wwPDB EM Validation Summary Report

Apr 1, 2025 – 09:18 pm BST

PDB ID	:	7ANE / pdb_00007ane
EMDB ID	:	EMD-11829
Title	:	Leishmania Major mitochondrial ribosome
Authors	:	Soufari, H.; Waltz, F.; Parrot, C.; Bochler, A.; Hashem, Y.
Deposited on	:	2020-10-11
Resolution	:	3.90 Å(reported)

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

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

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

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

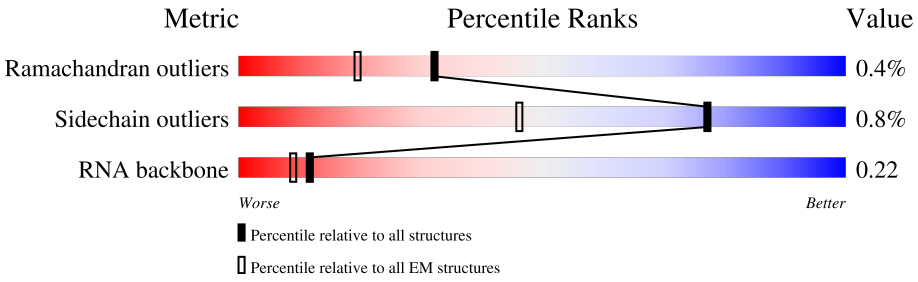
EMDB validation analysis	:	0.0.1.dev117
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1	18998	94%
1	2	18998	97%
2	h	166	16% 95% 5%
3	aw	139	24% 100%
4	m	325	24% 88% 11%
5	f	371	15% 39% 60%
6	s	179	25% 92% 8%
7	au	247	32% 96%

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Mol	Chain	Length	Quality of chain
8	am	313	30% 87% 13%
9	n	171	27% 83% 17%
10	ae	655	20% 89% 11%
11	ay	169	21% 83% 17%
12	ag	564	34% 98%
13	aj	397	10% 80% 20%
14	e	822	26% 98%
15	d	351	19% 97%
16	az	163	14% 94% 6%
17	ax	184	26% 88% 12%
18	r	467	17% 97%
19	af	835	16% 70% 30%
20	u	890	26% 79% 21%
21	aa	1813	24% 83% 16%
22	ab	1177	34% 98%
23	ak	325	36% 82% 18%
24	ac	1267	32% 87% 12%
25	ad	811	31% 85% 14%
26	an	302	21% 99%
27	ao	291	17% 65% 34%
28	ap	245	17% 97%
29	aq	295	48% 72% 28%
30	as	270	47% 91% 9%
31	at	397	42% 50% 49%
32	y	485	15% 58% 42%

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Mol	Chain	Length	Quality of chain
33	w	190	54% 81% 18%
34	v	214	9% 29% 71%
35	t	267	41% 85% 15%
36	p	321	11% 72% 26%
37	j	189	42% 95% 5%
38	l	677	32% 80% 19%
39	ar	282	32% 89% 11%
40	av	236	35% 63% 36%
41	ai	379	23% 100%
42	x	268	19% 94% 5%
43	i	429	18% 62% 38%
44	g	192	31% 52% 48%
45	o	604	35% 72% 27%
46	c	311	32% 80% 19%
47	k	312	12% 37% 63%
48	q	425	9% 46% 54%
49	b	159	25% 96%
50	a	431	35% 94% 5%
51	ba	94	27% 28% 72%
52	z	1169	19% 83% 17%
53	bd	89	13% 44% 54%
54	A	466	35% 77% 21%
55	B	435	31% 98%
56	C	261	15% 81% 19%
57	D	204	41% 61% 37%

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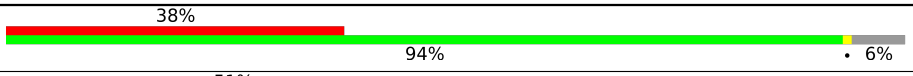
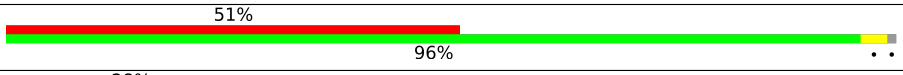
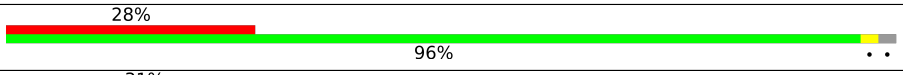
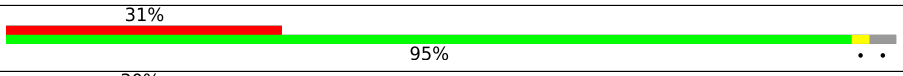
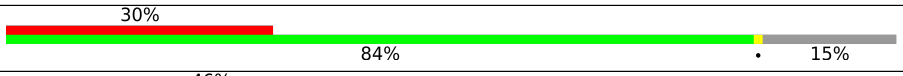
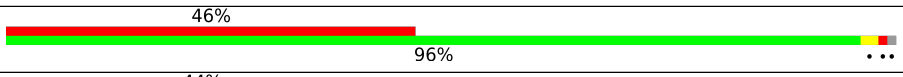
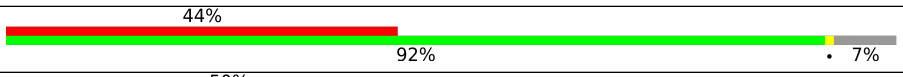
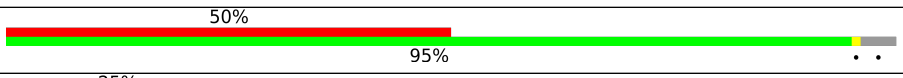
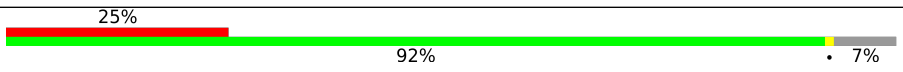
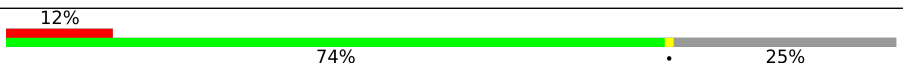
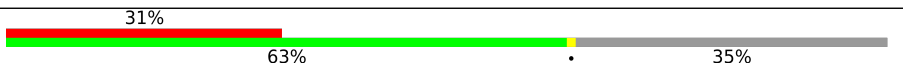
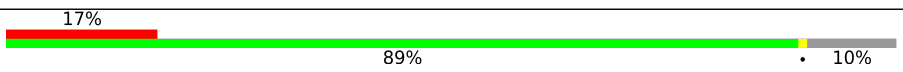
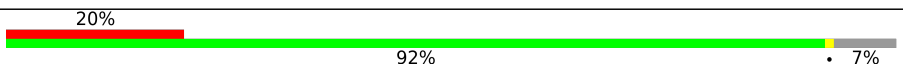
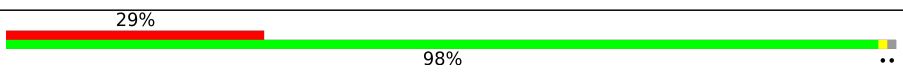
Mol	Chain	Length	Quality of chain
58	E	345	
59	F	171	
60	G	373	
61	H	167	
62	I	304	
63	J	143	
64	K	193	
65	L	185	
66	M	278	
67	N	251	
68	O	475	
69	P	184	
70	Q	233	
71	R	479	
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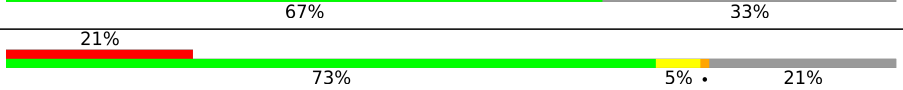
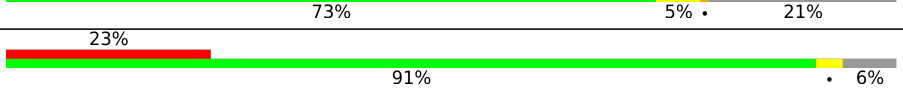
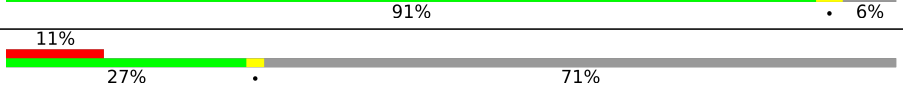
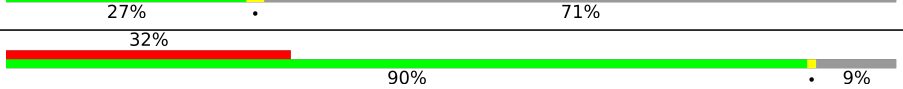
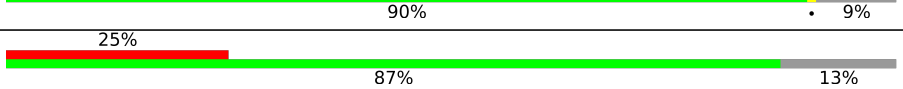
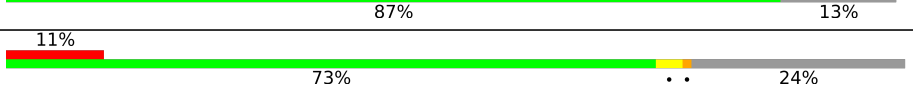
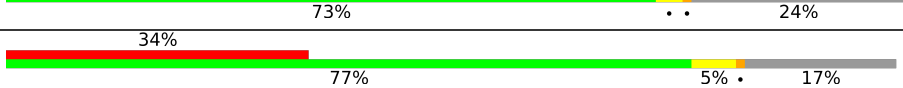
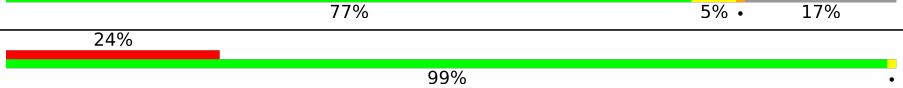
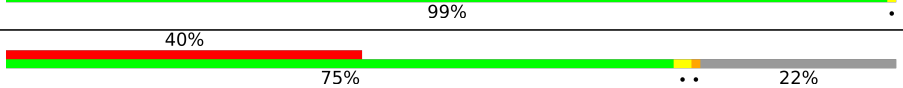
73	T	82	
74	U	117	
75	V	150	
76	W	185	
77	X	512	
78	Y	292	
79	Z	197	
80	BA	167	
81	UA	203	
82	BB	156	

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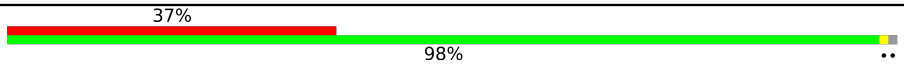
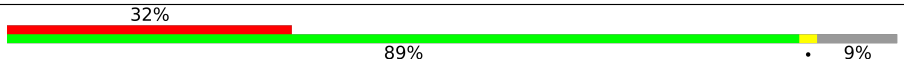
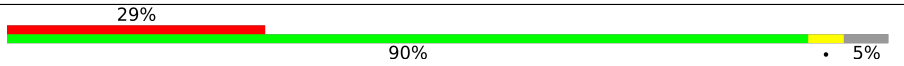
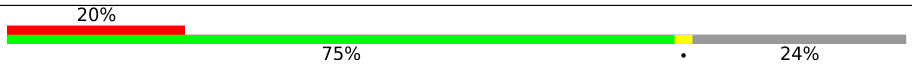
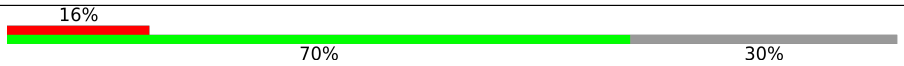
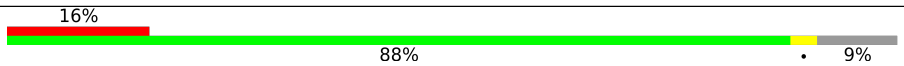
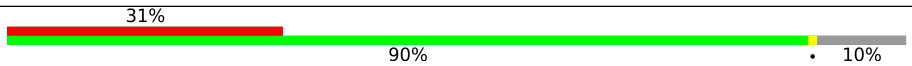
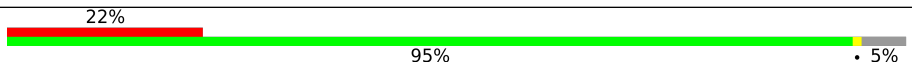
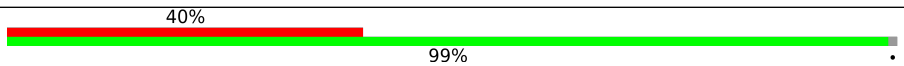
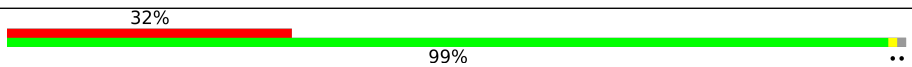
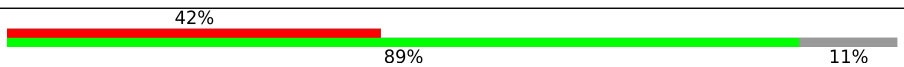
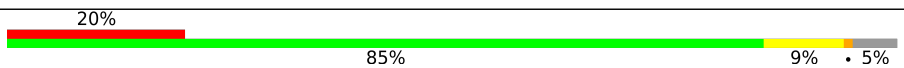
Mol	Chain	Length	Quality of chain
83	Aw	187	
84	Bj	185	
85	An	331	
86	Al	346	
87	BI	266	
88	Az	152	
89	At	183	
90	BC	147	
91	Ab	262	
92	Ai	479	
93	Ap	240	
94	Au	186	
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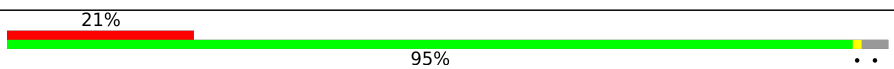
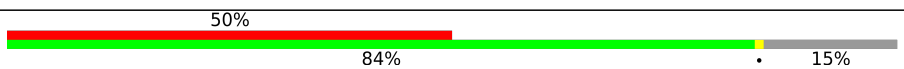
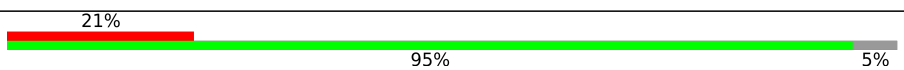
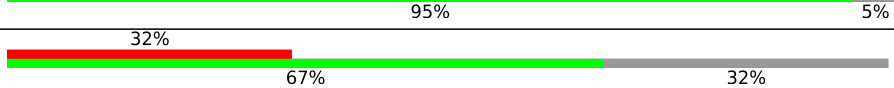
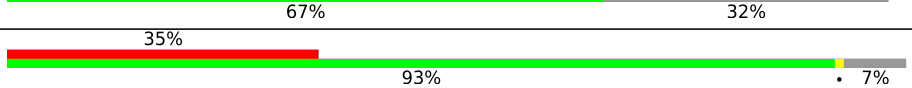
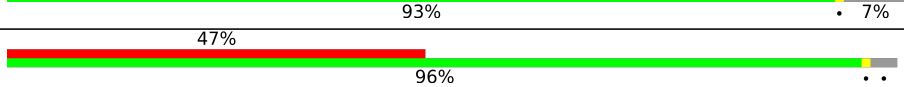
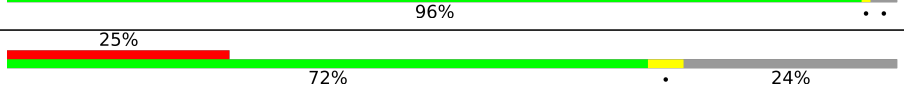
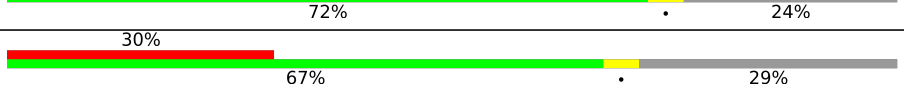
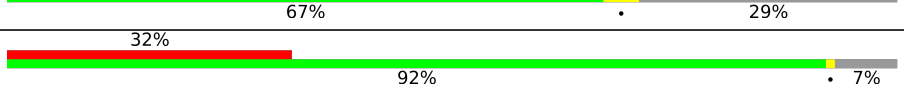
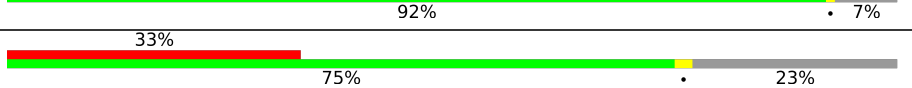
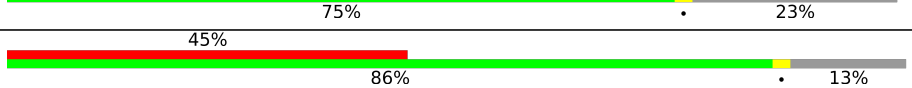
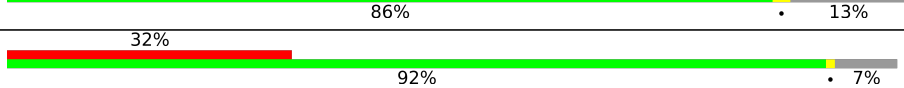
96	Ao	284	
97	BM	457	
98	Ar	205	
99	Aj	503	
100	BH	229	
101	Am	340	
102	Aq	341	
103	BE	118	
104	Ak	323	
105	BP	254	
106	Ad	237	
107	BF	109	

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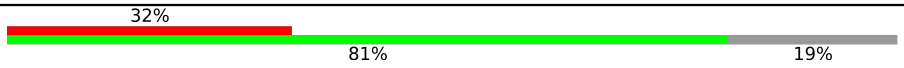
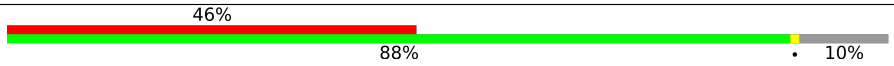
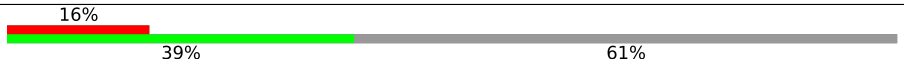
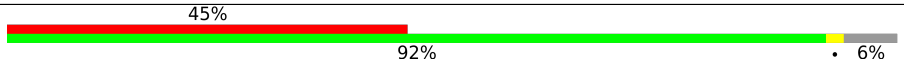
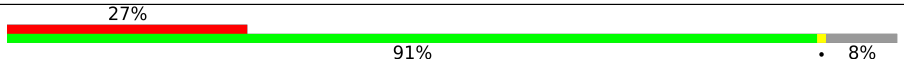
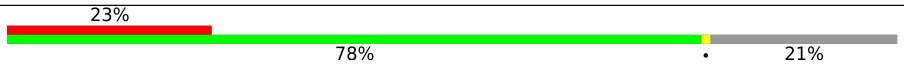
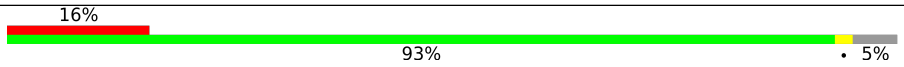
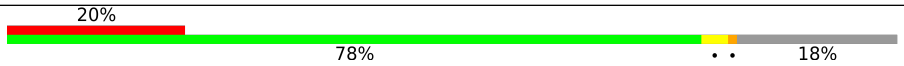
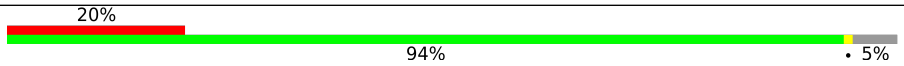
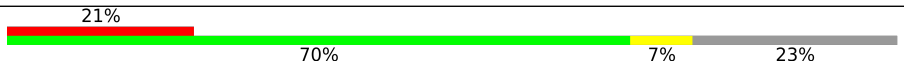
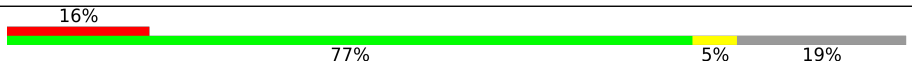
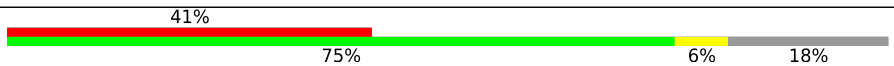
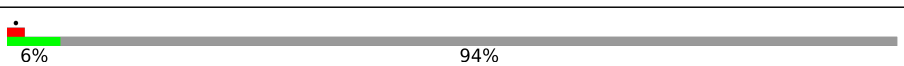
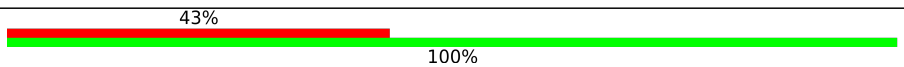
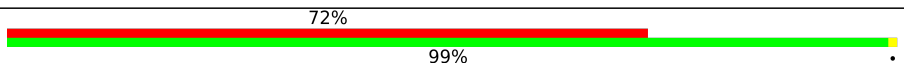
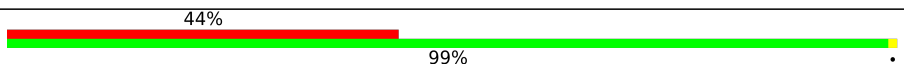
Mol	Chain	Length	Quality of chain
108	Av	192	
109	Af	155	
110	As	249	
111	Ae	311	
112	Ac	291	
113	Ah	570	
114	BD	102	
115	Ay	174	
116	Ag	244	
117	Ax	216	
118	BL	380	
119	BO	190	
120	BG	1347	
121	UB	67	
122	UC	144	
123	UD	95	

2 Entry composition (i)

There are 126 unique types of molecules in this entry. The entry contains 303111 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 Large ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	604	Total 12723	C 5725	N 2119	O 4275	P 604	0	0
1	1	1084	Total 22858	C 10292	N 3832	O 7650	P 1084	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	612	U	A	conflict	GB 1756572068
2	613	U	A	conflict	GB 1756572068
2	615	U	G	conflict	GB 1756572068
1	1840	U	A	conflict	GB 1756572068
1	1841	U	A	conflict	GB 1756572068
1	1843	U	G	conflict	GB 1756572068

- Molecule 2 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	h	157	Total 1311	C 831	N 248	O 224	S 8	0	0

- Molecule 3 is a protein called mS69.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	aw	139	Total 1144	C 723	N 209	O 204	S 8	0	0

- Molecule 4 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	m	288	Total 2368	C 1495	N 435	O 427	S 11	0	0

- Molecule 5 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	148	Total	C	N	O	S	0	0
			1213	764	231	216	2		

- Molecule 6 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	s	165	Total	C	N	O	S	0	0
			1349	852	251	239	7		

- Molecule 7 is a protein called Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	au	239	Total	C	N	O	S	0	0
			2066	1322	366	368	10		

- Molecule 8 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	am	272	Total	C	N	O	S	0	0
			2198	1398	404	386	10		

- Molecule 9 is a protein called uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	n	142	Total	C	N	O	S	0	0
			1176	760	210	201	5		

- Molecule 10 is a protein called mS53.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ae	584	Total	C	N	O	S	0	0
			4593	2888	856	830	19		

- Molecule 11 is a protein called mS71.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	ay	141	Total	C	N	O	S	0	0
			1187	756	222	204	5		

- Molecule 12 is a protein called mS55.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	ag	557	Total	C	N	O	S	0	0
			4521	2827	849	821	24		

- Molecule 13 is a protein called mS57.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	aj	316	Total	C	N	O	S	0	0
			2560	1643	449	453	15		

- Molecule 14 is a protein called uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	e	809	Total	C	N	O	S	0	0
			6413	4040	1128	1218	27		

- Molecule 15 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	d	343	Total	C	N	O	S	0	0
			2715	1716	474	511	14		

- Molecule 16 is a protein called mS72.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	az	154	Total	C	N	O	S	0	0
			1301	834	246	214	7		

- Molecule 17 is a protein called mS70.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	ax	161	Total	C	N	O	S	0	0
			1356	864	261	224	7		

- Molecule 18 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	451	Total	C	N	O	S	0	0
			3703	2380	646	660	17		

- Molecule 19 is a protein called Excreted/secreted protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	af	585	Total	C	N	O	S	0	0
			4698	2963	853	857	25		

- Molecule 20 is a protein called mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	706	Total	C	N	O	S	0	0
			5564	3497	1017	1025	25		

- Molecule 21 is a protein called mS48.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	aa	1514	Total	C	N	O	S	0	0
			12070	7616	2166	2249	39		

- Molecule 22 is a protein called mS49.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	ab	1151	Total	C	N	O	S	0	0
			9209	5726	1711	1744	28		

- Molecule 23 is a protein called mS58.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	ak	268	Total	C	N	O	S	0	0
			2141	1337	403	394	7		

- Molecule 24 is a protein called mS50.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	ac	1116	Total	C	N	O	S	0	0
			8700	5454	1568	1644	34		

- Molecule 25 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	ad	694	Total	C	N	O	S	0	0
			5676	3607	1012	1023	34		

- Molecule 26 is a protein called mS60.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	an	302	Total	C	N	O	S	0	0
			2480	1560	484	427	9		

- Molecule 27 is a protein called mS61.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	ao	191	Total	C	N	O	S	0	0
			1535	980	271	274	10		

- Molecule 28 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	ap	240	Total	C	N	O	S	0	0
			1893	1180	341	360	12		

- Molecule 29 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	aq	212	Total	C	N	O	S	0	0
			1794	1147	318	320	9		

- Molecule 30 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	as	247	Total	C	N	O	S	0	0
			1954	1246	352	348	8		

- Molecule 31 is a protein called mS66.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	at	204	Total	C	N	O	S	0	0
			1631	1008	313	300	10		

- Molecule 32 is a protein called mS43.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	y	283	Total	C	N	O	S	0	0
			2152	1345	395	398	14		

- Molecule 33 is a protein called Protein FYV4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	w	155	Total	C	N	O	S	0	0
			1279	815	227	233	4		

- Molecule 34 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	v	63	Total	C	N	O	S	0	0
			486	294	89	97	6		

- Molecule 35 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	226	Total	C	N	O	S	0	0
			1776	1128	308	336	4		

- Molecule 36 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	p	236	Total	C	N	O	S	0	0
			1954	1241	346	360	7		

- Molecule 37 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	180	Total	C	N	O	S	0	0
			1506	963	280	254	9		

- Molecule 38 is a protein called mS52.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	545	Total	C	N	O	S	0	0
			4438	2809	821	796	12		

- Molecule 39 is a protein called AKAP7_NLS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	ar	252	Total	C	N	O	S	0	0
			1993	1249	376	356	12		

- Molecule 40 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	av	150	Total	C	N	O	S	0	0
			1237	777	219	236	5		

- Molecule 41 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	ai	379	Total	C	N	O	S	0	0
			3068	1957	534	565	12		

- Molecule 42 is a protein called Putative superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	x	255	Total	C	N	O	S	0	0
			2034	1299	351	375	9		

- Molecule 43 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	267	Total	C	N	O	S	0	0
			2221	1406	403	402	10		

- Molecule 44 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	g	99	Total	C	N	O	S	0	0
			818	513	161	141	3		

- Molecule 45 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	438	Total	C	N	O	S	0	0
			3736	2395	658	664	19		

- Molecule 46 is a protein called uS8m.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	c	251	Total	C	N	O	S	0	0
			2038	1279	379	370	10		

- Molecule 47 is a protein called 30S Ribosomal protein S17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	116	Total	C	N	O	S	0	0
			951	614	169	163	5		

- Molecule 48 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	196	Total	C	N	O	S	0	0
			1699	1077	317	297	8		

- Molecule 49 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	b	155	Total	C	N	O	S	0	0
			1290	816	232	238	4		

- Molecule 50 is a protein called Ribosomal_S5_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	a	408	Total	C	N	O	S	0	0
			3298	2084	610	587	17		

- Molecule 51 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	ba	26	Total	C	N	O	S	0	0
			223	147	36	39	1		

- Molecule 52 is a protein called mS47.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z	971	Total	C	N	O	S	0	0
			7713	4847	1378	1454	34		

- Molecule 53 is a protein called uS3m.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	bd	41	Total	C	N	O	0	0
			350	245	52	53		

- Molecule 54 is a protein called Ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	A	368	Total	C	N	O	S	0	0
			2996	1929	496	556	15		

- Molecule 55 is a protein called uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B	435	Total	C	N	O	S	0	0
			3513	2237	615	642	19		

- Molecule 56 is a protein called RIBOSOMAL_L9 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	C	212	Total	C	N	O	S	0	0
			1772	1144	303	321	4		

- Molecule 57 is a protein called uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	D	128	Total	C	N	O	S	0	0
			1036	656	198	177	5		

- Molecule 58 is a protein called Putative ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	E	326	Total	C	N	O	S	0	0
			2668	1704	480	470	14		

- Molecule 59 is a protein called 50S ribosomal protein L13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	F	170	Total	C	N	O	S	0	0
			1435	919	261	243	12		

- Molecule 60 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	G	365	Total	C	N	O	S	0	0
			3012	1917	555	531	9		

- Molecule 61 is a protein called Ribosomal_L16 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	H	162	Total	C	N	O	S	0	0
			1305	836	239	226	4		

- Molecule 62 is a protein called Putative 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	I	257	Total	C	N	O	S	0	0
			2153	1362	406	372	13		

- Molecule 63 is a protein called bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	J	141	Total	C	N	O	S	0	0
			1146	727	211	202	6		

- Molecule 64 is a protein called bL20m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	K	179	Total	C	N	O	S	0	0
			1467	910	289	258	10		

- Molecule 65 is a protein called bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	L	178	Total	C	N	O	S	0	0
			1419	907	257	250	5		

- Molecule 66 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	M	259	Total	C	N	O	S	0	0
			2116	1345	385	371	15		

- Molecule 67 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	N	189	Total	C	N	O	S	0	0
			1599	1031	296	269	3		

- Molecule 68 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	O	307	Total	C	N	O	S	0	0
			2537	1600	455	475	7		

- Molecule 69 is a protein called bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	P	165	Total	C	N	O	S	0	0
			1367	856	266	238	7		

- Molecule 70 is a protein called bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Q	217	Total	C	N	O	S	0	0
			1785	1127	331	316	11		

- Molecule 71 is a protein called uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	R	472	Total	C	N	O	S	0	0
			3755	2377	662	704	12		

- Molecule 72 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	S	150	Total	C	N	O	S	0	0
			1244	782	247	207	8		

- Molecule 73 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	T	55	Total	C	N	O	S	0	0
			487	311	93	78	5		

- Molecule 74 is a protein called bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	U	92	Total	C	N	O	S	0	0
			744	472	142	125	5		

- Molecule 75 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	V	141	Total	C	N	O	S	0	0
			1202	755	242	197	8		

- Molecule 76 is a protein called bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	W	54	Total	C	N	O	S	0	0
			465	299	89	74	3		

- Molecule 77 is a protein called mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	X	468	Total	C	N	O	S	0	0
			3733	2365	657	694	17		

- Molecule 78 is a protein called mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Y	255	Total	C	N	O	S	0	0
			2067	1287	373	402	5		

- Molecule 79 is a protein called mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Z	150	Total	C	N	O	S	0	0
			1223	784	224	211	4		

- Molecule 80 is a protein called mL94.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BA	138	Total	C	N	O	S	0	0
			1038	648	188	197	5		

- Molecule 81 is a protein called UA.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	UA	203	Total	C	N	O	0	0
			1015	609	203	203		

- Molecule 82 is a protein called mL95.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	BB	122	Total	C	N	O	0	0
			1028	663	189	176		

- Molecule 83 is a protein called mL89.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Aw	185	Total	C	N	O	S	0	0
			1509	949	289	268	3		

- Molecule 84 is a protein called bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bj	168	Total	C	N	O	S	0	0
			1358	865	255	231	7		

- Molecule 85 is a protein called mL76.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	An	314	Total	C	N	O	S	0	0
			2605	1643	487	470	5		

- Molecule 86 is a protein called mL74.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Al	264	Total	C	N	O	S	0	0
			2152	1371	374	399	8		

- Molecule 87 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	BI	186	Total	C	N	O	S	0	0
			1409	895	242	264	8		

- Molecule 88 is a protein called mL93.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	Az	138	Total	C	N	O	S	0	0
			1215	782	216	211	6		

- Molecule 89 is a protein called mL86.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	At	165	Total	C	N	O	S	0	0
			1346	824	260	254	8		

- Molecule 90 is a protein called mL96.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	BC	140	Total	C	N	O	S	0	0
			1114	693	205	207	9		

- Molecule 91 is a protein called L51_S25_CI-B8 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	Ab	260	Total	C	N	O	S	0	0
			2185	1365	416	397	7		

- Molecule 92 is a protein called mL69.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	Ai	476	Total	C	N	O	S	0	0
			3789	2419	654	694	22		

- Molecule 93 is a protein called mL80.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	Ap	214	Total	C	N	O	S	0	0
			1775	1111	327	328	9		

- Molecule 94 is a protein called mL87.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	Au	176	Total	C	N	O	S	0	0
			1490	945	292	245	8		

- Molecule 95 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	Aa	178	Total	C	N	O	S	0	0
			1417	884	270	256	7		

- Molecule 96 is a protein called mL79.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	Ao	275	Total	C	N	O	S	0	0
			2276	1433	429	402	12		

- Molecule 97 is a protein called mL70.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	BM	389	Total	C	N	O	S	0	0
			3069	1954	548	551	16		

- Molecule 98 is a protein called mL84.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	Ar	195	Total	C	N	O	S	0	0
			1644	1054	295	288	7		

- Molecule 99 is a protein called mL72.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	Aj	341	Total	C	N	O	S	0	0
			2766	1756	508	491	11		

- Molecule 100 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	BH	214	Total	C	N	O	S	0	0
			1659	1050	290	310	9		

- Molecule 101 is a protein called mL75.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	Am	330	Total	C	N	O	S	0	0
			2708	1727	491	474	16		

- Molecule 102 is a protein called mL82.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	Aq	258	Total	C	N	O	S	0	0
			2074	1296	406	360	12		

- Molecule 103 is a protein called mL98.

Mol	Chain	Residues	Atoms				AltConf	Trace
103	BE	84	Total	C	N	O	0	0
			700	447	125	128		

- Molecule 104 is a protein called mL73.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	Ak	300	Total	C	N	O	S	0	0
			2352	1489	421	429	13		

- Molecule 105 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	BP	195	Total	C	N	O	S	0	0
			1593	1014	288	288	3		

- Molecule 106 is a protein called mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	Ad	207	Total	C	N	O	S	0	0
			1632	1049	289	286	8		

- Molecule 107 is a protein called mL99.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	BF	101	Total	C	N	O	S	0	0
			851	530	165	154	2		

- Molecule 108 is a protein called mL88.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	Av	155	Total	C	N	O	S	0	0
			1300	828	230	234	8		

- Molecule 109 is a protein called mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	Af	139	Total	C	N	O	S	0	0
			1132	709	215	207	1		

- Molecule 110 is a protein called mL85.

Mol	Chain	Residues	Atoms					AltConf	Trace
110	As	97	Total	C	N	O	S	0	0
			787	495	139	148	5		

- Molecule 111 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	Ae	291	Total	C	N	O	S	0	0
			2359	1526	418	404	11		

- Molecule 112 is a protein called MRP-L46 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	Ac	268	Total	C	N	O	S	0	0
			2174	1375	389	405	5		

- Molecule 113 is a protein called mL68.

Mol	Chain	Residues	Atoms					AltConf	Trace
113	Ah	452	Total	C	N	O	S	0	0
			3686	2338	651	679	18		

- Molecule 114 is a protein called mL97.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	BD	97	Total	C	N	O	S	0	0
			807	499	160	140	8		

- Molecule 115 is a protein called C2H2-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	Ay	142	Total	C	N	O	S	0	0
			1226	774	228	217	7		

- Molecule 116 is a protein called mL59/64.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	Ag	231	Total	C	N	O	S	0	0
			1916	1211	356	340	9		

- Molecule 117 is a protein called LIM zinc-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	Ax	167	Total	C	N	O	S	0	0
			1388	876	268	233	11		

- Molecule 118 is a protein called Putative ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	BL	309	Total	C	N	O	S	0	0
			2497	1594	464	427	12		

- Molecule 119 is a protein called Putative ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	BO	155	Total	C	N	O	S	0	0
			1239	772	253	205	9		

- Molecule 120 is a protein called mL100.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	BG	85	Total	C	N	O	S	0	0
			643	400	122	115	6		

- Molecule 121 is a protein called UB.

Mol	Chain	Residues	Atoms				AltConf	Trace
121	UB	67	Total	C	N	O	0	0
			335	201	67	67		

- Molecule 122 is a protein called UC.

Mol	Chain	Residues	Atoms				AltConf	Trace
122	UC	144	Total	C	N	O	0	0
			720	432	144	144		

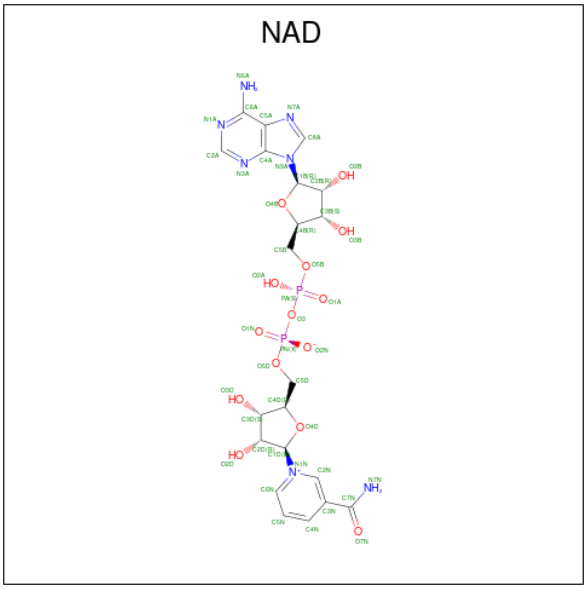
- Molecule 123 is a protein called UD.

Mol	Chain	Residues	Atoms				AltConf	Trace
123	UD	95	Total	C	N	O	0	0
			475	285	95	95		

- Molecule 124 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
124	T	1	Total Zn 1 1	0
124	W	1	Total Zn 1 1	0
124	BD	1	Total Zn 1 1	0
124	Ax	2	Total Zn 2 2	0
124	BG	1	Total Zn 1 1	0

- Molecule 125 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms	AltConf
125	Ag	1	Total C N O P 44 21 7 14 2	0

- Molecule 126 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

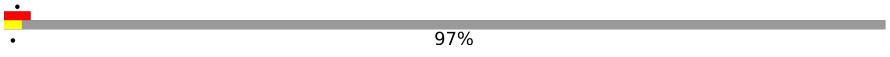
Mol	Chain	Residues	Atoms	AltConf
126	1	2	Total Mg 2 2	0

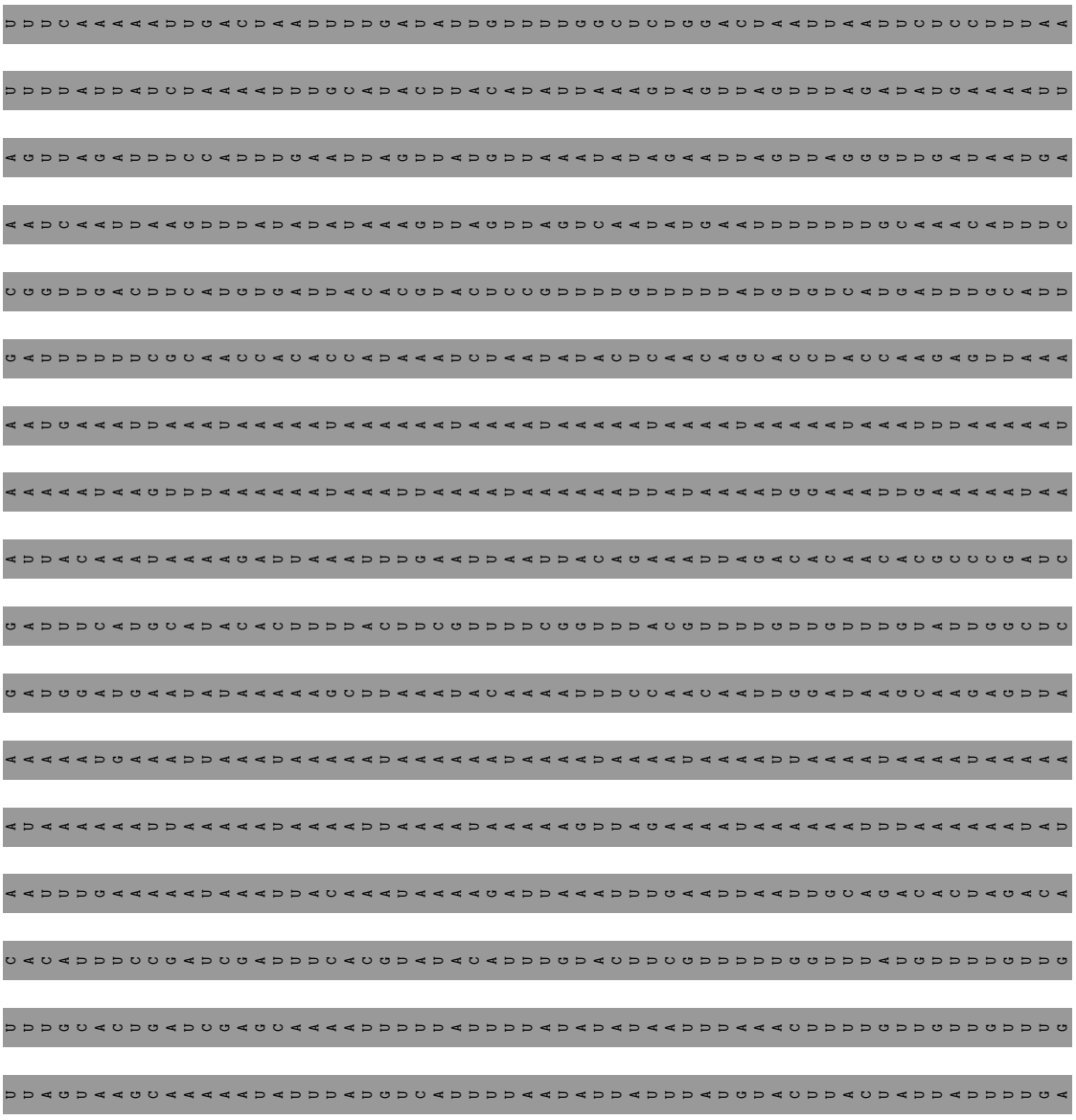
3 Residue-property plots (i)

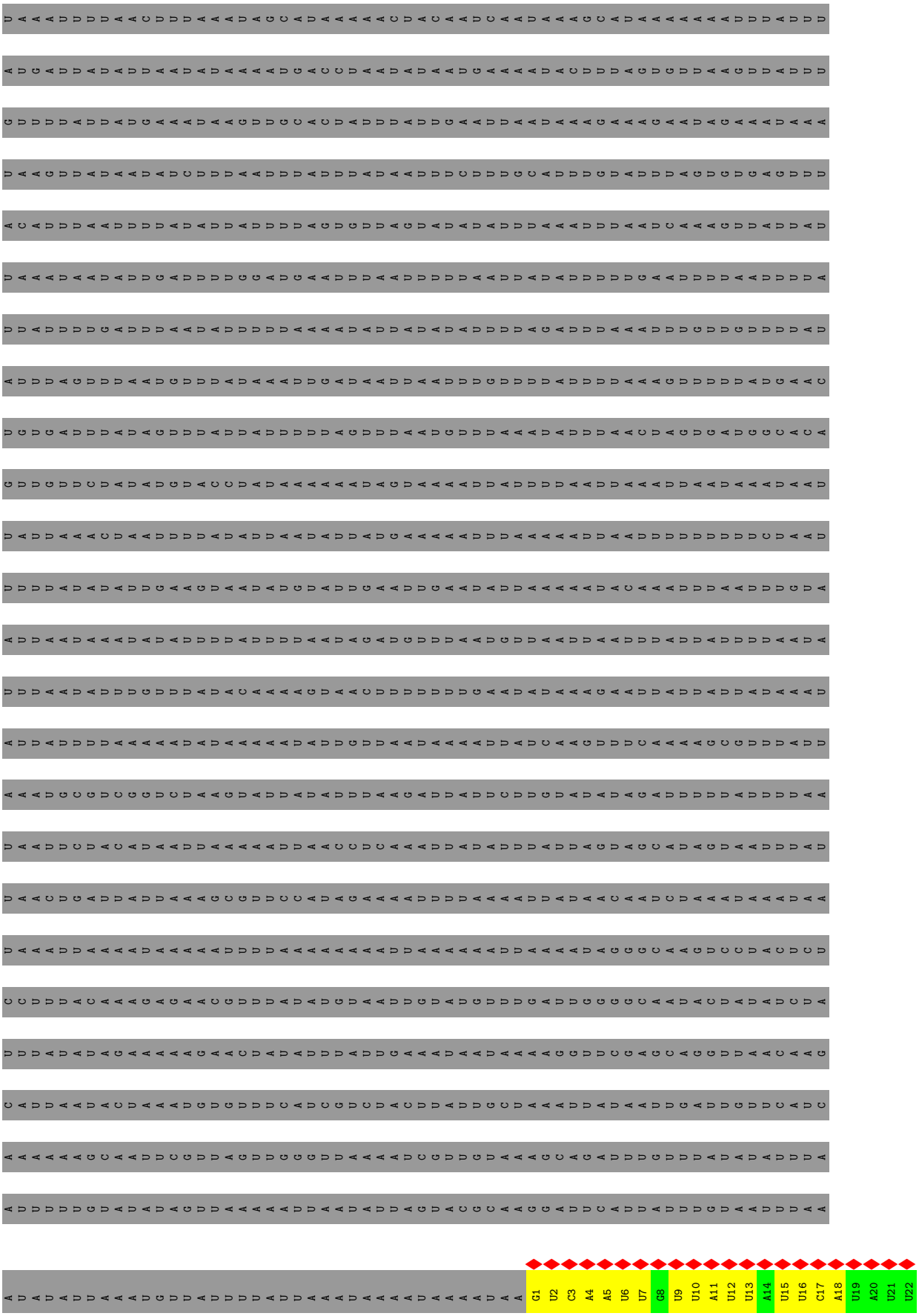
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

Chain 2:



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C3
A4
A5
U6
U7
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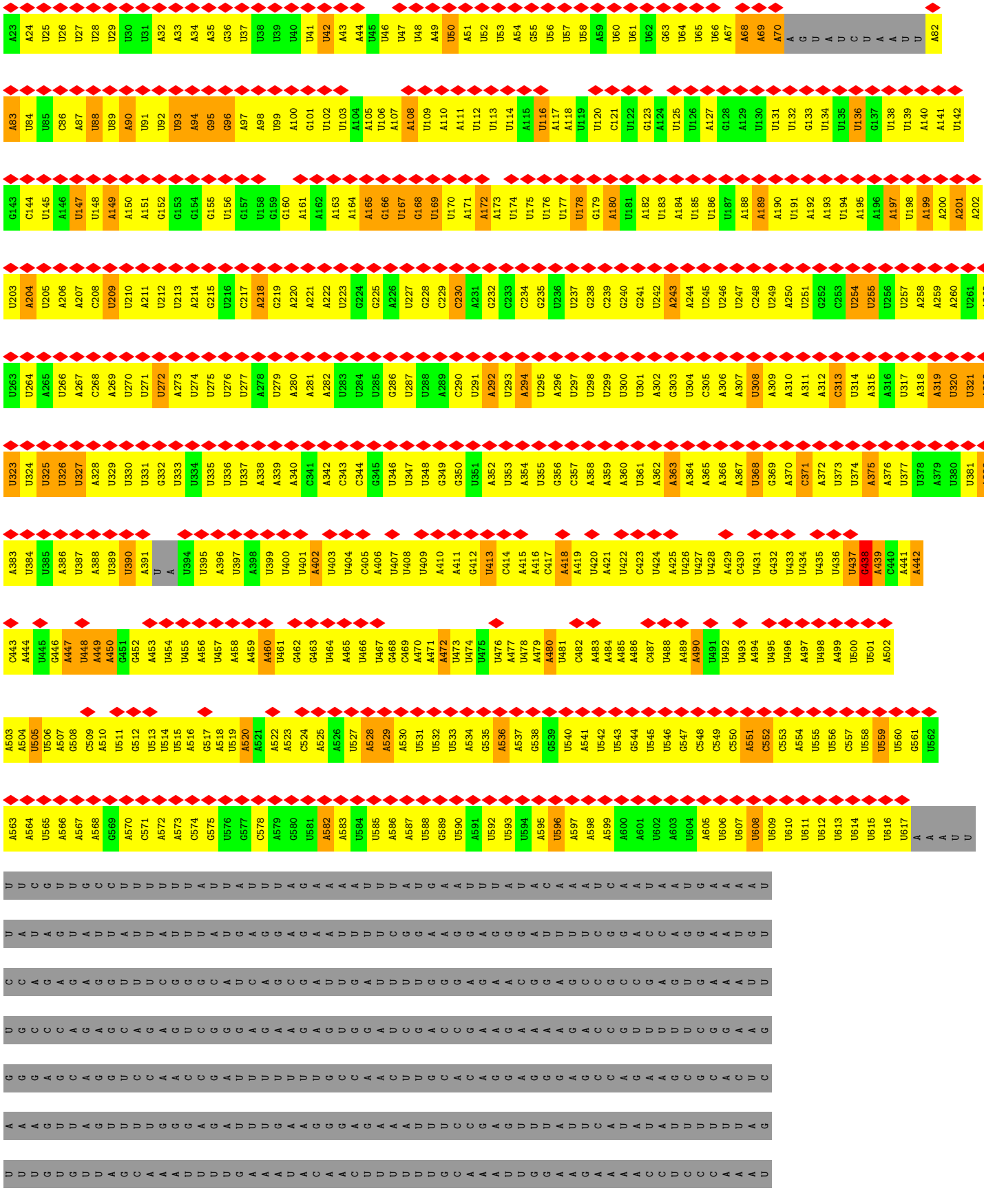
U16
C17
A18
U19
A20
U21
U22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A83 U84 U85 C86 A87 U88 U89 A90 U91 U92 U93 A94 G95 G96 A97 A98 U99 A100 G101 U102 U103 A104 A105 U106 A107 A108 U109 A110 A111 U112 U113 U114 A115 U116 A117 A118 U119 U120 C121 U122 G123 A124 U125 U126 A127 G128 A129 U130 U131 U132 G133 U134 U135 U136 G137 U138 U139 A140 A141 U142
G143 C144 U145 A146 U147 U148 A149 A150 A151 G152 G153 G154 G155 U156 G157 U158 G159 G160 A161 A162 A163 A164 A165 G166 U167 G168 U169 U170 A171 A172 A173 U174 U175 U176 U177 U178 G179 A180 U181 A182 U183 A184 U185 U186 U187 A188 A189 A190 U191 A192 A193 U194 A195 A196 A197 U198 A199 A200 A201 A202
U203 A204 U205 A206 A207 C208 U209 U210 A211 U212 U213 A214 G215 U216 C217 A218 G219 A220 A221 A222 U223 G224 G225 A226 U227 G228 C229 C230 A231 G232 C233 C234 G235 U236 U237 G238 C239 G240 G241 U242 A243 A244 U245 U246 U247 C248 U249 A250 U251 G252 C253 U254 U255 U256 U257 A258 A259 A260 U261 A262
U263 U264 A265 U266 A267 C268 A269 U270 U271 U272 A273 U274 U275 U276 U277 A278 U279 A280 A281 A282 U283 U284 U285 G286 U287 U288 A289 C290 U291 A292 U293 A294 U295 A296 U297 U298 U299 U300 U301 A302 G303 U304 C305 A306 A307 U308 A309 A310 A311 A312 C313 U314 A315 A316 U317 A318 A319 U320 U321 A322
U323 U324 U325 U326 U327 A328 U329 U330 U331 G332 U333 U334 U335 U336 U337 A338 A339 A340 C341 A342 C343 C344 G345 U346 U347 U348 G349 G350 U351 A352 U353 A354 U355 G356 C357 A358 A359 A360 U361 A362 A363 A364 A365 A366 A367 U368 G369 A370 C371 A372 U373 U374 A375 A376 U377 U378 A379 U380 U381 A382
A383 U384 U385 A386 U387 A388 U389 U390 A391 U A U394 U395 A396 U397 A398 U399 U400 U401 A402 U403 U404 C405 A406 U407 U408 U409 A410 A411 G412 U413 C414 A415 A416 C417 A418 A419 U420 A421 U422 C423 U424 A425 U426 U427 U428 A429 C430 U431 G432 U433 U434 U435 U436 U437 G438 A439 C440 A441 A442
C443 A444 U445 G446 A447 U448 A449 A450 G451 G452 A453 U454 U455 A456 U457 A458 A459 A460 U461 G462 G463 U464 A465 U466 U467 G468 C469 A470 A471 A472 U473 U474 U475 U476 A477 U478 A479 A480 U481 C482 A483 A484 A485 A486 C487 U488 A489 A490 U491 U492 U493 A494 U495 U496 A497 U498 A499 U500 U501 A502
A503 A504 U505 U506 A507 G508 C509 A510 U511 G512 U513 U514 U515 A516 G517 A518 U519 A520 A521 A522 A523 C524 A525 A526 U527 A528 A529 A530 U531 U532 U533 A534 G535 A536 A537 G538 G539 U540 A541 U542 U543 G544 U545 U546 G547 C548 C549 C550 A551 C552 C553 A554 U555 U556 C557 U558 U559 U560 G561 U562
A563 A564 U565 A566 A567 A568 G569 A570 C571 A572 A573 C574 G575 U576 G577 C578 A579 G580 U581 A582 A583 U584 U585 A586 A587 U588 G589 U590 A591 U592 U593 U594 A595 U596 A597 A598 A599 A600 A601 U602 A603 U604 A605 U606 U607 U608 U609 U610 U611 U612 U613 U614 U615 U616 U617 A A A U U
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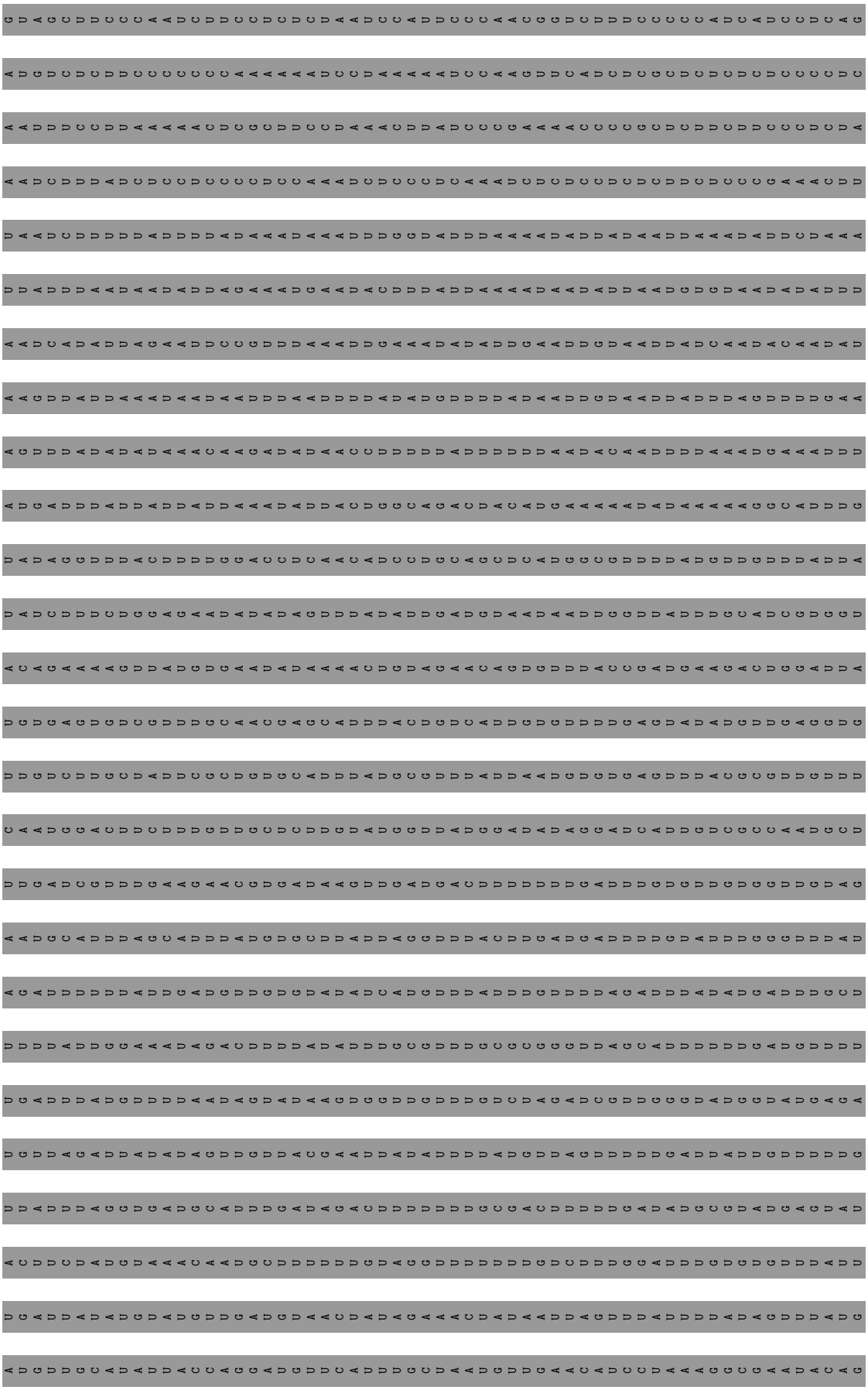
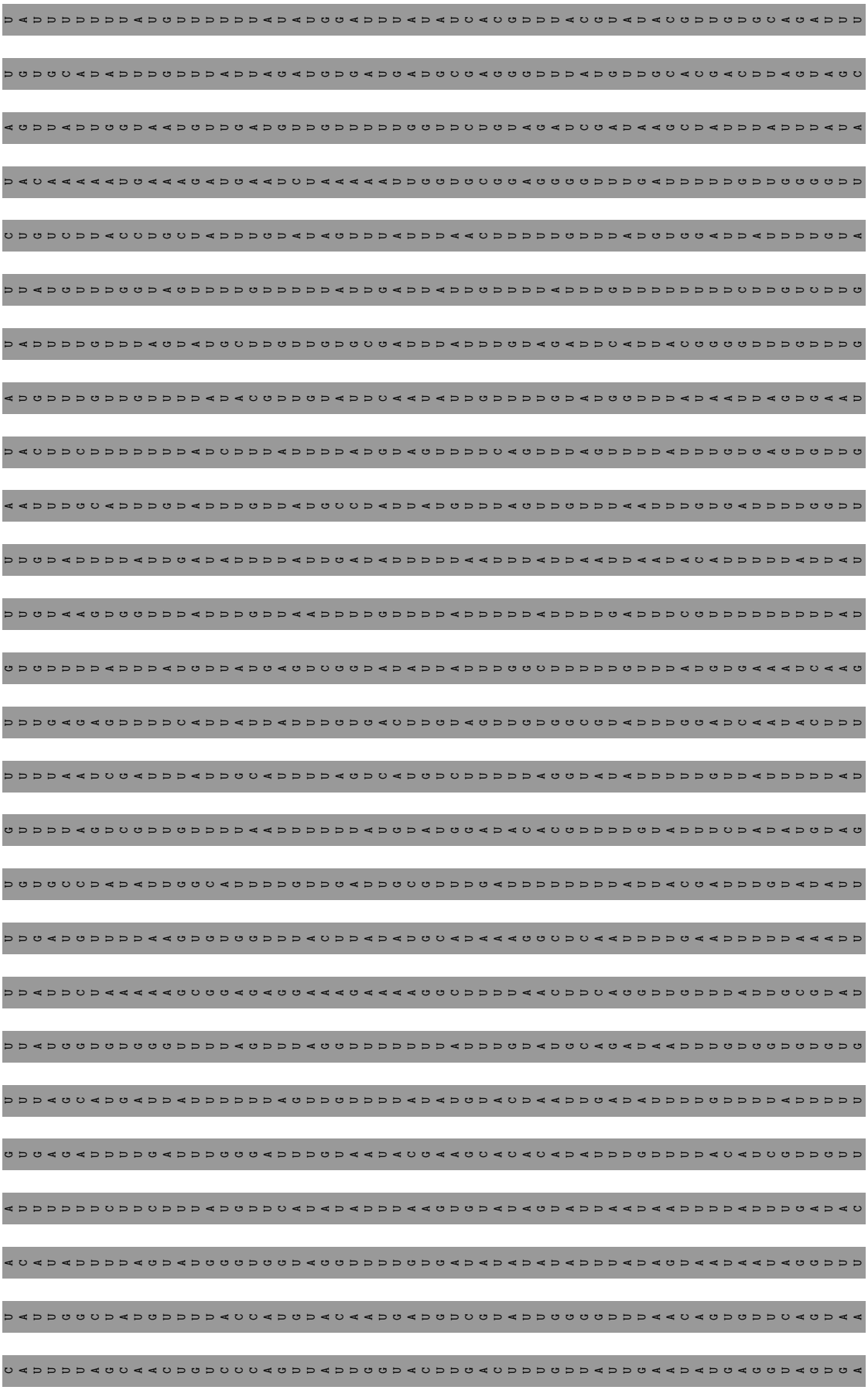
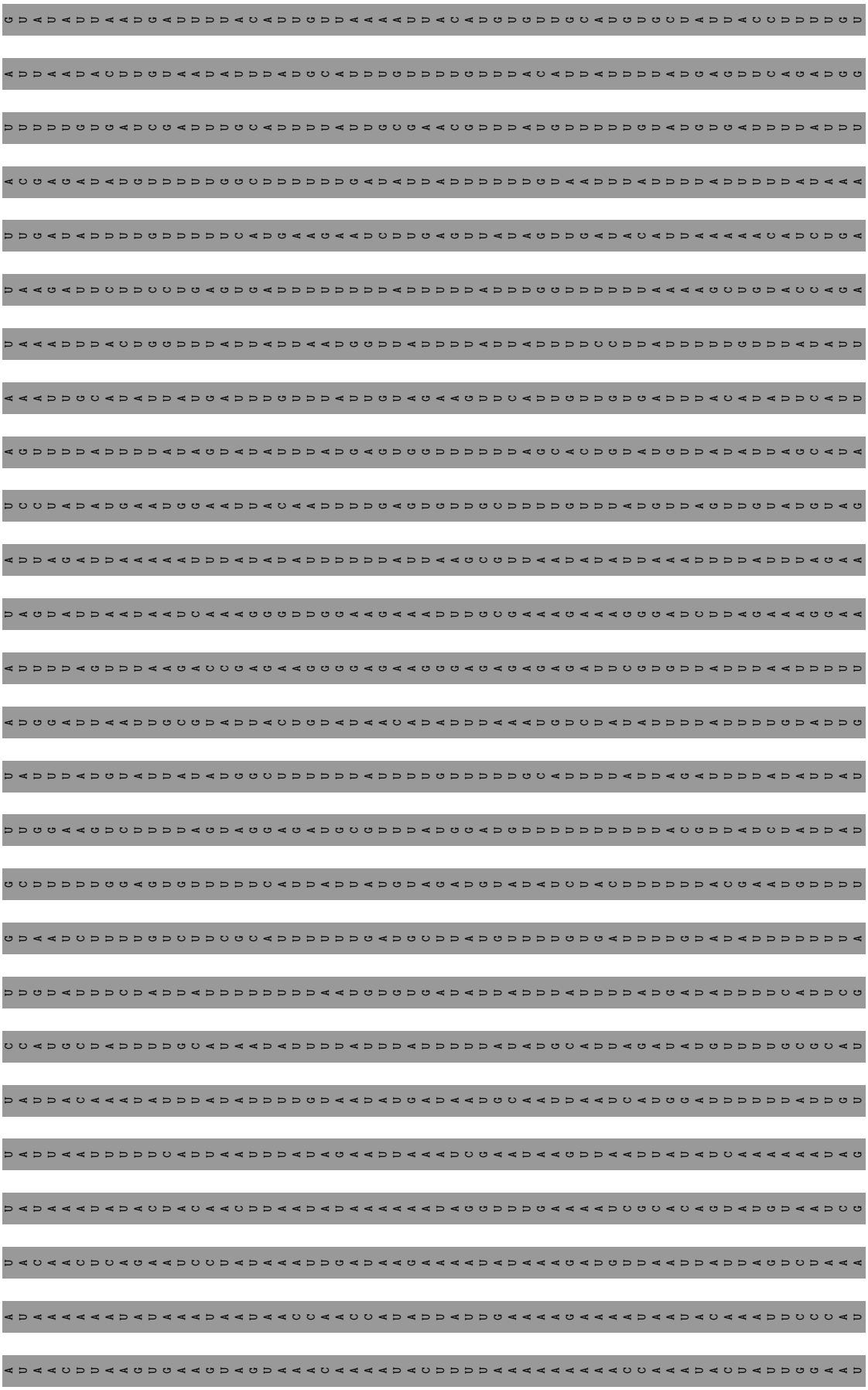
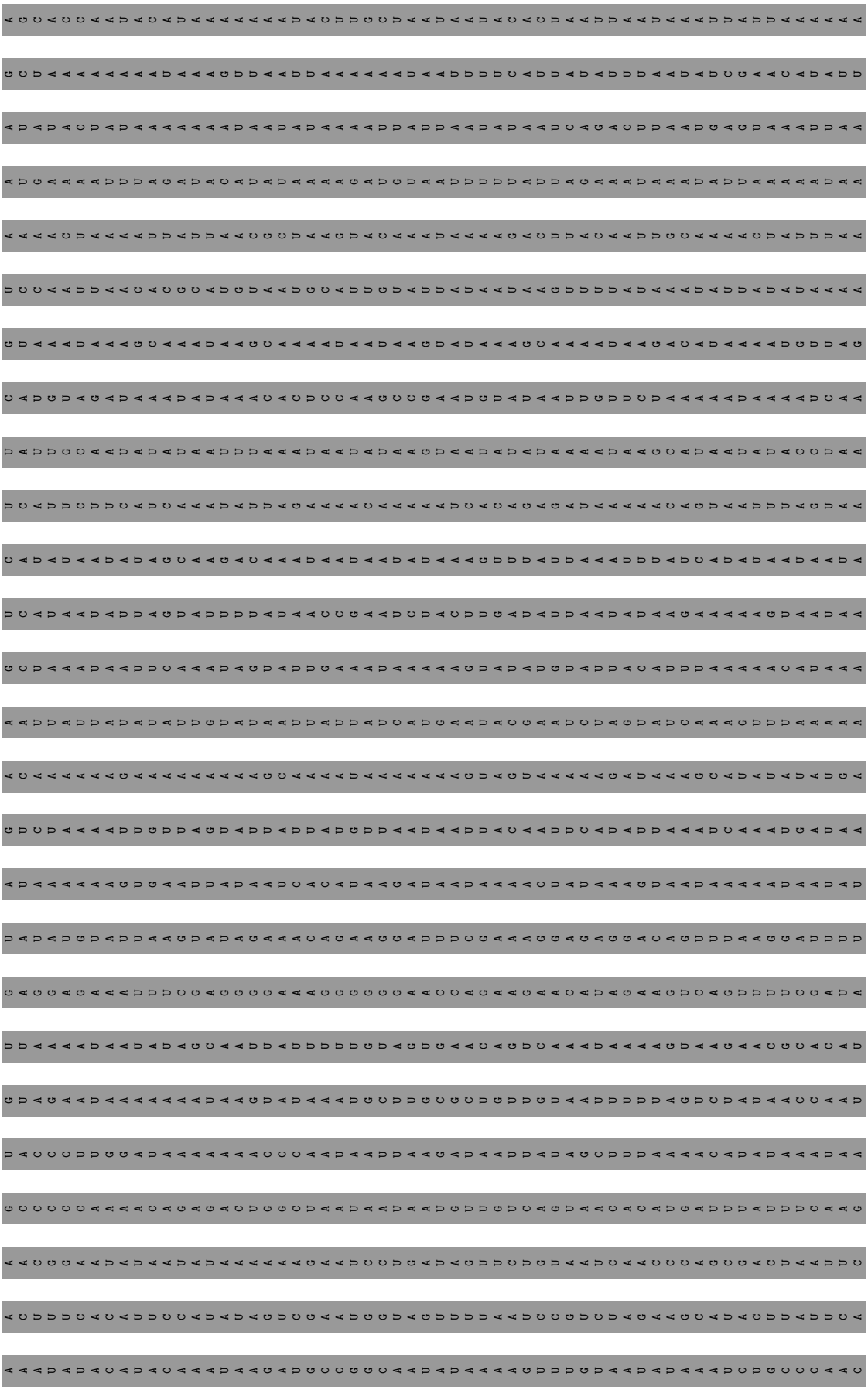
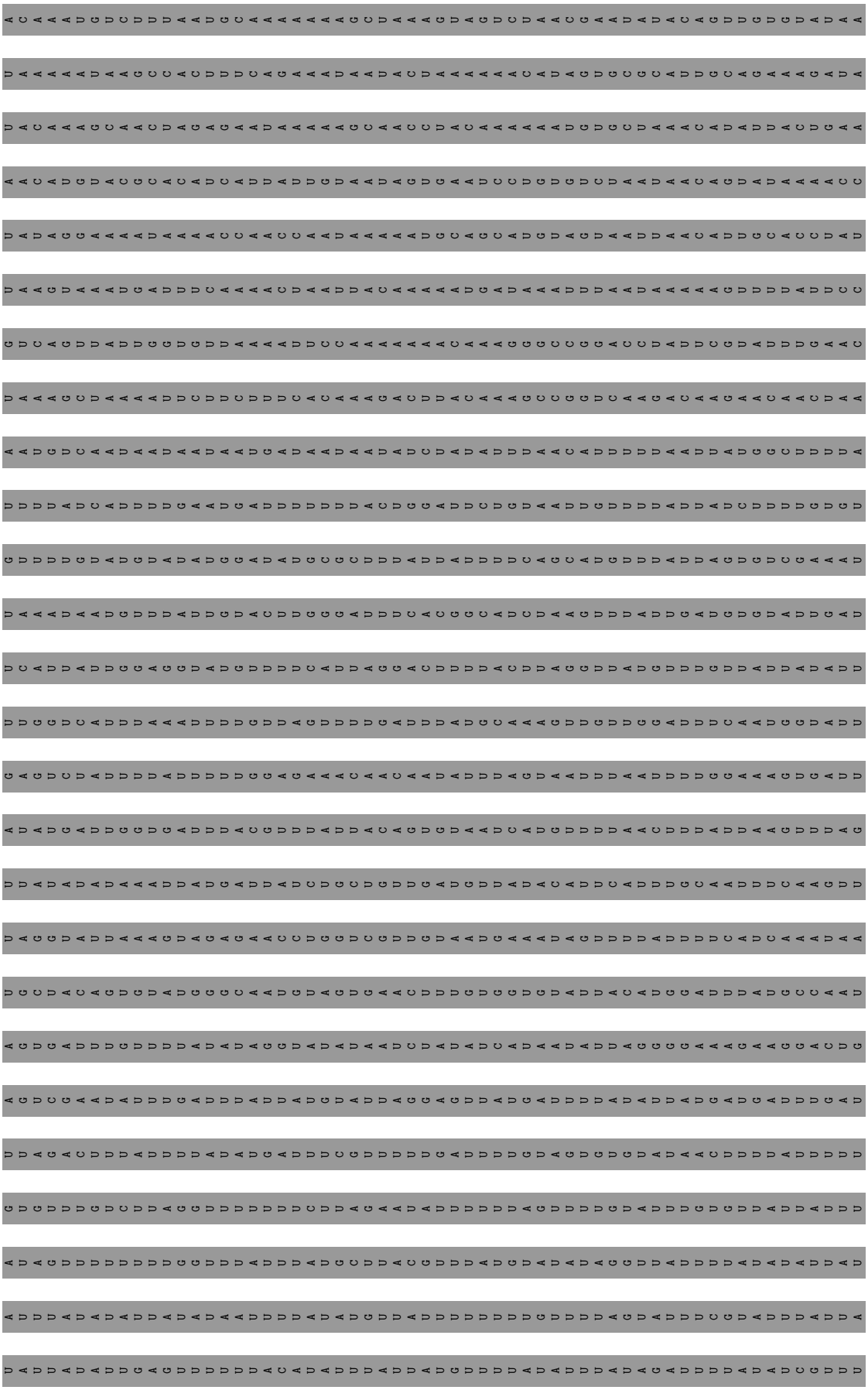
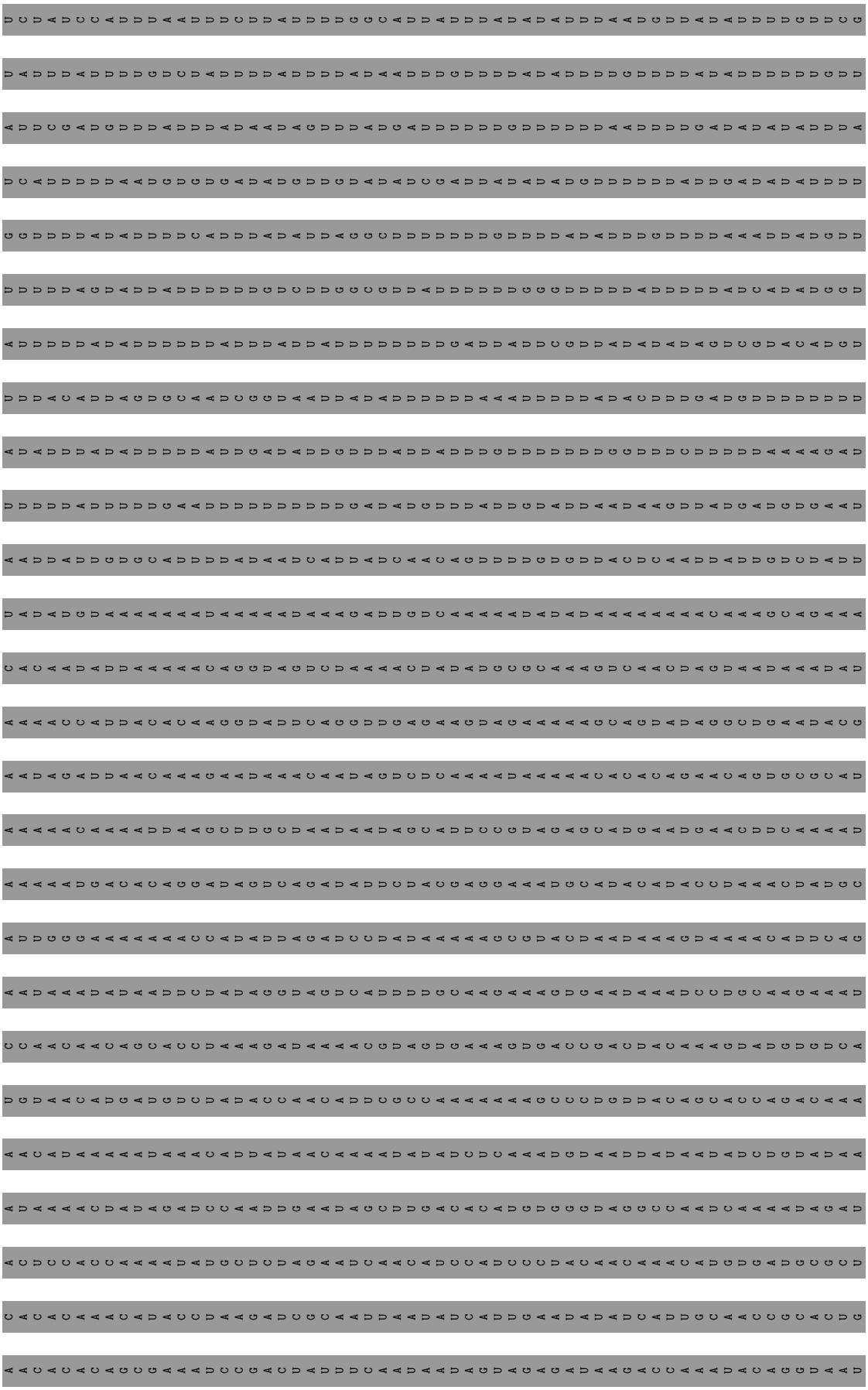


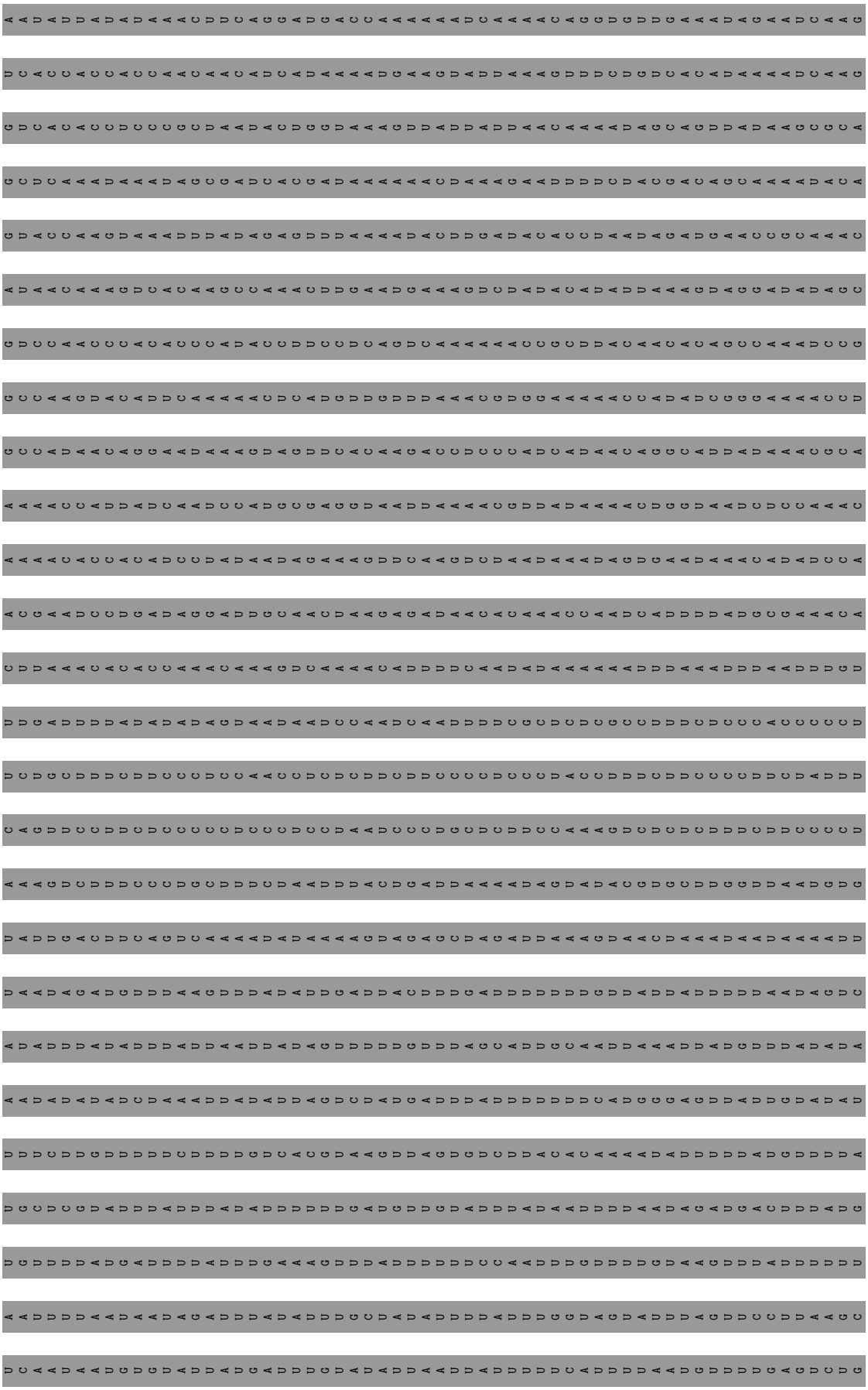


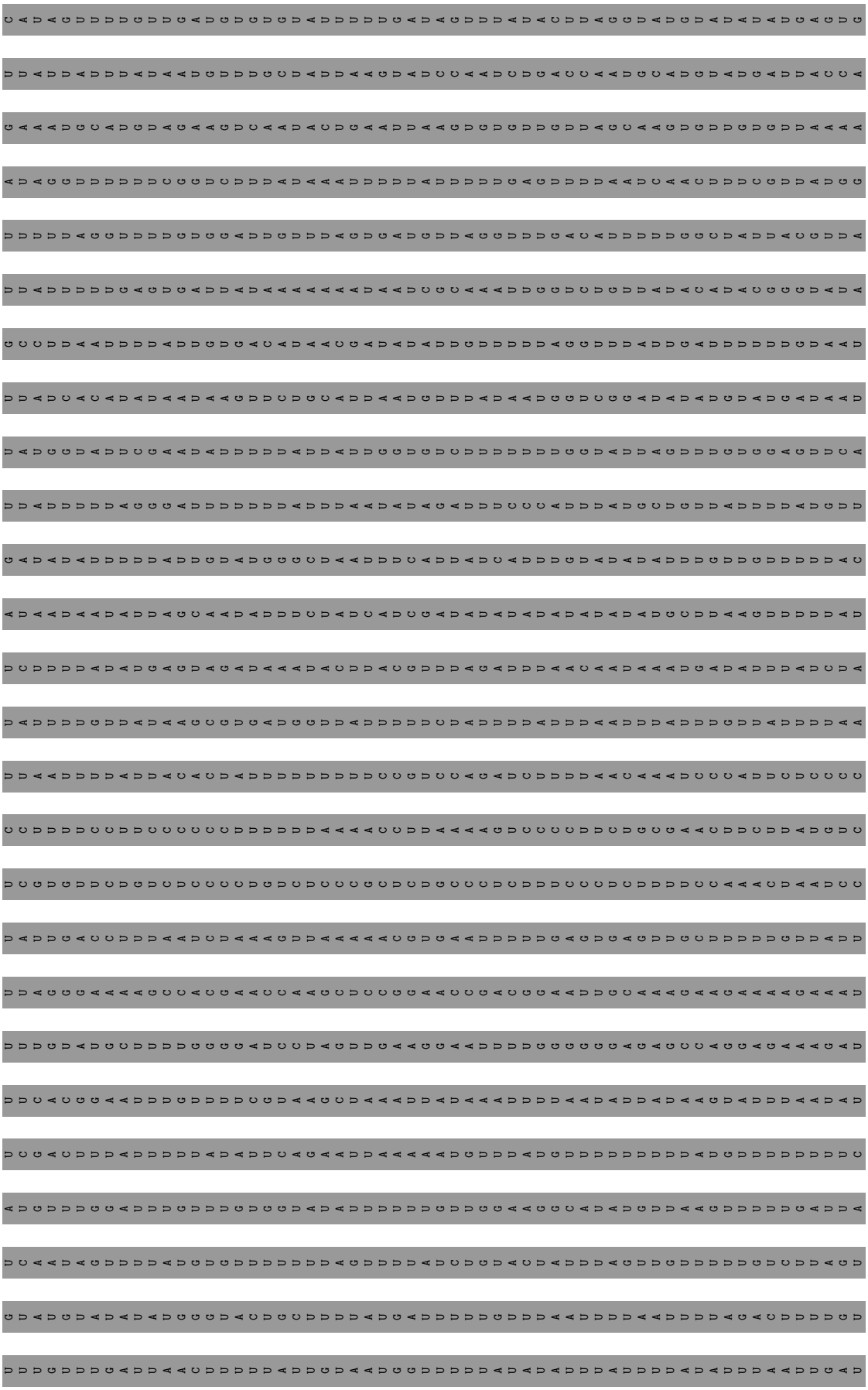


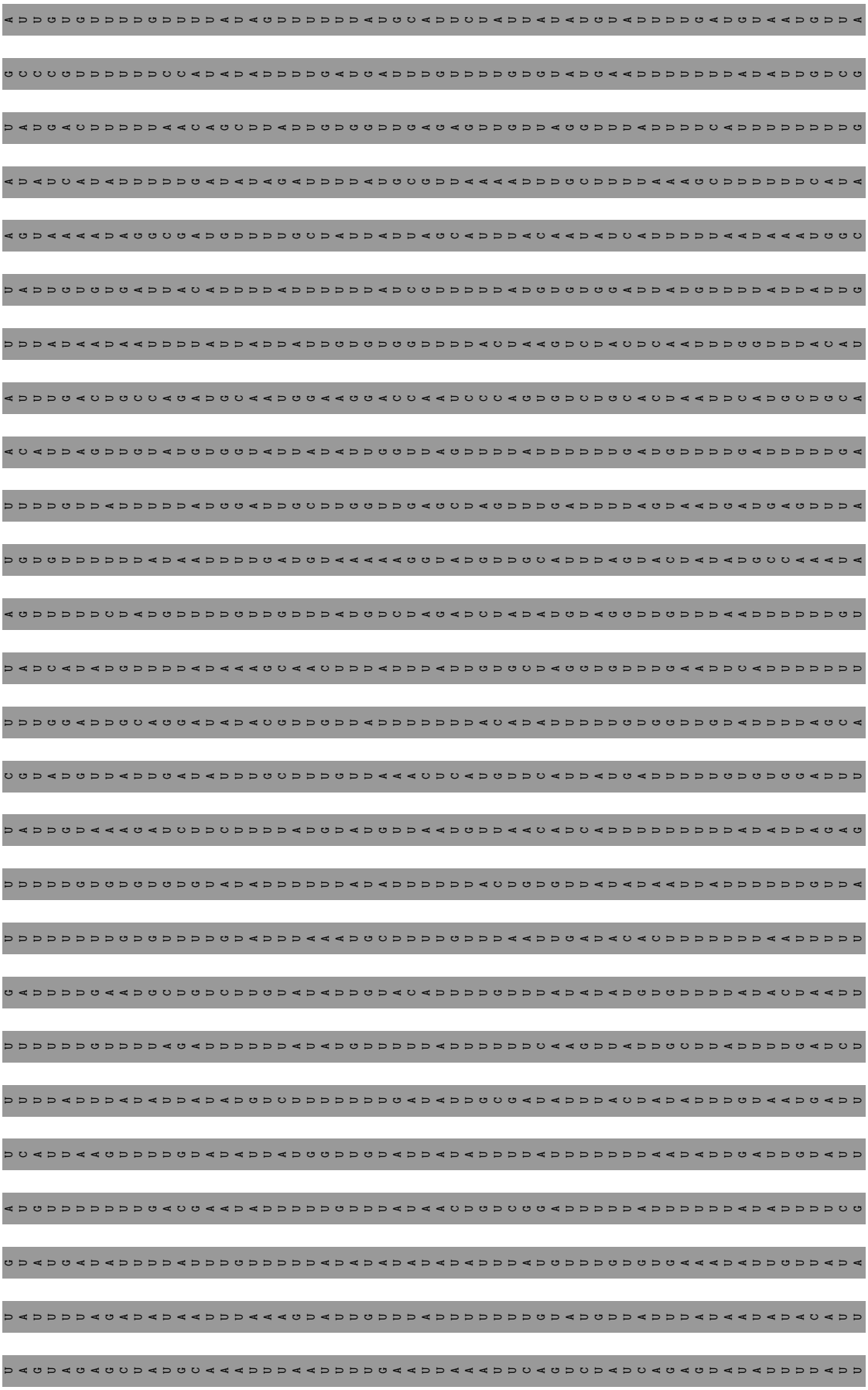


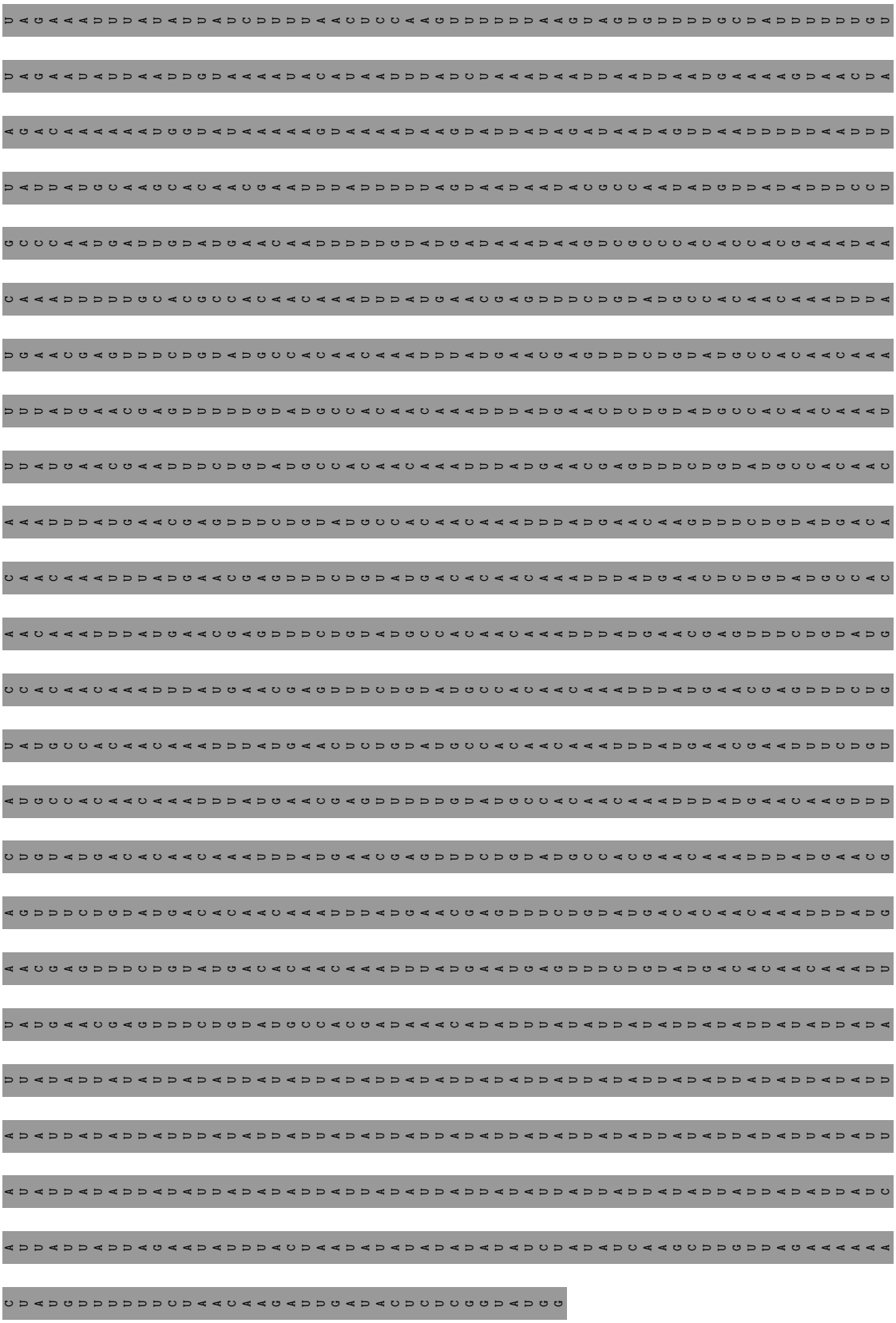






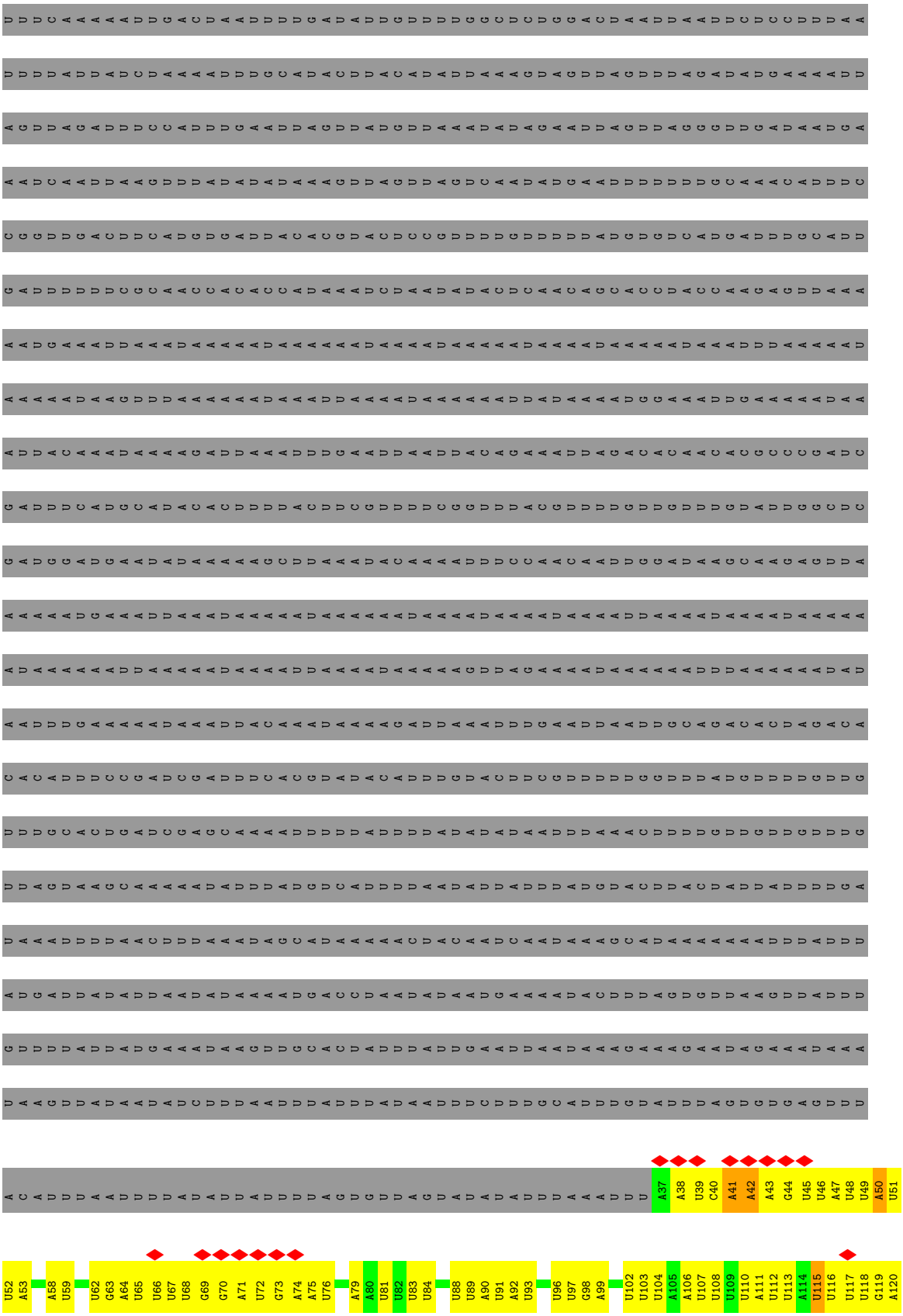






• Molecule 1: Large ribosomal RNA

Chain 1: 94%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A105
A106
U107
U108
U109
U110
A111
U112
U113
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U115
U116
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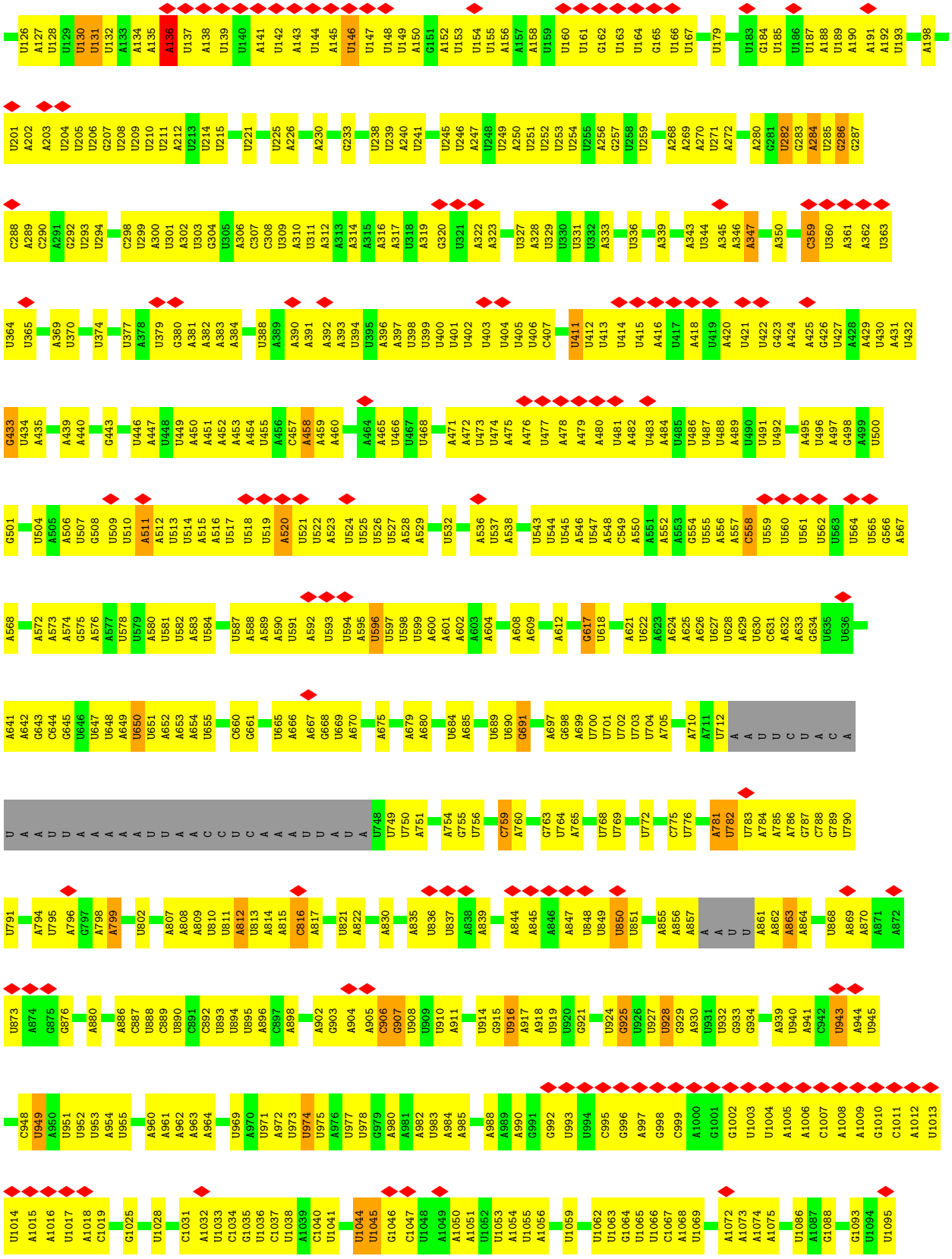
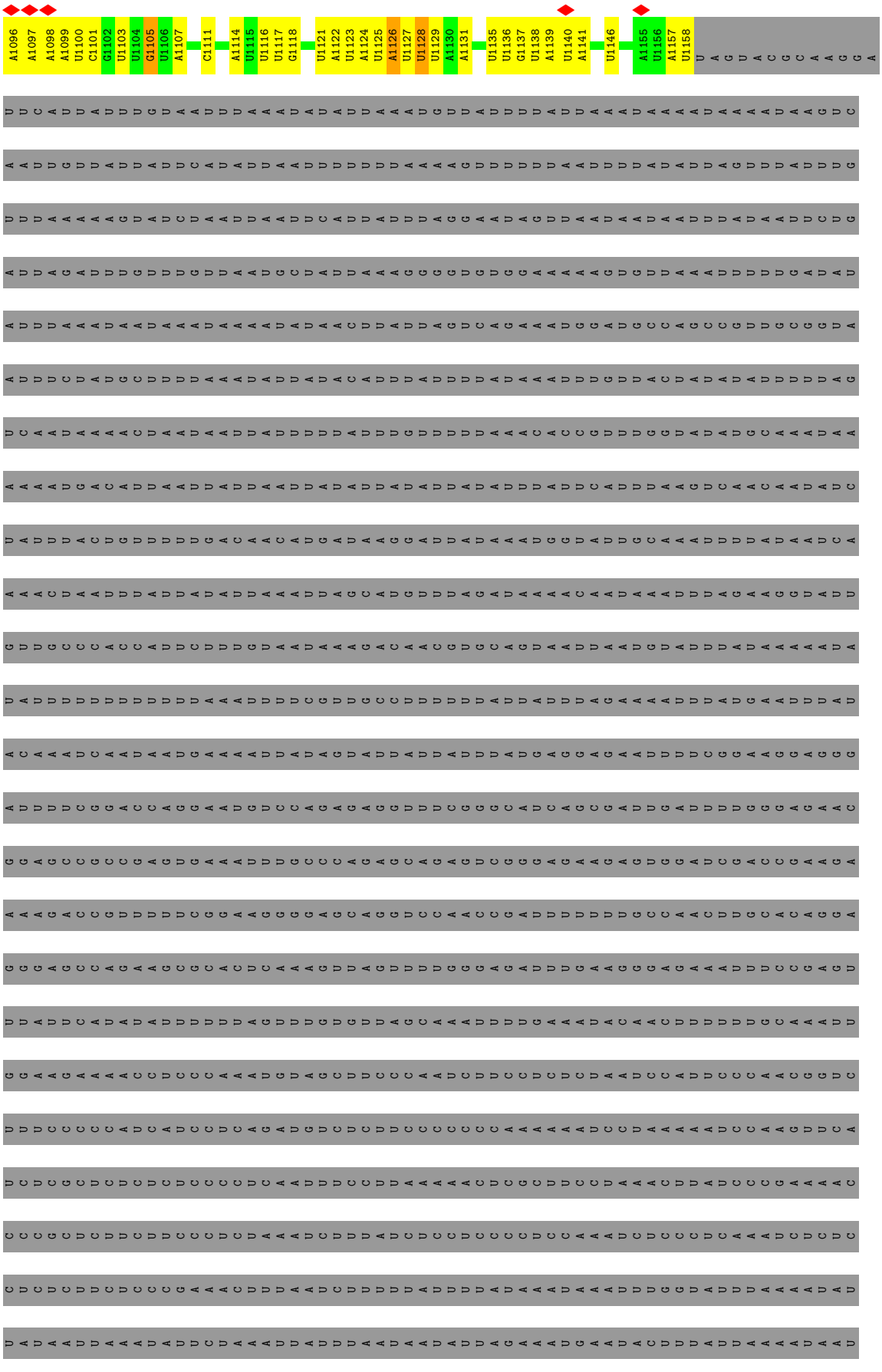
A120

