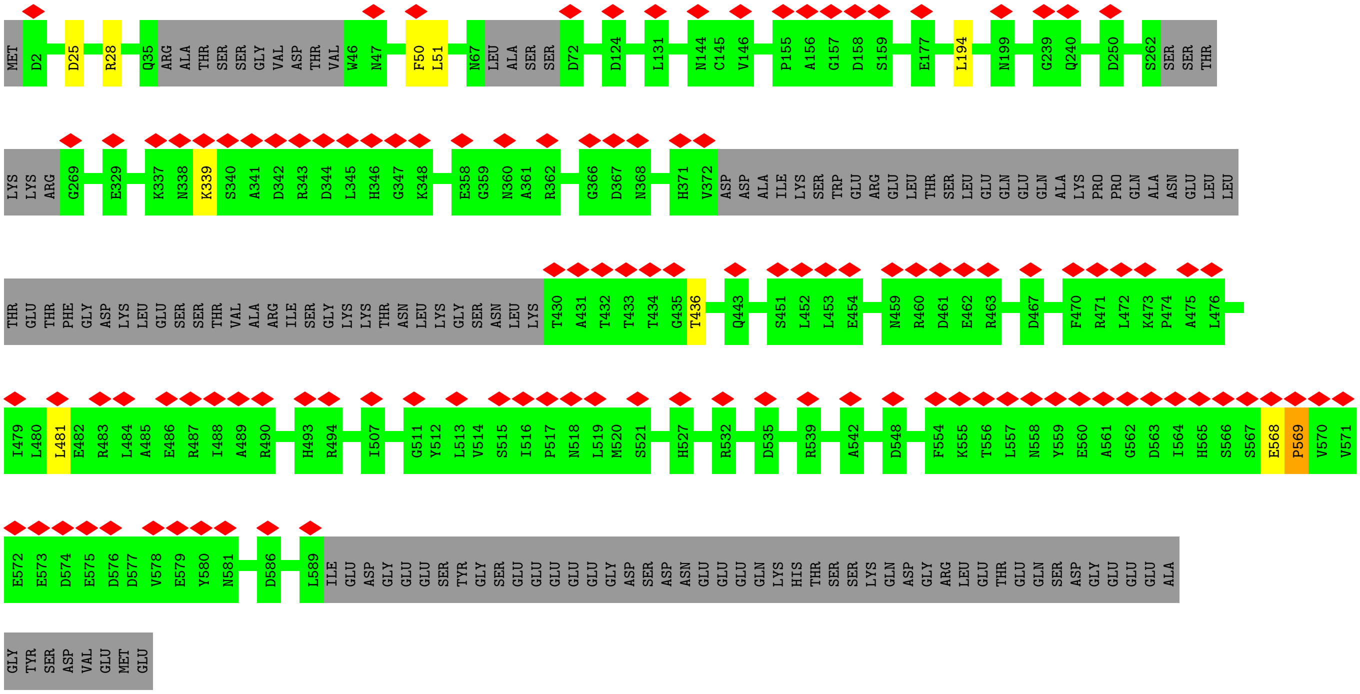
- Molecule 27: U3 small nucleolar RNA-associated protein 4





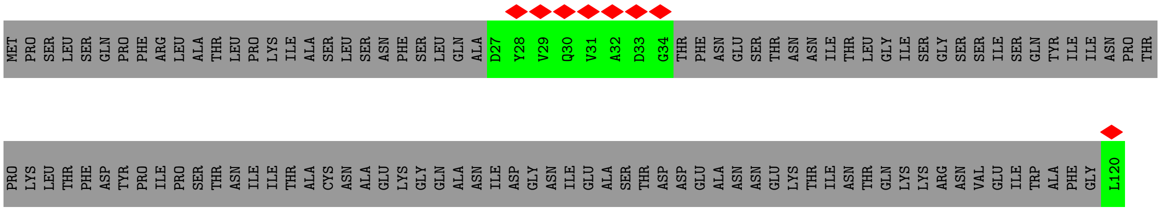
- Molecule 28: U3 small nucleolar RNA-associated protein 5

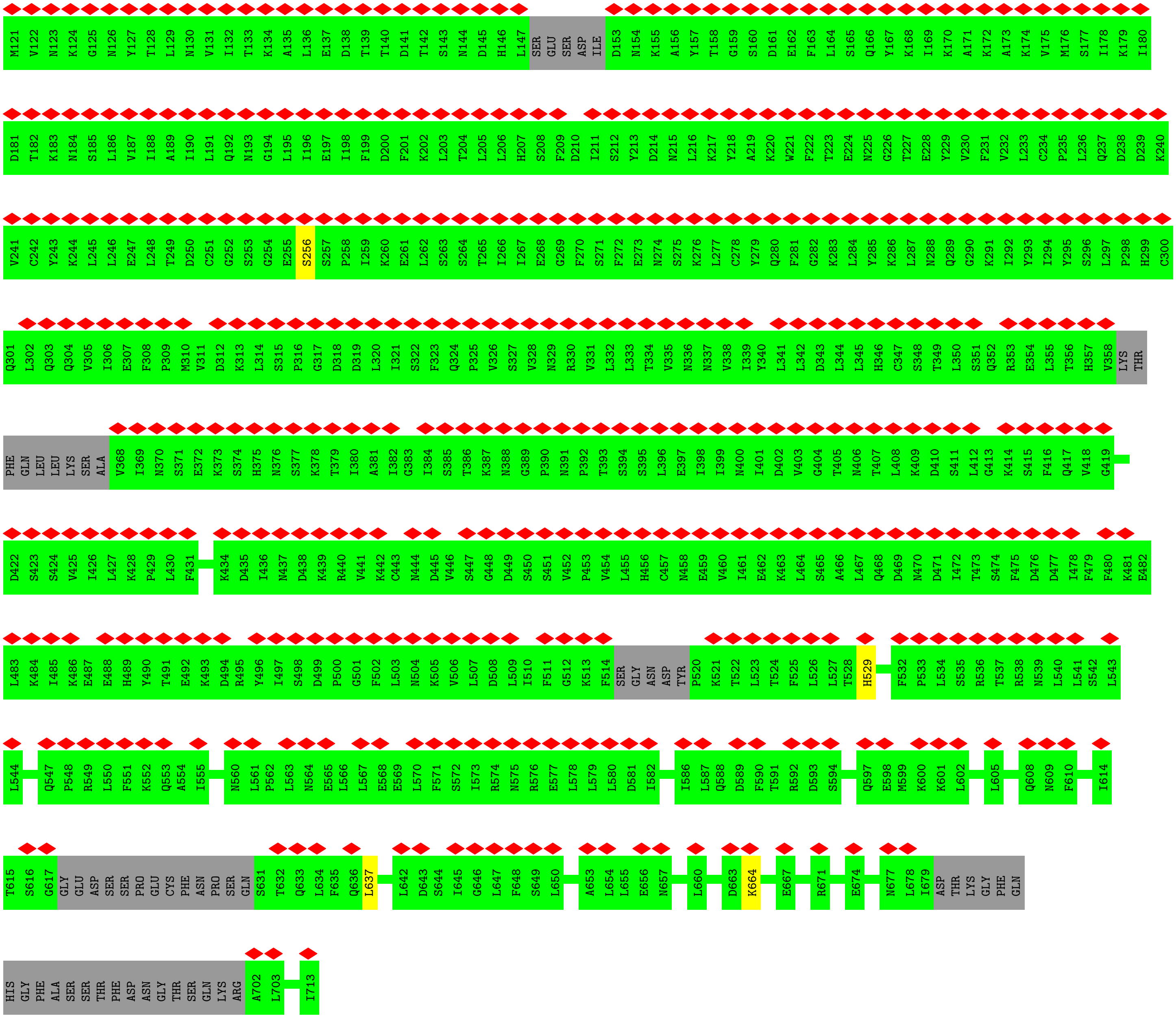
Chain A5:



- Molecule 29: U3 small nucleolar RNA-associated protein 8

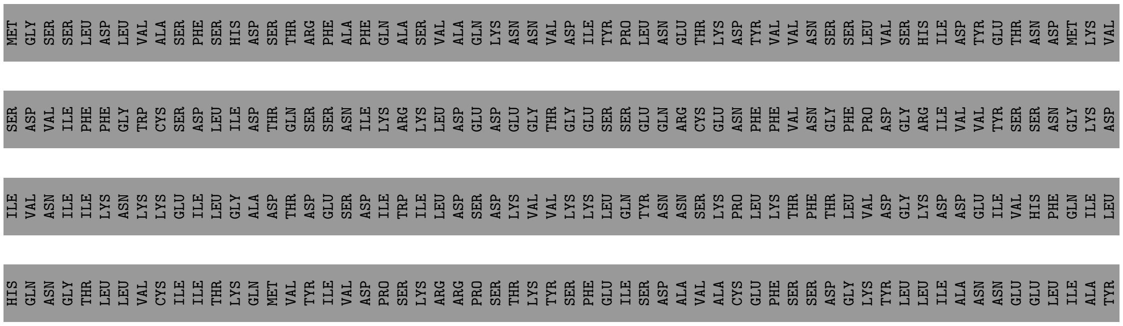
Chain A8:

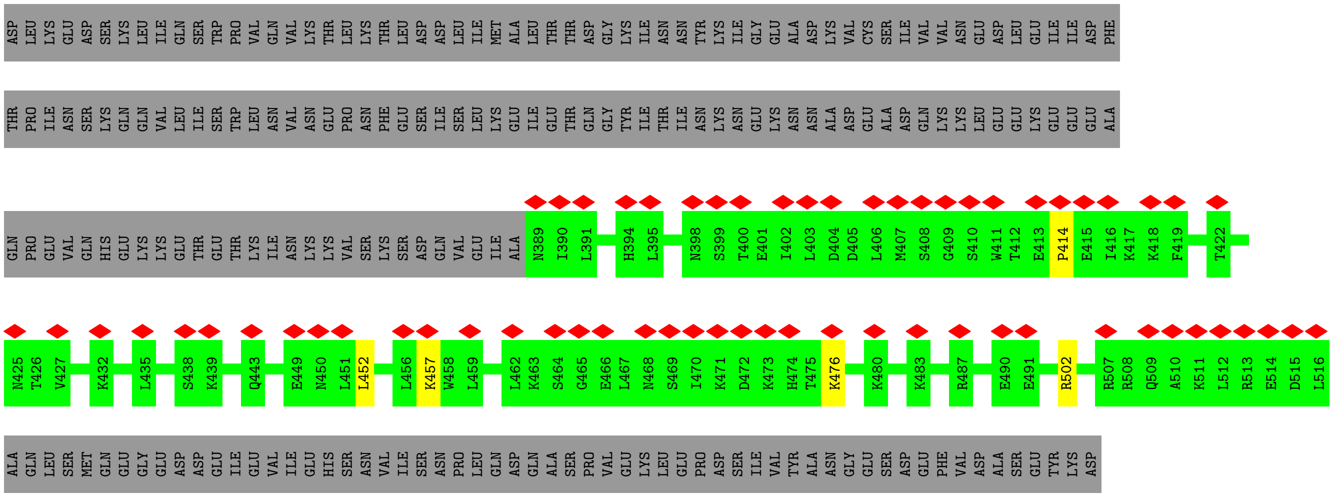




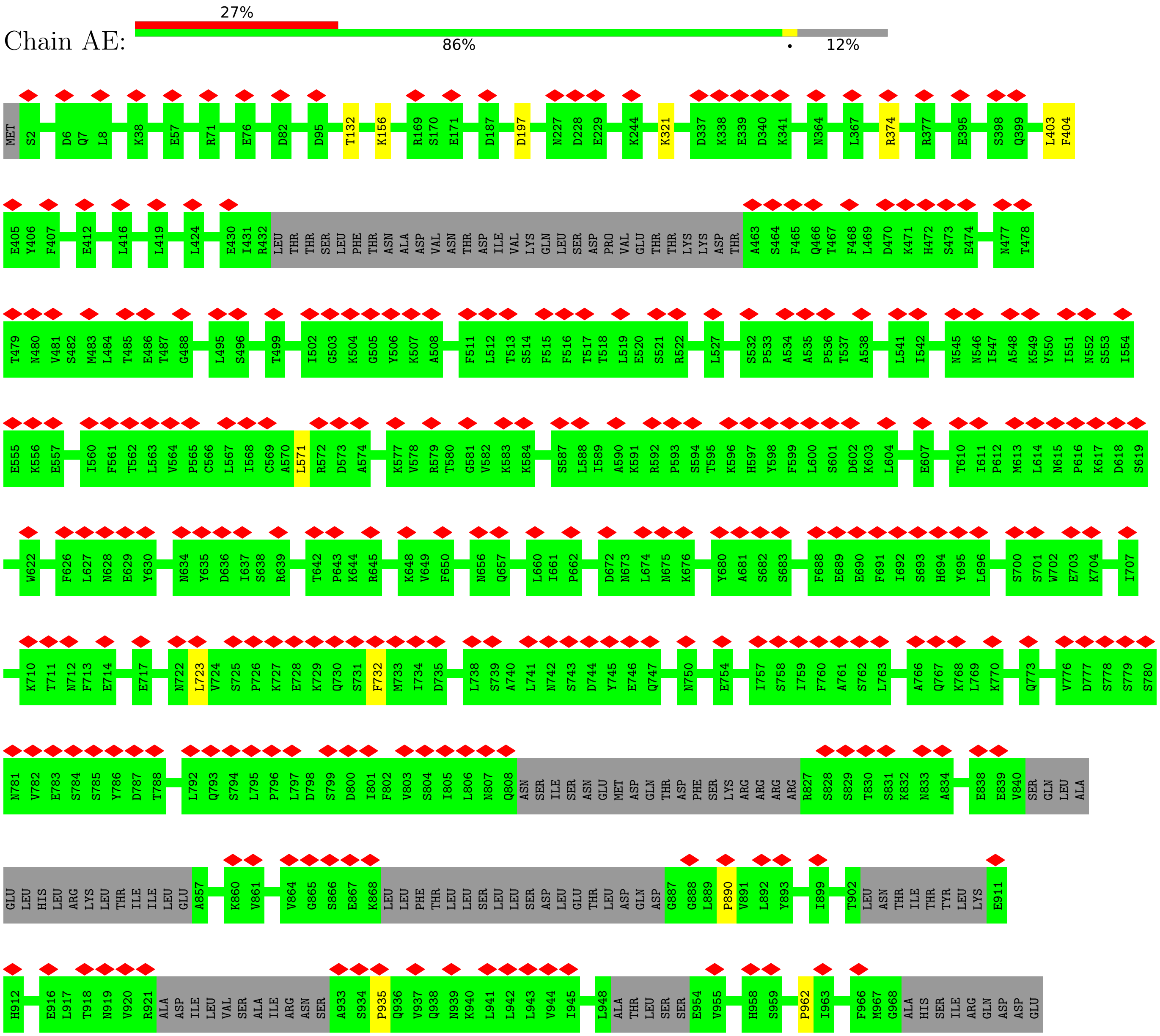
- Molecule 30: U3 small nucleolar RNA-associated protein 9

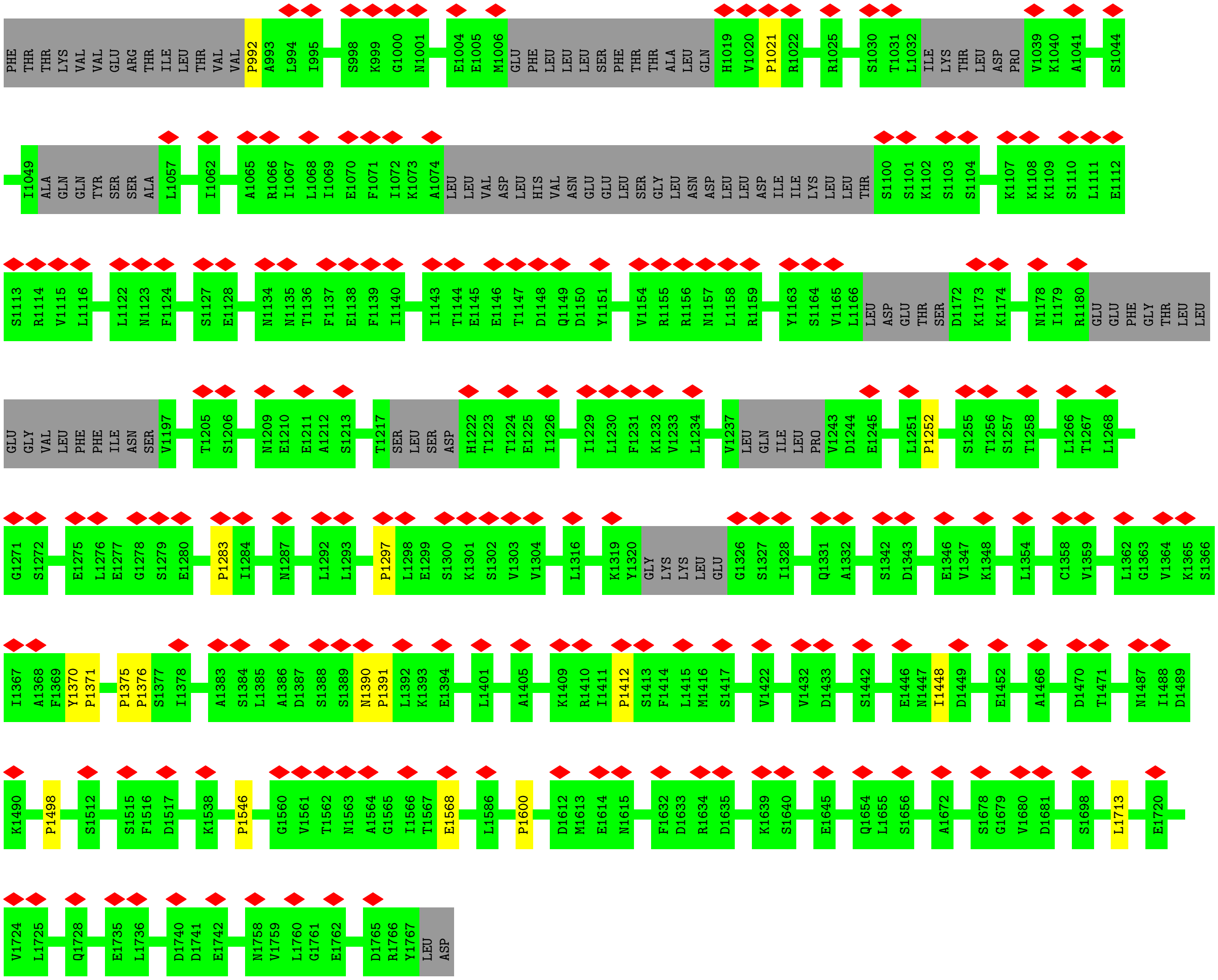
Chain A9:





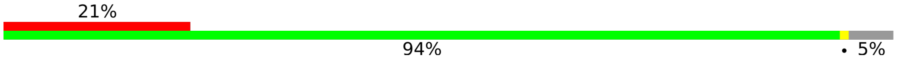
- Molecule 31: U3 small nucleolar RNA-associated protein 10

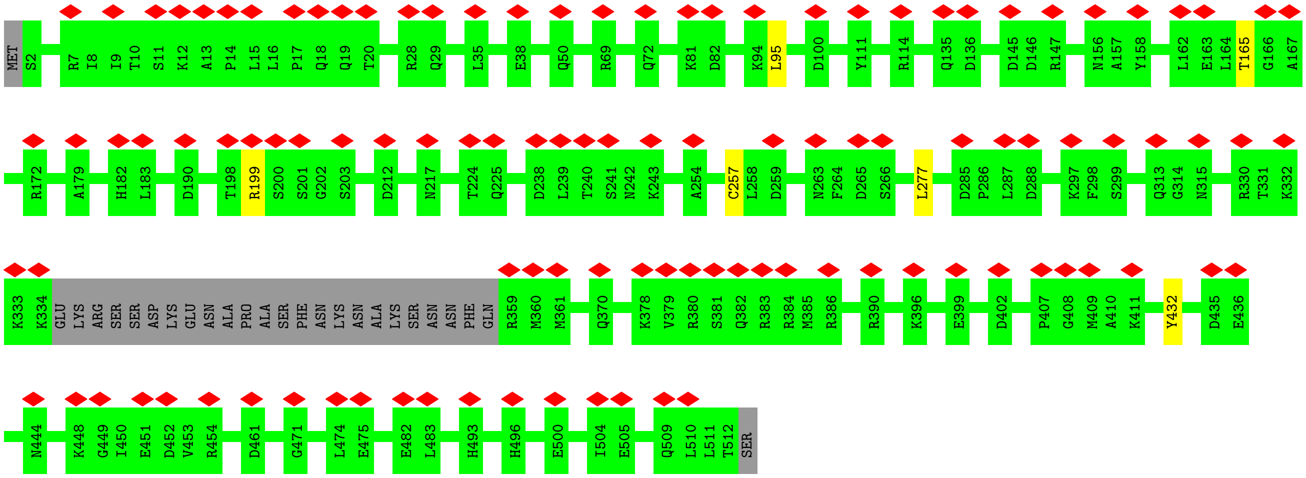




- Molecule 32: U3 small nucleolar RNA-associated protein 15

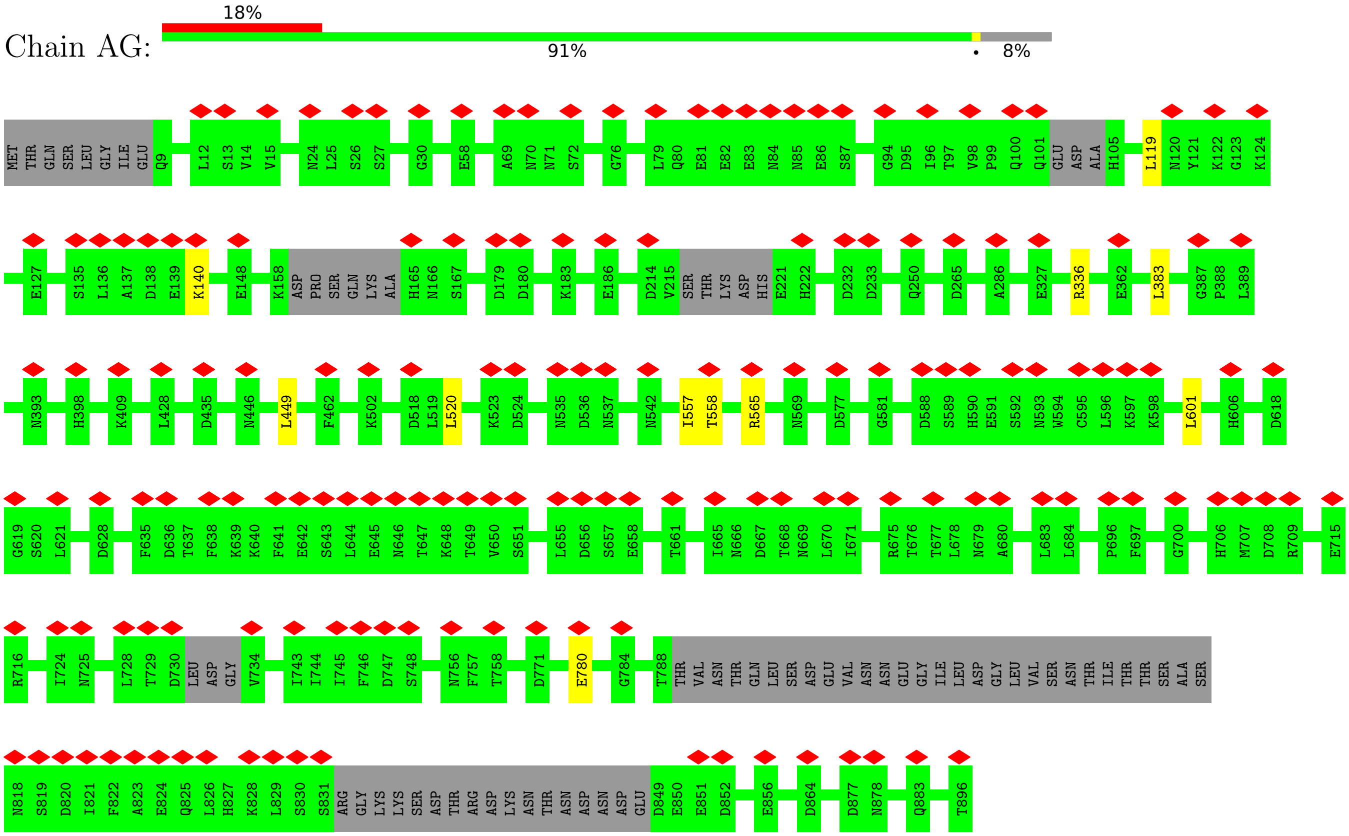
Chain AF:





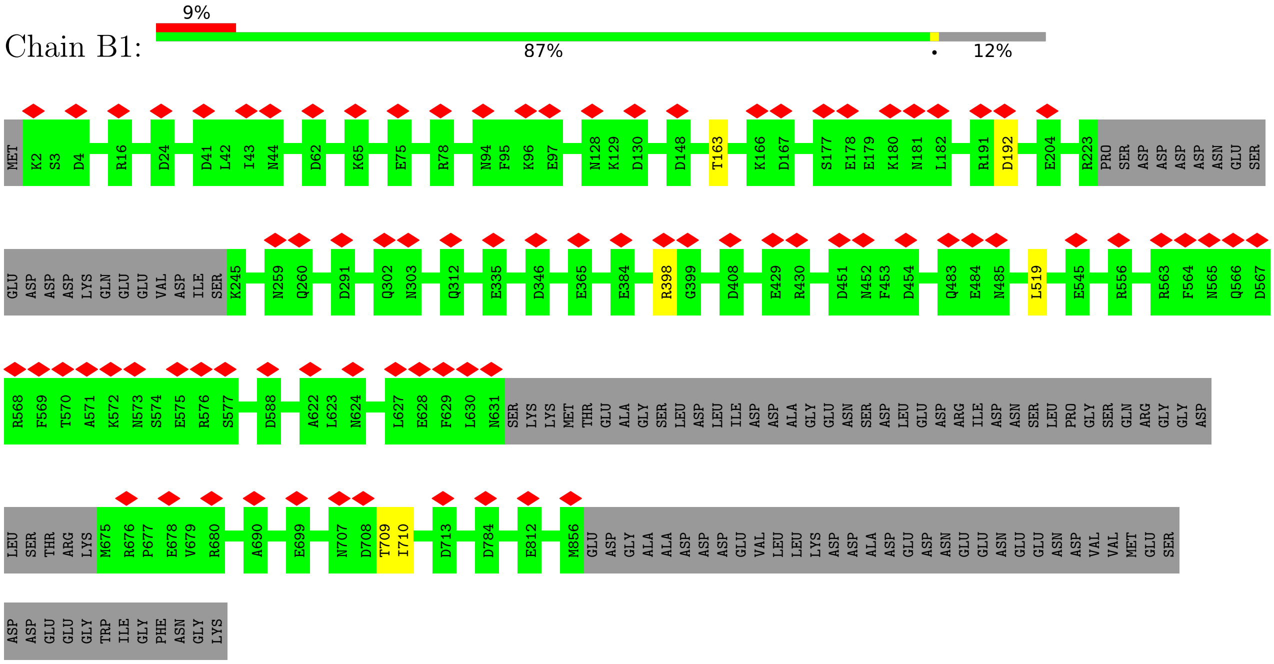
- Molecule 33: NET1-associated nuclear protein 1

Chain AG:



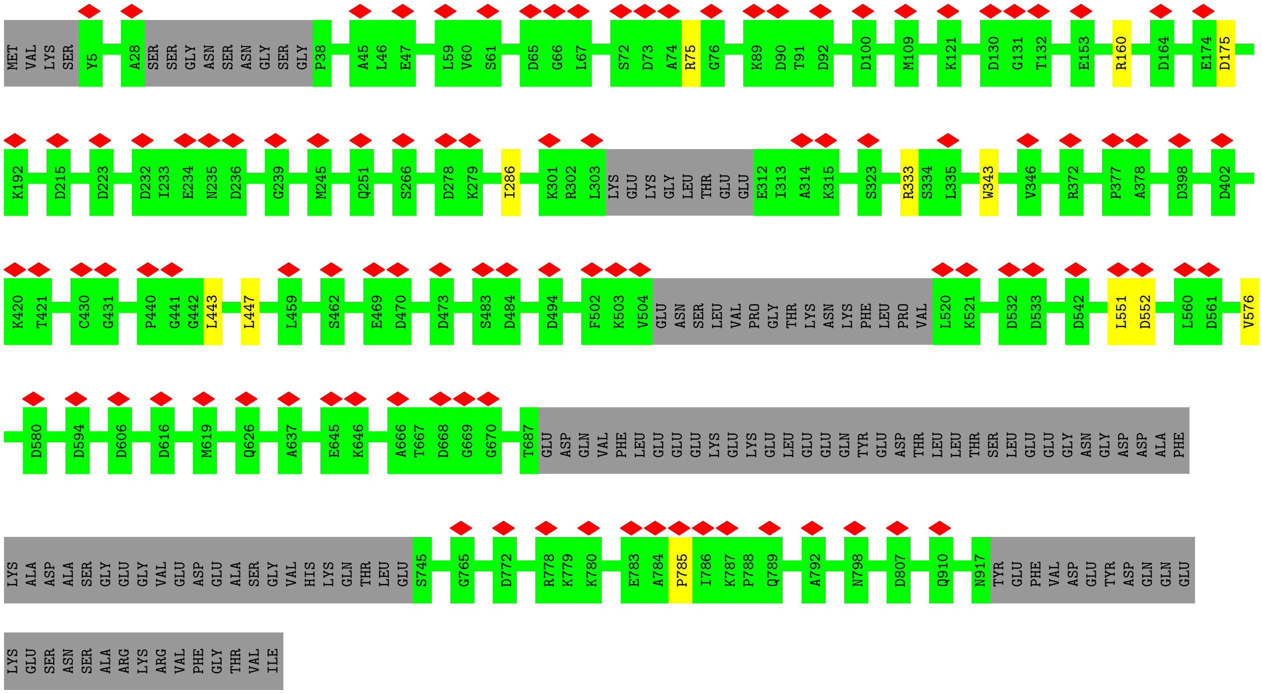
- Molecule 34: Periodic tryptophan protein 2

