wwPDB EM Validation Summary Report (i)

Mar 17, 2026 – 08:20 PM UTC

PDB ID	:	6LQS / pdb_00006lqs
EMDB ID	:	EMD-0952
Title	:	Cryo-EM structure of 90S small subunit preribosomes in transition states (State D)
Authors	:	Du, Y.; Ye, K.
Deposited on	:	2020-01-14
Resolution	:	3.80 Å(reported)
Based on initial model	:	6LQP

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

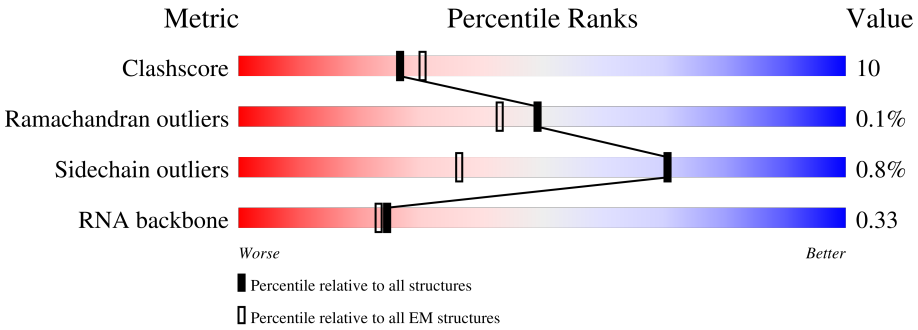
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

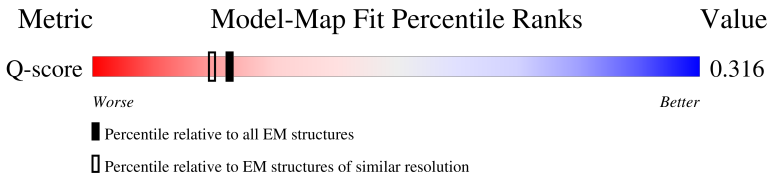
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 Å.

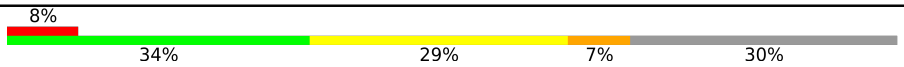
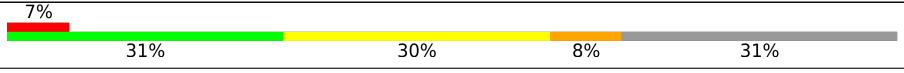
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	1809	

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Mol	Chain	Length	Quality of chain
4	SC	255	69% 21% 9%
5	SF	261	75% 20%
6	SG	225	81% 13% 5%
7	SH	236	13% 56% 21% 23%
8	SI	190	5% 57% 27% 14%
9	SJ	200	9% 52% 18% 30%
10	SK	197	68% 19% 13%
11	SM	156	28% 63% 25% 12%
12	SO	151	69% 19% 11%
13	SP	137	66% 20% 14%
14	SR	143	69% 18% 13%
15	SX	130	70% 28%
16	SY	145	59% 14% 27%
17	SZ	135	69% 21% 9%
18	Sc	82	68% 28%
19	Sd	67	85% 9% 6%
20	3B	327	53% 20% 27%
20	3C	327	7% 46% 22% 31%
21	3D	504	60% 15% 25%
22	3E	511	65% 19% 15%
23	3F	573	55% 21% 24%
24	3G	126	72% 24%
24	3H	126	70% 26%
25	A4	776	54% 31% 14%
26	A5	643	18% 58% 21% 21%

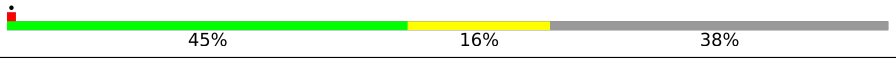
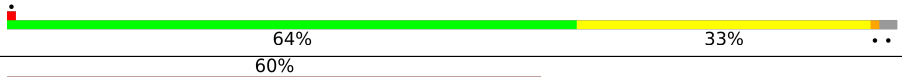
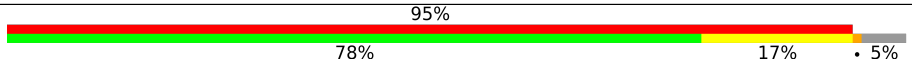
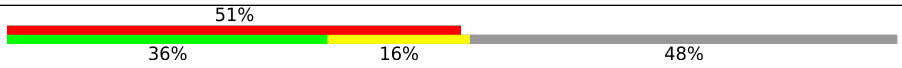
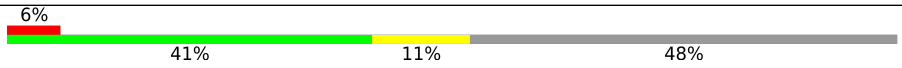
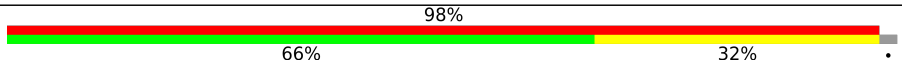
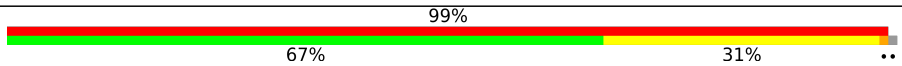
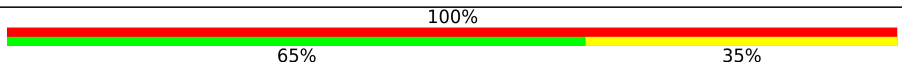
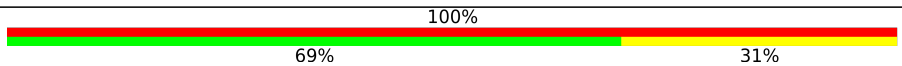
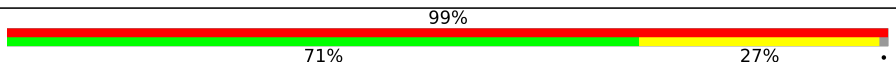
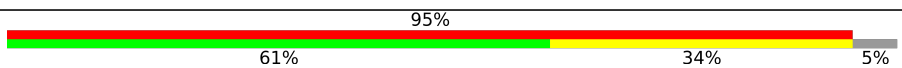
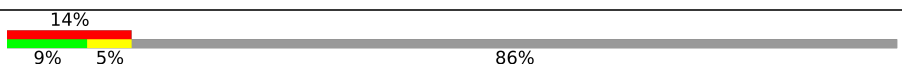
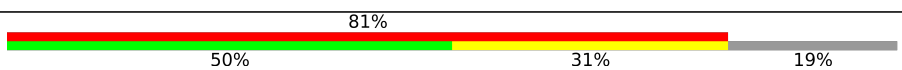
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Mol	Chain	Length	Quality of chain
27	A8	713	48% 67% 10% 23%
28	A9	575	7% 17% 5% 78%
29	AE	1769	20% 75% 11% 13%
30	AF	513	17% 66% 28% 7%
31	AG	896	6% 62% 29% 8%
32	B1	900	68% 21% 10%
33	B2	943	62% 25% 13%
34	B3	817	64% 28% 7%
35	B8	594	59% 21% 20%
36	BE	939	63% 24% 12%
37	B6	440	71% 14% 15%
38	5B	214	13% 22% 6% 72%
39	5C	554	66% 16% 17%
40	5D	250	32% 64% 17% 18%
41	5E	593	24% 8% 67%
42	5F	183	76% 23%
43	5G	290	56% 19% 26%
44	5H	610	11% 88%
45	5I	489	68% 25% 6%
46	5J	217	5% 50% 12% 38%
47	5K	189	72% 16% 12%
48	RD	1729	11% 16% 82%
49	RE	1237	62% 25% 12%
50	RF	297	7% 59% 21% 19%
51	RG	252	81% 58% 27% 14%

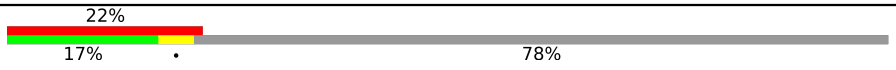
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Mol	Chain	Length	Quality of chain
51	RH	252	
52	RJ	1183	
53	RK	367	
54	RN	810	
55	RO	552	
56	RP	2493	
57	RQ	899	
58	RS	480	
59	RT	326	
60	RW	206	
61	X1	347	
62	X2	694	
63	R5	305	
64	R1	246	
65	R3	394	
66	R6	223	
67	R2	265	
68	M3	250	
69	R0	240	
70	r4	359	
71	C4	292	
72	R4	1001	
73	r6	733	
74	R7	184	
75	M4	1073	

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Mol	Chain	Length	Quality of chain
76	M6	186	

2 Entry composition (i)

There are 79 unique types of molecules in this entry. The entry contains 238320 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	234	4962	2220	863	1645	234	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5A	152	3260	1455	593	1060	152	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1249	26609	11894	4706	8760	1249	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	232	1848	1168	339	337	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	250	1930	1232	354	341	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
			1457	917	273	266	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	SI	164	Total	C	N	O	0	0
			1310	847	222	241		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	140	Total	C	N	O	S	0	0
			1104	689	211	202	2		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	106	Total 807	C 515	N 148	O 142	S 2	0	0

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3D	378	Total	C	N	O	S	0	0
			2974	1886	511	568	9		

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3E	432	Total	C	N	O	S	0	0
			3041	1895	545	592	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3F	437	Total	C	N	O	S	0	0
			3498	2227	609	652	10		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A4	664	Total	C	N	O	S	0	0
			5243	3320	912	990	21		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AE	1534	Total	C	N	O	S	0	0
			9956	6243	1771	1923	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	479	Total	C	N	O	S	0	0
			3807	2395	685	715	12		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B1	806	Total	C	N	O	S	0	0
			6427	4104	1099	1205	19		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BE	823	Total	C	N	O	S	0	0
			6475	4107	1119	1228	21		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5D	204	Total	C	N	O	S	0	0
			1733	1082	340	306	5		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5G	216	Total	C	N	O	S	0	0
			1732	1093	321	312	6		

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

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

- Molecule 45 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5I	460	Total	C	N	O	S	0	0
			3756	2349	685	706	16		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	134	Total	C	N	O	S	0	0
			1127	712	205	207	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5K	166	Total	C	N	O	S	0	0
			1323	849	238	226	10		

- Molecule 48 is a protein called rRNA biogenesis protein RRP5.

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

- Molecule 49 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 50 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 51 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 52 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RJ	731	Total	C	N	O	S	0	0
			5935	3812	1051	1046	26		

- Molecule 53 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 54 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RN	553	Total	C	N	O	S	0	0
			4088	2590	731	758	9		

- Molecule 55 is a protein called Nucleolar complex protein 4.

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

- Molecule 56 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RP	2180	Total	C	N	O	S	0	0
			12716	7827	2389	2484	16		

- Molecule 57 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RQ	226	Total	C	N	O	S	0	0
			1655	1026	314	313	2		

- Molecule 58 is a protein called Essential nuclear protein 1.

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

- Molecule 59 is a protein called Pno1.

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

- Molecule 60 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	RW	150	Total	C	N	O	0	0
			747	447	150	150		

- Molecule 61 is a protein called Unassigned helices 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	X1	80	Total	C	N	O	0	0
			400	240	80	80		

- Molecule 62 is a protein called Unassigned helices 2.

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

- Molecule 63 is a protein called Exosome complex component RRP45.

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

- Molecule 64 is a protein called Exosome complex component SKI6.

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

- Molecule 65 is a protein called Exosome complex component RRP43.

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

- Molecule 66 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	R6	223	Total	C	N	O	S	0	0
			1696	1067	285	334	10		

- Molecule 67 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	R2	265	Total	C	N	O	S	0	0
			2030	1296	334	395	5		

- Molecule 68 is a protein called Exosome complex component MTR3.

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

- Molecule 69 is a protein called Exosome complex component RRP40.

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

- Molecule 70 is a protein called Exosome complex component RRP4.

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

- Molecule 71 is a protein called Exosome complex component CSL4.

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

- Molecule 72 is a protein called Exosome complex exonuclease DIS3.

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

- Molecule 73 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	r6	104	Total	C	N	O	S	0	0
			802	496	144	157	5		

- Molecule 74 is a protein called Exosome complex protein LRP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	R7	85	Total	C	N	O	S	0	0
			681	428	117	132	4		

- Molecule 75 is a protein called ATP-dependent RNA helicase DOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	M4	874	Total	C	N	O	S	0	0
			6814	4354	1166	1254	40		

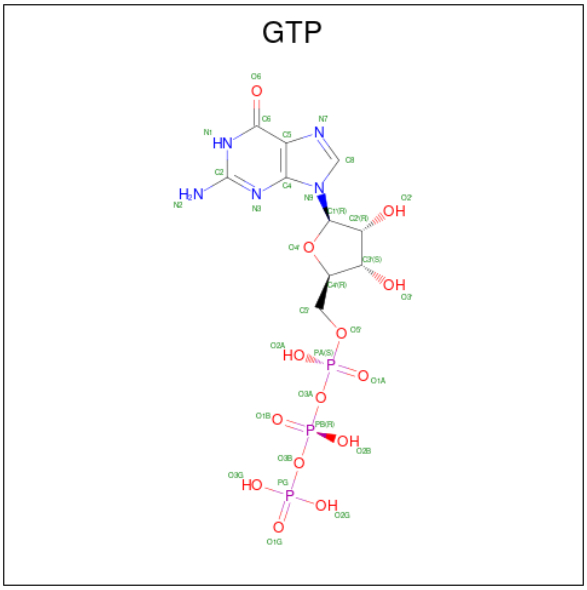
- Molecule 76 is a protein called M-phase phosphoprotein 6 homolog.

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

- Molecule 77 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
77	Sc	1	Total Zn 1 1	0
77	5K	1	Total Zn 1 1	0

- Molecule 78 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

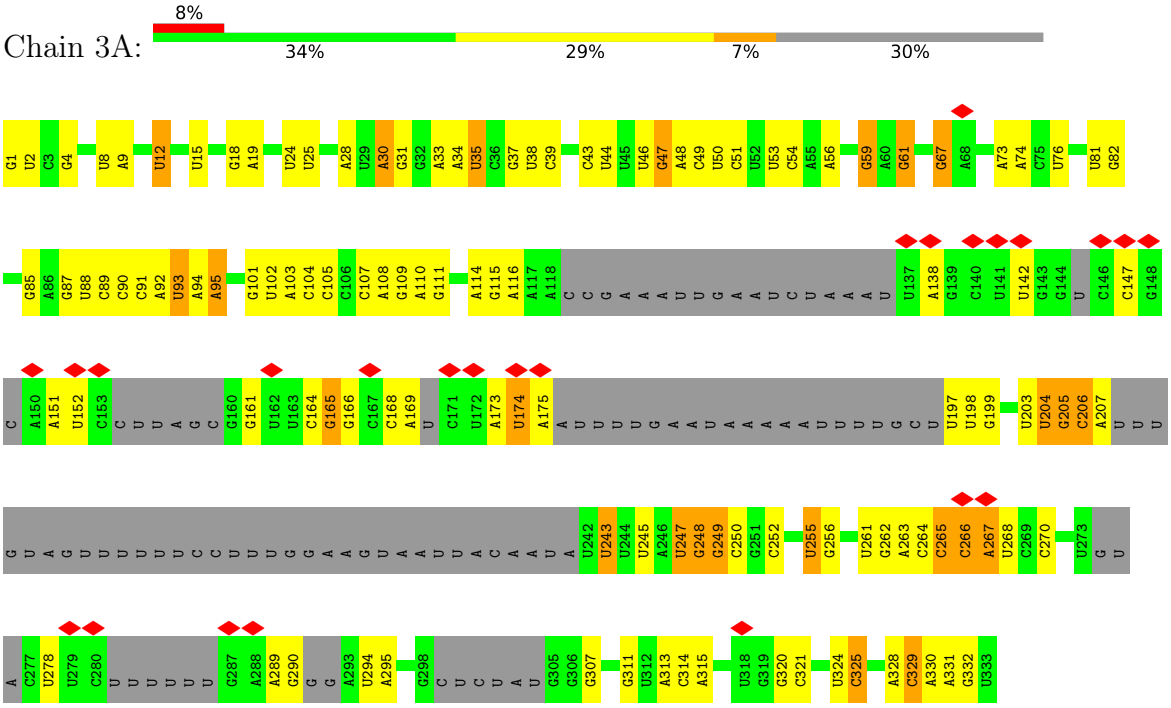
Mol	Chain	Residues	Atoms	AltConf
79	RJ	1	Total Mg 1 1	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

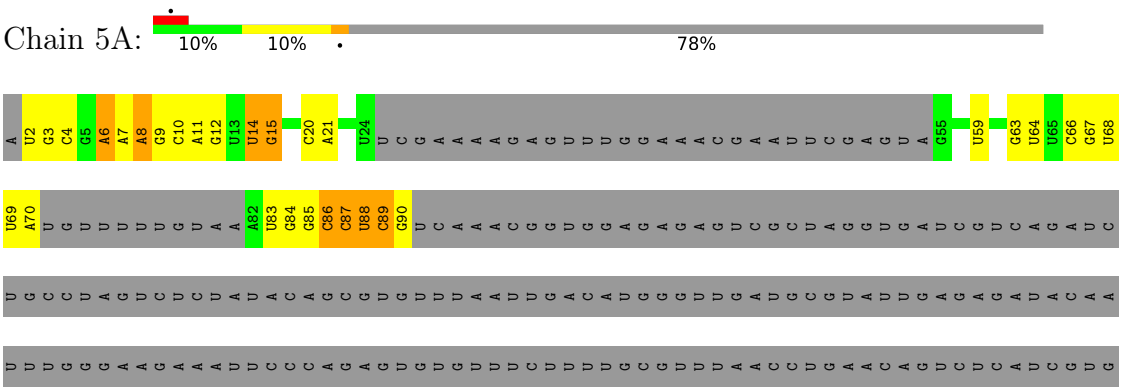
- Molecule 1: U3 snoRNA

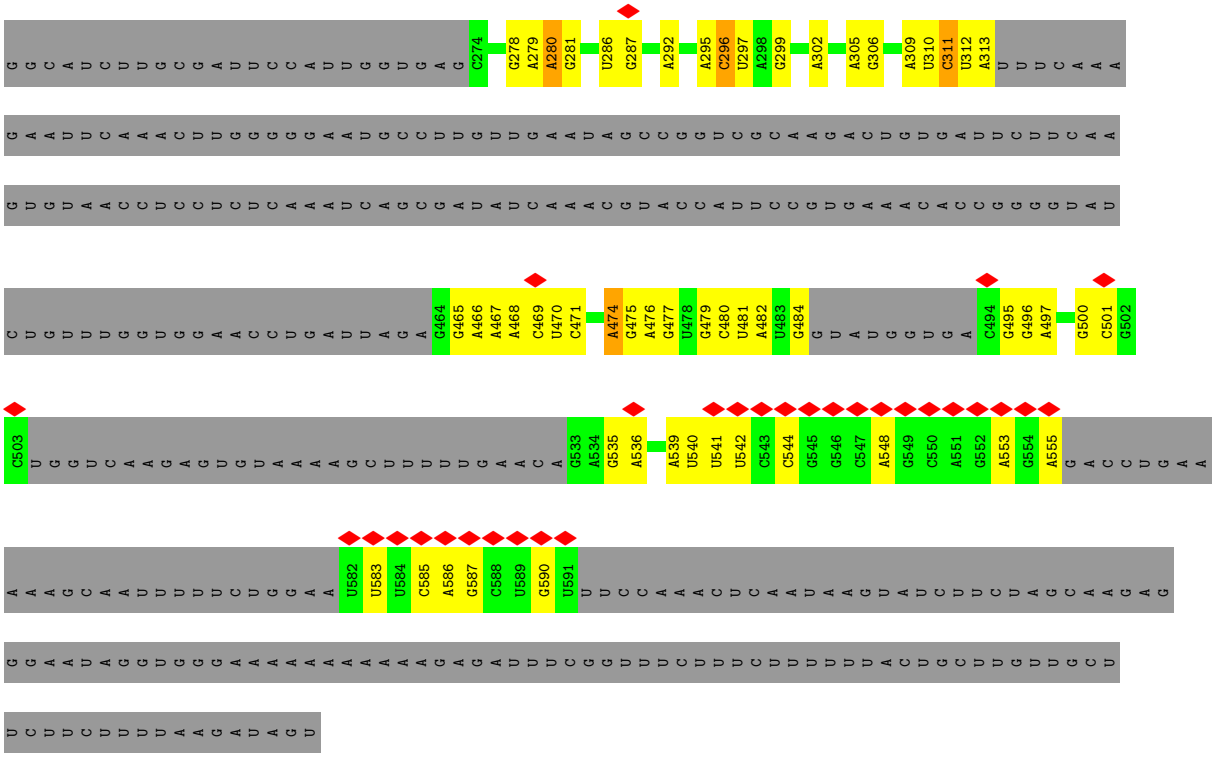
Chain 3A:



- Molecule 2: 5' ETS

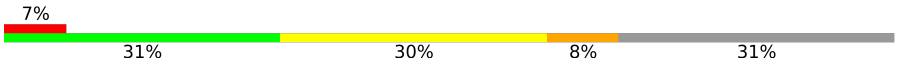
Chain 5A:

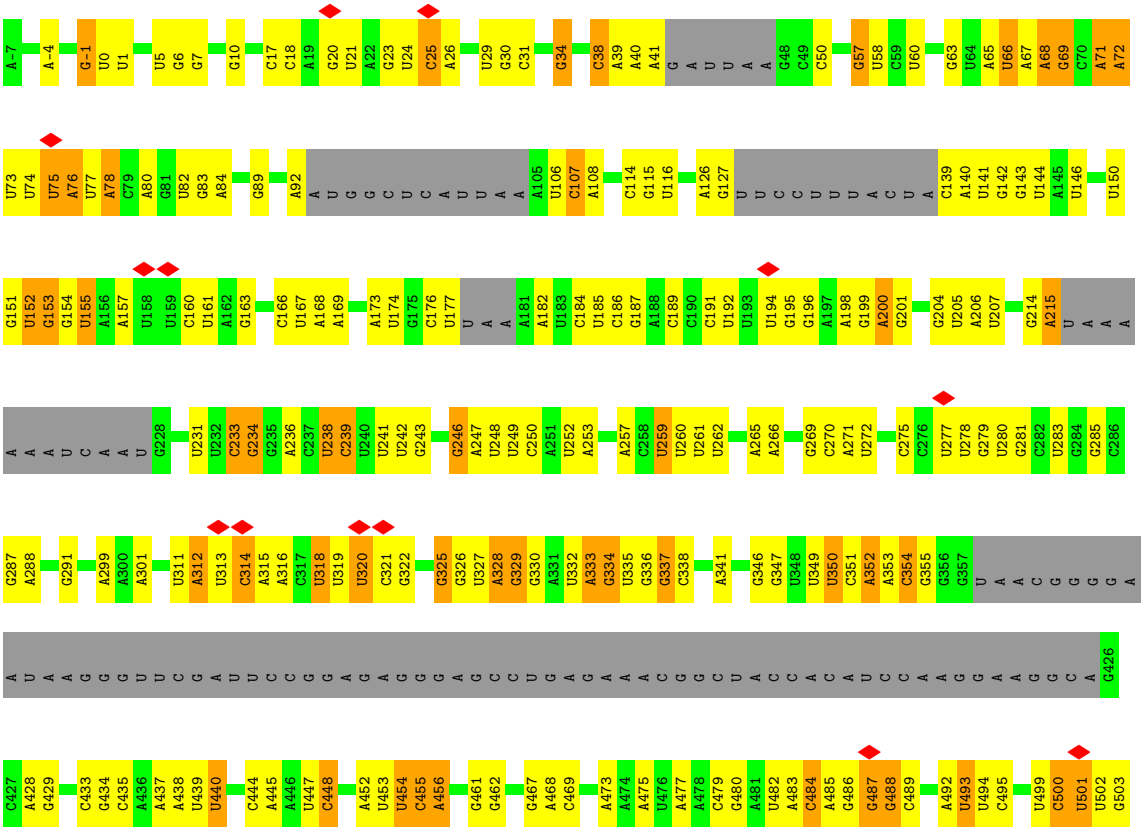


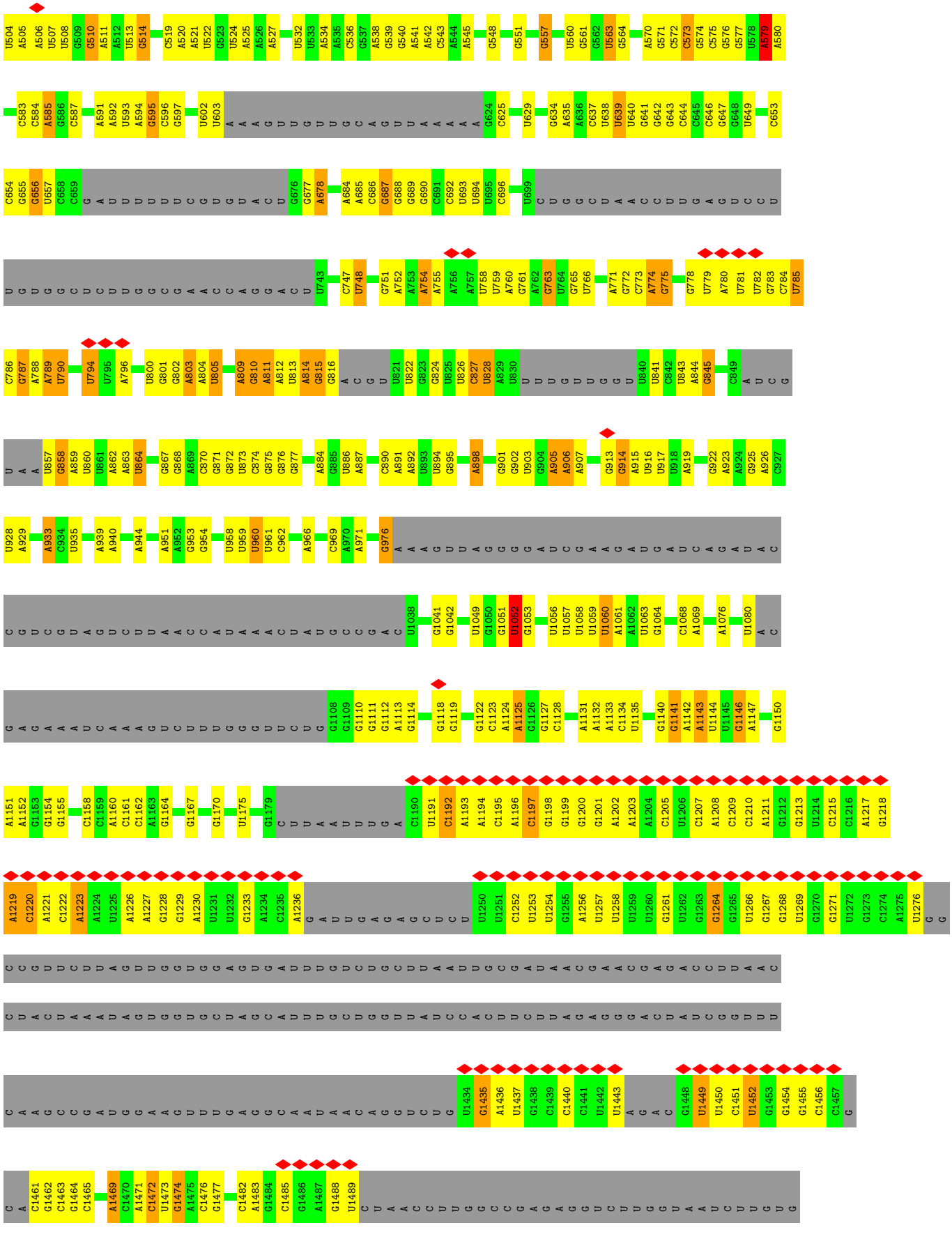


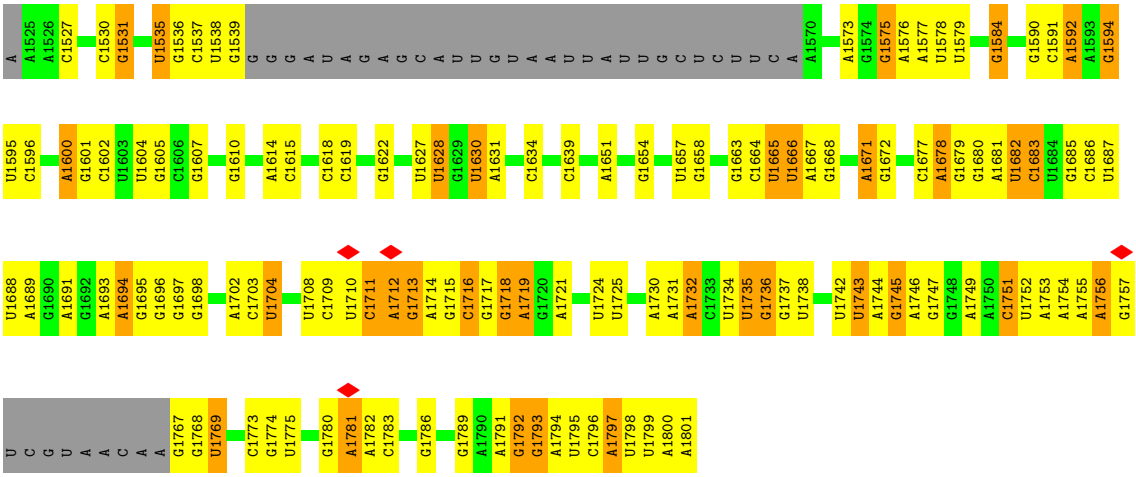
• Molecule 3: 18S pre-rRNA

Chain SA:





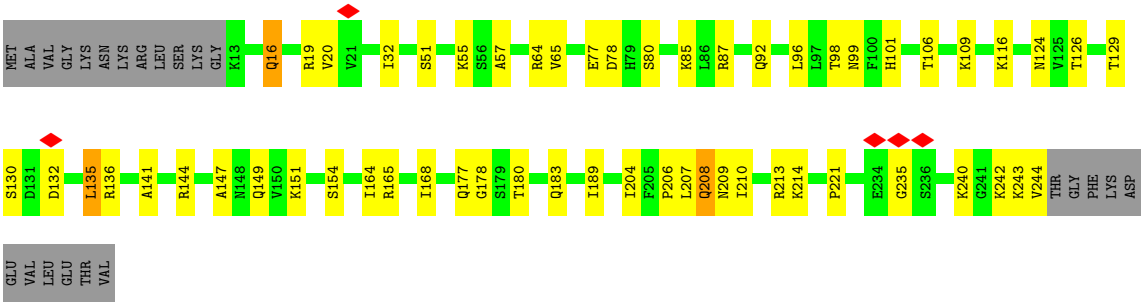




• Molecule 4: 40S ribosomal protein S1-A

Chain SC:

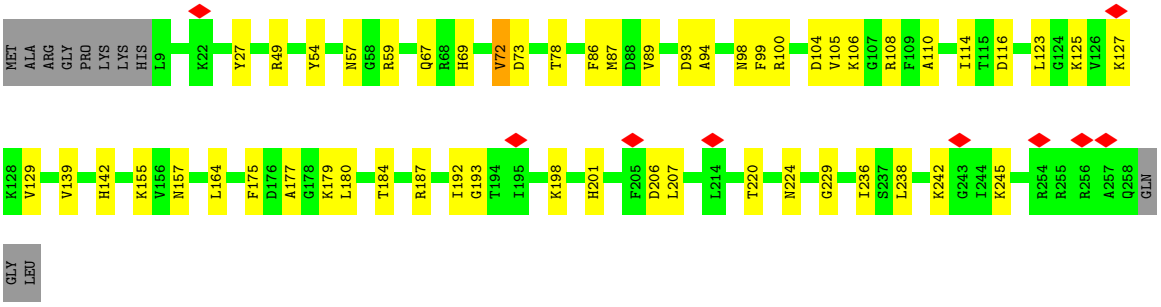




• Molecule 5: 40S ribosomal protein S4-A

Chain SF:

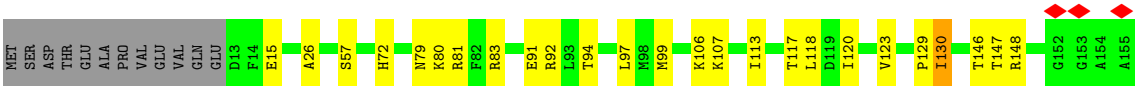




• Molecule 6: 40S ribosomal protein S5

Chain SG:



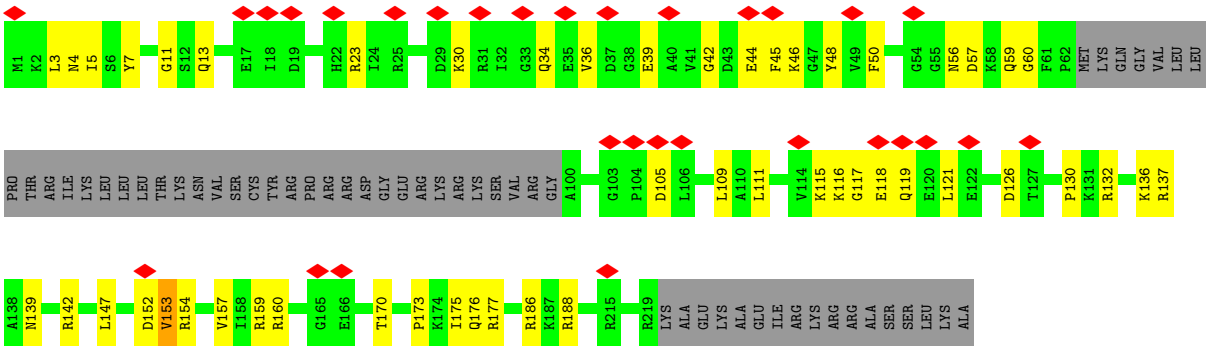




• Molecule 7: 40S ribosomal protein S6-A

Chain SH:

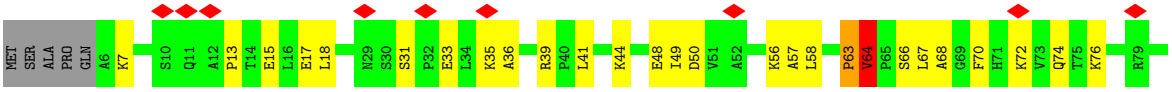


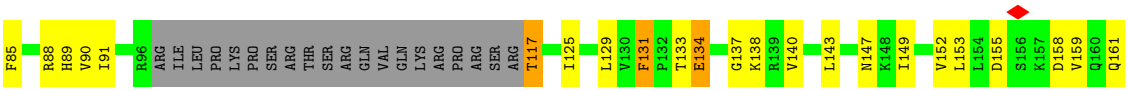


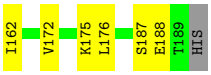
• Molecule 8: 40S ribosomal protein S7-A

Chain SI:



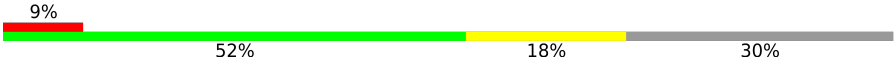


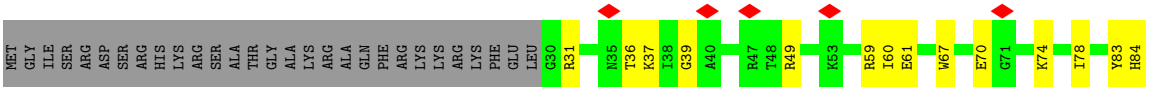


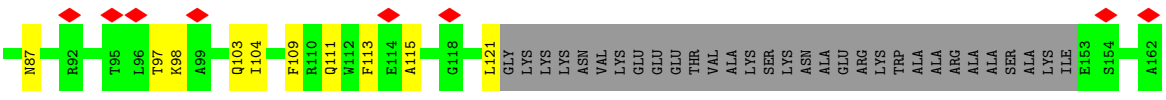


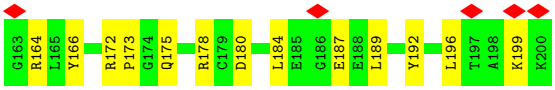
• Molecule 9: 40S ribosomal protein S8-A