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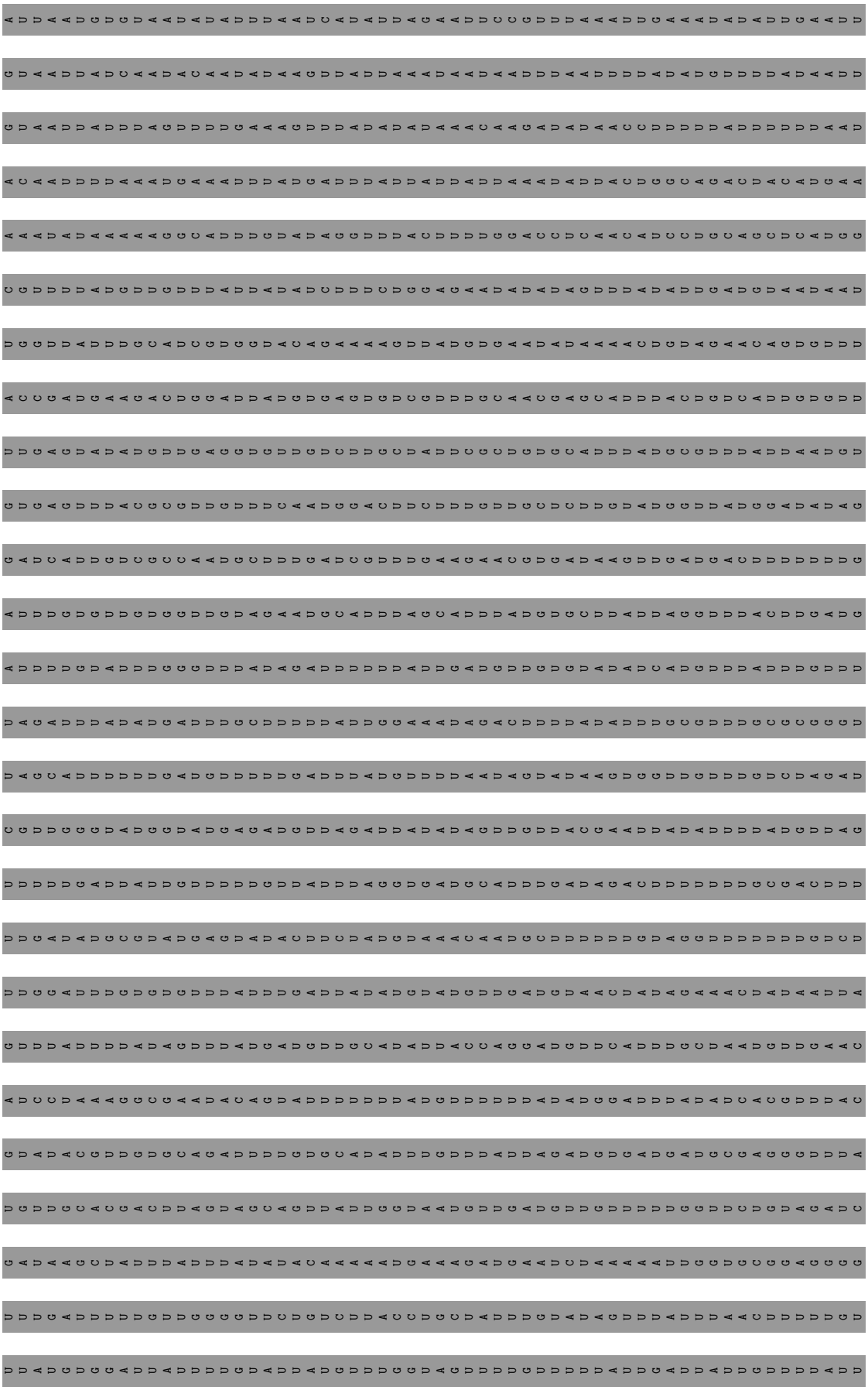
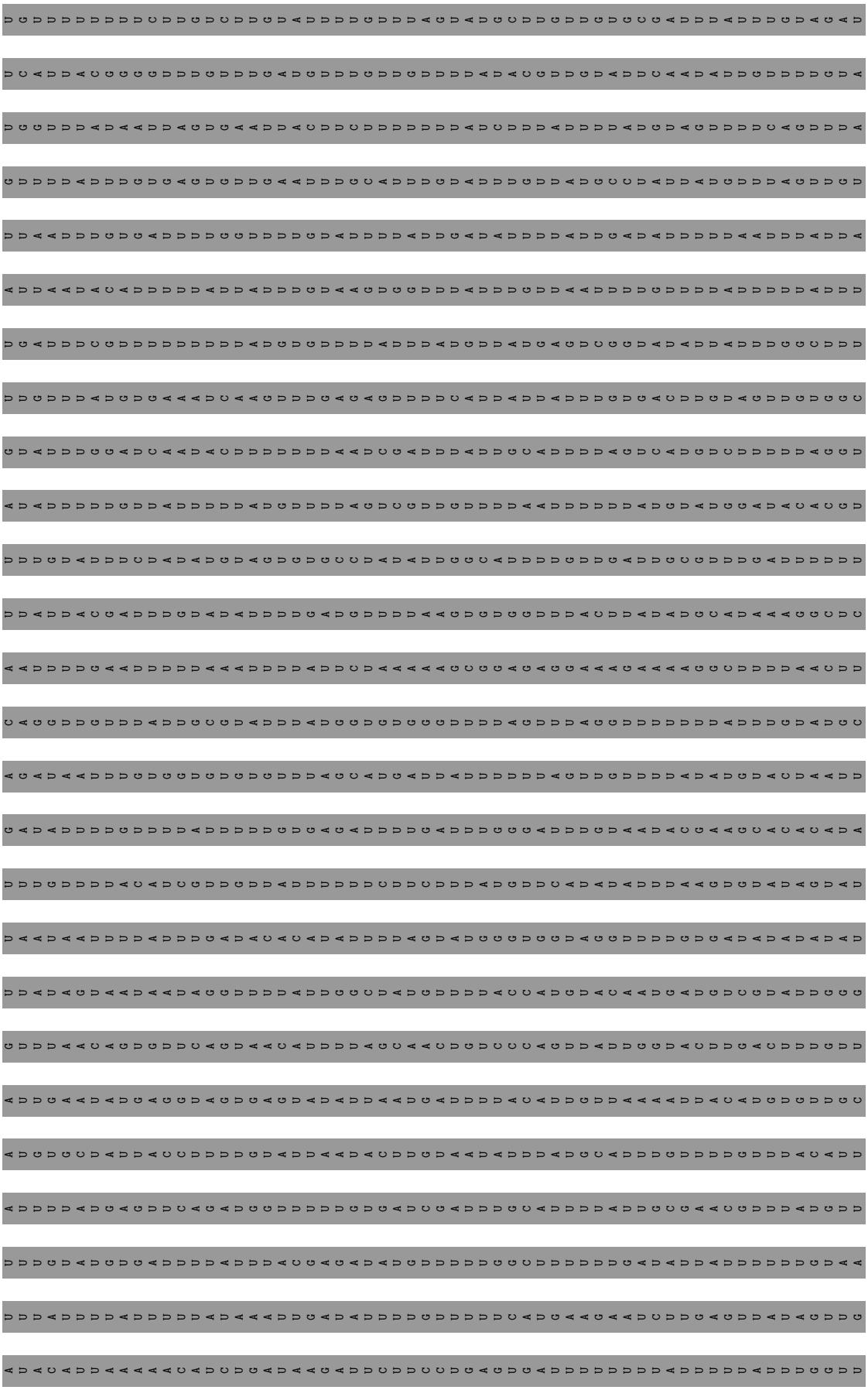
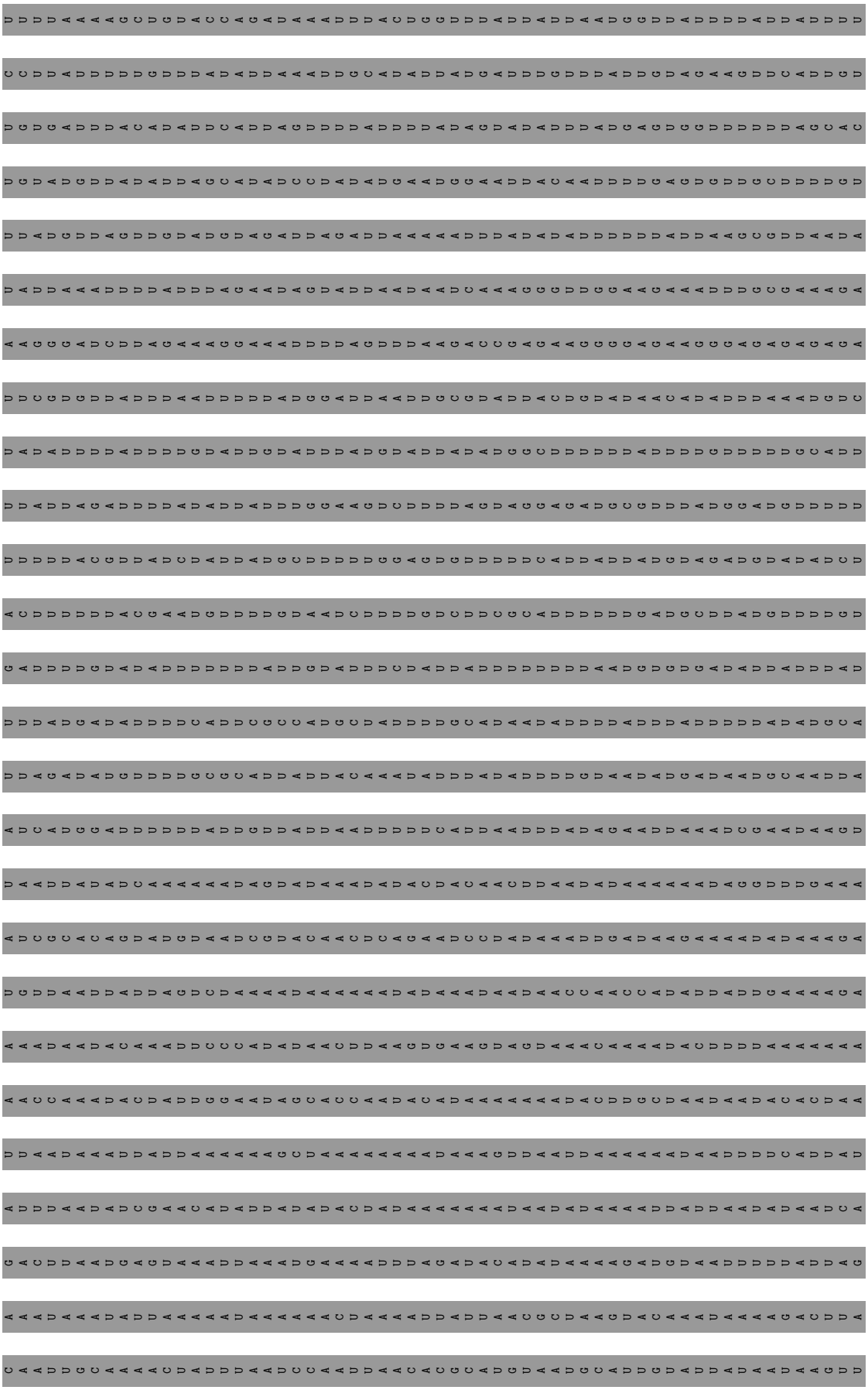
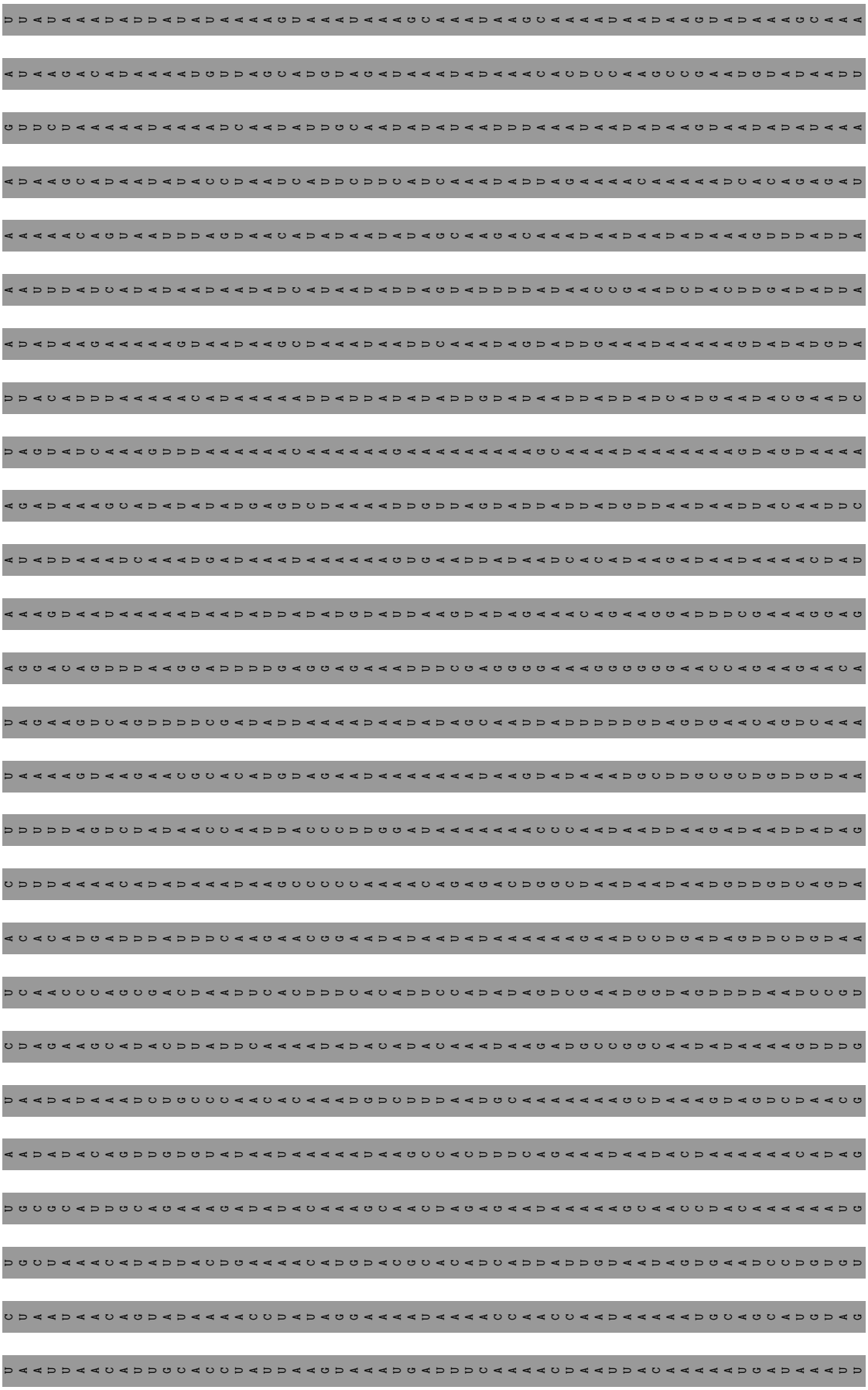
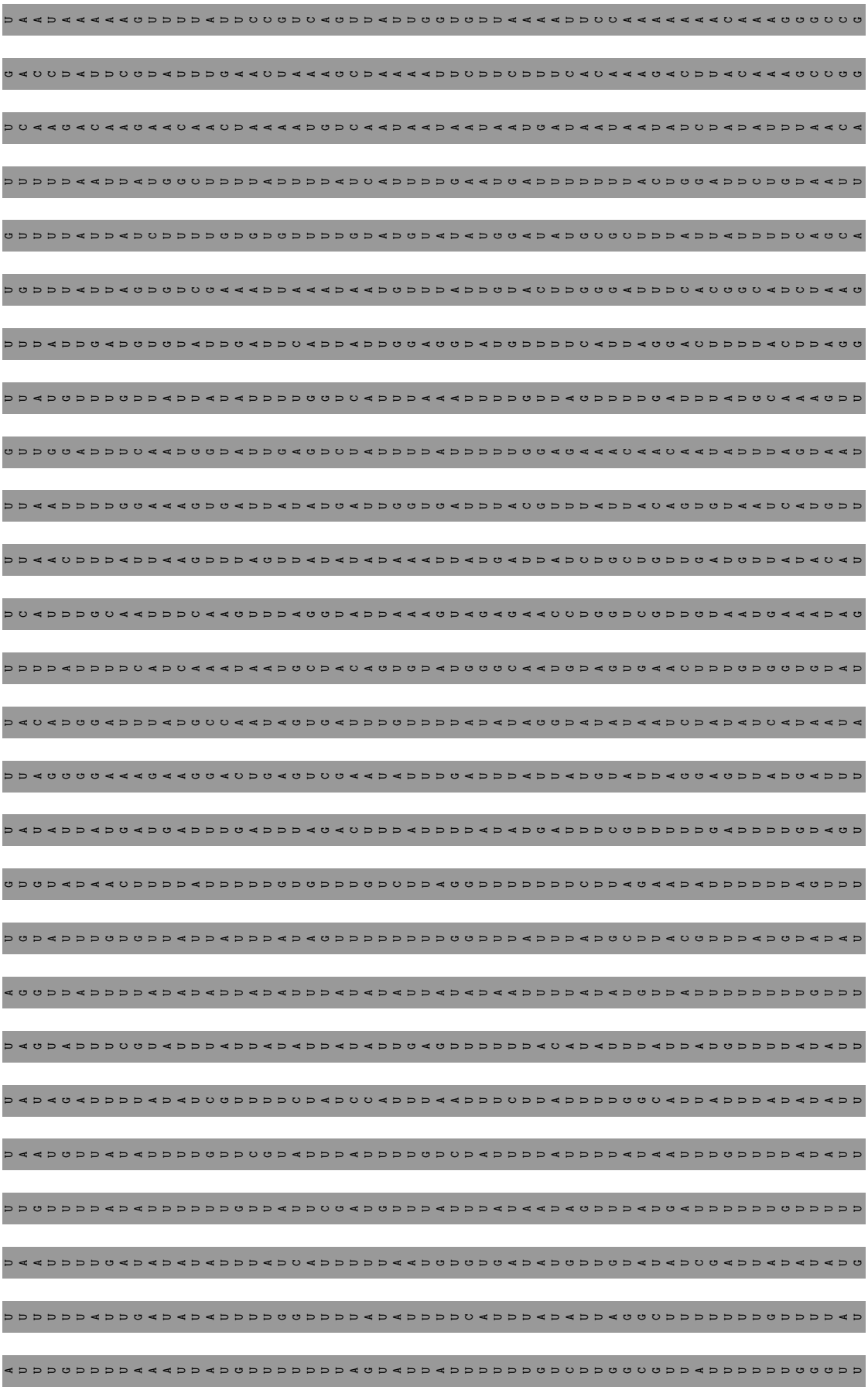
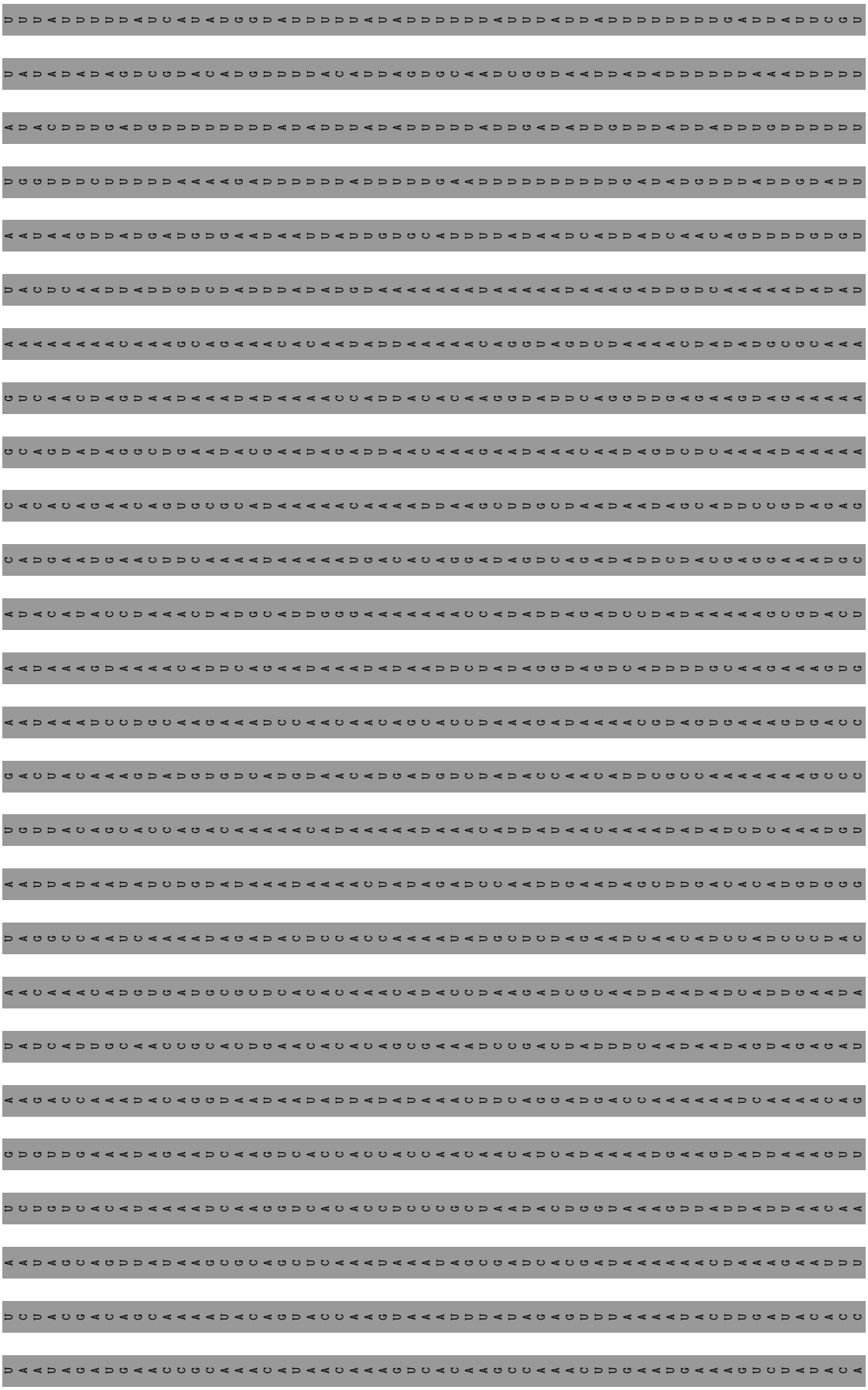


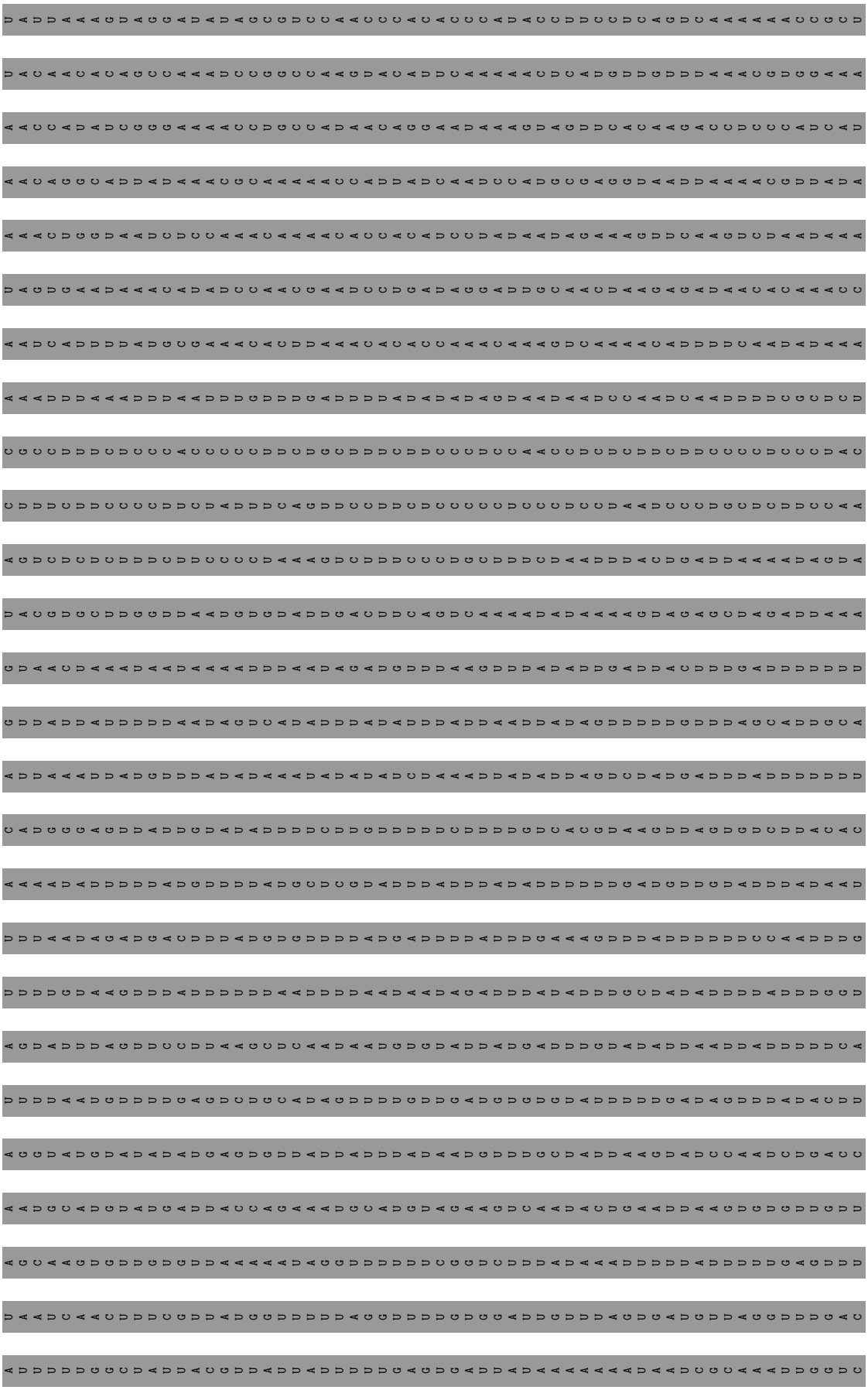


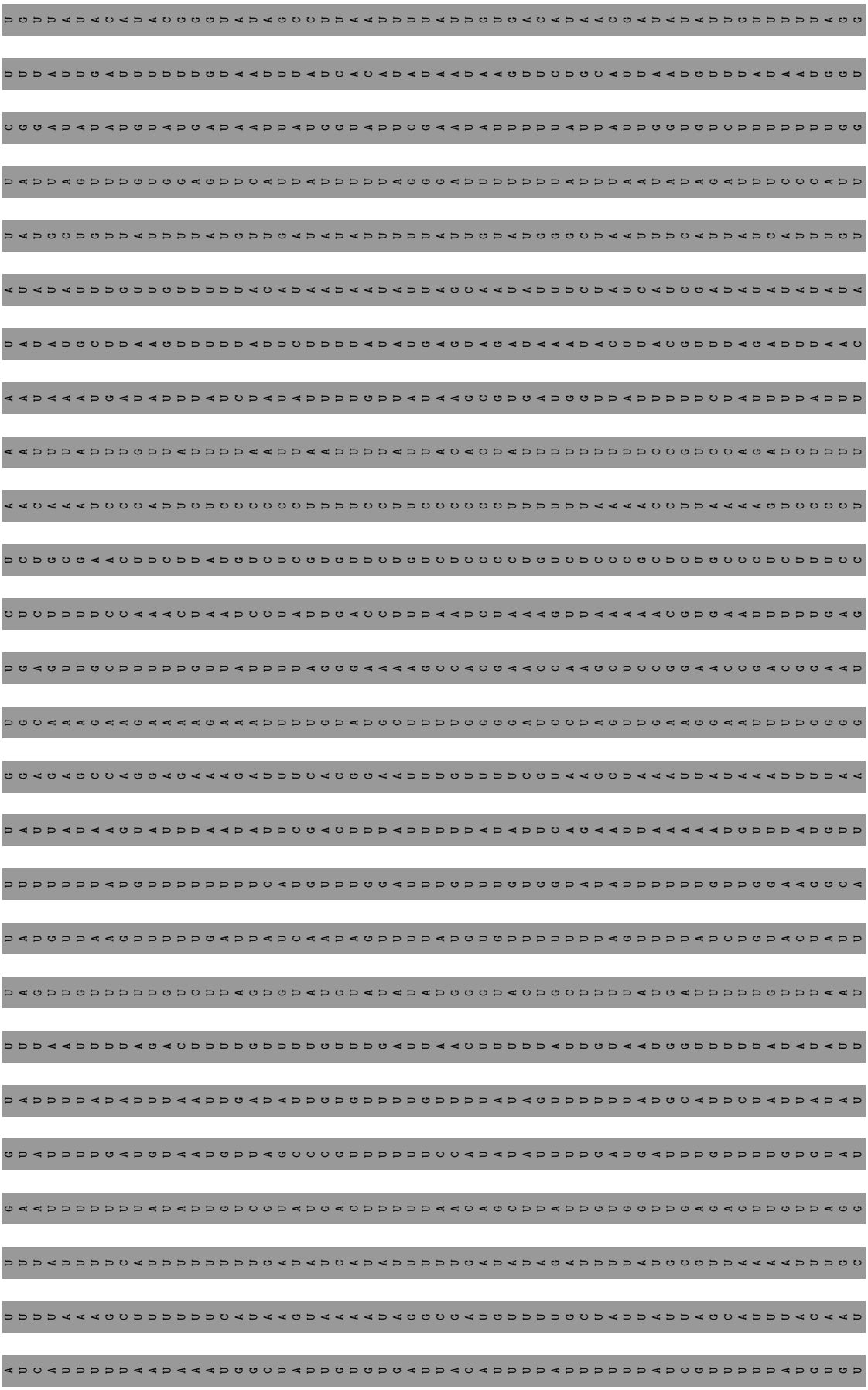


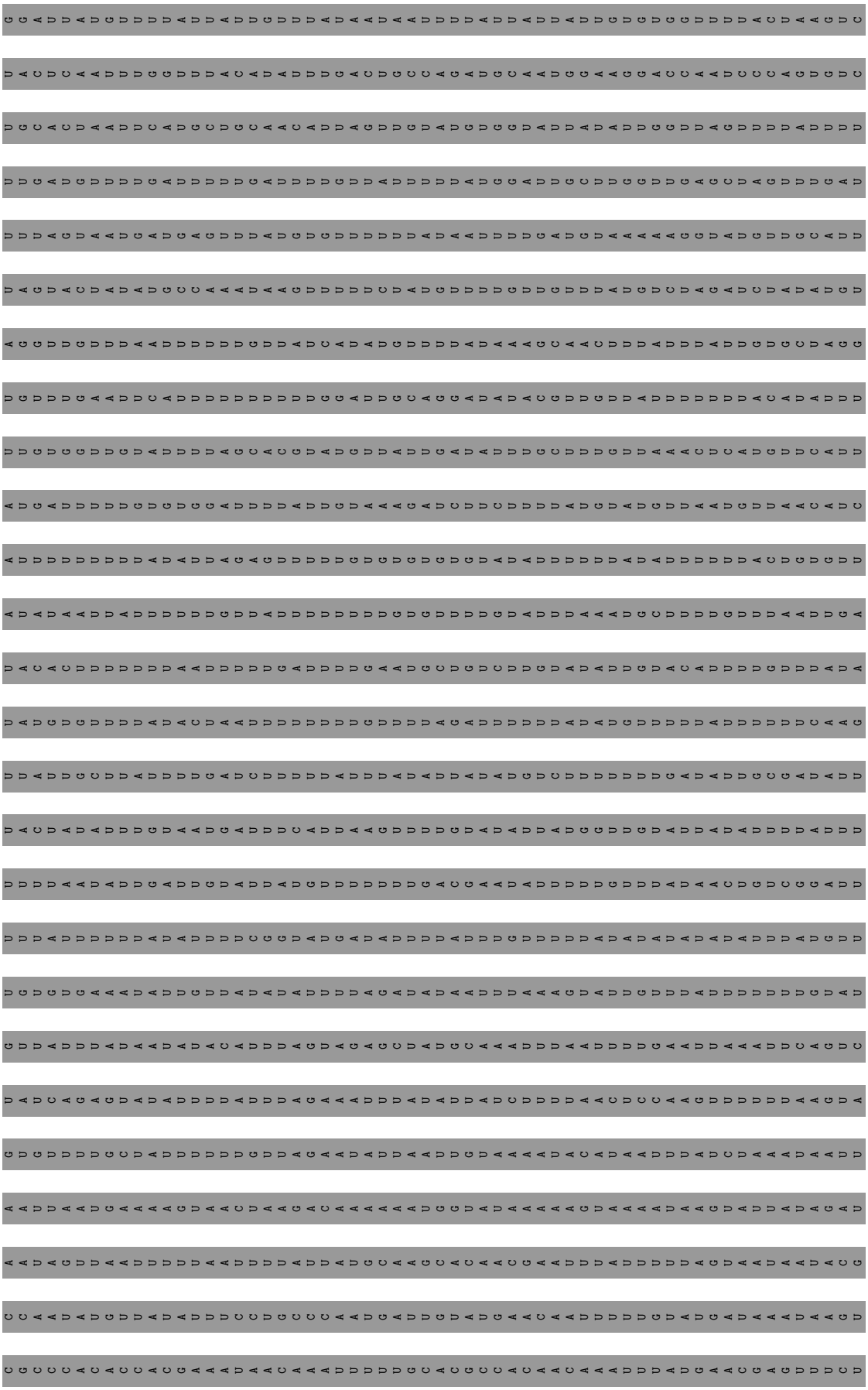


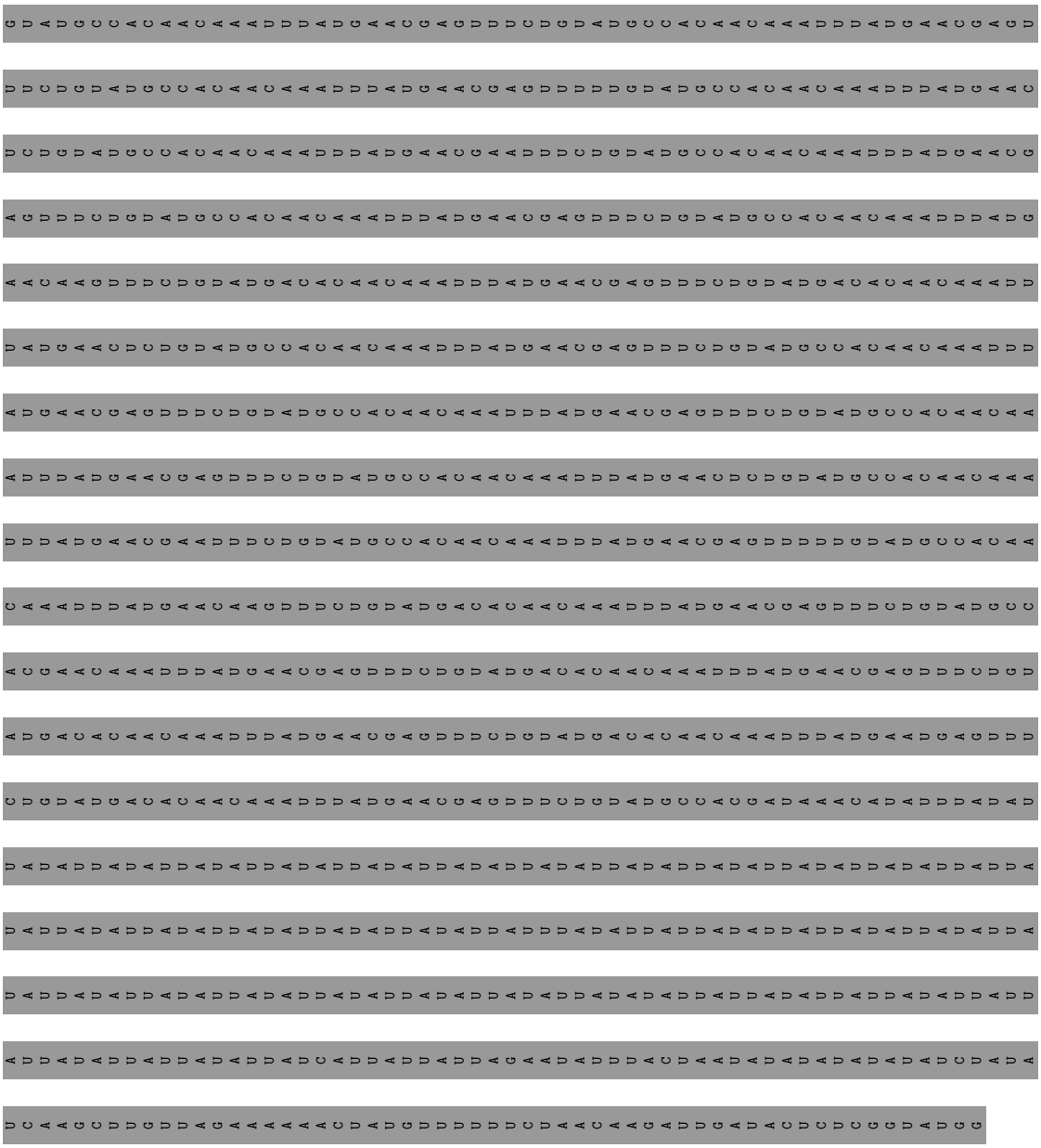






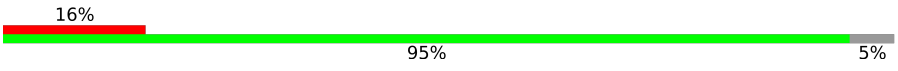


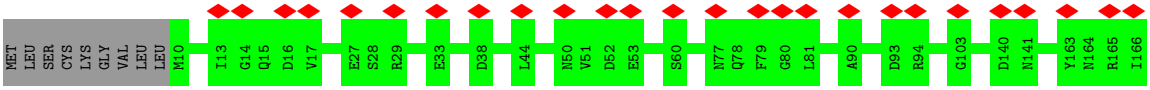




• Molecule 2: uS14m

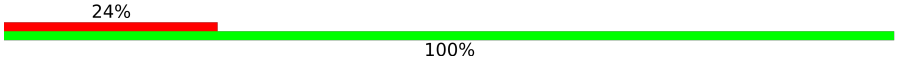
Chain h:

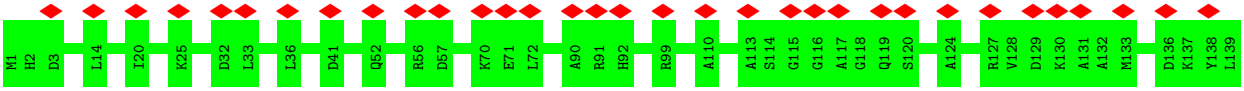




• Molecule 3: mS69

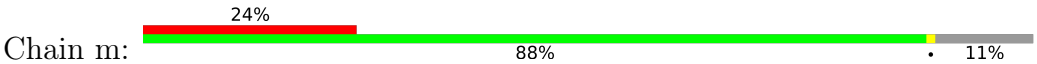
Chain aw:

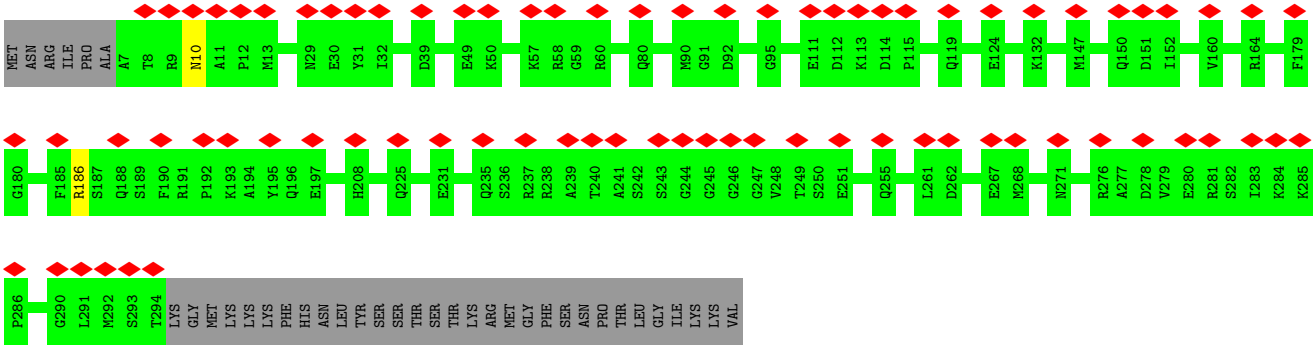




• Molecule 4: bS18m

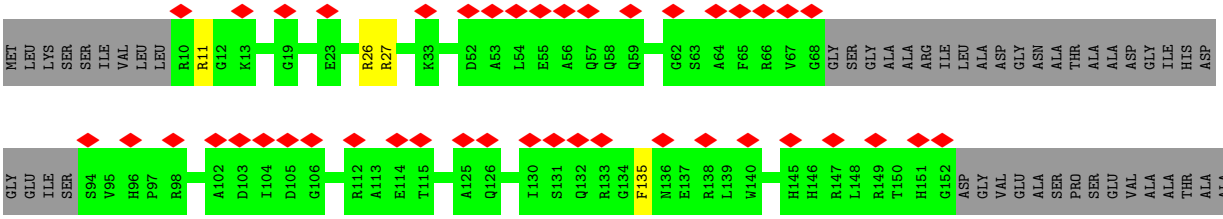
Chain m:





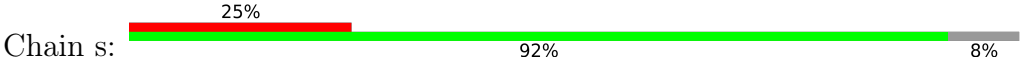
• Molecule 5: uS11m

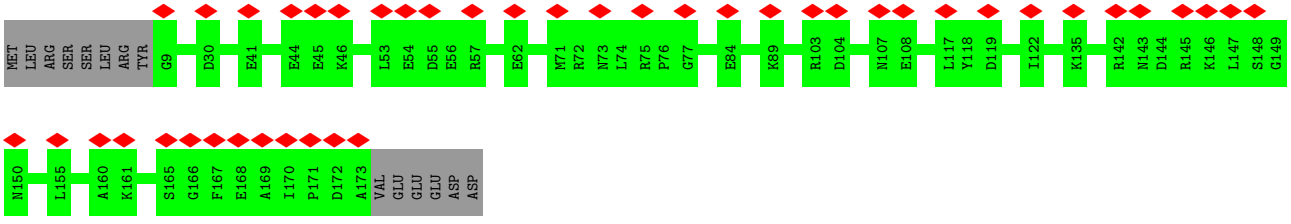
Chain f:



• Molecule 6: mS33

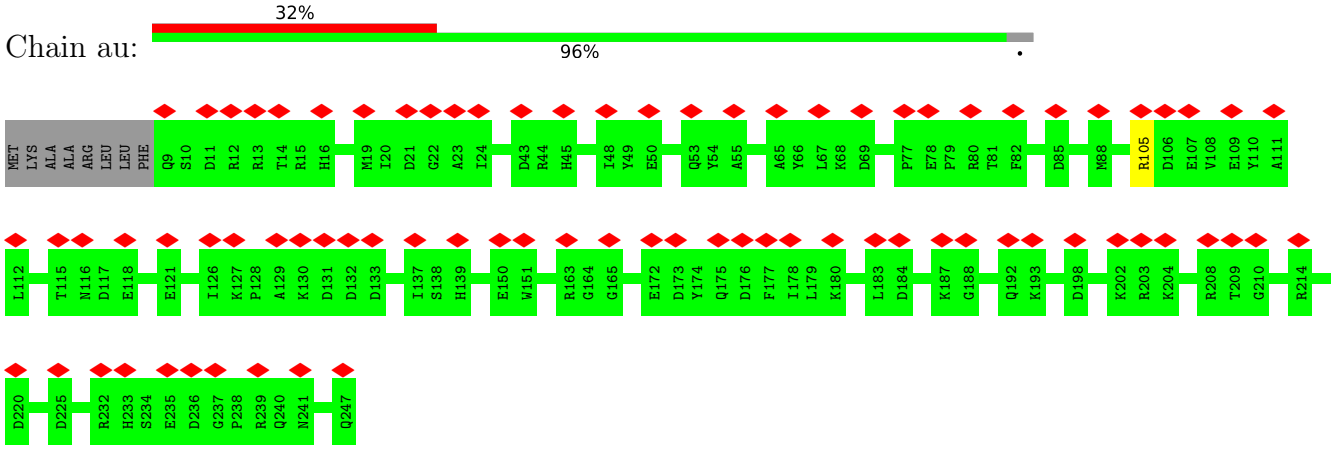
Chain s:





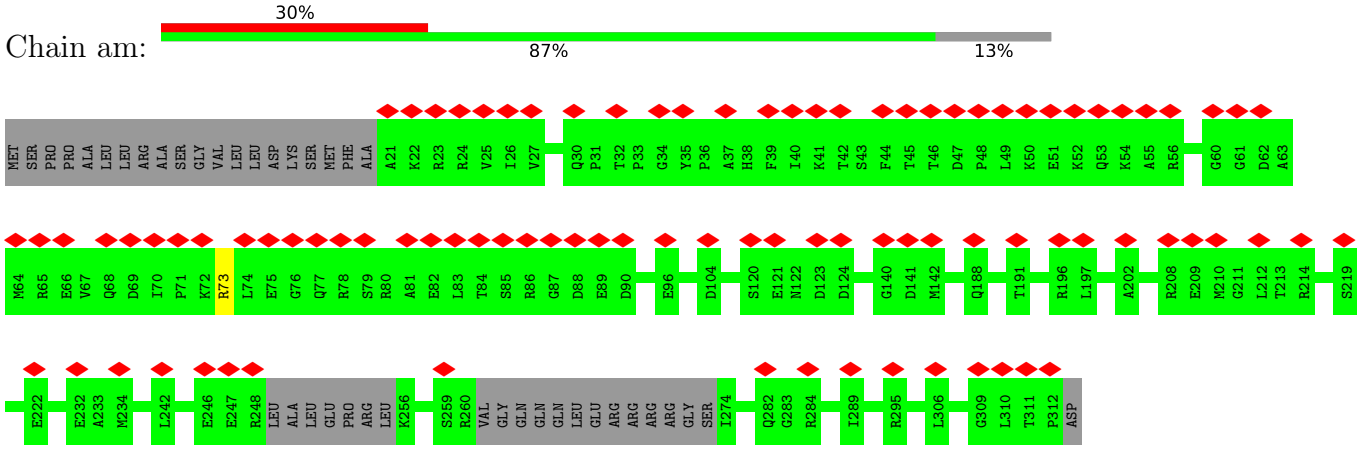
• Molecule 7: Rhodanese domain-containing protein

Chain au:



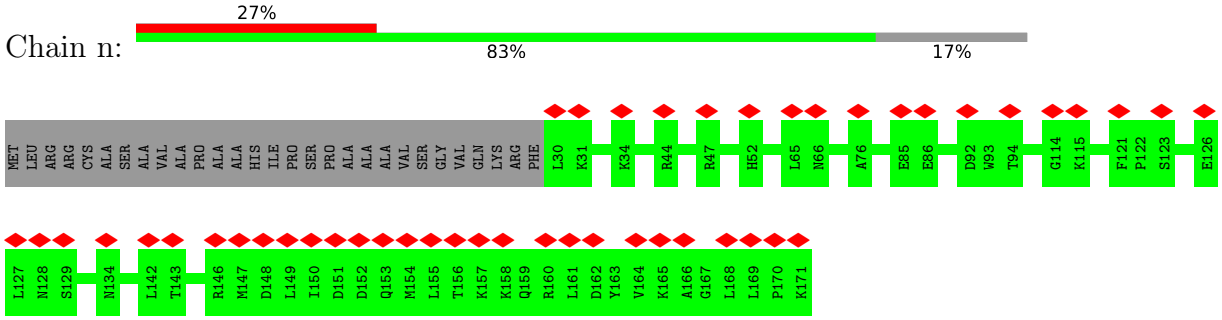
• Molecule 8: mS59

Chain am:



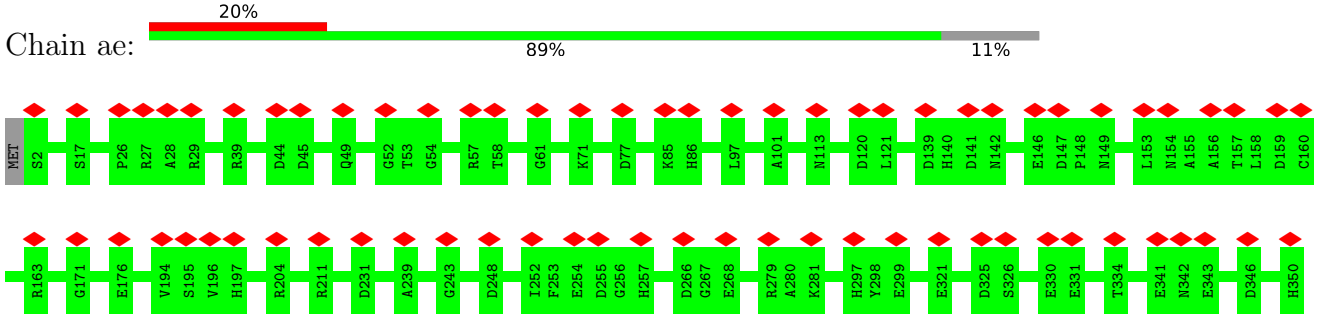
• Molecule 9: uS19m

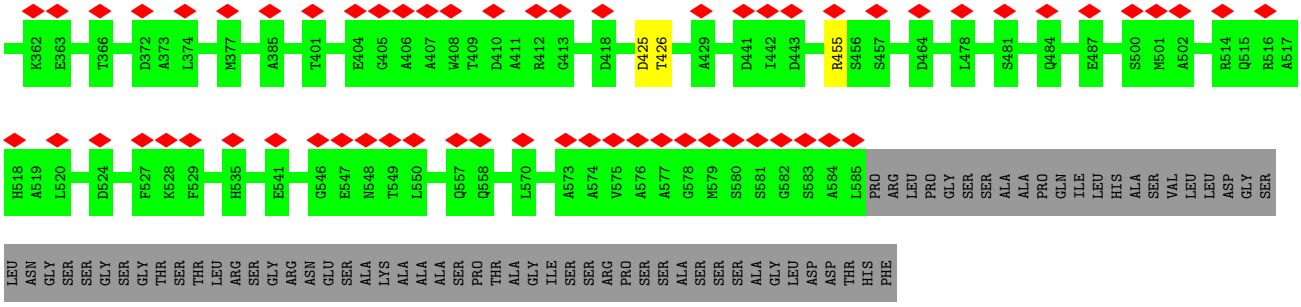
Chain n:



• Molecule 10: mS53

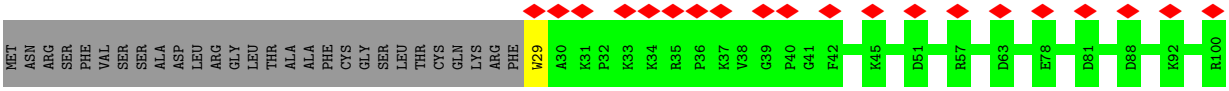
Chain ae:

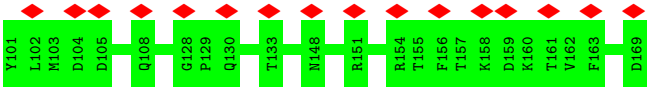




• Molecule 11: mS71

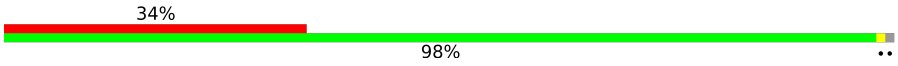
Chain ay:

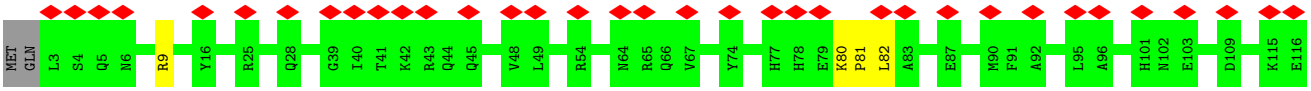


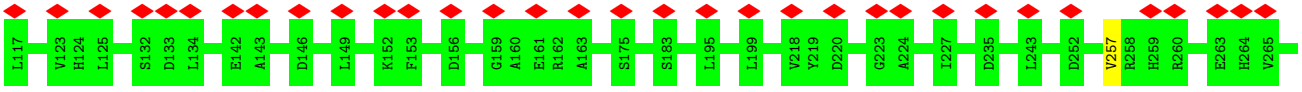


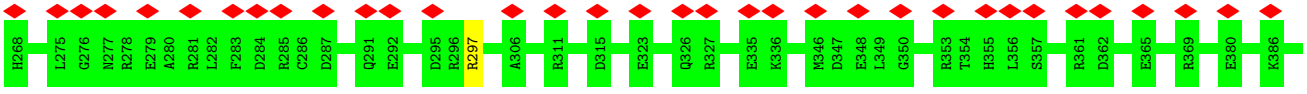
• Molecule 12: mS55

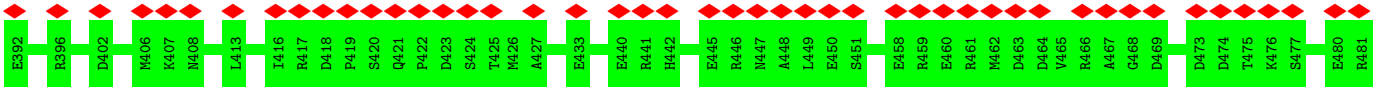
Chain ag:

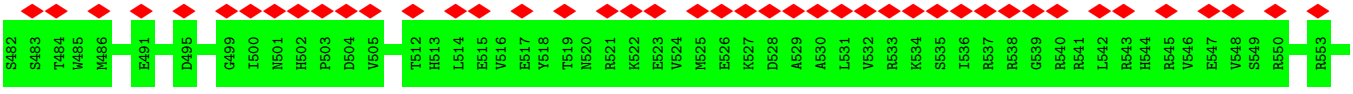


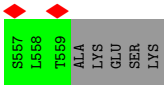






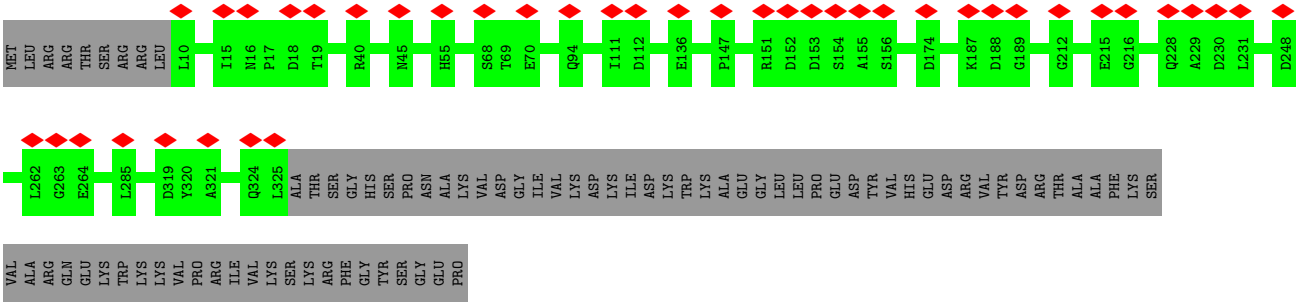






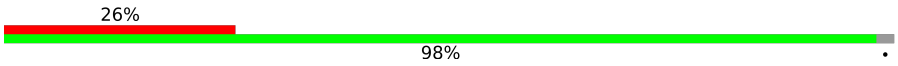
• Molecule 13: mS57

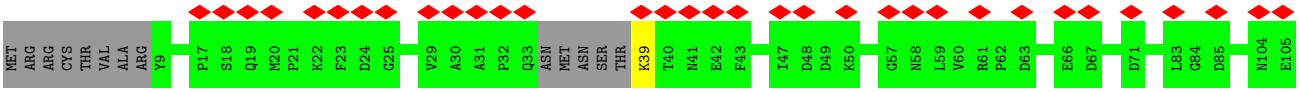
Chain aj:

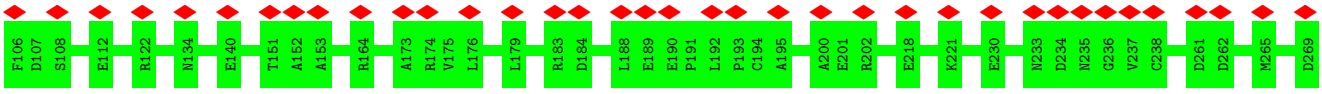


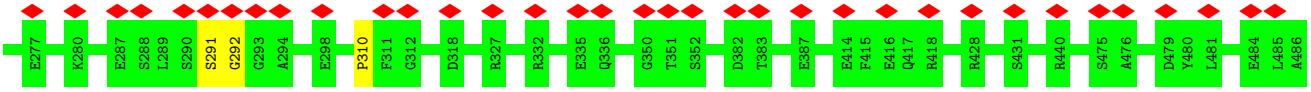
- Molecule 14: uS10m

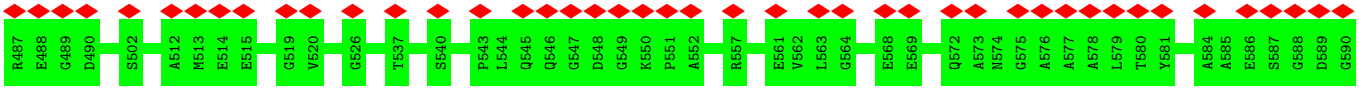
Chain e:

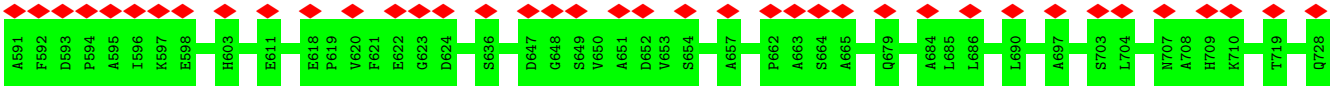


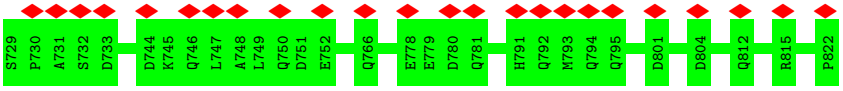






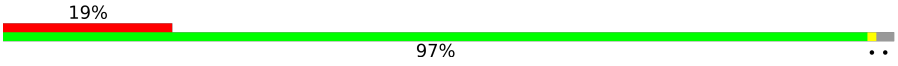


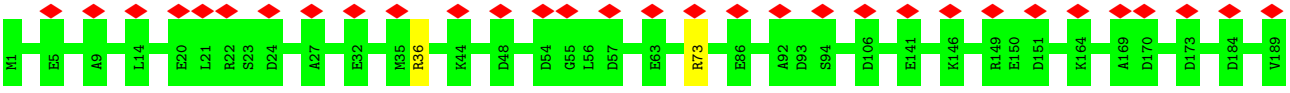


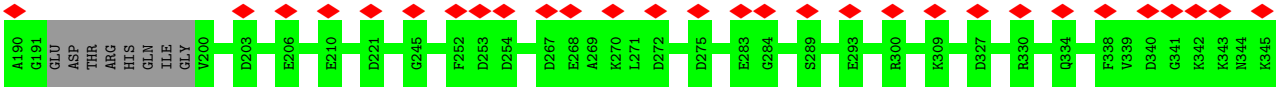


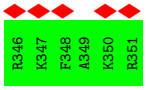
- Molecule 15: uS9m

Chain d:



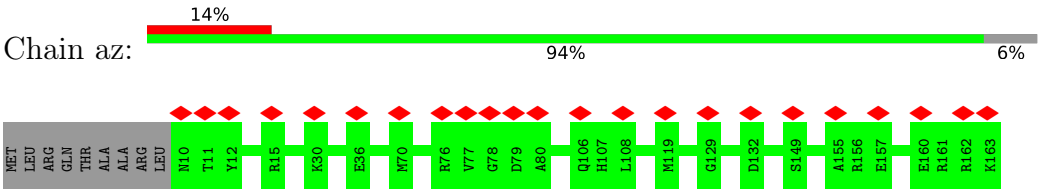






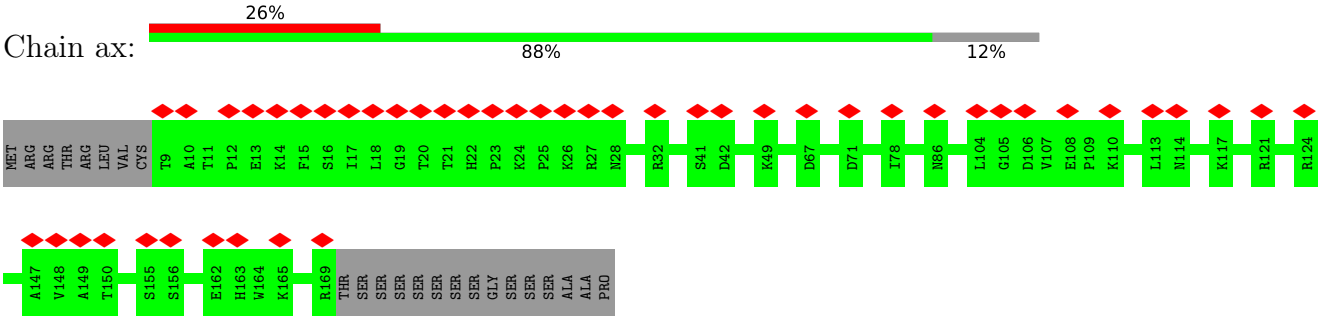
• Molecule 16: mS72

Chain az:



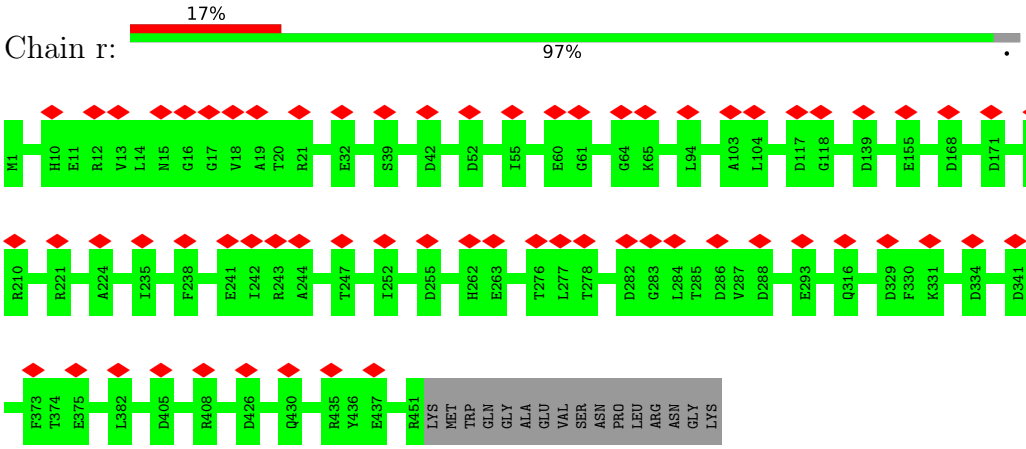
• Molecule 17: mS70

Chain ax:



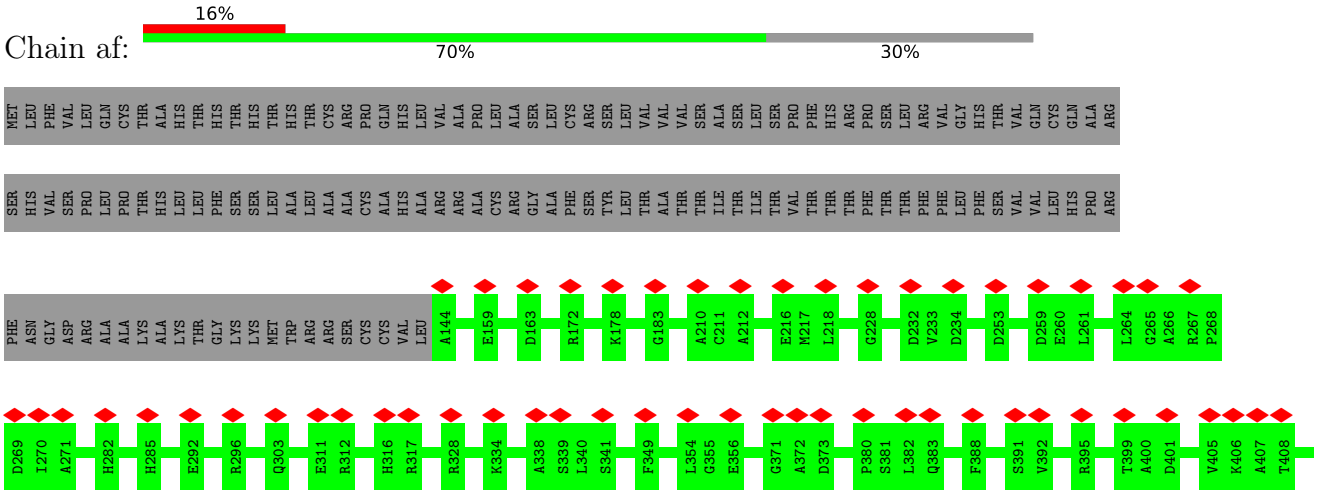
• Molecule 18: mS29

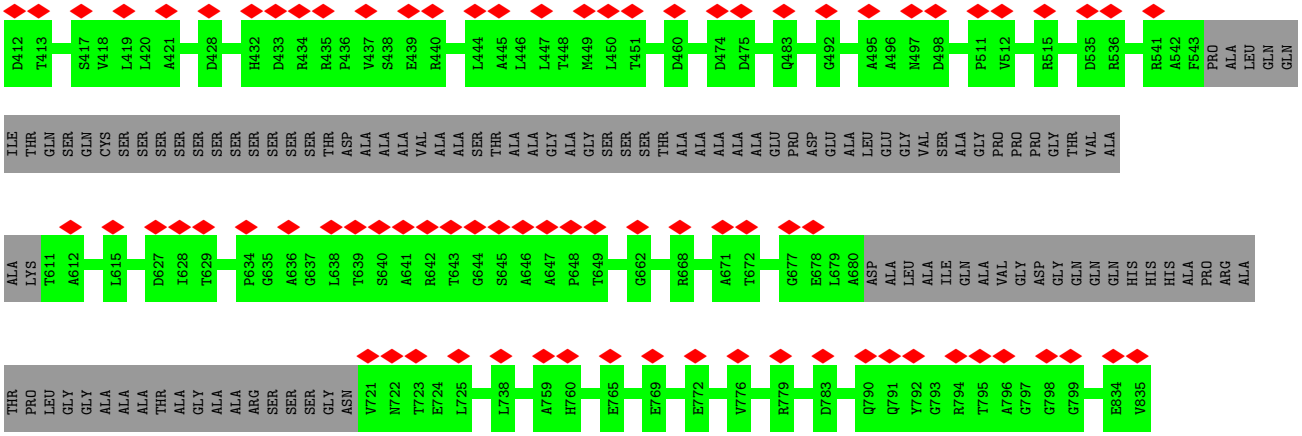
Chain r:



• Molecule 19: Excreted/secreted protein 15

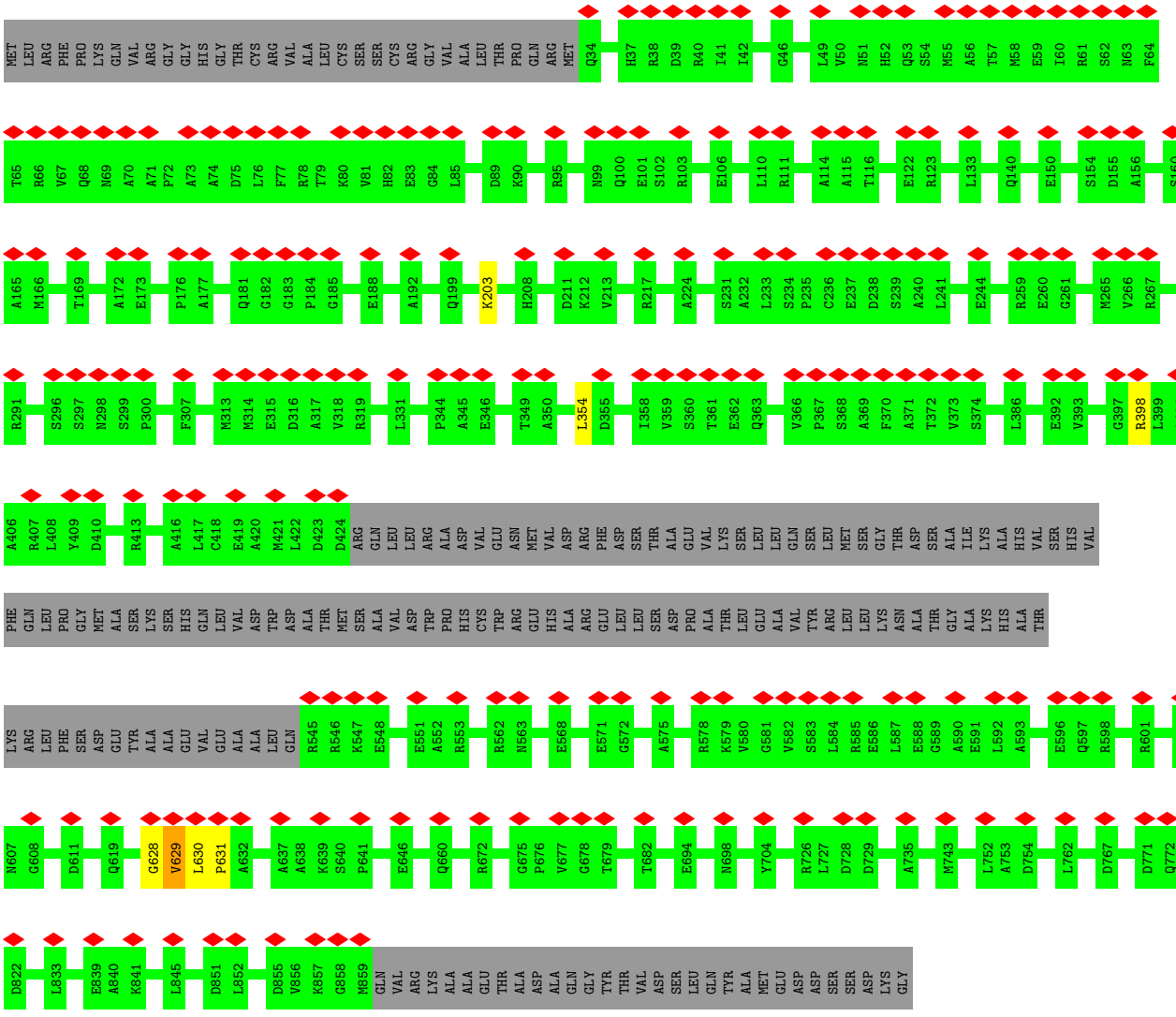
Chain af:





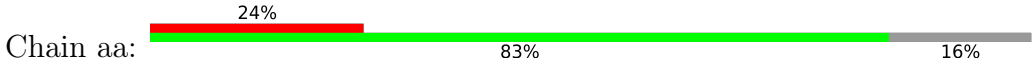
• Molecule 20: mS35

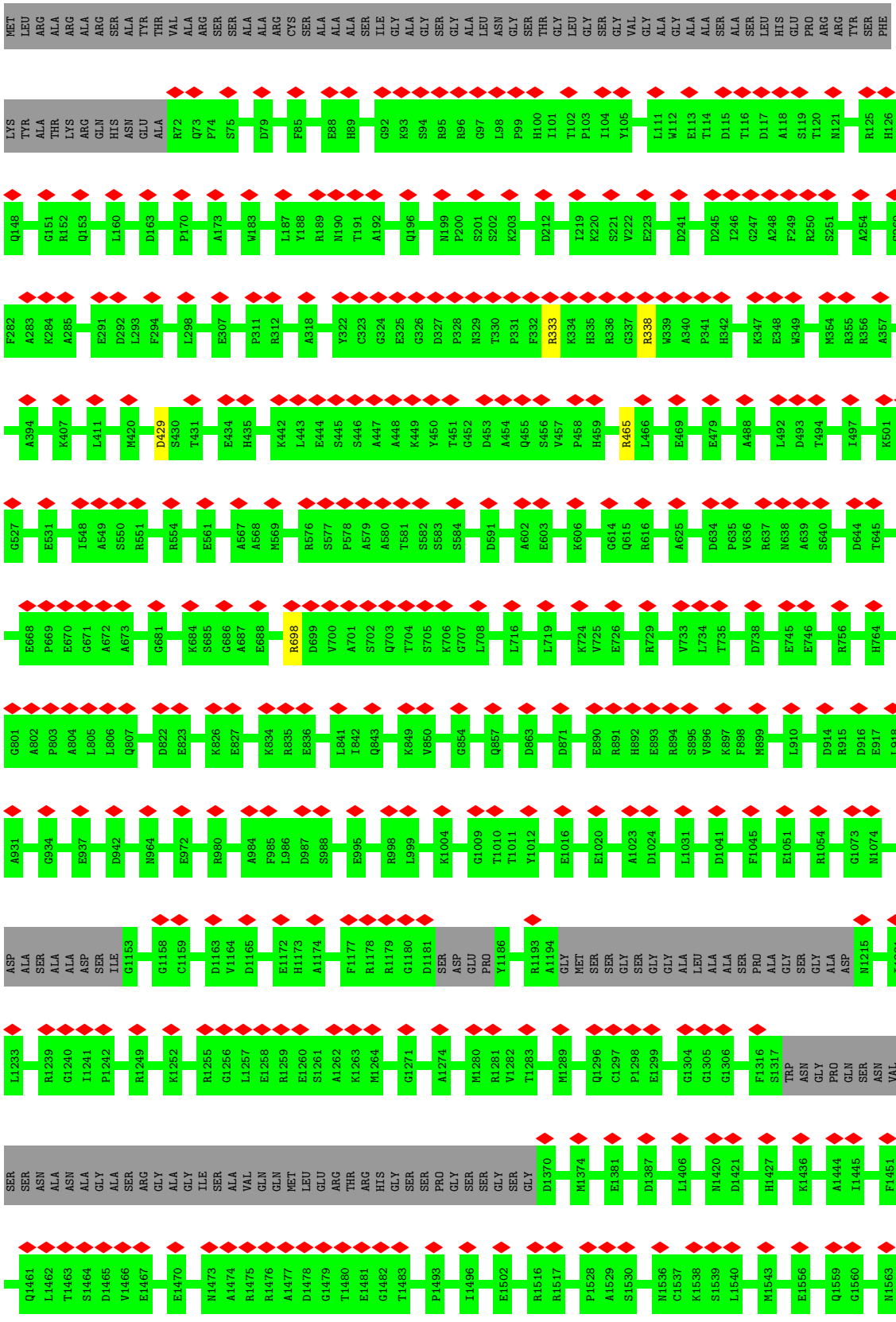
Chain u:

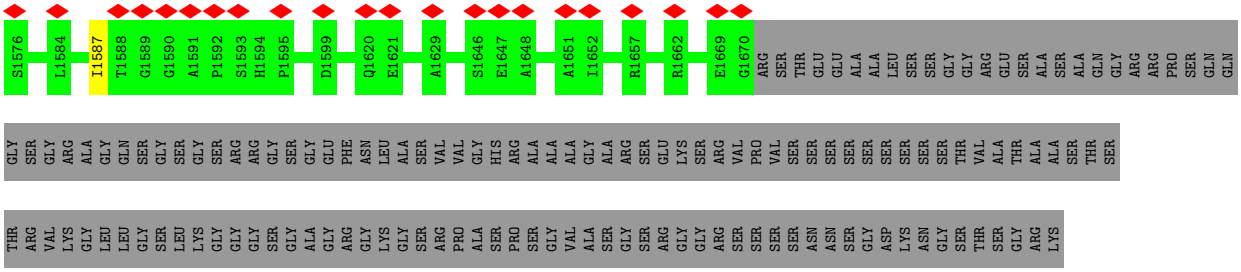


• Molecule 21: mS48

Chain aa:

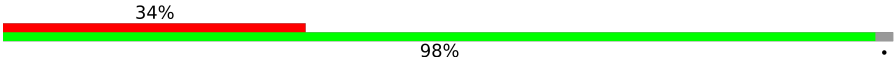

24%
83%
16%

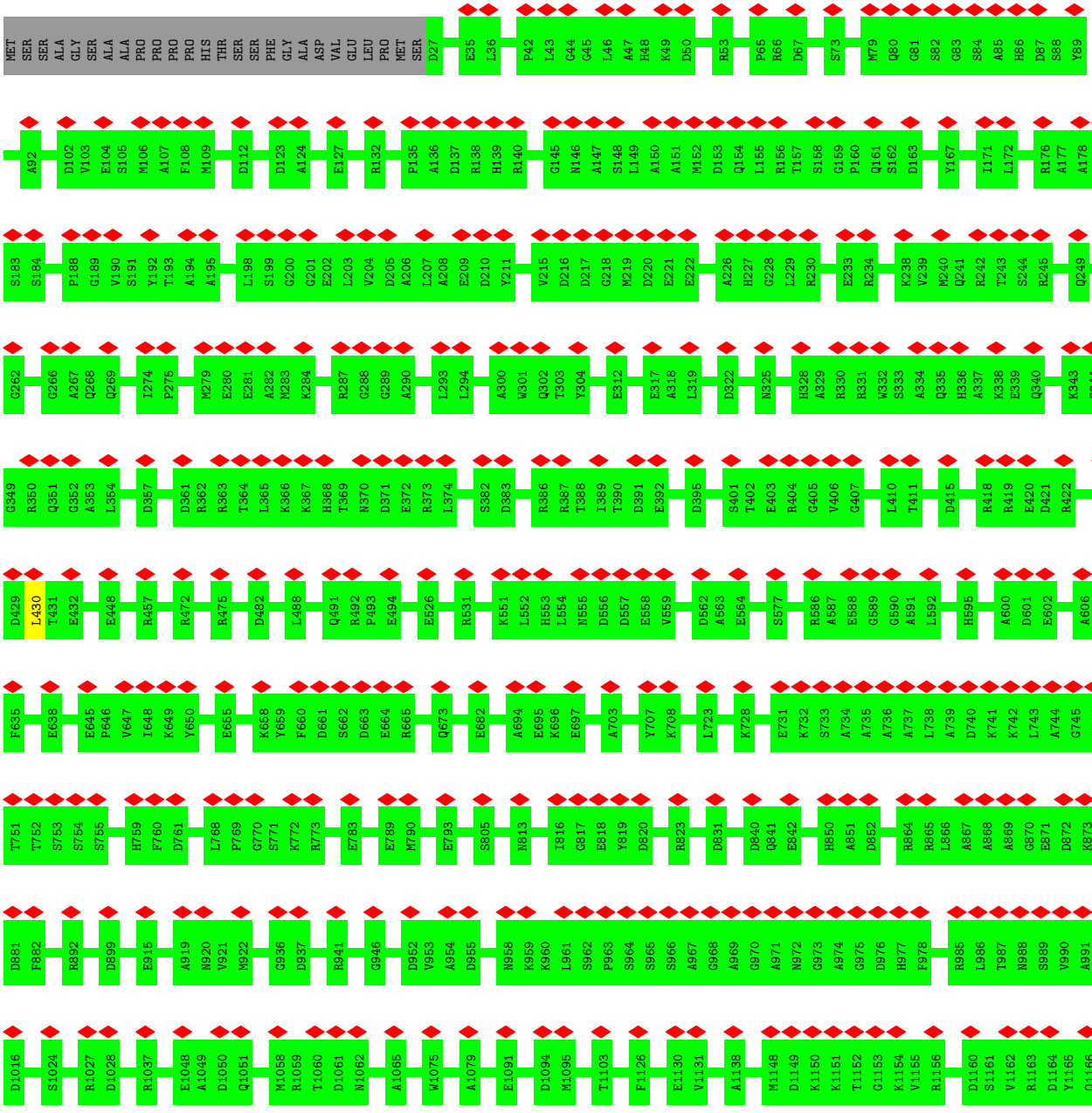

MET LEU ARG ALA ARG ALA ARG SER ALA TYR THR VAL ALA ARG SER SER ALA ALA ALA ARG CYS SER ALA ALA ALA SER ILE GLY ALA GLY SER GLY ALA LEU ASN GLY SER THR GLY LEU GLY SER GLY VAL GLY ALA GLY ALA ALA SER ALA SER LEU HIS GLU PRO ARG ARG TYR SER PHE
LYS TYR ALA THR LYS ARG GLN HIS ASN GLU ALA R72 Q73 P74 S75 D79 F85 E88 H89 G92 K93 S94 R95 R96 G97 L98 P99 H100 I101 T102 P103 I104 Y105 L111 W112 E113 T114 D115 T116 D117 A118 S119 T120 N121 R125 H126 F129 G143 F144 E145 A146 D147
Q148 G151 R152 Q153 L160 D163 P170 A173 W183 L187 Y188 R189 N190 T191 A192 Q196 N199 P200 S201 S202 K203 D212 I219 K220 S221 V222 E223 D241 D245 I246 G247 A248 F249 R250 S251 A254 S269 S270 F271 D272 F273 R276 Q281
F282 A283 K284 A285 E291 D292 L293 F294 L298 E307 P311 R312 A318 Y322 C323 G324 E325 G326 D327 P328 N329 T330 P331 F332 R333 K334 H335 R336 G337 R338 W339 A340 P341 H342 K347 E348 W349 M354 R355 R356 A357 E366 D367 F370 G371 T372 T373 A374 K391
A394 K407 L411 M420 D429 S430 T431 E434 H435 K442 L443 E444 S445 S446 A447 A448 K449 Y450 T451 G452 D453 A454 Q455 S456 V457 P458 H459 R465 L466 E469 E479 A488 L492 D493 T494 I497 K501 V502 D503 P504 Q505 T506 F523 L524
G527 E531 I548 A549 S550 R551 R554 E561 A567 A568 M569 R576 S577 P578 A579 A580 T581 S582 S583 S584 D591 A602 E603 K606 G614 Q615 R616 A625 D634 P635 V636 R637 N638 A639 S640 D644 T645 E648 G654 G655 F656 E657 S658 G659 E660
E668 P669 E670 G671 A672 A673 G681 K684 S685 G686 A687 E688 R698 D699 V700 A701 S702 Q703 T704 S705 K706 G707 L708 L716 L719 K724 V725 E726 R729 V733 L734 T735 D738 E745 E746 R756 H764 S771 E772 Y791 K792 D798 A799 D800
G801 A802 P803 A804 L805 L806 Q807 D822 E823 K826 E827 K834 R835 E836 L841 I842 Q843 K849 V850 G854 Q857 D863 D871 E890 R891 H892 E893 R894 S895 V896 K897 F898 M899 L910 D914 R915 D916 E917 L918 E919 E924 A925 E926 E927 I928 S929 D930
A931 G934 E937 D942 N964 E972 R980 A984 F985 L986 D987 S988 E995 R998 L999 K1004 G1009 T1010 T1011 Y1012 E1016 E1020 A1023 D1024 L1031 D1041 F1045 E1051 R1054 G1073 N1074 E1100 R1114 D1126 C1143 ALA
ASP ALA SER ALA ALA ASP SER ILE G1153 G1158 C1159 D1163 V1164 D1165 E1172 H1173 A1174 F1177 R1178 R1179 G1180 D1181 SER ASP GLU PRO Y1186 R1193 A1194 GLY MET SER SER GLY SER GLY GLY ALA LEU ALA ALA SER PRO ALA GLY SER GLY ALA ASP N1215 I1221 D1224
L1233 R1239 G1240 I1241 P1242 R1249 K1252 R1255 G1256 L1257 E1258 R1259 E1260 S1261 A1262 K1263 M1264 G1271 A1274 M1280 R1281 V1282 T1283 M1289 Q1296 C1297 P1298 E1299 G1304 G1305 G1306 F1316 S1317 TRP ASN GLY PRO GLN SER ASN VAL SER ALA ALA THR SER ASN SER SER
SER SER ASN ALA ASN ALA GLY ALA SER ARG GLY ALA GLY ILE SER ALA VAL GLN GLN MET LEU GLU ARG THR ARG HIS GLY SER SER PRO GLY SER SER GLY SER GLY D1370 M1374 E1381 D1387 L1406 N1420 D1421 H1427 K1436 A1444 I1445 F1451 T1457 H1458
Q1461 L1462 T1463 S1464 D1465 V1466 E1467 E1470 N1473 A1474 R1475 R1476 A1477 D1478 G1479 T1480 E1481 G1482 T1483 P1493 I1496 E1502 R1516 R1517 P1528 A1529 S1530 N1536 C1537 K1538 S1539 L1540 M1543 E1556 Q1559 G1560 N1563 S1567 S1568 A1569 L1570 F1571 K1572 S1573 I1574 A1575

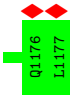


• Molecule 22: mS49

Chain ab:

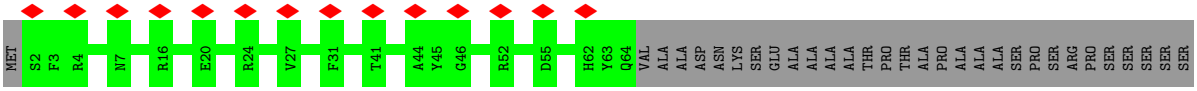


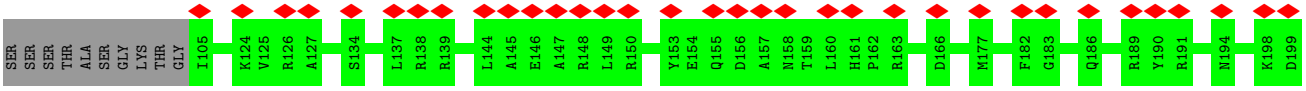


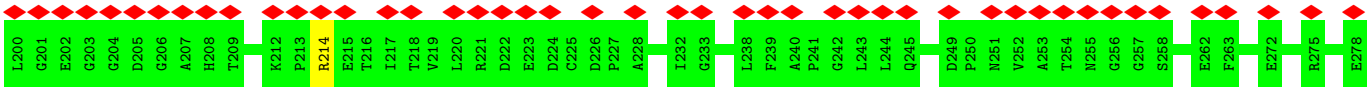


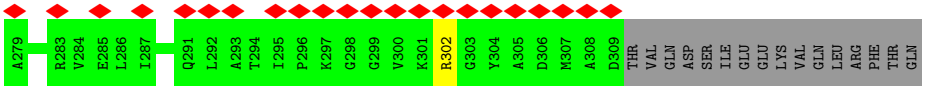
- Molecule 23: mS58

Chain ak:



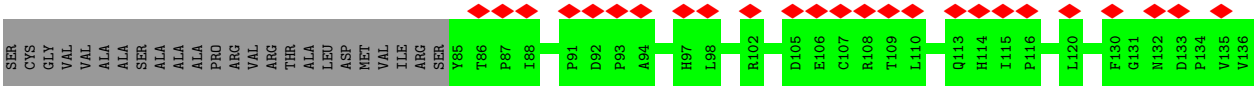


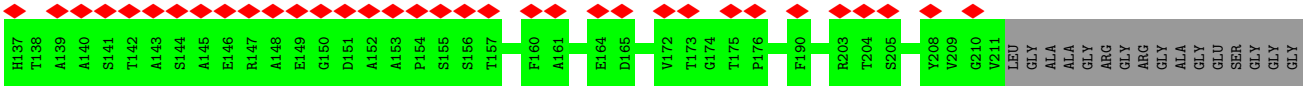


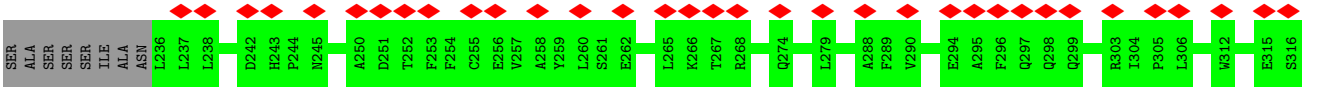


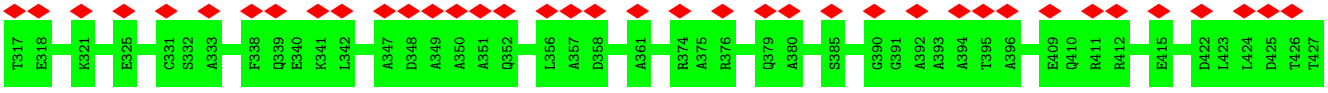
- Molecule 24: mS50

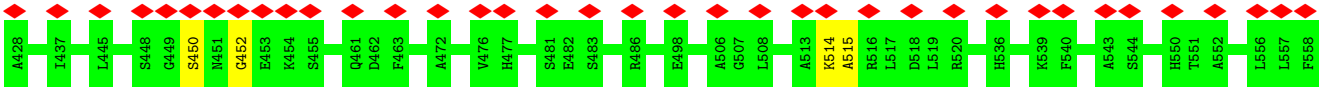
Chain ac:

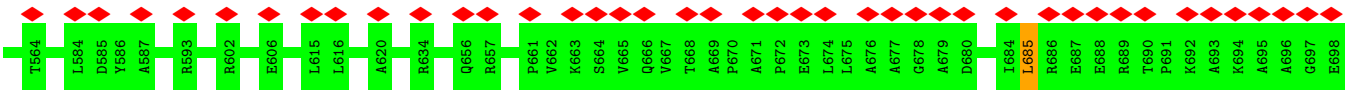


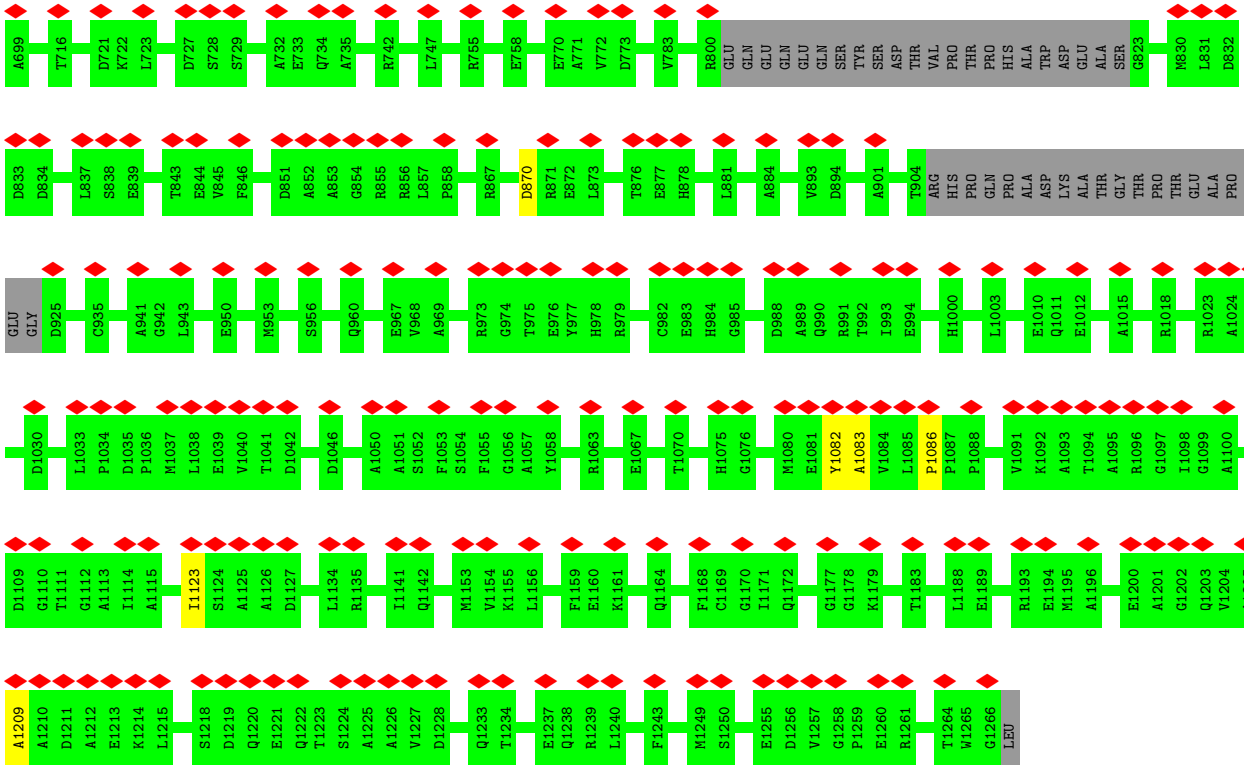






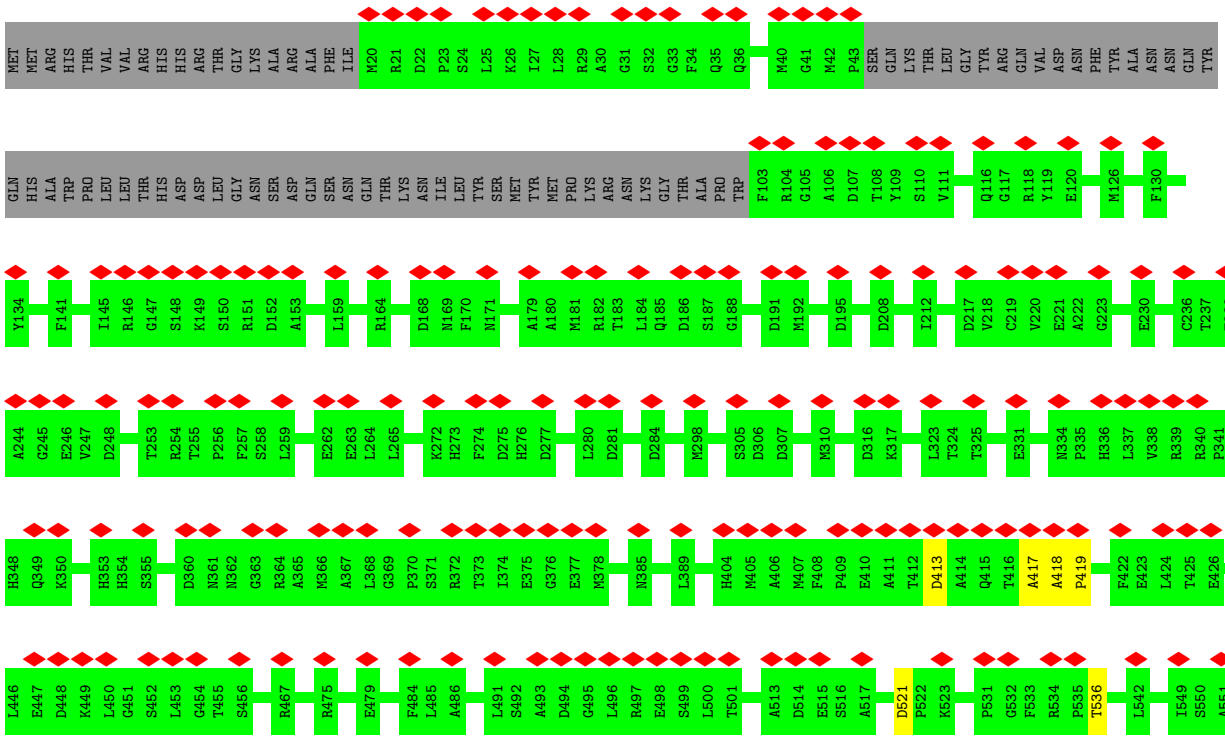


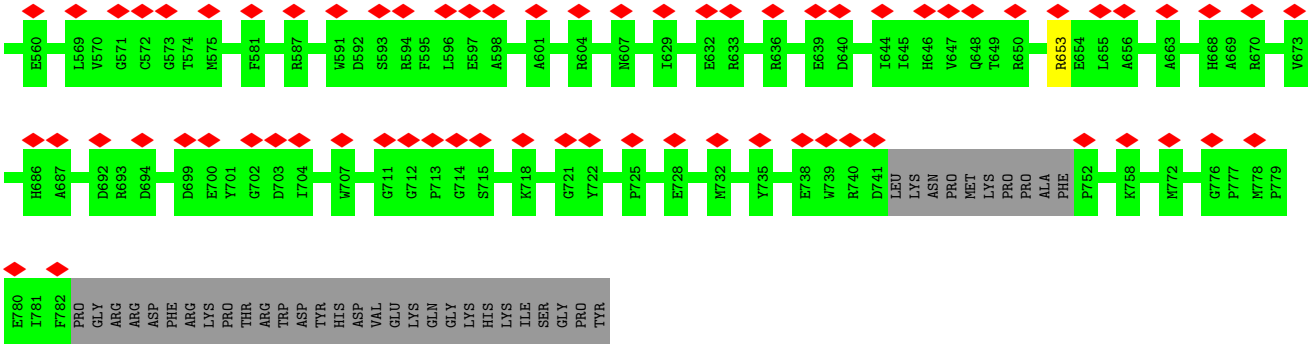




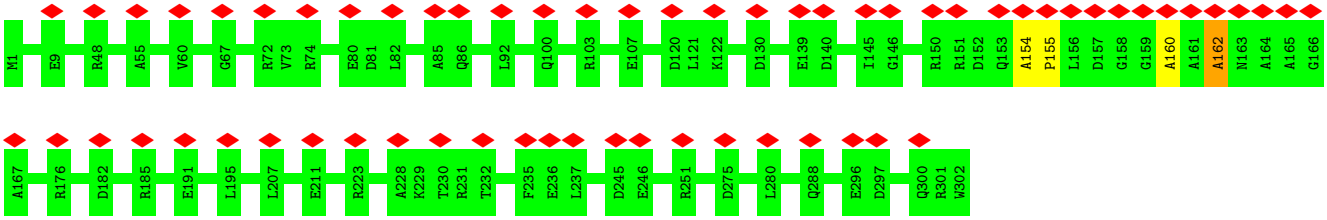
• Molecule 25: mS51

Chain ad:

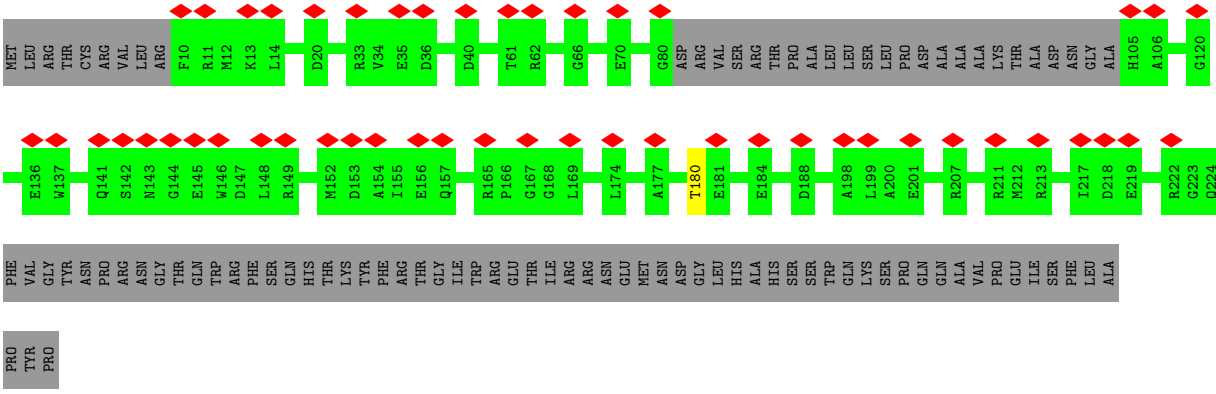




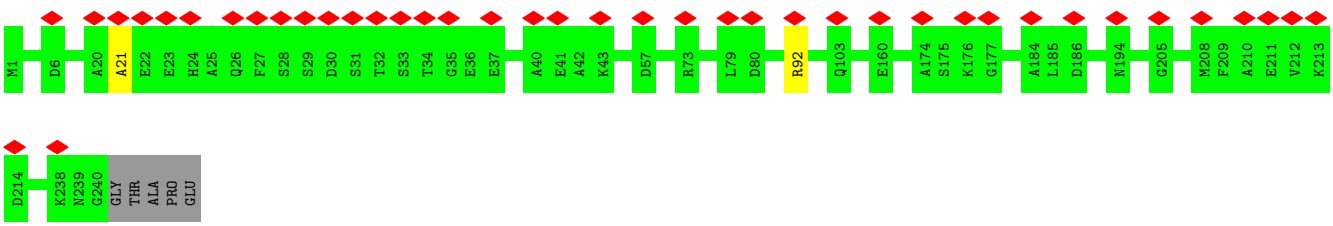
• Molecule 26: mS60



• Molecule 27: mS61

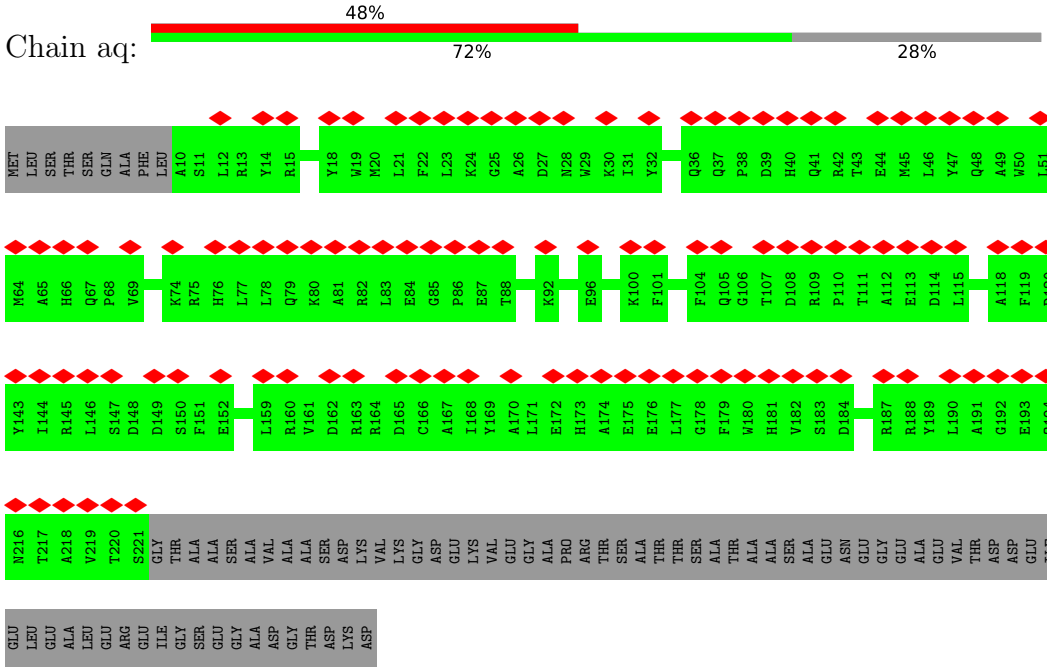


• Molecule 28: mS62



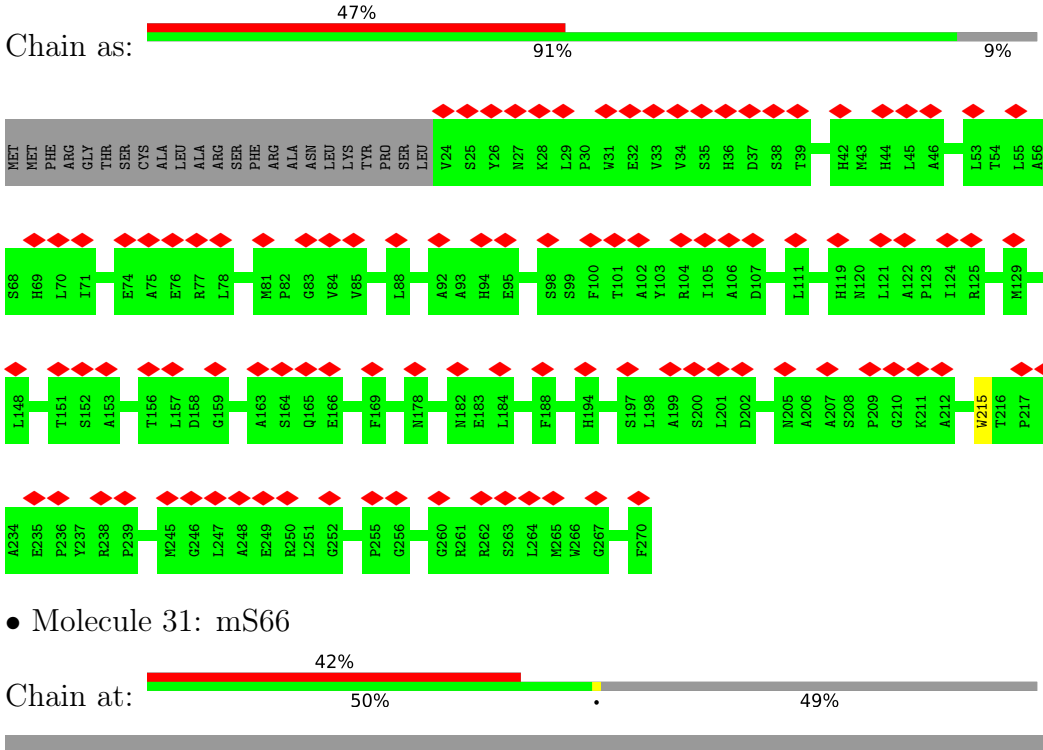
• Molecule 29: mS63

Chain aq:



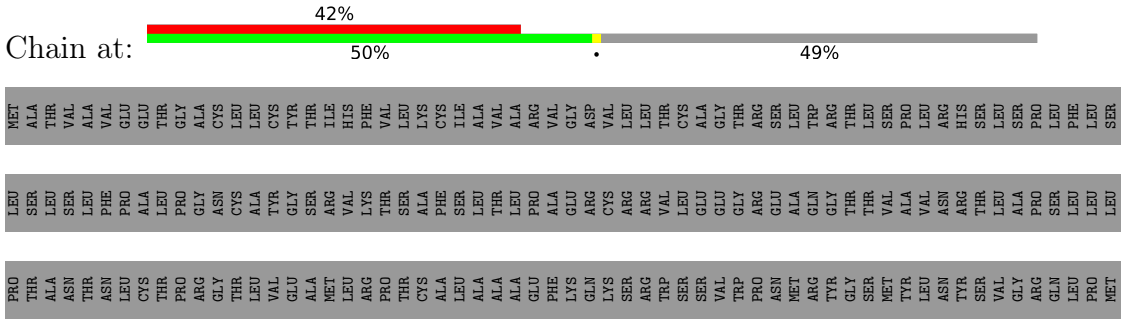
• Molecule 30: mS65

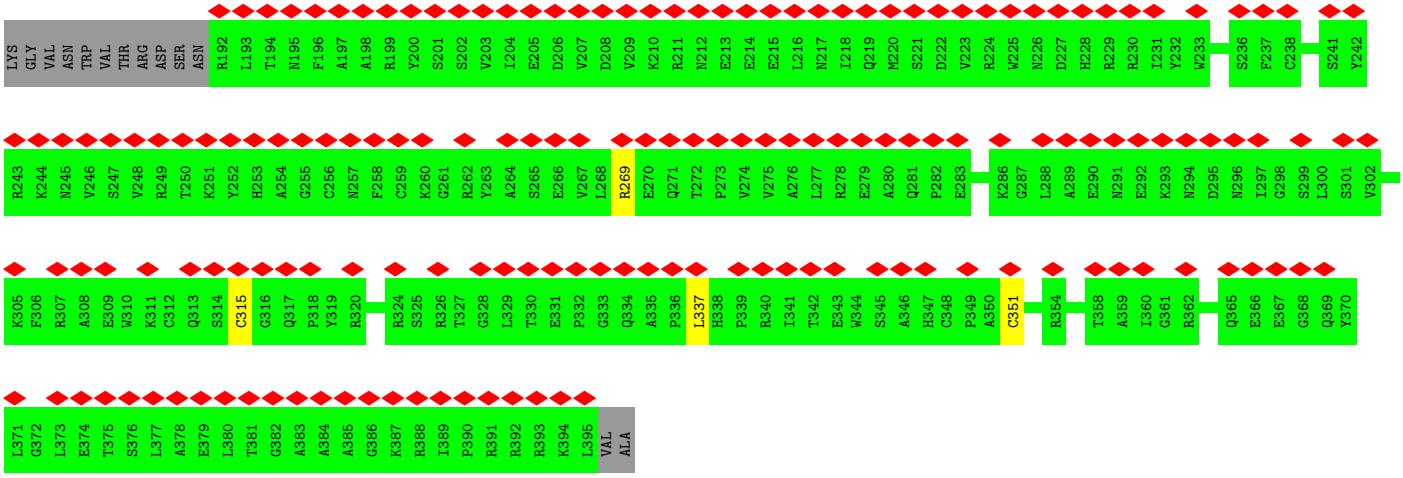
Chain as:



• Molecule 31: mS66

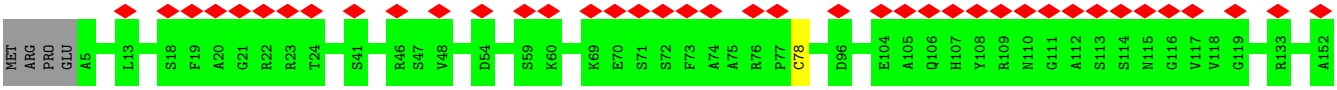
Chain at:

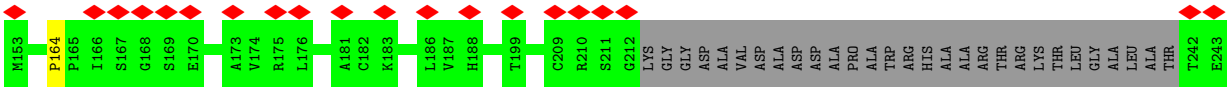


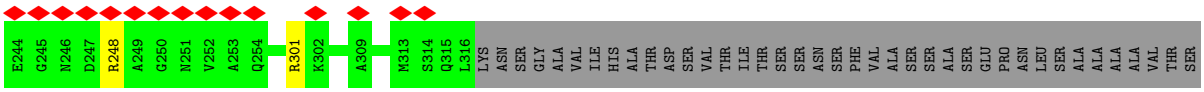


- Molecule 32: mS43

Chain y:

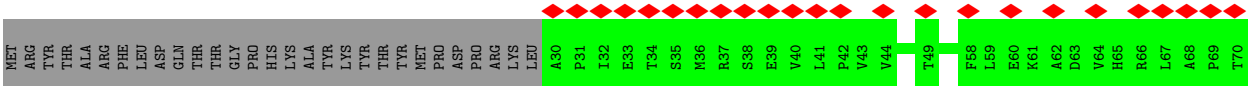


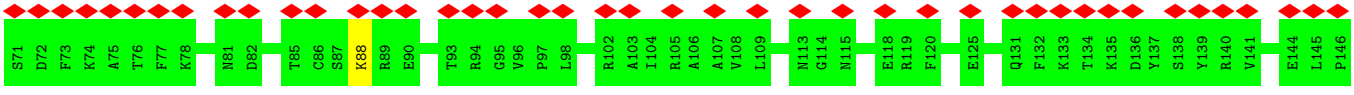


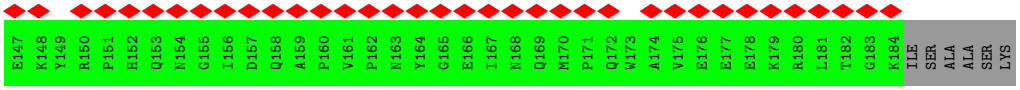


- Molecule 33: Protein FYV4, mitochondrial

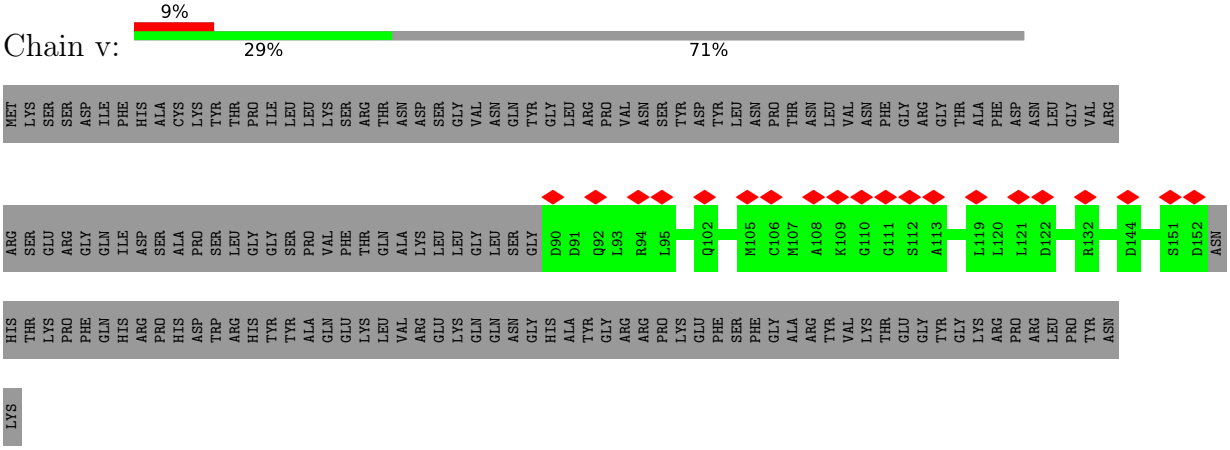
Chain w:



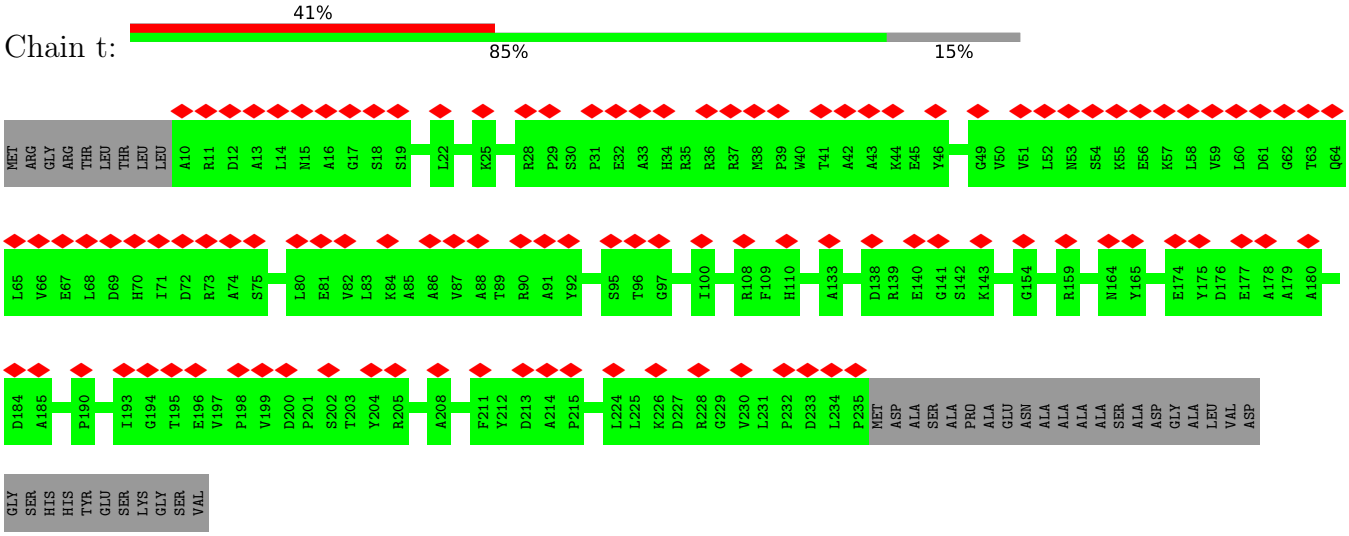




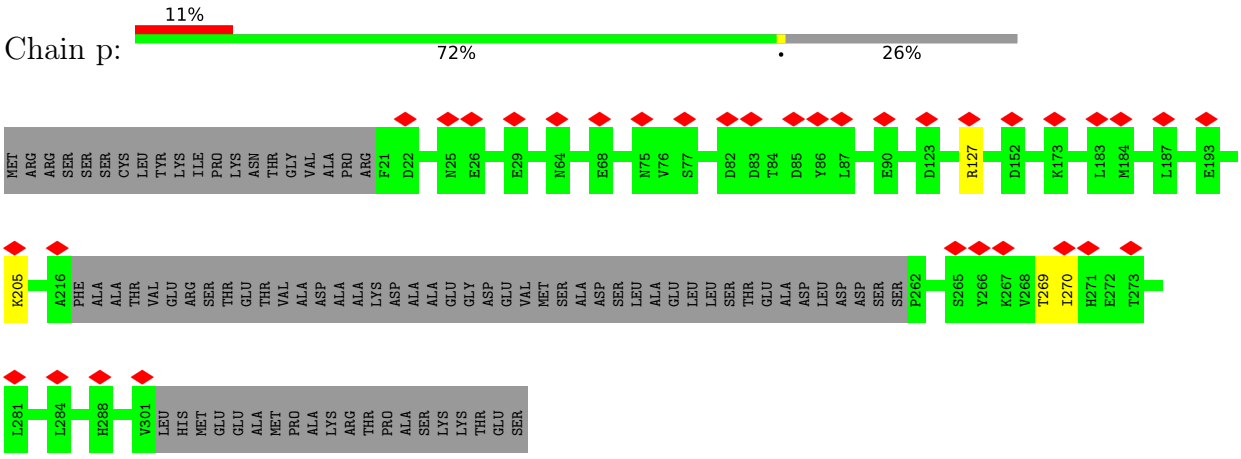
• Molecule 34: mS37



• Molecule 35: mS34

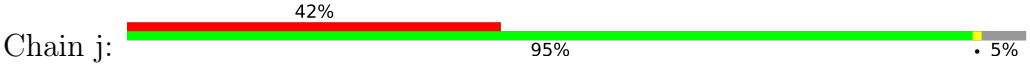


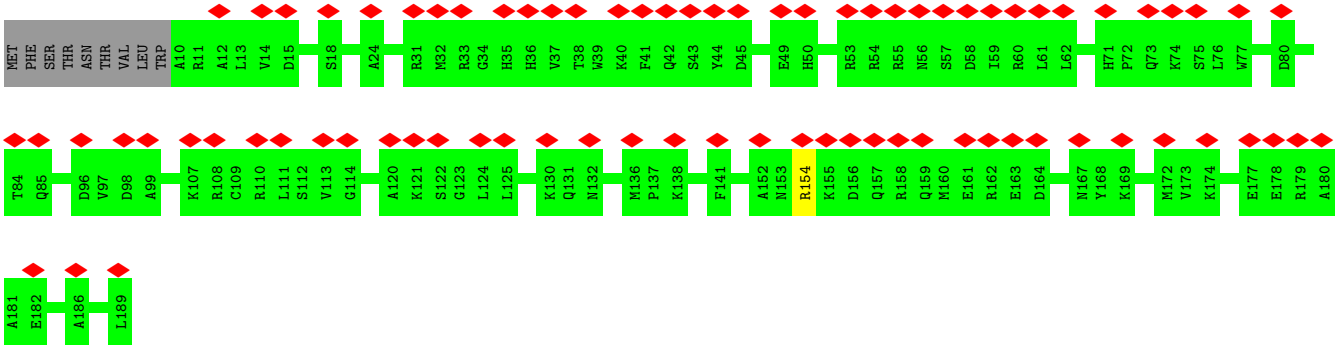
• Molecule 36: mS23



• Molecule 37: bS16m

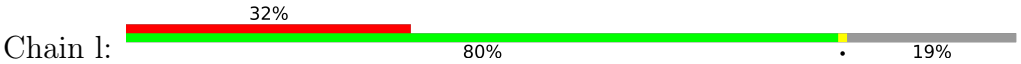
Chain j:

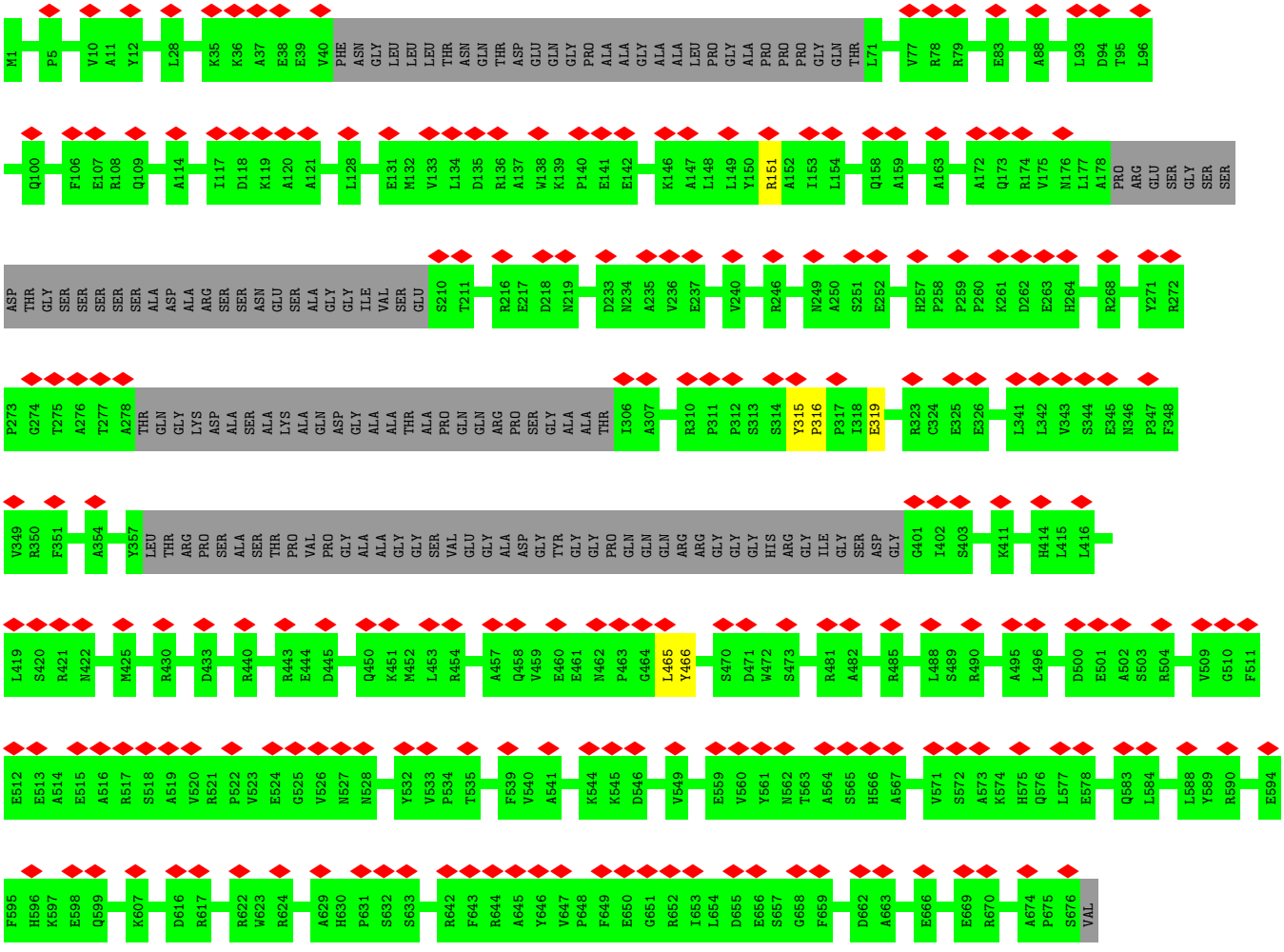




• Molecule 38: mS52

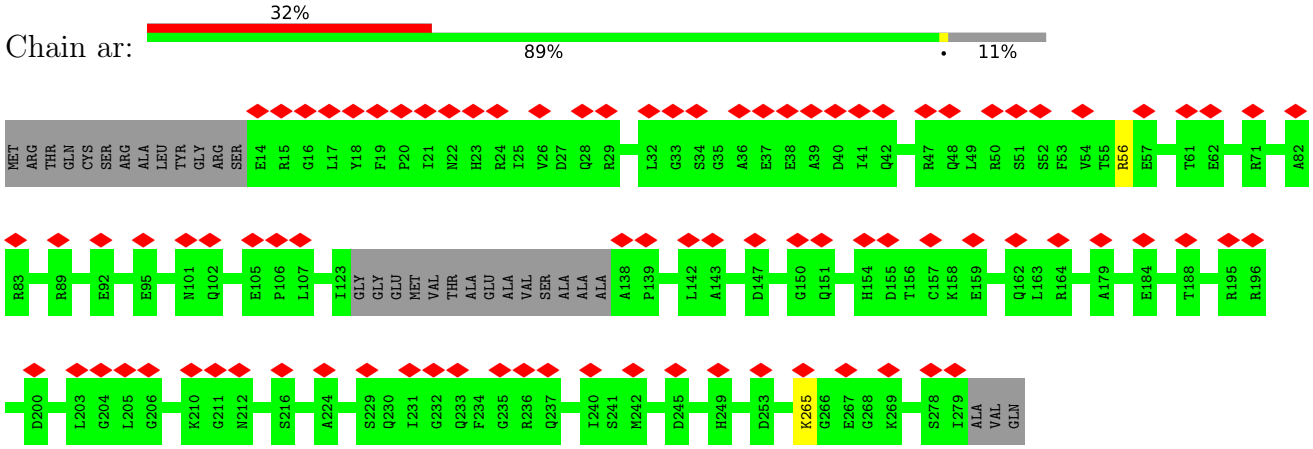
Chain l:





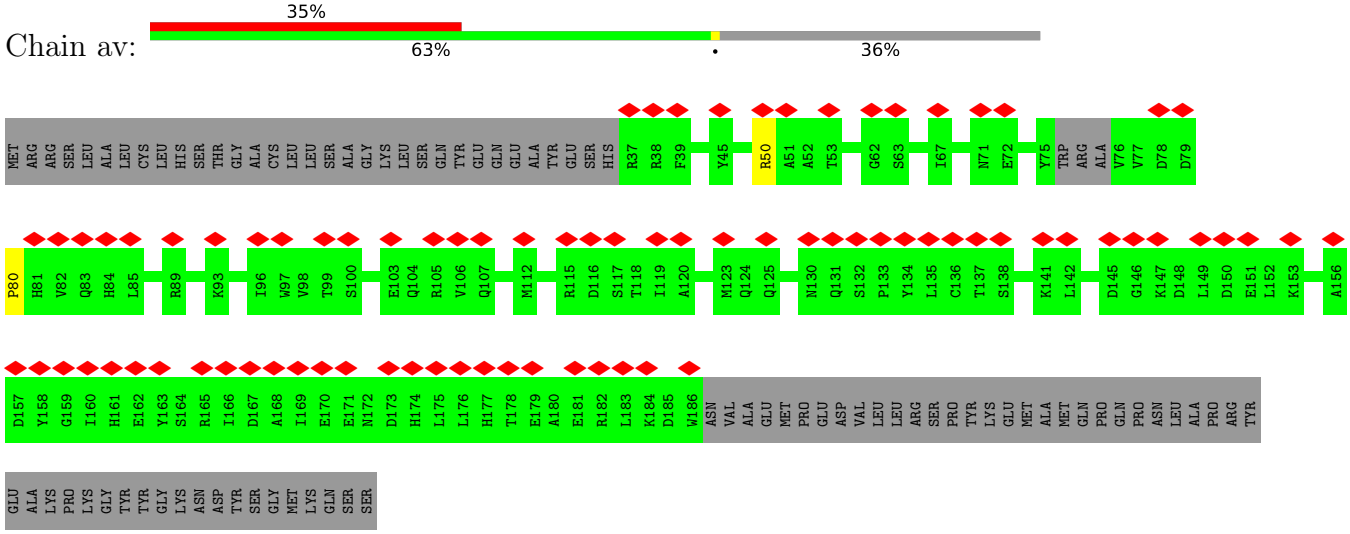
• Molecule 39: AKAP7_NLS domain-containing protein

Chain ar:



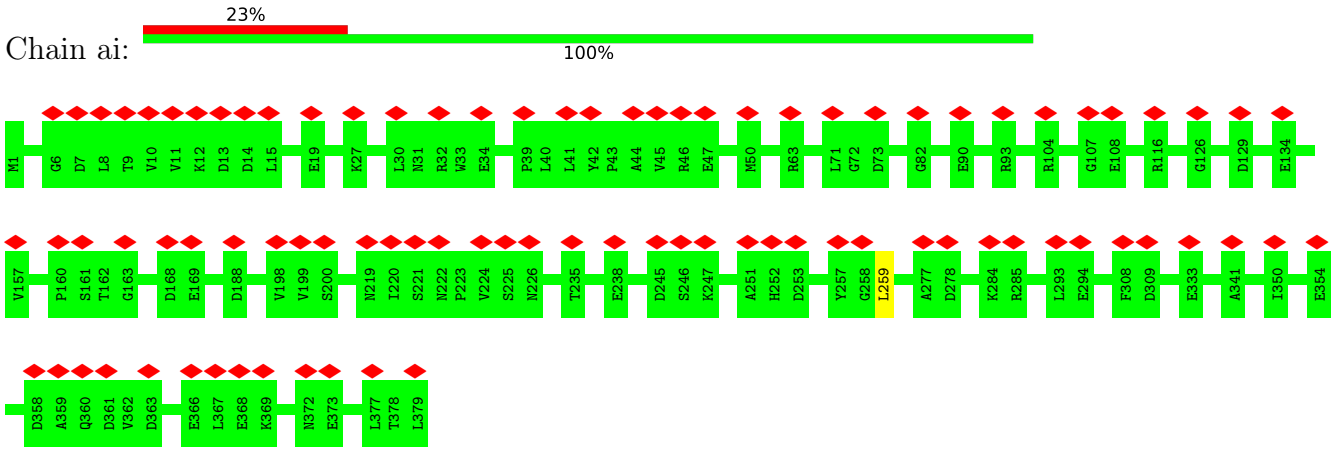
- Molecule 40: Ubiquitin-like domain-containing protein

Chain av:



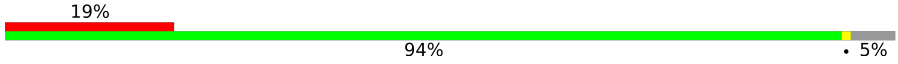
- Molecule 41: mS56

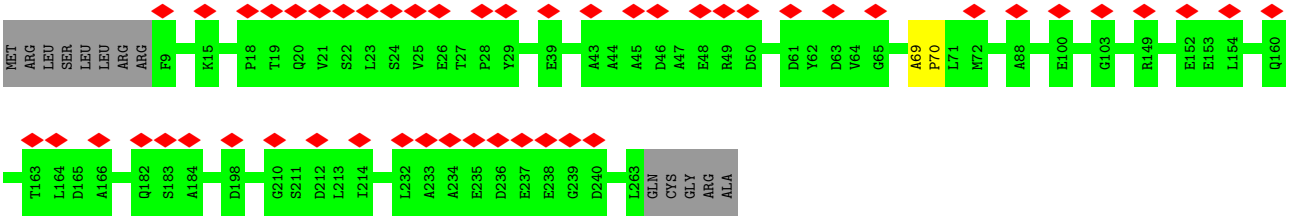
Chain ai:



- Molecule 42: Putative superoxide dismutase

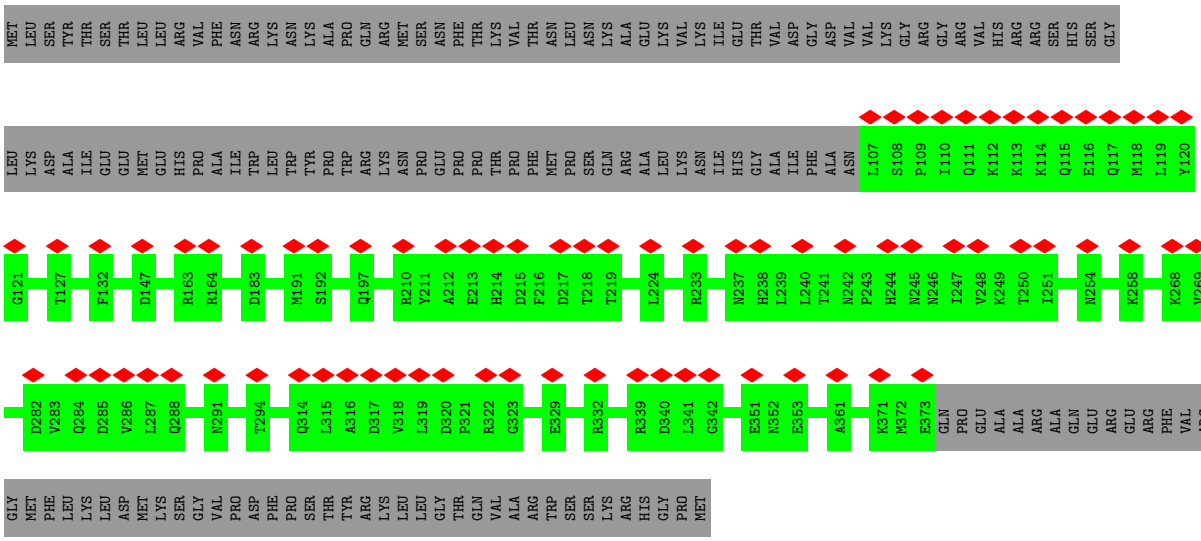
Chain x:





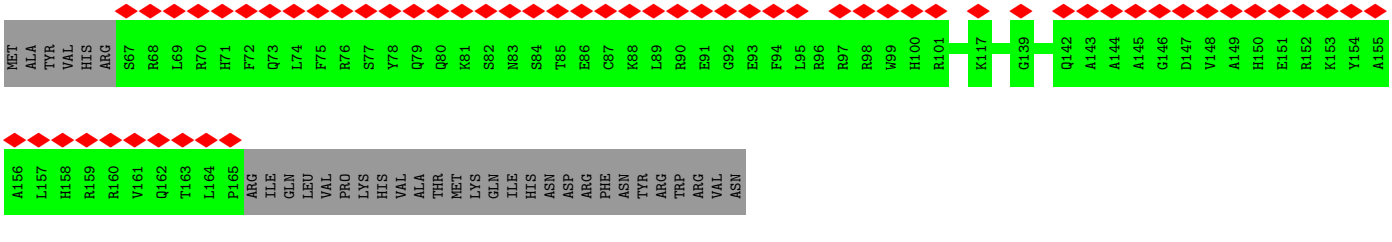
• Molecule 43: uS15m

Chain i:



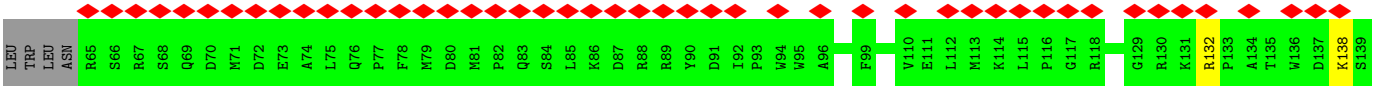
• Molecule 44: bS21m

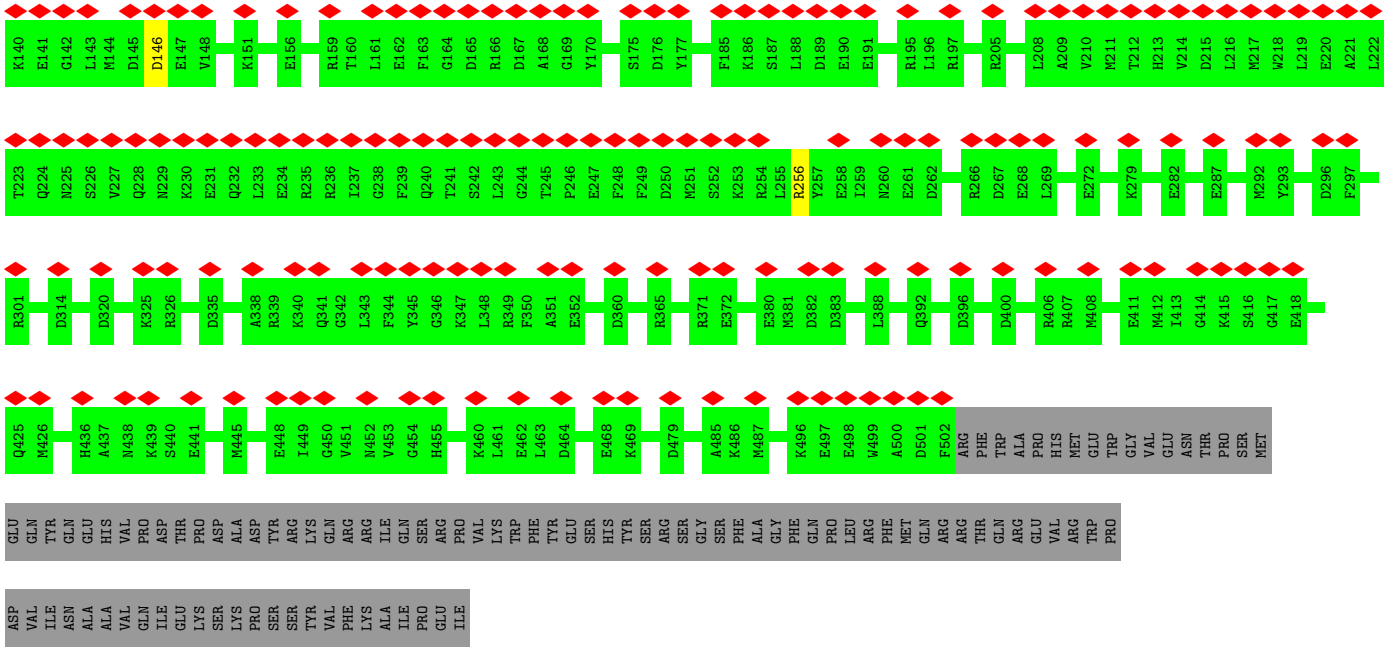
Chain g:



• Molecule 45: mS22

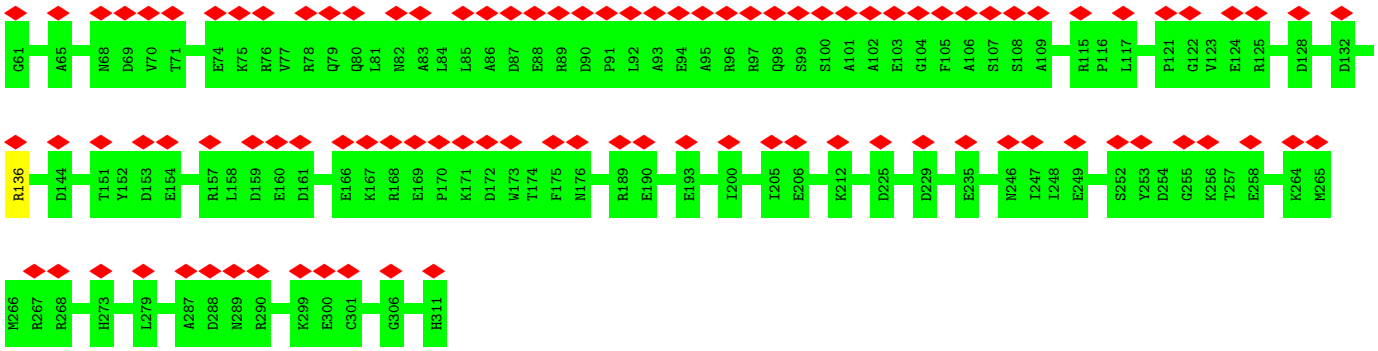
Chain o:





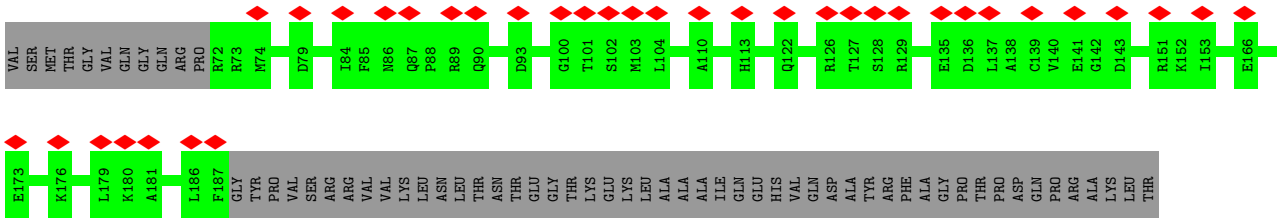
- Molecule 46: uS8m

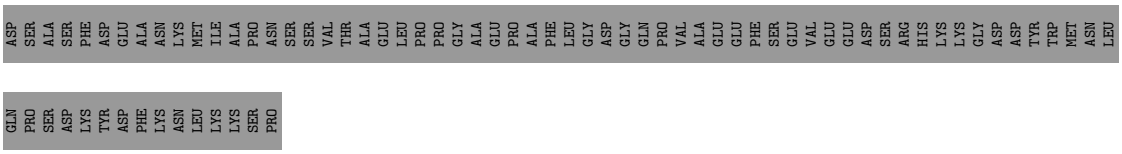
Chain c:



- Molecule 47: 30S Ribosomal protein S17-like protein

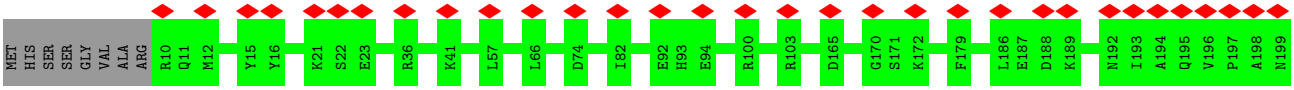
Chain k:

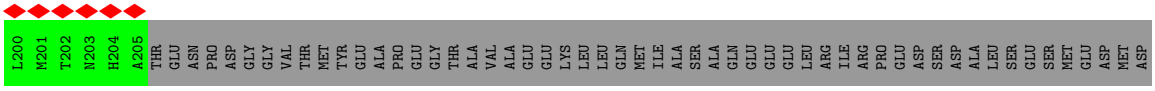


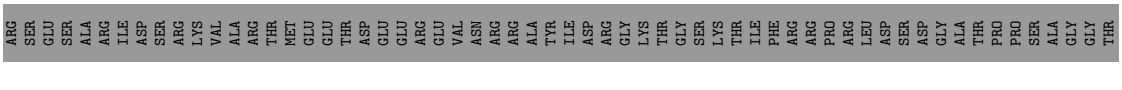


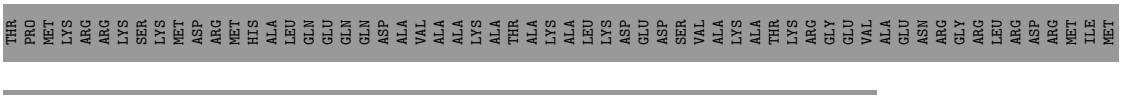
• Molecule 48: mS26

Chain q:



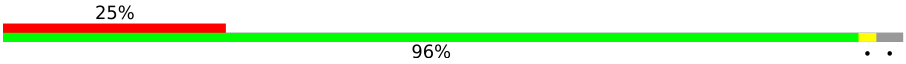


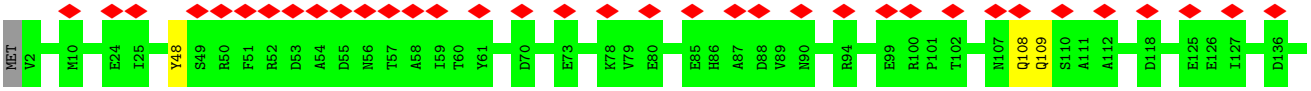


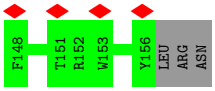


• Molecule 49: bS6m

Chain b:

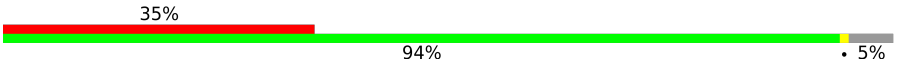


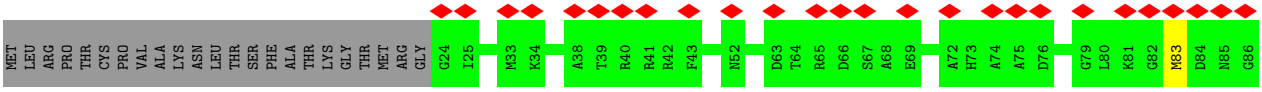


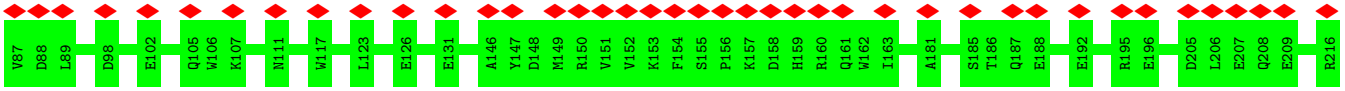


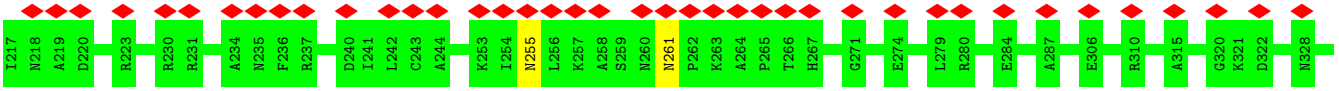
• Molecule 50: Ribosomal_S5_C domain-containing protein

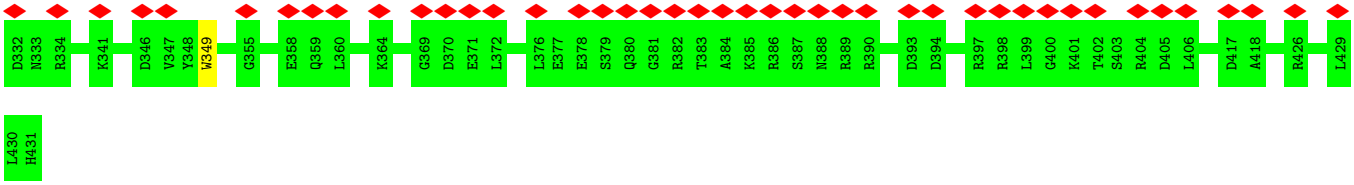
Chain a:





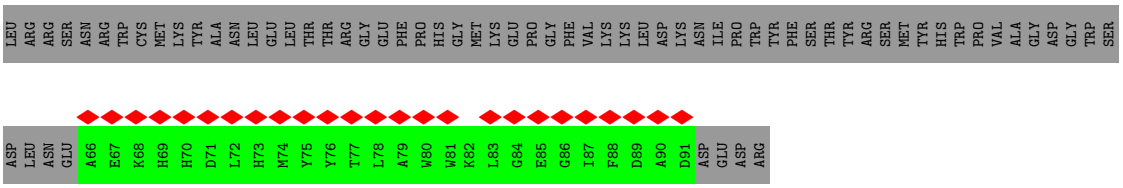






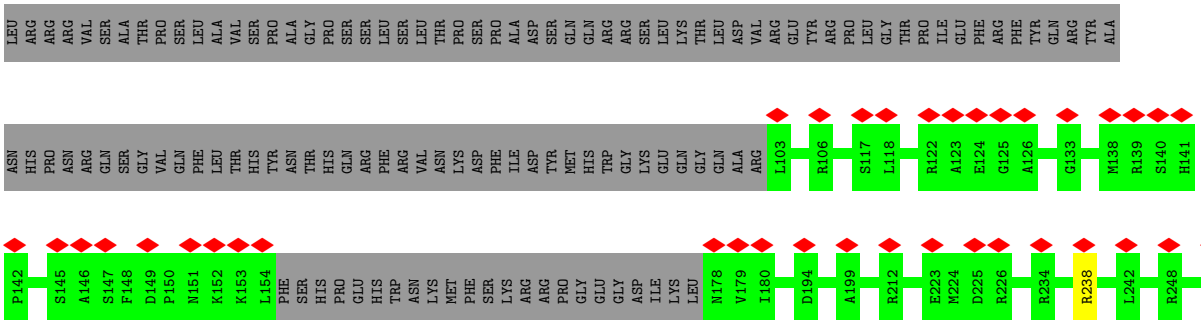
• Molecule 51: mS73

Chain ba:



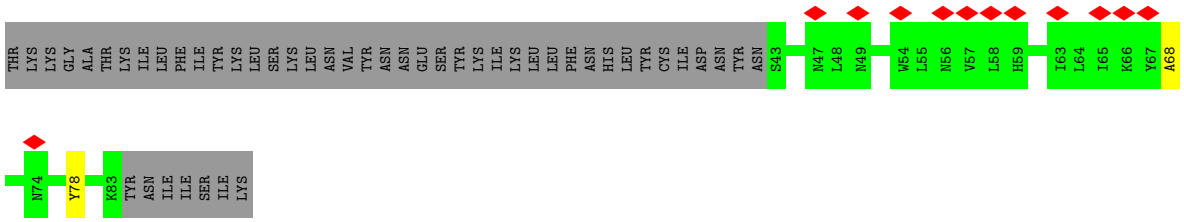
• Molecule 52: mS47

Chain z:



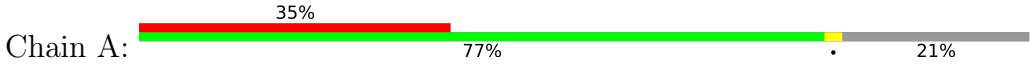
• Molecule 53: uS3m

Chain bd:



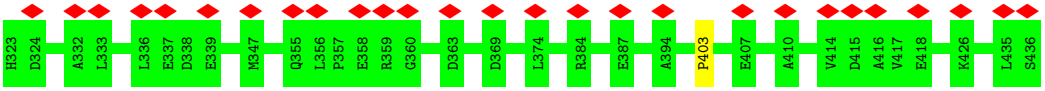
• Molecule 54: Ribosomal protein L3-like protein

Chain A:



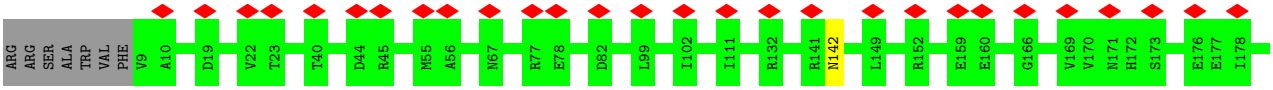
• Molecule 55: uL4m

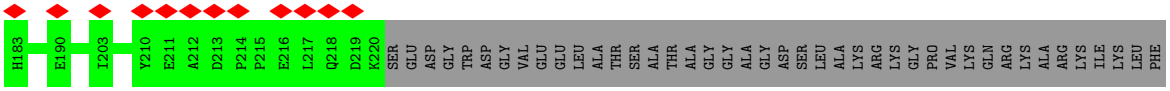
Chain B:



• Molecule 56: RIBOSOMAL_L9 domain-containing protein

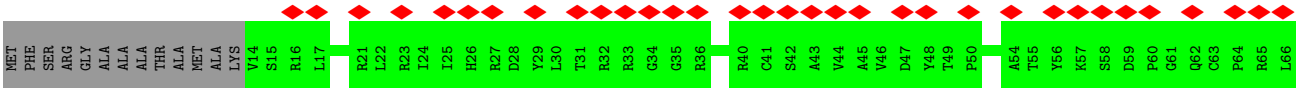
Chain C:

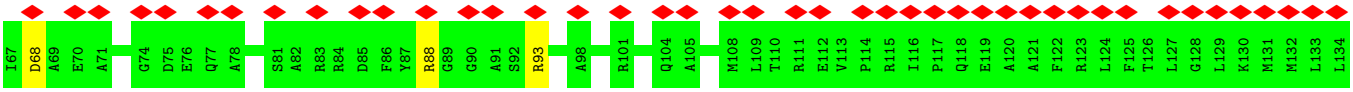


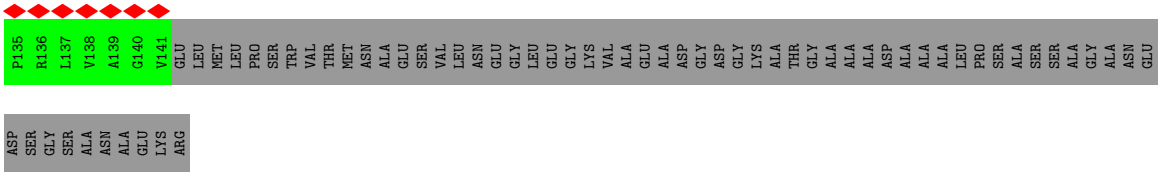


• Molecule 57: uL10m

Chain D:

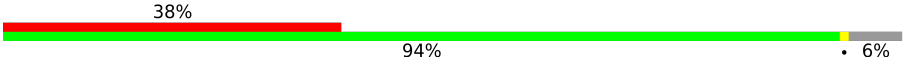


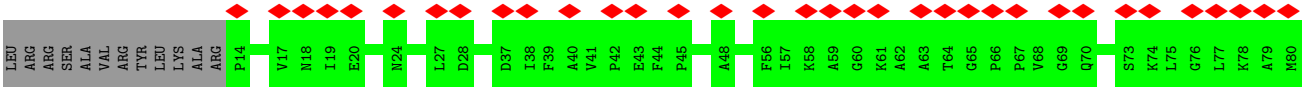


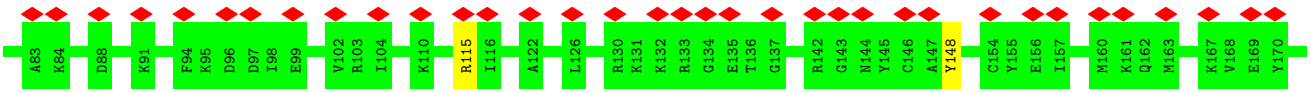


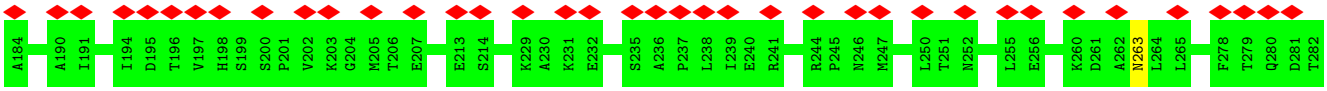
• Molecule 58: Putative ribosomal protein L11

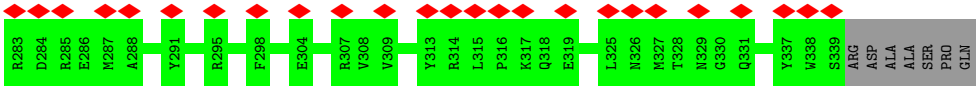
Chain E:





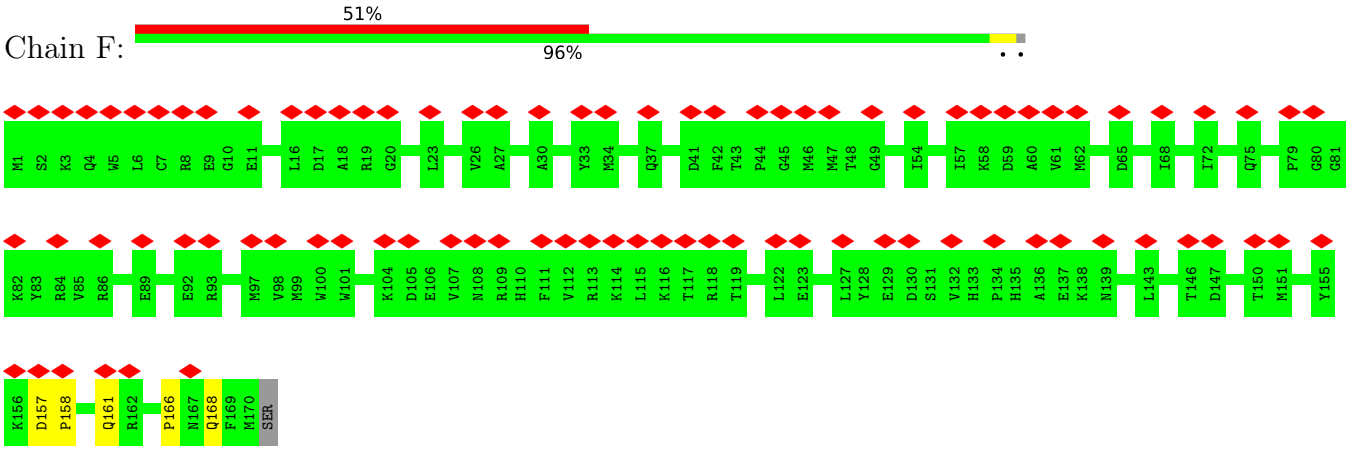






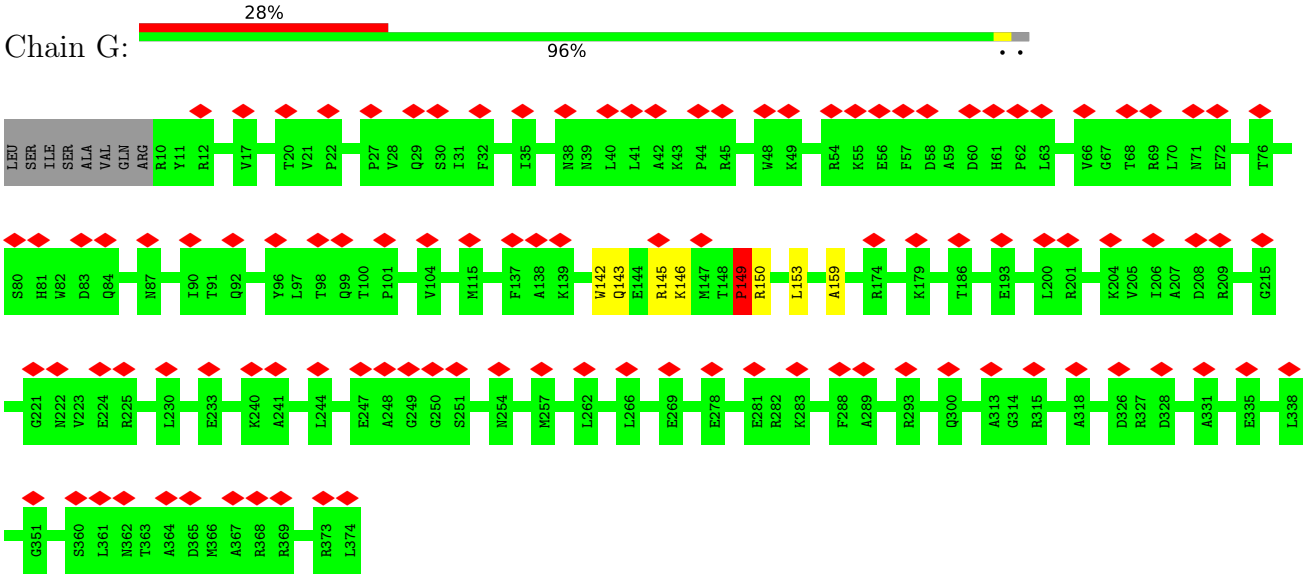
• Molecule 59: 50S ribosomal protein L13-like protein

Chain F:



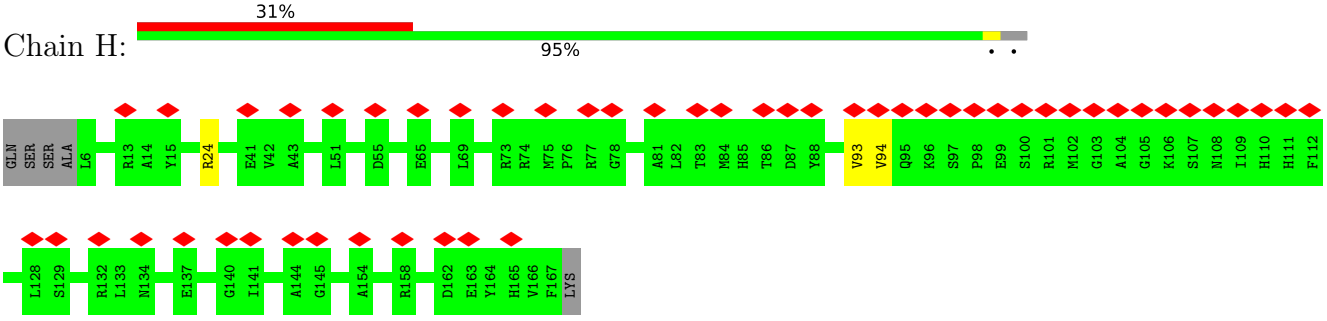
• Molecule 60: Ribosomal_L18e/L15P domain-containing protein

Chain G:



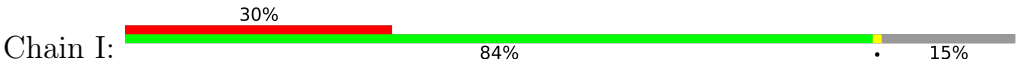
• Molecule 61: Ribosomal_L16 domain-containing protein

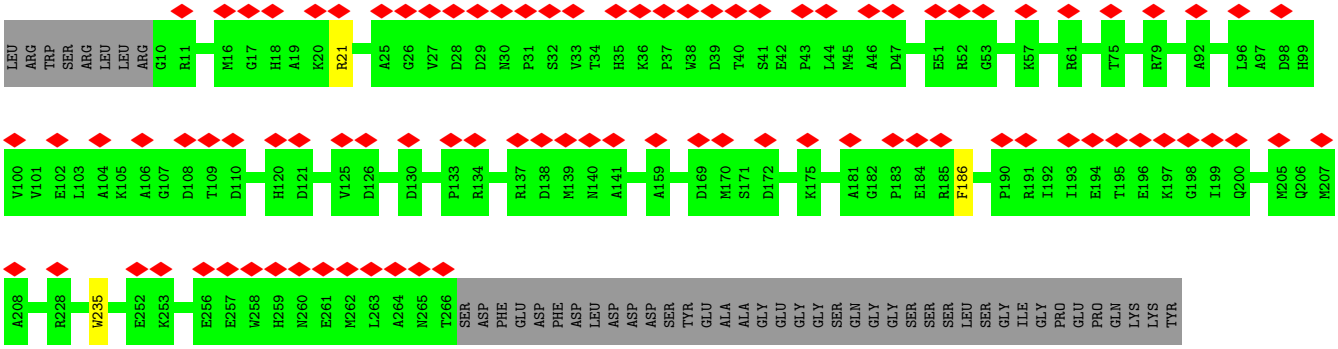
Chain H:



• Molecule 62: Putative 50S ribosomal protein L17

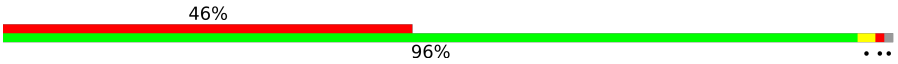
Chain I:

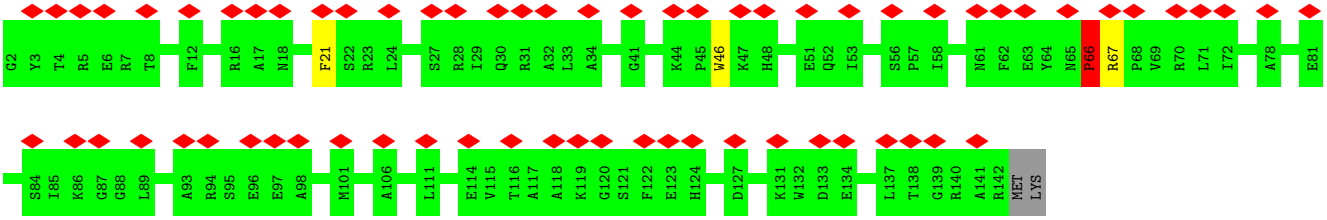




- Molecule 63: bL19m

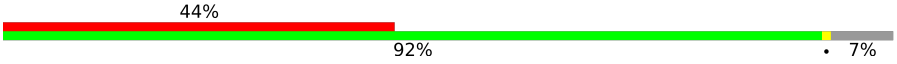
Chain J:

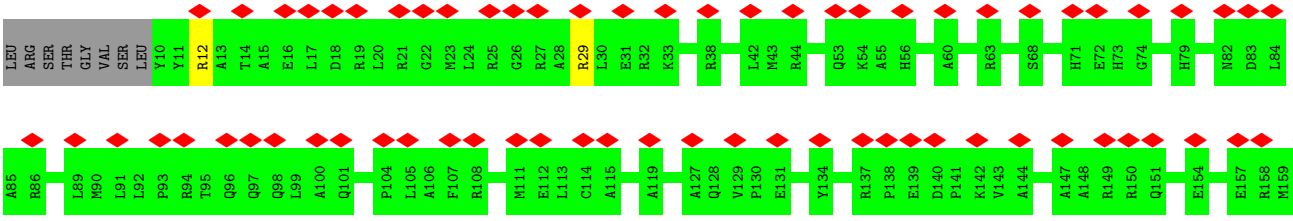


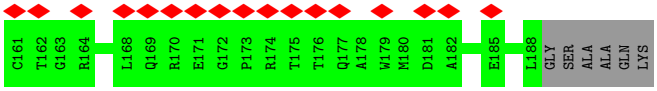


- Molecule 64: bL20m

Chain K:

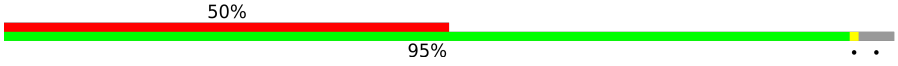


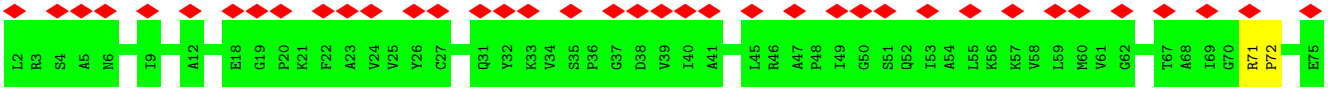


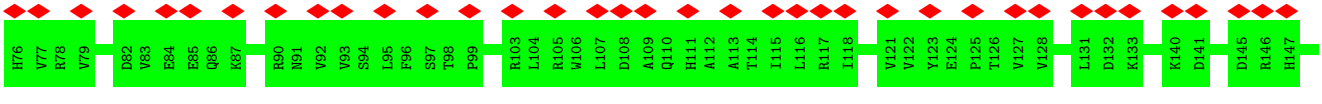


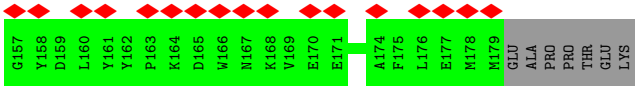
- Molecule 65: bL21m

Chain L:



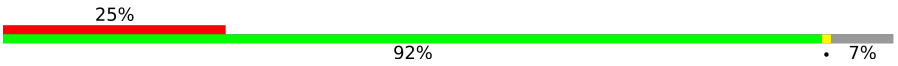


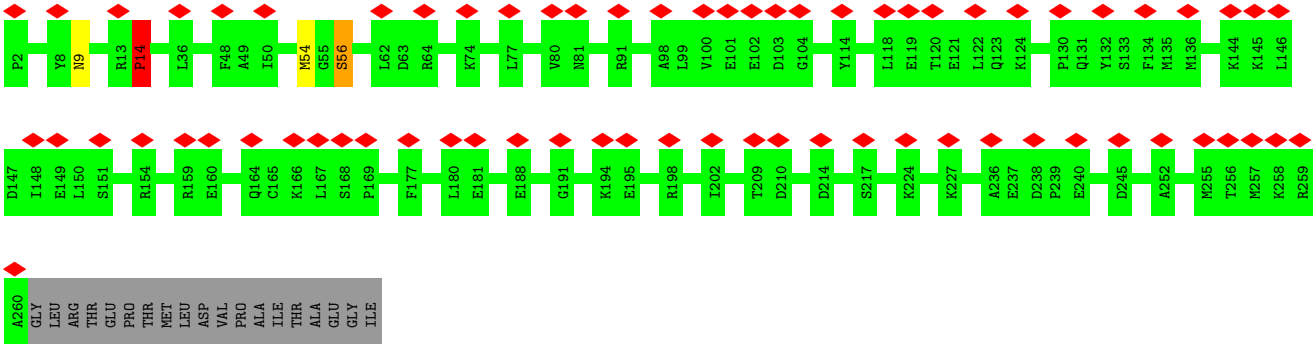




• Molecule 66: uL22m

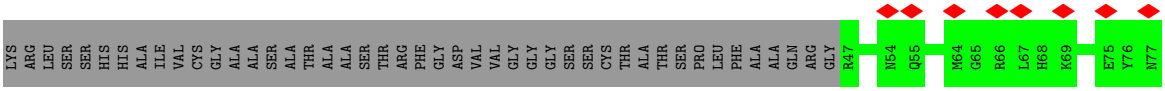
Chain M:

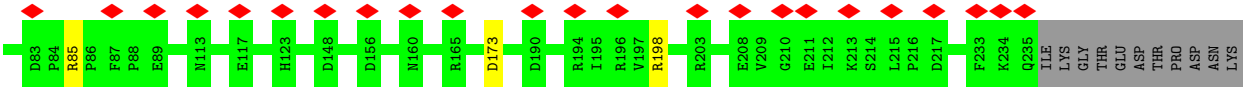




• Molecule 67: uL23m

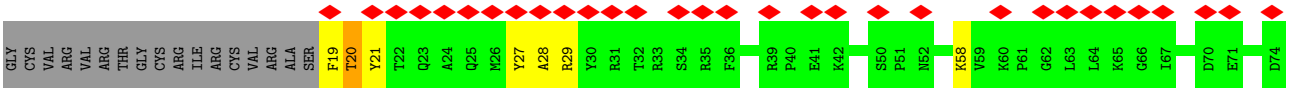
Chain N:

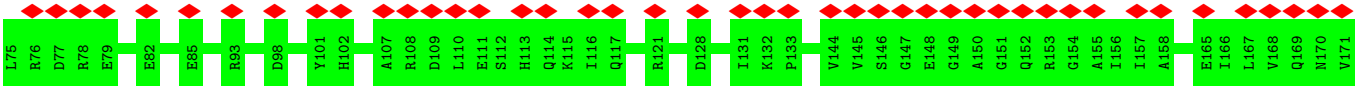


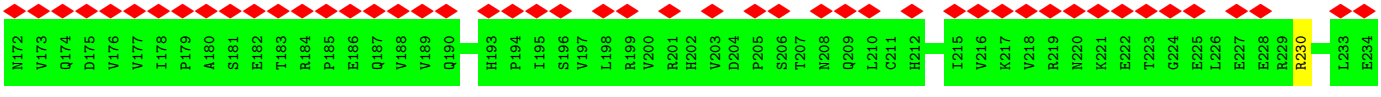


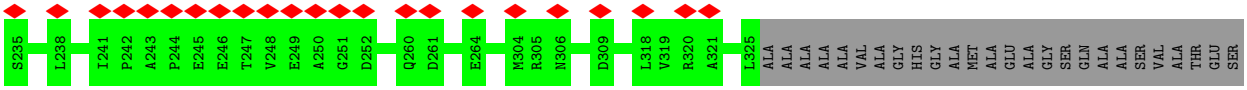
• Molecule 68: uL24m

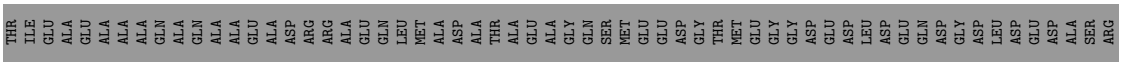
Chain O:





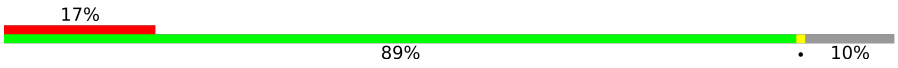


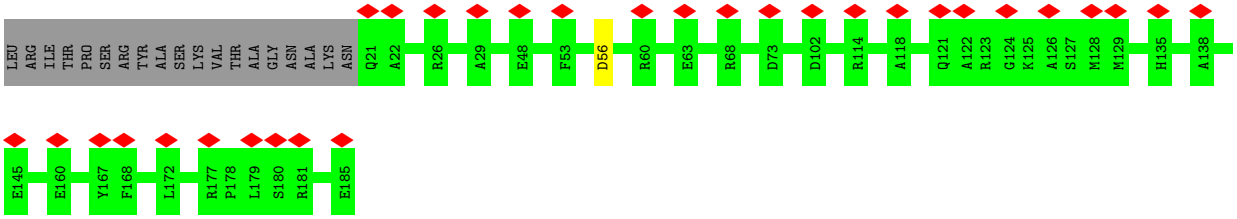




• Molecule 69: bL27m

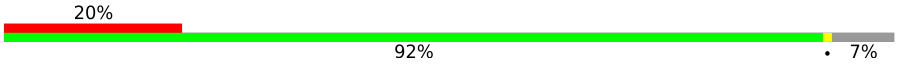
Chain P:

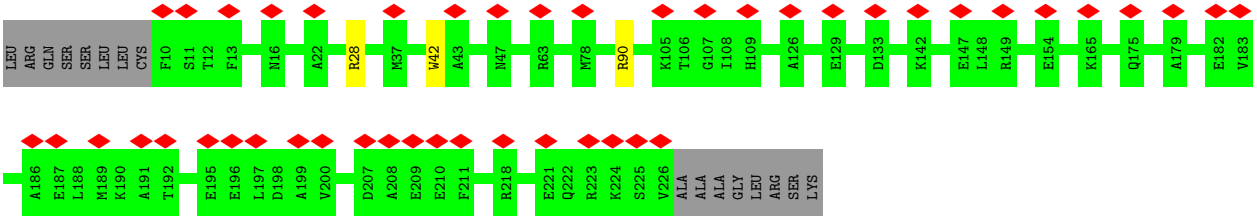




• Molecule 70: bL28m

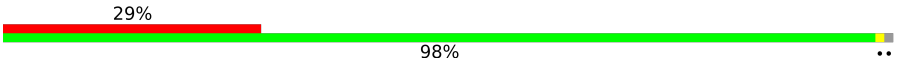
Chain Q:

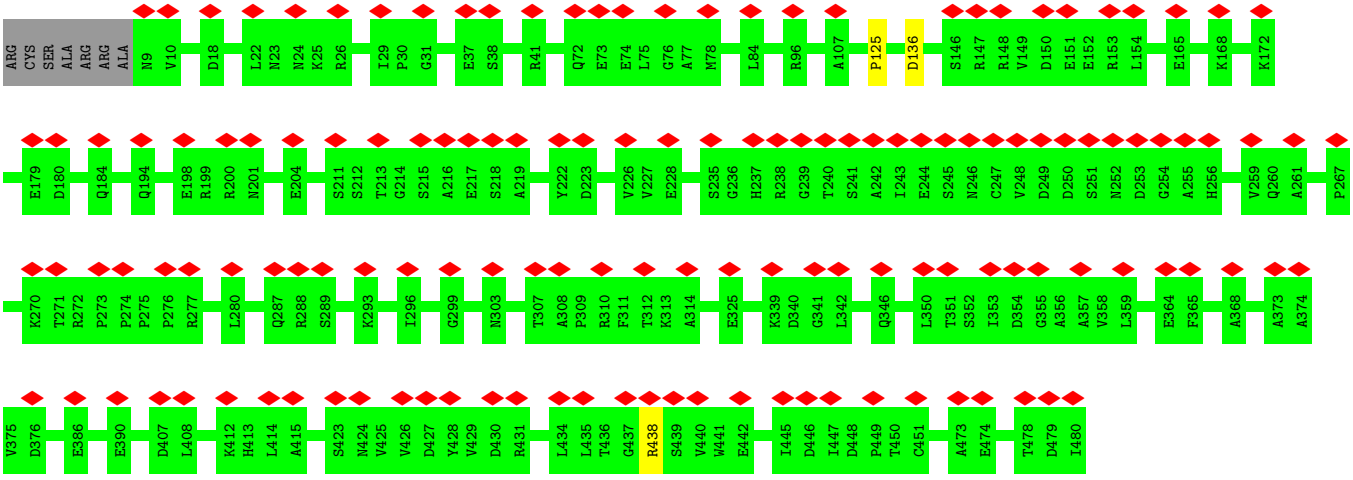




• Molecule 71: uL29m

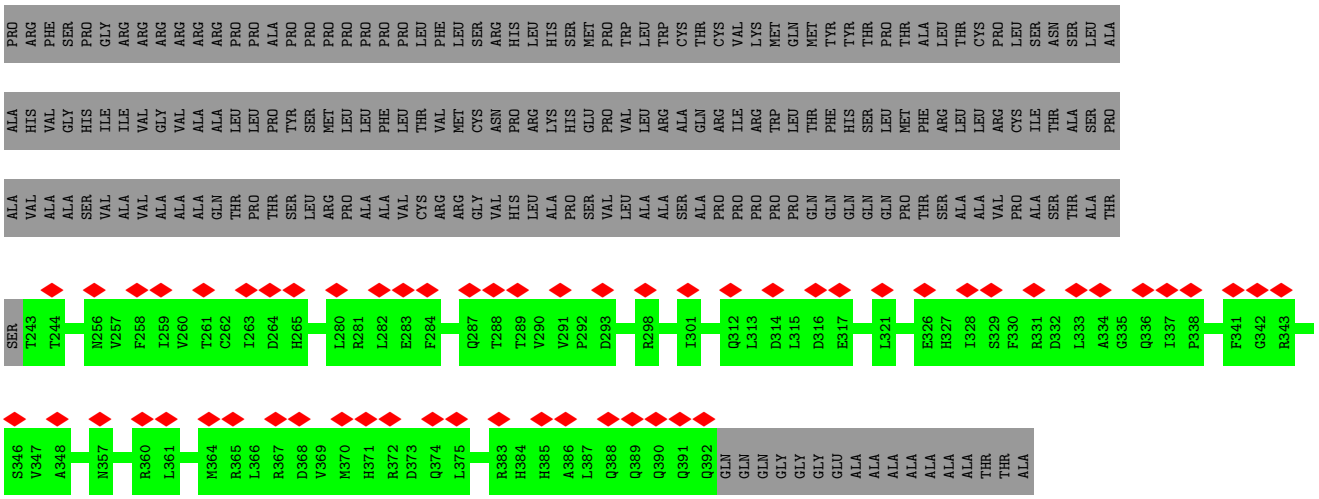
Chain R:





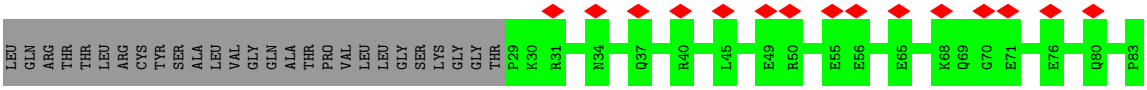
• Molecule 72: uL30m

Chain S:



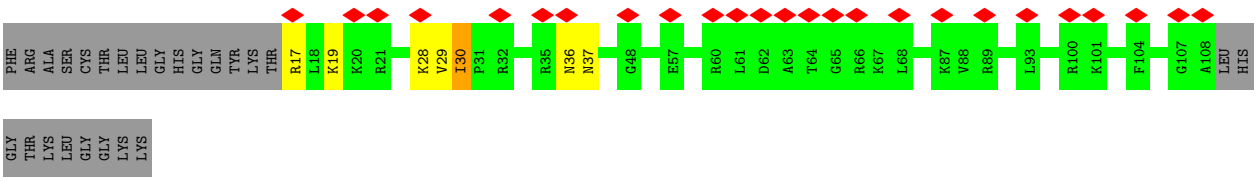
• Molecule 73: bL32m

Chain T:



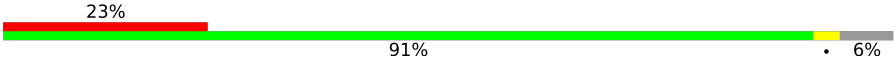
• Molecule 74: bL33m

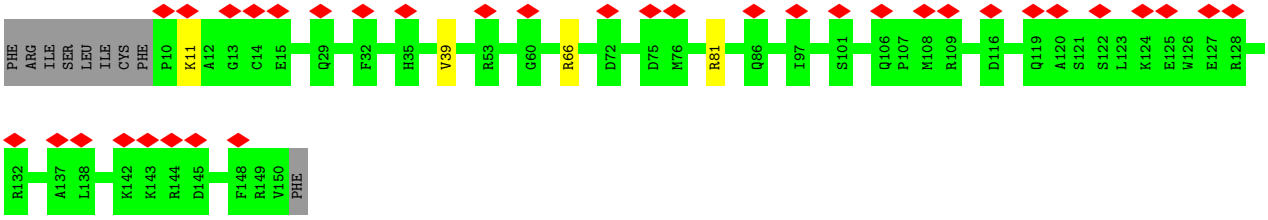
Chain U:



• Molecule 75: bL35m

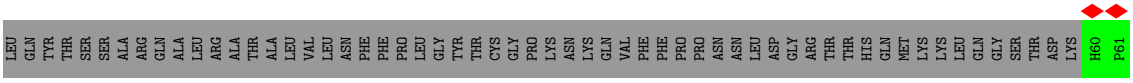
Chain V:

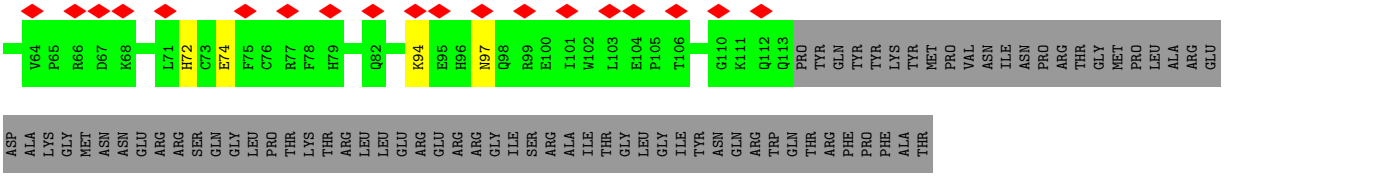




• Molecule 76: bL36m

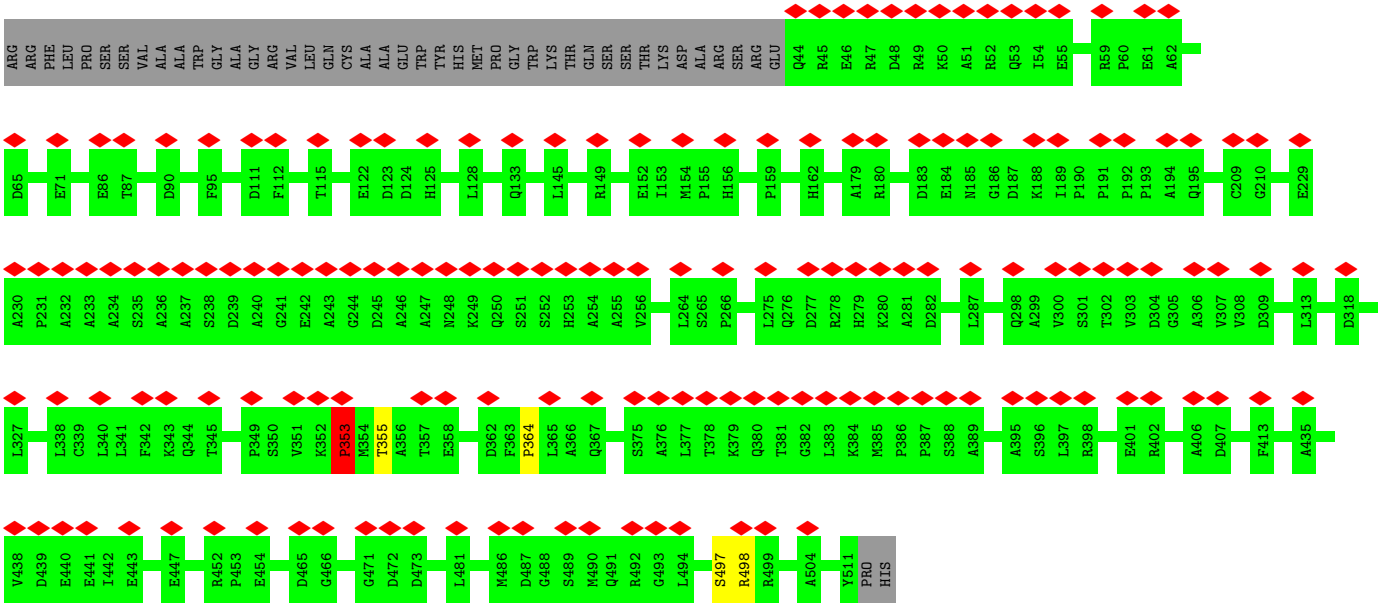
Chain W:





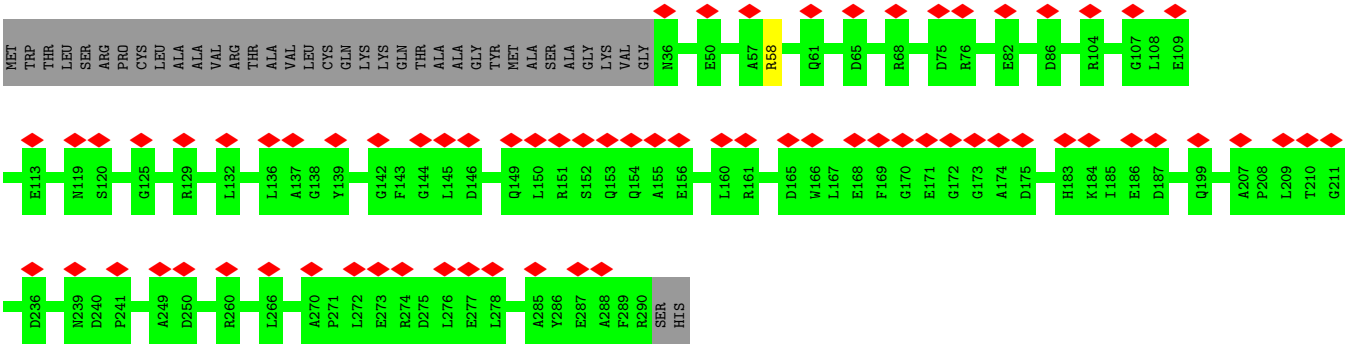
• Molecule 77: mL38

Chain X:



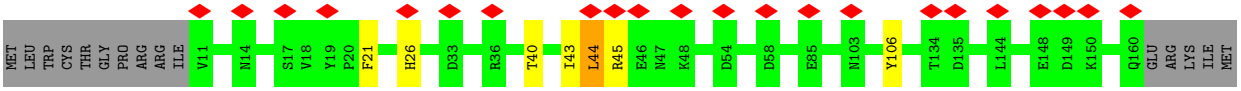
• Molecule 78: mL40

Chain Y:



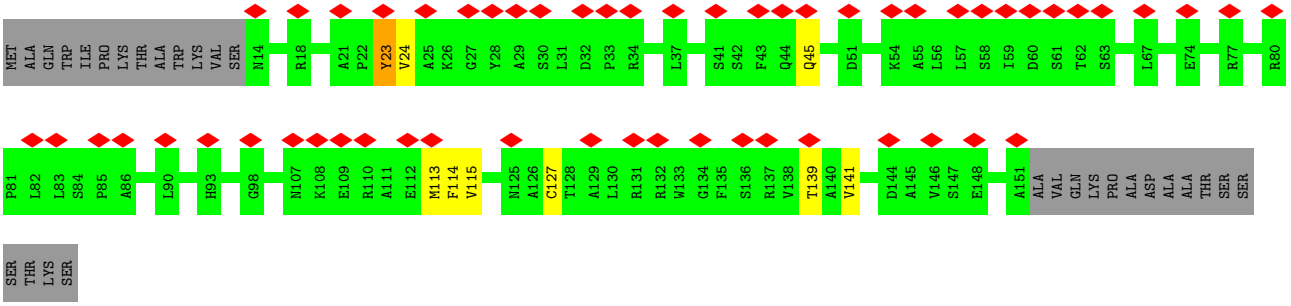
• Molecule 79: mL41

Chain Z:



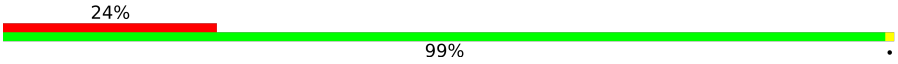
• Molecule 80: mL94

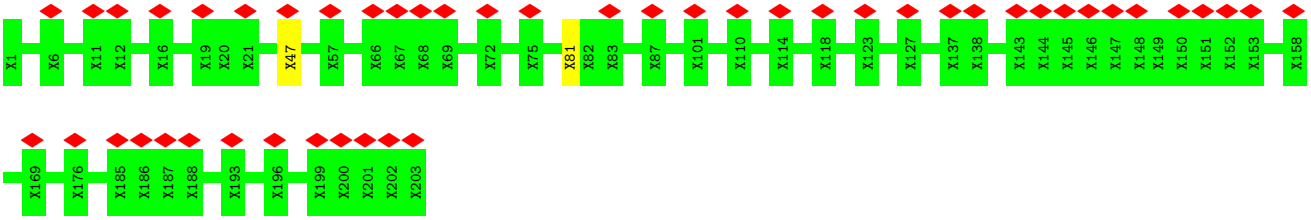
Chain BA:



• Molecule 81: UA

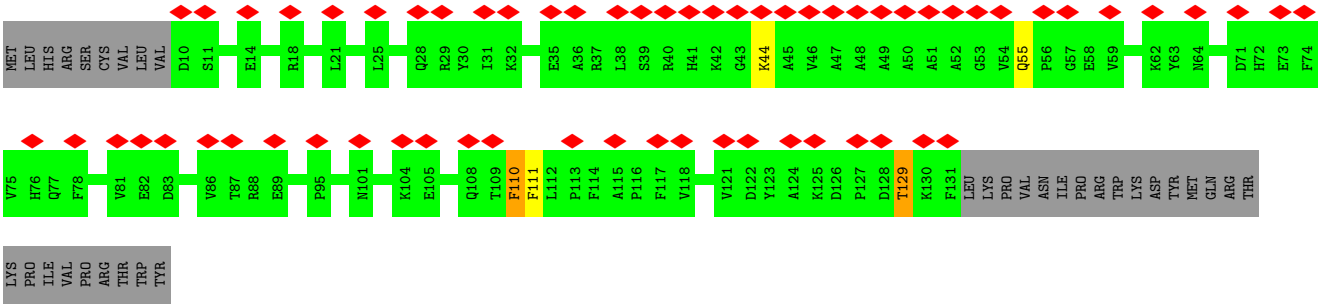
Chain UA:





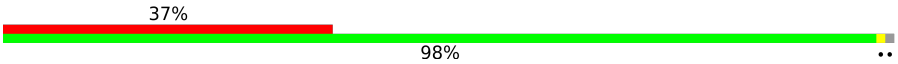
• Molecule 82: mL95

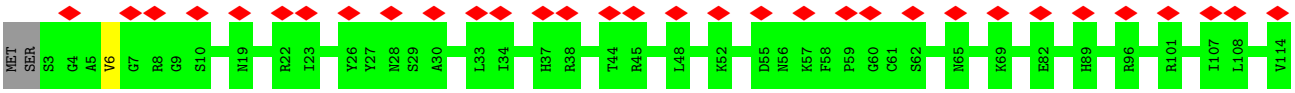
Chain BB:

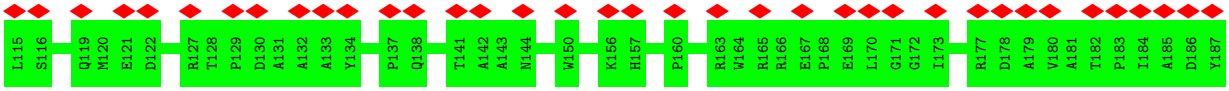


• Molecule 83: mL89

Chain Aw:

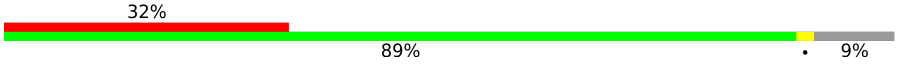


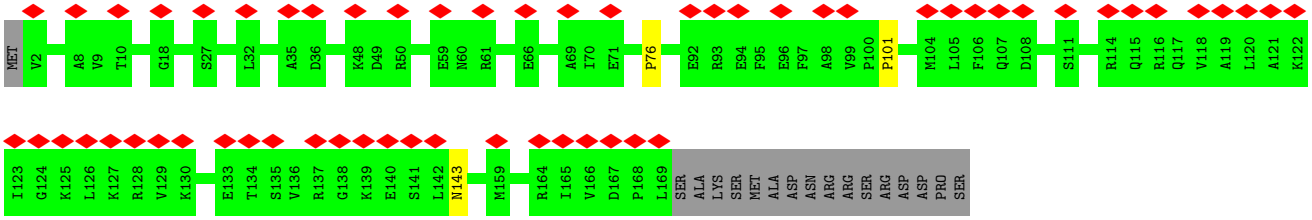




• Molecule 84: bL31m

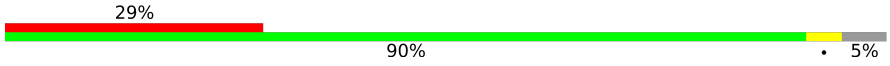
Chain Bj:

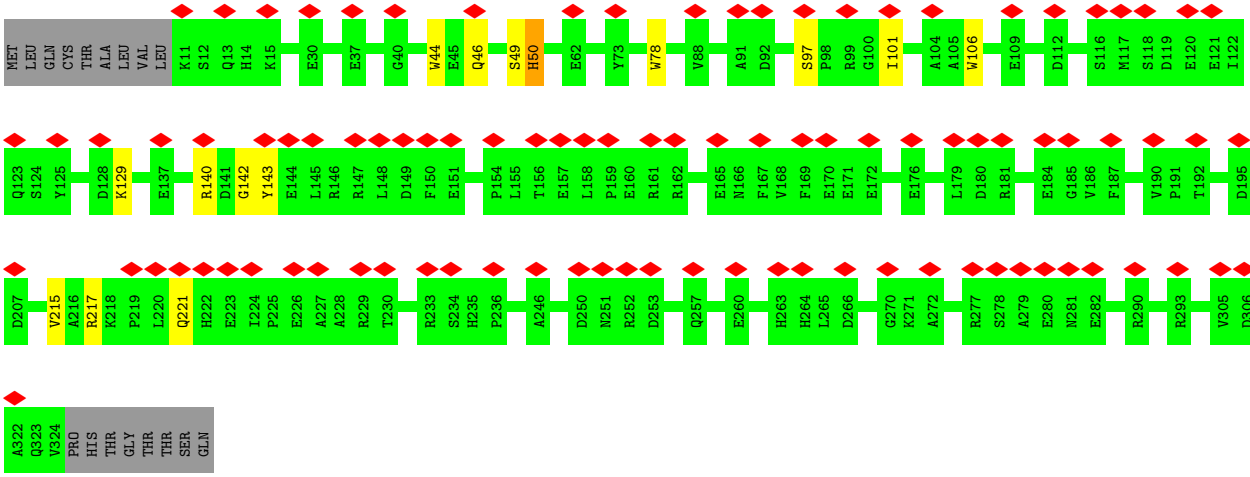




• Molecule 85: mL76

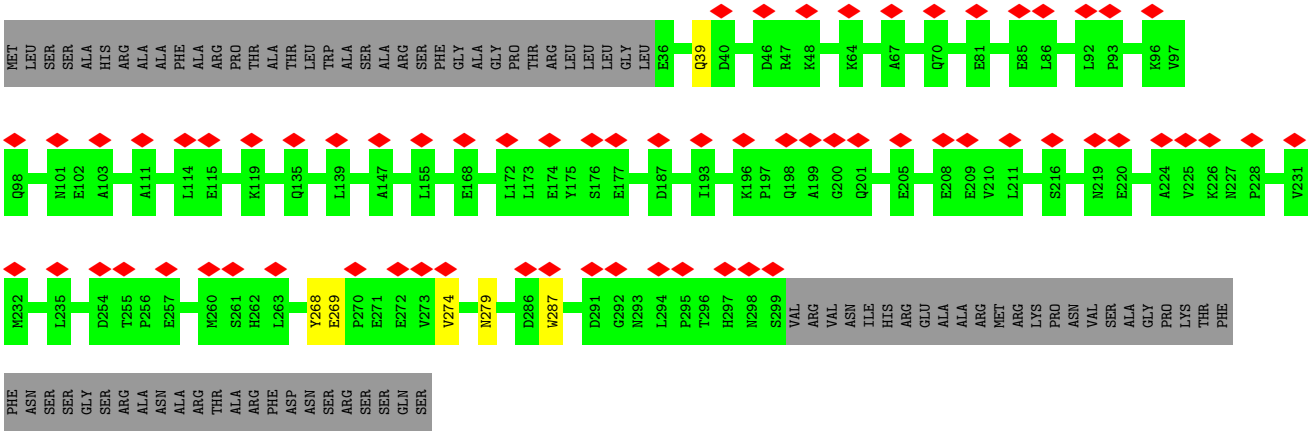
Chain An:





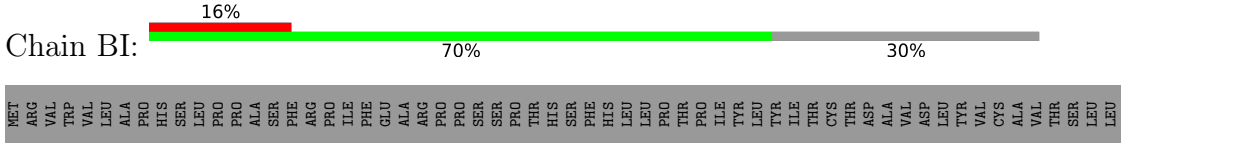
• Molecule 86: mL74

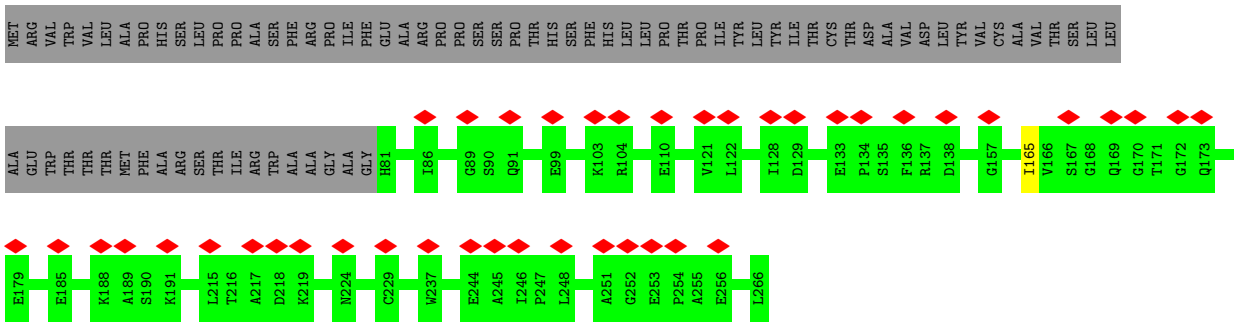
Chain Al:



• Molecule 87: Peptidyl-prolyl cis-trans isomerase

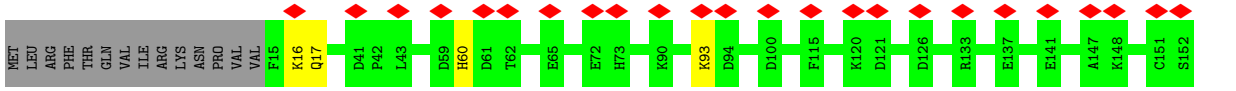
Chain BI:





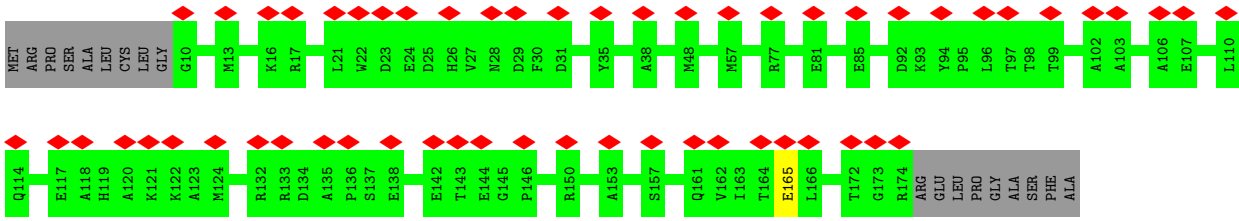
• Molecule 88: mL93

Chain Az:



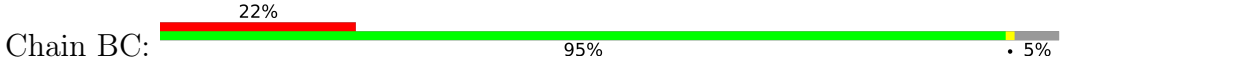
• Molecule 89: mL86

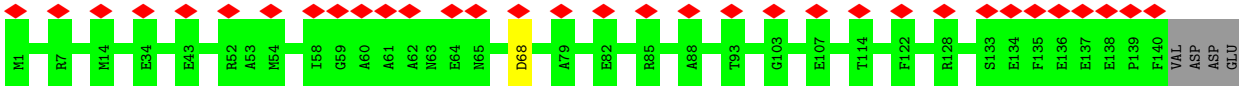
Chain At:



• Molecule 90: mL96

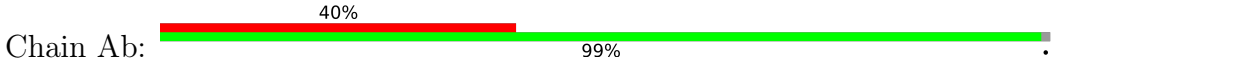
Chain BC:

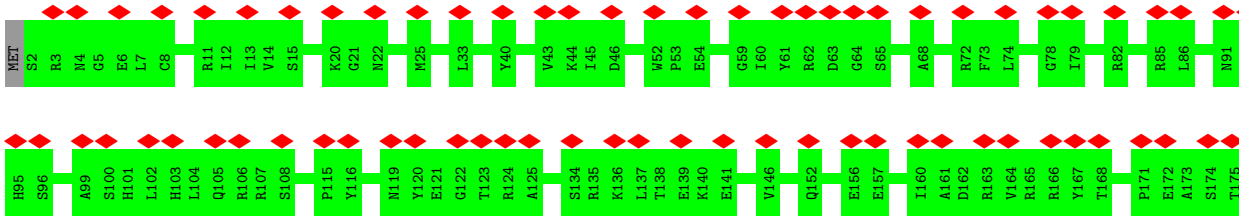


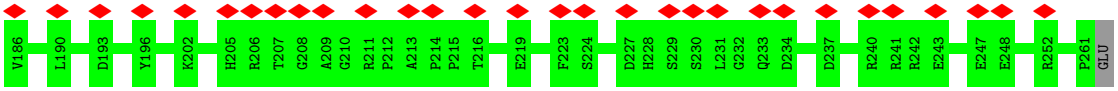


• Molecule 91: L51_S25_CI-B8 domain-containing protein

Chain Ab:

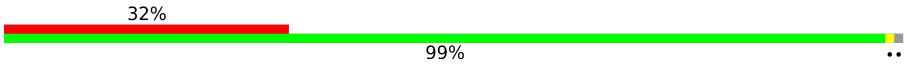


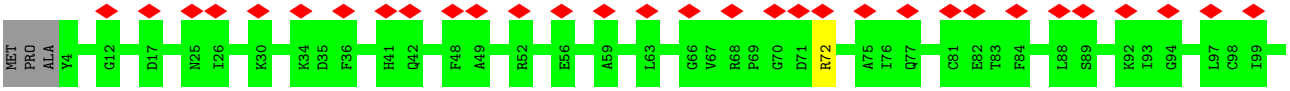


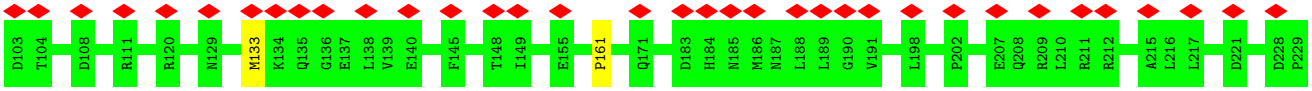


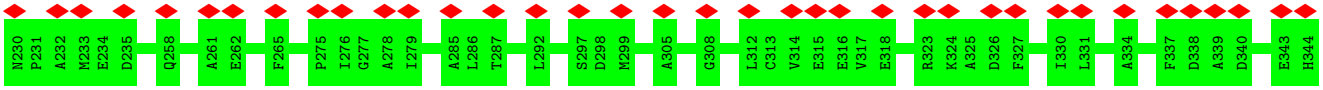
• Molecule 92: mL69

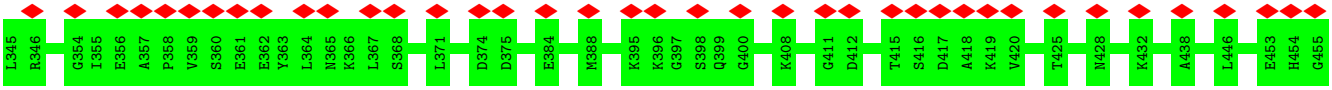
Chain Ai:

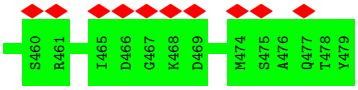






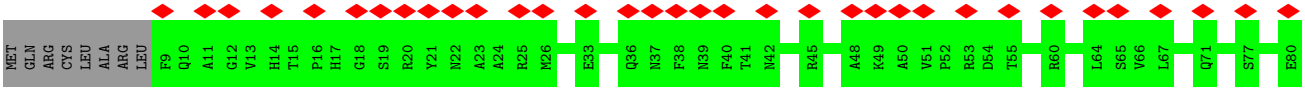


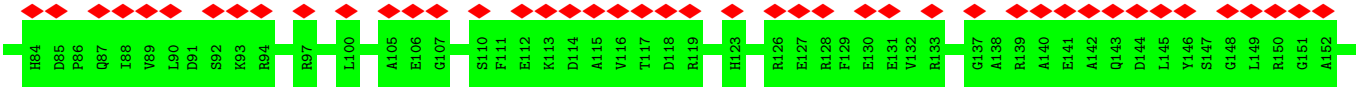




• Molecule 93: mL80

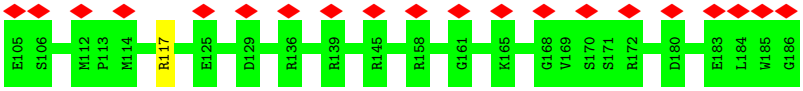
Chain Ap:





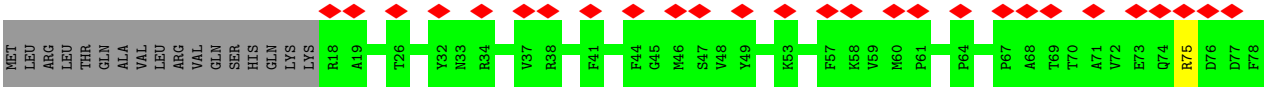
• Molecule 94: mL87

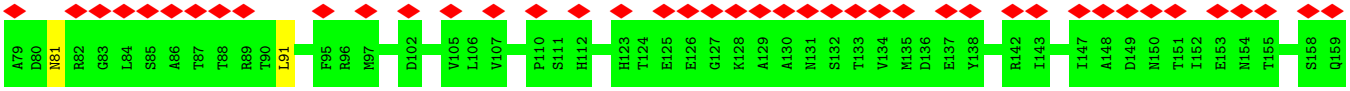
Chain Au:

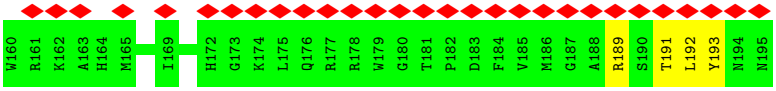


• Molecule 95: mL42

Chain Aa:

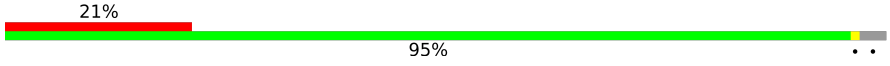


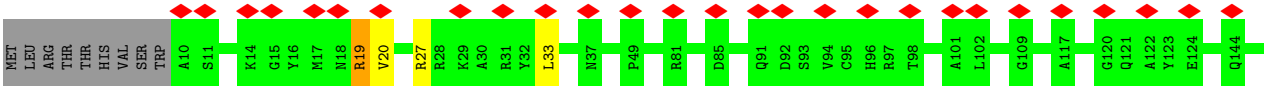


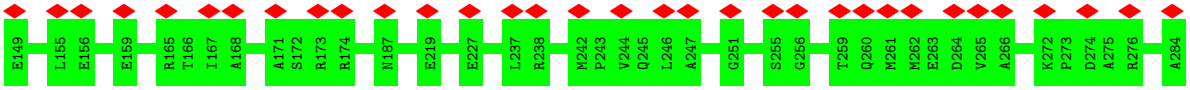


• Molecule 96: mL79

Chain Ao:

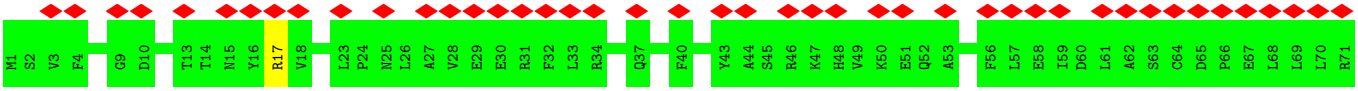


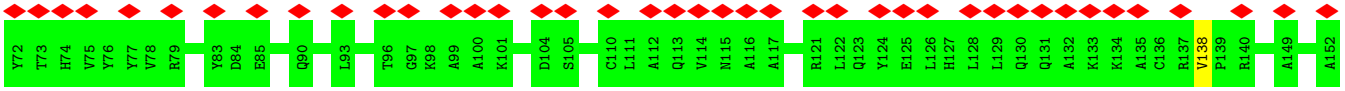


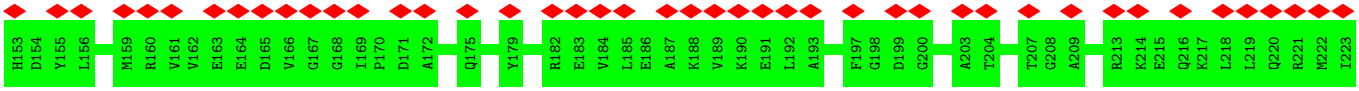


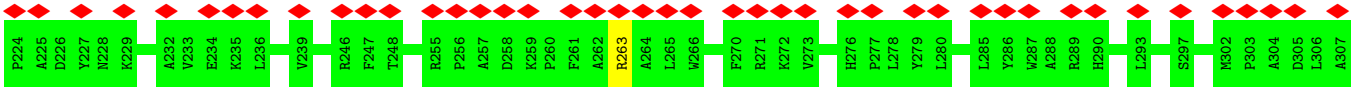
• Molecule 97: mL70

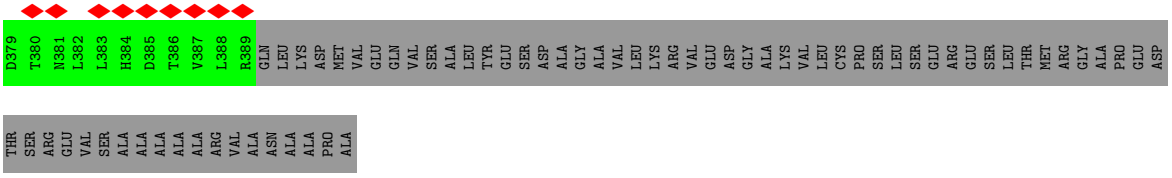
Chain BM:





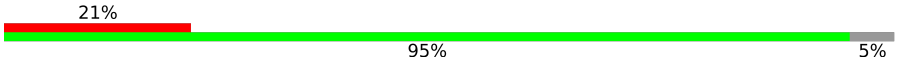


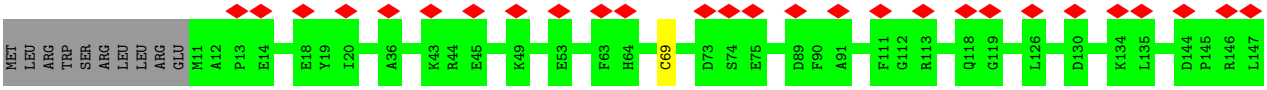


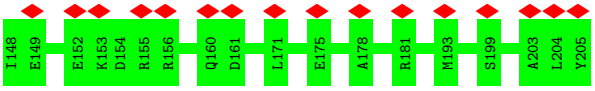


• Molecule 98: mL84

Chain Ar:

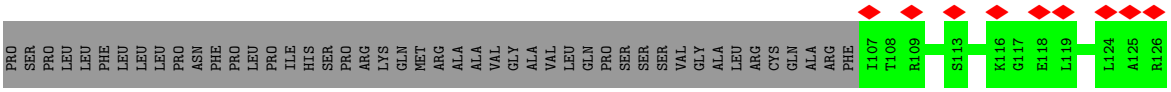


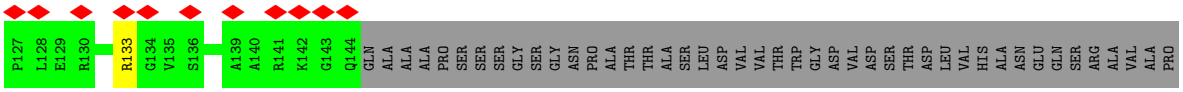


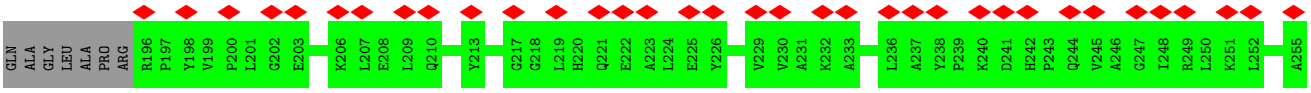


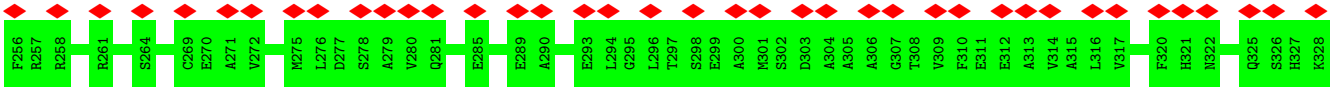
• Molecule 99: mL72

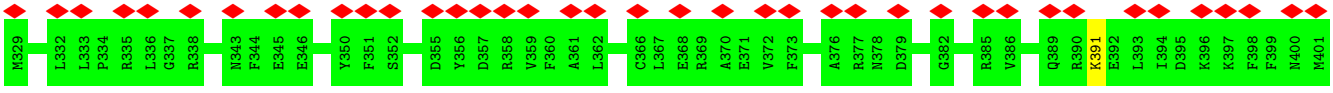
Chain Aj:

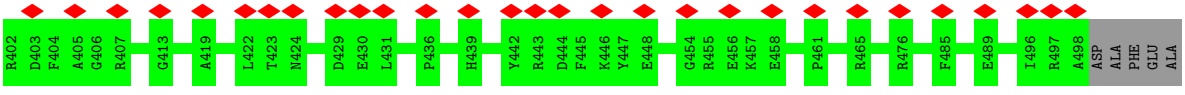






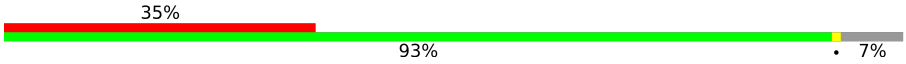


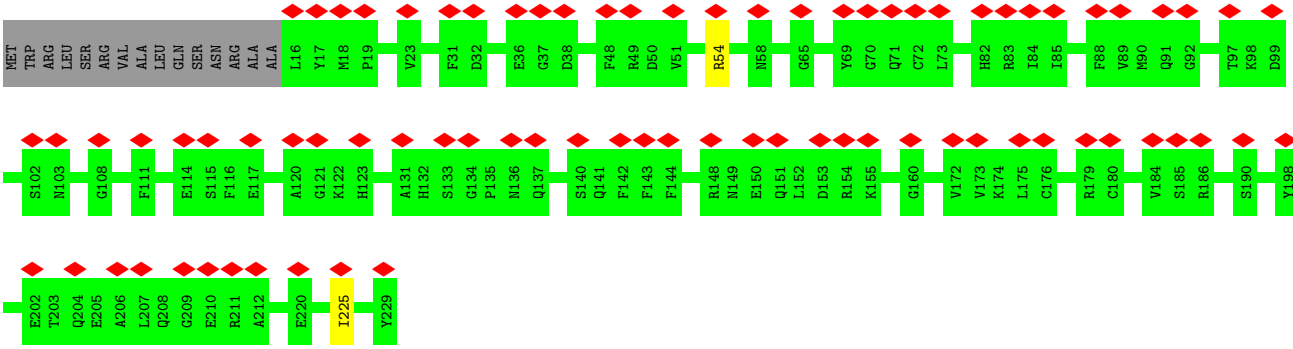




• Molecule 100: Peptidyl-prolyl cis-trans isomerase

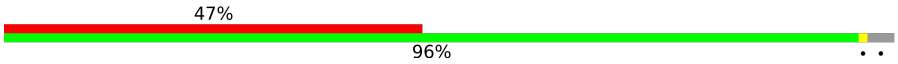
Chain BH:

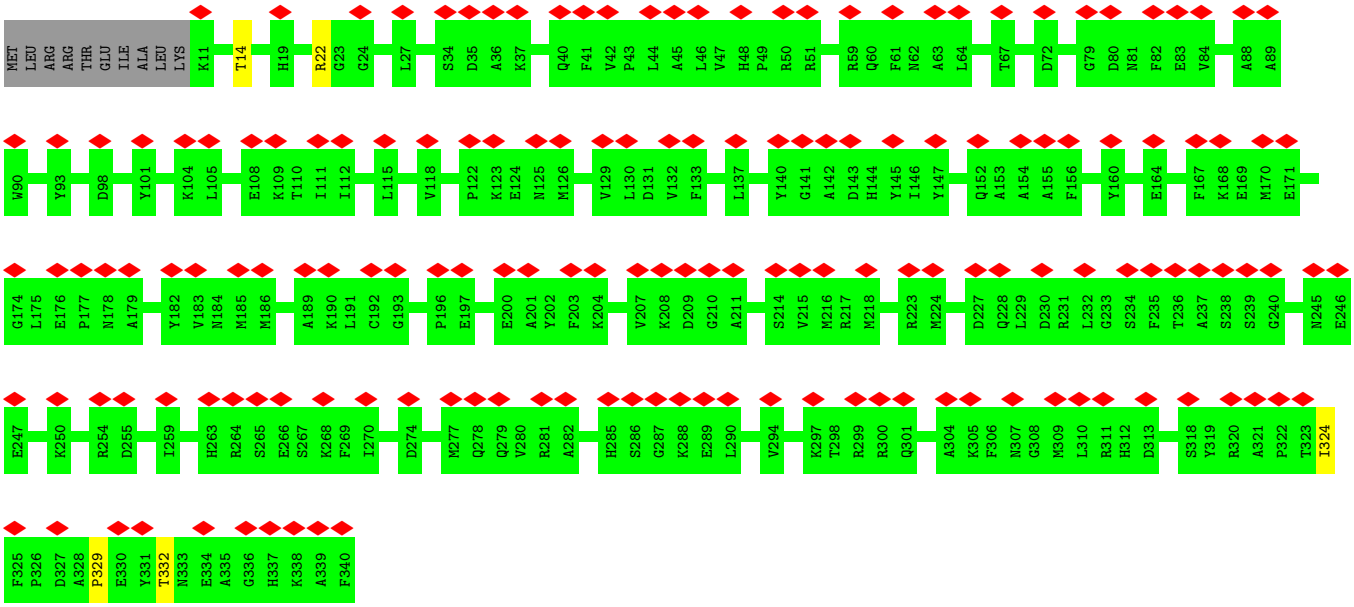




• Molecule 101: mL75

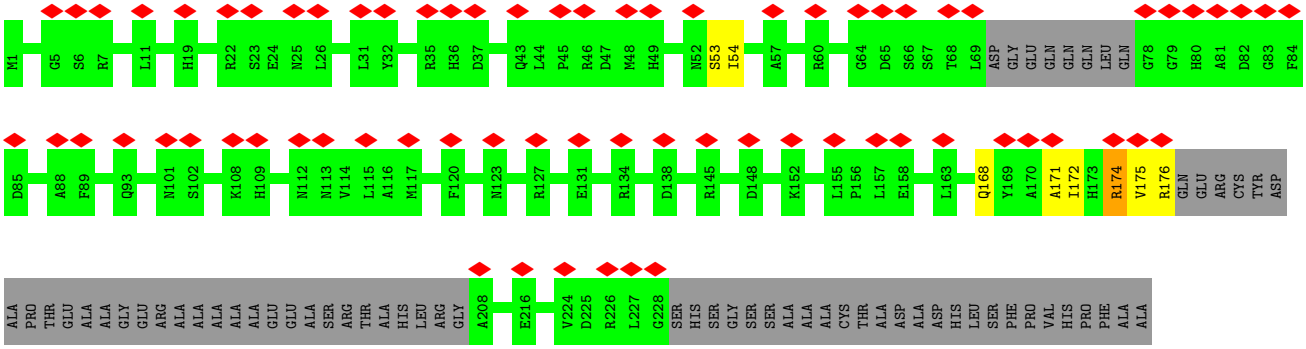
Chain Am:

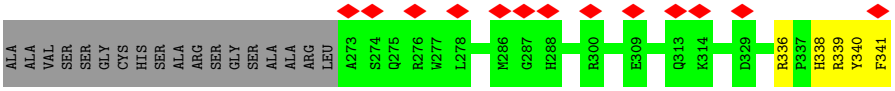




• Molecule 102: mL82

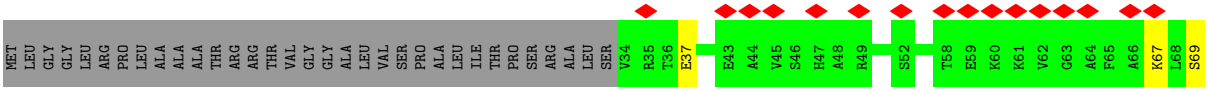
Chain Aq:

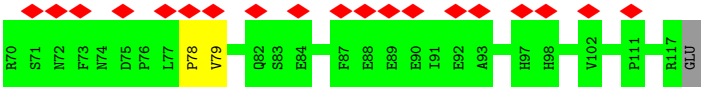




• Molecule 103: mL98

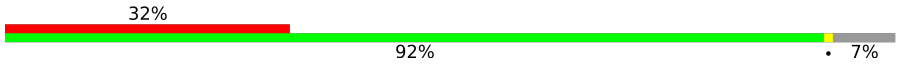
Chain BE:

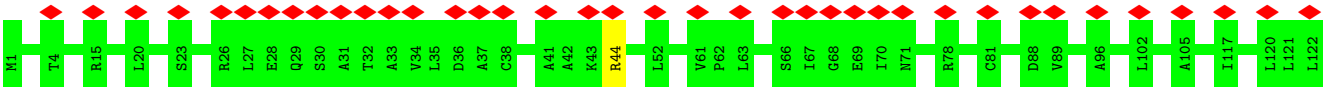


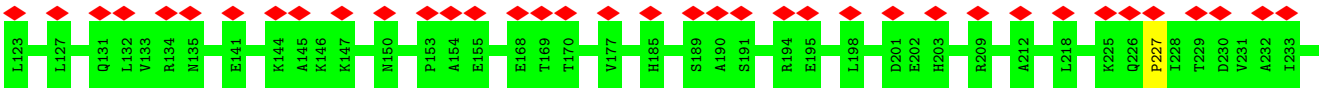


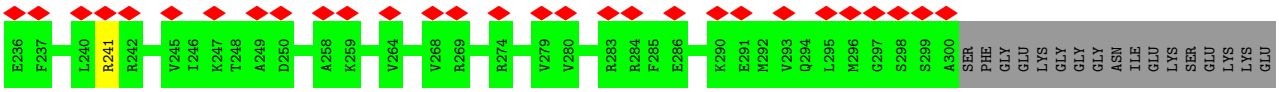
• Molecule 104: mL73

Chain Ak:



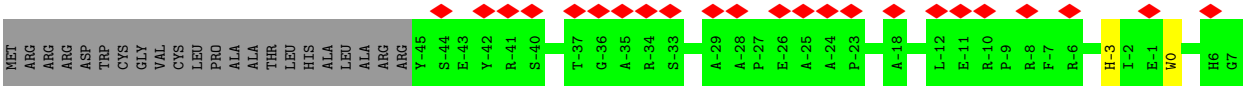


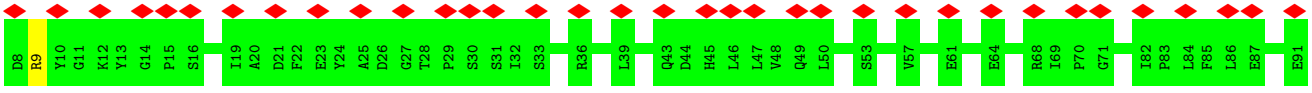


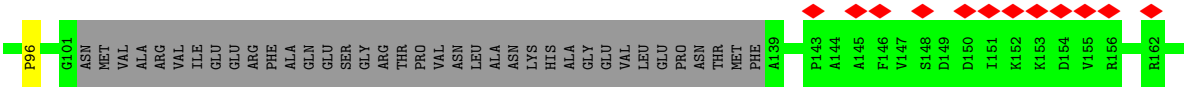


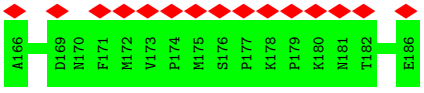
• Molecule 105: mL52

Chain BP:



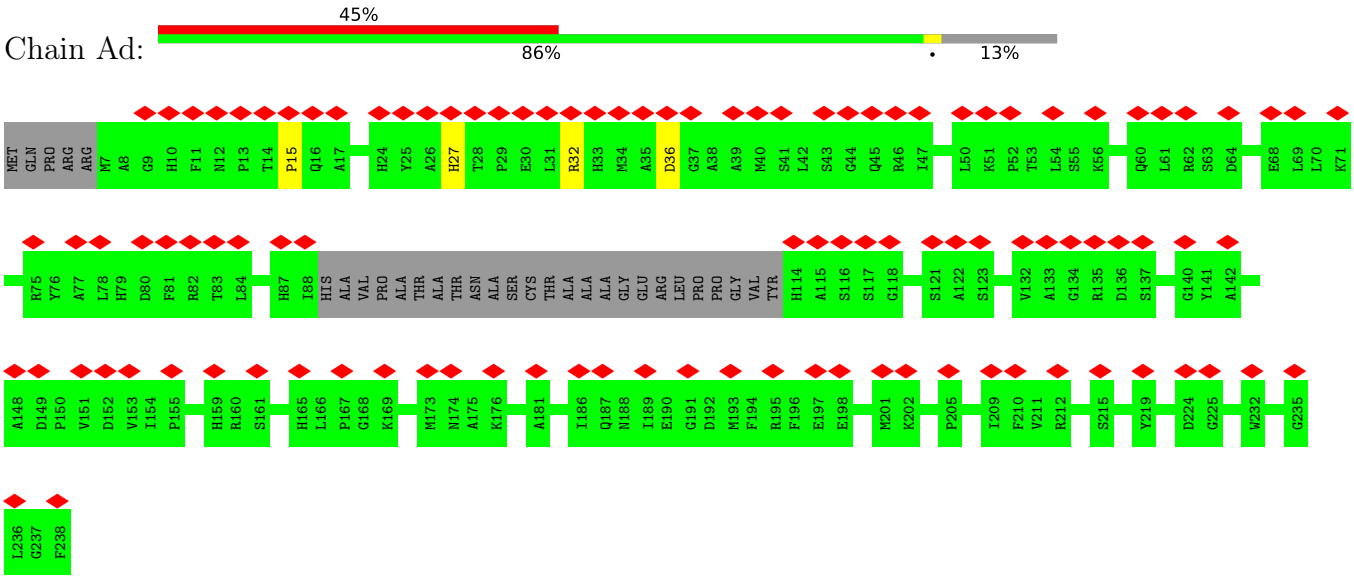






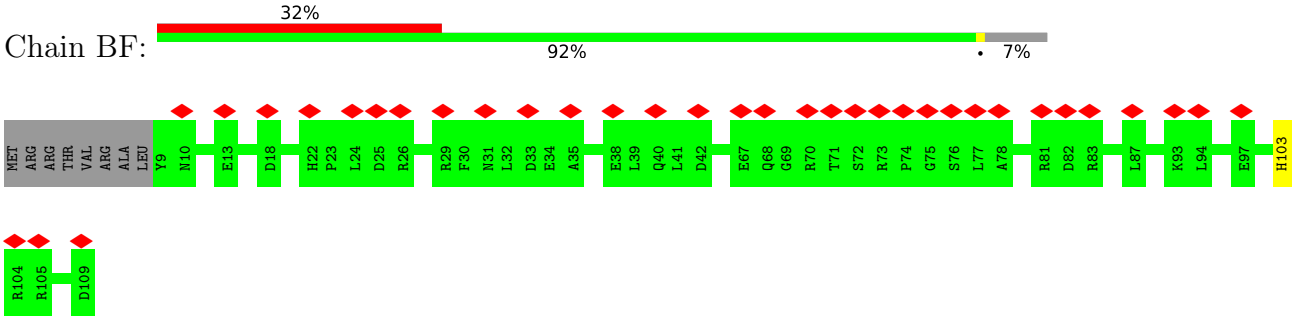
• Molecule 106: mL49

Chain Ad:



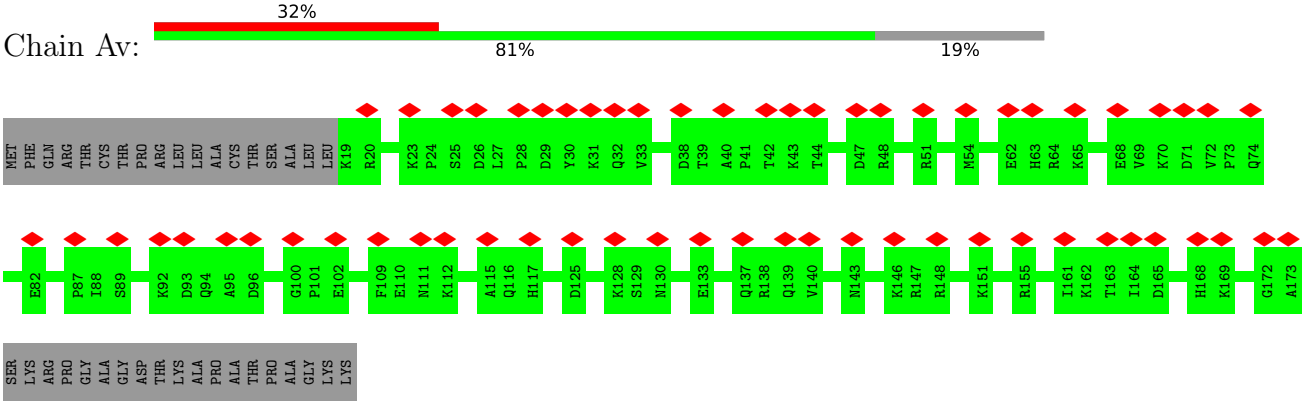
• Molecule 107: mL99

Chain BF:



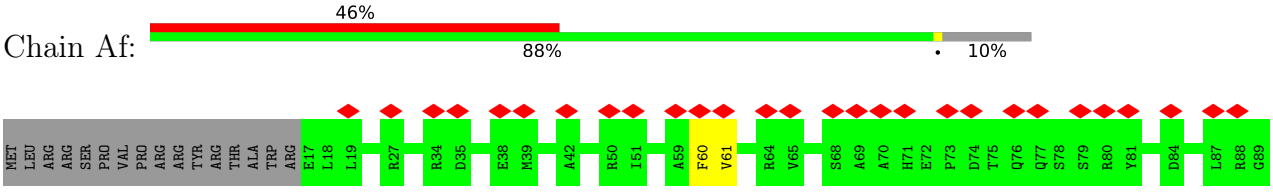
• Molecule 108: mL88

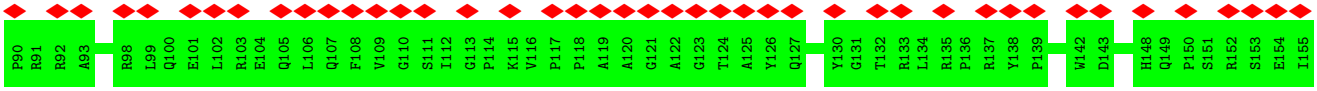
Chain Av:



• Molecule 109: mL63

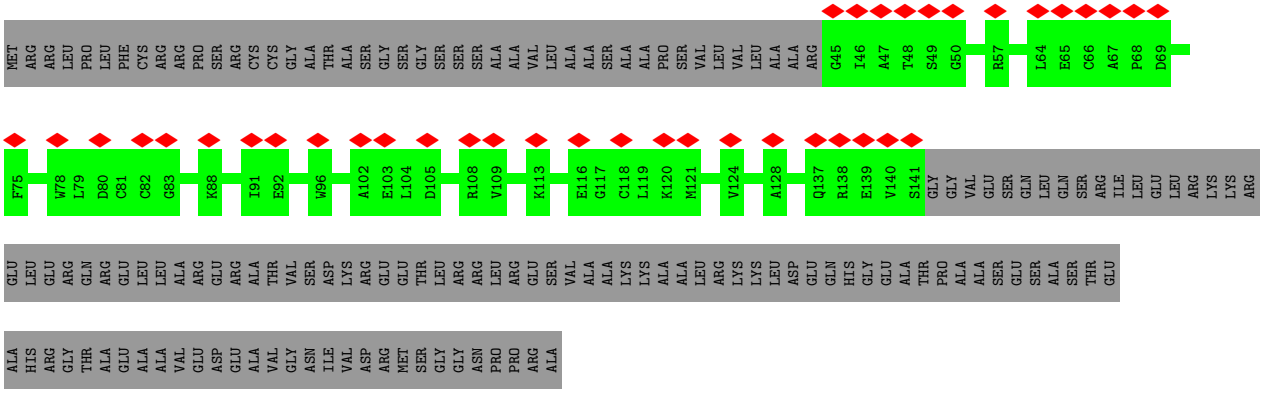
Chain Af:





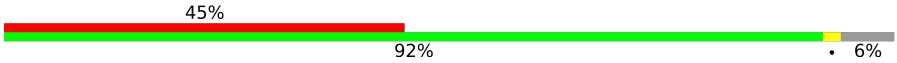
• Molecule 110: mL85

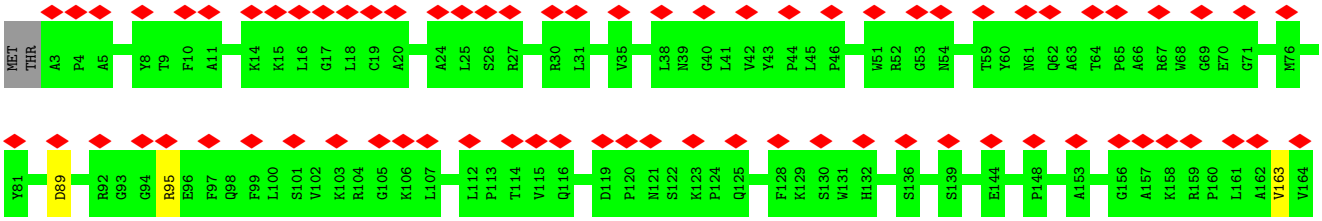
Chain As:



• Molecule 111: mL53

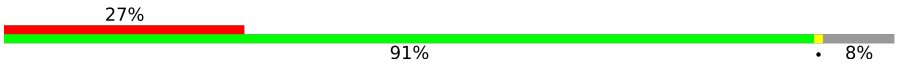
Chain Ae:

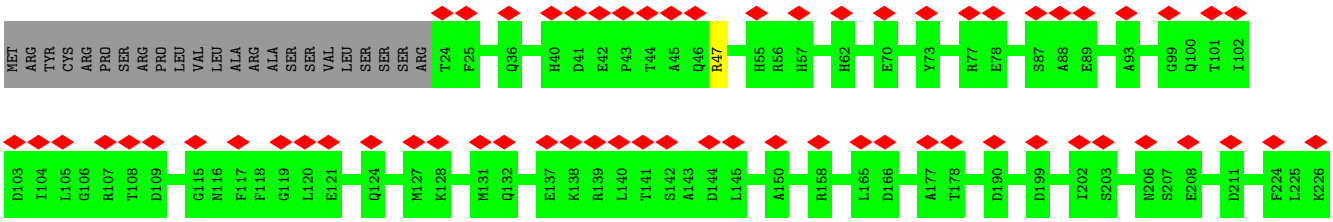


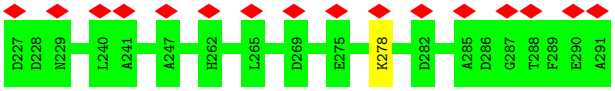


• Molecule 112: MRP-L46 domain-containing protein

Chain Ac:

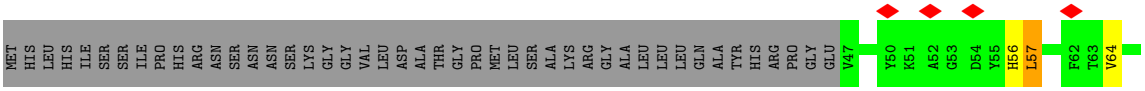


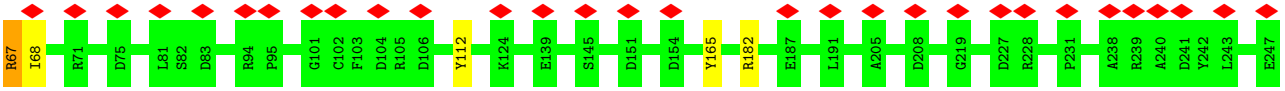


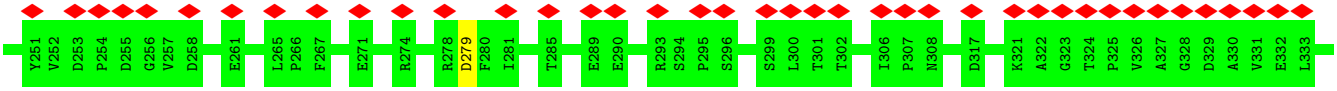


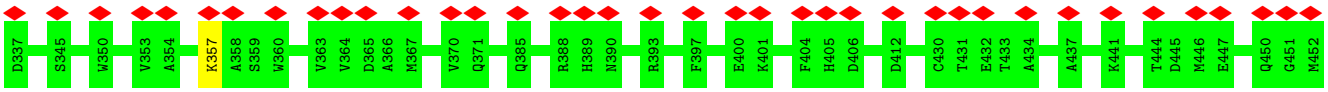
• Molecule 113: mL68

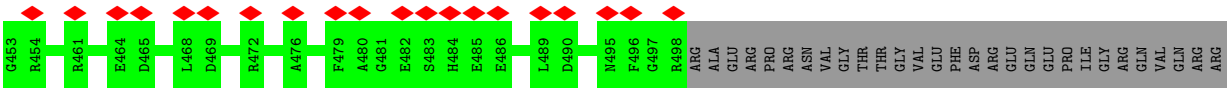
Chain Ah:





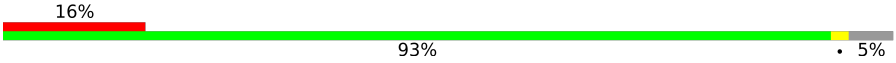






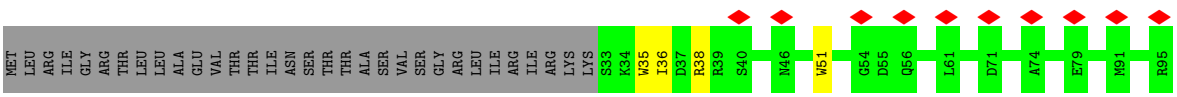
• Molecule 114: mL97

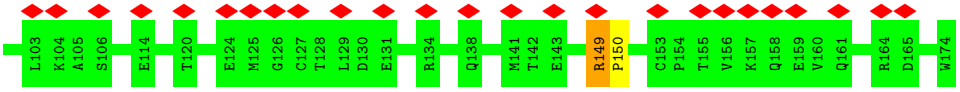
Chain BD:



• Molecule 115: C2H2-type domain-containing protein

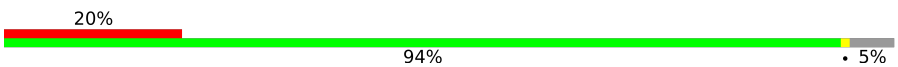
Chain Ay:

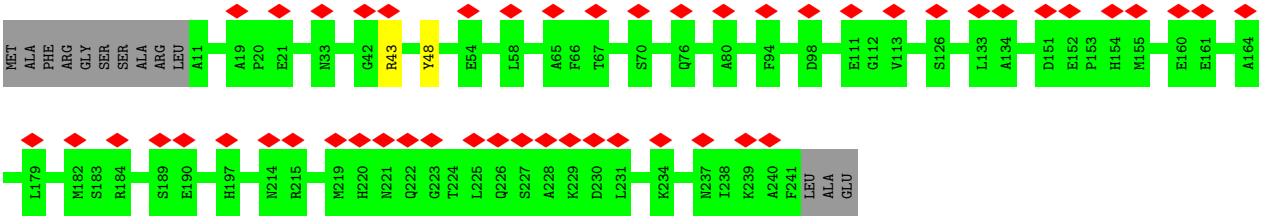




• Molecule 116: mL59/64

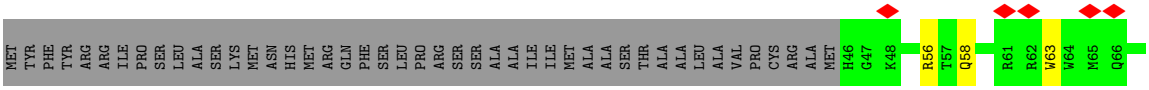
Chain Ag:

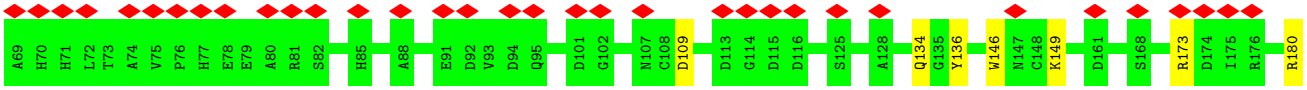




• Molecule 117: LIM zinc-binding domain-containing protein

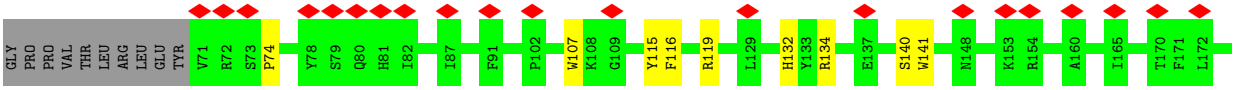
Chain Ax:

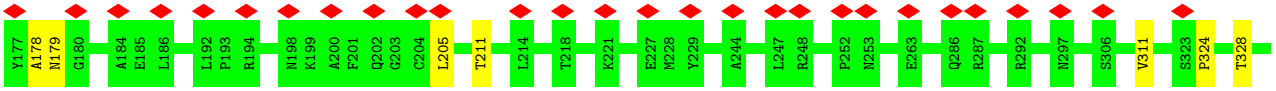


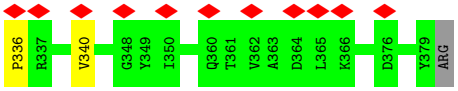


• Molecule 118: Putative ribosomal protein L2

Chain BL:

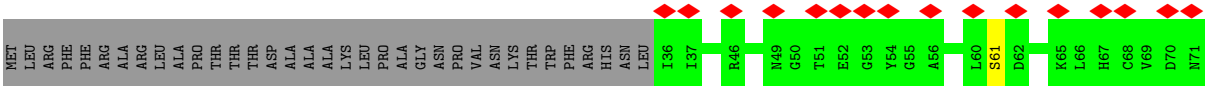


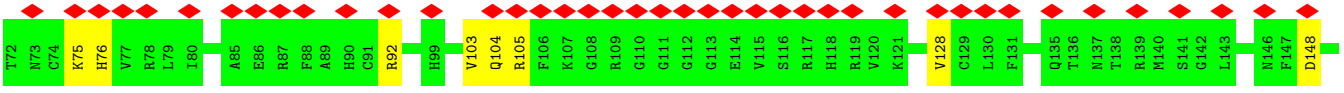




• Molecule 119: Putative ribosomal protein L14

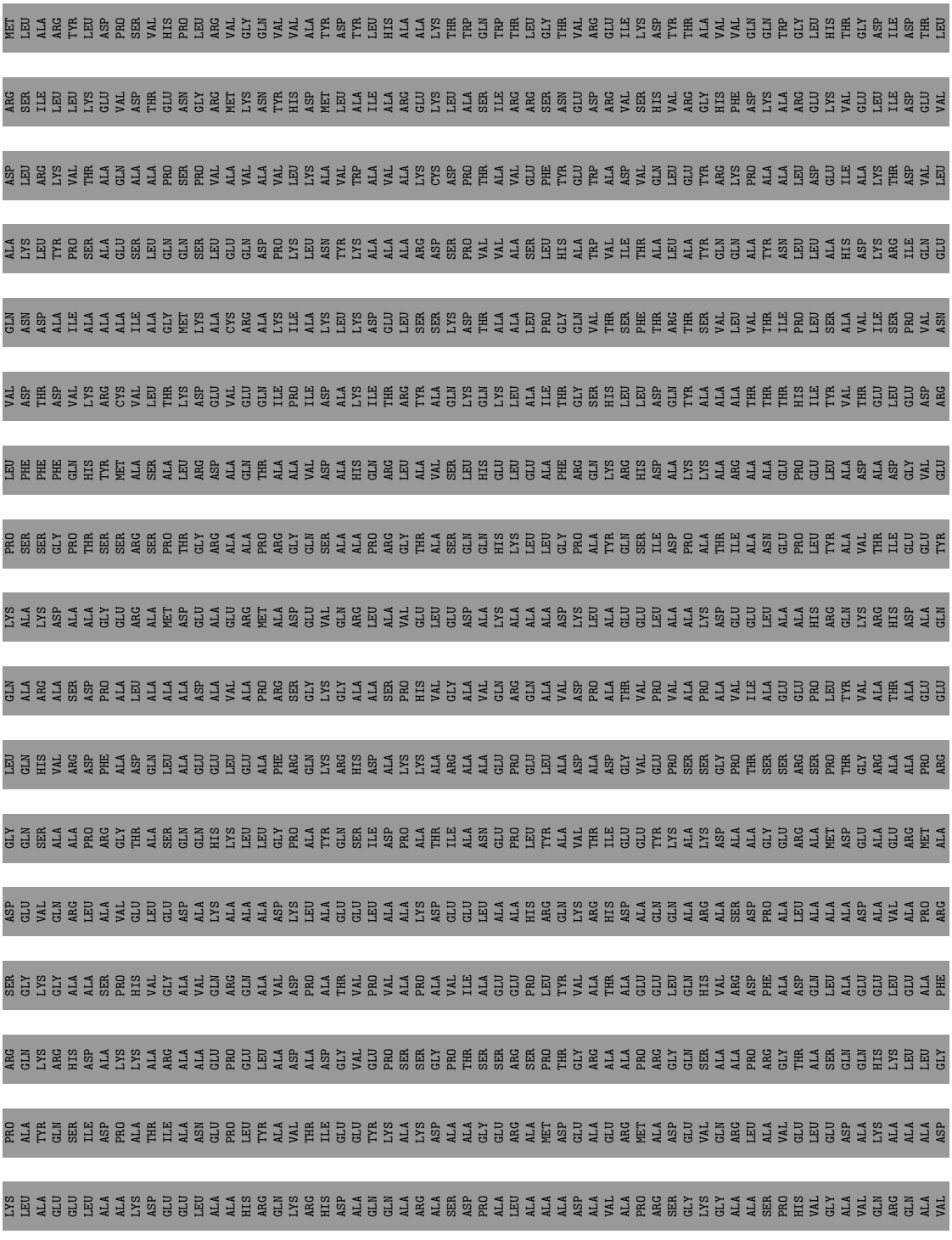
Chain BO:

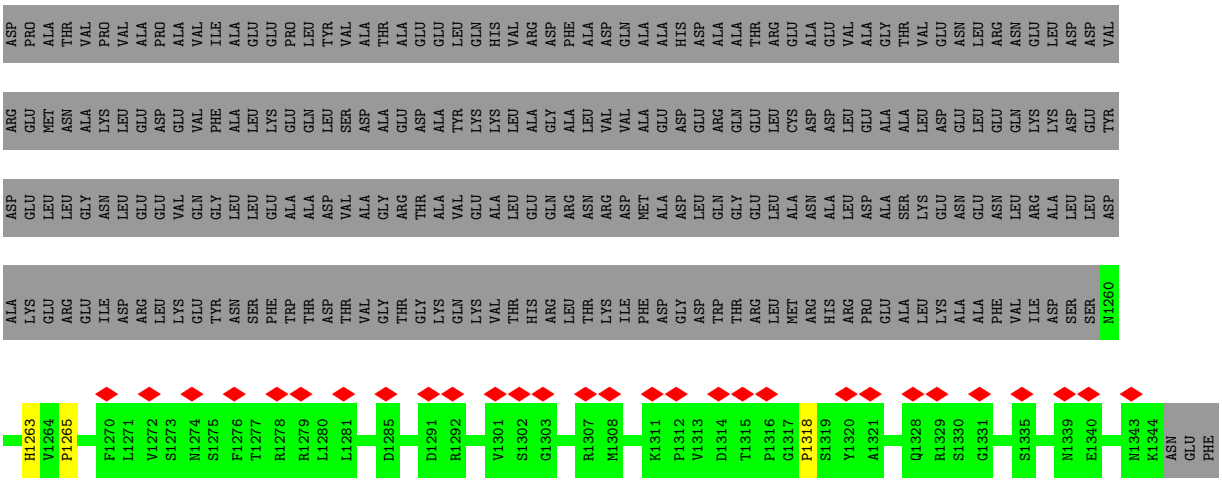




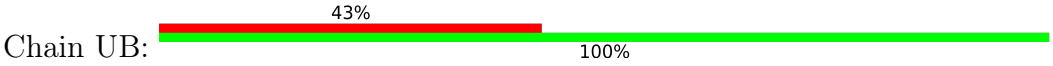
• Molecule 120: mL100

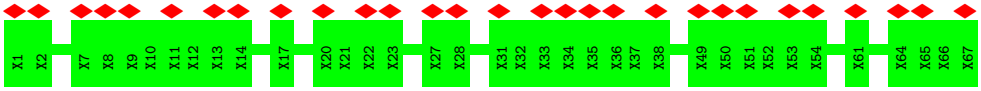
Chain BG: 6% 94%



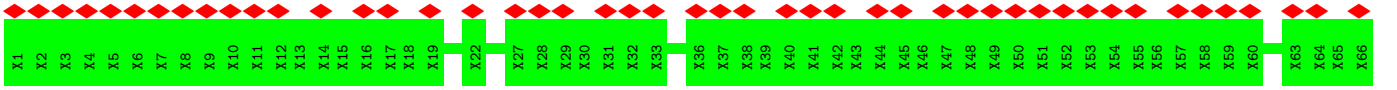


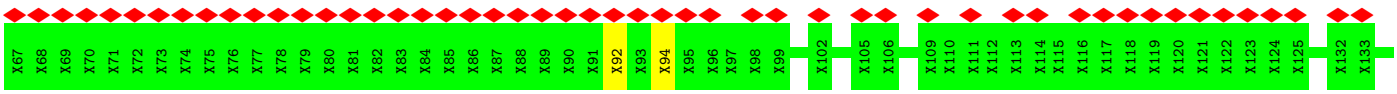
• Molecule 121: UB

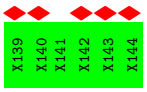




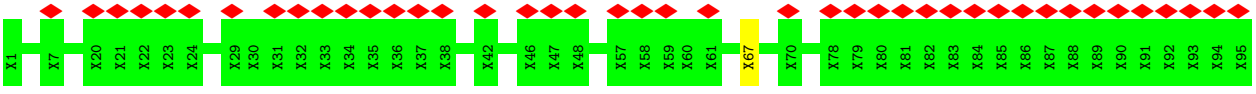
• Molecule 122: UC







• Molecule 123: UD



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	82060	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.195	Depositor
Minimum map value	-0.108	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.045	Depositor
Map size (Å)	476.00003, 476.00003, 476.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	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: ZN, NAD, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1	0.91	7/25559 (0.0%)	1.09	102/39736 (0.3%)
1	2	0.89	81/14217 (0.6%)	1.04	51/22099 (0.2%)
2	h	0.32	0/1347	0.42	0/1819
3	aw	0.32	0/1172	0.44	0/1578
4	m	0.31	0/2437	0.44	0/3300
5	f	0.29	0/1239	0.48	0/1660
6	s	0.31	0/1389	0.43	0/1877
7	au	0.30	0/2140	0.41	0/2899
8	am	0.32	0/2252	0.46	0/3035
9	n	0.29	0/1209	0.45	0/1625
10	ae	0.29	0/4698	0.44	0/6385
11	ay	0.31	0/1223	0.42	0/1653
12	ag	0.30	0/4627	0.43	0/6260
13	aj	0.29	0/2641	0.41	0/3591
14	e	0.32	0/6598	0.45	0/8991
15	d	0.31	0/2771	0.42	0/3733
16	az	0.33	0/1343	0.42	0/1815
17	ax	0.29	0/1405	0.42	0/1906
18	r	0.31	0/3818	0.42	0/5177
19	af	0.29	0/4802	0.42	0/6515
20	u	0.29	0/5673	0.44	0/7675
21	aa	0.28	0/12362	0.43	0/16747
22	ab	0.30	0/9432	0.44	0/12775
23	ak	0.28	0/2187	0.43	0/2963
24	ac	0.27	0/8897	0.46	3/12093 (0.0%)
25	ad	0.38	1/5837 (0.0%)	0.46	4/7913 (0.1%)
26	an	0.30	0/2545	0.44	0/3443
27	ao	0.30	0/1574	0.47	0/2141
28	ap	0.29	0/1927	0.45	0/2593
29	aq	0.27	0/1847	0.43	0/2506
30	as	2.26	6/2013 (0.3%)	0.57	4/2745 (0.1%)
31	at	0.27	0/1664	0.52	2/2243 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	y	0.28	0/2191	0.44	0/2965
33	w	0.27	0/1315	0.43	0/1787
34	v	0.26	0/490	0.45	0/656
35	t	0.28	0/1826	0.46	0/2488
36	p	0.32	0/2002	0.43	0/2704
37	j	0.29	0/1553	0.44	0/2098
38	l	0.28	0/4544	0.45	1/6158 (0.0%)
39	ar	0.27	0/2038	0.45	0/2758
40	av	0.28	0/1265	0.50	0/1716
41	ai	0.29	0/3133	0.45	1/4241 (0.0%)
42	x	0.33	0/2091	0.44	0/2844
43	i	0.30	0/2271	0.42	0/3065
44	g	0.26	0/834	0.37	0/1115
45	o	1.17	1/3847 (0.0%)	0.45	2/5196 (0.0%)
46	c	0.31	0/2084	0.44	0/2815
47	k	0.33	0/977	0.45	0/1319
48	q	0.31	0/1748	0.42	0/2354
49	b	0.32	0/1319	0.47	0/1787
50	a	0.90	6/3377 (0.2%)	0.48	0/4558
51	ba	0.24	0/232	0.39	0/314
52	z	0.30	0/7898	0.44	0/10712
53	bd	0.38	0/358	0.62	0/487
54	A	0.58	0/3098	0.53	0/4217
55	B	0.52	0/3623	0.54	1/4931 (0.0%)
56	C	0.52	0/1831	0.53	0/2498
57	D	0.42	0/1062	0.53	0/1438
58	E	0.41	0/2734	0.48	0/3687
59	F	0.52	0/1485	0.56	1/2019 (0.0%)
60	G	0.51	0/3110	0.56	1/4223 (0.0%)
61	H	0.46	0/1338	0.57	0/1808
62	I	0.50	0/2220	0.53	0/2998
63	J	0.48	0/1175	0.61	1/1582 (0.1%)
64	K	0.46	0/1499	0.50	0/2026
65	L	0.52	0/1452	0.55	0/1970
66	M	0.50	0/2168	0.60	1/2928 (0.0%)
67	N	0.55	0/1650	0.51	0/2242
68	O	0.41	0/2591	0.54	1/3507 (0.0%)
69	P	0.51	0/1402	0.52	0/1892
70	Q	0.50	0/1827	0.52	0/2463
71	R	0.44	0/3852	0.49	0/5243
72	S	0.48	0/1271	0.50	0/1712
73	T	0.50	0/501	0.48	0/665
74	U	0.49	0/756	0.73	1/1011 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
75	V	0.56	0/1231	0.56	0/1645
76	W	0.51	0/483	0.69	0/657
77	X	0.49	0/3846	0.56	3/5250 (0.1%)
78	Y	0.40	0/2116	0.46	0/2866
79	Z	0.53	0/1268	0.66	0/1725
80	BA	0.42	0/1056	0.59	0/1435
82	BB	0.53	0/1061	0.60	0/1438
83	Aw	0.50	0/1552	0.52	0/2107
84	Bj	0.45	0/1389	0.50	0/1878
85	An	0.49	0/2677	0.61	0/3633
86	Al	0.49	0/2212	0.56	0/3013
87	BI	0.42	0/1440	0.53	0/1953
88	Az	0.61	0/1259	0.53	0/1700
89	At	0.45	0/1373	0.51	1/1848 (0.1%)
90	BC	0.38	0/1135	0.49	0/1532
91	Ab	0.48	0/2249	0.49	0/3044
92	Ai	0.48	0/3879	0.51	0/5258
93	Ap	0.40	0/1819	0.47	0/2458
94	Au	0.53	0/1542	0.62	0/2082
95	Aa	0.52	1/1454 (0.1%)	0.63	1/1968 (0.1%)
96	Ao	0.52	0/2351	0.55	0/3196
97	BM	0.30	0/3136	0.51	0/4259
98	Ar	0.55	0/1689	0.54	0/2280
99	Aj	0.47	0/2826	0.50	0/3807
100	BH	0.50	0/1700	0.53	0/2301
101	Am	0.48	0/2791	0.52	1/3775 (0.0%)
102	Aq	0.44	0/2128	0.59	1/2876 (0.0%)
103	BE	0.47	0/723	0.63	0/981
104	Ak	0.38	0/2403	0.50	0/3265
105	BP	0.48	0/1648	0.55	0/2238
106	Ad	0.52	0/1682	0.60	0/2283
107	BF	0.47	0/871	0.52	0/1170
108	Av	0.40	0/1335	0.48	0/1797
109	Af	0.48	0/1165	0.55	0/1585
110	As	0.42	0/804	0.53	0/1093
111	Ae	0.48	0/2441	0.51	0/3324
112	Ac	0.41	0/2236	0.49	0/3038
113	Ah	0.44	0/3780	0.55	1/5125 (0.0%)
114	BD	0.49	0/826	0.47	0/1109
115	Ay	0.49	0/1269	0.52	0/1724
116	Ag	0.52	0/1968	0.50	0/2661
117	Ax	0.56	0/1439	0.79	3/1952 (0.2%)
118	BL	0.53	0/2572	0.65	1/3482 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
119	BO	0.51	0/1266	0.67	0/1702
120	BG	0.46	0/657	0.68	0/888
All	All	0.54	103/311630 (0.0%)	0.61	189/430089 (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
1	1	2	0
1	2	1	1
4	m	0	1
10	ae	0	1
12	ag	0	1
14	e	0	1
20	u	0	2
24	ac	0	6
25	ad	0	3
26	an	0	3
27	ao	0	1
28	ap	0	1
32	y	0	1
36	p	0	1
38	l	0	1
42	x	0	1
49	b	0	1
50	a	0	1
52	z	0	2
53	bd	0	1
54	A	0	1
56	C	0	1
59	F	0	1
62	I	0	1
65	L	0	1
71	R	0	2
79	Z	0	1
80	BA	0	2
81	UA	0	2
82	BB	0	2
84	Bj	0	1
85	An	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
94	Au	0	3
96	Ao	0	1
101	Am	0	1
102	Aq	0	2
103	BE	0	3
104	Ak	0	1
106	Ad	0	1
109	Af	0	1
115	Ay	0	1
118	BL	0	3
119	BO	0	5
122	UC	0	2
123	UD	0	1
All	All	3	72

The worst 5 of 103 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	as	215	TRP	CE3-CZ3	72.01	2.60	1.38
45	o	132	ARG	CB-CG	70.18	3.42	1.52
30	as	215	TRP	CZ3-CH2	45.96	2.13	1.40
30	as	215	TRP	CE2-CZ2	32.69	1.95	1.39
50	a	349	TRP	CE3-CZ3	32.57	1.93	1.38

The worst 5 of 189 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	438	G	N9-C1'-C2'	-17.25	91.57	114.00
1	1	136	A	C2'-C3'-O3'	-17.05	71.99	109.50
1	2	438	G	C4'-C3'-O3'	12.40	137.80	113.00
1	1	146	U	N1-C1'-C2'	-11.88	98.56	114.00
1	2	529	A	N9-C1'-C2'	11.32	128.72	114.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	2	529	A	C2'
1	1	136	A	C4',C3'