Chain B1:



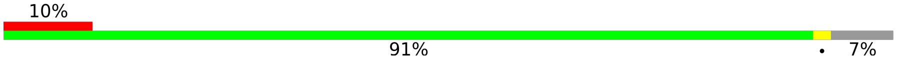
- Molecule 35: U3 small nucleolar RNA-associated protein 12

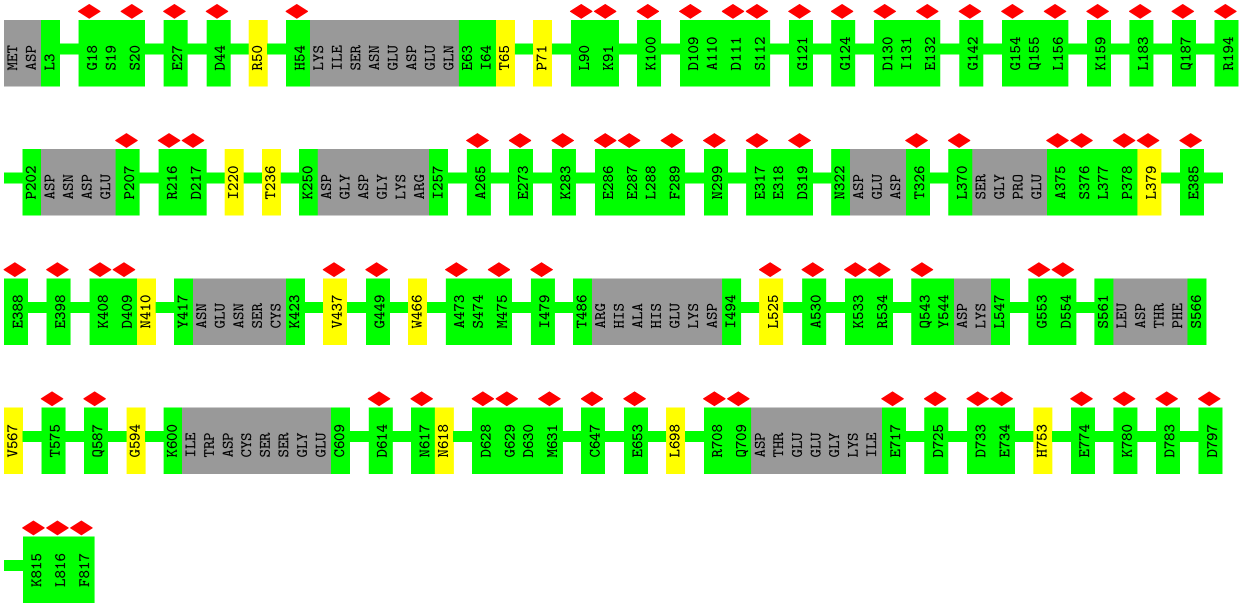
Chain B2:



- Molecule 36: U3 small nucleolar RNA-associated protein 13

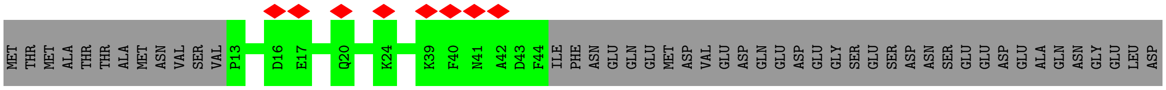
Chain B3:

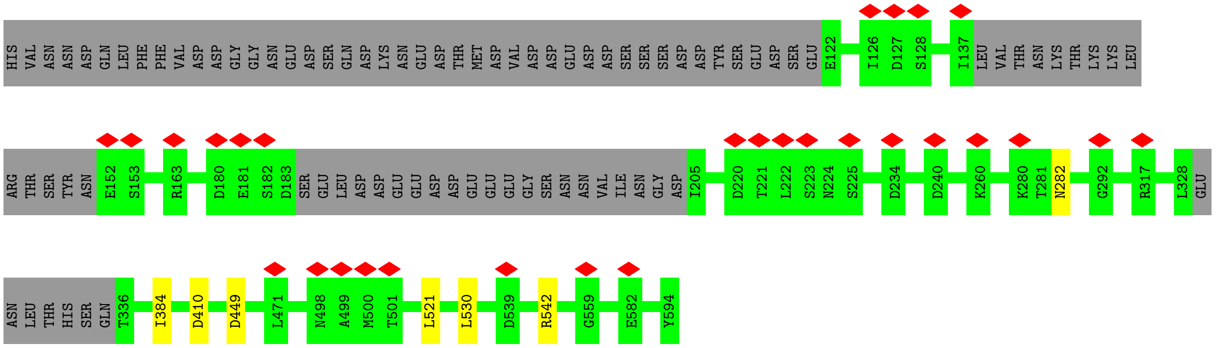




- Molecule 37: U3 small nucleolar RNA-associated protein 18

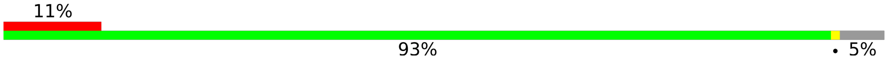
Chain B8:

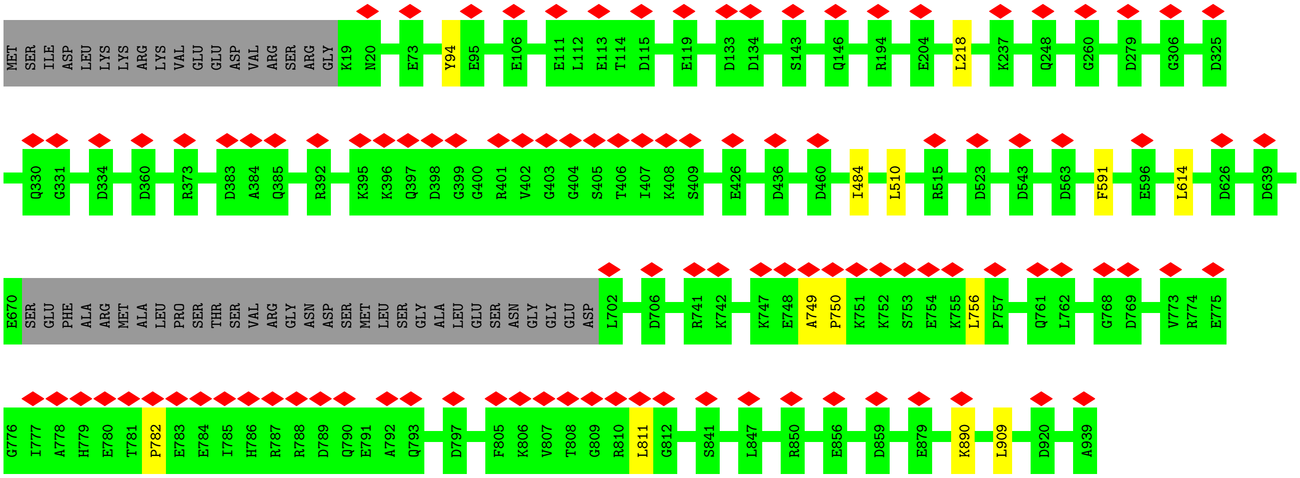




- Molecule 38: U3 small nucleolar RNA-associated protein 21

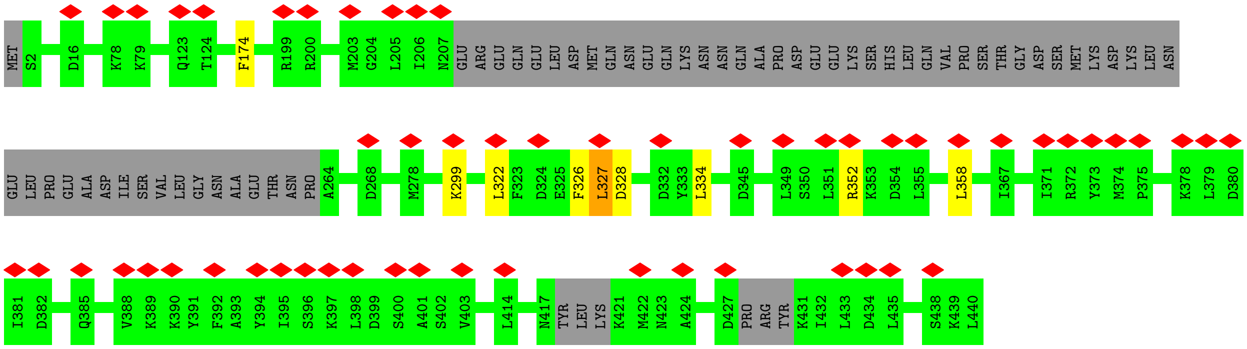
Chain BE:





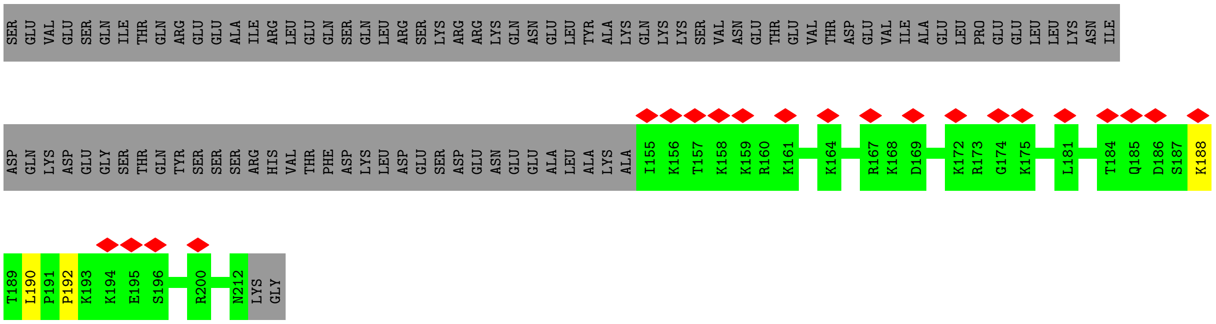
- Molecule 39: U3 small nucleolar RNA-associated protein 6

Chain B6:

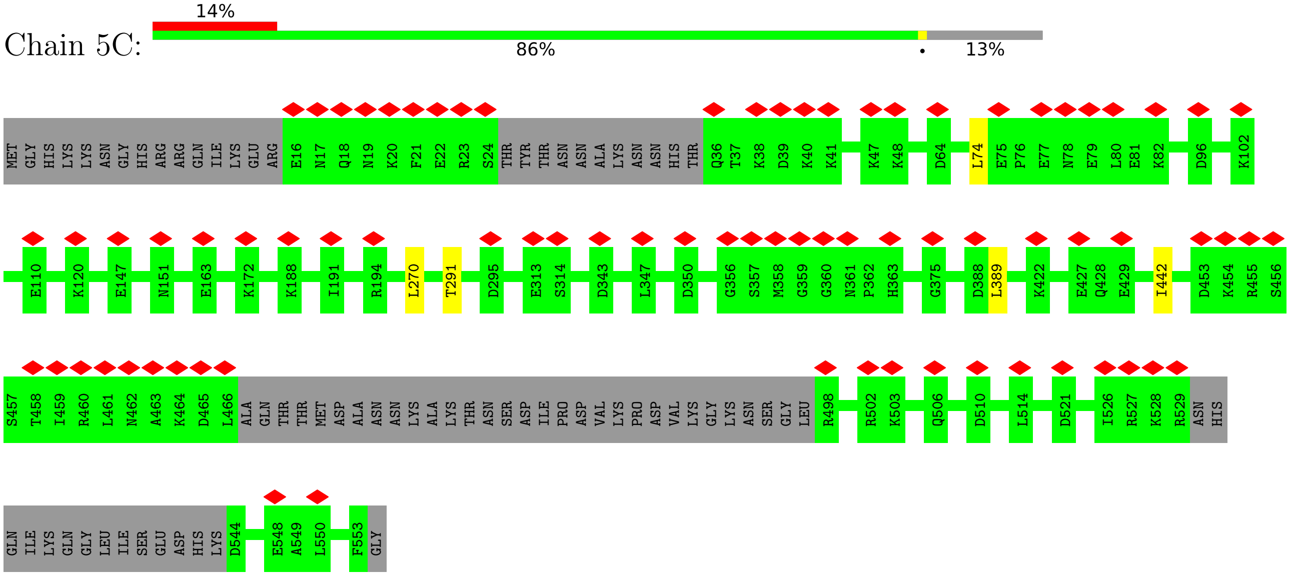


- Molecule 40: Bud site selection protein 21

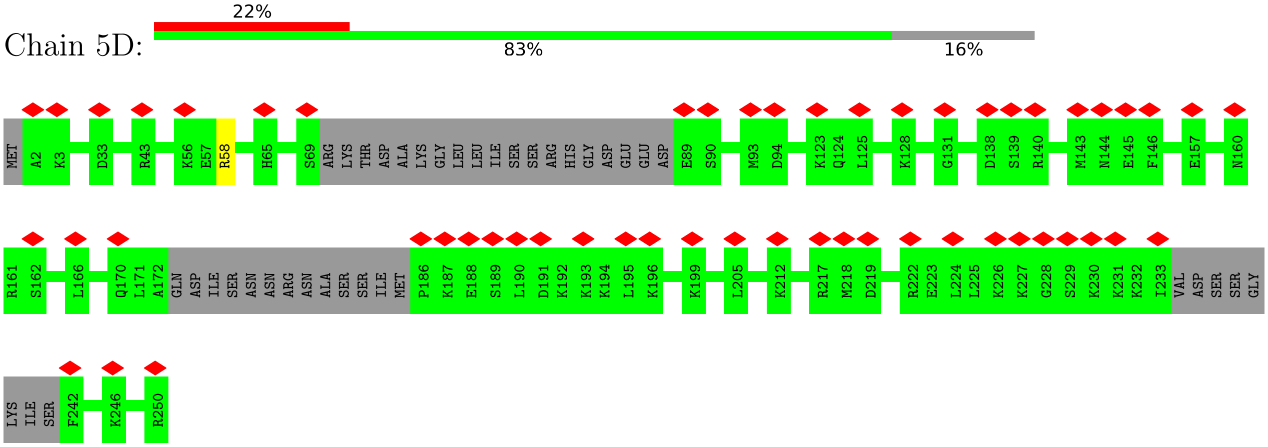
Chain 5B:



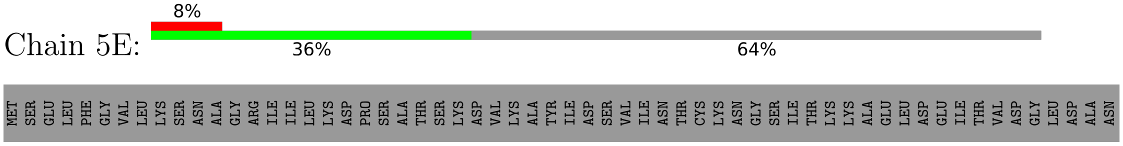
- Molecule 41: U3 small nucleolar RNA-associated protein 7

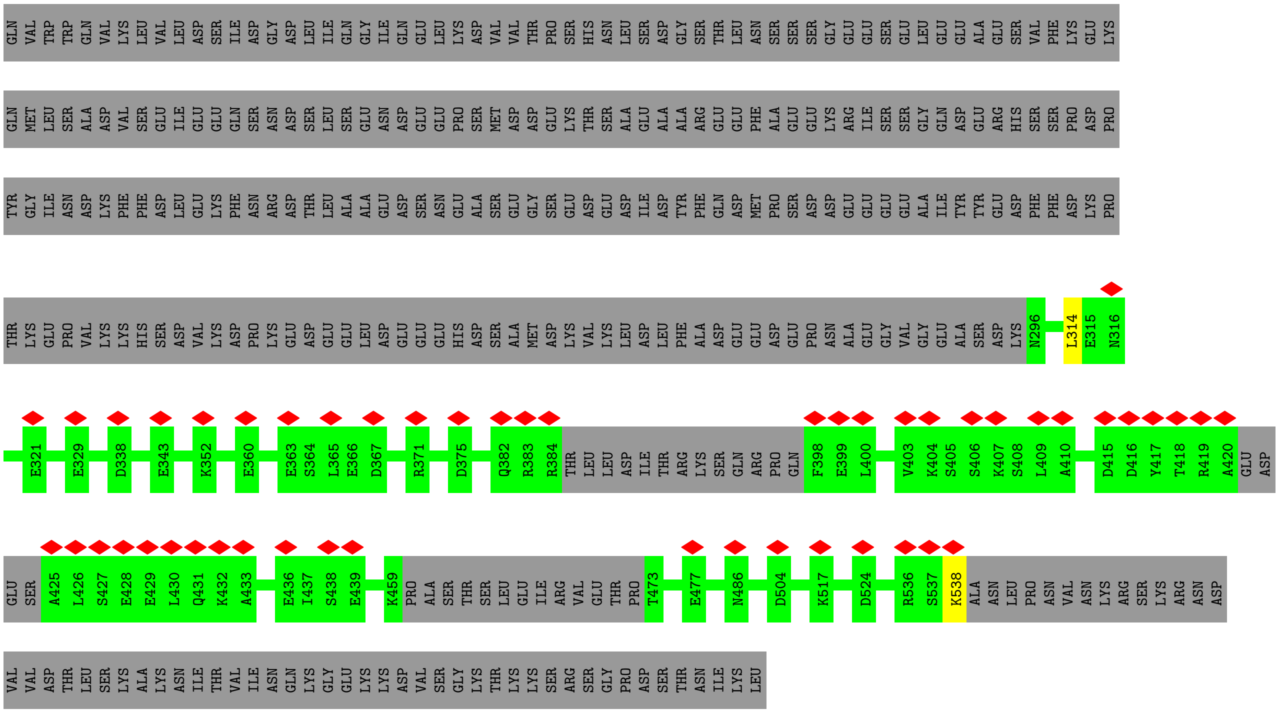


- Molecule 42: U3 small nucleolar RNA-associated protein 11



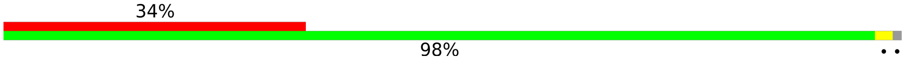
- Molecule 43: U3 small nucleolar RNA-associated protein MPP10

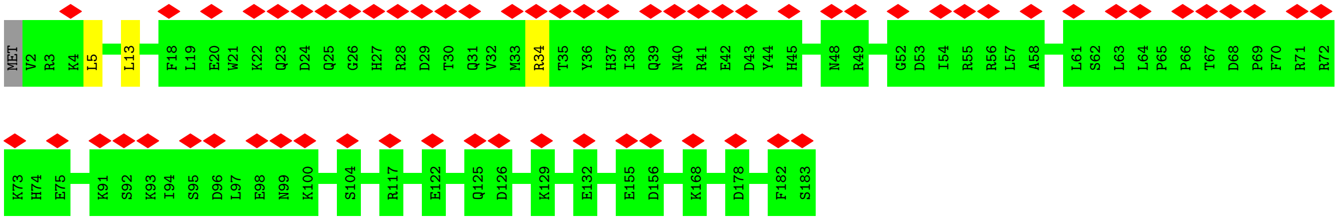




- Molecule 44: U3 small nucleolar ribonucleoprotein protein IMP3

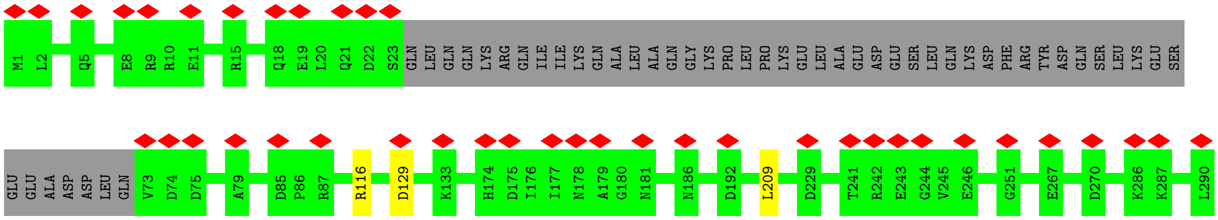
Chain 5F:





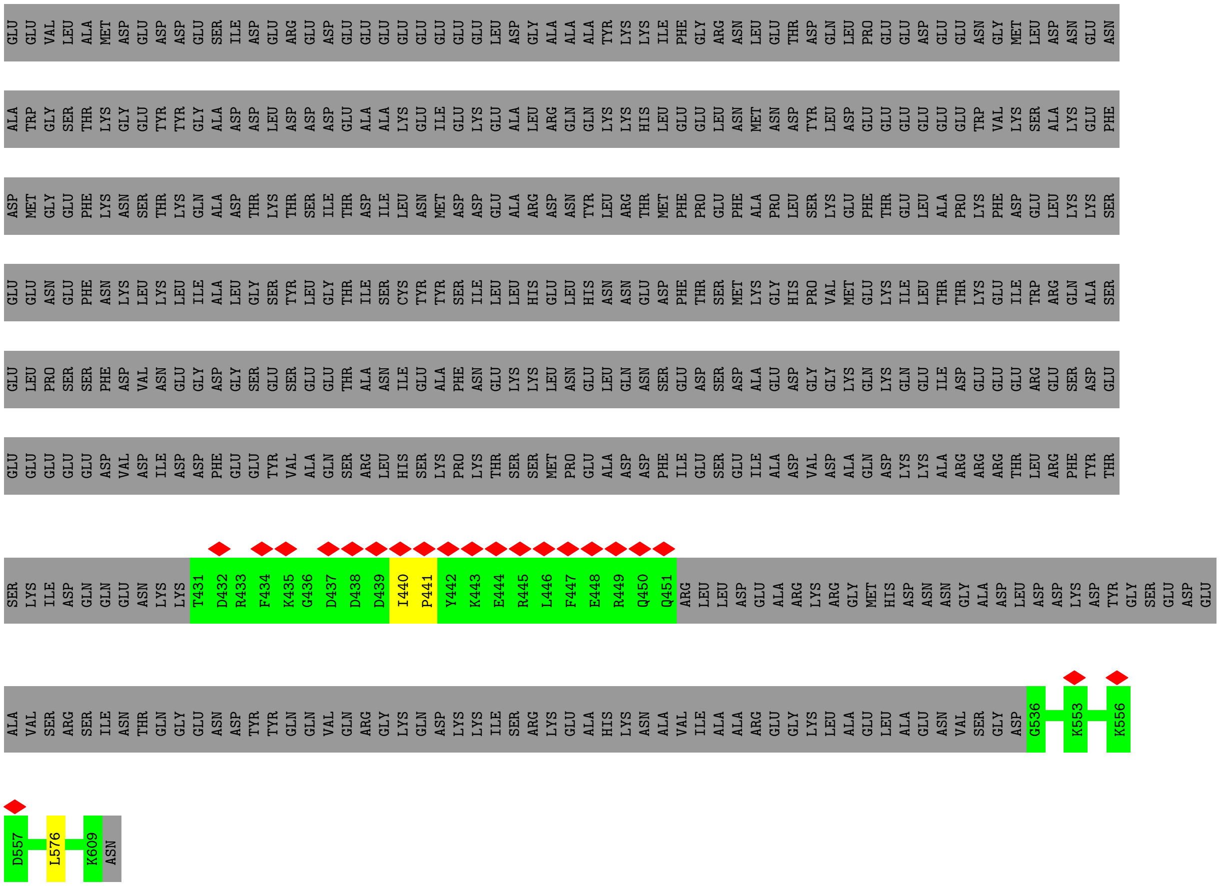
- Molecule 45: U3 small nucleolar ribonucleoprotein protein IMP4

Chain 5G:



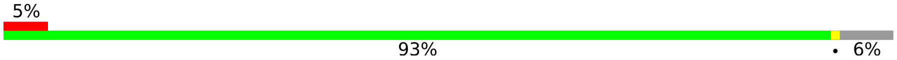
- Molecule 46: Something about silencing protein 10

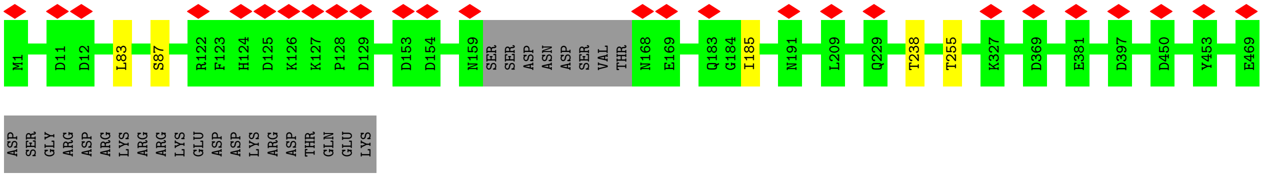
Chain 5H:



- Molecule 47: Protein SOF1

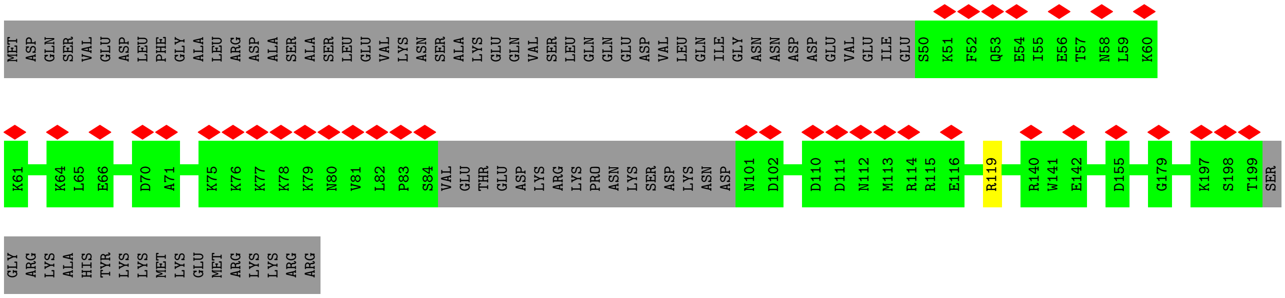
Chain 5I:





- Molecule 48: rRNA-processing protein FCF2

Chain 5J:



- Molecule 49: rRNA-processing protein FCF1

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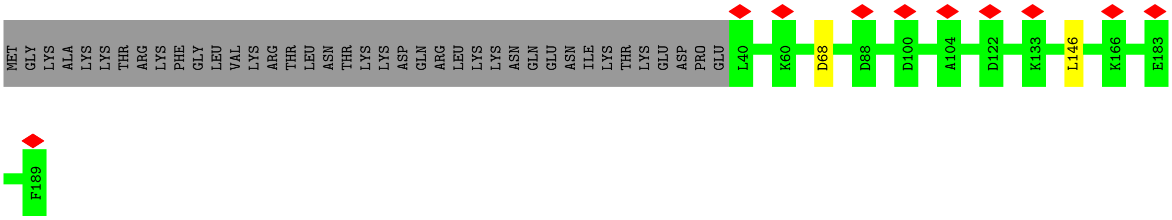
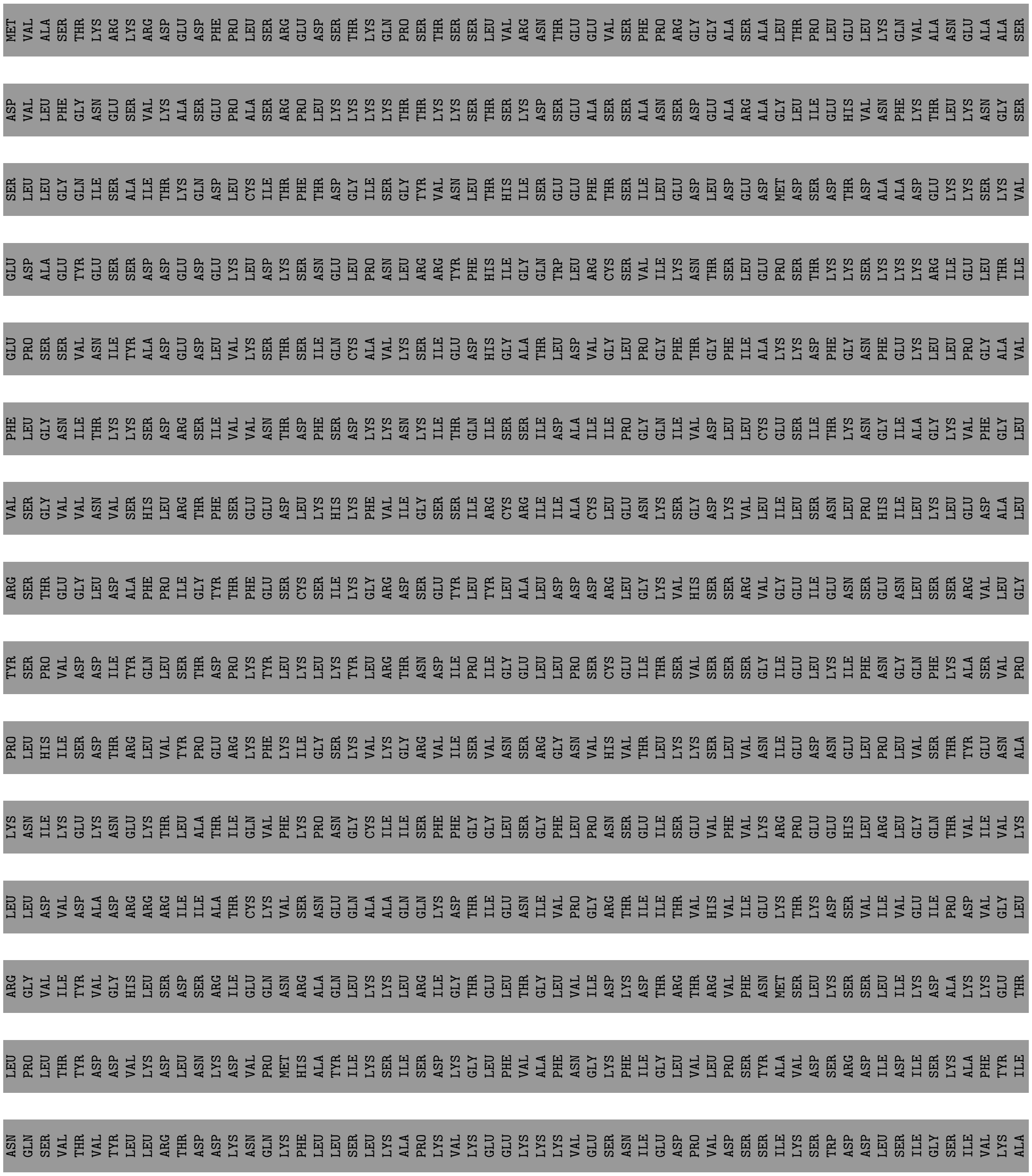
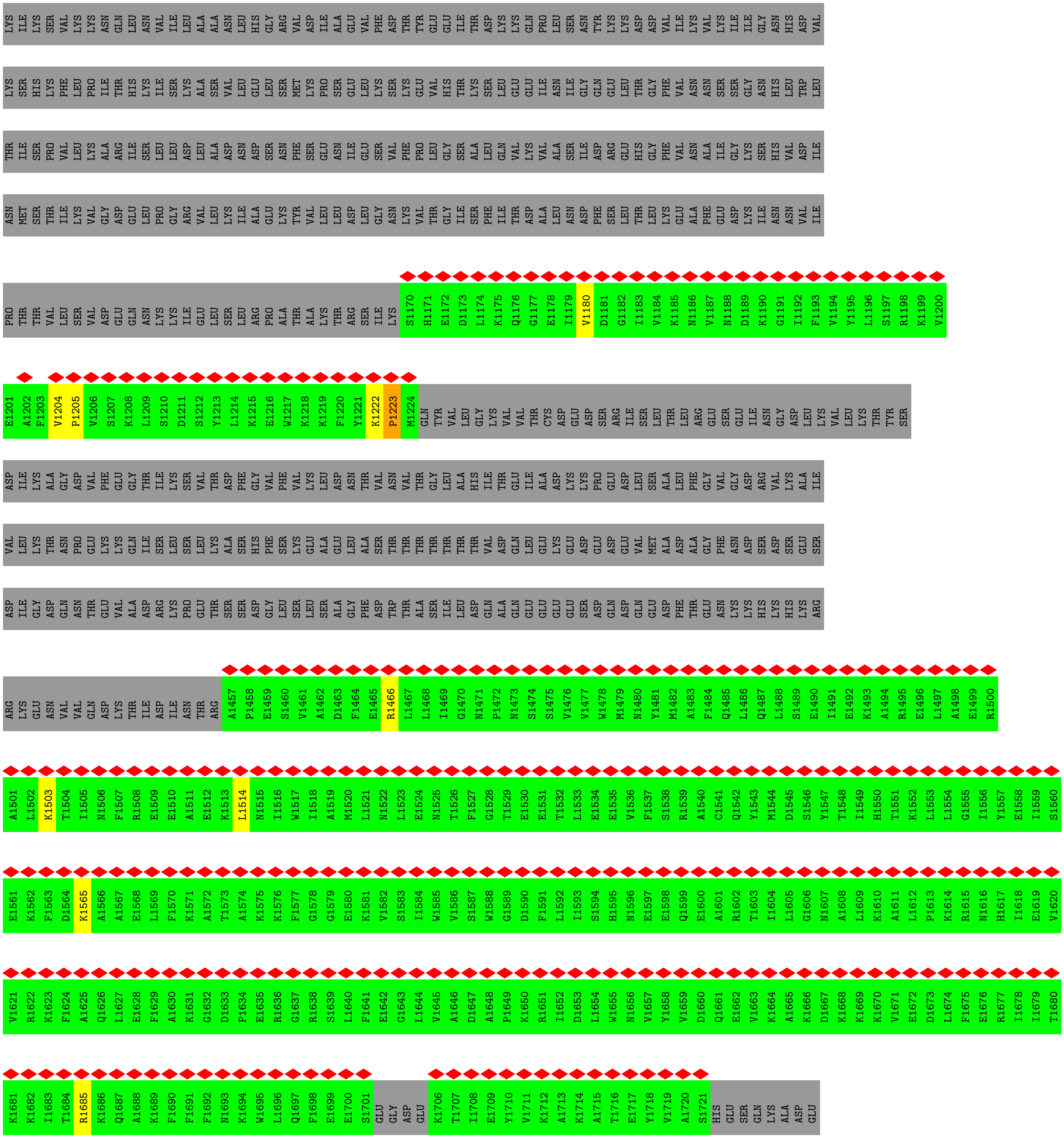


- Molecule 50: rRNA biogenesis protein RRP5

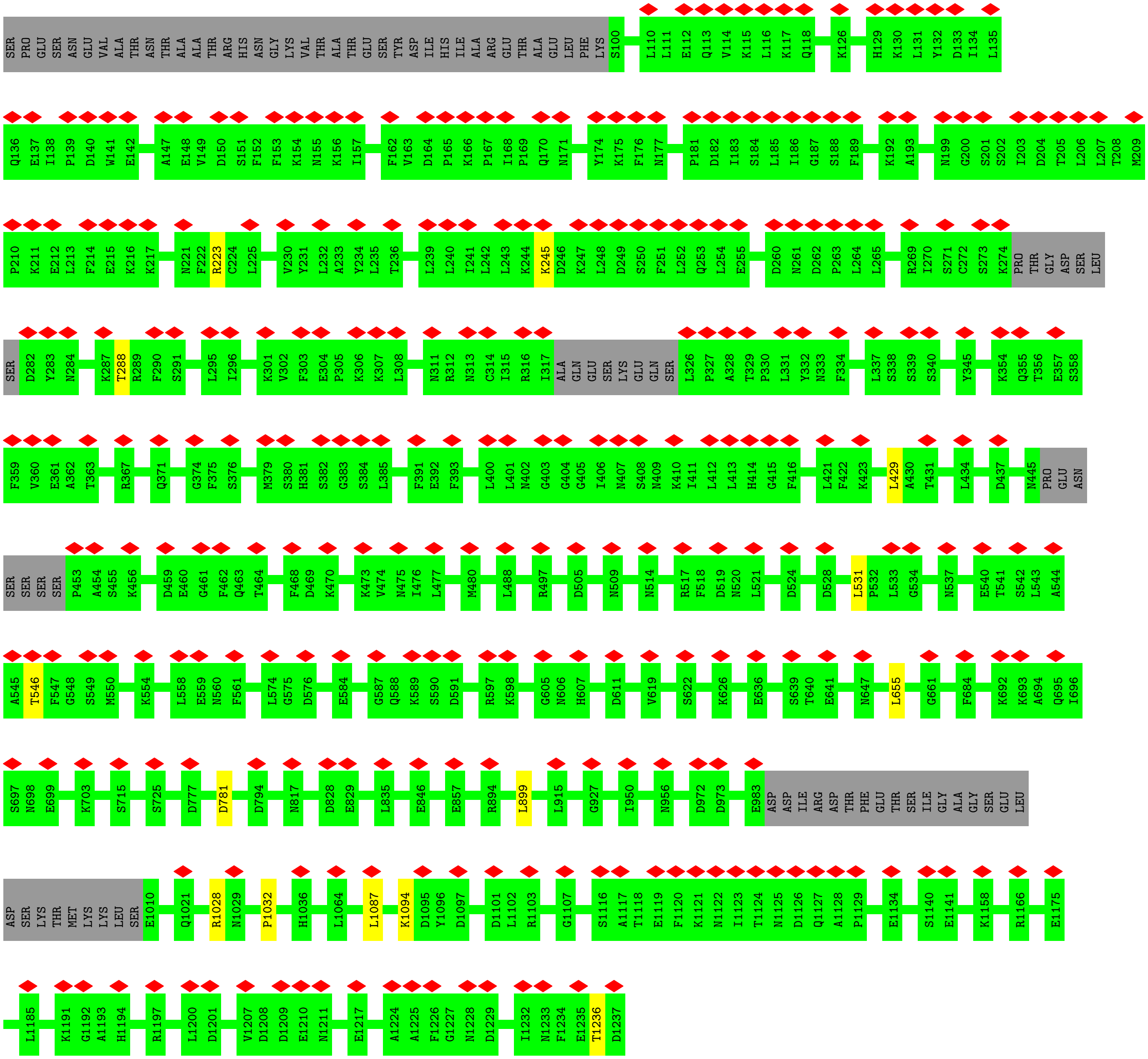
Chain RD:





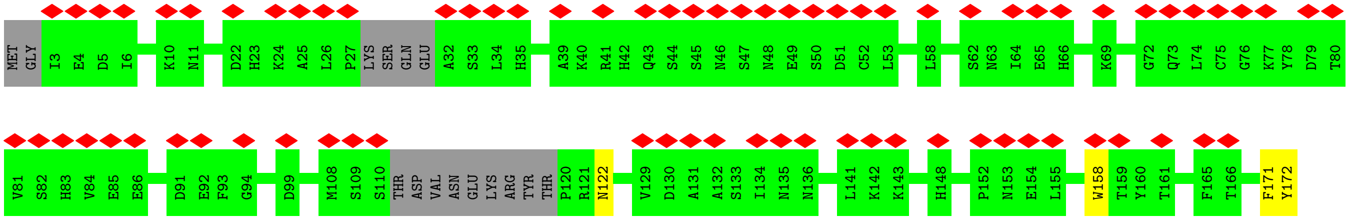
- Molecule 51: U3 small nucleolar RNA-associated protein 22

Chain RE:



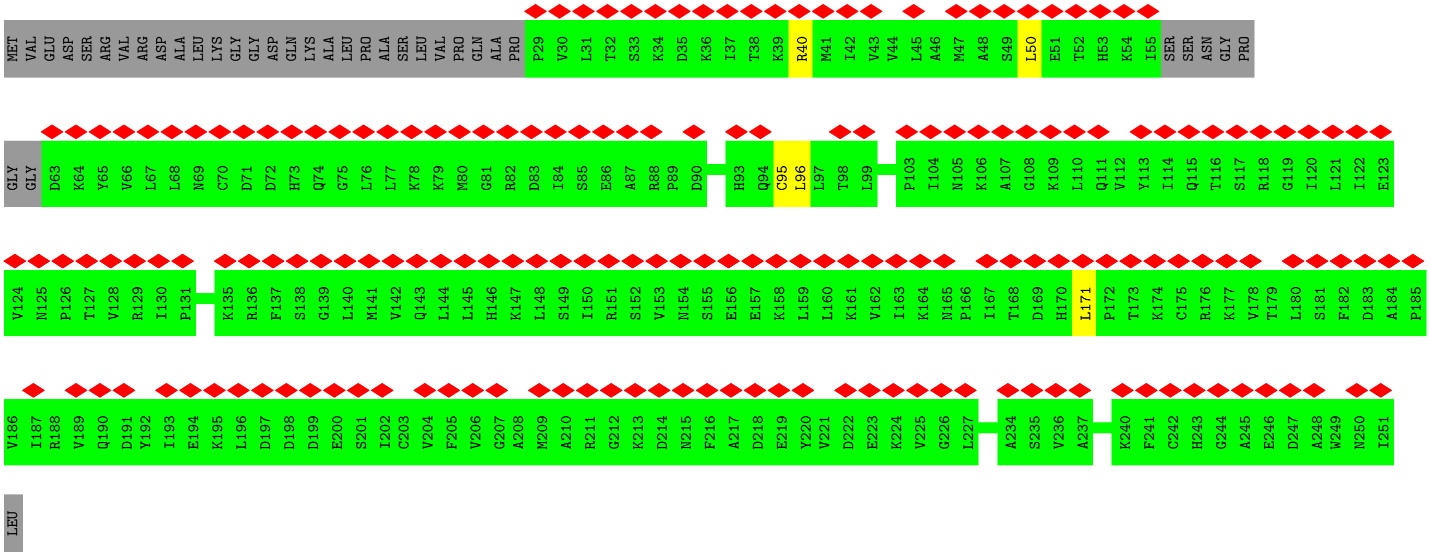
- Molecule 52: Ribosomal RNA-processing protein 7

Chain RF:



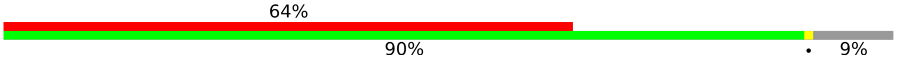
- Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

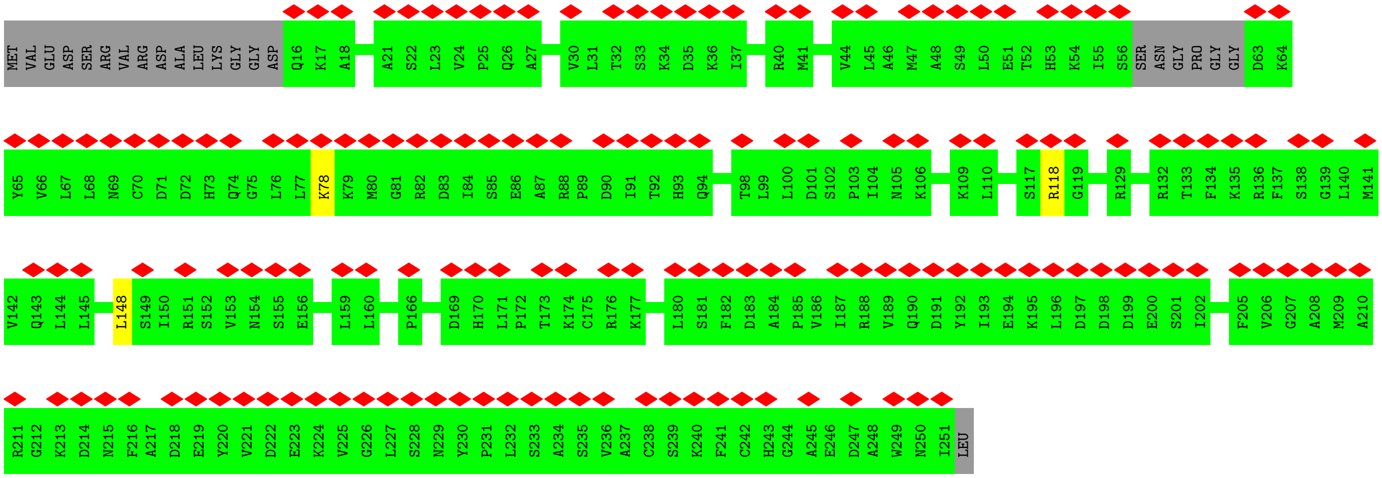
Chain RG:



- Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

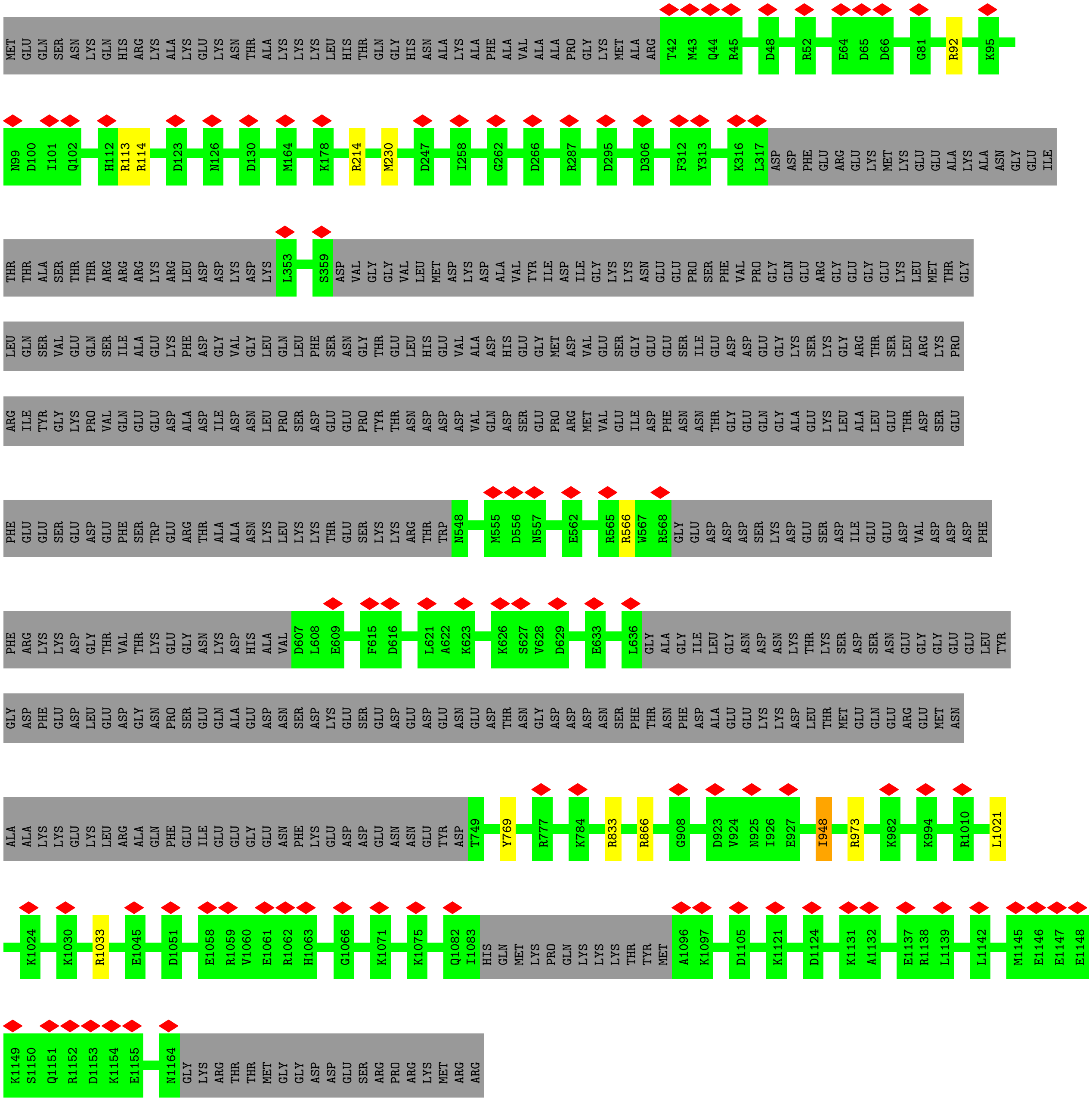
Chain RH:





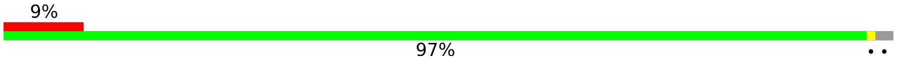
- Molecule 54: Ribosome biogenesis protein BMS1

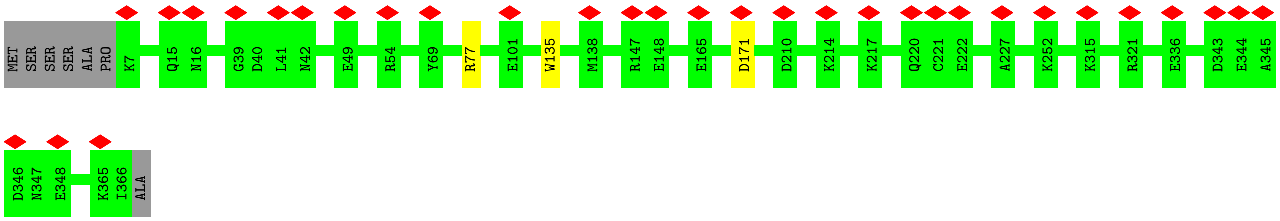
Chain RJ:



- Molecule 55: RNA 3'-terminal phosphate cyclase-like protein

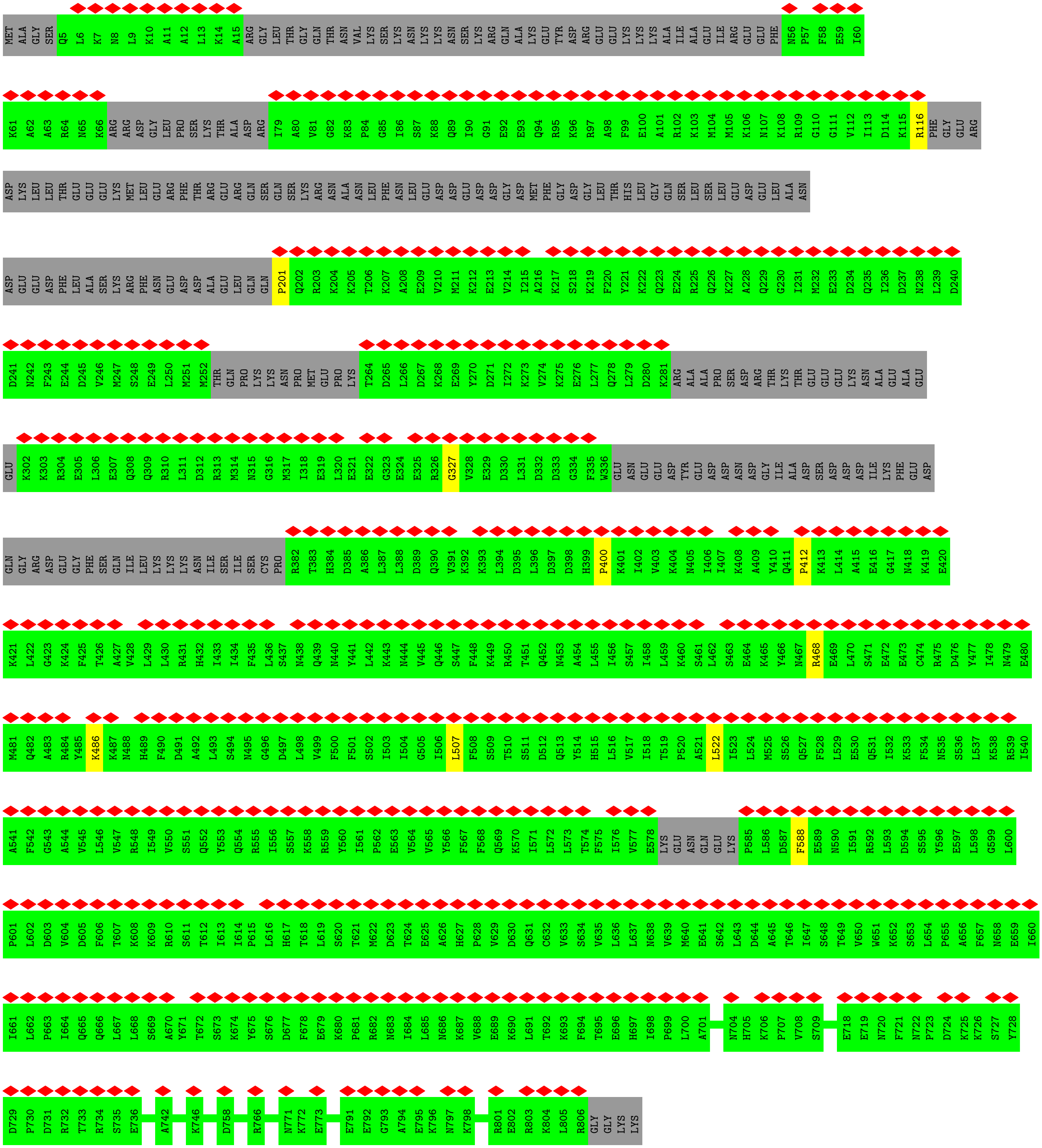
Chain RK:





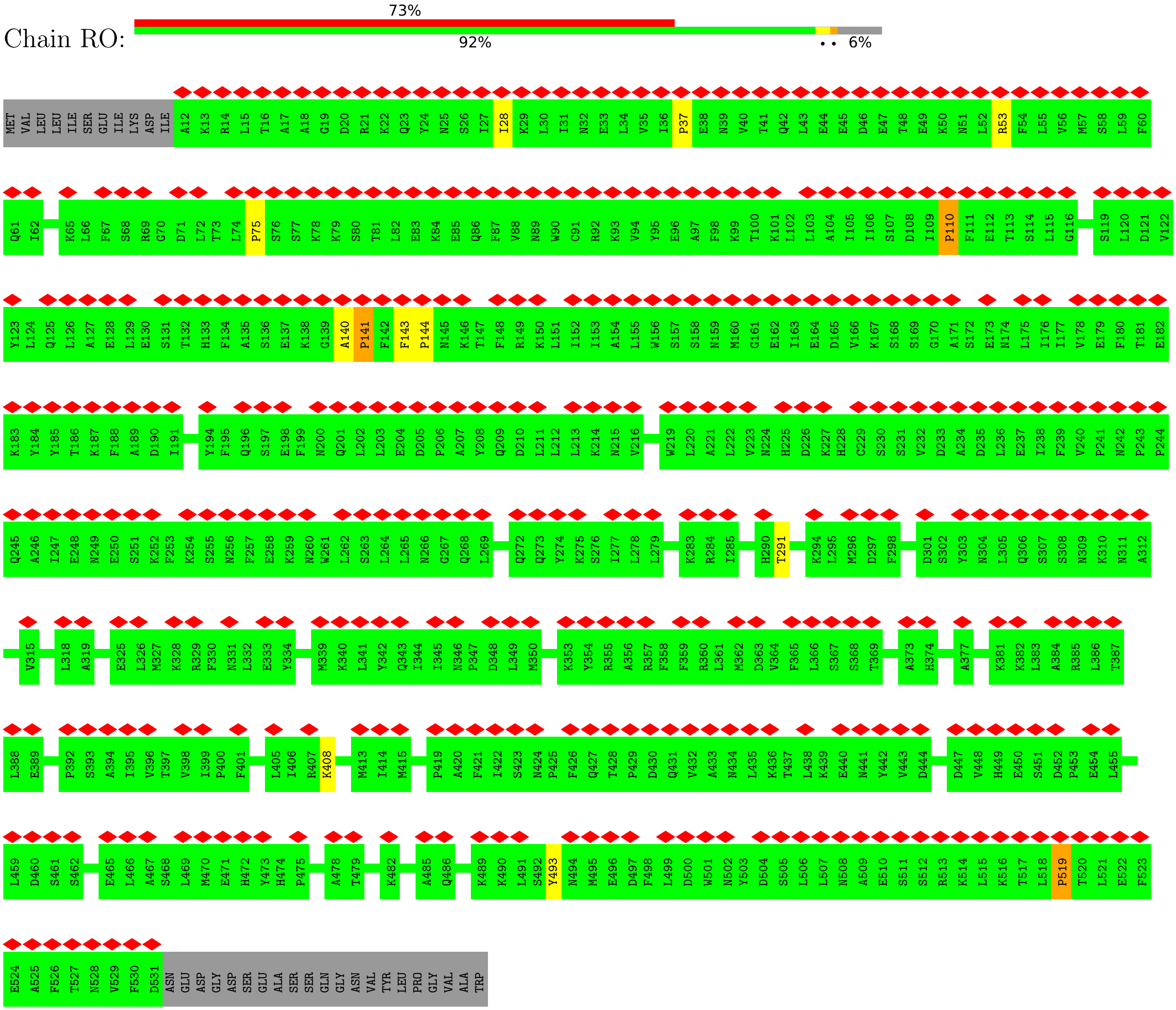
- Molecule 56: Nucleolar complex protein 14

Chain RN:



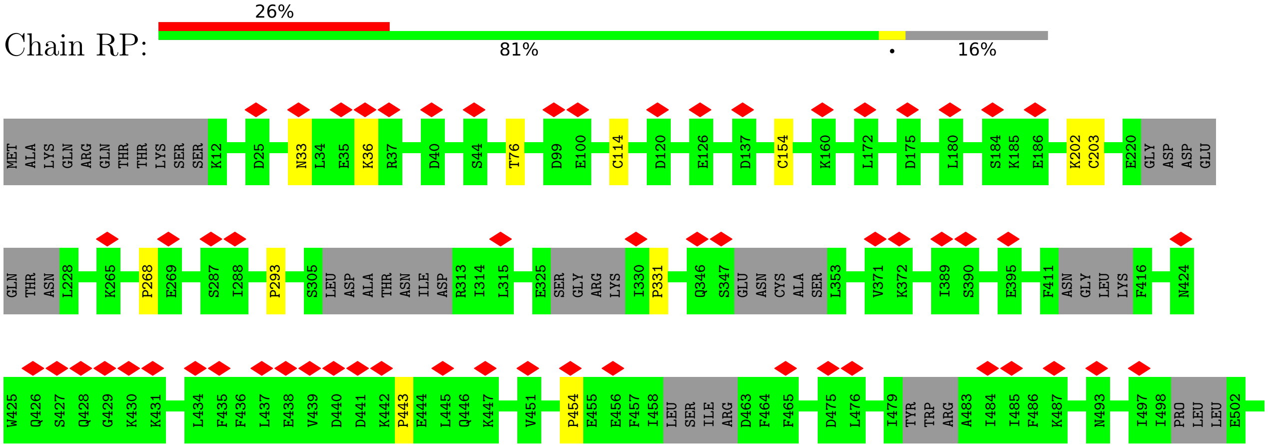
- Molecule 57: Nucleolar complex protein 4