Chain SJ:





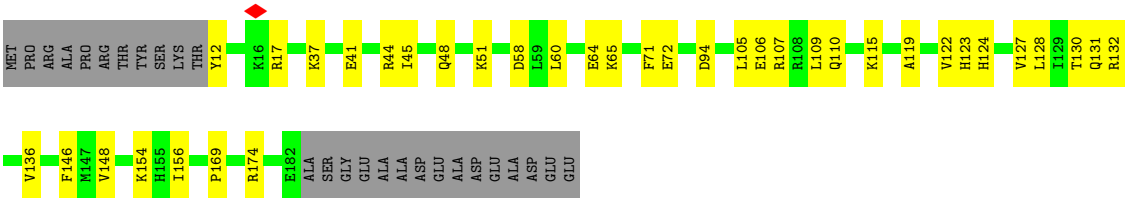




• Molecule 10: 40S ribosomal protein S9-A

Chain SK:

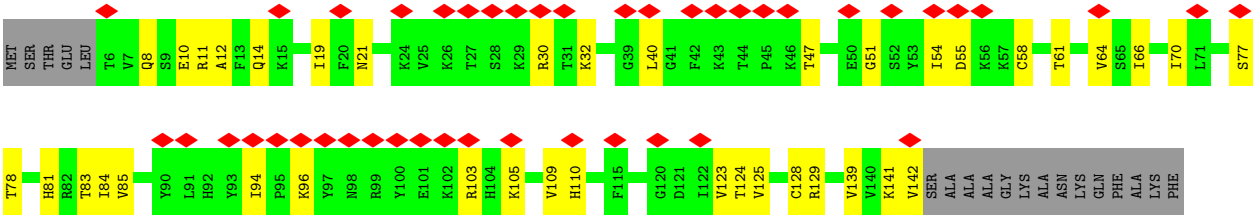




• Molecule 11: 40S ribosomal protein S11-A

Chain SM:

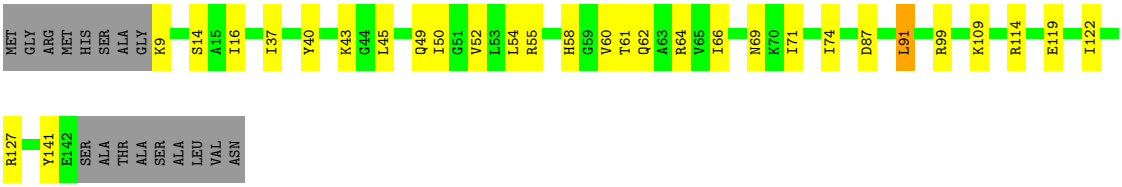




• Molecule 12: 40S ribosomal protein S13

Chain SO:

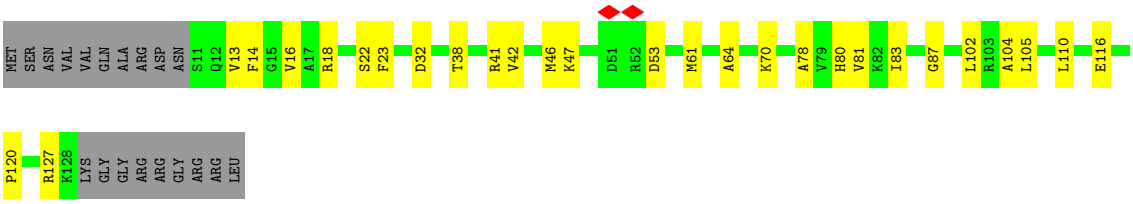




• Molecule 13: 40S ribosomal protein S14-A

Chain SP:

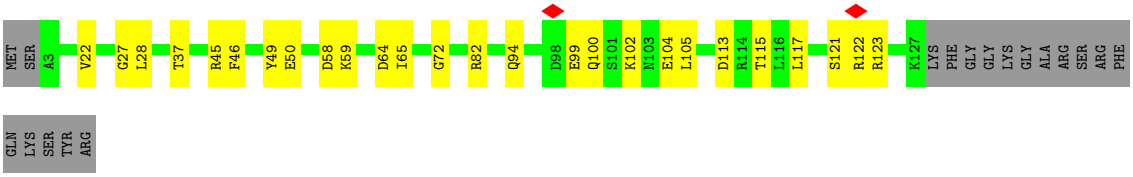




• Molecule 14: 40S ribosomal protein S16-A

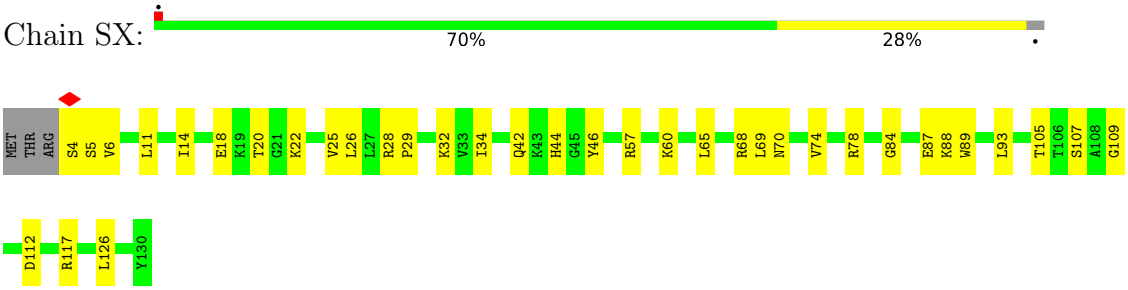
Chain SR:





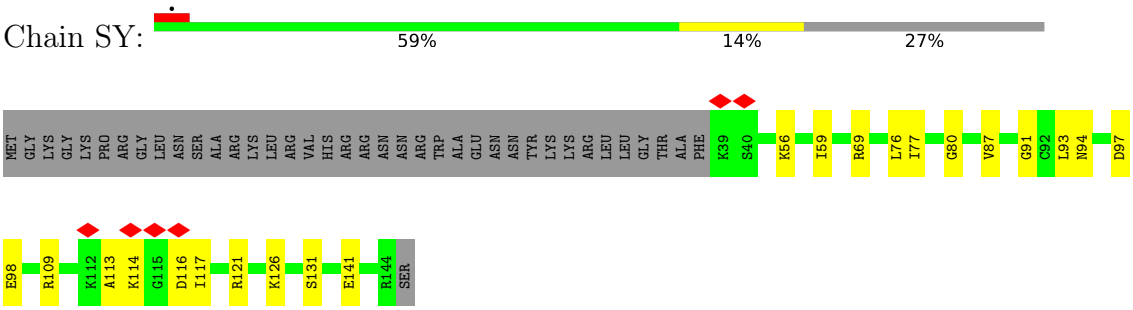
• Molecule 15: 40S ribosomal protein S22-B

Chain SX:



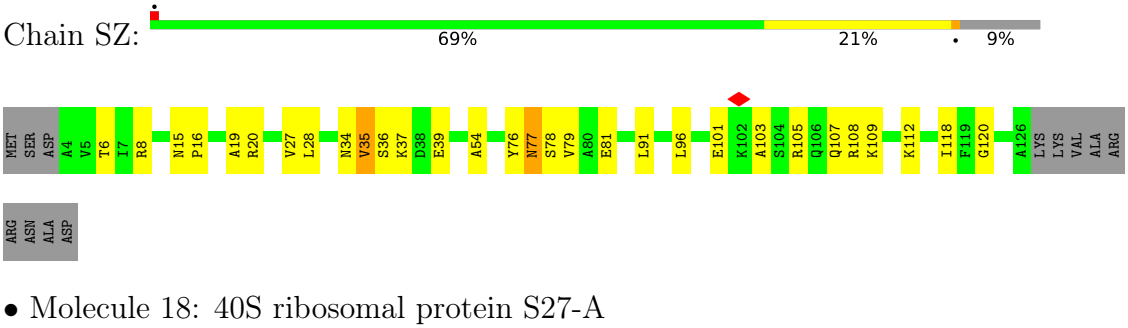
• Molecule 16: 40S ribosomal protein S23-A

Chain SY:



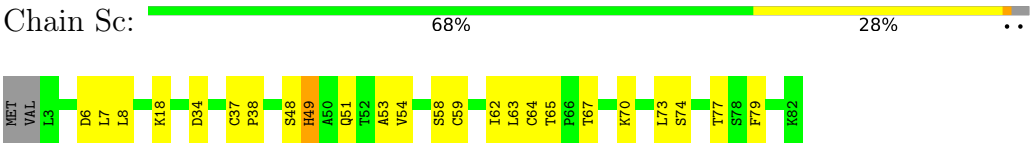
• Molecule 17: 40S ribosomal protein S24-A

Chain SZ:



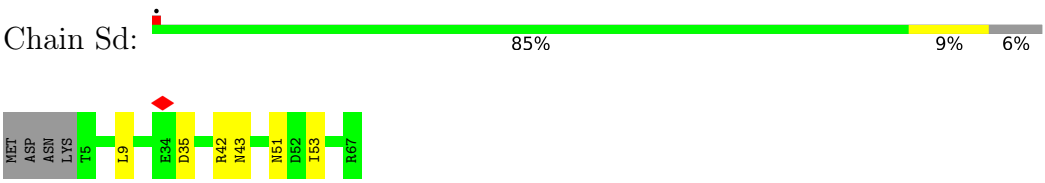
• Molecule 18: 40S ribosomal protein S27-A

Chain Sc:



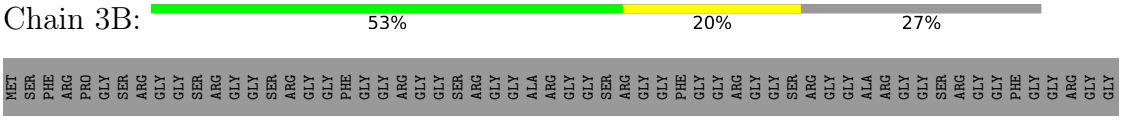
• Molecule 19: 40S ribosomal protein S28-A

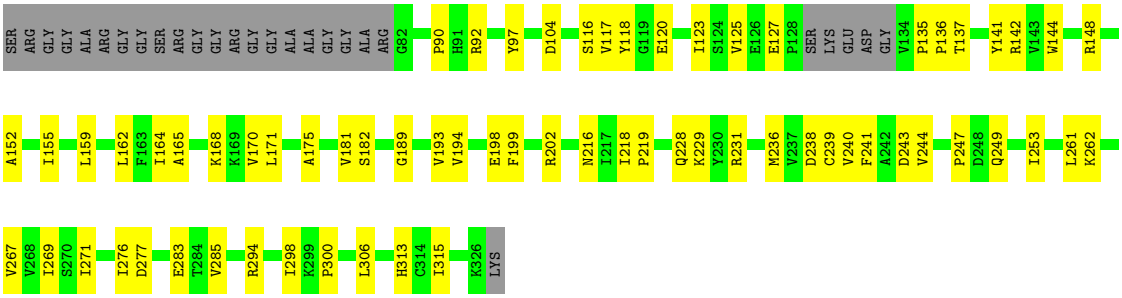
Chain Sd:

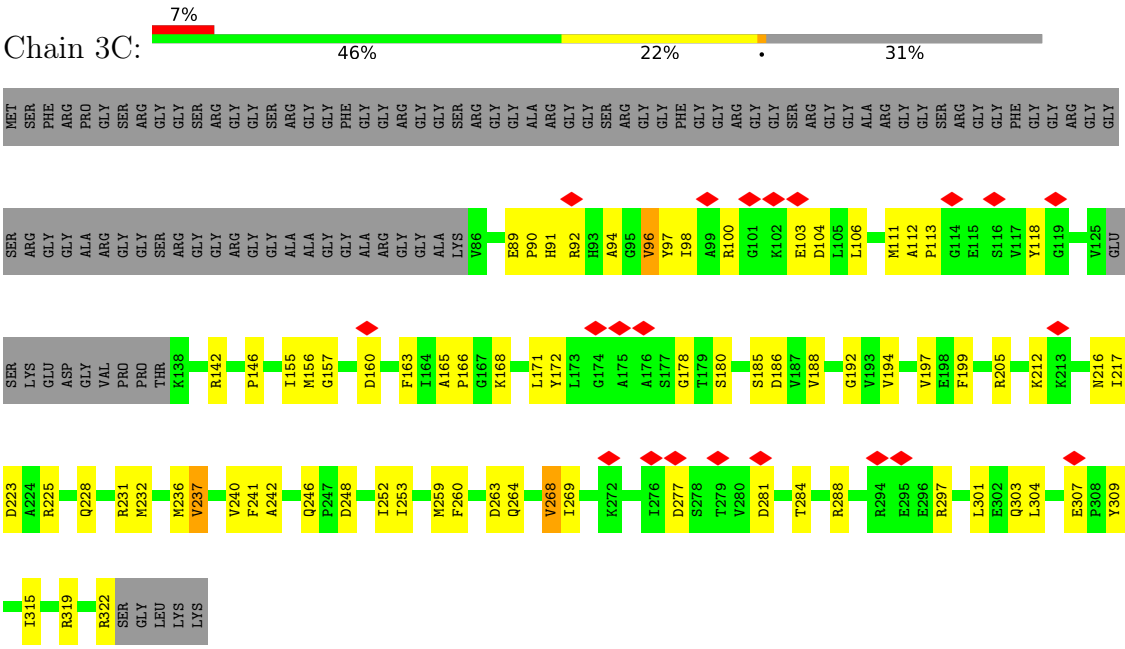


• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3B:







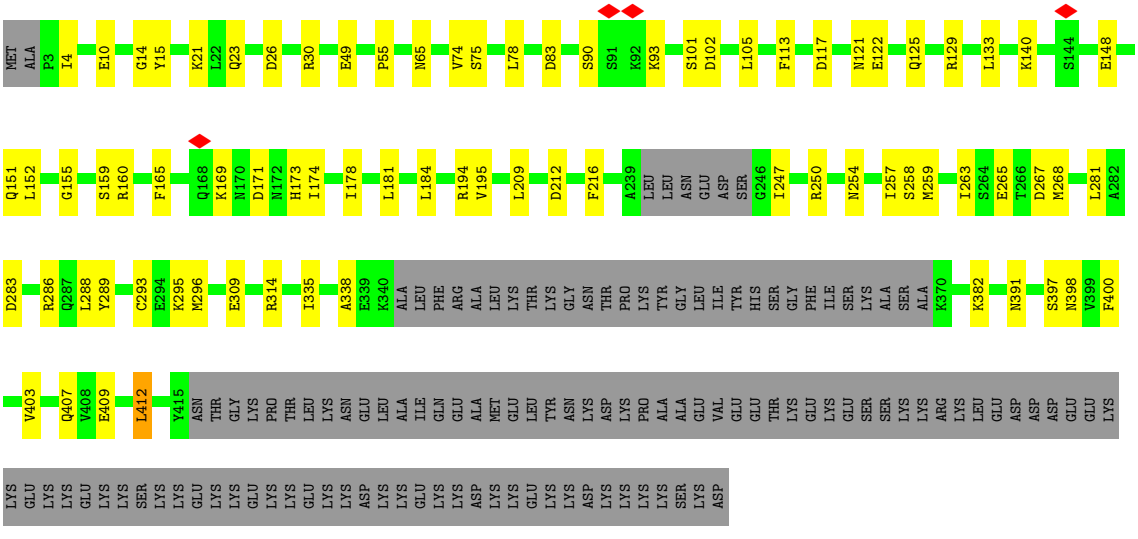
• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3C:

• Molecule 21: Nucleolar protein 56

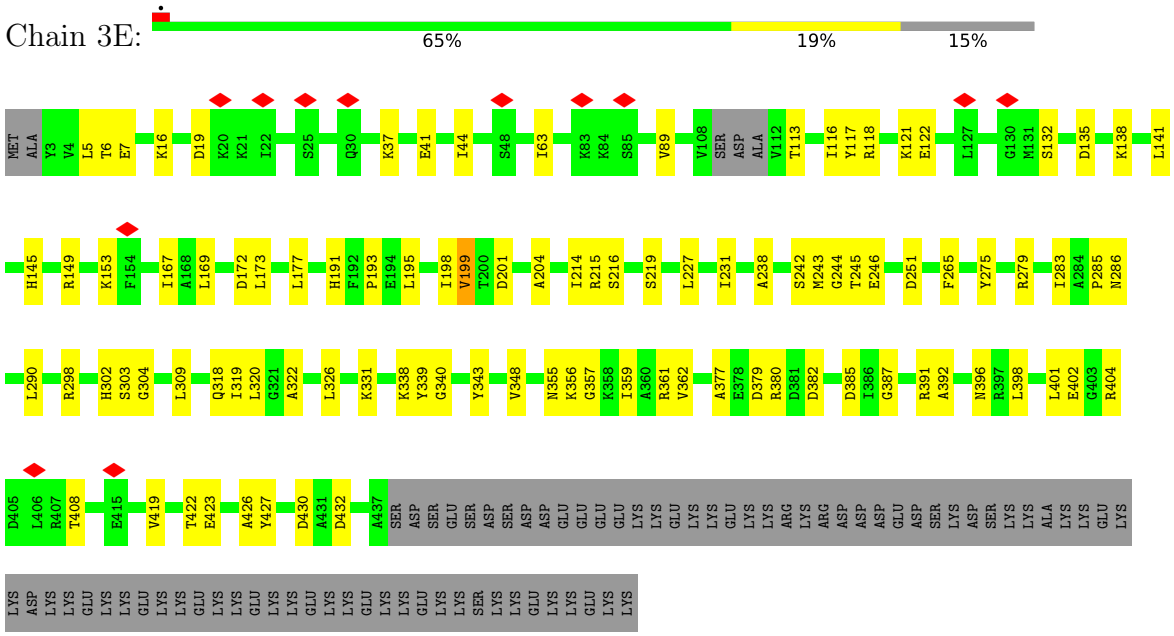
Chain 3D:





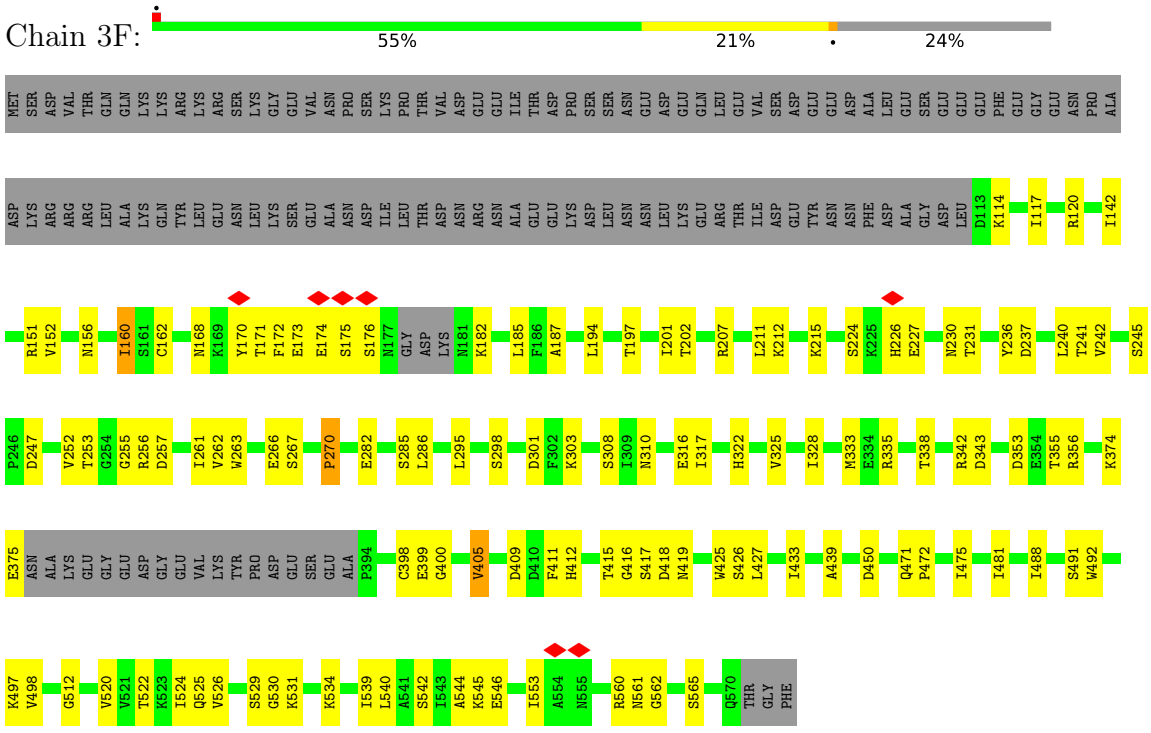
• Molecule 22: Nucleolar protein 58

Chain 3E:



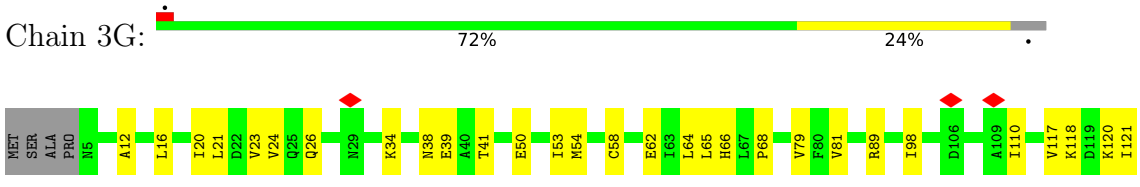
• Molecule 23: Ribosomal RNA-processing protein 9

Chain 3F:



• Molecule 24: 13 kDa ribonucleoprotein-associated protein

Chain 3G:

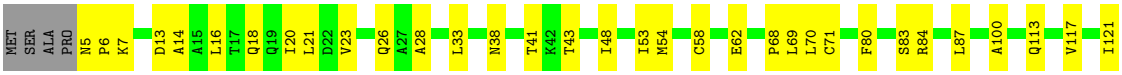




• Molecule 24: 13 kDa ribonucleoprotein-associated protein

Chain 3H:



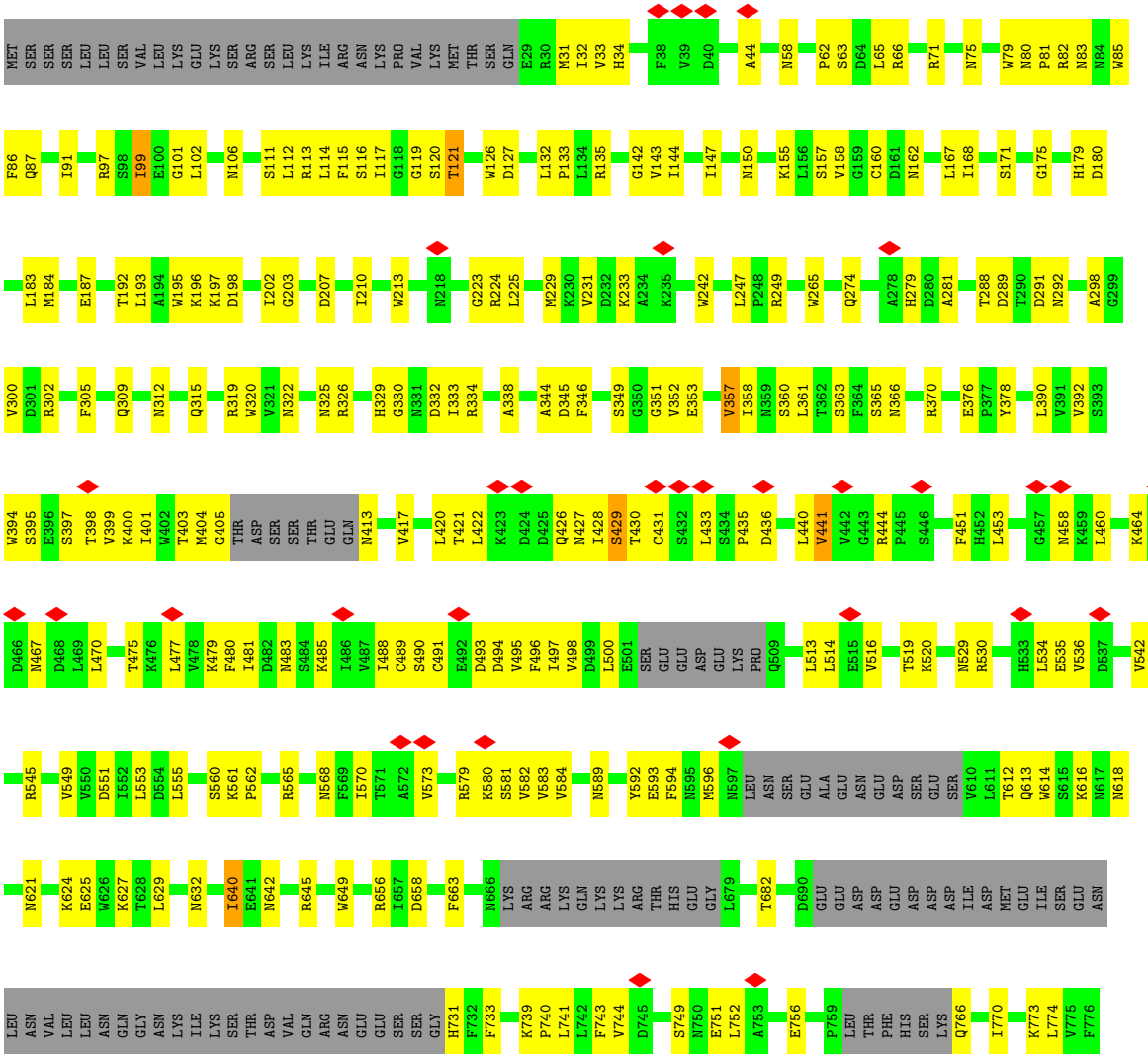




• Molecule 25: U3 small nucleolar RNA-associated protein 4

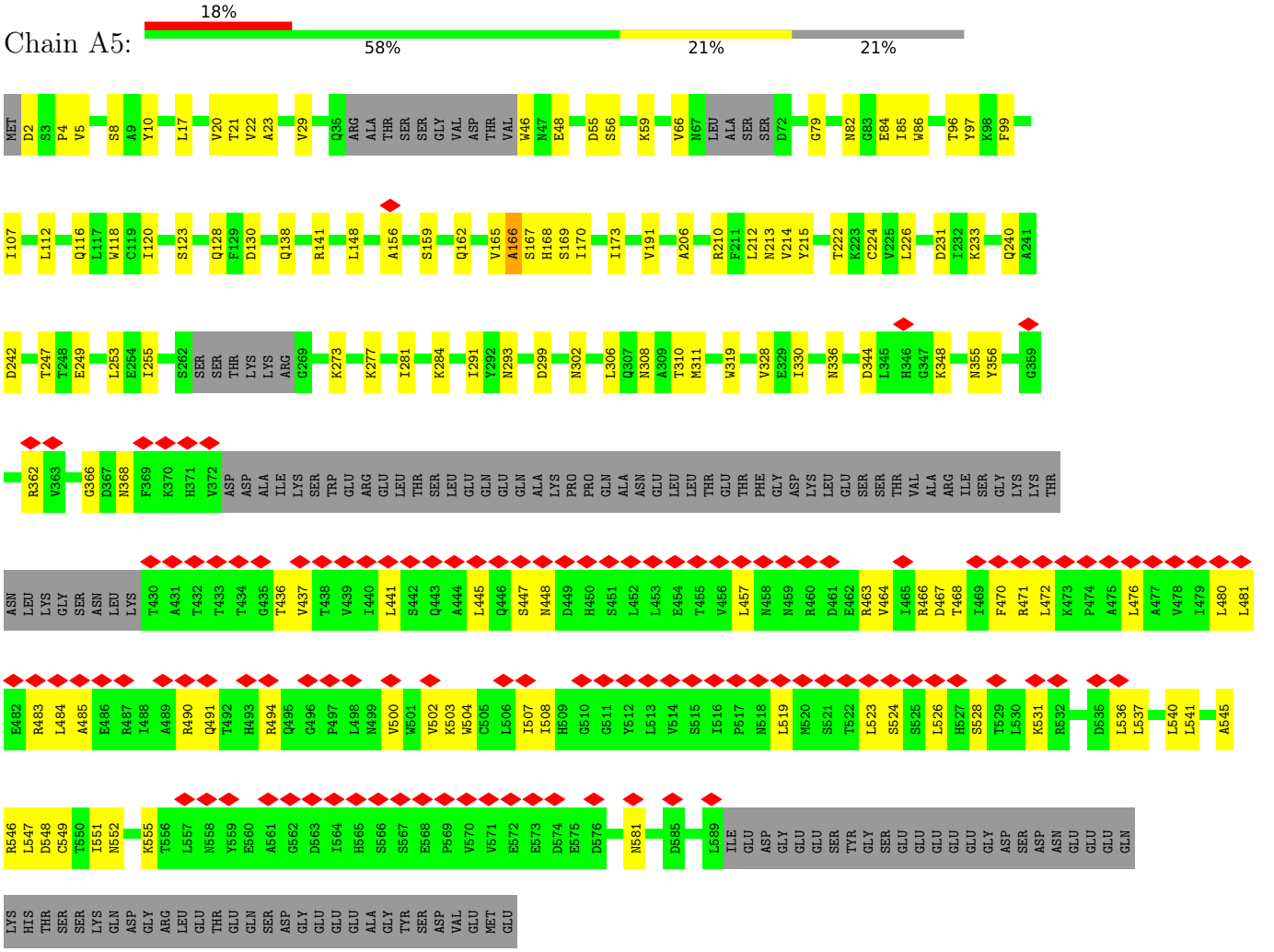
Chain A4:





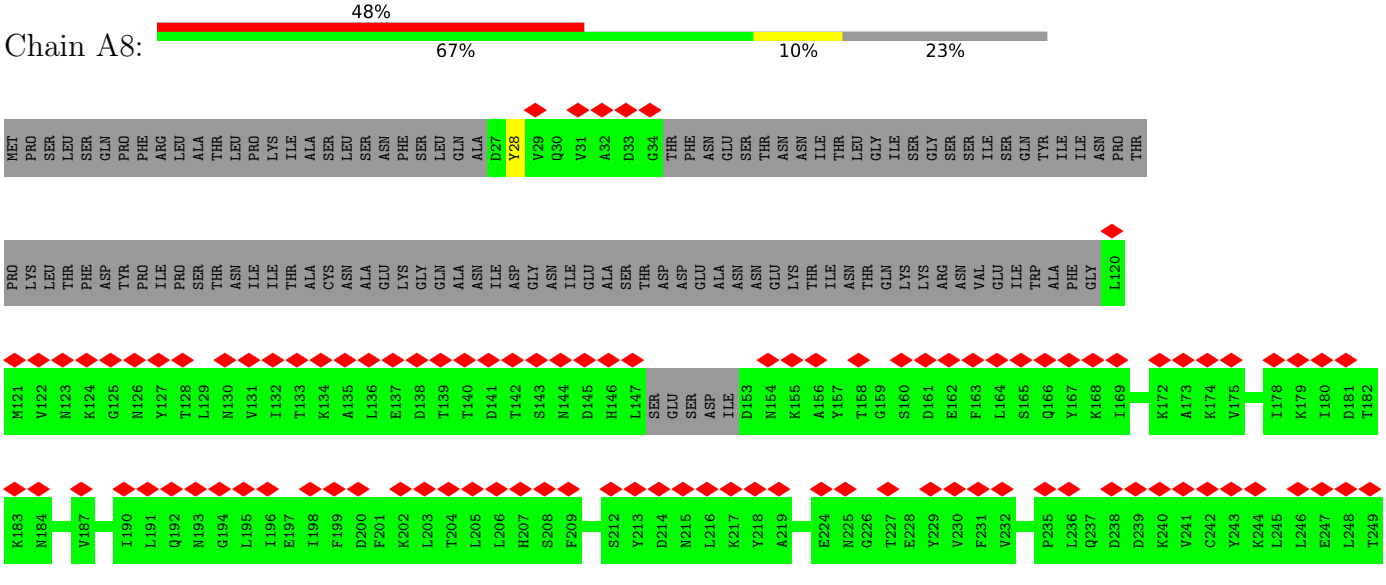
• Molecule 26: U3 small nucleolar RNA-associated protein 5

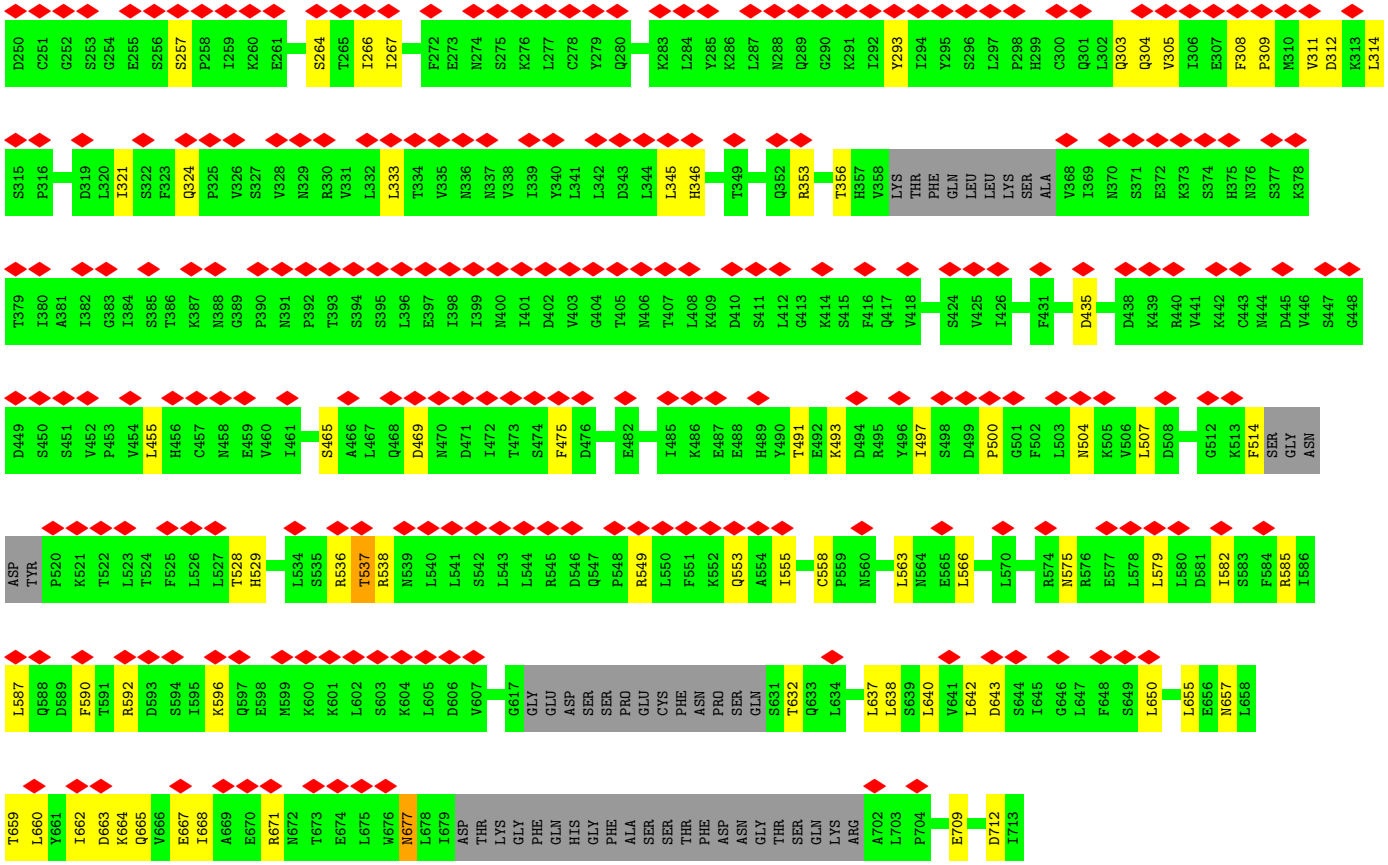
Chain A5:



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

Chain A8:

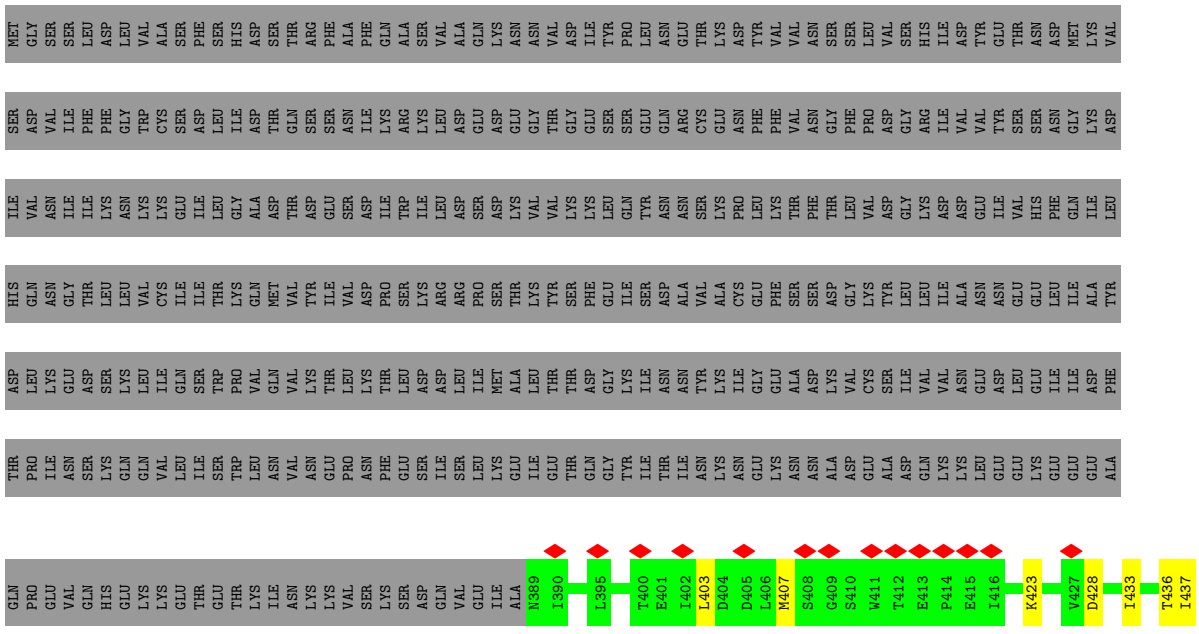


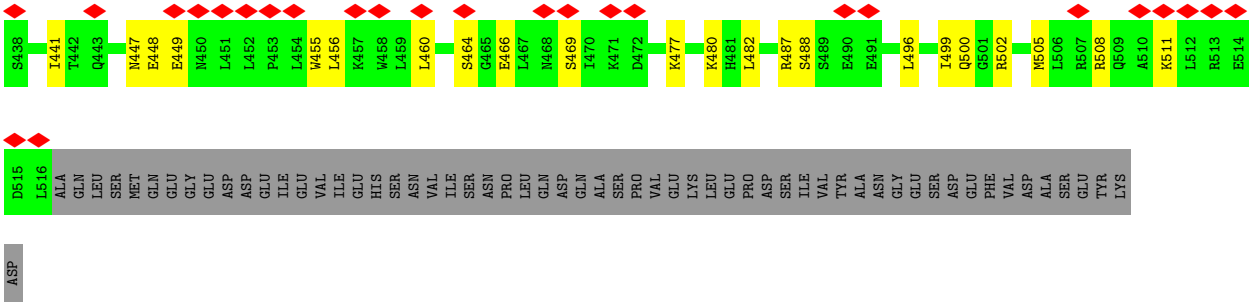


• Molecule 28: U3 small nucleolar RNA-associated protein 9

Chain A9:



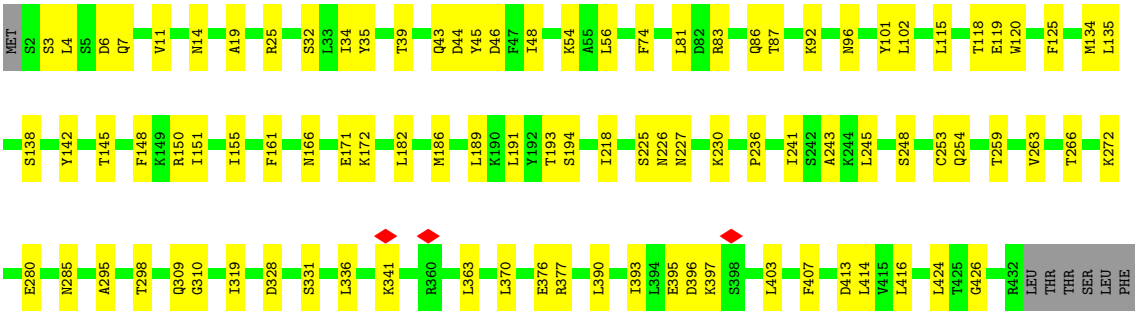


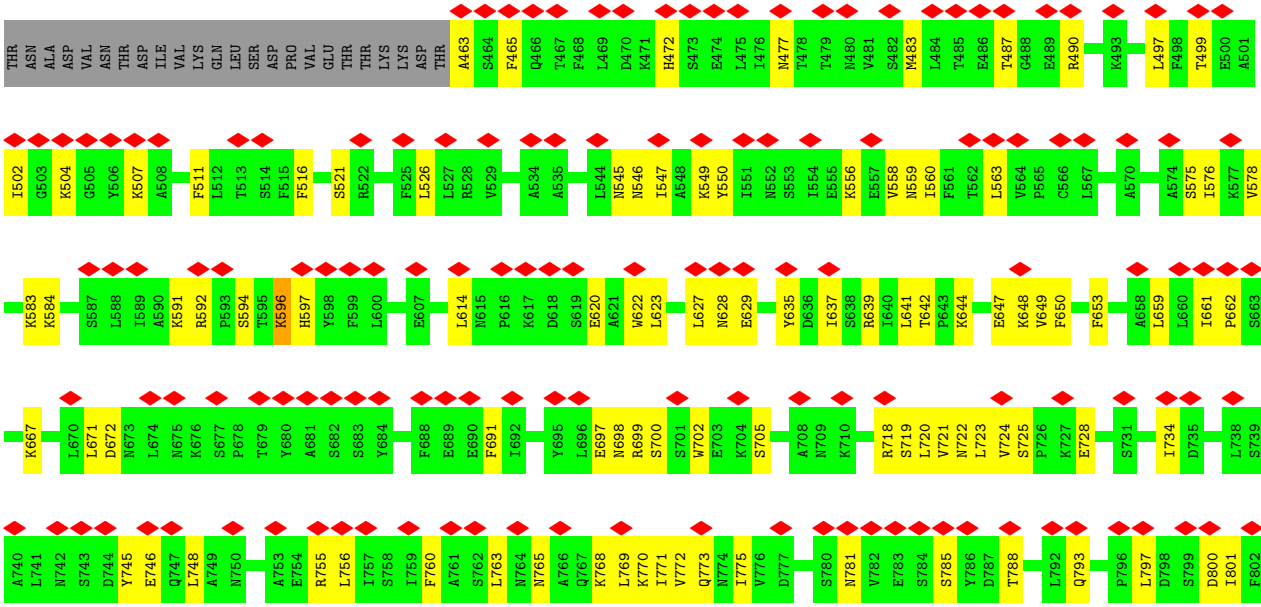


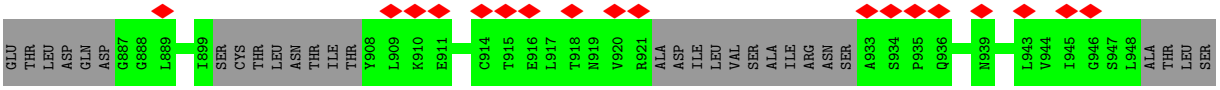
• Molecule 29: U3 small nucleolar RNA-associated protein 10

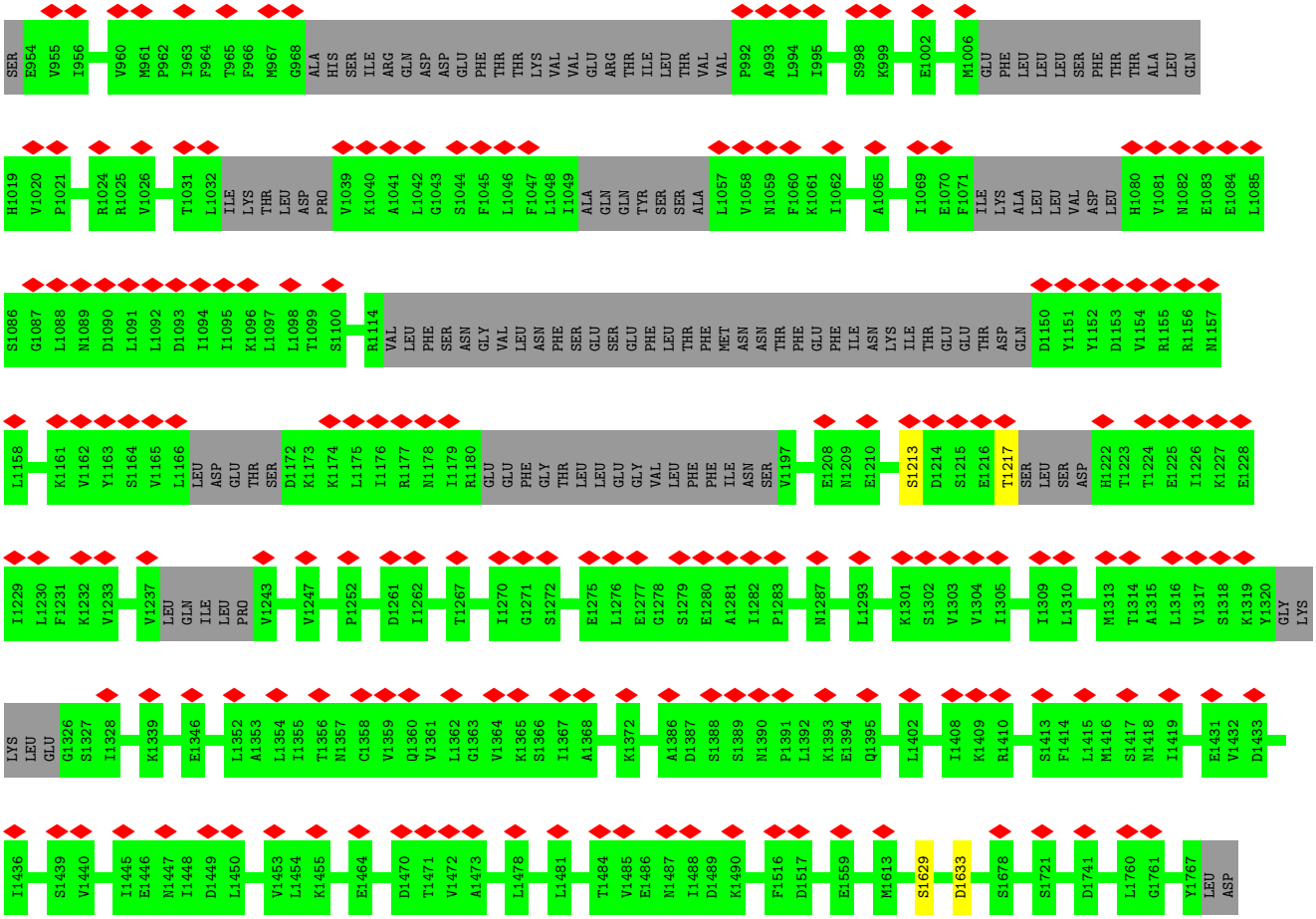
Chain AE:







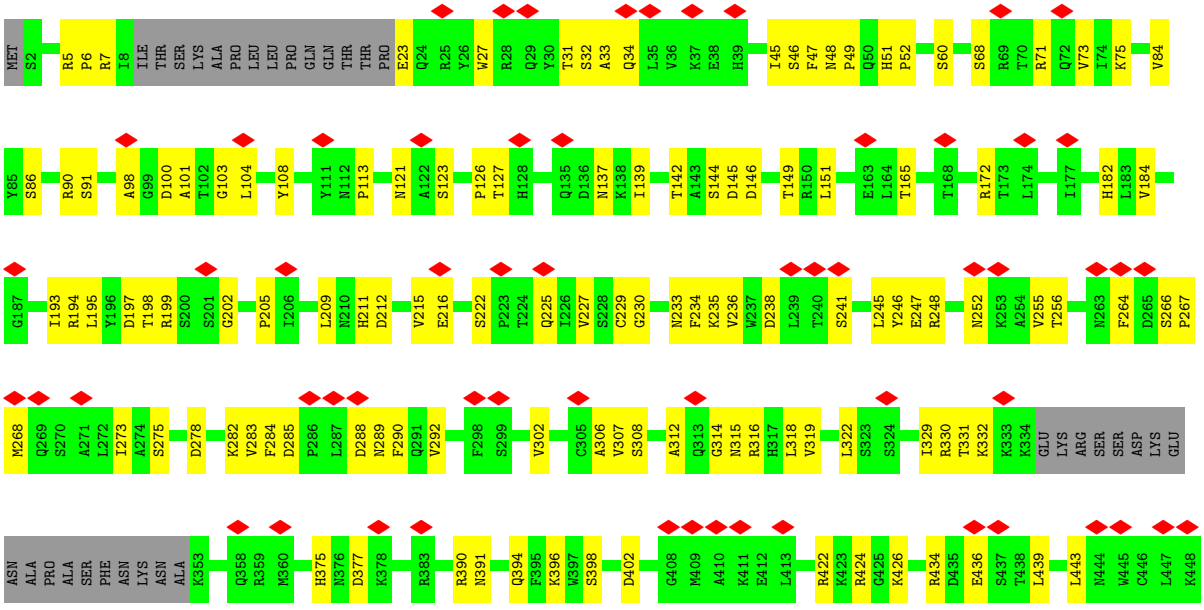


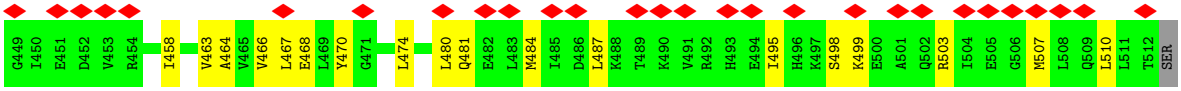


• Molecule 30: U3 small nucleolar RNA-associated protein 15

Chain AF:



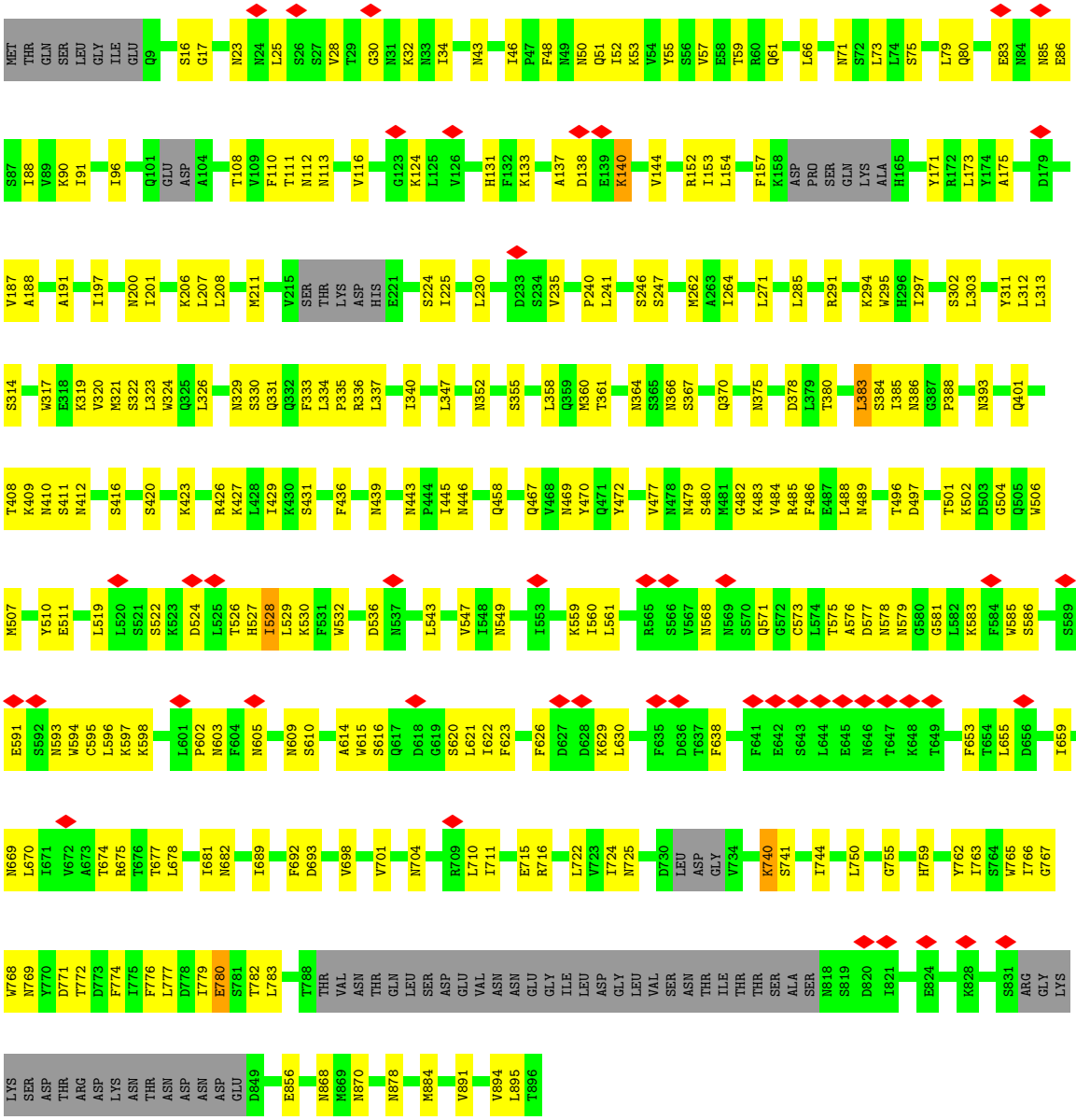




• Molecule 31: NET1-associated nuclear protein 1

Chain AG:

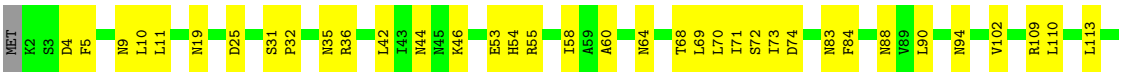


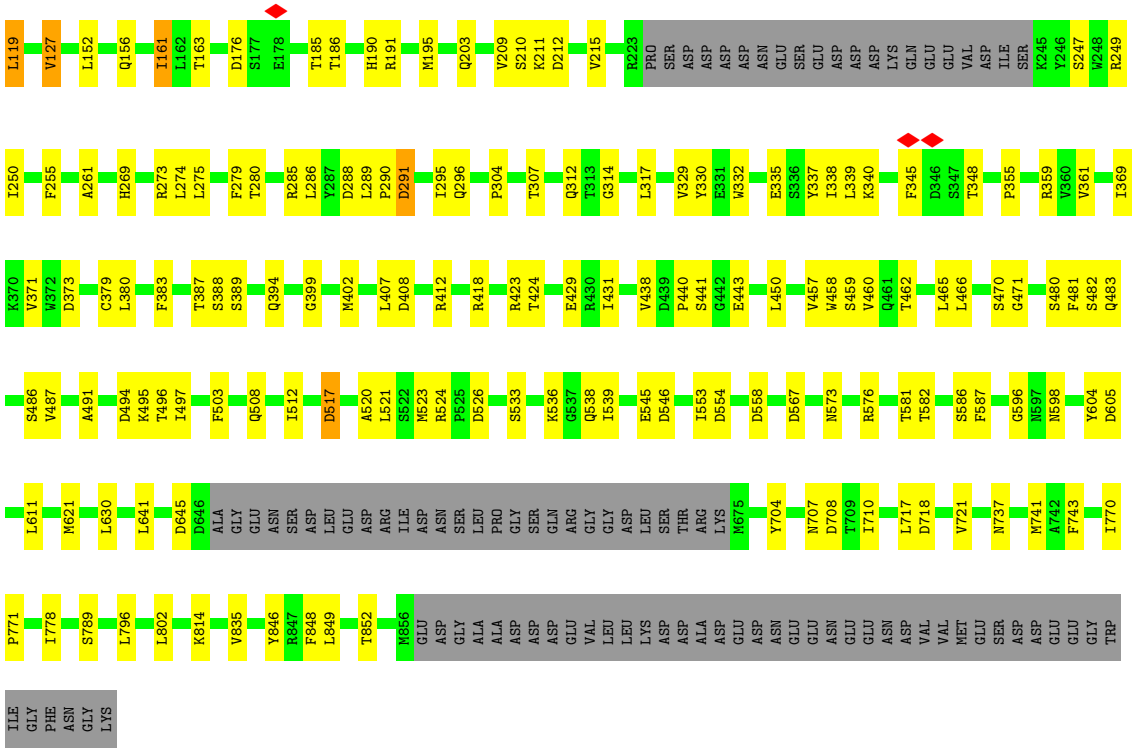


• Molecule 32: Periodic tryptophan protein 2

Chain B1:



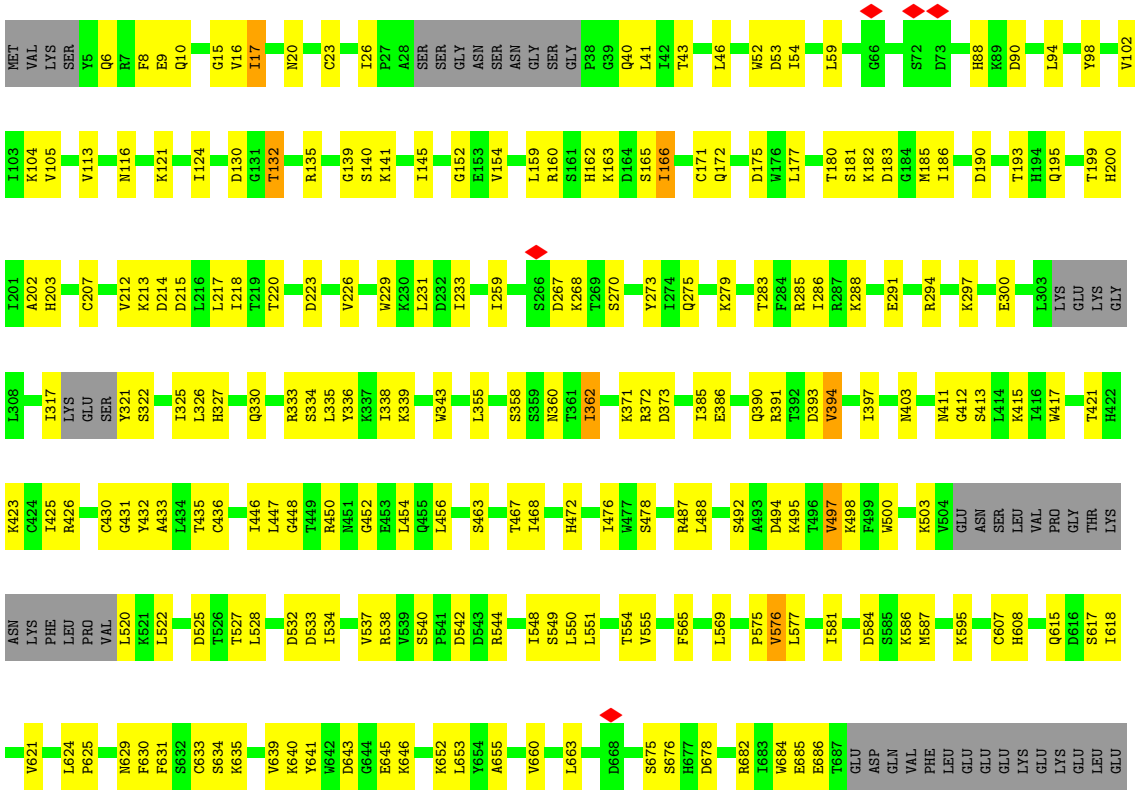


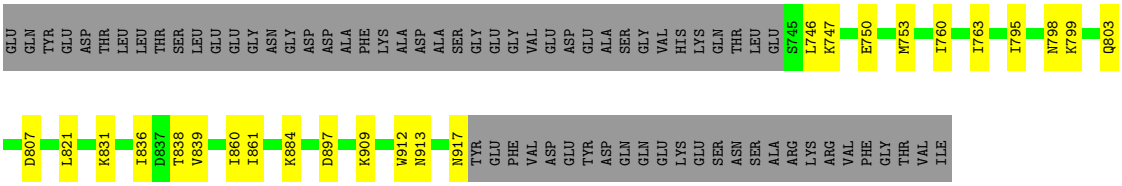


• Molecule 33: U3 small nucleolar RNA-associated protein 12

Chain B2:



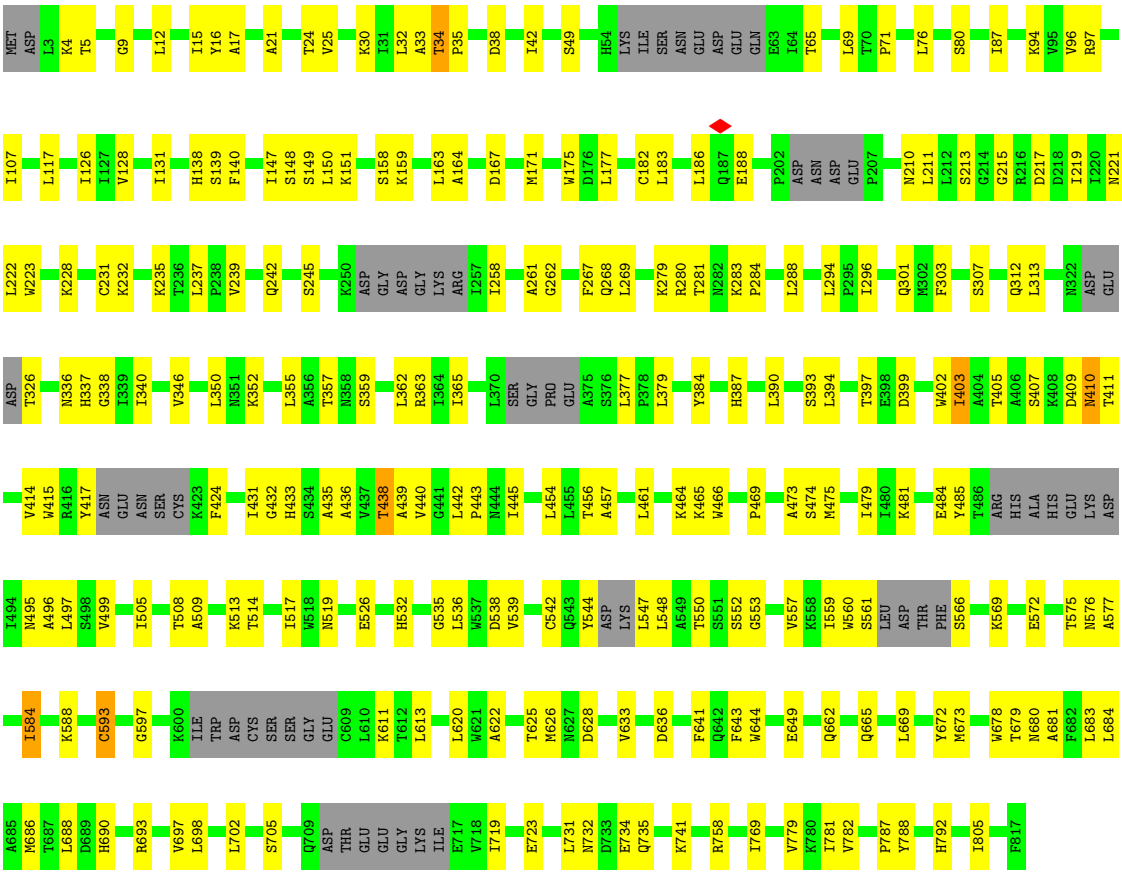




• Molecule 34: U3 small nucleolar RNA-associated protein 13

Chain B3:

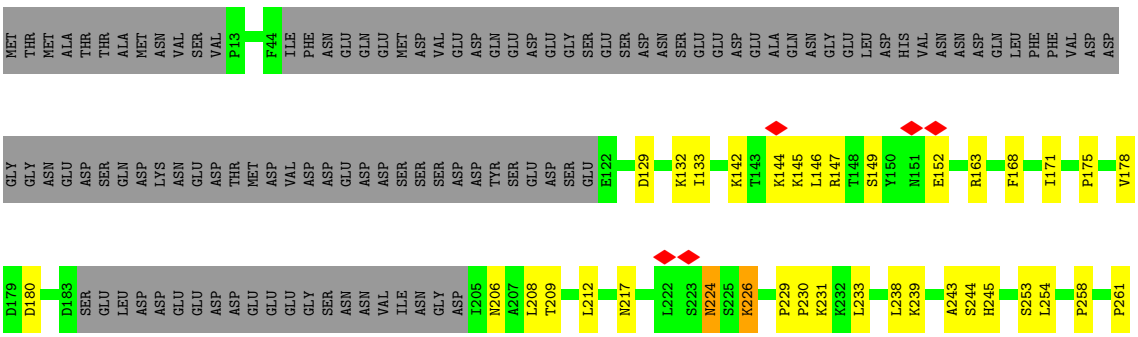


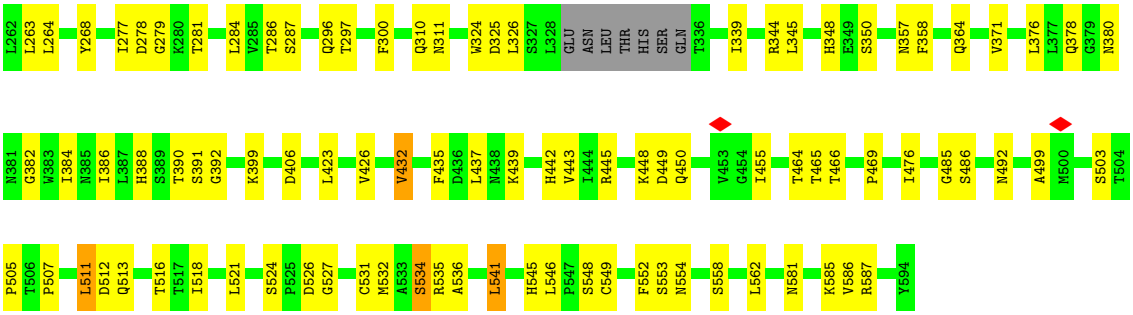


• Molecule 35: U3 small nucleolar RNA-associated protein 18

Chain B8:



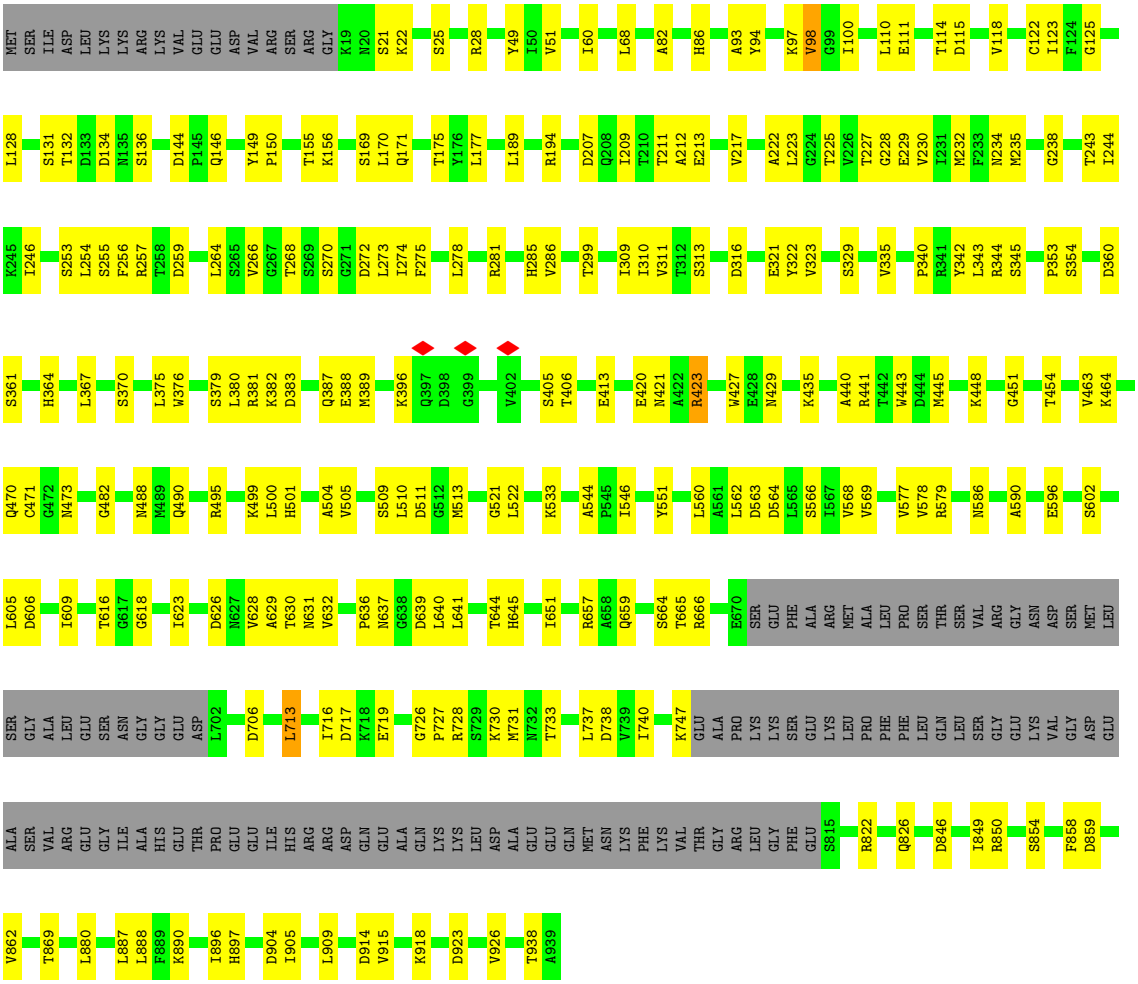




• Molecule 36: U3 small nucleolar RNA-associated protein 21

Chain BE:

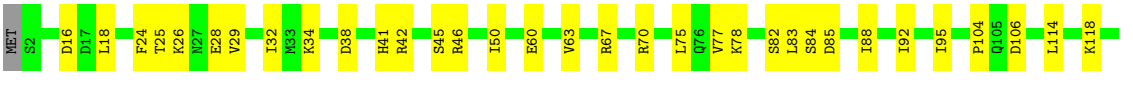


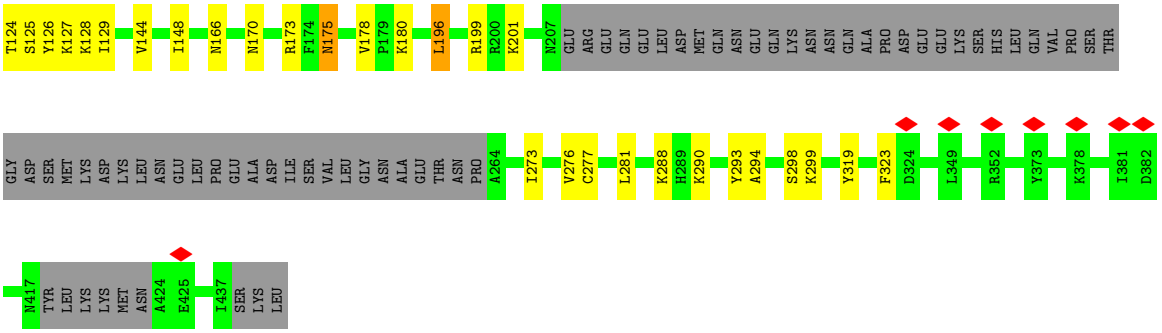


• Molecule 37: U3 small nucleolar RNA-associated protein 6

Chain B6:



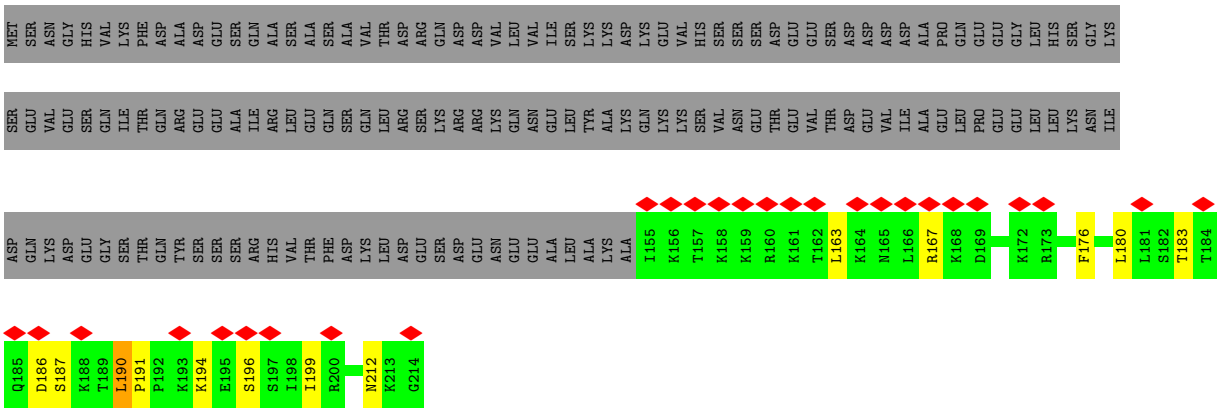




• Molecule 38: Bud site selection protein 21

Chain 5B:

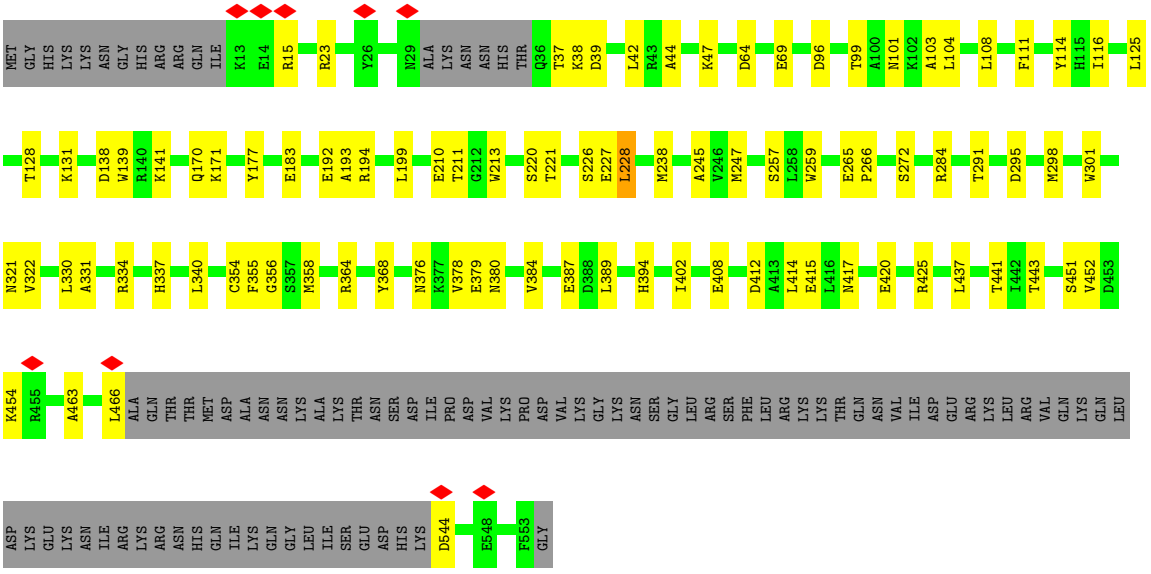




• Molecule 39: U3 small nucleolar RNA-associated protein 7

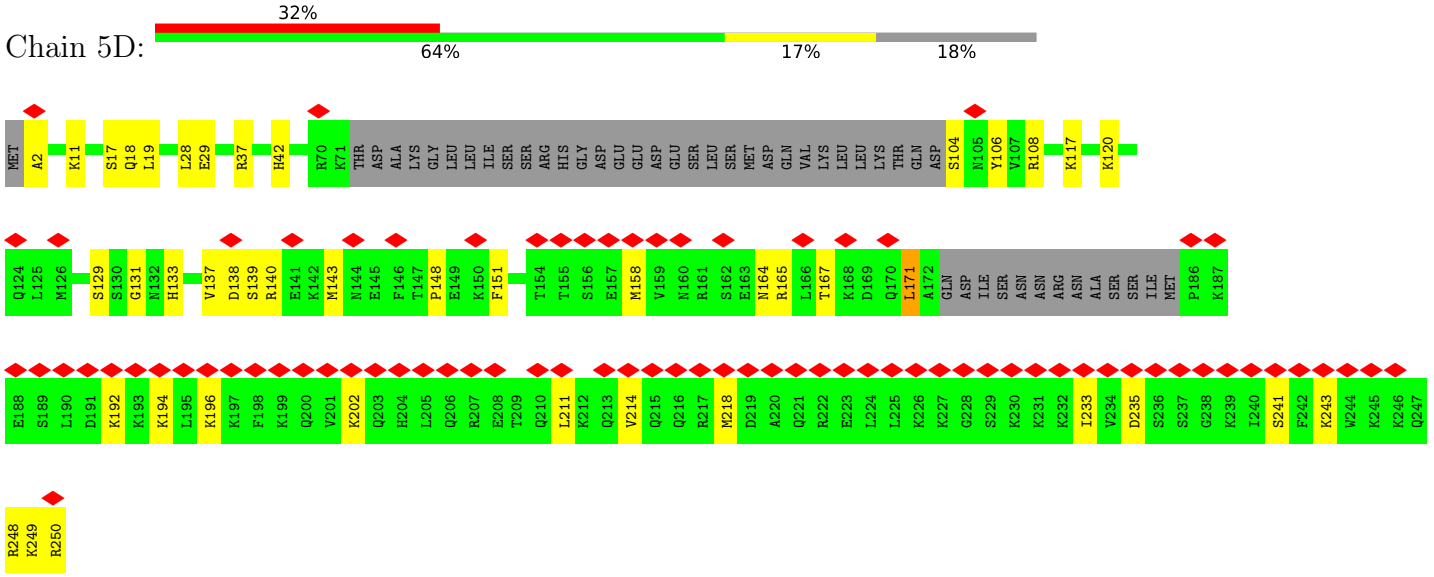
Chain 5C:





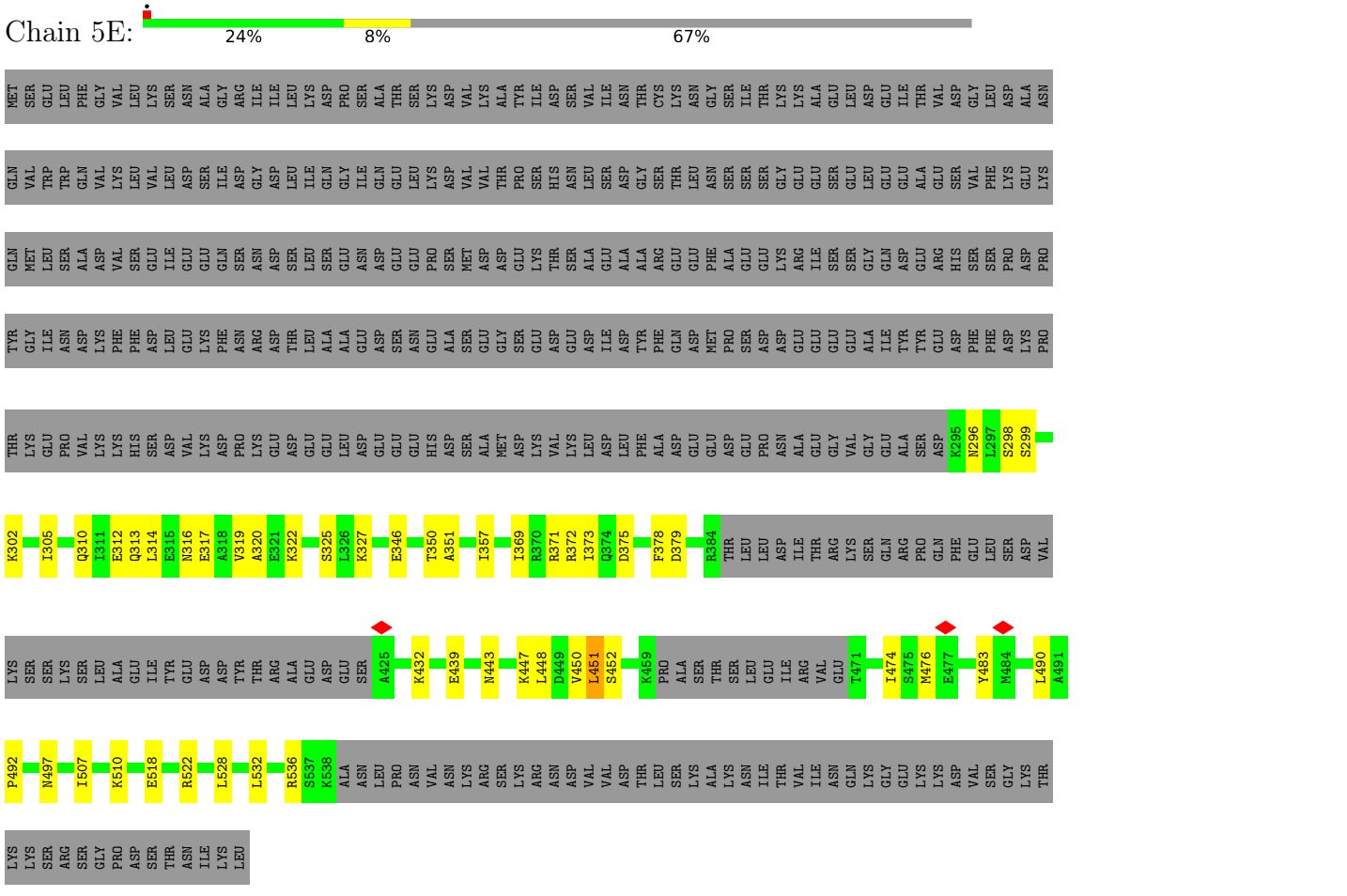
• Molecule 40: U3 small nucleolar RNA-associated protein 11

Chain 5D:



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

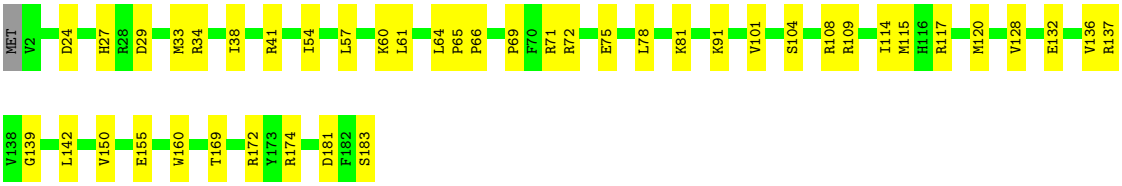
Chain 5E:



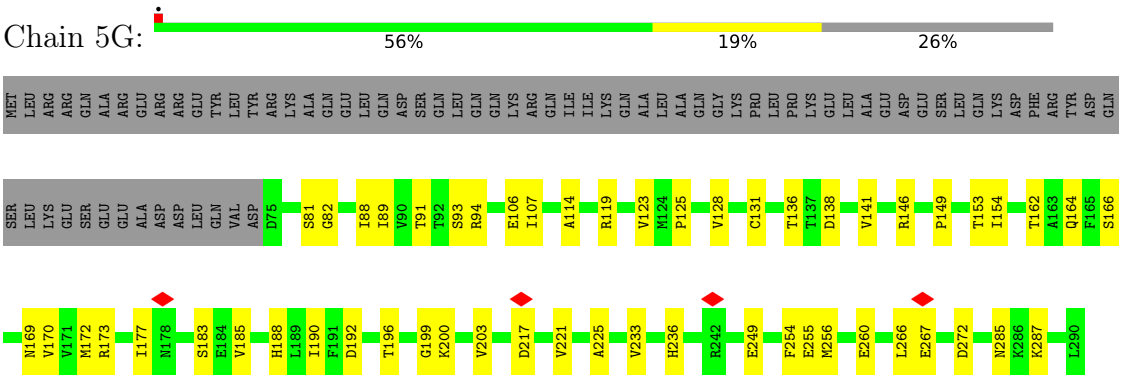
• Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

Chain 5F:

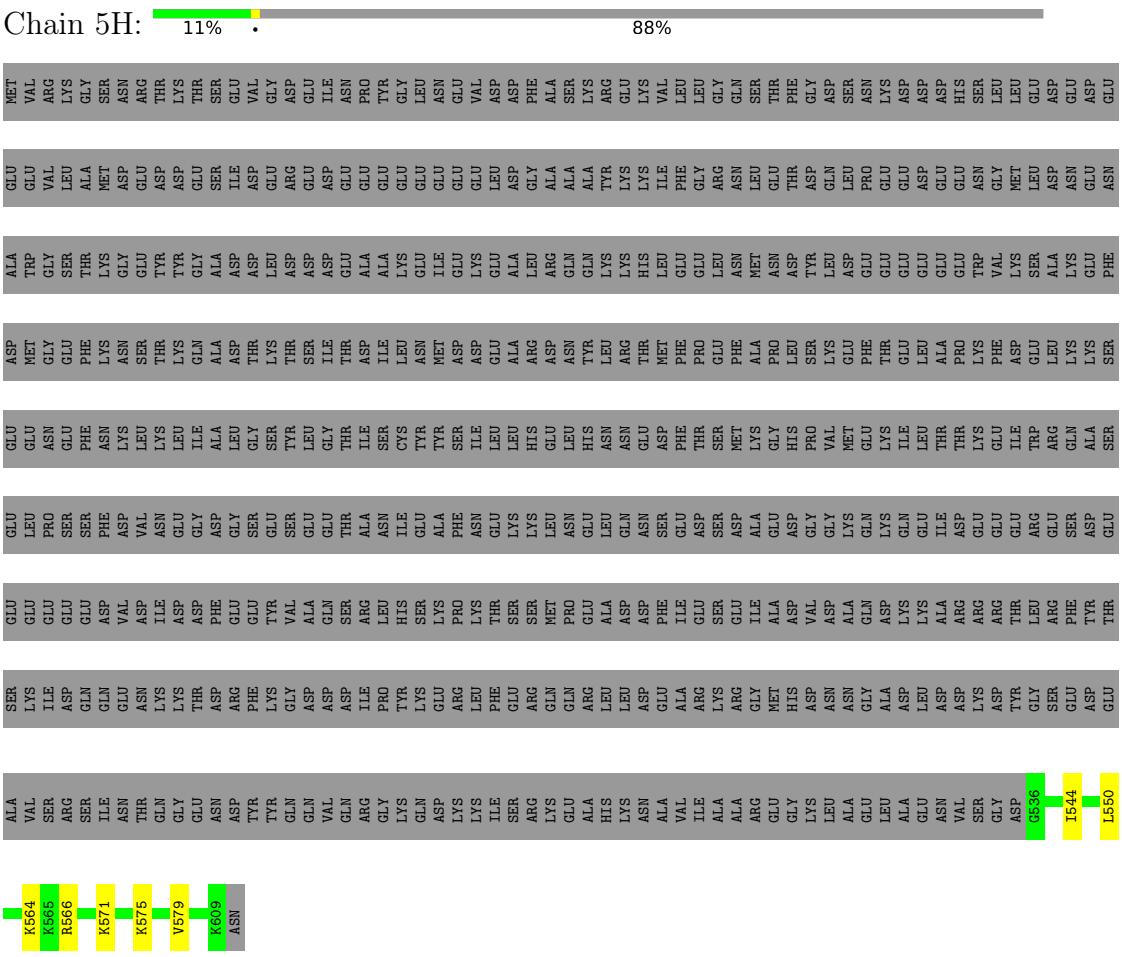




• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

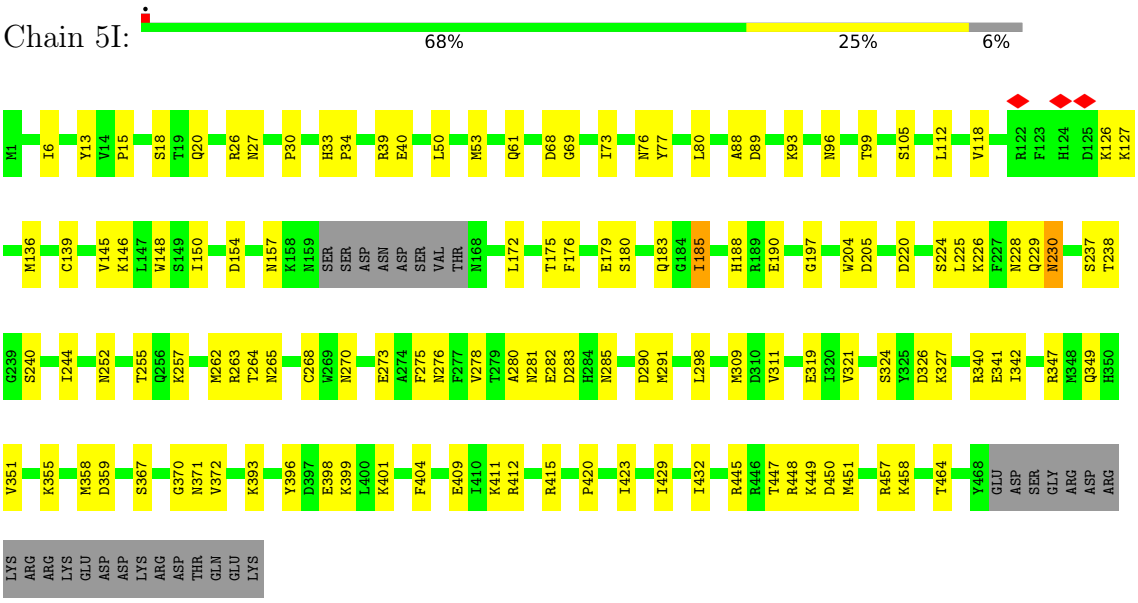


• Molecule 44: Something about silencing protein 10



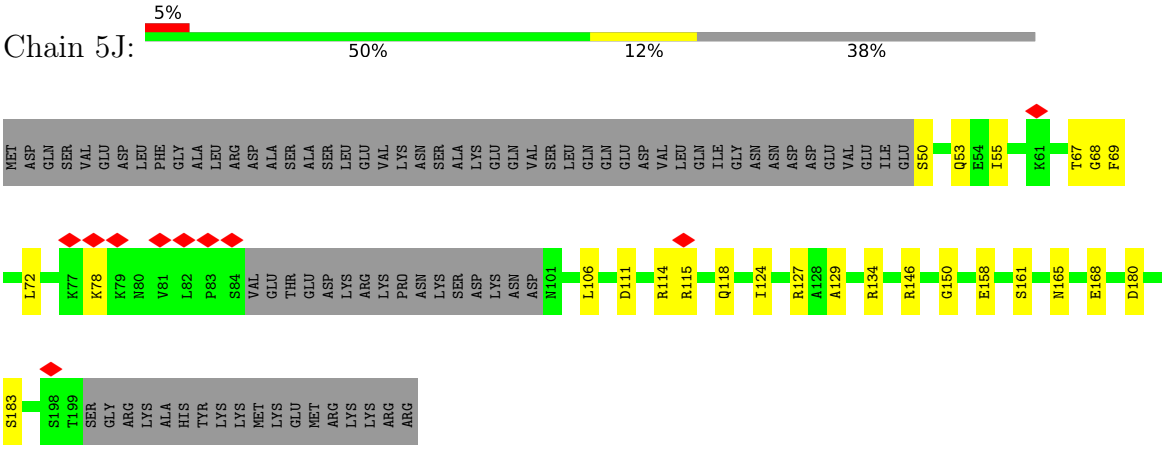
• Molecule 45: Protein SOF1

Chain 5I:



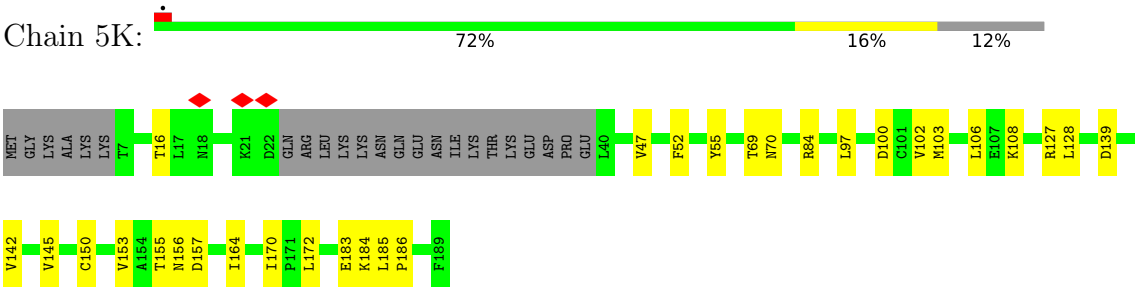
• Molecule 46: rRNA-processing protein FCF2

Chain 5J:



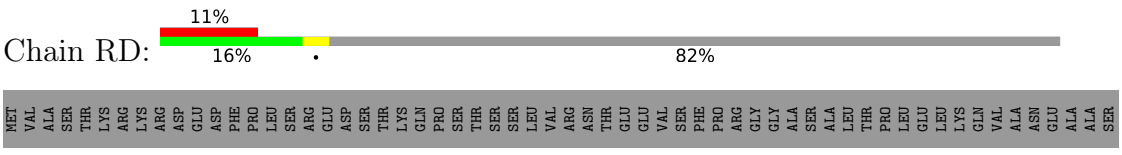
• Molecule 47: rRNA-processing protein FCF1

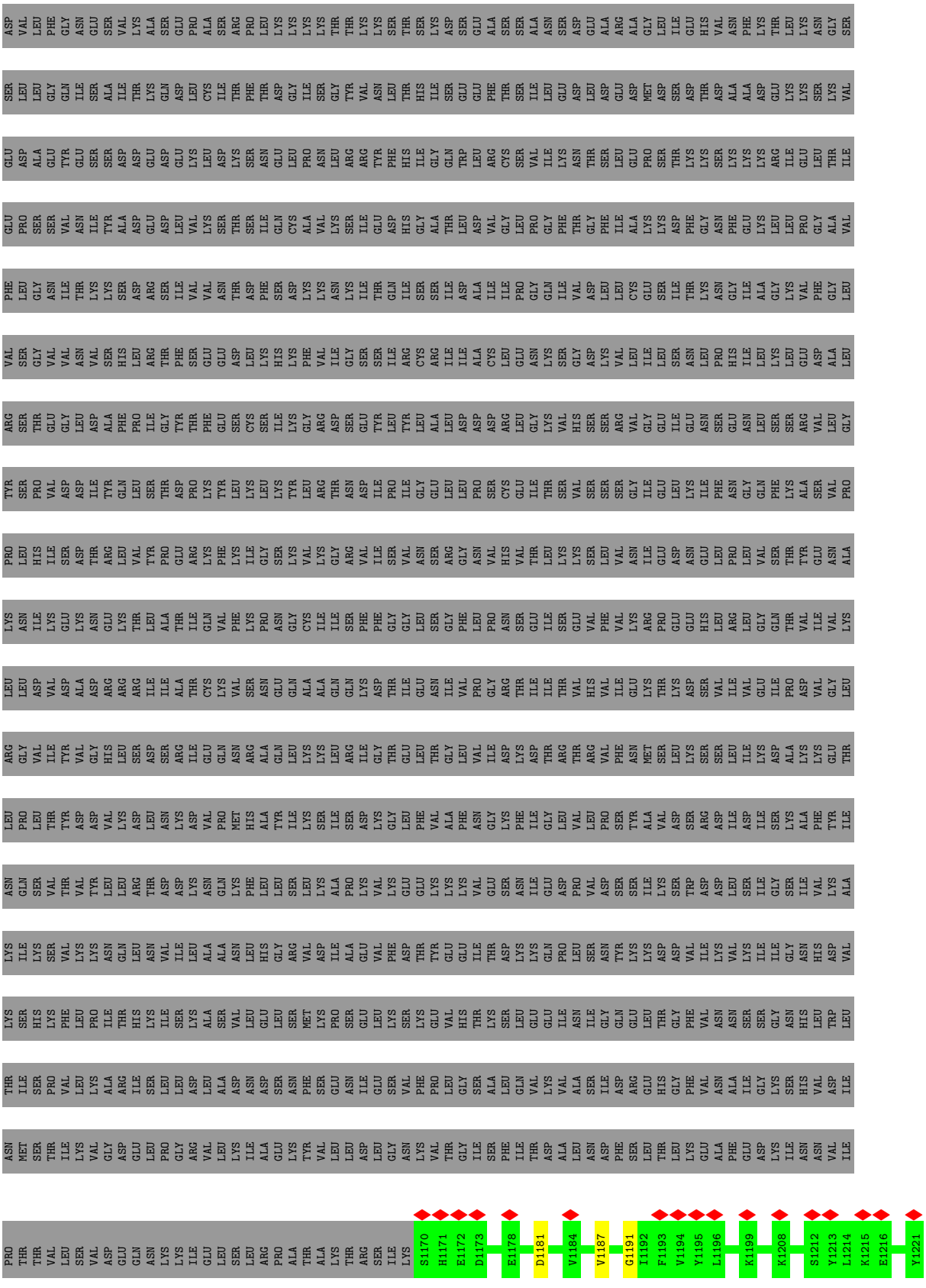
Chain 5K:

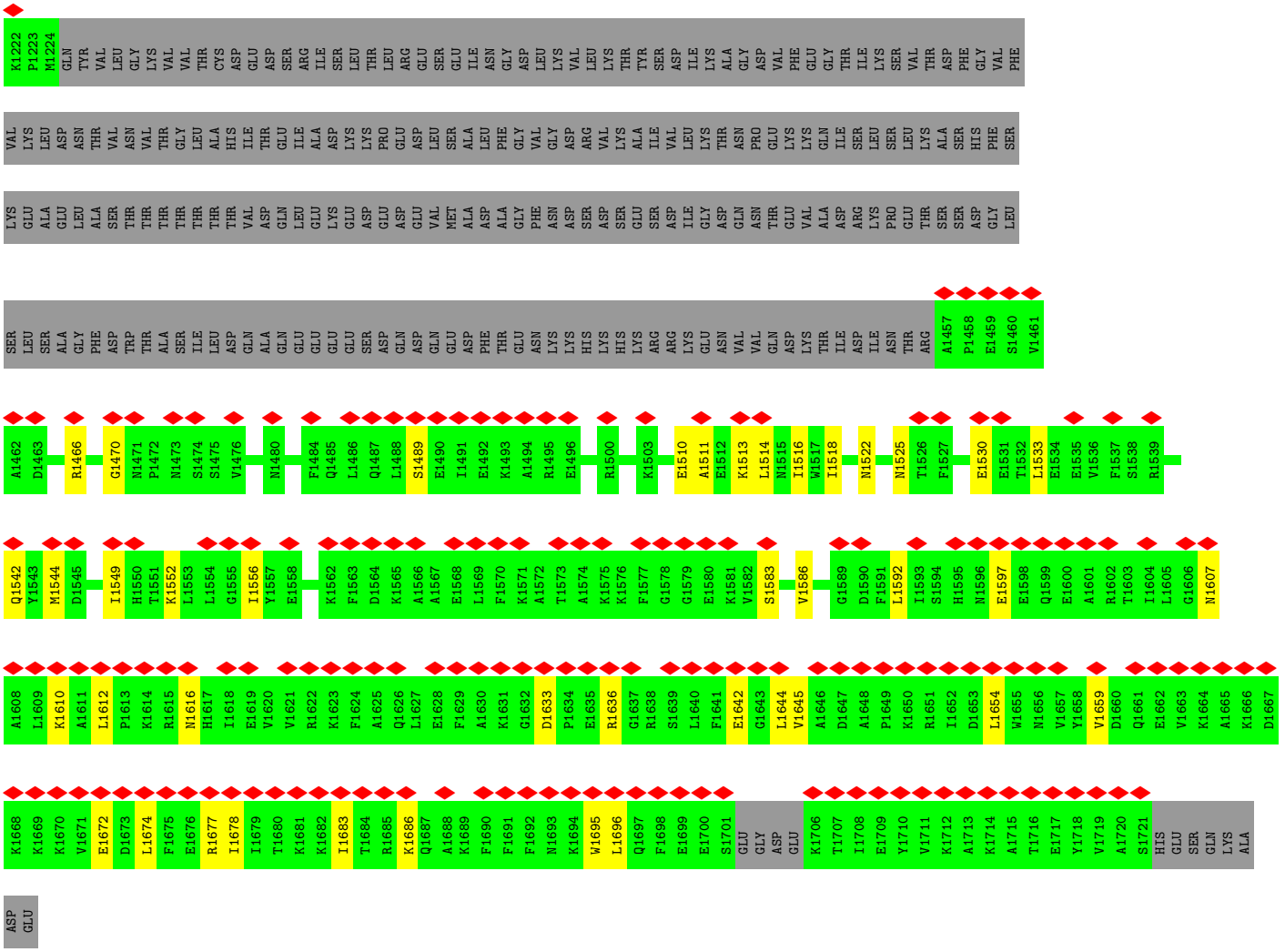


• Molecule 48: rRNA biogenesis protein RRP5

Chain RD:



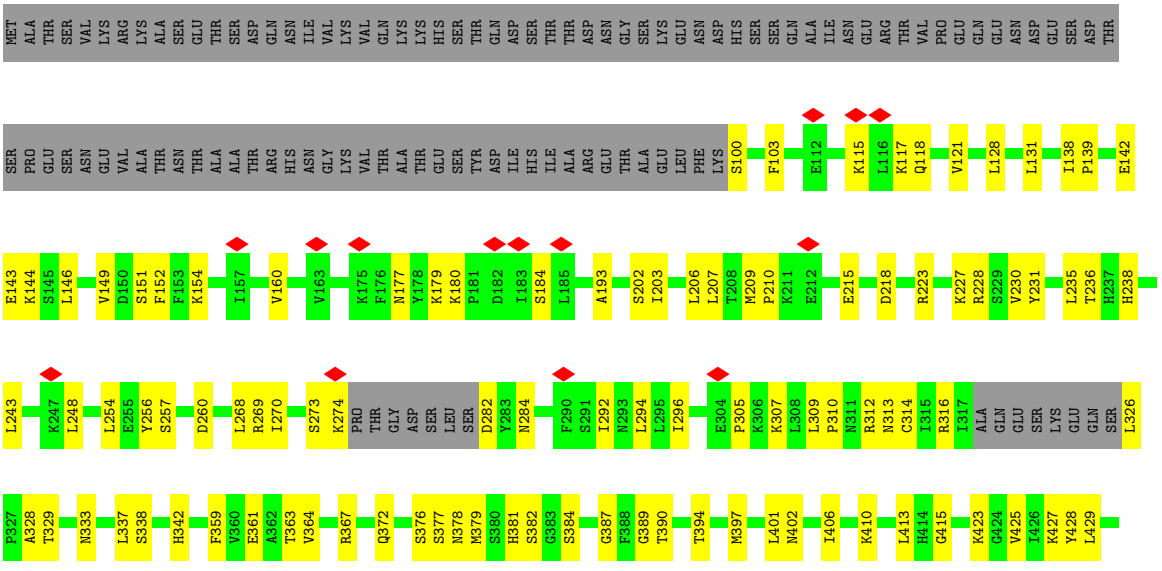

S1170
H1171
E1172
D1173
E1178
D1181
V1184
V1187
G1191
I1192
F1193
V1194
Y1195
L1196
K1199
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S1212
Y1213
L1214
K1215
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Y1221

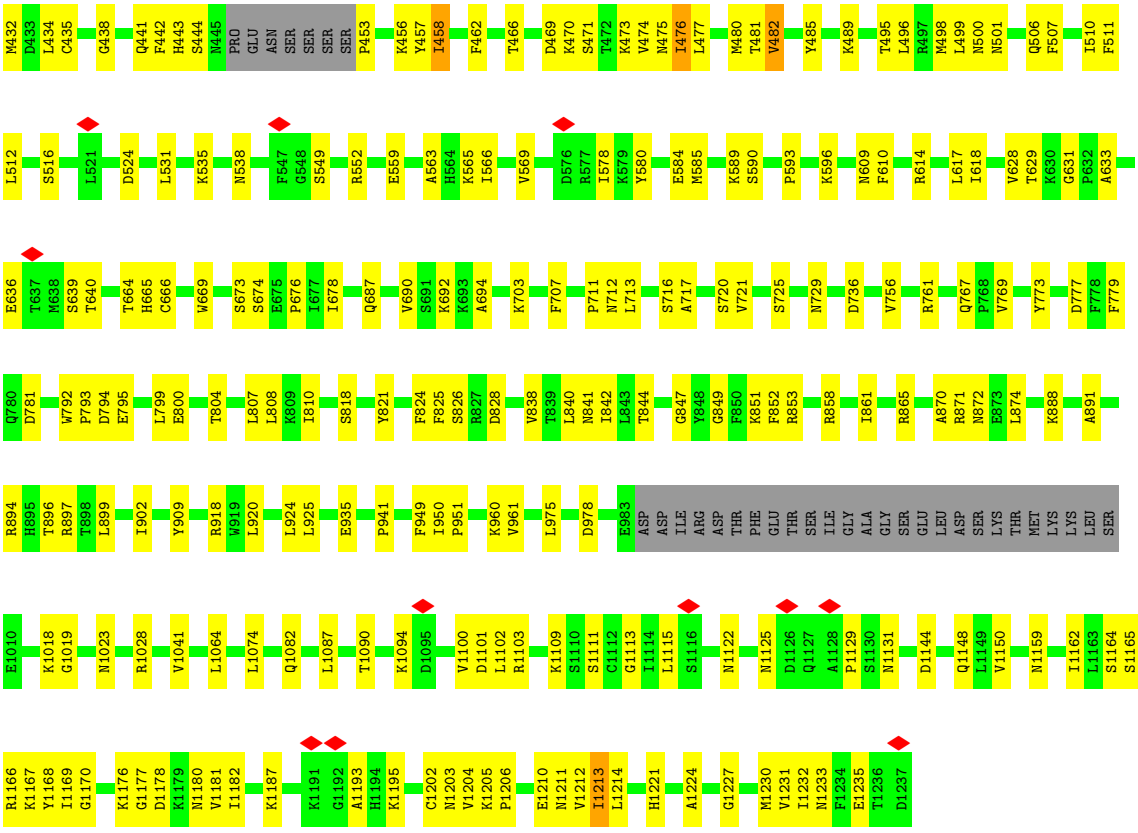


• Molecule 49: U3 small nucleolar RNA-associated protein 22

Chain RE:



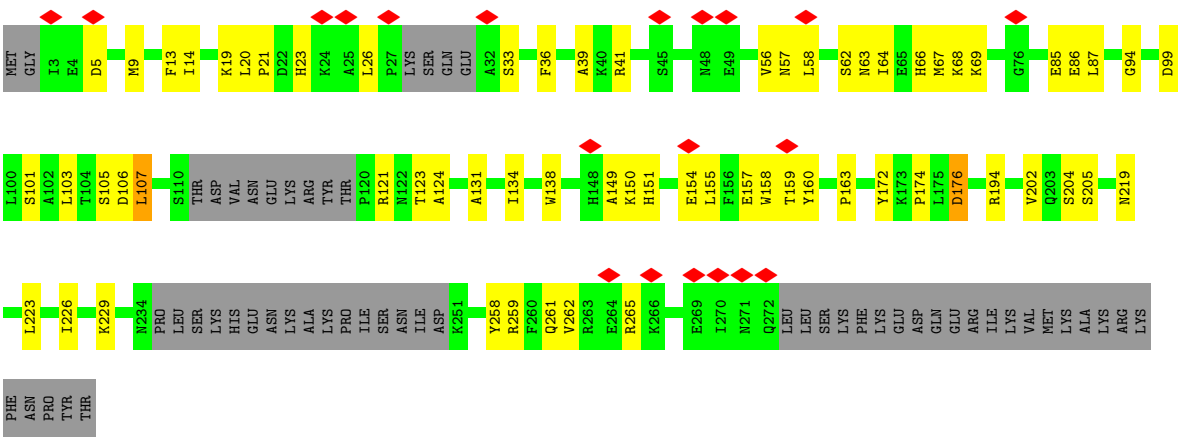




• Molecule 50: Ribosomal RNA-processing protein 7

Chain RF:

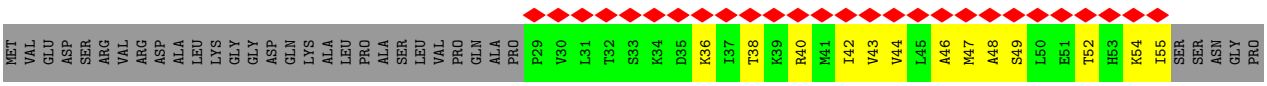




• Molecule 51: Ribosomal RNA small subunit methyltransferase NEP1

Chain RG:



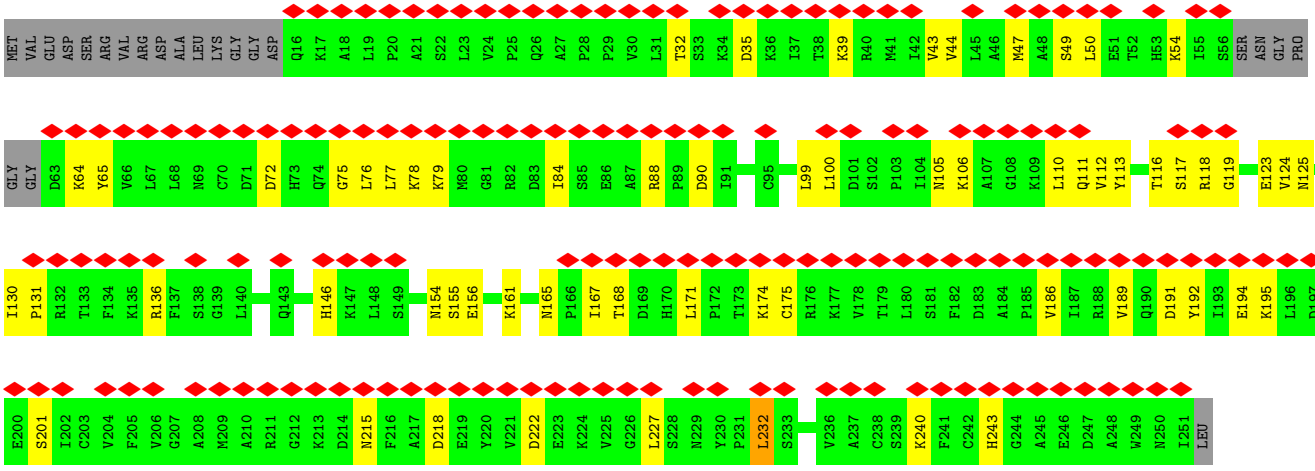




• Molecule 51: Ribosomal RNA small subunit methyltransferase NEP1

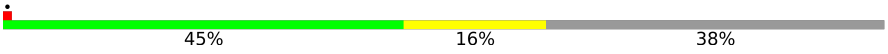
Chain RH:

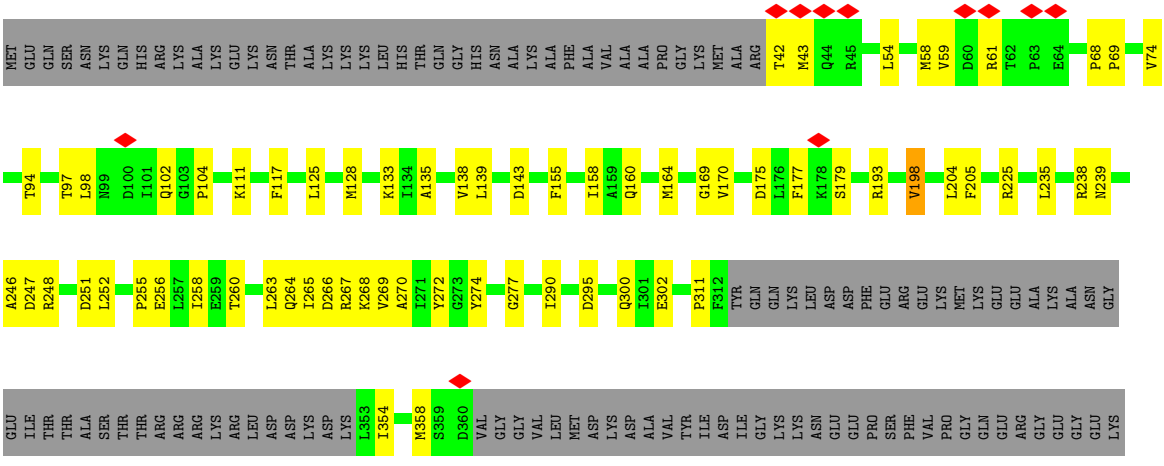


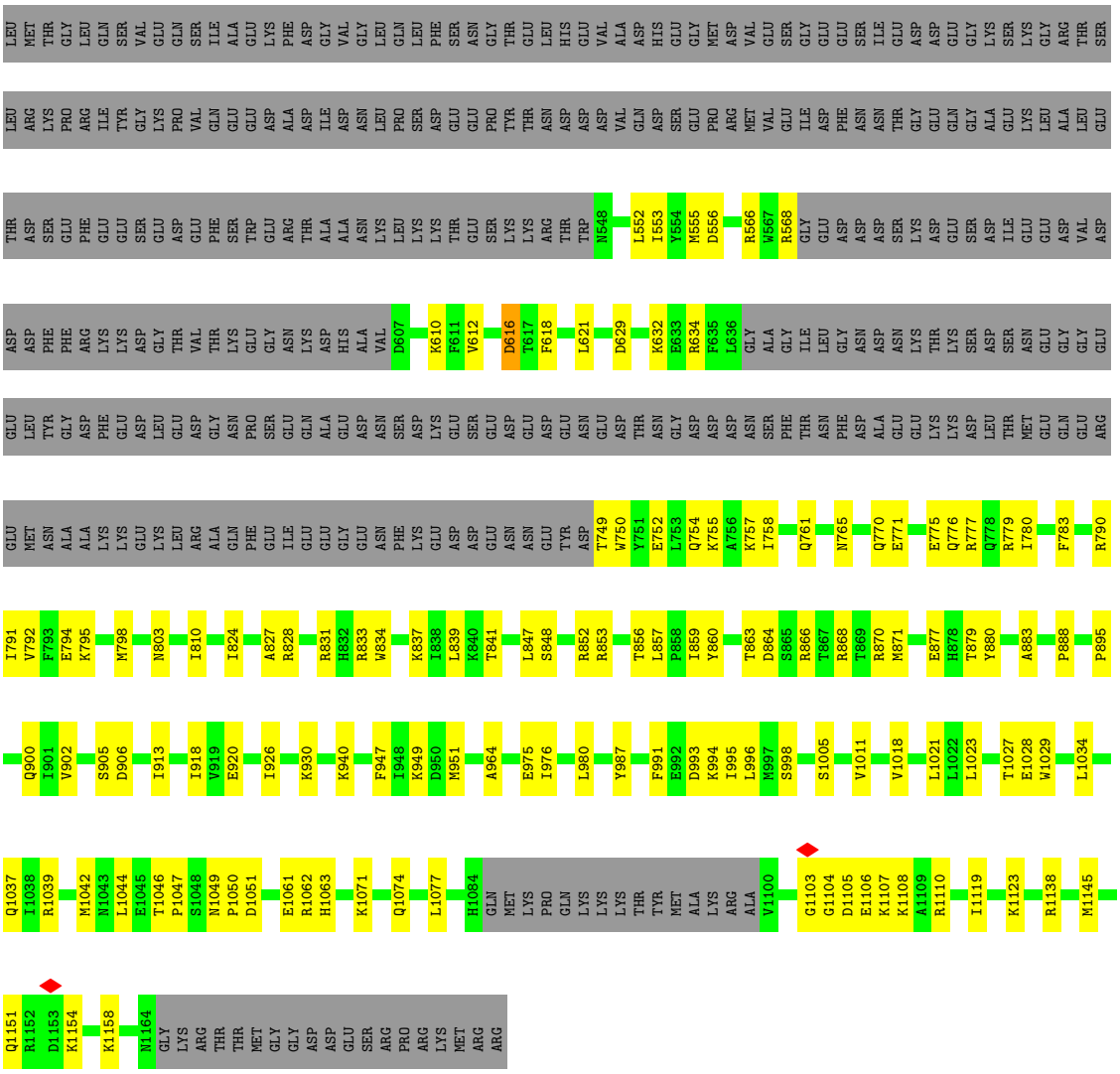


• Molecule 52: Ribosome biogenesis protein BMS1

Chain RJ:



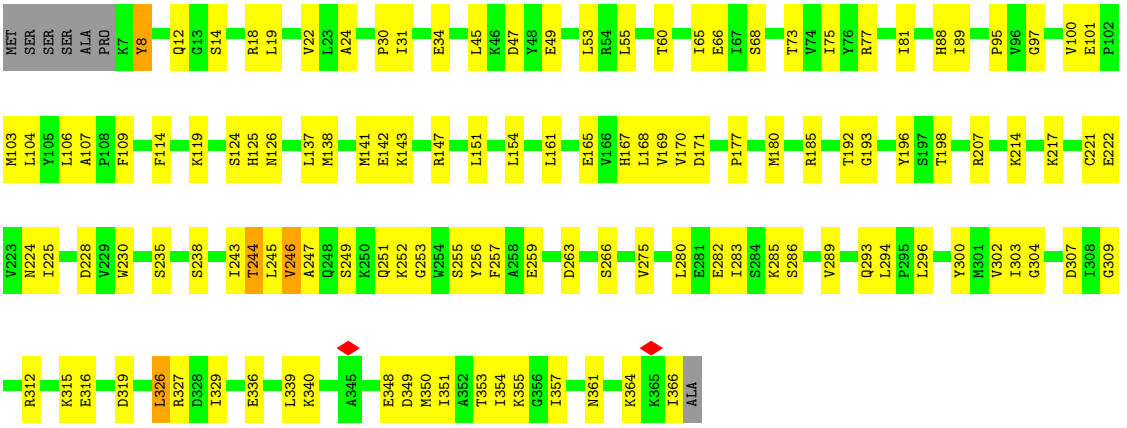




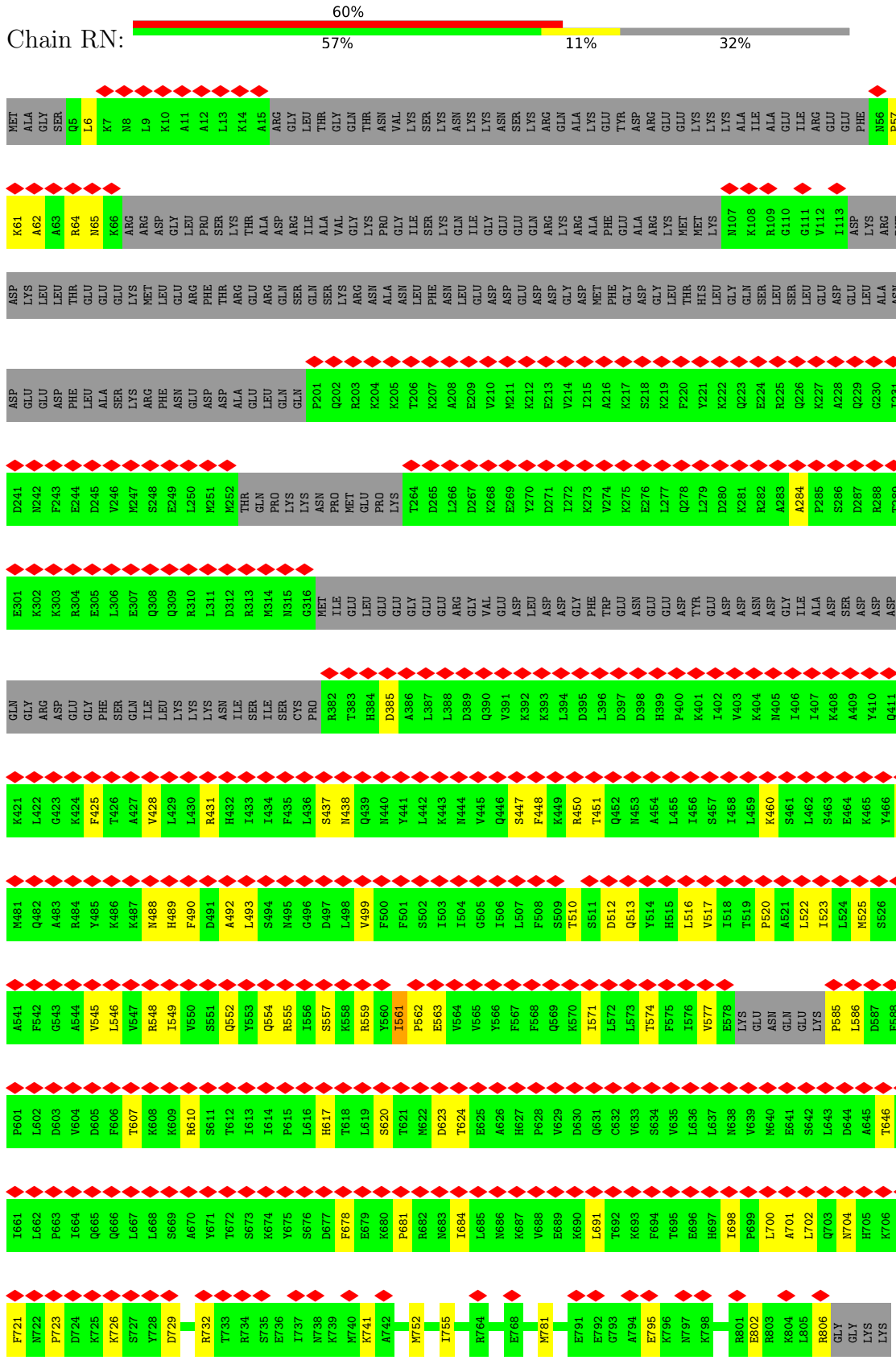
• Molecule 53: RNA 3'-terminal phosphate cyclase-like protein

Chain RK:



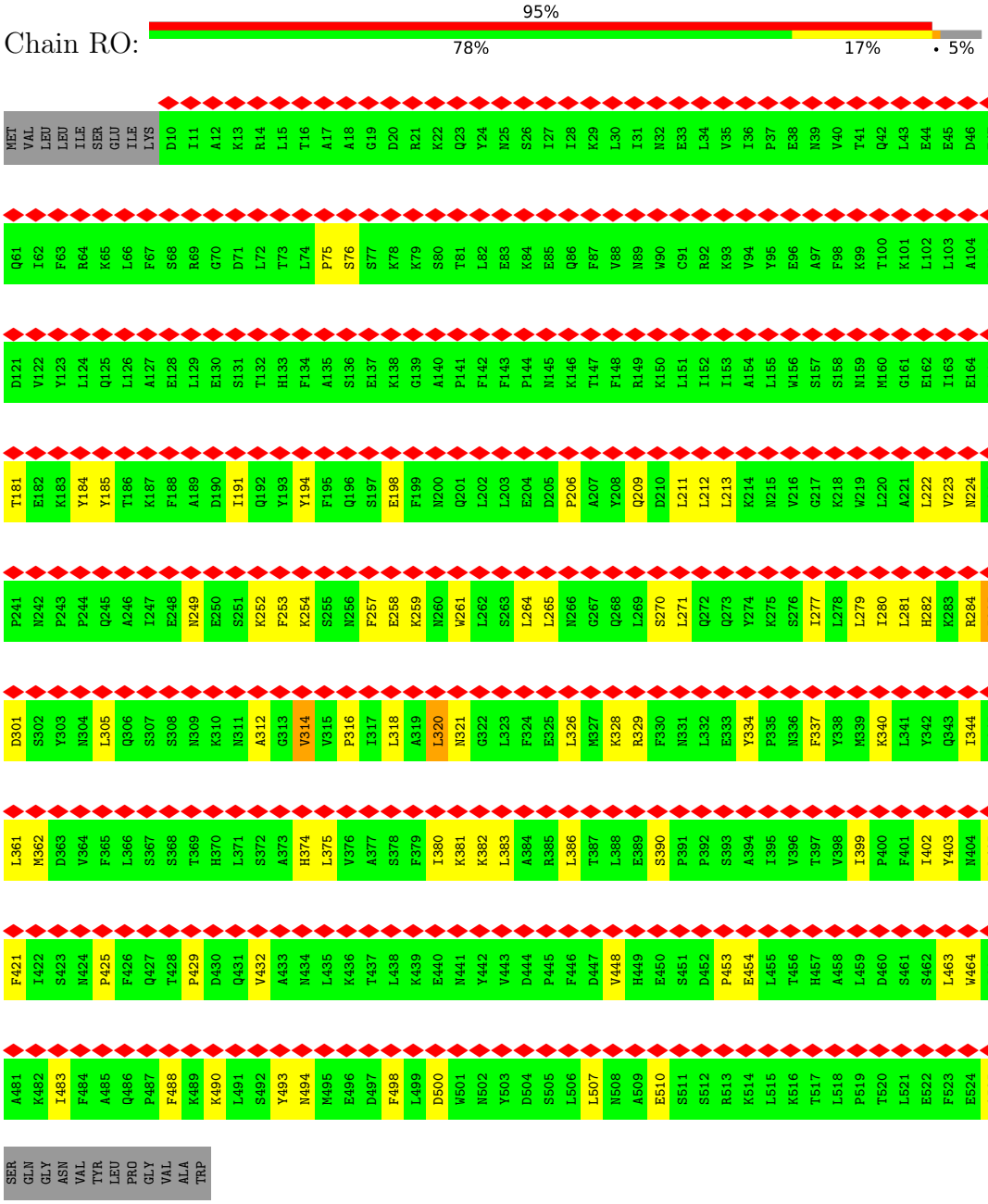


• Molecule 54: Nucleolar complex protein 14



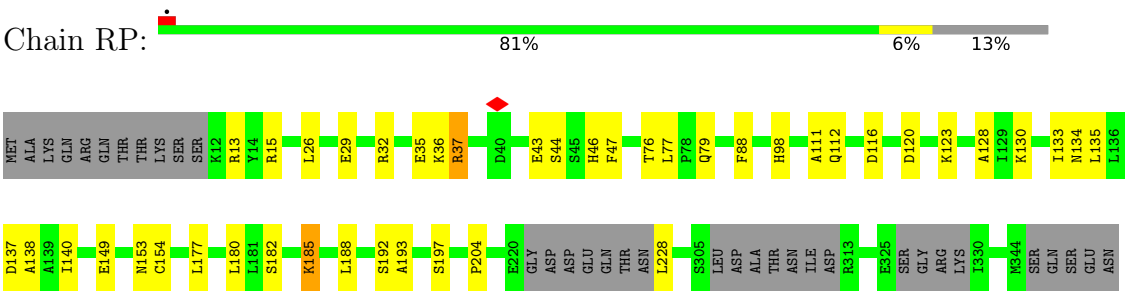
• Molecule 55: Nucleolar complex protein 4

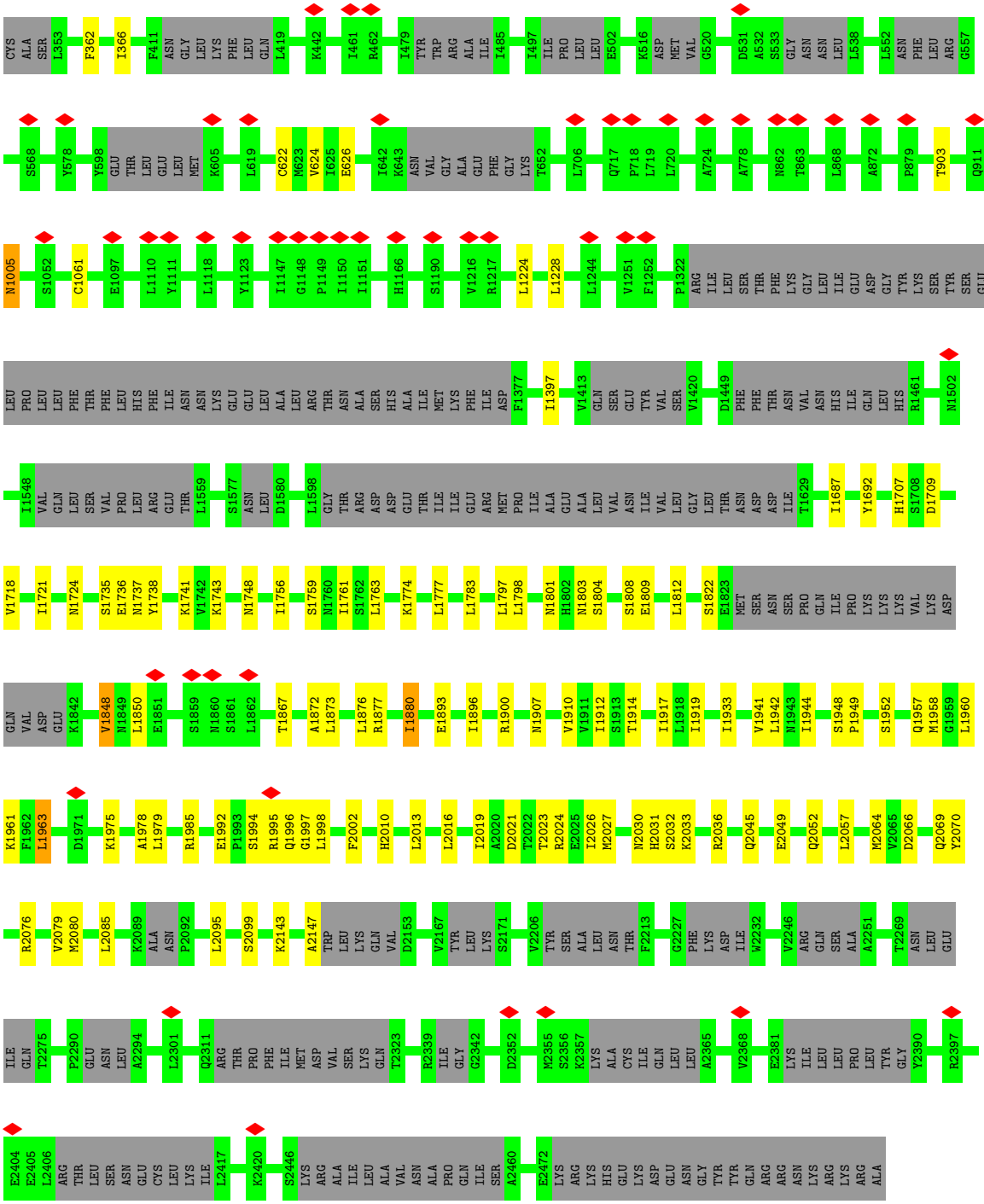
Chain RO:



• Molecule 56: U3 small nucleolar RNA-associated protein 20

Chain RP:

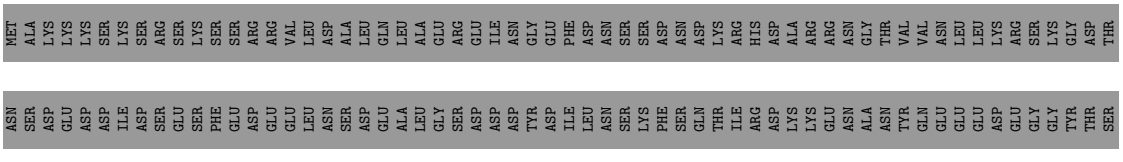


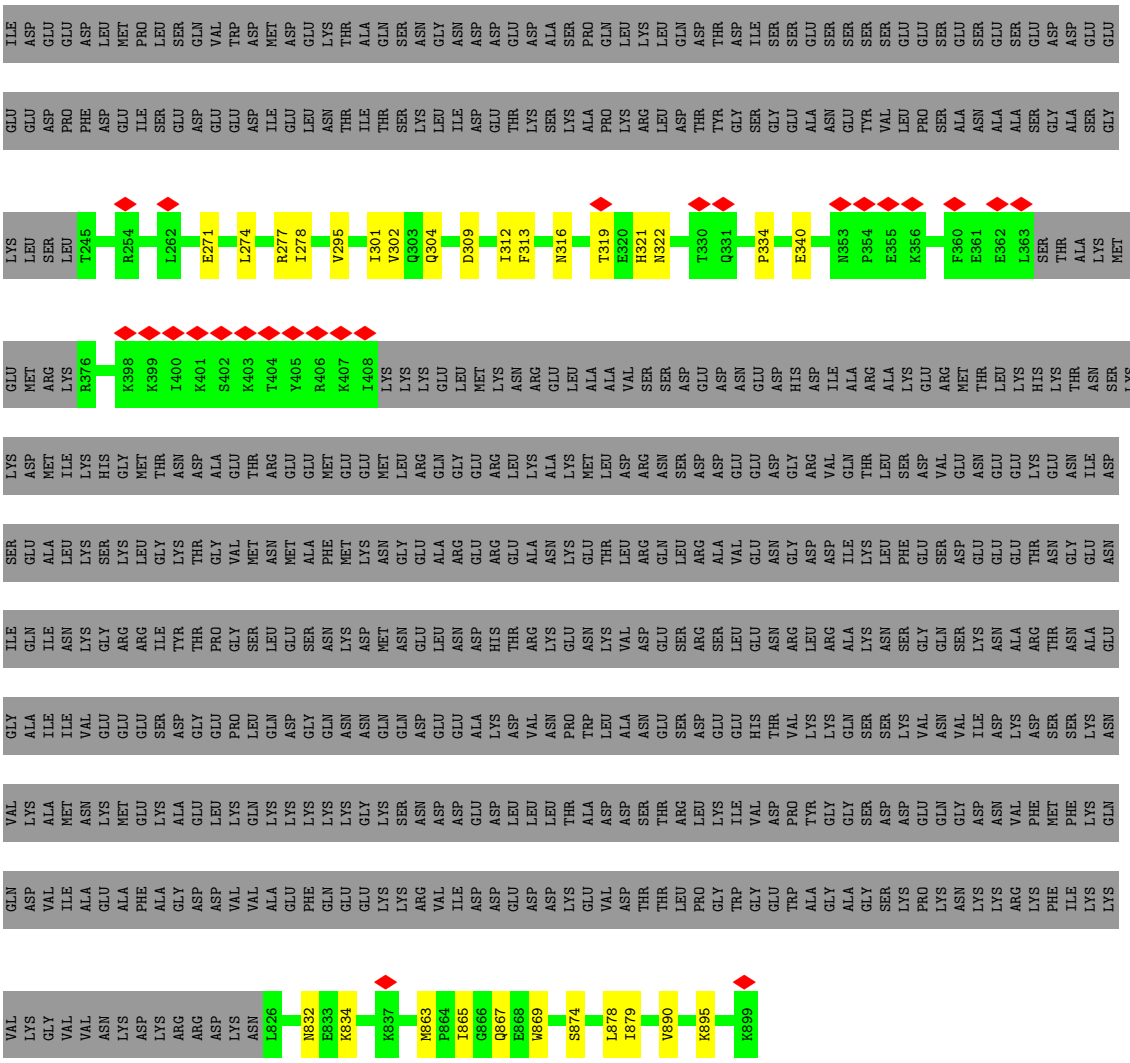


• Molecule 57: U3 small nucleolar RNA-associated protein 14

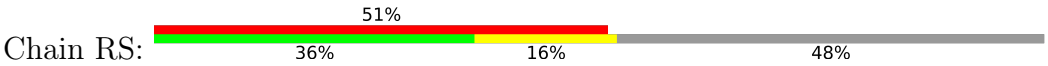
Chain RQ:

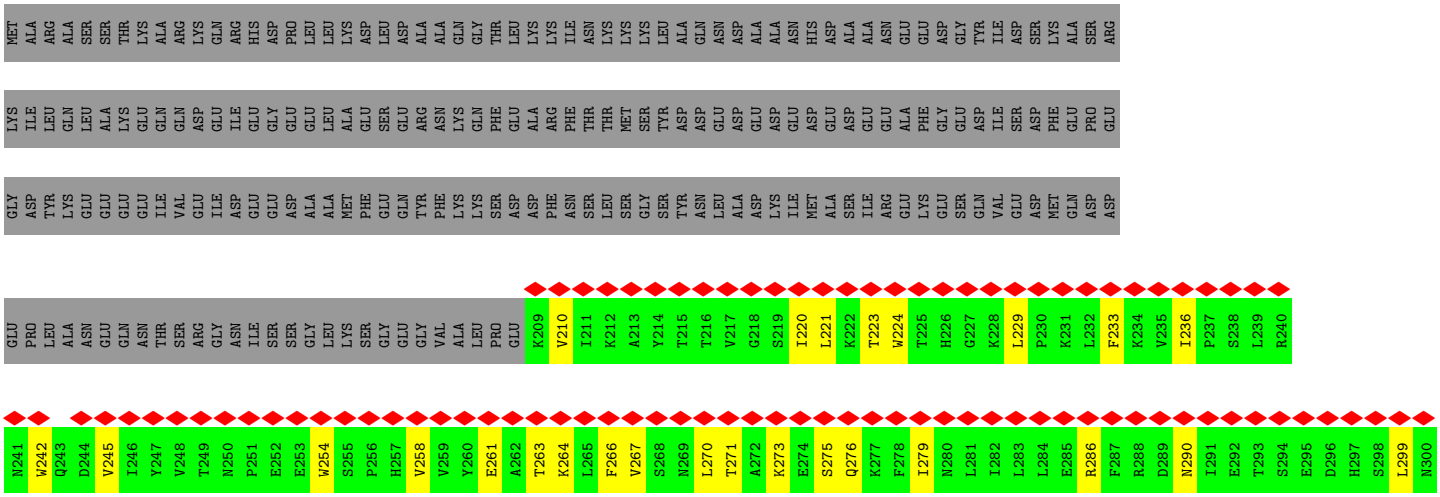


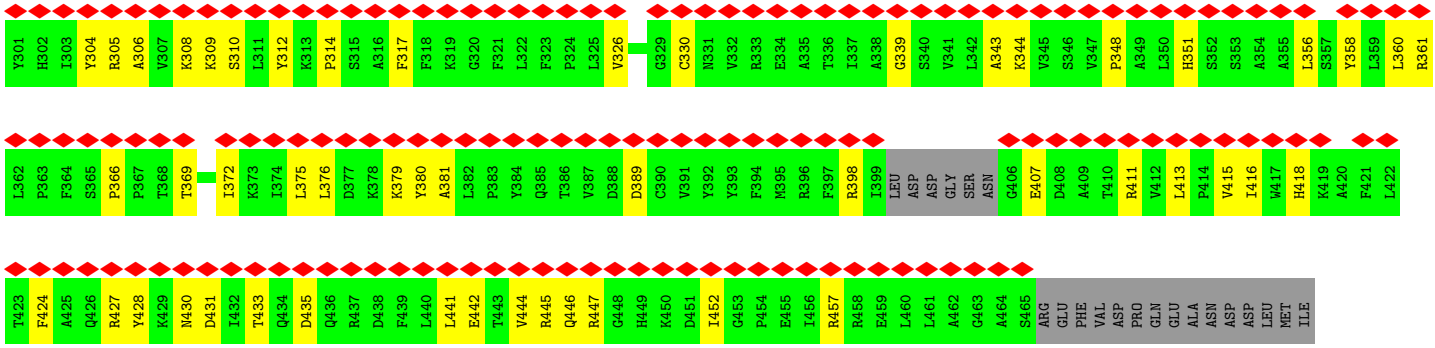




• Molecule 58: Essential nuclear protein 1

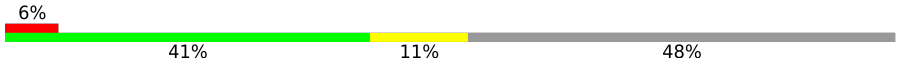


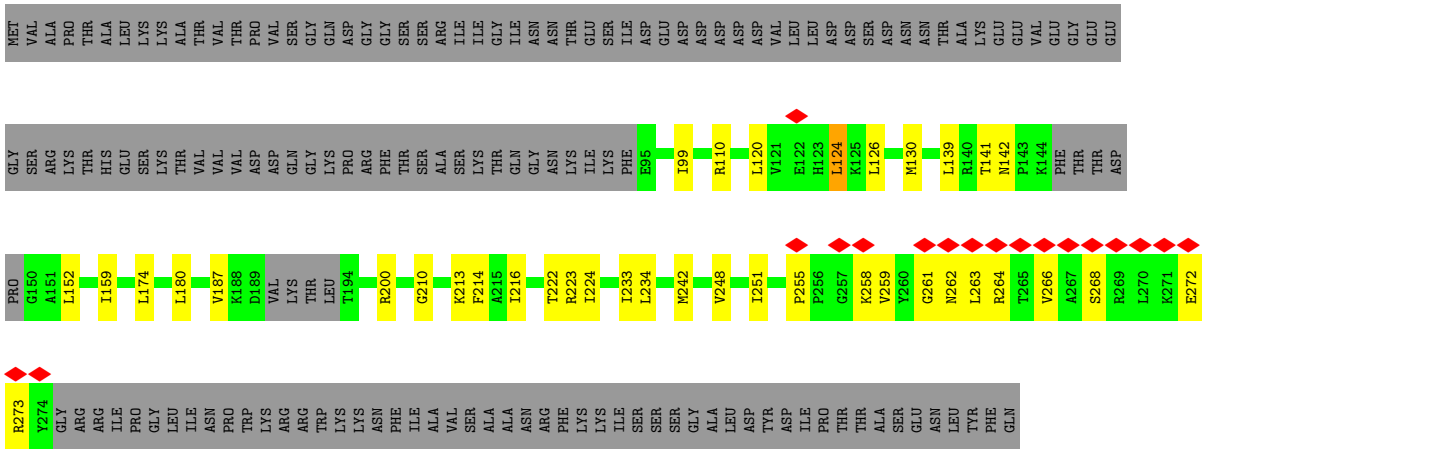




• Molecule 59: Pno1

Chain RT:

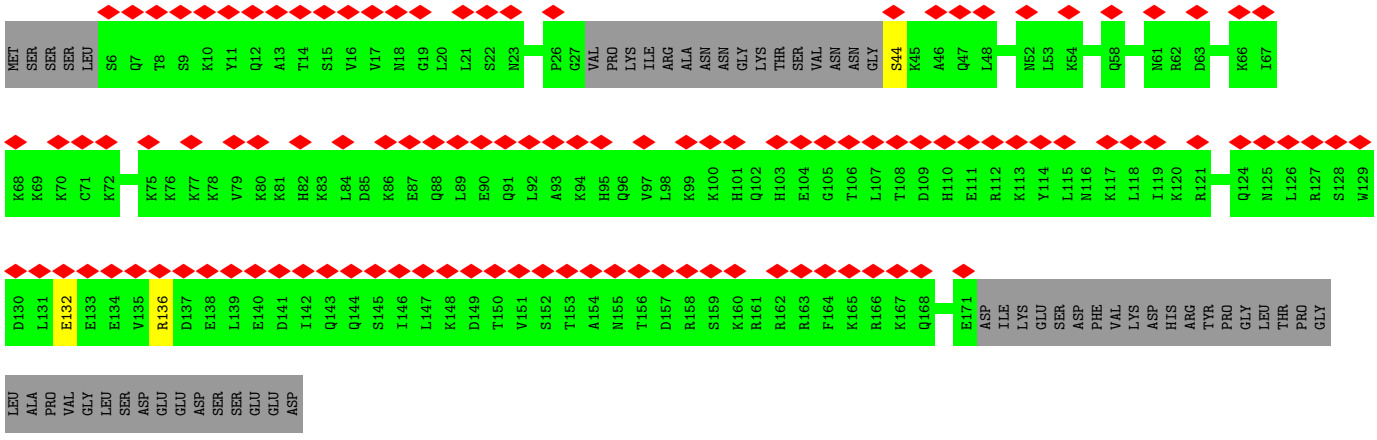




• Molecule 60: Regulator of rDNA transcription protein 14

Chain RW:

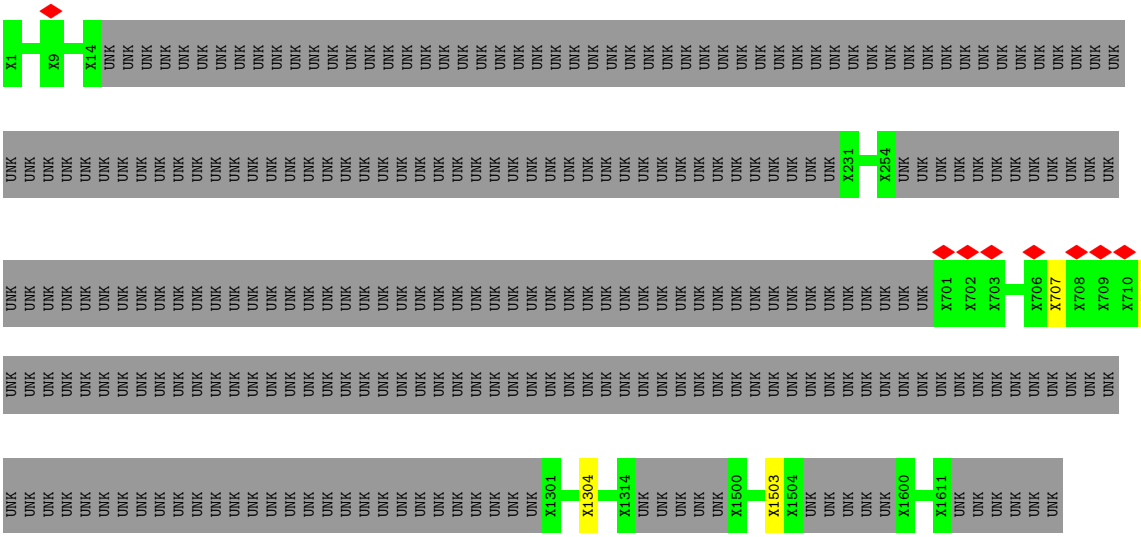




• Molecule 61: Unassigned helices 1

Chain X1:

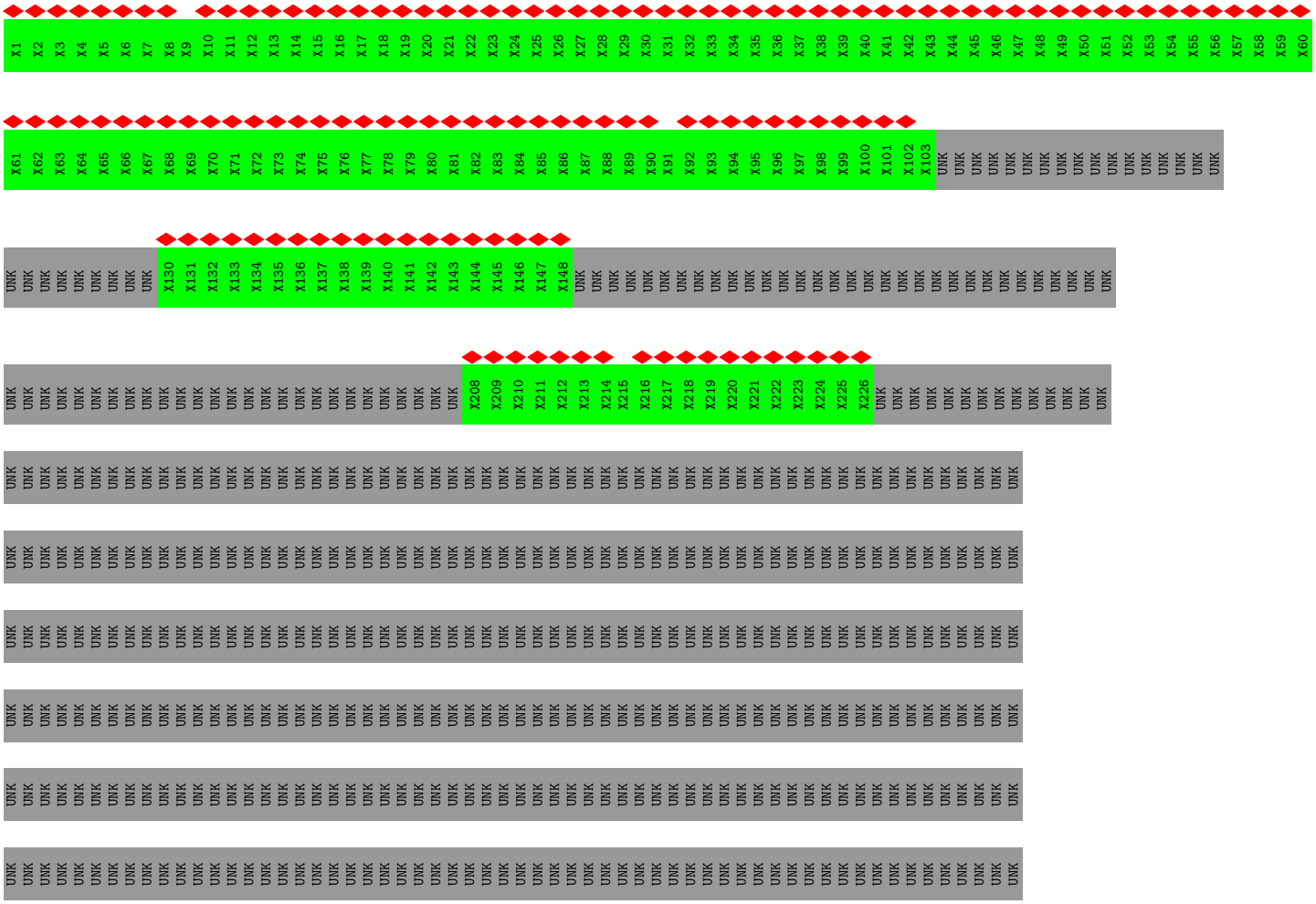


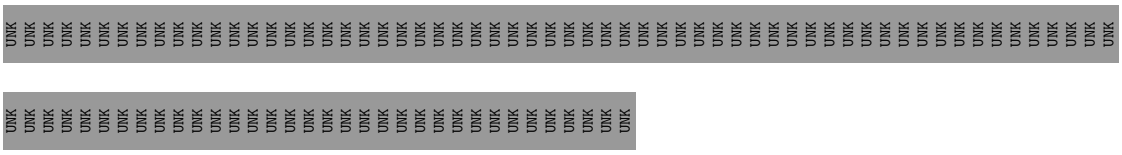


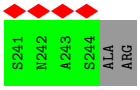
• Molecule 62: Unassigned helices 2

Chain X2:





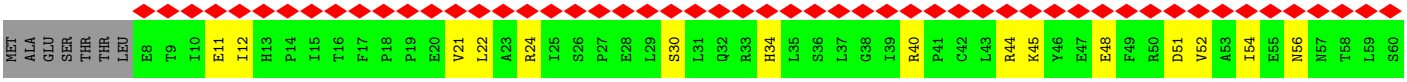

UNK UNK UNK

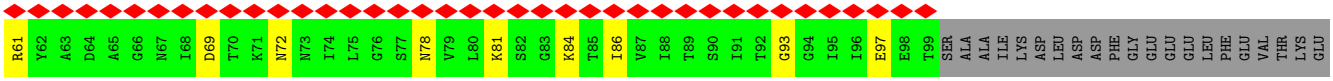


• Molecule 65: Exosome complex component RRP43

Chain R3:

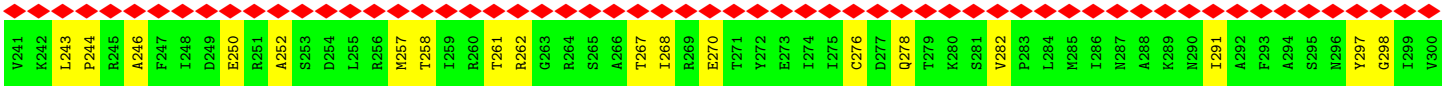


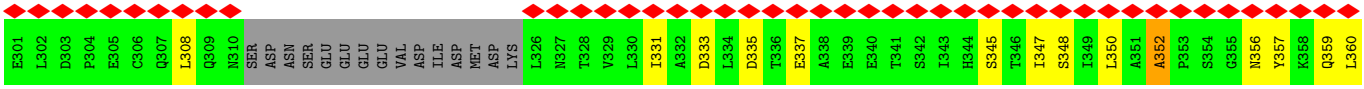


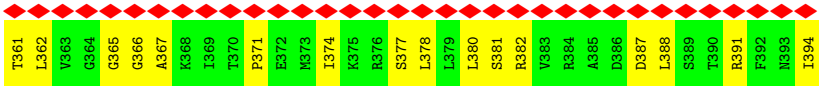








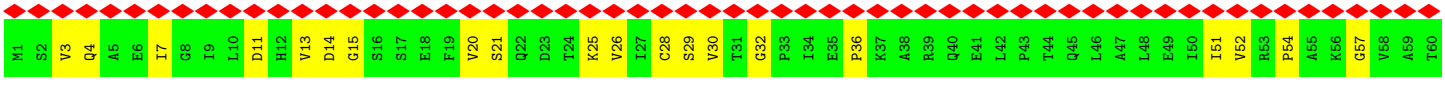


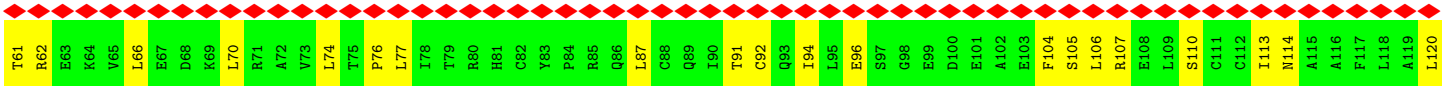


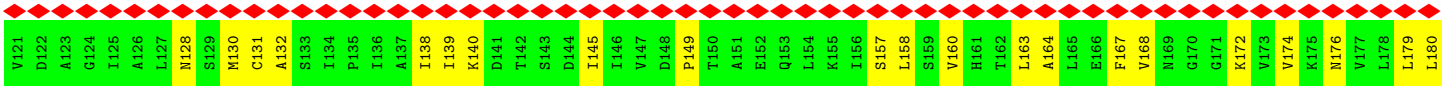
• Molecule 66: Exosome complex component RRP46

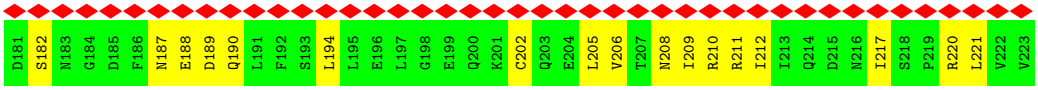
Chain R6:





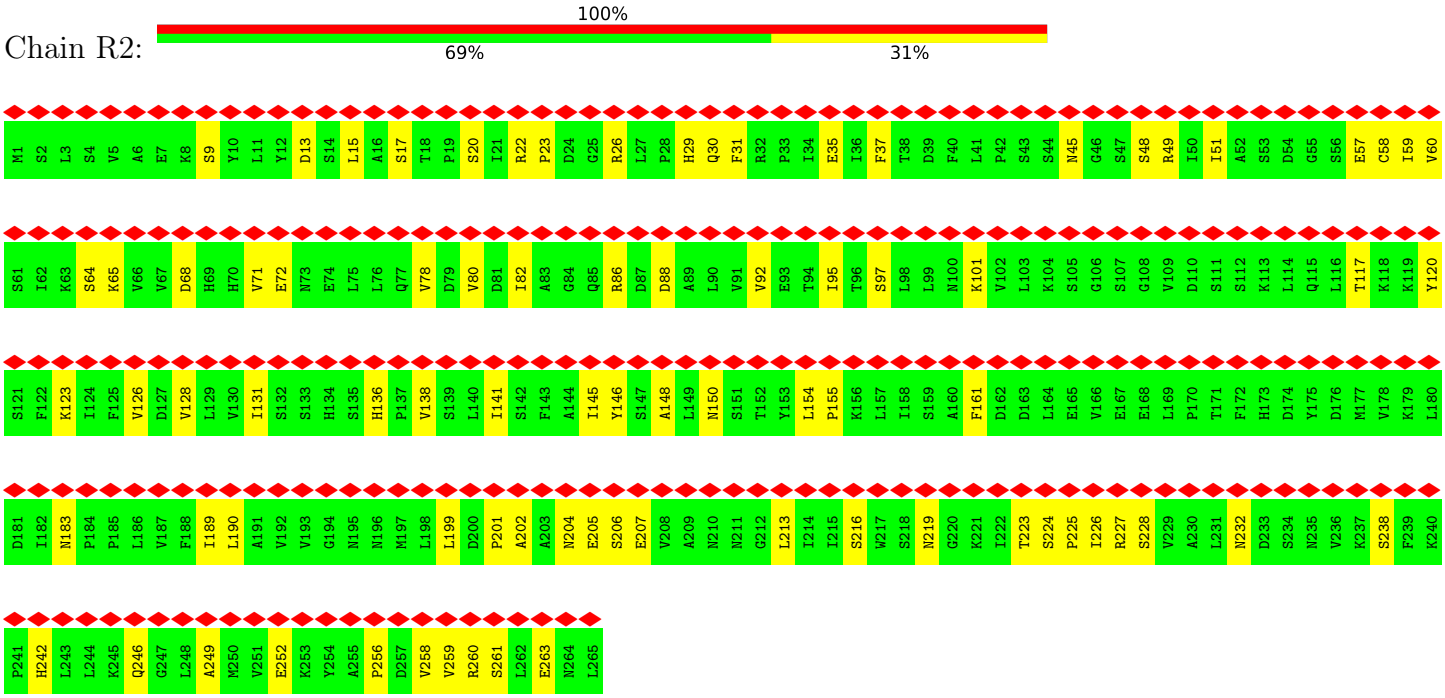






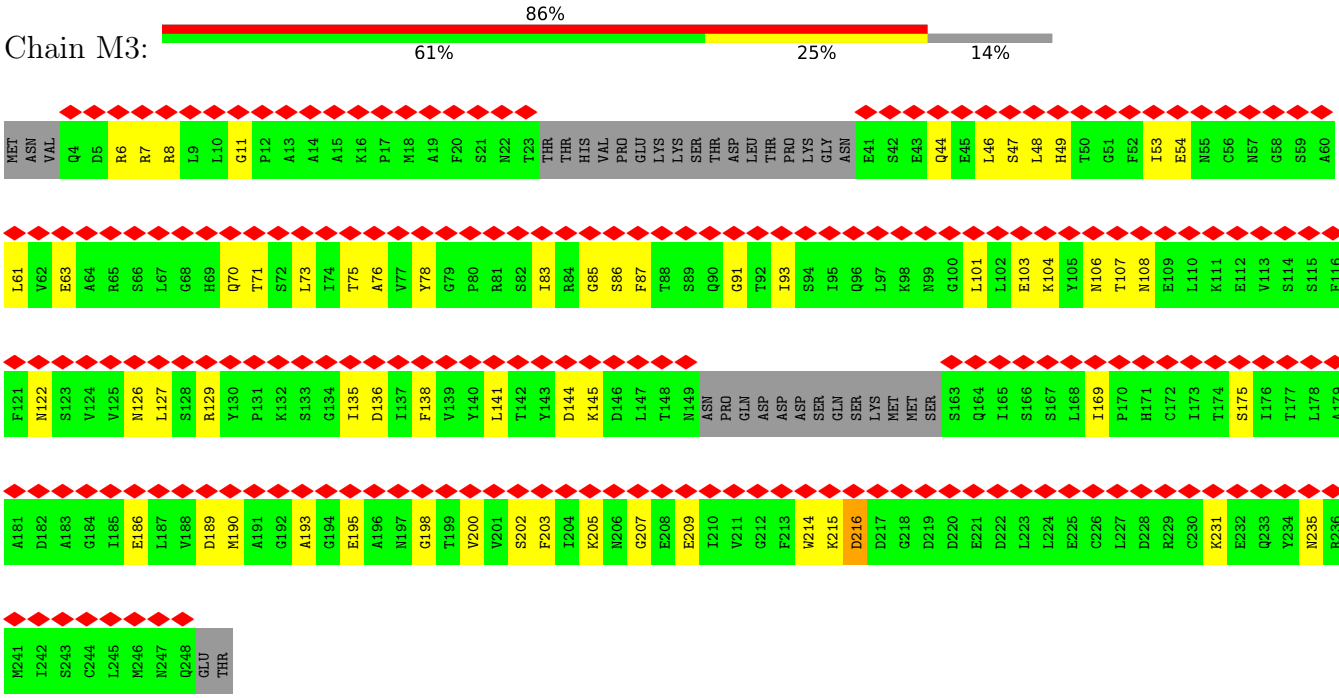
• Molecule 67: Exosome complex component RRP42

Chain R2:



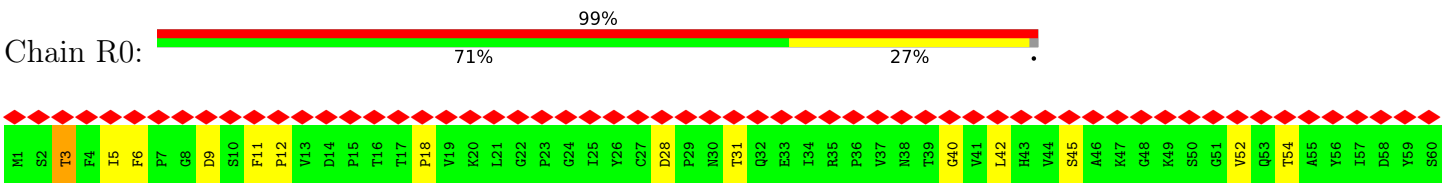
• Molecule 68: Exosome complex component MTR3

Chain M3:



• Molecule 69: Exosome complex component RRP40

Chain R0:

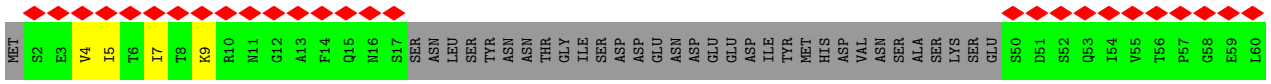


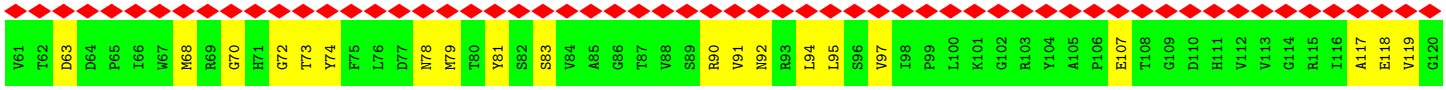


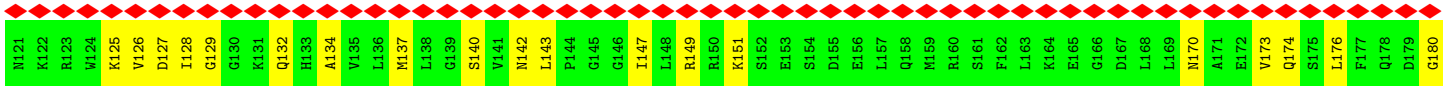
• Molecule 70: Exosome complex component RRP4

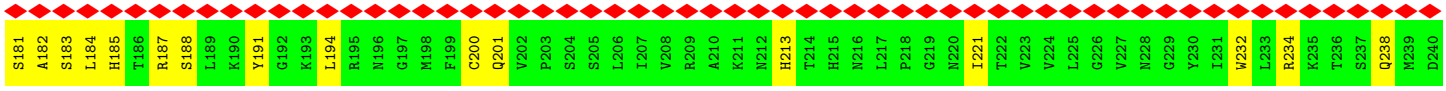
Chain r4:

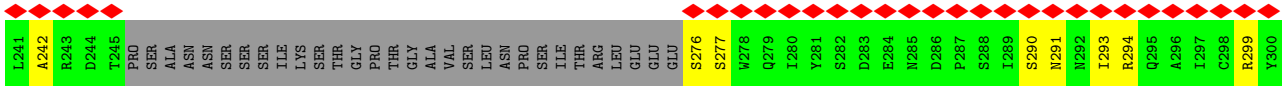


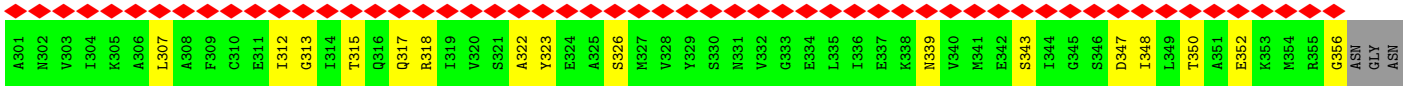










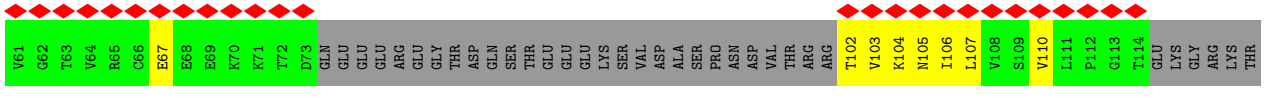


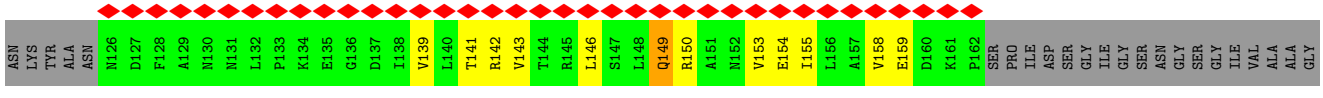
• Molecule 71: Exosome complex component CSL4

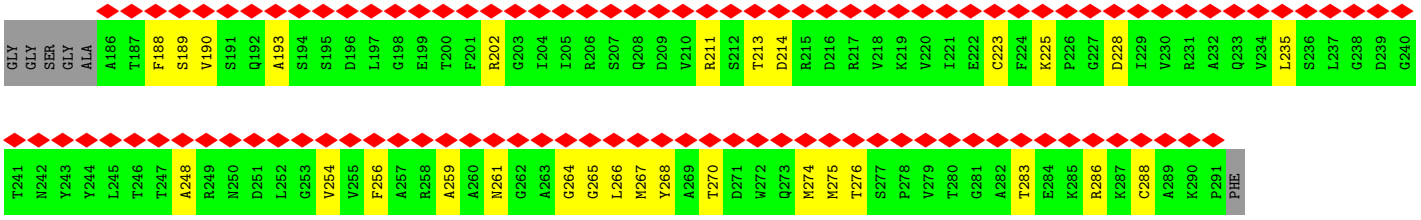
Chain C4:





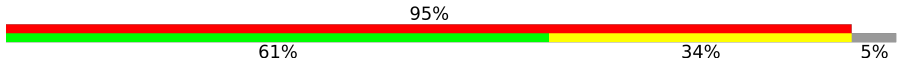


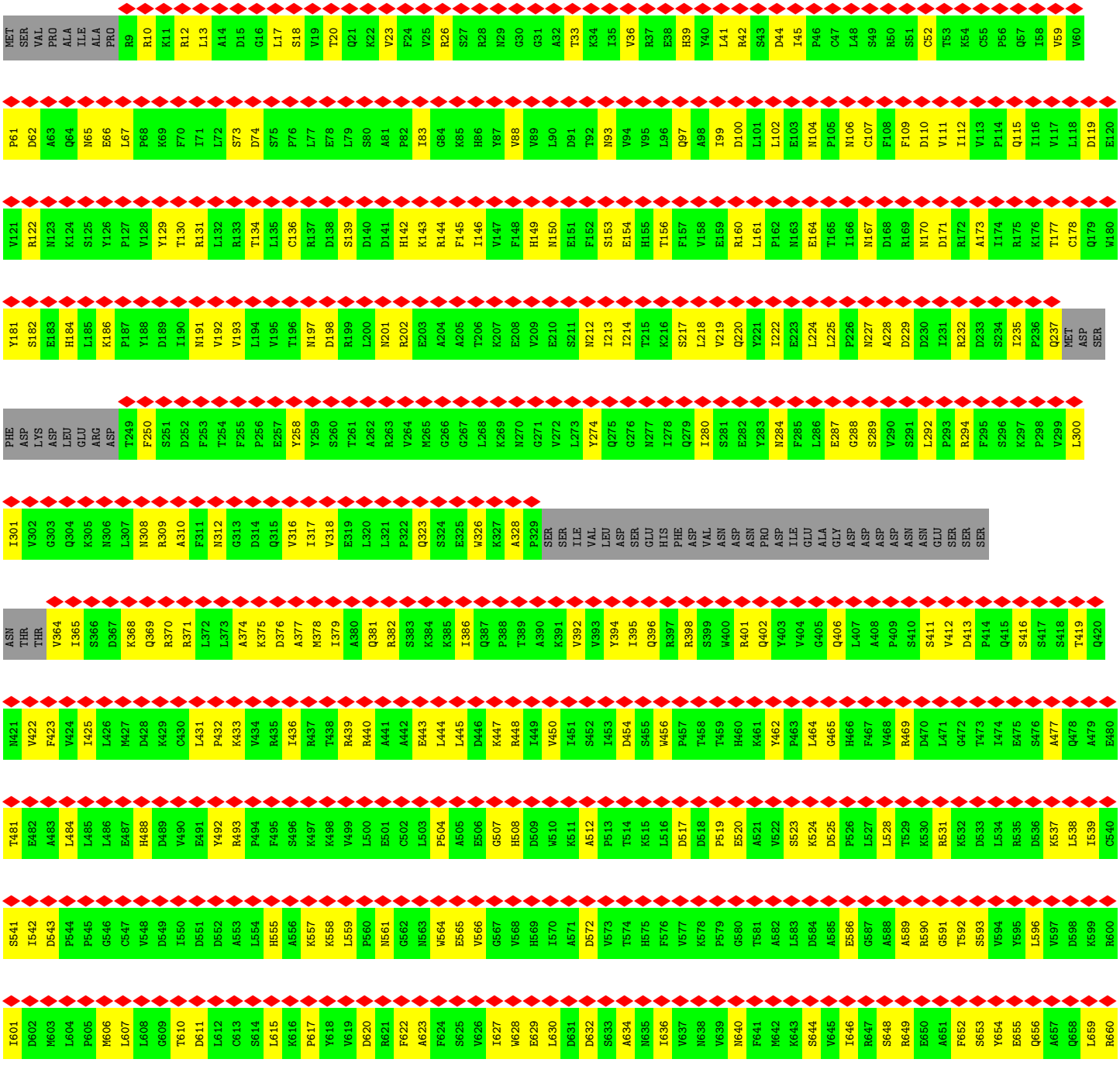


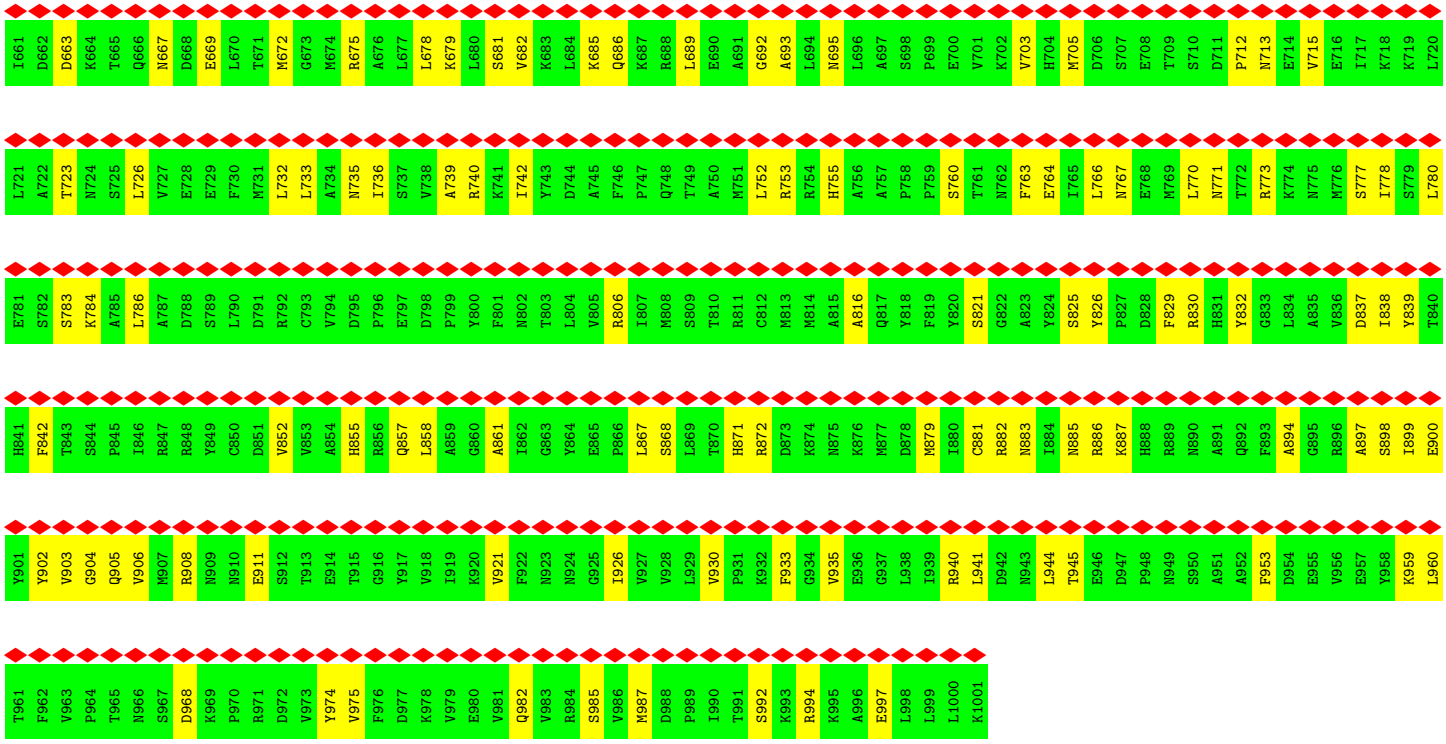


• Molecule 72: Exosome complex exonuclease DIS3

Chain R4:



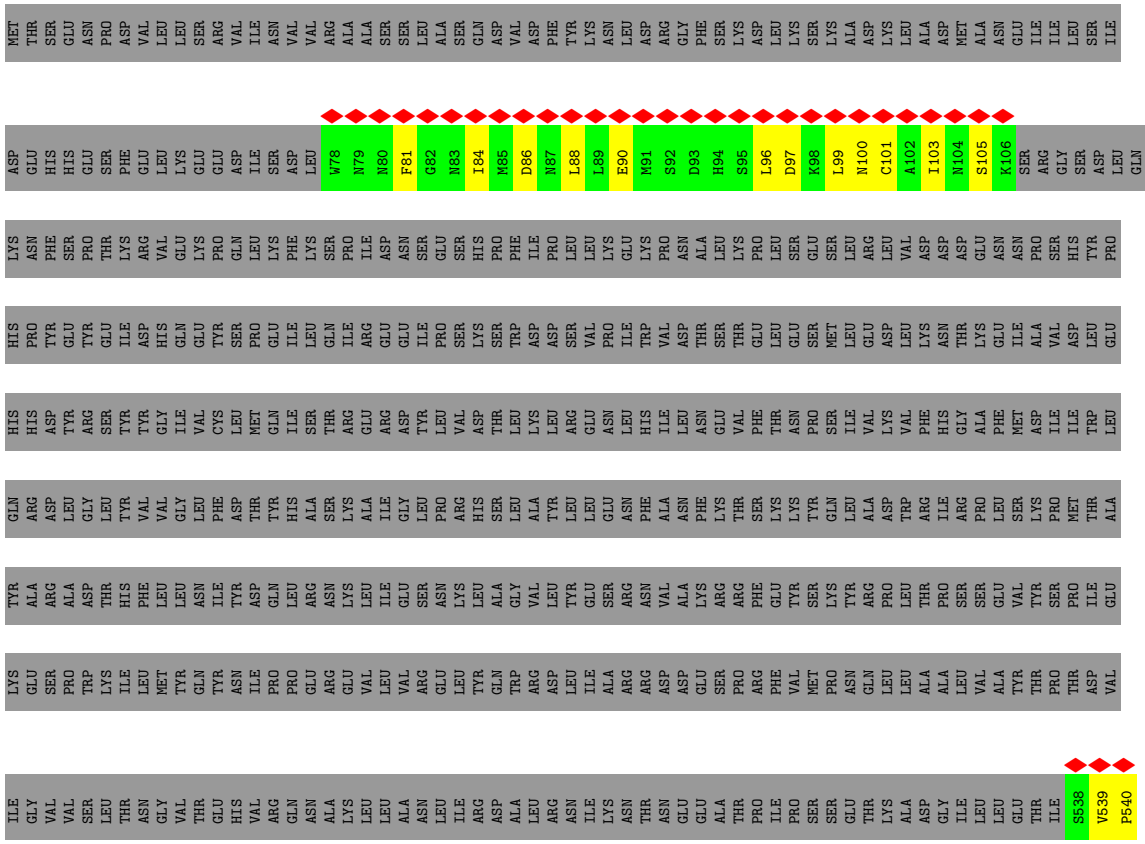


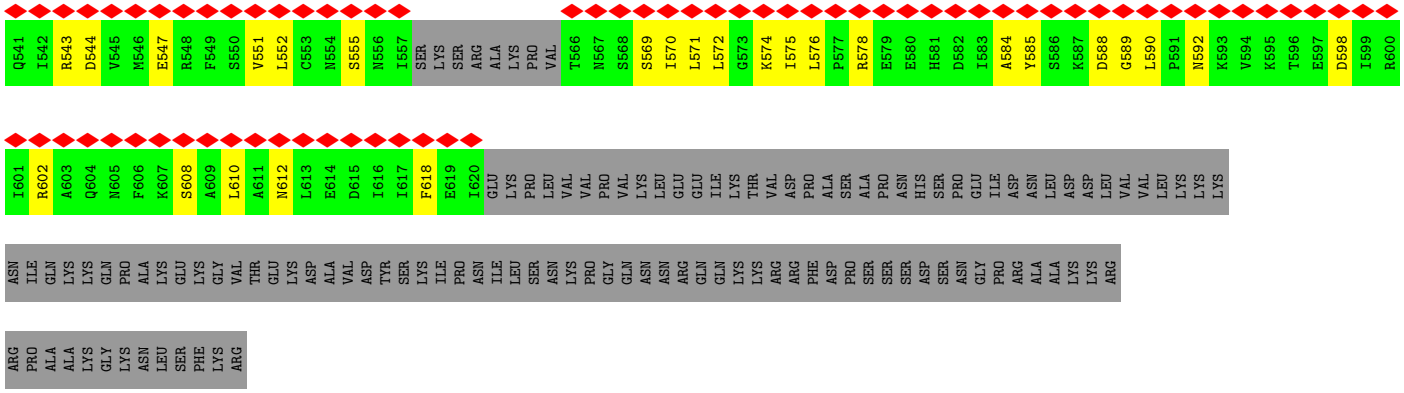


- Molecule 73: Exosome complex exonuclease RRP6

Chain r6:



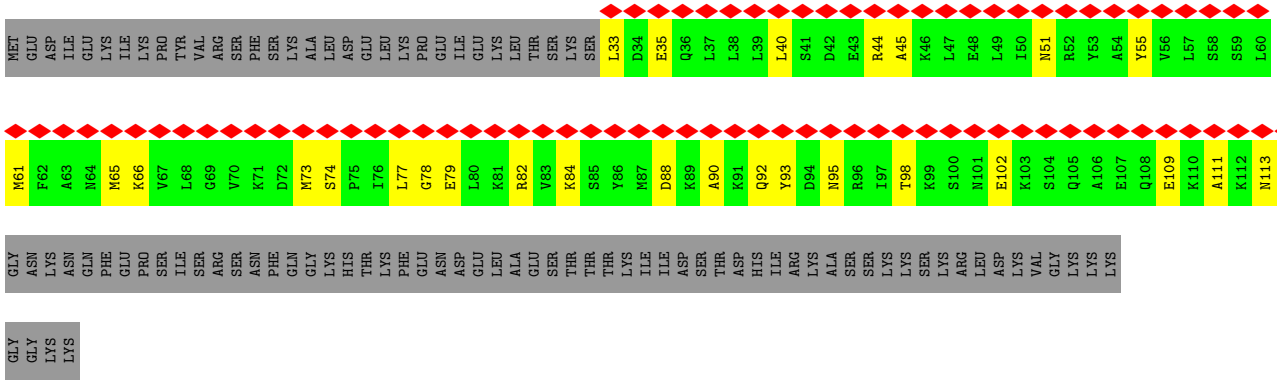




• Molecule 74: Exosome complex protein LRP1

Chain R7:

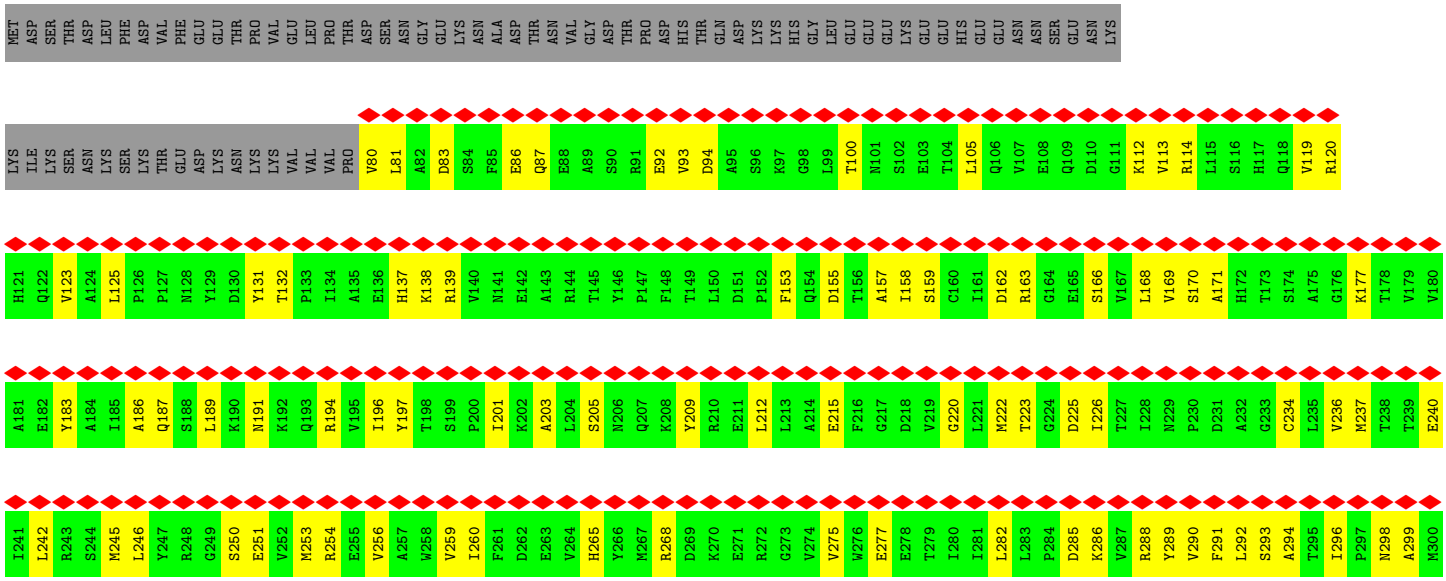


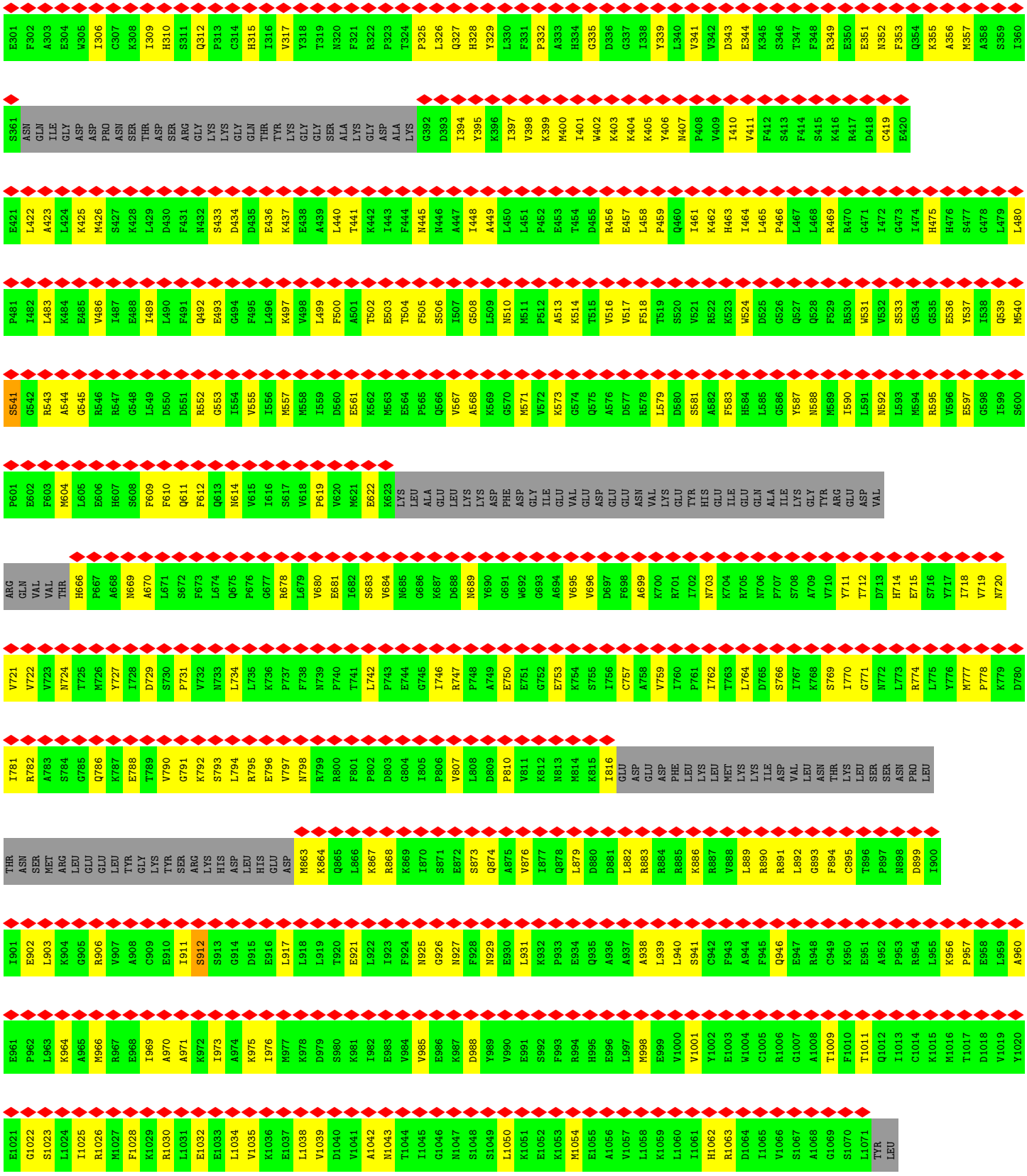


• Molecule 75: ATP-dependent RNA helicase DOB1

Chain M4:



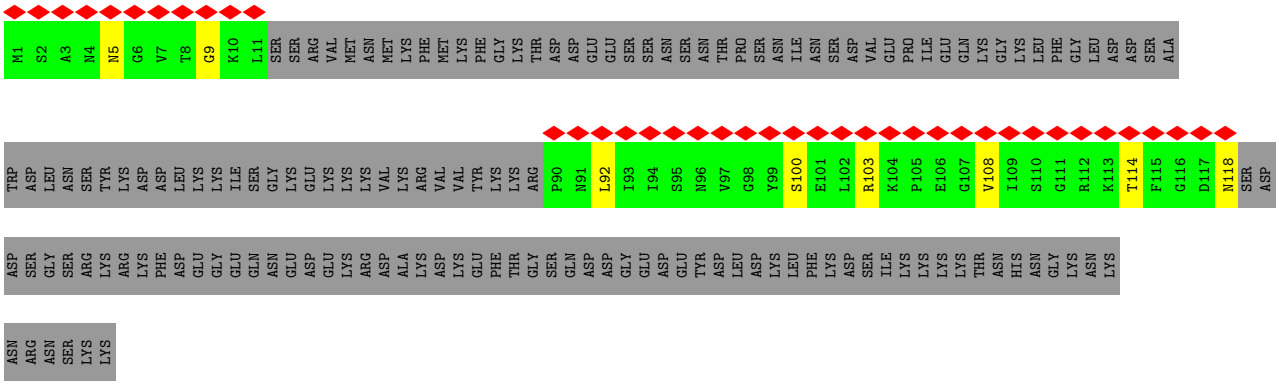




• Molecule 76: M-phase phosphoprotein 6 homolog

Chain M6:


22%
17%
78%


M1 S2 A3 N4 N5 G6 V7 T8 G9 K10 L11 SER SER ARG VAL MET ASN MET LYS PHE MET LYS PHE GLY LYS THR ASP ASP GLU GLU SER SER ASN SER ASN THR PRO SER ASN ILE ASN SER ASP VAL GLU PRO ILE GLU GLN LYS GLY LYS LEU PHE GLY LEU ASP ASP SER ALA
TRP ASP LEU ASN SER TYR LYS ASP ASP LEU LYS LYS ILE SER GLY LYS GLU LYS LYS LYS VAL LYS ARG VAL VAL TYR LYS LYS ARG P90 N91 L92 I93 I94 S95 N96 V97 G98 Y99 S100 E101 L102 R103 K104 P105 E106 G107 V108 I109 S110 G111 R112 K113 T114 F115 G116 D117 N118 SER ASP
ASP SER GLY SER ARG LYS ARG LYS PHE ASP GLU GLY GLU GLN ASN GLU ASP GLU LYS ARG ASP ALA LYS ASP LYS GLU PHE THR GLY SER GLN ASP ASP GLY GLU ASP GLU TYR ASP LEU ASP LYS LEU PHE LYS ASP SER ILE LYS LYS LYS LYS THR ASN HIS ASN GLY LYS ASN LYS
ASN ARG ASN SER LYS LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75404	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 ($e^-/Å^2$)	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	0.146	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.33	0/5532	0.47	1/8585 (0.0%)
2	5A	0.27	0/3643	0.46	1/5663 (0.0%)
3	SA	0.32	0/29737	0.46	4/46285 (0.0%)
4	SC	0.43	0/1874	0.81	3/2512 (0.1%)
5	SF	0.36	0/1969	0.78	3/2661 (0.1%)
6	SG	0.41	0/1690	0.67	0/2285
7	SH	0.24	0/1477	0.59	0/1977
8	SI	0.36	0/1330	0.77	5/1792 (0.3%)
9	SJ	0.25	0/1124	0.66	0/1510
10	SK	0.48	0/1410	0.69	0/1888
11	SM	0.25	0/1139	0.60	0/1535
12	SO	0.41	0/1109	0.72	0/1495
13	SP	0.37	0/879	0.68	1/1186 (0.1%)
14	SR	0.48	0/990	0.77	0/1335
15	SX	0.45	0/1020	0.70	0/1371
16	SY	0.38	0/819	0.69	0/1093
17	SZ	0.43	0/1000	0.72	0/1334
18	Sc	0.43	0/613	0.77	0/828
19	Sd	0.47	0/499	0.80	0/670
20	3B	0.50	0/1901	0.71	0/2567
20	3C	0.31	0/1796	0.69	0/2424
21	3D	0.41	0/3020	0.67	0/4066
22	3E	0.35	0/3072	0.62	0/4169
23	3F	0.46	0/3569	0.73	0/4806
24	3G	0.37	0/928	0.75	0/1262
24	3H	0.51	0/928	0.74	0/1262
25	A4	0.32	0/5338	0.69	3/7230 (0.0%)
26	A5	0.40	0/4021	0.64	0/5462
27	A8	0.24	0/3328	0.64	0/4565
28	A9	0.24	0/951	0.68	0/1287
29	AE	0.30	1/10050 (0.0%)	0.58	0/13739
30	AF	0.26	0/3885	0.63	2/5261 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
31	AG	0.28	0/6699	0.63	1/9077 (0.0%)
32	B1	0.51	0/6570	0.70	2/8892 (0.0%)
33	B2	0.38	0/6628	0.70	2/8954 (0.0%)
34	B3	0.34	0/6014	0.77	2/8137 (0.0%)
35	B8	0.40	0/3848	0.66	2/5218 (0.0%)
36	BE	0.51	0/6606	0.71	0/8935
37	B6	0.38	0/2849	0.64	0/3853
38	5B	0.23	0/499	0.61	0/659
39	5C	0.50	0/3690	0.68	0/4991
40	5D	0.28	0/1757	0.59	0/2320
41	5E	0.35	0/1580	0.72	0/2115
42	5F	0.47	0/1559	0.72	0/2097
43	5G	0.47	0/1768	0.72	0/2392
44	5H	0.41	0/601	0.69	0/789
45	5I	0.59	0/3835	0.75	0/5162
46	5J	0.32	0/1147	0.60	0/1531
47	5K	0.47	0/1346	0.66	0/1812
48	RD	0.25	0/2454	0.63	1/3310 (0.0%)
49	RE	0.31	0/9015	0.65	0/12195
50	RF	0.29	0/2004	0.67	0/2697
51	RG	0.24	0/1727	0.68	0/2329
51	RH	0.24	0/1828	0.61	1/2470 (0.0%)
52	RJ	0.40	0/6067	0.66	3/8170 (0.0%)
53	RK	0.35	0/2832	0.66	0/3825
54	RN	0.26	0/4146	0.62	0/5604
55	RO	0.25	0/3849	0.63	1/5261 (0.0%)
56	RP	0.25	0/12777	0.58	6/17558 (0.0%)
57	RQ	0.39	0/1682	0.68	1/2286 (0.0%)
58	RS	0.32	1/2104 (0.0%)	0.73	0/2854
59	RT	0.29	0/1379	0.67	0/1853
60	RW	0.16	0/745	0.37	0/1038
63	R5	0.58	1/2340 (0.0%)	0.74	0/3161
64	R1	0.58	0/1910	0.76	0/2579
65	R3	0.51	0/2628	0.77	0/3569
66	R6	0.56	0/1714	0.77	0/2328
67	R2	0.52	0/2069	0.76	0/2817
68	M3	0.54	0/1661	0.75	0/2243
69	R0	0.55	0/1828	0.80	2/2486 (0.1%)
70	r4	0.53	0/2269	0.77	0/3066
71	C4	0.48	0/1676	0.77	0/2277
72	R4	0.38	0/7575	0.69	1/10290 (0.0%)
73	r6	0.48	0/810	0.71	0/1091
74	R7	0.38	0/686	0.70	0/916

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
75	M4	0.49	0/6945	0.78	4/9400 (0.0%)
76	M6	0.45	0/277	0.94	1/371 (0.3%)
All	All	0.38	3/244634 (0.0%)	0.65	53/339083 (0.0%)

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	4
7	SH	0	1
8	SI	0	4
12	SO	0	1
18	Sc	0	2
19	Sd	0	1
20	3C	0	1
23	3F	0	1
26	A5	0	1
27	A8	0	6
29	AE	0	1
30	AF	0	1
31	AG	0	5
32	B1	0	1
33	B2	0	2
34	B3	0	5
38	5B	0	1
41	5E	0	1
45	5I	0	3
49	RE	0	3
50	RF	0	3
51	RH	0	1
52	RJ	0	1
53	RK	0	1
55	RO	0	4
56	RP	0	11
57	RQ	0	2
59	RT	0	1
64	R1	0	1
65	R3	0	3
66	R6	0	1
67	R2	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
68	M3	0	2
70	r4	0	1
71	C4	0	1
72	R4	0	1
75	M4	0	3
All	All	0	83

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	R5	250	LYS	CA-CB	-7.14	1.43	1.53
29	AE	642	THR	C-N	5.40	1.39	1.33
58	RS	344	LYS	CA-C	5.30	1.60	1.52

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	B3	584	ILE	CA-C-N	6.54	134.03	121.54
34	B3	584	ILE	C-N-CA	6.54	134.03	121.54
48	RD	1187	VAL	N-CA-C	-6.43	106.54	111.62
25	A4	480	PHE	N-CA-C	6.27	118.25	110.91
76	M6	108	VAL	N-CA-C	-6.11	104.70	113.07

There are no chirality outliers.

5 of 83 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	135	LEU	Peptide
4	SC	16	GLN	Peptide
4	SC	177	GLN	Peptide
4	SC	208	GLN	Peptide
7	SH	152	ASP	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	4962	0	2519	57	0
2	5A	3260	0	1643	36	0
3	SA	26609	0	13415	318	0
4	SC	1848	0	1940	40	0
5	SF	1930	0	1950	32	0
6	SG	1669	0	1724	25	0
7	SH	1457	0	1504	39	0
8	SI	1310	0	1374	36	0
9	SJ	1104	0	1107	28	0
10	SK	1388	0	1467	28	0
11	SM	1113	0	1181	28	0
12	SO	1087	0	1152	27	0
13	SP	868	0	894	20	0
14	SR	973	0	1029	20	0
15	SX	1003	0	1040	25	0
16	SY	807	0	865	16	0
17	SZ	986	0	1042	19	0
18	Sc	603	0	621	14	0
19	Sd	497	0	535	5	0
20	3B	1865	0	1910	46	0
20	3C	1763	0	1805	53	0
21	3D	2974	0	3001	57	0
22	3E	3041	0	2831	73	0
23	3F	3498	0	3515	83	0
24	3G	916	0	964	17	0
24	3H	916	0	964	24	0
25	A4	5243	0	5216	194	0
26	A5	3953	0	3894	86	0
27	A8	3307	0	2316	45	0
28	A9	939	0	898	26	0
29	AE	9956	0	7969	130	0
30	AF	3807	0	3791	91	0
31	AG	6570	0	6473	190	0
32	B1	6427	0	6329	131	0
33	B2	6502	0	6493	154	0
34	B3	5919	0	6007	151	0
35	B8	3764	0	3757	83	0
36	BE	6475	0	6453	160	0
37	B6	2800	0	2517	43	0
38	5B	495	0	561	11	0
39	5C	3612	0	3578	69	0
40	5D	1733	0	1815	37	0
41	5E	1564	0	1592	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	5F	1530	0	1572	31	0
43	5G	1732	0	1744	38	0
44	5H	596	0	661	8	0
45	5I	3756	0	3708	92	0
46	5J	1127	0	1150	17	0
47	5K	1323	0	1401	20	0
48	RD	2413	0	2264	29	0
49	RE	8805	0	8911	200	0
50	RF	1963	0	1942	43	0
51	RG	1701	0	1767	48	0
51	RH	1799	0	1872	46	0
52	RJ	5935	0	6100	136	0
53	RK	2781	0	2878	79	0
54	RN	4088	0	3798	64	0
55	RO	3766	0	3269	65	0
56	RP	12716	0	8235	94	0
57	RQ	1655	0	1461	22	0
58	RS	2051	0	2096	46	0
59	RT	1357	0	1426	22	0
60	RW	747	0	312	2	0
61	X1	400	0	99	3	0
62	X2	705	0	151	0	0
63	R5	2304	0	2265	63	0
64	R1	1886	0	1904	58	0
65	R3	2588	0	2607	78	0
66	R6	1696	0	1744	47	0
67	R2	2030	0	2047	58	0
68	M3	1639	0	1592	46	0
69	R0	1792	0	1747	41	0
70	r4	2236	0	2215	55	0
71	C4	1653	0	1616	44	0
72	R4	7430	0	7346	223	0
73	r6	802	0	776	35	0
74	R7	681	0	707	17	0
75	M4	6814	0	6792	236	0
76	M6	275	0	254	6	0
77	5K	1	0	0	0	0
77	Sc	1	0	0	0	0
78	RJ	32	0	12	0	0
79	RJ	1	0	0	0	0
All	All	238320	0	212092	4452	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 4452 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:741:LEU:HD11	25:A4:744:VAL:CG2	1.48	1.42
25:A4:740:PRO:O	25:A4:756:GLU:HG2	1.44	1.16
25:A4:741:LEU:HD11	25:A4:744:VAL:HG21	1.16	1.13
25:A4:741:LEU:HD21	25:A4:744:VAL:HG23	1.39	1.04
25:A4:741:LEU:CD1	25:A4:744:VAL:CG2	2.39	1.00

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	SC	230/255 (90%)	190 (83%)	39 (17%)	1 (0%)	30 62
5	SF	248/261 (95%)	211 (85%)	37 (15%)	0	100 100
6	SG	211/225 (94%)	194 (92%)	17 (8%)	0	100 100
7	SH	178/236 (75%)	158 (89%)	17 (10%)	3 (2%)	7 34
8	SI	160/190 (84%)	136 (85%)	24 (15%)	0	100 100
9	SJ	136/200 (68%)	113 (83%)	23 (17%)	0	100 100
10	SK	169/197 (86%)	155 (92%)	14 (8%)	0	100 100
11	SM	135/156 (86%)	119 (88%)	16 (12%)	0	100 100
12	SO	132/151 (87%)	119 (90%)	13 (10%)	0	100 100
13	SP	116/137 (85%)	103 (89%)	13 (11%)	0	100 100
14	SR	123/143 (86%)	110 (89%)	13 (11%)	0	100 100
15	SX	125/130 (96%)	114 (91%)	11 (9%)	0	100 100
16	SY	104/145 (72%)	91 (88%)	13 (12%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	SZ	121/135 (90%)	104 (86%)	17 (14%)	0	100	100
18	Sc	78/82 (95%)	66 (85%)	12 (15%)	0	100	100
19	Sd	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	204 (92%)	17 (8%)	0	100	100
21	3D	372/504 (74%)	343 (92%)	29 (8%)	0	100	100
22	3E	428/511 (84%)	389 (91%)	39 (9%)	0	100	100
23	3F	431/573 (75%)	365 (85%)	65 (15%)	1 (0%)	43	73
24	3G	119/126 (94%)	109 (92%)	10 (8%)	0	100	100
24	3H	119/126 (94%)	112 (94%)	6 (5%)	1 (1%)	16	48
25	A4	650/776 (84%)	583 (90%)	67 (10%)	0	100	100
26	A5	501/643 (78%)	453 (90%)	48 (10%)	0	100	100
27	A8	534/713 (75%)	423 (79%)	109 (20%)	2 (0%)	30	62
28	A9	126/575 (22%)	114 (90%)	12 (10%)	0	100	100
29	AE	1496/1769 (85%)	1372 (92%)	124 (8%)	0	100	100
30	AF	473/513 (92%)	427 (90%)	46 (10%)	0	100	100
31	AG	812/896 (91%)	694 (86%)	118 (14%)	0	100	100
32	B1	800/900 (89%)	720 (90%)	80 (10%)	0	100	100
33	B2	813/943 (86%)	731 (90%)	82 (10%)	0	100	100
34	B3	733/817 (90%)	608 (83%)	123 (17%)	2 (0%)	36	67
35	B8	469/594 (79%)	423 (90%)	45 (10%)	1 (0%)	43	73
36	BE	817/939 (87%)	746 (91%)	71 (9%)	0	100	100
37	B6	368/440 (84%)	343 (93%)	25 (7%)	0	100	100
38	5B	58/214 (27%)	52 (90%)	6 (10%)	0	100	100
39	5C	452/554 (82%)	400 (88%)	52 (12%)	0	100	100
40	5D	198/250 (79%)	172 (87%)	25 (13%)	1 (0%)	24	57
41	5E	187/593 (32%)	173 (92%)	14 (8%)	0	100	100
42	5F	180/183 (98%)	165 (92%)	15 (8%)	0	100	100
43	5G	214/290 (74%)	196 (92%)	18 (8%)	0	100	100
44	5H	72/610 (12%)	63 (88%)	9 (12%)	0	100	100
45	5I	456/489 (93%)	422 (92%)	33 (7%)	1 (0%)	43	73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	5J	130/217 (60%)	121 (93%)	9 (7%)	0	100	100
47	5K	162/189 (86%)	149 (92%)	13 (8%)	0	100	100
48	RD	310/1729 (18%)	278 (90%)	32 (10%)	0	100	100
49	RE	1080/1237 (87%)	996 (92%)	84 (8%)	0	100	100
50	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
51	RG	212/252 (84%)	193 (91%)	19 (9%)	0	100	100
51	RH	226/252 (90%)	208 (92%)	18 (8%)	0	100	100
52	RJ	719/1183 (61%)	649 (90%)	69 (10%)	1 (0%)	48	79
53	RK	358/367 (98%)	335 (94%)	23 (6%)	0	100	100
54	RN	539/810 (66%)	482 (89%)	57 (11%)	0	100	100
55	RO	523/552 (95%)	473 (90%)	49 (9%)	1 (0%)	43	73
56	RP	2112/2493 (85%)	1903 (90%)	203 (10%)	6 (0%)	36	67
57	RQ	220/899 (24%)	197 (90%)	23 (10%)	0	100	100
58	RS	247/480 (52%)	218 (88%)	29 (12%)	0	100	100
59	RT	165/326 (51%)	152 (92%)	13 (8%)	0	100	100
60	RW	146/206 (71%)	140 (96%)	6 (4%)	0	100	100
63	R5	297/305 (97%)	276 (93%)	21 (7%)	0	100	100
64	R1	242/246 (98%)	225 (93%)	17 (7%)	0	100	100
65	R3	332/394 (84%)	304 (92%)	27 (8%)	1 (0%)	36	67
66	R6	221/223 (99%)	208 (94%)	13 (6%)	0	100	100
67	R2	263/265 (99%)	249 (95%)	14 (5%)	0	100	100
68	M3	209/250 (84%)	190 (91%)	19 (9%)	0	100	100
69	R0	235/240 (98%)	216 (92%)	19 (8%)	0	100	100
70	r4	287/359 (80%)	262 (91%)	25 (9%)	0	100	100
71	C4	214/292 (73%)	198 (92%)	16 (8%)	0	100	100
72	R4	942/1001 (94%)	875 (93%)	67 (7%)	0	100	100
73	r6	98/733 (13%)	91 (93%)	7 (7%)	0	100	100
74	R7	83/184 (45%)	82 (99%)	1 (1%)	0	100	100
75	M4	866/1073 (81%)	806 (93%)	60 (7%)	0	100	100
76	M6	36/186 (19%)	32 (89%)	4 (11%)	0	100	100
All	All	26369/36145 (73%)	23774 (90%)	2573 (10%)	22 (0%)	49	79

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	B8	226	LYS
55	RO	75	PRO
24	3H	6	PRO
27	A8	309	PRO
56	RP	37	ARG

5.3.2 Protein sidechains (i)

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	205/224 (92%)	205 (100%)	0	100	100
5	SF	199/222 (90%)	196 (98%)	3 (2%)	57	69
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	79
7	SH	153/201 (76%)	153 (100%)	0	100	100
8	SI	145/170 (85%)	143 (99%)	2 (1%)	59	70
9	SJ	114/161 (71%)	114 (100%)	0	100	100
10	SK	147/166 (89%)	146 (99%)	1 (1%)	76	77
11	SM	124/137 (90%)	124 (100%)	0	100	100
12	SO	117/128 (91%)	115 (98%)	2 (2%)	53	67
13	SP	90/105 (86%)	89 (99%)	1 (1%)	65	73
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	108 (100%)	0	100	100
16	SY	88/120 (73%)	86 (98%)	2 (2%)	44	63
17	SZ	103/113 (91%)	101 (98%)	2 (2%)	50	66
18	Sc	69/71 (97%)	65 (94%)	4 (6%)	18	44
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	199 (99%)	2 (1%)	68	74
20	3C	190/240 (79%)	186 (98%)	4 (2%)	47	64
21	3D	322/435 (74%)	321 (100%)	1 (0%)	86	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
22	3E	265/433 (61%)	264 (100%)	1 (0%)	84 83
23	3F	382/503 (76%)	372 (97%)	10 (3%)	40 60
24	3G	100/104 (96%)	98 (98%)	2 (2%)	48 65
24	3H	100/104 (96%)	100 (100%)	0	100 100
25	A4	593/713 (83%)	585 (99%)	8 (1%)	61 71
26	A5	431/574 (75%)	429 (100%)	2 (0%)	81 81
27	A8	174/657 (26%)	174 (100%)	0	100 100
28	A9	89/533 (17%)	89 (100%)	0	100 100
29	AE	708/1633 (43%)	704 (99%)	4 (1%)	78 79
30	AF	424/454 (93%)	421 (99%)	3 (1%)	76 77
31	AG	750/826 (91%)	747 (100%)	3 (0%)	84 83
32	B1	707/789 (90%)	699 (99%)	8 (1%)	65 73
33	B2	712/832 (86%)	702 (99%)	10 (1%)	59 70
34	B3	665/719 (92%)	659 (99%)	6 (1%)	70 74
35	B8	421/529 (80%)	413 (98%)	8 (2%)	50 66
36	BE	721/819 (88%)	713 (99%)	8 (1%)	65 73
37	B6	251/414 (61%)	248 (99%)	3 (1%)	63 72
38	5B	57/196 (29%)	56 (98%)	1 (2%)	51 67
39	5C	394/480 (82%)	391 (99%)	3 (1%)	73 76
40	5D	192/234 (82%)	191 (100%)	1 (0%)	81 81
41	5E	175/535 (33%)	174 (99%)	1 (1%)	78 79
42	5F	171/172 (99%)	171 (100%)	0	100 100
43	5G	191/258 (74%)	189 (99%)	2 (1%)	68 74
44	5H	63/538 (12%)	63 (100%)	0	100 100
45	5I	415/443 (94%)	410 (99%)	5 (1%)	63 72
46	5J	124/200 (62%)	123 (99%)	1 (1%)	73 76
47	5K	148/169 (88%)	148 (100%)	0	100 100
48	RD	226/1544 (15%)	225 (100%)	1 (0%)	84 83
49	RE	994/1125 (88%)	987 (99%)	7 (1%)	76 77
50	RF	221/274 (81%)	219 (99%)	2 (1%)	70 74
51	RG	195/222 (88%)	193 (99%)	2 (1%)	68 74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	RH	206/222 (93%)	206 (100%)	0	100	100
52	RJ	649/1039 (62%)	643 (99%)	6 (1%)	70	74
53	RK	307/312 (98%)	302 (98%)	5 (2%)	55	68
54	RN	379/732 (52%)	378 (100%)	1 (0%)	86	84
55	RO	329/506 (65%)	326 (99%)	3 (1%)	70	74
56	RP	550/2307 (24%)	546 (99%)	4 (1%)	76	77
57	RQ	149/808 (18%)	149 (100%)	0	100	100
58	RS	225/421 (53%)	220 (98%)	5 (2%)	45	63
59	RT	148/282 (52%)	147 (99%)	1 (1%)	76	77
63	R5	255/266 (96%)	252 (99%)	3 (1%)	63	72
64	R1	210/218 (96%)	209 (100%)	1 (0%)	81	81
65	R3	282/349 (81%)	282 (100%)	0	100	100
66	R6	195/197 (99%)	195 (100%)	0	100	100
67	R2	236/240 (98%)	236 (100%)	0	100	100
68	M3	181/219 (83%)	180 (99%)	1 (1%)	78	79
69	R0	194/209 (93%)	193 (100%)	1 (0%)	81	81
70	r4	243/311 (78%)	241 (99%)	2 (1%)	73	76
71	C4	174/240 (72%)	174 (100%)	0	100	100
72	R4	812/901 (90%)	812 (100%)	0	100	100
73	r6	89/671 (13%)	89 (100%)	0	100	100
74	R7	76/168 (45%)	75 (99%)	1 (1%)	61	71
75	M4	729/953 (76%)	729 (100%)	0	100	100
76	M6	25/168 (15%)	25 (100%)	0	100	100
All	All	20418/31979 (64%)	20257 (99%)	161 (1%)	70	76

5 of 161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	RD	1683	ILE
56	RP	1756	ILE
49	RE	482	VAL
52	RJ	616	ASP
58	RS	312	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 378 such sidechains are listed below:

Mol	Chain	Res	Type
45	5I	392	ASN
52	RJ	770	GLN
48	RD	1515	ASN
49	RE	743	GLN
54	RN	552	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	222/333 (66%)	86 (38%)	3 (1%)
2	5A	144/700 (20%)	62 (43%)	2 (1%)
3	SA	1227/1809 (67%)	466 (37%)	20 (1%)
All	All	1593/2842 (56%)	614 (38%)	25 (1%)

5 of 614 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	4	G
1	3A	12	U
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	579	A
3	SA	685	A
3	SA	1754	A
3	SA	637	C
3	SA	773	C

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
78	GTP	RJ	1201	79	33,34,34	0.85	1 (3%)	50,54,54	1.63	9 (18%)

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
78	GTP	RJ	1201	79	-	1/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	RJ	1201	GTP	C2-N3	2.01	1.38	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
78	RJ	1201	GTP	C5-C4-N3	-5.13	120.23	128.39
78	RJ	1201	GTP	C2-N3-C4	4.71	120.41	112.30
78	RJ	1201	GTP	C2-N1-C6	-3.20	119.31	125.11
78	RJ	1201	GTP	N9-C4-N3	3.14	132.23	125.95
78	RJ	1201	GTP	N9-C8-N7	-2.91	108.00	113.40

There are no chirality outliers.