5 of 72 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	438	G	Sidechain
10	ae	425	ASP	Peptide
12	ag	257	VAL	Peptide
14	e	291	SER	Peptide
4	m	10	ASN	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	h	155/166 (93%)	148 (96%)	7 (4%)	0	100	100
3	aw	137/139 (99%)	123 (90%)	14 (10%)	0	100	100
4	m	286/325 (88%)	267 (93%)	19 (7%)	0	100	100
5	f	140/371 (38%)	118 (84%)	22 (16%)	0	100	100
6	s	163/179 (91%)	148 (91%)	15 (9%)	0	100	100
7	au	237/247 (96%)	225 (95%)	12 (5%)	0	100	100
8	am	264/313 (84%)	242 (92%)	22 (8%)	0	100	100
9	n	140/171 (82%)	129 (92%)	11 (8%)	0	100	100
10	ae	582/655 (89%)	542 (93%)	39 (7%)	1 (0%)	44	75
11	ay	139/169 (82%)	129 (93%)	10 (7%)	0	100	100
12	ag	555/564 (98%)	520 (94%)	33 (6%)	2 (0%)	30	65
13	aj	314/397 (79%)	297 (95%)	17 (5%)	0	100	100
14	e	805/822 (98%)	736 (91%)	67 (8%)	2 (0%)	44	75
15	d	339/351 (97%)	317 (94%)	22 (6%)	0	100	100
16	az	152/163 (93%)	148 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	ax	159/184 (86%)	147 (92%)	12 (8%)	0	100	100
18	r	449/467 (96%)	423 (94%)	26 (6%)	0	100	100
19	af	579/835 (69%)	541 (93%)	38 (7%)	0	100	100
20	u	702/890 (79%)	652 (93%)	47 (7%)	3 (0%)	30	65
21	aa	1504/1813 (83%)	1411 (94%)	92 (6%)	1 (0%)	48	80
22	ab	1149/1177 (98%)	1070 (93%)	79 (7%)	0	100	100
23	ak	264/325 (81%)	244 (92%)	20 (8%)	0	100	100
24	ac	1108/1267 (88%)	1014 (92%)	89 (8%)	5 (0%)	25	60
25	ad	688/811 (85%)	643 (94%)	43 (6%)	2 (0%)	37	70
26	an	300/302 (99%)	272 (91%)	26 (9%)	2 (1%)	19	54
27	ao	187/291 (64%)	170 (91%)	17 (9%)	0	100	100
28	ap	238/245 (97%)	213 (90%)	25 (10%)	0	100	100
29	aq	210/295 (71%)	202 (96%)	8 (4%)	0	100	100
30	as	245/270 (91%)	213 (87%)	32 (13%)	0	100	100
31	at	202/397 (51%)	185 (92%)	17 (8%)	0	100	100
32	y	279/485 (58%)	250 (90%)	29 (10%)	0	100	100
33	w	153/190 (80%)	143 (94%)	10 (6%)	0	100	100
34	v	61/214 (28%)	55 (90%)	6 (10%)	0	100	100
35	t	224/267 (84%)	210 (94%)	14 (6%)	0	100	100
36	p	232/321 (72%)	210 (90%)	21 (9%)	1 (0%)	30	65
37	j	178/189 (94%)	158 (89%)	20 (11%)	0	100	100
38	l	535/677 (79%)	489 (91%)	44 (8%)	2 (0%)	30	65
39	ar	248/282 (88%)	235 (95%)	13 (5%)	0	100	100
40	av	148/236 (63%)	124 (84%)	23 (16%)	1 (1%)	19	54
41	ai	377/379 (100%)	346 (92%)	31 (8%)	0	100	100
42	x	253/268 (94%)	236 (93%)	16 (6%)	1 (0%)	30	65
43	i	265/429 (62%)	248 (94%)	17 (6%)	0	100	100
44	g	97/192 (50%)	94 (97%)	3 (3%)	0	100	100
45	o	436/604 (72%)	412 (94%)	23 (5%)	1 (0%)	44	75
46	c	249/311 (80%)	223 (90%)	26 (10%)	0	100	100
47	k	114/312 (36%)	107 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	q	194/425 (46%)	189 (97%)	5 (3%)	0	100	100
49	b	153/159 (96%)	127 (83%)	25 (16%)	1 (1%)	19	54
50	a	406/431 (94%)	373 (92%)	32 (8%)	1 (0%)	44	75
51	ba	24/94 (26%)	23 (96%)	1 (4%)	0	100	100
52	z	965/1169 (82%)	891 (92%)	73 (8%)	1 (0%)	48	80
53	bd	39/89 (44%)	30 (77%)	9 (23%)	0	100	100
54	A	366/466 (78%)	311 (85%)	50 (14%)	5 (1%)	9	39
55	B	433/435 (100%)	380 (88%)	52 (12%)	1 (0%)	44	75
56	C	210/261 (80%)	179 (85%)	31 (15%)	0	100	100
57	D	126/204 (62%)	109 (86%)	17 (14%)	0	100	100
58	E	324/345 (94%)	293 (90%)	31 (10%)	0	100	100
59	F	168/171 (98%)	153 (91%)	14 (8%)	1 (1%)	22	57
60	G	363/373 (97%)	314 (86%)	47 (13%)	2 (1%)	22	57
61	H	160/167 (96%)	144 (90%)	14 (9%)	2 (1%)	10	41
62	I	255/304 (84%)	224 (88%)	31 (12%)	0	100	100
63	J	139/143 (97%)	102 (73%)	36 (26%)	1 (1%)	19	54
64	K	177/193 (92%)	158 (89%)	19 (11%)	0	100	100
65	L	176/185 (95%)	157 (89%)	18 (10%)	1 (1%)	22	57
66	M	257/278 (92%)	217 (84%)	38 (15%)	2 (1%)	16	51
67	N	187/251 (74%)	163 (87%)	24 (13%)	0	100	100
68	O	305/475 (64%)	273 (90%)	29 (10%)	3 (1%)	13	46
69	P	163/184 (89%)	145 (89%)	17 (10%)	1 (1%)	22	57
70	Q	215/233 (92%)	192 (89%)	22 (10%)	1 (0%)	25	60
71	R	470/479 (98%)	405 (86%)	65 (14%)	0	100	100
72	S	148/408 (36%)	132 (89%)	16 (11%)	0	100	100
73	T	53/82 (65%)	50 (94%)	3 (6%)	0	100	100
74	U	90/117 (77%)	76 (84%)	12 (13%)	2 (2%)	5	32
75	V	139/150 (93%)	120 (86%)	19 (14%)	0	100	100
76	W	52/185 (28%)	46 (88%)	6 (12%)	0	100	100
77	X	466/512 (91%)	417 (90%)	46 (10%)	3 (1%)	22	57
78	Y	253/292 (87%)	233 (92%)	20 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
79	Z	148/197 (75%)	114 (77%)	31 (21%)	3 (2%)	6 33
80	BA	136/167 (81%)	103 (76%)	29 (21%)	4 (3%)	3 27
82	BB	120/156 (77%)	95 (79%)	23 (19%)	2 (2%)	7 36
83	Aw	183/187 (98%)	161 (88%)	22 (12%)	0	100 100
84	Bj	166/185 (90%)	143 (86%)	22 (13%)	1 (1%)	22 57
85	An	312/331 (94%)	253 (81%)	52 (17%)	7 (2%)	5 32
86	Al	262/346 (76%)	219 (84%)	43 (16%)	0	100 100
87	BI	184/266 (69%)	155 (84%)	29 (16%)	0	100 100
88	Az	136/152 (90%)	110 (81%)	24 (18%)	2 (2%)	8 39
89	At	163/183 (89%)	145 (89%)	18 (11%)	0	100 100
90	BC	138/147 (94%)	129 (94%)	9 (6%)	0	100 100
91	Ab	258/262 (98%)	226 (88%)	32 (12%)	0	100 100
92	Ai	474/479 (99%)	413 (87%)	60 (13%)	1 (0%)	44 75
93	Ap	212/240 (88%)	188 (89%)	24 (11%)	0	100 100
94	Au	174/186 (94%)	131 (75%)	37 (21%)	6 (3%)	3 25
95	Aa	176/195 (90%)	142 (81%)	31 (18%)	3 (2%)	7 36
96	Ao	273/284 (96%)	232 (85%)	39 (14%)	2 (1%)	19 54
97	BM	387/457 (85%)	326 (84%)	61 (16%)	0	100 100
98	Ar	193/205 (94%)	168 (87%)	25 (13%)	0	100 100
99	Aj	337/503 (67%)	292 (87%)	45 (13%)	0	100 100
100	BH	212/229 (93%)	185 (87%)	27 (13%)	0	100 100
101	Am	328/340 (96%)	275 (84%)	53 (16%)	0	100 100
102	Aq	250/341 (73%)	201 (80%)	43 (17%)	6 (2%)	5 30
103	BE	82/118 (70%)	56 (68%)	25 (30%)	1 (1%)	11 43
104	Ak	298/323 (92%)	254 (85%)	44 (15%)	0	100 100
105	BP	191/254 (75%)	161 (84%)	28 (15%)	2 (1%)	13 46
106	Ad	203/237 (86%)	163 (80%)	38 (19%)	2 (1%)	13 46
107	BF	99/109 (91%)	79 (80%)	20 (20%)	0	100 100
108	Av	153/192 (80%)	128 (84%)	25 (16%)	0	100 100
109	Af	137/155 (88%)	117 (85%)	19 (14%)	1 (1%)	19 54
110	As	95/249 (38%)	87 (92%)	8 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
111	Ae	289/311 (93%)	253 (88%)	36 (12%)	0	100 100
112	Ac	266/291 (91%)	234 (88%)	32 (12%)	0	100 100
113	Ah	450/570 (79%)	386 (86%)	60 (13%)	4 (1%)	14 48
114	BD	95/102 (93%)	85 (90%)	10 (10%)	0	100 100
115	Ay	140/174 (80%)	118 (84%)	18 (13%)	4 (3%)	3 27
116	Ag	229/244 (94%)	204 (89%)	25 (11%)	0	100 100
117	Ax	165/216 (76%)	129 (78%)	33 (20%)	3 (2%)	7 35
118	BL	307/380 (81%)	233 (76%)	67 (22%)	7 (2%)	5 31
119	BO	153/190 (80%)	104 (68%)	46 (30%)	3 (2%)	6 33
120	BG	83/1347 (6%)	57 (69%)	23 (28%)	3 (4%)	3 24
All	All	32374/40717 (80%)	28909 (89%)	3346 (10%)	119 (0%)	32 65

5 of 119 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	ac	685	LEU
54	A	289	ARG
54	A	290	MET
61	H	94	VAL
63	J	66	PRO

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
2	h	138/146 (94%)	138 (100%)	0	100 100
3	aw	120/120 (100%)	120 (100%)	0	100 100
4	m	250/283 (88%)	249 (100%)	1 (0%)	89 91
5	f	122/292 (42%)	118 (97%)	4 (3%)	33 56
6	s	143/157 (91%)	143 (100%)	0	100 100
7	au	217/223 (97%)	216 (100%)	1 (0%)	86 90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
8	am	228/262 (87%)	227 (100%)	1 (0%)	89 91
9	n	127/147 (86%)	127 (100%)	0	100 100
10	ae	479/532 (90%)	478 (100%)	1 (0%)	92 94
11	ay	126/149 (85%)	125 (99%)	1 (1%)	79 84
12	ag	478/484 (99%)	475 (99%)	3 (1%)	84 88
13	aj	275/345 (80%)	275 (100%)	0	100 100
14	e	688/700 (98%)	687 (100%)	1 (0%)	92 95
15	d	289/296 (98%)	287 (99%)	2 (1%)	81 86
16	az	137/144 (95%)	137 (100%)	0	100 100
17	ax	146/166 (88%)	146 (100%)	0	100 100
18	r	396/409 (97%)	396 (100%)	0	100 100
19	af	486/676 (72%)	486 (100%)	0	100 100
20	u	582/733 (79%)	579 (100%)	3 (0%)	86 90
21	aa	1266/1465 (86%)	1261 (100%)	5 (0%)	89 91
22	ab	951/971 (98%)	950 (100%)	1 (0%)	92 95
23	ak	224/268 (84%)	222 (99%)	2 (1%)	75 83
24	ac	889/1002 (89%)	888 (100%)	1 (0%)	92 95
25	ad	595/699 (85%)	593 (100%)	2 (0%)	91 92
26	an	248/248 (100%)	248 (100%)	0	100 100
27	ao	167/253 (66%)	167 (100%)	0	100 100
28	ap	191/194 (98%)	190 (100%)	1 (0%)	86 90
29	aq	190/249 (76%)	190 (100%)	0	100 100
30	as	207/226 (92%)	207 (100%)	0	100 100
31	at	172/334 (52%)	170 (99%)	2 (1%)	67 78
32	y	230/379 (61%)	227 (99%)	3 (1%)	65 76
33	w	140/170 (82%)	139 (99%)	1 (1%)	81 86
34	v	53/182 (29%)	53 (100%)	0	100 100
35	t	186/214 (87%)	186 (100%)	0	100 100
36	p	209/278 (75%)	207 (99%)	2 (1%)	73 81
37	j	163/172 (95%)	162 (99%)	1 (1%)	84 88
38	l	465/552 (84%)	463 (100%)	2 (0%)	89 91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
39	ar	217/237 (92%)	215 (99%)	2 (1%)	75 83
40	av	136/208 (65%)	135 (99%)	1 (1%)	81 86
41	ai	338/338 (100%)	338 (100%)	0	100 100
42	x	211/222 (95%)	211 (100%)	0	100 100
43	i	241/383 (63%)	241 (100%)	0	100 100
44	g	84/168 (50%)	84 (100%)	0	100 100
45	o	393/546 (72%)	391 (100%)	2 (0%)	86 90
46	c	217/260 (84%)	216 (100%)	1 (0%)	86 90
47	k	104/272 (38%)	104 (100%)	0	100 100
48	q	177/363 (49%)	177 (100%)	0	100 100
49	b	140/144 (97%)	139 (99%)	1 (1%)	81 86
50	a	346/365 (95%)	345 (100%)	1 (0%)	91 92
51	ba	21/82 (26%)	21 (100%)	0	100 100
52	z	817/979 (84%)	814 (100%)	3 (0%)	89 91
53	bd	39/85 (46%)	38 (97%)	1 (3%)	41 61
54	A	314/393 (80%)	313 (100%)	1 (0%)	91 92
55	B	380/380 (100%)	375 (99%)	5 (1%)	65 76
56	C	190/226 (84%)	190 (100%)	0	100 100
57	D	106/154 (69%)	103 (97%)	3 (3%)	38 59
58	E	285/300 (95%)	282 (99%)	3 (1%)	70 79
59	F	151/152 (99%)	149 (99%)	2 (1%)	65 76
60	G	315/322 (98%)	308 (98%)	7 (2%)	47 65
61	H	138/142 (97%)	137 (99%)	1 (1%)	81 86
62	I	223/261 (85%)	221 (99%)	2 (1%)	75 83
63	J	119/121 (98%)	115 (97%)	4 (3%)	32 55
64	K	151/161 (94%)	149 (99%)	2 (1%)	65 76
65	L	151/157 (96%)	151 (100%)	0	100 100
66	M	226/241 (94%)	222 (98%)	4 (2%)	54 71
67	N	175/219 (80%)	172 (98%)	3 (2%)	56 72
68	O	278/396 (70%)	273 (98%)	5 (2%)	54 71
69	P	147/162 (91%)	147 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
70	Q	191/203 (94%)	189 (99%)	2 (1%)	73 81
71	R	406/411 (99%)	405 (100%)	1 (0%)	92 94
72	S	135/335 (40%)	135 (100%)	0	100 100
73	T	52/73 (71%)	52 (100%)	0	100 100
74	U	80/99 (81%)	75 (94%)	5 (6%)	15 40
75	V	125/134 (93%)	121 (97%)	4 (3%)	34 56
76	W	50/163 (31%)	46 (92%)	4 (8%)	10 33
77	X	402/437 (92%)	399 (99%)	3 (1%)	81 86
78	Y	209/236 (89%)	208 (100%)	1 (0%)	86 90
79	Z	132/172 (77%)	128 (97%)	4 (3%)	36 58
80	BA	112/135 (83%)	108 (96%)	4 (4%)	30 54
82	BB	106/140 (76%)	103 (97%)	3 (3%)	38 59
83	Aw	157/159 (99%)	156 (99%)	1 (1%)	84 88
84	Bj	150/165 (91%)	149 (99%)	1 (1%)	81 86
85	An	274/289 (95%)	267 (97%)	7 (3%)	41 61
86	Al	236/299 (79%)	230 (98%)	6 (2%)	42 62
87	BI	153/221 (69%)	152 (99%)	1 (1%)	81 86
88	Az	129/143 (90%)	127 (98%)	2 (2%)	58 73
89	At	140/153 (92%)	140 (100%)	0	100 100
90	BC	117/124 (94%)	116 (99%)	1 (1%)	75 83
91	Ab	233/235 (99%)	233 (100%)	0	100 100
92	Ai	408/410 (100%)	406 (100%)	2 (0%)	86 90
93	Ap	189/208 (91%)	188 (100%)	1 (0%)	86 90
94	Au	154/164 (94%)	145 (94%)	9 (6%)	17 42
95	Aa	150/166 (90%)	148 (99%)	2 (1%)	65 76
96	Ao	236/245 (96%)	234 (99%)	2 (1%)	79 84
97	BM	319/370 (86%)	316 (99%)	3 (1%)	75 83
98	Ar	169/179 (94%)	168 (99%)	1 (1%)	84 88
99	Aj	286/420 (68%)	284 (99%)	2 (1%)	81 86
100	BH	177/189 (94%)	175 (99%)	2 (1%)	70 79
101	Am	278/287 (97%)	275 (99%)	3 (1%)	70 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
102	Aq	221/276 (80%)	216 (98%)	5 (2%)	45 64
103	BE	76/100 (76%)	75 (99%)	1 (1%)	65 76
104	Ak	254/272 (93%)	252 (99%)	2 (1%)	79 84
105	BP	167/215 (78%)	165 (99%)	2 (1%)	67 78
106	Ad	172/193 (89%)	171 (99%)	1 (1%)	84 88
107	BF	88/95 (93%)	87 (99%)	1 (1%)	70 79
108	Av	141/169 (83%)	141 (100%)	0	100 100
109	Af	120/135 (89%)	120 (100%)	0	100 100
110	As	88/204 (43%)	88 (100%)	0	100 100
111	Ae	249/261 (95%)	244 (98%)	5 (2%)	50 68
112	Ac	232/253 (92%)	230 (99%)	2 (1%)	75 83
113	Ah	385/485 (79%)	378 (98%)	7 (2%)	54 71
114	BD	85/90 (94%)	83 (98%)	2 (2%)	44 63
115	Ay	130/158 (82%)	128 (98%)	2 (2%)	60 74
116	Ag	202/211 (96%)	200 (99%)	2 (1%)	73 81
117	Ax	150/190 (79%)	141 (94%)	9 (6%)	16 41
118	BL	268/329 (82%)	261 (97%)	7 (3%)	41 61
119	BO	130/158 (82%)	126 (97%)	4 (3%)	35 56
120	BG	67/1047 (6%)	67 (100%)	0	100 100
All	All	27983/34364 (81%)	27759 (99%)	224 (1%)	77 84

5 of 224 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
79	Z	40	THR
119	BO	128	VAL
88	Az	93	LYS
118	BL	328	THR
114	BD	62	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 648 such sidechains are listed below:

Mol	Chain	Res	Type
79	Z	13	HIS

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Mol	Chain	Res	Type
101	Am	152	GLN
85	An	24	HIS
78	Y	282	GLN
92	Ai	142	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1082/18998 (5%)	638 (58%)	129 (11%)
1	2	602/18998 (3%)	481 (79%)	200 (33%)
All	All	1684/37996 (4%)	1119 (66%)	329 (19%)

5 of 1119 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	U
1	2	3	C
1	2	6	U
1	2	7	U
1	2	9	U

5 of 329 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	249	U
1	1	703	U
1	1	309	U
1	1	519	U
1	1	849	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 8 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	$\#\|Z\| > 2$
125	NAD	Ag	301	-	42,48,48	0.61	0	50,73,73	1.12	5 (10%)

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
125	NAD	Ag	301	-	-	11/26/62/62	0/5/5/5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
125	Ag	301	NAD	O4D-C1D-C2D	-4.10	100.93	106.93
125	Ag	301	NAD	C3D-C2D-C1D	3.28	105.91	100.98
125	Ag	301	NAD	C6N-N1N-C2N	-2.20	119.97	121.97
125	Ag	301	NAD	C5A-C6A-N6A	2.15	123.62	120.35
125	Ag	301	NAD	O4B-C4B-C3B	-2.09	100.98	105.11

There are no chirality outliers.

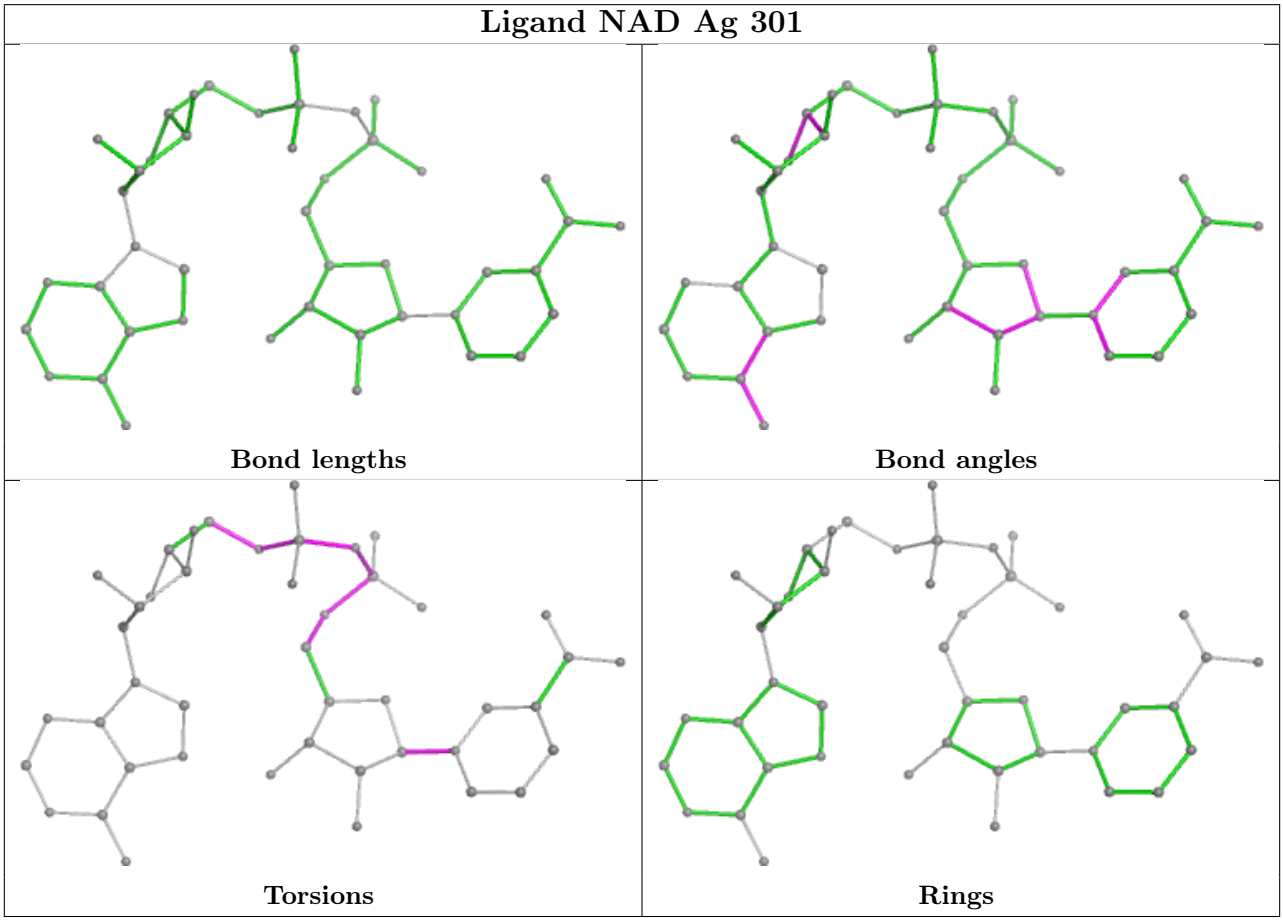
5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
125	Ag	301	NAD	C5B-O5B-PA-O3
125	Ag	301	NAD	C2D-C1D-N1N-C2N
125	Ag	301	NAD	C4B-C5B-O5B-PA
125	Ag	301	NAD	PN-O3-PA-O5B
125	Ag	301	NAD	PA-O3-PN-O5D

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	am	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	am	121:GLU	C	122:ASN	N	3.38

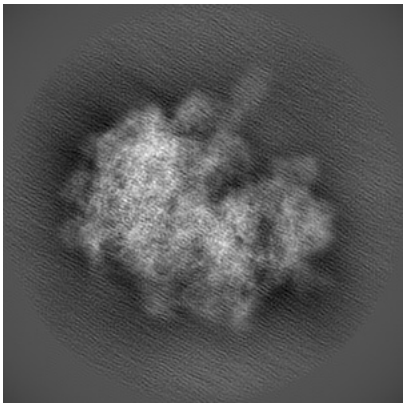
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11829. These allow visual inspection of the internal detail of the map and identification of artifacts.

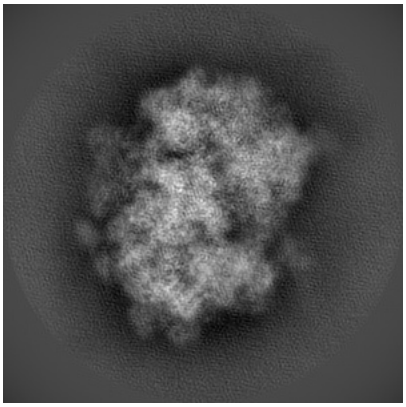
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

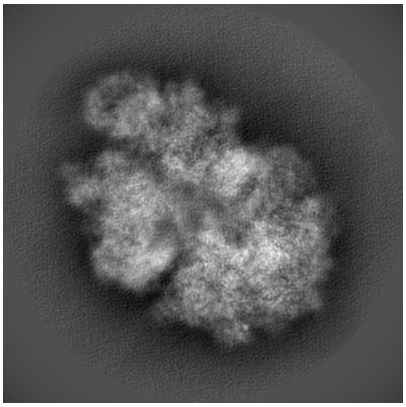
6.1.1 Primary map



X



Y

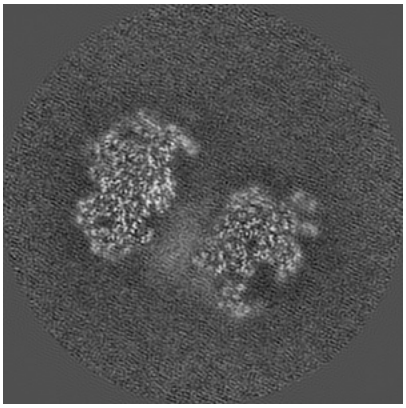


Z

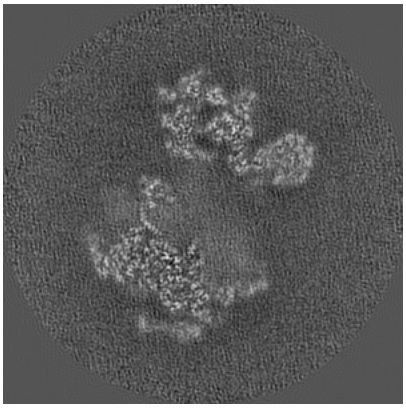
The images above show the map projected in three orthogonal directions.

6.2 Central slices

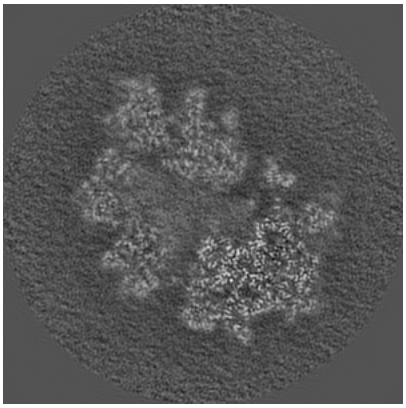
6.2.1 Primary map



X Index: 200



Y Index: 200

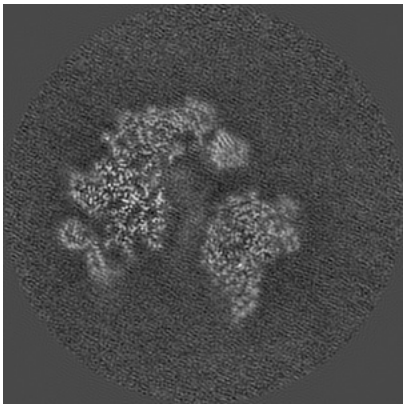


Z Index: 200

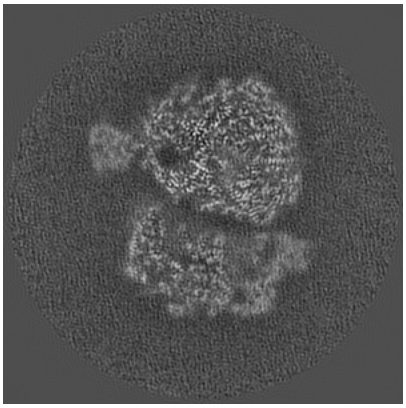
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

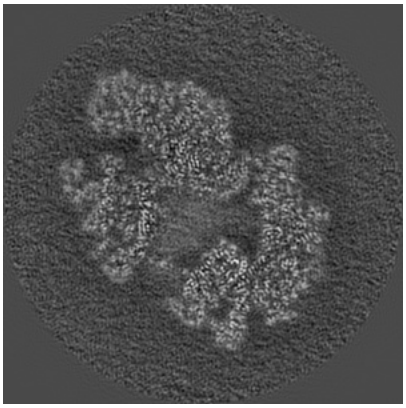
6.3.1 Primary map



X Index: 224



Y Index: 150

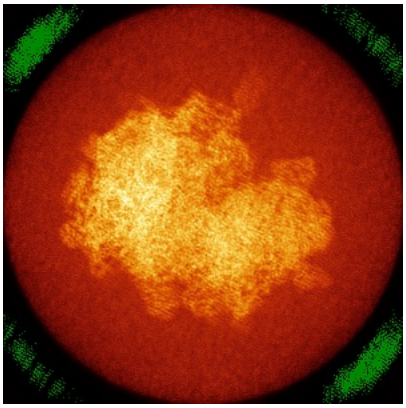


Z Index: 173

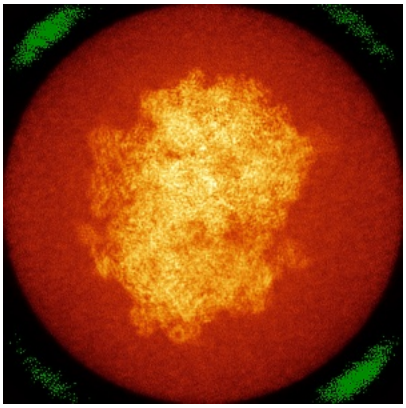
The images above show the largest variance slices of the map in three orthogonal directions.

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

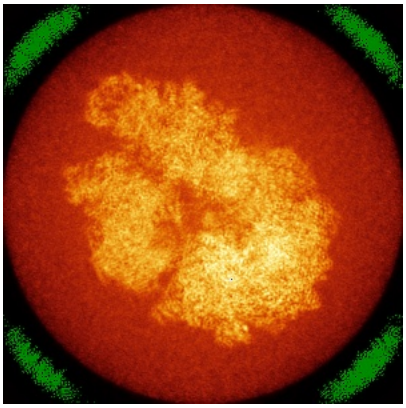
6.4.1 Primary map



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

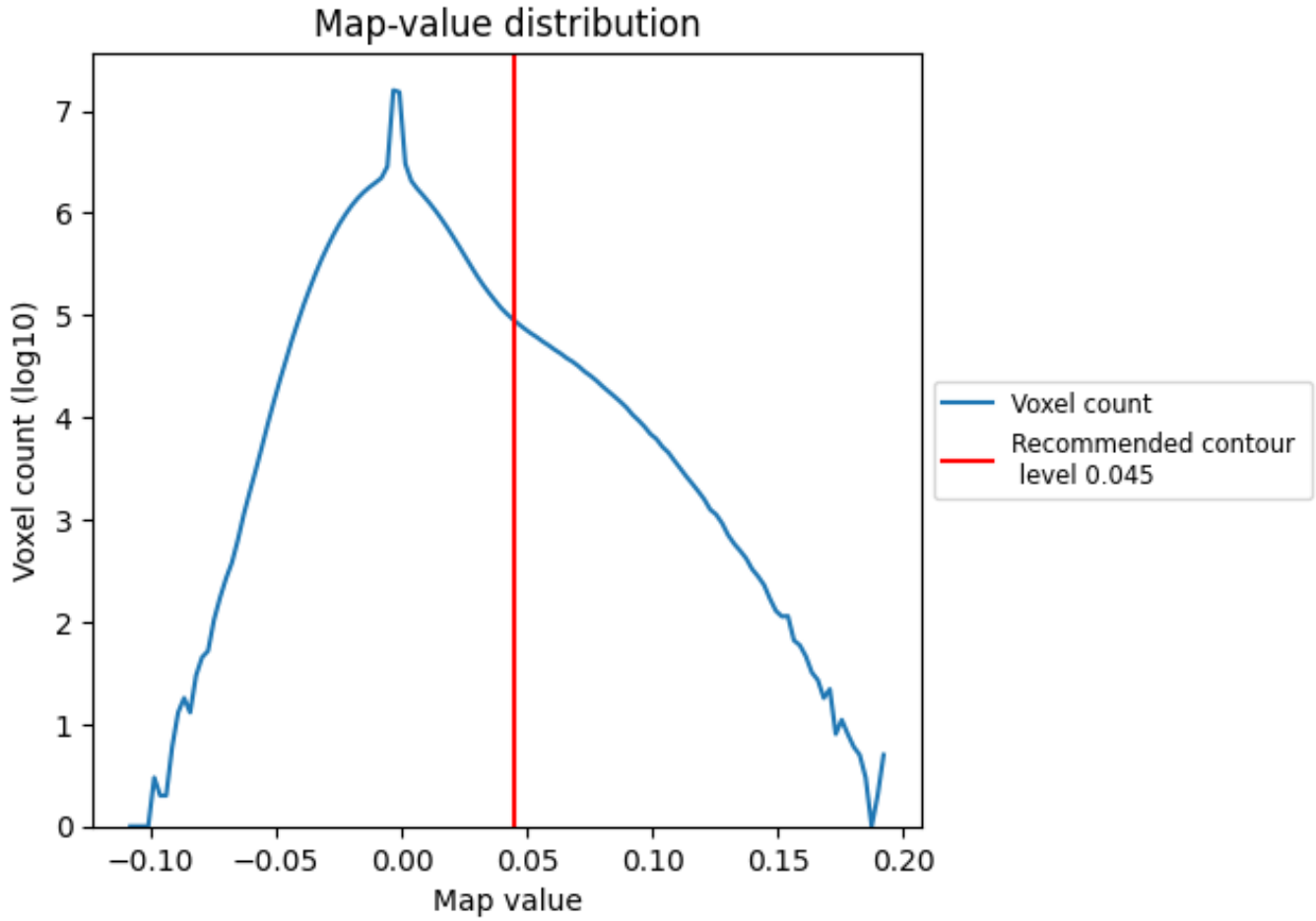
6.6 Mask visualisation (i)

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

7 Map analysis

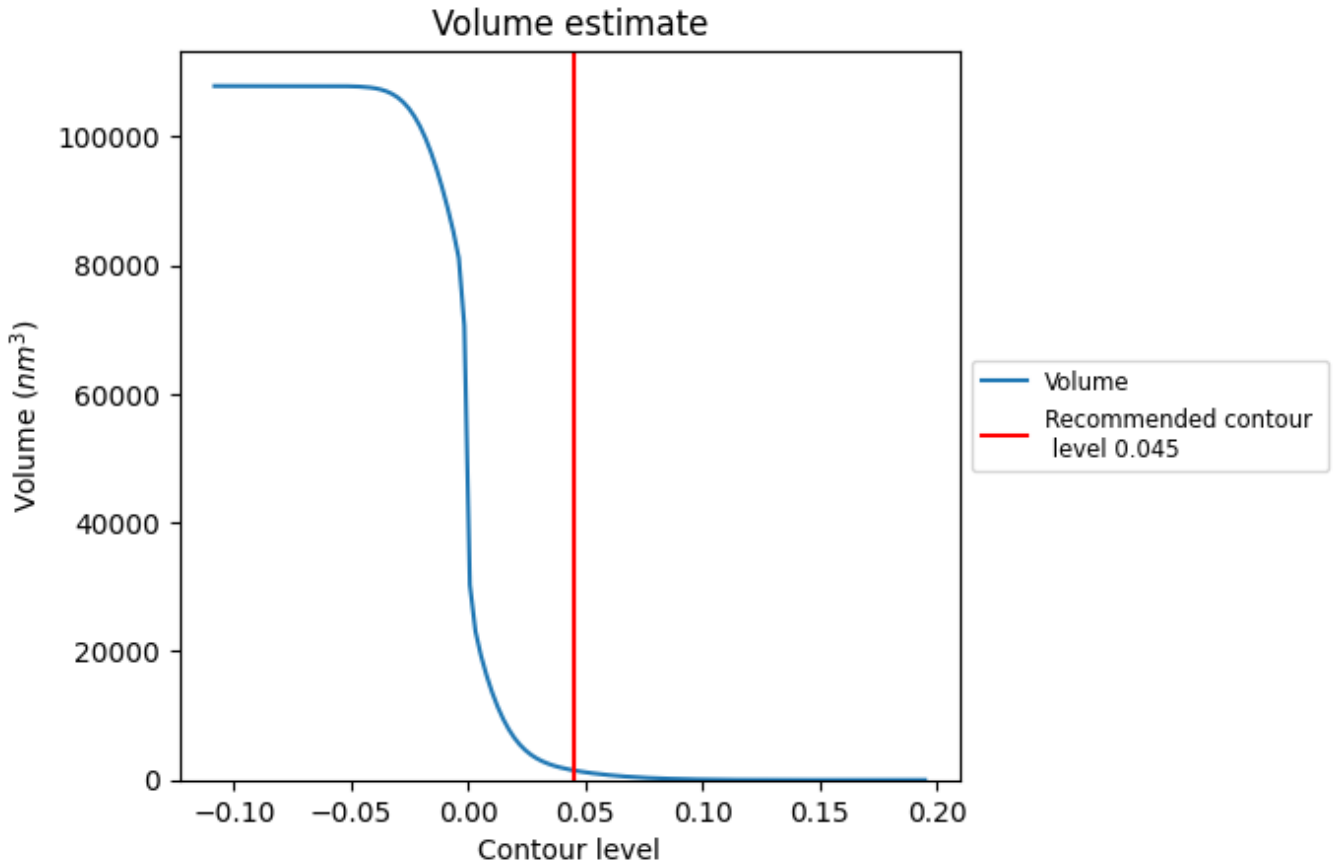
This section contains the results of statistical analysis of the map.

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.

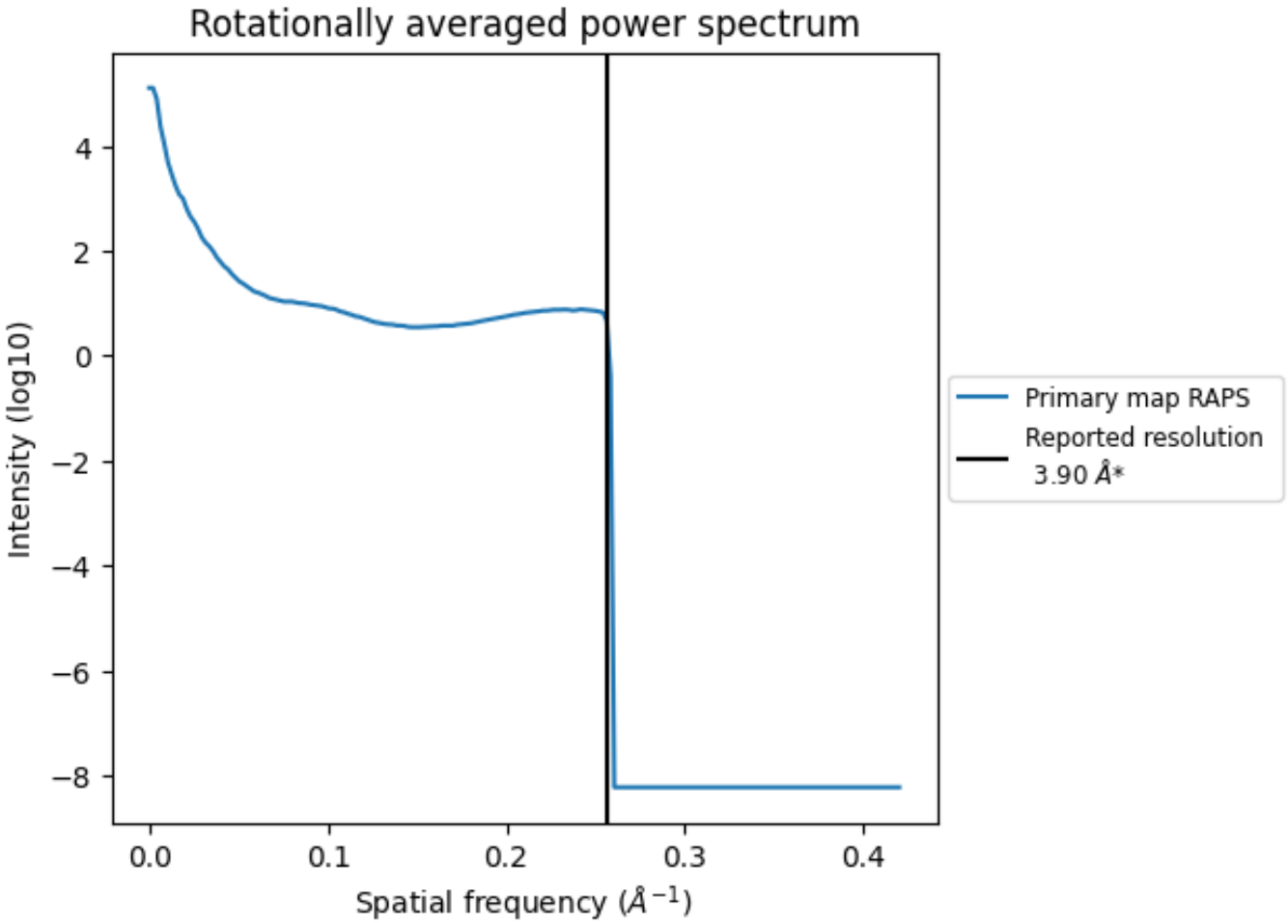
7.2 Volume estimate (i)



The volume at the recommended contour level is 1487 nm^3; this corresponds to an approximate mass of 1343 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 0.256 Å^{-1}

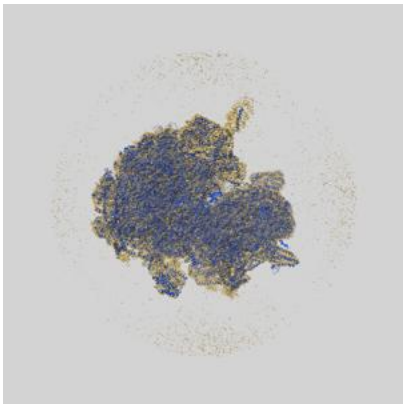
8 Fourier-Shell correlation

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

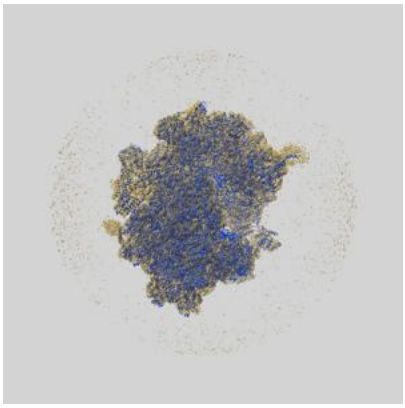
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-11829 and PDB model 7ANE. Per-residue inclusion information can be found in section 3 on page 27.

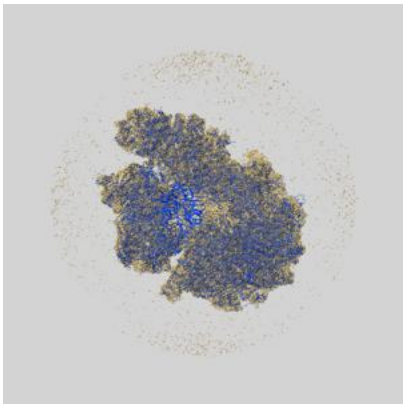
9.1 Map-model overlay



X



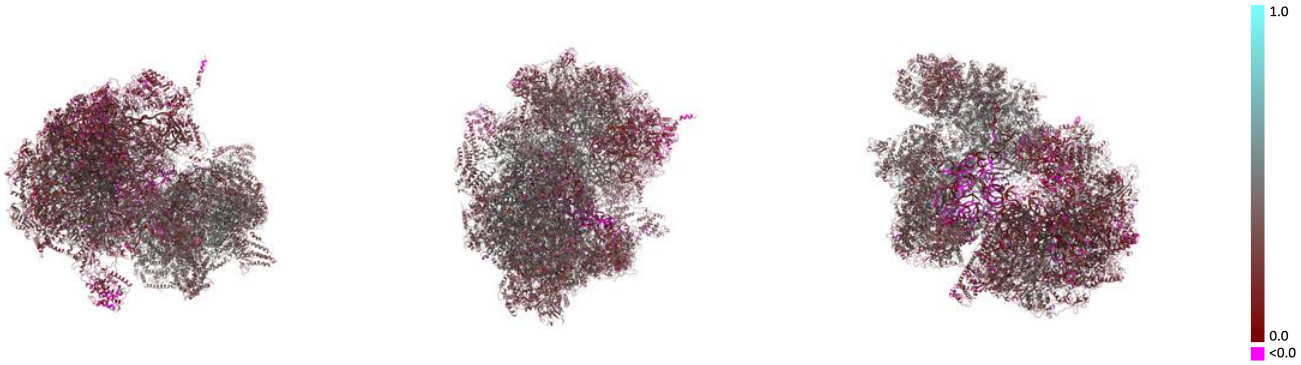
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

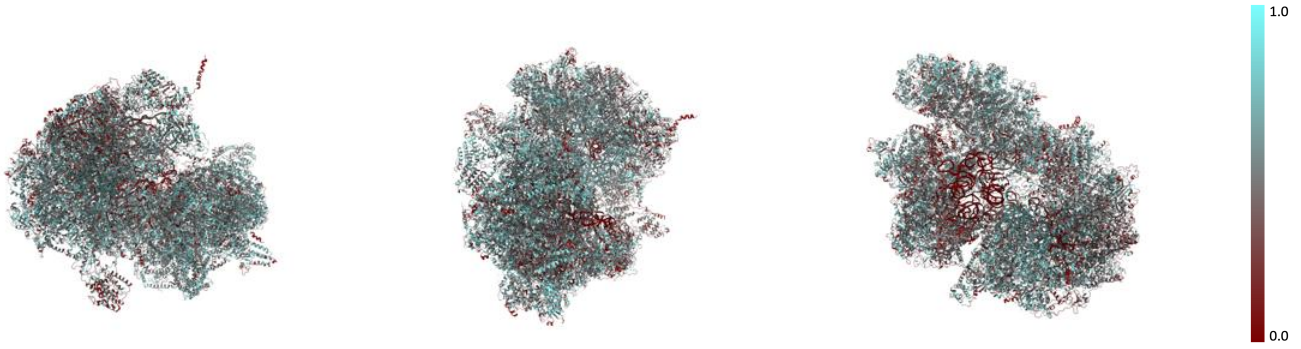
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

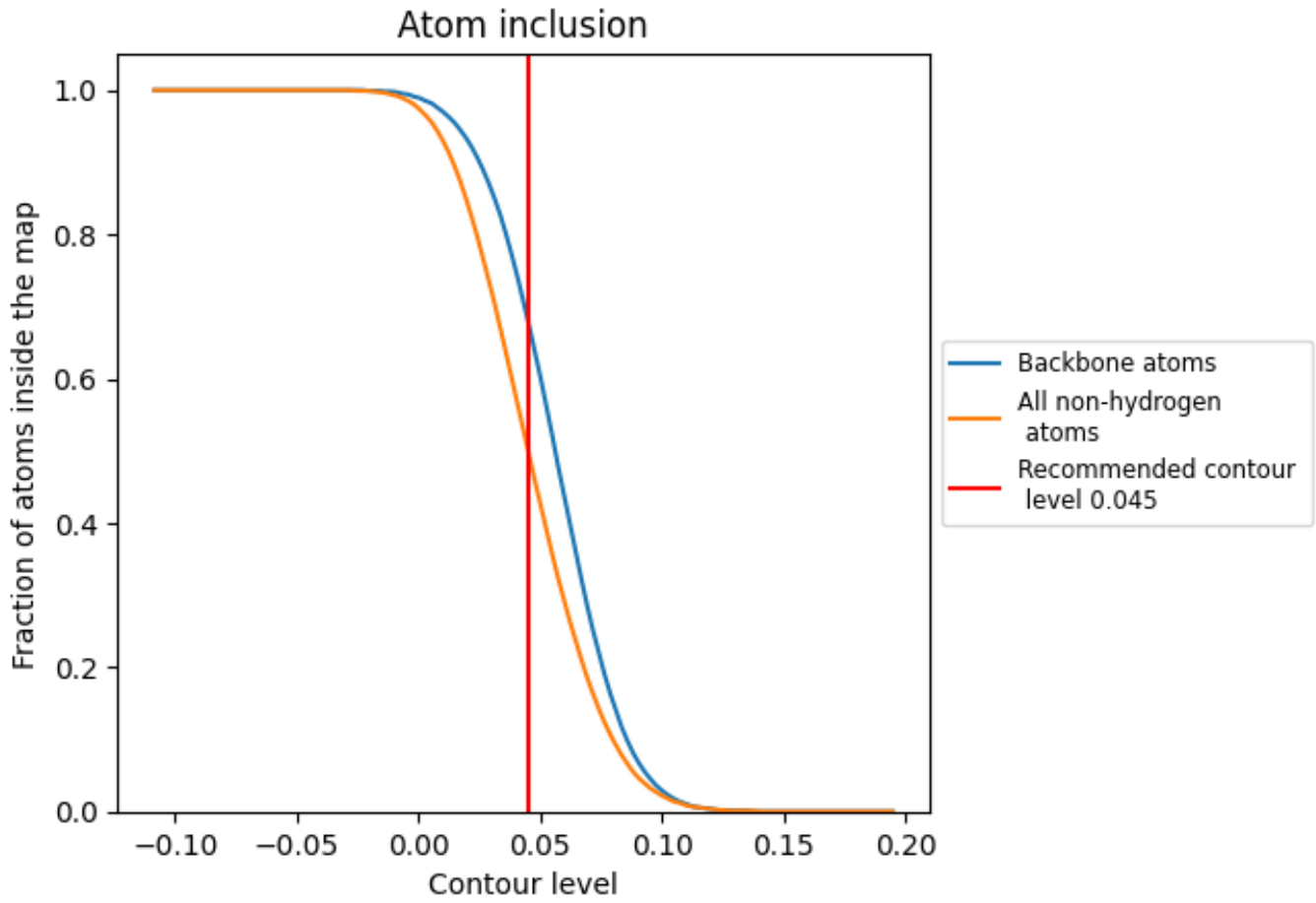
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 50% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5010	0.3210
1	0.6440	0.3250
2	0.1120	0.0360
A	0.4610	0.2040
Aa	0.3690	0.2020
Ab	0.4850	0.2250
Ac	0.5310	0.3030
Ad	0.4300	0.2790
Ae	0.4230	0.1760
Af	0.4190	0.2100
Ag	0.5820	0.3550
Ah	0.5310	0.2640
Ai	0.5150	0.2900
Aj	0.4460	0.2260
Ak	0.5080	0.2390
Al	0.5480	0.2700
Am	0.4360	0.1610
An	0.5300	0.2960
Ao	0.5800	0.3180
Ap	0.4250	0.1900
Aq	0.5120	0.3570
Ar	0.5580	0.3460
As	0.4710	0.1780
At	0.5100	0.2510
Au	0.5970	0.3460
Av	0.4840	0.2070
Aw	0.5140	0.2570
Ax	0.5600	0.3310
Ay	0.5790	0.2930
Az	0.6210	0.3700
B	0.5050	0.2890
BA	0.4840	0.2390
BB	0.4210	0.1810
BC	0.5510	0.3630
BD	0.5930	0.3220

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Chain	Atom inclusion	Q-score
BE	0.4470	0.1690
BF	0.5210	0.3430
BG	0.5290	0.3080
BH	0.4620	0.2390
BI	0.5840	0.2960
BL	0.5730	0.3350
BM	0.3460	0.1220
BO	0.4170	0.2090
BP	0.4470	0.2500
Bj	0.4920	0.3330
C	0.5840	0.3250
D	0.3250	0.1210
E	0.4720	0.1750
F	0.4170	0.2200
G	0.5290	0.3200
H	0.4850	0.3200
I	0.4870	0.2790
J	0.4400	0.1980
K	0.4380	0.2300
L	0.4190	0.2030
M	0.5270	0.3060
N	0.6120	0.4010
O	0.4020	0.2560
P	0.5730	0.3810
Q	0.5820	0.3370
R	0.5320	0.2830
S	0.4750	0.2740
T	0.5820	0.3010
U	0.5240	0.3610
UA	0.6670	0.2890
UB	0.5370	0.3040
UC	0.3280	0.1890
UD	0.5030	0.1910
V	0.5590	0.3960
W	0.4600	0.2770
X	0.4890	0.2890
Y	0.5370	0.3210
Z	0.6180	0.3990
a	0.4880	0.4310
aa	0.5240	0.3740
ab	0.5000	0.4030
ac	0.4990	0.3150

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Chain	Atom inclusion	Q-score
ad	0.4910	0.3690
ae	0.5580	0.3940
af	0.5580	0.3690
ag	0.4930	0.4050
ai	0.5610	0.3960
aj	0.6130	0.4020
ak	0.4450	0.3460
am	0.4960	0.4470
an	0.5890	0.4180
ao	0.5520	0.4140
ap	0.6240	0.3810
aq	0.3490	0.2790
ar	0.4900	0.3620
as	0.4150	0.3030
at	0.2090	0.2680
au	0.5050	0.3990
av	0.3970	0.3520
aw	0.5600	0.4370
ax	0.5370	0.4190
ay	0.5480	0.4160
az	0.6230	0.4420
b	0.5500	0.3990
ba	0.0730	0.3450
bd	0.4940	0.4070
c	0.4700	0.4340
d	0.5590	0.4430
e	0.5400	0.4250
f	0.4810	0.3670
g	0.3030	0.3410
h	0.5830	0.4480
i	0.5020	0.4050
j	0.4610	0.3630
k	0.5070	0.4440
l	0.4720	0.3280
m	0.5350	0.4250
n	0.4920	0.4150
o	0.4140	0.3920
p	0.5950	0.4110
q	0.5720	0.3820
r	0.6050	0.4200
s	0.5520	0.4360
t	0.4240	0.3090

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Chain	Atom inclusion	Q-score
u	0.5160	0.3860
v	0.5070	0.3990
w	0.2920	0.2890
x	0.5900	0.4250
y	0.5590	0.3560
z	0.5650	0.4190