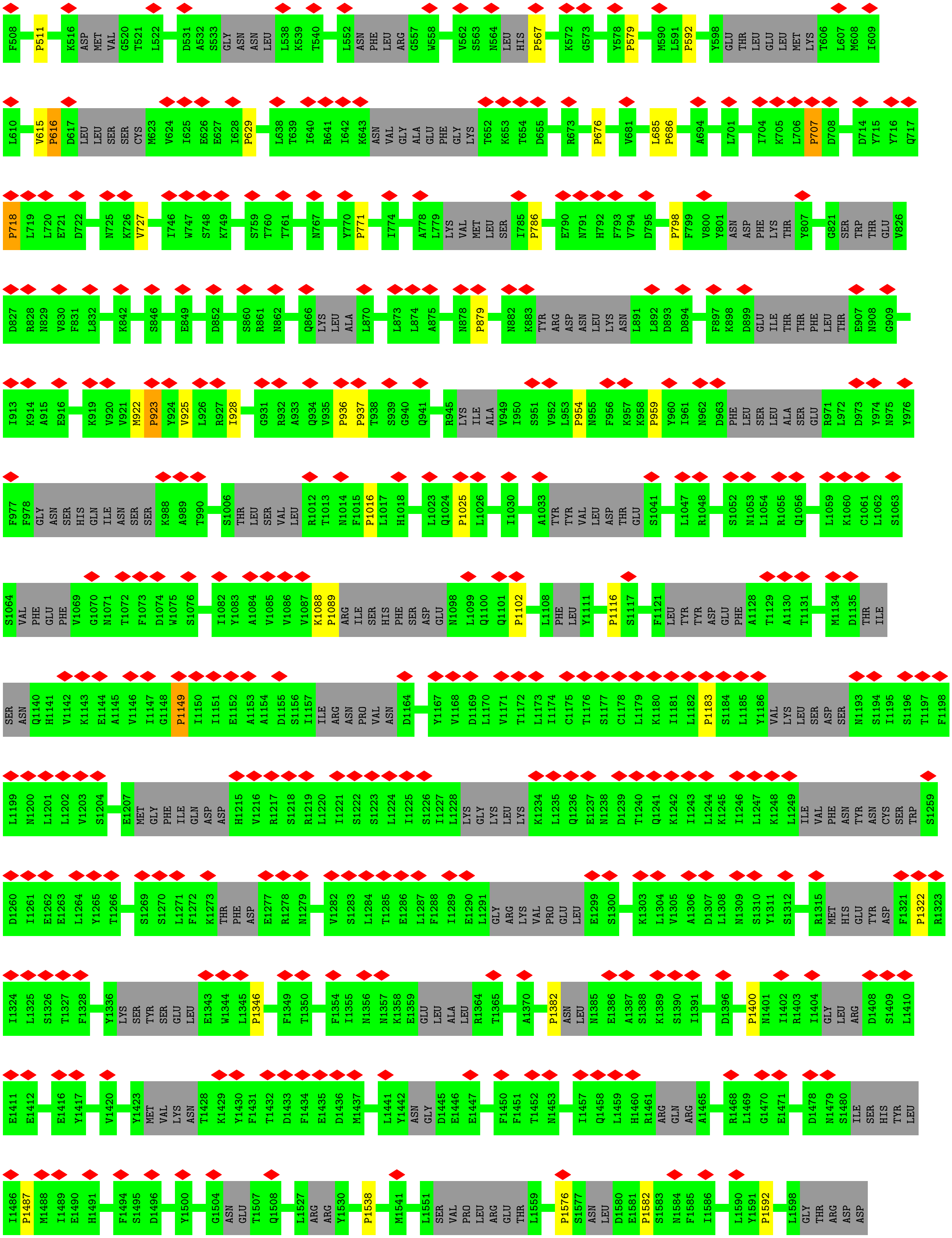
Chain RO:

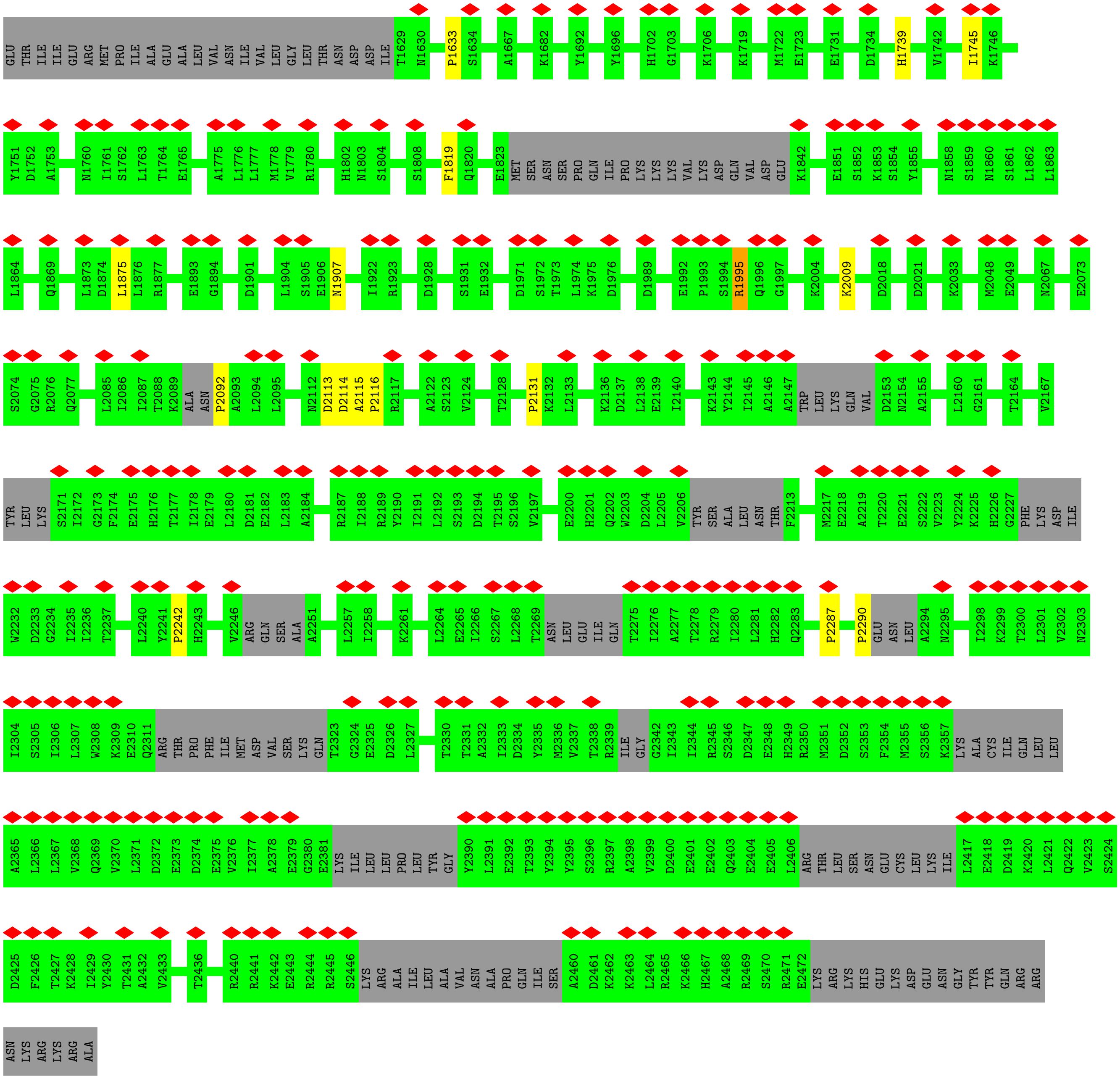


- Molecule 58: U3 small nucleolar RNA-associated protein 20

Chain RP:

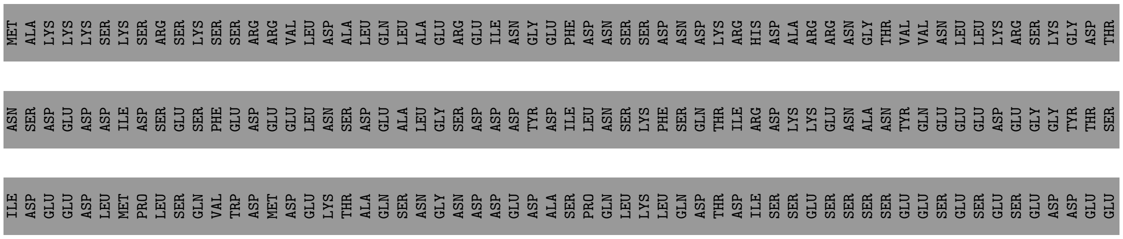


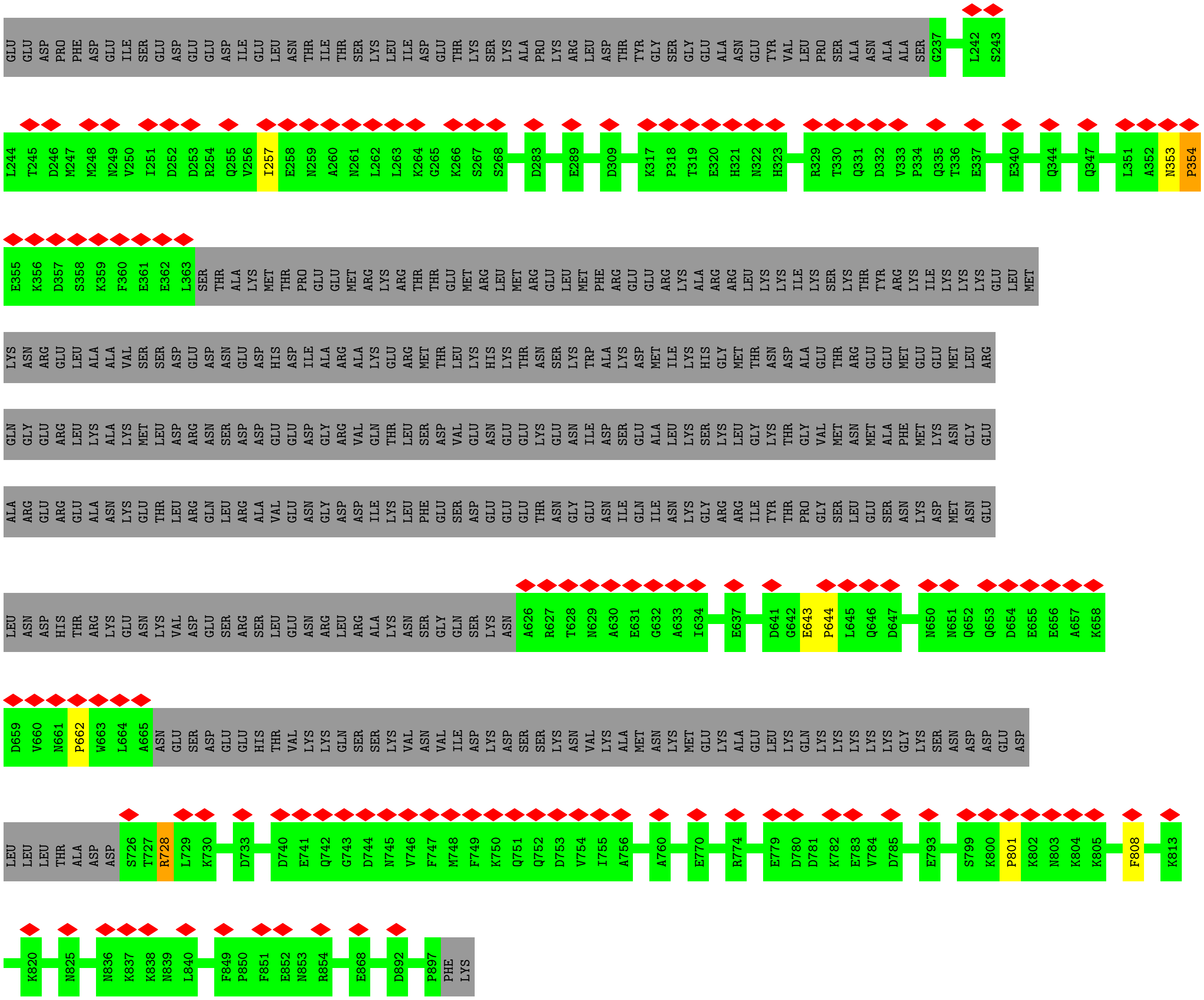

F508 P511 K516 ASP MET VAL G520 T521 L522 D531 A532 S533 GLY ASN ASN LEU L538 K539 T540 L552 ASN PHE LEU ARG G557 W558 V562 S563 N564 LEU HIS P567 K572 G573 Y578 P579 M590 L591 P592 Y598 GLU THR LEU GLU LEU MET LYS T606 L607 M608 I609
L610 V615 P616 D617 LEU LEU SER SER CYS M623 V624 I625 E626 E627 I628 P629 L638 T639 I640 R641 I642 K643 ASN VAL GLY ALA GLU PHE GLY LYS T652 K653 T654 D655 R673 P676 V681 L685 P686 A694 L701 I704 K705 L706 P707 D708 D714 Y715 Y716 Q717
P718 L719 L720 E721 D722 N725 K726 V727 I746 W747 S748 K749 S759 T760 T761 N767 Y770 P771 I774 A778 L779 LYS VAL MET LEU SER I785 P786 E790 N791 H792 F793 V794 D795 P798 F799 V800 Y801 ASN ASP PHE LYS THR Y807 G821 SER TRP THR GLU V826
D827 R828 N829 V830 F831 L832 K842 S846 E849 D852 S860 R861 N862 Q866 LYS LEU ALA L870 L873 L874 A875 N878 P879 N882 K883 TYR ARG ASP ASN LEU LYS ASN L891 L892 D893 D894 F897 K898 D899 GLU ILE THR THR PHE LEU THR E907 N908 G909
I913 K914 A915 E916 K919 V920 V921 M922 P923 Y924 V925 L926 R927 I928 G931 R932 A933 Q934 V935 P936 P937 T938 S939 G940 Q941 R945 LYS ILE ALA V949 I950 S951 V952 L953 P954 N955 F956 K957 K958 P959 Y960 I961 N962 D963 PHE LEU SER LEU ALA SER GLU R971 L972 D973 Y974 N975 Y976
F977 F978 GLY ASN SER HIS GLN ILE ASN SER SER K988 A989 T990 S1006 THR LEU SER VAL LEU R1012 T1013 N1014 F1015 P1016 L1017 H1018 L1023 Q1024 P1025 L1026 I1030 A1033 TYR TYR VAL LEU ASP THR GLU S1041 L1047 R1048 S1052 N1053 L1054 R1055 Q1056 L1059 K1060 C1061 L1062 S1063
S1064 VAL PHE GLU PHE V1069 G1070 N1071 T1072 F1073 D1074 W1075 S1076 I1082 Y1083 A1084 V1085 V1086 V1087 K1088 P1089 ARG ILE SER HIS PHE SER ASP GLU N1098 L1099 Q1100 Q1101 P1102 L1108 PHE LEU Y1111 P1116 S1117 F1121 LEU TYR TYR ASP GLU PHE A1128 T1129 A1130 T1131 M1134 D1135 THR ILE
SER ASN Q1140 H1141 V1142 K1143 E1144 A1145 V1146 I1147 G1148 P1149 I1150 I1151 E1152 A1153 A1154 D1155 S1156 I1157 ILE ARG ASN PRO VAL ASN D1164 Y1167 V1168 D1169 L1170 V1171 T1172 L1173 I1174 C1175 T1176 S1177 C1178 L1179 K1180 I1181 L1182 P1183 S1184 L1185 Y1186 VAL LYS LEU SER ASP SER N1193 S1194 I1195 S1196 T1197 F1198
L1199 N1200 L1201 L1202 V1203 S1204 E1207 MET GLY PHE ILE GLN ASP ASP H1215 V1216 R1217 S1218 R1219 L1220 I1221 S1222 S1223 L1224 I1225 S1226 I1227 L1228 LYS GLY LYS LEU LYS K1234 L1235 Q1236 E1237 N1238 D1239 T1240 Q1241 K1242 I1243 L1244 K1245 I1246 L1247 K1248 L1249 ILE VAL PHE ASN TYR ASN CYS SER TRP S1259
D1260 I1261 E1262 E1263 L1264 Y1265 T1266 S1269 S1270 L1271 F1272 K1273 THR PHE ASP E1277 R1278 N1279 V1282 S1283 L1284 T1285 E1286 L1287 F1288 I1289 E1290 L1291 GLY ARG LYS VAL PRO GLU LEU E1299 S1300 K1303 L1304 V1305 A1306 D1307 L1308 N1309 S1310 Y1311 S1312 R1315 MET HIS GLU TYR ASP F1321 P1322 R1323
I1324 L1325 S1326 T1327 F1328 Y1336 LYS SER TYR SER GLU LEU E1343 W1344 L1345 P1346 F1349 T1350 F1354 I1355 N1356 N1357 K1358 E1359 GLU LEU ALA LEU R1364 T1365 A1370 P1382 ASN LEU N1385 E1386 A1387 S1388 K1389 S1390 I1391 D1396 P1400 N1401 I1402 R1403 I1404 GLY LEU ARG D1408 S1409 L1410
E1411 E1412 E1416 Y1417 V1420 Y1423 MET VAL LYS ASN T1428 K1429 Y1430 F1431 T1432 D1433 F1434 E1435 D1436 M1437 L1441 Y1442 ASN GLY D1445 E1446 E1447 F1450 F1451 T1452 N1453 I1457 Q1458 L1459 H1460 R1461 ARG GLN ARG A1465 R1468 L1469 G1470 E1471 D1478 N1479 S1480 ILE SER HIS TYR LEU
I1486 P1487 M1488 I1489 E1490 H1491 F1494 S1495 D1496 Y1500 G1504 ASN GLU T1507 Q1508 L1527 ARG ARG Y1530 P1538 M1541 L1551 SER VAL PRO LEU ARG GLU THR L1559 P1576 S1577 ASN LEU D1580 E1581 P1582 S1583 N1584 F1585 I1586 L1590 Y1591 P1592 L1598 GLY THR ARG ASP ASP



- Molecule 59: U3 small nucleolar RNA-associated protein 14

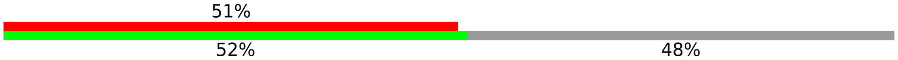
Chain RQ:

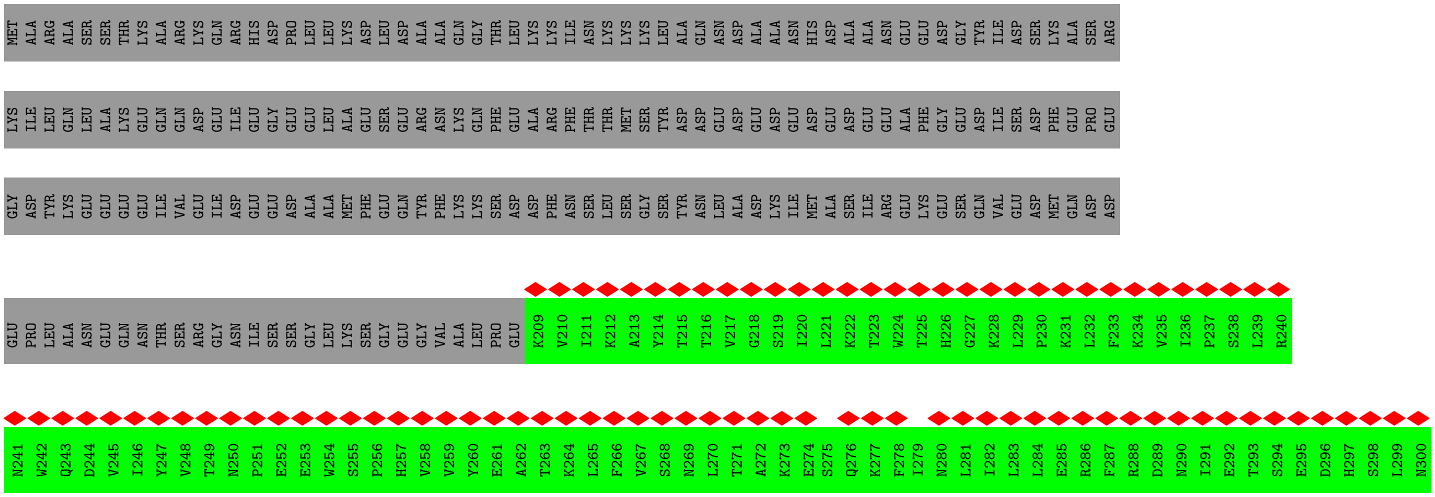


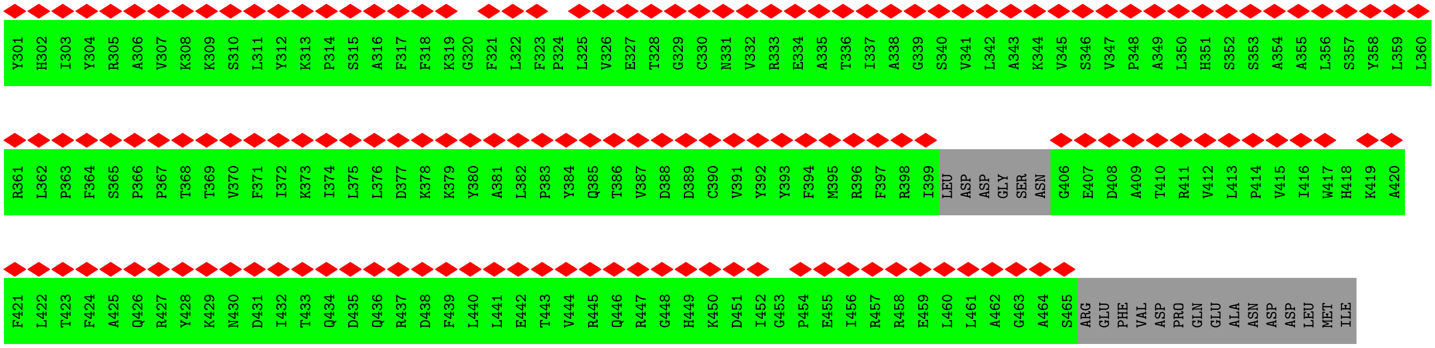


- Molecule 60: Essential nuclear protein 1

Chain RS:

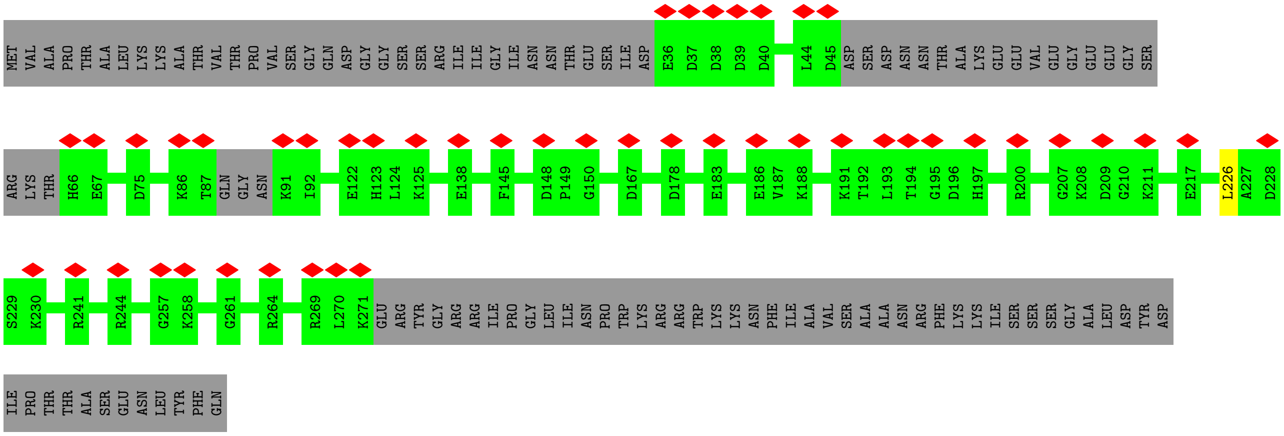






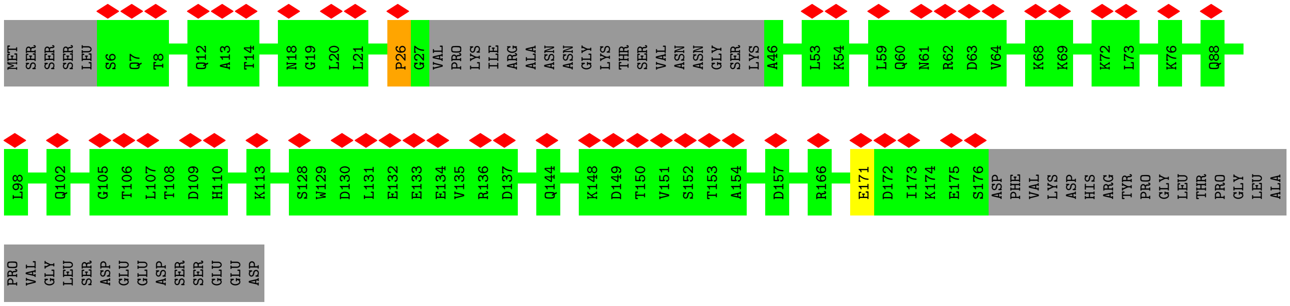
- Molecule 61: Pno1

Chain RT:



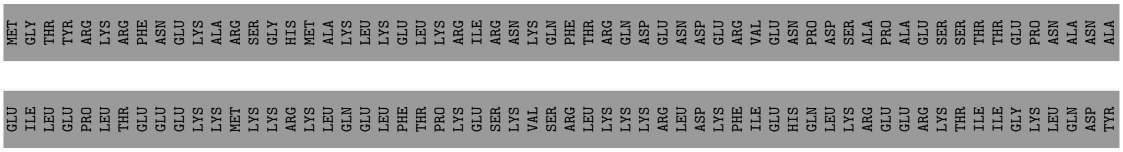
- Molecule 62: Regulator of rDNA transcription protein 14

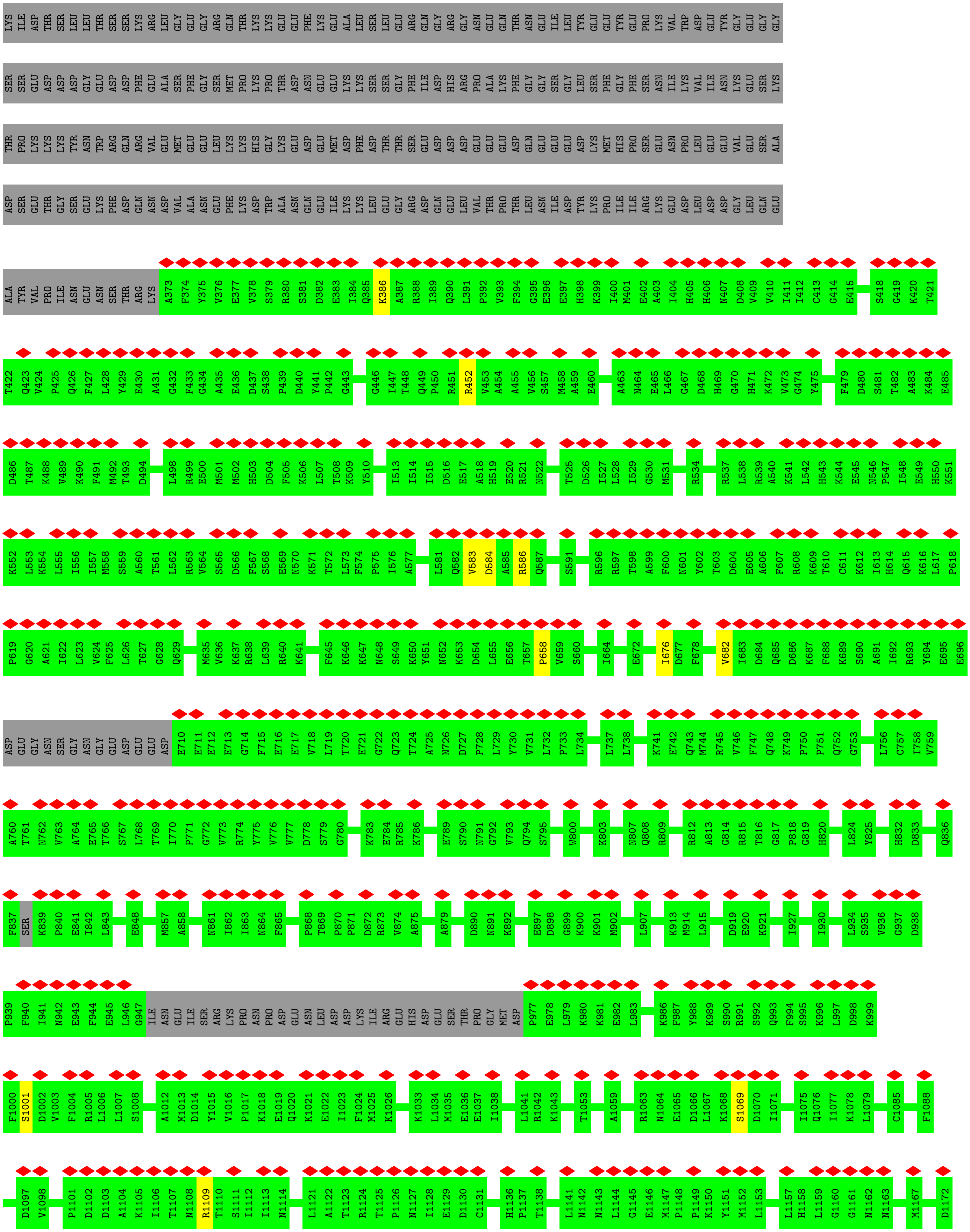
Chain RW:



- Molecule 63: Probable ATP-dependent RNA helicase DHR1

Chain RZ:

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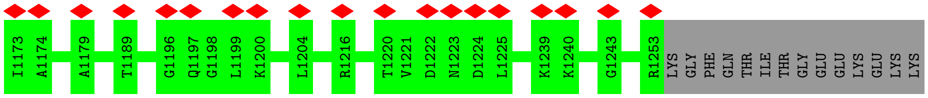
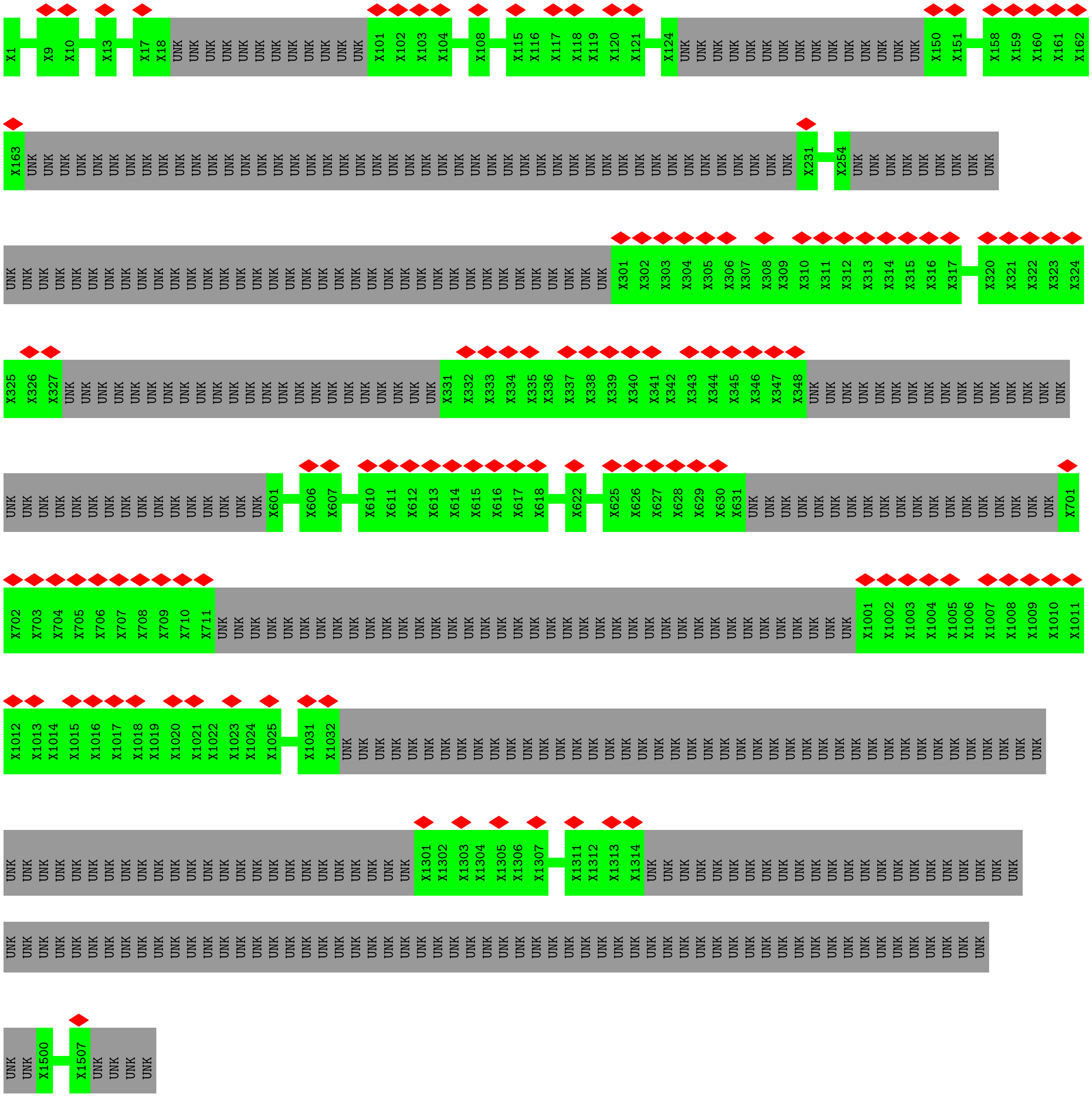
SER SER GLU ASP ASP ASP GLY GLU ASP ASP PHE GLU ALA SER PHE GLY SER MET PRO LYS PRO THR ASP ASN GLU GLU LYS LYS SER SER GLY PHE ILE ASP HIS ARG PRO ALA LYS PHE GLY GLY SER GLY LEU SER PHE GLY PHE SER ASN ILE LYS VAL ILE ASN LYS GLU SER LYS
THR PRO LYS LYS TYR ASN TRP ARG GLN ARG VAL GLU MET GLU GLU LEU LYS LYS HIS GLY LYS GLU ASP GLU MET ASP PHE ASP THR THR SER GLU ASP ASP GLU GLU GLU ASP GLN GLU GLU GLU ASP LYS MET HIS PRO SER GLU ASN PRO LEU GLU GLU VAL GLU SER ALA
ASP SER GLU THR GLY SER GLU LYS PHE ASP GLN ASN ASP VAL ALA ASN GLU PHE LYS SER ASP TRP ALA ASN GLN GLU ILE LYS LYS LEU GLU GLY ARG GLN ASP GLN LEU VAL THR PRO THR LEU ASN ILE ASP TYR LYS PRO ILE ILE ARG LYS GLU ASP LEU ASP ASP GLY LEU GLN GLU
ALA TYR VAL PRO ILE ASN GLU ASN SER THR ARG LYS A373 F374 Y375 V376 E377 V378 S379 R380 S381 D382 E383 I384 Q385 K386 A387 R388 I389 Q390 L391 P392 V393 F394 G395 E396 E397 H398 K399 I400 M401 E402 A403 I404 H405 H406 N407 D408 V409 V410 I411 I412 G413 G414 E415 S418 G419 K420 T421
T422 Q423 V424 P425 Q426 F427 L428 Y429 E430 A431 G432 F433 G434 A435 E436 D437 S438 P439 D440 Y441 P442 G443 G446 I447 T448 Q449 P450 R451 R452 V453 A454 A455 V456 S457 M458 A459 E460 A463 N464 E465 L466 G467 D468 H469 G470 H471 K472 V473 G474 Y475 F479 D480 S481 T482 A483 K484 E485
D486 T487 K488 V489 K490 F491 M492 T493 D494 L498 R499 E500 M501 M502 H503 D504 F505 K506 L507 T508 K509 Y510 I513 I514 I515 D516 E517 A518 H519 E520 R521 N522 T525 D526 I527 L528 I529 G530 M531 R534 R537 L538 R539 A540 K541 L542 H543 K544 E545 N546 P547 I548 E549 H550 K551
K552 L553 K554 L555 I556 I557 M558 S559 A560 T561 L562 R563 V564 S565 D566 F567 S568 E569 N570 K571 T572 L573 F574 P575 I576 A577 L581 Q582 V583 D584 A585 R586 Q587 S591 R596 R597 T598 A599 F600 N601 Y602 T603 D604 E605 A606 F607 R608 K609 T610 C611 K612 I613 H614 Q615 K616 L617 P618
P619 G620 A621 I622 L623 V624 F625 L626 T627 G628 Q629 M635 V636 K637 R638 L639 R640 K641 F645 K646 K647 N648 S649 K650 Y651 N652 K653 D654 L655 E656 T657 P658 V659 S660 I664 E672 I676 D677 F678 V682 I683 D684 Q685 D686 K687 F688 K689 S690 A691 I692 R693 Y694 E695 E696
ASP GLU GLY ASN SER GLY ASN GLY GLU ASP GLU ASP E710 E711 E712 E713 G714 F715 E716 E717 V718 L719 T720 E721 G722 Q723 T724 A725 N726 D727 P728 L729 Y730 V731 L732 P733 L734 L737 L738 K741 E742 Q743 M744 R745 V746 F747 Q748 K749 P750 P751 Q752 G753 L756 C757 I758 V759
A760 T761 N762 V763 A764 E765 T766 S767 L768 T769 I770 P771 G772 V773 R774 Y775 V776 V777 D778 S779 G780 K783 E784 R785 K786 E789 S790 N791 G792 V793 Q794 S795 W800 K803 N807 Q808 R809 R812 A813 G814 R815 T816 G817 P818 G819 H820 L824 Y825 H832 D833 Q836
F837 SER K839 P840 E841 I842 L843 E848 M857 A858 N861 I862 I863 N864 F865 P868 T869 P870 P871 D872 R873 V874 A875 A879 D890 N891 K892 E897 D898 G899 K900 K901 M902 L907 K913 M914 L915 D919 E920 K921 I927 I930 L934 S935 V936 G937 D938
P939 F940 I941 N942 E943 F944 E945 L946 G947 ILE ASN GLU ILE SER ARG LYS PRO ASN PRO ASP GLU ASN LEU ASP LYS ILE ARG GLU HIS ASP GLU SER THR PRO GLY MET ASP P977 E978 L979 K980 K981 E982 L983 K986 F987 Y988 K989 S990 R991 S992 Q993 F994 S995 K996 L997 D998 K999
F1000 S1001 D1002 V1003 F1004 R1005 L1006 L1007 S1008 A1012 M1013 D1014 Y1015 V1016 P1017 K1018 E1019 Q1020 K1021 E1022 I1023 F1024 M1025 K1026 K1033 L1034 M1035 E1036 E1037 I1038 L1041 R1042 K1043 T1053 A1059 R1063 N1064 E1065 D1066 L1067 K1068 S1069 D1070 I1071 I1075 Q1076 I1077 K1078 L1079 C1085 F1088
D1097 V1098 P1101 D1102 D1103 A1104 K1105 I1106 T1107 N1108 R1109 T1110 S1111 I1112 I1113 N1114 L1121 A1122 T1123 R1124 T1125 P1126 N1127 I1128 E1129 D1130 C1131 H1136 P1137 T1138 L1141 N1142 N1143 L1144 G1145 E1146 M1147 P1148 P1149 K1150 Y1151 M1152 L1153 L1157 H1158 L1159 G1160 G1161 N1162 N1163 M1167 D1172



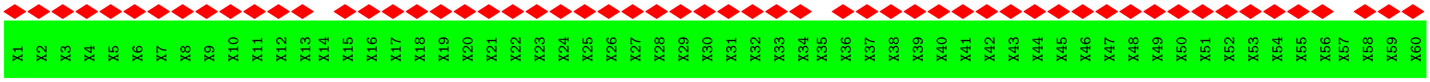
- Molecule 64: Unassigned peptides 1

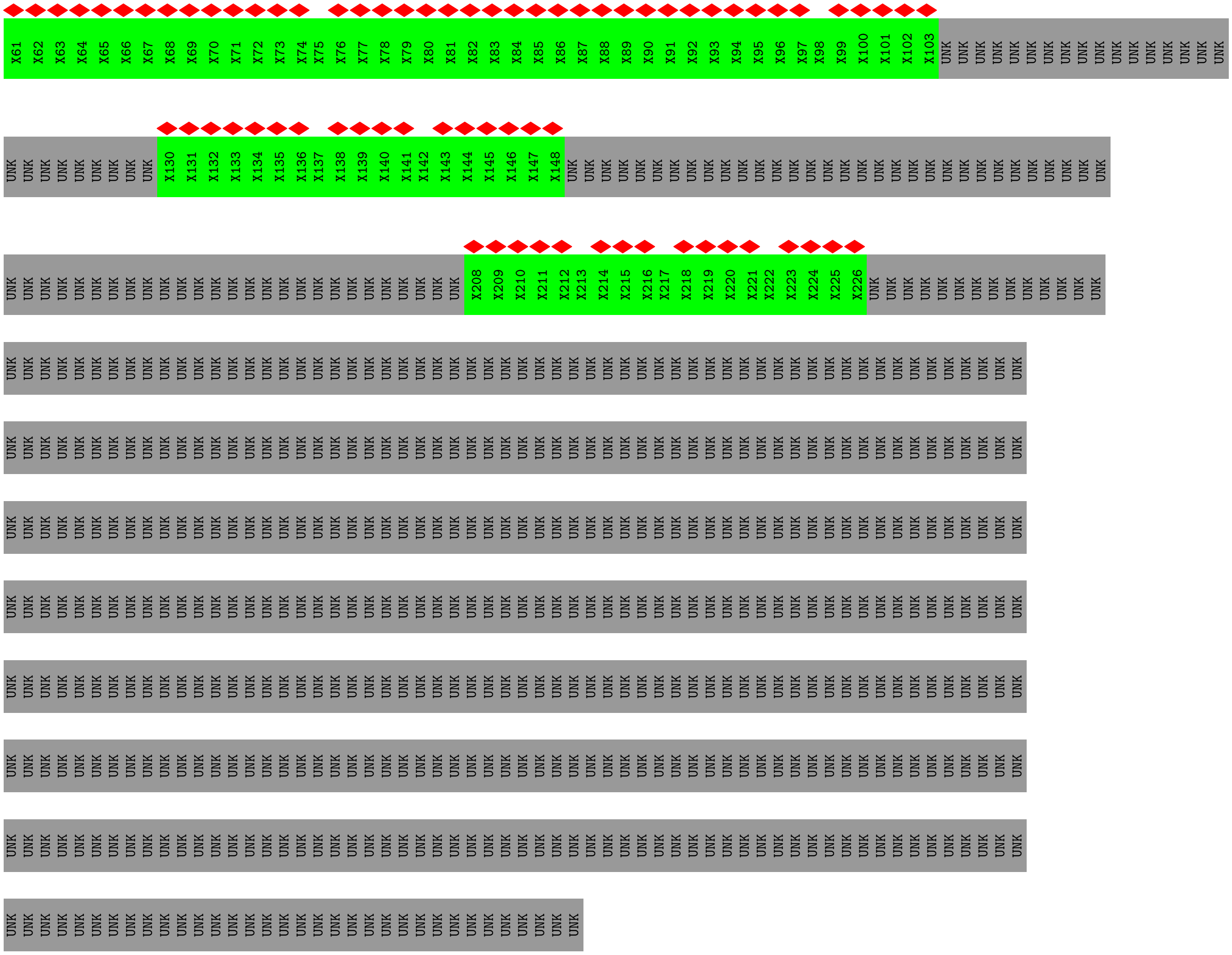
Chain X1:



- Molecule 65: Unassigned peptides 2

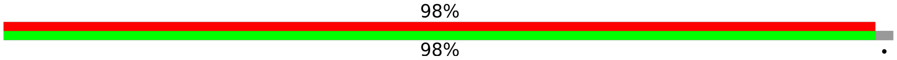
Chain X2:

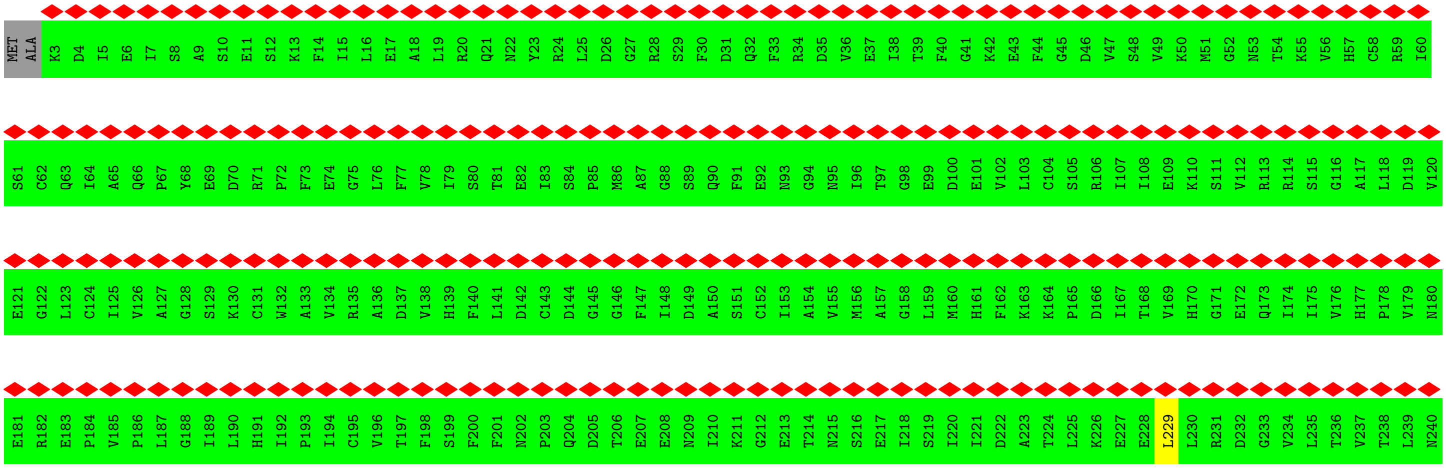




- Molecule 66: Exosome complex component RRP45

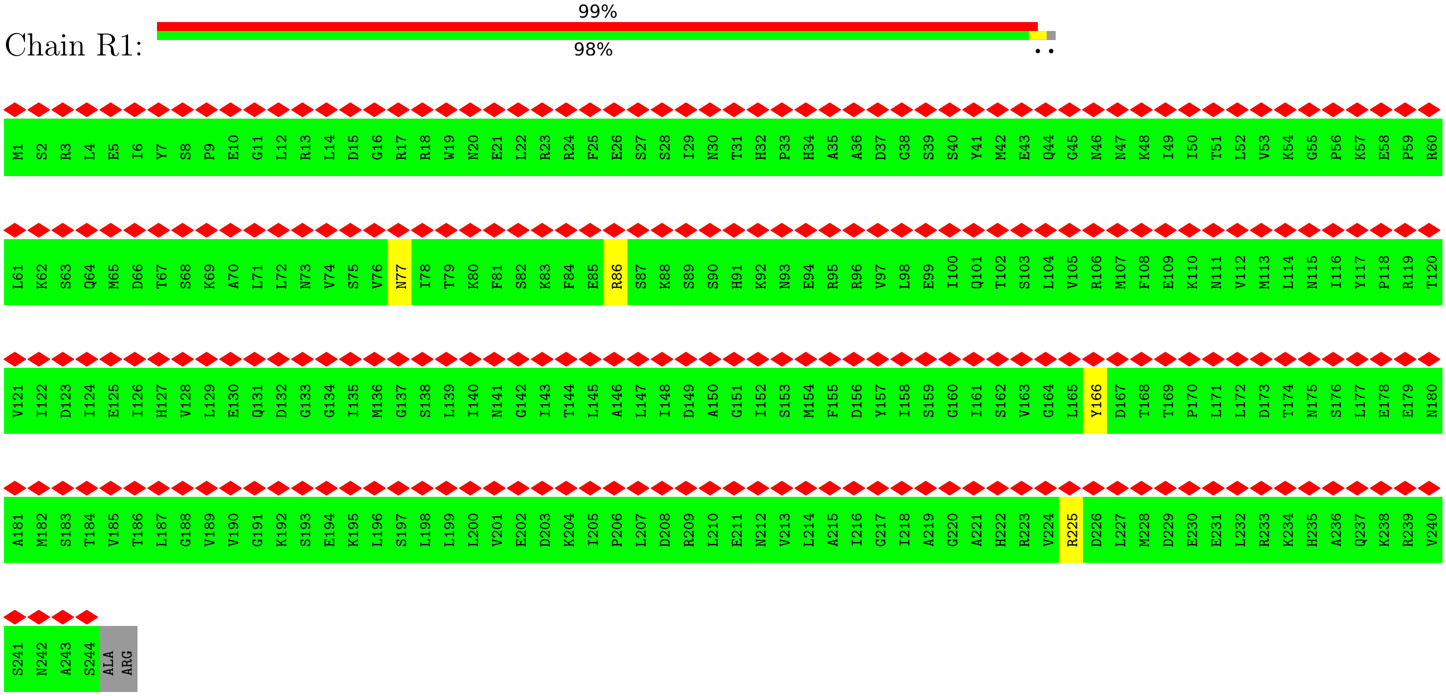
Chain R5:





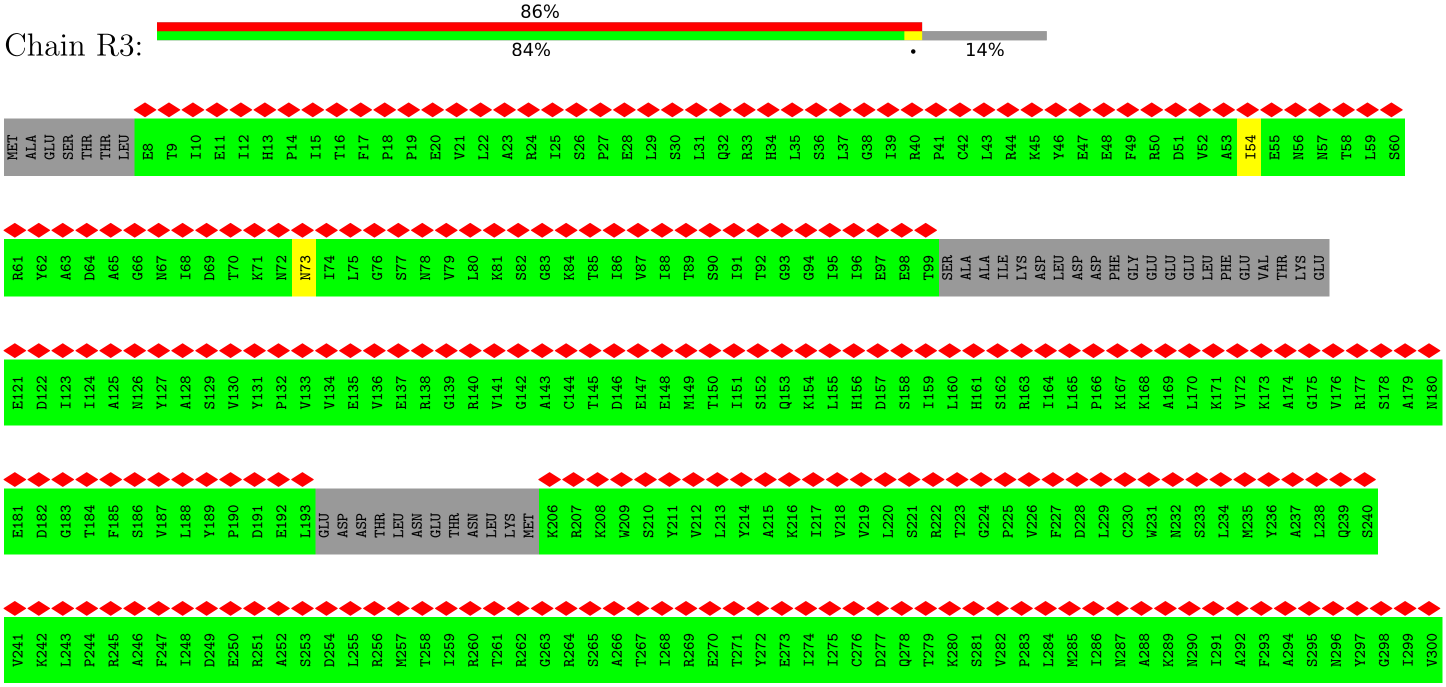
- Molecule 67: Exosome complex component SKI6

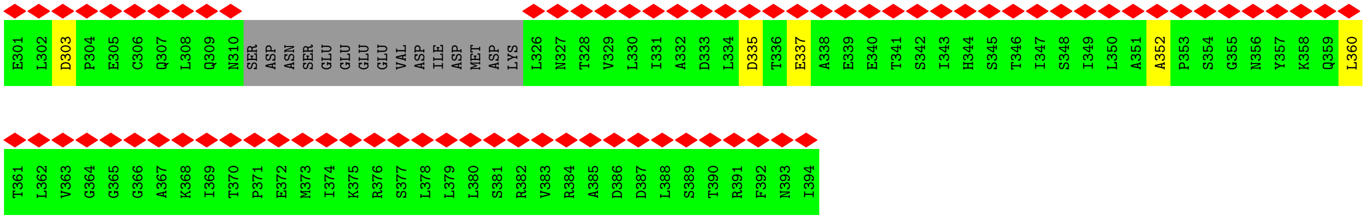
Chain R1:



- Molecule 68: Exosome complex component RRP43

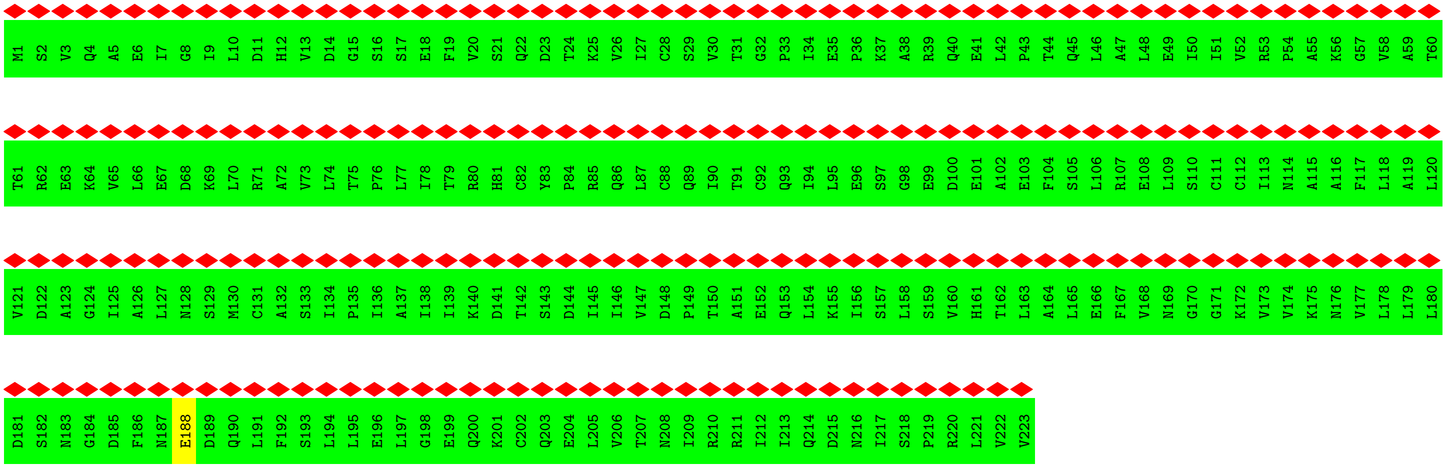
Chain R3:





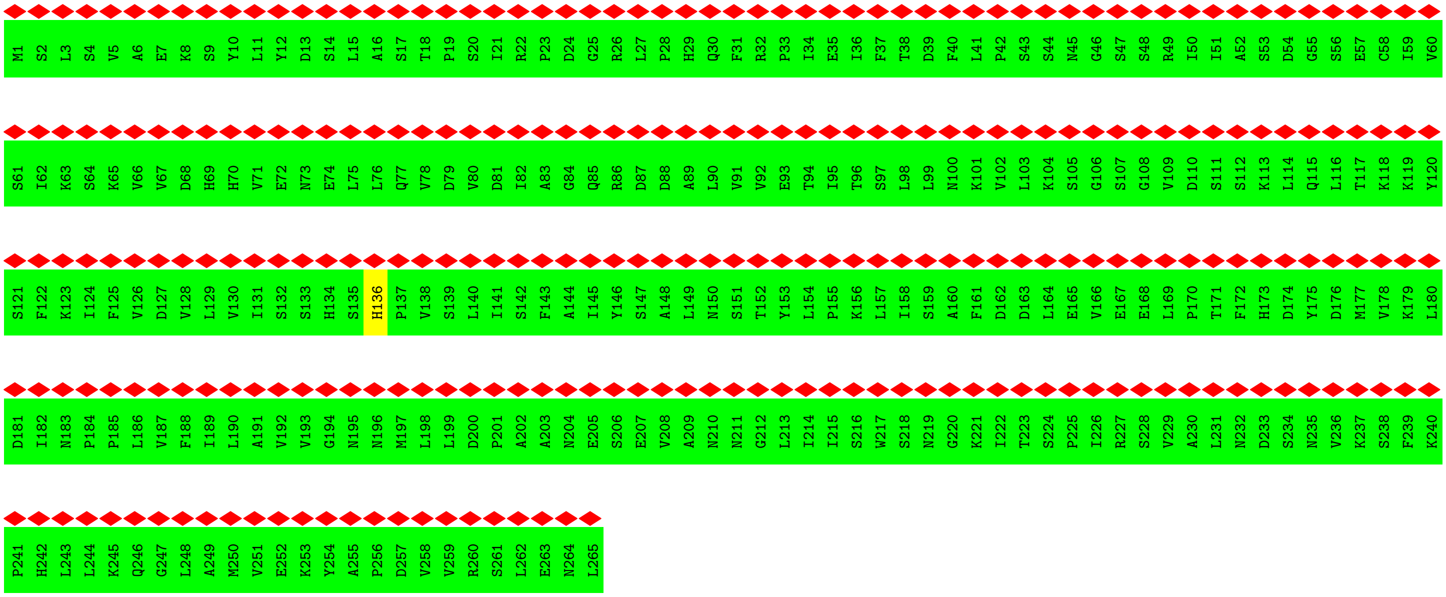
- Molecule 69: Exosome complex component RRP46

Chain R6:



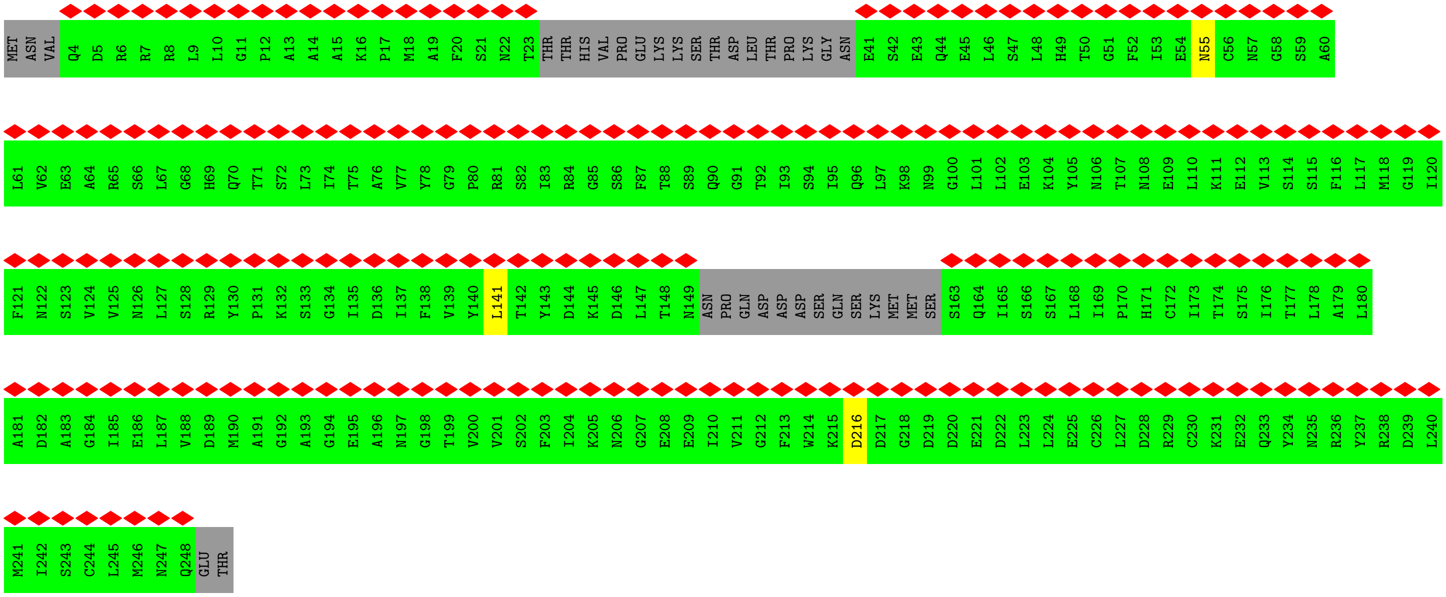
- Molecule 70: Exosome complex component RRP42

Chain R2:



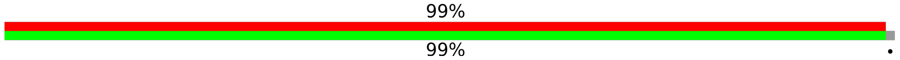
- Molecule 71: Exosome complex component MTR3

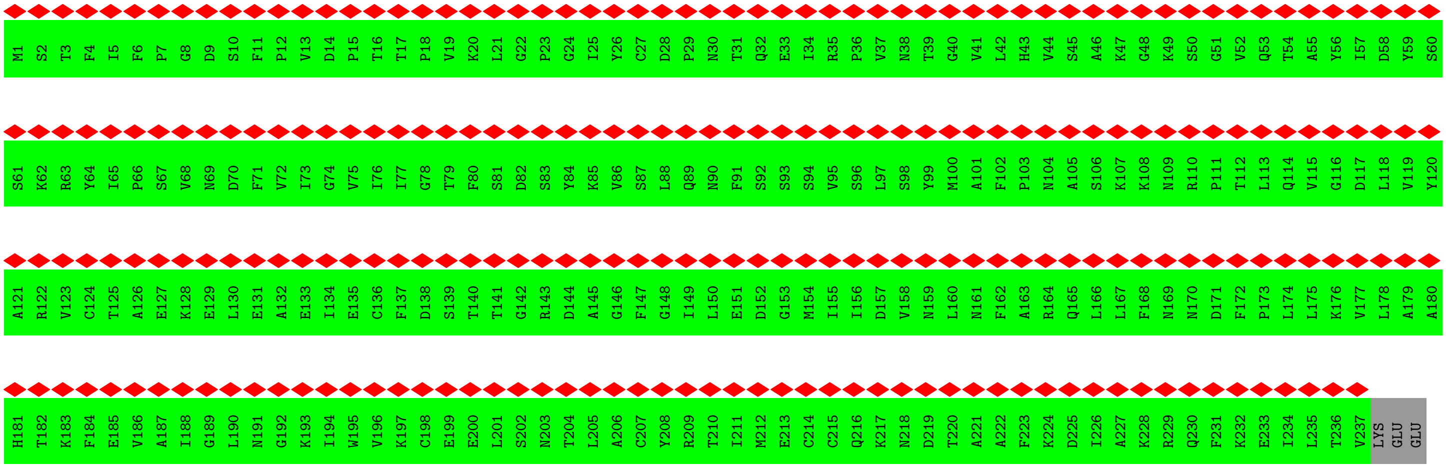
Chain M3:



• Molecule 72: Exosome complex component RRP40

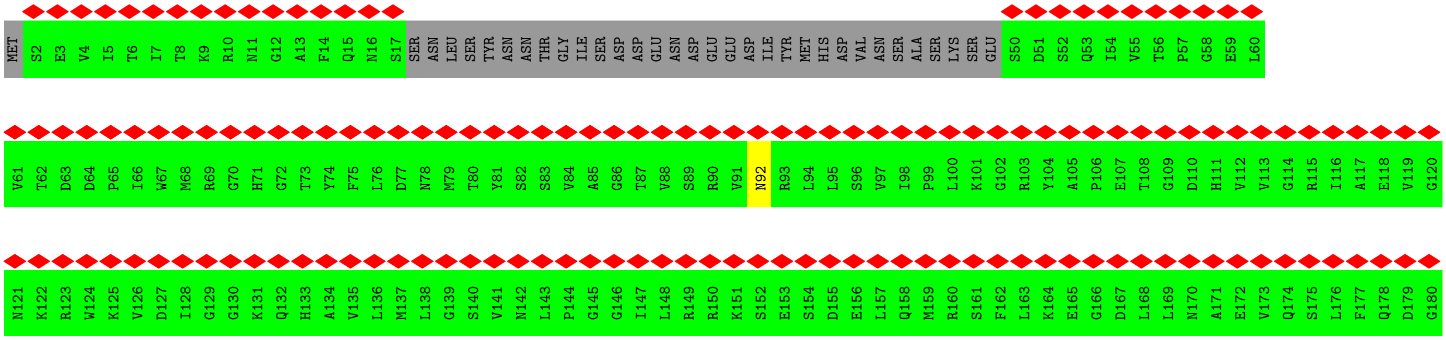
Chain R0:

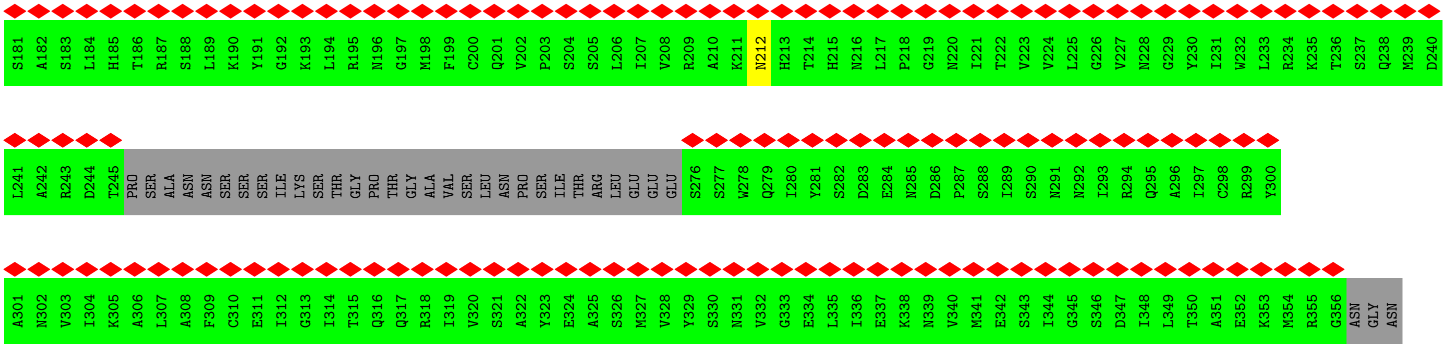




• Molecule 73: Exosome complex component RRP4

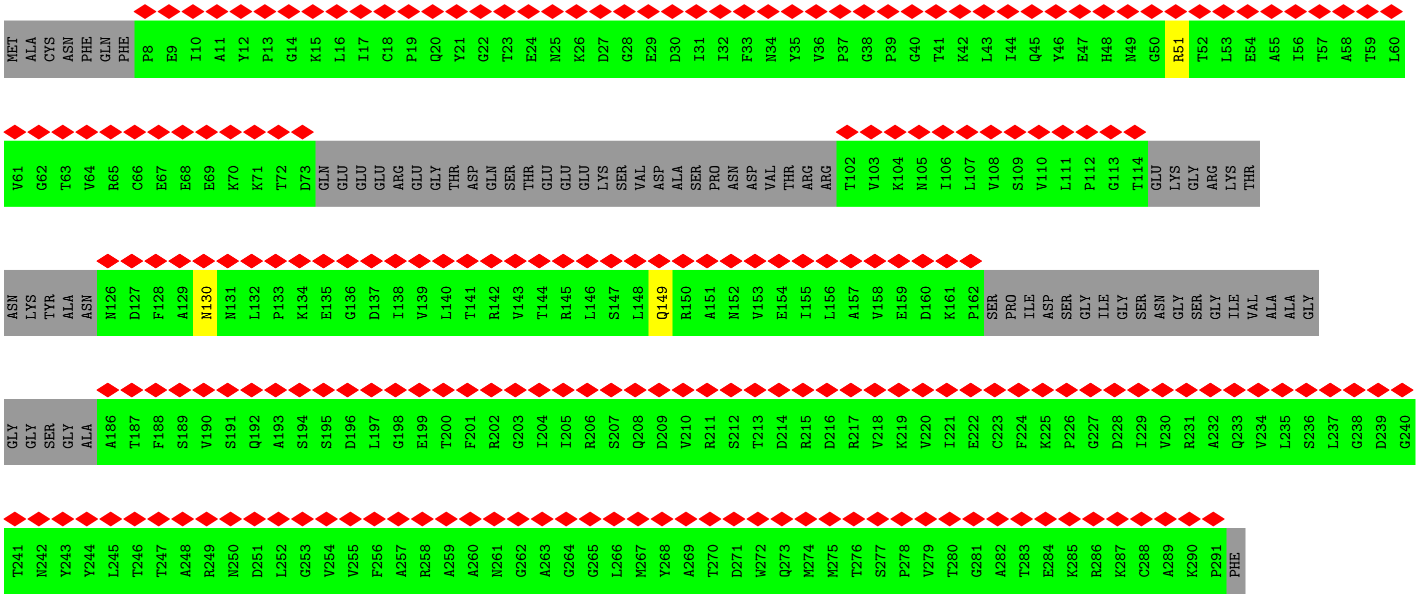
Chain r4:





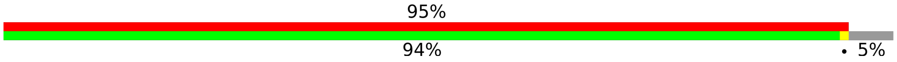
- Molecule 74: Exosome complex component CSL4

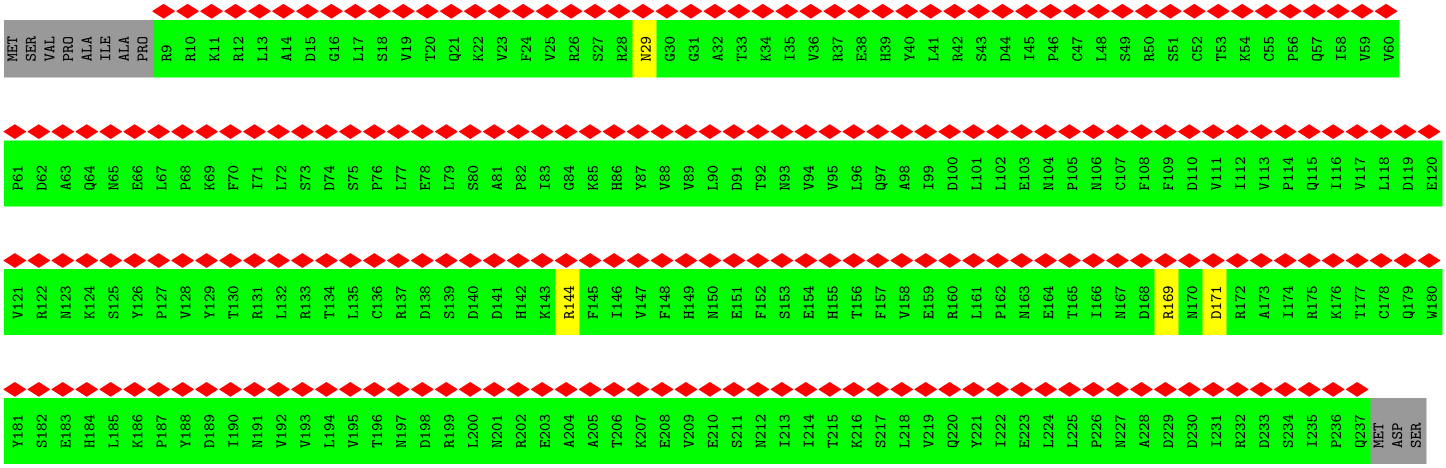
Chain C4:

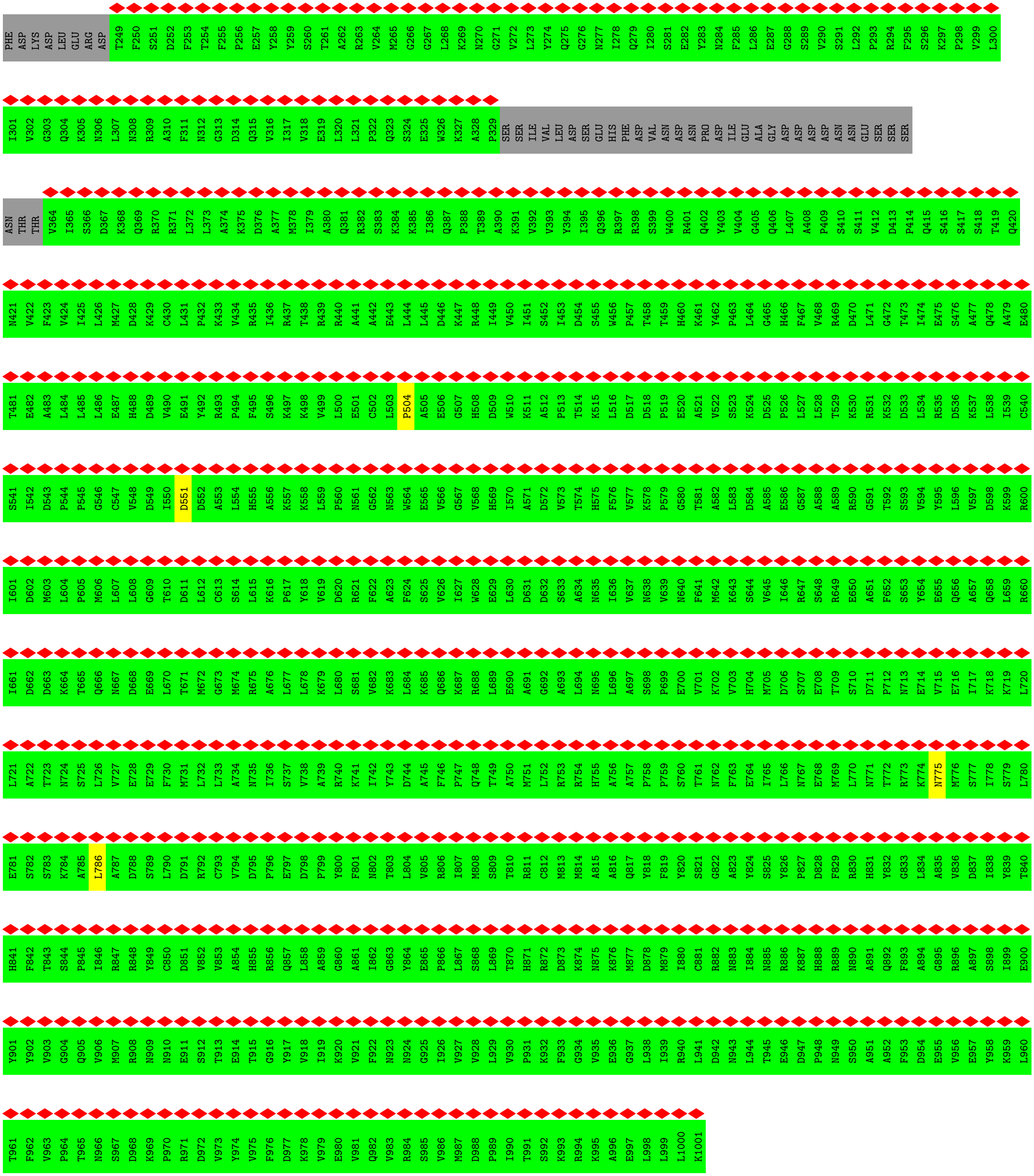


- Molecule 75: Exosome complex exonuclease DIS3

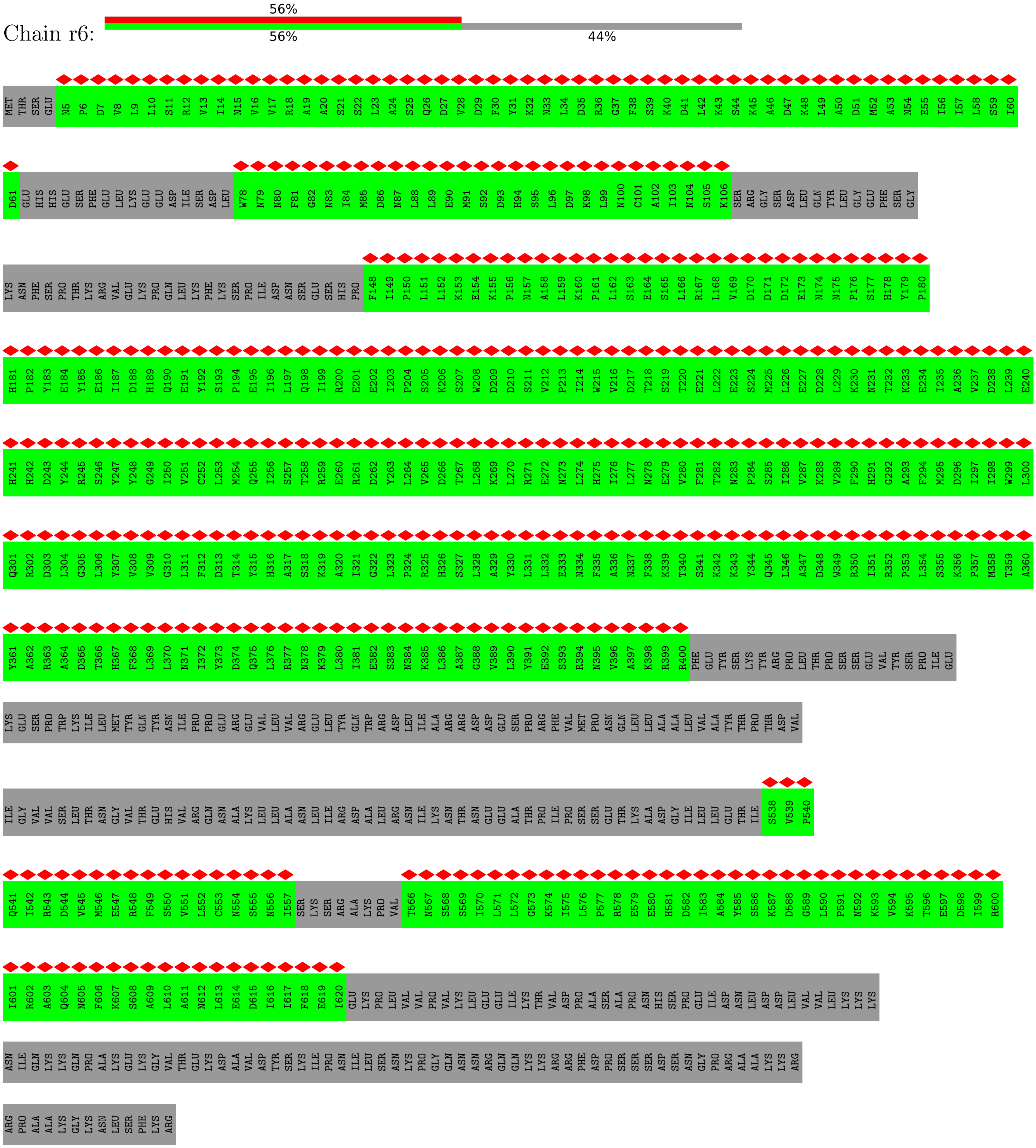
Chain R4:



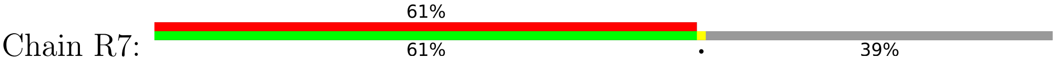


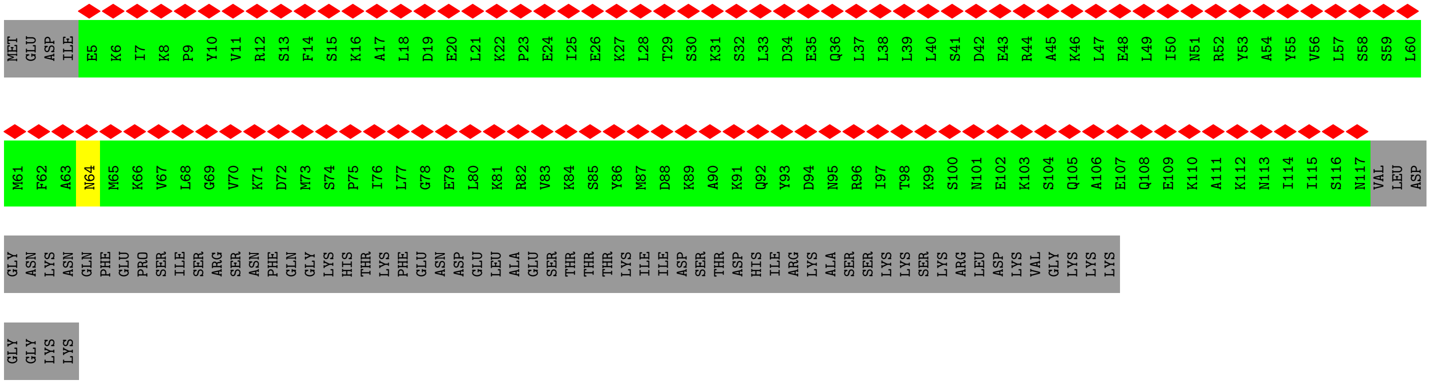


- Molecule 76: Exosome complex exonuclease RRP6

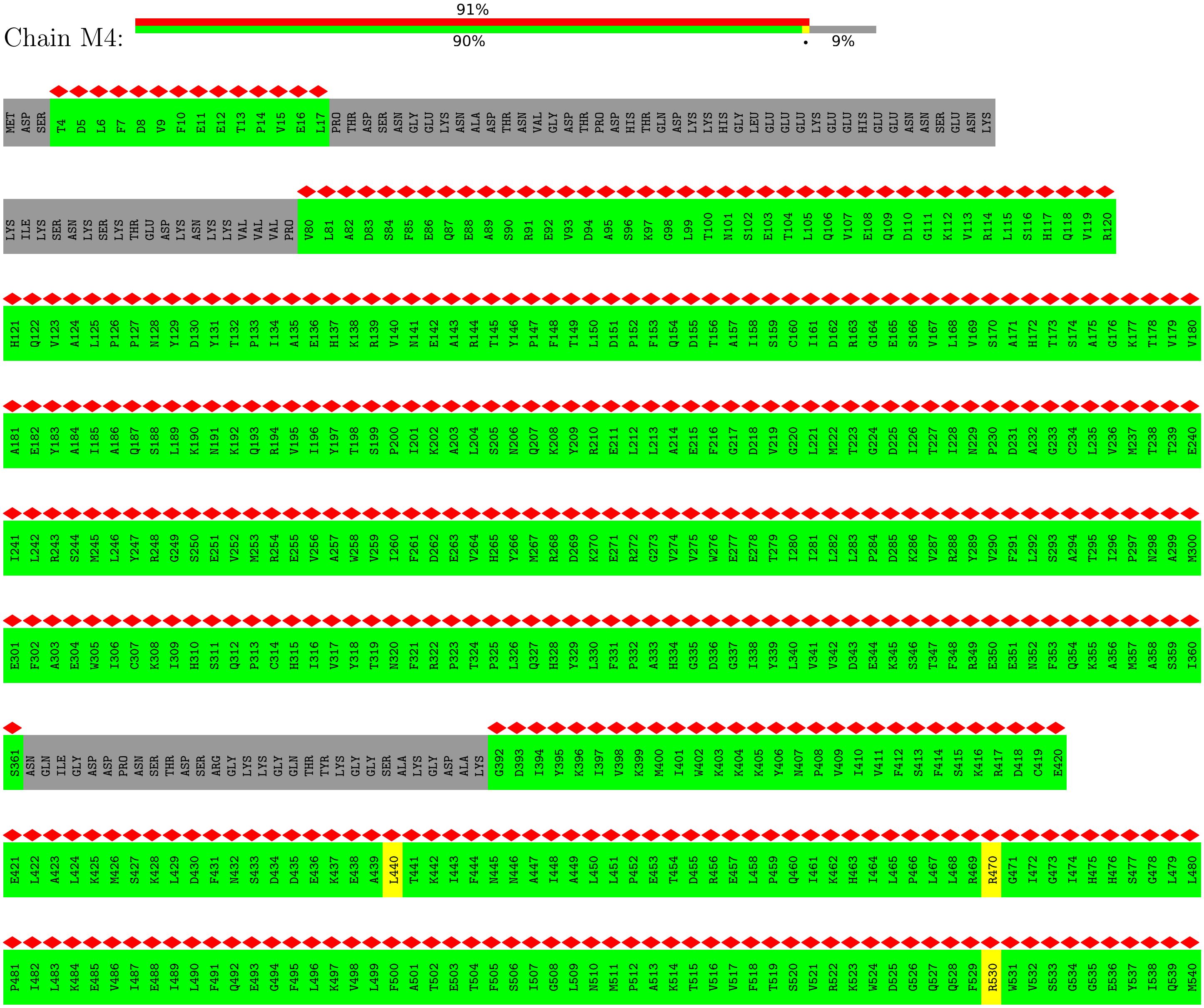


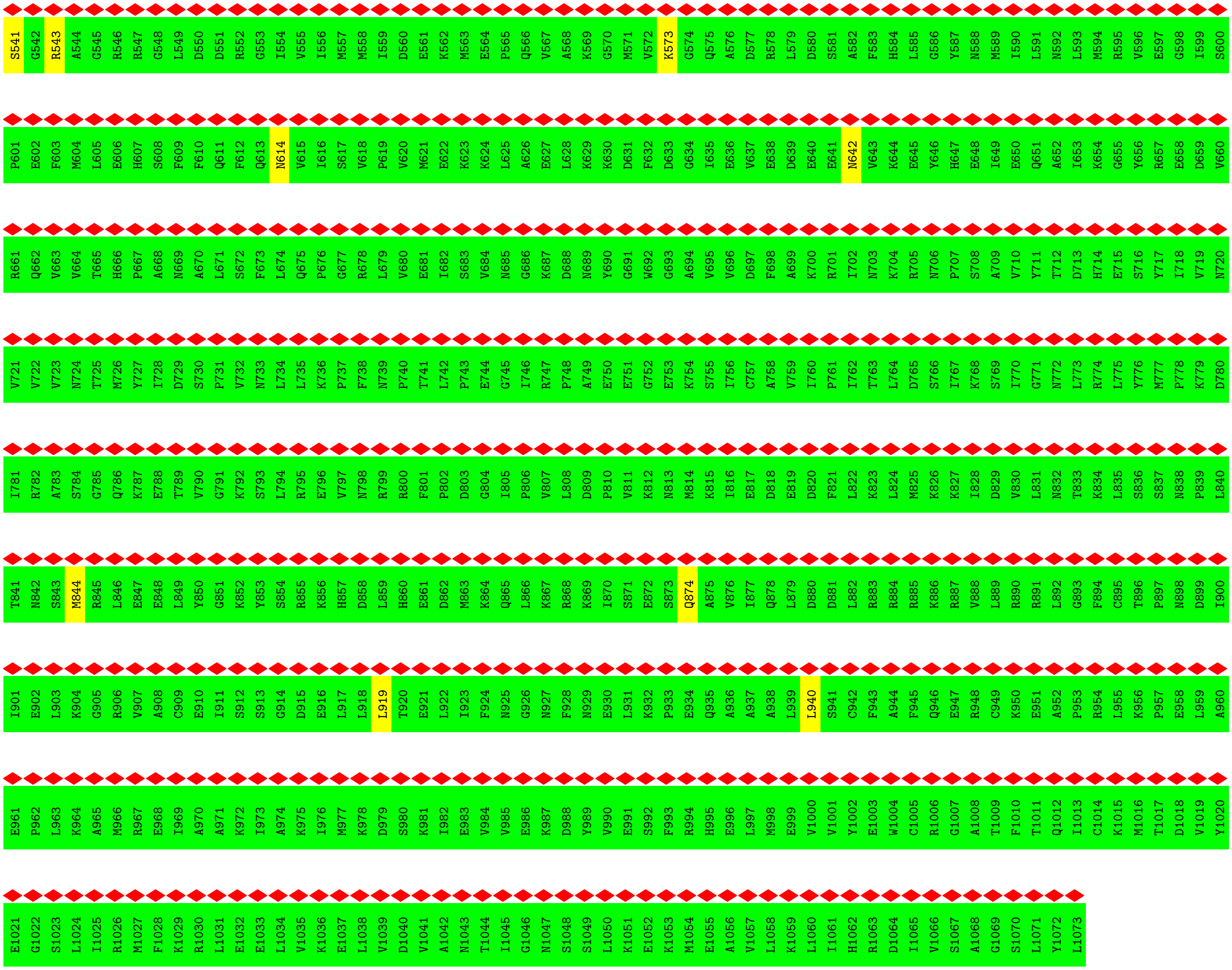
- Molecule 77: Exosome complex protein LRP1