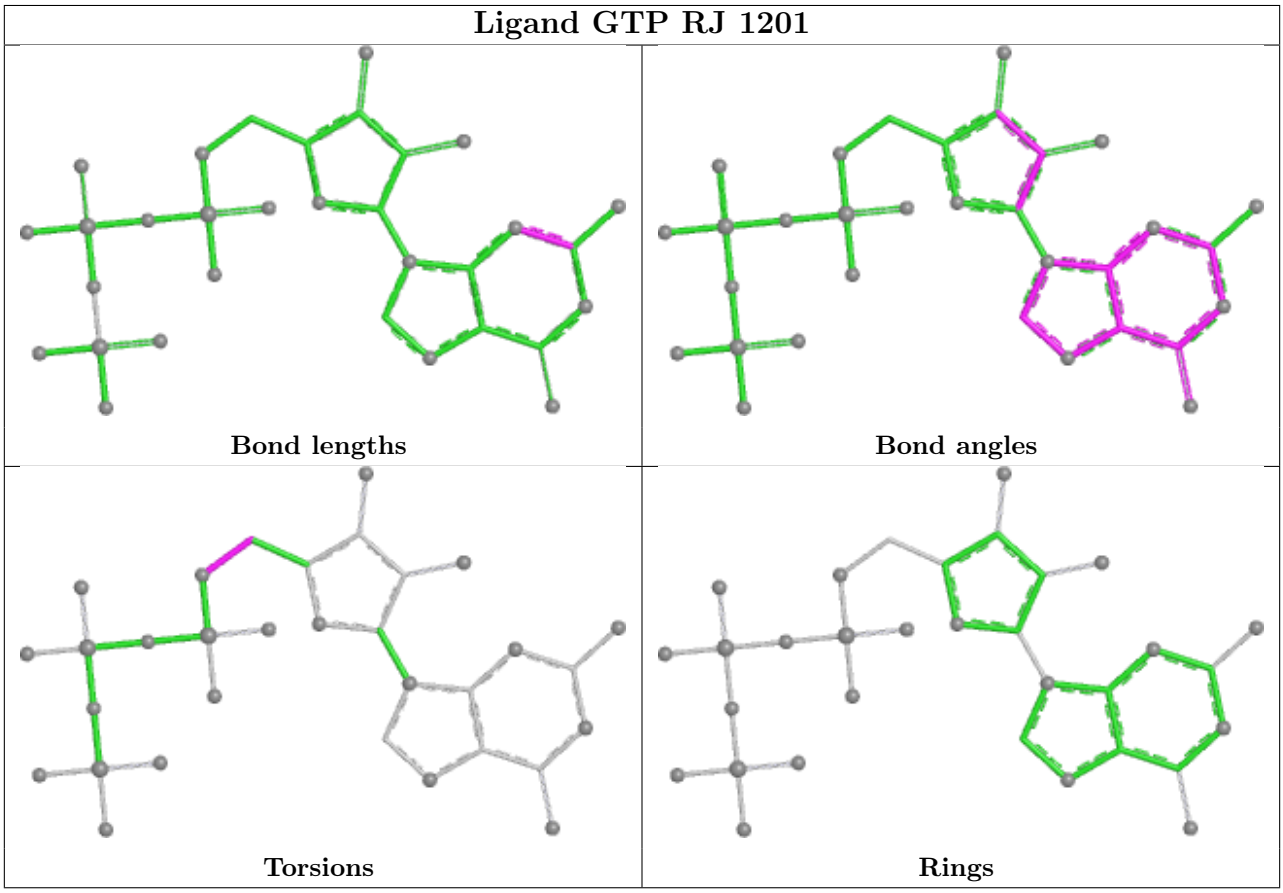
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
78	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

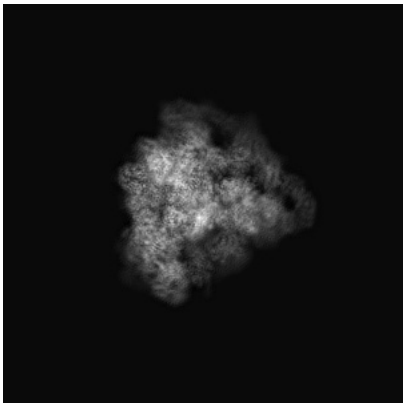
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0952. These allow visual inspection of the internal detail of the map and identification of artifacts.

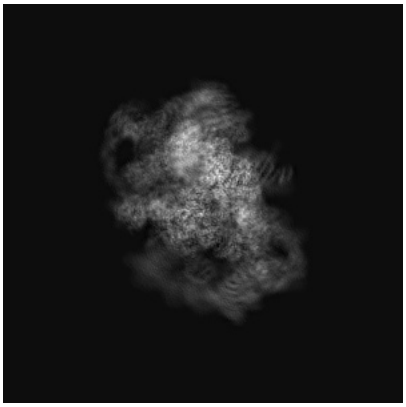
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

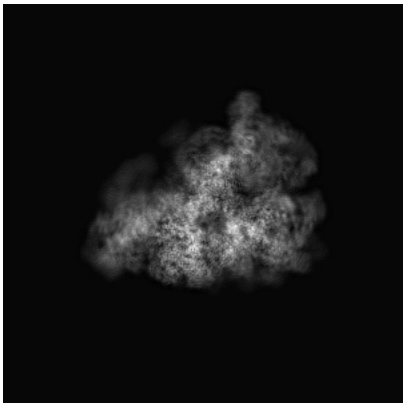
6.1.1 Primary map



X



Y

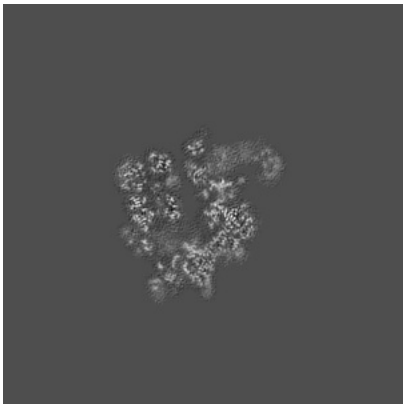


Z

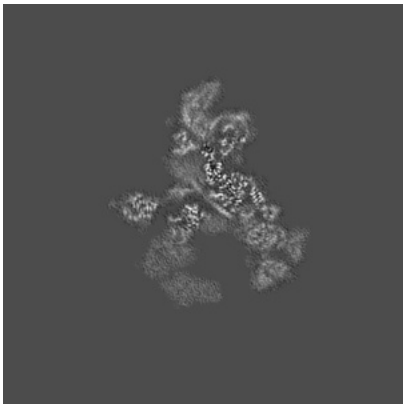
The images above show the map projected in three orthogonal directions.

6.2 Central slices

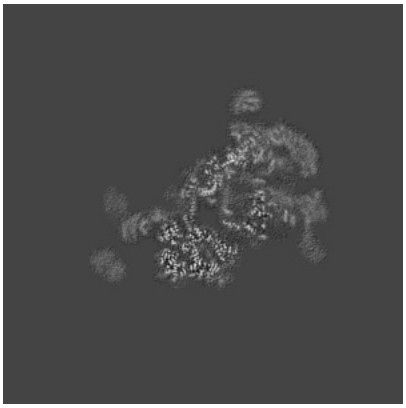
6.2.1 Primary map



X Index: 224



Y Index: 224



Z Index: 224

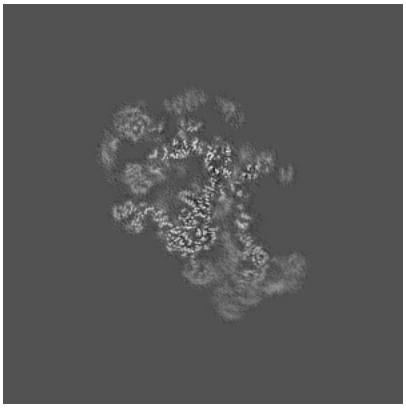
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

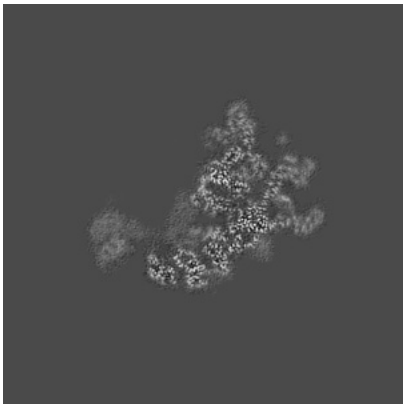
6.3.1 Primary map



X Index: 212



Y Index: 189

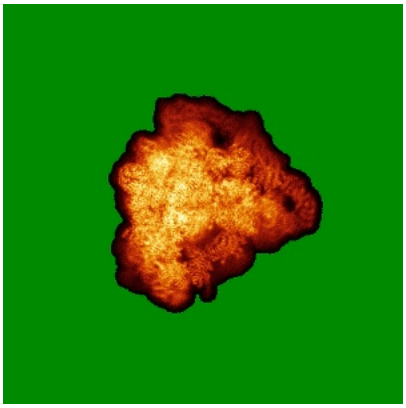


Z Index: 245

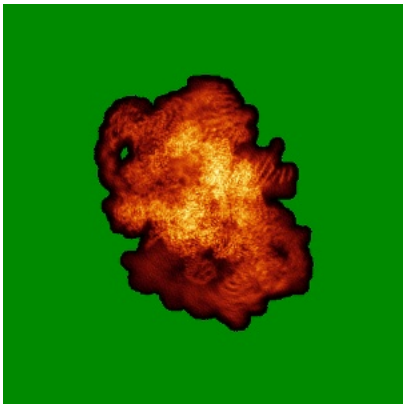
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

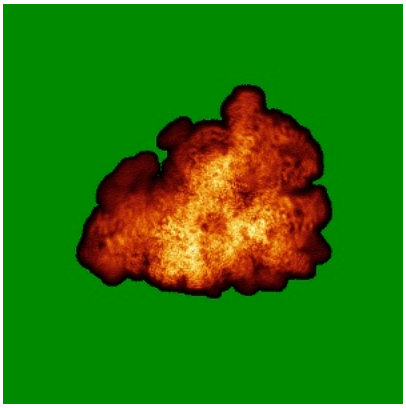
6.4.1 Primary map



X



Y

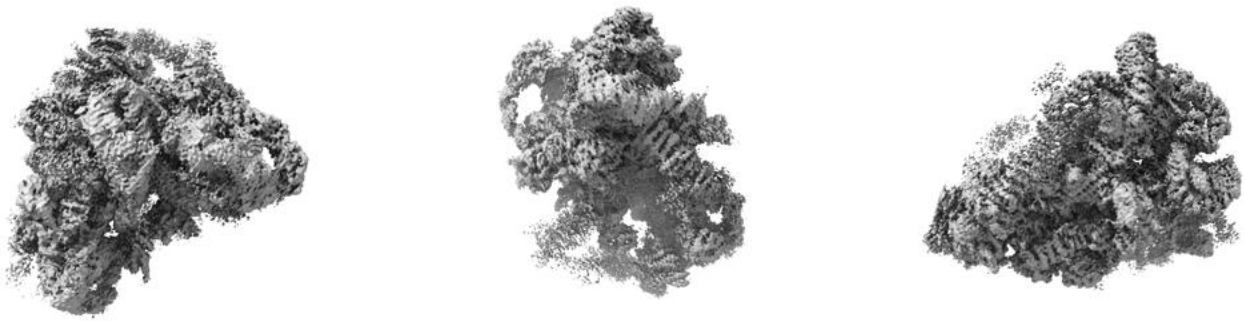


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

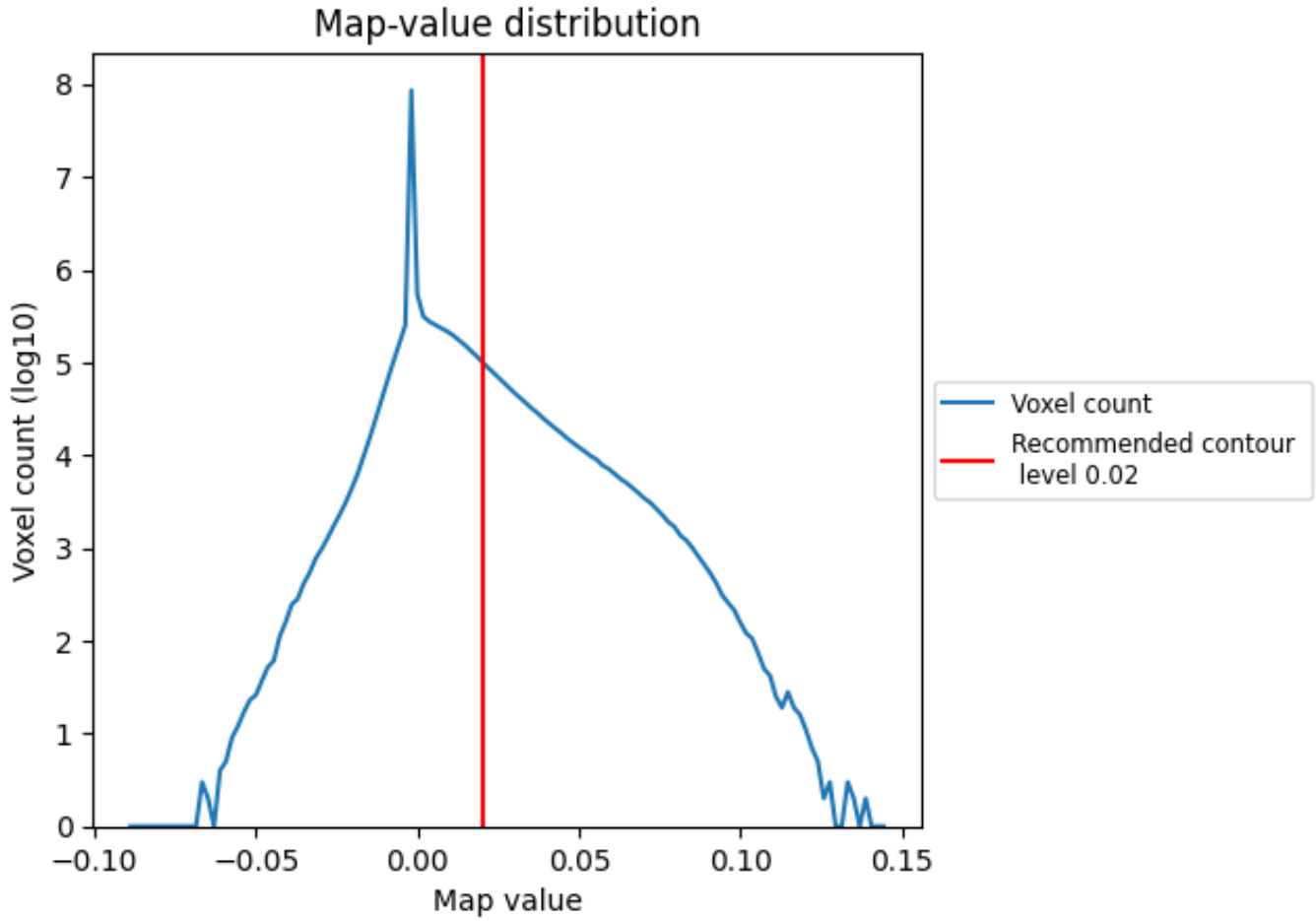
6.6 Mask visualisation (i)

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

7 Map analysis

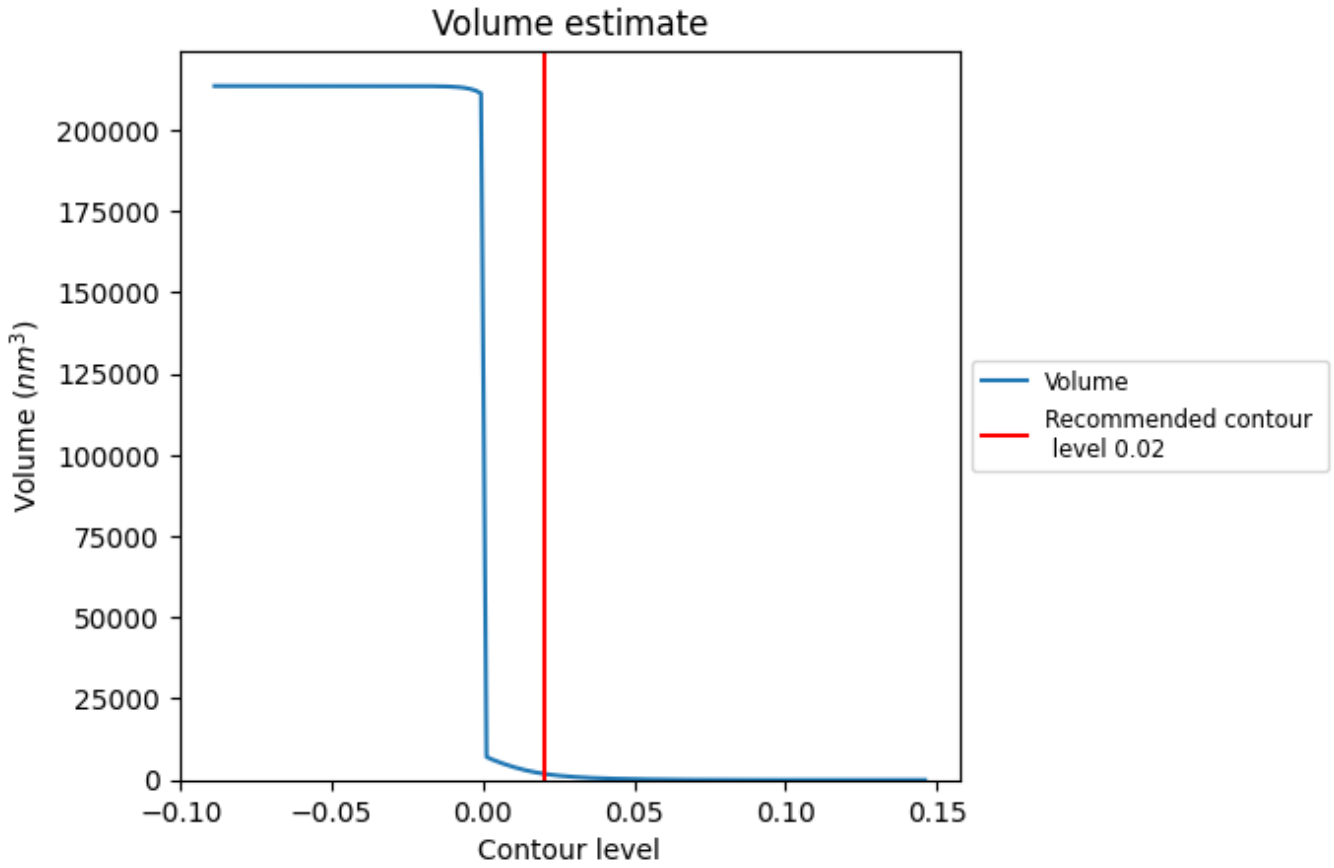
This section contains the results of statistical analysis of the map.

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.

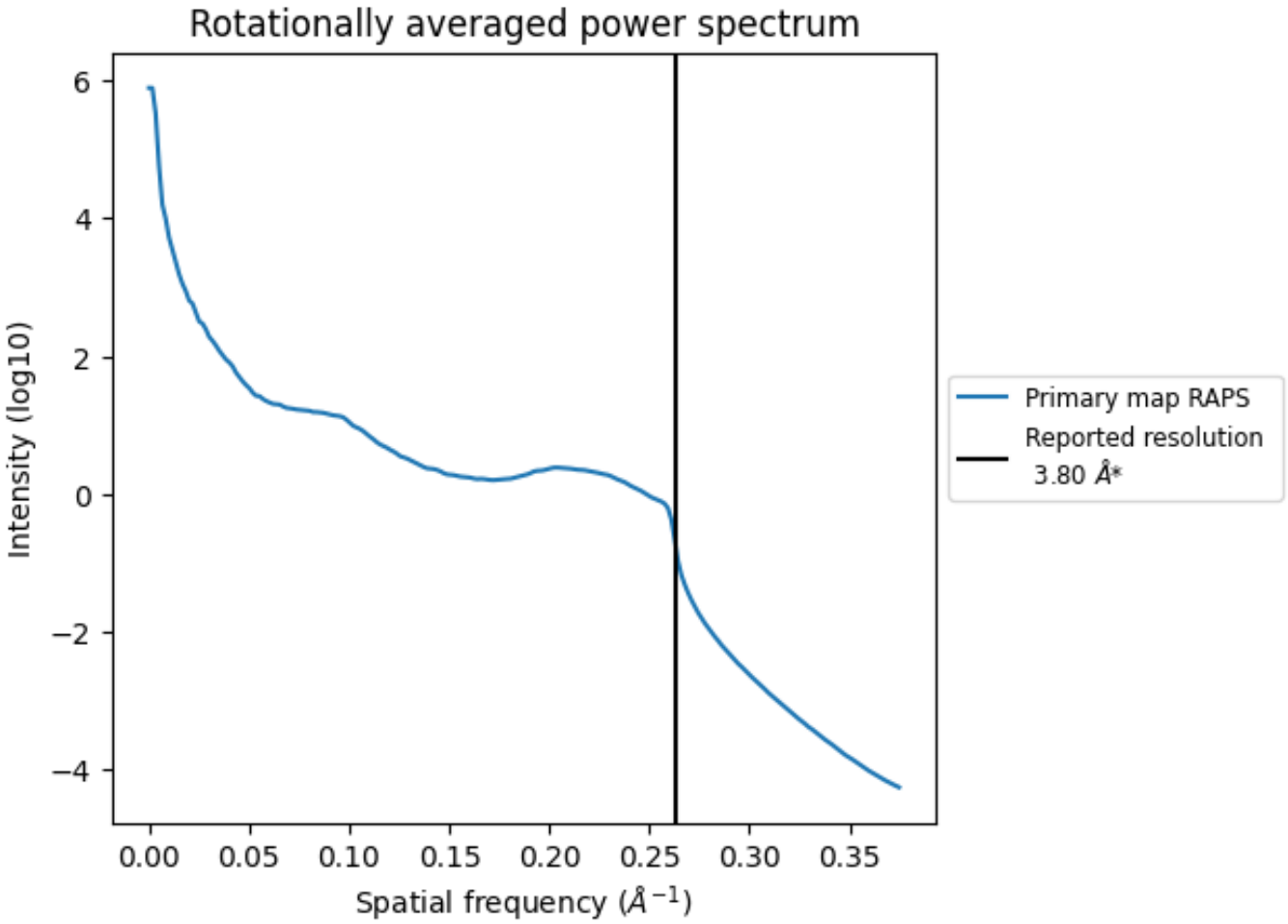
7.2 Volume estimate (i)



The volume at the recommended contour level is 1925 nm^3; this corresponds to an approximate mass of 1739 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

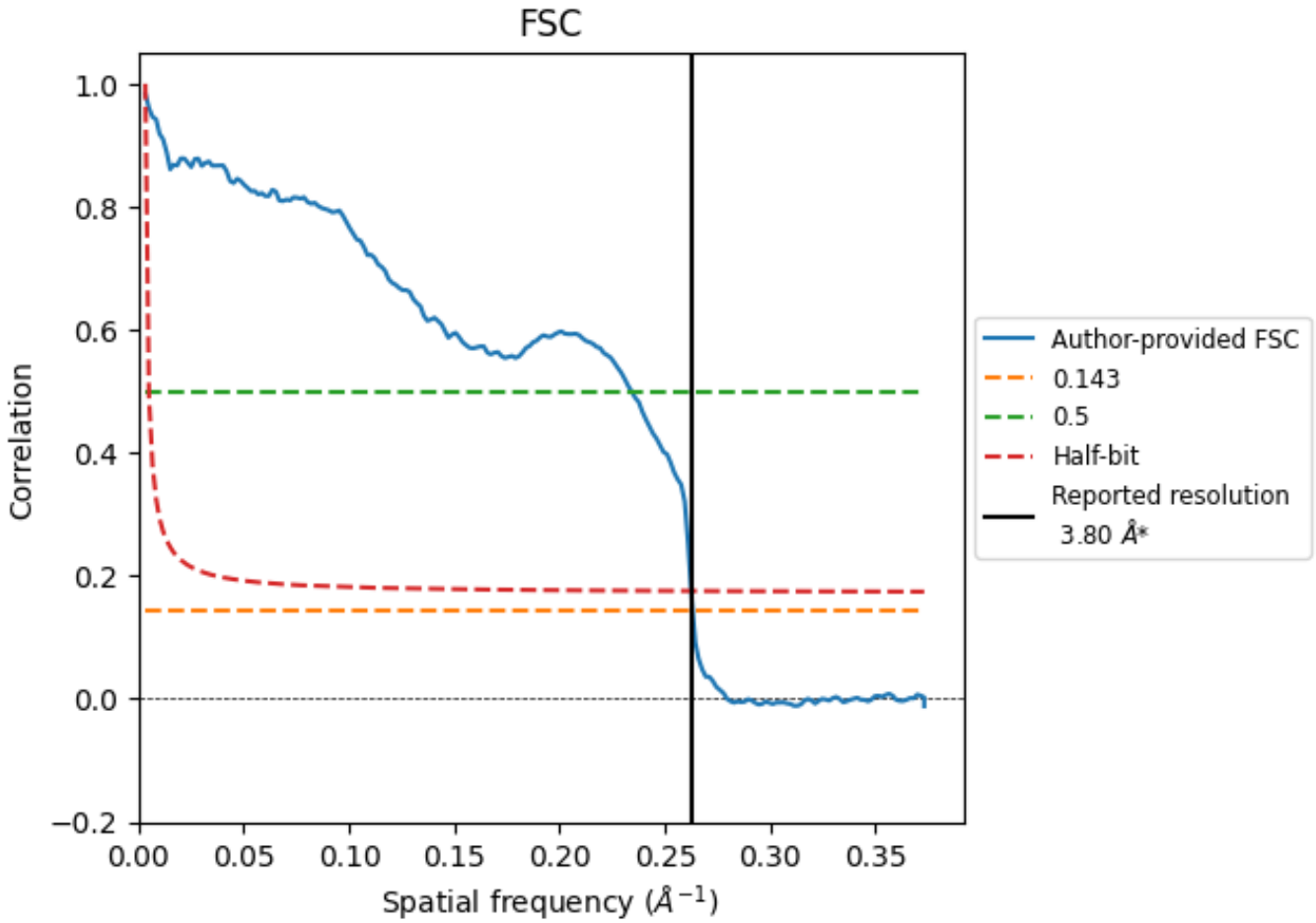


*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8.2 Resolution estimates (i)

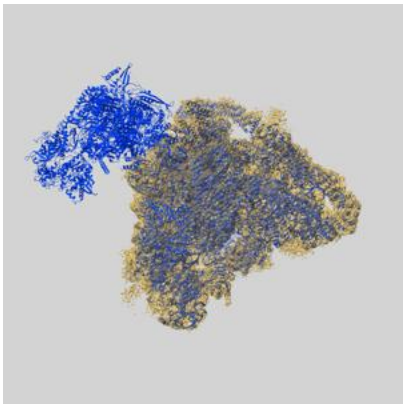
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.80	4.27	3.81
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

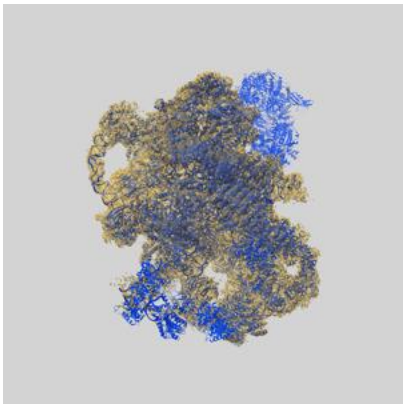
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-0952 and PDB model 6LQS. Per-residue inclusion information can be found in section 3 on page 19.

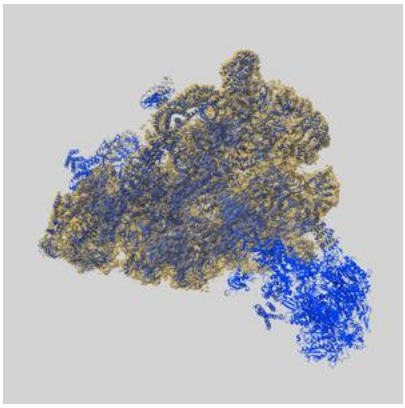
9.1 Map-model overlay



X



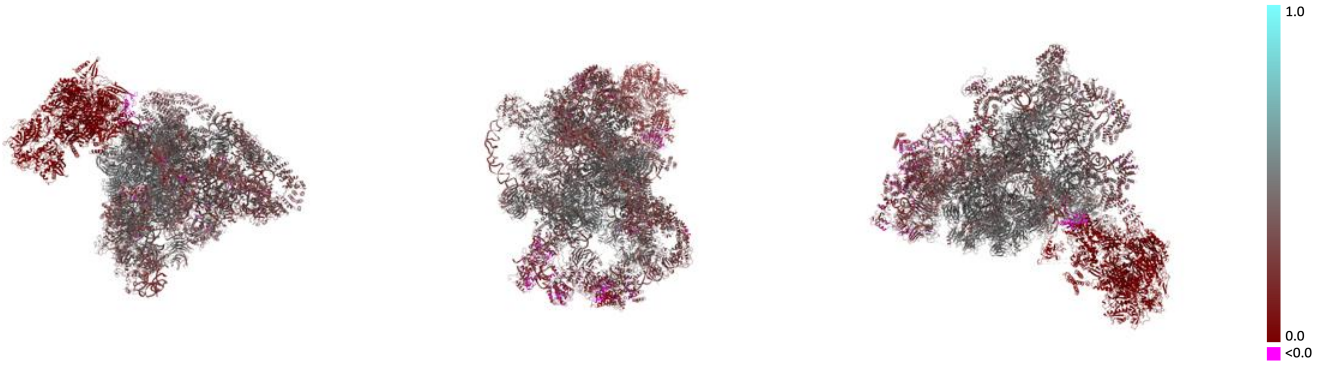
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

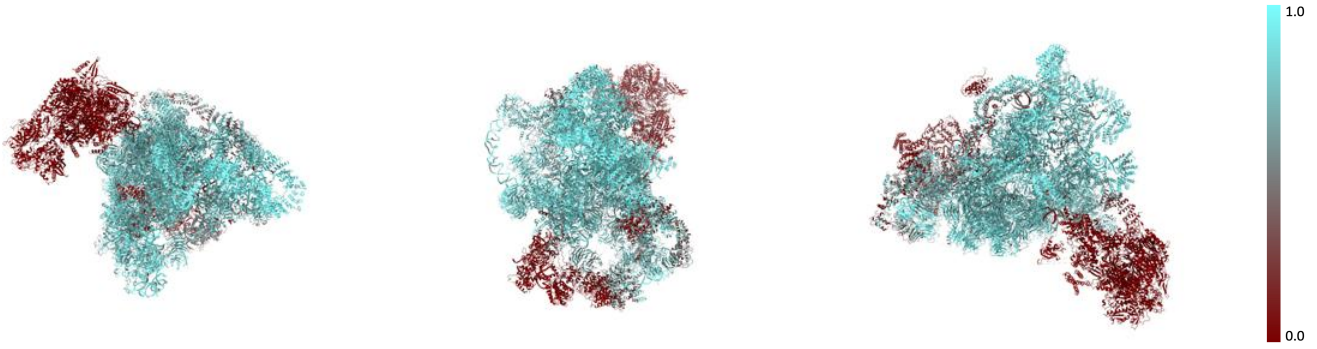
9.2 Q-score mapped to coordinate model (i)



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.

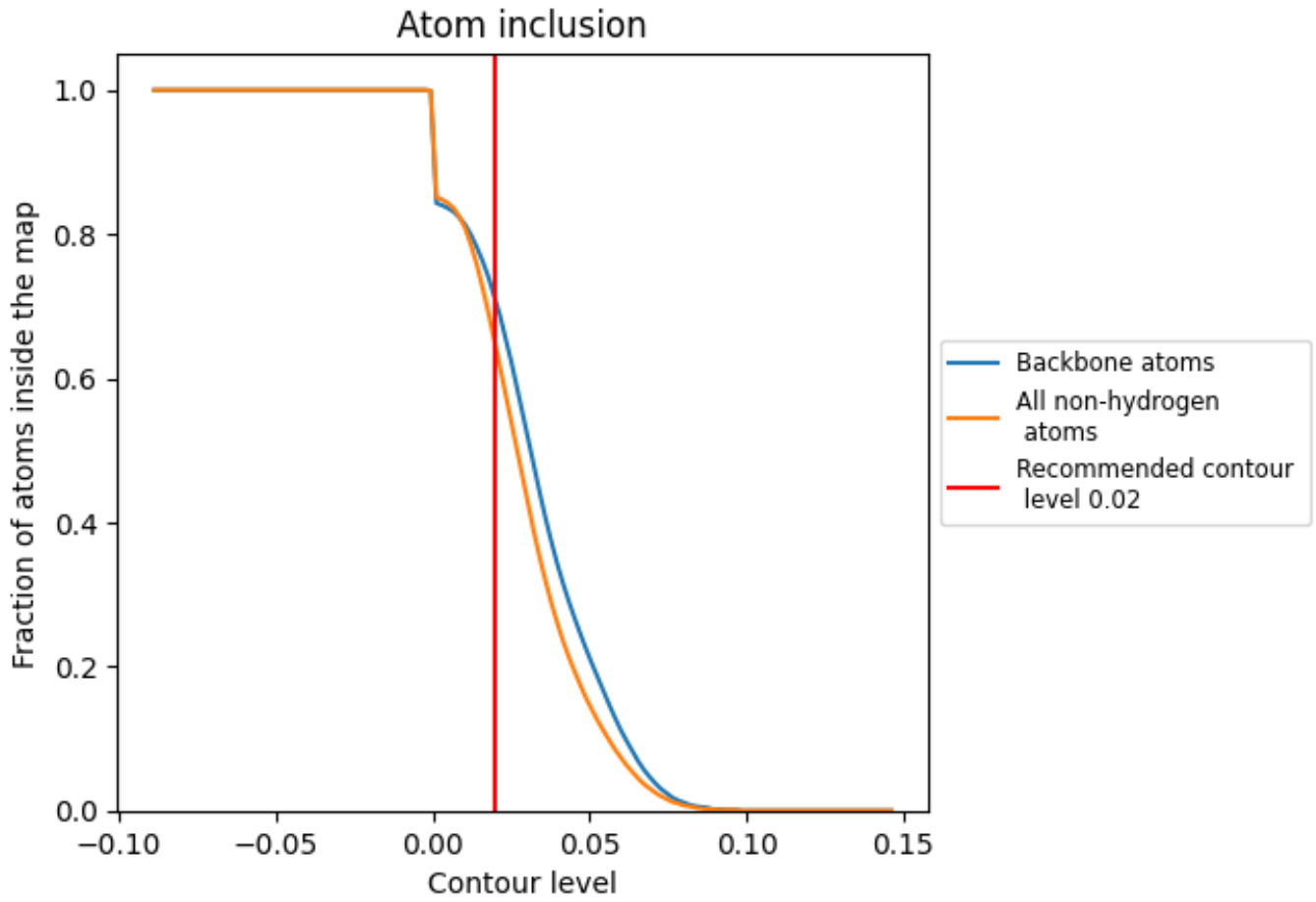
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6450	0.3160
3A	0.7970	0.3500
3B	0.8650	0.4750
3C	0.7380	0.3690
3D	0.8620	0.4290
3E	0.8280	0.3910
3F	0.8760	0.4550
3G	0.8010	0.3890
3H	0.8550	0.4590
5A	0.7230	0.2890
5B	0.4290	0.3480
5C	0.8620	0.4790
5D	0.5030	0.3770
5E	0.8250	0.4170
5F	0.8530	0.4590
5G	0.8430	0.4690
5H	0.8860	0.4730
5I	0.9090	0.4910
5J	0.7600	0.4050
5K	0.8640	0.4790
A4	0.7920	0.3530
A5	0.7020	0.3800
A8	0.3990	0.2010
A9	0.5750	0.2150
AE	0.6750	0.3380
AF	0.6480	0.2880
AG	0.7940	0.3350
B1	0.8910	0.4750
B2	0.8750	0.4080
B3	0.8640	0.3710
B6	0.8660	0.4110
B8	0.8570	0.4480
BE	0.9020	0.4730
C4	0.0000	0.0000
M3	0.0000	0.0000



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Chain	Atom inclusion	Q-score
M4	0.0000	-0.0040
M6	0.0000	0.0000
R0	0.0000	0.0000
R1	0.0000	0.0000
R2	0.0000	0.0000
R3	0.0000	0.0000
R4	0.0000	0.0000
R5	0.0000	0.0000
R6	0.0000	0.0000
R7	0.0000	0.0000
RD	0.3260	0.2790
RE	0.8000	0.3500
RF	0.7710	0.3320
RG	0.1070	0.2420
RH	0.2340	0.2920
RJ	0.8410	0.4200
RK	0.8420	0.4100
RN	0.1150	0.1970
RO	0.0210	0.1810
RP	0.8800	0.3400
RQ	0.7950	0.4200
RS	0.0490	0.1750
RT	0.6990	0.3620
RW	0.2640	0.3010
SA	0.8380	0.3440
SC	0.8500	0.4530
SF	0.8280	0.3990
SG	0.8520	0.4490
SH	0.6680	0.3150
SI	0.7830	0.3650
SJ	0.6470	0.2950
SK	0.8750	0.4690
SM	0.5590	0.2910
SO	0.8750	0.4310
SP	0.8570	0.4260
SR	0.8830	0.4690
SX	0.8700	0.4550
SY	0.8140	0.4470
SZ	0.8770	0.4470
Sc	0.9040	0.4690
Sd	0.8850	0.4670
X1	0.8530	0.3890

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Chain	Atom inclusion	Q-score
X2	0.0840	0.2990
r4	0.0000	0.0000
r6	0.0000	0.0000