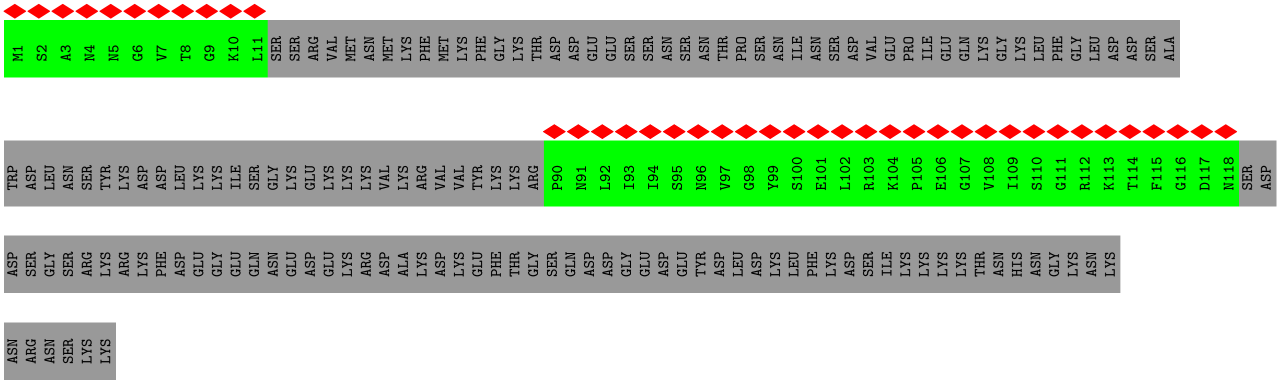
- Molecule 78: ATP-dependent RNA helicase DOB1





- Molecule 79: M-phase phosphoprotein 6 homolog

Chain M6:



4 Experimental information (i)

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	219545	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	0.120	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	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, GTP, ZN, ADP

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	0.61	0/5088	1.20	47/7888 (0.6%)
2	5A	0.44	0/2833	1.13	12/4401 (0.3%)
3	SA	0.56	0/31829	1.17	228/49545 (0.5%)
4	SC	0.39	0/1949	0.66	2/2609 (0.1%)
5	SF	0.37	0/1954	0.65	1/2640 (0.0%)
6	SG	0.38	0/1690	0.61	0/2285
7	SH	0.29	0/1476	0.56	1/1975 (0.1%)
8	SI	0.36	0/1341	0.76	3/1806 (0.2%)
9	SJ	0.30	0/1202	0.58	0/1610
10	SK	0.41	0/1432	0.65	2/1917 (0.1%)
11	SM	0.29	0/1139	0.52	0/1535
12	SO	0.37	0/1109	0.57	0/1495
13	SP	0.37	0/859	0.63	0/1161
14	SR	0.46	0/990	0.63	0/1335
15	ST	0.30	0/914	0.59	0/1229
16	SU	0.34	0/1092	0.55	0/1466
17	SX	0.39	0/1020	0.64	0/1371
18	SY	0.40	0/804	0.57	0/1074
19	SZ	0.44	0/1000	0.66	0/1334
20	Sc	0.38	0/613	0.62	0/828
21	Sd	0.41	0/499	0.60	0/670
22	3B	0.50	0/1914	0.66	1/2582 (0.0%)
22	3C	0.41	0/1787	0.66	2/2413 (0.1%)
23	3D	0.41	0/3020	0.60	2/4066 (0.0%)
24	3E	0.37	0/3088	0.61	1/4193 (0.0%)
25	3F	0.45	0/3569	0.62	0/4806
26	3G	0.42	0/928	0.74	2/1262 (0.2%)
26	3H	0.46	0/928	0.74	2/1262 (0.2%)
27	A4	0.41	0/5282	0.65	2/7154 (0.0%)
28	A5	0.37	0/4021	0.65	4/5462 (0.1%)
29	A8	0.27	0/3328	0.59	2/4565 (0.0%)
30	A9	0.28	0/951	0.65	2/1287 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	AE	0.33	0/10367	0.57	18/14163 (0.1%)
32	AF	0.33	0/3941	0.59	1/5344 (0.0%)
33	AG	0.36	0/6694	0.62	4/9070 (0.0%)
34	B1	0.43	0/6459	0.63	0/8744
35	B2	0.38	0/6624	0.65	3/8950 (0.0%)
36	B3	0.37	0/6001	0.66	3/8120 (0.0%)
37	B8	0.44	0/3730	0.63	3/5058 (0.1%)
38	BE	0.42	0/7012	0.63	5/9493 (0.1%)
39	B6	0.40	0/3138	0.60	2/4226 (0.0%)
40	5B	0.32	0/486	0.71	1/643 (0.2%)
41	5C	0.40	0/3902	0.61	3/5265 (0.1%)
42	5D	0.34	0/1801	0.57	0/2379
43	5E	0.34	0/1745	0.62	1/2335 (0.0%)
44	5F	0.37	0/1559	0.60	0/2097
45	5G	0.42	0/1993	0.65	2/2689 (0.1%)
46	5H	0.40	0/704	0.59	1/931 (0.1%)
47	5I	0.49	0/3844	0.61	0/5174
48	5J	0.37	0/1147	0.56	0/1531
49	5K	0.44	0/1213	0.63	1/1638 (0.1%)
50	RD	0.30	0/2454	0.56	3/3310 (0.1%)
51	RE	0.34	0/9015	0.58	4/12195 (0.0%)
52	RF	0.32	0/2004	0.62	0/2697
53	RG	0.27	0/1727	0.62	2/2329 (0.1%)
53	RH	0.32	0/1828	0.61	1/2470 (0.0%)
54	RJ	0.41	0/6126	0.59	1/8247 (0.0%)
55	RK	0.38	0/2832	0.61	0/3825
56	RN	0.30	0/4521	0.58	5/6083 (0.1%)
57	RO	0.29	0/3824	0.59	6/5226 (0.1%)
58	RP	0.31	0/12292	0.58	48/16822 (0.3%)
59	RQ	0.35	0/2443	0.62	4/3317 (0.1%)
60	RS	0.30	0/2104	0.58	0/2854
61	RT	0.34	0/1679	0.63	1/2261 (0.0%)
62	RW	0.30	0/760	0.46	1/1059 (0.1%)
63	RZ	0.31	0/6730	0.58	1/9088 (0.0%)
66	R5	0.57	0/2340	0.64	1/3161 (0.0%)
67	R1	0.54	0/1910	0.68	0/2579
68	R3	0.50	0/2628	0.69	2/3569 (0.1%)
69	R6	0.54	0/1722	0.70	0/2339
70	R2	0.51	0/2077	0.69	0/2828
71	M3	0.53	0/1661	0.65	0/2243
72	R0	0.55	0/1828	0.68	0/2486
73	r4	0.52	0/2269	0.66	0/3066
74	C4	0.48	0/1676	0.66	0/2277

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
75	R4	0.42	0/7575	0.61	3/10290 (0.0%)
76	r6	0.35	0/2540	0.51	0/3497
77	R7	0.39	0/903	0.58	0/1210
78	M4	0.49	0/7772	0.66	3/10521 (0.0%)
79	M6	0.43	0/277	0.66	0/371
All	All	0.42	0/259526	0.74	450/359296 (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	2
5	SF	0	1
7	SH	0	2
8	SI	0	2
14	SR	0	1
17	SX	0	1
19	SZ	0	1
20	Sc	0	1
25	3F	0	3
26	3G	0	2
26	3H	0	1
27	A4	0	1
28	A5	0	2
29	A8	0	2
33	AG	0	4
34	B1	0	2
35	B2	0	2
36	B3	0	7
38	BE	0	3
39	B6	0	2
40	5B	0	1
46	5H	0	1
47	5I	0	2
49	5K	0	1
51	RE	0	2
52	RF	0	1
54	RJ	0	1
56	RN	0	1
57	RO	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
58	RP	0	9
59	RQ	0	1
62	RW	0	1
63	RZ	0	2
67	R1	0	1
68	R3	0	3
69	R6	0	1
70	R2	0	1
71	M3	0	2
73	r4	0	1
74	C4	0	1
75	R4	0	1
78	M4	0	3
All	All	0	81

There are no bond length outliers.

The worst 5 of 450 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	5A	494	C	C2-N1-C1'	14.08	134.28	118.80
3	SA	185	U	C2-N1-C1'	10.48	130.27	117.70
1	3A	269	C	C2-N1-C1'	10.38	130.22	118.80
3	SA	185	U	N1-C2-O2	10.12	129.88	122.80
3	SA	1473	U	C2-N1-C1'	10.10	129.82	117.70

There are no chirality outliers.

5 of 81 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	16	GLN	Peptide
4	SC	18	LYS	Peptide
5	SF	207	LEU	Peptide
7	SH	147	LEU	Peptide
7	SH	152	ASP	Peptide

5.2 Too-close contacts ⓘ

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

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	SC	240/255 (94%)	210 (88%)	30 (12%)	0	100	100
5	SF	245/261 (94%)	198 (81%)	47 (19%)	0	100	100
6	SG	211/225 (94%)	194 (92%)	17 (8%)	0	100	100
7	SH	178/236 (75%)	159 (89%)	15 (8%)	4 (2%)	6	37
8	SI	161/190 (85%)	137 (85%)	24 (15%)	0	100	100
9	SJ	144/200 (72%)	126 (88%)	18 (12%)	0	100	100
10	SK	172/197 (87%)	154 (90%)	17 (10%)	1 (1%)	25	63
11	SM	135/156 (86%)	117 (87%)	18 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	114/137 (83%)	96 (84%)	18 (16%)	0	100	100
14	SR	123/143 (86%)	110 (89%)	13 (11%)	0	100	100
15	ST	107/146 (73%)	91 (85%)	16 (15%)	0	100	100
16	SU	136/144 (94%)	123 (90%)	13 (10%)	0	100	100
17	SX	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
18	SY	102/145 (70%)	88 (86%)	14 (14%)	0	100	100
19	SZ	121/135 (90%)	106 (88%)	15 (12%)	0	100	100
20	Sc	78/82 (95%)	66 (85%)	12 (15%)	0	100	100
21	Sd	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
22	3B	238/327 (73%)	215 (90%)	23 (10%)	0	100	100
22	3C	220/327 (67%)	200 (91%)	20 (9%)	0	100	100
23	3D	372/504 (74%)	342 (92%)	30 (8%)	0	100	100
24	3E	433/511 (85%)	392 (90%)	40 (9%)	1 (0%)	47	79
25	3F	431/573 (75%)	394 (91%)	37 (9%)	0	100	100
26	3G	119/126 (94%)	114 (96%)	5 (4%)	0	100	100
26	3H	119/126 (94%)	110 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	A4	643/776 (83%)	568 (88%)	75 (12%)	0	100	100
28	A5	501/643 (78%)	447 (89%)	52 (10%)	2 (0%)	34	71
29	A8	534/713 (75%)	407 (76%)	127 (24%)	0	100	100
30	A9	126/575 (22%)	111 (88%)	15 (12%)	0	100	100
31	AE	1516/1769 (86%)	1374 (91%)	138 (9%)	4 (0%)	41	75
32	AF	483/513 (94%)	440 (91%)	43 (9%)	0	100	100
33	AG	811/896 (90%)	726 (90%)	84 (10%)	1 (0%)	51	84
34	B1	785/900 (87%)	709 (90%)	75 (10%)	1 (0%)	51	84
35	B2	814/943 (86%)	716 (88%)	98 (12%)	0	100	100
36	B3	733/817 (90%)	585 (80%)	147 (20%)	1 (0%)	51	84
37	B8	453/594 (76%)	397 (88%)	56 (12%)	0	100	100
38	BE	886/939 (94%)	804 (91%)	81 (9%)	1 (0%)	51	84
39	B6	369/440 (84%)	341 (92%)	26 (7%)	2 (0%)	29	67
40	5B	56/214 (26%)	51 (91%)	5 (9%)	0	100	100
41	5C	474/554 (86%)	424 (90%)	50 (10%)	0	100	100
42	5D	201/250 (80%)	175 (87%)	26 (13%)	0	100	100
43	5E	205/593 (35%)	187 (91%)	18 (9%)	0	100	100
44	5F	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
45	5G	237/290 (82%)	215 (91%)	22 (9%)	0	100	100
46	5H	91/610 (15%)	81 (89%)	9 (10%)	1 (1%)	14	51
47	5I	457/489 (94%)	413 (90%)	44 (10%)	0	100	100
48	5J	130/217 (60%)	117 (90%)	13 (10%)	0	100	100
49	5K	148/189 (78%)	134 (90%)	14 (10%)	0	100	100
50	RD	310/1729 (18%)	281 (91%)	25 (8%)	4 (1%)	12	48
51	RE	1080/1237 (87%)	998 (92%)	81 (8%)	1 (0%)	51	84
52	RF	233/297 (78%)	205 (88%)	26 (11%)	2 (1%)	17	55
53	RG	212/252 (84%)	191 (90%)	21 (10%)	0	100	100
53	RH	226/252 (90%)	207 (92%)	19 (8%)	0	100	100
54	RJ	726/1183 (61%)	670 (92%)	56 (8%)	0	100	100
55	RK	358/367 (98%)	332 (93%)	26 (7%)	0	100	100
56	RN	568/810 (70%)	513 (90%)	55 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	RO	518/552 (94%)	462 (89%)	50 (10%)	6 (1%)	13	49
58	RP	1948/2493 (78%)	1778 (91%)	156 (8%)	14 (1%)	22	61
59	RQ	333/899 (37%)	287 (86%)	42 (13%)	4 (1%)	13	49
60	RS	247/480 (52%)	224 (91%)	23 (9%)	0	100	100
61	RT	207/326 (64%)	188 (91%)	19 (9%)	0	100	100
62	RW	149/206 (72%)	135 (91%)	13 (9%)	1 (1%)	22	61
63	RZ	831/1267 (66%)	737 (89%)	91 (11%)	3 (0%)	34	71
66	R5	297/305 (97%)	275 (93%)	22 (7%)	0	100	100
67	R1	242/246 (98%)	224 (93%)	18 (7%)	0	100	100
68	R3	332/394 (84%)	304 (92%)	27 (8%)	1 (0%)	41	75
69	R6	222/223 (100%)	209 (94%)	13 (6%)	0	100	100
70	R2	264/265 (100%)	250 (95%)	14 (5%)	0	100	100
71	M3	209/250 (84%)	192 (92%)	17 (8%)	0	100	100
72	R0	235/240 (98%)	216 (92%)	19 (8%)	0	100	100
73	r4	287/359 (80%)	263 (92%)	24 (8%)	0	100	100
74	C4	214/292 (73%)	198 (92%)	16 (8%)	0	100	100
75	R4	942/1001 (94%)	875 (93%)	67 (7%)	0	100	100
76	r6	404/733 (55%)	367 (91%)	37 (9%)	0	100	100
77	R7	111/184 (60%)	108 (97%)	3 (3%)	0	100	100
78	M4	972/1073 (91%)	908 (93%)	64 (7%)	0	100	100
79	M6	36/186 (19%)	32 (89%)	4 (11%)	0	100	100
All	All	28063/37702 (74%)	25255 (90%)	2753 (10%)	55 (0%)	50	79

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	A5	569	PRO
50	RD	1223	PRO
57	RO	141	PRO
57	RO	519	PRO
58	RP	707	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	213/224 (95%)	210 (99%)	3 (1%)	67	81
5	SF	199/222 (90%)	197 (99%)	2 (1%)	76	86
6	SG	180/191 (94%)	178 (99%)	2 (1%)	73	85
7	SH	153/201 (76%)	151 (99%)	2 (1%)	69	82
8	SI	146/170 (86%)	144 (99%)	2 (1%)	67	81
9	SJ	122/161 (76%)	118 (97%)	4 (3%)	38	62
10	SK	150/166 (90%)	149 (99%)	1 (1%)	84	90
11	SM	124/137 (90%)	124 (100%)	0	100	100
12	SO	117/128 (91%)	117 (100%)	0	100	100
13	SP	88/105 (84%)	86 (98%)	2 (2%)	50	70
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	ST	99/129 (77%)	99 (100%)	0	100	100
16	SU	111/116 (96%)	111 (100%)	0	100	100
17	SX	108/111 (97%)	107 (99%)	1 (1%)	78	88
18	SY	86/120 (72%)	86 (100%)	0	100	100
19	SZ	103/113 (91%)	103 (100%)	0	100	100
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	55 (98%)	1 (2%)	59	77
22	3B	201/240 (84%)	199 (99%)	2 (1%)	76	86
22	3C	189/240 (79%)	188 (100%)	1 (0%)	88	93
23	3D	322/435 (74%)	320 (99%)	2 (1%)	86	92
24	3E	265/433 (61%)	264 (100%)	1 (0%)	91	94
25	3F	382/503 (76%)	379 (99%)	3 (1%)	81	89
26	3G	100/104 (96%)	99 (99%)	1 (1%)	76	86
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	587/713 (82%)	581 (99%)	6 (1%)	76	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	A5	431/574 (75%)	428 (99%)	3 (1%)	84	90
29	A8	174/657 (26%)	173 (99%)	1 (1%)	86	92
30	A9	89/533 (17%)	86 (97%)	3 (3%)	37	61
31	AE	770/1633 (47%)	761 (99%)	9 (1%)	71	84
32	AF	431/454 (95%)	426 (99%)	5 (1%)	71	84
33	AG	750/826 (91%)	748 (100%)	2 (0%)	92	95
34	B1	694/789 (88%)	691 (100%)	3 (0%)	91	94
35	B2	712/832 (86%)	705 (99%)	7 (1%)	76	86
36	B3	659/719 (92%)	655 (99%)	4 (1%)	86	92
37	B8	407/529 (77%)	403 (99%)	4 (1%)	76	86
38	BE	741/819 (90%)	737 (100%)	4 (0%)	88	93
39	B6	323/414 (78%)	319 (99%)	4 (1%)	71	84
40	5B	56/196 (29%)	55 (98%)	1 (2%)	59	77
41	5C	418/480 (87%)	416 (100%)	2 (0%)	88	93
42	5D	198/234 (85%)	197 (100%)	1 (0%)	88	93
43	5E	193/535 (36%)	192 (100%)	1 (0%)	88	93
44	5F	171/172 (99%)	168 (98%)	3 (2%)	59	77
45	5G	214/258 (83%)	213 (100%)	1 (0%)	88	93
46	5H	63/538 (12%)	63 (100%)	0	100	100
47	5I	416/443 (94%)	413 (99%)	3 (1%)	84	90
48	5J	124/200 (62%)	123 (99%)	1 (1%)	81	89
49	5K	133/169 (79%)	133 (100%)	0	100	100
50	RD	226/1544 (15%)	222 (98%)	4 (2%)	59	77
51	RE	994/1125 (88%)	987 (99%)	7 (1%)	84	90
52	RF	221/274 (81%)	220 (100%)	1 (0%)	88	93
53	RG	195/222 (88%)	192 (98%)	3 (2%)	65	80
53	RH	206/222 (93%)	204 (99%)	2 (1%)	76	86
54	RJ	654/1039 (63%)	642 (98%)	12 (2%)	59	77
55	RK	307/312 (98%)	304 (99%)	3 (1%)	76	86
56	RN	435/732 (59%)	431 (99%)	4 (1%)	78	88
57	RO	329/506 (65%)	327 (99%)	2 (1%)	86	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	RP	556/2307 (24%)	550 (99%)	6 (1%)	73	85
59	RQ	206/808 (26%)	204 (99%)	2 (1%)	76	86
60	RS	225/421 (53%)	225 (100%)	0	100	100
61	RT	178/282 (63%)	178 (100%)	0	100	100
63	RZ	717/1140 (63%)	712 (99%)	5 (1%)	84	90
66	R5	255/266 (96%)	255 (100%)	0	100	100
67	R1	210/218 (96%)	207 (99%)	3 (1%)	67	81
68	R3	282/349 (81%)	281 (100%)	1 (0%)	91	94
69	R6	196/197 (100%)	196 (100%)	0	100	100
70	R2	237/240 (99%)	237 (100%)	0	100	100
71	M3	181/219 (83%)	180 (99%)	1 (1%)	86	92
72	R0	194/209 (93%)	194 (100%)	0	100	100
73	r4	243/311 (78%)	242 (100%)	1 (0%)	91	94
74	C4	174/240 (72%)	172 (99%)	2 (1%)	73	85
75	R4	812/901 (90%)	808 (100%)	4 (0%)	88	93
76	r6	150/671 (22%)	150 (100%)	0	100	100
77	R7	99/168 (59%)	98 (99%)	1 (1%)	76	86
78	M4	810/953 (85%)	804 (99%)	6 (1%)	84	90
79	M6	25/168 (15%)	25 (100%)	0	100	100
All	All	21859/33364 (66%)	21691 (99%)	168 (1%)	82	89

5 of 168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	RJ	92	ARG
59	RQ	808	PHE
54	RJ	230	MET
56	RN	116	ARG
67	R1	86	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 291 such sidechains are listed below:

Mol	Chain	Res	Type
57	RO	472	HIS

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Mol	Chain	Res	Type
78	M4	832	ASN
59	RQ	876	GLN
70	R2	183	ASN
34	B1	128	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	202/333 (60%)	78 (38%)	4 (1%)
2	5A	110/700 (15%)	42 (38%)	0
3	SA	1315/1812 (72%)	510 (38%)	20 (1%)
All	All	1627/2845 (57%)	630 (38%)	24 (1%)

5 of 630 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	3	C
1	3A	4	G
1	3A	23	U
1	3A	24	U
1	3A	25	U

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	773	C
3	SA	1063	U
3	SA	1052	U
3	SA	1490	C
3	SA	136	C

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 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
81	GTP	RJ	1201	82	26,34,34	1.20	1 (3%)	32,54,54	1.70	7 (21%)
83	ADP	RZ	1301	-	24,29,29	0.96	1 (4%)	29,45,45	1.37	4 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	GTP	RJ	1201	82	-	5/18/38/38	0/3/3/3
83	ADP	RZ	1301	-	-	4/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	RJ	1201	GTP	C5-C6	-4.23	1.38	1.47
83	RZ	1301	ADP	C5-C4	2.45	1.47	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	RJ	1201	GTP	PA-O3A-PB	-4.49	117.41	132.83
81	RJ	1201	GTP	PB-O3B-PG	-4.12	118.69	132.83
83	RZ	1301	ADP	N3-C2-N1	-3.40	123.36	128.68
81	RJ	1201	GTP	C5-C6-N1	3.36	119.88	113.95
81	RJ	1201	GTP	C8-N7-C5	3.10	108.89	102.99

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

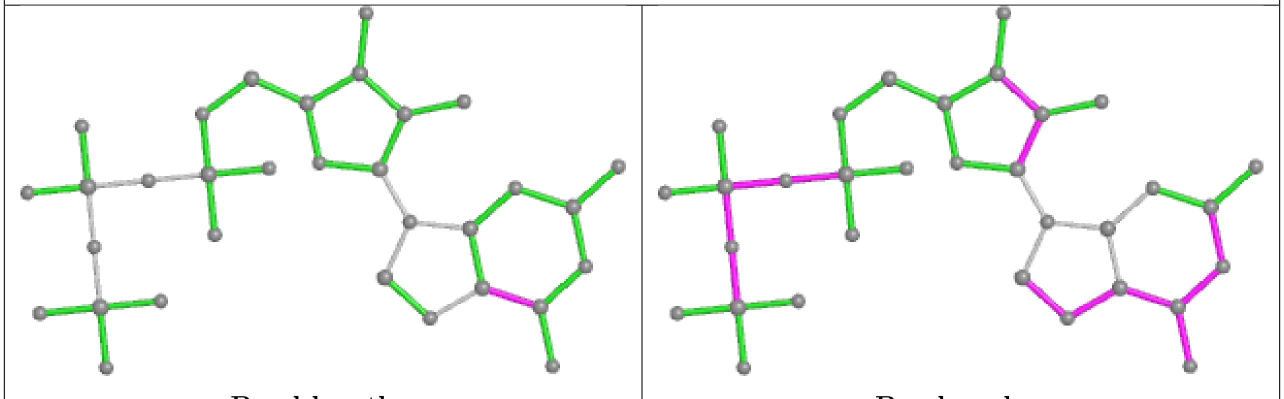
Mol	Chain	Res	Type	Atoms
83	RZ	1301	ADP	C5'-O5'-PA-O2A
83	RZ	1301	ADP	C5'-O5'-PA-O3A
81	RJ	1201	GTP	O4'-C4'-C5'-O5'
81	RJ	1201	GTP	C3'-C4'-C5'-O5'
81	RJ	1201	GTP	PA-O3A-PB-O2B

There are no ring outliers.

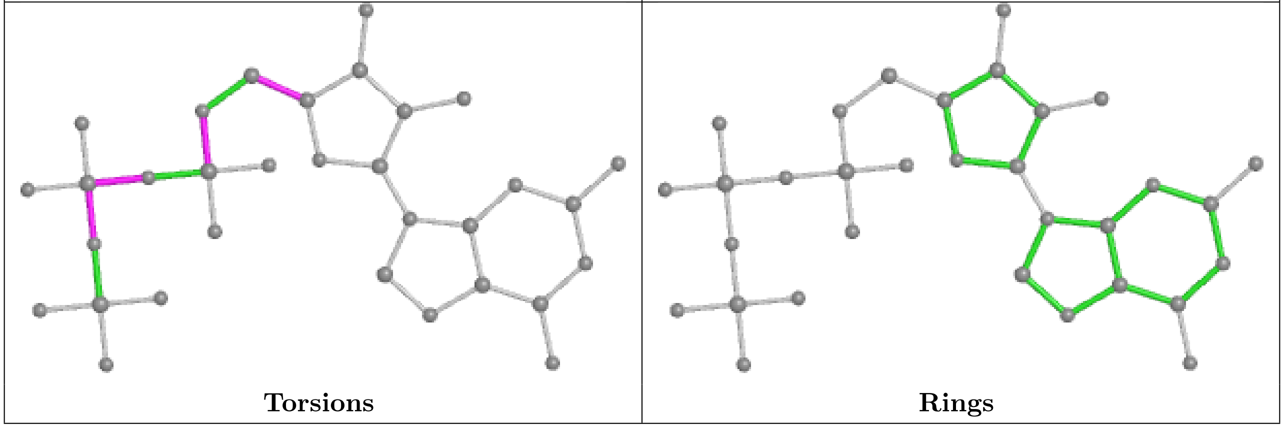
No monomer is involved in short contacts.

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 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.

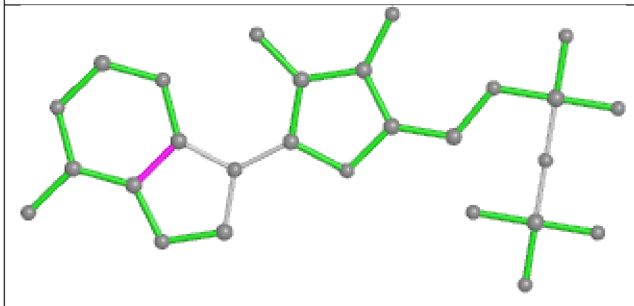
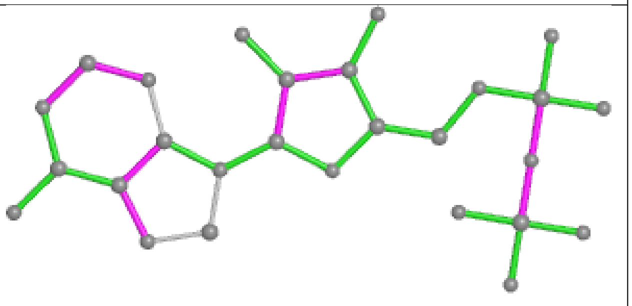
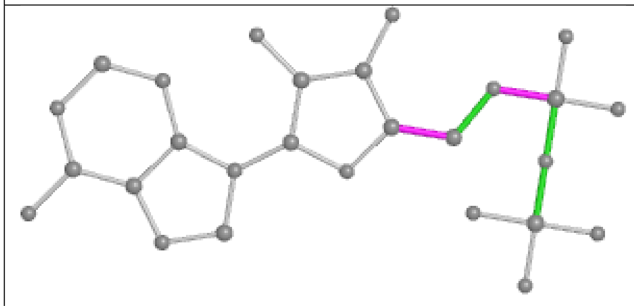
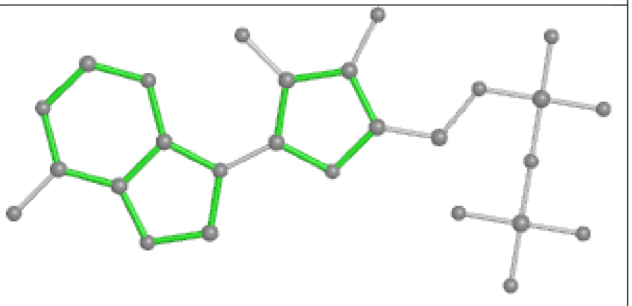
Ligand GTP RJ 1201



Bond lengths **Bond angles**



Torsions **Rings**

Ligand ADP RZ 1301	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.

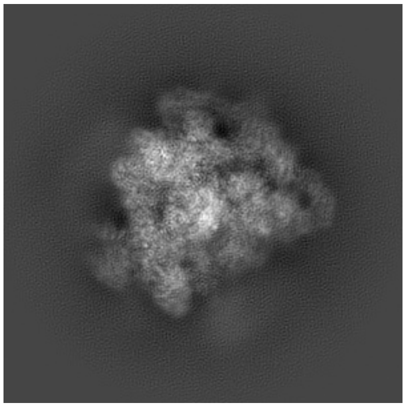
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-30574. These allow visual inspection of the internal detail of the map and identification of artifacts.

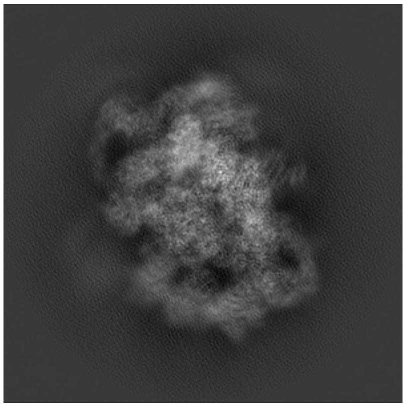
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

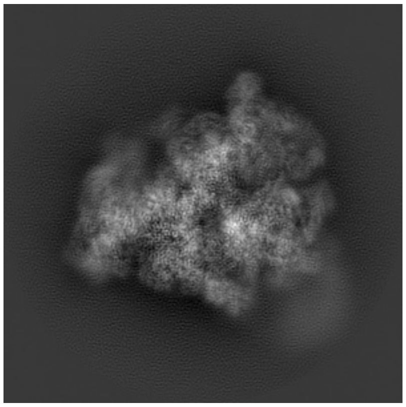
6.1.1 Primary map



X



Y

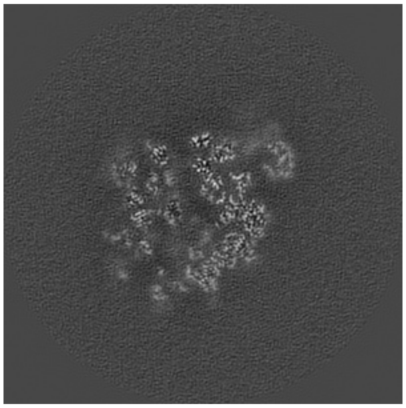


Z

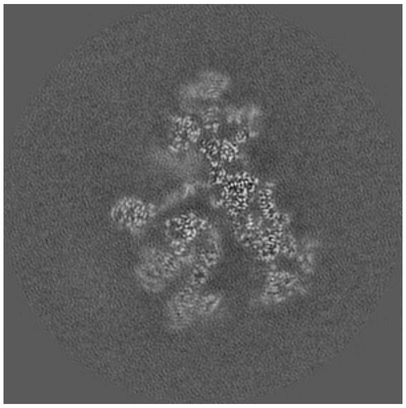
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

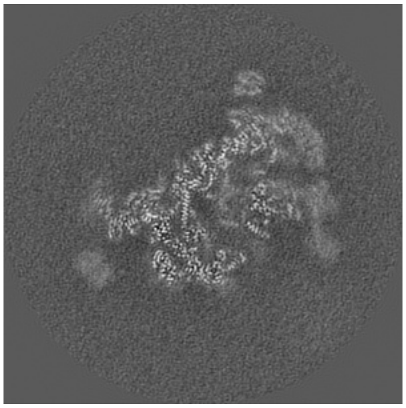
6.2.1 Primary map



X Index: 200



Y Index: 200

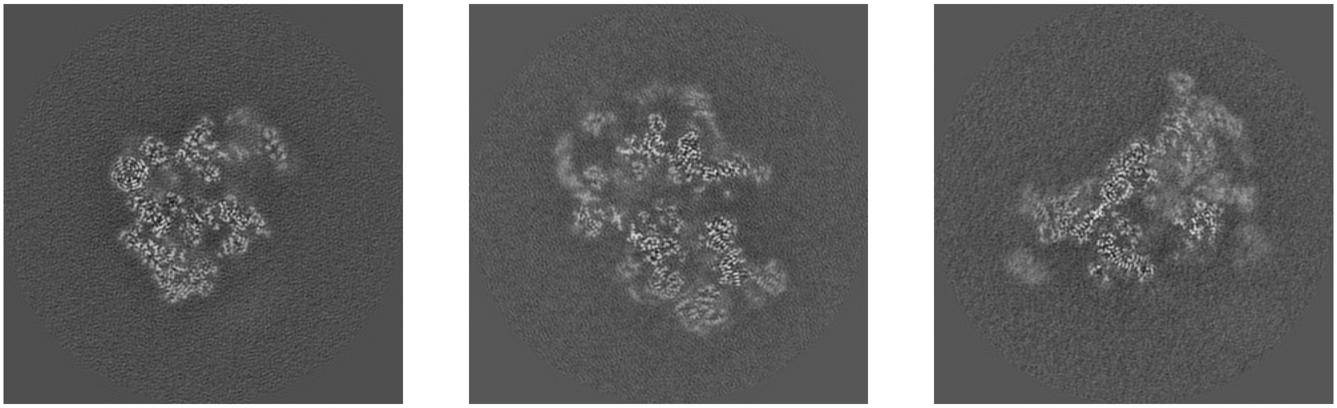


Z Index: 200

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: 186

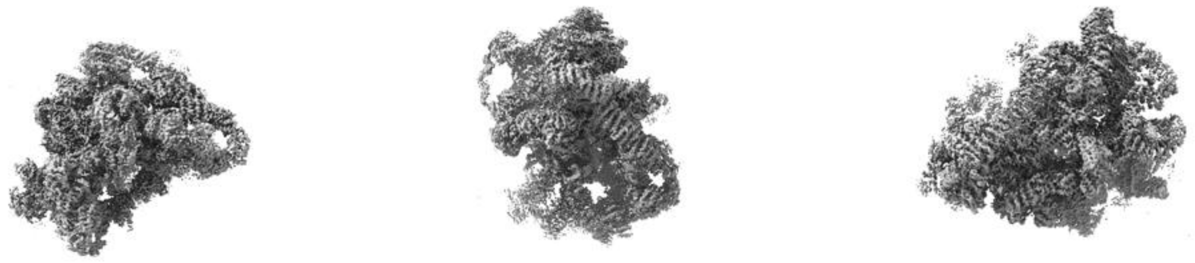
Y Index: 178

Z Index: 192

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

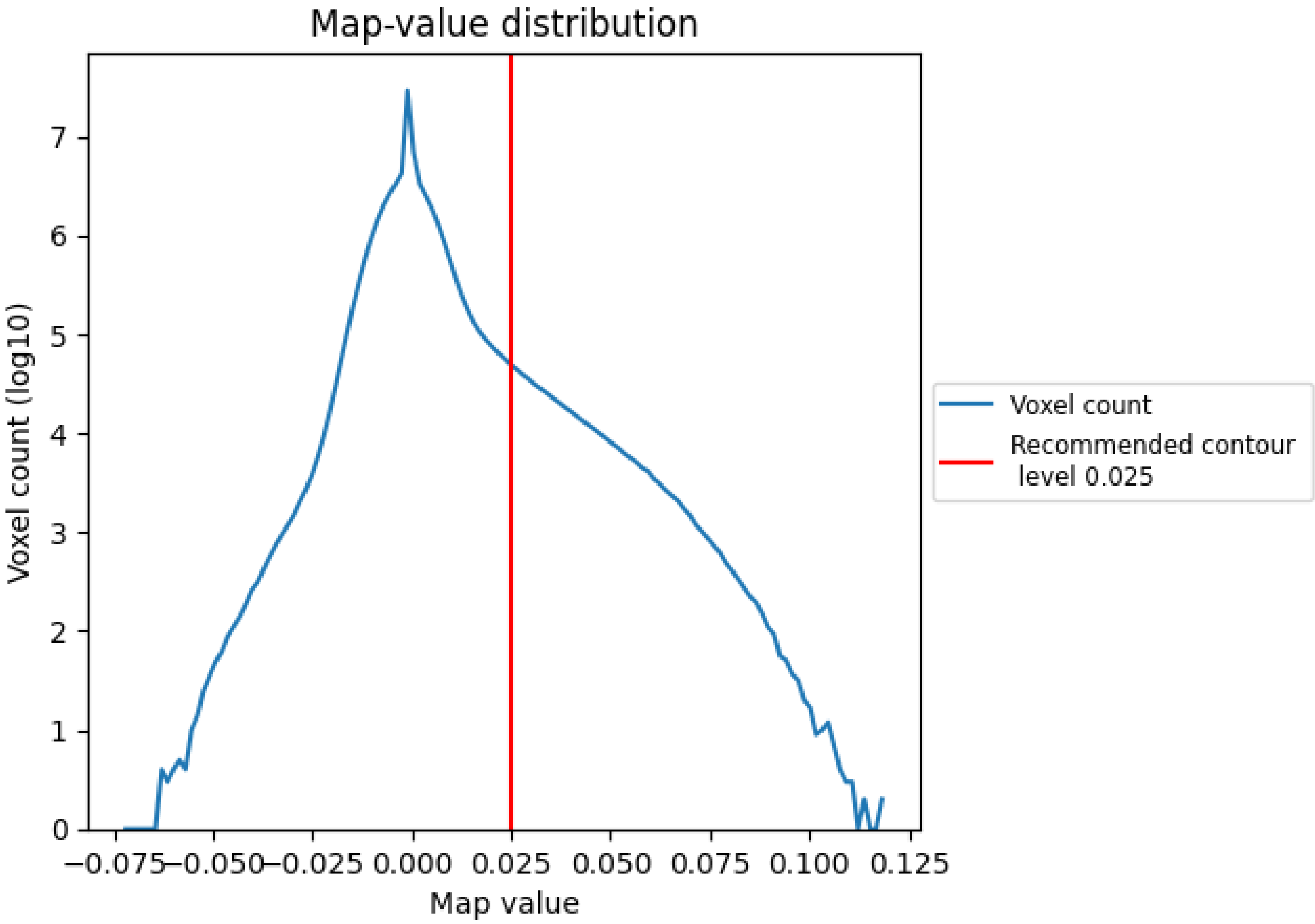
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

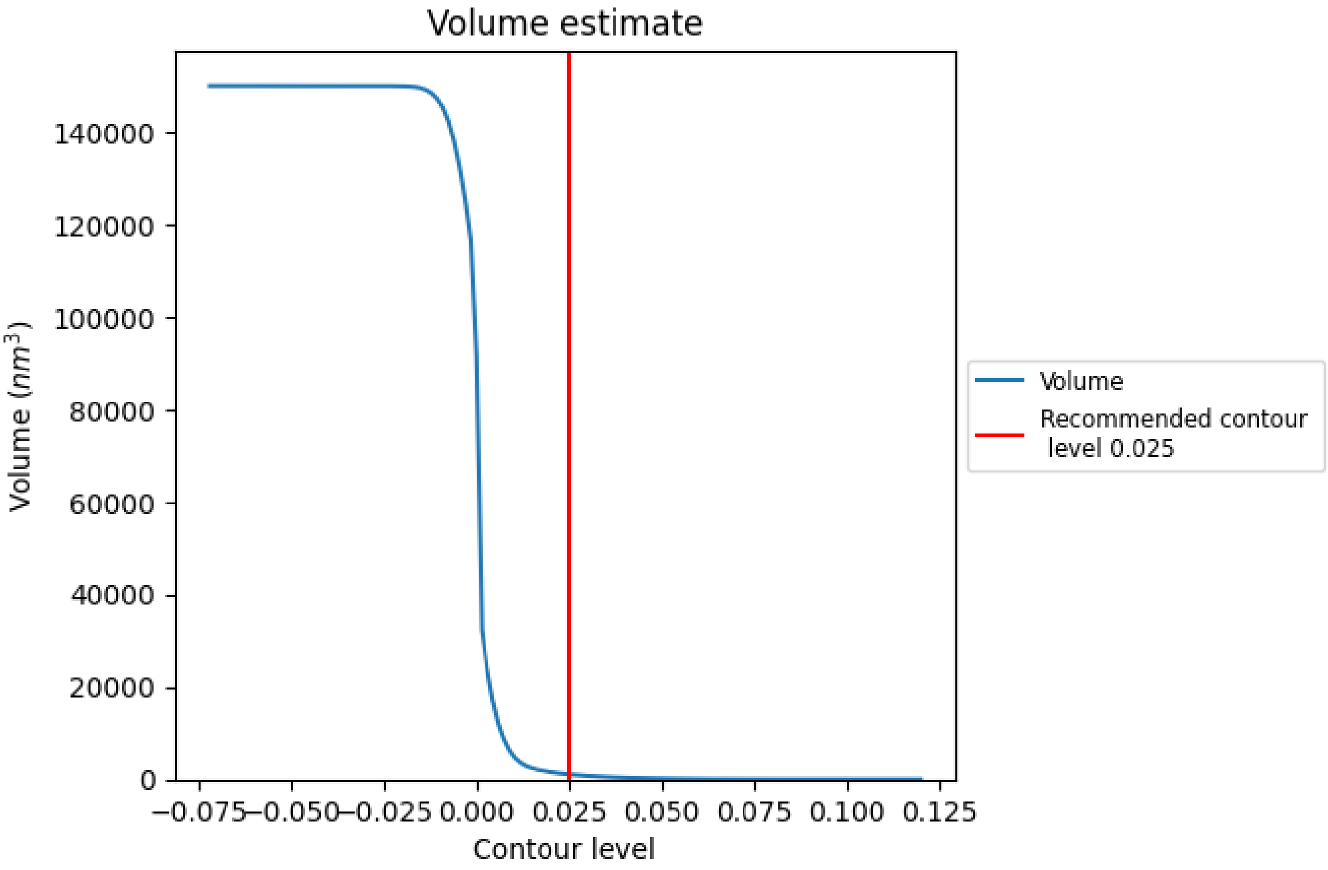
This section contains the results of statistical analysis of the map.

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.

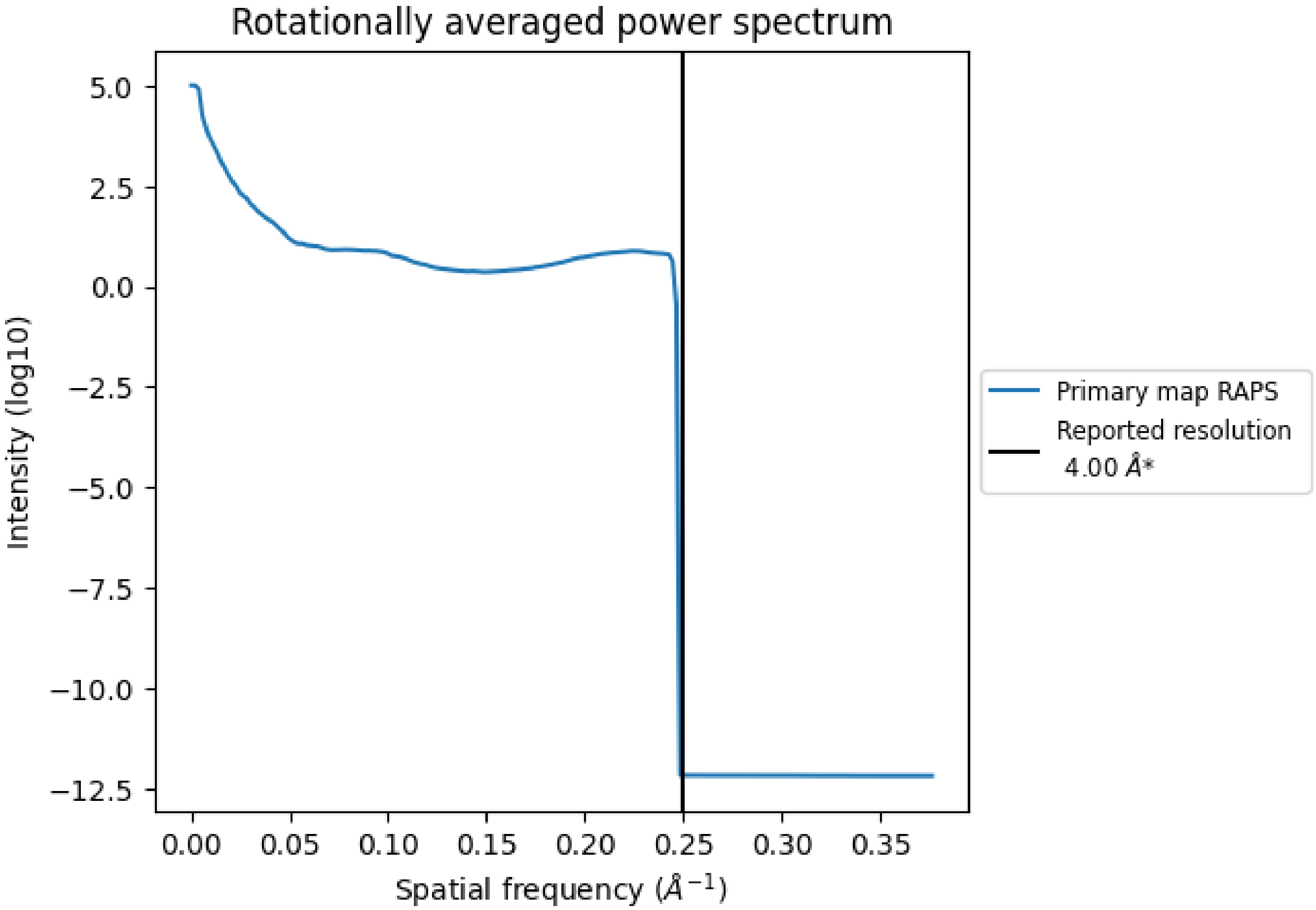
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1074 nm^3; this corresponds to an approximate mass of 970 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 0.250 Å^{-1}

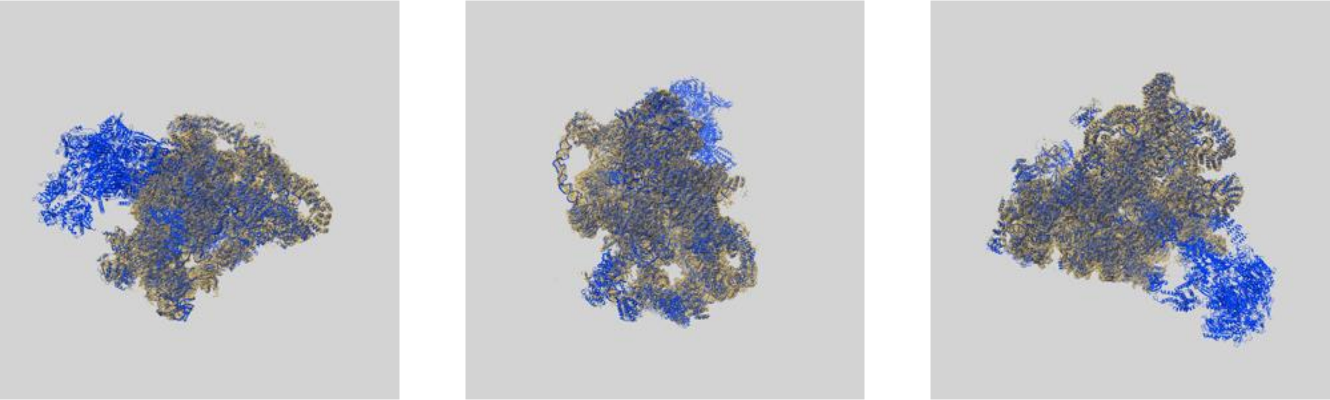
8 Fourier-Shell correlation ⓘ

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-30574 and PDB model 7D4I. Per-residue inclusion information can be found in section 3 on page 20.

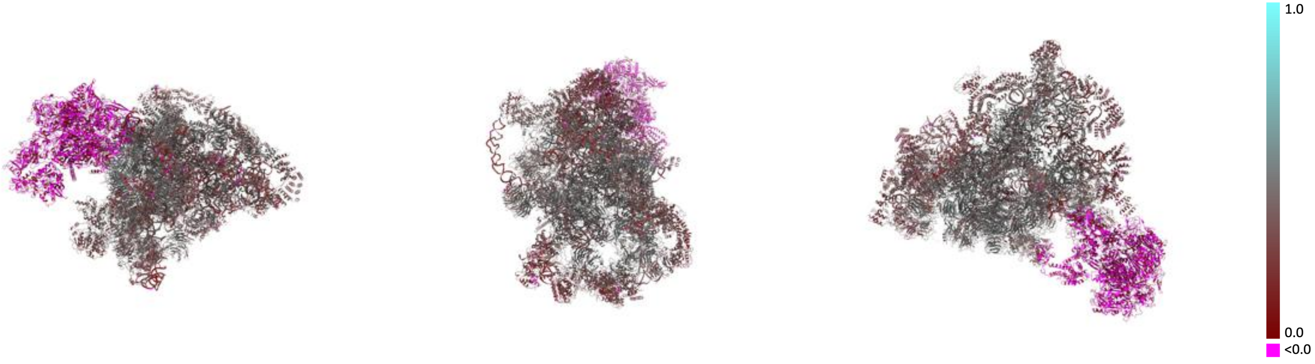
9.1 Map-model overlay



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.025 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.

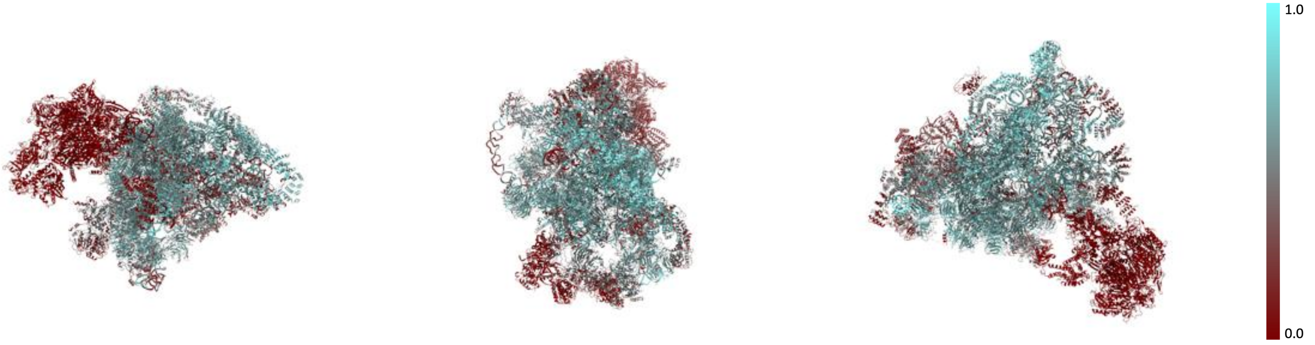
9.2 Q-score mapped to coordinate model ⓘ



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.

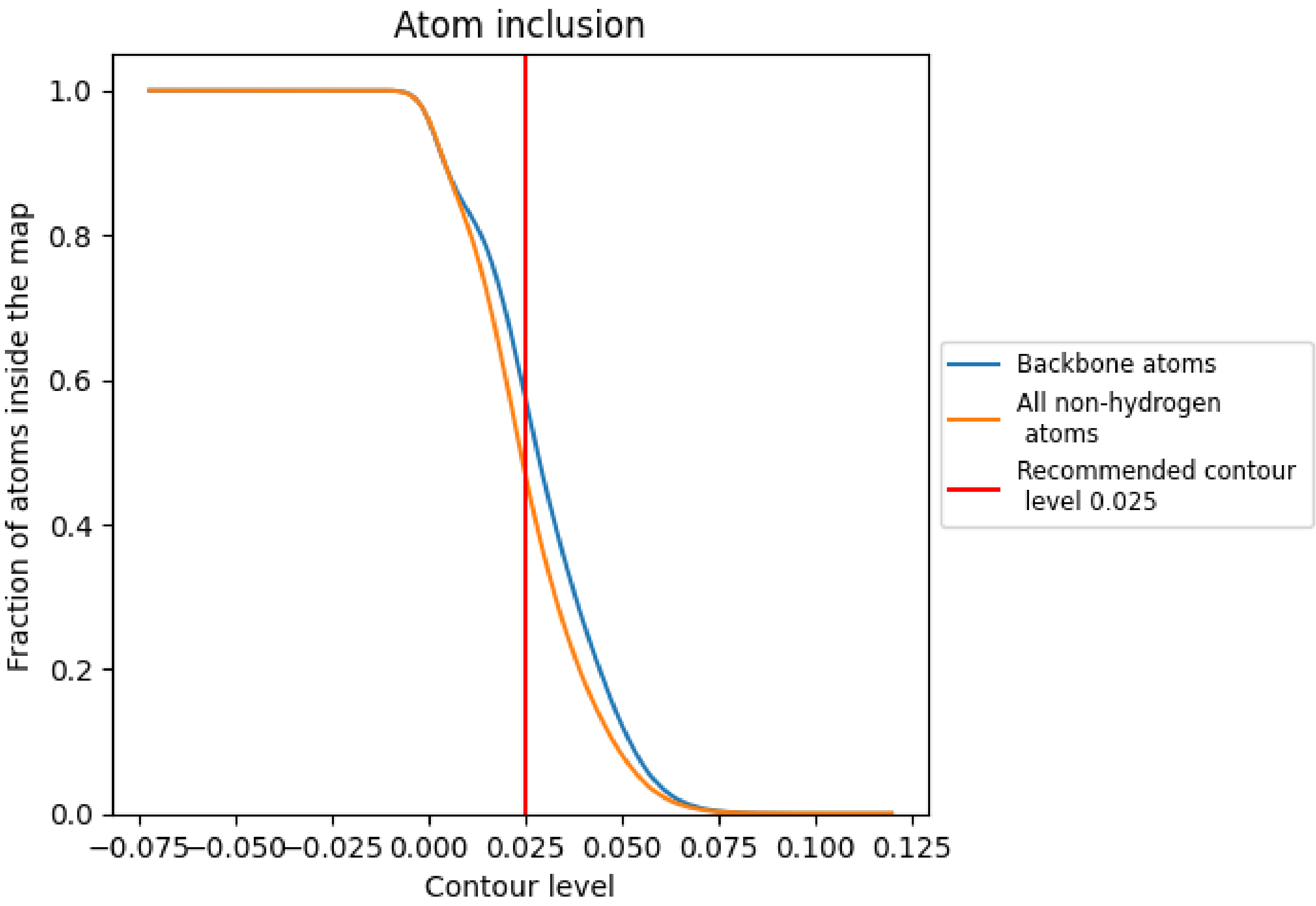
9.3 Atom inclusion mapped to coordinate model ⓘ



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 (0.025).

9.4 Atom inclusion ⓘ



At the recommended contour level, 58% of all backbone atoms, 47% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4723	0.3390
3A	0.6875	0.3800
3B	0.7032	0.4820
3C	0.6511	0.4460
3D	0.6824	0.4450
3E	0.6469	0.4270
3F	0.6890	0.4600
3G	0.6460	0.4550
3H	0.6858	0.4620
5A	0.4290	0.2980
5B	0.4732	0.4040
5C	0.6099	0.4530
5D	0.5588	0.4350
5E	0.5352	0.4230
5F	0.4976	0.4190
5G	0.6040	0.4550
5H	0.6422	0.4620
5I	0.6999	0.4760
5J	0.5669	0.4540
5K	0.6692	0.4760
A4	0.6528	0.4270
A5	0.5791	0.4240
A8	0.1932	0.3060
A9	0.4449	0.3310
AE	0.5486	0.3640
AF	0.5387	0.4190
AG	0.5808	0.4120
B1	0.6430	0.4640
B2	0.6441	0.4170
B3	0.6321	0.4210
B6	0.6328	0.4130
B8	0.6833	0.4570
BE	0.6634	0.4540
C4	0.0000	0.0140
M3	0.0000	0.0020

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Chain	Atom inclusion	Q-score
M4	0.0000	0.0070
M6	0.0000	-0.0180
R0	0.0000	0.0240
R1	0.0000	-0.0040
R2	0.0000	-0.0020
R3	0.0000	-0.0050
R4	0.0000	-0.0040
R5	0.0000	-0.0020
R6	0.0000	0.0200
R7	0.0000	-0.0180
RD	0.0438	0.2830
RE	0.5242	0.3780
RF	0.4603	0.3590
RG	0.1548	0.3120
RH	0.2784	0.3730
RJ	0.6415	0.4430
RK	0.6323	0.4350
RN	0.1619	0.3150
RO	0.2538	0.3260
RP	0.5767	0.3540
RQ	0.4825	0.4150
RS	0.0673	0.2410
RT	0.5494	0.4390
RW	0.5617	0.3770
RZ	0.3569	0.3490
SA	0.6215	0.3510
SC	0.6416	0.4550
SF	0.5579	0.4330
SG	0.6223	0.4540
SH	0.2821	0.3650
SI	0.4954	0.3850
SJ	0.2726	0.3480
SK	0.6779	0.4600
SM	0.1885	0.3280
SO	0.6663	0.4340
SP	0.6449	0.4560
SR	0.6688	0.4730
ST	0.3580	0.3880
SU	0.4626	0.4250
SX	0.6487	0.4510
SY	0.6184	0.4530
SZ	0.6587	0.4520

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Chain	Atom inclusion	Q-score
Sc	▬ 0.6706	▬ 0.4620
Sd	▬ 0.6625	▬ 0.4830
X1	▬ 0.4407	▬ 0.3940
X2	▬ 0.1574	▬ 0.3330
r4	▬ 0.0000	▬ 0.0010
r6	▬ 0.0000	▬ 0.0010